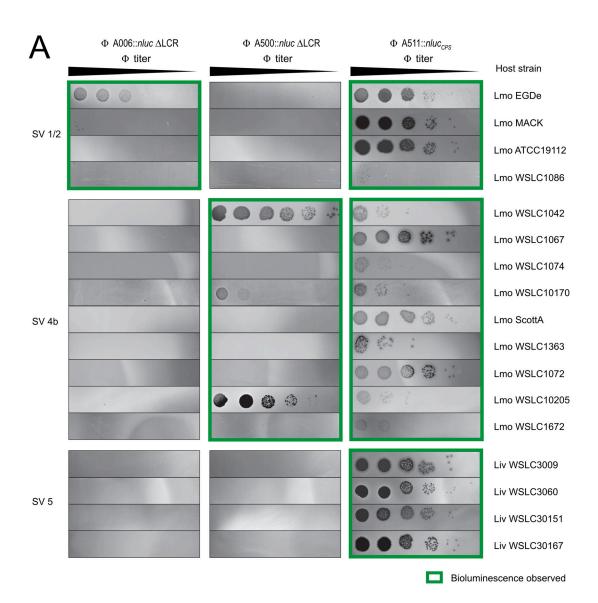
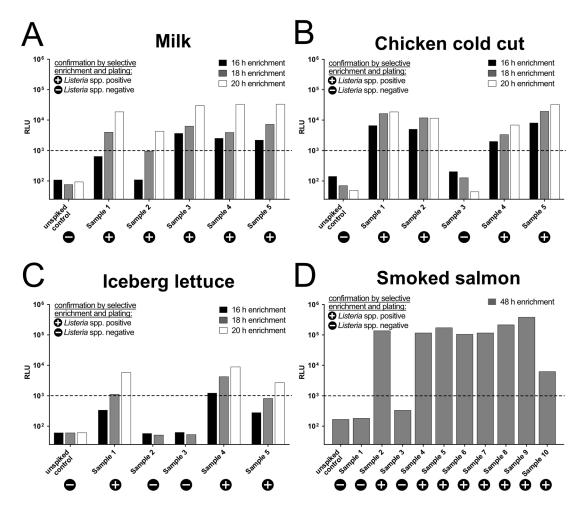


Supplementary Figure S1: Genotypic and phenotypic analysis of engineered phages used in this study. PCR verification and plaque morphologies of A006-derived phages (**A**) and A500-derived phages (**B**) are shown. Deletions of the lysogeny control regions (LCR-PCR) and correct insertion of luciferase sequences (Luciferase-PCR) were verified by PCR and plaque morphologies visualized from soft-agar overlays after 24 h of incubation. (**C**) Upon CRISPR-Cas-mediated counterselection, five individual plaques were picked and insertion of the heterologous *nluc* gene sequence into the *ply*- or *cps*-locus of A511-derived candidates was verified by PCR ("PLY locus PCR" and "CPS locus PCR", respectively). Primers are listed in Table S1.



Supplementary Figure S2: Phagetyping and SV differentiation of *Listeria* spp. by bioluminescence measurements and spot-on-the-lawn plaque assays. (A) Indicated strains covering *Listeria* SVs 1/2, 4b, and 5 were infected with serial dilutions of the indicated phage using spot-on-the-lawn assays and plaque formation was visualized 24 h p.i. Host strains that produced a positive signal with the indicated phages in the bioluminescence assays are highlighted within green boxes.



Supplementary Figure S3: Bioluminescence-based detection of *Listeria* in artificially contaminated foods. Bioluminescence (RLU) of artificially spiked milk (A), chicken cold cut (B), and iceberg lettuce (C) are shown after selective enrichment in full LEB (16, 18, and 20 h) and compared to results from culture-based detection of the same samples. Spiked salmon samples (D) were enriched for 48 h in 1/4 LEB. For each food matrix, one unspiked control was included. (+) culture positive for *Listeria*; (-) culture negative for *Listeria*. Samples were contaminated with \pm 1 CFU / 25 g of food (quantified values: 1.4 \pm 0.3 in milk, 1.1 \pm 0.1 in chicken cold cut, 1.4 \pm 0.1 in iceberg lettuce and 1.0 \pm 0.2 in smoked salmon, errors are STDEV of technical triplicates). Dotted lines = threshold for positive samples.

