

Table S1. Primer set used for the qPCR and PMA-qPCR for *Lactobacillus* strains.

Target organism	Forward primer (5' → 3')	Reverse primer (5' → 3')	Amplicon length (bp)	Concentration (Forward/Reverse) (μM)	C _t gDNA <i>L. rhamnosus</i>	C _t gDNA <i>S. cerevisiae</i>
<i>L. rhamnosus</i> ATCC 9595 <i>L. rhamnosus</i> RW-9595M <i>L. rhamnosus</i> R0011	CATGGCCCAATGCCACAA	CAACGATGTATTCAACACCAACTT	42	5/5	17	Undet.

Table S2. Gene targets and parameters for RT-qPCR analysis by TaqMan for strains of *L. rhamnosus* and the assessment of specificity towards *L. rhamnosus* strains and *S. cerevisiae*.

Metabolic pathway	Gene ^a	Locus tag	Probe	Primer sequences		Amplicon Length (bp)	Efficiency	C _t Value with gDNA of	
				Forward primer	Reverse primer			<i>L.rhamnosus</i>	<i>S.cerevisiae</i>
Carbohydrate catabolism	galactokinase	<i>R0011_09418</i>	TGACCGGAATTGA GTTGGACACCTTGT	GCGTCTCCTTGGCT TTTGAT	CACACCACGTTG CTCAAAG	56	1.84	18.44	27.77
	Beta-galactosidase	<i>R0011_RS0113525</i>	GCATGGCTGTTGA CGAAGAAGATGCGT	AGTGGGAGTTTGG CGGATTT	CGCCGTGGGTA ACTTGATGA	121	1.90	18.96	27.04
	UDP-glucose 4-epimerase	<i>R0011_09423</i>	AGATTGTCTTCTCG TCAACTGCTGCCACA	CGGCATGATTACG CTGCTTG	ATCGGTTTCCTT GATCGGCA	68	2.04	20.63	30.34
	Transcription antiterminator lacT	<i>R0011_09393</i>	AGCGTGCGGATGT GATTCCGGC	AAGCGTTGTAA GGGACGG	TTCTGGCGGGAA GTTTCACT	73	1.81	16.89	26.20
	Galactose operon repressor	<i>R0011_09433</i>	TTGGTTTCTTGGC GGATTGGAAACGAGC	TATGCTGGCGTTTG ATTGCG	GAAACTGTTGCG GTCCACTG	51	1.95	17.19	26.31
	tagatose 1,6-diphosphate aldolase	<i>R0011_RS04275</i>	CTTGCTGTACATTG ACCCTGACGAACCTGA	TGGCCGTTTCCCAG ATTTGA	GCACCAACCCG TTCAACAAA	60	1.85	14.41	28.121
	putative fructose-1,6-bisphosphatase	<i>R0011_RS01155</i>	TGGCTGTTTGGC ACGGTTGACCC	ATCATCGGTTGCTG CTGGAT	ACCTCTTGCTCC TCCTCCAA	63	1.81	19.79*	undet
	acetate kinase		CGCCCCGACACAT CCGCGC	GTTCGTGATCTTGA AGCCGC	AACGCCATTGAT TAAGGCCG	97	1.85	15.54	30.20
	pyruvate kinase	<i>R0011_02305</i>	CCGAAGCAGTGGG TCAGAGTGTGCA	TGAATACACCGAA GCAGCCA	AACACCAAGGT TACGAGCCG	50	1.81	18.32	28.6

