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Supplemental Information

Active Lysogeny in *Listeria Monocytogenes*
Is a Bacteria-Phage Adaptive Response
in the Mammalian Environment

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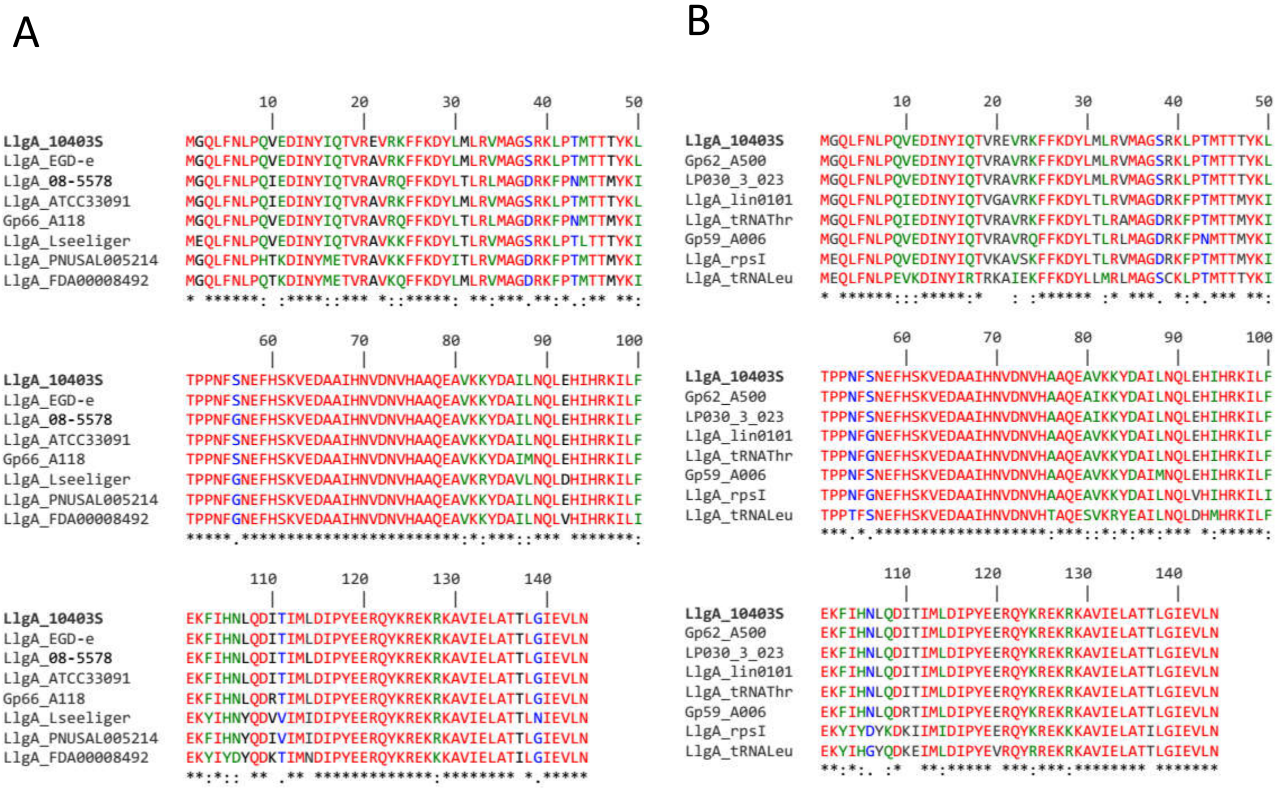

A

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                              10        20        30        40        50
                               |         |         |         |         |
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LlgA_EGD-e            MGQLFNLPQVEDINYIQTVRAVRKFFKDYLMLRVMAGSRKLPTMTTTYKL
LlgA_08-5578          MGQLFNLPQIEDINYIQTVRAVRQFFKDYLTLRLMAGDRKFPNMTTMYKI
LlgA_ATCC33091        MGQLFNLPQIEDINYIQTVRAVRKFFKDYLMLRVMAGSRKLPTMTTTYKL
Gp66_A118             MGQLFNLPQVEDINYIQTVRAVRQFFKDYLTLRLMAGDRKFPNMTTMYKI
LlgA_Lseeliger        MEQLFNLPQVEDINYIQTVRAVKKFFKDYLTLRVMAGSRKLPTLTTTYKI
LlgA_PNUSAL005214     MGQLFNLPHTKDINYMETVRAVKKFFKDYITLRVMAGDRKFPTMTTMYKI
LlgA_FDA00008492      MGQLFNLPQTKDINYMETVRAVKQFFKDYLMLRVMAGDRKFPTMTTMYKI
                      * ******: :****::*** *::*****: **:***.**:*.:** **:

