Supplementary Information

Table S1. List of yeast strains and genomes used in this study.

Table S2. List of yeasts and GenBank numbers used for the rDNA phylogenetic analysis.

Table S3. The phenotypic characteristics of newly reclassified *Candida* and related taxa in *Saccharomycotina*.

Table S4. The antifungal resistance profiles of *Candida* species assigned to the newly created genera in this study.

Figure S1. The expanded phylogenomic tree inferred using 526 single-copy orthologue proteins showing the phylogenetic relationship between *Candida* and related taxa in *Dipodascomycetes*. Bootstrap percentages of maximum likelihood analysis from 1 000 bootstrap replicates are shown on the major branches. *Trigonopsis variabilis* and *Tortispora ganteri* were used as outgroups. Bar = 0.2 substitutions per nucleotide position.

Figure S2. The expanded phylogenomic tree inferred using 545 single-copy orthologue proteins showing the phylogenetic relationship between *Candida* species and related taxa in *Pichiales* (*Pichiomycetes*). Bootstrap percentages of maximum likelihood analysis from 1 000 bootstrap replicates are shown on the major branches. *Nakazawaea holstii* and *Pachysolen tannophilus* were used as outgroups. Bar = 0.2 substitutions per nucleotide position.

Figure S3. The expanded phylogenomic tree inferred using 652 single-copy orthologue proteins showing the phylogenetic relationship between *Candida* species and *Barnettozyma*, *Millerago*, *Phaffomyces* and *Wickerhamomyces* in *Phaffomycetales* (*Saccharomycetes*). Bootstrap percentages of maximum likelihood analysis from 1 000 bootstrap replicates are shown on the major branches. *Ascoidea rubescens* and *Saccharomycopsis capsularis* were used as outgroups. Bar = 0.2 substitutions per nucleotide position.

Figure S4. The expanded phylogenomic tree inferred using 583 single-copy orthologue proteins showing the phylogenetic relationship between *Candida* species and related taxa in *Debaryomycetaceae* (*Serinales*, *Pichiomycetes*). Bootstrap percentages of maximum likelihood analysis from 1 000 bootstrap replicates are shown on the major branches. *Nakazawaea holstii* and *Pachysolen tannophilus* were used as outgroups. Bar = 0.05 substitutions per nucleotide position.

Figure S5. Phylogenetic tree inferred using LSU showing the phylogenetic relationship between *Candida incommunis*, *Candida bentonensis* and related undescribed species. Bootstrap percentages of ML analysis over 50 % from 1 000 bootstrap replicates are shown on the major branches. Bar = 0.2 substitutions per nucleotide position.

Figure S6. Phylogenetic tree inferred using LSU showing the phylogenetic relationship between *Candida* species and the genera *Diddensiella*, *Spencermartinsiella*, *Sugiyamaella* and *Zygoascus*. Bootstrap percentages of ML analysis over 50 % from 1 000 bootstrap replicates are shown on the major branches. Bar = 0.1 substitutions per nucleotide position.

Figure S7. Phylogenetic tree inferred using LSU showing the phylogenetic relationship between *Candida* species and the genus *Starmerella*. Bootstrap percentages of ML analysis over 50 % from 1000 bootstrap replicates are shown on the major branches. Bar = 0.05 substitutions per nucleotide position.

Figure S8. Phylogenetic tree inferred using LSU showing the phylogenetic relationship between *Candida hispaniensis* and related undescribed strains. Bootstrap percentages of ML analysis over 50 % from 1000 bootstrap replicates are shown on the major branches. Bar = 0.1 substitutions per nucleotide position.

Figure S9. Phylogenetic tree inferred using LSU showing the phylogenetic relationship between *Candida* species and related taxa in *Pichiales* (*Pichiomycetes*). Bootstrap percentages of ML analysis over 50 % from 1 000 bootstrap replicates are shown on the major branches. Bar = 0.2 substitutions per nucleotide position.

Figure S10. Phylogenetic tree inferred using ITS showing the phylogenetic relationship of *Candida boidinii* and related unpublished strains. Bootstrap percentages of ML analysis over 50 % from 1000 bootstrap replicates are shown on the major branches. Bar = 0.05 substitutions per nucleotide position.

Figure S11. Phylogenetic tree inferred using LSU showing the phylogenetic relationship between *Candida* species and related taxa in *Debaryomycetaceae*

(*Serinales*, *Pichiomycetes*). Bootstrap percentages of ML analysis over 50 % from 1000 bootstrap replicates are shown on the major branches. Bar = 0.5 substitutions per nucleotide position.

Figure S12. Phylogenetic tree inferred using ITS showing the phylogenetic relationship of *Candida multigemmis* and related unpublished strains. Bootstrap percentages of ML analysis over 50 % from 1000 bootstrap replicates are shown on the major branches. Bar = 0.05 substitutions per nucleotide position.

Figure S13. Phylogenetic tree inferred using LSU showing the phylogenetic relationship between *Candida* species and related taxa in *Phaffomycetaceae* (*Phaffomycetales*, *Saccharomycetes*). Bootstrap percentages of ML analysis over 50 % from 1000 bootstrap replicates are shown on the major branches. Bar = 0.1 substitutions per nucleotide position.

Table S1. List of yeast strains and genomes used in this study

Taxa	Strain	Assembly	Complete BUSCOs (C)	Complete and single-copy BUSCOs (S)	Complete and duplicated BUSCOs (D)	Fragmented BUSCOs (F)	Missing BUSCOs (M)
Dipodascomycetes							
Blastobotrys adeninivorans	TMCC 70007	GCA 016162255.1	99.00%	98.70%	0.30%	0.50%	0.50%
Blastobotrys americana	NRRL Y-6844	GCA 003705795.2	99.20%	99.10%	0.10%	0.30%	0.50%
Blastobotrys arbuscula	NRRL Y-17585	GCA 030564365.1	97.20%	96.70%	0.50%	0.40%	2.40%
Blastobotrys attinorum	NRRL Y-27639	GCA 030564265.1	98.30%	98.00%	0.30%	0.50%	1.20%
Blastobotrys buckinghamii	NRRL Y-63727	GCA 030579975.1	96.70%	96.40%	0.30%	0.40%	2.90%
Blastobotrys capitulata	NRRL Y-17573	GCA 030564325.1	96.30%	96.20%	0.10%	0.70%	3.00%
Blastobotrys chiropterorum	NRRL Y-17071	GCA 030570055.1	98.80%	98.70%	0.10%	0.40%	0.80%
Blastobotrys elegans	NRRL Y-17572	GCA 030564235.1	97.60%	97.50%	0.10%	0.40%	2.00%
Blastobotrys illinoisensis	NRRL YB-1343	GCA 030558835.1	98.60%	97.00%	1.60%	0.40%	1.00%
Blastobotrys indianensis	NRRL YB-1950	GCA 030558855.1	97.30%	97.00%	0.30%	0.40%	2.30%
Blastobotrys malaysiensis	NRRL Y-6417	GCA 030558815.1	98.10%	97.40%	0.70%	0.50%	1.40%
Blastobotrys mokoenaii	NRRL Y-27120	GCA 003705765.2	98.70%	98.30%	0.40%	0.40%	0.90%
Blastobotrys muscicola	NRRL Y-7993	GCA 003705745.2	98.60%	98.20%	0.40%	0.40%	1.00%

Table S1. List of yeast strains and genomes used in this study (Continue)

Taxa	Strain	Assembly	Complete BUSCOs (C)	Complete and single-copy BUSCOs (S)	Complete and duplicated BUSCOs (D)	Fragmented BUSCOs (F)	Missing BUSCOs (M)
Blastobotrys niveus	NRRL Y-17581	GCA 003707525.2	66.30%	66.00%	0.30%	17.70%	16.00%
Blastobotrys parvus	NRRL Y-1004	GCA 030564285.1	97.90%	97.60%	0.30%	0.50%	1.60%
Blastobotrys peoriensis	NRRL YB-2290	GCA 003705735.2	98.40%	98.30%	0.10%	0.90%	0.70%
Blastobotrys persicus	CBS 14259	GCA 030585065.1	99.00%	98.30%	0.70%	0.70%	0.30%
Blastobotrys proliferans	NRRL Y-17577	GCA 003707485.2	98.10%	97.60%	0.50%	0.00%	1.90%
Blastobotrys raffinosifermentans	NRRL Y-27150	GCA 003705705.1	99.00%	95.00%	4.00%	0.50%	0.50%
Blastobotrys robertii	NRRL Y-27775	GCA 030564385.1	97.60%	97.10%	0.50%	0.70%	1.70%
Blastobotrys serpentis	NRRL Y-48249	GCA 003705695.1	99.50%	99.20%	0.30%	0.10%	0.40%
Blastobotrys terrestris	NRRL Y-17704	GCA 030674225.1	98.30%	84.80%	13.50%	0.80%	0.90%
Candida bentonensis	NRRL YB-2364	GCA 030561725.1	95.70%	95.60%	0.10%	0.50%	3.80%
Candida hispaniensis	NRRL Y-5580	GCA 030574015.1	95.20%	95.10%	0.10%	0.70%	4.10%
Candida incommunis	NRRL Y-17085	GCA 003706695.3	95.40%	95.10%	0.30%	0.70%	3.90%
Candida kazuoi	JCM 12558	GCA 030555755.1	77.70%	77.60%	0.10%	7.10%	15.20%
Candida lundiana	CBS 12271	GCA 030563415.1	98.10%	97.60%	0.50%	0.10%	1.80%

Table S1. List of yeast strains and genomes used in this study (Continue)

Taxa	Strain	Assembly	Complete BUSCOs (C)	Complete and single-copy BUSCOs (S)	Complete and duplicated BUSCOs (D)	Fragmented BUSCOs (F)	Missing BUSCOs (M)
Candida patagonica	CBS 10443	GCA 030580475.1	97.50%	96.70%	0.80%	0.50%	2.00%
Candida suthepensis	CBS 12270	GCA 030568895.1	97.60%	97.10%	0.50%	0.70%	1.70%
Candida tunisiensis	CBS 12513	GCA 030407195.1	96.50%	96.20%	0.30%	2.40%	1.10%
Crinitomyces ghanaensis	NRRL YB-1486	GCA 030581755.1	97.10%	97.10%	0.00%	0.70%	2.20%
Deakozyma indianensis	NRRL YB-1937	GCA 003706415.3	96.40%	96.30%	0.10%	0.80%	2.80%
Diddensiella caesifluorescens	NRRL Y-48781	GCA 030558955.1	99.10%	98.70%	0.40%	0.30%	0.60%
Diddensiella santjacobensis	NRRL Y-17667	GCA 030574215.1	98.30%	97.90%	0.40%	0.40%	1.30%
Diddensiella transvaalensis	NRRL Y-27140	GCA 030555955.1	98.10%	97.80%	0.30%	0.90%	1.00%
Dipodascus aggregatus	NRRL Y-17564	GCA 030564925.1	98.90%	84.70%	14.20%	0.00%	1.10%
Dipodascus albidus	NRRL Y-12859	GCA 003707475.1	97.50%	92.20%	5.30%	0.40%	2.10%
Dipodascus armillariae	NRRL Y-17580	GCA 030674515.1	81.30%	72.30%	9.00%	10.40%	8.30%
Dipodascus australiensis	NRRL Y-17565	GCA 030563945.1	98.30%	94.20%	4.10%	0.10%	1.60%
Dipodascus carabidarus	NRRL Y-27727	GCA 030556585.1	99.00%	83.40%	15.60%	0.00%	1.00%
Dipodascus cucujoidarus	NRRL Y-27731	GCA 030566025.1	98.20%	87.50%	10.70%	0.90%	0.90%

Table S1. List of yeast strains and genomes used in this study (Continue)

Taxa	Strain	Assembly	Complete BUSCOs (C)	Complete and single-copy BUSCOs (S)	Complete and duplicated BUSCOs (D)	Fragmented BUSCOs (F)	Missing BUSCOs (M)
Dipodascus fermentans	NRRL Y-1492	GCA 030564905.1	98.90%	82.80%	16.10%	0.40%	0.70%
Dipodascus geniculatus	NRRL Y-17628	GCA 003708655.1	97.80%	92.90%	4.90%	0.40%	1.80%
Dipodascus ghanensis	CBS 11010	GCA 022023575.1	97.00%	92.00%	5.00%	0.40%	2.60%
Dipodascus histeridarus	NRRL Y-27729	GCA 030566085.1	98.90%	83.60%	15.30%	0.10%	1.00%
Dipodascus klebahnii	NRRL Y-17568	GCA 030570935.1	98.70%	79.40%	19.30%	0.30%	1.00%
Dipodascus macrosporus	NRRL Y-17586	GCA 030463045.1	96.80%	87.30%	9.50%	1.20%	2.00%
Dipodascus restrictus	CBS 111234	GCA 030563985.1	98.40%	84.20%	14.20%	0.10%	1.50%
Dipodascus siamensis	CBS 10929	GCA 030568955.1	96.20%	91.70%	4.50%	0.90%	2.90%
Galactomyces geotrichum	NRRL Y-17569	GCA 030558905.1	98.70%	91.70%	7.00%	0.30%	1.00%
Galactomyces reessii	NRRL Y-17566	GCA 030570815.1	98.20%	90.90%	7.30%	0.50%	1.30%
Geotrichum candidum	CLIB 918	GCA 001402995.1	98.30%	91.20%	7.10%	0.10%	1.60%
Geotrichum citri-aurantii	CBS 176.89	GCA 030463015.1	98.60%	91.70%	6.90%	0.40%	1.00%
Geotrichum europaeum	CBS 866.68	GCA 030567025.1	96.70%	90.10%	6.60%	1.30%	2.00%
Geotrichum phurueaensis	CBS 11418	GCA 030558065.1	98.30%	91.20%	7.10%	0.40%	1.30%

Table S1. List of yeast strains and genomes used in this study (Continue)

Taxa	Strain	Assembly	Complete BUSCOs (C)	Complete and single-copy BUSCOs (S)	Complete and duplicated BUSCOs (D)	Fragmented BUSCOs (F)	Missing BUSCOs (M)
Groenewaldozyma auringiensis	NRRL Y-17674	GCA 030574195.1	97.10%	97.00%	0.10%	1.20%	1.70%
Groenewaldozyma salmanticensis	NRRL Y-17090	GCA 003708315.3	97.60%	97.50%	0.10%	0.80%	1.60%
Groenewaldozyma sp.	yHMH443	GCA 030580275.1	97.20%	97.10%	0.10%	0.80%	2.00%
Groenewaldozyma tartarivorans	NRRL Y-27291	GCA 030574255.1	97.50%	97.40%	0.10%	0.70%	1.80%
Magnusiomyces capitatus	NRRL Y-17686	GCA 900497725.1	96.90%	96.80%	0.10%	0.10%	3.00%
Magnusiomyces clavatus	CNRMA 12.647	GCA 000817185.1	97.10%	96.80%	0.30%	0.40%	2.50%
Magnusiomyces ingens	NRRL Y-17630	GCA 900497715.1	92.60%	92.50%	0.10%	1.50%	5.90%
Magnusiomyces magnusii	NRRL Y-17563	GCA 030570155.1	87.70%	39.80%	47.90%	4.90%	7.40%
Magnusiomyces starmeri	NRRL Y-17816	GCA 030578655.1	94.10%	93.80%	0.30%	1.80%	4.10%
Magnusiomyces tetraspermus	NRRL Y-7288	GCA 030578715.1	96.70%	79.90%	16.80%	0.30%	3.00%
Middelhovenomyces tepae	NRRL Y-17670	GCA 003708105.3	98.30%	98.20%	0.10%	0.50%	1.20%
Nadsonia commutata	NRRL Y-7950	GCA 030563525.1	98.70%	95.10%	3.60%	0.70%	0.60%
Nadsonia fulvescens var. elongata	DSM 6958	GCA 001661315.1	96.30%	93.10%	3.20%	2.10%	1.60%
Nadsonia fulvescens var. fulvescens	NRRL Y-12810	GCA 003705595.2	98.60%	95.30%	3.30%	0.40%	1.00%

Table S1. List of yeast strains and genomes used in this study (Continue)

Taxa	Strain	Assembly	Complete BUSCOs (C)	Complete and single-copy BUSCOs (S)	Complete and duplicated BUSCOs (D)	Fragmented BUSCOs (F)	Missing BUSCOs (M)
Nadsonia starkeyi-henricii	UCD142	GCA 003123035.1	99.20%	95.90%	3.30%	0.10%	0.70%
Saprochaete fungicola	N/A	GCA 900654225.1	96.80%	96.80%	0.00%	0.10%	3.10%
Saprochaete ingens	CBS 517.90	GCA 902498895.1	95.40%	95.30%	0.10%	0.70%	3.90%
Saprochaete suaveolens	N/A	GCA 900642975.1	96.00%	75.30%	20.70%	0.30%	3.70%
Spencermartinsiella europaea	NRRL Y-48265	GCA 030579595.1	98.70%	98.00%	0.70%	0.50%	0.80%
Spencermartinsiella ligniputridi	NRRL Y-48818	GCA 030583385.1	99.20%	98.90%	0.30%	0.30%	0.50%
Starmerella apicola	NRRL Y-50540	GCA 001005415.1	80.60%	80.60%	0.00%	2.10%	17.30%
Starmerella apis	NRRL Y-2482	GCA 030564665.1	85.40%	85.40%	0.00%	1.10%	13.50%
Starmerella asiatica	CBS 14173	GCA 030572815.1	80.70%	80.60%	0.10%	2.10%	17.20%
Starmerella bacillaris	CBS 9494	GCA 003260575.1	76.10%	76.10%	0.00%	2.80%	21.10%
Starmerella bombi	NRRL Y-17081	GCA 030579915.1	79.00%	79.00%	0.00%	2.40%	18.60%
Starmerella bombicola	NRRL Y-17069	GCA 004124885.1	81.40%	81.40%	0.00%	2.80%	15.80%
Starmerella cellae	NRRL Y-27860	GCA 030579775.1	78.80%	78.80%	0.00%	2.50%	18.70%
Starmerella davenportii	CBS 9069	GCA 004124985.1	69.00%	68.90%	0.10%	4.90%	26.10%