EPS Operon	similar to polysaccharide co-polymerase	<i>eps gene cluster</i>	ACCCCTGTCACTC CTAACCTAAAGAT CGCT	GAGCAAAGGATGT CGCCAAC	TCTCGAATCAGA CCGACAGT	89	1.96	18.35	28
	putative membrane-anchored protein	<i>eps gene cluster</i>	GGATACGAGCACT GCAACATAAACGC CG	TCAATCCGAGTCT GGAAGCTT	TCGGCAGGTTTCG TGTCTTTC	90	1.88	16.5	30.4
	similar to dTDP-glucose pyrophosphorylase	<i>eps gene cluster</i>	ACTGGGGCGACGG TGTTTGGC	TGGTGCAGACTTT ATTGGGGA	CCCAAAACGCT CAGGGTCAT	51	1.81	13.89	24
	similar to dTDP-4-keto-L-rhamnose reductase	<i>eps gene cluster</i>	GATCTGGATATTA CCGATGAAGCCGC CGT	CACTTATTGGATGC ACGCGG	TCGGCTTTATCA ACGGCTGT	104	1.80	20.25	31.04
	transcriptional regulator of polysaccharide biosynthesis	<i>eps gene cluster</i>	CGAGAACTTCAAG GCGTCACTGCCGT	TGACGGCCATAAT CCCCTTG	CGTCACAGTAA CCTCGCCAT	100	1.89	19.28	30.13
	similar to phosphoprotein phosphatase and exopolysaccharide biosynthesis genes; EspB	<i>eps gene cluster</i>	CGGTTTGCTTTATC AGATGGTTGAGCG CG	TCTGACGATGTGC CGCTTTA	TAGCCGTCACCT GTGCAAAA	53	1.88	19.87	30.84
	Undecaprenyl-phosphate galactosephosphotransferase	<i>eps gene cluster</i>	ACGGGATTGTGGC AGGTTTCGGGA	TGGACCAAGACCT CCGTTG	TGACCATTTCAT CAAACTTAATT CGT	55	1.81	18.08	30.31
	similar to negative regulator of proteolysis NrpR1 from <i>L. plantarum</i>	<i>eps gene cluster</i>	TGGATGAACGCCG ACTGTTGTTTGGGT	GCGGTTGATTGT GGCAGA	GCCGGACTTCAC GTGGTAAA	72	1.84	19.14	30.01
Amino acid transport and lipid metabolism	cysteine synthase	<i>R0011_09088</i>	CAAGCACAAGATT CAAGGGATCTCAG CCGG	CCAATGCTAAAAG AAGGCCAT	TGATGTCTTGAT AGAGGTTTCGTAT C	74	1.83	18.32	28.6
	dipeptidyl aminopeptidases/acylamioacyl peptidases	<i>R0011_04490</i>	TCTGGTGTCAATG CAAAGTCCGTCAC ATGA	CTGCTCTTCTTCCG ATGCCA	GCCTTTGATTGA TGGTCGGC	51	1.85	18.49	28.01
	cystathionine gamma-synthase	<i>R0011_09103</i>	CAAGAGTCCGCTG GCACCCGTG	AGATGGTGCCAAG TGAGTCG	TTGCCCACGTTT ACTACCCC	86	2.05	14.5	26.31
	homoserine O-succinyltransferase	<i>R0011_09083</i>	GGCTCCCCGATTG AAACGCTGGAATT TG	TGGATATTCACGA AGCGGCA	ACAGGTACATTT GGTTGGGCA	106	1.97	22.7	34.45
	N-acetylmuramoyl-L-alanine amidase	<i>R0011_03100</i>	AGAGCGTCAATGT TCGGCTAGGTCCC	CGCTATTGTTTGGC GTTGG	TTCACCTGACCC ATGATGCC	58	1.88	15.84	27.09

