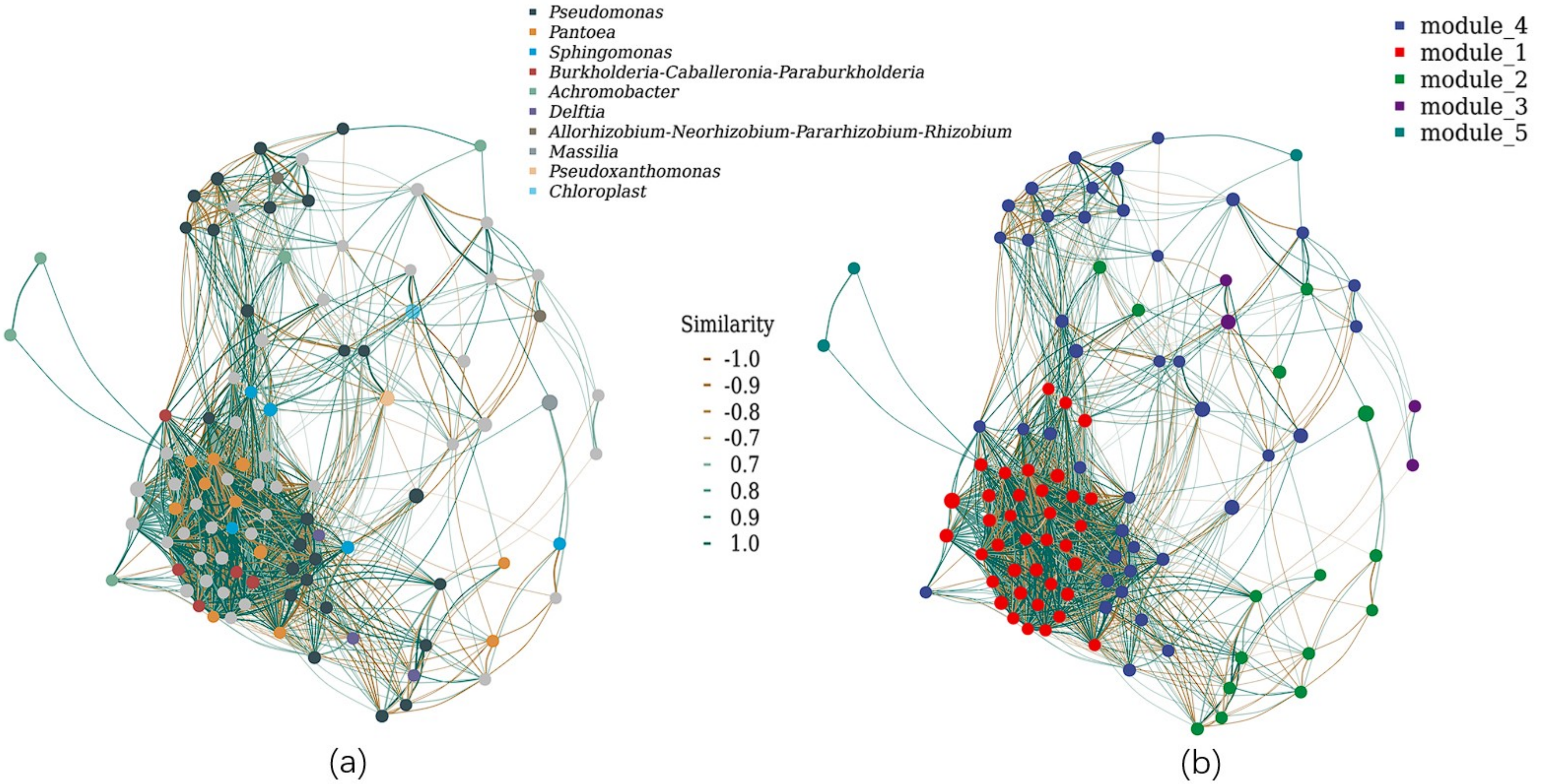

Figure S1 SparCC was used to construct ASVs correlation network. (a) correlation (|Simalarity| > 0.7) between different ASVs. (b) Multi-level Modularity optimization is used to divide the network into five modules.

Table S1 Relative abundance of bacteria at the genus level in simulate wastewater(%)

Group	Monoculture					Frist stage				Second stage	
Genus	Micractinium sp.	Desmodesmus sp.	Pediastrum sp.	Scenedesmus obliquus	Nannochloropsis oceanica	PS	PM	DS	DM	PMN	PMp
Chloroplast	49.8	0.0	0.1	58.3	28.5	41.7	15.9	28.1	44.1	27.8	1.2
Pseudomonas	0.1	56.6	90.3	0.0	0.0	12.9	0.0	3.7	3.6	0.5	0.0
Paraburkholderia	1.8	0.1	0.1	23.7	10.9	8.9	4.8	7.6	13.0	14.3	2.5
Sphingomonas	2.4	5.1	0.7	0.4	3.9	6.9	3.7	1.1	15.2	27.6	10.2
Pantoea	26.6	0.0	0.1	3.2	17.5	0.2	11.7	1.5	2.5	0.1	0.0
Cupriavidus	0.0	0.0	0.0	0.0	0.0	1.6	0.7	2.5	0.2	3.7	41.8
Ralstonia	0.3	0.3	0.0	0.0	0.1	14.2	1.1	18.6	2.6	2.9	0.1
Hydrotalea	0.0	0.0	0.0	0.0	0.0	1.1	2.0	2.1	0.1	3.5	30.9
Massilia	0.0	0.0	0.0	0.0	0.0	0.0	0.0	23.1	0.9	0.3	0.0
Novosphingobium	3.1	0.1	0.0	0.1	0.0	0.2	1.7	0.3	0.4	1.1	2.8
Buttiauxella	0.2	0.0	0.0	2.6	0.5	0.1	2.4	0.5	0.6	1.7	0.1
Delftia	0.0	1.4	1.5	0.0	0.0	1.8	0.0	1.0	0.7	0.2	0.0
Mesorhizobium	0.0	4.9	0.0	0.0	0.0	0.1	0.1	0.2	0.4	0.0	0.0
Achromobacter	1.2	0.7	0.4	0.0	0.0	0.4	0.2	0.4	1.0	0.5	0.0
Rhizobium	0.0	4.3	0.0	0.0	0.0	0.1	0.0	0.1	0.1	0.0	0.0
Curvibacter	0.0	4.6	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Bradyrhizobium	0.9	0.2	0.0	2.4	0.1	0.0	0.5	0.1	0.2	0.0	0.0
Caulobacter	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	3.5
Terrimonas	0.0	0.0	0.1	0.0	0.0	2.0	0.0	0.6	0.0	0.0	0.7
Paludisphaera	2.1	0.5	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.2	0.1
Others	11.4	21.2	6.3	9.3	38.4	7.6	55.0	8.8	14.5	15.6	6.1