

**Enhancement of microbial and metabolic mechanisms in an aerobic bioreactor  
with immobilized microflora by simple and complex electron donors**

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**Table S1** Alpha Diversity Statistics of different samples

Sample	Shannon	chao1	observed species	PD whole tree
AS1-1	3.4277	623.5	556	36.7217
AS1-2	3.1697	682.0574	600	39.0487
AS1-3	3.2112	651.0811	572	38.8872
AS7-1	3.777	542.2143	455	32.6993
AS7-2	4.2201	700.6	607	41.0423
AS7-3	5.1828	771.2959	679	42.1885
BS1-1	4.2151	817.25	726	50.0964
BS1-2	4.06	773	702	44.5495
BS1-3	4.3244	766.4576	684	45.9731
BS7-1	6.1407	805.1135	792	50.1924
BS7-2	6.4204	1172.66	1090	62.798
BS7-3	7.0871	1316.07	1211	62.6754

**Table S2** Microbial difference between AS1 group and AS7 group in genus level

Taxa	Mean (AS1)	Mean (AS7)	p value	q value	diff
<i>Acinetobacter</i>	0.452	0.1016	0.0081	0.3561	down
<i>Aquaspirillum</i>	0.4213	0.1686	0.02	0.4469	down
<i>Alishewanella</i>	0.004	0.0891	0.0186	0.4409	up
<i>Azonexus</i>	0.0024	0.0457	0.0095	0.3561	up
<i>Hydrogenophaga</i>	0.0015	0.022	0.0104	0.3561	up
<i>Brevundimonas</i>	0.0006	0.0079	0.0005	0.1481	up
<i>Dechloromonas</i>	0.0037	0.0128	0.0251	0.493	up
<i>Erysipelothrix</i>	0.001	0.0115	0.0114	0.3691	up
<i>Paracoccus</i>	0.0006	0.0088	0.0067	0.3561	up
<i>Rhodobacter</i>	0.0009	0.0125	0.0144	0.4149	up
<i>Flavobacterium</i>	0.0000629	0.0082	0.01	0.3561	up
<i>Azoarcus</i>	0.0015	0.012	0.0018	0.237	up
<i>Thauera</i>	0.0004	0.0051	0.0152	0.4149	up

**Table S3** Microbial difference between BS1 group and BS7 group in genus level

Taxa	Mean (BS1)	Mean (BS7)	p value	q value	diff
<i>Acinetobacter</i>	0.861	0.2333	0.0028	0.1228	down
<i>Aquaspirillum</i>	0.0028	0.0096	0.0101	0.1518	up
<i>Alishewanella</i>	0.0005	0.0235	0.009	0.15	up
<i>Azonexus</i>	0.0009	0.0778	0.0053	0.1284	up
<i>Pedobacter</i>	0.0004	0.0413	0.0153	0.1708	up
<i>Hydrogenophaga</i>	0.0008	0.034	0.0011	0.1081	up
<i>Brevundimonas</i>	0.0007	0.0213	0.0025	0.1216	up
<i>Dechloromonas</i>	0.0007	0.0189	0.0042	0.1267	up
<i>Erysipelothrix</i>	0.0006	0.0205	0.0008	0.1013	up
<i>Paracoccus</i>	0.0004	0.0179	0.0059	0.129	up
<i>Rhodobacter</i>	0.0003	0.0191	0.0031	0.1238	up
<i>Pseudomonas</i>	0.0058	0.0081	0.0363	0.2274	up
<i>Flavobacterium</i>	0.0003	0.0131	0.0151	0.1708	up
<i>Azoarcus</i>	0.0002	0.0061	0.0006	0.0901	up
<i>Hyphomonas</i>	0.0002	0.0103	0.0093	0.15	up
<i>Gemmobacter</i>	0.0009	0.0098	0.0045	0.1272	up
<i>Marivita</i>	0.0017	0.0082	0.0047	0.1276	up
<i>Sphingopyxis</i>	0.0003	0.0066	0.0159	0.1708	up
<i>Acidovorax</i>	0.001	0.0063	0.0003	0.0676	up
<i>Cloacibacterium</i>	0.0005	0.0059	0.0039	0.1261	up

