

Supplementary information

The mechanical scouring of bio-carriers improves phosphorous removal and mediates functional microbiome in membrane bioreactors

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Table caption

Table S1 Compositions of the synthetic wastewater.

Table S2 Variation of biopolymers in bulk sludge of the two MBRs.

Table S3 Biodiversity of the 16S rRNA sequences of the total (unstained) and active (PMA stained) bacterial communities.

Table S4 The relative abundances of all the identified genera in total and active microbial community of bulk sludge from the control MBR and carrier-dosed MBR.

Figure caption

Figure S1 Experimental set-up of the control MBR and carrier-dosed MBR and picture of the carrier used in this work.

Figure S2 Variations in COD, TN, TP , NO_3^- -N and NO_2^- -N during the operation of the control MBR and carrier-dosed MBR.

Figure S3 Particle size distribution and MLSS development during the operation of the MBRs. Particle size distribution of the bulk sludge from the control MBR and carrier-dosed MBR- were measured in triplicate. Averages of the triplicate measures were used to plot the profiles.

Figure S4 Venn diagrams of bacterial genera present in total and active microbial community in bulk sludge from the control MBR and carrier-dosed MBR, respectively.

Table S1 Compositions of the synthetic wastewater.

Substrates	mg/L	Trace elements	mg/L
Na-acetate	35	FeSO ₄ ·7H ₂ O	2.50
KH ₂ PO ₄	40	ZnCl ₂	0.06
(NH ₄) ₂ SO ₄	150	MnCl ₂ ·4H ₂ O	0.06
Starch	160	NaMoO ₄ ·2H ₂ O	0.19
Milk powder	200	CoCl ₂ ·6H ₂ O	0.13
Sucrose	140	NiCl ₂ ·6H ₂ O	0.04
Urea	50	CuSO ₄	0.06
Peptone	32	CaCl ₂	0.44
Yeast extract	70	H ₃ BO ₃	0.06
Beef extract	80	MgCl ₂ ·6H ₂ O	0.19
NaHCO ₃	80		

Table S2 Variation of biopolymers in bulk sludge of the two MBRs.*

	Items	MBR-A	MBR-B	<i>P</i> -value
Biopolymers (mg/g-MLVSS)	EPS-PS	24.0±5.7	18.4±4.3	0.01
	EPS-PN	49.8±14.2	43.1±7.0	0.12
	EPS	73.8±17.5	61.4±5.9	0.02
	SMP-PS	3.0±1.1	3.3±1.1	0.45
	SMP-PN	1.1±1.0	0.9±1.0	0.59
	SMP	4.1±1.6	4.2±1.7	0.85

*PN and PS denote proteins and polysaccharides, respectively; sample numbers n = 15; the data were given as mean ± standard deviation.

Table S3 Biodiversity of the 16S rRNA sequences of the total (unstained) and active (PMA stained) bacterial communities. *

Sample name		Observed species	Shannon	Simpson	Chao1	ACE	goods coverage	PD whole tree
Control MBR	Total	1173	6.791	0.973	1267	1296	0.996	128
sludge	Active	746	6.462	0.975	819	821	0.998	78
Carrier-dosed MBR	Total	1163	6.978	0.977	1261	1261	0.997	98
sludge	Active	891	6.445	0.97	975	1002	0.997	91
Carrier-dosed MBR	Total	1091	6.858	0.97	1118	1156	0.998	96
biofilm	Active	858	6.305	0.959	915	948	0.998	88

*Total and Active represent the total and active bacterial communities, respectively, of biomass sample (i.e., control MBR sludge, carrier-dosed MBR sludge and carrier-dosed MBR biofilm).

Table S4 The relative abundances of all the identified genera in total and active microbial community of bulk sludge from the control MBR and carrier-dosed MBR.

Taxonomy	MBR-control sludge		MBR-carrier sludge	
	Total	Active	Total	Active
<i>unidentified_Nitrospiraceae</i>	0.029455	0.033536	0.018346	0.042926
<i>Phaeodactylibacter</i>	0.037882	0.042057	0.06745	0.083661
<i>Candidatus_Accumulibacter</i>	0.023787	0.02817	0.070813	0.085796
<i>Candidatus_Competibacter</i>	0.04593	0.056794	0.062406	0.07616
<i>Thiothrix</i>	0.094373	0.052656	0.034878	0.020235
<i>Roseiflexus</i>	0.026224	0.021331	0.017061	0.04782
<i>Sarcina</i>	0.038089	7.56E-05	0.003854	0.004459
<i>Byssovorax</i>	0.00376	0.005441	0.003911	0.005895

