

Additional file 5. List of the down-regulated genes involved in carbohydrates metabolism after *ccpA* inactivation and their putative CcpA binding sites (CREs) [§]

Gene locus	Annotation	Gene name	Expression ratio (824 <i>ccpA</i> /824WT)				CcpA-binding sites (CREs)		
			M	L	T	S	Sequence	Position [†]	Score
CAC0539	Mannanase-like protein, contains ChW-repeats	<i>manB</i>	0.11	0.14	0.22	0.17			
CAC0540									
CAC0570	PTS IIBC, glucose specific	<i>glcG</i>	0.16	0.20	0.11	0.19			
CAC1351	Periplasmic sugar-binding protein		0.21	0.30	0.22				
CAC1353	PTS IICB, glucose specific		0.07	0.07	0.11	0.20	ttgtaaacgatgtaa	-219	1.7
CAC1354	PTS IIA, glucose specific		0.25	0.44			tttacatcgttacaa	-214	1.7
CAC2237	Glucose-1-phosphate adenylyltransferase	<i>glgC</i>	0.44	0.37	0.43	0.34			
CAC2238									
CAC2239	Glycogen synthase	<i>glgA</i>		0.39	0.47	0.48			
CAC2240	Cyclomaltodextrin glucanotransferase			0.44	0.39	0.48			
CAC3087	Phosphoenolpyruvate-protein kinase	<i>ptsI</i>	0.32		0.11	0.17			

Notes:

[§]The black arrows indicate the transcription direction of the predicted operon obtained from DOOR database [1, 2].

[†]The +1 position is defined as the first nucleotide of coding sequence.

References

1. Mao F, Dam P, Chou J, Olman V, Xu Y: **DOOR: a database for prokaryotic operons.** *Nucleic Acids Res* 2009, **37**:D459-463.
2. Dam P, Olman V, Harris K, Su ZC, Xu Y: **Operon prediction using both genome-specific and general genomic information.** *Nucleic Acids Research* 2007, **35**:288-298.