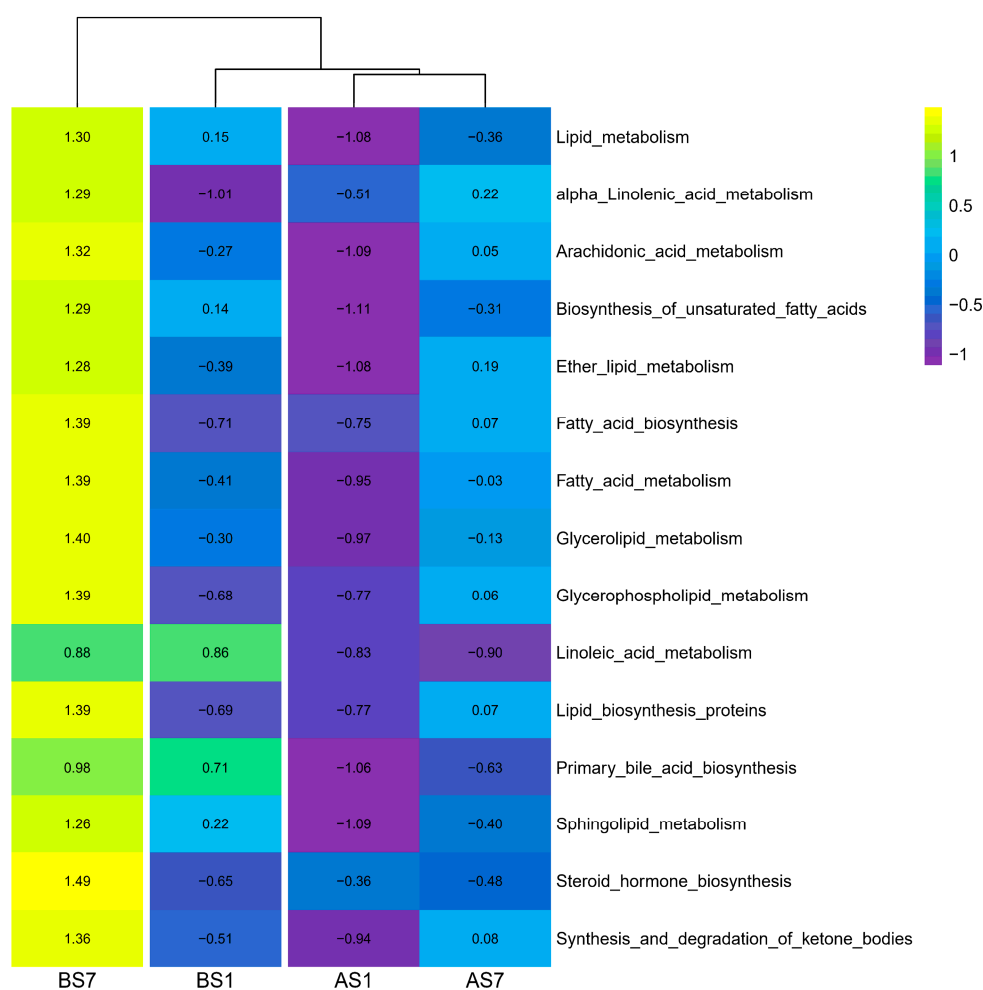
**Table S4** Microbial difference between AS1 group and BS1 group in genus level

Taxa	Mean (AS1)	Mean (BS1)	p value	q value	diff
<i>Acinetobacter</i>	0.452	0.861	0.0033	0.3337	up
<i>Aquaspirillum</i>	0.4213	0.0028	0.0017	0.3337	down