<i>Haliangium</i>	0.016343	0.026092	0.005347	0.004346
<i>Leeia</i>	0.025676	0.001965	0.009371	0.000246
<i>Ruminococcaceae_UCG-005</i>	0.010467	0.000302	0.017647	0.006745
<i>Clostridium_sensu_stricto_1</i>	0.003004	0.017042	0.005177	0.000246
<i>Ideonella</i>	0.01213	0.016645	0.011601	0.012224
<i>Eubacterium_coprostanoligenes_group</i>	0.006688	0.000132	0.014907	0.003212
<i>Tolumonas</i>	0.008823	0.013868	0.008105	0.007085
<i>Phaselicystis</i>	0.007784	0.013547	0.005063	0.006707
<i>Mycoplasma</i>	0.000586	0	0	0.000113
<i>Lactobacillus</i>	0.009749	0.006499	0.005744	0.000416
<i>Rikenellaceae_RC9_gut_group</i>	0.007539	9.45E-05	0.011204	0.003269
<i>Streptococcus</i>	0.003099	0.004742	0.006575	0.004686
<i>Nitrosomonas</i>	0.00444	0.003231	0.00342	0.00257
<i>Romboutsia</i>	0.007557	0.004912	0.008729	0.002022
<i>Ruminococcaceae_UCG-014</i>	0.008011	0.000756	0.00614	0.001171
<i>Ruminococcaceae_UCG-010</i>	0.005668	0	0.007973	3.78E-05
<i>Dechloromonas</i>	0.002834	0.004893	0.003949	0.007727
<i>Aeromonas</i>	0.005063	0.006934	0.005781	0.005763
<i>Nannocystis</i>	0.005536	0.006443	0.001568	0.00119
<i>Ruminococcus_2</i>	0.004988	0.000151	0.002192	0.001455
<i>unidentified_Saprospiraceae</i>	0.005763	0.005196	0.005045	0.003892
<i>Prevotellaceae_NK3B31_group</i>	0.000359	0	5.67E-05	0.005649
<i>Lewinella</i>	0.004327	0.005422	0.002777	0.003873
<i>Haliscomenobacter</i>	0.00529	0.004175	0.004497	0.003911
<i>Turicibacter</i>	0.004497	0.002381	0.005215	0.000246
<i>Opitutus</i>	0.000321	0.00051	0.000302	0.000567
<i>Prostheco bacter</i>	0.002267	0.005063	0.001455	0.003684
<i>Alistipes</i>	0.00478	0	0.004308	1.89E-05
<i>Enterobacter</i>	0.002211	0.004383	0.00257	0.002532
<i>unidentified_GR-WP33-30</i>	7.56E-05	0.000246	0.000113	0.000151
<i>Bryobacter</i>	0.000246	0.000472	0.000416	0.000642
<i>Christensenellaceae_R-7_group</i>	0.00274	0.000227	0.004119	0.001606
<i>Blastocatella</i>	0.00034	0.000907	0.000812	0.00085
<i>Hydrogenophaga</i>	0.000699	0.000246	0.004043	0.003987
<i>Propionicicella</i>	0.002796	0.003741	0.003646	0.003817
<i>Zoogloea</i>	0.000945	0.003382	0.0017	0.000642
<i>Cloacibacterium</i>	0.002324	0.001153	0.002872	0.002399
<i>Ruminococcaceae_UCG-013</i>	0.002399	0.000113	0.003344	0.00051
<i>Piscinibacter</i>	0.002702	0.003193	0.000907	0.001474
<i>Pseudobutyrvibrio</i>	0.000661	0.000265	0.000869	0.002985
<i>Rubellimicrobium</i>	0.00187	0.002966	0.00153	0.001304
<i>Lachnospiraceae_XPB1014_group</i>	0.000132	3.78E-05	0.002947	0.002173
<i>Exiguobacterium</i>	0.001228	0.001455	0.002626	0.002929
<i>Woodsholea</i>	0.000151	0.000189	0.000227	0.000132

<i>Terrimonas</i>	0.002815	0.001625	0.002551	0.001927
<i>Acinetobacter</i>	0.001757	0.002343	0.00119	0.002796
<i>unidentified_Syntrophaceae</i>	0.000529	0.000529	0.001889	0.00274
<i>Lachnospiraceae_AC2044_group</i>	0.00102	0.000265	0.002551	0.000945
<i>Sandaracinus</i>	0.001115	0.002551	0.001266	0.001304
<i>Stella</i>	0.000964	0.002494	0.000775	0.000623
<i>Prevotellaceae_UCG-003</i>	0.002418	0.000132	0.001568	0.000189
<i>Prevotella_9</i>	0.000265	0	9.45E-05	0.002192
<i>unidentified_Rickettsiaceae</i>	0.001001	0.002135	0.000491	0.000189
<i>Subdoligranulum</i>	0.002135	0.000302	0.001077	0.000302
<i>Defluviicoccus</i>	0.001587	0.002097	0.000982	0.001304
<i>Rhodobacter</i>	0.000869	0.002097	0.000548	0.000586
<i>Treponema_2</i>	0.002078	0	0.001398	0.001115
<i>Ferruginibacter</i>	0.001625	0.001304	0.001115	0.000794
<i>Pseudomonas</i>	0.000321	0.000586	0.000623	0.000378
<i>Ruminiclostridium_6</i>	0.00051	0	0.00085	0.001965
<i>Bacteroides</i>	0.001965	3.78E-05	0.001852	7.56E-05
<i>Candidatus_Microthrix</i>	0.000359	0.000378	0.000982	0.001266
<i>Turneriella</i>	0.001228	0.001549	0.000623	0.000718
<i>Ruminiclostridium_5</i>	0.000831	1.89E-05	0.001776	9.45E-05
<i>CL500-29_marine_group</i>	0.001323	0.001738	0.000907	0.001757
<i>Dongia</i>	0.001001	0.001625	0.000283	0.000208
<i>Ruminococcus_1</i>	0.001039	3.78E-05	0.000642	0.001587
<i>dgA-11_gut_group</i>	0.000737	0	0.001568	0
<i>Halomonas</i>	0.000756	0.001171	0.001511	0.00102
<i>Propioniciclava</i>	0.000302	0.000321	0.001436	0.001209
<i>Lysobacter</i>	0.000548	0.001417	0.000661	0.000661
<i>Desulfomicrobium</i>	0.000435	0.000453	0.001077	0.001417
<i>Ruminococcaceae_NK4A214_group</i>	0.000737	0.000113	0.001417	0.000246
<i>Roseburia</i>	0.00017	0	7.56E-05	0.000113
<i>Runella</i>	0.00119	0.000586	0.001058	0.000661
<i>Alloprevotella</i>	0.000888	0	0.000964	0.00136
<i>Lachnospiraceae_UCG-005</i>	0.001266	0	3.78E-05	0.001058
<i>SM1A02</i>	7.56E-05	0.000227	0.000208	0.000132
<i>Bosea</i>	3.78E-05	0.00017	5.67E-05	5.67E-05
<i>Chryseobacterium</i>	0.000265	0.00017	0.000642	0.000831
<i>Rubrivivax</i>	0.000132	9.45E-05	0.000397	0.000416
<i>Ruminococcaceae_UCG-002</i>	0.001096	0	0.000699	0.000794
<i>Coprococcus_3</i>	0.000453	0.000132	0.001077	0.000113
<i>Bradyrhizobium</i>	0.00017	0.000283	0.000151	0.000132
<i>Prevotella_1</i>	0.000246	5.67E-05	0.000151	0.001001
<i>Gordonia</i>	1.89E-05	0	7.56E-05	7.56E-05
<i>Ruminococcaceae_UCG-009</i>	0.000623	0	0.001001	0.000189
<i>unidentified_OPB35_soil_group</i>	0.000246	0.000586	0.000246	0.000945

