TABLE S1.Histidine kinase and response regulators identified in *L. casei* genomes

System	Gene tag		Family	Most similar sequence[1]
	BL23	**ATCC334**		
TC01	LCABL_02090	LSEI_0220	IIIA	LSA0278 (*L. sakei*)
	LCABL_02080	LSEI_0219	OmpR	LSA0277 (*L. sakei*)
TC02	LCABL_05270	LSEI_0461	IIIA	RBAM_005810 (*B. amyloliquefaciens*)
	LCABL_05260	LSEI_0460	OmpR	CD0486 (*C. difficile*)
TC03	LCABL_07770	LSEI_0712	IIIA	LVIS_0355 (*L. brevis*)
	LCABL_07760	LSEI_0711	OmpR	llrF (*Lc. lactis*)
TC04	LCABL_10490	LSEI_0935	IIIA	LSA0501 (*L. sakei*)
	LCABL_10480	LSEI_0934	OmpR	LSA0500 (*L. sakei*)
TC05	LCABL_10650	LSEI_0951	IIIA	CLI_0968 (*C. botulinum*)
	LCABL_10640	LSEI_0950	OmpR	CLI_0967 (*C. botulinum*)
TC06	LCABL_12060	LSEI_1042	IIIA	LSA1214 (*L. sakei*)
	LCABL_12050	LSEI_1041	ompR	LVIS_1316 (*L. brevis*)
TC07	LCABL_14270	LSEI_1208	IIIA	CTC00159 (*C. tetani*)
	LCABL_14280	LSEI_1209	OmpR	SMU.1038c (*S. mutans*)
TC08	LCABL_14440	LSEI_1223	II	Lp_1943 (*L. plantarum*)
	LCABL_14430	LSEI_1222	NarL	Lp_1942 (*L. plantarum*)
TC09	LCABL_16420	LSEI_1419	IIIA	STER_1309 (*S. thermophilus*)
	LCABL_16430	LSEI_1420	OmpR	SAG0976 (*S. agalactiae*)
TC10	LCABL_18840	LSEI_1666	II	LSA1370 (*L. sakei*)
	LCABL_18830	LSEI_1665	NarL	EF2911 (*E. faecalis*)
TC11	LCABL_18970	LSEI_1678	IIIA	Hpk5 (*L. plantarum*)
	LCABL_18980	LSEI_1679	OmpR	LSA1384 (*L. sakei*)
TC12	LCABL_19610	LSEI_1741	IIIA	LSA1455 (*L. sakei*)
	LCABL_19600	LSEI_1740	OmpR	LSA1454 (*L. sakei*)

TC13	Pseudogene	Pseudogene		
	LCABL_25620	LSEI_2389	lytT	*pltR* (*L. plantarum*)
TC14	LCABL_27660	LSEI_2600		TDE0032 (*T. denticola*)
	LCABL_27650	LSEI _2599	lytT	CAC1581 (*C. acetobutylicum*)
TC15	LCABL_28710	LSEI _2680	IIIA	OEOE_0489 (*O. oeni*)
	LCABL_28720	LSEI_2681	OmpR	LP_0283 (*L. plantarum*)
TC16	LCABL_30120	LSEI_2807	IIIA	LSA0078 (*L. sakei*)
	LCABL_30130	LSEI_2808	OmpR	LSA0077 (*L. sakei*)
TC17	LCABL_30710	LSEI_2868	CitA	EF1209 (*E. faecalis*)
	LCABL_30720	LSEI_2869	CitB (IV)	*dpiA* (*S. pyogenes*)

[1] Sequences of *L. casei* or *Lactobacillus rhamnosus* are not considered.

TABLE S2. Bacterial strains and plasmids used in this study

Strain or plasmid	Relevant characteristics[a]	Ref. or source
E. coli DH5α	F$^-$ *endA1 hsdR17 gyrA96 thi-1 recA1 relA1 supE44* Δ*lacU169* (Φ 80 *lacZ*ΔM15)	Stratagene
L. casei BL23	Wild type	B. Chassy, U. Illinois
L. casei TC01	LCABL_02080 mutant; pRV02080 Ery^r	This study
L. casei TC02	LCABL_05260 mutant; pRV05260 Ery^r	This study
L. casei TC03	LCABL_07760 mutant; pRV07760 Ery^r	This study
L. casei TC04	LCABL_10480 mutant; pRV10480 Ery^r	This study
L. casei TC05	LCABL_10640 mutant; pRV10640 Ery^r	This study
L. casei TC06	LCABL_12050 mutant; pRV12050 Ery^r	This study
L. casei TC07	LCABL_14280 mutant; pRV14280 Ery^r	This study
L. casei TC08	LCABL_14430 mutant; pRV14430Ery^r	This study
L. casei TC09	LCABL_16430 mutant; pRV16430 Ery^r	This study
L. casei TC10	LCABL_18830 mutant; pRV18830 Ery^r	This study
L. casei TC11	LCABL_18980 mutant; pRV18980 Ery^r	This study
L. casei TC12	LCABL_19600 mutant; pRV19600 Ery^r	This study
L. casei TC13	LCABL_25620 mutant; pRV25620 Ery^r	This study
L. casei TC14	LCABL_27650 mutant; pRV27650 Ery^r	This study
L. casei TC15	LCABL_28720 mutant; pRV28720 Ery^r	This study
L. casei TC16	LCABL_30130 mutant; pRV30130 Ery^r	This study
L. casei TC17	BL23 Δ*maeR*	BL315 (1)
L. casei ΔRR01	BL23 Δ*rrp11* (LCABL_2080)	This study