	acyltransferase	R0011_RS11250	GTCGGTGACTCAG TTATGCTTGACGG TGA	ATCCAGATACGCT TCGCAGG	CGGCATCAATC ACCGCTTTT	73	1.85	19.912	29.22
	Cyclopropane-fatty-acyl- phospholipid synthase	R0011_RS01535	TGGGTCAGATTTT CCGCCATCCCAGG GCGTCGGGTCATC	AGTCGTCCAACGT CATAACCG	ATGGGATTACAC GGCAGCAA	100	1.84	15.24	28.57
	Acyl-ACP thioesterase	R0011_13115	AGGGTCACGT GCCAAAGTTCAAG CAGAGATTCCCGC G	CTCGGCATTACCT GGTCAT	CGGGGCGCAGA TATTCGATA	88	1.84	21.95	undet
	3-oxoacyl-acyl carrier protein reductase	R0011_00195	AGCCGTCACCACC AAAATGA	CCGCATCCTTGG CAACCA	91	1.86	20.69	34.9	
Genes stress and lipid metabolism	<i>ATP synthase subunit D F0F1-type ATP synthase. delta subunit</i>	R0011_01330	GCCCCAATTTTCAG CCGCAGACAAAG C	TCAAAGAAAATCC AACAATCCTGACA A	TGGGCTTGCATC CTTGGTC	63	1.84	15.83	29.86
	molecular chaperone	R0011_RS10250	CACGGGTAAAGT GCGTTCCAAGTGC A	ACTGGCACCTTGG TCTTAGC	TGTGACCCAGA CGCAAATCA	83	1.82	15.49	29.55
	<i>S</i> -ribosylhomocysteinase	R0011_09878	TGGGGAACACAC AGCACCACGGA	GATTGATACTGCC GGGTTGC	TCGCTTCAAGGC TGGACTTC	58	1.97	16.734	26.73
	chaperonin	R0011_RS00900	CTTTGCCGGTTTGC GGTTTCTGTTTGC TGCACAAATTCGG	CGCCTTCACCTAC AGCAACA	ATCGCGTGATTG TCGAGGTC	96	2.00	14.06	16.06
	alkyl hydroperoxide reductase. subunit C	R0011_11250	TATCCTCAGAAGC GGA	GGACTCGTCTCTGC CCATG	CCCACAGAACT AGGCGATTG	95	2.02	19.66	26.48
	<i>F0F1 ATP synthase subunit alpha</i>	R0011_01315	TTGGCTCTGACTTG GATGCAGCTACAC A	CTGGCATCCTTCCG TGAAC	TACCGGCTGCTT CAACACTT	80	2.00	14.07	26.58
	<i>ATP-dependent clp protease ATP-binding subunit</i>	R0011_04300	AAATTTCAGGAAAC TGCC	CGGTGATTGGCCG TGATC	CGTCCGCCGACT CAAAATT	38	2.00	15.20	26.71
Others functions and cellular responses to diverse environments	<i>L</i> -rhamnose isomerase	RhaA	TGCGTGCGATCAA GATAACCGTCCCG	GCGTCAAAGAAGT CAAGGCC	TCAGCGCCTTC TTCCCATT	148	1.95	24.5	32.8
	Xylanase/ chitin deacylated	R0011_11803	CGGGTCGGCTGCA GGAATATGGGT	TTTGGGGCGGTGAT CTCTTG	CCATTACGCCT CGGTTCGTA	151	2.00	20.62	30.19
	Carboxymucunolactone decarboxylase	R0011_02165	CGCCGCGCTAAAT GATGATGTCTTGTT CG	GCAGGAAGAAAA CAGTTAGGCG	CAGGTGTGCTT TTAACTGGG	136	1.85	20.33	29.86

References genes	16S rRNA		AGACACGGCCCA AACTCCTACGGG	CTGAGAGGTTGAT CGGCCAC	TTGCTCCATCAG ACTTGCGT	73	2	10	27.04
	DNA gyrase subunit A	R0011_06607	TCCTGATGCCACC ACCGCCGA	TCCCGAATCTGCTG GTCAAC	ACTTGCCCATGA CAACACCA	80	1.89	18.57	Undet
	elongation factor Tuf	R0011_02150	GGTCGTGGTACCG TTGCTTCTGGTCG	TCGTGAAACCGAC AAGCCTT	CATCGCCGACCT TAACCGTA	58	2.03	15.52	28.23
	D-lactate dehydrogenase	R0011_RS06380	CGGTAAACTGGCT GGCGTCGGG	GAAGCCAAGCGTG ATTGTGG	CGCGAGCAGTTC ATCCCATA	112	1.86	17.87	Undet.
	recombinase A	R0011_RS13145	CCAGGTGGTCGGG CGCTGAAGT	AAGTTGTCTGGGG CGATCAA	TTCCATACGCAC AGTGGCAT	45	1.87	19.50	27.39
	glyceraldehyde-3-phosphate dehydrogenase	R0011_00425	TGTTGCTTGACGG CCCAGTTCGTG	CACCGTTCATGCCT ACACCT	CCAGTGCTGTGA GGAATCGT	82	1.93	12.91	25.15

Table S3. Reference genes identified by the software geNorm for each time point of the fermentation for the three strains of *Lactobacillus rhamnosus*.

Strain of <i>Lactobacillus rhamnosus</i>	Time of Fermentation (h)				
	6	9	12	15	24
R0011	<i>tuf, recA, gapdh</i>	<i>gyrA, ldh, gapdh</i>	<i>gyrA, recA, ldh</i>	<i>tuf, ldh, recA</i>	<i>ldh, recA, gapdh</i>
ATCC9595	<i>gyrA, recA, gapdh</i>	<i>gyrA, recA, gapdh</i>	<i>gyrA, tuf, recA</i>	<i>gyrA, tuf, gapdh</i>	<i>gyrA, tuf, recA</i>
RW-9595M	<i>gyrA, tuf, gapdh</i>	<i>gyrA, tuf, gapdh</i>	<i>gyrA, tuf, gapdh</i>	<i>gyrA, tuf, gapdh</i>	<i>gyrA, tuf, recA</i>

Table S4. Changes in the profile of phenolic acids by *Lactobacillus rhamnosus* R0011, ATCC 9595 and RW-9595M in mono and co-culture during 48 h of fermentation.