                              60        70        80        90       100
                               |         |         |         |         |
LlgA_10403S           TPPNFSNEFHSKVEDAAIHNVDNVHAAQEAVKKYDAILNQLEHIHRKILF
LlgA_EGD-e            TPPNFSNEFHSKVEDAAIHNVDNVHAAQEAVKKYDAILNQLEHIHRKILF
LlgA_08-5578          TPPNFGNEFHSKVEDAAIHNVDNVHAAQEAVKKYDAILNQLEHIHRKILF
LlgA_ATCC33091        TPPNFSNEFHSKVEDAAIHNVDNVHAAQEAVKKYDAILNQLEHIHRKILF
Gp66_A118             TPPNFSNEFHSKVEDAAIHNVDNVHAAQEAVKKYDAIMNQLEHIHRKILF
LlgA_Lseeliger        TPPNFGNEFHSKVEDAAIHNVDNVHAAQEAVKRYDAVLNQLDHIHRKILF
LlgA_PNUSAL005214     TPPNFGNEFHSKVEDAAIHNVDNVHAAQEAVKKYDAILNQLEHIHRKILF
LlgA_FDA00008492      TPPNFGNEFHSKVEDAAIHNVDNVHAAQEAVKKYDAILNQLVHIHRKILI
                      *****.************************:*:***::*** *******:

                             110       120       130       140
                               |         |         |         |
LlgA_10403S           EKFIHNLQDITIMLDIPYEERQYKREKRKAVIELATTLGIEVLN
LlgA_EGD-e            EKFIHNLQDITIMLDIPYEERQYKREKRKAVIELATTLGIEVLN
LlgA_08-5578          EKFIHNLQDITIMLDIPYEERQYKREKRKAVIELATTLGIEVLN
LlgA_ATCC33091        EKFIHNLQDITIMLDIPYEERQYKREKRKAVIELATTLGIEVLN
Gp66_A118             EKFIHNLQDRTIMLDIPYEERQYKREKRKAVIELATTLGIEVLN
LlgA_Lseeliger        EKYIHNYQDVVIMIDIPYEERQYKREKRKAVIELATTLNIEVLN
LlgA_PNUSAL005214     EKFIHNYQDIVIMIDIPYEERQYKREKRKAVIELATTLGIEVLN
LlgA_FDA00008492      EKYIYDYQDKTIMNDIPYEERQYKREKKKAVIELATILGIEVLN
                      **:*:: ** .** *************:******** *.*****
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B

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                              10        20        30        40        50
                               |         |         |         |         |
LlgA_10403S           MGQLFNLPQVEDINYIQTVREVRKFFKDYLMLRVMAGSRKLPTMTTTYKL
Gp62_A500             MGQLFNLPQVEDINYIQTVRAVRKFFKDYLMLRVMAGSRKLPTMTTTYKL
LP030_3_023           MGQLFNLPQVEDINYIQTVRAVRKFFKDYLMLRVMAGSRKLPTMTTTYKL
LlgA_lin0101          MGQLFNLPQIEDINYIQTVGAVRKFFKDYLTLRVMAGDRKFPTMTTMYKI
LlgA_tRNAThr          MGQLFNLPQIEDINYIQTVRAVRKFFKDYLTLRAMAGDRKFPTMTTMYKI
Gp59_A006             MGQLFNLPQVEDINYIQTVRAVRQFFKDYLTLRLMAGDRKFPNMTTMYKI
LlgA_rpsI             MEQLFNLPQVEDINYIQTVKAVSKFFKDYLTLRVMAGDRKFPTMTTMYKI
LlgA_tRNALeu          MEQLFNLPEVKDINYIRTRKAIEKFFKDYLLMRLMAGSCKLPTMTTTYKI
                      * ******:::*****:*   : :****** :* ***. *:*.*** **:

                              60        70        80        90       100
                               |         |         |         |         |
LlgA_10403S           TPPNFSNEFHSKVEDAAIHNVDNVHAAQEAVKKYDAILNQLEHIHRKILF
Gp62_A500             TPPNFSNEFHSKVEDAAIHNVDNVHAAQEAIKKYDAILNQLEHIHRKILF
LP030_3_023           TPPNFSNEFHSKVEDAAIHNVDNVHAAQEAIKKYDAILNQLEHIHRKILF
LlgA_lin0101          TPPNFGNEFHSKVEDAAIHNVDNVHAAQEAVKKYDAILNQLEHIHRKILF
LlgA_tRNAThr          TPPNFGNEFHSKVEDAAIHNVDNVHAAQEAVKKYDAILNQLEHIHRKILF
Gp59_A006             TPPNFSNEFHSKVEDAAIHNVDNVHAAQEAVKKYDAIMNQLEHIHRKILF
LlgA_rpsI             TPPNFGNEFHSKVEDAAIHNVDNVHAAQEAVKKYDAILNQLVHIHRKILI
LlgA_tRNALeu          TPPTFSNEFHSKVEDAAIHNVDNVHTAQESVKRYEAILNQLDHMHRKILF
                      ***.*.*******************.***::*:*:**:*** *:*****:

