

TABLE S1. Primers used in this study

Primer	Gene	Sequence (5' - 3') ^a
Cloning		
RG037	LCABL_08550	AGTCAAGCTTGTTCAGATTATTCGCGCACC
RG038	LCABL_08550	GACTACTAGTCTGACACTTGATTGCCTTGC
RG039	LCABL_24490	AGTCAAGCTTTTCCGCTATCGTCTGTCTTG
RG040	LCABL_24490	GACTACTAGTTGAAGGTCGTCTAGCAAAGC
RG047	LCABL_16400	CTATAGGGCGAATTG GGTACCGCAAGCCTTCAGTAT CGCCG
RG048	LCABL_16400	CTCGAGGGGGGGCCCG GTACCTCAGCCGCGTTTTGA TAGCG
RG049	LCABL_19580	CTATAGGGCGAATTG GGTACCGCATTGCTGGCGTCG TTTTG
RG050	LCABL_19580	CTCGAGGGGGGGCCCG GTACCGCCGGTCGGGAAAAG ATTGG
RG058	LCABL_16440	TTTTCTCGAGTAAAATATAACCAGCCAACAGCGG
RG059	LCABL_16440/ LCABL_16430 intergenic region and LCABL_16420	CGAGCGGCAATAAGCTTTCATCATCTCGTATACATC CCCTTGGGTATC
RG060	LCABL_16420 and intergenic region LCABL_16440 / LCABL_16430	GATACCCAAGGGGATGTATACGAGATGATGAAAGCT TATTGCCGCTCG
RG061	LCABL_16420	AAAAGAATTCTGTCACTAATAACAGTTGGCAATGG

Cloning checking

pRV300.fw	pRV300 plasmid	GTTTTCCAGTCACGAC
pRV300.rv	pRV300 plasmid	CAGGAAACAGCTATGAC
RG003	LCABL_19580	GTCCGATCACTGACAAGC
RG066	LCABL_16420	GCAATTGTTCAAAAATAAAATGCAGCC
RG067	LCABL_16440	GATGGCCAACGCGGCAGATAAG
RG074	LCABL_16440	CATATTGCAACCCGGCGAGA
RG075	LCABL_16420	CACCGCGTTTGGGGAAAATG
LSEI1418R	LCABL_16410	GTCAACATTACTTAAATTAAAAA

qRT-PCR

lepA-F	lepA	CACATTGATCACGGGAAGTC
lepA-R	lepA	GTAATGCCACGTTACGTTTC
ileS-F	ileS	ACCATTCCGGCTAACTATGG
ileS-R	ileS	TCAGGATCTTCGGATTTTCC
pcrA-F	pcrA	CGGCCAATAATGTGATTCAG
pcrA-R	pcrA	TCATCAGTTTCGCTTTGAGC
pyrG-F	pyrG	AATTGCGCTTTTCACTGATG
pyrG-R	pyrG	CGAAATGATCGACCACAATC
RG006	LCABL_19580	GGGAACGCGCATTTCATTGTG
RG007	LCABL_19580	TCTCGCGCTGAACAAGATCC
RG008	LCABL_21670	TTGCCGGTATTTTGGTCGGG
RG009	LCABL_21670	ATGTCCACAATACGGCTGGC
RG019	LCABL_08550	TGGTCGAGGTTTTCTTGGGC

RG020	LCABL_08550	CCGGTGTATGGGCAACATCC
RG021	LCABL_24490	GCCGGATCAGCCAAGACTTG
RG022	LCABL_24490	TTAGCATCGGTGTAACGGCG
RG027	LCABL_19590	TAGCTTTCAGGTCAACGCGG
RG028	LCABL_19590	CTTGGCGTCTCAATCGTTGC
RG029	LCABL_19600	GGCAATGAATATGGGCGCTG
RG030	LCABL_19600	TAGGTTCGTCTGAAGCAAGGC
RG031	LCABL_21680	CACCCGCATTGAAAGGTGTC
RG032	LCABL_21680	GCAAGGTCGTTTTCCCTGAAC
RG033	LCABL_16410	GGACAGGATCTGAGCAACGTC
RG034	LCABL_16410	ATTGAAGGTGTCAAGCAAGTCG
RG054	LCABL_16400	GTACCGTCCTTTCCCGCATC
RG055	LCABL_16400	CCGATGGTAATGATCCCGGC
RG056	LCABL_16430	AGCGAGTTACGCAAACACAG
RG057	LCABL_16430	CGGCTCCTAAGTTCATCGCC

^a Restriction sites are underlined. Sequences highlighted in boldface type are the sequences for the CloneEZ PCR reaction. See materials and methods for details.

TABLE S2. BceRS-BceAB like resistance modules identified in *L. casei* BL23

	Descriptive name in this article	Loci	Phylogenetic group ^a	Induced by nisin?	Resistance substrates ^b	ABC regulated by TCS?	ABC required for sensing?
Resistance module	TCS09: <i>hk09-rr09</i>	LCABL_16420-16430	II	No	Bac, Nis, Plec, Sub	Yes (TCS09)	Yes
	ABC09: <i>permease09-ATPase09</i>	LCABL_16400-16410	II	Yes			
	TCS12: <i>rr12-hk12</i>	LCABL_19600-19610	V	No	Bac, Nis, Mer, Plec, Sub, Van	No	Yes
	ABC12: <i>permease12-ATPase12</i>	LCABL_19580-19590	No group assigned	No			
	Orphan ABC: <i>orphan permease-orphan ATPase</i>	LCABL_21670-21680	VI	Yes	n.d.	Yes (TCS12)	n.d.

^aPhylogenetic group assigned according to Dintner *et al.* 2011 (1) classification of Pep7E-type permeases and BceS-like HKs.

^b Bac, bacitracin; Nis, nisin; Mer, mersacidin; Plec, plectasin; Sub, subtilin; Van, vancomycin.

n.d. not determined

1. **Dintner S, Staroń A, Berchtold E, Petri T, Mascher T, Gebhard S.** 2011. Coevolution of ABC transporters and two-component regulatory systems as resistance modules against antimicrobial peptides in *Firmicutes* Bacteria. *J. Bacteriol.* **193**:3851-3862.