Table S1. List of yeast strains and genomes used in this study (Continue)

Taxa	Strain	Assembly	Complete BUSCOs (C)	Complete and single-copy BUSCOs (S)	Complete and duplicated BUSCOs (D)	Fragmented BUSCOs (F)	Missing BUSCOs (M)
Starmerella etchellsii	NRRL Y-17084	GCA 030490775.1	76.10%	76.00%	0.10%	4.40%	19.50%
Starmerella floricola	NRRL Y-17676	GCA 030579735.1	82.40%	82.30%	0.10%	2.00%	15.60%
Starmerella floris	NRRL Y-48255	GCA 030555655.1	73.20%	71.00%	2.20%	4.60%	22.20%
Starmerella geochares	NRRL Y-17073	GCA 004125165.1	80.60%	80.60%	0.00%	4.10%	15.30%
Starmerella gropengiesseri	NRRL Y-17142	GCA 030579755.1	49.10%	49.10%	0.00%	19.80%	31.10%
Starmerella khaoyaiensis	NBRC 104213	GCA 030563285.1	81.80%	81.80%	0.00%	1.50%	16.70%
Starmerella kuoi	NRRL Y-27208	GCA 004124915.1	83.90%	83.90%	0.00%	1.60%	14.50%
Starmerella lactis-condensi	NRRL Y-1515	GCA 030568935.1	73.10%	73.10%	0.00%	2.60%	24.30%
Starmerella magnoliae	PYCC 2903	GCA 003033435.1	76.50%	76.50%	0.00%	4.70%	18.80%
Starmerella potacharoeniae	NBRC 106439	GCA 030566975.1	69.40%	69.10%	0.30%	5.10%	25.50%
Starmerella powellii	CBS 8795	GCA 030568915.1	81.80%	81.80%	0.00%	2.10%	16.10%
Starmerella ratchasimensis	CBS 10611	GCA 004124975.1	60.80%	60.70%	0.10%	5.10%	34.10%
Starmerella riodocensis	NRRL Y-27859	GCA 004124955.1	72.70%	72.70%	0.00%	6.30%	21.00%
Starmerella roubikii	CBS 15148	GCA 030584945.1	79.60%	79.60%	0.00%	2.10%	18.30%

Table S1. List of yeast strains and genomes used in this study (Continue)

Taxa	Strain	Assembly	Complete BUSCOs (C)	Complete and single-copy BUSCOs (S)	Complete and duplicated BUSCOs (D)	Fragmented BUSCOs (F)	Missing BUSCOs (M)
Starmerella scarabaei	CBS 14174	GCA 030565305.1	82.30%	82.30%	0.00%	1.70%	16.00%
Starmerella sirachaensis	NBRC 108605	GCA 030578495.1	82.60%	82.60%	0.00%	1.80%	15.60%
Starmerella sorbosivorans	CBS 8768	GCA 004125005.1	78.40%	78.40%	0.00%	3.70%	17.90%
Starmerella stellata	NRRL Y-1446	GCA 030674195.1	76.50%	76.50%	0.00%	2.40%	21.10%
Starmerella stigmatis	CBS 11464	GCA 030563545.1	81.60%	81.50%	0.10%	2.60%	15.80%
Starmerella tilneyi	CBS 8794	GCA 004125055.1	83.50%	83.40%	0.10%	2.00%	14.50%
Starmerella vaccinii	NRRL Y-17684	GCA 004125185.1	84.00%	83.90%	0.10%	1.80%	14.20%
Starmerella vitae	CBS 15147	GCA 030584925.1	78.50%	78.50%	0.00%	2.80%	18.70%
Sugiyamaella americana	NRRL YB-2067	GCA 030583405.1	99.00%	98.90%	0.10%	0.70%	0.30%
Sugiyamaella boreocaroliniensis	NRRL YB-1835	GCA 030575195.1	98.10%	98.00%	0.10%	0.40%	1.50%
Sugiyamaella castrensis	NRRL Y-17329	GCA 030583505.1	98.90%	98.40%	0.50%	0.50%	0.60%
Sugiyamaella chiloensis	NRRL Y-17643	GCA 030578775.1	92.60%	92.10%	0.50%	0.90%	6.50%
Sugiyamaella floridensis	NRRL YB-3827	GCA 030556845.1	98.40%	98.30%	0.10%	0.30%	1.30%
Sugiyamaella grinbergsii	NRRL Y-27117	GCA 030579895.1	99.00%	98.90%	0.10%	0.10%	0.90%

Table S1. List of yeast strains and genomes used in this study (Continue)

Taxa	Strain	Assembly	Complete BUSCOs (C)	Complete and single-copy BUSCOs (S)	Complete and duplicated BUSCOs (D)	Fragmented BUSCOs (F)	Missing BUSCOs (M)
Sugiyamaella japonica	NRRL YB-2798	GCA 030583365.1	99.20%	99.10%	0.10%	0.10%	0.70%
Sugiyamaella lignohabitans	CBS 10342	GCA 001640025.2	81.80%	81.70%	0.10%	6.70%	11.50%
Sugiyamaella marilandica	NRRL YB-1847	GCA 030563205.1	98.80%	98.50%	0.30%	0.10%	1.10%
Sugiyamaella marionensis	NRRL YB-1336	SRR16988754	98.60%	98.30%	0.30%	0.40%	1.00%
Sugiyamaella mastotermitis	CBS 14182	GCA 030572735.1	99.20%	98.90%	0.30%	0.40%	0.40%
Sugiyamaella neomexicana	NRRL YB-2450	GCA 030555635.1	98.70%	98.20%	0.50%	0.10%	1.20%
Sugiyamaella novakii	NRRL Y-27346	GCA 030575175.1	98.80%	98.50%	0.30%	0.10%	1.10%
Sugiyamaella paludigena	NRRL Y-12697	GCA 030579875.1	97.70%	97.40%	0.30%	0.70%	1.60%
Sugiyamaella pinicola	NRRL YB-2263	GCA 030565085.1	99.10%	98.80%	0.30%	0.30%	0.60%
Sugiyamaella qingdaonensis	CBS 11390	GCA 030569235.1	98.80%	98.50%	0.30%	0.30%	0.90%
Sugiyamaella smithiae	NRRL Y-17850	GCA 030579815.1	99.20%	98.80%	0.40%	0.40%	0.40%
Sugiyamaella sp.	yHKS617	GCA 030580325.1	98.30%	98.20%	0.10%	0.30%	1.40%
Sugiyamaella valdiviana	NRRL Y-7791	GCA 030570555.1	98.60%	98.30%	0.30%	0.30%	1.10%
Sugiyamaella xylanicola	CBS 12683	GCA 001939105.2	99.00%	98.90%	0.10%	0.30%	0.70%

Table S1. List of yeast strains and genomes used in this study (Continue)

Taxa	Strain	Assembly	Complete BUSCOs (C)	Complete and single-copy BUSCOs (S)	Complete and duplicated BUSCOs (D)	Fragmented BUSCOs (F)	Missing BUSCOs (M)
Tardiomyces blankii	NRRL Y-17068	GCA 030573285.1	98.50%	96.70%	1.80%	0.70%	0.80%
Tardiomyces depauwii	NCPF13064	GCA 038086965.1	98.00%	97.60%	0.40%	0.80%	1.20%
Tardiomyces digboiensis	CBS 9800	GCA 030570855.1	86.00%	68.10%	17.90%	8.30%	5.70%
Trichomonascus apis	NRRL Y-48475	GCA 030557665.1	98.50%	97.40%	1.10%	0.50%	1.00%
Trichomonascus ciferrii	NRRL Y-10943	GCA 030573635.1	99.20%	98.40%	0.80%	0.10%	0.70%
Trichomonascus petasosporus	NRRL YB-2092	GCA 030580095.1	98.20%	97.90%	0.30%	0.30%	1.50%
Trichomonascus vanleenenianus	CBS 14902	GCA 030572835.1	98.60%	98.30%	0.30%	0.80%	0.60%
Wickerhamiella allomyrinae	CBS 13167	GCA 030581455.1	92.10%	91.80%	0.30%	1.20%	6.70%
Wickerhamiella alocasiicola	PYCC 8427	GCA 022577715.1	87.40%	86.50%	0.90%	1.30%	11.30%
Wickerhamiella australiensis	NRRL Y-27360	GCA 030579635.1	87.30%	87.30%	0.00%	2.10%	10.60%
Wickerhamiella azymoides	CBS 10508	GCA 030563245.1	84.80%	84.70%	0.10%	2.50%	12.70%
Wickerhamiella bombiphila	NRRL Y-27640	GCA 030561035.1	86.10%	86.00%	0.10%	1.80%	12.10%
Wickerhamiella brachini	CBS 14176	GCA 030565285.1	91.30%	91.20%	0.10%	1.30%	7.40%
Wickerhamiella cacticola	NRRL Y-27362	GCA 003705615.1	88.10%	83.10%	5.00%	1.30%	10.60%

Table S1. List of yeast strains and genomes used in this study (Continue)

Taxa	Strain	Assembly	Complete BUSCOs (C)	Complete and single-copy BUSCOs (S)	Complete and duplicated BUSCOs (D)	Fragmented BUSCOs (F)	Missing BUSCOs (M)
Wickerhamiella dianesei	PYCC 8330	GCA 022577725.1	85.90%	85.90%	0.00%	1.70%	12.40%
Wickerhamiella domercqiae	NRRL Y-6692	GCA 004125175.1	84.40%	84.40%	0.00%	1.70%	13.90%
Wickerhamiella galacta	NRRL Y-17645	GCA 003045245.1	92.20%	92.10%	0.10%	0.80%	7.00%
Wickerhamiella hasegawae	JCM 12559	GCA 004125105.1	90.80%	90.50%	0.30%	1.80%	7.40%
Wickerhamiella infanticola	NRRL Y-17858	GCA 004125145.1	90.30%	89.80%	0.50%	0.90%	8.80%
Wickerhamiella kurtzmanii	PYCC 8437	GCA 022577765.1	87.10%	87.10%	0.00%	1.10%	11.80%
Wickerhamiella lipophila	NRRL Y-27367	GCA 030582055.1	86.80%	86.80%	0.00%	1.80%	11.40%
Wickerhamiella musiphila	CBS 10697	GCA 030558175.1	85.10%	85.00%	0.10%	1.30%	13.60%
Wickerhamiella nectarea	PYCC 8436	GCA 022577815.1	85.80%	85.80%	0.00%	2.00%	12.20%
Wickerhamiella occidentalis	NRRL Y-27364	GCA 004125095.1	86.80%	86.50%	0.30%	2.10%	11.10%
Wickerhamiella pararugosa	NRRL Y-17089	GCA 004125235.1	78.30%	78.20%	0.10%	7.30%	14.40%
Wickerhamiella parazyma	PYCC 8426	GCA 022577825.1	82.40%	82.10%	0.30%	2.80%	14.80%
Wickerhamiella qilinensis	CBS 13929	GCA 030556915.1	89.80%	89.70%	0.10%	1.50%	8.70%
Wickerhamiella sergipiensis	CBS 9567	GCA 030563925.1	90.10%	90.00%	0.10%	2.10%	7.80%

Table S1. List of yeast strains and genomes used in this study (Continue)

Taxa	Strain	Assembly	Complete BUSCOs (C)	Complete and single-copy BUSCOs (S)	Complete and duplicated BUSCOs (D)	Fragmented BUSCOs (F)	Missing BUSCOs (M)
Wickerhamiella shivajii	CBS 15893	GCA 030585105.1	87.60%	87.60%	0.00%	1.20%	11.20%
Wickerhamiella siamensis	CBS 13331	GCA 030571815.1	91.10%	90.80%	0.30%	1.50%	7.40%
Wickerhamiella slavikovae	CBS 12417	GCA 030571795.1	81.90%	81.80%	0.10%	2.40%	15.70%
Wickerhamiella sorbophila	DS02	GCA 002251995.2	91.80%	91.00%	0.80%	0.80%	7.40%
Wickerhamiella spandovensis	PYCC 8431	GCA 022577695.1	90.50%	90.40%	0.10%	1.20%	8.30%
Wickerhamiella vanderwaltii	PYCC 3671	GCA 022577775.1	88.10%	88.00%	0.10%	1.30%	10.60%
Wickerhamiella versatilis	NRRL Y-6652	GCA 004125065.1	86.50%	86.10%	0.40%	1.80%	11.70%
Yarrowia alimentaria	CBS 10151	GCA 900518985.1	96.70%	96.60%	0.10%	0.70%	2.60%
Yarrowia brassicae	CBS 15225	GCA 030585005.1	97.70%	97.60%	0.10%	0.40%	1.90%
Yarrowia bubula	NRRL Y-63668	GCA 003707035.1	96.40%	95.30%	1.10%	0.80%	2.80%
Yarrowia deformans	CBS 2071	GCA 900519085.1	97.60%	97.60%	0.00%	0.80%	1.60%
Yarrowia galli	CBS 9722	GCA 900519055.1	97.50%	97.20%	0.30%	0.40%	2.10%
Yarrowia hollandica	CBS 4855	GCA 900519065.1	98.30%	98.20%	0.10%	0.30%	1.40%
Yarrowia keelungensis	CBS 11062	GCA 900519035.1	96.40%	96.40%	0.00%	1.10%	2.50%

Table S1. List of yeast strains and genomes used in this study (Continue)

Taxa	Strain	Assembly	Complete BUSCOs (C)	Complete and single-copy BUSCOs (S)	Complete and duplicated BUSCOs (D)	Fragmented BUSCOs (F)	Missing BUSCOs (M)
Yarrowia lipolytica	CGMCC7326	GCA 020826875.1	97.50%	97.50%	0.00%	0.50%	2.00%
Yarrowia osloensis	CBS 10146	GCA 900519015.1	96.50%	96.40%	0.10%	0.50%	3.00%
Yarrowia phangngaensis	CBS 10407	GCA 900519005.1	98.00%	98.00%	0.00%	0.50%	1.50%
Yarrowia porcina	CBS 12935	GCA 900519025.1	97.10%	97.00%	0.10%	0.80%	2.10%
Yarrowia yakushimensis	CBS 10253	GCA 900518995.1	97.30%	97.20%	0.10%	0.50%	2.20%
Zygoascus biomembranicola	CBS 14157	GCA 030556875.1	98.90%	98.80%	0.10%	0.00%	1.10%
Zygoascus bituminiphia	CBS 8813	GCA 030705125.1	99.00%	98.90%	0.10%	0.10%	0.90%
Zygoascus flipseniorum	CBS 14876	GCA 030565365.1	98.10%	98.00%	0.10%	0.70%	1.20%
Zygoascus hellenicus	NRRL Y-7136	GCA 030564625.1	94.10%	93.80%	0.30%	0.50%	5.40%
Zygoascus meyerae	NRRL Y-17319	GCA 003707935.2	97.30%	97.20%	0.10%	0.30%	2.40%
Zygoascus ofunaensis	NRRL Y-10998	GCA 003707925.2	98.30%	98.30%	0.00%	0.00%	1.70%
Zygoascus polysorbophila	NRRL Y-27161	GCA 030563625.1	98.80%	98.50%	0.30%	0.00%	1.20%
Zygoascus tannicola	NRRL Y-17392	GCA 030569095.1	97.50%	97.40%	0.10%	0.00%	2.50%
Pichiomycetes							
Alaninales							

Table S1. List of yeast strains and genomes used in this study (Continue)

Taxa	Strain	Assembly	Complete BUSCOs (C)	Complete and single-copy BUSCOs (S)	Complete and duplicated BUSCOs (D)	Fragmented BUSCOs (F)	Missing BUSCOs (M)
Nakazawaea holstii	NRRL Y-2155	GCA 003706265.1	96.40%	95.60%	0.80%	0.50%	3.10%
Pachysolen tannophilus	NRRL Y-2460	GCA 030573675.1	96.50%	96.00%	0.50%	0.50%	3.00%
Pichiales							
Allodekkera sacchari	CBS 14167	GCA 030565225.1	93.80%	93.70%	0.10%	0.70%	5.50%
Ambrosiozyma ambrosiae	NRRL Y-7524	GCA 003705185.2	93.30%	93.30%	0.00%	0.70%	6.00%
Ambrosiozyma angophorae	NRRL Y-7118	GCA 030567475.1	86.80%	86.70%	0.10%	0.90%	12.30%
Ambrosiozyma cicatricosa	NRRL Y-17594	GCA 030579935.1	92.10%	91.70%	0.40%	0.50%	7.40%
Ambrosiozyma kamigamensis	NRRL Y-63629	GCA 030572235.1	90.50%	90.50%	0.00%	1.30%	8.20%
Ambrosiozyma kashinagicola	JCM 15019	GCA 001599075.1	95.10%	95.10%	0.00%	0.40%	4.50%
Ambrosiozyma llanquihuensis	NRRL Y-17657	GCA 030568425.1	92.20%	92.20%	0.00%	1.30%	6.50%
Ambrosiozyma maleeae	NRRL Y-63635	GCA 003706635.1	93.80%	93.70%	0.10%	0.70%	5.50%
Ambrosiozyma monospora	JCM 7599	GCA 001599995.1	89.60%	88.30%	1.30%	1.20%	9.20%
Ambrosiozyma neoplatypodis	NRRL Y-63630	GCA 030567495.1	92.30%	92.20%	0.10%	1.10%	6.60%
Ambrosiozyma oregonensis	NRRL Y-6106	GCA 003706315.2	93.90%	93.90%	0.00%	0.40%	5.70%

