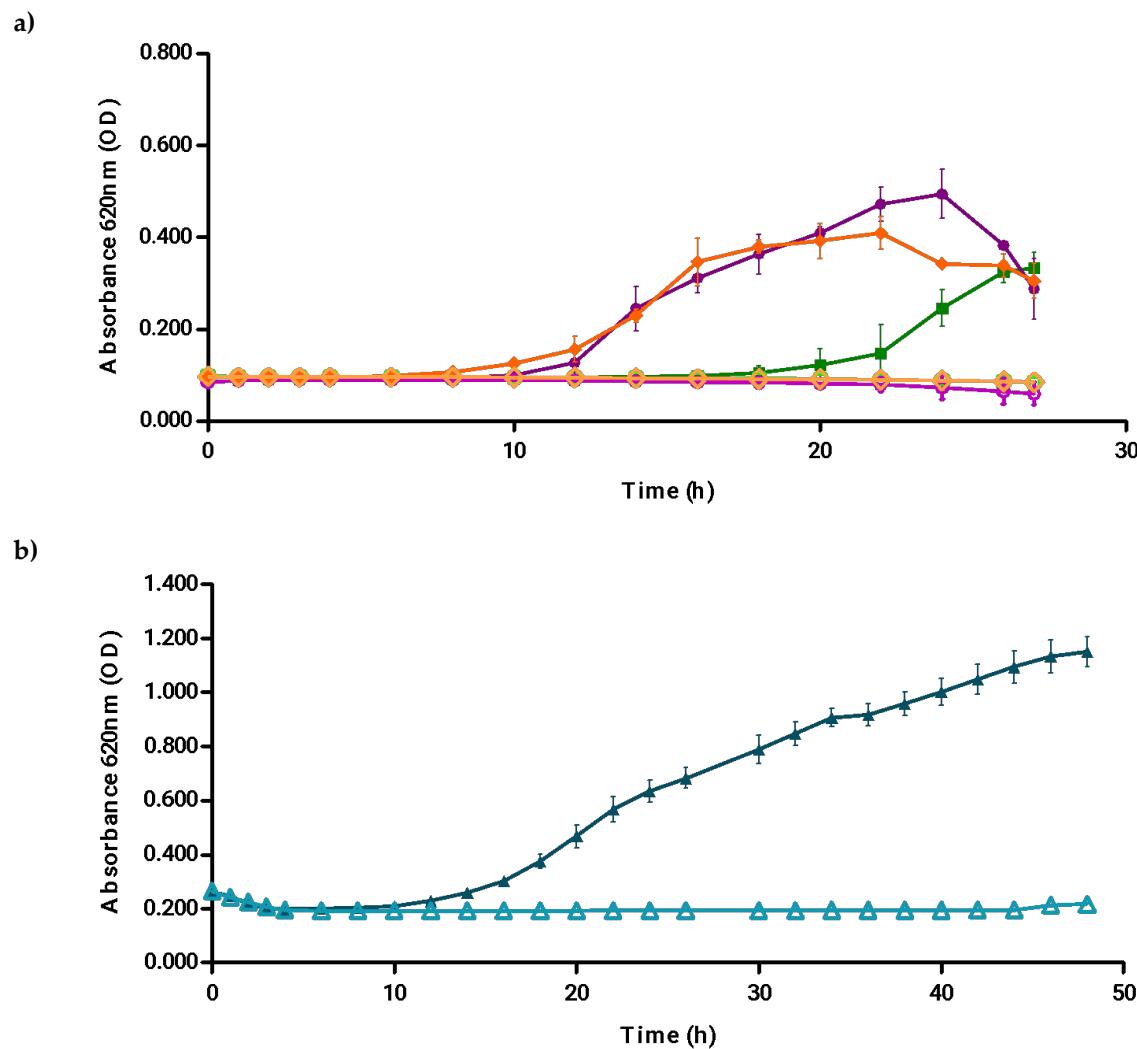


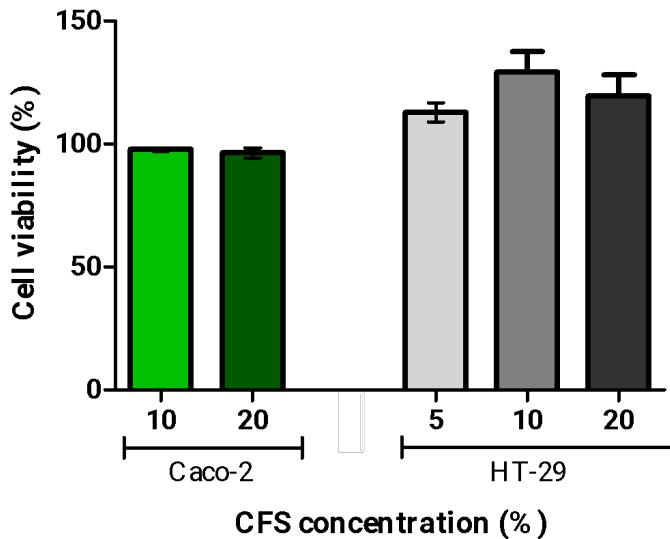
**Figure S1.** Depiction of the inhibition zone achieved by each tested culture-free supernatant, including the well diameter: < 9.2 mm (white), 9.2 mm ≤ inhibition zone < 15.0 mm (green), 15.0 mm ≤ inhibition zone < 25.0 mm (red), ≥ 25.0 mm (blue).

Tested bacterial species: K.m. = *Kluyveromyces marxianus* CNTA.1649, P.f. = *Pseudomonas fluorescens* CNTA 571, L.p. = *Lentilactobacillus parabuchneri* DSMZ 5987, R.m. = *Rothia mucilaginosa* DSMZ 18184, P.a. = *Pseudomonas aeruginosa* CECT 110T, L.m. = *Listeria monocytogenes* CECT 7467, B.c.193 = *Bacillus cereus* CECT 193, B.c.503 = *Bacillus cereus* CNTA 503, S.T. = *Salmonella Typhimurium* CECT 443, S.a. = *Staphylococcus aureus* CECT 976, E.c. = *Escherichia coli* DSMZ 19206.

A dendrogram showing the taxonomic hierarchical relationship between the different tested strains is also shown. 1 = *Lactiplantibacillus plantarum*, 2 = *Lactiplantibacillus pentosus*, 3 = *Lactiplantibacillus paraplanitarum*, 4 = *Pediococcus acidilactici*, 5 = *Pediococcus pentosaceus*, 6 = *Pediococcus parvulus*, 7 = *Lacticaseibacillus paracasei*, 8 = *Lacticaseibacillus casei*, 9 = *Lacticaseibacillus rhamnosus*, 10 = *Lacticaseibacillus manihotivorans*, 11 = *Lacticaseibacillus saniviri*, 12 = *Levilactobacillus brevis*, 13 = *Leuconostoc mesenteroides*, 14 = *Leuconostoc pseudomenteroides*, 15 = *Leuconostoc citreum*, 16 = *Leuconostoc suinucom*, 17 = *Limosilactobacillus fermentum*, 18 = *Limosilactobacillus reuteri*, 19 = *Lentilactobacillus parabuchneri*, 20 = *Lentilactobacillus buchneri*, 21 = *Latilactobacillus curvatus*, 22 = *Latilactobacillus sakei*, 23 = *Lactobacillus delbrueckii*, 24 = *Lactobacillus johnsonii*, 25 = *Lactobacillus acidophilus*, 26 = *Weissella confusa*, 27 = *Weissella cibaria*, 28 = *Loigolactobacillus coryniformis*, 29 = *Companilactobacillus alimentarius*, 30 = *Liquorilactobacillus nagelii*, 31 = *Oenococcus oeni*, 32 = *Ligilactobacillus salivarius*, 33 = *Furfurilactobacillus rossiae*, 34 = *Streptococcus thermophilus*, 35 = *Streptococcus salivarius*, 36 = *Lactococcus lactis*, 37 = *Lactococcus cremoris*, 38 = *Enterococcus faecalis*, 39 = *Enterococcus faecium*, 40 = *Enterococcus mundtii*, 41 = *Bacillus subtilis*, 42 = *Bifidobacterium animalis* subsp. *lactis*, 43 = *Bifidobacterium pseudocatenulatum*, 44 = *Bifidobacterium longum*