L. casei ΔRR01-c	BL23 Δ*rrp11* harbouring plasmid pT1-RR01	This study
L. casei ΔRR06	BL23 Δ*rrp7* (LCABL_12050)	This study
L. casei ΔRR06-c	BL23 Δ*rrp7* harbouring plasmid pT1-RR06	This study
L. casei ΔRR12	BL23 Δ*rrp1* (LCABL_19600)	This study
pRV300	Insertional vector for *Lactobacillus*, Amp^r, Ery^r	(2)
pRV02080	pRV300 containing a 372-pb internal fragment of LCABL_02080	This study
pRV05260	pRV300 containing a 368-pb internal fragment of LCABL_05260	This study
pRV07760	pRV300 containing a 369-pb internal fragment of LCABL_07760	This study
pRV10480	pRV300 containing a 399-pb internal fragment of LCABL_10480	This study
pRV10640	pRV300 containing a 367-pb internal fragment of LCABL_10640	This study
pRV12050	pRV300 containing a 422-pb internal fragment of LCABL_12050	This study
pRV14280	pRV300 containing a 406-pb internal fragment of LCABL_14280	This study
pRV14430	pRV300 containing a 347-pb internal fragment of LCABL_14430	This study
pRV16430	pRV300 containing a 354-pb internal fragment of LCABL_16430	This study
pRV18830	pRV300 containing a 349-pb internal fragment of LCABL_18830	This study
pRV18980	pRV300 containing a 378-pb internal fragment of LCABL_18980	This study
pRV19600	pRV300 containing a 382-pb internal fragment of LCABL_19600	This study
pRV25620	pRV300 containing a 373-pb internal fragment of LCABL_25620	This study
pRV27650	pRV300 containing a 365-pb internal fragment of LCABL_27650	This study
pRV28720	pRV300 containing a 383-pb internal fragment of LCABL_28720	This study
pRV30130	pRV300 containing a 364-pb internal fragment of LCABL_30130	This study
pRVRR01	pRV300 containing fused flanking fragments upstream and downstream of LCABL_02080	This study
pRVRR06	pRV300 containing fused flanking fragments upstream and downstream of LCABL_12050	This study

pRVRR12	pRV300 containing fused flanking fragments upstream and downstream of LCABL_19600	This study
pT1NX	Expression vector for Gram-positive bacteria harboring the constitutive P1 promoter, Ery^r	(3)
pT1-RR01	pT1NX with cloned LCABL_02080 (RR01) expressed from the P1 promoter	This study
pT1-RR06	pT1NX with cloned LCABL_12050 (RR06) and its promoter region	This study
pT1-RR12	pT1NX with cloned LCABL_19600 (RR12) and its promoter region	This study

[a] Amp^r, ampicillin resistance; Ery^r, erythromycin resistance.

TABLE S3. Oligonucleotides used in this study.