Table S1. List of yeast strains and genomes used in this study (Continue)

Taxa	Strain	Assembly	Complete BUSCOs (C)	Complete and single-copy BUSCOs (S)	Complete and duplicated BUSCOs (D)	Fragmented BUSCOs (F)	Missing BUSCOs (M)
Ambrosiozyma philentoma	NRRL Y-7523	GCA 003707675.2	93.00%	92.70%	0.30%	0.40%	6.60%
Ambrosiozyma platypodis	NRRL Y-7524	GCA 003705185.2	93.40%	93.40%	0.00%	0.70%	5.90%
Ambrosiozyma pseudovanderkliftii	NRRL Y-63632	GCA 003707895.2	94.30%	94.30%	0.00%	0.70%	5.00%
Ambrosiozyma vanderkliftii	NRRL Y-63633	GCA 003705225.1	94.00%	93.90%	0.10%	0.30%	5.70%
Brettanomyces anomalus	NRRL Y-17522	GCA 018344455.1	91.40%	87.30%	4.10%	0.80%	7.80%
Brettanomyces bruxellensis	NRRL Y-12961	GCA 018346845.1	80.40%	67.30%	13.10%	5.80%	13.80%
Brettanomyces custersianus	NRRL Y-6653	GCA 003705215.2	92.20%	91.80%	0.40%	0.90%	6.90%
Brettanomyces naardenensis	NRRL Y-17526	GCA 018344465.1	93.50%	84.00%	9.50%	0.80%	5.70%
Brettanomyces nanus	CBS 1945	GCA 011074865.2	89.50%	89.40%	0.10%	1.20%	9.30%
Brettanomyces sp.	kh3	GCA 016906875.1	88.40%	83.80%	4.60%	1.80%	9.80%
Candida arabinofermentans	NRRL YB-2248	GCA 030567675.1	95.90%	95.60%	0.30%	0.50%	3.60%
Candida awuae	CBS 11011	GCA 030563725.1	85.50%	85.40%	0.10%	0.80%	13.70%
Candida boidinii	NRRL Y-2332	GCA 003243125.1	93.90%	93.80%	0.10%	0.70%	5.40%
Candida cabralensis	CBS 11679	GCA 030569495.1	84.10%	84.00%	0.10%	1.10%	14.80%

Table S1. List of yeast strains and genomes used in this study (Continue)

Taxa	Strain	Assembly	Complete BUSCOs (C)	Complete and single-copy BUSCOs (S)	Complete and duplicated BUSCOs (D)	Fragmented BUSCOs (F)	Missing BUSCOs (M)
Candida californica	Olga-1	GCA 016584265.1	86.60%	86.50%	0.10%	1.30%	12.10%
Candida ethanolica	NRRL Y-12615	GCA 030570435.1	88.30%	88.00%	0.30%	1.50%	10.20%
Candida inconspicua	CBS 180	GCA 004931855.1	86.00%	85.90%	0.10%	1.70%	12.30%
Candida insectalens	NRRL Y-7778	GCA 030574155.1	92.60%	92.60%	0.00%	0.90%	6.50%
Candida krabiensis	NRRL Y-27965	GCA 030582815.1	96.10%	95.80%	0.30%	0.40%	3.50%
Candida maris	NRRL Y-6696	GCA 030557505.1	94.40%	94.30%	0.10%	0.50%	5.10%
Candida mattraensis	CBS 12097	GCA 030564055.1	95.70%	95.60%	0.10%	0.80%	3.50%
Candida methanosorbosa	NRRL Y-17320	GCA 030570755.1	96.00%	95.90%	0.10%	0.40%	3.60%
Candida nanaspora	NRRL Y-17679	GCA 030557475.1	94.90%	94.60%	0.30%	0.70%	4.40%
Candida nemodendra	NRRL Y-7779	GCA 030567775.1	95.40%	95.30%	0.10%	0.80%	3.80%
Candida nitratophila	NRRL YB-3654	GCA 030567875.1	94.60%	94.30%	0.30%	1.10%	4.30%
Candida ortonii	NRRL Y-48038	GCA 030561785.1	92.20%	92.10%	0.10%	1.10%	6.70%
Candida ovalis	NRRL Y-17662	GCA 030556425.1	95.80%	95.40%	0.40%	0.40%	3.80%
Candida phayaonensis	NBRC 108868	GCA 030558305.1	84.80%	84.70%	0.10%	1.70%	13.50%

Table S1. List of yeast strains and genomes used in this study (Continue)

Taxa	Strain	Assembly	Complete BUSCOs (C)	Complete and single-copy BUSCOs (S)	Complete and duplicated BUSCOs (D)	Fragmented BUSCOs (F)	Missing BUSCOs (M)
Candida piceae	NRRL YB-2107	GCA 030567815.1	95.70%	95.40%	0.30%	0.30%	4.00%
Candida pignaliae	NRRL Y-17664	GCA 030570775.1	95.60%	95.30%	0.30%	0.70%	3.70%
Candida pini	NRRL Y-2023	GCA 030567935.1	94.20%	93.90%	0.30%	0.80%	5.00%
Candida pseudolambica	NRRL Y-17318	GCA 030569595.1	78.40%	78.00%	0.40%	5.30%	16.30%
Candida rishiriensis	NBRC 105027	GCA 030569615.1	95.00%	94.20%	0.80%	0.80%	4.20%
Candida rugopelliculosa	NRRL Y-17079	GCA 030570335.1	83.70%	83.40%	0.30%	0.90%	15.40%
Candida silvatica	NRRL Y-7777	GCA 030564685.1	90.20%	90.20%	0.00%	0.80%	9.00%
Candida sithepensis	JCM 12265	GCA 030564825.1	95.10%	95.00%	0.10%	0.70%	4.20%
Candida sonorensis	NRRL Y-7800	GCA 030567855.1	95.20%	94.90%	0.30%	0.70%	4.10%
Candida sorboxylosa	NRRL Y-17669	GCA 030564865.1	81.90%	81.90%	0.00%	2.10%	16.00%
Candida sp.	NRRL Y-12764	GCA 030579995.1	93.80%	93.70%	0.10%	1.20%	5.00%
Candida succiphila	JCM 9445	GCA 001599255.1	93.00%	92.90%	0.10%	0.80%	6.20%
Candida suzukii	NRRL Y-27593	GCA 030568155.1	94.70%	94.60%	0.10%	0.70%	4.60%
Candida thaimueangensis	NBRC 101967	GCA 030569635.1	87.00%	86.90%	0.10%	1.20%	11.80%

Table S1. List of yeast strains and genomes used in this study (Continue)

Taxa	Strain	Assembly	Complete BUSCOs (C)	Complete and single-copy BUSCOs (S)	Complete and duplicated BUSCOs (D)	Fragmented BUSCOs (F)	Missing BUSCOs (M)
Candida xyloterini	CBS 11547	GCA 030573155.1	92.50%	92.00%	0.50%	1.50%	6.00%
Citeromyces hawaiiensis	NRRL Y-11581	GCA 030567395.1	94.00%	93.90%	0.10%	1.80%	4.20%
Citeromyces matritensis	NRRL Y-2407	GCA 030570875.1	94.60%	91.60%	3.00%	0.70%	4.70%
Citeromyces nyonsensis	CBS 12700	GCA 030580415.1	93.90%	93.00%	0.90%	1.20%	4.90%
Citeromyces siamensis	NRRL Y-27975	GCA 003706365.1	90.10%	65.30%	24.80%	3.20%	6.70%
Komagataella kurtzmanii	VKPM Y-727	GCA 022533605.1	93.90%	93.80%	0.10%	0.80%	5.30%
Komagataella mondaviorum	CBS 15017	GCA 023213015.1	95.10%	95.00%	0.10%	0.80%	4.10%
Komagataella pastoris	ATCC 28485	GCA 001708105.1	94.30%	94.20%	0.10%	0.90%	4.80%
Komagataella phaffii	CBS 7435	GCA 900235035.2	96.40%	96.30%	0.10%	0.50%	3.10%
Komagataella populi	NRRL YB-455	GCA 003705255.2	93.90%	93.80%	0.10%	1.20%	4.90%
Komagataella pseudopastoris	NRRL Y-27603	GCA 003671595.2	94.00%	93.90%	0.10%	0.70%	5.30%
Komagataella ulmi	CBS 12361	GCA 023213065.1	95.20%	95.10%	0.10%	0.70%	4.10%
Kregervanrija delftensis	NRRL Y-7119	GCA 003707205.2	92.70%	92.60%	0.10%	0.70%	6.60%
Kregervanrija fluxuum	NRRL YB-4273	GCA 003707275.2	93.30%	93.00%	0.30%	0.70%	6.00%

Table S1. List of yeast strains and genomes used in this study (Continue)

Taxa	Strain	Assembly	Complete BUSCOs (C)	Complete and single-copy BUSCOs (S)	Complete and duplicated BUSCOs (D)	Fragmented BUSCOs (F)	Missing BUSCOs (M)
Kregervanrija pseudodelftensis	NRRL Y-5494	GCA 030580115.1	93.60%	93.50%	0.10%	0.70%	5.70%
Kuraishia borneana	CBS 12507	GCA 030569035.1	94.60%	94.30%	0.30%	1.50%	3.90%
Kuraishia capsulata	CBS 1993	GCA 000576695.1	95.60%	95.30%	0.30%	0.90%	3.50%
Kuraishia cidri	NRRL Y-27078	GCA 030557465.1	98.50%	98.20%	0.30%	0.10%	1.40%
Kuraishia floccosa	NRRL Y-27951	GCA 030567535.1	96.20%	96.20%	0.00%	0.70%	3.10%
Kuraishia hungarica	NRRL Y-27594	GCA 030567555.1	97.80%	97.80%	0.00%	0.50%	1.70%
Kuraishia molischiana	NRRL Y-27899	GCA 003706305.2	96.70%	96.60%	0.10%	0.80%	2.50%
Kuraishia ogatae	NRRL Y-48474	GCA 003706285.2	97.90%	97.60%	0.30%	0.40%	1.70%
Kuraishia piskuri	NRRL YB-2544	GCA 030567595.1	97.40%	97.10%	0.30%	0.40%	2.20%
Martiniozyma abietophila	NRRL Y-11514	GCA 030564585.1	85.10%	82.50%	2.60%	2.10%	12.80%
Martiniozyma asiatica	NRRL Y-63747	GCA 030572475.1	83.00%	83.00%	0.00%	2.40%	14.60%
Ogataea allantospora	NRRL Y-48267	GCA 030572655.1	94.20%	94.10%	0.10%	0.80%	5.00%
Ogataea angusta	CBS 2575	GCA 019207455.1	92.60%	92.60%	0.00%	2.10%	5.30%
Ogataea chonburiensis	CBS 10363	GCA 030578415.1	90.20%	90.20%	0.00%	1.20%	8.60%

Table S1. List of yeast strains and genomes used in this study (Continue)

Taxa	Strain	Assembly	Complete BUSCOs (C)	Complete and single-copy BUSCOs (S)	Complete and duplicated BUSCOs (D)	Fragmented BUSCOs (F)	Missing BUSCOs (M)
Ogataea corticis	NBRC 1794	GCA 030555865.1	95.90%	95.60%	0.30%	0.80%	3.30%
Ogataea degrootiae	UCD465	GCA 019232045.1	95.30%	95.00%	0.30%	0.70%	4.00%
Ogataea dorogensis	NRRL Y-27599	GCA 030568015.1	92.70%	92.70%	0.00%	1.10%	6.20%
Ogataea ganodermae	CBS 10646	GCA 030569375.1	95.60%	95.50%	0.10%	0.90%	3.50%
Ogataea glucozyma	NRRL YB-2185	GCA 003706155.1	96.10%	90.00%	6.10%	0.70%	3.20%
Ogataea haglerorum	83-474-2	GCA 019206905.1	91.40%	91.40%	0.00%	2.10%	6.50%
Ogataea henricii	NRRL YB-2194	GCA 003705115.1	95.30%	95.00%	0.30%	0.90%	3.80%
Ogataea kodamae	NRRL Y-17234	GCA 003706165.2	91.80%	91.80%	0.00%	1.30%	6.90%
Ogataea methanolica	JCM 10240	GCA 001600755.1	95.40%	94.90%	0.50%	0.80%	3.80%
Ogataea methylovora	NRRL Y-17250	GCA 003706205.1	97.50%	90.50%	7.00%	0.50%	2.00%
Ogataea minuta	NRRL Y-411	GCA 003706195.1	93.00%	92.90%	0.10%	1.20%	5.80%
Ogataea naganishii	NRRL Y-7654	GCA 003706235.1	94.70%	94.60%	0.10%	1.10%	4.20%
Ogataea nakhonphanomensis	CBS 10362	GCA 030564965.1	93.10%	93.10%	0.00%	0.90%	6.00%
Ogataea neopini	AB440274	GCA 030578575.1	93.40%	93.30%	0.10%	0.80%	5.80%

Table S1. List of yeast strains and genomes used in this study (Continue)

Taxa	Strain	Assembly	Complete BUSCOs (C)	Complete and single-copy BUSCOs (S)	Complete and duplicated BUSCOs (D)	Fragmented BUSCOs (F)	Missing BUSCOs (M)
Ogataea nitratoaversa	NRRL Y-48449	GCA 003705625.1	95.20%	94.90%	0.30%	0.70%	4.10%
Ogataea nonfermentans	NRRL YB-2203	GCA 003706255.1	95.00%	77.80%	17.20%	0.90%	4.10%
Ogataea paradorogensis	CBS 10978	GCA 030555885.1	93.00%	92.90%	0.10%	0.80%	6.20%
Ogataea paraovalis	CBS 14697	GCA 030565405.1	95.70%	95.40%	0.30%	0.70%	3.60%
Ogataea parapolymorpha	CBS 12304	GCA 019207935.1	93.40%	93.40%	0.00%	1.30%	5.30%
Ogataea philodendri	NRRL Y-7210	GCA 003706115.2	90.90%	90.90%	0.00%	1.30%	7.80%
Ogataea pilisensis	NRRL Y-27598	GCA 003707685.1	95.70%	95.60%	0.10%	0.40%	3.90%
Ogataea pini	NRRL Y-11528	GCA 003707665.1	95.90%	95.80%	0.10%	0.40%	3.70%
Ogataea polymorpha	NCYC 495 leu1.1	GCA 001664045.1	90.00%	90.00%	0.00%	2.40%	7.60%
Ogataea populialbae	NRRL Y-48632	GCA 030579375.1	96.30%	96.20%	0.10%	0.40%	3.30%
Ogataea ramenticola	NRRL YB-1985	GCA 003706105.2	95.70%	95.60%	0.10%	0.80%	3.50%
Ogataea salicorniae	NRRL Y-12834	GCA 030557545.1	95.10%	95.00%	0.10%	0.50%	4.40%
Ogataea saltuana	NRRL Y-48448	GCA 030674545.1	96.00%	95.60%	0.40%	0.70%	3.30%
Ogataea siamensis	NRRL Y-27963	GCA 030574315.1	90.90%	90.90%	0.00%	1.60%	7.50%

Table S1. List of yeast strains and genomes used in this study (Continue)

Taxa	Strain	Assembly	Complete BUSCOs (C)	Complete and single-copy BUSCOs (S)	Complete and duplicated BUSCOs (D)	Fragmented BUSCOs (F)	Missing BUSCOs (M)
Ogataea sp.	NRRL YB-2437	GCA 030570735.1	96.50%	96.20%	0.30%	0.50%	3.00%
Ogataea sp.	NRRL Y-27170	GCA 030567915.1	94.70%	94.60%	0.10%	0.50%	4.80%
Ogataea sp.	NRRL YB-2442	GCA 030567955.1	92.30%	92.30%	0.00%	0.50%	7.20%
Ogataea sp.	NRRL Y-27166	GCA 030563385.1	93.90%	93.80%	0.10%	0.90%	5.20%
Ogataea sp.	NRRL YB-1238	GCA 030567895.1	95.40%	95.30%	0.10%	0.50%	4.10%
Ogataea sp.	yHMJ1	GCA 030571015.1	94.40%	94.30%	0.10%	0.80%	4.80%
Ogataea thermomethanolica	NRRL Y-27981	GCA 030674565.1	93.10%	93.10%	0.00%	0.90%	6.00%
Ogataea thermophila	NCAIM Y.01608	GCA 020536115.1	92.90%	92.90%	0.00%	1.70%	5.40%
Ogataea trehaloabstinens	NRRL Y-27595	GCA 003706095.1	94.60%	94.50%	0.10%	0.80%	4.60%
Ogataea trehalophila	NRRL Y-6781	GCA 003707645.1	95.50%	95.40%	0.10%	0.50%	4.00%
Ogataea wickerhamii	NRRL YB-4943	GCA 030559035.1	93.90%	93.80%	0.10%	0.80%	5.30%
Ogataea zsoltii	NRRL Y-27601	GCA 003709205.2	95.80%	95.50%	0.30%	0.80%	3.40%
Pichia cactophila	NRRL Y-10963	GCA 030563965.1	86.40%	86.30%	0.10%	1.50%	12.10%
Pichia cephalocereana	NRRL Y-17225	GCA 030565065.1	86.50%	86.40%	0.10%	1.80%	11.70%

Table S1. List of yeast strains and genomes used in this study (Continue)