<i>Phenylobacterium</i>	9.45E-05	0.000189	0	0.000189
<i>Lacibacter</i>	0.000435	0.000945	0.000265	0.000208
<i>Candidatus_Odyssella</i>	0.000283	0.000208	0.000926	0.000812
<i>Meganema</i>	0.000208	0.000189	0.000642	0.000888
<i>Blautia</i>	0.000548	0.000189	0.000208	0.000132
<i>Ferrovibrio</i>	0.000208	7.56E-05	5.67E-05	5.67E-05
<i>Erysipelotrichaceae_UCG-006</i>	0.000869	3.78E-05	0.000416	3.78E-05
<i>Comamonas</i>	0.000453	0.000737	0.00085	0.000435
<i>Collinsella</i>	0.000397	7.56E-05	0.000831	3.78E-05
<i>Shewanella</i>	0.000283	0.000567	0.000416	0.000529
<i>Sorangium</i>	0.000359	0.000775	0.000321	0.000491
<i>Zymomonas</i>	3.78E-05	5.67E-05	0	5.67E-05
<i>unidentified_Neisseriaceae</i>	0.000794	0.000737	0.000416	0.00034
<i>Phascolarctobacterium</i>	0.000132	0	5.67E-05	0.000756
<i>Holdemanella</i>	0.000737	0.000113	0.000359	3.78E-05
<i>Phreatobacter</i>	3.78E-05	3.78E-05	1.89E-05	3.78E-05
<i>Candidatus_Alysiosphaera</i>	0.000265	0.000491	0.000113	5.67E-05
<i>unidentified_Chloroplast</i>	3.78E-05	0.000661	0.000189	0.000718
<i>Escherichia-Shigella</i>	0.000283	0.000113	0.00068	0.000227
<i>Hyphomicrobium</i>	0.000265	0.000359	0.000378	0.000661
<i>Sphingosinicella</i>	0.000132	0.000529	0.00017	0.000208
<i>Coprococcus_1</i>	0.000378	3.78E-05	0.000605	3.78E-05
<i>Ruminiclostridium</i>	0.000642	0	0	3.78E-05
<i>Lachnospira</i>	0.00017	0	5.67E-05	0.000623
<i>Actinobacillus</i>	5.67E-05	0	0.000586	1.89E-05
<i>Prevotellaceae_UCG-004</i>	0.000586	0	0.000529	0
<i>Campylobacter</i>	0.000586	0	0.000113	0
<i>Bdellovibrio</i>	0.000132	0.000113	7.56E-05	1.89E-05
<i>Chitinophaga</i>	0.000359	0.000548	0.000246	0.000151
<i>Family_XIII_AD3011_group</i>	0.00034	3.78E-05	0.000548	1.89E-05
<i>Ruminococcaceae_UCG-008</i>	9.45E-05	0.000227	0.000151	1.89E-05
<i>Chloronema</i>	3.78E-05	9.45E-05	0.000132	0.000529
<i>Peptoclostridium</i>	9.45E-05	0.00051	0.000472	9.45E-05
<i>Parabacteroides</i>	0.000378	0	0.00034	0.00051
<i>Flavobacterium</i>	0.000491	0.000321	0.000472	0.000208
<i>Mycobacterium</i>	0	9.45E-05	5.67E-05	7.56E-05
<i>Delftia</i>	0.00017	0.000265	9.45E-05	9.45E-05
<i>Cetobacterium</i>	0	0	1.89E-05	0
<i>Lachnospiraceae_UCG-003</i>	3.78E-05	5.67E-05	3.78E-05	0
<i>Faecalibacterium</i>	0.000472	7.56E-05	0.000246	0.000246
<i>Hirschia</i>	0.000132	0.000283	7.56E-05	3.78E-05
<i>Pseudoxanthomonas</i>	0.000151	0.000453	1.89E-05	3.78E-05
<i>Anaerotruncus</i>	0.000453	0	0.000265	0.000397
<i>Sphaerochaeta</i>	0.000435	1.89E-05	1.89E-05	0.000208

