

Supplementary data

**Evolution of bacterial consortia in an integrated tannery wastewater treatment
process**

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Summary

Figure S1 Phylogenetic tree of bacterial communities based on the partial 16S gene sequences recovered from the DGGE gel. The scale bar represents evolutionary distance (10 substitutions per 100 nucleotides).

Figure S2 Rarefaction curves at the 3% distance cutoff indicating the observed number of operational taxonomic units (OTUs) within samples.

Figure S3 Heatmap describing the 35 most abundant genera of bacterial community for each sample. The relative abundance are indicated by color intensity with the legend at the top right corner.

Table S1 Species richness and diversity indices based on the $OTU_{0.03}$ obtained from HiSeq sequencing data.

Table S2 SRCCs between the microbial composition and environmental parameters (SRCC: Spearman's rank correlation coefficient; RE: removal efficiency; * indicate $p < 0.05$, two tailed, SRCC values with $p < 0.05$ are shown in red).

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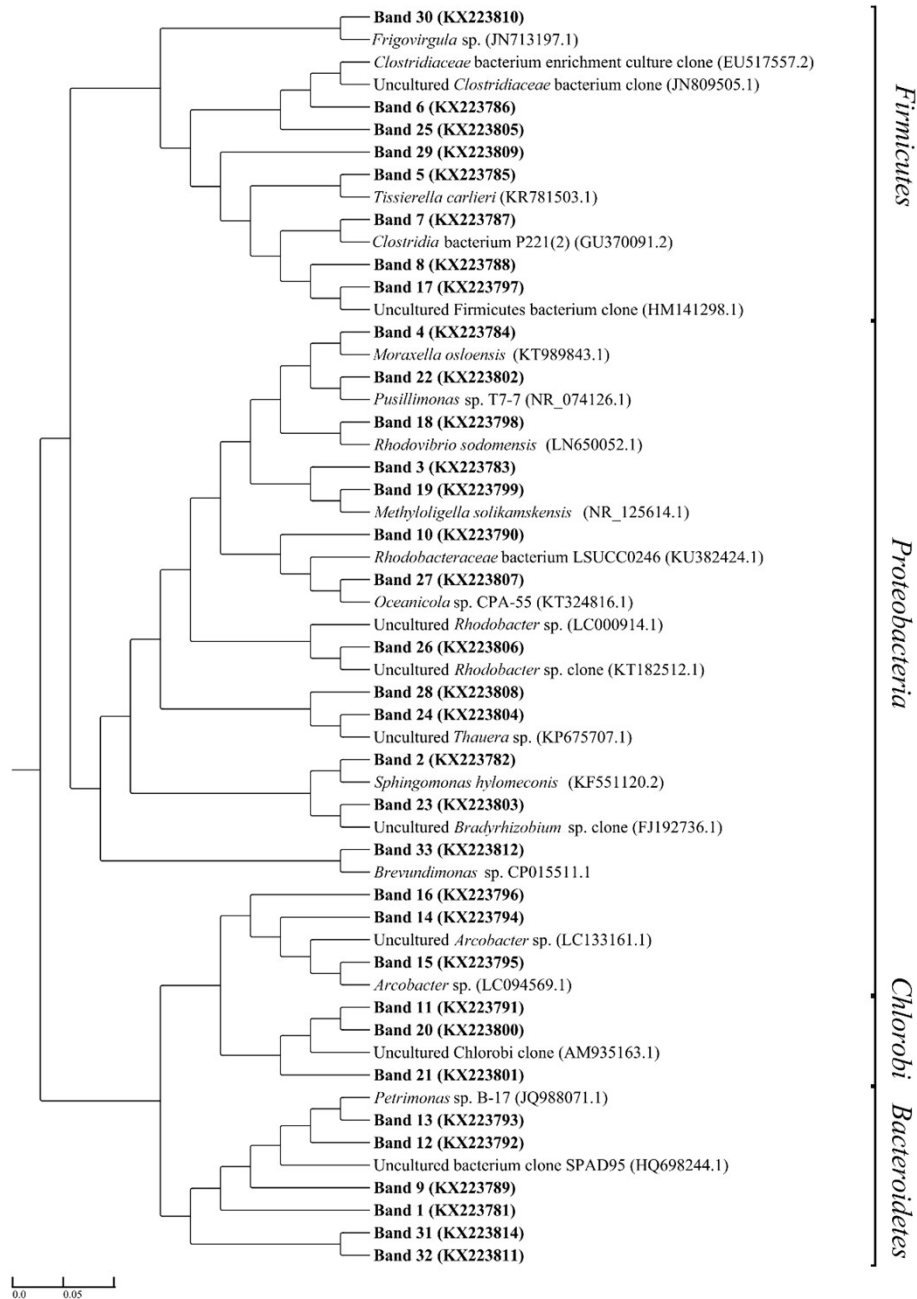


Figure S2 Rarefaction curves at the 3% distance cutoff indicating the observed number of operational taxonomic units (OTUs) within samples.

