

Table S4. Amino acid sequence based comparative analysis of the *bcs* genes among the *Komagataeibacter oboediens* samples

Gene name	<i>K. oboediens</i> /iKMC Seq-length	<i>K. oboediens</i> /tKMC				
		Length	Blast against <i>K. oboediens</i> /iKMC			
			Coverage	Identity	Positive	gaps
			Operon I			
<i>cmcax</i>	359	359	100%	359/359(100%)	359/359(100%)	0/359(0%)
<i>ccpAx</i>	342	342	100%	342/342(100%)	342/342(100%)	0/342(0%)
<i>bcsA</i>	745	745	100%	745/745(100%)	745/745(100%)	0/745(0%)
<i>bcsB</i>	809	809	100%	809/809(100%)	809/809(100%)	0/809(0%)
<i>bcsC</i>	1325	1325	100%	1325/1325(100%)	1325/1325(100%)	0/1325(0%)
<i>bcsD</i>	156	156	100%	156/156(100%)	156/156(100%)	0/156(0%)
<i>bglAx</i>	733	733	100%	733/733(100%)	733/733(100%)	0/733(0%)
			Operon II			
<i>bcsAB-II</i>	1240	1240	100%	1240/1240(100%)	1240/1240(100%)	0/1240(0%)
<i>bcsX</i>	223	223	100%	223/223(100%)	223/223(100%)	0/223(0%)
<i>bcsY</i>	386	386	100%	386/386(100%)	386/386(100%)	0/386(0%)
<i>bcsC-II</i>	1307	1307	100%	1307/1307(100)	1307/1307(100)	0/1307(0%)
			Operon III			
<i>bcsAB-II</i>	1495	1495	100%	1495/1495(100%)	1495/1495(100%)	0/1495(0%)
<i>bcsC-II</i>	1234	1234	100%	1234/1234(100%)	1234/1234(100%)	0/1234(0%)
			Operon IV			
<i>bcsAB-II</i>	1538	1538	100%	1538/1538(100%)	1538/1538(100%)	0/1538(0%)