                             110       120       130       140
                               |         |         |         |
LlgA_10403S           EKFIHNLQDITIMLDIPYEERQYKREKRKAVIELATTLGIEVLN
Gp62_A500             EKFIHNLQDITIMLDIPYEERQYKREKRKAVIELATTLGIEVLN
LP030_3_023           EKFIHNLQDITIMLDIPYEERQYKREKRKAVIELATTLGIEVLN
LlgA_lin0101          EKFIHNLQDITIMLDIPYEERQYKREKRKAVIELATTLGIEVLN
LlgA_tRNAThr          EKFIHNLQDITIMLDIPYEERQYKREKRKAVIELATTLGIEVLN
Gp59_A006             EKFIHNLQDRTIMLDIPYEERQYKREKRKAVIELATTLGIEVLN
LlgA_rpsI             EKYIYDYKDKIIMIDIPYEERQYKREKKKAVIELATILGIEVLN
LlgA_tRNALeu          EKYIHGYQDKEIMLDIPYEVRQYRREKRKAVIELATTLGIEVLN
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Figure S1. Comparison of ϕ10403S LlgA orthologs. Related to Figure 6. **A.** Comparison of ϕ10403S LlgA orthologs encoded by selected *comK* associated prophages of *Listeria*. Alignment length: 144 residues. Identical residues (marked with asterisks and shown in red) are 75.69 % (109/144), strongly similar residues (marked with colons and shown in green) are 13.89 % (20/144), weakly similar (marked with dots and shown in blue) are 3.47 % (5/144), and different are 6.94 % (10/144). LlgA_10403S (LMRG_01529, 144 aa), *comK* associated prophage ϕ10403S, *L. monocytogenes* str. 10403S. LlgA_EGD-e (lmo2303, 144 aa), *comK* associated prophage, *L. monocytogenes* str. EGD-e. LlgA_08-5578 (LM5578_2501, 144 aa), *comK* associated prophage, *L. monocytogenes* str. 08-5578. LlgA_ATCC33091 (EHN62215.1, 144 aa), *comK* associated prophage, *L. innocua* str. ATCC 33091. Gp66_A118 (Gp66, NP_463531.1, 144 aa), *comK* associated *Listeria* phage A118. LlgA_Lseeliger (OLQ23568.1, 144 aa), *comK* associated prophage, *L. seeligeri* str. BCW_4759. LlgA_PNUSAL005214 (ECK6838613.1, 144 aa), *comK* associated prophage, *L. monocytogenes* str. PNUSAL005214. LlgA_FDA00008492 (EAC8843104.1, 144 aa), *L. monocytogenes* str. FDA00008492. **B.** Comparison of ϕ10403S LlgA orthologs encoded by selected non-*comK* associated prophages of *Listeria*. Alignment length: 144 residues. Identical residues (marked with asterisks and shown in red) are 70.14 % (101/144), strongly similar residues (marked with colons and shown in green) are 15.97 % (23/144), weakly similar (marked with dots and shown in blue) are 3.47 % (5/144), and different are 10.42 % (15/144). LlgA_10403S (144 aa, LMRG_01529), *comK* gene prophage ϕ10403S, *L. monocytogenes* str. 10403S. Gp62_A500 (144 aa, Gp62, YP_001468447.1), tRNA-Lys gene *Listeria* phage A500. LP030_3_023 (144 aa, YP_009044669.1), tRNA-Lys gene *Listeria* phage LP-030-3. LlgA_lin0101 (144 aa, lin0101), tRNA-Lys gene prophage, *L. innocua* str. Clip11262. LlgA_tRNAThr (144 aa, LMOSLCC7179_2533), tRNA-Thr gene prophage, *L. monocytogenes* SLCC 7179 (serotype 3a). Gp59_A006 1 (144 aa, Gp59, YP_001468899.1), tRNA-Arg gene *Listeria* phage A006. LlgA_rpsI (144 aa, EAV9834825.1), *rpsI* gene prophage, *L. monocytogenes* L7-0863. LlgA_tRNALeu (144 aa, EAC7181297.1), tRNA-Leu prophage, *L. monocytogenes* PNUSAL001712 (serotype 4b).

Table S1. Lytic induction of ϕ10403S and ϕEGDe *comK*-prophages by mitomycin C. Related to Figure 1.

Strain/treatment	**PFU/ml**	**STD**
Lm 10403S -MC	108,500	48,000
Lm 10403S +MC	444,500,000	55,700,00
Lm EGDe -MC	0	0
Lm EGDe +MC	15	21

Table S2: A list of ϕ10403S genes and annotations. Related to Figure 2A.

