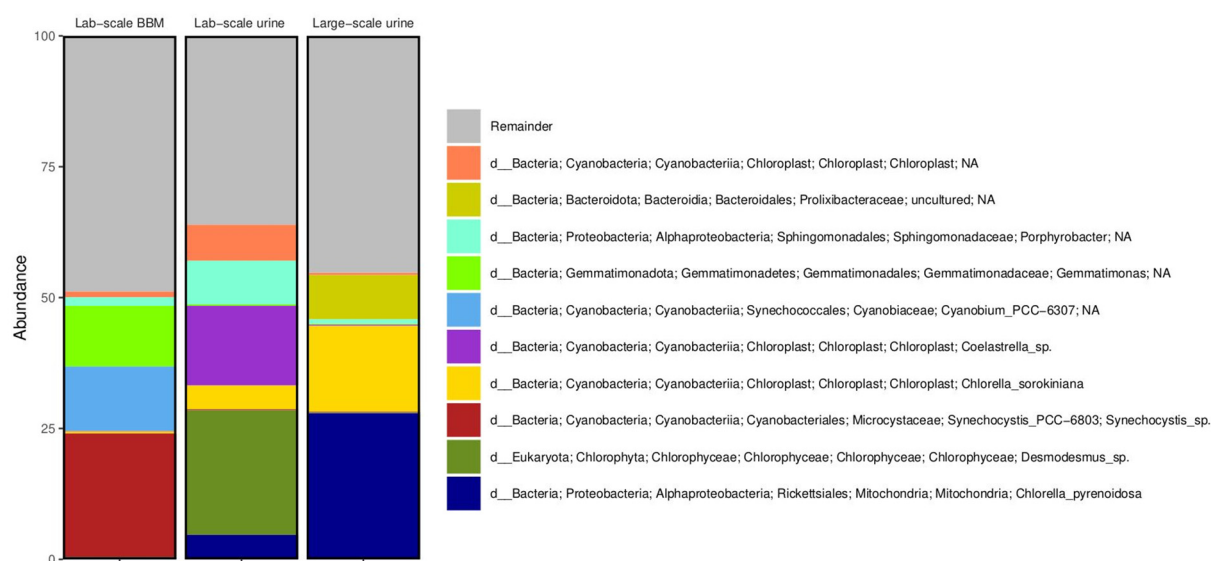


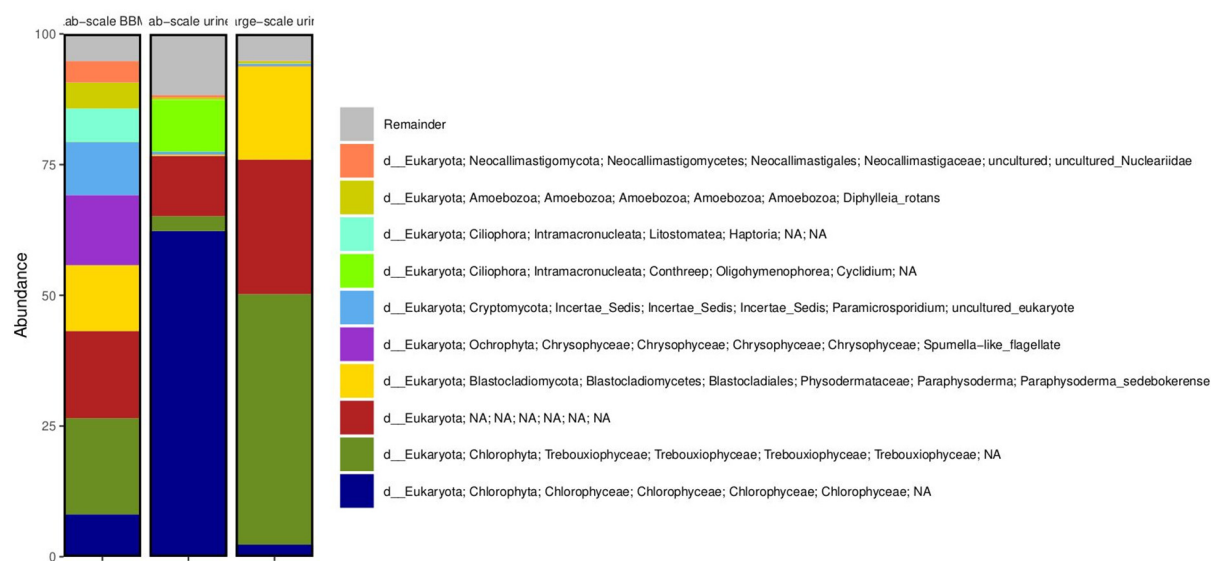
**Tech.phi2 Table S1.** Sequence information from QIIME 2 (2022.8 version) processing of NGS amplicon reads

