

## Supplementary Materials

**Table S1.** Identity of yeast isolates from traditional sourdoughs around Botswana using the ITS region. All sequences were last blasted on the 31st of July 2024.

Sample name	Yeast isolate	No. of bases	Query cover	% Identity	Accession number	Repository Accession number
FJ1-A1	<i>Saccharomyces cerevisiae</i>	817	99%	99.26%	CP006426.1	PP864082
FJ2-A1	<i>Saccharomyces cerevisiae</i>	800	99%	99.87%	KY596697.1	PP864080
FJ2-A2	<i>Wickerhamomyces anomalus</i> <sup>aff</sup>	565	96%	81.72%	KT175191.1	None
FJ2-A3	<i>Saccharomyces cerevisiae</i>	815	99%	99.25%	CP006426.1	PP864081
GT1-A1	<i>Saccharomyces cerevisiae</i> <sup>aff</sup>	682	99%	98.02%	OP764057.1	PP864083
GA1-A1	<i>Pichia kudriavzevii</i>	636	95%	90.30%	OP764057.1	PP864074
MN1-A1	<i>Saccharomyces cerevisiae</i>	805	99%	99.50%	KY596697.1	PP864084
MN1-A2	<i>Pichia membranifaciens</i>	444	99%	100%	KY495728.1	PP864091
MN1-A3	<i>Saccharomyces cerevisiae</i>	799	99%	99.62%	KY596697.1	PP864078
GD1-A1	<i>Saccharomyces cerevisiae</i>	797	99%	99.62%	KT958553.1	PP864079
GD1-A2	<i>Pichia kudriavzevii</i>	479	98%	99.58%	CP039617.1	PP864085
GD1-A3	<i>Pichia kudriavzevii</i>	478	99%	99.58%	KY457575.1	PP864086
GD1-A4	<i>Saccharomyces cerevisiae</i>	493	97%	99.38%	KU500417.1	
TB1-A1	<i>Saccharomyces cerevisiae</i>	801	99%	99.62%	KY495744.1	PP864076
TB1-A2	<i>Saccharomyces cerevisiae</i>	799	99%	99.25%	LC576585.1	PP864077
RK1-A1	<i>Saccharomyces cerevisiae</i>	846	96%	99.14%	CP006426.1	PP864075
RK1-A2	<i>Saccharomyces cerevisiae</i> <sup>aff</sup>	601	100%	87.52%	MW856066.1	None

ME1-A1	<i>Kazachstania unispora</i>	693	99%	100%	MK268124.1	PP864089
ME1-A2	<i>Kazachstania unispora</i>	694	99%	100%	MK268124.1	PP864090
UK1-A1	<i>Kazachstania humilis</i>	655	99%	99.51%	LS974436.1	PP864087
UK1-A2	<i>Kazachstania humilis</i>	688	99%	99.52%	JQ726600.1	PP864088
Baker's yeast	<i>Saccharomyces cerevisiae</i> <sup>aff</sup>	629	100%	97.82%	KF447149.1	

**Table S2.** Identity of lactic acid bacteria from traditional sourdoughs around Botswana using 16S region. All sequences were last blasted on the 31<sup>th</sup> of July 2024.

Sample name	Bacterium	No. of bases	Query cover	% Identity	Accession	Repository Accession no.
GD1-B1	<i>Lactiplantibacillus plantarum</i>	967	99%	99.38%	MT463431.1	PP860773
GD1-B2	<i>Lactiplantibacillus Plantarum</i>	896	100 %	99.41 %	MT611900.1	PP860774
GD1-B3	<i>Lactiplantibacillus plantarum</i>	1013	99%	99.51%	CP052869.1	PP860775
GD1-B4	<i>Lactiplantibacillus plantarum</i>	825	100%	100%	OR520803.1	PP860791
GA1-B1	<i>Lacticaseibacillus paracasei</i>	964	100%	99.48%	MT538398.1	PP860776
RK1-B4	<i>Liquorilactobacillus nageli</i>	540	99%	99.07%	ON705146.1	PP860792
FJ2-B3	<i>Lacticaseibacillus paracasei</i>	867	99%	86.72%	AB759528.1	PP860789
ME1-B1	<i>Lentilactobacillus parabuchneri</i>	1095	99%	88.56%	ON125464.1	PP860788
ME1-B2	<i>Liquorilactobacillus nageli</i>	804	100%	100%	MT597696.1	PP860787
GT1-B1	<i>Lactiplantibacillus Plantarum</i>	972	99%	96.60%	ON384540.1	

**Table S3.** Identity of *Bacillus* and other bacteria from traditional sourdoughs around Botswana using 16S region. All sequences were last blasted on the 31<sup>th</sup> of July 2024.

Sample name	Bacillus and other bacteria	No. of bases	Query cover (%)	% identity	Accession	Repository Accession no.
GA1-B2	<i>Bacillus cereus</i>	1063	99%	99.43%	ON740901.1	PP860777
RK1-B1	<i>Bacillus carboniphilus</i>	1020	100%	99.32%	KC494304.1	PP860780
RK1-B2	<i>Bacillus siamensis</i>	1066	99%	98.91%	AB813716.1	PP860778
RK1-B3	<i>Bacillus cereus</i>	1034	100%	99.52%	MK479915.1	PP860779
FJ1-B1	<i>Bacillus pumilus</i>	993	100%	99.80%	KT970980.1	PP860781
FJ2-B1	<i>Bacillus zhangzhouensis</i>	913	100%	100%	CP119300.1	PP860782
FJ2-B2	<i>Bacillus cereus</i>	1057	100%	99.34%	OP984781.1	PP860783
MN1-B1	<i>Bacillus stratosphericus</i>	1093	99%	99.09%	MG561355.1	PP860784
MN1-B2	<i>Bhagavaea ginsengi</i>	1098	99%	99.65%	MN121192.1	PP860785
TB1-B1	<i>Lysinibacillus halotolerans</i>	1136	99%	97.33%	OM142568.1	PP860786
UK1-B1	<i>Bacillus thuringiensis</i>	964	99%	85.49%	OR741996.1	PP860793
UK1-B2	<i>Bacillus licheniformis</i>	1064	99%	87.02%	MW282868.1	PP860794

**Table S4.** Identity of Acetic acid bacteria from traditional sourdough around Botswana. All sequences were last blasted on the 10th of June 2024

Sample name	Acetic acid bacteria	No. of bases	Query cover (%)	% identity	Accession	Repository Accession no.
GA1-C1	<i>Acetobacter pasteurianus</i>	820	99 %	99.63 %	MH845625.1	PP864057
FJ1-C1	<i>Acetobacter pasteurianus</i>	813	99 %	99.88 %	EU096228.1	PP864057
GD1-C1	<i>Acetobacter indonesiensis</i>	537	95 %	84.27 %	AB906412.1	None
UK1-C1	<i>Acetobacter malorum</i>	813	99 %	99.97 %	EU096228.1	PP864058

**Table S5.** Yeast isolates and sequences used for phylogenetic analysis and PCR-RFLP

Yeast isolates	Sequence
> <i>Saccharomyces cerevisiae</i> (FJ2-A1)	AATTTTAATAATTTTGAAATGGATTTTTTTTTTGTGTTTGGCAAGAGCATG AGAGCTTTTACTGGGCAAGAAGACAAGAGATGGAGAGTCCAGCCGGG CCTGCGCTTAAGTGC GCGGTCTTGCTAGGCTTGTAAGTTTCTTTCTTGCT ATTCCAAACGGTGAGAGATTTCTGTGCTTTTGTTATAGGACAATTAAAA CCGTTTCAATACAACACACTGTGGAGTTTTTCATATCTTTGCAACTTTTT CTTTGGGCATTCGAGCAATCGGGGCCAGAGGTAACAAACACAAACAA TTTTATCTATTCATTAAATTTTTGTCAAAAACAAGAATTTTCGTAAGTG GAAATTTTAAAATATTA AAAACTTTCAACAACGGATCTCTTG GTTCTCG CATCGATGAAGAACGCAGCGAAATGCGATACGTAATGTGAATTGCAGA ATTCCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCCCTTGGTATT CCAGGGGGCATGCCTGTTTGAGCGTCATTTCTTCTCAAACATTCTGTT TGGTAGTGAGTGATACTCTTTGGAGTTAACTTGAAATTGCTGGCCTTTT TCATTGGATGTTTTTTTTTCCAAAGAGAGGTTTCTCTGCGTGCTTGAGGT ATAATGCAAGTACGGTCGTTTTAGGTTTTACCAACTGCGGCTAATCTTT TTTATACTGAGCGTATTGGAACGTTATCGATAAGAAGAGAGCGTCTAG GCGAACAATGTTCTTAAAGTTTGACCTCAAATCAGGTAGGAGTACCCG CTGA ACTTAAGCATATCA
> <i>Wickerhamomyces anomalus</i> (FJ2-A2)	ATAATGAATTCTATTGCCAGCGCTTATTGCGCGGGCGATAACCTTACACA CATTGTCTAGTTTTTTTTGAACTTTGCTTTGGGTGGTGAGCCTGGCTTACT GCCCAAAGGTCTAAACACATTTTTTTTTATGGTTAAACCTTTACCCATT ATCCTTAAAATTTTTTACCAAATTA AAAATTTTTCAA AATTTTCACCAC

	CGAACCTTTGGGTCCCCCACCATAAAAAACCCACCAAATGGCAATC CTAATGGGAATTGGCAAATTTCTGAAACCTCCAAACCTTTAAACCCCT TGGCCCCCCCCGGAATCCCAAAGGGAATGCCGGTTTAACCGCCTTTTTT CTCTCAACCCCTTCGGGTGGGATTTAAGGGATACCCTGCCAGGGGTAA CCTGGAATAATGGACTAACCAAAAGGGAACAATAAACCATCCTTCTTA AAAAAAGGAATAAGGTCCCTCCACTCCGTATTATCACCTAGGCGGGTT AAAAAGAATTTAAGGTCCGGTTAACCAACCATTAACCTAAAAGTTGAAC CCCAAACCAGGAAGAATAACCCCTTAACTT
> <i>Saccharomyces cerevisiae</i> (FJ2-A3)	GAATTTATAATTTTGAAATGGATTTTTTTTTTTGTTTTGGCAAGAGCATG AGAGCTTTTACTGGGCAAGAAGACAAGAGATGGAGAGTCCAGCCGGG CCTGCGCTTAAGTGCGCGGTCTTGCTAGGCTTGTAAGTTTCTTTCTTGCT ATTCCAAACGGTGAGAGATTTCTGTGCTTTTGTATAGGACAATTA CCGTTTCAATACAACACACTGTGGAGTTTTTCATATCTTTGCAACTTTTT CTTTGGGCATTCGAGCAATCGGGGCCAGAGGTAACAAACACAAACAA TTTTATCTATTCATTAAATTTTTGTCAAAAACAAGAATTTTCGTA GAAATTTTAAAATATTA AAAAACTTTCAACAACGGATCTCTTGGTTCTCG CATCGATGAAGAACGCAGCGAAATGCGATACGTAATGTGAATTGCAGA ATTCCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCCCTTGGTATT CCAGGGGGCATGCCTGTTTGAGCGTCATTTCCCTTCTCAAACATTCTGTT TGGTAGTGAGTGATACTCTTTGGAGTTAACTTGAAATTGCTGGCCTTTT TCATTGGATGTTTTTTTTTCCAAAGAGAGGTTTCTCTGCGTGCTTGAGGT ATAATGCAAGTACGGTCGTTTTAGGTTTTACCAACTGCGGCTAATCTTT TTTATACTGAGCGTATTGGAACGTTATCGATAAGAAGAGAGCGTCTAG GCGAACAATGTTCTTAAAGTTTGACCTCAAATCAGGTAGGAGTACCCG CTGAACCTTAAGCATATCATAAGGCGGAGGAAGGA
> <i>Saccharomyces cerevisiae</i> (FJ1-A1)	CAAAGATTTAATAATTTTGAAATGGATTTTTTTTTTTGTTTTGGCAAGAGC ATGAGAGCTTTTACTGGGCAAGAAGACAAGAGATGGAGAGTCCAGCC GGGCCTGCGCTTAAGTGCGCGGTCTTGCTAGGCTTGTAAGTTTCTTTCT TGCTATTCCAAACGGTGAGAGATTTCTGTGCTTTTGTATAGGACAATT AAAACCGTTTCAATACAACACACTGTGGAGTTTTTCATATCTTTGCAAC TTTTTCTTTGGGCATTCGAGCAATCGGGGCCAGAGGTAACAAACACA AACAATTTTATCTATTCATTAAATTTTTGTCAAAAACAAGAATTTTCGT AACTGGAAATTTTAAAATATTA AAAAACTTTCAACAACGGATCTCTTGGT TCTCGCATCGATGAAGAACGCAGCGAAATGCGATACGTAATGTGAATT GCAGAATTCCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCCCTTG GTATTCCAGGGGGCATGCCTGTTTGAGCGTCATTTCCCTTCTCAAACATT CTGTTTGGTAGTGAGTGATACTCTTTGGAGTTAACTTGAAATTGCTGGC CTTTTTCATTGGATGTTTTTTTTTCCAAAGAGAGGTTTCTCTGCGTGCTT GAGGTATAATGCAAGTACGGTCGTTTTAGGTTTTACCAACTGCGGCTAA TCTTTTTTATACTGAGCGTATTGGAACGTTATCGATAAGAAGAGAGCGT CTAGGCGAACAATGTTCTTAAAGTTTGACCTCAAATCAGGTAGGAGTA CCCGCTGAACCTTAAGCATATCATAAAGCGGAGGAAGG
> <i>Saccharomyces cerevisiae</i> (MN1-A1)	GAATTTAATAATTTTGAAAATGGATTTTTTTTTTTGTTTTGGCAAGAGCAT GAGAGCTTTTACTGGGCAAGAAGACAAGAGATGGAGAGTCCAGCCGG GCCTGCGCTTAAGTGCGCGGTCTTGCTAGGCTTGTAAGTTTCTTTCTTG CTATTCCAAACGGTGAGAGATTTCTGTGCTTTTGTATAGGACAATTAA