Gene	Strand	Annotation/Putative function	Detected transcripts (by RNA-seq)	Ortholog in A118
LMRG_01560	+	N-terminus of competence regulator ComK		
LMRG_01559	-	Conserved hypothetical protein	+	-
LMRG_01558	-	Conserved hypothetical protein	+	-
rli43-like*	-	Ortholog of Rli43 of *Lm* EGDe	-	-
LMRG_01557	-	Putative secreted protein	-	-
rli34-like*	+	Rli34 ortholog of *Lm* EGDe	-	-
LMRG_01556	-	Putative acetyltransferase	+	gp27
LMRG_01555	-	Conserved hypothetical protein	+	gp26
LMRG_01554	-	Endolysin	+	gp25
LMRG_01553	-	Holin	+	gp24
LMRG_01552	-	Membrane-associated protein	+	gp23
LMRG_01551	-	Conserved hypothetical protein	+	gp22
LMRG_01550	-	Hypothetical protein	+	gp21
LMRG_01549	-	Secreted receptor-binding protein (RBP)	+	gp20
LMRG_01548	-	Secreted pectin-lyase-fold protein	+	gp19
LMRG_01547	-	Tail or base plate protein with a putative endopeptidase activity	+	gp18
LMRG_01546	-	Tail protein	+	gp17
LMRG_01545	-	Tape-measure protein	+	gp16
LMRG_01544	-	Conserved hypothetical protein	+	gp15
LMRG_01543	-	Tail assembly chaperone protein	+	gp14
LMRG_01542	-	Cell surface and adhesion associated protein	+	gp13
LMRG_01541	-	Conserved hypothetical protein	+	gp12
LMRG_01540	-	Minor capsid protein	+	gp11
LMRG_01539	-	Minor capsid protein	+	gp10
LMRG_01538	-	Minor capsid protein	+	gp9
LMRG_01537	-	Head-tail connector protein YqbG	+	gp8
LMRG_01536	-	Capsid protein	+	-
LMRG_01535	-	Minor structural protein of GP20-family, scaffolding protein	+	gp5
LMRG_01534	-	Minor capsid protein	+	gp4
LMRG_01533	-	Portal protein	+	gp3
LMRG_01532	-	Terminase large subunit, TerL, XtmB family	+	gp2
LMRG_01531	-	Terminase small subunit, TerS, XtmA family	+	gp1
LMRG_01530	-	Membrane-associated protein	+	gp68
rliG-like*	-	RliG ortholog of *Lm* EGDe	+	*
LMRG_01529	-	Late lytic genes activator, LlgA, transcriptional regulatory protein of the ArpU family	+	gp66
LMRG_01528	-	Conserved hypothetical protein	+	gp65
LMRG_02921	-	Conserved hypothetical protein	+	-
LMRG_01527	-	Conserved hypothetical protein	+	-
LMRG_01526	-	DnaD-like DNA replication protein, replicase	+	gp49
LMRG_01525	-	Recombinational DNA repair protein RecT, recombinase	+	gp48
LMRG_01524	-	Predicted endonuclease	+	gp47
rli99-like*	+	Rli99 ortholog of *Lm* EGDe	-	-
rli140-like*	-	Rli140 ortholog of *Lm* EGDe	+	-
gp46-like*	-	Hypothetical protein	-	gp46
LMRG_01510	+	C-terminus of competence regulator ComK		

Table S2: continued

LMRG_01523	-	Conserved tail-fibre system protein	+	gp45
LMRG_01522	-	Recombination Directionality Factor (RDF)	+	gp44
LMRG_01521	-	Conserved hypothetical protein	+	gp43
LMRG_02920	-	Putative anti-repressor protein	+	gp42
lasRNA-like*	+	Long anti-sense RNA of LMRG_01516-01517-01518-02984 as identified in EGDe *comK*-prophage. Includes a putative ORF similar to gp41-1 of A118	+	-
LMRG_02984	-	Putative membrane-associated protein	+	*
LMRG_01518	-	Hypothetical protein	+	gp41
LMRG_01517	-	Conserved hypothetical protein	+	-
LMRG_01516	-	Conserved hypothetical protein	+	-
LMRG_01515	-	Cro-like transcriptional regulator, XRE-family protein	+	gp36-1**
LMRG_01514	+	CI-like transcriptional regulator, XRE-family protein	+	gp36**
rli141-like*	+	Rli141 ortholog of *Lm* EGDe	-	-
LMRG_02918	+	Conserved hypothetical protein	+	-
LMRG_01513	+	Putative secreted Lpt-like lipoprotein	+	gp32
LMRG_01512	+	Putative DNA helicase	+	-
LMRG_01511	+	Site-specific phage serine integrase	+	gp31

***   present but not annotated**
**** low similarity**

Table S3. ϕ10403S transcriptional response under lysogenic and lytic conditions. Related to Figure 2B-C.

Transcription Start	Translation Start	Translation Stop	Transcription Stop	Strand	Genes	**Time post UV irradiation**					
						0h	**1h**	**2h**	**3h**	**4h**	**5h**
	2357429	2357878		+	comk C'	7	7	9	5	4	1
	2356053	2357411	2357411	+	LMRG_01511	58	40	40	49	50	24
2354478	2354478	2355992	2355992	+	LMRG_01512	29	33	26	27	31	15
2353710	2353710	2354246		+	LMRG_01513	41	77	59	31	31	21
2353494	2353494	2353661		+	LMRG_02918	24	55	38	24	24	16
2352860	2352860	2353336	2353336	+	LMRG_01514	79	134	102	34	31	20
2352691	2352691	2352488	2352488	-	LMRG_01515	14	32	109	195	312	226
2352487	2352455	2352261	2352250	-	LMRG_01516	16	37	120	268	427	318
2352249	2352249	2351965	2351947	-	LMRG_01517	19	50	149	336	520	397
2351946	2351939	2351658	2351653	-	LMRG_01518	15	43	130	302	450	371
2351632			2351664	+	lasRNA	388	83	125	283	371	452
2351652	2351652	2351377		-	LMRG_02984	17	52	161	351	579	438
	2351395	2350616	2350576	-	LMRG_02920	25	53	176	379	554	425
2350510	2350494	2349961		-	LMRG_01521	15	35	121	229	333	259
	2349964	2349749	2349743	-	LMRG_01522	9	16	66	151	253	197
2349647	2349640	2349452	2349446	-	LMRG_01523	9	17	74	176	276	201
2349421			2349324	-	rli140	21	37	155	320	485	368
2349221	2349219	2348260		-	LMRG_01524	14	31	124	280	402	324
	2348260	2347445	2347426	-	LMRG_01525	23	56	206	437	620	485
2347425	2347425	2346499		-	LMRG_01526	21	46	163	359	509	389
	2346502	2346251	2346251	-	LMRG_01527	16	39	144	295	426	344
2346250	2346248	2345724	2345704	-	LMRG_02921	14	43	137	286	434	331

