

**Table S1.** Primers for construction in this study.

Purpose	Oligo name	5' to 3'
<i>csrA</i> Arg6His mutants construction	pSW7848_fwd	GTCTGATTTCGTTACCAATTATGACAAC
	pSW7848_rev	GAATTCGATATCAAGCTTATCGATAC
	<i>csrAR6H</i> -up_fwd	ATAAGCTTGATATCGAATTCTGCACGCTCGCTTACCGG
	<i>csrAR6H</i> -up_rev	AAATTAGCATTCTTTGCTCCTTGAGTAATCTCTAAATTTTCTTGC
	<i>csrAR6H</i> -down_fwd	GGAGCAAAGAATGCTAATTTTGACTCACCG
	<i>csrAR6H</i> -down_rev	TAATTGGTAACGAATCAGACAGGATTCGAACCTCCGAC
	Del-check-pSW7848-F	TCACTGTCCCTTATTCGCACC
	Del-check-pSW7848-R	CTGCTTTTGAGCACTACCCG
	del-check- <i>csrA</i> -F	CACCCGAATGTGTGGATACAGC
	del-check- <i>csrA</i> -R	CTGGCTTAACCGTTGCTGATTTAAT
over expression of CsrA construction	over- <i>csrA</i> _fwd	GTCTGATTTCGTTACCAATTATGACAAC
	over- <i>csrA</i> _rev	GAATTCGATATCAAGCTTATCGATAC
	over_pSCT32_fwd	ATAAGCTTGATATCGAATTCTGCACGCTCGCTTACCGG
	over_pSCT32_rev	AAATTAGCATTCTTTGCTCCTTGAGTAATCTCTAAATTTTCTTGC
	pSCT32-over-check-F	GGAGCAAAGAATGCTAATTTTGACTCACCG
	pSCT3-over-check-R	TAATTGGTAACGAATCAGACAGGATTCGAACCTCCGAC

Table S2. Primers for qPCR.

Oligo name	5' to 3'
q-aceE-F	TTTCCAGTCTTCTGCTGCGT
q-aceE-R	CATCAGTTTAGGGTGCGGGT
q-acnB-F	TTCAACGCGTAACCTCCCGA
q-acnB-R	CGTAGCGTCGATTTGCTTCG
q-alaS-F	CTTCCACAAGTTGGTTGGCG
q-alaS-R	TTAAGTCAGCTGGGAAGCCG
q-ald-F	TGGGTCGTTTGCCACTGTTA
q-ald-R	AATAGTGACGTCAGCGCGAA
q-avtA-F	GCGTGCGTATTGATTGTCC
q-avtA-R	TTCGCGGTAAGCCTTTTCCA
q-eno-F	AAGACGCAGGTTACACAGCA
q-eno-R	CACGGTCAGAACGGCTCATA
q-fbp-F	CGTGATTTACGGCTCCTCCA
q-fbp-R	CACCCCTTGAGGGAAACGAA
q-flaC2-F	TTGAACGGCTCATTGCGTGA
q-flaC2-R	TGGGTCAACGCTCCAGTTTT
q-flgC1-F	CCCTTGCAAACGAAGAAGGC
q-flgC1-R	ATTGACCCATCTGCAGCGTA
q-flgC2-F	CAGAGAAGCGTTTTGAGCCG
q-flgC2-R	AGCAGACCTTGCTGCATACT
q-fruA-F	TGAACGGCCTGACTGACTTC
q-fruA-R	CTTTGTTTACCGGGCCTCCT
q-gcvP-F	CTTCACGCCGAACGTGATTC
q-gcvP-R	GCGTTCGCGATTTCCATACC
q-glxA-F	CGCGCAGGACTTAGTTGGTA
q-glxA-R	AGCTTTCTTCCCTTGCGACA
q-cs-F	GCGGATAAGAAAGCGACCCCT
q-cs-R	ACCATTGGCTCCCAGCTTAC
q-lafA-F	GCACACTAACTACGCTTCGC
q-lafA-R	TGTTTGCGCTTCTAGACGGT
q-pdhA-F	CAATGTGCCGCCGATTTCTT
q-pdhA-R	GATGAGTGTTGCGCCTTTCC
q-pfkA-F	AATCGGTGGTGATGGTTCGT
q-pfkA-R	TCACGTAGACGGTCGATTGC
q-proB-F	ACGAGATGGCGAGTAAGCAG
q-proB-R	TCGCAACGGCATCATTTTCG
q-proQ-F	AAACCAGGTGCAGTACGTGT
q-proQ-R	GGTTTCGCTTTCGCCTTACC
q-proV-F	ACTTGCCGGCATCGATGTTA
q-proV-R	CAGGCTAACGCTCTCGCTAA
q-putA-F	CAGGCTGTAAACCGTCTGGT
q-putA-R	GTGAAACCTTTGTCGCGCAT
q-sdaA-F	AACGCGTCTATCTCTGGTGC
q-sdaA-R	ACCTGAACCTGACCTGCAAC
q-sdaB-F	GGCAAGTCGTCACCTTCTCCA
q-sdaB-R	CAACTTCTCCCTGACACCCC
q-sdaC-F	AACCCTGAAGCGGACATCAC
q-sdaC-R	ACCGAATACTACGCCTGCTG
q-serA-F	AGAGGGACTCCACCCTTCTT