<i>Deinococcus</i>	0	5.67E-05	1.89E-05	0
<i>Lactococcus</i>	9.45E-05	9.45E-05	0.000321	0.000208
<i>Sphingopyxis</i>	1.89E-05	0	1.89E-05	0
<i>Devosia</i>	0.000113	0.000227	0.000113	9.45E-05
<i>Peptococcus</i>	0.000397	1.89E-05	5.67E-05	0
<i>Brevundimonas</i>	1.89E-05	1.89E-05	1.89E-05	3.78E-05
<i>Solobacterium</i>	0.000378	5.67E-05	0.000227	0.000208
<i>Candidatus_Soleaferrea</i>	0.000208	0	0.000378	1.89E-05
<i>Oscillospira</i>	0.000132	0	0.000208	0.000378
<i>Weissella</i>	0.000113	0.000378	3.78E-05	1.89E-05
<i>Succinivibrio</i>	7.56E-05	0	0	0
<i>Megasphaera</i>	0	0	0.000378	3.78E-05
<i>Pedomicrobium</i>	0	7.56E-05	0	7.56E-05
<i>Intestinimonas</i>	0.00017	0	0.00034	7.56E-05
<i>Ruminococcaceae_UCG-004</i>	9.45E-05	9.45E-05	0.000321	0
<i>Blvii28_wastewater-sludge_group</i>	0.000321	0.000321	0.000151	9.45E-05
<i>Olsenella</i>	1.89E-05	0	0.000321	1.89E-05
<i>Filimonas</i>	0.000302	0.000113	0.000189	0.000113
<i>Acidaminobacter</i>	3.78E-05	0.000302	5.67E-05	1.89E-05
<i>Denitratisoma</i>	3.78E-05	0.000113	9.45E-05	0.000113
<i>Prevotellaceae_UCG-001</i>	0.000302	0	1.89E-05	1.89E-05
<i>Bauldia</i>	0.000132	0.000302	9.45E-05	3.78E-05
<i>Reyranella</i>	3.78E-05	1.89E-05	0	1.89E-05
<i>Serratia</i>	0	0	0.000283	0
<i>Sutterella</i>	0.000283	0	3.78E-05	5.67E-05
<i>Helicobacter</i>	0.000283	0	0	0
<i>Rheinheimera</i>	9.45E-05	0.000227	7.56E-05	3.78E-05
<i>Desulfovibrio</i>	3.78E-05	0.000132	0.000113	0.000265
<i>Veillonella</i>	3.78E-05	0.000151	0.00017	0.000189
<i>Ruminiclostridium_1</i>	0.000151	0	0.000265	0
<i>Vibrio</i>	3.78E-05	0.000227	0	0
<i>Microbacterium</i>	9.45E-05	3.78E-05	0.000246	0.000113
<i>Thauera</i>	0.00017	0.000151	0.000151	0.000151
<i>Eubacterium_brachy_group</i>	0.000132	0	0.000246	0
<i>Gemmata</i>	5.67E-05	1.89E-05	3.78E-05	1.89E-05
<i>Candidatus_Captivus</i>	0.000189	0.000246	0.000208	5.67E-05
<i>Legionella</i>	0.000151	0.000246	5.67E-05	5.67E-05
<i>Anaerorhabdus_furcosa_group</i>	0.000151	0	0.000246	0
<i>Peredibacter</i>	0.000132	0.000246	0.000151	0.000151
<i>Fibrobacter</i>	0.000132	0	0	0.000246
<i>Gemmatimonas</i>	9.45E-05	0.000246	0.000113	0.000113
<i>Dokdonella</i>	1.89E-05	5.67E-05	0.000132	0.000113
<i>Desulfobulbus</i>	5.67E-05	0.000189	7.56E-05	0.000132
<i>Luteimonas</i>	0	0	0	0

<i>Paludibacter</i>	0.000227	0.000189	0.00017	0.000189
<i>Rhodococcus</i>	0.000132	1.89E-05	0	3.78E-05
<i>Oceanisphaera</i>	0	0	0	0
<i>unidentified_OPB56</i>	0	3.78E-05	1.89E-05	7.56E-05
<i>Candidatus_Solibacter</i>	3.78E-05	1.89E-05	1.89E-05	3.78E-05
<i>Bacillus</i>	0	0	3.78E-05	0
<i>Micromonospora</i>	0	0	0	0
<i>Elusimicrobium</i>	0	0	0	0.000208
<i>Gemella</i>	0.000151	0.000132	0	0
<i>Polynucleobacter</i>	0.000132	0.000189	3.78E-05	3.78E-05
<i>Stenotrophomonas</i>	0	0.000151	0.000189	5.67E-05
<i>Massilia</i>	3.78E-05	9.45E-05	0.000132	3.78E-05
<i>Butyrivibrio</i>	9.45E-05	1.89E-05	0.000189	0
<i>Nocardioides</i>	0	0.000113	0	1.89E-05
<i>Sphingomonas</i>	9.45E-05	0.000132	0	1.89E-05
<i>Dorea</i>	0.000113	7.56E-05	7.56E-05	0
<i>Roseomonas</i>	1.89E-05	0.000113	0	0
<i>Arenimonas</i>	0	3.78E-05	0	0
<i>Anaeroplasma</i>	9.45E-05	0	0.000151	3.78E-05
<i>unidentified_Blfdi19</i>	1.89E-05	5.67E-05	7.56E-05	0.000151
<i>Candidatus_Saccharimonas</i>	0.000113	1.89E-05	0.000132	0.000151
<i>unidentified_Xanthomonadaceae</i>	5.67E-05	0.000151	5.67E-05	1.89E-05
<i>Leadbetterella</i>	7.56E-05	7.56E-05	0.000151	7.56E-05
<i>Oxalobacter</i>	0	0	1.89E-05	0.000151
<i>Propionivibrio</i>	1.89E-05	0.000113	0.000132	3.78E-05
<i>Erysipelotrichaceae_UCG-001</i>	5.67E-05	0	9.45E-05	5.67E-05
<i>Sporolactobacillus</i>	1.89E-05	3.78E-05	7.56E-05	1.89E-05
<i>Cellulosilyticum</i>	0	0	1.89E-05	0
<i>Lachnospiraceae_UCG-010</i>	0.000132	5.67E-05	7.56E-05	1.89E-05
<i>Brevibacterium</i>	0	0	0	0
<i>Adhaeribacter</i>	0	0.000113	0	0
<i>Rothia</i>	3.78E-05	0.000113	0	3.78E-05
<i>Sulfurospirillum</i>	1.89E-05	7.56E-05	0.000113	0
<i>Defluviitaleaceae_UCG-011</i>	0.000113	0	0.000113	0
<i>Lachnospiraceae_NK3A20_group</i>	1.89E-05	0	1.89E-05	0.000113
<i>Lachnoclostridium_10</i>	0.000113	0	0.000113	0
<i>Prevotella_2</i>	0	0	0	9.45E-05
<i>unidentified_Saccharibacteria</i>	1.89E-05	0.000113	0	0
<i>Dielma</i>	0	0.000113	3.78E-05	0
<i>unidentified_Coriobacteriaceae</i>	1.89E-05	5.67E-05	9.45E-05	3.78E-05
<i>Macellibacteroides</i>	0.000113	0	0	0
<i>Psychrobacter</i>	3.78E-05	7.56E-05	0	0.000113
<i>Singulisphaera</i>	5.67E-05	5.67E-05	0	0
<i>Planctomyces</i>	0	9.45E-05	1.89E-05	1.89E-05