Supplementary Table S1. *Listeria* detection in potentially contaminated food samples from commercial sources. Exclusion = experimental clarification of unclear selective plating results; - = no growth or negative results; + = growth or positive results; +/- = some growth, untypical morphology; *C. citreum* = *Curtobacterium citreum*.

Food sample	3M	Selectiv	e plating	Repor	ter phage	Exclusion	API test
(anonym. vendor)	MDS	Oxford	ALOA	Result	FC-value	· 	API® Listeria
Pineapple pieces	-	-	-	-	1.42	nA	
Salad with beans and pomegranate	-	-	-	-	2.15	nA	
Alfa-alfa sprouts	-	_	-	_	1.20	nA	
Cheese "Mostkäse"				_	1.80	nA	
Salad with carots,	-	-	-	-	1.50	nA	
shaker Salad, organic		-	_	_	0.05	nA	
Spicy thai basil	-				1.36	nA	
Cress	-	-	-	-			
	<u> </u>	<u> </u>	<u> </u>	<u> </u>	0.8	nA	
Mixed salad, organic	+	+	+	+	172222.22	nA	L.grayi
Onion sprouts	-	-	-	-	2.00	nA	
Rocket sprouts	-	-	•	-	2.09	nA	
Sprouts	-	-	-	-	1.65	nA	
Salmon	+	+	+	+	55.71	nA	L.welshimer
Thai coriander	-	-	-	-	3.41	nA	
Greek salad	-	-	-	-	3.43	nA	
Mungbean sprouts, organic	-	-	-	-	3.41	nA	
Salad, organic	-	_	_	_	3.67	nA	
Coriander	-	-	-	-	3.39	nA	
Mixed salad	-	-	+/-	-	1.50	16S sequence (C. citreum)	
Salad	+	+	+	+	8150.00	nA	L.welshimer
Microgreens	-	-	-	-	3.89	nA	
Mungbean sprouts	-	-	-	-	4.95	nA	
Mixed sprouts	-	-	-	-	1.70	nA	
Sweet basil	-		_	_	1.77	nA	
Mixed salad	-		+/-	_	1.49	Spore-forming	
Mixed sprouts				_	1.90	nA	
Cheese and ham salad	-	-	-	-	3.32	nA	
Thai coriander	-	-	-	-	2.00	nA	
Parsley	-	-	-	-	4.90	nA	
Salad	-	-	-	-	3.75	nA	
Thai celery	-	-	-	-	2.33	nA	
Basil	-		-	_	2.19	nA	
Rice sandwich with	-	-	-	-	1.67	nA	
smoked salmon Filled pimiento					2.30	nA	
Coriander	<u> </u>	-	-	-	2.79	nA	
Thai basil					2.19	nA	
Salad, organic	+	+	+	+	19500.00	nA	L innocua
Fleur-de-lis sprouts	T	T	T		1.51	nA	Lilliocua
Smoked salmon	-	-	-	-	2.22	nA	
Cicorino rosso	-	-	-	-	1.30	nA	
Chicken salad	-	-	-	-	1.30		
Vietnamese coriander	-	-	-	-		nA	
Mixed sprouts (alfa-	-	-	+/-	-	2.17 1.98	nA Spore-forming	
alfa and rocket) Crayfish salad					1 50	nΛ	
	-	-	-	-	1.52	nA	
Mixed sprouts	-	-	-	-	2.08	nA	
Salad Smoked salmon with	-	-	+/-	-	1.02 1.84	Spore-forming nA	
herbs Egg and chicken salad	_		_	_	1.49	nA	
	-	-	-	-	1.70	11/7	

Supplementary Table S2. Primers and templates used for phage genome fragmentation, modification,

PCR-based insert validations, and sequencing of phages and plasmids.