	AACCGTTTCAATACAACACACTGTGGAGTTTTTCATATCTTTGCAACTT TTTCTTTGGGCATTTCGAGCAATCGGGGCCAGAGGTAACAAACACAAA CAATTTTATCTATTCATTAAATTTTTGTCAAAAACAAGAATTTTCGTAA CTGGAAATTTTAAAATATTA AAAA ACTTTCAACAACGGATCTCTTGGTTC TCGCATCGATGAAAAACGCAGCGAAATGCGATACGTAATGTGAATTGC AAAATTCCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCCCTTGGT ATTCCAGGGGGCATGCCTGTTTGAGCGTCATTTCCCTTCTCAAACATTCT GTTTGGTAGTGAGTGATACTCTTTGGAGTTAACTTGAAATTGCTGGCCT TTTTCATTGGATGTTTTTTTTTCCAAAAAGAGGTTTCTCTGCGTGCTTGA GGTATAATGCAAGTACGGTCGTTTTAGGTTTTACCAACTGCGGCTAATC TTTTTTATACTGAGCGTATTGGAACGTTATCGATAAGAAGAGAGCGTCT AGGCGAACAAATGTTCTTAAAGTTTGACCTCAAATCAGGTAGGAGTACC CGCTGAACTTAAGCATATCATAAGG
> <i>Pichia membranifaciens</i> (MN1-A2)	ATAACCAACACCACACTGTGTGGGCGCACAAAACACCTAAACCTGGAG TATACACACGTCAACAAAAGATCTAAAAGAATAAACTTTCAACAACG GATCTCTTGGTTCTCGCATCGATGAAGAGCGCAGCGAAATGCGATACC TAGTGTGAATTGCAGCCATCGTGAATCATCGAGTTCTTGAACGCACATT GCGCCCGTCGGTATTCCGGCGGGGCATGCCTGTCTGAGCGTCGTTTCCTT CTTGTGCACCGGGGGTCTTTGCTGATCTTCTGTGCGCAGAGCTGGCCGT GCCACTGGCCCGGCCGAAAAGAAACGTTGCGGACGAAGCGAACTACA TCGGGACGCTTTGGCCGCCGAGCGAAAAAACACCATTGAGCTCGACCT CAGATCAGGTAGGAGTACCCGCTGAACTTAAGCATATCAATAAGCGGA GGAAGATATT
> <i>Saccharomyces cerevisiae</i> (MN1-A3)	AATTTAATAATTTTGAAATGGATTTTTTTTTTTGTTTTGGCAAGAGCATG AGAGCTTTTACTGGGCAAGAAGACAAGAGATGGAGAGTCCAGCCGGG CCTGCGCTTAAGTGCGCGGTCTTGCTAGGCTTGTAAGTTTCTTTCTTGCT ATTCCAAACGGTGAGAGATTTCTGTGCTTTTGTTATAGGACAATTA AAA CCGTTTCAATACAACACACTGTGGAGTTTTTCATATCTTTGCAACTTTTT CTTTGGGCATTTCGAGCAATCGGGGCCAGAGGTAACAAACACAAACAA TTTTATCTATTCATTAAATTTTTGTCAAAAACAAGAATTTTCGTA ACTG GAAATTTTAAAATATTA AAAA ACTTTCAACAACGGATCTCTTGGTTCTCG CATCGATGAAAAACGCAGCGAAATGCGATACGTAATGTGAATTGCAGA ATTCCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCCCTTGGTATT CCAGGGGGCATGCCTGTTTGAGCGTCATTTCCCTTCTCAAACATTCTGTT TGGTAGTGAGTGATACTCTTTGGAGTTAACTTGAAATTGCTGGCCTTTT TCATTGGATGTTTTTTTTTCCAAAAAGAGGTTTCTCTGCGTGCTTGAGGT ATAATGCAAGTACGGTCGTTTTAGGTTTTACCAACTGCGGCTAATCTTT TTTATACTGAGCGTATTGGAACGTTATCGATAAGAAGAGAGCGTCTAG GCGAACAAATGTTCTTAAAGTTTGACCTCAAATCAGGTAGGAGTACCCG CTGAACTTAAGCATATCA
> <i>Saccharomyces cerevisiae</i> (GD1-A1)	GAATTTAATAATTTTGAAATGGATTTTTTTTTGTTTTGGCAAGAGCATGAG AGCTTTTACTGGGCAAGAAGACAAGAGATGGAGAGTCCAGCCGGGCCT GCGCTTAAGTGCGCGGTTTTGCTAGGCTTGTAAGTTTCTTTCTTGCTATT CCAAACGGTGAGAGATTTCTGTGCTTTTGTTATAGGACAATTA AAAACCG TTTCAATACAACACACTGTGGAGTTTTTCATATCTTTGCAACTTTTTCTTT GGGCATTTCGAGCAATCGGGGCCAGAGGTAACAAACACAAACAATTTT

	<p>ATTTATTCATTAAATTTTTGTCAAAAACAAGAATTTTCGTAACCTGGAAA  TTTTAAAATATTA AAAA ACTTTCAACAACGGATCTCTTGGTTCTCGCATC  GATGAAGAACGCAGCGAAATGCGATACGTAATGTGAATTGCAGAATTC  CGTGAATCATCGAATCTTTGAACGCACATTGCGCCCCTTGGTATTCCAG  GGGGCATGCCTGTTTGAGCGTCATTTCCTTCTCAAACATTCTGTTTGGT  AGTGAGTGATACTCTTTGGAGTTAACTTGAAATTGCTGGCCTTTTCATT  GGATGTTTTTTTTTCCAAAGAGAGGTTTCTCTGCGTGCTTGAGGTATAAT  GCAAGTACGGTCGTTTTAGGTTTTACCAACTGCGGCTAATCTTTTTTAT  ACTGAGCGTATTGGAACGTTATCGATAAGAAGAGAGCGTCTAGGCGAA  CAATGTTCTTAAAGTTTGACCTCAAATCAGGTAGGAGTACCCGCTGAA  CTTAAGCATATCATAA</p>
> <i>Pichia kudriavzeii</i> (GD1-A2)	<p>GGGGATTACTACTACACATGCGTGAGCGGAACGAAAACAACAACACCT  AAATGTGGAATATAGCATATAGTCGACAAGAGAAATCTACGAAAAAA  CAAACAAAACCTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  AGCGCAGCGAAATGCGATACCTAGTGTGAATTGCAGCCATCGTGAATC  ATCGAGTTCTTGAACGCACATTGCGCCCCTCGGCATTCCGGGGGGCAT  GCCTGTTTGAGCGTCGTTTCCATCTTGCGCGTGCGCAGAGTTGGGGGAG  CGGAGCGGACGACGTGTAAAGAGCGTCGGAGCTGCGACTCGCCTGAA  AGGGAGCGAAGCTGGCCGAGCGAACTAGACTTTTTTTTCAGGGACGCTT  GGCGGCCGAGAGCGAGTGTTGCGAGACAACAAAAAGCTCGACCTCAA  ATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGA  A</p>
> <i>Pichia kudriavzeii</i> (GD1-A3)	<p>GGGAATTTACTACTACTGCGTGAGCGGACGAAAACAACAACACCTA  AAATGTGGAATATAGCATATAGTCGACAAGAGAAATCTACGAAAAAC  AAACAAAACCTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAGA  GCGCAGCGAAATGCGATACCTAGTGTGAATTGCAGCCATCGTGAATCA  TCGAGTTCTTGAACGCACATTGCGCCCCTCGGCATTCCGGGGGGCATG  CCTGTTTGAGCGTCGTTTCCATCTTGCGCGTGCGCAGAGTTGGGGGAGC  GGAGCGGACGACGTGTAAAGCGCGTCGGAGCTGCGACTCGCCTGAAA  GGGAGCGAAGCTGGCCGAGCGAACTAGACTTTTTTTTCAGGGACGCTTG  GCGGCCGAGAGCGAGTGTTGCGAGACAACAAAAAGCTCGACCTCAAA  TCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAA</p>
> <i>Saccharomyces cerevisiae</i> (GD1-A4)	<p>CAAGAATTTAATAATTTTGAAATGGGTTTTTTTTTTTTTTTGTTTTGGAAA  AGCATGAAAGCTTTTCCGGGGGCAAAAAAACA AAAAAGGGAAAGCCCC  CCCGGGCCCGCCCTTAAGGGCGCGGCCTTGCTAGGCTTGTAAGTTTCTT  TCTTGTTTTTCCAAACGGGGAAAAATTTCTGGGTTTTTGTATAGGACA  ATAAAAACCGTTTCAAAACACCCCCCGGGGGAGTTTTTCATATCTTTC  ACCTTTTTTCTTTGGGCATTCAACCAACCGGGGCCCAAAGGAAACAAAC  CCAAACAATTTTATCTATTCTTTAAATTTTTGTCAAAAACA AAAATTTT  CGAAACGGGAAATTTTAAAAAATAAAAAACTTTCAACACCGGATCTCT  TGGTTCCCCCTCAATAAAAAACCCCCCAAAAGGCGAAACGAAAGGG  GAATTGCAAAATCCCGGGAATCCCCAAATCTTTGAACCCCTTTGCCCC  CCTGGGTTTTTCCGGGGGGCATGCCGTTTGAGCGCCTTTTCCTTCCCAA  ACATTCTGTTGGGGAGGGAGGGAAACTCTTTGGAGTAACTTGAAATT  GCGGCCCTTTTTCTTTGAAGGTTTTTTTTTTTTTCCAAAAAAGGTTTTT  CCGG</p>

> <i>Pichia kudriavzevii</i> (GA1-A1)	GGGGAAATTACTACTACACTGCGTGAGCGGACGAAAACAACAACACCT AAATGTGGAATATAGCATATAGTCGACAAGAGAAATCTACGAAAAAA CAAACAAAACCTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG AGCGCAGCGAAATGCGATACCTAGTGTGAATTGCAGCCATCGTGAATC ATCGAGTTCTTGAACGCACATTGCGCCCCCTCGGCATTCCGGGGGGCAT GCCTGTTTGAGCGTCGTTTCCATCTTGCGCGTGCGCAGAGTTGGGGGAG CGGAGCGGACGACGTGTAAAGAGCGTCGGAGCTGCGACTCGCCTGAA AGGGAGCGAAGCTGGCCGAGCGAACTAGACTTTTTTTCAGGGACGCTT GGCGGCCGAGAGCGAGTGTTGCGAGACAACAAAAAGCTCGACCTCAA ATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGA AAGGATCAGTACTGT
> <i>Saccharomyces cerevisiae</i> (RK1-A1)	TAGGAAATTTTAATAAATTTTGAAATGGATTTTTTTTTTTGTTTTGGCAAG AGCATGAGAGCTTTTACTGGGCAAGAAGACAAGAGATGGAGAGTCCA GCCGGGCCTGCGCTTAAGTGCGCGGTCTTGCTAGGCTTGTAAGTTTCTT TCTTGCTATTCCAAACGGTGAGAGATTTCTGTGCTTTTGTTATAGGACA ATTAAAACCGTTTCAATACAACACACTGTGGAGTTTTTCATATCTTTGC AACTTTTTCTTTGGGCATTCGAGCAATCGGGGCCCAGAGGTAACAAAC ACAAACAATTTTATCTATTCATTAAATTTTTGTCAAAAACAAGAATTTT CGTAACTGGAAATTTTAAAATATTA AAAA ACTTTCAACAACGGATCTCTT GGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATACGTAATGTGA ATTGCAGAATTCCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCC TTGGTATTCCAGGGGGGCATGCCTGTTTGAGCGTCATTTCTCTCAAAC ATTCTGTTTGGTAGTGAGTGATACTCTTTGGAGTTAACTTGAAATTGCT GGCCTTTTTTCATTGGATGTTTTTTTTTTCCAAAGAGAGGTTTCTCTGCGTG CTTGAGGTATAATGCAAGTACGGTCGTTTTAGGTTTTACCAACTGCGGC TAATCTTTTTTATACTGAGCGTATTGGAACGTTATCGATAAGAAGAGAG CGTCTAGGCGAACAATGTTCTTAAAGTTTGACCTCAAATCAGGTAGGA GTACCCGCTGAACTTAAGCATATCATAAAGCGGAGGAAAGATCAATAG GAACTTTAATAATTTGA
> <i>Saccharomyces cerevisiae</i> (RK1-A2)	TTAATAATTTTGAAATGGATTTTTTTTTTTGTTTGGGCAAAACCTTGAAA CTTTTTCCGGGGGCAAAAAAACA AAAAAGGGAAAGCCCACCCGGGCCG GCCCTTAAGGGCCCGGCCTGGTTAGGTTGGAAAGTTCCTTTCTGGTTTT CCCAACCGGGGAAAAATTCCGGGGTTTTTGTATTAGGACAATAAAACC CGTTCCAAACACCCCCCGGGGAAGTTTTTCTTATCTTTGCACTTTTTTC TTGGGGCTTCCAACCAACCGGGGCCCAAAGGCACCAACCCCAACCAAT TTTTTCTTTTCTTTAAATTTTGCCAAAACCAAAAATTTCCGAACCGGA AAATTTTAAAAAATAAAAAACTTTTACCACCGAACCCCTGGGTCCCCC CTCCAATAAAAAACCCACCAATGGCAAACCGAATGGGGAATGGCAA AATCCCGGGAACCAACCAACCTTTAAACCCCTTGCCCCCCTGGGAA TCCCAGGGGGCTGGCCGGTTTAACCGCCTTTCTTCTCCAACCTTTTCGG TTTGAAGGGAGGGATACCCTTGGAAGTAACTTTGAAATGGTGGGCTT TTTCTTGGAAGGTTTTTTTTT
> <i>Saccharomyces cerevisiae</i> (TB1-A1)	AAAATTTAATAATTTTGAAATGGATTTTTTTTTGTTTTGGCAAGAGCAT GAGAGCTTTTACTGGGCAAGAAGACAAGAGATGGAGAGTCCAGCCGG GCCTGCGCTTAAGTGCGCGGTCTTGCTAGGCTTGTAAGTTTCTTTCTTG CTATTCCAAACGGTGAGAGATTTCTGTGCTTTTGTTATAGGACAATTAA