	Samples	Number of reads	Number of sequences after denoising with Dada2	Number of observed ASVs
16S rRNA	1	53725	49269	415
	2	67913	61667	357
	10	63615	59403	394
18S rRNA	1	97940	95098	69
	2	96266	93876	74
	10	68905	67319	64
23S rRNA	1	113771	110267	82
	2	112697	109131	73
	10	96778	94580	51
tufA	1	31673	27026	97
	2	35074	29654	51
	10	11132	9465	64

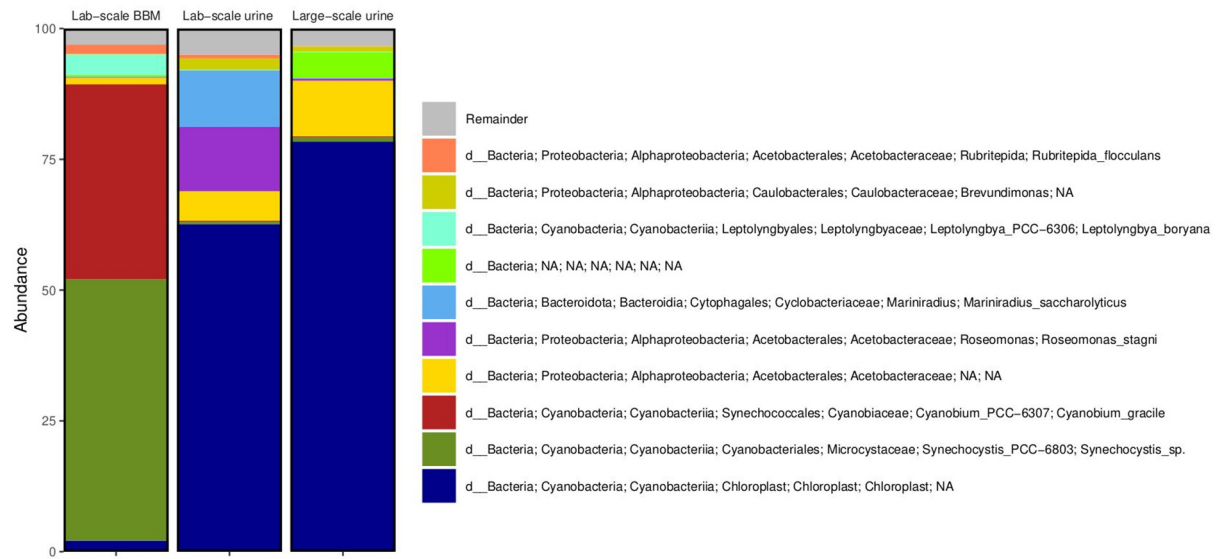
(a)



(b)



(c)