Supplementary Table S2: Primers	s and templates used for p Fragment ID	phage genome fragmentation, Template	, modification, PCR-based Primer 1	Suprlementary Table S.2 Priners and templates used for plagge genome fragmentation, modification, PCR-based insert valkations, and sequencing of plagges and plasmids. Prinner 1 PI sequence 15:31	Primer 2	P2 sequence [5':31]	Amplicon size [bp]
	A500 ft	AS00 gDNA	A500 fl fwd	ATGCTACAGAAGCCGCTCGTC	A500 fl rev	CATCACCTAAACCGACTCTAAACAGTT	8492
	A500 luc f2	A500 ALCR gDNA	A500 f2 fwd	CAGCTTGGCACGGAACTGTTTAGA	A500 luc f2 rev	ATATATATTACCTCCTCTTATTTTAAGAAGTATTCTGCTGTGTAATACC	
ΦΑ500:r/uc ΔLCR assembly	A500 rluc f3A	rhe string	A500 rluc BA fwd	CAGAATACTICTTAAAATAAGAGGAGGTAAATATATGGGTGGTC	A500 rluc f3A rev	AAAATGCGAGGCCAATAGTTTTATTGTTCGTTTTTTAAAACACGTTCAACGAAAG	1112
	A500 fluc 13B	A500 aDNA	A 500 fd fwd		A 500 fd rev	AAGIGICIIGIAACGIIICIGIGICIA TTCGAACTATAACCAGCAAGAAGAAG	9138
	A500 fi	AS00 gDNA	A500 fl fwd	ATGCTACAGAAGCCGCTCGTC	A500 fl rev	CATCACCTAAACCGACTCTAAACAGTT	8492
	A500 luc f2	A500 ALCR gDNA	A500 f2 fwd	CAGCTTGGCACGGAACTGTTTAGA	A500 luc f2 rev	ATATATATTTACCTCCTCTTATTTTAAGAAGTATTCTGCTGTGTAATACC	12373
ΦΑ500::gluc ΔLCR assembly	A500 gluc f3A	gluc string	A500 glue f3A fwd	CAGAATACTTCTTAAAATAAGAGGAGGTAAATATATATGGGTGTTAAAGT	A500 gluc f3A rev	AAAATGCGAGGCAATAGTTTTAATCACCACCAGCACCTTTGATTTTA	614
	A500 gluc f3B	A 500 ALCR gDNA	A500 gluc ISB fwd	AAGGTGCTGGTGGTGATTAAACTATTGCCCTCGCATTTTGCG	A500 f3 rev	AAGTGTCTTGTAACGTTTCTGTGTCTA TTCGAACTATAACCAGCAAGACGAG	9929
	A500 fl	ASOU GDNA	A500 Fl favd	ATGCCGGAGGGGCGCTCGTC	A 500 F1 rev	CATCACCTAAACCGACTCTAAACATT	8497
	A500 luc 17	A 500 ALCR ODNA	A 500 f7 fwd	CAGCITGGCACGGAACIGTTAGA	A 500 lite (7 rev	ATATATATTACCTCTCTATTTAAGAGTATTCTGCTGTGTAATACC	17373
ΦA500:n/uc ALCR assembly	A500 nluc f3A	nhc string	A500 nluc f3A fwd	CAGAATACTTCTTAAAATAAGAGGAGGTAAATATATATGGTTTTCACTT	A500 nluc f3A rev	AAAATGCGAGGCAATAGTTTTAAGCTAAGATACGTTCACATAAACGC	572
	A500 nluc f3B	A500 ALCR gDNA	A500 nluc f3B fwd	GTGAACGTATCTTAGCTTAAAACTATTGCCCTCGCATTTTGCG	A500 f3 rev	AAGTGTCTTGTAACGTTTCTGTGTCTA	9929
	A500 f4	A500 gDNA	A500 f4 fwd	ATGGCGGAGGACTTAGACACAGA	A500 f4 rev	TTCGAACTATAACCAGCAAGACGAG	9016
