Supporting information

Title: Kitchen waste compost leachate as compensatory carbon sources intensify nitrogen removal in sewage treatments

Table S1 Water quality of CL from 4 kitchen waste disposal sites in Hangzhou.

Source of leachate	pH	TN (mg/L)	NH_4^+-N (mg/L)	COD (mg/L)	Oil content (%)
Eshan	5.29	470.2	234.0	37894	0.39
Tonglu	4.59	1174.5	503.0	21034	0.26
Shangcheng 1# site	5.43	771.0	362.0	42854	0.20
Shangcheng 2# site	5.34	430.6	238.0	22221	0.53
Average	5.16±0.39	711.6±344.0	334.3±127.2	31001±11022	0.35±0.15

Table S2 The water quality of effluent from each pool in Fuchun sewage plant.

Sample	COD (mg/L)	NH_4^+-N (mg/L)	NO_3^--N (mg/L)	TN (mg/L)	TP (mg/L)	pH	DO (mg/L)	Salinity (%)
Adjusting pool	112	12.65	0.02	20.6	0.32	7.04	4.9	0. 02
SBR pool	12	1.58	2.89	9.6	0.25	6.77	9.2	0. 02
Clarifier	64	0.66	2.63	11.2	0.16	6.49	8.6	0. 02
Denitrification pool	NA	1.26	0.1	10.3	0.15	6.45	9.3	0. 02

Note: NA is below the detection limit

Table S3 The main physicochemical properties of CL and domestic sewage.

Sample	COD (mg/L)	NH_4^+-N (mg/L)	NO_3^--N (mg/L)	TN (mg/L)	TP (mg/L)	pH	DO (mg/L)	Salinity (%)	TS (g/L)	TDS (g/L)	TOC (mg/L)
CL	38225	134	148.6	765	0.47	5.20	1.05	0.26	41.65	28.2	10850
Domestic sewage	112	12.65	0.02	20.6	0.32	7.14	4.9	0.02	0.3	0.1	1.03

Table S4 The water quality of influent both raw and pre-treated CL addition into the actual sewage with varying proportions.

Addition ratio	NH_4^+-N (mg/L)	NO_3^--N (mg/L)	TN (mg/L)	COD (mg/L)	TP (mg/L)	pH*
0.25%	12.93	0.39	22.9	145	0.321	6.92
0.50%	13.24	0.76	24.2	244	0.322	6.83
0.75%	13.7	1.38	26.9	339	0.323	6.74
1.00%	13.93	1.5	28.9	445	0.324	6.66
1.25%	14.27	1.86	30.2	547	0.326	6.57
1.50%	14.62	2.64	32.4	652	0.328	6.49
2.00%	15.42	3.48	35.8	810	0.331	6.35
2.50%	16.59	4.35	38.1	1169	0.336	6.27
3.00%	17.75	6.43	42.2	1220	0.344	6.12

*pH values were measured immediately after mixing CL with domestic sewage (initial influent pH).

Table S5 Bacterial biomarkers identified by LEfSe analysis among CK, S1 and S2 groups, basing on the Kruskall–Wallis test with threshold LDA > 3.5 and $p < 0.05$.

Level	Name	group	LDA	*p*
Phylum	Firmicutes	S2	4.74	0.03
Phylum	Actinobacteriota	S2	4.61	0.03
Phylum	Patescibacteria	CK	3.68	0.04
Class	Actinobacteria	S2	4.77	0.03
Class	Bacilli	S2	4.77	0.03
Class	Acidimicrobiia	CK	4.08	0.04
Class	Thermoleophilia	CK	3.99	0.03
Class	JG30-KF-CM66	CK	3.65	0.04
Class	Phycisphaerae	CK	3.55	0.03
Order	Rhodobacterales	S1	3.92	0.03
Order	Actinomycetales	S2	4.12	0.03
Order	Lactobacillales	S2	4.75	0.03
Order	IMCC26256	CK	3.71	0.04
Order	Microtrichales	CK	3.65	0.04
Order	Solirubrobacterales	CK	3.90	0.03
Order	norank_c_JG30-KF-CM66	CK	3.67	0.04
Family	Rhodocyclaceae	S1	4.10	0.04
Family	Rhodobacteraceae	S1	3.90	0.03
Family	Actinomycetaceae	S2	4.13	0.03
Family	Saccharimonadaceae	S2	3.53	0.03
Family	Solirubrobacteraceae	CK	3.67	0.03
Family	norank_o_IMCC26256	CK	3.80	0.04
Family	67-14	CK	3.51	0.03
Family	norank_o_JG30-KF-CM66	CK	3.59	0.04
Genus	*Micropruina*	S1	4.10	0.02
Genus	*unclassified*_f_Rhodobacteraceae	S1	3.82	0.03
Genus	*unclassified*_f_Rhodocyclaceae	S1	3.66	0.04
Genus	*Propioniciclava*	S2	4.20	0.04
Genus	*TM7a*	S2	3.55	0.03
Genus	*norank*_f_Actinomycetaceae	S2	4.11	0.03
Genus	*unclassified*_f_Solirubrobacteraceae	CK	3.50	0.03
Genus	*norank*_f_Steroidobacteraceae	CK	3.66	0.04
Genus	*norank*_f_IMCC26256	CK	3.76	0.04
Genus	*norank*_f_JG30-KF-CM66	CK	3.65	0.04

