Table S1. Primers Used for the Generation of Response Regulator Null Mutants

Strain designation	*Gene*	*Primer Name*	*Primer sequences 5′ to 3′*[a]
B4-007	*lisRK*[b]	KDBlisRKSoeA	**CGG** *GGTACC* TCTTAAAAACTTACTACTTGATCC
		KDBlisRKSoeB	TATTCTATTCATTTGGCCTAACCC
		KDBlisRKSoeC	GGGTTAGGCCAAATGAATAGAATA ATGCGTACATGACGACTAGCC
		KDBlisRKSoeD	**CGC** *GGATCC* ATTATCATCTGCTACAATCGGCAT
B2-078	*agrA*	CRL01agrAsoeA	**G** *GAATT* CGCTCAAGAGTTGAAAATTGATGC
		CRL02agrAsoeB	CGGTAGCATAAATTCATCCCC
		CRL03agrAsoeC	GGGGATGAATTTATGCTACCG AGCTTGAGTTTATAAAAGTGGCC
		CRL04agrAsoeD	**CG** *GGATCC* CACTACGCTTAATCCGATACGT
B2-080	*resD*	SRMresDSoeA	**CGC** *GGATCC* AAACGAAAGATAAAGCCATTG
		SRMresDSoeB	CACTCTAACTTGTTCACTC
		SRMresDSoeC	GAGTGAACAAGTTAGAGTG GGATATAAATTTGAAGTTCCAG
		SRMresDSoeD	**CGG** *GGTACC* TGTCTTGAATTAATTTATTGGC
B2-086	*lmo1022*	BB7 lmo1022SoeA	**GG** *GGTACCT* GCCAATCGAAGTAGAATGGC
		BB8 lmo1022SoeB	TATCATTCGCTTTCCACGTCC
		BB9 lmo1022SoeC	GGACGTGGAAAGCGAATGATA GACCTAGTAGAAAAAAAGTAGCA
		BB10 lmo1022SoeD	**GG** *AAGCTT* GGCATGCTTATCATTTGTCGC
B2-096	*lmo1060*	BB11 lmo1060SoeA	**GG** *GGTACC* AACACCAGAAAAAACACGTG
		BB12 lmo1060SoeB	GAGTATTTTTTCCATATTTGCC
		BB13 lmo1060SoeC	GGCAAATATGGAAAAAATACTC AAAATTCAAACGATTAGAGGT
		BB14 lmo1060SoeD	**G** *TCTAGA* ATTTTTTGTTTCTGTTCCACC
C5-017	*lmo2010*	YC10 lmo2010A	**A** *GGATCC* CCAAGGTTTGCTCTGCAG
		YC11 lmo2010B	ACCTTTGAGAATAAGGGGCTC
		YC12 lmo2010C	GAGCCCCTTATTCTCAAAGGT TCTGGTTATACCGATATGGCTTAT
		YC13 lmo2010D	**C** *GAATTC* CACCCAGTCACTGCTCAT
C5-019	*lmo2583*	YC6 lmo2583A	**G** *GGATCC* CGGCACTATGTAGTTCAGC
		YC7 lmo2583B	CACAAGTTTAAGTATATGCCGATC
		YC8 lmo2583C	GATCGGCATATACTTAAACTTGTG CCCGTGAAAGAATTTGAGCT
		YC9 lmo2583D	**T** *GAATTC* AAAGAAATCGTAGCATTTGACTCG
B2-100	*phoP*	WS5 phoPA	**GA** *GGTACC* CACGGATTGAAATACCAACG
		WS6 phoPB	TTCGGTTATAAAATGGAGAACG
		WS7 phoPC	GTTCTCCATTTTATAACCGAA AAGAATTTTTACCAACGTACTTCC
		WS8 phoPD	**CT** *AAGCTT* GCTTGTAGTTTTGGGTGC
C5-041	*virR*	YC41 lmo1745A	**G** *GGATCC* ACTTCAAATTAGTTACAGATGCTG
		YC42 lmo1745B	TACTACACCAATCTCAAATCCC
		YC43 lmo1745C	GGGATTTGAGATTGGTGTAGTA GCAGAAATTGGTTTGAGCG
		YC44 lmo1745D	**T** *GAATTC* CTCAACTAAAGCTCGACCT
C5-036	*lmo1507*	YC35 lmo1507A	**A** *GGATCC* GCCGATTGAATGGTAAAACCTGA
		YC36 lmo1507B	CGCTTCATAACCCATTTTGCC
		YC37 lmo1507C	GGCAAAATGGGTTATGAAGCG CGTTTACGCCAAAAAATCGC
		YC38 lmo1507D	**GTA** *GTCGAC* GAGAAATCCTTAGGTAAAGGCTGA
C5-033	*degU*	YC29 lmo2515A	**G** *GGATCC* GTGTTTTCCATCGCTATGGATG
		YC30 lmo2515B	AATTCGCTTGATACCTTCGC
		YC31 lmo2515C	GCGAAGGTATCAAGCGAATT GTAACGGCAATCAAGCACG
		YC32 lmo2515D	**CAT** *GTCGAC* CAATGGCTCGTTTGCCAA
B2-104	*kdpE*	WS1 lmo2678A	**CT** *GGTACC* CCATACGATTCTCCAGCGAG
		WS2 lmo2678B	GTTGGGGTTGGATACCGG
		WS3 lmo2678C	CCGGTATCCAACCCCAAC TAGCACAAGCCGCTTGCTG
		WS4 lmo2678D	**GT** *AAGCTT* GACACTGATTGAGCAAGTGC
B2-105	*cheY*	BB27 cheYSoeA	**G** *TCTAGA* CAACTAAAGCATCTGCTTC
		BB28 cheYSoeB	ATTCTTAATCATCGTACGCAT
		BB29 cheYSoeC	ATGCGTACGATGATTAAGAAT GACCGAGTTTTAGAGGCG
		BB30 cheYSoeD	**GG** *GGTACC* AATTTGAATGGCAATACGGTA
B2-102	*cesR*	BB3 cesRSoeA	**GG** *GGTACC* CTGTCATCGCAATTCTAACGG
		BB4 cesRSoeB	AGAAGTTGTCATACTCATTGTCC
		BB5 cesRSoeC	GGACAATGAGTATGACAACTTCT TACAAAATTGAAATCTAAACTGG
		BB6 cesRSoeD	**G** *TCTAGA* GTTCCCGCATATTTTCGATG

