

Supplementary materials:

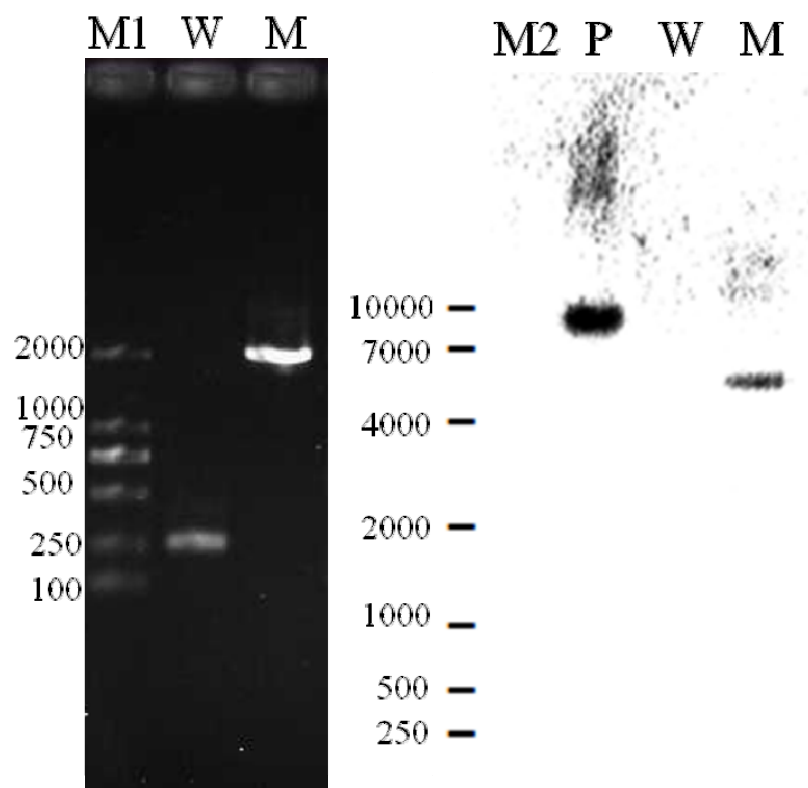


Figure S1 The mutagenesis for *csrA*. A, The generation of integrant; B, Southern blot testing; M1, DL2000; M2, DL10000; W, wild type; M, $\Delta csrA$ strain; P, pMTL007C-E2.

