

Supplementary Information

The Csr system regulates genome-wide mRNA stability and transcription and thus gene expression in *Escherichia coli*

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Figure S1. Phenotypic characterization of the MG1655(*csrA51*) mutant strain. (A) Glycogen staining assay in the MG1655, MG1655(*csrA51*) and *csrA+* strains. (B) Motility and biofilm formation assays in the MG1655 and MG1655(*csrA51*) strains. (C) Level of CsrB and CsrC in the MG1655 and MG1655(*csrA51*) strains in Northern blots of total RNA probed for CsrB and CsrC.

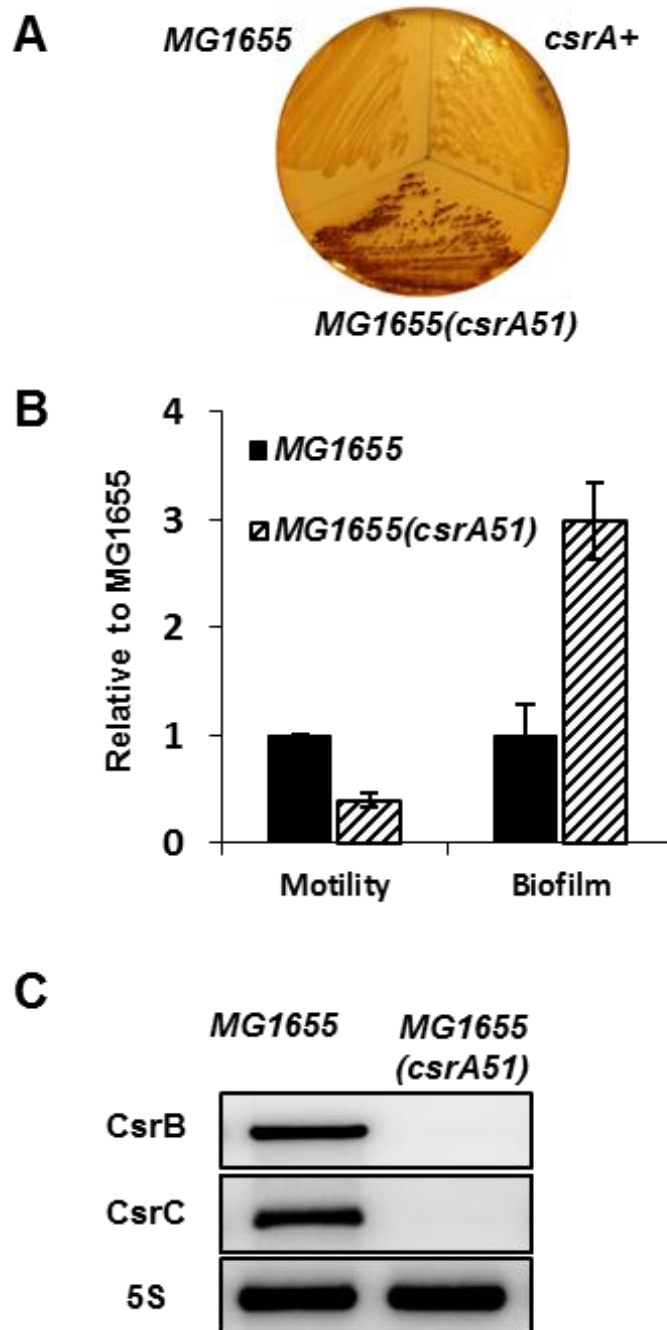


Figure S2. Effect of the $\Delta csrD$ mutation on the stability of CsrB and CsrC sRNAs. CsrB and CsrC stability in MG1655 and MG1655($\Delta csrD$) strains was measured in Northern blot and quantified by PhosphorImager. All experiments were repeated at least twice.