Taxa	Strain	Assembly	Complete BUSCOs (C)	Complete and single-copy BUSCOs (S)	Complete and duplicated BUSCOs (D)	Fragmented BUSCOs (F)	Missing BUSCOs (M)
Pichia deserticola	NRRL Y-12918	GCA 030570135.1	88.80%	88.70%	0.10%	0.70%	10.50%
Pichia eremophila	NRRL Y-17224	GCA 030579415.1	85.70%	85.40%	0.30%	1.60%	12.70%
Pichia exigua	NRRL Y-10920	GCA 003707355.1	86.20%	86.10%	0.10%	1.30%	12.50%
Pichia fermentans	fo MP 02	GCA 003339355.1	82.60%	82.60%	0.00%	1.80%	15.60%
Pichia gijzenarium	CBS 15024	GCA 030556995.1	82.60%	82.60%	0.00%	2.50%	14.90%
Pichia heedii	NRRL Y-10967	GCA 003705525.2	86.30%	86.00%	0.30%	1.60%	12.10%
Pichia insulana	CBS 11169	GCA 030558495.1	87.30%	87.30%	0.00%	1.30%	11.40%
Pichia kluyveri	B7036	GCA 023629335.1	82.90%	81.10%	1.80%	2.50%	14.60%
Pichia kudriavzevii	NRRL Y-5396	GCA 003705515.2	88.90%	87.20%	1.70%	0.40%	10.70%
Pichia mandshurica	NRRL Y-27978T	GCA 030578975.1	89.20%	88.90%	0.30%	1.30%	9.50%
Pichia membranifaciens	KS47-1	GCA 001950575.1	64.80%	64.80%	0.00%	5.40%	29.80%
Pichia nakasei	NRRL Y-7686	GCA 003705495.1	78.40%	78.10%	0.30%	3.40%	18.20%
Pichia nanzhaoensis	CBS 15346	GCA 030573035.1	82.50%	82.50%	0.00%	1.70%	15.80%
Pichia norvegensis	NRRL Y-7687	GCA 003705465.1	86.90%	85.40%	1.50%	1.60%	11.50%

Table S1. List of yeast strains and genomes used in this study (Continue)

Taxa	Strain	Assembly	Complete BUSCOs (C)	Complete and single-copy BUSCOs (S)	Complete and duplicated BUSCOs (D)	Fragmented BUSCOs (F)	Missing BUSCOs (M)
Pichia occidentalis	NRRL Y-7552	GCA 003705455.2	89.60%	89.20%	0.40%	1.20%	9.20%
Pichia paraexigua	CBS 15237	GCA 030573095.1	85.50%	85.20%	0.30%	1.80%	12.70%
Pichia pseudocactophila	NRRL Y-17239	GCA 030580035.1	81.70%	81.70%	0.00%	2.20%	16.10%
Pichia scutulata	NRRL Y-7663	GCA 030560845.1	84.30%	84.30%	0.00%	1.70%	14.00%
Pichia sp.	NRRL Y-12824	GCA 030560915.1	82.30%	82.20%	0.10%	2.00%	15.70%
Pichia sp.	NRRL Y-12827	GCA 030570315.1	86.20%	85.90%	0.30%	1.80%	12.00%
Pichia sp.	NRRL Y-12830	GCA 030564565.1	85.60%	85.50%	0.10%	1.30%	13.10%
Pichia sp.	NRRL Y-27259	GCA 030563085.1	88.70%	88.40%	0.30%	1.50%	9.80%
Pichia sp.	NRRL Y-27261	GCA 030569835.1	85.90%	38.80%	47.10%	2.00%	12.10%
Pichia sp.	NRRL YB-4149	GCA 030556025.1	73.00%	73.00%	0.00%	1.10%	25.90%
Pichia sp.	yHKS168	GCA 030571145.1	88.90%	88.80%	0.10%	0.80%	10.30%
Pichia sp.	yHMH446	GCA 030555725.1	83.80%	83.80%	0.00%	1.80%	14.40%
Pichia sporocuriosa	NRRL Y-27347	GCA 030574275.1	88.60%	88.50%	0.10%	1.60%	9.80%
Pichia terricola	NRRL YB-4310	GCA 030581875.1	85.80%	85.50%	0.30%	0.80%	13.40%

Table S1. List of yeast strains and genomes used in this study (Continue)

Taxa	Strain	Assembly	Complete BUSCOs (C)	Complete and single-copy BUSCOs (S)	Complete and duplicated BUSCOs (D)	Fragmented BUSCOs (F)	Missing BUSCOs (M)
Saturnispora ahearnii	NRRL Y-7555	GCA 030564945.1	86.60%	86.50%	0.10%	0.80%	12.60%
Saturnispora besseyi	NRRL Y-63574	GCA 030571455.1	86.40%	86.30%	0.10%	1.10%	12.50%
Saturnispora bothae	yHDO578	GCA 030462855.1	83.80%	83.80%	0.00%	1.80%	14.40%
Saturnispora dispora	NRRL Y-1447	GCA 003708095.2	86.20%	86.10%	0.10%	1.30%	12.50%
Saturnispora diversa	NRRL Y-5713	GCA 030560905.1	86.80%	86.80%	0.00%	0.70%	12.50%
Saturnispora galanensis	CBS 15223	GCA 030584985.1	85.00%	85.00%	0.00%	1.30%	13.70%
Saturnispora gosingensis	NRRL Y-48718	GCA 030570395.1	86.60%	86.50%	0.10%	1.20%	12.20%
Saturnispora hagleri	NRRL Y-27828	GCA 003707255.1	86.20%	86.10%	0.10%	0.90%	12.90%
Saturnispora halmiae	CBS 11009	GCA 030563645.1	84.00%	83.90%	0.10%	0.90%	15.10%
Saturnispora kantuleensis	CBS 15217	GCA 030557035.1	84.80%	84.70%	0.10%	1.50%	13.70%
Saturnispora mendoncae	NRRL Y-11515	GCA 003705365.1	79.70%	79.30%	0.40%	2.20%	18.10%
Saturnispora quitensis	CBS 12184	GCA 030581435.1	86.20%	86.10%	0.10%	1.20%	12.60%
Saturnispora saitoi	NRRL Y-6671	GCA 003707305.1	86.00%	85.90%	0.10%	1.20%	12.80%
Saturnispora sanitii	CBS 10864	GCA 030563185.1	82.50%	82.50%	0.00%	1.80%	15.70%

Table S1. List of yeast strains and genomes used in this study (Continue)

Taxa	Strain	Assembly	Complete BUSCOs (C)	Complete and single-copy BUSCOs (S)	Complete and duplicated BUSCOs (D)	Fragmented BUSCOs (F)	Missing BUSCOs (M)
Saturnispora sekii	CBS 10931	GCA 030563565.1	85.50%	85.40%	0.10%	1.50%	13.00%
Saturnispora serradocipensis	NRRL Y-48717	GCA 003705415.1	85.60%	85.50%	0.10%	1.30%	13.10%
Saturnispora silvae	NRRL Y-6725	GCA 003707315.2	83.90%	83.90%	0.00%	1.80%	14.30%
Saturnispora zaruensis	NRRL Y-7008	GCA 003705435.1	86.50%	86.40%	0.10%	0.90%	12.60%
Serinales							
Aciculoconidium aculeatum	NRRL YB-4298	GCA 030579395.1	95.70%	95.60%	0.10%	0.70%	3.60%
Australozyma bambusicola	CBS 11723	GCA 030563705.1	92.60%	92.60%	0.00%	0.50%	6.90%
Australozyma nongkhaiensis	CBS 11724	GCA 030563825.1	92.90%	92.90%	0.00%	0.50%	6.60%
Australozyma picinguabensis	NRRL Y-27814	GCA 030582875.1	93.30%	93.30%	0.00%	0.40%	6.30%
Australozyma robnettiae	CBS 8580	GCA 030568975.1	92.30%	92.30%	0.00%	0.50%	7.20%
Australozyma saccharicola	CBS 12575	GCA 030569455.1	93.10%	93.10%	0.00%	0.50%	6.40%
Australozyma saopauloensis	NRRL Y-27815	GCA 030582915.1	93.00%	93.00%	0.00%	0.70%	6.30%
Australozyma succicola	CBS 11726	GCA 030563905.1	93.00%	93.00%	0.00%	0.70%	6.30%
Australozyma touchengensis	CBS 10585	GCA 030566735.1	92.30%	92.30%	0.00%	0.50%	7.20%

Table S1. List of yeast strains and genomes used in this study (Continue)

Taxa	Strain	Assembly	Complete BUSCOs (C)	Complete and single-copy BUSCOs (S)	Complete and duplicated BUSCOs (D)	Fragmented BUSCOs (F)	Missing BUSCOs (M)
Babjeviella inositovora	NRRL Y-12698	GCA 030561425.1	94.20%	93.90%	0.30%	0.10%	5.70%
Candida aaseri	B8007	GCA 023623315.1	92.60%	92.60%	0.00%	1.30%	6.10%
Candida africana	CEC4854	GCA 019359905.1	79.70%	79.20%	0.50%	0.80%	19.50%
Candida alai	NRRL Y-27739	GCA 030572135.1	96.10%	96.00%	0.10%	0.30%	3.60%
Candida albicans	SC5314	GCA 000784655.1	95.50%	92.60%	2.90%	0.80%	3.70%
Candida andamanensis	CBS 10859	GCA 030569055.1	93.40%	93.40%	0.00%	0.80%	5.80%
Candida anglica	NRRL Y-27079	GCA 030557785.1	88.30%	87.90%	0.40%	0.40%	11.30%
‘Candida anglica’	VS III C KN 3	GCA 019775655.1	97.00%	96.70%	0.30%	0.10%	2.90%
Candida anutae	NRRL Y-27374	GCA 030566955.1	92.90%	92.90%	0.00%	0.80%	6.30%
Candida argentea	CBS 12358	GCA 030581555.1	90.30%	90.20%	0.10%	1.10%	8.60%
Candida ascalaphidarum	NRRL Y-27908	GCA 003708745.2	94.70%	94.60%	0.10%	0.50%	4.80%
Candida atlantica	NRRL Y-17759	GCA 030561325.1	92.40%	92.30%	0.10%	1.30%	6.30%
Candida atmosphaerica	NRRL Y-17642	GCA 030574775.1	95.40%	95.30%	0.10%	0.40%	4.20%
Candida aurita	CBS 9724	GCA 030566905.1	96.00%	95.90%	0.10%	0.30%	3.70%

Table S1. List of yeast strains and genomes used in this study (Continue)

Taxa	Strain	Assembly	Complete BUSCOs (C)	Complete and single-copy BUSCOs (S)	Complete and duplicated BUSCOs (D)	Fragmented BUSCOs (F)	Missing BUSCOs (M)
Candida blackwelliae	CBS 10843	GCA 030579015.1	92.00%	91.60%	0.40%	2.40%	5.60%
Candida blattariae	NRRL Y-27703	GCA 030581595.1	93.50%	93.50%	0.00%	0.70%	5.80%
Candida bohioensis	NRRL Y-27737	GCA 030582535.1	95.70%	95.60%	0.10%	0.10%	4.20%
Candida boleticola	NRRL Y-17080	GCA 030570215.1	95.30%	95.00%	0.30%	0.50%	4.20%
Candida broadrunensis	CBS 11838	GCA 030563665.1	96.10%	95.80%	0.30%	0.30%	3.60%
Candida buenavistaensis	NRRL Y-27734	GCA 030582575.1	93.60%	90.00%	3.60%	2.40%	4.00%
Candida buinensis	NRRL Y-11706	GCA 030571035.1	92.00%	92.00%	0.00%	0.40%	7.60%
Candida caryicola	NRRL YB-1499	GCA 030568635.1	95.60%	95.60%	0.00%	0.50%	3.90%
Candida cerambycidarum	NRRL Y-27706	GCA 030574835.1	95.00%	95.00%	0.00%	0.50%	4.50%
Candida chauliodis	NRRL Y-27909	GCA 030557115.1	95.10%	95.10%	0.00%	0.40%	4.50%
Candida chilensis	NRRL Y-17141	GCA 030573195.1	99.50%	99.20%	0.30%	0.00%	0.50%
Candida citri	CBS 11858	GCA 030571295.1	93.70%	93.70%	0.00%	0.70%	5.60%
Candida coleopterorum	CBS 14180	GCA 030565325.1	93.80%	93.70%	0.10%	0.70%	5.50%
Candida conglobata	NRRL Y-1504	GCA 030572275.1	95.40%	95.30%	0.10%	0.30%	4.30%

Table S1. List of yeast strains and genomes used in this study (Continue)

Taxa	Strain	Assembly	Complete BUSCOs (C)	Complete and single-copy BUSCOs (S)	Complete and duplicated BUSCOs (D)	Fragmented BUSCOs (F)	Missing BUSCOs (M)
Candida corydali	NRRL Y-27910	GCA 003706475.2	94.30%	89.60%	4.70%	0.30%	5.40%
Candida danieliae	CBS 8533	GCA 030579135.1	92.60%	92.60%	0.00%	0.70%	6.70%
Candida dendronema	NRRL Y-7781	GCA 030572355.1	94.30%	94.30%	0.00%	1.10%	4.60%
Candida diddensiae	NRRL Y-7589	GCA 030563465.1	94.30%	94.30%	0.00%	1.10%	4.60%
Candida diospyri	CBS 9769	GCA 030579195.1	93.90%	93.90%	0.00%	0.80%	5.30%
Candida dubliniensis	CD36	GCA 000026945.1	96.90%	96.40%	0.50%	0.30%	2.80%
Candida endomychidarum	NRRL Y-27708	GCA 030582775.1	93.50%	93.50%	0.00%	0.40%	6.10%
Candida fluviatilis	NRRL Y-7711	GCA 030560825.1	96.60%	96.60%	0.00%	0.30%	3.10%
Candida friedrichii	NRRL Y-17653	GCA 030565865.1	94.20%	94.20%	0.00%	0.50%	5.30%
Candida frijolesensis	NRRL Y-48060	GCA 030557105.1	92.60%	89.60%	3.00%	1.20%	6.20%
Candida germanica	NRRL Y-27064	GCA 030574815.1	93.00%	93.00%	0.00%	1.20%	5.80%
Candida gigantensis	NRRL Y-27736	GCA 030557085.1	94.10%	93.40%	0.70%	1.30%	4.60%
Candida glaebosa	NRRL Y-6949	GCA 030564305.1	96.20%	96.20%	0.00%	0.00%	3.80%
Candida glucosophila	NRRL Y-17219	GCA 030572315.1	95.10%	4.60%	90.50%	0.30%	4.60%

Table S1. List of yeast strains and genomes used in this study (Continue)

Taxa	Strain	Assembly	Complete BUSCOs (C)	Complete and single-copy BUSCOs (S)	Complete and duplicated BUSCOs (D)	Fragmented BUSCOs (F)	Missing BUSCOs (M)
Candida golubevii	NRRL Y-48707	GCA 003708755.1	93.80%	93.80%	0.00%	1.10%	5.10%
Candida gorgasii	NRRL Y-27707	GCA 003708985.2	95.10%	95.10%	0.00%	0.50%	4.40%
Candida hainanensis	NRRL Y-48715	GCA 030561765.1	91.80%	91.70%	0.10%	1.70%	6.50%
Candida insectorum	NRRL Y-7787	GCA 030574895.1	95.00%	95.00%	0.00%	0.70%	4.30%
Candida jaroonii	CLIB 1444	GCA 943733655.1	95.80%	95.80%	0.00%	0.50%	3.70%
Candida jiufengensis	CBS 10846	GCA 024610255.1	95.30%	95.30%	0.00%	0.10%	4.60%
Candida kanchanaburiensis	NBRC 104475	GCA 030555785.1	92.50%	92.50%	0.00%	1.10%	6.40%
Candida khao-thaluensis	CBS 8535	GCA 030563265.1	95.40%	95.30%	0.10%	0.40%	4.20%
Candida koratica	NBRC 103208	GCA 030572455.1	92.90%	92.90%	0.00%	0.80%	6.30%
Candida labiduridarum	NRRL Y-27940	GCA 030572435.1	95.40%	94.50%	0.90%	0.10%	4.50%
Candida lessepsii	NRRL Y-27766	GCA 030563485.1	95.40%	95.40%	0.00%	0.50%	4.10%
Candida loeiensis	CBS 11899	GCA 030563775.1	92.20%	92.10%	0.10%	1.30%	6.50%
Candida lyxosophila	NRRL Y-17539	GCA 030582855.1	95.00%	93.90%	1.10%	0.70%	4.30%
Candida maltosa	Xu316	GCA 000344705.1	95.20%	95.10%	0.10%	0.50%	4.30%

Table S1. List of yeast strains and genomes used in this study (Continue)

Taxa	Strain	Assembly	Complete BUSCOs (C)	Complete and single-copy BUSCOs (S)	Complete and duplicated BUSCOs (D)	Fragmented BUSCOs (F)	Missing BUSCOs (M)
Candida manassasensis	CBS 12534	GCA 030569175.1	96.70%	96.60%	0.10%	0.30%	3.00%
Candida margitis	CBS 14175	GCA 024628925.1	94.80%	94.10%	0.70%	0.10%	5.10%
Candida membranifaciens	NRRL Y-2089	GCA 030572415.1	95.00%	95.00%	0.00%	0.30%	4.70%
Candida membranifaciens subsp. flavinogenes	IST 626	GCA 022457055.1	95.00%	95.00%	0.00%	0.30%	4.70%
Candida mesenterica	UWOPS91-121.2	GCA 015708695.1	95.90%	95.60%	0.30%	0.40%	3.70%
Candida metapsilosis	ATCC 96143	GCA 008904905.1	86.20%	83.20%	3.00%	2.40%	11.40%
Candida michaelii	NRRL Y-27705	GCA 030572395.1	94.30%	94.30%	0.00%	0.90%	4.80%
Candida morakotiae	NRRL Y-48708	GCA 030564645.1	93.10%	93.00%	0.10%	1.10%	5.80%
Candida multigemmis	NRRL Y-17659	GCA 030572295.1	93.10%	93.00%	0.10%	0.70%	6.20%
Candida neerlandica	NRRL Y-27057	GCA 030557875.1	94.90%	94.20%	0.70%	0.30%	4.80%
Candida nonsorbophila	CBS 10862	GCA 030578515.1	94.00%	93.90%	0.10%	1.60%	4.40%
Candida oceani	2020i151	GCA 020281285.1	94.20%	94.10%	0.10%	0.90%	4.90%
Candida oleophila	NRRL Y-2317	GCA 030563865.1	95.20%	94.90%	0.30%	0.70%	4.10%
Candida orthopsilosis	Co 90-125	GCA 000315875.1	96.40%	96.40%	0.00%	0.30%	3.30%

