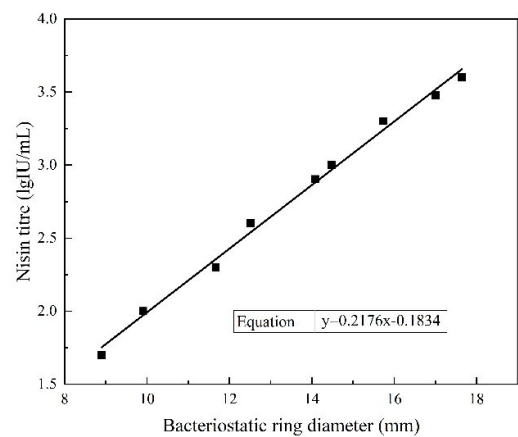## Supplementary Materials

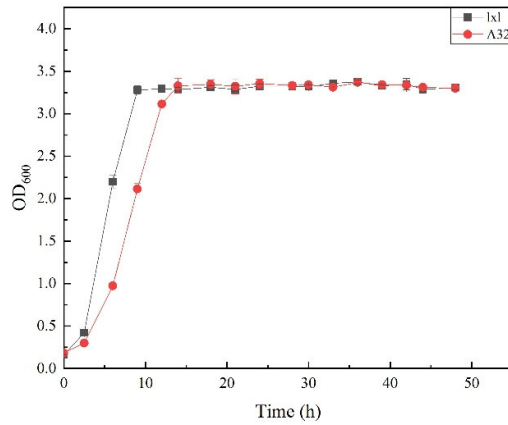**Figure S1** Nisin titre standard curve

Figure S2 Biomass curve of *L. lactis* A32 and lxl with increasing fermentation times

Table S1. Results of the nisin production stability of strains *L. lactis* A32 and A225.

Generation / Mutant strain	F3	F6	F9	F12	F15	F18	F20
A32 (IU/mL)	5089	5081	5095	5109	5075	5083	5091
A225 (IU/mL)	2589	2481	2395	2309	2275	2183	2091

Table S2. Statistics of the genome sequencing data of *L. lactis* A32 and lxl.

Item	A32	lxl
Raw bases (bp)	1087723800	1132569600
Raw reads	7251492	7550464
Raw Q20 (%)	1061634089 (97.6%)	1103022678 (97.39%)
Raw Q30 (%)	1010309134 (92.88%)	1046233103 (92.38%)
Raw N (%)	33223 (0.0%)	34905 (0.0%)
Raw GC (%)	374802794 (34.46%)	391690432 (34.58%)
Clean bases (bp)	1086215124	1130798432
Clean reads	7244702	7542298
Clean Q20 (%)	1060475729 (97.63%)	1101675644 (97.42%)
Clean Q30 (%)	1009294227 (92.92%)	1045061090 (92.42%)
Clean N (%)	16312 (0.0%)	24835 (0.0%)
Clean GC (%)	374135882 (34.44%)	390898883 (34.57%)

Table S3. GO functional categories of *L. lactis* A32 and lxl.

GO ontology	GO functional category	No. A32 Genes	No. lxl Genes
	Cellular process	1583	1577
	Metabolic process	1447	1443
	Single-organism process	1368	1366
	Localization	512	511
Biological Process	Response to stimulus	464	466
	Cellular component organization or biogenesis	457	457
	Biological regulation	454	453
	Regulation of biological process	415	414
	Multiorganism process	157	157

	Developmental process	129	130
	Negative regulation of biological process	97	96
	Growth	88	88
	Reproduction	79	80
	Signalling	76	78
	Multicellular organismal process	75	76
	Locomotion	39	40
	Positive regulation of biological process	32	32
	Detoxification	20	20
	Biological adhesion	19	19
	Immune system process	9	9
	Reproductive process	6	6
	Rhythmic process	3	3
	Cell aggregation	2	2
	Cell killing	1	1
	Presynaptic process involved in synaptic transmission	1	1
	Catalytic activity	1339	1335
	Binding	1085	1084
	Transporter activity	377	375
	Nucleic acid binding transcription factor activity	143	143
	Structural molecule activity	123	123
	Transcription factor activity, protein binding	43	40
	Signal transducer activity	36	38
Molecular Function	Molecular function regulator	29	29
	Antioxidant activity	27	27
	Molecular transducer activity	27	27
	Electron carrier activity	23	24
	Metallochaperone activity	3	3
	Translation regulator activity	3	3
	D-alanyl carrier activity	1	1
	Nutrient reservoir activity	1	1
	Cell	1086	1085
	Cell part	1084	1083
	Membrane	639	638
	Macromolecular complex	471	469
	Membrane part	467	465
	Organelle	218	217
	Organelle part	157	155
	Extracellular region	42	43
	Membrane-enclosed lumen	35	33
Cellular Component	Virion	22	22
	Nucleoid	16	16
	Virion part	13	13
	Extracellular region part	10	11
	Viral occlusion body	5	5
	Other organism	2	2
	Other organism part	2	2
	Synapse	1	1
	Supramolecular fibre	1	1

Table S4. Numbers and lengths of reads and numbers of expressed genes detected by transcriptome sequencing in control and acid-treated samples.

Sample name	Total clean reads (million)	Clean Data (Gb)	Q20 (%)	Q30 (%)	No. expressed genes
A1[1]	16.05	2.14	96.8	91.31	2205
A2[1]	12.60	1.65	96.76	91.22	2183
A3[1]	13.86	1.82	97.03	91.74	2185
B1[1]	16.33	2.15	96.92	91.54	2190
B2[1]	14.32	1.88	97.06	91.8	2182
B3[1]	14.99	1.94	97.11	91.91	2193

[1] A1-A3 are three parallel groups of the original strain atcc11454; B1-B3 are three parallel groups of mutant A32.