Name	Secuence (5´→ 3´)[a]	Application
Lsei219RF	GATGCCTAATATGTCTGGGATG	Amplification of *rrp11* internal fragment (RR01)
Lsei219RR	CTCATCAGCCGAGAAAACAC	
Lsei460RF	CAACTTACCTGATACTGACG	Amplification of *spaR* internal fragment (RR02)
Lsei460RR	GTTCACGACTAAAGACTTGCC	
Lsei711RF	GCCAGAATTAAATGGTTTTGACG	Amplification of *llrF* internal fragment (RR03)
Lsei711RR	CCCACAAACGATCAAAAATCTG	
Lsei934RF	GCTGCCGAGTCTGAGCGGC	Amplification of *rrp2* internal fragment (RR04)
Lsei934RR	CCCCGTTCAATAAAGCATCTCG	
Lsei950RF	CTGAGCATGCCCGATGGTG	Amplification of LCABL_10640 internal fragment (RR05)
Lsei950RR	GCGTGTCCCACAAGGCTGC	
Lsei1041RF	TTTTGTCGACCTCAATCTGCCAAAAATGGAC	Amplification of *rrp7* internal fragment (RR06)
Lsei1041RR	TTTTCTGCAGCCAATTGCAGTAATTGTTCACG	
Lsei1209RF	GCTGCCAAACGTCACCGGTG	Amplification of LCABL_14280 internal fragment (RR07)
Lsei1209RR	GCGTTCATGAACGGCTCGCC	
Lsei1222RF	GAGATGCCCAAGTTAACCGG	Amplification of *rrp6* internal fragment (RR08)
Lsei1222RR	GTTCCTTCCGAGAGAAACAGC	
Lsei1420RF	CAGTCTGCCATATTTTAATGG	Amplification of LCABL_16430 internal fragment (RR09)
Lsei1420RR	CAGCGCTGAACAAAAGACTC	
Lsei1665RF	TTTTGTCGACGGATCYCGTGATGCCGGTG	Amplification of LCABL_18830 internal fragment (RR10)
Lsei1665RR	TTTTCTGCAGCTGTCGCAATTTCTTGATTCG	
Lsei1679RF	GATGTTGCCAGAATTAAACGG	Amplification of *rrp5* internal fragment (RR11)
Lsei1679RR	CGTCACGAGCCAAAACAACG	
Lsei1740RF	CCAGTTTTTGACGGCTATTATTGG	Amplification of *rrp1* internal fragment (RR12)
Lsei1740RR	GCCATAAGTCCTTTAATAACC	
Lsei2389RF	CCCTGGATCTTCTGTAAGTGG	Amplification of *pltR* internal fragment (RR13)
Lsei2389RR	GCAAAATGCTTCGATGACAGC	
Lsei2599RF	CAAGTTAGGTTCAGGCATGG	Amplification of LCABL_27650 internal fragment (RR14)
Lsei2599RR	CGTCGAGTTGAGGAAGAAAC	
Lsei2681RF	GGATGCTGCCTAAACTAGACG	Amplification of *rrp2* internal fragment (RR15)
Lsei2681RR	CAAGTCATCCCTCGAACAAGC	
Lsei2808RF	GATGTTACCAAAAATTGATGGG	Amplification of *rrp3* internal fragment
Lsei2808RR	CAAGGTGTCGAGCAAGGTAG	

		(RR16)
DEL_219AF	TTTTGTCGACGCGCAGTTCATTCAAATTACC	Amplification of *rr01up* fragment
DEL_219AR	GATTTTTTCGCTCATGATCGTGTATTGGCTCCGTTTATG	
DEL_219BF	CATAAACGGAGCCAATACACGATCATGAGCGAAAAAGTC	Amplification of *rr01down* fragment
DEL_219BR	TTTTCTGCAGCCTCAACGCGATAAAAACG	
PT219FOR	TTTTAGATCTCATAAACGGAGCCAATACAATG	Amplification of *rr01* gene
PT219REV	TTTTACTAGTCGTTAGGCCTCAACCTTATAG	
DEL1041AF	TTTTGTCGACGCTTTTGTCTGCTAGGTGAC	Amplification of *rr06up* fragment
DEL1041AR	GCTGGTAGAGCATTTTCATCGATGTACCCCTCATTTCACAG	
DEL1041BR	TTTTCTGCAGGATGTTATCAAGATCCGTGC	
DEL1041BF	CTGTGAAATGAGGGGTACATCGATGAAAATGCTCTACCAGC	Amplification of *rr06down* fragment
PT1041FOR	TTTTAGATCTGAAATGAGGGGTACATCATG	Amplification of *rr06* gene
PT1041REV	TTTTACTAGTGCATTTTCATCGATCAAGCC	
CP1041FOR	TTTTGAATTCGATTAAGGTGCAAACGTTATG	Amplification of promoter region and *rr06* gene
CP1041REV	TTTTACTAGTATCGATCAAGCCCCGAATCATC	
DEL1740AF	TTTTAAGCTTCTTCCATATCAATAATTCGGTC	Amplification of *rr12up* fragment
DEL1740AR	GAAACCGCATCTGCCAGCCTCGATTTTAAACACGTGACCAAC	
DEL1740BR	TTTTACTAGTGTACCTTGATTGATTACCGAGG	
DEL1740BF	GTTGGTCACGTGTTTAAAATCGAGGCTGGCAGATGCGGTTTC	Amplification of *rr12down* fragment
PT1740FOR	TTTTAGATCTGAAATGGAGTTGGTCACGTG	Amplification of *rr12* gene
PT1740REV	TTTTACTAGTCCAGCCTCCTAAGGAACG	
CP1740FOR	TTTTGAATTCATGCATGTGCTGCCAACTCC	Amplification of promoter region and *rr12* gene
CP1740REV	TTTTTCTAGATGCCAGCCTCCTAAGGAACG	
External primers		
C94-68754	CTAGCCCTGTTTTCTTAGGC	Screening of *rrp11* mutants (RR01)
C87-24906	CGTGTTGCAAGCGATTCCG	Screening of SpaR mutants (RR02)
C87-10203	GGATCATTATGAGAGTTACAGC	Screening of *llrF* mutants (RR03)
C85-48527	CAACCTATTGCCGCTTGCGG	Screening of *rrp2* mutants (RR04)
C85-65285	GACTATCCGGACTTTTTCGG	Screening of LCABL_10640 mutants (RR05)
C93-82083	GCAAGCCCATGATGCACTGCC	Screening of *rrp7* mutants (RR06)
C73-25455	GTGGCCTTGGGTGTGATGG	Screening of LCABL_14280

