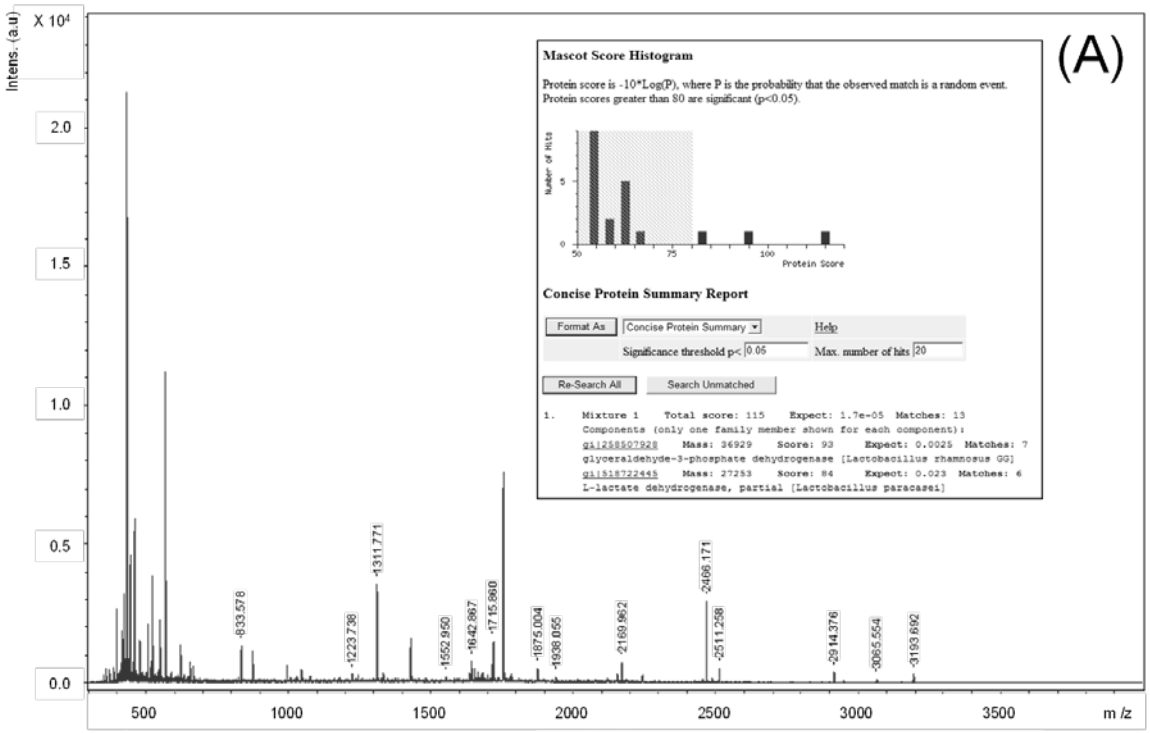
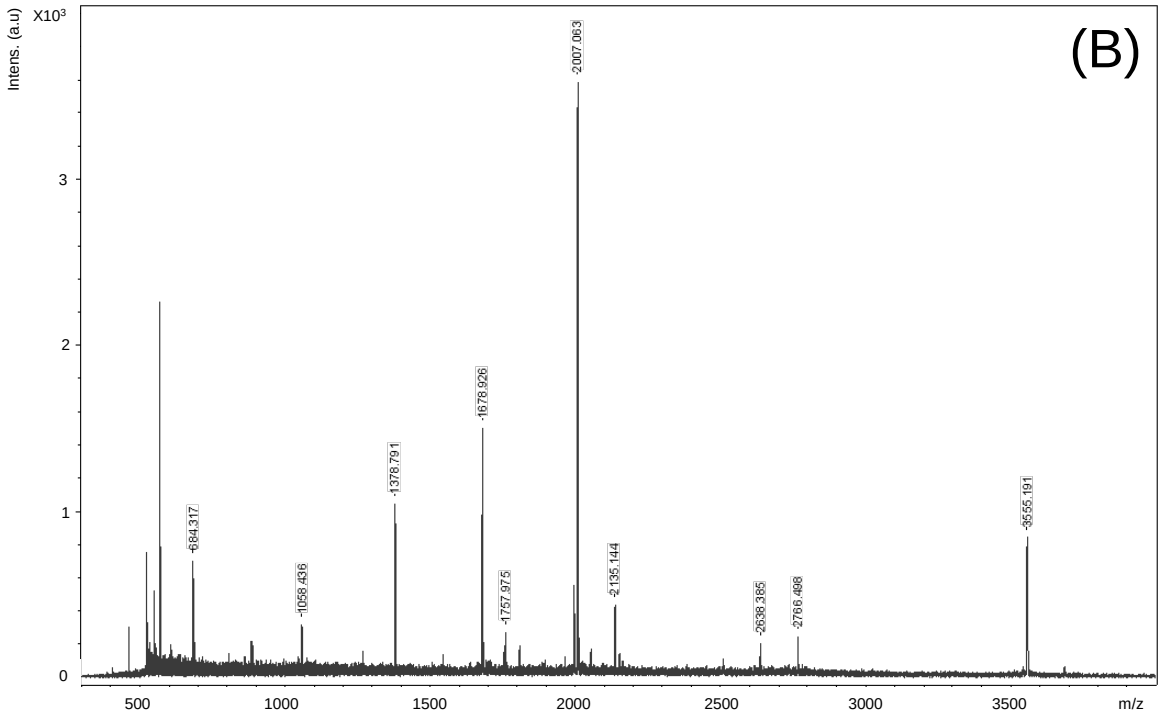
Table S1. Cell viabilities and extracted cell surface protein amounts of *Lactobacillus rhamnosus* FSMM15 and FSMM22.