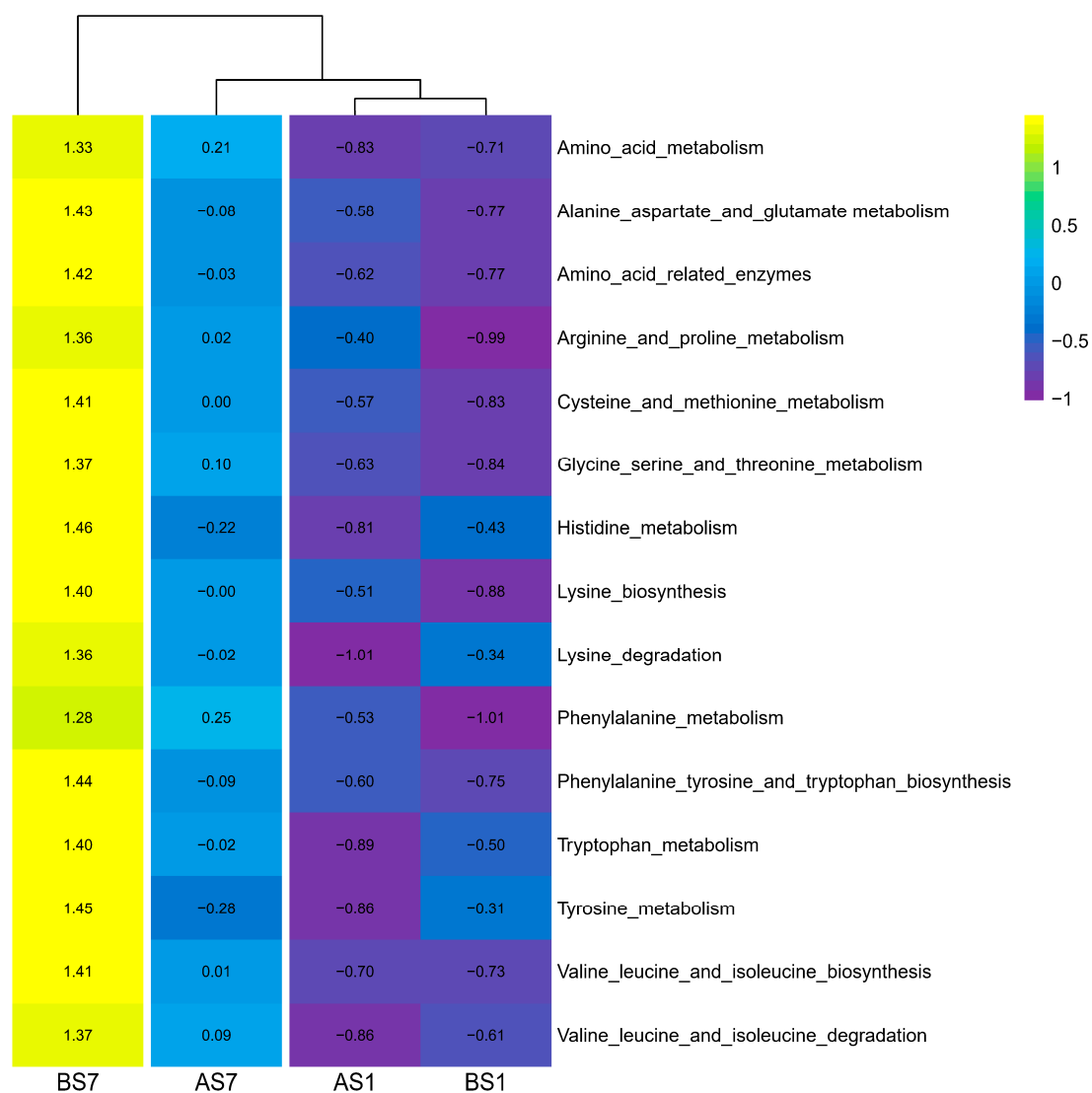
**Table S5** Microbial difference between AS7 group and BS7 group in genus level