		mutants (RR07)
C73-15384	CAACGTATGAAAGAAGTTAATGG	Screening of *rrp6* mutants (RR08)
C83-40666	CAGTTAGAATAGAAACTGTCC	Screening of LCABL_16430 mutants (RR09)
C68-7694	CTTGCAAATATCAAGGAACGTGC	Screening of LACBL_18830 mutants (RR10)
C92-145449	GTCAAAATGAGAAAACTGTGC	Screening of *rrp5* mutants (RR11)
C92-59224	CCTAAAAGCCGGACAAACCC	Screening of *rrp1* mutants (RR12)
C89-64634	GCACGGCAATGGCTTGACC	Screening of *pltR* mutants (RR13)
C96-12266	GCTGACTCACTCTAGTCAGC	Screening of LCABL_27650 mutants (RR14)
C96-50721	GTCACCTTCTCTAAGGCTGC	Screening of *rrp2* mutants (RR15)
C91-15689	CCTGCATATAAGAACCCC	Screening of *rrp3* mutants (RR16)

1

TABLE S4. Maximum specific growth rates and $\Delta O.D\ 595_{nm}$ of different *L. casei* BL23 mutants grown in MRS broth in microplates.

Strain	Maximum specific growth rate, μmax (h^{-1})	$O.D_{max}$-$O.D_{min}$
BL23	0.279 ± 0.005	2.422 ± 0.06
TC01	0.271 ± 0.006	2.344 ± 0.14
TC02	0.291 ± 0.012	2.224 ± 0.08
TC03	0.284 ± 0.005	2.285 ± 0.11
TC04	0.239 ± 0.007 (P<0.01)[a]	2.390 ± 0.09
TC05	0.268 ± 0.015	2.386 ± 0.06
TC06	0.280 ± 0.006	2.154 ± 0.12
TC07	0.274 ± 0.010	2.316 ± 0.08
TC08	0.275 ± 0.001	2.445 ± 0.09
TC09	0.279 ± 0.015	2.400 ± 0.03
TC10	0.282 ± 0.006	2.382 ± 0.14
TC11	0.213 ± 0.002 (P<0.01)	2.318 ± 0.08
TC12	0.285 ± 0.004	1.883 ± 0.06 (P<0.01)
TC13	0.284 ± 0.010	2.246 ± 0.12
TC14	0.277 ± 0.004	2.377 ± 0.13
TC15	0.266 ± 0.016	2.269 ± 0.18
TC16	0.276 ± 0.005	2.249 ± 0.16
TC17	0.281 ± 0.014	2.341 ± 0.18

[a] Significant difference (P<0.01; one way ANOVA) between the wild-type and the mutant strain.

TABLE S5A. Maximal growth rate (μ_{max}) values and pairwise two way ANOVA under different stress conditions[a].