Table S3 **continued**

2345686	2345676	2345512	2345512	-	LMRG_01528	13	35	106	244	375	297
2345511	2345493	2345059	2345000	-	LMRG_01529	15	41	146	278	412	304
2344909			2344775	-	rliG	126	496	1366	1943	1944	1327
2344696	2344692	2343982	2343982	-	LMRG_01530	14	32	78	215	332	190
2343898	2343898	2343356		-	LMRG_01531	11	23	74	184	321	181
	2343387	2342056	2342044	-	LMRG_01532	8	19	55	150	263	145
2342043	2342043	2340553	2340553	-	LMRG_01533	14	32	100	251	443	257
2340552	2340547	2339408	2339408	-	LMRG_01534	16	38	115	296	503	293
2339388	2339329	2338739		-	LMRG_01535	31	79	256	757	1343	807
	2338739	2337738	2337738	-	LMRG_01536	29	73	238	733	1261	754
2337737	2337719	2337324		-	LMRG_01537	23	70	211	710	1235	755
	2337324	2336962		-	LMRG_01538	22	67	211	667	1161	717
	2336962	2336624		-	LMRG_01539	31	89	272	860	1490	914
	2336624	2336217	2336215	-	LMRG_01540	22	59	186	648	1085	695
2336214	2336214	2335777	2335777	-	LMRG_01541	25	69	223	672	1132	729
2335776	2335754	2335515	2335515	-	LMRG_01542	28	83	255	808	1370	876
2335514	2335460	2335038	2335038	-	LMRG_01543	14	31	117	381	700	371
2335034	2335032	2334430	2334425	-	LMRG_01544	12	30	100	317	591	309
2334419	2334419	2329056	2329056	-	LMRG_01545	10	22	73	220	430	243
2329055	2329054	2328236	2328228	-	LMRG_01546	8	24	66	201	403	294
2328227	2328227	2327202		-	LMRG_01547	8	23	63	204	396	272
	2327201	2326173		-	LMRG_01548	7	20	54	168	334	242
	2326173	2325100	2325100	-	LMRG_01549	6	19	48	140	288	214
2325093	2325088	2324771	2324771	-	LMRG_01550	4	13	38	124	276	199
2324770	2324766	2324608	2324590	-	LMRG_01551	6	16	51	163	357	262
2324579	2324579	2324214	2324214	-	LMRG_01552	3	11	33	109	241	197
2324213	2324201	2323920		-	LMRG_01553	3	12	35	104	230	187

Table S3 **continued**

	2323920	2323069	2323069	-	LMRG_01554	5	20	54	172	343	301
2322830	2322830	2322654		-	LMRG_01555	300	273	249	197	333	241
	2322667	2322068	2322068	-	LMRG_01556	184	185	150	119	187	160
	2321545	2320622		-	LMRG_01557	2	2	2	2	3	0
2320365	2320365	2320132		-	LMRG_01558	29	318	295	194	261	211
	2320135	2319938	2319937	-	LMRG_01559	47	400	360	298	370	330
	2319659	2319937	2319937	+	comK N'	7	16	10	7	5	4

Table S4: A list of ϕ10403S nCounter probes. Related to Figure 3.