<i>unidentified_Mitochondria</i>	0	5.67E-05	5.67E-05	9.45E-05
<i>Olivibacter</i>	0	0	0	0
<i>Buchnera</i>	3.78E-05	0	0	0
<i>unidentified_Nitrosomonadaceae</i>	1.89E-05	1.89E-05	1.89E-05	0
<i>Saccharofermentans</i>	9.45E-05	0	3.78E-05	0
<i>Eubacterium_hallii_group</i>	5.67E-05	9.45E-05	7.56E-05	1.89E-05
<i>Anaeroarcus</i>	1.89E-05	9.45E-05	7.56E-05	1.89E-05
<i>Asteroleplasma</i>	9.45E-05	0	5.67E-05	0
<i>Lautropia</i>	3.78E-05	5.67E-05	3.78E-05	0
<i>Anaerovibrio</i>	0	0	0	9.45E-05
<i>Enterococcus</i>	9.45E-05	0	9.45E-05	0
<i>Marvinbryantia</i>	5.67E-05	1.89E-05	0	0
<i>Bifidobacterium</i>	9.45E-05	3.78E-05	0	1.89E-05
<i>Mogibacterium</i>	0	9.45E-05	0	0
<i>Mitsuokella</i>	0	0	0	9.45E-05
<i>Slackia</i>	0	0	0	3.78E-05
<i>Geobacillus</i>	0	0	0	0
<i>Phocaeicola</i>	9.45E-05	0	9.45E-05	0
<i>Papillibacter</i>	0	0	7.56E-05	0
<i>Staphylococcus</i>	1.89E-05	7.56E-05	1.89E-05	0
<i>Pseudofulvimonas</i>	0	7.56E-05	0	3.78E-05
<i>hgcI_clade</i>	0	7.56E-05	0	0
<i>Pirellula</i>	0	3.78E-05	0	3.78E-05
<i>Tessaracoccus</i>	1.89E-05	0	7.56E-05	7.56E-05
<i>Achromobacter</i>	0	1.89E-05	7.56E-05	3.78E-05
<i>Catenibacterium</i>	7.56E-05	0	0	5.67E-05
<i>Corynebacterium_1</i>	0	7.56E-05	1.89E-05	1.89E-05
<i>Chlorobium</i>	3.78E-05	1.89E-05	7.56E-05	7.56E-05
<i>Eubacterium_ruminantium_group</i>	1.89E-05	0	7.56E-05	7.56E-05
<i>Gardnerella</i>	0	0	7.56E-05	0
<i>Arthrobacter</i>	0	1.89E-05	0	0
<i>Propionibacterium</i>	0	7.56E-05	7.56E-05	0
<i>Telmatobacter</i>	0	7.56E-05	0	0
<i>Butyricicoccus</i>	7.56E-05	3.78E-05	3.78E-05	5.67E-05
<i>Anaerosporobacter</i>	5.67E-05	0	7.56E-05	0
<i>Chlorobaculum</i>	3.78E-05	7.56E-05	7.56E-05	7.56E-05
<i>Thalassospira</i>	0	0	0	0
<i>Ezakiella</i>	5.67E-05	0	0	0
<i>Erysipelotrichaceae_UCG-003</i>	5.67E-05	0	3.78E-05	0
<i>unidentified_Actinobacteria</i>	0	0	0	0
<i>Prevotellaceae_Ga6A1_group</i>	5.67E-05	0	0	0
<i>Methylobacterium</i>	5.67E-05	0	1.89E-05	0
<i>Ignavibacterium</i>	1.89E-05	0	3.78E-05	1.89E-05
<i>Desulfobacula</i>	0	5.67E-05	5.67E-05	1.89E-05

<i>Anaerovorax</i>	5.67E-05	0	5.67E-05	0
<i>Moraxella</i>	3.78E-05	3.78E-05	0	5.67E-05
<i>Peptostreptococcus</i>	3.78E-05	5.67E-05	0	0
<i>Cellvibrio</i>	3.78E-05	1.89E-05	3.78E-05	5.67E-05
<i>Sediminibacterium</i>	1.89E-05	1.89E-05	0	5.67E-05
<i>CL500-3</i>	0	0	0	0
<i>Lachnospiraceae_FCS020_group</i>	3.78E-05	0	0	3.78E-05
<i>Desulfocapsa</i>	0	0	5.67E-05	0
<i>Tahibacter</i>	0	0	0	0
<i>unidentified_Acidobacteria</i>	3.78E-05	5.67E-05	0	0
<i>Skermanella</i>	0	5.67E-05	0	0
<i>Tyzzerella</i>	5.67E-05	0	0	0
<i>Porphyromonas</i>	0	0	5.67E-05	0
<i>Coprococcus_2</i>	0	0	0	5.67E-05
<i>Erysipelatoclostridium</i>	0	0	3.78E-05	0
<i>Allisonella</i>	5.67E-05	0	0	1.89E-05
<i>Proteus</i>	0	5.67E-05	3.78E-05	0
<i>unidentified_Gracilibacteria</i>	0	0	5.67E-05	0
<i>Clostridium_sensu_stricto_15</i>	0	0	0	5.67E-05
<i>Fusicatenibacter</i>	0	1.89E-05	0	0
<i>Ralstonia</i>	5.67E-05	0	0	0
<i>Thermomonas</i>	1.89E-05	1.89E-05	0	3.78E-05
<i>Leptolinea</i>	0	0	3.78E-05	0
<i>Dysgonomonas</i>	1.89E-05	0	3.78E-05	0
<i>Sphingobacterium</i>	0	0	0	0
<i>Peptoniphilus</i>	3.78E-05	0	0	0
<i>Sedimentibacter</i>	3.78E-05	0	0	0
<i>Mucispirillum</i>	3.78E-05	0	0	0
<i>Dyella</i>	3.78E-05	3.78E-05	0	3.78E-05
<i>Chlamydia</i>	0	0	1.89E-05	0
<i>Parvularcula</i>	0	1.89E-05	0	3.78E-05
<i>Cytophaga</i>	0	0	0	0
<i>Parasegetibacter</i>	3.78E-05	0	0	0
<i>Paenalcaligenes</i>	0	0	0	0
<i>Erysipelotrichaceae_UCG-004</i>	0	0	3.78E-05	0
<i>Odoribacter</i>	3.78E-05	0	1.89E-05	0
<i>Enterorhabdus</i>	1.89E-05	0	0	3.78E-05
<i>Iamia</i>	1.89E-05	1.89E-05	0	0
<i>Family_XIII_UCG-001</i>	1.89E-05	0	3.78E-05	0
<i>Rubrobacter</i>	1.89E-05	0	1.89E-05	0
<i>Flavihumibacter</i>	0	3.78E-05	1.89E-05	0
<i>Limnohabitans</i>	0	0	3.78E-05	0
<i>Dyadobacter</i>	0	0	0	0
<i>Truepera</i>	0	0	0	0