Strain	0.5% bile			0.6 M NaCl			pH 3.75			T 42°C		
		ANOVA[b]			ANOVA			ANOVA			ANOVA	
	μ_{max}	Strain	Int.[c]	μ_{max}	Strain	Int.	μ_{max}	Strain	Int.	μ_{max}	Strain	Int.
BL23	0.17±<10^{-2}			0.23±0.01			0.07±<10^{-2}			0.26±0.01		
TC01	NG[d]	-[e]	-	NG	-	-	0.03±<10^{-2}	**<0.001**	**<0.001**	0.24±<10^{-2}	<0.001	0.030
TC02	0.17±0.01	0.778	0.010	0.23±0.01	0.097	0.056	0.05±<10^{-2}	0.902	0.005	0.25±0.02	0.725	0.051
TC03	0.17±<10^{-2}	0.848	0.070	0.20±0.01	**0.002**	**<0.001**	0.06±<10^{-2}	0.179	0.003	0.25±0.01	0.368	0.010
TC04	0.13±0.01	<0.001	0.307	0.16±0.01	**<0.001**	**<0.001**	0.05±<10^{-2}	**<0.001**	**<0.001** (-)[f]	0.23±0.01	<0.001	0.033
TC05	0.17±<10^{-2}	0.154	0.201	0.22±0.02	0.037	0.560	0.05±0.01	0.002	0.289	0.24±0.01	0.006	0.444
TC06	NG	-	-	NG	-	-	0.03±0.01	**<0.001**	**<0.001**	0.17±0.01	**<0.001**	**<0.001**
TC07	0.18±0.01	0.472	0.459	0.23±<10^{-2}	0.077	0.743	0.04±0.01	**<0.001**	**0.009**	0.26±0.01	0.452	0.511
TC08	0.19±0.01	0.153	0.009	0.23±0.01	0.163	0.911	0.07±<10^{-2}	0.439	0.005	0.25±<10^{-2}	0.007	0.333
TC09	0.18±<10^{-2}	0.557	0.556	0.22±<10^{-2}	0.209	0.205	0.07±<10^{-2}	0.049	0.062	0.26±0.01	0.735	0.726
TC10	0.15±<10^{-2}	**<0.001**	**<0.001**	0.22±0.01	0.135	0.019	0.05±<10^{-2}	0.014	0.002	0.24±0.01	**0.003**	**<0.001**
TC11	0.13±<10^{-2}	**<0.001**	**0.001** (-)	0.17±0.01	<0.001	0.591	0.05±<10^{-2}	**<0.001**	**<0.001** (-)	0.20±0.01	<0.001	0.110
TC12	0.08±<10^{-2}	**<0.001**	**<0.001**	0.21±0.01	**0.009**	**<0.001**	NG	-	-	0.22±0.02	**0.005**	**<0.001**
TC13	0.17±0.01	0.971	0.135	0.25±0.01	0.031	0.260	0.04±<10^{-2}	**0.001**	**0.008**	0.24±0.01	0.017	0.001
TC14	0.19±0.01	0.108	0.037	0.22±0.01	0.047	0.144	0.05±<10^{-2}	**0.001**	**0.006**	0.24±0.01	0.007	0.020
TC15	0.16±0.01	0.002	0.559	0.22±0.01	0.012	0.828	0.04±<10^{-2}	0.025	0.487	0.24±0.01	0.003	0.515

TC16	0.17±0.01	0.162	0.624	0.21±0.02	0.015	0.046	0.05±<10^{-2}	**<0.001**	**0.004**	0.24±0.01	0.043	0.166
TC17	0.16±0.01	0.252	0.123	0.20±0.02	0.015	0.008	0.06±<10^{-2}	0.254	0.063	0.24±0.01	0.092	0.042

[a] Contribution of treatment is omitted since it was always significant; significant differences are indicated in bold characters.

[b] P values

[c] Interaction.

[d] No growth.

[e] Analysis not performed.

[f] Negative interaction.

1

2 TABLE S5 B. Increment in optical density (Δ O.D.) values and pairwise two way ANOVA at different stress conditions[a].

Strain	0.5% bile			0.6 M NaCl			pH 3.75			T 42°C		
		ANOVA			ANOVA			ANOVA			ANOVA	
	Δ O.D.	Strain	Int.	Δ O.D.	Strain	Int.	Δ O.D.	Strain	Int.	Δ O.D.	Strain	Int.
BL23	1.15±0.14			1.83±0.04			0.56±0.07			2.19±0.10		
TC01	NG	-	-	NG	-	-	0.19±0.06	**<0.001**	**<0.005**	2.07±0.15	0.112	0.741
TC02	1.16±0.10	0.061	0.046	1.86±0.05	0.010	0.003	0.40±0.02	<0.001	0.569	1.97±0.08	<0.001	0.848
TC03	1.13±0.03	0.114	0.240	1.75±0.05	0.003	0.419	0.35±0.02	<0.001	0.337	2.11±0.17	0.072	0.591
TC04	0.85±0.07	0.004	0.014	1.81±0.02	0.404	0.873	0.38±0.04	0.006	0.043	2.18±0.07	0.653	0.751
TC05	1.21±0.09	0.781	0.317	1.88±0.07	0.911	0.174	0.37±0.04	0.001	0.015	2.15±0.15	0.420	0.962
TC06	NG	-	-	NG	-	-	0.14±0.01	**<0.001**	**0.009**	0.46±0.03	**<0.001**	**<0.001**
TC07	1.11±0.07	0.126	0.495	1.84±0.01	0.128	0.086	0.40±0.02	0.001	0.037	2.02±0.11	0.008	0.489
TC08	1.11±0.05	0.820	0.484	1.88±0.08	0.304	0.725	0.41±0.02	0.086	0.025	2.10±0.12	0.409	0.192
TC09	1.23±0.10	0.632	0.375	1.91±0.03	0.278	0.056	0.40±0.02	0.007	0.027	2.12±0.10	0.287	0.579
TC10	0.98±0.03	0.070	0.245	1.82±0.03	0.516	0.685	0.36±0.04	0.022	0.111	2.14±0.14	0.425	0.927
TC11	1.09±0.11	0.135	0.730	1.73±0.11	0.023	0.966	0.32±0.02	<0.001	0.071	2.11±0.12	0.082	0.805
TC12	0.52±0.03	<0.001	0.297	1.81±0.03	**<0.001**	**<0.001** (-)	NG	-	-	1.02±0.05	**<0.001**	**<0.001**
TC13	1.15±0.05	0.132	0.138	1.89±0.03	0.114	-0.008	0.34±0.01	<0.001	0.622	2.16±0.08	0.054	0.156
TC14	1.13±0.02	0.549	0.847	1.79±0.06	0.316	0.930	0.45±0.04	0.097	0.477	2.14±0.09	0.359	0.991