Supplementary Table S1 Oligonucleotide primers used in this study

Primer name	Sequence (5'-3')	Description
Cac-csrA-97s-IBS	AAAAAAGCTTATAATTATCCTTATCTGTCAAATAGTGCG CCCAGATAGGGTG	csrA ClosTron primer
Cac-csrA-97s-EBS1d	CAGATTGTACAAATGTGGTGATAACAGATAAGTCAAAT AGCTAACTTACCTTTCTTTGT	csrA ClosTron primer
Cac-csrA-97s- EBS2	TGAACGCAAGTTTCTAATTTTCGGTTACAGATCGATAGAGG AAAGTGTCT	csrA ClosTron primer
csrA -ID-for	TAAAGGAGTGACTTAAATGT	Screening primer
csrA -ID-rev	CTCGTTTTATACTTATTTCTTTAG	Screening primer
EBS universal	CGAAATTAGAACTTGC GTTCAGTAAAC	Universal ClosTron primer
SalI-R1	ATTACTGTGACTGGTTTGCACCACCCTCTTCG	Used for generation of Southern blot probe
Cac- csrA -Not/F	ATAAGAATGCGGCCGCTTATGTTAAGGCAGACTATGAAG	<i>csrA</i> promoter forward primer
Cac- csrA -NcoI/R	GGCCATGGTTATTTCTTTAGAGTTAATTCCTT	<i>csrA</i> reverse primer
lacZ_ NheI/F	AAAAAAGCTAGCATGAGAAAGATTATTCCTATTA	<i>lacZ</i> forward primer
lacZ_ NcoI/R	AAAAAACCATGGTTATTCAACTTTTATCATTAC	<i>lacZ</i> reverse primer
Cac- rib_ Pst I/ F	AAAAAACTGCAGGAATCTATAGAATCTAAAAG	Riboflavin forward primer
Cac- rib_ Nhe I/ R	AAAAAAGCTAGCGCAAATAAAAAAATCTCCAA	Riboflavin reverse primer
Cac- spo_ Pst I/ F	AAAAAACTGCAGAGAAACAATAAGAGTTGATAC	Spore forward primer
Cac- spo_ Nhe I/ R	AAAAAAGCTAGCGAAAAGATATCTTCAAGGTTTCAT	Spore reverse primer
Cac- fla_ Pst I/ F	AAAAAACTGCAGTTATCTAAAAATTTTATAAAAAC	Flagellar forward primer
Cac- fla_ Nhe I/ R	AAAAAAGCTAGCATACTGCTCACATCCATCAT	Flagellar reverse primer
Cac- fru_ Pst I/ F	AAAAAACTGCAGGAGAGATAAATAATATGCTG	Fructose PTS forward primer
Cac- fru_ Nhe I/ R	AAAAAAGCTAGCACTAATATTACATATCTCAT	Fructose PTS reverse primer
Cac- Fe_ Pst I/ F	AAAAAACTGCAGCAATAATATAAATGAGATAAAAAG	Ferric uptaking forward primer
Cac- Fe_ Nhe I/ R	AAAAAAGCTAGCAGACCTATACCTTTTGTTCAT	Ferric uptaking reverse primer
CA_C0712RT/F	CGGACTAAGCGTAGGACTTC	CA_C0712 qRT-PCR primer
CA_C0712RT/R	TTATCTTTGTAAGCGATTGA	
CA_C1347 RT/F	AGTAACAACCTAATCCTTCCCTT	CA_C1347 qRT-PCR primer
CA_C1347 RT/R	TATCATTCCTTCAGCGTCTA	
CA_C2612 RT/F	CGAGTAAGTGGTGGAGGTGC	CA_C2612 qRT-PCR primer
CA_C2612 RT/R	TATTGCTACGCCAAGTGCTG	
CA_C3635 RT/F	TTCAGGAGGAACTTGGACTT	CA_C3635 qRT-PCR primer
CA_C3635 RT/R	GGGTGAAGCGGATTATTGTA	
CA_C3181 RT/F	CTACCGAATACCTTTCCCTT	CA_C3181 qRT-PCR primer
CA_C3181 RT/R	GCCGCATTTATCATATTTCC	
CA_C1457 RT/F	ATTTCAAGGATTAGAGGACG	CA_C1457 qRT-PCR primer
CA_C1457 RT/R	ACTGCTGTAGTCAAAGGAGA	
CA_C2957 RT/F	TATCAGGTTGTAGCAGATGCAATG	CA_C2957 qRT-PCR primer
CA_C2957 RT/R	GCTCCTGCTTCAACGACTGG	

CA_C0232 RT/F	ACTGACATTATAGATGGAGCAA	
CA_C0232 RT/R	AACTGGAAC TACCAAACCCT	CA_C0232 qRT-PCR primer
CA_C3288 RT/F	GGAAAGCCAATAAAGCTAAT	
CA_C3288 RT/R	TTCTCCACCTGAGAAACCTA	CA_C3288 qRT-PCR primer
CA_C2151 RT/F	ACATGCAAAATGGTAGGTTT	
CA_C2151 RT/R	CCTCATCGGTAAGTTCCTTA	CA_C2151 qRT-PCR primer
CA_C0122 RT/F	AATCCAGAGGCTAAGGTGGTA	
CA_C0122 RT/R	CAAACGGCTTGGCAATAAAA	CA_C0122 qRT-PCR primer
CA_C0590 RT/F	TTGGAGGAAATCATGCTGAG	
CA_C0590 RT/R	TATTCCCGCTTTAACTACCG	CA_C0590 qRT-PCR primer
CA_C2087 RT/F	CTGGAGGGAAAAGAACAACC	
CA_C2087 RT/R	TGCTCCTTCTGCCACAACAC	CA_C2087 qRT-PCR primer
CA_C2679 RT/F	ATACTGGGTAAAAGAATATC	
CA_C2679 RT/R	TCCCAGCCTTCTCCATACAA	CA_C2679 qRT-PCR primer