[a]Clamp sequences for SOE-A and SOE-D primers are bolded; restriction sites for SOE-A and SOE-D primers are italicized; overhangs complementary to SOE-B primers are underlined.

[b]This mutant includes an internal deletion of the *lisR* gene, which also removed a portion of the ribosome binding site of *lisK* sensory kinase gene.

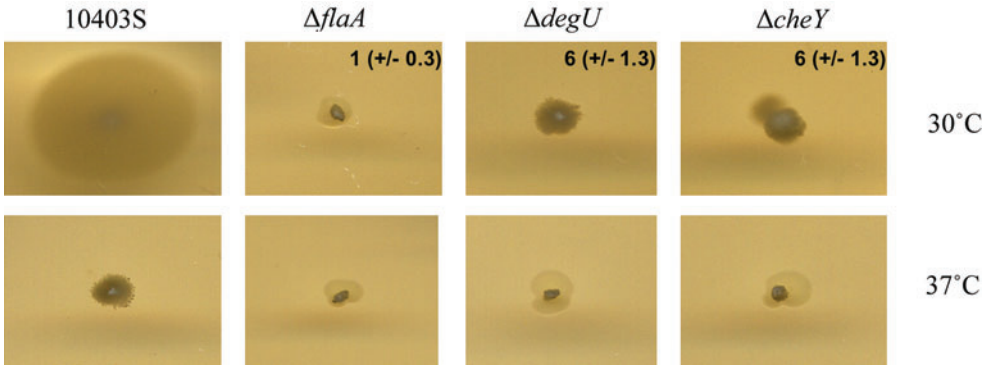

FIG S1. Swarming behavior of parent strain, Δ*degU*, Δ*cheY*, and Δ*flaA* strains grown at 24°C, 30°C, or 37°C. Three independent trials of the motility assays were performed and each strain was tested in triplicate in a given trial. Images show representative results. Pixel counts of the swarming areas were determined to quantitate swarming areas and relative swarming of the mutant strain was expressed relative to parent strain swarming (which was set at 100%). Relative swarming is shown for mutant strains grown at 30°C (values shown represent average +/− standard deviation). No detectable swarming was observed for the mutants at 37°C and hence no relative swarming values are shown.

TABLE S2. SUMMARY OF GENE DELETION EFFECTS ON TRANSCRIPTION LEVELS OF VARIOUS *LISTERIA MONOCYTOGENES* STRESS AND VIRULENCE GENES

	p-Values for the effects of various gene deletion effects on L. monocytogenes *gene transcription measured in stationary phase at:*					
	30°C			*37°C*		
Gene	*sigB*[a]	*prfA*	*sigB*prfA*	*sigB*	*prfA*	*sigB*prfA*
inlA	<0.0001[b]	0.2961	0.3139	<0.0001[b]	0.1282	0.0799
flaA	0.0003[b]	0.7317	0.7263	0.4051	0.9589	0.4016
plcA	0.0475	0.6952	0.5122	0.2593	<0.0001[b]	0.1808
gadA	<0.0001[b]	0.9887	0.8895	<0.0001[b]	0.6512	0.8698

[a]The variables listed in this column represent either a single gene deletions (e.g., "sigB") or interactions between two gene deletions (e.g., "sigB*prfA"). The *p*-values for the single gene deletions measure the individual effect of deleting each respective gene. The "gene*gene" variable measures synergistic deletion effects by comparing the effect of deleting both genes to the effect of deleting either one gene or the other; significant values are marked with [b](p-value ≤ 0.001). The actual data used for these analyses are presented in Figure 4.