	AACCGTTTCAATACAACACACTGTGGAGTTTTTCATATCTTTGCAACTTT TTCTTTGGGCATTTCGAGCAATCGGGGCCAGAGGTAACAAACACAAAC AATTTTATCTATTCATTAAATTTTTGTCAAAAACAAGAATTTTCGTAAC TGGAAATTTTAAAATATTA AAAA ACTTTCAACAACGGATCTCTTGGTTCT CGCATCGATGAAGAACGCAGCGAAATGCGATACGTAATGTGAATTGCA GAATTCCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCCTTGGTA TTCCAGGGGGCATGCCTGTTTGAGCGTCATTTCTTCTCAAACATTCTG TTTGGTAGTGAGTGATACTCTTTGGAGTTAACTTGAAATTGCTGGCCTT TTCATTGGATGTTTTTTTTTCCAAAGAAAGGTTTCTCTGCGTGCTTGAGGT ATAATGCAAGTACGGTCGTTTTAGGTTTTACCAACTGCGGCTAATCTTT TTTTATACTGAGCGTATTGGAACGTTATCGATAAGAAGAGAGCGTCTA GGCGAACAATGTTCTTAAAGTTTGACCTCAATCAGGTAGGAGTACCCG CTGA ACTTAAGCATATCATAGG
> <i>Saccharomyces cerevisiae</i> (TB1-A2)	AATTTATAATTTTGAAATGGATTTTTTTTTGTTTTGGCAAGAGCATGAGA GCTTTTACTGGGCAAGAAGACAAGAGATGGAGAGTCCAGCCGGGCCTG CGCTTAAGTGCGCGGTCTTGCTAGGCTTGTAAGTTTCTTCTTGCTATTC CAAACGGTGAGAGATTTCTGTGCTTTTGTTATAGGACAATTA AAACCGT TTCAATACAACACACTGTGGAGTTTTTCATATCTTTGCAACTTTTTCTTTG GGCATTTCGAGCAATCGGGGCCAGAGGTAACAAACACAAACAATTTTA TTTATTCATTAAATTTTTGTCAAAAACAAGAATTTTCGTA ACTGGAAAT TTTAAATATTA AAAA ACTTTCAACAACGGATCTCTTGGTTCTCGCATCG ATGAAGAACGCAGCGAAATGCGATACGTAATGTGAATTGCAGAATTCC GTGAATCATCGAATCTTTGAACGCACATTGCGCCCCTTGGTATTCCAGG GGGCATGCCTGTTTGAGCGTCATTTCTTCTCAAACATTCTGTTTGGTA GTGAGTGATACTCTTTGGAGTTAACTTGAAATTGCTGGCCTTTTCATTG GATGTTTTTTTTTCCAAAAGAGGTTTCTCTGCGGGCTTGAGGTATAAT GCAAGAACGGCCGTTTTAGGTTTTACCAACTGCGGCTAATCTTTTTTAT ACTGAGCGTATTGGAACGTTATCGATAAGAAGAGAGCGTCTAGGCGAA CAATGTTCTTAAAGTTTGACCTCAAATCAGGTAGGAGTACCCGCTGAA CTTAAGCATATCAATAAG
> <i>Pichia kudriavzevii</i> (GT1-A1)	GGGGAAATTACTACTACACTGCGTGAGCGGACGAAAACAACAACACCT AAATGTGGAATATAGCATATAGTCGACAAGAGAAATCTACGAAAAAA CAAACAAA ACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG AGCGCAGCGAAATGCGATACCTAGTGTGAATTGCAGCCATCGTGAATC ATCGAGTTCTTGAACGCACATTGCGCCCCTCGGCATTCCGGGGGGCAT GCCTGTTTGAGCGTCGTTTCCATCTTGCGCGTGCGCAGAGTTGGGGGAG CGGAGCGGACGACGTGTAAAGAGCGTCGGAGCTGCGACTCGCCTGAA AGGGAGCGAAGCTGGCCGAGCGAACTAGACTTTTTTTCAGGGACGCTT GGCGGCCGAGAGCGAGTGTTGCGAGACAACAAAAGCTCGACCTCAA ATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGA AAGGATCAGTACTGT
> <i>Kazachstania unispora</i> (ME1-A1)	AATTATTCGTTGCTTTGCTTGGAGACACATACTGCCGAACCAGCGCTTA ATTGCGCGGTTTGGTGGGTCTCTGTAGCTCAGTAGCACTATTACACACT GTGGAGATTTTATAATTCTTTGCATGCTTCTTTGGGCAGCTTCGGCAGC CCAGAGGTAACAAACACAAACA ACTTTGTAATATTTTTAACCAGTCA AAACCAGAATTCCAGAAAGATTTATCTTTTTGTAATATTATAACAAATA

	<p>TTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAAC  GCAGCGAAATGCGATACGTAATGTGAATTGCAGAATTCCGTGAATCAT  CGAATCTTTGAACGCACATTGCGCCCCCTTGGTATTCCAGGGGGCATGCC  TGTTTGAGCGTCATTTCTTCTCAAACAGCAATGTTTGGTTGTGAGTGA  TACTCATTTCGAGTTAGCTTGAAATTGCTGGCCGATGGCTGTTGTGGCTG  AGTGTCTCCCTCGGGAGAGCACTTGCTGCGTTAGGGACGTCCTGCTGG  ACATCTTCGTACTAGGTTTTACCAATTTCGAGGACGGTTAGCGAGGCGG  CCTGCAGTGAGTGTAGTGCTTGACTACGTTGCACCATGGCGAACAGTG  TTCTTTTAAGTTTGACCTCAAATCAGGTAGGAGTACCCGCTGAACTTAA  GCATATCAATAG</p>
> <i>Kazachstania unispora</i> (ME1-A2)	<p>TAATTATTCGTTGCTTTGCTTGGAGACACATACTGCCGAACCAGCGCTT  AATTGCGCGGTTTGGTGGGTCTCTGTAGCTCAGTAGCACTATTACACAC  TGTGGAGATTTTATAATTCTTTGCATGCTTCTTTGGGCAGCTTCGGCAG  CCCAGAGGTAACAAACACAAACAACCTTTGTAATATTTTAAACCCAGTC  AAAACCAGAATTCCAGAAAGATTTATCTTTTTTGTAAATATTATAACAAAT  ATTCAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAA  CGCAGCGAAATGCGATACGTAATGTGAATTGCAGAATTCCGTGAATCA  TCGAATCTTTGAACGCACATTGCGCCCCCTTGGTATTCCAGGGGGCATGC  CTGTTTGAGCGTCATTTCTTCTCAAACAGCAATGTTTGGTTGTGAGTG  ATACTCATTTCGAGTTAGCTTGAAATTGCTGGCCGATGGCTGTTGTGGCT  GAGTGTCTCCCTCGGGAGAGCACTTGCTGCGTTAGGGACGTCCTGCTG  GACATCTTCGTACTAGGTTTTACCAATTTCGAGGACGGTTAGCGAGGCG  GCCTGCAGTGAGTGTAGTGCTTGACTACGTTGCACCATGGCGAACAGT  GTTCTTTTAAGTTTGACCTCAAATCAGGTAGGAGTACCCGCTGAACTTA  AGCATATCAATAG</p>
> <i>Kazachstania humilis</i> (UK1-A1)	<p>TGATTGGGGGAGCCCGCCTGCGCTTAGCTGCGCGGTGGCGTTCCACCT  CTTACACACAGTGGAGTAATTACTTATTCTTGGGCTGAGCGAAAGCTCT  GCTCGCCAAACACAAACAACCTATTTTTTATTATACAATGTCATCAAATC  TGCTTACGCAGTAACCAAAATATTCAAACTTTCAACAACGGATCTCTT  GGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATACGTAATGTGA  ATTGCAGAATTCCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCC  TTGGTATTCCAGGGGGCATGCCTGTTTGAGCGTCATTTCTTCTCAAGC  ACCTGTGCTTGGTTGTGGGTGACACTCTCTCGAGTTAGCTTGAAATTGC  TGGCCGCACTGCGGTGGAGCAGTTGGCTTGCTGTCTGTCGTGCGCGGTGCCT  CGGCGCCGGGCGTGGCTGGCATGCGATTGTCGTACTAGGTTTTACCAA  TTCGGCAGGAGCGTGCTGGGCAGAGAGACAATAACAACCGCCCTCCCC  TGGCTAACAGTACTCTTTAAGTTTGACCTCAAATCAGGTAGGAATACCC  GCTGAACTTAAGCATATCAATAAGGCGGAGGAACATTAAGAATGATTG  GGGAGCCCGCCTGCGCTTACTC</p>
> <i>Kazachstania humilis</i> (UK1-A2)	<p>TAAAAATGATTGGGGGAGCCGCCTGCGCTTAGCTGCGCGGTGGCGTTC  CACCTCTTACACACAGTGGAGTAATTACTTATTCTTGGGCTGAGCGAAA  GCTCTGCTCGCCAAACACAAACAACCTATTTTTTATTATACAATGTCATC  AAATCTGCTTACGCAGTAACCAAAATATTCAAACTTTCAACAACGGA  TCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATACGTA  ATGTGAATTGCAGAATTCCGTGAATCATCGAATCTTTGAACGCACATTG  CGCCCTTGGTATTCCAGGGGGCATGCCTGTTTGAGCGTCATTTCTTCTC</p>

	TCAAGCACCTGTGCTTGGTTGTGGGTGACACTCTCTCGAGTTAGCTTGA AATTGCTGGCCGCACTGCGGTGGAGCAGTTGGCTTGTCTGTCGTGCGC GGTGCCTCGGCGCCGGGCGTGGCTGGCATGCGATTGTCGTACTAGGTT TTACCAATTCGGCAGGAGCGTGCTGGGCAGAGAGACAATACAACCGCC CTCCCCCTGGCTAACAGTACTCTTTAAGTTTGACCTCAAATCAGGTAGG AATACCCGCTGAACTTAAGCATATCAATAAGGCGGAGGAATCTTAAAG AAATGATTGGGGGAGCCCCGCTGCGCTTAGCTGCGCGG
> <i>Saccharomyces cerevisiae</i> (BY)	TAAAAATTTTAATAATTTTGAAATGGATTTTTTTTTTTTTTTGGGAAAG AATGAGAGATTTTTCTGGGCAAAAAACACAAAAAGGGGAGACCCCC CCCGGCCCCGCTTTAAAGCGCGGGCTTGTGCGGGGTGTGAATTTCTTTT TTGTGATTCCCACGGGGAGAAAATTCTCTGCTTTTTTTTTTATGACAAA AAAAACCCCTTCCCAACACCACCCTGTGGGGATTTCTCATCTTTGCGCC TTTTTCTTTGGGGGTTCCTCGCACACGGGGCCCCCAGGGGAAAAAAACC AAAAACTTTTTTTTTTTCTTTAAATTTTTTTCAAAAAAATAATTTCCC AAAGGGGAAATTTAAAAAATAAAAAAATTTTCCAACCGGGCCCCCTCGG GCCCCCCCCCCCCAAAAAAACCCCCAAAAAGGGAAACCCATGGGGAA TTTGGAATAATCCCCGAAAACCCCAAATTTTTAAACCCCTTTGCCCCC CGGGTTTCCCGGGGGGGGGCCCCGTTTTGGGGCCTTTTCCCCTCCAAAAA TTTGGTTGGGGGAGGGGGGAACCCTTTGAAGAAAACCTCAAATGGTG GCCCCCTTCCGGAAGATTTTTTTTTTTCCAAAAAAGAGGTTTTTCTC

**Table S6.** Sequences for type strains/materials used for phylogenetic analysis.

Type strain/material	Sequences
>NR_111007.1 <i>Saccharomyces cerevisiae</i> CBS 1171 ITS	AAAGAAATTTAATAATTTTGAAAATGGATTTTTTTGTTTTGGCAAGA GCATGAGAGCTTTTACTGGGCAAGAAGACAAGAGATGGAGAGTCC AGCCGGGCTGCGCTTAAGTGCGCGGTCTTGCTAGGCTTGTAAGTT TCTTTCTTGCTATTCCAAACGGTGAGAGATTTCTGTGCTTTTGTTATA GGACAATTTAAACCGTTTCAATACAACACACTGTGGAGTTTTTCATA TCTTTGCAACTTTTTCTTTGGGCATTCGAGCAATCGGGGCCAGAGG TAACAAACACAAACAATTTTATCTATTCATTAAATTTTTGTCAAAAA CAAGAATTTTCGTAACCTGGAAATTTTAAAAATATTTAAACCTTTCA ACAACGGATCTCTTGTTCTCGCATCGATGAAGAACGCAGCGAAAT GCGATACGTAATGTGAATTGCAGAATTCCGTGAATCATGAATCTTT GAACGCACATTGCCCCCTTGGTATTCCAGGGGGCATGCCTGTTTGA GCGTCATTTCTTCTCAAACATTCTGTTTGGTAGTGAGTGATACTCT TTGGAGTTAACTTGAAATTGCTGGCCTTTTCATTGGATGTTTTTTTC CAAAGAGAGGTTTCTCTGCGTGCTTGAGGTATAATGCAAGTACGGT CGTTTTAGGTTTTACCAACTGCGGCTAATCTTTTTTATACTGAGCGT ATTGGAACGTTATCGATAAGAAGAGAGCGTCTAGGCAACAATGTTC TTAAAGT
>NR_111210.1 <i>Wickerhamomyces anomalus</i> CBS 5759	TTCTATTGCCAGCGCTTAATTGCGCGGCGATAAACCTTACACACATT GTCTAGTTTTTTTTGAACTTTGCTTTGGGTGGTGAGCCTGGCTTACTG CCCAAAGGTCTAAACACATTTTTTTTTAATGTAAAACCTTTAACC TAGTCATGAAAATTTTTAACAAAAATTTAAATCTTCAAACTTTCA ACAACGGATCTCTTGTTCTCGCAACGATGAAGAACGCAGCGAAAT