Supplementary Table S2 Expression profiles of genes involved in flagella assembly.
FDR = false discovery rate

Accession	Annotation	FDR	Folds
CA_C2139	flagella basal body rod protein FlgG	9.09E-63	-1.1
CA_C2140	flagella basal body rod protein FlgG	1.17E-32	-1.2
CA_C2141	hypothetical protein	9.26E-06	-1.6
CA_C2142	hypothetical protein	3.40E-39	-1.1
CA_C2143	sigma factor of SigD/WhiG family	3.96E-21	-1.5
CA_C2144	hypothetical protein	2.22E-12	-0.5
CA_C2145	chromosome partitioning ATPase	1.54E-07	-0.6
CA_C2146	flagella biosynthesis regulator FlhF	0.0001315	-0.26
CA_C2147	flagella biosynthesis protein FlhA	4.18E-06	-0.47
CA_C2148	bifunctional flagella biosynthesis protein FliR/FlhB	5.53E-05	-0.97
CA_C2149	flagella biosynthesis protein FliQ	0.3485852	-1.0
CA_C2150	flagella biosynthesis protein FliP	3.55E-06	-4.37
CA_C2151	flagella biosynthesis protein FliZ	0.008649	-3.9
CA_C2152	flagella protein FliL	0.0001582	-1.2
CA_C2153	flagella protein flbD	0.0001176	-1.3
CA_C2154	flagella hook protein FlgE	7.91E-15	-0.83
CA_C2155	hypothetical protein	4.39E-08	-1.6
CA_C2156	flagella hook assembly protein FlgD	1.43E-08	-1.9

CA_C2157	flagella hook-length control protein fliK	9.57E-14	-1.7
CA_C2158	flagella protein FliJ	1.90E-06	-1.5
CA_C2159	flagella-Type ATPase	2.51E-22	-1.7
CA_C2160	flagella assembly protein FliH	1.90E-13	-1.5
CA_C2161	flagella motor switch protein G	2.79E-20	-1.5
CA_C2162	flagella MS-ring protein	3.49E-23	-1.2
CA_C2163	flagella hook-basal body protein FliE	4.97E-07	-1.2
CA_C2164	flagella basal body rod protein FlgC	9.92E-10	-1.6
CA_C2165	flagella basal-body rod protein FlgB	1.08E-21	-1.1
CA_C2166	nucleoside-diphosphate-sugar epimerase	0.0060478	-0.82
CA_C2167	flagellin family protein	0.1443435	0.31

Supplementary Table S3 Expression profiles of genes involved in oligopeptide, PTS and Iron transport system. FDR = false discovery rate

Accession	Annotation	FDR	Folds
ABC transporters			
CA_C3634	oligopeptide ABC transporter periplasmic substrate-binding component	3.27E-274	1.9
CA_C3635	oligopeptide ABC transporter ATPase	9.66E-57	2.0
CA_C3636	oligopeptide ABC transporter ATPase	8.02E-27	1.7
CA_C3637	oligopeptide ABC transporter permease	1.24E-16	1.9
CA_C3638	oligopeptide ABC transporter permease	6.52E-28	1.6
CA_C3628	oligopeptide ABC transporter ATPase	0.445426	-0.11
CA_C3629	oligopeptide ABC transporter ATPase	0.098892	-0.31
CA_C3630	oligopeptide ABC transporter permease	0.666337	-0.10
CA_C3631	oligopeptide ABC transporter permease	0.109226	-0.46
CA_C3632	oligopeptide ABC transporter periplasmic substrate-binding component	2.96E-54	0.59
CA_C3633	hypothetical protein	0.283894	0.89
CA_C3641	oligopeptide ABC transporter ATPase	0.044623	0.32
CA_C3642	oligopeptide ABC transporter ATPase	0.429352	0.29
CA_C3643	oligopeptide ABC transporter permease	0.719418	0.38
CA_C3644	oligopeptide ABC transporter permease	0.027025	-1.4
CA_C0177	oligopeptide transport permease	0.988522	-0.01
CA_C0178	oligopeptide transport permease	0.000611	-0.66