Strain	Extraction method	Cell viability (x 10^8 CFUs/ ml)		Protein yield (µg/ml)
		Before extraction	After extraction	
FSMM22	PBS	1.23 ± 0.15	1.10 ± 0.36	920 ± 60
	0.2 M Glycine (pH 3)	1.65 ± 0.22	1.62 ± 0.23	380 ± 30
	2 M GndCl**	1.48 ± 0.19	0*	4010 ± 620
	1 M LiCl	1.26 ± 0.22	1.18 ± 0.20	580 ± 60
	2 mg/ml lysozyme solution**	1.49 ± 0.14	1.43 ±0.06	940 ± 310
	2 mg/ml lysozyme solution-1 M LiCl**	1.15 ±0.0 5	1.12 ± 0.18	1450 ± 150
FSMM15	PBS	1.46 ± 0.30	1.44 ± 0.24	195 ± 44
	2 M GndCl	1.68 ± 0.22	0*	2347 ± 358
	1 M LiCl	1.59 ± 0.13	1.47 ±0.08	143 ± 12

*Cell viabilities decreased significantly after treatment of extraction buffer ($p < 0.05$, $n = 3$).

**Extraction with 2 M guanidine hydrochloride, 2 mg mL^{-1} lysozyme, and 2 mg mL^{-1} lysozyme in combination with 1 M LiCl gave several times higher protein yield, but these were avoided because they led the significant low cell viability or interference on mass spectrometry analysis.


(A)
Intens. (a.u)
X 10⁴
2.0
1.5
1.0
0.5
0.0
Mascot Score Histogram
Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 80 are significant (p<0.05).
Number of Hits
Protein Score
Concise Protein Summary Report
Format As
Concise Protein Summary
Help
Significance threshold p<
0.05
Max. number of hits
20
Re-Search All
Search Unmatched
1. Mixture 1 Total score: 115 Expect: 1.7e-05 Matches: 13
Components (only one family member shown for each component):
gi|258507928 Mass: 36929 Score: 93 Expect: 0.0025 Matches: 7
glyceraldehyde-3-phosphate dehydrogenase [Lactobacillus rhamnosus GG]
gi|518722445 Mass: 27253 Score: 84 Expect: 0.023 Matches: 6
L-lactate dehydrogenase, partial [Lactobacillus paracasei]
833.578
1223.736
1311.771
1552.950
1642.867
1715.860
1875.004
1938.055
2169.962
2466.171
2511.258
2914.376
3065.554
3193.692
500
1000
1500
2000
2500
3000
3500
m /z


(B)
Intens. (a.u)
X10³
3
2
1
0
2007.063
1678.926
1378.791
684.317
1056.436
1757.975
2135.144
2638.385
2786.498
3555.191
500
1000
1500
2000
2500
3000
3500
m/z