Table S1. List of yeast strains and genomes used in this study (Continue)

Taxa	Strain	Assembly	Complete BUSCOs (C)	Complete and single-copy BUSCOs (S)	Complete and duplicated BUSCOs (D)	Fragmented BUSCOs (F)	Missing BUSCOs (M)
Candida oxycetoniae	CBS 10844	GCA 023343755.1	94.10%	94.10%	0.00%	0.40%	5.50%
Candida palmioleophila	NRRL Y-17323	GCA 030560805.1	96.30%	95.80%	0.50%	0.40%	3.30%
Candida palmyrensis	CBS 11546	GCA 030558275.1	93.90%	93.90%	0.00%	0.80%	5.30%
Candida parablackwelliae	CBS 15228	GCA 030585045.1	93.40%	90.20%	3.20%	0.50%	6.10%
Candida parachauliodis	CBS 13928	GCA 030565145.1	94.60%	94.60%	0.00%	0.70%	4.70%
Candida parapsilosis	ATCC 22019	GCA 015344875.1	94.90%	94.90%	0.00%	0.80%	4.30%
Candida pseudoaaseri	CBS 11170	GCA 030674785.1	94.60%	94.60%	0.00%	0.70%	4.70%
Candida pseudocylindracea	CBS 10854	GCA 030558265.1	82.30%	82.30%	0.00%	3.40%	14.30%
Candida pseudofarinosa	NCYC 386	GCA 030556505.1	95.90%	95.90%	0.00%	0.10%	4.00%
Candida pseudoglaebosa	NRRL Y-17911	GCA 030705115.1	94.10%	94.10%	0.00%	0.30%	5.60%
Candida pseudojiufengensis	CBS 10847	GCA 024610245.1	92.10%	92.10%	0.00%	0.90%	7.00%
Candida pseudoviswanathii	CBS 13916	GCA 030565125.1	95.60%	95.50%	0.10%	0.30%	4.10%
Candida psychrophila	FYBW01	GCA 900186205.1	96.70%	96.60%	0.10%	0.40%	2.90%
Candida railenensis	CLIB 1423	GCA 935541525.1	96.30%	95.90%	0.40%	0.70%	3.00%

Table S1. List of yeast strains and genomes used in this study (Continue)

Taxa	Strain	Assembly	Complete BUSCOs (C)	Complete and single-copy BUSCOs (S)	Complete and duplicated BUSCOs (D)	Fragmented BUSCOs (F)	Missing BUSCOs (M)
Candida saitoana	NRRL Y-17316	GCA 030557765.1	89.70%	89.70%	0.00%	4.40%	5.90%
Candida sakaeoensis	CBS 12318	GCA 030569255.1	93.00%	92.90%	0.10%	1.70%	5.30%
Candida sake	NRRL Y-1622	GCA 030572495.1	96.80%	96.80%	0.00%	0.50%	2.70%
Candida santamariae	NRRL Y-6656	GCA 030578175.1	94.10%	93.80%	0.30%	0.10%	5.80%
Candida sanyaensis	CBS 12637	GCA 030562985.1	92.10%	85.50%	6.60%	2.90%	5.00%
Candida schatavii	NRRL Y-17078	GCA 003707405.1	95.20%	92.00%	3.20%	0.40%	4.40%
Candida silvanorum	NRRL Y-7782	GCA 030574095.1	96.10%	96.00%	0.10%	0.50%	3.40%
Candida sinolaborantium	LESF1467	GCA 039762375.1	91.40%	91.40%	0.00%	2.20%	6.40%
Candida smagusa	CBS 11430	GCA 030566775.1	94.60%	93.90%	0.70%	0.70%	4.70%
Candida sojae	GF41	GCA 001442715.1	76.40%	74.30%	2.10%	1.60%	22.00%
Candida songkhlaensis	NBRC 103214	GCA 030570975.1	93.90%	93.90%	0.00%	0.80%	5.30%
Candida sophiae-reginae	NRRL Y-17668	GCA 030564725.1	92.50%	92.20%	0.30%	1.80%	5.70%
Candida sp.	UFMG-CM-Y605	GCA 030705185.1	97.10%	97.10%	0.00%	0.30%	2.60%
Candida sp.	AC06	GCA 026724345.1	83.00%	20.70%	62.30%	5.10%	11.90%

Table S1. List of yeast strains and genomes used in this study (Continue)

Taxa	Strain	Assembly	Complete BUSCOs (C)	Complete and single-copy BUSCOs (S)	Complete and duplicated BUSCOs (D)	Fragmented BUSCOs (F)	Missing BUSCOs (M)
Candida sp.	LDI48194	GCA 001005365.1	82.70%	67.50%	15.20%	1.30%	16.00%
Candida sp.	LN1	GCA 019280635.1	96.00%	95.50%	0.50%	0.40%	3.60%
Candida sp.	yHKB357	GCA 030580355.1	84.30%	83.90%	0.40%	3.80%	11.90%
Candida sp.	gmt3-3-4	NMDC20301685#	96.30%	96.30%	0.00%	0.30%	3.40%
Candida sp.	XZY238F3	NMDC20301686#	96.00%	96.00%	0.00%	0.30%	3.70%
Candida sp.	Y128-05C	GCA 037042315.1	93.70%	17.30%	76.40%	2.00%	4.30%
Candida sp.	Y128-05E	GCA 037042355.1	92.50%	16.20%	76.30%	2.80%	4.70%
Candida spencermartinsiae	NRRL Y-48663	GCA 030582355.1	95.40%	95.30%	0.10%	0.70%	3.90%
Candida sphagnicola	CBS 11774	GCA 030569075.1	96.20%	96.20%	0.00%	0.50%	3.30%
Candida subhashii	CBS 10753	GCA 019202705.1	94.50%	94.10%	0.40%	1.20%	4.30%
Candida tallmaniae	CBS 8575	GCA 030569655.1	94.10%	94.10%	0.00%	0.40%	5.50%
Candida tammaniensis	NRRL Y-8257	GCA 003708705.1	93.30%	93.30%	0.00%	0.80%	5.90%
Candida taylorii	NRRL Y-27213	GCA 030583035.1	93.80%	93.50%	0.30%	0.70%	5.50%
Candida tetrigidarum	NRRL Y-48142	GCA 030557055.1	93.30%	88.40%	4.90%	1.70%	5.00%

Table S1. List of yeast strains and genomes used in this study (Continue)

Taxa	Strain	Assembly	Complete BUSCOs (C)	Complete and single-copy BUSCOs (S)	Complete and duplicated BUSCOs (D)	Fragmented BUSCOs (F)	Missing BUSCOs (M)
Candida theae	CBS 12239	GCA 024610275.1	94.30%	94.20%	0.10%	0.50%	5.20%
Candida tibetensis	CBS 10298	GCA 030570835.1	96.60%	96.60%	0.00%	0.30%	3.10%
Candida tropicalis	MYA-3404	GCA 017315405.1	94.40%	93.50%	0.90%	1.30%	4.30%
Candida trypodendroni	NRRL Y-6488	GCA 030572515.1	94.10%	94.10%	0.00%	0.90%	5.00%
Candida vaughaniae	CBS 8583	GCA 030569695.1	94.60%	94.60%	0.00%	1.10%	4.30%
Candida verbasci	CBS 12699	GCA 030569305.1	93.70%	93.70%	0.00%	0.70%	5.60%
Candida viswanathii	NRRL Y-6660	GCA 030566835.1	94.20%	93.70%	0.50%	0.50%	5.30%
Candida wancherniae	NRRL Y-48709	GCA 003708715.2	89.40%	89.40%	0.00%	1.80%	8.80%
Candida xiaguanensis	CBS 13923	GCA 030555925.1	93.80%	93.80%	0.00%	0.40%	5.80%
Candida xylanilytica	NBRC 106499	GCA 030563365.1	94.60%	84.20%	10.40%	1.10%	4.30%
Candida zeylanoides	NRRL Y-1774	GCA 030564465.1	89.50%	89.10%	0.40%	2.20%	8.30%
Candidozyma auris	CBS 10913	GCA 030581515.1	93.10%	93.00%	0.10%	0.80%	6.10%
Candidozyma chanthaburiensis	CBS 10926	GCA 030579055.1	91.30%	91.20%	0.10%	0.90%	7.80%
Candidozyma duobushaemuli	NRRL Y-17802	GCA 030575055.1	91.40%	91.30%	0.10%	1.20%	7.40%

Table S1. List of yeast strains and genomes used in this study (Continue)

Taxa	Strain	Assembly	Complete BUSCOs (C)	Complete and single-copy BUSCOs (S)	Complete and duplicated BUSCOs (D)	Fragmented BUSCOs (F)	Missing BUSCOs (M)
Candidozyma haemuli	NRRL Y-6693	GCA 030569475.1	93.10%	93.00%	0.10%	1.10%	5.80%
Candidozyma heveicola	NRRL Y-48716	GCA 003708405.2	91.50%	91.20%	0.30%	0.90%	7.60%
Candidozyma konsanensis	CBS 12666	GCA 030563505.1	91.70%	91.60%	0.10%	0.80%	7.50%
Candidozyma pseudohaemuli	NRRL Y-48733	GCA 030573385.1	91.40%	91.30%	0.10%	1.20%	7.40%
Candidozyma ruelliae	NRRL Y-48703	GCA 030582895.1	89.40%	89.30%	0.10%	1.10%	9.50%
Candidozyma vulturna	CBS 14366	GCA 030585165.1	93.10%	93.00%	0.10%	0.90%	6.00%
Cephaloascus albidus	NRRL Y-7343	GCA 030575015.1	98.40%	97.90%	0.50%	0.30%	1.30%
Cephaloascus fragrans	NRRL Y-6742	GCA 003707825.3	98.90%	98.80%	0.10%	0.10%	1.00%
Clavispora asparagi	CBS 9770	GCA 030573135.1	92.30%	92.30%	0.00%	1.60%	6.10%
Clavispora carvajalis	NRRL Y-48694	GCA 030581635.1	92.50%	92.50%	0.00%	1.20%	6.30%
Clavispora fructus	NRRL Y-17072	GCA 003707795.2	91.30%	90.80%	0.50%	1.60%	7.10%
Clavispora fructus	NRRL Y-17088	GCA 030557895.1	90.20%	90.20%	0.00%	1.50%	8.30%
Clavispora lusitaniae	NRRL Y-11827	GCA 030449025.1	94.80%	94.30%	0.50%	1.10%	4.10%
Clavispora opuntiae	NRRL Y-11820	GCA 030574075.1	94.70%	94.60%	0.10%	0.80%	4.50%

Table S1. List of yeast strains and genomes used in this study (Continue)

Taxa	Strain	Assembly	Complete BUSCOs (C)	Complete and single-copy BUSCOs (S)	Complete and duplicated BUSCOs (D)	Fragmented BUSCOs (F)	Missing BUSCOs (M)
Clavispora phyllophila	CBS 12671	GCA 030674715.1	92.10%	92.10%	0.00%	2.00%	5.90%
Clavispora vitiphila	CBS 12672	GCA 030557995.1	93.40%	93.40%	0.00%	1.10%	5.50%
Danielia oregonensis	NRRL Y-5850	GCA 003707785.3	95.50%	95.50%	0.00%	0.80%	3.70%
Danielia reshetovae	CBS 11556	GCA 030558395.1	94.30%	93.90%	0.40%	0.40%	5.30%
Danielozyma ontarioensis	NRRL YB-1246	GCA 003706395.2	97.10%	97.00%	0.10%	0.40%	2.50%
Debaryomyces coudertii	NRRL Y-7425	GCA 030564605.1	98.00%	97.90%	0.10%	0.10%	1.90%
Debaryomyces fabryi	NRRL Y-17914	GCA 003708665.2	98.30%	98.20%	0.10%	0.30%	1.40%
Debaryomyces hansenii	NRRL Y-7426	GCA 006942235.1	97.60%	97.50%	0.10%	0.30%	2.10%
Debaryomyces maramus	NRRL Y-2171	GCA 003708605.2	98.30%	98.20%	0.10%	0.00%	1.70%
Debaryomyces nepalensis	NRRL Y-7108	GCA 003708585.1	98.10%	97.80%	0.30%	0.30%	1.60%
Debaryomyces prosopidis	NRRL Y-27369	GCA 003708935.1	97.90%	91.00%	6.90%	0.30%	1.80%
Debaryomyces robertsiae	NRRL Y-6670	GCA 030566065.1	96.90%	96.80%	0.10%	0.30%	2.80%
Debaryomyces singareniensis	CBS 10405	GCA 030558045.1	91.00%	91.00%	0.00%	1.20%	7.80%
Debaryomyces subglobosus	NRRL Y-6666	GCA 003708965.1	98.30%	98.00%	0.30%	0.30%	1.40%

Table S1. List of yeast strains and genomes used in this study (Continue)

Taxa	Strain	Assembly	Complete BUSCOs (C)	Complete and single-copy BUSCOs (S)	Complete and duplicated BUSCOs (D)	Fragmented BUSCOs (F)	Missing BUSCOs (M)
Debaryomyces udenii	NRRL Y-17354	GCA 030556595.1	97.50%	97.40%	0.10%	0.50%	2.00%
Diutina catenulata	WY3-10-4	GCA 003285555.1	75.70%	75.70%	0.00%	4.50%	19.80%
Diutina mesorugosa	CBS 12656	GCA 030674695.1	85.00%	85.00%	0.00%	1.60%	13.40%
Diutina neorugosa	CBS 12627	GCA 030578555.1	88.40%	88.40%	0.00%	1.10%	10.50%
Diutina pseudorugosa	CBS 10433	GCA 030580175.1	85.20%	85.20%	0.00%	2.00%	12.80%
Diutina ranongensis	CBS 10861	GCA 030569815.1	89.20%	89.10%	0.10%	1.20%	9.60%
Diutina rugosa	CBS 613	GCA 008704595.1	92.10%	92.10%	0.00%	1.10%	6.80%
Diutina scorzettiae	NRRL Y-27665	GCA 030563345.1	90.70%	90.60%	0.10%	0.50%	8.80%
Diutina siamensis	CBS 13388	GCA 030580155.1	90.90%	90.60%	0.30%	0.70%	8.40%
Gaillardinia entomophila	NRRL Y-7783	GCA 030555945.1	94.30%	94.30%	0.00%	0.90%	4.80%
Helenozyma baotianmanensis	CBS 11898	GCA 030556145.1	87.90%	87.90%	0.00%	2.50%	9.60%
Helenozyma melibiosica	NRRL Y-17076	GCA 030563325.1	86.80%	86.80%	0.00%	3.30%	9.90%
Helenozyma rhizophorensis	NRRL Y-48382	GCA 030573355.1	89.80%	89.80%	0.00%	1.30%	8.90%
Hemisphaericaspora insectamans	NRRL Y-7786	GCA 030578955.1	85.80%	85.10%	0.70%	4.20%	10.00%

Table S1. List of yeast strains and genomes used in this study (Continue)

Taxa	Strain	Assembly	Complete BUSCOs (C)	Complete and single-copy BUSCOs (S)	Complete and duplicated BUSCOs (D)	Fragmented BUSCOs (F)	Missing BUSCOs (M)
Hemisphaericaspora nanyangensis	CBS 13020	GCA 030557635.1	96.80%	96.70%	0.10%	0.30%	2.90%
Hermanozyma aechmeae	NRRL Y-48456	GCA 030583085.1	92.30%	92.30%	0.00%	0.90%	6.80%
Hermanozyma ubatubensis	NRRL Y-27812	GCA 030567085.1	90.80%	90.80%	0.00%	1.30%	7.90%
Hyphopichia burtonii	NRRL Y-1933	GCA 018343885.1	96.40%	96.30%	0.10%	0.30%	3.30%
Hyphopichia buzzinii	CBS 14300	GCA 030556945.1	96.00%	95.90%	0.10%	0.70%	3.30%
Hyphopichia fennica	NRRL Y-7505	GCA 030444945.1	97.30%	97.20%	0.10%	0.30%	2.40%
Hyphopichia homilentoma	JCM 1507	GCA 001599095.1	95.40%	95.30%	0.10%	0.50%	4.10%
Hyphopichia khmerensis	CBS 9784	GCA 030569195.1	96.30%	96.20%	0.10%	0.00%	3.70%
Hyphopichia pseudoburtonii	makgeolli 2	GCA 003856775.1	96.50%	96.40%	0.10%	0.40%	3.10%
Hyphopichia wangnamkhiaoensis	CBS 11695	GCA 030578475.1	97.30%	97.20%	0.10%	0.10%	2.60%
Isabelozyma gotoi	NRRL Y-27225	GCA 003708205.1	96.60%	96.60%	0.00%	0.30%	3.10%
Isabelozyma heimii	NRRL Y-7502	GCA 003706925.2	97.10%	97.00%	0.10%	0.40%	2.50%
Isabelozyma pseudorhagii	NRRL YB-2076	GCA 030449045.1	97.00%	97.00%	0.00%	0.40%	2.60%
Isabelozyma rhagii	NRRL Y-2594	GCA 003708185.2	96.80%	96.80%	0.00%	0.10%	3.10%

Table S1. List of yeast strains and genomes used in this study (Continue)