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q- <i>serA</i> -R	CGGGAGCGGATACCAATGAA
q- <i>tdh</i> -F	AATCGGTGACCGCGTATCTG
q- <i>tdh</i> -R	AAGTGCTGTGTGTACTGCGT
q- <i>thrA</i> -F	CCGCAGGTAACGAGAAAGGT
q- <i>thrA</i> -R	TTCCACTAAACGAGGGTCGC
q- <i>ppc</i> -F	TGCGCATGTTAGGCCACTTA
q- <i>ppc</i> -R	GCTGTCCCTGTCTGCTTGAT
q- <i>pckA</i> -F	CGCCCGACAGAAGAAGAGTT
q- <i>pckA</i> -R	GATAAGTTGCATGCGCTCGG
q- <i>sdhA</i> -F	ATGCGTTGGGAAAACAGCAC
q- <i>sdhA</i> -R	AGACTTGTCCGCTAGATGCG
q- <i>sucA</i> -F	AGCATCCTACACCACGCAAA
q- <i>sucA</i> -R	AGTCTACAGAGTGCAACGCC
q- <i>sucC</i> -F	ACCAAAC TGACGCTAACGGT
q- <i>sucC</i> -R	GGCGTTTCTTCCGCAACTTT
q- <i>fbxA</i> -F	CAGTGGGCTACTTGGGATGG
q- <i>fbxA</i> -R	CCATACGCGTGGATCGTAGT
q- <i>gltD</i> -F	GTATGACGCGCTGCCATTTT
q- <i>gltD</i> -R	TTGAGGTACGAACGCAGTCC
q- <i>gltB</i> -F	TTGTTGCCATTCTTGGTGCG
q- <i>gltB</i> -R	CAGCATGACTCGACCCTGTT
q- <i>ppsA</i> -F	TCAGAAGGTGAAACGGGCTACG
q- <i>ppsA</i> -R	TCAAGACGAGCAAGACCAAC
q- <i>pykA</i> -F	CACTACGCTGGGTCCTTCAA
q- <i>pykA</i> -R	TGGTACGGACTTTGTTTCGCA
q-16S-F	CTGGAAC TGAGACACGGTCC
q-16S-R	CTCGCACCCCTCCGTATTACC
q- <i>recA</i> -F	TCTTCATCAACCAAATCCGTA
q- <i>recA</i> -R	GCTGCAATCTTATTCTTAACAATT
q- <i>csrA</i> -F	AATTTTGACTCGCCGCGTAGG
q- <i>csrA</i> -R	TGAATGCGCATGTAGATTCTTCACG

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**Table S3.** Genes for q-PCR and mRNA stability experiments.