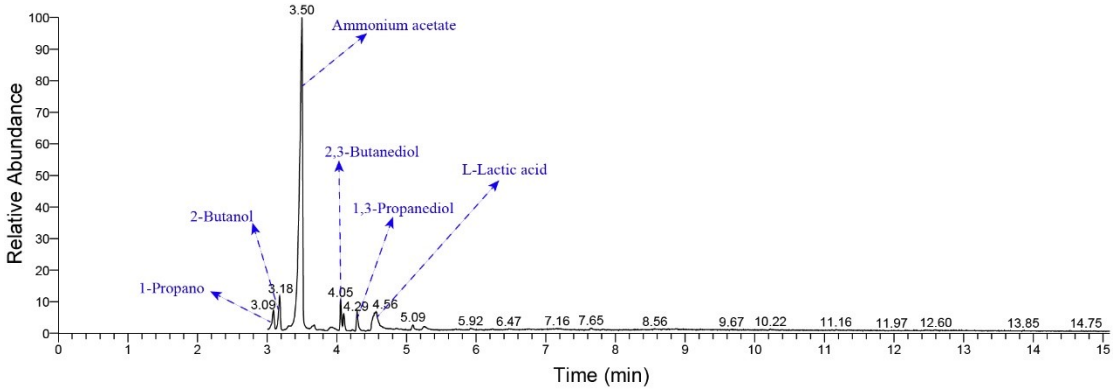

Figure S1 Components of organic carbon in CL, determined by Gas Chromatography and Mass Spectrometry (GC-MS, TRACE1300-ISQ7000, Thermo Fisher Scientific).