Gene	Probe sequence
LMRG_01559	TACGTCTGCTACGTAGAAGGAAAAGATAAAGCTATAGAAAAGCTGTTTGCCGAATTATTTGAAACAAGAAAGTTAAAGACCTTACAAAGGCGTATAAAAA
LMRG_01558	ATAGTATTAGCAGACGCGCTTAGGCGCAATTGGTCAATAGAAGTACTGTTTTTAAAGAACAATCATCACGTGCGATACAAGTATGTCGTGCCTGTCCACA
LMRG_01557	TGGTTTAACTATGCGTTATACTTCAAAGGCAGGAACTTGGGATACTTCGGCATGGAAAGTAGTTTCCGCCAGTACTAAAACGACAGATAAATATGCGCAG
LMRG_01556	GGAGTAATCGAGTTTACAAGAAGAAACGATAAATTTGTCCGGCATACACCGGGTTTTGATAGTAATACTATGTTTGCTGATGGAGGGAATCAAACCTATC
LMRG_01555	TTTCGGAAAGAAAAGCAATTGCTAGTATAAGAGAGAATTTTGCACAAATTCCAAAGATGAACATTACTAATGACAAGAGATAA
LMRG_01554	TTGGGGCGCTTATCGTTCAGATAAAGGCAAGAAATTTGTGGCAAAAGCGAAGGCACTTGGATTTGAATGGGGCGGTGATTGGTCTGGATTTGTAGACAAT
LMRG_01553	GTGGCTTCCGACTGTTAGCATACTTATTGGTGCTATTCTGGGCGCATTAGCAACGTTTTTGGATGGCTCTGGATCGCTTGCAACGATGATTTGGGCAGGT
LMRG_01552	TATAAGTACGATGAACGAACAACAGCGATTGATGGATAGGCAAAATGACATGATGAAACAGCAACAACAATCAATTGACAGCTTGTCTAAATCAGTCGGA
LMRG_01551	ATTGAAGAAGTTCCTGCGAATTTACGAGGTCAGGTAAAAGCAAAAGTGGATGAGTTAAAACAAGAACAACAACGAATACAGTCAGAAGAAATAGAAGCCG
LMRG_01550	ACCTTCCATAATAGAAAACGGCATAGCAAGAGCAATGTATTATCCGCGTTGGGATGGGGATGATTGGGACGAAGACAAGACGAGATGGGAATTAGAAAAC
LMRG_01549	AACACAAGCATTCATGTGACAATGACTGATAAAACGAATTGGAATGCAAAAGAAAATACCGCGGGATCGCAAGCAAAAGCGGATAGTGCATTAAACTCTG
LMRG_01548	AACTTCGAATGTCGGCTTAAAAGCTGCTAGCGGAGGCATTTTGGTTAAGTCTGGTACGCCAGTTTTAAACGCTACTACCGCAGAATTGAAACAAGCGGGA
LMRG_01547	ACACTGTTGCAGGTAATATGCAACGGCGTCTTAAGCTAGAATTACAAGACTATCCAGCGACGACAGGAAGTGTGACCTTAAAACAATACTACGATTGTGG
LMRG_01546	CATTCTAAAACGCCTGGTAAAAAATATAGAGTACATCCGAGTGGCGTTGGTATTGACCGCAAAGCGCCGGGATACGCAGATTTGACACTTGAATTCGATG
LMRG_01545	ACAGCAGTGATAGGGTCTGTAGTGGCAGTTCTTTATGGCATGTATACCGCCTTCAAGGAAAACACGGCAGGGATTAAAGGCTTTTTATCTGGTATGTGGG
LMRG_01544	GATGGTTTGCTTTATGATATCGACGGAAACAAGATGCCAAGCGCTACAAACAATGAGGATGCGGAAGAAATTGCTTCATATTCATTAACGCAAGATGCGG
LMRG_01543	ACTGGACAAATTGGATAAATACAACTTAGACGAATTAGGCGAAATGACTATAAATGATTACGATGTCTTAATGGACAATGTCAGAGAGGCGCTCAAACAC
LMRG_01542	GTAACTTTCACTTCTTCAAACCCACCAAAGGCAAAAGTAAATGCTGCTGGAGTGGTTGAAGGTGTAGCAGAAGGAACAGCAAATATTACTGTCGCATCTA
LMRG_01541	GATGGGTCAGATAACACCGAAGAGCAAGGCGATTATGACGGTGATGGCAACGAAAAAACGGTTGTGCTAGGTTACTCAGAAGCTTACACATTCGAAGGGA
LMRG_01540	GAAATTAAGAACAGCGATATTAAAACCTGAATCGATTGCTTTGCTACTGACTCCAAATAACGCCAAACAAGGTTATCAAGACGGCTCTTATGAGCGGTCT
LMRG_01539	CCGATTAAAGTACGTGTAGACCTCTCGAAAGCAAAAGGGAGCGTAAAAAAGGCGAAAGAAAGAGGTCAGTTTGCTTTAATTAACCAAGCGGCTGCGGATA
LMRG_01538	CAAATCGCGGGATTATCTGATAGTGATAGATATGATGCGGTTATTTTTATTGATGCAGTGAATAGTATGAACGTGCCAGATAACTTTATAAGTAGATCTA
LMRG_01537	TACAGTTAGCTACTTGTAATCAAATCGAGTATTTCAAAGAGGCTGGCGGAACAAGTGAGTTAGCTGTTTCTAAGCCGGATAACGTATCAATCGGAAGAAC
LMRG_01536	AACGAACTTGCGGCGGTCATTTCAGGAGACGACCCTTTAGACGCTTTAATGGGCAAAATCGCTTCTTGGTGGATGCGTCGAGAGCAAACTGTACTAATTT
LMRG_01535	ACGGTAAGGACATTACAGCTGCTAAACAACAATTATCTGAGGTGGAAGCAGAGAGAGATGGCTTAAAAAGCCAGCTAACACAACGGGACAAAGATATTGA
LMRG_01534	CGCTTGTGGATAAAGCTAATAAGCGATGGACGCCGGAATCATACGTTAAAACAGTAACTAGGACAACCGTCAACAGCGTTTATAACAGCATTGAAGACGA
LMRG_01533	TGTTAAAACGGCTGTTAACCTAGACGGCTCAACCACGCAGTATTTCGATTCAACTGATGAAGCATTCTTTTTATATCAAGGTGACCAAGACGACAACGGC