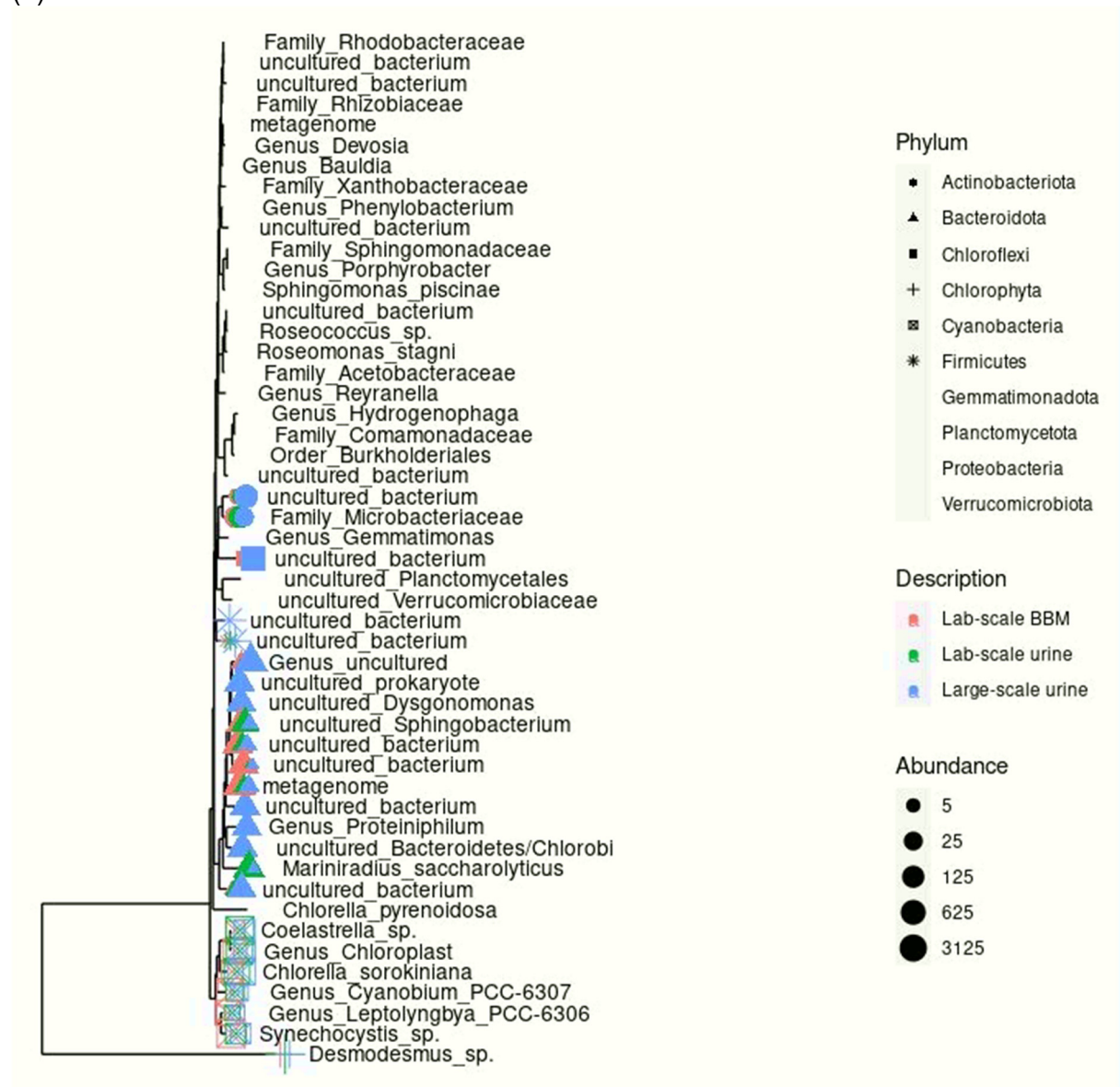


(d)