Taxa	Strain	Assembly	Complete BUSCOs (C)	Complete and single-copy BUSCOs (S)	Complete and duplicated BUSCOs (D)	Fragmented BUSCOs (F)	Missing BUSCOs (M)
Kodamaea alishanica	CBS 11429	GCA 030563745.1	94.80%	94.70%	0.10%	0.70%	4.50%
Kodamaea anthophila	UWOPS95-602.1	GCA 015708815.1	90.90%	90.90%	0.00%	1.70%	7.40%
Kodamaea arcana	NRRL Y-27712	GCA 030574295.1	94.10%	93.70%	0.40%	0.70%	5.20%
Kodamaea derodonti	NRRL Y-27711	GCA 030570035.1	94.70%	94.30%	0.40%	0.30%	5.00%
Kodamaea fukazawae	JCM 1641	GCA 030572255.1	90.60%	90.60%	0.00%	1.20%	8.20%
Kodamaea fungicola	JCM 10142	GCA 030560575.1	94.60%	94.10%	0.50%	1.10%	4.30%
Kodamaea hsintzibuensis	CBS 11427	GCA 030568835.1	95.50%	95.10%	0.40%	0.50%	4.00%
Kodamaea jinghongensis	CBS 14700	GCA 030556895.1	95.00%	95.00%	0.00%	0.50%	4.50%
Kodamaea kakaduensis	CBS 8611	GCA 030558435.1	92.90%	92.90%	0.00%	1.50%	5.60%
Kodamaea kaohsiungensis	CBS 11435	GCA 030558205.1	94.10%	93.70%	0.40%	0.70%	5.20%
Kodamaea laetipori	NRRL Y-27713	GCA 003705675.1	95.90%	95.60%	0.30%	0.90%	3.20%
Kodamaea leandrae	NRRL Y-27757	GCA 030564445.1	94.10%	94.10%	0.00%	1.20%	4.70%
Kodamaea lidongshanica	CBS 11426	GCA 030562865.1	95.00%	94.90%	0.10%	0.90%	4.10%
Kodamaea neixiangensis	CBS 14699	GCA 030565385.1	95.00%	95.00%	0.00%	0.80%	4.20%

Table S1. List of yeast strains and genomes used in this study (Continue)

Taxa	Strain	Assembly	Complete BUSCOs (C)	Complete and single-copy BUSCOs (S)	Complete and duplicated BUSCOs (D)	Fragmented BUSCOs (F)	Missing BUSCOs (M)
Kodamaea nitidulidarum	NRRL Y-27353	GCA 030674215.1	94.60%	94.50%	0.10%	0.80%	4.60%
Kodamaea ohmeri	NRRL Y-1932	GCA 003708155.1	95.30%	95.30%	0.00%	0.90%	3.80%
Kodamaea plutei	NRRL Y-27715	GCA 030705055.1	94.60%	94.10%	0.50%	1.10%	4.30%
Kodamaea restingae	NRRL Y-27358	GCA 003707425.3	93.90%	93.90%	0.00%	0.90%	5.20%
Kodamaea sagamina	JCM 10144	GCA 030556545.1	93.80%	93.50%	0.30%	0.80%	5.40%
Kodamaea sp.	yHQL449	GCA 030582715.1	89.80%	89.70%	0.10%	0.80%	9.40%
Kodamaea sp.	yHQL451	GCA 030578635.1	96.40%	96.40%	0.00%	0.30%	3.30%
Kodamaea suecica	NRRL Y-12943	GCA 030558315.1	93.30%	93.00%	0.30%	0.80%	5.90%
Kurtzmaniella cleridarum	NRRL Y-48386	GCA 003707135.1	94.90%	94.90%	0.00%	0.70%	4.40%
Kurtzmaniella fragi	NRRL Y-17910	GCA 003706895.1	95.10%	95.10%	0.00%	0.70%	4.20%
Kurtzmaniella natalensis	NRRL Y-17680	GCA 030574355.1	93.50%	93.40%	0.10%	0.40%	6.10%
Kurtzmaniella quercitrusa	NRRL Y-5392	GCA 030570095.1	94.30%	94.20%	0.10%	0.50%	5.20%
Kurtzmaniella quercitrusa var. comoensis	1112	GCA 020280125.1	94.90%	94.20%	0.70%	0.40%	4.70%
Kurtzmaniella quercitrusa var. filamentosus	1120	GCA 020280135.1	94.20%	94.20%	0.00%	0.90%	4.90%

Table S1. List of yeast strains and genomes used in this study (Continue)

Taxa	Strain	Assembly	Complete BUSCOs (C)	Complete and single-copy BUSCOs (S)	Complete and duplicated BUSCOs (D)	Fragmented BUSCOs (F)	Missing BUSCOs (M)
Limtongozyma cylindracea	NRRL Y-17506	GCA 030572215.1	85.10%	84.80%	0.30%	3.00%	11.90%
Lodderomyces beijingensis	CBS 14171	GCA 030565245.1	93.80%	93.80%	0.00%	0.40%	5.80%
Lodderomyces elongisporus	NRRL YB-4239	GCA 030557865.1	88.00%	88.00%	0.00%	1.50%	10.50%
Metschnikowia aberdeeniae	SUB 05-213.1	GCA 002370615.1	92.50%	92.50%	0.00%	0.80%	6.70%
Metschnikowia agaves	UWOPS 92-210.1	GCA 008065255.1	93.80%	93.80%	0.00%	0.80%	5.40%
Metschnikowia andauensis	CBS 10809	GCA 030568715.1	73.80%	72.60%	1.20%	10.00%	16.20%
Metschnikowia anglica	CBS 15342	GCA 030573055.1	95.30%	95.30%	0.00%	0.40%	4.30%
Metschnikowia arizonensis	UWOPS 99-103.4	GCA 002370875.1	93.70%	93.70%	0.00%	0.70%	5.60%
Metschnikowia australis	W7-5	GCA 019285895.1	90.50%	90.50%	0.00%	1.20%	8.30%
Metschnikowia baotianmanensis	CBS 15869	GCA 030565705.1	90.70%	75.10%	15.60%	2.40%	6.90%
Metschnikowia bicuspidata var. bicuspidata	NRRL YB-4993	GCA 030570515.1	79.00%	79.00%	0.00%	5.10%	15.90%
Metschnikowia bicuspidata var. californica	NRRL Y-17916	GCA 030555835.1	78.00%	78.00%	0.00%	4.50%	17.50%
Metschnikowia bicuspidata var. chathamia	NRRL Y-17917	GCA 030556055.1	81.40%	81.40%	0.00%	5.00%	13.60%
Metschnikowia borealis	SUB 99-207.1	GCA 002374385.1	91.20%	91.20%	0.00%	2.80%	6.00%

Table S1. List of yeast strains and genomes used in this study (Continue)

Taxa	Strain	Assembly	Complete BUSCOs (C)	Complete and single-copy BUSCOs (S)	Complete and duplicated BUSCOs (D)	Fragmented BUSCOs (F)	Missing BUSCOs (M)
Metschnikowia bowlesiae	UWOPS 04-243x5	GCA 002374615.1	90.70%	90.40%	0.30%	1.80%	7.50%
Metschnikowia caudata	EBD-CdVSA 57-2	GCA 008065175.1	86.50%	86.50%	0.00%	2.40%	11.10%
Metschnikowia cerradonensis	UFMG 03-T67.1	GCA 002370635.1	94.30%	94.30%	0.00%	0.50%	5.20%
Metschnikowia chrysomelidarum	NRRL Y-27749	GCA 030582795.1	92.30%	91.80%	0.50%	1.20%	6.50%
Metschnikowia chrysoperlae	NRRL Y-27615	GCA 030674525.1	83.00%	83.00%	0.00%	6.50%	10.50%
Metschnikowia colocasiae	UWOPS 03-202.1	GCA 002370175.1	92.50%	92.50%	0.00%	1.20%	6.30%
Metschnikowia continentalis	UWOPS 95-402.1	GCA 002370835.1	93.40%	93.30%	0.10%	0.50%	6.10%
Metschnikowia corniflorae	NRRL Y-27750	GCA 030581935.1	88.50%	87.20%	1.30%	3.20%	8.30%
Metschnikowia dekortorum	UWOPS 03-172.2	GCA 002370735.1	91.80%	91.70%	0.10%	1.50%	6.70%
Metschnikowia drakensbergensis	EBD-CdVSA 10-2A	GCA 002370475.1	92.90%	92.90%	0.00%	1.10%	6.00%
Metschnikowia drosophilae	UWOPS83-1 143.1	GCA 002893705.1	92.00%	92.00%	0.00%	1.10%	6.90%
Metschnikowia fructicola	NRRL Y-27328	GCA 030556695.1	84.20%	65.30%	18.90%	4.20%	11.60%
Metschnikowia gelsemii	NRRL Y-48212	GCA 030561745.1	94.00%	93.70%	0.30%	0.70%	5.30%
Metschnikowia gruessii	NRRL Y-17809	GCA 030563445.1	91.60%	91.60%	0.00%	2.90%	5.50%

Table S1. List of yeast strains and genomes used in this study (Continue)

Taxa	Strain	Assembly	Complete BUSCOs (C)	Complete and single-copy BUSCOs (S)	Complete and duplicated BUSCOs (D)	Fragmented BUSCOs (F)	Missing BUSCOs (M)
Metschnikowia hamakuensis	UWOPS 04-199.1	GCA 002370815.1	92.00%	92.00%	0.00%	0.90%	7.10%
Metschnikowia hawaiiana	NRRL Y-27473	GCA 003708615.1	93.00%	93.00%	0.00%	0.80%	6.20%
Metschnikowia hawaiiensis	UWOPS 87-2203.2	GCA 002370325.1	90.60%	90.60%	0.00%	1.10%	8.30%
Metschnikowia henanensis	CBS 12677	GCA 030674755.1	83.70%	66.40%	17.30%	6.30%	10.00%
Metschnikowia hibisci	UWOPS 95-797.2	GCA 002374725.1	93.90%	93.90%	0.00%	0.30%	5.80%
Metschnikowia ipomoeae	NRRL Y-27455	GCA 030566495.1	92.70%	92.60%	0.10%	0.90%	6.40%
Metschnikowia kamakouana	UWOPS 04-112.5	GCA 002374535.1	93.00%	93.00%	0.00%	1.10%	5.90%
Metschnikowia kipukae	UWOPS 00-669.2	GCA 002370135.1	93.70%	93.70%	0.00%	0.40%	5.90%
Metschnikowia kofuensis	NRRL Y-27226	GCA 030564885.1	89.00%	79.60%	9.40%	3.60%	7.40%
Metschnikowia koreensis	CBS 8854	GCA 030569435.1	93.40%	93.40%	0.00%	1.10%	5.50%
Metschnikowia krissii	NRRL Y-5389	GCA 030561945.1	91.30%	91.30%	0.00%	1.30%	7.40%
Metschnikowia kunwiensis	NRRL Y-48698	GCA 030583255.1	86.10%	86.00%	0.10%	2.10%	11.80%
Metschnikowia lachancei	NRRL Y-27242	GCA 030572615.1	92.30%	88.50%	3.80%	2.20%	5.50%
Metschnikowia laotica	CBS 12961	GCA 030563125.1	85.40%	85.40%	0.00%	5.00%	9.60%

Table S1. List of yeast strains and genomes used in this study (Continue)

Taxa	Strain	Assembly	Complete BUSCOs (C)	Complete and single-copy BUSCOs (S)	Complete and duplicated BUSCOs (D)	Fragmented BUSCOs (F)	Missing BUSCOs (M)
Metschnikowia leonuri	CBS 15341	GCA 030573075.1	52.50%	37.10%	15.40%	21.90%	25.60%
Metschnikowia lochheadii	UWOPS 99-661.1	GCA 002370915.1	94.10%	94.10%	0.00%	0.70%	5.20%
Metschnikowia lopburiensis	CBS 12574	GCA 030563105.1	92.30%	92.20%	0.10%	0.90%	6.80%
Metschnikowia lunata	NRRL Y-7131	GCA 030583235.1	94.30%	94.30%	0.00%	0.90%	4.80%
Metschnikowia matae	NRRL Y-63736	GCA 030674615.1	92.80%	92.10%	0.70%	1.20%	6.00%
Metschnikowia matae var. maris	UFMG-CM-Y397	GCA 002370695.1	93.70%	93.70%	0.00%	0.90%	5.40%
Metschnikowia matae var. matae	UFMG-CM-Y391	GCA 002370655.1	93.70%	93.70%	0.00%	0.90%	5.40%
Metschnikowia mauinuiana	UWOPS 04-190.1	GCA 002374555.1	92.00%	92.00%	0.00%	1.10%	6.90%
Metschnikowia noctiluminum	NRRL Y-27753	GCA 030578735.1	93.30%	92.10%	1.20%	0.40%	6.30%
Metschnikowia orientalis	UWOPS99-745.6	GCA 002893665.1	91.70%	91.70%	0.00%	0.90%	7.40%
Metschnikowia peoriensis	CBS 15345	GCA 030573015.1	92.90%	82.20%	10.70%	2.00%	5.10%
Metschnikowia persimmonesis	KIOM G15050	GCA 014905795.1	81.00%	76.00%	5.00%	7.00%	12.00%
Metschnikowia picachoensis	NRRL Y-27607	GCA 030556465.1	92.80%	89.80%	3.00%	0.80%	6.40%
Metschnikowia pimensis	NRRL Y-27619	GCA 030556455.1	92.60%	92.20%	0.40%	1.50%	5.90%

Table S1. List of yeast strains and genomes used in this study (Continue)

Taxa	Strain	Assembly	Complete BUSCOs (C)	Complete and single-copy BUSCOs (S)	Complete and duplicated BUSCOs (D)	Fragmented BUSCOs (F)	Missing BUSCOs (M)
Metschnikowia proteae	EBD-T1Y1T	GCA 002370515.1	93.10%	93.10%	0.00%	1.10%	5.80%
Metschnikowia pulcherrima	NRRL Y-7111	GCA 030583425.1	92.50%	92.50%	0.00%	1.30%	6.20%
Metschnikowia reukaufii	MR1 2	GCA 003401635.1	90.00%	90.00%	0.00%	1.50%	8.50%
Metschnikowia rubicola	CBS 15344	GCA 030557065.1	88.60%	83.50%	5.10%	2.10%	9.30%
Metschnikowia santaceciliae	UWOPS 01-517a1	GCA 002374485.1	93.60%	93.50%	0.10%	0.70%	5.70%
Metschnikowia shanxiensis	NRRL Y-48710	GCA 030578695.1	88.10%	78.20%	9.90%	4.10%	7.80%
Metschnikowia shivogae	UWOPS 04-310.1	GCA 002374645.1	92.60%	92.60%	0.00%	0.70%	6.70%
Metschnikowia similis	UWOPS 03-133.4	GCA 002370765.1	90.50%	90.40%	0.10%	2.00%	7.50%
Metschnikowia sinensis	NRRL Y-48711	GCA 030583125.1	91.60%	91.20%	0.40%	1.60%	6.80%
Metschnikowia sp.	yHJM9	GCA 030444895.1	92.90%	92.90%	0.00%	0.80%	6.30%
Metschnikowia sp.	yHQL527	GCA 030578455.1	94.10%	94.10%	0.00%	0.90%	5.00%
Metschnikowia sp.	yHKB443	GCA 030444905.1	79.80%	79.40%	0.40%	2.10%	18.10%
Metschnikowia torresii	CBS 5152	GCA 002893725.1	92.10%	92.00%	0.10%	1.10%	6.80%
Metschnikowia vanudenii	NRRL Y-17036	GCA 030583145.1	95.00%	95.00%	0.00%	0.40%	4.60%

Table S1. List of yeast strains and genomes used in this study (Continue)

Taxa	Strain	Assembly	Complete BUSCOs (C)	Complete and single-copy BUSCOs (S)	Complete and duplicated BUSCOs (D)	Fragmented BUSCOs (F)	Missing BUSCOs (M)
Metschnikowia viticola	NRRL Y-48693	GCA 030556725.1	85.10%	85.00%	0.10%	5.50%	9.40%
Metschnikowia zizyphicola	NRRL Y-48712	GCA 030578815.1	62.70%	51.50%	11.20%	19.00%	18.30%
Metschnikowia zobellii	CALNDW01	GCA 939531315.1	91.20%	90.80%	0.40%	0.70%	8.10%
Meyerozyma athensensis	NRRL Y-27644	GCA 003705555.1	95.60%	95.60%	0.00%	0.70%	3.70%
Meyerozyma caribbica	NRRL Y-27274	GCA 003707125.2	95.40%	95.40%	0.00%	1.20%	3.40%
Meyerozyma carpophila	JCM 9396	GCA 001599235.1	95.00%	95.00%	0.00%	1.10%	3.90%
Meyerozyma elateridarum	NRRL Y-27647	GCA 030574335.1	95.40%	95.40%	0.00%	0.30%	4.30%
Meyerozyma guilliermondii	ATCC 6260	GCA 006942155.1	96.00%	96.00%	0.00%	0.40%	3.60%
Meyerozyma smithsonii	NRRL Y-27642	GCA 030570235.1	94.70%	94.70%	0.00%	0.90%	4.40%
Millerozyma acaciae	JCM 10732	GCA 001600675.1	97.10%	97.00%	0.10%	0.10%	2.80%
Millerozyma farinosa	NRRL Y-7553	GCA 030557775.1	96.40%	96.40%	0.00%	0.10%	3.50%
Millerozyma miso	CBS 2004	GCA 030569015.1	95.90%	95.90%	0.00%	0.30%	3.80%
Nematodospora anomalae	CBS 13927	GCA 030572795.1	95.90%	95.80%	0.10%	0.10%	4.00%
Nematodospora valgi	CBS 12562	GCA 030565165.1	95.90%	95.80%	0.10%	0.10%	4.00%

