

Suppl. Table 6. Down 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>gadBC</i>		
<i>gadB</i>	-1.870	glutamate decarboxylase isozyme
<i>gadC</i>	-1.259	acid sensitivity protein
<i>hdeAB-yhiD</i>		
<i>hdeA</i>	-1.819	acid-resistance protein
<i>hdeB</i>	-1.627	acid-resistance protein
<i>entCEBAH</i>		
<i>entC</i>	-1.531	isochorismate synthase
<i>entE</i>	-1.804	2,3-dihydroxybenzoate-AMP ligase component of enterobactin synthase multienzyme complex
<i>entB</i>	-1.191	2,3-dihydro-2,3-dihydroxybenzoate synthetase
<i>gadAXW</i>		
<i>gadA</i>	-1.156	glutamate decarboxylase isozyme
<i>gadX</i>	-1.718	DNA-binding transcriptional regulator GadX
<i>ybaST</i>		
<i>ybaS</i>	-1.548	glutaminase
<i>puuRDCBE</i>		
<i>puuR</i>	-1.263	DNA-binding transcriptional repressor PuuR
<i>puuD</i>	-1.288	gamma-glutamyl-gamma-aminobutyrate hydrolase
<i>puuC</i>	-1.465	gamma-glutamyl-gamma-aminobutyraldehyde dehydrogenase
<i>puuB</i>	-1.420	gamma-Glu-putrescine oxidase, FAD
<i>talA-tktB</i>		
<i>tktB</i>	-1.268	transketolase
<i>yeaGH</i>		
<i>yeaG</i>	-1.180	hypothetical protein
<i>acs-yjcH-actP</i>		
<i>acs</i>	-1.153	acetyl-CoA synthetase
<i>gadE-mdtEF</i>		
<i>gadE</i>	-1.149	hypothetical protein
<i>fadBA</i>		
<i>fadB</i>	-1.126	multifunctional fatty acid oxidation complex subunit alpha
monocistronic operons		
<i>mscS</i>	-1.160	mechanosensitive channel MscS
<i>katE</i>	-1.114	hydroperoxidase II
<i>yciE</i>	-1.114	hypothetical protein
<i>entF</i>	-1.112	enterobactin synthase multienzyme complex component, ATP-dependent
<i>hchA</i>	-1.103	chaperone protein HchA
<i>pfkB</i>	-1.760	6-phosphofructokinase 2
<i>fiu</i>	-1.477	catecholate siderophore receptor Fiu
<i>hdeD</i>	-1.376	acid-resistance membrane protein
<i>cirA</i>	-1.241	colicin I receptor
<i>ydiZ</i>	-1.153	hypothetical protein
<i>ydhS</i>	-1.131	hypothetical protein
<i>ygiW</i>	-1.487	hypothetical protein