	A500 fl	A500 gDNA	A500 fl fwd	ATGCTACAGAAGCCGCTCGTC	A500 fl rev	CATCACCTAAACCGACTCTAAACAGTT	8492
	A500 luc f2	A500 ALCR gDNA	A500 f2 fwd		A500 luc f2 rev	ATATATATTAGCTCCTCTTATTTAAGAAGTATTCTGCTGTGTAATACC	12373
ΦΑ500://ux/B ΔLCR assembly A500 luxAB I3A	A500 luxAB f3A	ASIL:hadB	A500 luxAB f3A fwd		A500 luxAB f3A rev	AAAATGCGAGGCAATAGTTTTACGAGTGGTATTTGACGATGTTG	2099
	A500 luxAB f3B	nho string	A500 hxAB f3B fwd	TCGTCAAATACCACTCGTAAAACTATTGCCCTCGCATTTTGCG	A500 f3 rev	AAGIGICTIGIAACGITTCIGIGICIA	6566
	A200 FI	A006 aDNA	A006 Fl fwd	TTCAGATAAGACAATGCCACTTGTG	A006 Fl rev	GAATATOCTAGOGAATGCGAAATAG	9008
	A006 £2	A006 eDNA	A006 f2 fwd	TGAACTATGTCGTCGTTTTCG	A006 f2 rev	AATAAATACTTACACCTGGAATG	9833
ΦA006 ΔLCR assembly	A006 DLCR BA	A006 gDNA	A006 ALCR IBA fwd		A006 ALCR 13A rev	AATATGAAAGTCAATGAAATAGTTAATGGACAAGATTAATGAAATTTAAAAC	3549
	A006 DLCR f3B	A006 gDNA	A006 ALCR f3B fwd		A006 ALCR f3B rev	CCAAAGATCATCAACAACCATCG	3686
	A006 f4	A006 gDNA	A006 f4 fwd	AAACATGGTTGAGAATCCGATGG	A006 f4 rev	CTTACTGGCAATTTTCACAAGTGG	9294
	A006 f1	A006 gDNA	A006 f1 fwd	TTCAGATAAGACAATGCCACTTGTG	A006 fl rev	GAATATCCTAGCGAATGCGAAATAG	9885
	A006 nluc f2A	A006 gDNA	A006 nluc f2A fwd	TGAACTATGTCGGTCCTATTTCG	A006 nluc f2A rev	CCATATATATTACCTCCTCCTAAATCTTTTTAACAAACTTCTT	9816
ΦΑ006:n/uc ΔLCR assembly	A006 nluc f2B	nluc string	A006 nluc f2B fwd	TTTGTTAAAAAGATTTAGGAGGAGGTAAATATATATGTTTTCACTTTAG	A006 nluc f2B rev	CGCGAGGGCTTTAAACTAAATCTTAAGCTAAGATACGTTCACATAAACG	572
	A006 nluc f3	A006 ALCR gDNA	A006 of 63	GAACGTATCTTAGCTTAAGATTTAGTTTAAAGCCCTCG	A006 f4 rev	CCAAAGATCATCAACAACCATCG	7308
	AU06 14	Auto guna	AUU6 14 TWG	TATOTTA CONTRACTOR AND TANDA CONTRACTOR CONT	A006 14 FeV	C AC GGCAA CACAAG GG	9294
pSK1_ply511_nluc	pSK.1 PL.1 Dackbone nluc ph/511	pSK1_pty211_tys-ms0 nluc string	psk.t ptysti twa ptysti nluc fwd	AGTTATCAAAAAATAAGAGGAGGTAAATATATATATGGTTTTCAC	pSK1 piy511 rev	TOTAGTTTACCICULATITAGCTAGGTAGCTGC	564
	pSK1 CPS backbone	pSK1 cps511 hys-his6	pSK1 cps511 fwd	CGTATCTTAGCTTAATAATTATAGGATAATTGAATAAAAACAGTATAGAG	pSK1 pb511 rev	CATATATATACCTCCTCTTAGTTGC	5371
