

Table S3. Nucleotide sequence based comparative analysis of the *bcs* operon genes among the *Komagataeibacter oboediens* samples

Gene name	<i>K. oboediens</i> / iKMC Seq-length	<i>K. oboediens</i> /tKMC			
		Blast against <i>K. oboediens</i> /iKMC			
		Operon I			
		Length	Coverage	Identity	gaps
<i>cmcax</i>	1080	1080	100%	1080/1080(100%)	0/1080(0%)
<i>ccpAx</i>	1029	1029	100%	1029/1029(100%)	0/1029(0%)
<i>bcsA</i>	2238	2238	100%	2238/2238(100%)	0/2238(0%)
<i>bcsB</i>	2430	2430	100%	2430/2430(100%)	0/2430(0%)
<i>bcsC</i>	3978	3978	100%	3978/3978(100%)	0/3978(0%)
<i>bcsD</i>	471	471	100%	471/471(100%)	0/471(0%)
<i>bglAx</i>	2202	2202	100%	2202/2202(100%)	0/2202(0%)
		Operon II			
<i>bcsAB-II</i>	3723	3723	100%	3723/3723(100%)	0/3723(0%)
<i>bcsX</i>	672	672	100%	672/672(100%)	0/672(0%)
<i>bcsY</i>	1161	1161	100%	1161/1161(100%)	0/1161(0%)
<i>bcsC-II</i>	3924	3924	100%	3924/3924(100%)	0/3924(0%)
		Operon III			
<i>bcsAB-II</i>	4488	4488	100%	4488/4488(100%)	0/4488(0%)
<i>bcsC-II</i>	3705	3705	100%	3705/3705(100%)	0/3705(0%)
		Operon IV			
<i>bcsAB-II</i>	4617	4617	100%	4617/4617(100%)	0/4617(0%)