	GCGATACGTATTGTGAATTGCAGATTTTCGTGAATCATCGAATCTTT GAACGCACATTGCACCCTCTGGTATTCCAGAGGGTATGCCTGTTTG AGCGTCATTTCTCTCTCAAACCTTCNNGTTTGGTATTGAGTGATACT CTGATCAAGGGTTAACTTGAAATATTGACTTAGCAAGAGTGTACTA ATAAGCAGTCTTTCTGAAATAATGTATTAGGTTCTTCCAACCTCGTTA TATCAGCTAGGCAGGTTTAGAAGTATTTTAGGCTCGGCTTAACAAC AATAACTAAAAGTTTGACCTCAAATCAGGTAGGACTACCCGCTGAA CTTAAGCATATCAT
>NR_131315.1 <i>Pichia kudriavzevii</i> ATCC 6258	AGGATCATTACTGTGATTTAGTACTACACTGCGTGAGCGGAACGAA AACAAACAACACCTAAAATGTGGAATATAGCATATAGTCGACAAGA GAAATCTACGAAAAACAAACAAAACCTTTCAACAACGGATCTCTTGG TTCTCGCATCGATGAAGAGCGCAGCGAAATGCGATACCTAGTGTGA ATTGCAGCCATCGTGAATCATCGAGTTCTTGAACGCACATTGCGCC CCTCGGCATTCCGGGGGGGCATGCCTGTTTGAGCGTCGTTTCCATCTT GCGCGTGCGCAGAGTTGGGGGAGCGGAGCGGACGACGTGTAAAGA GCGTCGGAGCTGCGACTCGCCTGAAAGGGAGCGAAGCTGGCCGAG CGAACTAGACTTTTTTTCAGGGACGCTTGGCGGCCGAGAGCGAGTG TTGCGAGACAACAAAAGCTCGACCTCAAATCAGGTAGGAATACC CGCTGAACCTTAAG
>NR_138187.1 <i>Kazachstania unispora</i> CBS 398	GCTTTGCTTGGAGACACATACTGCCGAACCAGCGCTTAATTGCGCG GTTTGGTGGGTCTCTGTAGCTCAGTAGCACTATTACACACTGTGGA GATTTTATAATTCTTTGCATGCTTCTTTGGGCAGCTTCGGCAGCCCA GAGGTAACAAACACAAACAACCTTTGTAATATTTTTTAACCCAGTCAA AACCAGAATTCCAGAAAGATTTATCTTTTTTGTAATATTATAACAAAT ATTCAAAACCTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAA GAACGCAGCGAAATGCGATACGTAATGTGAATTGCAGAATTCCGTG AATCATCGAATCTTTGAACGCACATTGCGCCCCCTTGGTATTCCAGG GGGCATGCCTGTTTGAGCGTCATTTCCTTCTCAAACAGCAATGTTTG GTTGTGAGTGATACTCATTCGAGTTAGCTTGAAATTGCTGCCGATGG CTGTTGTGGCTGAGTGTCTCCCTCGGGAGAGCACTTGCTGCGTTAG GGACGTCCTGCTGGACATCTTCGTACTAGGTTTTACCAATTTCGAGG ACGGTTAGCGAGGCGGCCTGCAGTGAGTGTAGTGCTTGACTACGTT GCACCATGGCGAACAGTGTTCTTTTAAGTTTGAACCTCAA
>AY046174.1 <i>Kazachstania humilis</i>	AAGAAATGATTGGGGGAGCCCGCCTGCGCTTAGCTGCGCGGTGGCG TTCCACCTCTTACACACAGTGGAGTAATTACTTATTCTTGGGCCGAG CGTAAGCTCAGCTCGCCAAACACAAACAACCTATTTTCTATTATACA ATGTCATCAAATCTGCTTACGCAGTAACCAAAATATTCAAAACCTT CAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAA ATGCGATACGTAATGTGAATTGCAGAATTCCGTGAATCATCGAATC TTTGAACGCACATTGCGCCCCCTTGGTATTCCAGGGGGGCATGCCTGTT TGAGCGTCATTTCCTTCTCAAGCACCTGTGCTTGGTTGTGGGTGACA CTCTCTCGAGTTAGCTTGAAATTGCTGGCCGCACTGCGGTGGAGCA GTTGGCTTGTCTGTCGTGCGCGGTGCCTCGGCGCCGGGCGTGGCTG GCATGCGATTGTCGTACTAGGTTTTACCAATTTCGGCAGGAGCATGG CAGACAGAGAGACAATAACAACCGCCCTCCCCCTGGCTAACAGTACT CTTTAAGT

>NR_111195.1 <i>Pichia membranifaciens</i> CBS 107	AACCTGCGGAAGGATCATTACTGTGATTATACCAACACCACACTGT GTGGGCGCACAAAACACCTAAACCTGGAGTATACACACGTCAACA AAAGATCTAAAAGAATAAAACTTTCAACAACGGATCTCTTGGTTCT CGCATCGATGAAGAGCGCAGCGAAATGCGATACCTAGTGTGAATTG CAGCCATCGTGAATCATCGAGTTCTTGAACGCACATTGCGCCCGTC GGTATTCCGGCGGGCATGCCTGTCTGAGCGTCGTTTCCTTCTTGTGC ACCGCGGGGTCTTTGCAGATCCTCTCTGCGCAGAGCTGGCCGTGCC ACTGGCCCGGCCGAAAAGAAACGTTGCGGACGAAGCGAACTACAT CGGGACGCTTTGGCCGCCGAGCGAAAAAAAACACCATTGAGCTC GACCTCAGATCAGGTAGGAGTACCCGCTGAACTTAA
>OW983270.1 <i>Schizosaccharomyces pombe</i>	GATCATTAGAAAAGTTATATGAAAAGGTTTTAAAAAATTTCCATCT TTTAACTTTTTTGGGAATTTTTTTTACCTTTTTTCTTCTTATCCATTTA CCTTTCTGTGAAAATGTAAAATATTTTCAATTTTGATTTTTTTTCTTT TTCTTTATATTTTTTTTATTAAAAAAAAGTGTTAGAAAAGAAAAAA GAAGAAAAAAAATGAAATTGTAAATATTACGAGTGGATGATTTT TGTTTGGGGGGTTTTTGTTCATGCCAAGCATATCATTACTTTTTTA CTATTTTATTTTATTTTATCATTTTTTCTATTCTTTTCYCTTTTTTTTAA ATATAAGGAAATTGGAAAARAAGCAAAATTAAATTATAAMCCTTG AAATTTGTTTTTGAAGTCTGAATTAATTATATCTAATATATAAAATT WTTTAAACCTTTCAGCAACGGATCTYTKGGCTCTCGCATCGATGAA RAACGCASCGAAATGCGATACGTAAKKGKAATTGCARAATTCCGKG AATCATCGAATYTTTGAACSCMCATTGCSCCTTKGGGTTYTMCCAA AGGCAYSCCTGTTTGAGKGTCAATACAATYTTYTCMAAAAAATKT TTTTTTTAAATATTTTTTGATGAGGTGTTGAACGAAAATTTGTTTTTTT TTTAAATATAAATTTAGTTTGAAATCGATTGGTGAAAACAAAAGG AAGATTGAAATTATTTTTCTATGCCTTTTTTTCATTTTTTTTTTCTATTG AACGTAATAGGTTTTACCACCTTTGTTTGATAGAAAAAAAGAAATTA GGAAAGAAAAATAACTAAAAAGTTTTAATCTCTTTTATATTTGAAC CTTAACGAAAAAAAAGTTATTTTTTTTCACAGT
<i>Saccharomyces cerevisiae</i> (AY)	ACATTGTTTCGCTAGACGCTCTCTTCTTATCGATAACGTTCCAATAC GCTCAGTATAAAAAAGATTAGCCGCAGTTGGTAAAACCTAAAACG ACCGTACTTGCATTATACCTCAAGCACCCAGAGAAACCTCTCTTTG GAAAAAAAACATCCAATGAAAAGGCCAGCAATTTCAAGTTAAC TCCAAAGAGTATCACTCACTACCAAACATAATGTTTGAGAAGGAAA TGACGCTCAAACAGGCATGCCCCCTGGAATACCAAGGGGCGCAAT GTGCGTTCAAAGATTCGATGATTCACGGAATTCTGCAATTCACATT ACGTATCGCATTTTCGCTGCGTTCTTCATCGATGCGGAGAACCAAGAG ATCCGTTGTTGAAAGTTTTTAATATTTTAAAATTTCCAGTTACAAAA ATTCTTGTTTTTGACAAAAATTTAATGAATAAAATAAAATTGTTTGTG TTTGTTACCCTTGGGGCCCCAATGGTTCAATTCCCCAAAAAAAATTT TGCAAAAAAATAAAACCTCCCCGGGGGGTGTGTTTGAACGGTTTTT ATTTGCCCTATACAAAAATTCCAAAAATCCTTCACCGTTTGAATAG GAAAAAAAATTACCAA
<i>Saccharomyces cerevisiae</i> (WY)	GGATTTTTTTTTTTTGGGCAGAGGAAGAAAGCTTTTACTGGGGAAA AAAACCAAAAAAGGGGAGTCCCGCCCGGCCGCGCTTAAATGCGC GGGCTTGCTTAGGTTGTGAGATTCTTTTTTGTATTCCCCACAGGGA

	GAGATTTCTGTGCTTTTGTATATGACAATTAAAACCGCTTCAATAC AACACACGTGGGGATTCTTATCTTTTCACTTTTTTTTTTGGGATTA GCAATCGGGGGCCCCAGGGGACAAACACAAACAAATTTATCTATTT TTTTTATTTTTTTCAAAAACAAAAAATTTCTCAACTGGGAAATTTTA AAAATTAAAAACTTTCTACAACAGATCTCTTGGGTCTCCCATCTATG AAAAAAACCCCGAAAGCGATACACAATGTGAATTGCGGAAATCCC CGAAACATCTAAACTTTTAACACACATTGCGCCCCCGGGATTCCC CGGGGGATGCCTGTTTGAGCGCCATTTCCCTCCTCAAACATTCTGTTT GGGAGTGAGGGAGACTCTTTGG
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**Table S7.** 26S rDNA region of isolated yeasts and their excision regions using three restriction endonucleases (*HaeIII*, *HinfI* and *GluI*) for PCR-RFLP.

Strain ID	<i>HaeIII</i> + <i>CfoI</i> + <i>HinfI</i>
<i>Saccharomyces cerevisiae</i> (FJ2-A1)	1. 178 bp 2. 157 bp 3. 104 bp 4. 80 bp 5. 33 bp 6. 21 bp 7. 12 bp 8. 10 bp 9. 8 bp 10. 6 bp
<i>Wickerhamomyces anomalus</i> (FJ2-A2)	557 bp
<i>Saccharomyces cerevisiae</i> (FJ2-A3)	1. 178 bp 2. 157 bp 3. 104 bp 4. 79 bp 5. 33 bp 6. 21 bp 7. 12 bp 8. 10 bp 9. 8 bp 10. 6 bp
<i>Saccharomyces cerevisiae</i> (FJ1-A1)	1. 178 bp 2. 157 bp 3. 104 bp 4. 79 bp 5. 33 bp 6. 21 bp 7. 12 bp 8. 10 bp

	9. 8 bp 10. 6 bp
<i>Pichia kudriavzevii</i> (GA1-A1)	1. 145 bp 2. 71 bp 3. 52 bp 4. 50 bp 5. 40 bp 6. 38 bp 7. 29 bp 8. 26 bp 9. 6 bp
<i>Saccharomyces cerevisiae</i> (TB1-A1)	1. 178 bp 2. 156 bp 3. 104 bp 4. 79 bp 5. 31 bp 6. 21 bp 7. 12 bp 8. 10 bp 9. 8 bp 10. 6 bp
<i>Saccharomyces cerevisiae</i> (TB1-A2)	1. 178 bp 2. 156 bp 3. 104 bp 4. 77 bp 5. 32 bp 6. 21 bp 7. 12 bp 8. 10 bp 9. 8 bp 10. 6 bp
<i>Saccharomyces cerevisiae</i> (GD1-A1)	1. 178 bp 2. 143 bp 3. 104 bp 4. 77 bp 5. 31 bp 6. 21 bp 7. 13 bp 8. 12 bp 9. 10 bp 10. 8 bp 11. 6 bp

<i>Pichia kudriavzevii</i> (GD1-A2)	<ol style="list-style-type: none"> <li>1. 147 bp</li> <li>2. 71 bp</li> <li>3. 52 bp</li> <li>4. 50 bp</li> <li>5. 40 bp</li> <li>6. 38 bp</li> <li>7. 29 bp</li> <li>8. 26 bp</li> <li>9. 6 bp</li> </ol>
<i>Pichia kudriavzevii</i> (GD1-A3)	<ol style="list-style-type: none"> <li>1. 145 bp</li> <li>2. 71 bp</li> <li>3. 52 bp</li> <li>4. 40 bp</li> <li>5. 38 bp</li> <li>6. 37 bp</li> <li>7. 29 bp</li> <li>8. 26 bp</li> <li>9. 13 bp</li> <li>10. 6 bp</li> </ol>
<i>Saccharomyces cerevisiae</i> (GD1-A4)	<ol style="list-style-type: none"> <li>1. 178 bp</li> <li>2. 154 bp</li> <li>3. 95 bp</li> <li>4. 67 bp</li> <li>5. 65bp</li> <li>6. 37 bp</li> <li>7. 16 bp</li> <li>8. 3 bp</li> </ol>
<i>Pichia kudriavzevii</i> (GT1-A1)	<ol style="list-style-type: none"> <li>1. 145 bp</li> <li>2. 71 bp</li> <li>3. 52 bp</li> <li>4. 50 bp</li> <li>5. 40 bp</li> <li>6. 38 bp</li> <li>7. 29bp</li> <li>8. 26 bp</li> <li>9. 6 bp</li> </ol>
<i>Kazachstania unispora</i> (ME1-A1)	<ol style="list-style-type: none"> <li>1. 280 bp</li> <li>2. 115 bp</li> <li>3. 105 bp</li> <li>4. 59 bp</li> <li>5. 26 bp</li> <li>6. 21 bp</li> <li>7. 10 bp</li> </ol>