<i>MSBL7</i>	0	3.78E-05	0	0
<i>Micrococcus</i>	0	3.78E-05	0	0
<i>Zavarzinella</i>	0	0	0	0
<i>Candidatus_Nitrotoga</i>	0	3.78E-05	0	0
<i>Coxiella</i>	0	1.89E-05	1.89E-05	1.89E-05
<i>Murdochiella</i>	0	0	0	3.78E-05
<i>Sodalis</i>	0	0	0	3.78E-05
<i>Niabella</i>	3.78E-05	0	3.78E-05	1.89E-05
<i>Arcobacter</i>	1.89E-05	0	1.89E-05	1.89E-05
<i>Oribacterium</i>	0	0	0	0
<i>Gaiella</i>	0	1.89E-05	0	0
<i>Family_XIII_UCG-002</i>	0	0	1.89E-05	0
<i>Sva0081_sediment_group</i>	0	0	0	0
<i>Vogesella</i>	1.89E-05	0	0	0
<i>NS10_marine_group</i>	1.89E-05	0	0	0
<i>Illumatobacter</i>	0	0	0	0
<i>unidentified_Erysipelotrichaceae</i>	0	1.89E-05	0	0
<i>Nocardia</i>	0	0	1.89E-05	1.89E-05
<i>Desulfuromonas</i>	1.89E-05	0	1.89E-05	0
<i>Geothrix</i>	0	0	0	0
<i>Chitinimonas</i>	0	0	1.89E-05	0
<i>Senegalimassilia</i>	0	0	0	0
<i>Uliginosibacterium</i>	0	1.89E-05	0	0
<i>Pir4_lineage</i>	0	0	0	0
Others	0.433532	0.537277	0.460834	0.457338

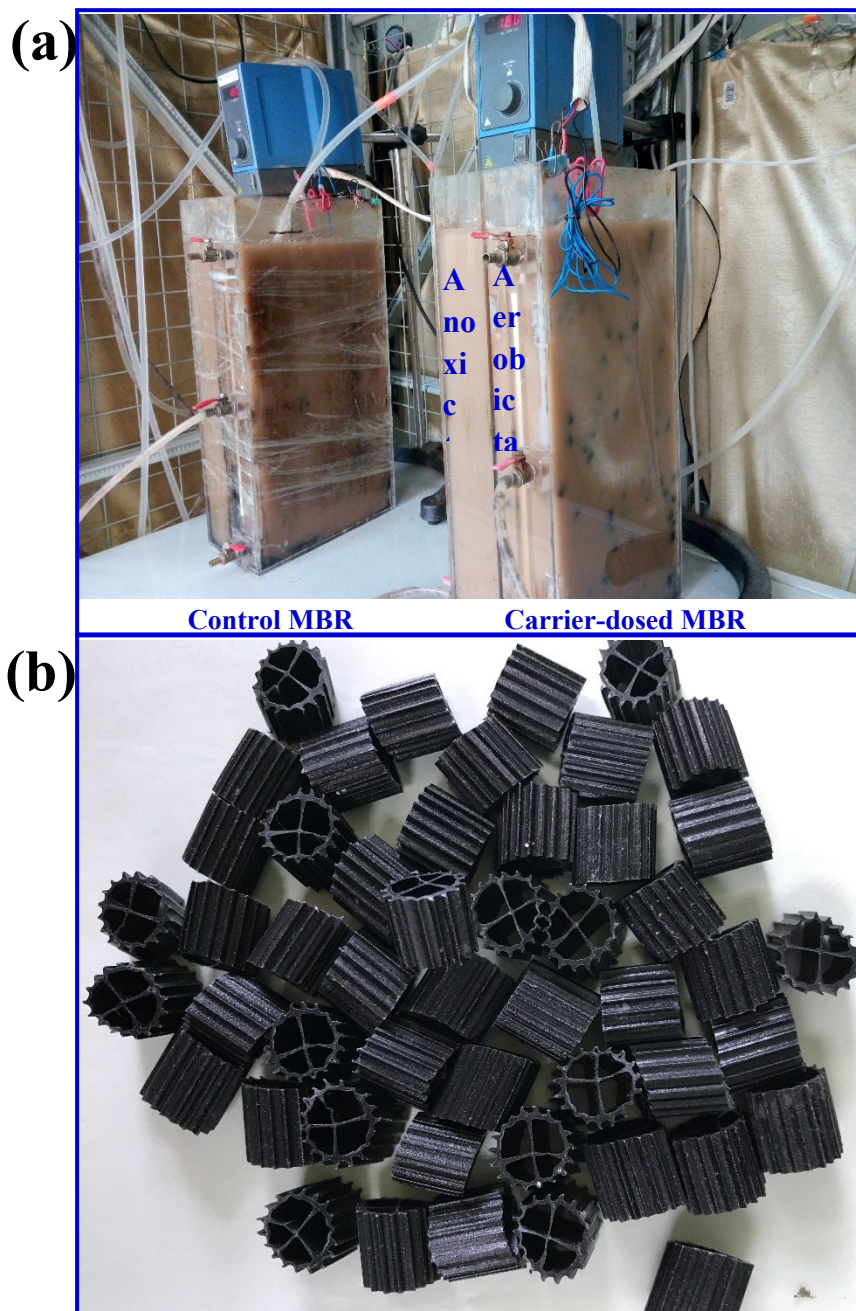


Figure S1 Experimental set-up of the control MBR and carrier-dosed MBR (a) and picture of the carrier used in this work (b).

