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CLUSTAL O(1.2.4) multiple sequence alignment
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L. sakei strain FAM18311	GTTTGTCCAAACATCAAGTGTTAACTTGTCGAAATCGTTACGACGACCAACACGTGTACT	60
L. sakei laboratory collection strain	GTTTGTCCAAACATCAAGTGTTAACTTGTCGAAATCGTTACGACGACCAACACGTGTACT	60
L. curvatus laboratory collection strain	----------ACATCAAGTGTTAACTTGTCGAAATCGTTACGACGACCAACACGTGTACT	50
L. curvatus strain MRS6	GTTTGTCCAAACATCAAGTGTTAACTTGTCGAAATCGTTACGACGACCAACACGTGTACT	60
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LscHRM-R

L. sakei strain FAM18311	TTCTACTTGATAGTTGACACGACTGATTGGGGTATAAATTGAGTCGATTGGTAAAACACC	120
L. sakei laboratory collection strain	TTCTACTTGATAGTTGACACGACTGATTGGGGTATAAATTGAGTCGATTGGTAAAACACC	120
L. curvatus laboratory collection strain	TTCTACTTGATAGTTGACACGACTGATTGGGGTATAAATTGAGTCGATTGGCAAAACACC	110
L. curvatus strain MRS6	TTCTACTTGATAGTTGACACGACTGATTGGGGTATAAATTGAGTCGATTGGCAAAACACC	120
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LscHRM-F

L. sakei strain FAM18311	AATTGGCATATCGTCTGACTTGTTTTGAACAGCAGCAACATAACCACGGCCTTTTTTAAC	180
L. sakei laboratory collection strain	AATTGGCATATCGTCTGACTTGTTTTGAACAGCAGCAACATAACCACGGCCTTTTTTAAC	180
L. curvatus laboratory collection strain	AATTGGCATATCGTCTGACTTGTTTTGATCAGCAGCAACATAACCACGGCCTTTTTTAAC	170
L. curvatus strain MRS6	AATTGGCATATCGTCTGACTTGTTTTGATCAGCAGCAACATAACCACGGCCTTTTTTAAC	180
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L. sakei strain FAM18311	TGTCATTCGCACGTGGAAATTGCCGCCTTCAGCTAC	216
L. sakei laboratory collection strain	TGTCATTCGCACGTGGAAATTGCCGCCTTC------	210
L. curvatus laboratory collection strain	TGTCATTCGCACGTGGAAATTGCCGCCTTCAGCTAC	206
L. curvatus strain MRS6	TGTCATTCGCACGTGGAAATTGCCGCCTTCAGCTAC	216
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Fig. S1. Alignment of the sequences of *Lactobacillus sakei* and *L. curvatus* laboratory strains with the respective sections of the *rpoA* gene from the strains in the NCBI database (*L. sakei* FAM18311 strain and *L. curvatus* MR56 strain) (*33*). SNPs are highlighted in red, primer (LscHRM-F and LscHRM-R) positions are marked
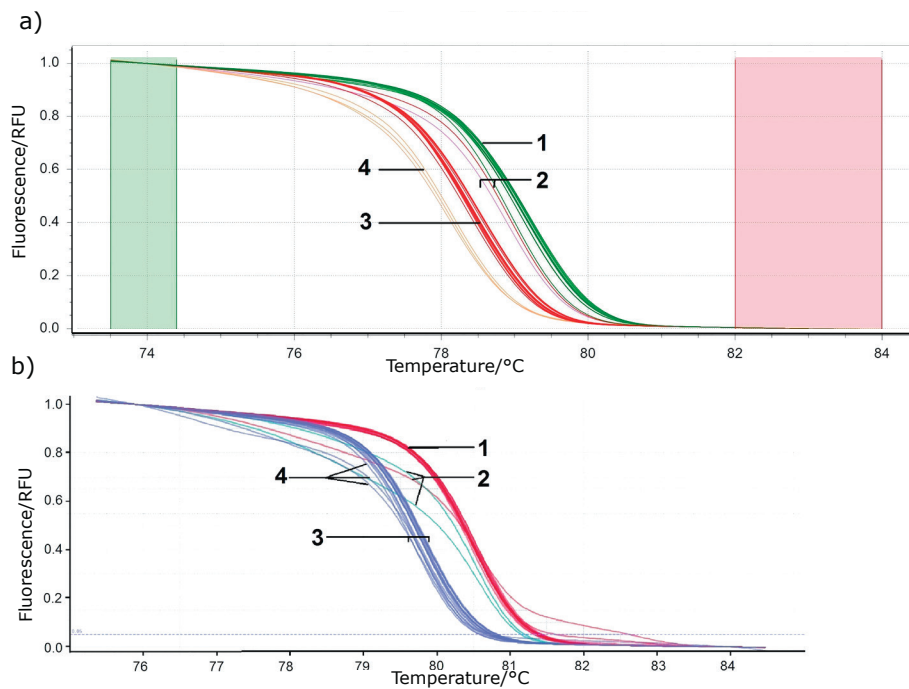