	8. 8 bp
<i>Kazachstania unispora</i> (ME1-A2)	1. 280 bp 2. 115 bp 3. 105 bp 4. 59 bp 5. 26 bp 6. 21 bp 7. 10 bp 8. 8 bp
<i>Saccharomyces cerevisiae</i> (MN1-A1)	1. 178 bp 2. 157 bp 3. 104 bp 4. 80 bp 5. 33 bp 6. 21 bp 7. 12 bp 8. 10 bp 9. 8 bp 10. 6 bp
<i>Pichia membranifaciens</i> (MN1-A2)	1. 101 bp 2. 82 bp 3. 65 bp 4. 48 bp 5. 40 bp 6. 29 bp 7. 24 bp 8. 12 bp 9. 9 bp 10. 5 bp
<i>Saccharomyces cerevisiae</i> (MN1-A3)	1. 178 bp 2. 157 bp 3. 104 bp 4. 80 bp 5. 33 bp 6. 21 bp 7. 12 bp 8. 10 bp 9. 8 bp 10. 6 bp
<i>Saccharomyces cerevisiae</i> (RK1-A1)	1. 178 bp 2. 157 bp 3. 104 bp 4. 81 bp

	5. 33 bp 6. 21 bp 7. 12 bp 8. 10 bp 9. 8 bp 10. 6 bp
<i>Saccharomyces cerevisiae</i> (RK1-A2)	1. 205 bp 2. 154 bp 3. 96 bp 4. 93 bp 5. 16 bp 6. 10 bp 7. 5 bp 8. 4 bp
<i>Kazachstania humilis</i> (UK1-A1)	1. 227 bp 2. 113 bp 3. 105 bp 4. 38 bp 5. 21 bp 6. 18 bp 7. 13 bp 8. 10 bp 9. 8 bp
<i>Kazachstania humilis</i> (UK1-A2)	1. 227 bp 2. 113 bp 3. 105 bp 4. 38 bp 5. 27 bp 6. 21 bp 7. 13 bp 8. 10 bp 9. 8 bp
<i>Saccharomyces cerevisiae</i> (BY)	1. 113 bp 2. 109 bp 3. 94 bp 4. 91 bp 5. 67 bp 6. 34 bp 7. 33 bp 8. 31 bp 9. 15 bp 10. 13 bp 11. 9 bp

## Bacteria

**Table S8.** Identity and sequences for lactic acid bacteria isolates used for phylogenetic analysis and PCR-RFLP.

Bacteria isolates	Sequence
> <i>Lactiplantibacillus plantarum</i> (GD1-B1)	GC GATG AGT AAC ACG TGG GA ACC TGC CCA GAA GCG GGG GAT C AC TGAAA CAAG CTTC CGC ATA ACA CT TA TGG TCC GAG CTT TC ACT TTT GGA TGG TCC CGC GGC GTA TTA GCTA GAT GGT GGG GTA ACG GCT CAC CAT GGC AAT GAT ACG TAG CCG ACC TGA GAG GGT AAT CG CCA CAT TGG GAC TGA C ACG GCC CAA ACT CT ACG GGA GGC AGC AG TAG GGA ATC TTC CAC AT GGA CAAG TCT GAT GGA GCA CG CCG CGT GAG TA AGA AGG GTT TCG GCT CGT AAA ACT CTTG TTA AAG AAAAC ATGA CGG TAT TTA ACC AGA AAG CCA CGG CTA ACT ACG TGC CAG CAG CG CGG T TCCG GAT TTA TTG GGC GTA AAG GA GCG CAG GCG GTT TTT AA GTC TGA TGT GAA AGC CTT CGG CTCA ACC GAA GAA GTG CAT
> <i>Lactiplantibacillus plantarum</i> (GD1-B2)	GC GATG AGT AAC ACG TGG GA ACC TGC CCA GAA GCG GGG GAT C AC TGAAA CAAG CTTC CGC ATA ACA CT TA TGG TCC GAG TTT TC ACT TTT GGA TGG TCC CGC GGC GTA TTA GCTA GAT GGT GAG GTA ACG GCT CAC CAT GGC AAT GAT ACG TAG CCG ACC TGA GAG GGT AAT CG CCA CAT TGG GAC TGA C ACG GCC CAA ACT CT ACG GGA GGC AGC AG TAG GGA ATC TTC CAC AT GGA CAAG TCT GAT GGA GCA CG CCG CGT GAG TA AGA AGG GTT TCG GCT CGT AAA ACT CTTG TTA AAG AAAAC ATGA CGG TAT TTA ACC AGA AAG CCA CGG CTA ACT ACG TGC CAG CAG CG CGG T TCCG GAT TTA TTG GGC GTA AAG GA GCG CAG GCG GTT TTT AA GTC TGA TGT GAA AGC CTT CGG CTCA ACC GAA GAA GTG CAT
> <i>Lactiplantibacillus plantarum</i> (GD1-B3)	GC GATG AGT AAC ACG TGG GA ACC TGC CCA GAA GCG GGG GAT C AC TGAAA CAAG CTTC CGC ATA ACA CT TA TGG TCC GAG TTT TC ACT TTT GGA TGG TCC CGC GGC GTA TTA GCTA GAT GGT GAG GTA ACG GCT CAC CAT GGC AAT GAT ACG TAG CCG ACC TGA GAG GGT AAT CG CCA CAT TGG GAC TGA C ACG GCC CAA ACT CT ACG GGA GGC AGC AG TAG GGA ATC TTC CAC AT GGA CAAG TCT GAT GGA GCA CG CCG CGT GAG TA AGA AGG GTT TCG GCT CGT AAA ACT CTTG TTA AAG AAAAC ATGA CGG TAT TTA ACC AGA AAG CCA CGG CTA ACT ACG TGC CAG CAG CG CGG T TCCG GAT TTA TTG GGC GTA AAG GA GCG CAG GCG GTT TTT AA GTC TGA TGT GAA AGC CTT CGG CTCA ACC GAA GAA GTG CAT
> <i>Lactiplantibacillus plantarum</i> (GD1-B4)	GC GGTG CTT AAT GCG TTA GT GCA GCA CTG AAG GGC GGA AAC C CC CACAC TTGA TTCT CGT TTA CGG AT GA GGG TAT CTA ATC TT TGC TAC CCA TAC TTT CGA GCC TCA GCG TCTT

	ACA GAC CAG ACA GCC GCC TTC GCC ACT GGG GTT CTT CCA TAT ATC TAC GCA TTT CAC CG CTA CAC ATG GAG TTC C ACT GTC CTC TTC TC ACT CAA GTT TCC AG TTT CCG ATG CAC TTC TC GGT TGAG CCG AAG GCT TTC CA TCA AAC TTA AA AAC CGC CTG CGC TCG CTT TAC GCC CAAA ATC CGG ACAAC GCGG CTG CTG GCA CGT AGT TAG CCG TGG CTT TCT GGT TAA ATA CCG TA ATA T CCTT TAA CAA CAG AGT TTT ACG GC CGA AAC CCT TCT TCA TC ACG CGG GGT TGC TCC ATC ACA CTCG TCC ATT GTG GAA GAT
> <i>Lactiplantibacillus_plantarum</i> (ME1-B1)	GC GGTG CTT AAT GCG TTA GT GCA GCA CTG AAG GGC GGA AAC C CC CACAC TTGA TTCT CGT TTA CGG AT GA GGG TAT CTA ATC TT TGC TAC CCA TAC TTT CGA GCC TCA GCG TCTT ACA GAC CAG ACA GCC GCC TTC GCC ACT GGT GTT CTT CCA TAT ATC TAC GCA TTT CAC CG CTA CAC ATG GAG TTC C ACT GTC CTC TTC TC ACT CAA GTT TCC AG TTT CCG ATG CAC TTC TC GGT TGAG CCG AAG GCT TTC CA TCA GAC TTA AA AAC CGC CTG CGC TCG CTT TAC GCC CAAA ATC CGG ACAAC GCGG CTG CTG GCA CGT AGT TAG CCG TGG CTT TCT GGT TAA ATA CCG TA ATA T CCTT TAA CAA CAG AGT TTT ACG GC CGA AAC CCT TCT TCA TC ACG CGG CGT TGC TCC ATC AGA CTCG TCC ATT GTG GAA GAT
> <i>Bacillus_carboniphilus</i> (RK1-B1)	GC GGTG CTT AAT GCG TTA AT TCA GCA CTA AAG GGC GGA AAC C CC TACAC TTGA CTCT CGT TTA CGG GT GA GGG TAT CTA ATC TT TGC TCC CCA CGC TTT CGC GCC TCA GTG TCTT ACA GAC CAG AAA GTC GCC TTC GCC ACT GGT GTT CCT CCA TAT CTC TAC GCA TTT CAC CG CTA CAC ATG GAA TTC C ACT TTC CTC TTC TC ACT CAA GTC TCC AG TTT CCA ATG ACC CTC CC GGT TGAG CCG TGG GCT TTC CA TCA GAC TTA AA AAC CAC CTG CGC GCG CTT TAC GCC CAAA TTC CGG ATAAC GCGG CTG CTG GCA CGT AGT TAG CCG TGG CTT TCT GGT TAG GTA CCG TA AGG T CCCC TAA CAA CAG AGT TTT ACG CC CGA AAG CCT TCA TCA TC ACG CGG CGT TGC TCC GTC AGA CTCG TCC ATT GCG GAA GAT
> <i>Bacillus_cereus</i> (FJ2-B2)	GC GGTG AGT AAC ACG TGG GA ACC TGC CCA TAA GAC TGG GAT C TC GGAAA CCGG CTTC CGG ATA ACA TT TA TGG TTC GAA ATT TC ACT TAT GGA TGG ACC CGC GTC GCA TTA GCTA GTT GGT GAG GTA ACG GCT CAC CAA GGC AAC GAT GCG TAG CCG ACC TGA GAG GGT GAT CG CCA CAC TGG GAC TGA C ACG GCC CAG ACT CT ACG GGA GGC AGC AG TAG GGA ATC TTC CGC AT GGA CAAG TCT GAC GGA GCA CG CCG CGT GAG TA TGA AGG CTT TCG GGT CGT AAA ACT CTTG TTA GGG AAAAC ATGA CGG TAC CTA ACC AGA AAG CCA CGG CTA ACT ACG

	TGC CAG CAG CG CGG T TCCG GAA TTA TTG GGC GTA AAG GC GCG CAG GTG GTT TCT AA GTC TGA TGT GAA AGC CCA CGG CTCA ACC GTG GAG GGT CAT
> <i>Bacillus_cereus</i> (GA1-B2)	GC GGTG AGT AAC ACG TGG GA ACC TGC CCA TAA GAC TGG GAT C TC GGAAA CCGG CTTC CGG ATA ACA TT TA TGG TTC GAA ATT TC ACT TAT GGA TGG ACC CGC GTC GCA TTA GCTA GTT GGT GAG GTA ACG GCT CAC CAA GGC AAC GAT GCG TAG CCG ACC TGA GAG GGT GAT CG CCA CAC TGG GAC TGA C ACG GCC CAG ACT CT ACG GGA GGC AGC AG TAG GGA ATC TTC CGC AT GGA CAAG TCT GAC GGA GCA CG CCG CGT GAG TA TGA AGG CTT TCG GGT CGT AAA ACT CTTG TTA GGG AAAAC ATGA CGG TAC CTA ACC AGA AAG CCA CGG CTA ACT ACG TGC CAG CAG CG CGG T TCCG GAA TTA TTG GGC GTA AAG GC GCG CAG GTG GTT TCT AA GTC TGA TGT GAA AGC CCA CGG CTCA ACC GTG GAG GGT CAT
> <i>Bacillus_cereus</i> (RK1-B3)	GC GGTG AGT AAC ACG TGG GA ACC TGC CCA TAA GAC TGG GAT C TC GGAAA CCGG CTTC CGG ATA ACA TT TA TGG TTC GAA ATT TC ACT TAT GGA TGG ACC CGC GTC GCA TTA GCTA GTT GGT GAG GTA ACG GCT CAC CAA GGC AAC GAT GCG TAG CCG ACC TGA GAG GGT GAT CG CCA CAC TGG GAC TGA C ACG GCC CAG ACT CT ACG GGA GGC AGC AG TAG GGA ATC TTC CGC AT GGA CAAG TCT GAC GGA GCA CG CCG CGT GAG TA TGA AGG CTT TCG GGT CGT AAA ACT CTTG TTA GGG AAAAC ATGA CGG TAC CTA ACC AGA AAG CCA CGG CTA ACT ACG TGC CAG CAG CG CGG T TCCG GAA TTA TTG GGC GTA AAG GC GCG CAG GTG GTT TCT AA GTC TGA TGT GAA AGC CCA CGG CTCA ACC GTG GAG GGT CAT
> <i>Bacillus_licheniformis</i> (UK1-B2)	GC GGTG CTT AAT GCG TTT GT GCA GCA CTA AAG GGC GGA AAC C CC TACAC TTGA CTCT CGT TTA CGG GT GA GGG TAT CTA ATC TT CGC TCC CCA CGC TTT CGC GCC TCA GCG TCTT ACA GAC CAG AGA GTC GCC TTC GCC ACT GGT GTT CCT CCA CAT CTC TAC GCA TTT CAC CG CTA CAC GTG GAA TTC C ACT CTC CTC TTCTC ACT CAA GTT CCC AG TTT CCA ATG ACC CTC CC GGT TGAG CCG GGG GCT TTC CA TCA GAC TTA AA AAC CGC CTG CGC GCG CTT TAC GCC CAAA TTC CGG ACAAC GCGG CTG CTG GCA CGT AGT TAG CCG TGG CTT TCT GGT TAG GTA CCG TA AGG T CCCC TAA CAA CAG AGT TTT ACG TC CGA AAA CCT TCA TCA TC ACG CGG CGT TGC TCC GTC AGA CTCG TCC ATT GCG GAA GAT
> <i>Bacillus_pumilus</i> (FJ1-B1)	GC GGTG AGT AAC ACG TGG GA ACC TGC CTG TAA GAC TGG GAT C TC GGAAA CCGG CTTC CGG ATA GTT CT TA TGG TTC AAG GAT TC ACT TAC AGA TGG ACC CGC GGC GCA TTA GCTA GTT GGT GGG GTA ATG GCT CAC CAA GGC GAC GAT GCG TAG CCG ACC TGA GAG GGT GAT CG CCA CAC TGG GAC TGA C ACG GCC CAG ACT CT ACG GGA GGC AGC AG TAG GGA ATC TTC CGC AT GGA CAAG TCT GAC GGA GCA CG CCG CGT GAG TA