TC15	1.16±0.08	0.261	0.220	1.89±0.02	0.328	-0.044	0.49±0.09	0.042	0.413	2.15±0.09	0.119	0.348
TC16	1.19±0.06	0.266	0.105	1.92±0.03	0.322	0.012	0.48±0.02	0.018	0.341	2.09±0.09	0.027	0.528
TC17	1.15±0.03	0.489	0.485	1.72±0.05	0.072	0.773	0.58±0.04	0.605	0.356	2.01±0.11	0.054	0.434

[a] Abbreviations and symbols as in Table 3 A.

TABLE S6. MIC values of *L. casei* BL23 and TCS-defective derivative mutants.

Strain	Bacitracin[a]	Vancomycin[b]	Gramicidin[a]	Nisin[a]
BL23	3	0.97[c]	>250	1
TC01	1	0.19[c]	>250	0.25
TC02	3	>1.2	>250	1
TC03	3	>1.2	>250	1
TC04	4	>1.2	>250	1.5
TC05	3	>1.2	>250	1
TC06	3	0.45[c]	>250	0.25
TC07	3	>1.2	>250	1
TC08	3	>1.2	>250	1
TC09	2	>1.2	>250	0.25
TC10	2	>1.2	>250	0.25
TC11	3	>1.2	>250	0.5
TC12	3	0.17[c]	>250	0.25
TC13	3	>1.2	>250	1
TC14	3	>1.2	>250	1
TC15	4	>1.2	>250	1
TC16	4	>1.2	>250	1
TC17	4	>1.2	>250	1
ΔRR01	1.5	0.29[c]	>250	0.25
ΔRR01-c	3	0.74[c]	>250	1
ΔRR06	3	0.43[c]	>250	0.5
ΔRR06-c	3	0.97[c]	>250	1

ΔRR12	3	0.45[c]	>250	0.125

[a] μg ml^{-1}

[b] mg ml^{-1}

[c] IC_{50} values are shown. MIC values higher than 1.2 mg ml^{-1}.

Supplementary references

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3. **Schotte, L., L. Steidler, J. Vandekerckhove, and E. Remaut**. 2000. Secretion of biologically active murine interleukin-10 by *Lactococcus lactis*. Enzyme Microb. Technol. **27**:761-765.