Fig. S2. Normalized melting curves analysed by: a) Precision Melt Analysis software (*40*), and b) LightCycler® 96 software (*39*). PCR was performed using LightCycler 480 HRM MasterMix. Samples: 1=1-10³ dilutions of *Lactobacillus curvatus*, 2=10⁴ dilution of *L. curvatus*, 3=1-10³ dilutions of *L. sakei*, and 4=10⁴ dilution of *L. sakei*. RFU=relative fluorescence unit

Table S1. Melting temperature (T_m) and threshold cycle values of positive controls and their dilutions obtained by CFX96 (40)

	Lactobacillus sakei			*Lactobacillus curvatus*	
Dilution	T_m/°C	Threshold cycle	Dilution	T_m/°C	Threshold cycle
		LightCycler 480 HRM master kit			
1	(78.5±0.1)[a]	(21.7±0.2)[a]	1	(79.1±0.1)[a]	(21.55±0.07)[a]
10^{-1}	(78.4±0.0)[a]	(25.09±0.03)[a]	10^{-1}	(79.0±0.0)[a]	(25.23±0.08)[a]
10^{-2}	(78.4±0.0)[a]	(28.47±0.09)[a]	10^{-2}	(79.1±0.1)[a]	(28.52±0.08)[a]
10^{-3}	(78.4±0.0)[a]	(32.2±0.2)[a]	10^{-3}	(79.0±0.0)[a]	(32.32±0.03)[a]
10^{-4}	(78.2±0.0)[a]	(35.9±0.6)[a]	10^{-4}	(79.0±0.0)[a]	(35.8±0.6)[a]
Total	(78.4±0.1)[b]		Total	(80.45±0.03)[b]	
		Real-time PCR reagent			
1	(79.4±0.0)[a]	(20.3±0.1)[a]	1	(80.0±0.0)[a]	(20.21±0.04)[a]
10^{-1}	(79.3±0.1)[a]	(24.07±0.08)[a]	10^{-1}	(79.8±0.0)[a]	(24.15±0.05)[a]
10^{-2}	(79.2±0.0)[a]	(28.5±0.1)[a]	10^{-2}	(79.8±0.0)[a]	(27.8±0.1)[a]
10^{-3}	(79.2±0.0)[a]	(31.6±0.3)[a]	10^{-3}	(79.8±0.0)[a]	(31.15±0.04)[a]
10^{-4}	(79.2±0.0)[a]	(35.3±0.2)[a]	10^{-4}	(79.8±0.0)[a]	(34.5±0.4)[a]
Total	(79.25±0.09)[b]		Total	(79.84±0.08)[b]	

Data represent the mean value±standard deviation ([a]*N*=3, [b]*N*=15). PCR=polymerase chain reaction

Table S2. The comparison of high-resolution melting analysis (HRM) and biochemical identification results of samples

Sample code	Species included in the composition of the starter culture	Microbiogical identification*	PCR with LscHRM primers	HRM differentation
		Starter culture		
A-1	*Lactobacillus sakei, Debaromyces hansenii, Pediococcus pentosaceus, Staphylococcus carnosus, S. xylosus*	*L. sakei*	+	*L. sakei*
A-2	*L. sakei, S. carnosus*	*L. sakei*	+	*L. sakei*
A-3	*L. sakei, S. carnosus*	*L. sakei*	+	*L. sakei*
A-4	*L. sakei, S. carnosus*	*L. sakei*	+	*L. sakei*
A-5	*L. sakei, S. carnosus*	*L. sakei*	+	*L. sakei*
A-6	*L. sakei, S. carnosus*	*L. sakei*	+	*L. sakei*
A-7	*L. sakei, S. carnosus, S. xylosus, P. pentosaceus, Candida famata*	*L. sakei*	+	*L. sakei*
A-8	*L. sakei, S. carnosus*	*L. sakei*	+	*L. sakei*
A-9	*L. curvatus, S. carnosus, S. xylosus, Lactococcus lactis, D. hansenii*	*L. curvatus*	+	*L. curvatus*
A-10	*L. curvatus*	*L. curvatus*	+	*L. curvatus*
A-11	*L. plantarum, L. rhamnosus, Kocuria varians*	*L. plantarum* (5 colonies) *L. rhamnosus* (1 colony)	-	
		Fermented sausage		
B-1		*L. sakei*	+	*L. sakei*
B-2		*L. sakei*	+	*L. sakei*
B-3		*L. sakei*	+	*L. sakei*
B-4		*L. sakei*	+	*L. sakei*
B-5		*L. sakei*	+	*L. sakei*
B-6		*L. sakei*	+	*L. sakei*
B-7		*L. sakei*	+	*L. sakei*
B-8		*L. sakei*	+	*L. sakei*
B-9		*L. sakei*	+	*L. sakei*
B-10		*L. curvatus*	+	*L. curvatus*
B-11		*L. curvatus*	+	*L. curvatus*
B-12		*L. curvatus*	+	*L. curvatus*
B-13		*L. plantarum*	-	
B-14		*L. plantarum*	-	
B-15		*P. pentosaceus*	-	

*According to API 50 CHL test system result of 6 isolated colonies from the Petri dishes of the last dilutions in which growth was observed; +=positive result, -=negative result, PCR=polymerase chain reaction