	TGA AGG TTT TCG GAT CGT AAA GCT CTTG TTA GGG AAAAC ATGA CGG TAC CTA ACC AGA AAG CCA CGG CTA ACT ACG TGC CAG CAG CG CGG T TCCG GAA TTA TTG GGC GTA AAG GC TCG CAG GCG GTT TCT AA GTC TGA TGT GAA AGC CCC CGG CTCA ACC GGG GAG GGT CAT
> <i>Bacillus_siamensis</i> (RK1-B2)	GC GGTG AGT AAC ACG TGG GA ACC TGC CTG TAA GAC TGG GAT C TC GGAAA CCGG CTTC CGG ATG CTT TT TA TGG TTC AGA CAT CC ACT TAC AGA TGG ACC CGC GGC GCA TTA GCTA GTT GGT GAG GTA ACG GCT CAC CAA GGC GAC GAT GCG TAG CCG ACC TGA GAG GGT GAT CG CCA CAC TGG GAC TGA C ACG GCC CAG ACT CT ACG GGA GGC AGC AG TAG GGA ATC TTC CGC AT GGA CAAG TCT GAC GGA GCA CG CCG CGT GAG TA TGA AGG TTT TCG GAT CGT AAA GCT CTTG TTA GGG AAAAC ATGA CGG TAC CTA ACC AGA AAG CCA CGG CTA ACT ACG TGC CAG CAG CG CGG T TCCG GAA TTA TTG GGC GTA AAG GC TCG CAG GCG GTT TCT AA GTC TGA TGT GAA AGC CCC CGG CTCA ACC GGG GAG GGT CAT
> <i>Bacillus_stratosphericus</i> (MN1-B1)	GC GGTG AGT AAC ACG TGG GA ACC TGC CTG TAA GAC TGG GAT C TC GGAAA CCGG CTTC CGG ATA GTT CT TA TGG TTC AAG GAT TC ACT TAC AGA TGG ACC CGC GGC GCA TTA GCTA GTT GGT GAG GTA ACG GCT CAC CAA GGC GAC GAT GCG TAG CCG ACC TGA GAG GGT GAT CG CCA CAC TGG GAC TGA C ACG GCC CAG ACT CT ACG GGA GGC AGC AG TAG GGA ATC TTC CGC AT GGA CAAG TCT GAC GGA GCA CG CCG CGT GAG TA TGA AGG TTT TCG GAT CGT AAA GCT CTTG TTA GGG AAAAC ATGA CGG TAC CTA ACC AGA AAG CCA CGG CTA ACT ACG TGC CAG CAG CG CGG T TCCG GAA TTA TTG GGC GTA AAG GC TCG CAG GCG GTT TCT AA GTC TGA TGT GAA AGC CCC CGG CTCA ACC GGG GAG GGT CAT
> <i>Bacillus_zhangzhouensis</i> (FJ2-B1)	GC GGTG AGT AAC ACG TGG GA ACC TGC CTG TAA GAC TGG GAT C TC GGAAA CCGG CTTC CGG ATA GTT CT TA TGG TTC AAG GAT TC ACT TAC AGA TGG ACC CGC GGC GCA TTA GCTA GTT GGT GGG GTA ATG GCT CAC CAA GGC GAC GAT GCG TAG CCG ACC TGA GAG GGT GAT CG CCA CAC TGG GAC TGA C ACG GCC CAG ACT CT ACG GGA GGC AGC AG TAG GGA ATC TTC CGC AT GGA CAAG TCT GAC GGA GCA CG CCG CGT GAG TA TGA AGG TTT TCG GAT CGT AAA GCT CTTG TTA GGG AAAAC ATGA CGG TAC CTA ACC AGA AAG CCA CGG CTA ACT ACG TGC CAG CAG CG CGG T TCCG GAA TTA TTG GGC GTA AAG GC TCG CAG GCG GTT TCT AA GTC TGA TGT GAA AGC CCC CGG CTCA ACC GGG GAG GGT CAT
> <i>Bhargavaea_ginsengi</i> (MN1-B2)	GC GGTG AGT AAC ACG TGG GA ACC TGC CTG TAA GAT CGG GAT C TC GGAAA CCGG CTTC CGG ATG GTT CT TA TGG AGG AAG GCG TC ACT TAC AGA TGG GCC CGC GGC GCA TTA GCTA GTT GGT GGG GTA ACG GCC TAC CAA GGC AAC GAT GCG TAG CCG ACC TGA GAG GGT GAT CG CCA CAC TGG GAC TGA C ACG

	GCC CAG ACT CT ACG GGA GGC AGC AG TAG GGA ATC TTC CGC AT GGA CAAG TCT GAC GGA GCA CG CCG CGT GAG CA AGA AGG CCT TCG GGT CGT AAA GCT CTTG TAA GGG AAAAC ATGA CGG TAC CTT ACC AGA AAG CCA CGG CTA ACT ACG TGC CAG CAG CG CGG T TCCG GAA TTA TTG GGC GTA AAG GC GCG CAG GCG GTC CTT AA GTC TGA TGT GAA AGC CCA CGG CTCA ACC GTG GAG GGT CAT
> <i>Liquorilactobacillus_nagelii</i> _(RK1-B4)	CC GGTG CTT AAT GCG TTT GT GCG GCA CTG AAG GGC GGA AAC C CC CACAC TTGA TTCT CGT TTA CAG GT GA GGG TAT CTA ATC TT TGC TAC CCA CGC TTT CGA ACC TCA GCG TCTT ACA GAC CAG AGA GCC GCT TTC GCC ACT GGT GTT CTT CCA TAT ATC TAC GCA TTT CAC CG CTA CAC ATG GAG TTC C ACT CTC CTC TTC TC ACT CAA GTC TCC AG TTT CCA ATG CAC GAC TC GGT TAAG CCG AAG GCT TTC CA TCA GAC TTA AA GAC CGC CTG CGT TCC CTT TAC GCC CAAA ATC CGG ACAAC GCGG CTG CTG GCA CGT AGT TAG CCG TGG CTT TCT GGC CAG ATA CCG TA CTG T CCTC TGA CAA CAG AGT TTT ACG TC CGA AAA CCT TCT TCA TC ACG CGG CGT TGC TCC ATC AGA CTCG TCC ATT GTG GAA GAT
> <i>Liquorilactobacillus_nagelii</i> _(ME1-B2)	GC GGTG CTT AAT GCG TTT GT GCG GCA CTG AAG GGC GGA AAC C CC CACAC TTGA TTCT CGT TTA CAG GT GA GGG TAT CTA ATC TT TGC TAC CCA CGC TTT CGA ACC TCA GCG TCTT ACA GAC CAG AGA GCC GCT TTC GCC ACT GGT GTT CTT CCA TAT ATC TAC GCA TTT CAC CG CTA CAC ATG GAG TTC C ACT CTC CTC TTC TC ACT CAA GTC TCC AG TTT CCA ATG CAC GAC TC GGT TAAG CCG AAG GCT TTC CA TCA GAC TTA AA GAC CGC CTG CGT TCC CTT TAC GCC CAAA ATC CGG ACAAC GCGG CTG CTG GCA CGT AGT TAG CCG TGG CTT TCT GGC CAG ATA CCG TA CTG T CCTC TGA CAA CAG AGT TTT ACG TC CGA AAA CCT TCT TCA TC ACG CGG CGT TGC TCC ATC AGA CTCG TCC ATT GTG GAA GAT
> <i>Lacticaseibacillus_paracasei</i> _(FJ2-B3)	GC GGTG CTT AAT GCG TTA GT GCG GCA CTG AAG GGC GGA AAC C CC CACAC CTGA TTCT CGT TTA CGG AT GA GGG TAT CTA ATC TT CGC TAC CCA TGC TTT CGA GCC TCA GCG TCTT ACA GAC CAG ACA GCC GCC TTC GCC ACT GGT GTT CTT CCA TAT ATC TAC GCA TTT CAC CG CTA CAC ATG GAG TTC C ACT GTC CTC TTC TC ACT CAA GTT TCC AG TTT CCG ATG CGC TTC CC GGT TGAG CCG AGG GCT TTC CA TCA GAC TTA AA AAC CGC CTG CGC TCG CTT TAC GCC CAAA ATC CGG ATAAC GCGG CTG CTG GCA CGT AGT TAG CCG TGG CTT TCT GGT TGG ATA CCG TA CTA T CCTC CAA CAA CAG AGT TTT ACG CC CGA AAG CCT TCT TCA TC ACG CGG CGT TGC TCC ATC AGA CTCG TCC ATT GTG GAA GAT
> <i>Lacticaseibacillus_paracasei</i> _(GA1-B1)	GC GGTG AGT AAC ACG TGG GA ACC TGC CCT TAA GTG GGG GAT C AT TGAAA CAAG CTTC CGC ATA GAT CA AA TGG TTC

	TTG GCT TC GCT TTT GGA TGG ACC CGC GGC GTA TTA GCTA GTT GGT GAG GTA ATG GCT CAC CAA GGC GAT GAT ACG TAG CCG AAC TGA GAG GTT GAT CG CCA CAT TGG GAC TGA C ACG GCC CAA ACT CT ACG GGA GGC AGC AG TAG GGA ATC TTC CAC AT GGA CAAG TCT GAT GGA GCA CG CCG CGT GAG TA AGA AGG CTT TCG GGT CGT AAA ACT CTTG TTG GAG AAAAT GTGA CGG TAT CCA ACC AGA AAG CCA CGG CTA ACT ACG TGC CAG CAG CG CGG T TCCG GAT TTA TTG GGC GTA AAG GA GCG CAG GCG GTT TTT AA GTC TGA TGT GAA AGC CCT CGG CTTA ACC GAG GAA GCG CAT
> <i>Lysinibacillus_halotolerans</i> _(TB1-B1)	GC GGTG AGT AAC ACG TGG GA ACC TGC CCT ATA GTT GGG GAT C TC GGAAA CCGG CTTC CGA ATA ATC AT TC TGA TGG AAT GTT TC GCT ATA GGA TGG GCC CGC GGC GCA TTA GCTA GTT GGT GAG GTA ACG GCT CAC CAA GGC GAC GAT GCG TAG CCG ACC TGA GAG GGT GAT CG CCA CAC TGG GAC TGA C ACG GCC CAG ACT CT ACG GGA GGC AGC AG TAG GGA ATC TTC CAC AT GGG CAAG CCT GAT GGA GCA CG CCG CGT GAG TA AGA AGG TTT TCG GAT CGT AAA ACT CTTG TAA GGG AAAAC ATGA CGG TAC CTT ATT AGA AAG CCA CGG CTA ACT ACG TGC CAG CAG CG CGG T TCCG GAA TTA TTG GGC GTA AAG GC GCG CAG GCG GTC CTT AA GTC TGA TGT GAA AGC CCA CGG CTCA ACC GTG GAG GGT CAT

**Table S9** Sequences for type strains/material used for PCR-RFLP of 16S rDNA region.

>KT025937.1 <i>Lactobacillus plantarum</i> ATCC 14917	GC GATG AGT AAC ACG TGG GA ACC TGC CCA GAA GCG GGG GAT C AC TGAAA CAAG CTTC CGC ATA ACA CT TA TGG TCC GAG CTT TC ACT TTT GGA TGG TCC CGC GGC GTA TTA GCTA GAT GGT GGG GTA ACG GCT CAC CAT GGC AAT GAT ACG TAG CCG ACC TGA GAG GGT AAT CG CCA CAT TGG GAC TGA C ACG GCC CAA ACT CT ACG GGA GGC AGC AG TAG GGA ATC TTC CAC AT GGA CAAG TCT GAT GGA GCA CG CCG CGT GAG TA AGA AGG GTT TCG GCT CGT AAA ACT CTTG TTA AAG AAAAC ATGA CGG TAT TTA ACC AGA AAG CCA CGG CTA ACT ACG TGC CAG CAG CG CGG T TCCG GAT TTA TTG GGC GTA AAG GA GCG CAG GCG GTT TTT AA GTC TGA TGT GAA AGC CTT CGG CTCA ACC GAA GAA GTG CAT
>NR_157729.1 <i>Bacillus albus</i> MCCC 1A02146	GC GGTG AGT AAC ACG TGG GA ACC TGC CCA TAA GAC TGG GAT C TC GGAAA CCGG CTTC CGG ATA ACA TT TA TGG TTC GAA ATT TC ACT TAT GGA TGG ACC CGC GTC GCA TTA GCTA GTT GGT GAG GTA ACG GCT CAC CAA GGC AAC GAT GCG TAG CCG ACC TGA GAG GGT GAT CG CCA CAC TGG GAC TGA C ACG GCC CAG ACT CT ACG GGA GGC AGC AG TAG GGA ATC TTC CGC AT GGA CAAG TCT GAC GGA GCA CG CCG CGT GAG TA TGA AGG CTT TCG GGT CGT AAA ACT CTTG TTA GGG AAAAC ATGA CGG TAC CTA ACC AGA AAG CCA CGG CTA ACT ACG TGC CAG CAG CG CGG T TCCG GAA TTA TTG GGC GTA



