

Table S7. R² values and Efficiency of standard curves used in qPCR analyses

Target gene	Annotation	R ²	Efficiency
<i>Primers used to quantify amplified versus non-amplified mRNA</i>			
<i>glyA*</i>	Serine hydroxymethyltransferase	1.0	0.89
<i>pykA*</i>	Pyruvate kinase	1.0	0.93
<i>tpiA</i>	Triosephosphate isomerase	1.0	0.96
<i>luxS</i>	S-ribosylhomocysteinase	1.0	0.86
<i>cirA</i>	ABC transporter ATP-binding protein	1.0	0.81
<i>hybB</i>	Hydrogenase 2 b cytochrome subunit	1.0	0.92
<i>fdxG</i>	Formate dehydrogenase	1.0	1.00
<i>tonB1</i>	Periplasmic protein	1.0	0.97
<i>tonB2</i>	TonB2 protein	1.0	1.01
<i>tbpA1</i>	Transferrin-binding protein 1	1.0	0.92
<i>hlyX</i>	Fumarate/nitrate reduction transcriptional regulator	1.0	0.90
<i>hyaA</i>	Hydrogenase 2 small subunit	1.0	1.07
<i>lldD</i>	L-lactate dehydrogenase	1.0	0.96
<i>Primers used to validate microarray data</i>			
<i>csrA*</i>	Carbon storage regulator	1.0	1.01
<i>manB*</i>	Phosphomannomutase	1.0	1.02
<i>yfhL</i>	Ferredoxin-like protein	1.0	1.00
<i>nusA</i>	Transcription elongation factor	1.0	1.01
<i>ywbN</i>	Putative iron dependent peroxidase	1.0	1.08
<i>hybB</i>	Putative hydrogenase 2 b cytochrome subunit	1.0	1.04
<i>ykgE</i>	Putative dehydrogenase subunit	1.0	0.92
<i>apxIIA</i>	RTX-II toxin determinant A	1.0	0.90
<i>apfB</i>	Fimbrial biogenesis protein	1.0	1.00
<i>nrfG</i>	Formate-dependent nitrite reductase complex subunit	1.0	0.90
<i>glpQ</i>	Glycerophosphodiester phosphodiesterase	1.0	1.00
<i>rraA</i>	Ribonuclease activity regulator protein	1.0	1.02
<i>kdsB</i>	Deoxy-manno-octulosonate cytidylyltransferase	1.0	1.02
<i>yegQ</i>	Uncharacterized protease	1.0	1.00
<i>ftsY</i>	Cell division protein	1.0	1.00
<i>ompP4</i>	Lipoprotein E	1.0	0.90
<i>hgbA</i>	Hemoglobin binding protein A	1.0	1.02
<i>wecD</i>	Putative TDP-D-fucosamine acetyltransferase	1.0	0.94
<i>wecE</i>	TDP-4-keto-6-deoxy-D-glucose transaminase	1.0	1.06
<i>nanA</i>	N-acetylneuraminate lyase	1.0	0.84
<i>neuA</i>	Acylneuraminate cytidylyltransferase	1.0	0.90
<i>nagB</i>	Glucosamine-6-phosphate deaminase	1.0	0.90

*Reference genes applied for data normalization.