Taxa	Mean (AS7)	Mean (BS7)	p value	q value	diff
<i>Aquaspirillum</i>	0.1686	0.0096	0.0107	0.1812	down
<i>Alishewanella</i>	0.0891	0.0235	0.0207	0.2276	down
<i>Azoarcus</i>	0.012	0.0061	0.003	0.1084	down
<i>Azonexus</i>	0.0457	0.0778	0.0274	0.2503	up
<i>Hydrogenophaga</i>	0.022	0.034	0.0263	0.2478	up
<i>Brevundimonas</i>	0.0079	0.0213	0.0027	0.1075	up
<i>Dechloromonas</i>	0.0128	0.0189	0.0479	0.2691	up
<i>Erysipelothrix</i>	0.0115	0.0205	0.015	0.212	up
<i>Paracoccus</i>	0.0088	0.0179	0.0183	0.2187	up
<i>Rhodobacter</i>	0.0125	0.0191	0.0444	0.2691	up
<i>Pedobacter</i>	0.0024	0.0413	0.0124	0.1931	up
<i>Sphingopyxis</i>	0.0004	0.0066	0.0129	0.1931	up
<i>Fusibacter</i>	0.0028	0.0092	0.0433	0.2691	up
<i>Hyphomonas</i>	0.0013	0.0103	0.0051	0.1401	up
<i>Gemmobacter</i>	0.0046	0.0098	0.0099	0.1812	up
<i>Marivita</i>	0.0029	0.0082	0.0097	0.1812	up
<i>Acinetobacter</i>	0.1016	0.2333	0.0473	0.2691	up
<i>Acidovorax</i>	0.0034	0.0063	0.0132	0.1931	up
<i>Cloacibacterium</i>	0.0022	0.0059	0.0042	0.1312	up

Red marked species were up regulated in Table S2, blue marked species were chosen as characteristic species of BS7.