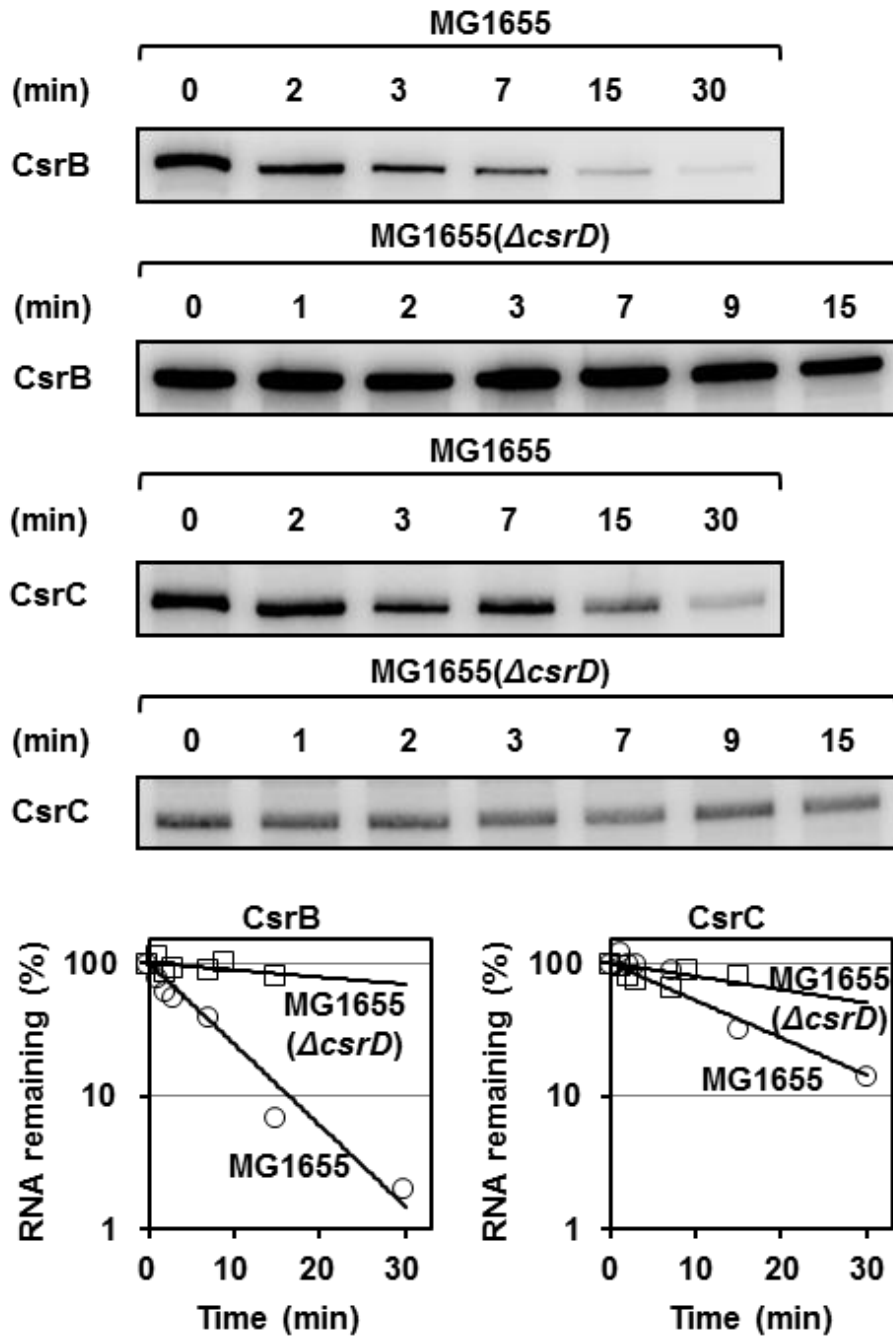


Table S4: Comparison of β -galactosidase activity of transcriptional fusions in the strains MG1655, MG1655(*csrA51*) and MG1655(Δ *csrD*). Ratios of β -galactosidase activity between two strains are given.

	MG1655(<i>csrA51</i>) / MG1655		MG1655(Δ <i>csrD</i>) / MG1655
glgB:: <i>lacZ</i>	1.55 \pm 0.13	<i>csrC</i> :: <i>lacZ</i>	0.48 \pm 0.00
ydeH:: <i>lacZ</i>	1.34 \pm 0.32	<i>fdrA</i> :: <i>lacZ</i>	0.44 \pm 0.03

Table S7. List of the 99 mRNAs for which direct regulation of stability by CsrA had an impact on quantity.