Table S4: continued

LMRG_01532	AGTCGCCAATGGAAATTGTCCACAAAACTTGGGGGACAGGCTTCTATTTCTCTGGTTGTGATGATCCCGCTAAACTAAAATCGATGAAAATTCCAGTCGG
LMRG_01531	ACGATTTGCGGATGAATATATAAAATGCGGTAATGCTACAGAAGCCGCTCGCTTGGCTGGTTATAGTTTGAAAACGGCTAATCGTATAGCGACCGAAAAC
LMRG_01530	GCTAGTATAGATGAGTTGGAAATATACGAAGCCATTATAAAAAAACACAGTATATCAGATTCTAAAGTGAAGACCCAGTTGGAAAAATACAGAATAAGCA
rliG	TATGATGATATAGCAGGAGATTGCTATGTTGCCCGGCAGAGGCTTTGTATCTGGCCACTAGTCTCAACAGATGACGACACTTCTGTTCAATCTCATATCC
LMRG_01529	TCAAAAGTAGAAGATGCTGCAATTCATAATGTCGATAACGTTCATGCAGCACAAGAAGCGGTTAAAAAATACGATGCTATTTTGAATCAGCTTGAGCACA
LMRG_02921	TGGGAAATGATTTCTTCACAACAGAGCCACCCCTTAATTGTGACTTAATGATTAGTAACCCGCCTTTTTCACAACAAAACGAAATAATAGAGCGTAGTTT

* presenting only probes that worked experimentally (52 in total)

Table S5. ϕ10403S transcriptional response during active lysogeny. Related to Figure 3.
Gene Expression Data Analysis generated by nSolver Analysis Software 4.0

Gene	RQ relative to lysogeny		
	Intracellular 2h vs. Log phase	Intracellular 4h vs. Log phase	Intracellular 6h vs. Log phase
LMRG_01511	0.93	0.57	0.59
LMRG_01512	1.10	0.99	0.6
LMRG_01513	1.39	1.13	0.74
LMRG_01514	1.59	1.5	1.46
LMRG_01515	1.78	2.19	6.82
LMRG_1516	1.91	2.25	6.69
LMRG_1517	1.78	1.96	6.06
LMRG_01518	1.82	2.08	6.53
lasRNA	0.47	0.19	0.15
LMRG_2984	2.28	1.87	5.58
LMRG_02920	1.83	1.65	4.85
LMRG_01521	1.71	1.58	5.48
LMRG_01522	1.76	1.65	5.62
LMRG_01523	1.62	1.68	6
rli140	2.29	2.42	7.74
LMRG_01524	1.75	1.51	5.3
LMRG_01525	1.53	1.23	4.74
LMRG_01526	1.82	1.47	5.72
LMRG_01527	1.87	1.46	5.79
LMRG_02921	2.39	1.82	5.97
LMRG_01529	1.82	1.36	5.64
rliG	0.78	0.54	1.23
LMRG_01530	2.26	1.94	3.86
LMRG_01531	2.37	0.79	1.21
LMRG_01532	2.13	0.73	1.04
LMRG_01533	1.96	0.49	0.76
LMRG_01534	1.90	0.43	0.81
LMRG_01535	0.91	0.22	0.32
LMRG_01536	0.91	0.2	0.26
LMRG_01537	0.92	0.21	0.29
LMRG_01538	0.89	0.21	0.24
LMRG_01539	0.92	0.22	0.31
LMRG_01540	0.91	0.22	0.27
LMRG_01541	0.94	0.22	0.27
LMRG_01542	1.01	0.24	0.36
LMRG_01543	0.96	0.25	0.32
LMRG_01544	1.11	0.3	0.41
LMRG_01545	1.30	0.35	0.67
LMRG_01546	1.26	0.38	0.63
LMRG_01547	1.49	0.46	0.72
LMRG_01548	2.03	0.61	1.05
LMRG_01549	1.59	0.5	0.89
LMRG_01550	1.43	0.54	0.98
LMRG_01551	1.37	0.43	0.63
LMRG_01552	1.37	0.4	0.62
LMRG_01553	1.16	0.39	0.64
LMRG_01554	1.56	0.49	0.73
LMRG_01555	1.82	1.99	1.63
LMRG_01556	2.26	2.13	1.74
LMRG_01557	1.61	1.78	1.08
LMRG_01558	14.10	15.85	21.69