Table S1. List of yeast strains and genomes used in this study (Continue)

Taxa	Strain	Assembly	Complete BUSCOs (C)	Complete and single-copy BUSCOs (S)	Complete and duplicated BUSCOs (D)	Fragmented BUSCOs (F)	Missing BUSCOs (M)
Osmozyma mogii	NRRL Y-17032	GCA 030573315.1	90.20%	90.20%	0.00%	1.60%	8.20%
Osmozyma tolerans	CBS 8613	GCA 030582955.1	92.10%	92.00%	0.10%	0.80%	7.10%
Priceomyces carsonii	NRRL YB-4275	GCA 003709225.2	97.20%	97.10%	0.10%	0.10%	2.70%
Priceomyces castillae	NRRL Y-7501	GCA 003706855.2	96.20%	95.30%	0.90%	0.70%	3.10%
Priceomyces fermenticarens	NRRL Y-17321	GCA 030574455.1	95.60%	95.60%	0.00%	0.30%	4.10%
Priceomyces haplophilus	JCM 1635	GCA 001599895.1	92.10%	92.00%	0.10%	1.20%	6.70%
Priceomyces medius	NRRL Y-7122	GCA 003705335.1	95.90%	95.90%	0.00%	0.70%	3.40%
Priceomyces melissophilus	NRRL Y-7585	GCA 030574515.1	95.90%	95.90%	0.00%	0.30%	3.80%
Scheffersomyces coipomensis	NRRL Y-17651	GCA 030578755.1	95.80%	95.80%	0.00%	0.30%	3.90%
Scheffersomyces cryptocercus	NRRL Y-48824	GCA 030555905.1	97.20%	97.10%	0.10%	0.10%	2.70%
Scheffersomyces ergatensis	NRRL Y-17652	GCA 030575095.1	95.70%	95.40%	0.30%	0.40%	3.90%
Scheffersomyces gosingicus	CBS 11433	GCA 030463055.1	95.10%	95.10%	0.00%	0.50%	4.40%
Scheffersomyces illinoinensis	NRRL Y-48827	GCA 030572695.1	95.40%	95.30%	0.10%	0.50%	4.10%
Scheffersomyces insectosa	NRRL Y-12854	GCA 030572575.1	96.50%	96.40%	0.10%	0.40%	3.10%

Table S1. List of yeast strains and genomes used in this study (Continue)

Taxa	Strain	Assembly	Complete BUSCOs (C)	Complete and single-copy BUSCOs (S)	Complete and duplicated BUSCOs (D)	Fragmented BUSCOs (F)	Missing BUSCOs (M)
Scheffersomyces lignicola	CBS 10612	GCA 030578435.1	96.40%	96.30%	0.10%	0.40%	3.20%
Scheffersomyces lignosus	JCM 9837	GCA 001599395.1	96.70%	96.60%	0.10%	0.10%	3.20%
Scheffersomyces parashehatae	CBS 12535	GCA 030571865.1	96.70%	96.60%	0.10%	0.30%	3.00%
Scheffersomyces quercinus	NRRL Y-48825	GCA 030556775.1	96.70%	96.60%	0.10%	0.30%	3.00%
Scheffersomyces segobiensis	DSM 27193	GCA 018489445.1	96.00%	95.90%	0.10%	0.10%	3.90%
Scheffersomyces shehatae	NBRC 1983	GCA 002118155.1	96.50%	96.40%	0.10%	0.40%	3.10%
Scheffersomyces spartinae	ARV 011	GCA 019049425.1	93.90%	93.90%	0.00%	0.70%	5.40%
Scheffersomyces stambukii	UFMG-CM-Y427	GCA 002245345.1	94.20%	94.10%	0.10%	0.90%	4.90%
Scheffersomyces stipitis	NRRL Y-7124	GCA 016859295.1	97.10%	95.90%	1.20%	0.00%	2.90%
Scheffersomyces titanus	CBS 13926	GCA 030565185.1	96.00%	95.90%	0.10%	0.00%	4.00%
Scheffersomyces virginianus	NRRL Y-48822	GCA 030565005.1	96.70%	96.60%	0.10%	0.30%	3.00%
Scheffersomyces xylosifermentans	CBS 12540	GCA 030571855.1	95.00%	94.90%	0.10%	0.00%	5.00%
Schwanniomyces capriottii	NRRL Y-7423	GCA 030674585.1	97.30%	97.20%	0.10%	0.40%	2.30%
Schwanniomyces etchellsii	NRRL Y-7121	GCA 030583275.1	94.90%	94.20%	0.70%	0.50%	4.60%

Table S1. List of yeast strains and genomes used in this study (Continue)

Taxa	Strain	Assembly	Complete BUSCOs (C)	Complete and single-copy BUSCOs (S)	Complete and duplicated BUSCOs (D)	Fragmented BUSCOs (F)	Missing BUSCOs (M)
Schwanniomyces occidentalis var. occidentalis	NRRL Y-10	GCA 030579795.1	97.80%	97.50%	0.30%	0.10%	2.10%
Schwanniomyces occidentalis var. persoonii	NRRL Y-7400	GCA 030556115.1	97.70%	97.60%	0.10%	0.30%	2.00%
Schwanniomyces polymorphus var. africanus	CBS 6741	GCA 030563145.1	97.30%	97.00%	0.30%	0.10%	2.60%
Schwanniomyces polymorphus var. polymorphus	NRRL Y-2022	GCA 030463025.1	96.50%	96.00%	0.50%	0.50%	3.00%
Schwanniomyces pseudopolymorphus	NRRL YB-4229	GCA 030583345.1	97.50%	97.20%	0.30%	0.10%	2.40%
Schwanniomyces sp.	yHMH407	GCA 030571215.1	96.20%	96.20%	0.00%	0.50%	3.30%
Schwanniomyces sp.	NRRL Y-7430	GCA 030462985.1	95.90%	95.40%	0.50%	1.10%	3.00%
Schwanniomyces vanrijiae var. vanrijiae	NRRL Y-7535	GCA 030556805.1	96.90%	96.60%	0.30%	0.40%	2.70%
Schwanniomyces vanrijiae var. yarrowii	NRRL Y-11714	GCA 030575115.1	96.40%	96.30%	0.10%	0.40%	3.20%
Schwanniomyces yamadae	NRRL Y-48658	GCA 030565025.1	96.80%	96.70%	0.10%	0.10%	3.10%
Soucietia sequanensis	NRRL Y-17682	GCA 030557975.1	94.70%	94.70%	0.00%	0.10%	5.20%
Spathaspora arborariae	UFMG-HM19.1AT	GCA 000497715.1	95.10%	95.10%	0.00%	0.40%	4.50%
Spathaspora boniae	UFMG-CM-Y306	GCA 002094185.1	95.40%	95.40%	0.00%	0.10%	4.50%
Spathaspora girioi	UFMG-CM-Y302	GCA 001657455.1	94.80%	94.50%	0.30%	0.80%	4.40%

Table S1. List of yeast strains and genomes used in this study (Continue)

Taxa	Strain	Assembly	Complete BUSCOs (C)	Complete and single-copy BUSCOs (S)	Complete and duplicated BUSCOs (D)	Fragmented BUSCOs (F)	Missing BUSCOs (M)
Spathaspora gorwiae	UFMG-CM-Y312	GCA 001655765.1	87.90%	86.70%	1.20%	4.70%	7.40%
Spathaspora hagerdaliae	UFMG-CM-Y303	GCA 001655755.1	94.40%	93.30%	1.10%	1.60%	4.00%
Spathaspora jeffriesii	NRRL Y-27738	GCA 030705235.1	73.70%	62.00%	11.70%	13.90%	12.40%
Spathaspora passalidarum	NRRL Y-27907	GCA 013620965.1	96.40%	96.30%	0.10%	0.10%	3.50%
Spathaspora xylofermentans	UFMG-HMD 23.3	GCA 002105455.1	96.30%	95.90%	0.40%	0.80%	2.90%
Suhomyces ambrosiae	NRRL YB-1316	GCA 030568575.1	93.50%	93.50%	0.00%	0.30%	6.20%
Suhomyces anneliseae	NRRL Y-27563	GCA 030568535.1	96.60%	96.60%	0.00%	0.50%	2.90%
Suhomyces atakaporum	NRRL Y-27570	GCA 030561405.1	97.00%	97.00%	0.00%	0.30%	2.70%
Suhomyces bokatorum	NRRL Y-27571	GCA 030568615.1	93.10%	93.10%	0.00%	1.20%	5.70%
Suhomyces bolitotheri	NRRL Y-27587	GCA 030568555.1	96.60%	96.60%	0.00%	0.50%	2.90%
Suhomyces bribrorum	NRRL Y-27572	GCA 030561385.1	96.60%	96.60%	0.00%	0.30%	3.10%
Suhomyces canberraensis	NRRL YB-2417	GCA 003706525.1	96.50%	96.40%	0.10%	0.40%	3.10%
Suhomyces chickasaworum	NRRL Y-27566	GCA 030568495.1	94.50%	94.50%	0.00%	0.80%	4.70%
Suhomyces choctaworum	NRRL Y-27584	GCA 030568475.1	96.40%	96.40%	0.00%	0.00%	3.60%

Table S1. List of yeast strains and genomes used in this study (Continue)

Taxa	Strain	Assembly	Complete BUSCOs (C)	Complete and single-copy BUSCOs (S)	Complete and duplicated BUSCOs (D)	Fragmented BUSCOs (F)	Missing BUSCOs (M)
Suhomyces coccinellae	CBS 14298	GCA 030565345.1	94.70%	94.70%	0.00%	0.70%	4.60%
Suhomyces emberorum	NRRL Y-27606	GCA 003707835.2	96.20%	96.20%	0.00%	0.40%	3.40%
Suhomyces faveliae	CBS 14299	GCA 030585145.1	97.10%	97.00%	0.10%	0.30%	2.60%
Suhomyces guaymorum	NRRL Y-27568	GCA 030568515.1	95.30%	95.30%	0.00%	0.80%	3.90%
Suhomyces kilbournensis	NRRL Y-17864	GCA 030563685.1	96.40%	96.40%	0.00%	0.40%	3.20%
Suhomyces kunorum	NRRL Y-27580	GCA 030561465.1	94.10%	94.10%	0.00%	0.50%	5.40%
Suhomyces maxii	NRRL Y-27588	GCA 030574995.1	96.30%	96.30%	0.00%	0.40%	3.30%
Suhomyces panamericanus	NRRL Y-27567	GCA 030582475.1	91.00%	91.00%	0.00%	1.20%	7.80%
Suhomyces prunicola	NRRL YB-869	GCA 030568655.1	96.30%	96.30%	0.00%	0.40%	3.30%
Suhomyces pyralidae	NRRL Y-27085	GCA 003706505.2	96.00%	96.00%	0.00%	0.40%	3.60%
Suhomyces sp.	yHKS641	GCA 030705105.1	96.50%	96.40%	0.10%	0.40%	3.10%
Suhomyces sp.	yHMH580	GCA 030580235.1	96.80%	96.80%	0.00%	0.30%	2.90%
Suhomyces sp.	yHQL142	GCA 030582675.1	96.50%	96.40%	0.10%	0.00%	3.50%
Suhomyces taliae	NRRL Y-27589	GCA 030572155.1	96.70%	96.70%	0.00%	0.50%	2.80%

Table S1. List of yeast strains and genomes used in this study (Continue)

Taxa	Strain	Assembly	Complete BUSCOs (C)	Complete and single-copy BUSCOs (S)	Complete and duplicated BUSCOs (D)	Fragmented BUSCOs (F)	Missing BUSCOs (M)
Suhomyces tanzawaensis	NRRL Y-17324	GCA 001661415.1	97.10%	97.00%	0.10%	0.00%	2.90%
Suhomyces terraborum	NRRL Y-27573	GCA 030582495.1	96.40%	96.40%	0.00%	0.40%	3.20%
Suhomyces vadensis	NRRL Y-27778	GCA 030575035.1	93.90%	93.90%	0.00%	0.80%	5.30%
Suhomyces wounanorum	NRRL Y-27574	GCA 030568695.1	96.60%	96.60%	0.00%	0.50%	2.90%
Suhomyces xylopsoci	NRRL Y-27066	GCA 030568675.1	96.20%	96.20%	0.00%	0.40%	3.40%
Suhomyces yuchorum	NRRL Y-27569	GCA 030571845.1	96.70%	96.70%	0.00%	0.50%	2.80%
Sungouiella berkhoutiae	CBS 11722	GCA 030578995.1	94.10%	94.10%	0.00%	0.70%	5.20%
Sungouiella blattae	NRRL Y-27698	GCA 003706955.3	80.70%	80.70%	0.00%	1.50%	17.80%
Sungouiella dosseyi	NRRL Y-27950	GCA 030573325.1	95.10%	95.10%	0.00%	0.90%	4.00%
Sungouiella ecuadorensis	CBS 12653	GCA 030579155.1	91.40%	91.40%	0.00%	1.60%	7.00%
Sungouiella ezoensis	CBS 11753	GCA 030569115.1	94.10%	94.10%	0.00%	0.90%	5.00%
Sungouiella flosculorum	NRRL Y-48731	GCA 030568875.1	95.60%	95.60%	0.00%	0.70%	3.70%
Sungouiella intermedia	NRRL Y-981	GCA 030575135.1	95.30%	95.30%	0.00%	0.50%	4.20%
Sungouiella inulinophila	CBS 11725	GCA 030562885.1	94.10%	94.10%	0.00%	0.70%	5.20%

Table S1. List of yeast strains and genomes used in this study (Continue)

Taxa	Strain	Assembly	Complete BUSCOs (C)	Complete and single-copy BUSCOs (S)	Complete and duplicated BUSCOs (D)	Fragmented BUSCOs (F)	Missing BUSCOs (M)
Sungouiella middelhoveniana	CBS 12306	GCA 030557965.1	95.30%	95.30%	0.00%	0.50%	4.20%
Sungouiella pseudoflosculorum	CBS 8584	GCA 030674735.1	94.20%	94.20%	0.00%	0.90%	4.90%
Sungouiella pseudointermedia	NRRL Y-10939	GCA 030557285.1	95.40%	95.40%	0.00%	0.50%	4.10%
Sungouiella sharkensis	NRRL Y-48380	GCA 030567015.1	96.30%	96.30%	0.00%	0.80%	2.90%
Sungouiella suratensis	CBS 10928	GCA 030566815.1	91.00%	91.00%	0.00%	1.10%	7.90%
Sungouiella thailandica	CBS 10610	GCA 030563845.1	92.20%	92.10%	0.10%	2.10%	5.70%
Sungouiella tsuchiyae	NRRL Y-17840	GCA 030566995.1	94.10%	94.10%	0.00%	0.70%	5.20%
Tanozyma kutaoensis	CBS 11388	GCA 030562905.1	83.10%	83.10%	0.00%	3.70%	13.20%
Teunomyces aglyptinius	NRRL Y-27935	GCA 030581575.1	94.90%	94.90%	0.00%	0.70%	4.40%
Teunomyces atbi	NRRL Y-27651	GCA 030574975.1	95.00%	95.00%	0.00%	0.90%	4.10%
Teunomyces barrocoloradensis	NRRL Y-27934	GCA 030568385.1	95.50%	95.50%	0.00%	0.70%	3.80%
Teunomyces cretensis	NRRL Y-27777	GCA 003706575.1	95.50%	95.50%	0.00%	0.50%	4.00%
Teunomyces funiuensis	CBS 13911	GCA 030558095.1	95.00%	95.00%	0.00%	0.30%	4.70%
Teunomyces gatunensis	NRRL Y-48064	GCA 003706565.2	95.40%	95.40%	0.00%	0.30%	4.30%

Table S1. List of yeast strains and genomes used in this study (Continue)

Taxa	Strain	Assembly	Complete BUSCOs (C)	Complete and single-copy BUSCOs (S)	Complete and duplicated BUSCOs (D)	Fragmented BUSCOs (F)	Missing BUSCOs (M)
Teunomyces kruisii	NRRL Y-17087	GCA 003706535.1	95.60%	86.00%	9.60%	0.30%	4.10%
Teunomyces lycoperdinae	NRRL Y-27658	GCA 030574955.1	94.60%	94.60%	0.00%	0.70%	4.70%
Teunomyces pallodes	NRRL Y-27653	GCA 030556435.1	95.10%	95.00%	0.10%	0.50%	4.40%
Teunomyces panamensis	NRRL Y-27657	GCA 030564025.1	94.70%	93.50%	1.20%	0.50%	4.80%
Teunomyces stri	NRRL Y-48063	GCA 030563165.1	95.40%	95.40%	0.00%	0.30%	4.30%
Teunomyces tritomae	NRRL Y-27650	GCA 030568455.1	94.90%	94.90%	0.00%	0.40%	4.70%
Wickerhamia fluorescens	NRRL YB-4819	GCA 030579855.1	95.40%	95.10%	0.30%	0.70%	3.90%
Wilhelminamyces savonicus	NRRL Y-17077	GCA 030570115.1	96.80%	96.70%	0.10%	0.40%	2.80%
Wilhelminamyces tanticharoeniae	CBS 11574	GCA 030558325.1	94.70%	94.60%	0.10%	0.90%	4.40%
Yamadazyma akitaensis	NRRL Y-7904	GCA 030581475.1	94.90%	94.90%	0.00%	0.50%	4.60%
Yamadazyma dushanensis	CBS 13914	GCA 030571835.1	94.30%	94.30%	0.00%	0.80%	4.90%
Yamadazyma endophytica	CBS 14163	GCA 030571075.1	95.30%	95.30%	0.00%	0.40%	4.30%
Yamadazyma epiphylla	CBS 13384	GCA 030571925.1	92.30%	92.20%	0.10%	1.30%	6.40%
Yamadazyma insecticola	CBS 13382	GCA 030571995.1	89.70%	89.70%	0.00%	1.70%	8.60%