CsrA regulation: (-) negative and (+) positive in the MG1655 cells

Degradational coefficient ρ_D value: if $\rho_D \geq 0,6$ (bold), mRNA amount is mainly controlled by degradation; if $\rho_D \leq 0,6$ (italic) mRNA amount is equally controlled by degradation and transcription or mainly controlled by transcription

Blattner	Gene Symbol	CsrA regulation	Fold change of half-lives MG1655(<i>csrA51</i>) / MG1655	Fold change of mRNA amounts MG1655(<i>csrA51</i>) / MG1655	Degradational coefficient ρ_D value
b0072	<i>leuC</i>	-	1.50	1.28	1.67
b0073	<i>leuB</i>	-	1.53	1.34	1.45
b0118	<i>acnB</i>	-	2.15	1.12	6.83
b0212	<i>gloB</i>	+	0.69	0.65	0.88
b0391	<i>yaiE</i>	+	0.68	0.62	0.82
b0406	<i>tgt</i>	+	0.54	0.82	3.01
b0476	<i>aes</i>	+	0.72	0.71	0.99
b0688	<i>pgm</i>	-	1.41	3.19	<i>0.29</i>
b0721	<i>sdhC</i>	-	1.17	1.13	1.28
b0897	<i>ycaC</i>	+	0.29	0.61	2.54
b1042	<i>csgA</i>	+	0.46	0.77	3.04
b1089	<i>rpmF</i>	+	0.63	0.79	1.97
b1092	<i>fabD</i>	-	1.40	1.85	<i>0.55</i>
b1095	<i>fabF</i>	-	1.61	1.28	1.94
b1178	<i>pliG</i>	+	0.56	0.65	1.33
b1219	<i>yehN</i>	+	0.72	0.58	0.60
b1324	<i>tpx</i>	+	0.54	0.77	2.31
b1380	<i>ldhA</i>	+	0.60	0.82	2.62
b1415	<i>aldA</i>	+	0.65	0.93	5.58
b1440	<i>ydcS</i>	+	0.78	0.50	<i>0.35</i>
b1461	<i>pptA</i>	+	0.53	0.61	1.27
b1479	<i>maeA</i>	-	1.41	1.32	1.25
b1538	<i>dcp</i>	+	0.79	0.78	0.92
b1602	<i>pntB</i>	-	1.55	1.32	1.56
b1603	<i>pntA</i>	-	1.54	1.21	2.25
b1612	<i>fumA</i>	-	1.32	1.12	2.48
b1619	<i>hdhA</i>	+	0.64	0.77	1.70
b1667	<i>ydhR</i>	+	0.53	0.19	<i>0.38</i>
b1692	<i>ydiB</i>	+	0.57	0.64	1.23
b1694	<i>ydiF</i>	+	0.60	0.76	1.84
b1695	<i>ydiO</i>	+	0.65	0.73	1.35
b1718	<i>infC</i>	-	1.37	1.29	1.23

b1719	<i>thrS</i>	-	1.64	1.59	1.06
b1779	<i>gapA</i>	-	1.66	1.39	1.54
b1782	<i>mipA</i>	-	1.41	1.36	1.12
b1800	<i>dmlA</i>	+	0.69	0.67	0.92
b1817	<i>manX</i>	-	2.02	1.71	1.32
b1818	<i>manY</i>	-	2.29	1.25	3.74
b1819	<i>manZ</i>	-	2.10	1.37	2.37
b1823	<i>cspC</i>	+	0.64	0.28	<i>0.35</i>
b1824	<i>yobF</i>	+	0.45	0.37	0.79
b1852	<i>zwf</i>	+	0.79	0.93	3.19
b1901	<i>araF</i>	+	0.54	0.51	0.90
b2001	<i>yeeR</i>	+	0.60	0.06	<i>0.18</i>
b2094	<i>gatA</i>	-	1.62	1.19	2.79
b2095	<i>gatZ</i>	-	1.84	1.22	3.06
b2245	<i>yfaU</i>	+	0.57	0.82	2.96
b2246	<i>rhmT</i>	+	0.48	0.69	2.02
b2360	<i>yfdQ</i>	+	0.68	0.49	<i>0.55</i>
b2463	<i>maeB</i>	-	2.26	1.40	2.43
b2521	<i>sseA</i>	-	1.32	3.10	<i>0.24</i>
b2542	<i>hcaD</i>	+	0.73	0.84	1.84
b2702	<i>srlA</i>	+	0.31	0.53	1.83
b2703	<i>srlE</i>	+	0.28	0.42	1.47
b2704	<i>srlB</i>	+	0.32	0.39	1.21
b2799	<i>fucO</i>	-	2.96	4.07	0.77
b2937	<i>speB</i>	+	0.53	0.73	2.02
b2938	<i>speA</i>	-	1.49	1.19	2.27
b2989	<i>yghU</i>	+	0.59	0.65	1.23
b3008	<i>metC</i>	+	0.64	0.73	1.41
b3011	<i>yqhD</i>	+	0.50	0.72	2.12
b3067	<i>rpoD</i>	-	2.79	1.26	4.37
b3077	<i>ebgC</i>	+	0.57	0.66	1.34
b3078	<i>ygjI</i>	+	0.52	0.68	1.69
b3089	<i>sstT</i>	-	1.35	2.32	<i>0.36</i>
b3091	<i>uxaA</i>	+	0.66	0.80	1.86
b3092	<i>uxaC</i>	+	0.52	0.80	2.93
b3133	<i>agaV</i>	+	0.67	0.70	1.10
b3134	<i>agaW</i>	+	0.73	0.75	1.12
b3253	<i>yhdH</i>	+	0.69	0.65	0.87
b3310	<i>rplN</i>	-	1.29	1.13	2.06
b3313	<i>rplP</i>	-	2.10	1.17	4.63
b3316	<i>rpsS</i>	-	1.93	1.11	6.10
b3371	<i>frlB</i>	+	0.59	0.67	1.30
b3403	<i>pck</i>	-	2.61	1.25	4.35
b3432	<i>glgB</i>	-	1.92	3.58	<i>0.51</i>
b3433	<i>asd</i>	-	1.47	1.84	0.63
b3460	<i>livJ</i>	+	0.20	0.48	2.20