**Figure S2.** Growth over time of the selected indicator microorganisms *Listeria monocytogenes* (a) or *Lentilactobacillus parabuchneri* (b) measured by absorbance at 620 nm in the presence of cell-free supernatant (CFS) at the maximum non-inhibitory concentration and the minimum inhibitory concentration of each strain: (a) *Pediococcus acidilactici* CNTA 1059 at 1.25% (■) and 2.5% (□), *Lactiplantibacillus plantarum* at 2.5% (●) and 5% (○) and *Bacillus subtilis* at 0.625% (◆) and 1.25% (◇); (b) *Lentilactobacillus brevis* CNTA 1374 at 0% (▲) and 0.15% (△) concentration. Data are mean  $\pm$  standard deviations (error bars) obtained from at least three independent experiments.



**Figure S3.** The cytotoxic effect of *Bacillus subtilis* CNTA 517 cell-free supernatant (CFS) on the cell viability of Caco-2 cell line (green colors) at different concentrations of CFS (10% and 20%) and on HT-29 cell line's (grey colors) viability at the CFS concentrations of 5%, 10% and 20%. Data are means  $\pm$  standard deviations (error bars) obtained from at least three independent experiments.

**Table S1.** Potential protective culture species from CNTA collection employed for the preliminary screening: number of strains of each species and origin of the isolation.

Potential protective culture species (number of strains)		
<i>Bacillus subtilis</i> (16) (a, b)	<i>Lacticaseibacillus</i> spp. (24) (a, c, d, e, f, g, h)	<i>Lentilactobacillus</i> spp. (10) (c, d, e, g)
<i>Bifidobacterium longum</i> (1) (c)	<i>Ligilactobacillus</i> spp. (4) (c)	<i>Streptococcus</i> spp. (5) (c, g)
<i>Bifidobacterium bifidum</i> (1) (d)	<i>Limosilactobacillus</i> spp. (14) (a, c, d, f, g, h)	<i>Lactococcus</i> spp. (4) (a, c, g)
<i>Bifidobacterium animalis</i> subsp.	<i>Loigolactobacillus</i> spp. (5) (a)	<i>Enterococcus</i> spp. (7) (a, g, i)
<i>Lactis</i> (7) (e)	<i>Latilactobacillus</i> spp. (8) (a, h, i)	<i>Oenococcus</i> sp. (1) (f)
<i>Bifidobacterium pseudocatenolatum</i> (2) (e)	<i>Companilactobacillus</i> spp. (4) (h)	<i>Pediococcus</i> spp. (35) (a, d, e, f, h, i)
<i>Lactiplantibacillus</i> spp. (39) (a, c, d, f, g, h)	<i>Liquorilactobacillus</i> spp. (2) (a)	<i>Leuconostoc</i> spp. (19) (a, c, d, f, h, i)
<i>Levilactobacillus</i> spp. (20) (a, c, d, f, g, h)	<i>Furfurilactobacillus</i> sp. (1) (c)	<i>Weisella</i> spp. (12) (d, f)
<i>Lactobacillus</i> spp. (7) (a, c)		

Origin of the isolation: a) Non-fermented vegetable product/subproduct, b) wasted paint, c) type or private collection, d) cryovial contamination, e) human feces, f) fermented vegetable product, g) dairy products, h) chorizo, i) cereals

**Table S2.** Potential protective culture microorganisms' growth conditions.

Potential protective culture	Growth conditions			
	Medium	Temperature (° C)	Oxygen conditions	Time (h)
Lactic Acid Bacteria	MRSb*	30	Anaerobic	24
Lactic Acid Bacteria	MRSb*	37	Anaerobic	24
<i>Bifidobacterium</i> sp.	MRSb*	37	Anaerobic	24
<i>Bacillus subtilis</i>	TSB-YE**	37	Aerobic	24

