

Suppl. Table 7. Up regulated genes ($\log_2$) in the *cobB* mutant compared with the wild type in glucose chemostat cultures (FDR<0.05).

Genes	Fold change	Description
policistronic operons		
<i>tar-tap-cheRBYZ</i>		
<i>tar</i>	4.448	methyl-accepting chemotaxis protein II
<i>tap</i>	4.204	methyl-accepting protein IV
<i>cheR</i>	3.524	chemotaxis methyltransferase CheR
<i>cheB</i>	3.344	chemotaxis-specific methylesterase
<i>cheY</i>	4.200	chemotaxis regulatory protein CheY
<i>cheZ</i>	3.538	chemotaxis regulator CheZ
<i>fliDST</i>		
<i>fliD</i>	4.944	flagellar capping protein
<i>fliS</i>	4.306	flagellar protein FliS
<i>fliT</i>	2.994	flagellar biosynthesis protein FliT
<i>motAB-cheAW</i>		
<i>motA</i>	3.933	flagellar motor protein MotA
<i>motB</i>	3.500	flagellar motor protein MotB
<i>cheA</i>	3.834	chemotaxis protein CheA
<i>cheW</i>	4.397	purine-binding chemotaxis protein
<i>flgKL</i>		
<i>flgK</i>	4.355	flagellar hook-associated protein FlgK
<i>flgL</i>	3.764	flagellar hook-associated protein FlgL
<i>fliAZY</i>		
<i>fliA</i>	4.497	flagellar biosynthesis sigma factor
<i>fliZ</i>	4.380	flagella biosynthesis protein FliZ
<i>fliY</i>		
<i>flgBCDEFGHIJ</i>		
<i>flgB</i>	3.415	flagellar basal body rod protein FlgB
<i>flgC</i>	3.185	flagellar basal body rod protein FlgC
<i>flgD</i>	3.626	flagellar basal body rod modification protein
<i>flgE</i>	2.778	flagellar hook protein
<i>flgF</i>	3.880	flagellar component of cell-proximal portion of basal-body rod
<i>flgG</i>	3.394	flagellar basal body rod protein FlgG
<i>flgH</i>	3.134	flagellar basal body L-ring protein
<i>flgI</i>	3.279	flagellar basal body P-ring protein
<i>flgJ</i>	2.981	flagellar rod assembly protein
<i>flgAMN</i>		
<i>flgA</i>	3.357	flagellar basal body P-ring biosynthesis protein FlgA
<i>flgM</i>	4.290	anti-sigma28 factor FlgM
<i>flgN</i>	3.864	flagella synthesis protein FlgN
<i>fliLMNOPQ</i>		
<i>fliL</i>	3.113	flagellar basal body-associated protein FliL
<i>fliM</i>	2.961	flagellar motor switch protein FliM
<i>fliN</i>	3.555	flagellar motor switch protein FliN
<i>fliO</i>	2.285	flagellar biosynthesis protein FliO
<i>fliP</i>	1.437	flagellar biosynthesis protein FliP
<i>fliQ</i>	1.676	flagellar biosynthesis protein FliQ
<i>fliFGHIJK</i>		
<i>fliF</i>	2.918	flagellar MS-ring protein
<i>fliG</i>	3.159	flagellar motor switch protein G
<i>fliH</i>		
<i>fliI</i>	2.785	flagellum-specific ATP synthase
<i>fliJ</i>	2.764	flagellar biosynthesis chaperone
<i>fliK</i>	2.704	flagellar hook-length control protein
<i>yjfAZ</i>		
<i>yjcZ</i>	2.754	hypothetical protein
<i>fliHBA</i>		
<i>fliH</i>	2.248	flagellar biosynthesis protein FliH
<i>fliA</i>	2.072	flagellar biosynthesis protein FliA
<i>fliHCD</i>		
<i>fliH</i>	2.873	transcriptional activator FliH
<i>fliD</i>	2.844	transcriptional activator FliD
<i>fimAICDEFGH</i>		
<i>fimA</i>	2.177	major type 1 subunit fimbrin (pilin)
<i>codAB</i>		
<i>codA</i>	1.524	cytosine deaminase
<i>codB</i>		
<i>modABC</i>		
<i>modC</i>	1.466	molybdate transporter ATP-binding protein
<i>upp-uraA</i>		
<i>upp</i>	1.454	uracil phosphoribosyltransferase
<i>uraA</i>		

<i>purMN</i>		
<i>purM</i>	1.414	phosphoribosylaminoimidazole synthetase
<i>ykfBFXGHWI</i>		
<i>ykfB</i>	2.088	CP4-6 prophage; predicted protein
<i>nuoMN</i>		
<i>nuoM</i>	1.560	NADH dehydrogenase subunit M
monocistronic operons		
<i>fliC</i>	4.418	flagellar filament structural protein (flagellin)
<i>tsr</i>	3.771	methyl-accepting chemotaxis protein I
<i>fliE</i>	1.591	flagellar hook-basal body protein FliE
<i>ndk</i>	1.621	nucleoside diphosphate kinase
<i>aer</i>	2.673	aerotaxis receptor
<i>ycfQ</i>	1.795	hypothetical protein
<i>ycgR</i>	3.577	hypothetical protein
<i>yecR</i>	2.139	hypothetical protein
<i>ymdA</i>	2.819	hypothetical protein
<i>ynjH</i>	2.970	hypothetical protein
<i>flxA</i>	3.543	Qin prophage; predicted protein
<i>yhjH</i>	3.395	EAL domain-containing protein