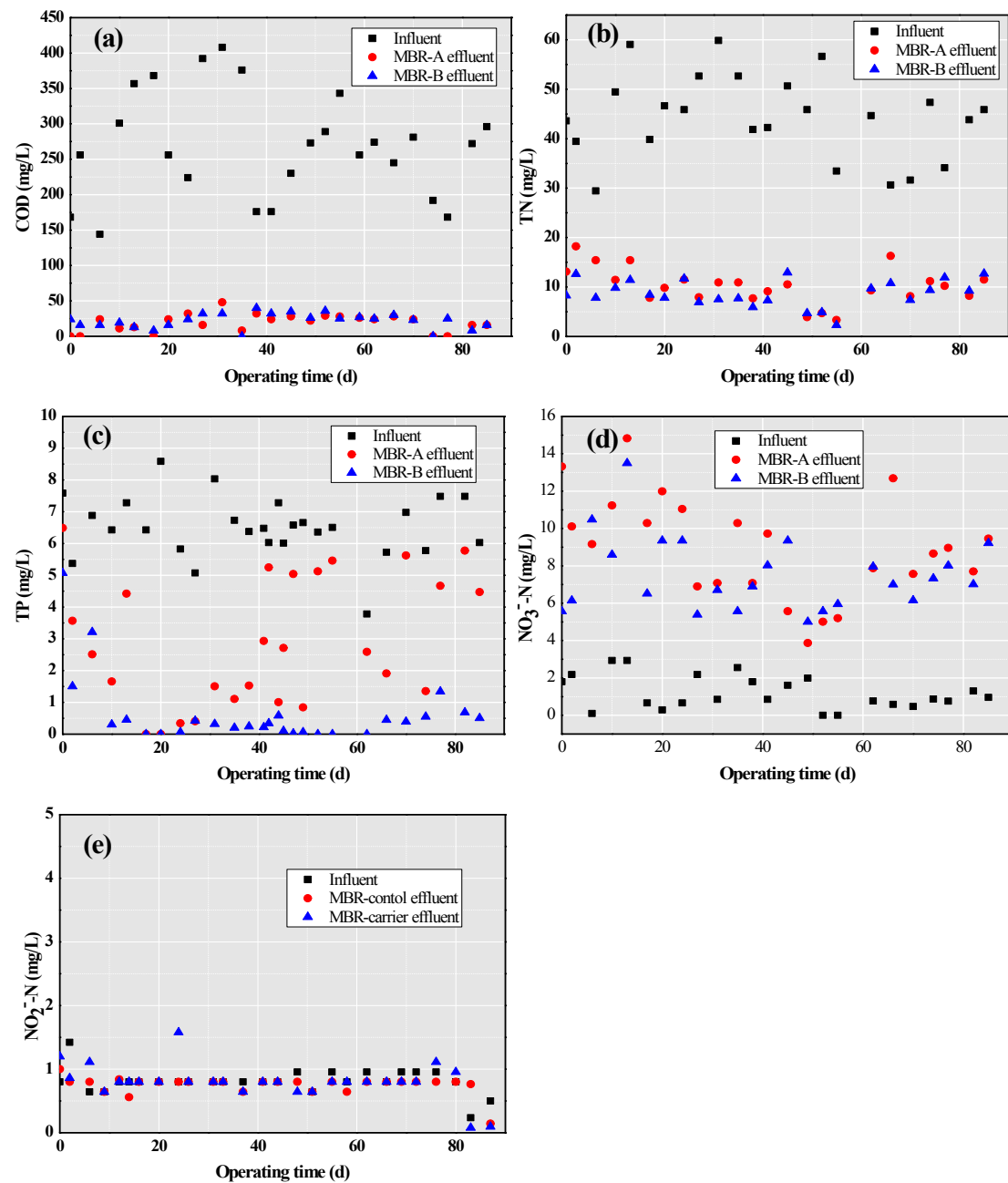


Figure S2 Variations of COD (a), TN (b), TP (c) NO₃-N (d) and NO₂-N (e) during the operation of the control MBR and carrier-dosed MBR.

