

Suppl. Table 5. Up regulated genes (log₂) in the *cobB* mutant compared with the wild type in glucose exponential phase cultures (FDR<0.05).

Genes	Fold change	Description
Policistronic operons		
<i>fliLMNOPQR</i>		
<i>fliL</i>	3.275	flagellar basal body-associated protein FliL
<i>fliM</i>	3.090	flagellar motor switch protein FliM
<i>fliN</i>	3.150	flagellar motor switch protein FliN
<i>fliO</i>	2.798	flagellar biosynthesis protein FliO
<i>fliP</i>	2.597	flagellar biosynthesis protein FliP
<i>fliQ</i>	2.294	flagellar biosynthesis protein FliQ
<i>fliR</i>	2.264	flagellar biosynthesis protein FliR
<i>fliFGIJK</i>		
<i>fliF</i>	3.081	flagellar MS-ring protein
<i>fliG</i>	3.200	flagellar motor switch protein G
<i>fliI</i>	2.849	flagellum-specific ATP synthase
<i>fliJ</i>	3.080	flagellar biosynthesis chaperone
<i>fliK</i>	2.797	flagellar hook-length control protein
<i>FlgBCDEFGHIJKL</i>		
<i>flgB</i>	3.617	flagellar basal body rod protein FlgB
<i>flgC</i>	3.484	flagellar basal body rod protein FlgC
<i>flgD</i>	3.354	flagellar basal body rod modification protein
<i>flgE</i>	3.477	flagellar hook protein
<i>flgF</i>	3.477	flagellar component of cell-proximal portion of basal-body rod
<i>flgG</i>	3.325	flagellar basal body rod protein FlgG
<i>flgH</i>	3.274	flagellar basal body L-ring protein
<i>flgI</i>	3.665	flagellar basal body P-ring protein
<i>flgJ</i>	3.293	flagellar rod assembly protein
<i>flgK</i>	3.853	flagellar hook-associated protein FlgK
<i>flgL</i>	3.526	flagellar hook-associated protein FlgL
<i>FlhBAE</i>		
<i>flhB</i>	2.341	flagellar biosynthesis protein FlhB
<i>flhA</i>	2.058	flagellar biosynthesis protein FlhA
<i>flhE</i>	2.322	flagellar protein
<i>FlgAMN</i>		
<i>flgA</i>	3.158	flagellar basal body P-ring biosynthesis protein FlgA
<i>flgM</i>	3.115	anti-sigma28 factor FlgM
<i>flgN</i>	3.447	flagella synthesis protein FlgN
<i>FliAZ</i>		
<i>fliA</i>	3.693	flagellar biosynthesis sigma factor
<i>fliZ</i>	3.572	flagella biosynthesis protein FliZ
<i>tar-tap-cheRYZ</i>		
<i>tar</i>	4.561	methyl-accepting chemotaxis protein II
<i>tap</i>	4.123	methyl-accepting protein IV
<i>cheR</i>	3.533	chemotaxis methyltransferase CheR
<i>cheB</i>	3.583	chemotaxis-specific methylesterase
<i>cheY</i>	3.618	chemotaxis regulatory protein CheY
<i>cheZ</i>	3.505	chemotaxis regulator CheZ
<i>fliDST</i>		
<i>fliD</i>	4.380	flagellar capping protein
<i>fliS</i>	3.981	flagellar protein FliS
<i>fliT</i>	3.054	flagellar biosynthesis protein FliT
<i>motAB-CheAW</i>		
<i>motA</i>	3.916	flagellar motor protein MotA
<i>motB</i>	4.004	flagellar motor protein MotB
<i>cheA</i>	4.175	chemotaxis protein CheA
<i>cheW</i>	4.149	purine-binding chemotaxis protein
<i>FlhCD</i>		
<i>flhC</i>	1.925	transcriptional activator FlhC
<i>flhD</i>	1.921	transcriptional activator FlhD
Monocistronic operons		
<i>fliC</i>	4.808	flagellar filament structural protein (flagellin)
<i>fliE</i>	2.907	flagellar hook-basal body protein FliE
<i>tsr</i>	3.883	methyl-accepting chemotaxis protein I
<i>ycgR</i>	3.717	hypothetical protein
<i>yhjH</i>	3.613	EAL domain-containing protein
<i>flxA</i>	3.519	Qin prophage; predicted protein
<i>yecR</i>	2.813	hypothetical protein
<i>ymdA</i>	2.688	hypothetical protein
<i>yjcZ</i>	2.630	hypothetical protein
<i>ynjH</i>	2.477	hypothetical protein
<i>aer</i>	1.467	aerotaxis receptor