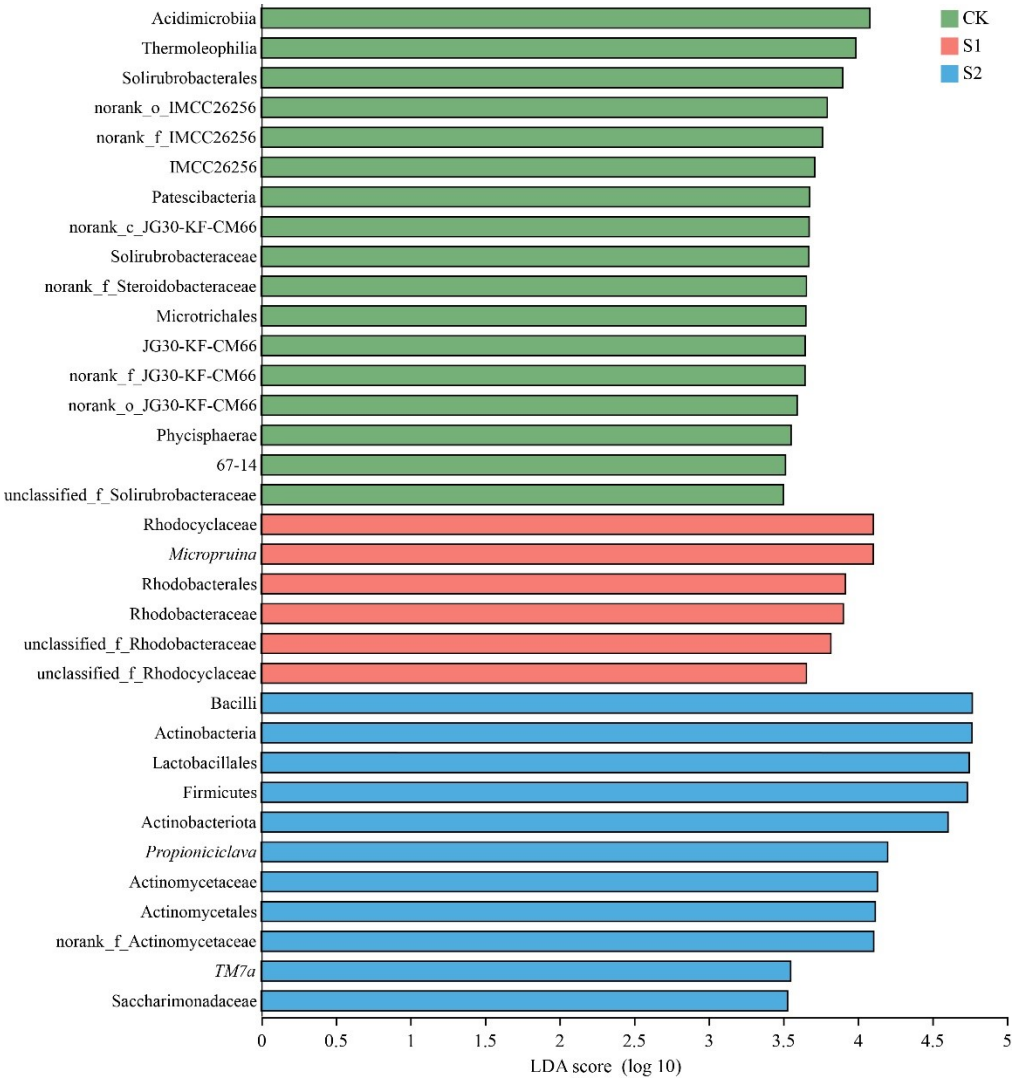

Figure S2 LDA score identified the size of sludge among CK, S1 and S2 groups, basing on the Kruskall–Wallis test with threshold LDA > 3.5 and p < 0.05.

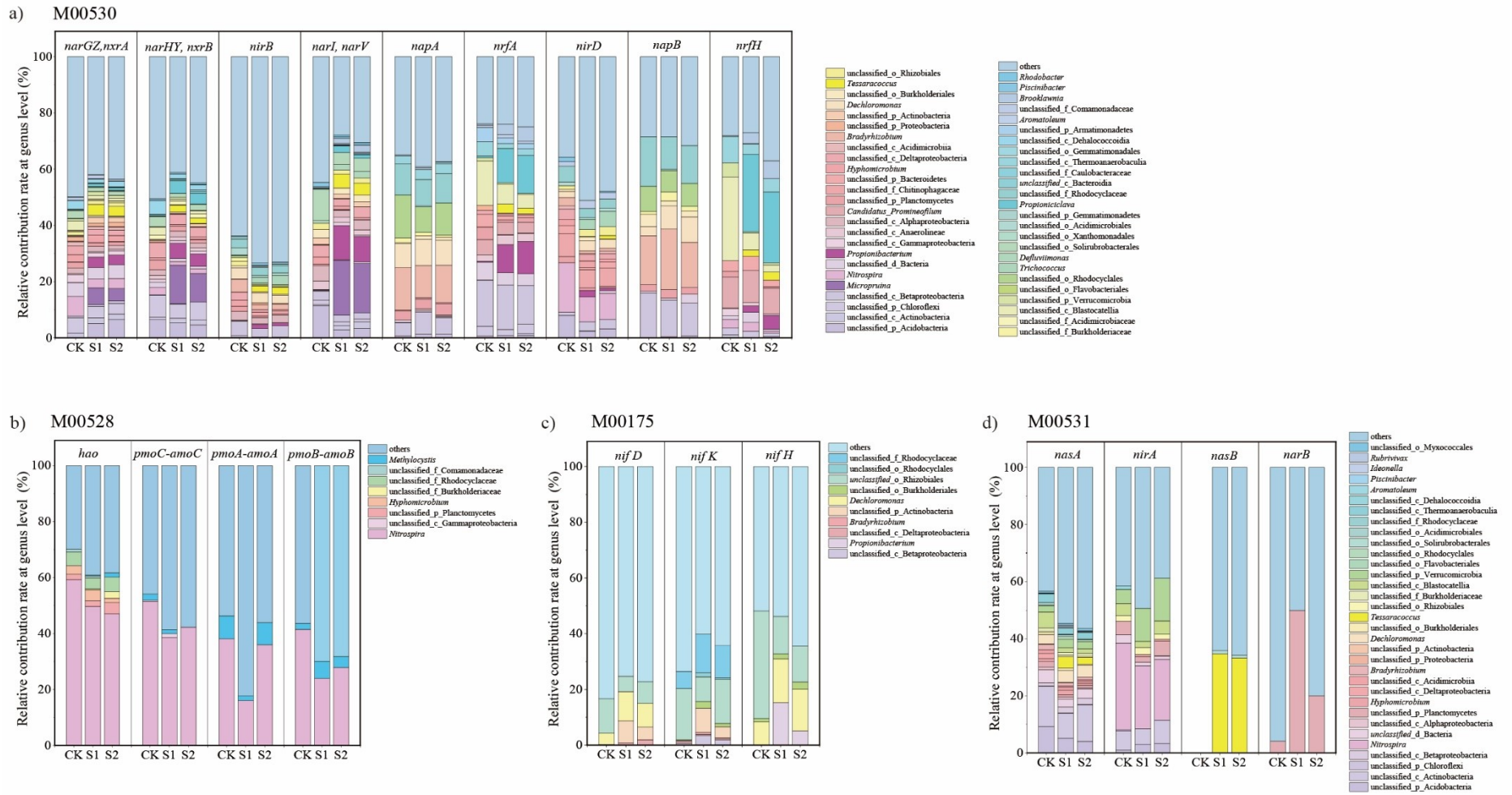

Figure S3 Relative contribution of microbes to N-metabolic pathways of different sludge groups. Panel (a)-(d) were the main functional bacteria relative contribution to nitrogen pathways, including DNRA (M00530), nitrification (M00528), nitrogen fixation (M00175) and assimilatory nitrate reduction (M00531) modules.