	AAG GC GCG CAG GTG GTT TCT AA GTC TGA TGT GAA AGC CCA CGG CTCA ACC GTG GAG GGT CAT
>AB021182.1 <i>Bacillus carboniphilus</i>	GC GGTG AGT AAC ACG TGG AA ACC TGC CTG TAA GAC TGG GAT C TC GGAAA CCGG CTTC CGG ATA TGA TT TA TGA ACT GAA ATG CC ACT TAC AGA TGG ATC CGC GGC GCA TTA GCTA GTT GGT GAG GTA ACG GCT CAC CAA GGC GAC GAT GCG TAG CCG ACC TGA GAG GGT GAT CG CCA CAC TGG GAC TGA C ACG GCC CAG ACT CT ACG GGA GGC AGC AG TAG GGA ATC TTC CGC AT GGA CAAG TCT GAC GGA GCA CG CCG CGT GAG TA TGA AGG TTT TCG GAT CGT AAA GCT CTTG TTA GGG AAAAC ATGA CGG TAC CTA ACC AGA AAG CCA CGG CTA ACT ACG TGC CAG CAG CG CGG T TCCG GAA TTA TTG GGC GTA AAG GC GCG CAG GCG GTT TCT AA GTC TGA TGT GAA AGC CCA CGG CTCA ACC GTG GAG GGT CAT
>NR_114582.1 <i>Bacillus cereus</i> ATCC 14579	GC GGTG AGT AAC ACG TGG GA ACC TGC CCA TAA GAC TGG GAT C TC GGAAA CCGG CTTC CGG ATA ACA TT TA TGG TTC GAA ATT TC ACT TAT GGA TGG ACC CGC GTC GCA TTA GCTA GTT GGT GAG GTA ACG GCT CAC CAA GGC AAC GAT GCG TAG CCG ACC TGA GAG GGT GAT CG CCA CAC TGG GAC TGA C ACG GCC CAG ACT CT ACG GGA GGC AGC AG TAG GGA ATC TTC CGC AT GGA CAAG TCT GAC GGA GCA CG CCG CGT GAG TA TGA AGG CTT TCG GGT CGT AAA ACT CTTG TTA GGG AAAAC ATGA CGG TAC CTA ACC AGA AAG CCA CGG CTA ACT ACG TGC CAG CAG CG CGG T TCCG GAA TTA TTG GGC GTA AAG GC GCG CAG GTG GTT TCT AA GTC TGA TGT GAA AGC CCA CGG CTCA ACC GTG GAG GGT CAT
>NR_074923.1 <i>Bacillus licheniformis</i> ATCC 14580	GC GGTG AGT AAC ACG TGG GA ACC TGC CTG TAA GAC TGG GAT C TC GGAAA CCGG CTTC CGG ATG CTT AT TA TGG TTC AAT CAT CC ACT TGC AGA TGG ACC CGC GGC GCA TTA GCTA GTT GGT GAG GTA ACG GCT CAC CAA GGC GAC GAT GCG TAG CCG ACC TGA GAG GGT GAT CG CCA CAC TGG GAC TGA C ACG GCC CAG ACT CT ACG GGA GGC AGC AG TAG GGA ATC TTC CGC AT GGA CAAG TCT GAC GGA GCA CG CCG CGT GAG TA TGA AGG TTT TCG GAT CGT AAA ACT CTTG TTA GGG AAAAC ATGA CGG TAC CTA ACC AGA AAG CCA CGG CTA ACT ACG TGC CAG CAG CG CGG T TCCG GAA TTA TTG GGC GTA AAG GC GCG CAG GCG GTT TCT AA GTC TGA TGT GAA AGC CCC CGG CTCA ACC GGG GAG GGT CAT
>NR_043242.1 <i>Bacillus pumilus</i> ATCC 7061	GC GGTG AGT AAC ACG TGG GA ACC TGC CTG TAA GAC TGG GAT C TC GGAAA CCGG CTTC CGG ATA GTT CT TA TGG TTC AAG GAT TC ACT TAC AGA TGG ACC CGC GGC GCA TTA GCTA GTT GGT GGG GTA ATG GCT CAC CAA GGC GAC GAT GCG TAG CCG ACC TGA GAG GGT GAT CG CCA CAC TGG GAC TGA C ACG GCC CAG ACT CT ACG GGA GGC AGC AG TAG GGA ATC TTC CGC AT GGA CAAG TCT GAC GGA GCA CG CCG CGT GAG TA TGA AGG TTT TCG GAT CGT AAA GCT CTTG TTA GGG AAAAC ATGA CGG TAC CTA ACC AGA AAG CCA CGG CTA ACT ACG TGC CAG CAG CG CGG T TCCG GAA TTA TTG GGC GTA AAG GC TCG CAG GCG GTT TCT AA GTC TGA TGT GAA AGC CCC CGG CTCA ACC GGG GAG GGT CAT

>NR_117274.1 <i>Bacillus siamensis</i> KCTC 13613	GC GGTG AGT AAC ACG TGG GA ACC TGC CTG TAA GAC TGG GAT C TC GGAAA CCGG CTTC CGG ATG GTT TT TA TGG TTC AGA CAT CC ACT TAC AGA TGG ACC CGC GGC GCA TTA GCTA GTT GGT GAG GTA ACG GCT CAC CAA GGC GAC GAT GCG TAG CCG ACC TGA GAG GGT GAT CG CCA CAC TGG GAC TGA C ACG GCC CAG ACT CT ACG GGA GGC AGC AG TAG GGA ATC TTC CGC AT GGA CAAG TCT GAC GGA GCA CG CCG CGT GAG TA TGA AGG TTT TCG GAT CGT AAA GCT CTTG TTA GGG AAAAC ATGA CGG TAC CTA ACC AGA AAG CCA CGG CTA ATT ACG TGC CAG CAG CG CGG T TCCG GAA TTA TTG GGC GTA AAG GC TCG CAG GCG GTT TCT AA GTC TGA TGT GAA AGC CCC CGG CTCA ACC GGG GAG GGT CAT
>AJ831841.2 <i>Bacillus stratosphericus</i>	GC GGTG AGT AAC ACG TGG GA ACC TGC CTG TAA GAC TGG GAT C TC GGAAA CCGG CTTC CGG ATA GTT CT TA TGG TTC AAG GAT TC ACT TAC AGA TGG ACC CGC GGC GCA TTA GCTA GTT GGT GAG GTA ACG GCT CAC CAA GGC GAC GAT GCG TAG CCG ACC TGA GAG GGT GAT CG CCA CAC TGG GAC TGA C ACG GCC CAG ACT CT ACG GGA GGC AGC AG TAG GGA ATC TTC CGC AT GGA CAAG TCT GAC GGA GCA CG CCG CGT GAG TA TGA AGG TTT TCG GAT CGT AAA GCT CTTG TTA GGG AAAAC ATGA CGG TAC CTA ACC AGA AAG CCA CGG CTA ACT ACG TGC CAG CAG CG CGG T TCCG GAA TTA TTG GGC GTA AAG GC TCG CAG GCG GTT TCT AA GTC TGA TGT GAA AGC CCC CGG CTCA ACC GGG GAG GGT CAT
>NR_148786.1 <i>Bacillus zhangzhouensis</i> MCCC 1A08372	GC GGTG AGT AAC ACG TGG GA ACC TGC CTG TAA GAC TGG GAT C TC GGAAA CCGG CTTC CGG ATA GTT CT TA TGG TTC AAG GAT TC ACT TAC AGA TGG ACC CGC GGC GCA TTA GCTA GTT GGT GGG GTA ATG GCT CAC CAA GGC GAC GAT GCG TAG CCG ACC TGA GAG GGT GAT CG CCA CAC TGG GAC TGA C ACG GCC CAG ACT CT ACG GGA GGC AGC AG TAG GGA ATC TTC CGC AT GGA CAAG TCT GAC GGA GCA CG CCG CGT GAG TA TGA AGG TTT TCG GAT CGT AAA GCT CTTG TTA GGG AAAAC ATGA CGG TAC CTA ACC AGA AAG CCA CGG CTA ACT ACG TGC CAG CAG CG CGG T TCCG GAA TTA TTG GGC GTA AAG GC TCG CAG GCG GTT TCT AA GTC TGA TGT GAA AGC CCC CGG CTCA ACC GGG GAG GGT CAT
>HQ424468.1 <i>Bacillus ginsengi</i>	GC GGTG AGT AAC ACG TGG GA ACC TGC CTG TAA GAT CGG GAT C TC GGAAA CCGG CTTC CGG ATG GTT CT TA TGG AGG AAG GCG TC ACT TAC AGA TGG GCC CGC GGC GCA TTA GCTA GTT GGT GGG GTA ATG GCC TAC CAA GGC AAC GAT GCG TAG CCG ACC TGA GAG GGT GAT CG CCA CAC TGG GAC TGA C ACG GCC CAG ACT CT ACG GGA GGC AGC AG TAG GGA ATC TTC CGC AT GGA CAAG TCT GAC GGA GCA CG CCG CGT GAG CA AGA AGG CCT TCG GGT CGT AAA GCT CTTG TAA GGG AAAAC ATGA CGG TAC CTT ACC AGA AAG CCA CGG CTA ACT ACG TGC CAG CAG CG CGG T TCCG GAA TTA TTG GGC GTA AAG GC GCG CAG GCG GTC CTT AA GTC TGA TGT GAA AGC CCA CGG CTCA ACC GTG GAG GGT CAT

>AB162131.1 <i>Liquorilactobacillus nagelii</i>	GC GATG AGT AAC ACG TGG GA ACC TGC CCC AAA GCG GGG GAT C AT TGAAA CAAG CTTC CGC ATA ACC CA GA TGG TTT CTG TGT TC ACT TTG GGA TGG ACC CGC GGC GTA TTA GCTA GTT GGT AAG GTA ATG GCT TAC CAA GGC AAT GAT ACG TAG CCG AAC TGA GAG GTT GAT CG CCA CAT TGG GAC TGA C ACG GCC CAA ACT CT ACG GGA GGC AGC AG TAG GGA ATC TTC CAC AT GGA CAAG TCT GAT GGA GCA CG CCC CGT GAG TA AGA AGG TTT TCG GAT CGT AAA ACT CTTG TCA GAG AAAAC GTGA CGG TAT CTG GCC AGA AAG CCA CGG CTA ACT ACG TGC CAG CAG CG CGG T TCCG GAT TTA TTG GGC GTA AAG GA ACG CAG GCG GTC TTT AA GTC TGA TGT GAA AGC CTT CGG CTTA ACC GAA GTC GTG CAT
>NR_117987.1 <i>Lacticaseibacillus paracasei</i> ATCC 25302	GC GGTG AGT AAC ACG TGG GA ACC TGC CCT TAA GTG GGG GAT C AT TGAAA CAAG CTTC CGC ATA GAT CA AA TGG TTC TTG GCT TC GCT TTT GGA TGG ACC CGC GGC GTA TTA GCTA GTT GGT GAG GTA ACG GCT CAC CAA GGC GAT GAT ACG TAG CCG AAC TGA GAG GTT GAT CG CCA CAT TGG GAC TGA C ACG GCC CAA ACT CT ACG GGA GGC AGC AG TAG GGA ATC TTC CAC AT GGA CAAG TCT GAT GGA GCA CG CCG CGT GAG TA AGA AGG CTT TCG GGT CGT AAA ACT CTTG TTG GAG AAAAT GTGA CGG TAT CCA ACC AGA AAG CCA CGG CTA ACT ACG TGC CAG CAG CG CGG T TCCG GAT TTA TTG GGC GTA AAG GA GCG CAG GCG GTT TTT AA GTC TGA TGT GAA AGC CCT CGG CTTA ACC GAG GAA GCG CAT
>KF443809.1 <i>Lysinibacillus halotolerans</i> LAM612	GC GGTG AGT AAC ACG TGG GA ACC TGC CCT ATA GTT GGG GAT C TC GGAAA CCGG CTTC CGA ATA ATA AT TC TGA TGA GAT GTT TC GCT ATA GGA TGG GCC CGC GGC GCA TTA GCTA GTT GGT GAG GTA ACG GCT CAC CAA GGC GAC GAT GCG TAG CCG ACC TGA GAG GGT GAT CG CCA CAC TGG GAC TGA C ACG GCC CAG ACT CT ACG GGA GGC AGC AG TAG GGA ATC TTC CAC AT GGG CAAG CCT GAT GGA GCA CG CCG CGT GAG TA AGA AGG TTT TCG GAT CGT AAA ACT CTTG TAA GGG AAAAC ATGA CGG TAC CTT ATT AGA AAG CCA CGG CTA ACT ACG TGC CAG CAG CG CGG T TCCG GAA TTA TTG GGC GTA AAG GC GCG CAG GCG GTC CTT AA GTC TGA TGT GAA AGC CCA CGG CTCA ACC GTG GAG GGT CAT
>NR_133708.1 <i>Bradyrhizobium paxllaeri</i> LMTR 21	GC AGTG AGT AAC GCG TGG GA ACG TAC CTT TTG GTT CGG AAC C CA GGAAA CTGG CTTC CGG ATA AGC CT TA CGG GGA AAG ATT TC GCC GAA AGA TCG GCC CGC GTC TGA TTA GCTA GTT GGT GAG GTA ATG GCT CAC CAA GGC GAC GAT CAG TAG CTG GTC TGA GAG GAT GAT CG CCA CAT TGG GAC TGA C ACG GCC CAA ACT CT ACG GGA GGC AGC AG TGG GGA ATA TTG GAC AT GGG CAAG CCT GAT CCA GCC TG CCG CGT GAG TA TGA AGG CCC TAG GGT TGT AAA GCT CTTG TGC GGG AAATA ATGA CGG TAC CGC AAG AAT AAG CCC CGG CTA ACT TCG TGC CAG CAG CG CGG T TTCG GAA TCA CTG GGC GTA AAG GT GCG TAG GCG GGT CTT AA GTC AGG GGT GAA ATC CTG GAG CTCA ACT CCA GAA CTG CCT

**Table S10.** 16S rDNA region of isolated lactic acid bacteria and their excision regions using three restriction endonucleases (*HaeIII*, *HinfI* and *GluI*) for PCR-RFLP.