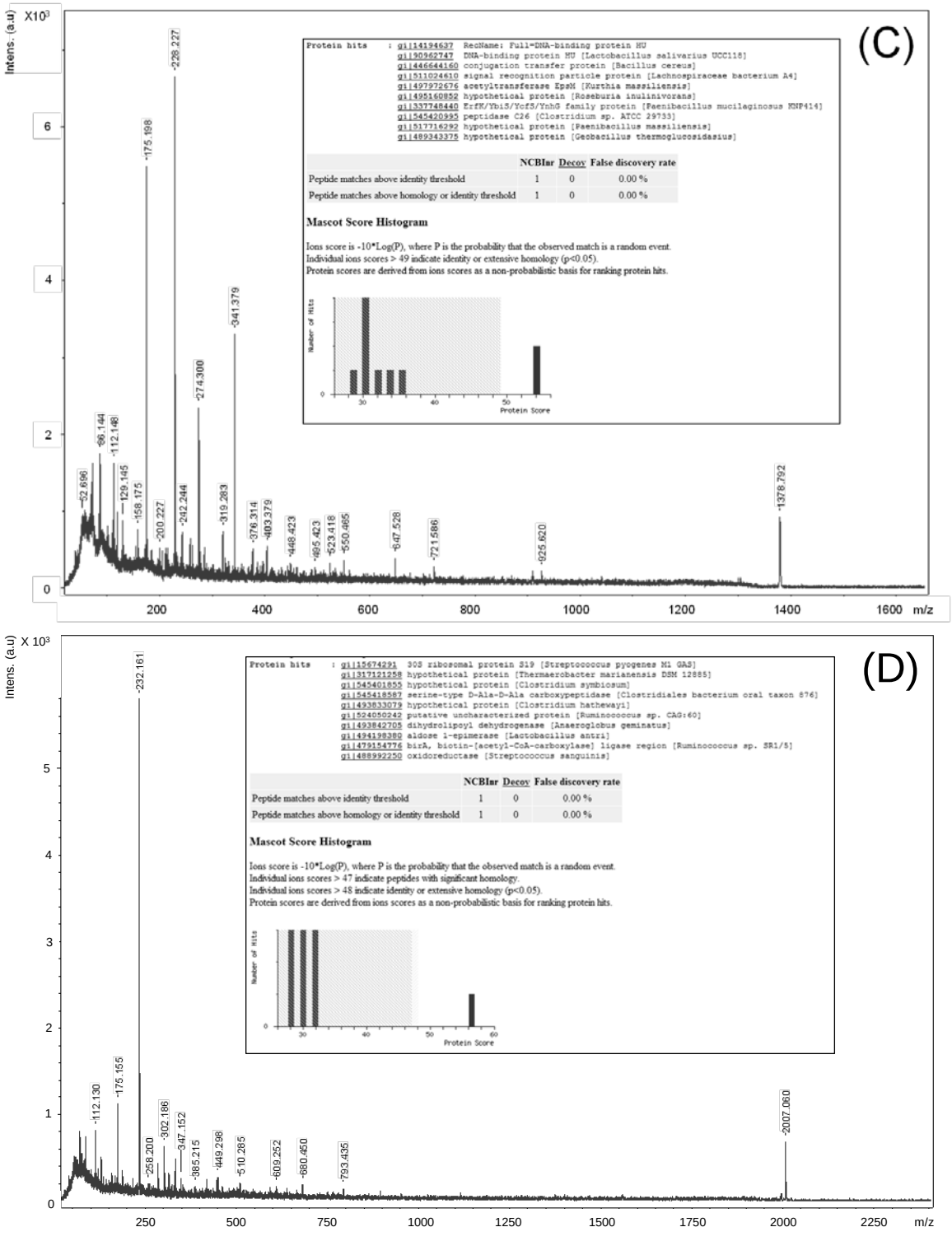


Fig. S1. Mass spectra used for the identification of the LBPs isolated from *L. rhamnosus* FSMM22. (A) Mass spectrum of peptides derived from band no. 5 (Fig.1). The fragmented peptides were identified as mixture of glycereldehyde-3-phosphate dehydrogenase (GAPDH) and lactate dehydrogenase (LDH) by Mascot search (inset). (B) Mass spectrum of peptides derived from band no.

8 (Fig.1). The peptide at *m/z* 2007.063 Da and 1378.791 Da were further analyzed by MS/MS analysis. (C) MS/MS spectrum of the parent peak at *m/z* 1378.791Da in panel (B). The peptide was identified as a DNA binding protein HU by Mascot search. (D) MS/MS spectrum of the parent peak at *m/z* 2007.063Da in panel (B). The peptide was identified as a 30S ribosomal protein S19 by Mascot search (insets). This peptide was correspondent to ^{38}STIFPSFIGYTIAVYDGR^{55}, which was completely conserved among RpsSs of *Streptococcus pyogenes* M1 and *Lactobacillus rhamnosus* GG.