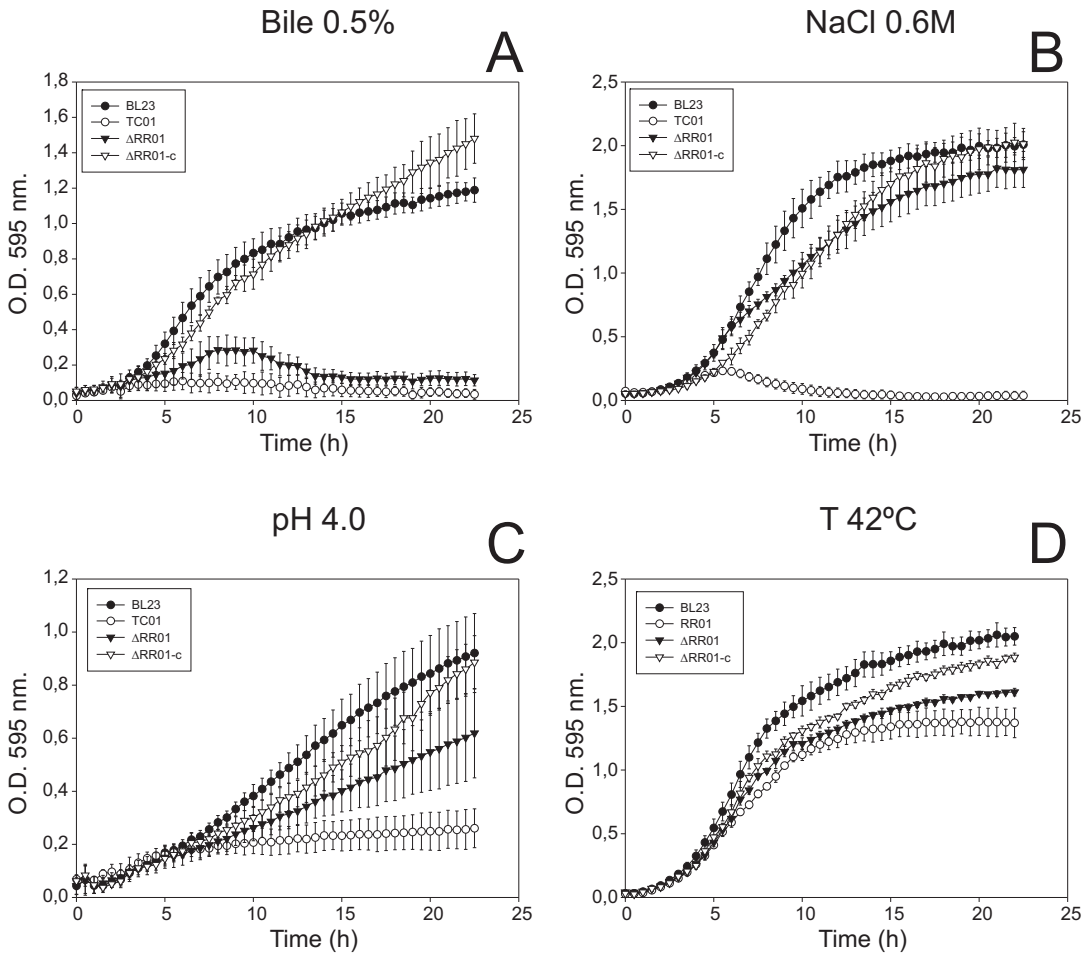
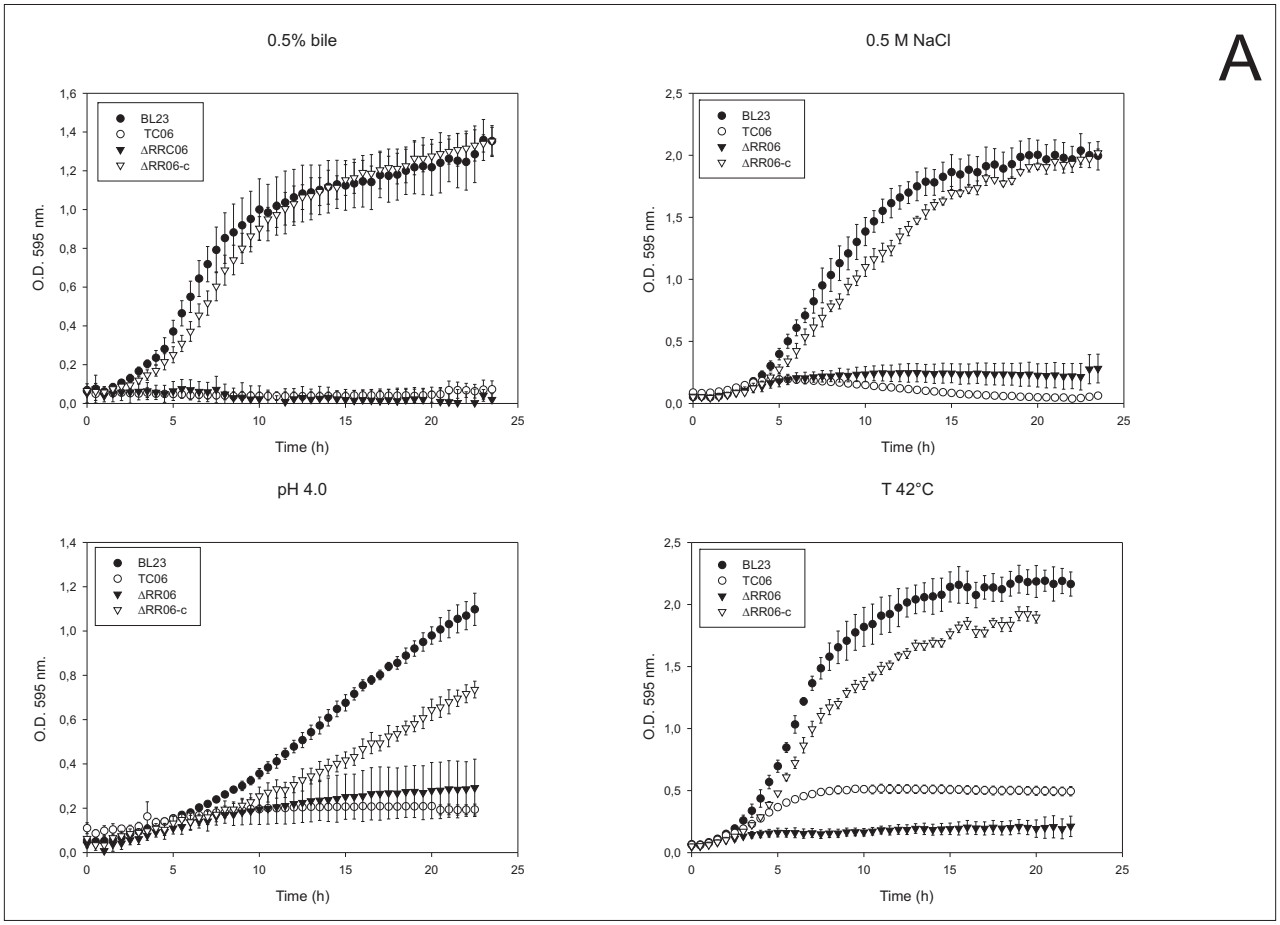