\*MRSb: Man, Rogosa and Sharpe Broth (Merck GmbH, Darmstadt, Germany)

\*\*TSB-YE: Tryptic Soy Broth – Yeast Extract (Scharlau, Barcelona, Spain)

**Table S3.** Pathogenic and spoilage microorganisms chosen as indicator strains and growth conditions.

Pathogenic/ spoilage microorganisms	Growth conditions			
	Medium	Temperature (° C)	Oxygen conditions	Time (h)
<i>Listeria monocytogenes</i> CECT 7467	TSB-YE*	37	Aerobic	18
<i>Escherichia coli</i> O157:H7 DSMZ 19206	TSB-YE*	37	Aerobic	18
<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar Typhimurium CECT 443	TSB-YE*	37	Aerobic	18
<i>Staphylococcus aureus</i> CECT 976	TSB-YE*	37	Aerobic	18
<i>Bacillus cereus</i> CECT 193	TSB-YE*	37	Aerobic	18
<i>Pseudomonas fluorescens</i> CNTA 571	PDA**	25	Aerobic	24
<i>Rhodotorula mucilaginosa</i> DSMZ 18184	PDA**	25	Aerobic	24
<i>Kluyveromyces marxianus</i> CNTA 1649	PDA**	25	Aerobic	24
<i>Lentilactobacillus parabuchneri</i> DSMZ 5987	MRSa***	37	Anaerobic	24

\*TSB-YE: Tryptic Soy Broth – Yeast Extract (Scharlau, Barcelona, Spain) (Tunçer and Karaçam, 2020)

\*\*PDA: Potato Dextrose Broth (Scharlau, Barcelona, Spain)

\*\*\*MRSa: Man, Rogosa and Sharpe Agar (Merck GmbH, Darmstadt, Germany)

**Table S4.** Antimicrobial activity of the cell-free supernatants (CFS) against pathogenic and spoilage strains with a well diameter of 7.20 mm. A bold typescript indicates the halo size achieved in the selected indicator microorganism.

Indicator strain	Halo diameter (mm)			
	<i>Pediococcus acidilactici</i> CNTA 1059	<i>Lactiplantibacillus plantarum</i> CNTA 600	<i>Levilactobacillus brevis</i> CNTA 1374	<i>Bacillus subtilis</i> CNTA 517
<i>Listeria monocytogenes</i> CECT 7467	<b>24.53 ± 0.21</b>	<b>22.35 ± 0.38</b>	7.20 ± 0.00	<b>28.52 ± 0.08</b>
<i>Staphylococcus aureus</i> CECT 976	7.20 ± 0.00	7.20 ± 0.00	7.20 ± 0.00	19.36 ± 0.07
<i>Salmonella</i> Typhimurium CECT 443	7.20 ± 0.00	7.20 ± 0.00	7.20 ± 0.00	7.20 ± 0.00
<i>Escherichia coli</i> DSMZ 19206	7.20 ± 0.00	7.20 ± 0.00	7.20 ± 0.00	7.20 ± 0.00
<i>Bacillus cereus</i> CECT 193	7.20 ± 0.00	<b>13.36 ± 0.67</b>	7.20 ± 0.00	7.20 ± 0.00
<i>Pseudomonas fluorescens</i> CNTA 571	7.20 ± 0.00	<b>10.78 ± 0.05</b>	7.20 ± 0.00	7.20 ± 0.00
<i>Rhodotorula mucilaginosa</i> DSMZ 18184	7.20 ± 0.00	7.20 ± 0.00	7.20 ± 0.00	7.20 ± 0.00
<i>Lentilactobacillus parabuchneri</i> DSMZ 5987	7.20 ± 0.00	7.20 ± 0.00	<b>32.20 ± 0.04</b>	7.20 ± 0.00
<i>Kluyveromyces marxianus</i> CNTA 1649	7.20 ± 0.00	<b>14.14 ± 0.12</b>	7.20 ± 0.00	7.20 ± 0.00

**Table S5.** Antibiotic resistance genes identified in *Bacillus subtilis* CNTA 517 after screening of contigs after whole genome sequencing for antimicrobial resistance genes using the CARD database (results from the Resfinder database are not shown to avoid duplicates).