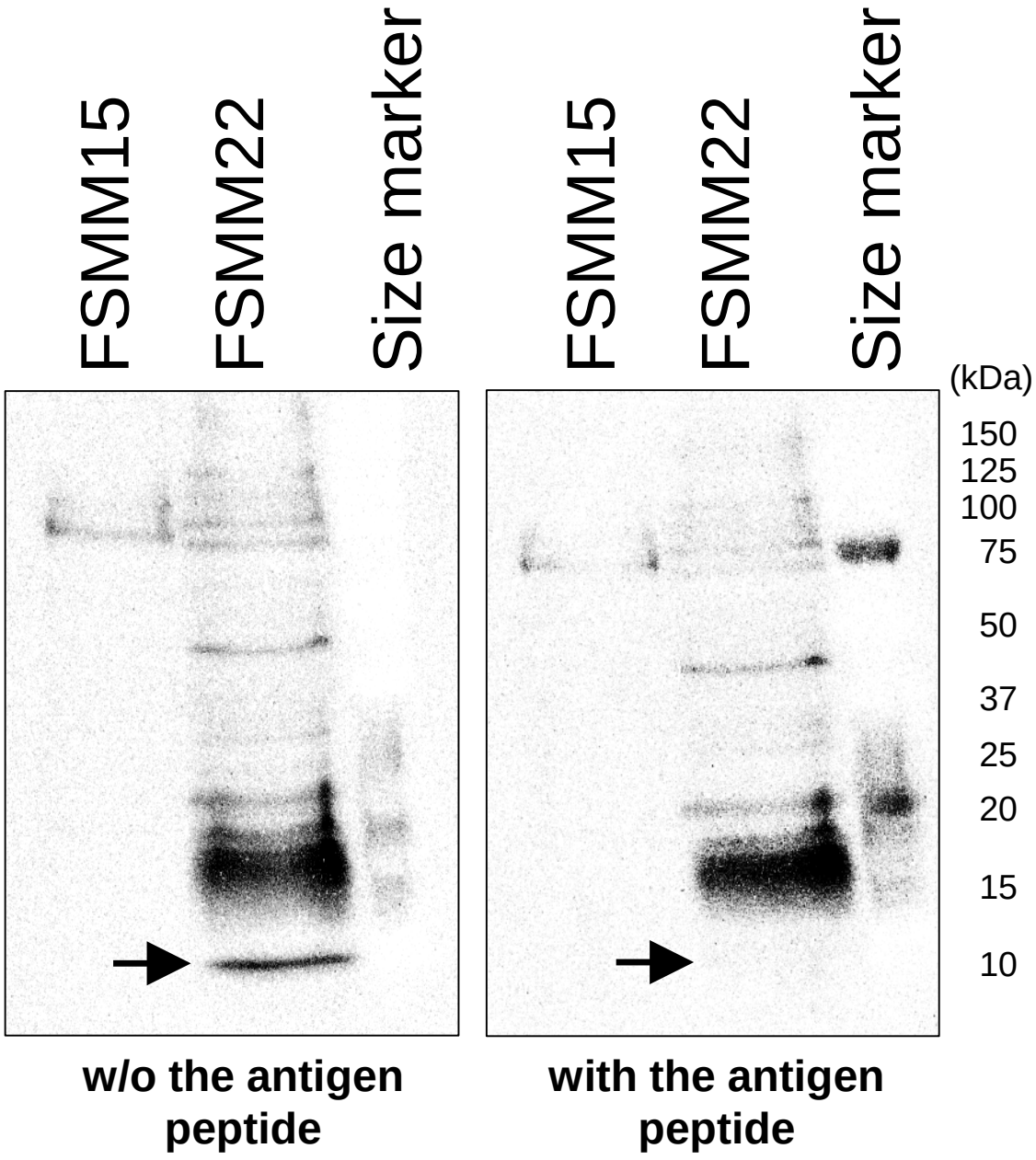


Fig. S2. Western blot analysis of CSPs extracted with 1 M LiCl from *L. rhamnosus* FSMM15 and FSMM22 without (left) and with (right) the antigen peptide, the N-terminal 19 amino acids of RpsS. Position of the RpsS was indicated by arrows.

Fig. S3. Anti-RpsS immunohistochemical staining of *L. rhamnosus* FSMM22 without (left) and with (right) the antigen peptide, the N-terminal 19 amino acids of RpsS.