Gene_ID	Symbol	Description
BAU10_RS22550	<i>lafA</i>	lateral flagellin LafA
BAU10_RS02985	<i>flgC1</i>	flagellar basal-body rod protein FlgC
BAU10_RS16785	<i>flgC2</i>	flagellar basal-body rod protein C
BAU10_RS03035	<i>flaC2</i>	flagellin
BAU10_RS04120	<i>glgA</i>	glycogen synthase
BAU10_RS00575	<i>fbp</i>	Fructose-1,6-bisphosphatase
BAU10_RS14165	<i>pfkA</i>	6-phosphofructokinase
BAU10_RS12575	<i>fbaA</i>	fructose-bisphosphate aldolase
BAU10_RS12400	<i>eno</i>	phosphopyruvate hydratase
BAU10_RS19230	<i>fruA</i>	PTS fructose transporter subunit IIBC
BAU10_RS12545	<i>serA</i>	<b>D-3-phosphoglycerate dehydrogenase</b>
BAU10_RS20470	<i>pdhA</i>	<b>ABC transporter permease</b>
BAU10_RS12140	<i>aceE</i>	<b>pyruvate dehydrogenase (acetyl-transferring), homodimeric type</b>
BAU10_RS12035	<i>acnB</i>	<b>bifunctional aconitate hydratase 2/2- methylisocitrate dehydratase</b>
BAU10_RS03265	<i>CS</i>	<b>citrate (Si)-synthase</b>
BAU10_RS13680	<i>ppc</i>	<b>phosphoenolpyruvate carboxylase</b>
BAU10_RS15770	<i>pckA</i>	<b>phosphoenolpyruvate carboxykinase</b>
BAU10_RS03280	<i>sdhA</i>	<b>succinate dehydrogenase catalytic subunit</b>
BAU10_RS03290	<i>sucA</i>	<b>2-oxoglutarate dehydrogenase, E1 component</b>
BAU10_RS03300	<i>sucC</i>	<b>succinyl-CoA synthetase subunit beta</b>
BAU10_RS17220	<i>ppsA</i>	<b>phosphoenolpyruvate synthase</b>
BAU10_RS09350	<i>pykA</i>	pyruvate kinase II
BAU10_RS08610	<i>sdaC</i>	serine transporter
BAU10_RS08615	<i>sdaA</i>	L-serine dehydratase 1
BAU10_RS16735	<i>sdaB</i>	L-serine ammonia-lyase
BAU10_RS19180	<i>gcvP</i>	glycine dehydrogenase (aminomethyl- transferring)
BAU10_RS01440	<i>thrA</i>	<b>bifunctional aspartate kinase /homoserine dehydrogenase I</b>
BAU10_RS22370	<i>tdh</i>	<b>L-threonine 3-dehydrogenase</b>
BAU10_RS06505	<i>proV</i>	<b>ABC superfamily (glycine/betaine/ proline transport protein)</b>
BAU10_RS07350	<i>proQ</i>	RNA chaperone ProQ
BAU10_RS02410	<i>proB</i>	gamma-glutamyl kinase
BAU10_RS23405	<i>putA</i>	<b>bifunctional proline dehydrogenase/L-glutamate gamma-semialdehyde dehydrogenase</b>
BAU10_RS04925	<i>ald</i>	<b>alanine dehydrogenase</b>
BAU10_RS12335	<i>alaS</i>	alanine--tRNA ligase
BAU10_RS15215	<i>avtA</i>	valine--pyruvate transaminase
BAU10_RS01380	<i>gltD</i>	<b>glutamate synthase</b>
BAU10_RS01385	<i>gltB</i>	<b>glutamate synthase</b>

Note: Bold letters (depicted in black) indicate the genes used for mRNA stability experiments.