Table S2. Summary of the sequence reads characteristics including the number of reads and base pairs of metagenomes retrieved from activated sludge and wastewater.

	Activated sludge			Wastewater		
	Reads count (bp)	Base pairs (bp)	Library fragment (bp)	Reads count (bp)	Base pairs (bp)	Library fragment (bp)
Max	8.68×10^7	2.60×10^{10}	602	8.27×10^7	2.48×10^{10}	302
Min	1.82×10^6	6.91×10^8	150	3.79×10^6	8.79×10^8	153
Ave	3.12×10^7	8.98×10^9	289.96	1.62×10^7	4.32×10^9	254.07
SD	1.80×10^7	5.48×10^7	69.69	1.72×10^7	5.29×10^9	52.63
Total	4.3×10^9	1.24×10^{12}	40014	4.36×10^8	1.17×10^{11}	6860