Table S6: List of strains and mutants used in this study. Related to all Figures

Strain	**Description**
XL-1 blue	*recA1 endA1 gyrA96 thi-1 hsdR17 supE44 relA1 lac* [F' *proAB lacIqZΔM15 Tn10* (*TetR*)]
SM-10	Conjugation donor; F-*thi*-1 *thr*-1 *leuB6 recA tonA21 lacY1 supE44 (Muc*+) λ-[*RP4-2*(*Tc::Mu*)] *Kan*^{R} *Tra*+
Lm 10403S	*Listeria monocytogenes* Wild Type, Strp^{R} (WT)
Bs PY79	*Bacillus subtilis* PY79 Wild type (AES101)
Δϕ	*Lm* 10403S cured of ϕ10403S (Cured strain) DPL-4056
Δ*comK*	*Lm* 10403S deleted of *comK* gene and cured of ϕ10403S
Bs-amyE::Phs-llgA-terS	*Bs* PY79 *amyE::Phs-RBS5-llgA-terS-spec*
WT-pPL2-*cI*-like	*Lm* 10403S harboring pPL2 integrative plasmid constitutively expressing ϕ10403S CI-like repressor (*LMRG_01514*) under Pconst promoter (Argov et al., 2017b)
Δ*LMRG_01511*	*Lm* 10403S Δ*LMRG_01511* (Rabinovich et al., 2012)
Δ*LMRG_01512*	*Lm* 10403S Δ*LMRG_01512*
Δ*LMRG_01513*	*Lm* 10403S Δ*LMRG_01513*
Δ*LMRG_02918*	*Lm* 10403S Δ*LMRG_02918*
Δ*LMRG_01515*	*Lm* 10403S Δ*LMRG_01515*
Δ*LMRG_01516*	*Lm* 10403S Δ*LMRG_01516*
Δ*LMRG_01517*	*Lm* 10403S Δ*LMRG_01517*
Δ*LMRG_01518*	*Lm* 10403S Δ*LMRG_01518*
Δ*LMRG_02984*	*Lm* 10403S Δ*LMRG_02984*
PlasRNA	*Lm* 10403S harboring a mutated -10 site (GCTATAA→ AGAGTAA) in the *lasRNA* promoter
Δ*LMRG_02920*	*Lm* 10403S Δ*LMRG_02920*
Δ*LMRG_01521*	*Lm* 10403S Δ*LMRG_01521*
Δ*LMRG_01522*	*Lm* 10403S Δ*LMRG_01522*
Δ*LMRG_01523*	*Lm* 10403S Δ*LMRG_01523*
Δ*LMRG_01524-25*	*Lm* 10403S Δ*LMRG_01524* and *LMRG_01525*
Δ*LMRG_01525*	*Lm* 10403S Δ*LMRG_01525*
Δ*LMRG_01526*	*Lm* 10403S Δ*LMRG_01526*
Δ*LMRG_01527*	*Lm* 10403S Δ*LMRG_01527*
Δ*LMRG_02921*	*Lm* 10403S Δ*LMRG_02921*
Δ*LMRG_01528*	*Lm* 10403S Δ*LMRG_01528*
Δ*LMRG_01529*	*Lm* 10403S Δ*LMRG_01529 (llgA)*
Δ*rliG*	*Lm* 10403S Δ*rliG*
Δ*LMRG_01530*	*Lm* 10403S Δ*LMRG_01530*
Δ*LMRG_01531*	*Lm* 10403S Δ*LMRG_01531*
Δ*LMRG_01535*	*Lm* 10403S Δ*LMRG_01535*
Δ*LMRG_01551*	*Lm* 10403S Δ*LMRG_01551*
Δ*LMRG_01552*	*Lm* 10403S Δ*LMRG_01552*
Δ*LMRG_01553*	*Lm* 10403S Δ*LMRG_01553*
Δ*LMRG_01554*	*Lm* 10403S Δ*LMRG_01554*
(*lysis*)ϕ	*Lm* 10403S Δ*LMRG_01552, LMRG_01553* and *LMRG_01554*
Δ*LMRG_01555-56*	*Lm* 10403S Δ*LMRG_01555* and *LMRG_01556*
Δ*LMRG_01557*	*Lm* 10403S Δ*LMRG_01557*
Δ*LMRG_01558-9*	*Lm* 10403S Δ*LMRG_01558* and *LMRG_01559*
WT-pPL2-PactA-*llgA*	*Lm* 10403S harboring pPL2 integrative plasmid expressing *llgA* (*LMRG_01529*) under the promoter of the *actA* gene
Δϕ-pPL2-PactA-*llgA*	*Lm* 10403S Δϕ (Cured strain) harboring pPL2 integrative plasmid expressing *llgA* (*LMRG_01529*) under the promoter of the *actA* gene
(*lysis*)ϕ-pPL2-PactA-*llgA*	*Lm* 10403S (*lysis*)ϕ harboring pPL2 integrative plasmid expressing *llgA* (*LMRG_01529*) under the promoter of the *actA* gene
WT-pPL2-P*tetR-llgA-his*	*Lm* 10403S harboring pPL2 integrative plasmid expressing *llgA* (*LMRG_01529*) tagged with C'-6His under the *tetR* inducible promoter
Δϕ-pPL2-P*tetR-llgA-his*	*Lm* 10403S Δϕ (Cured strain) harboring pPL2 integrative plasmid expressing *llgA* (*LMRG_01529*) tagged with C'-6His under the *tetR* inducible promoter
(*lysis*)ϕ-pPL2-P*tetR-llgA-his*	*Lm* 10403S Δ*LMRG_01552-01554* harboring pPL2 integrative plasmid expressing *llgA* (*LMRG_01529*) tagged with C'-6His under the *tetR* inducible promoter
WT-ϕ*pheS*Km*	*Lm* 10403S with *pheS** (mutated phenylalanyl-tRNA synthetase) and Kanamycin resistance gene inserted in the ϕ10403s genome downstream to *LMRG_01556* (Argov et al., 2017b)
LMRG_01526-ϕ*pheS*Km*	*LMRG_01526* with *pheS** (mutated phenylalanyl-tRNA synthetase) and Kanamycin resistance gene inserted in the ϕ10403S genome downstream to *LMRG_01556*