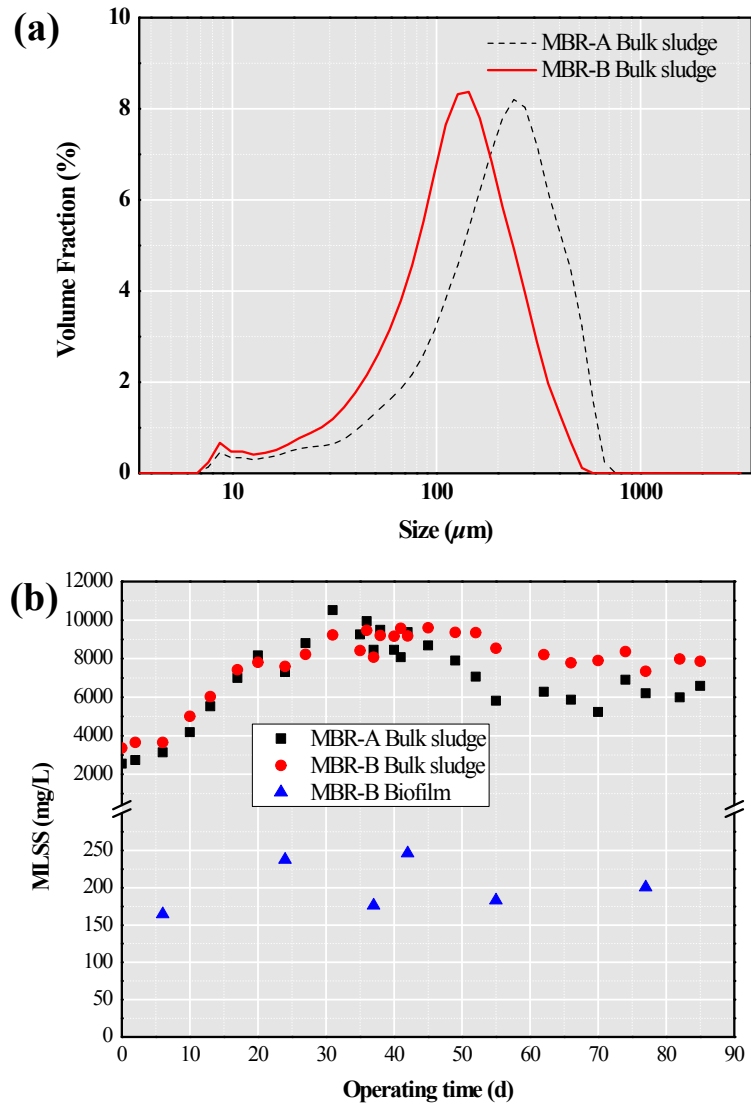


Figure S3 Particle size distribution (a) and MLSS development (b) during the MBRs operation. Particle size distribution of the bulk sludge from MBR-control and MBR-carrier were measured in triplicate. Averages of the triplicate measures were used to plot the profiles.

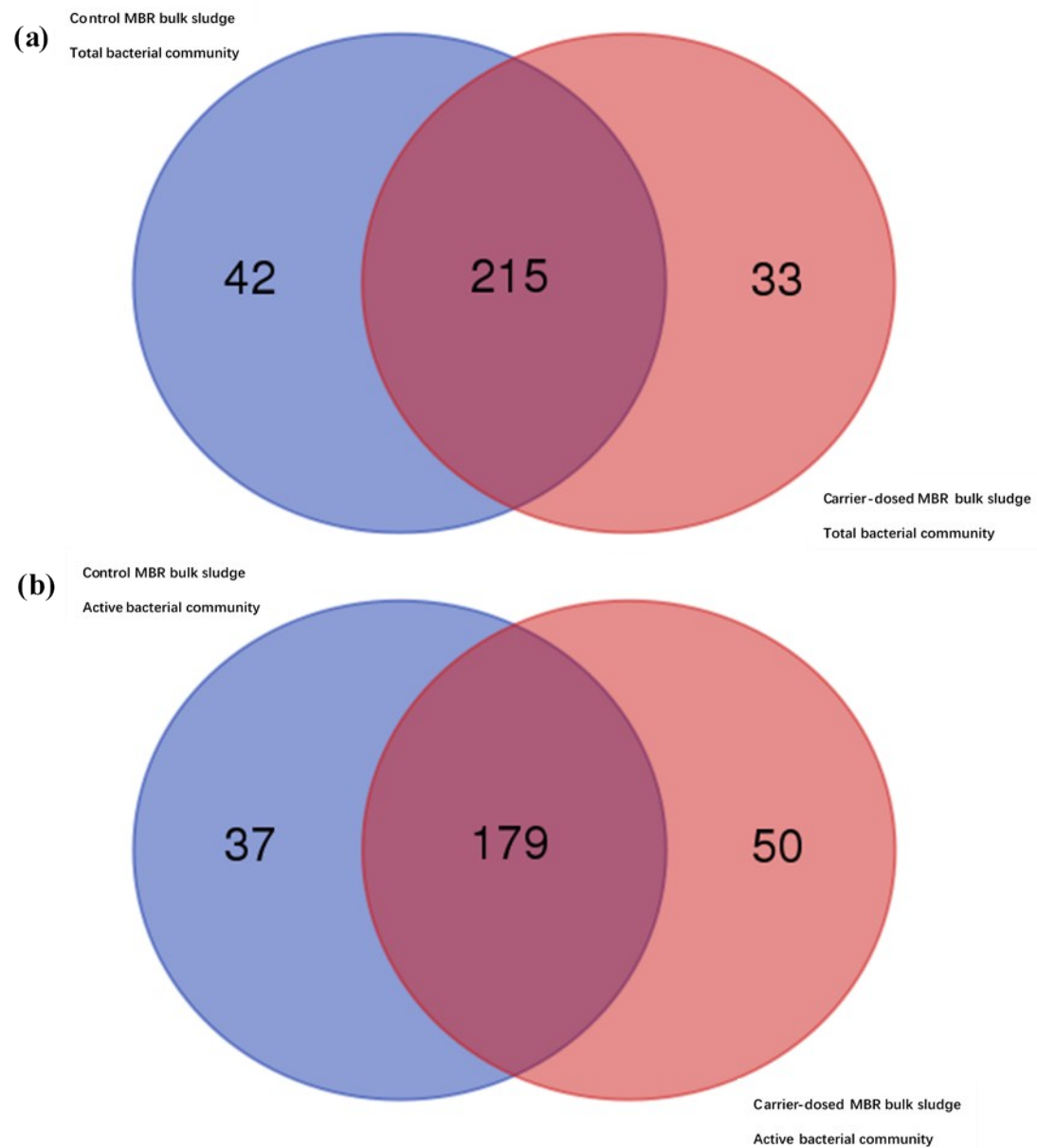


Figure S4 Venn diagrams of bacterial genera present in total (a) and active (b) microbial community in bulk sludge from the control MBR and carrier-dosed MBR.