pSK1_cps511_nluc	nluc cps511	nluc string	cps511 nluc fwd	TTCATAGCAACTAAGAGGAGGTAAATATATATGGTTTTCAC	cps511 nluc rev	AATTATCCTATAATTATTAAGCTAAGATACGTTCACATAAACG	562
	A500	A500					484
	A500 ALCR	A500 ALCR					484
A500 Luciferase PCR,	A500 rluc	A500:rluc ALCR	A500 LCR fwd	AGCTTTTGCGATGTTGTAGC	A500 LCR rev	TATCATAACTAATCCCACAACC	1557
sednencmg	A 500 oho	A500:niuc ALCK A500:oiuc ALCR					1010
	A500 luxAB	A500:hazdB ALCR					2544
	A500	V200					3191
	A500 ALCR	A500 ALCR					619
A500 LCR PCR	A500 rluc	A 500 mile ALCR	A500 luc fwd	CATAMACCGCGTAACAAAGCC	A500 luc fwd	GTTTTTCATTTTCCACCCTC	619
	A 500 other	A500-aduc ALCR					619
	A500 luxAB	A500:hax4B ALCR					619
	A006	A006					451
A006 Luciferase PCR, secuencing	A006 ALCR	A006 ALCR	A006 luc fwd	CCATCGACAAGCAA	A006 luc rev	GGTAAAGATACTCTTCCTCTAGCCA	451
	A006 nac	A006:77mc ALCK					990
A006 LCR PCR, sequencing	A006 ALCR	A006 ALCR	A006 LCR fwd	CCTGGTAATAATCAAGGCTAGTTATATATAGTA	A006 LCR rev	ATATATTGCATTTTAGTATCTTTGCCAAAAGAGGC	681
	A006 nhc	A006::nluc ALCR					189
	A511	ASII					1177
A511 PLY locus PCR	A511 nluc PLY	ASII:ntuc pry	AS11 PLY fwd	I AAGC I AGGAAGAACAC	A511 PLY fwd	GCT CTGCCGT AGC	1709
	A511	A511					1346
A511 CPS locus PCR	A511 nluc PLY	A511:mluc pry	A511 CPS fwd	AACTTGTTCGCGATAACGG	A511 CPS fwd	TATGATTGTAGAAGGTGTCTC	1346
	A511 nluc CPS	A511:nluc cPS					1912
	n/a		pSK1 fwd	GAGAAATGGAAGTTAAG	n/a	r/a	n/a
Sequencing pEdit PLY	n/a n/a	pSK1_pty511_ntuc	pSK1 rev	A AC GCAA CGGA G	n/a n/o	D/a 2/4	n/a n/s
	n/a		nSK1 fwd	GAGAAATGGAAGTTGAATTAAG	n/a	7.0	n/a
Sequencing pEdit CPS	n/a	pSK1 cps511 nluc	pSK1 rev	TTTATACTGCAATCGGATG	n/a	D/a	n/a
	n/a		A511 CPS fwd-2	GTTTATGGTATGGCGCATTAGC	n/a	n/a	n/a
	n/a		ASH PLY fwd	TAAGCTAGGAGAACAACAC	n/a	n/a	n/a
Sequencing ASTERnuc per	n/a n/a	ASH PLY locus PCK	A511 PLY TWG-2 A511 PLY 1034	AGAGGAACGG G A A A C G C C A T T T C C T T T C T T T C T C T T T C T C T T C T C T T C T C T T C T	n/a n/s	D/a	n/a n/a
	n/a		A511 CPS fwd	AACTTGTTCGCGATAACGG	n/a	17/3	n/a
Sequencing A511:nluc cps	n/a	A511 CPS locus PCR	A511 CPS fwd-2	GTTTTATGGTATGGCGCATTAGC	n/a	n/a	n/a
	n/a		A511 CPS rev	TGTTTCAGGGTCTACTACACG	n/a	n/a	n/a
n/a = not applicable.							