CA_C0179	oligopeptide transport ATP-binding protein	0.004133	-0.32
CA_C0180	oligopeptide ABC transporter ATP-binding protein	0.016131	-0.48
CA_C2374	oligopeptide ABC-type transporter permease component OPPC	0.964831	0.02
CA_C2375	oligopeptide ABC-type transporter permease	0.02043	-1.3
CA_C2377	oligopeptide ABC-type transporter periplasmic binding component (frameshift)	2.51E-07	-1.2
CA_C3179	oligopeptide ABC transporter periplasmic binding component	0.657066	0.38
CA_C3180	oligopeptide ABC transporter permease	0.702929	-0.43
CA_C3181	oligopeptide ABC transporter permease	0.384517	0.97
CA_C3182	oligopeptide ABC transporter ATPase	0.745794	0.38
CA_C3183	oligopeptide ABC transporter ATPase	0.98555	-0.01
CA_C0790	ferrichrome-binding periplasmic protein FhuD	8.93E-06	-1.5
CA_C0791	ferrichrome ABC transporter ATP-binding protein	0.0008719	-1.5

Phosphotransferase system (PTS)

CA_C0423	PTS, beta-glucosides specific IIABC component	4.33E-21	1.5
CA_C1407	PTS, beta-glucosides-specific transporter subunit IIABC	1.35E-08	1.9
CA_C1457	PTS, fructose(mannose)-specific transporter subunit IIA	4.24E-106	3.3

CA_C1458	PTS, fructose(mannose)-specific transporter subunit IIB	5.52E-125	3.0
CA_C1459	PTS, fructose(mannose)-specific transporter subunit IIC	6.31E-39	2.5
CA_C1460	PTS, fructose(mannose)-specific transporter subunit IID	2.82E-15	1.9
CA_C1461	hypothetical protein	0.0001216	1.4
CA_C1462	levanase/invertase	8.86E-77	2.1
CA_C1463	transcriptional regulator	9.28E-06	3.0
CA_C2956	PTS, galactitol/fructose specific transporter subunit IIC	2.80E-07	2.1
CA_C2957	PTS, galactitol/fructose specific transporter subunit IIB	1.31E-06	3.0
CA_C2958	PTS, galactitol/fructose specific transporter subunit IIBC	8.86E-14	2.4
CA_C0231	transcriptional regulator of sugar metabolism	2.02E-203	-1.9
CA_C0232	1-phosphofructokinase	5.10E-83	-1.4
CA_C0233	PTS, transporter subunit IIA	2.09E-222	-1.9
CA_C0234	PTS, fructose-specific transporter subunit IIBC	0	-1.3
Iron-uptaking system			
CA_C1029	FeoA-like protein, involved in iron transport	6.22E-24	-2.0
CA_C1030	FeoA-like protein, involved in iron transport	5.94E-08	-1.2
CA_C1031	FeoB-like GTPase, responsible for iron uptake	1.82E-58	-1.7

CA_C1032

transcriptional regulator

1.16E-18

-1.6

Supplementary Table S4 Expression profiles of genes involved in stage III sporulation and spore coat protein. FDR = false discovery rate