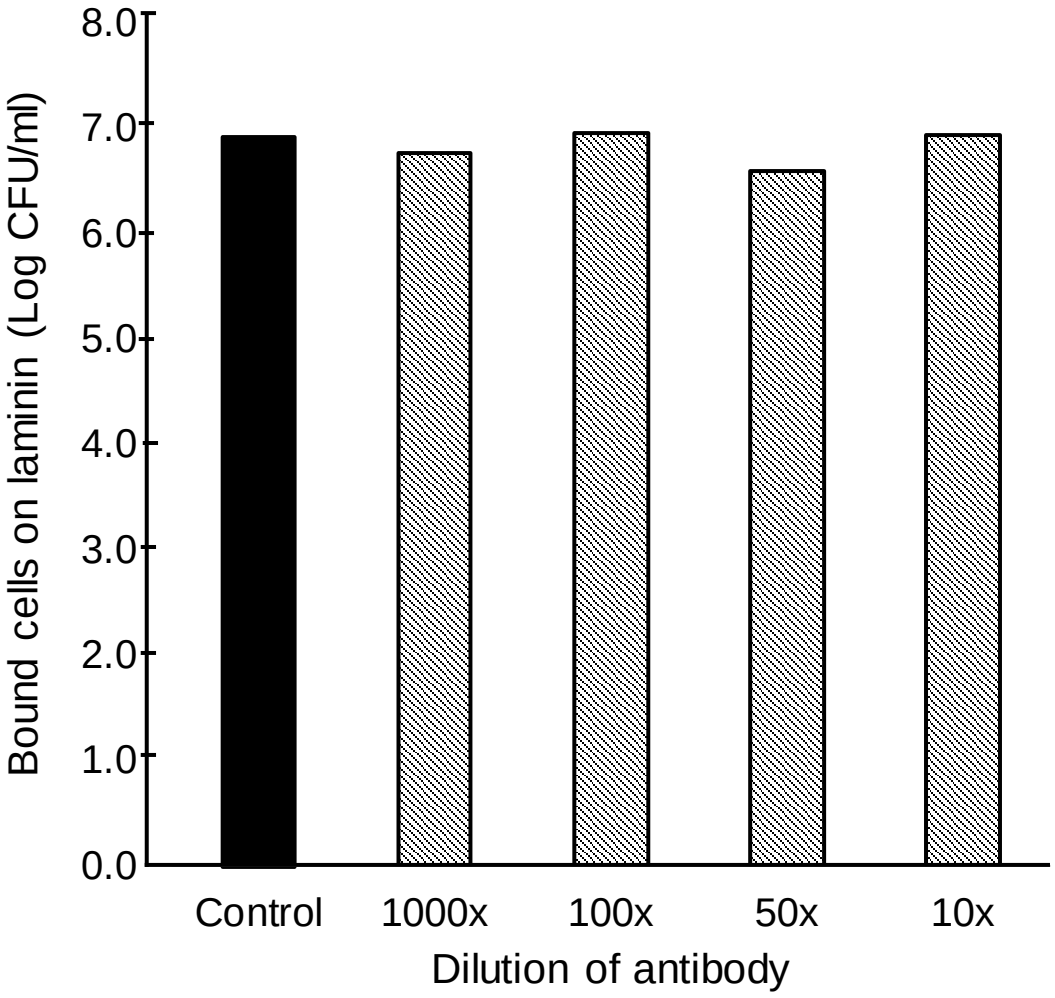


Fig. S4. Inhibition the adherence of FSMM22 to immobilize laminin using anti-RpsS antibody. Filled bar, bound bacterial cell to laminin without incubation with antibody, diagonal bars, binding of bacterial cells in presence of anti-RpsS antibody. About 1 x 10^9 CFU/ml of bacterial cells were incubated for 1h at 37°C in the absence or in the presence of serial diluted anti-RpsS antibody as described in the graph. After blocking with 1% BSA in PBS for 1 h at RT, immobilized laminin was incubated with 100 µl of each cells suspension for 1 h at 37°C. Subsequently, the unbound bacteria were removed and the wells were washed 3 times with 0.1% BSA in PBS. The bound bacteria on laminin were further collected by addition of 100 µl 0.01% Triton X-100 in PBS by vigorous pipetting. The serial dilution of cells suspension was plated on MRS agar and incubated as previous. The enumerated adherence bacteria were expressed in Log CFU/ml. There was no obvious decreasing bacterial adhesion to laminin was observed in correspondence to the increasing antibodies concentration. The experiment was conducted in one replication. The repeatability assay was not conducted because the preliminary data showed negative result.