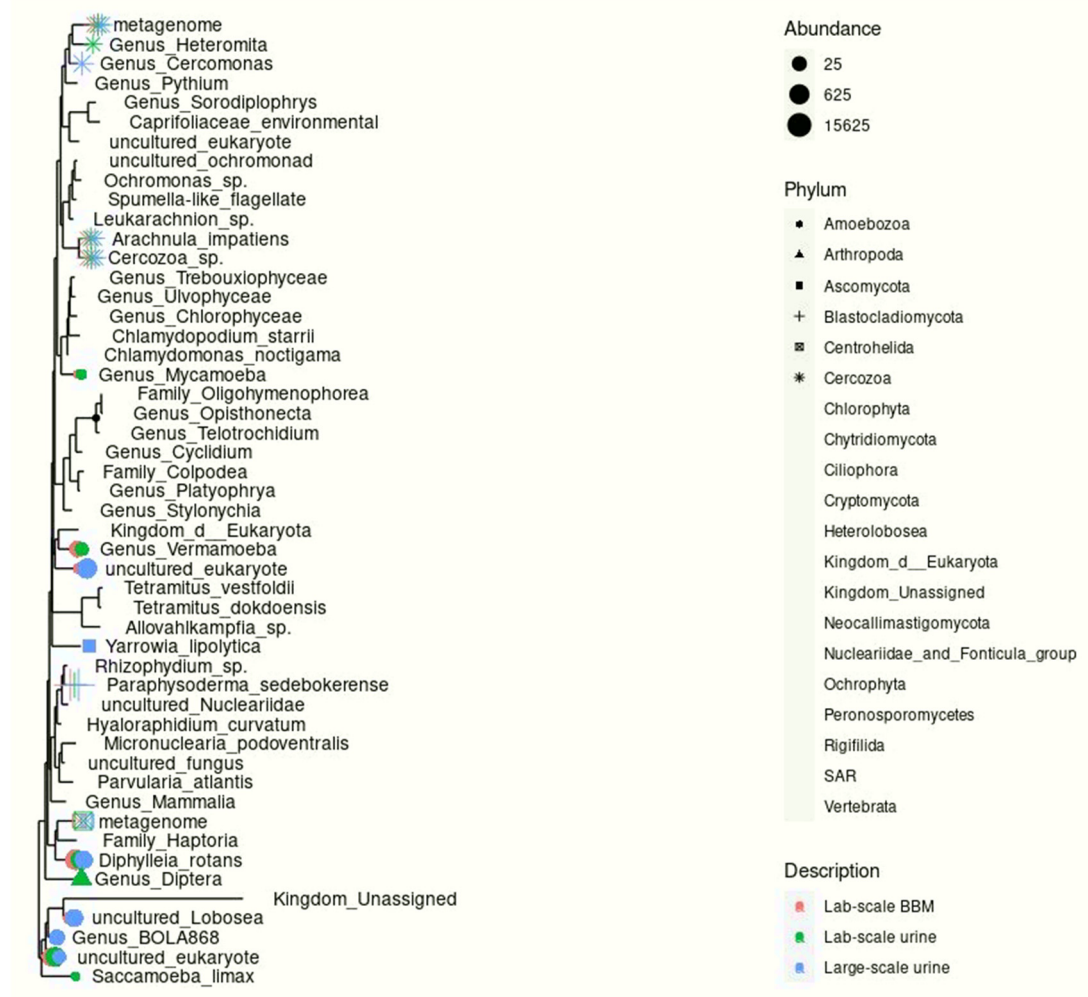


**Figure S1.** Bar plots showing variation in the relative abundances of taxonomies up to species level in lab-scale (urine and BBM) and large-scale urine microbial communities. Colors represent microbial taxonomy classified by Silva taxonomy (release\_138) with using (a) 16S rDNA marker regions, (b) 18S rDNA marker regions and (c) 23S rDNA marker regions, by (d) tufA database [Sauvage et al., 2016] [50].

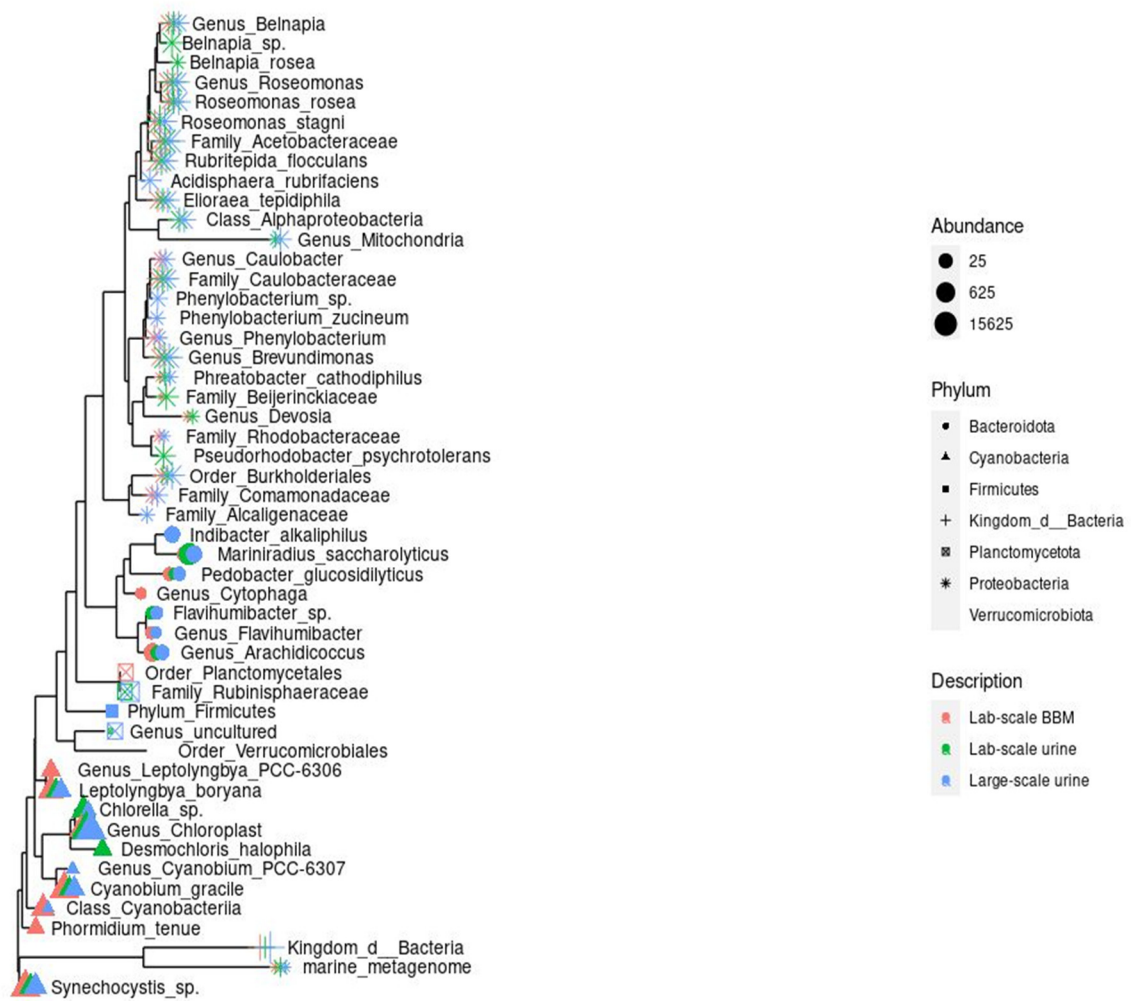
(a)