Supplementary Table S3. Synthetic, codon-optimized luciferase DNA strings.

Supplementary Table S3: Synthetic, codon-optimized luciferase DNA strings.

String	Sequence [5'-3']	Size [bp]
rluc	ATCACTAGAGGAGGTAAATATATATG GGTGGTCGTCGTGTTCGTTGGGAAGTTTAC ATCTCTCGTGCTTTATGGTTAACTCGTGAACCAACTGCTTACTGGTTAATCGAAATCA ACACTACTCATTACCGTGGTTCTGCTACTATGGCTTCTAAAGTTTACGATCCAGAACA ACGTAAACGTATGATCACTGGTCCACAATGGTGGGCTCGTTGTAAACAAATGAACGT TTTAGATTCTTTCATCAACTACTACGATTCTGAAAAACATGCTGAAAACACACTTCTTACATGGTAACGCTGTTATCT TCTTACATGGTAACGCTACTTCTTCTTACTTATGGCGTCATGTTGTTCCACATATCGA ACCAGTTGCTCGTTGTATCATCCCAGATTTAATCGGTAATCTGGTAAATCT GGTAACGGTTCTTACCGTTTATTAGATCATTACAAATACTTAACTGCTTGGTTCGAAT TATTAAACTTACCAAAAAAAAATCATCTTCGTTGGTCATGGTTCATATGGAATCT GTTGTTGATGTTATCGAACATCAAGATCGTACAAAGCTATCGTTCATATGGAATCT GTTGTTGATGTTATCGAACATCAGGGTTTGGCCAGATATCGAAGAAGAATTAGCT TTAATCAAATCTGAAGAAGGTGAAAAAAATGGTTTTAGAAAACAACTTCTTCGTTGAAAC TTTATTACCATCTAAAATCATGCGTAAATTAGAACCAGAAGAATTCGCTGCTTACTTA	1085
gluc	ATCACTA GAGGAGGTAAATATATATG GGTGTTAAAGTTTTATTCGCTTTAATCTGTAT CGCTGTTGCTGAAGCTAAACCAACTGAAAACAACGAAGATTTCAACATCGTTGCTGTT GCTTCTAACTTCGCTACTACTACTGATTTAGATGCTGATCGTGGTAAAATTACCAGGTAAAA AATTACCATTAGAAGTTTTAAAAGAAATGGAAGCTAACGCTCGTAAAGCTGGTTGTAC TCGTGGCTGTTAATCTGTTTATCTCATATCAAATGTACTCCAAAAATGAAAAAATTCA TCCCAGGTCGTTGATATCTCAGAAGGTGATAAAGAATCTGCTCAAGGTGGTATCG GTGAAGCTATCGTTGATATCCCAGAAATCCCAGGTTTCAAAGATTTAGAACCAATGGA ACAATTCATCGCTCAAGTTGATTTATGTGTTGATTGTACTACTGGTTGTTTAAAAAGGT TTAGCTAACGTTCAATGTTCTGATTTATTAAAAAAAATCAAAGGTGCTGGTGGTGAT TAA ATCATA	587
nluc	ATCACTAGAGGAGGTAAATATATATG GTTTTCACTTTAGAAGATTTCGTTGGTGATTG GCGTCAAACTGCTGGTTACAACTTAGATCAAGTTTTAGAACAAGGTGGTGTTTCTCTTTATTCCAAAACTTAGGTGTTTCTGTTACTCCAATCCAACGTATCGTTTATCTGGTG AAAACGGTTTAAAAATCGATATCCATGTTATCATCCCATACGAAGGTTTATCTGGTGA TCAAATGGGTCAAATCGAAAAAATCTTCAAAGTTGTTTACCCAGTTGATGATCATCATT TCAAAGTTATCTTACATTACGGTACTTTAGTTATCGATGGTAAAAAAATCACT GATTACTTCGGTCGTCCATACGAAGGTATCGCTGTTTTCGATGGTAAAAAAAA	545

Bold = RBS; italics = coding sequence; red = start and stop codon.