b3491	<i>yhiM</i>	+	0.57	0.76	2.05
b3774	<i>ilvC</i>	+	0.82	0.80	0.88
b3831	<i>udp</i>	+	0.51	0.63	1.47
b3870	<i>glnA</i>	-	1.71	1.33	1.88
b3919	<i>tpiA</i>	+	0.83	0.76	0.71
b3926	<i>glpK</i>	+	0.65	0.41	<i>0.49</i>
b3927	<i>glpF</i>	+	0.57	0.28	0.44
b3981	<i>secE</i>	-	1.34	1.35	0.98
b3990	<i>thiH</i>	+	0.55	0.87	4.30
b4034	<i>malE</i>	+	0.51	0.59	1.26
b4079	<i>fdhF</i>	+	0.75	0.65	0.65
b4088	<i>alsB</i>	+	0.66	0.62	0.86
b4120	<i>melB</i>	+	0.66	0.76	1.53
b4138	<i>dcuA</i>	-	1.99	4.33	<i>0.47</i>
b4211	<i>qorB</i>	+	0.67	0.83	2.17
b4216	<i>ytfJ</i>	+	0.54	0.66	1.48
b4234	<i>yjgA</i>	+	0.55	0.82	2.99
b4265	<i>idnT</i>	+	0.64	0.86	2.96
b4266	<i>idnO</i>	+	0.67	0.46	<i>0.51</i>
b4267	<i>idnD</i>	+	0.61	0.56	0.86
b4525	<i>ymjC</i>	+	0.59	0.87	3.89

Table S8. DNA oligonucleotides used in this study.

Primer Name	Sequence (5' to 3')
OKT-24	TGAGGGTGCCTCACCATAAAGATGAGACGCGAAAGACTTGAGCGATTGTGTAGGCT
OKT-25	GAAGGAAGTTTCTGTTACCCGTGAAGAGATCTACCAGCGTTAATCCATCCAGTCTATTAT
OCT-29	GGAGGTCTGACAGATAGTAG
OCT-30	TCACGGCATTGCGATTAACG
OCT-50	GCGTTAAAGGACACCTCCAGG
OCT-51	GTAATACGACTCACTATAGGTTTCGTTTCGAGCATTCCAG
OCT-52	GAGGACGCTAACAGGAACAATG
OCT-53	GTAATACGACTCACTATAGGTTTACAATCCTTGAGGC
MBO-59	ACTACCATCGGCGCTACGGC
MBO-139	TTACTTAGGATCCCCGACGTCGCGATTATACCTGAAC
MBO-140	CCTGTCCGGTGCCCTCTATGGGTGCTACTTTACGCC
MBO-197	TTACTTAGGATCCCCGCGCTATTCTAACGAGAGAAAAGC
MBO-198	CCTGTCCGGTGCCCTCGCGTAATTTGATTTCTCACAAG
MBO-199	GGGGATCCTAAGTAAGTAAGGAG
MBO-200	AGGGCACCGGACAGGTCG
MBO-203	TTACTTAGGATCCCCCTTAAAGAATAGCCAATGCTCTATTTAAC
MBO-204	CCTGTCCGGTGCCCTTCTGTGAGCCTTTACCGTGG
MBO-207	TTACTTAGGATCCCCATTCCACTGCTCCTTTATAGGTAC
MBO-208	CCTGTCCGGTGCCCTGCAACGCGACGGCGAGAC