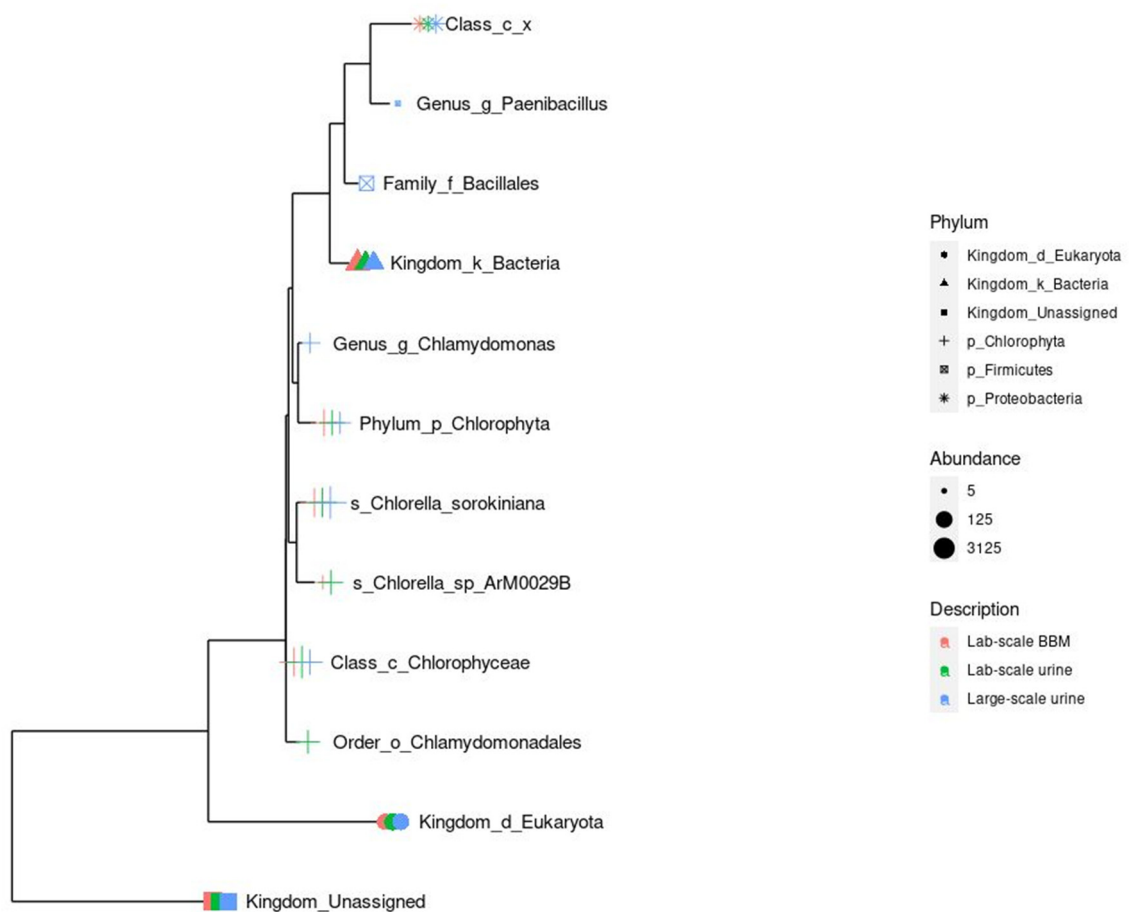
(b)



(c)



(d)



**Figure S2.** Phylogenetic trees showing the relationship of (a) 16S rRNA, (b) 18S RNA, (c) 23S rRNA and (d) *tufA* gene sequences. All the phylogenetic trees were constructed for top 50 taxa for better visualization.