

Table 1. Comparison of relative abundance (median %) of urinary microbiome between first voided urine group and midstream urine group at all taxonomic levels.

Taxa		First Voided Urine	Midstream Urine	P
Phylum	Firmicutes	32.54	33.79	Ns
	Proteobacteria	32.44	31.14	Ns
	Bacteroidetes	13.88	16.59	Ns
	Actinobacteria	11.28	11.87	Ns
	Tenericutes	4.8	4.56	Ns
Class	Gammaproteobacteria	22.34	20.31	Ns
	Bacilli	19.18	17.46	Ns
	Bacteroidia	12.20	14.79	Ns
	Actinobacteria	10.77	11.55	Ns
	Clostridia	9.46	10.72	0.041
	Mollicutes	4.89	4.34	Ns
	Alphanobacteria	5.34	5.49	Ns
	Betaproteobacteria	4.40	3.46	Ns
	Negativicutes	1.38	1.65	Ns
	Flavobacteriia	1.33	1.02	Ns
Order	Enterobacteriales	15.61	13.27	Ns
	Lactobacillales	14.03	13.07	Ns
	Bacteriodales	12.20	14.79	Ns
	Actinomycetales	9.84	10.12	Ns
	Clostridiales	9.46	10.72	0,041
	Mycoplasmatales	4.86	4.34	Ns
	Bacillales	4.12	3.57	Ns

	Xanthomonadales	3.17	3.49	Ns
	Burkholderiales	2.78	2.26	Ns
	Rhizobiales	2.11	2.34	Ns
	Pseudomonadales	1.95	1.70	Ns
	Selenomonadales	1.38	1.65	Ns
	Flavobacteriales	1.33	1.02	Ns
	Sphingomonadales	1.26	1.31	Ns
Family				
	Enterobacteriaceae	15.62	13.27	Ns
	Porphyromonadaceae	10.42	11.82	Ns
	Corynebacteriaceae	4.79	4.29	Ns
	Mycoplasmataceae	4.79	4.34	Ns
	Lachnospiraceae	4.23	4.77	Ns
	Xanthomonadaceae	3.17	3.51	Ns
	Lactobacillaceae	2.77	3.46	Ns
	Clostridiales Incertae Sedis XI	1.57	2.45	Ns
	Actinomycetaceae	1.54	1.71	Ns
	Streptococcaceae	1.48	3.33	Ns
	Moraxellaceae	1.45	1.04	Ns
	Veillonellaceae	1.39	1.74	Ns
	Flavobacteriaceae	1.33	1.02	Ns
	Prevotellaceae	1.33	1.51	Ns
	Sphingomonadaceae	1.09	1.26	Ns
	Rhodobacteraceae	0.60	1.52	Ns
	Ruminococceae	0.52	107	Ns

Bacterial taxa with a relative abundance >1% were included. P-value; Ns, not significant (based on $P < 0.05$).