Accession	Annotation	FDR	Folds
CA_C2086	stage III sporulation protein AH	1.14E-89	0.91
CA_C2087	stage III sporulation protein AG	4.67E-156	1.7
CA_C2088	stage III sporulation protein AF	6.39E-284	1.7
CA_C2089	stage III sporulation protein AE	1.20E-20	1.9
CA_C2090	stage III sporulation protein AD	1.03E-05	0.84821
CA_C2091	stage III sporulation protein AC	0.0889767	0.66
CA_C2092	stage III sporulation protein SpoAB	6.34E-106	1.7
CA_C2093	stage III sporulation protein AA	1.35E-265	1.8
CA_C0613	spore coat protein CotF	1.94E-05	0.43
CA_C0614	spore coat protein CotF	6.28E-18	0.62

CA_C1335	spore coat protein F (cof) related protein	0.435467	0.18
CA_C1336	hypothetical protein	0	2.2
CA_C1337	spore coat protein CotJB	0	2.3
CA_C1338	spore coat protein CotJC	0	2.0
CA_C2906	spore coat protein cotS related	0	1.7
CA_C2907	glycosyltransferase	1.40E-12	1.4
CA_C2908	spore coat protein cotS related	2.61E-204	1.9
CA_C2909	spore coat protein CotS-like protein	2.52E-200	2.3
CA_C2910	spore coat protein cotS related	3.01E-202	2.4

Supplementary Table S5 Expression profiles of genes involved in central carbon

metabolism. FDR = false discovery rate

Accession	Annotation	FDR	Folds
EMP pathway			
CA_C3021	phosphoglycerate mutase	1.83E-13	-1.3
CA_C0712	phosphoglyceromutase	0	-1.3
CA_P0064	fructose-1,6-bisphosphate aldolase	4.68E-39	1.3
TCA cycle			
CA_C2458	2-oxoglutarate ferredoxin oxidoreductase subunit beta	8.14E-17	-1.1
Pentose phosphate pathway			
CA_C1347	transaldolase	6.04E-97	1.3
CA_C2018	aldehyde:ferredoxin oxidoreductase	3.55E-23	-1.6
CA_C2973	keto-hydroxyglutarate-aldolase/keto-deoxy-phosph ogluconate aldolase	2.34E-08	-1.3
Pentose and glucuronate interconversions pathway			
CA_C1341	L-ribulose-5-phosphate 4-epimerase	6.89E-24	1.6
CA_C1342	L-arabinose isomerase	5.56E-95	1.5
CA_C2612	xylulose kinase	3.24E-12	-1.4
Starch and sucrose metabolism			
CA_C1664	glycogen phosphorylase	1.11E-42	-0.64

CA_C2239	glycogen synthase	5.27E-05	0.41
CA_P0098	alpha-amylase	7.16E-23	-1.1
CA_P0168	alpha-amylase	4.12E-18	0.47

Supplementary Table S6 The expression information of selected genes for qRT-PCR in *ΔcsrA* strain and wild type.

Gene ID	Gene function	Fold change (log2)	
		RNA-seq	qRT-PCR
CA_C0712	phosphoglyceromutase	-1.30	-2.4
CA_C1347	transaldolase	1.25	3.02
CA_C2612	xylulose kinase	-1.37	-1.53
CA_C3635	oligopeptide ABC transporter ATPase	2.00	1.87
CA_C3181	oligopeptide ABC transporter permease	0.38	0.88
CA_C1457	PTS, fructose(mannose)-specific transporter subunit IIA	3.35	4.48
CA_C2957	PTS, galactitol/fructose specific transporter subunit IIB	2.97	2.68
CA_C0232	1-phosphofructokinase	-1.36	-1.21
CA_C3288	Iron-regulated ABC transporter ATPase	-1.27	-2.19
CA_C2151	flagellar biosynthesis protein FliZ	-3.94	-4.59
CA_C0122	chemotaxis respons regulator (cheY)	-1.98	-2.46
CA_C0590	riboflavin biosynthesis protein RIBD (pirimidine deaminase and pirimidine reductase)	-1.36	-2.36
CA_C2087	stage III sporulation protein AG	1.69	2.33