Stain ID	
<i>Lactiplantibacillus plantarum</i> (GD1-B1)	1. 370 bp 2. 115 bp 3. 63 bp 4. 51 bp 5. 30 bp 6. 22 bp
<i>Lactiplantibacillus plantarum</i> (GD1-B2)	1. 370 bp 2. 165 bp 3. 63 bp 4. 30 bp 5. 22 bp
<i>Lactiplantibacillus plantarum</i> (GD1-B3)	1. 370 bp 2. 166 bp 3. 63 bp 4. 30 bp 5. 22 bp
<i>Lactiplantibacillus plantarum</i> (GD1-B4)	1. 496 bp 2. 24 bp 3. 20 bp
<i>Lactiplantibacillus plantarum</i> (ME1-B1)	1. 497 bp 2. 23 bp 3. 22 bp
<i>Bacillus carboniphilus</i> (RK1-B1)	1. 463 bp 2. 133 bp 3. 129 bp 4. 71 bp 5. 63 bp 6. 33 bp 7. 33 bp 8. 25 bp 9. 22 bp 10. 5 bp
<i>Bacillus cereus</i> (FJ2-B2)	1. 426 bp 2. 166 bp 3. 109 bp 4. 63 bp 5. 34 bp 6. 25 bp 7. 22 bp 8. 17 bp 9. 5 bp
<i>Bacillus cereus</i> (GA1-B2)	1. 424 bp

	2. 166 bp 3. 109 bp 4. 63 bp 5. 26 bp 6. 25 bp 7. 22 bp 8. 17 bp 9. 7 bp 10. 5 bp
<i>Bacillus_cereus</i> (RK1-B3)	1. 426 bp 2. 166 bp 3. 109 bp 4. 63 bp 5. 33 bp 6. 25 bp 7. 22 bp 8. 17 bp 9. 5 bp
<i>Bacillus thuringiensis</i> (UK1-B1)	1. 414 bp 2. 174 bp 3. 106 bp 4. 65 bp 5. 63 bp 6. 25 bp 7. 22 bp 8. 8 bp
<i>Bacillus_licheniformis</i> (UK1-B2)	1. 372 bp 2. 148 bp 3. 139 bp 4. 63 bp 5. 62 bp 6. 33 bp 7. 25 bp 8. 22 bp 9. 8 bp
<i>Bacillus_pumilus</i> (FJ1-B1)	1. 300 bp 2. 129 bp 3. 108 bp 4. 88 bp 5. 77 bp 6. 71 bp 7. 67 bp 8. 63 bp 9. 25 bp 10. 22 bp 11. 5 bp

<i>Bacillus_siamensis</i> (RK1-B2)	1. 301 bp 2. 165 bp 3. 135 bp 4. 128 bp 5. 71 bp 6. 68 bp 7. 63 bp 8. 38 bp 9. 25 bp 10. 22 bp 11. 5 bp
<i>Bacillus_stratosphericus</i> (MN1-B1)	1. 300 bp 2. 136 bp 3. 129 bp 4. 88 bp 5. 77 bp 6. 71 bp 7. 70 bp 8. 68 bp 9. 63 bp 10. 25 bp 11. 22 bp 12. 5 bp
<i>Bacillus_zhangzhouensis</i> (FJ2-B1)	1. 300 bp 2. 135 bp 3. 129 bp 4. 88 bp 5. 77 bp 6. 71 bp 7. 67 bp 8. 63 bp 9. 25 bp 10. 22 bp 11. 11 bp 12. 5 bp
<i>Bhargavaea_ginsengi</i> (MN1-B2)	1. 428 bp 2. 146 bp 3. 125 bp 4. 67 bp 5. 55 bp 6. 46 bp 7. 44 bp 8. 34 bp 9. 25 bp 10. 22 bp 11. 19 bp

	12. 16 bp 13. 15 bp 14. 5 bp 15. 4 bp
<i>Liquorilactobacillus_nagelii</i> _(RK1-B4)	1. 391 bp 2. 161 bp 3. 127 bp 4. 63 bp 5. 33 bp 6. 22 bp 7. 2 bp
<i>Liquorilactobacillus_nagelii</i> _(ME1-B2)	1. 396 bp 2. 161 bp 3. 127 bp 4. 63 bp 5. 33 bp 6. 22 bp
<i>Lacticaseibacillus_paracasei</i> _(FJ2-B3)	1. 497 bp 2. 63 bp 3. 33 bp 4. 22 bp 5. 21 bp 6. 15 bp
<i>Lacticaseibacillus_paracasei</i> _(GA1-B1)	1. 499 bp 2. 133bp 3. 63 bp 4. 41 bp 5. 33 bp 6. 30 bp 7. 22 bp
<i>Lysinibacillus_halotolerans</i> _(TB1-B1)	1. 500 bp 2. 150 bp 3. 89 bp 4. 68 bp 5. 67 bp 6. 63 bp 7. 44 bp 8. 25 bp 9. 22 bp 10. 15 bp 11. 5 bp

**Table S11.** Identity and sequences for acetic acid bacteria isolates used for phylogenetic analysis and PCR-RFLP.

<i>Acetobacter_indonesiensis</i> (GD1-C1)	GG CGTG CTT ATC GCG TTA GT ACA ACA CTG AAT AAC TAG AAT A CC CCCAT CCAA CTTT CGT TTA CCG GA GC AGG GAT CTA ATC GT TGC TCC CCA CTA TTT CCC GCC TCA GCG GCTA ATG AGA CCA GAT GCC GGC TTC GCC ACC GGG GGT CTT CCC AAT ATC TAC CAA TTT CAC CT CTA CCA TGG GAA TTC C ACA ACC CTC TCT CT GCT CTA ATC TGC CA TCT CAA ATG CAG CTT CA TGT TAAG ACC GGG GAT TTT CA TCT GAC TGT AA AAC CGC CTA CAC GCC CTT TTA CCC CACA TTC CCA GAACG GCGG CTG CTG GCA CAA AGT TAT CCG GGG CTT CTT CTG CGG GTA CCG GA TCA T CCTG AAG CCG ACT CGC TTT ATA TC CTT CTA CCT TCT TCA AC ACT AGG AAT TGA TGG ATC ACG GCCC CCC ATT GTC CAA TAT
<i>Acetobacter_pasterius</i> (FJ1-C1)	GC GGTG CTT ATC GCG TTA GT ACG ACA CTG AGT AAC TAA GTT A CC CACAT CCGA CACT CGT TTA CAG GT GA GGG TAT CTA ATC TT TGC TCC CCA CGC TTT CGC GCC TCA GCG TCTA ATG AGC CAG GTT GCC GCC TTC GCC ACC GGT GTT CTT CCC AAT ATC TAC GAA TTT CAC CT CTA CAC TGG GAA TTC C ACA ACC CTC TCT CC ACT CTA GTC TGC CG TAT TAA ATG CAG CTC CA GGT TAAG CCC GGG GAT TTC CA TCT AAC TGT AA AAC CGC CTA CAC GCC CTT TAC GCC CACA TTC CGA GCAAC GCGG CTG CTG GCA CGA AGT TAG CCG GGGCTT CTT CTG CGG GTA CCG TA TCA T CCCC CGC CGA AAG TGC TTT ACA TC CGA AAA CCT TCT TCA AC ACG CGG CAT TGC TGG ATC AGG GTCC CCC ATT GTC CAA TAT
<i>Acetobacter_pasterius</i> (GA1-C1)	CCCCAGGGCGGTGTGCTTAACGCGTTAACTGCGACACTGAATGACTAA GTCACCCAACATCTAGCACACATCGTTTACAGCGTGGACTACCAGGGTA TCTAATCCTGTTTGTCTCCCCACGCTTTCGCGCCTCAGCGTCAGTAATGAG CCAGGTTGCCGCCTTCGCCACCGGTGTTCTTCCCAATATCTACGAATTTT ACCTCTACACTGGGAATTCCACAACCCTCTCTCACACTCTAGTCTGCAC GTATCAAATGCAGCTCCCAGGTTAAGCCCGGGGATTTACATCTGACTG TACAAACCGCCTACACGCCCTTTACGCCAGTCATTCCGAGCAACGCTA GCCCCCTTCGTATTACCGCGGCTGCTGGCACGAAGTTAGCCGGGGCTTC TTCTACGGGTACCGTCATCATCGTCCCCGTCGAAAGTGCTTTACAATCC GAAGACCTTCTTCACACACGCGGCATTGCTGGATCAGGGTTGCCCCCAT TGTCCAATATTCCCCACTGCTGCCTCCCGTAGGAGTCTGGGCGCGTGTCTC AGTCCCAGTGTGGCTGATCATCCTCTCAAACCAGCTATTGATCATCGCC TTGGTAGGCCTTTACCCACCAACTAGCTAATCAAACGCAGGCTCCTCC ACAGGCGACTTGCGCCTTTGACCCTCAGGTGTCATGCGGTATTAGCACC AGTTTCCCAGTGTTATCCCCACCCATGGATAGATACCTACGCGTTACTC ACCCGTCCGCCACTAAAGCCGAAGCCTTCGTGCGACTTGTCATGTGTAA GCATGCCGCCAGCGTTTCGCTCTGAGCCATGAT
<i>Acetobacter_malorum</i> (UK1-C1)	GCGGGTGTGCTTATCGCGTTAGCTACGACACTGAGTAACTAAGTTACCC AACATCCAGCACACATCGTTTACAGCGTGGACTACCAGGGTATCTAATC CTGTTTGCTCCCCACGCTTTCGCGCCTCAGCGTCAGTAATGAGCCAGGTT GCCGCCTTCGCCACCGGTGTTCTTCCCAATATCTACGAATTTACCTCTA CACTGGGAATTCCACAACCCTCTCTCACACTCTAGTCTGCACGTATTAA



	ATGCAGCTCCCAGGTTAAGCCCGGGGATTTACATCTAACTGTACAAAC CGCCTACACGCCCTTTACGCCAGTCATTCCGAGCAACGCTAGCCCCCT TCGTATTACCGCGGCTGCTGGCACGAAGTTAGCCGGGGCTTCTTCTGCG GGTACCGTCATCATCGTCCCCGCCGAAAGTGCTTTACAATCCGAAAACC TTCTTCACACACGCGGCATTGCTGGATCAGGGTTGCCCCCATTGTCCAA TATTCCCCACTGCTGCCTCCCGTAGGAGTCTGGGCCGTGTCTCAGTCCC AGTGTGGCTGATCATCCTCTCAGACCAGCTATTGATCATCGCCTTGGA GGCCATTACCCACCAACAAGCTAATCAAACGCAGGCTCCTCCACAGG CGACTTGCGCCTTTGACCCTCAGGTATCATGCGGTATTAGCTCCAGTTTC CCGGAGTTATCCCCACCCATGGATAGATTCTTACGCGTTACTCACCCG TCCGCCACTAAAGCCGAAGCCTTCGTGCGACTTGCATGTGTAAAGCATG CCGCCAGCGTTTCGCTCTGAGCCATGAT
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**Table S12.** Sequences for type strains/material used for PCR-RFLP of the 16S rDNA for acetic acid bacteria.

AB032356.1 <i>Acetobacter indonesiensis</i>	GC GGTG AGT AAC GCG TAG GA ATC TAT CCG TGG GTG GGG GAT C TT GGAAA CTGG CTTC CGC ATG ACA CT GA GGG TCA AAG GCG TC GCC TGC GGA GGA GCC TGC GTT TGA TTA GCTT GTT GGT GGG GTA ATG GCC TAC CAA GGC GAT GAT CAA TAG CTG GTC TGA GAG GAT GAT CG CCA CAC TGG GAC TGA C ACG GCC CAG ACT CT ACG GGA GGC AGC AG TGG GGA ATA TTG GAC AT GGG GAAC CCT GAT CCA GCA TG CCG CGT GTG TA AGA AGG TTT TCG GAT TGT AAA GCA CTCG GCG GGG ACATG ATGA CGG TAC CCG CAG AAG AAG CCC CGG CTA ACT TCG TGC CAG CAG CG CGG T TTCG GAA TGA CTG GGC GTA AAG GC GTG TAG GCG GTT TGT CA GTC AGA TGT GAA ATC CCC GGG CTTA ACC TGG GAG CTG CAT
AJ419844.1 <i>Acetobacter_malorum</i>	GC GGTG AGT AAC GCG TAG GA ATC TAT CCA CGG GTG GGG GAT C TC GGAAA CTGG CTTC CGC ATG ATA CT GA GGG TCA AAG GCG TC GCC TGT GGA GGA GCC TGC GTT TGA TTA GCTT GTT GGT GGG GTA ATG GCC TAC CAA GGC GAT GAT CAA TAG CTG GTC TGA GAG GAT GAT CG CCA CAC TGG GAC TGA C ACG GCC CAG ACT CT ACG GGA GGC AGC AG TGG GGA ATA TTG GAC AT GGG GAAC CCT GAT CCA GCA TG CCG CGT GTG TA AGA AGG TTT TCG GAT TGT AAA GCA CTCG GCG GGG ACATG ATGA CGG TAC CCG CAG AAG AAG CCC CGG CTA ACT TCG TGC CAG CAG CG CGG T TTCG GAA TGA CTG GGC GTA AAG GC GTG TAG GCG GTT TGT CA GTT AGA TGT GAA ATC CCC GGG CTTA ACC TGG GAG CTG CAT
>AJ635216.1 Acetobacter pasteurianus DSM 3509T	GATGGTCTGTATACCCTGAACGGCAAGTTCTGGTACGGTATCCCCG GCCCACTGGGTGCGCATAACTTTA TGGCCATGGCCTACAGCCCCAAAACGCACCTGGTCTATATCCCCGGC TCACCAGATTCCGTTTGGTTATAA AAACCAGGTTGGTGGCTTTAAGCCGCATGCGGATTCCTGGAACGTT GGTCTGGACATGACCAAGAACGGT

	CTGCCTGATACCCCAGAAGCCCGTACCGCTTACATCAAGGATCTGC ACGGCTGGCTGCTGGCATGGGATC CGGTCAAGATGGAAACGGTCTGGAAGATTGACCACAAAGGTCCGT GGAACGGCGGCATTCTGGCCACCGG CGGTGATCTTCTGTTCCAAGGCTTGGCCAATGGTGAATTCCACGCC TATGACGCCACGAACGGTAGCGAC CTTTACAAGTTTGACGCACAGAGCGGCATTATCGCTCCGCCTATGA CCTATAGCGTCAACGGCAAGCA
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**Table S13.** 16S rDNA region of isolated acetic acid bacteria and their excision regions using three restriction endonucleases (*SSPI*, *BsgI* and *KpnI*) for PCR-RFLP.

Strain ID	<i>SSPI</i> , <i>BsgI</i> , <i>KpnI</i>
<i>Acetobacter_indonesiensis</i> _(GD1-C1)	1. 233 bp 2. 222 bp 3. 169 bp 4. 93 bp
<i>Acetobacter_pasterionus</i> _(FJ1-C1)	1. 236 bp 2. 225 bp 3. 177 bp 4. 98 bp
<i>Acetobacter_pasterionus</i> (GA1-C1)	1. 236 bp 2. 225 bp 3. 177 bp 4. 98 bp
<i>Acetobacter_malorum</i> (UK1-C1)	1. 236 bp 2. 218 bp 3. 177 bp 4. 98 bp