47 **Supplementary Table S4.** Experimental set-up for measurement of reporter phage-induced

48 bioluminescence.

Supplementary Table S4: Experimental set-up for measurement of reporter phage-induced bioluminescence.

Substrate	L. monocytogenes host strain	Infection time [min]	Culture Temp. [°C]	Substrate volume [µL]	Culture volume [µL]
Nonanal ¹⁾	WSLC 1042	180	30/20	5	95
Coelenterazine ²⁾	WSLC 1042	140	30	50	50
Coelenterazine ²⁾	WSLC 1042	140	30	50	50
Furimazine ³⁾	WSLC 1042	180	30	50	50
$Coelenterazine^{2)} \\$		140	30	50	50
Furimazine ³⁾	WSLC 1042	180	30	50	50
Nonanal ¹⁾		180	20	5	95
Nonanal ¹⁾	EGDe	180	20	5	95
Furimazine ³⁾	EGDe	180	30	50	50
Furimazine ³⁾	EGDe	180	30	50	50
Furimazine ³⁾	ECDo	180	30	50	50
Nonanal ¹⁾	ECIDE		20	5	95
Furimazine ²⁾	EGDe	180	30	50	50
Furimazine ²⁾	EGDe	180	30	50	50
	Nonanal ¹⁾ Coelenterazine ²⁾ Coelenterazine ³⁾ Furimazine ³⁾ Coelenterazine ²⁾ Furimazine ³⁾ Nonanal ¹⁾ Nonanal ¹⁾ Furimazine ³⁾	Nonanal ¹⁾ WSLC 1042 Coelenterazine ²⁾ WSLC 1042 Coelenterazine ²⁾ WSLC 1042 Furimazine ³⁾ WSLC 1042 Coelenterazine ²⁾ Furimazine ³⁾ WSLC 1042 Nonanal ¹⁾ Nonanal ¹⁾ EGDe Furimazine ³⁾ EGDe	Substrate L. monocytogenes host strain time [min] Nonanal ¹ WSLC 1042 180 Coelenterazine ² WSLC 1042 140 Coelenterazine ² WSLC 1042 140 Furimazine ³ WSLC 1042 180 Coelenterazine ² 140 Furimazine ³ WSLC 1042 180 Nonanal ¹ 180 Nonanal ¹ EGDe 180 Furimazine ³ EGDe 180 Furimazine ³ EGDe 180 Furimazine ³ EGDe 180 Furimazine ³ EGDe 180 Furimazine ² EGDe 180	Substrate L. monocytogenes host strain time [min] Temp. [°C] Nonanal ¹ WSLC 1042 180 30/20 Coelenterazine ² WSLC 1042 140 30 Coelenterazine ² WSLC 1042 140 30 Furimazine ³ WSLC 1042 180 30 Furimazine ³ WSLC 1042 180 30 Nonanal ¹ 180 20 Nonanal ¹ EGDe 180 30 Furimazine ³ EGDe 180 30 Furimazine ² EGDe 180 30 Furimazine ² EGDe 180 30	Substrate L. monocytogenes host strain time [min] Temp. [pC] volume [μL] Nonanal ¹⁾ WSLC 1042 180 30/20 5 Coelenterazine ²⁾ WSLC 1042 140 30 50 Coelenterazine ²⁾ WSLC 1042 140 30 50 Furimazine ³⁾ WSLC 1042 180 30 50 Furimazine ³⁾ WSLC 1042 180 30 50 Nonanal ¹⁾ 180 20 5 Nonanal ¹⁾ EGDe 180 30 50 Furimazine ³⁾ EGDe 180 30 50 Furimazine ³⁾ EGDe 180 30 50 Furimazine ³⁾ EGDe 180 30 50 Furimazine ²⁾ EGDe 180 30 50 Furimazine ²⁾ EGDe 180 30 50

^{1) 0.35%} nonanal in 70% EtOH

49

²⁾ Renilla Luciferase Assay System(Promega)

³⁾ Nano-Glo® Luciferase Assay System (Promega)