Fig. S1. Growth of BL23 and TC01-defective mutants under different conditions (TC01, insertional mutant; RR01, deletion mutant; RR01-c, deletion mutant complemented with plasmid pT1-RR01). Error bars indicate SD (at least three replicates).



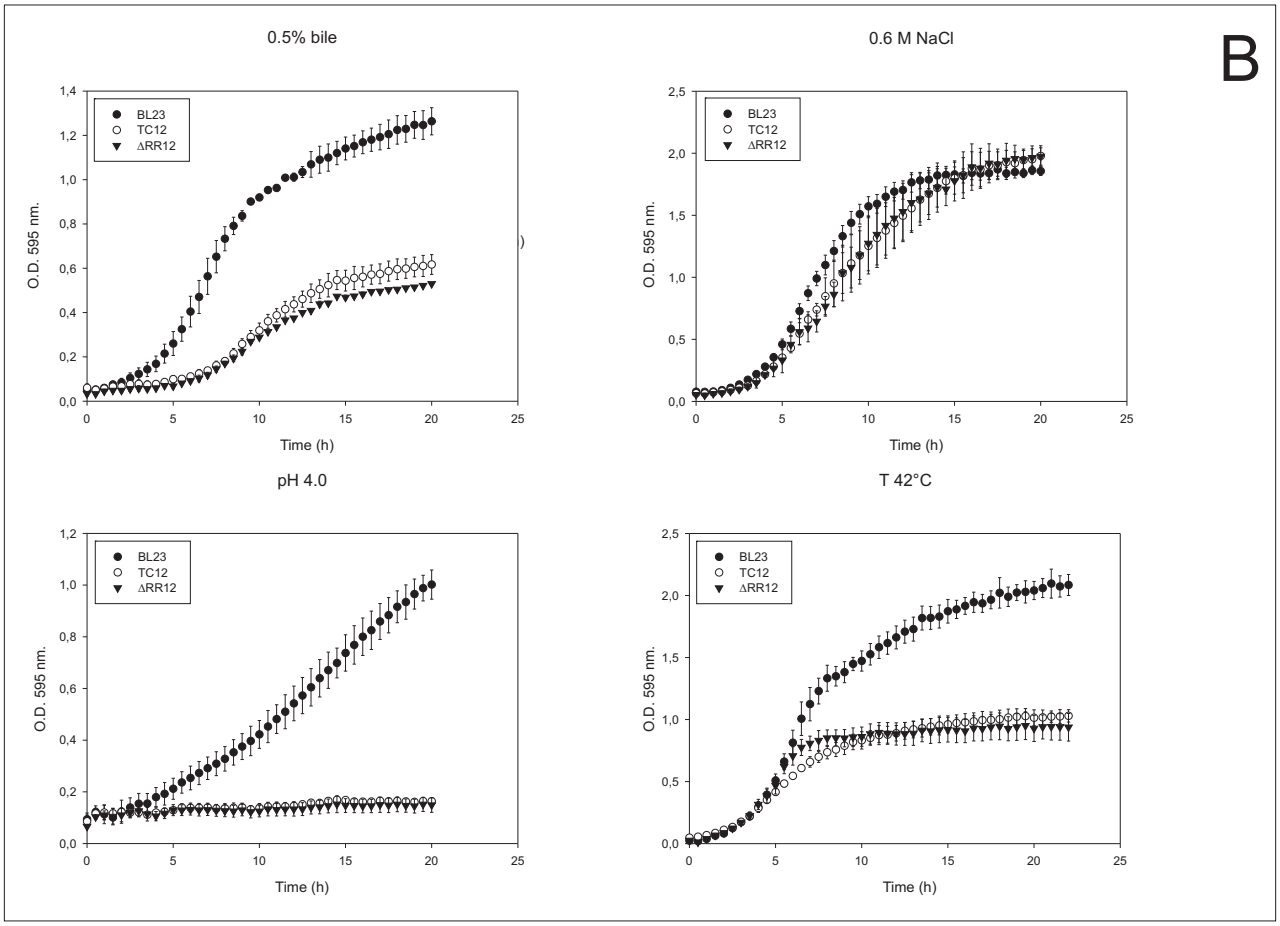


Fig. S2. Growth of *L. casei* BL23 and TC06-defective mutants (A) or TC12-defective mutants (B) under different conditions. Error bars indicate SD (at least three replicates).