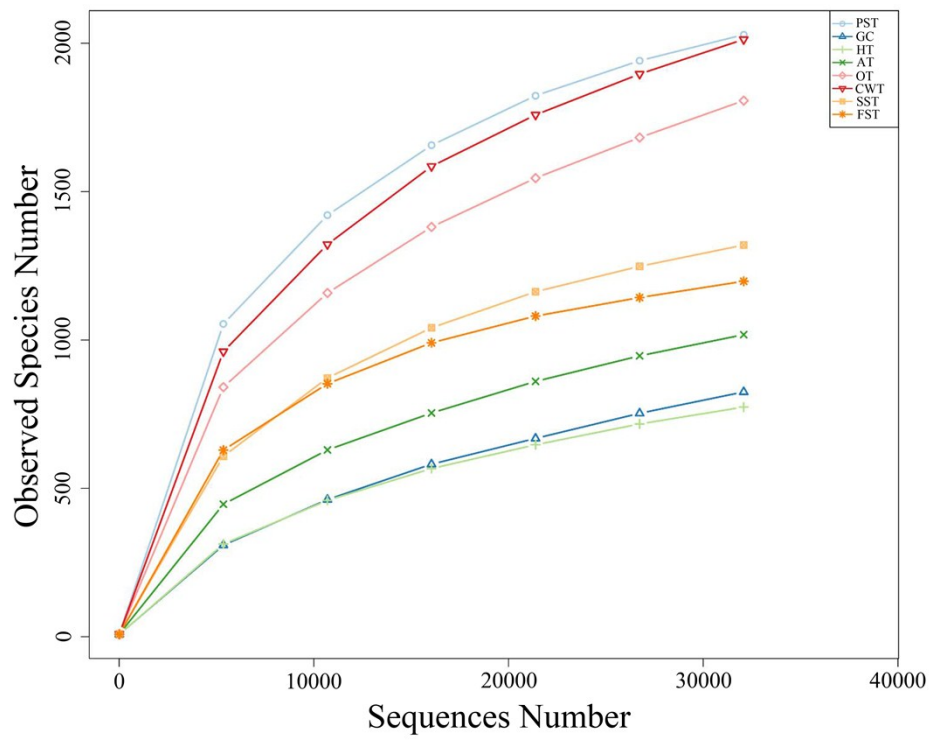


Table S1 Species richness and diversity indices based on the OTU_{0.03} obtained from HiSeq sequencing data.

Sample	Raw Tags	Effective Tags	OTUs	Shannon	Simpson	Chao1	ACE	Goods coverage
GC	65916	64655	1097	5.22	0.928	1335.907	1433.658	0.988
HT	52020	51176	995	4.782	0.897	1101.925	1131.541	0.99
PST	53326	50897	2295	8.572	0.99	2238.338	2356.215	0.986
AT	58819	56168	1315	6.212	0.963	1405.005	1487.069	0.988
SST	47129	44267	1589	6.67	0.968	1568.236	1637.057	0.988
OT	34644	33770	1807	7.663	0.981	3994.778	2712.138	0.978
FST	39771	37047	1426	6.494	0.929	1338.695	1366.364	0.992
CWT	60439	58890	2361	8.057	0.978	2578.047	2594.131	0.981

Table S2 SRCCs between the microbial composition and environmental parameters

(SRCC: Spearman's rank correlation coefficient; RE: removal efficiency; * indicate p<0.05, two tailed, SRCC values with p<0.05 are shown in red).

		COD	NH ₄ ⁺ -N	pH	COD RE (%)	NH ₄ ⁺ -N RE (%)
<i>Proteobacteria</i>	SRCC	0.000	0.048	-0.238	0.321	-0.179
	p values	1.000	0.911	0.570	0.482	0.702
<i>Bacteroidetes</i>	SRCC	0.619	0.762*	-0.381	0.143	-0.750
	p values	0.102	0.028	0.352	0.760	0.052
<i>Firmicutes</i>	SRCC	0.381	-0.286	0.643	-0.429	0.286
	p values	0.352	0.493	0.086	0.337	0.535
<i>Others</i>	SRCC	-0.810*	-0.667	0.071	-0.143	0.679
	p values	0.015	0.071	0.867	0.760	0.094
<i>Actinobacteria</i>	SRCC	-0.548	-0.071	-0.310	0.714	0.107
	p values	0.160	0.867	0.456	0.071	0.819
<i>Chloroflexi</i>	SRCC	-0.643	-0.357	-0.333	0.429	0.214
	p values	0.086	0.385	0.420	0.337	0.645
<i>[Thermi]</i>	SRCC	-0.714*	-0.381	0.190	0.250	0.786*
	p values	0.047	0.352	0.651	0.589	0.036
<i>Planctomycetes</i>	SRCC	-0.571	-0.333	-0.143	0.000	0.286
	p values	0.139	0.420	0.736	1.000	0.535
<i>Acidobacteria</i>	SRCC	-0.643	-0.167	-0.595	0.464	0.000
	p values	0.086	0.693	0.120	0.294	1.000
<i>TM7</i>	SRCC	-0.500	0.357	-0.429	0.321	-0.214
	p values	0.207	0.385	0.289	0.482	0.645
<i>Gemmatimonadetes</i>	SRCC	-0.643	-0.310	-0.357	0.071	0.179
	p values	0.086	0.456	0.385	0.879	0.702
<i>Nitrospirae</i>	SRCC	-0.524	-0.286	-0.381	0.036	0.000
	p values	0.183	0.493	0.352	0.939	1.000
<i>Tenericutes</i>	SRCC	0.405	0.500	-0.119	0.143	-0.357
	p values	0.320	0.207	0.779	0.760	0.432
<i>OD1</i>	SRCC	-0.323	0.156	-0.216	0.198	-0.108
	p values	0.435	0.713	0.608	0.670	0.818
<i>Spirochaetes</i>	SRCC	0.452	-0.214	0.262	-0.464	-0.107
	p values	0.260	0.610	0.531	0.294	0.819