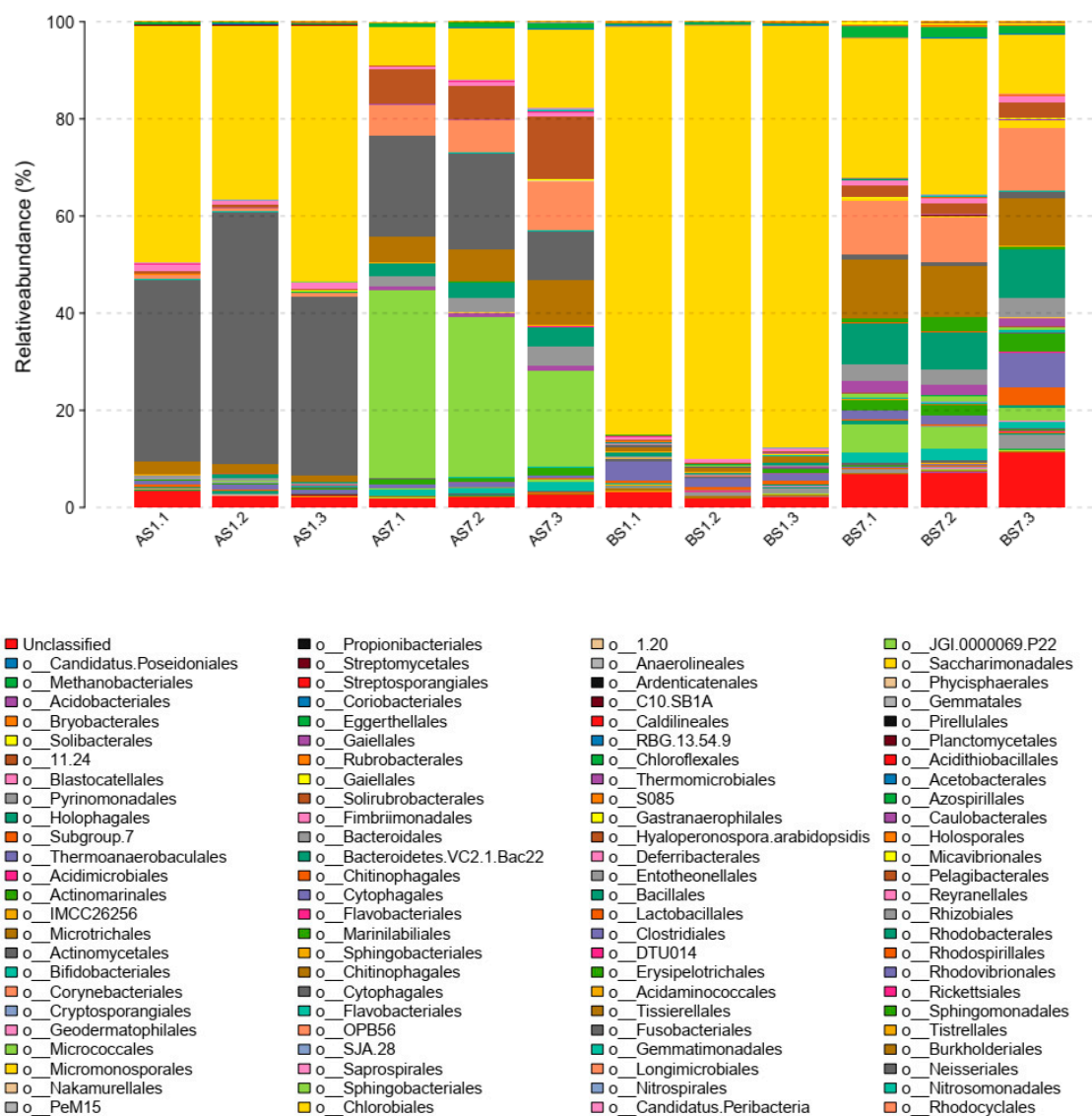


**Figure S1** Heatmap showing clustering among different samples based on relative abundance of lipid metabolisms from KEGG database.

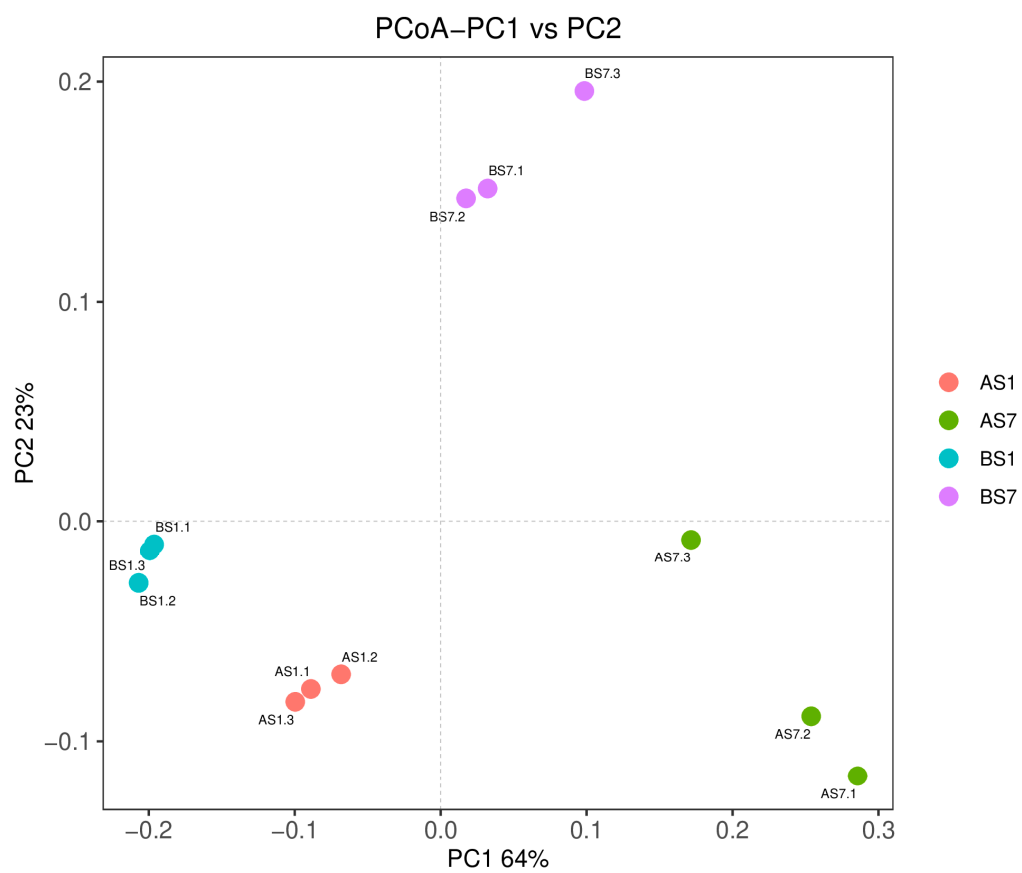


**Figure S2** Heatmap showing clustering among different samples based on relative abundance of amino acid metabolisms from KEGG database.





**Figure S3** Stacked column chart of relative abundance in the activated sludges at the order level.



**Figure S4** PCoA analysis of different sample groups based on weighted unifracc.