Time (h)	R0011				ATCC 9595				RW-9595M			
	Mono		Co-culture		Mono		Co-culture		Mono		Co-culture	
	Mean	STD	Mean	STD	Mean	STD	Mean	STD	Mean	STD	Mean	STD
4-Hydroxybenzoic acid												
0	808.9	68.8	957.4	148.7	243.0	72.7	1105.7	29.1	484.9	0.0	687.2	450.3
6	987.6	88.5	1305.3	275.0	843.7	47.0	542.8	83.3	1824.2	369.6	1168.3	17.7
12	1157.1	55.0	1145.9	384.9	1080.6	54.3	906.4	46.7	1553.1	15.5	942.4	130.1
24	1355.5	512.5	1829.0	495.2	1457.4	195.6	1024.1	62.3	1997.4	724.5	1557.9	53.0
48	1363.8	159.4	1483.4	294.9	1620.6	250.1	603.5	135.8	2152.3	854.7	1949.3	536.0
p-Coumaric acid												
0	1811.6	509.2	1737.7	432.2	2723.1	250.0	2510.4	50.2	2830.2	330.7	3042.9	206.9
6	2830.8	85.4	2487.5	298.0	1832.3	585.1	3652.5	240.4	4938.0	372.8	4112.8	0.0
12	4671.2	703.9	3233.3	1521.4	3261.7	134.0	3306.9	742.9	3261.9	630.1	5082.9	501.2
24	3117.0	726.6	3472.9	828.7	3982.7	396.9	2354.6	307.5	3415.1	531.8	2939.3	679.2
48	3971.5	595.3	4137.9	155.4	4458.8	835.5	4581.3	198.1	2941.4	809.3	3288.8	979.1
Caffeic acid												
0	1412.1	484.4	1428.5	317.4	1937.0	808.2	1662.6	844.7	1808.8	439.3	1218.0	442.1
6	1315.3	554.1	1488.7	308.5	1614.7	554.4	1066.2	119.0	1475.0	224.3	1456.5	557.3
12	2731.6	715.6	1935.1	906.3	3802.5	669.8	4224.8	841.5	3924.2	222.7	4420.2	921.3
24	2328.2	954.3	3529.4	606.2	3438.7	1226.9	3458.2	661.9	3588.4	1177.2	5284.1	232.9
48	3160.5	244.7	3538.9	917.7	3802.6	180.0	4431.1	636.9	4444.4	16.2	3247.6	319.5
Ferulic acid												
0	1026.5	66.2	1061.9	197.1	0.0	0.0	0.0	0.0	1030.9	143.8	1081.4	148.3
6	869.4	146.1	1033.3	151.7	886.3	136.2	1014.0	155.4	1003.6	317.2	915.1	148.6
12	578.8	81.6	495.4	43.2	261.6	79.2	268.0	28.6	202.8	85.8	206.2	57.8
24	434.7	8.6	575.2	56.3	132.2	18.6	210.5	61.6	164.0	89.1	68.3	18.3
48	466.2	36.3	302.2	13.0	355.1	15.0	175.4	36.0	244.2	64.3	118.7	0.0
Protocatechuic acid												
0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
6	69.0	0.8	109.5	0.0	303.7	196.7	138.3	0.0	125.3	27.4	300.4	0.0

12	718.7	59.5	729.8	49.6	1128.0	1.2	555.5	90.4	995.8	364.8	784.6	82.4
24	1206.4	57.6	1021.1	127.1	905.7	46.2	525.4	61.8	736.6	316.2	600.4	122.3
48	625.2	49.5	869.3	203.4	631.1	70.8	753.2	16.4	693.4	149.2	494.6	3.8

The values are the average of three fermentations.