Gene	% Coverage	% Identity	Resistance
<i>Bacillus_subtilis_mprF</i>	100.00	97.90	Cationic peptides (eg defensins)
<i>vmlR</i>	100.00	96.53	Lincosamide, streptogramin, pleuromutilin, virginiamycin
<i>tet(L)</i>	99.93	80.04	Tetracycline
<i>blt</i>	100.00	99.00	Fluoroquinolone, acridine dye
<i>aadK</i>	99.77	98.83	Aminoglycoside
<i>bmr</i>	100.00	98.97	Fuoroquinolone, nucleoside, phenicol, acridine dye
<i>ykkD</i>	100.00	99.69	Aminoglycoside, phenicol, tetracycline
<i>ykkC</i>	100.00	99.70	Aminoglycoside, phenicol, tetracycline
<i>tmrB</i>	100.00	97.98	Tunicamycin (nucleoside)
<i>lmrB</i>	100.00	99.51	Lincosamide
<i>mphK</i>	100.00	99.13	Macrolide
<i>rphB</i>	97.78	80.33	Rifamycin

**Table S6.** Antimicrobial activity of the cell-free supernatants (CFS) after a heat treatment of 110 °C and 121 °C at different times, considering the 0.00 mm as 7.20 mm (no halo).

Temperature (°C)	CFS	Halo diameter (mean ± SD mm)				
		0 min	10 min	60 min	90 min	120 min
110	<i>P. acidilactici</i> CNTA 1059	16.73 ± 0.29	15.59 ± 0.33	12.95 ± 0.37	11.93 ± 0.93	9.26 ± 0.93
	<i>L. plantarum</i> CNTA 600	15.13 ± 0.38	12.25 ± 0.19	11.47 ± 0.32	8.08 ± 0.03	4.66 ± 0.61
	<i>L. brevis</i> CNTA 1374	25.00 ± 0.04	22.54 ± 1.48	20.11 ± 0.64	19.75 ± 0.63	17.70 ± 0.20
	<i>B. subtilis</i> CNTA 517	21.78 ± 0.08	17.03 ± 0.61	11.42 ± 1.09	3.75 ± 0.45	0.00 ± 0.00
121	<i>P. acidilactici</i> CNTA 1059	16.73 ± 0.29	14.06 ± 0.42	11.70 ± 0.05	7.99 ± 0.19	2.98 ± 0.73
	<i>L. plantarum</i> CNTA 600	15.13 ± 0.38	10.49 ± 0.60	6.89 ± 0.02	2.97 ± 0.39	0.00 ± 0.00
	<i>L. brevis</i> CNTA 1374	25.00 ± 0.04	22.38 ± 0.45	18.63 ± 0.32	15.53 ± 0.20	13.83 ± 0.47
	<i>B. subtilis</i> CNTA 517	21.78 ± 0.08	16.07 ± 1.53	0.00 ± 0.00	0.00 ± 0.00	0.00 ± 0.00

**Table S7.** Lost antimicrobial activity of the cell-free supernatants (CFS) after heat treatments at 110 °C and 121 °C.

CFS of	Temperature (°C)	Equation	R <sup>2</sup>
<i>Pediococcus acidilactici</i> CNTA 1059	110	0.3432x + 1.333	0.98
	121	0.6105x + 1.9034	0.95
<i>Lactiplantibacillus plantarum</i> CNTA 600	110	0.4975x + 3.9658	0.91
	121	0.7545x + 10.853	0.96
<i>Levilactobacillus brevis</i> CNTA 1374	110	0.2098x + 4.1638	0.92
	121	0.3579x + 3.6514	0.98
<i>Bacillus subtilis</i> CNTA 517	110	0.7987x + 5.7009	0.98
	121	1.6050x + 4.6284	0.99