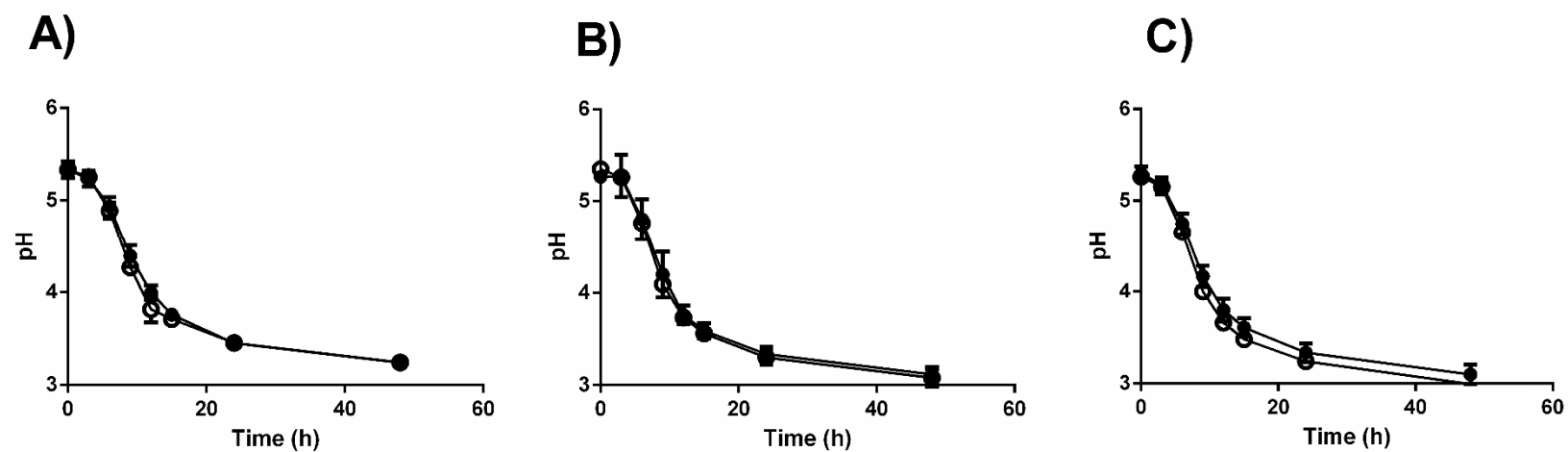


Figure S1. Change in pH of medium fermented by *Lactobacillus rhamnosus* R0011, ATCC 9595 and RW-9595M in mono (solid) and co-culture (open) fermentation. The values are the average of three fermentations and the bars represent the standard error deviation.

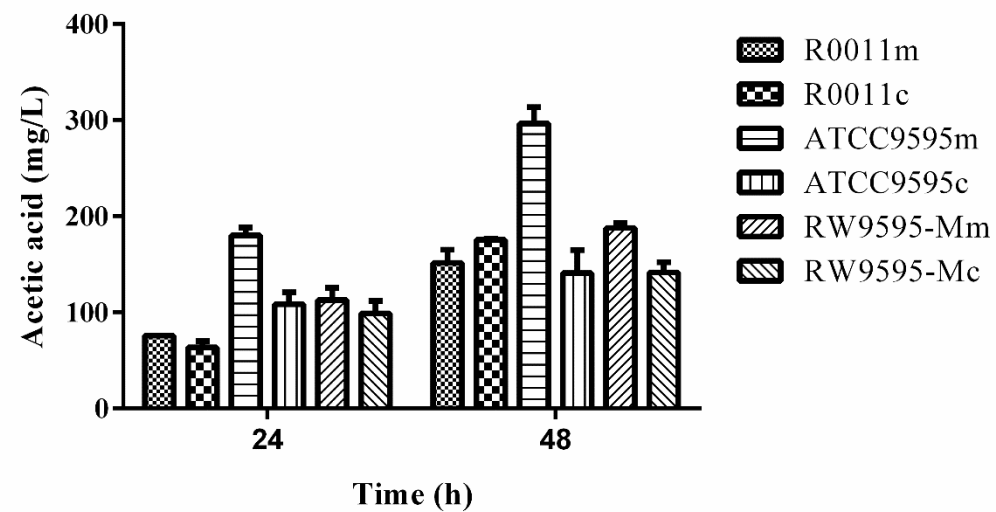


Figure S2. Acetic acid produced by *Lactobacillus rhamnosus* R0011, ATCC 9595 and RW-9595M in mono (m) and co-culture (c) at 24 and 48 h of fermentation. The values are the average of three fermentations and the bars represent the standard error deviation.