Table S1. List of yeast strains and genomes used in this study (Continue)

Taxa	Strain	Assembly	Complete BUSCOs (C)	Complete and single-copy BUSCOs (S)	Complete and duplicated BUSCOs (D)	Fragmented BUSCOs (F)	Missing BUSCOs (M)
Yamadazyma kitorensis	JCM 31005	GCA 030572015.1	92.00%	92.00%	0.00%	1.60%	6.40%
Yamadazyma laniorum	yHMH7	GCA 002109505.1	95.00%	95.00%	0.00%	0.70%	4.30%
Yamadazyma mexicana	NRRL Y-11818	GCA 030569415.1	94.70%	94.70%	0.00%	0.70%	4.60%
Yamadazyma nakazawae	NRRL Y-7903	GCA 003706715.1	94.60%	94.60%	0.00%	0.80%	4.60%
Yamadazyma olivae	CBS 11171	GCA 030571975.1	93.80%	93.80%	0.00%	0.90%	5.30%
Yamadazyma paraphyllophila	CBS 9928	GCA 030563605.1	95.00%	94.90%	0.10%	0.40%	4.60%
Yamadazyma philogaea	NRRL Y-7813	GCA 003706995.2	93.80%	93.80%	0.00%	0.50%	5.70%
Yamadazyma phyllophila	CBS 12572	GCA 030571955.1	94.70%	94.60%	0.10%	0.70%	4.60%
Yamadazyma scolyti	NRRL Y-5512	GCA 003707025.1	92.70%	92.70%	0.00%	1.10%	6.20%
Yamadazyma siamensis	CBS 12573	GCA 030581535.1	93.60%	93.50%	0.10%	1.10%	5.30%
Yamadazyma sp.	yHKB15	GCA 030555745.1	94.50%	94.50%	0.00%	1.10%	4.40%
Yamadazyma sp.	yHKS699	GCA 030580295.1	94.60%	94.60%	0.00%	0.90%	4.50%
Yamadazyma sp.	yHMH393	GCA 030580255.1	92.10%	90.10%	2.00%	0.30%	7.60%
Yamadazyma sp.	yHMH685	GCA 030571055.1	94.70%	94.70%	0.00%	0.80%	4.50%

Table S1. List of yeast strains and genomes used in this study (Continue)

Taxa	Strain	Assembly	Complete BUSCOs (C)	Complete and single-copy BUSCOs (S)	Complete and duplicated BUSCOs (D)	Fragmented BUSCOs (F)	Missing BUSCOs (M)
Yamadazyma takamatsuzukensis	NBRC 104391	GCA 030572035.1	94.40%	94.30%	0.10%	0.90%	4.70%
Yamadazyma tenuis	ATCC 10573	GCA 029203305.1	94.70%	94.60%	0.10%	0.50%	4.80%
Yamadazyma triangularis	NRRL Y-5714	GCA 030573955.1	94.40%	10.60%	83.80%	0.70%	4.90%
Yamadazyma tumulicola	NBRC 104392	GCA 030578535.1	93.40%	93.40%	0.00%	0.50%	6.10%
Yamadazyma ubonensis	CBS 12859	GCA 030572075.1	93.20%	93.10%	0.10%	0.90%	5.90%
Saccharomycetes							
Ascoideales							
Ascoidea rubescens	DSM 1968	GCA 001661345.1	90.50%	89.30%	1.20%	2.00%	7.50%
Saccharomycopsis capsularis	NRRL Y-17639	GCA 003705375.1	93.70%	92.50%	1.20%	0.80%	5.50%
Phaffomycetales							
Barnettozyma botsteinii	1118	GCA 020280145.1	93.80%	93.70%	0.10%	0.90%	5.30%
Barnettozyma californica	NRRL Y-17395	GCA 003706655.2	96.00%	95.90%	0.10%	0.90%	3.10%
Barnettozyma hawaiiensis	NRRL Y-27270	GCA 003706665.1	96.40%	96.30%	0.10%	0.40%	3.20%
Barnettozyma populi	NRRL Y-12728	GCA 003706705.2	96.10%	96.00%	0.10%	0.30%	3.60%
Barnettozyma pratensis	NRRL Y-12696	GCA 003707865.1	95.20%	95.10%	0.10%	0.50%	4.30%

Table S1. List of yeast strains and genomes used in this study (Continue)

Taxa	Strain	Assembly	Complete BUSCOs (C)	Complete and single-copy BUSCOs (S)	Complete and duplicated BUSCOs (D)	Fragmented BUSCOs (F)	Missing BUSCOs (M)
Barnettozyma salicaria	NRRL Y-6780	GCA 003707885.1	96.80%	90.10%	6.70%	0.40%	2.80%
Barnettozyma siamensis	CBS 13392	GCA 030579035.1	94.30%	94.20%	0.10%	0.80%	4.90%
Barnettozyma sp.	yHDO593	GCA 030580455.1	95.70%	95.60%	0.10%	0.50%	3.80%
Barnettozyma sucrosica	CBS 11512	GCA 030558145.1	96.10%	96.00%	0.10%	0.70%	3.20%
Barnettozyma vustinii	CBS 11554	GCA 030569515.1	96.50%	96.40%	0.10%	0.40%	3.10%
Barnettozyma wickerhamii	NRRL Y-2435	GCA 030574915.1	96.10%	95.80%	0.30%	0.90%	3.00%
Candida adriatica	CBS 12504	GCA 030558135.1	95.50%	95.40%	0.10%	1.10%	3.40%
Candida berthetii	NRRL Y-17644	GCA 030564525.1	95.60%	92.60%	3.00%	2.40%	2.00%
Candida coquimbonensis	CBS 12348	GCA 030566895.1	93.40%	93.10%	0.30%	1.30%	5.30%
Candida dajiaensis	CBS 10590	GCA 030579075.1	97.30%	97.00%	0.30%	0.30%	2.40%
Candida dendrica	NRRL Y-7775	GCA 030570475.1	92.20%	92.10%	0.10%	4.10%	3.70%
Candida easanensis	JCM 12476	GCA 030580135.1	96.90%	96.80%	0.10%	0.30%	2.80%
Candida ficus	CBS 12638	GCA 030557985.1	92.30%	92.00%	0.30%	1.50%	6.20%
Candida freyschussii	NRRL Y-7957A	GCA 003707735.2	98.50%	98.00%	0.50%	0.10%	1.40%

Table S1. List of yeast strains and genomes used in this study (Continue)

Taxa	Strain	Assembly	Complete BUSCOs (C)	Complete and single-copy BUSCOs (S)	Complete and duplicated BUSCOs (D)	Fragmented BUSCOs (F)	Missing BUSCOs (M)
Candida galis	NRRL Y-48037	GCA 030568845.1	96.10%	96.00%	0.10%	0.50%	3.40%
Candida hungchunana	CBS 12243	GCA 030563225.1	98.60%	98.30%	0.30%	0.00%	1.40%
Candida jianshihensis	CBS 10591	GCA 030562945.1	97.10%	96.70%	0.40%	1.10%	1.80%
Candida maesae	CBS 12240	GCA 030563305.1	97.70%	97.60%	0.10%	0.10%	2.20%
Candida montana	NRRL Y-17326	GCA 003706615.3	93.90%	93.80%	0.10%	0.80%	5.30%
Candida namnaoensis	CBS 12175	GCA 030563805.1	95.10%	95.10%	0.00%	0.70%	4.20%
Candida norvegica	NRRL Y-17660	GCA 030567455.1	96.20%	96.20%	0.00%	0.40%	3.40%
Candida odintsovae	NRRL Y-17760	GCA 030557705.1	98.10%	97.80%	0.30%	0.50%	1.40%
Candida orba	NRRL Y-27336	GCA 003708145.2	95.40%	95.10%	0.30%	0.80%	3.80%
Candida peoriensis	NRRL YB-1497	GCA 030574875.1	98.10%	97.80%	0.30%	0.10%	1.80%
Candida ponderosae	NRRL YB-2307	GCA 003706755.2	96.70%	96.00%	0.70%	0.30%	3.00%
Candida qinlingensis	CBS 9768	GCA 030563005.1	95.60%	95.50%	0.10%	0.50%	3.90%
Candida quercuum	NRRL Y-12942	GCA 030556525.1	98.10%	97.80%	0.30%	0.30%	1.60%
Candida sanyiensis	CBS 10592	GCA 030569275.1	96.00%	95.60%	0.40%	0.30%	3.70%

Table S1. List of yeast strains and genomes used in this study (Continue)

Taxa	Strain	Assembly	Complete BUSCOs (C)	Complete and single-copy BUSCOs (S)	Complete and duplicated BUSCOs (D)	Fragmented BUSCOs (F)	Missing BUSCOs (M)
Candida silvicultrix	NRRL Y-7789	GCA 030574755.1	98.80%	98.70%	0.10%	0.40%	0.80%
Candida solani	NRRL Y-2224	GCA 030462955.1	60.70%	59.90%	0.80%	22.00%	17.30%
Candida sp.	XZY480-2	NMDC2030 1684[#]	93.00%	92.90%	0.10%	0.90%	6.10%
Candida sp.	NRRL Y-27127	GCA 030574675.1	97.30%	96.80%	0.50%	0.50%	2.20%
Candida sp.	NRRL YB-4088	GCA 030567155.1	98.20%	97.90%	0.30%	0.00%	1.80%
Candida stauntonica	CBS 12241	GCA 030558335.1	98.20%	97.80%	0.40%	0.40%	1.40%
Candida takata	CBS 12244	GCA 030564145.1	97.70%	97.40%	0.30%	0.40%	1.90%
Candida taoyuanica	CBS 12242	GCA 030567055.1	98.40%	98.30%	0.10%	0.40%	1.20%
Candida ulmi	CBS 8670	GCA 030569675.1	98.20%	97.90%	0.30%	0.30%	1.50%
Candida subsp. tiovaarae	NRRL Y-6701	GCA 003708265.2	97.90%	97.60%	0.30%	0.30%	1.80%
Candida yuanshanica	CBS 10589	GCA 030569295.1	98.50%	98.40%	0.10%	0.40%	1.10%
Cyberlindnera americana	NRRL Y-2156	GCA 003708795.2	99.00%	98.90%	0.10%	0.30%	0.70%
Cyberlindnera amylophila	NRRL YB-1287	GCA 030557155.1	92.40%	92.30%	0.10%	2.00%	5.60%
Cyberlindnera bimundalis	NRRL Y-5343	GCA 030569745.1	98.80%	98.70%	0.10%	0.50%	0.70%

Table S1. List of yeast strains and genomes used in this study (Continue)

Taxa	Strain	Assembly	Complete BUSCOs (C)	Complete and single-copy BUSCOs (S)	Complete and duplicated BUSCOs (D)	Fragmented BUSCOs (F)	Missing BUSCOs (M)
Cyberlindnera euphorbiae	NRRL Y-17232	GCA 030567115.1	93.10%	93.10%	0.00%	1.20%	5.70%
Cyberlindnera euphorbiiphila	NRRL Y-12742	GCA 030556625.1	96.70%	96.40%	0.30%	0.30%	3.00%
Cyberlindnera fabianii	NRRL Y-1871	GCA 018343965.1	98.70%	98.40%	0.30%	0.30%	1.00%
Cyberlindnera galapagoensis	CBS 13997	GCA 030565205.1	98.60%	98.30%	0.30%	0.10%	1.30%
Cyberlindnera jadinii	NRRL Y-1542	GCA 001661405.1	97.40%	96.20%	1.20%	1.10%	1.50%
Cyberlindnera japonica	NRRL YB-2750	GCA 030557175.1	97.70%	97.60%	0.10%	0.70%	1.60%
Cyberlindnera lachancei	NRRL Y-27008	GCA 030567175.1	98.00%	96.00%	2.00%	0.40%	1.60%
Cyberlindnera maclurae	NRRL Y-5377	GCA 003708355.2	98.30%	97.90%	0.40%	0.70%	1.00%
Cyberlindnera maritima	NRRL Y-17775	GCA 030557345.1	98.60%	98.50%	0.10%	0.00%	1.40%
Cyberlindnera meyerae	NRRL Y-17236	GCA 030462915.1	92.60%	92.30%	0.30%	2.40%	5.00%
Cyberlindnera mississippiensis	NRRL YB-1294	GCA 030581715.1	95.70%	95.60%	0.10%	0.80%	3.50%
Cyberlindnera misumaiensis	NRRL Y-17389	GCA 003707745.1	97.70%	96.80%	0.90%	0.40%	1.90%
Cyberlindnera mrakii	NRRL Y-1364	GCA 003706445.2	98.80%	98.40%	0.40%	0.00%	1.20%
Cyberlindnera mycetangii	NRRL Y-6843	GCA 003708295.2	99.20%	98.90%	0.30%	0.10%	0.70%

Table S1. List of yeast strains and genomes used in this study (Continue)

Taxa	Strain	Assembly	Complete BUSCOs (C)	Complete and single-copy BUSCOs (S)	Complete and duplicated BUSCOs (D)	Fragmented BUSCOs (F)	Missing BUSCOs (M)
Cyberlindnera nakhonratchasimensis	JCM 12474	GCA 030572335.1	98.80%	98.50%	0.30%	0.00%	1.20%
Cyberlindnera petersonii	NRRL YB-3808	GCA 003706915.2	98.60%	98.30%	0.30%	0.70%	0.70%
Cyberlindnera rhodanensis	NRRL Y-7854	GCA 030569395.1	98.10%	97.80%	0.30%	0.70%	1.20%
Cyberlindnera samutprakarnensis	CBS 12528	GCA 030569715.1	98.10%	97.80%	0.30%	0.30%	1.60%
Cyberlindnera sargentensis	SHA 17.2	GCA 020995425.1	97.90%	97.60%	0.30%	0.30%	1.80%
Cyberlindnera saturnus	NRRL Y-17396	GCA 003709245.2	98.30%	95.00%	3.30%	0.40%	1.30%
Cyberlindnera sp.	NRRL Y-7615	GCA 030557335.1	98.90%	98.80%	0.10%	0.10%	1.00%
Cyberlindnera sp.	NRRL Y-27103	GCA 030567185.1	98.00%	97.60%	0.40%	0.40%	1.60%
Cyberlindnera sp.	NRRL Y-27267	GCA 030572555.1	97.40%	97.10%	0.30%	0.40%	2.20%
Cyberlindnera suaveolens	NRRL Y-17391	GCA 003708225.2	98.50%	98.40%	0.10%	0.40%	1.10%
Cyberlindnera subsufficiens	NG8.2	GCA 017948575.1	98.40%	98.30%	0.10%	0.40%	1.20%
Cyberlindnera veronae	NRRL Y-7818	GCA 030563065.1	98.30%	98.20%	0.10%	0.40%	1.30%
Cyberlindnera xishuangbannaensis	CBS 14692	GCA 030585085.1	98.50%	98.20%	0.30%	0.40%	1.10%
Cyberlindnera xylosilytica	NRRL YB-2097	GCA 003708285.1	98.90%	94.90%	4.00%	0.10%	1.00%

Table S1. List of yeast strains and genomes used in this study (Continue)

Taxa	Strain	Assembly	Complete BUSCOs (C)	Complete and single-copy BUSCOs (S)	Complete and duplicated BUSCOs (D)	Fragmented BUSCOs (F)	Missing BUSCOs (M)
Millerago phaffii	UFMG-CM-Y7052	GCA 040802125.1	87.80%	87.70%	0.10%	2.40%	9.80%
Phaffomyces antillensis	NRRL Y-12881	GCA 003707195.1	94.70%	94.60%	0.10%	0.70%	4.60%
Phaffomyces opuntiae	NRRL Y-11707	GCA 003707165.1	93.80%	93.40%	0.40%	1.10%	5.10%
Phaffomyces thermotolerans	NRRL Y-11709	GCA 003707215.1	95.10%	95.00%	0.10%	0.70%	4.20%
Starmera amethionina	NRRL Y-10978	GCA 003708085.1	89.00%	88.50%	0.50%	1.50%	9.50%
Starmera caribaea	NRRL Y-17468	GCA 030565045.1	91.70%	89.30%	2.40%	1.50%	6.80%
Starmera dryadoides	NRRL Y-10990	GCA 030579655.1	98.00%	97.60%	0.40%	0.50%	1.50%
Starmera pachycereana	NRRL Y-10981	GCA 030570535.1	89.40%	89.10%	0.30%	1.60%	9.00%
Starmera quercuum	NRRL YB-4281	GCA 003705275.1	97.70%	96.00%	1.70%	0.70%	1.60%
Starmera sp.	NRRL Y-17713	GCA 030570575.1	95.50%	95.40%	0.10%	0.70%	3.80%
Starmera stellimalicola	NRRL Y-17912	GCA 003707265.1	95.50%	95.40%	0.10%	0.50%	4.00%
Wickerhamomyces alni	NRRL Y-11625	GCA 003707985.2	97.90%	97.50%	0.40%	0.40%	1.70%
Wickerhamomyces anomalus	NRRL Y-366-8	GCA 001661255.1	96.20%	94.90%	1.30%	1.70%	2.10%
Wickerhamomyces bisporus	VH7 F	GCA 024271855.1	97.50%	97.20%	0.30%	0.70%	1.80%

Table S1. List of yeast strains and genomes used in this study (Continue)

Taxa	Strain	Assembly	Complete BUSCOs (C)	Complete and single-copy BUSCOs (S)	Complete and duplicated BUSCOs (D)	Fragmented BUSCOs (F)	Missing BUSCOs (M)
Wickerhamomyces bovis	NRRL YB-4184	GCA 003707945.2	98.10%	97.60%	0.50%	0.30%	1.60%
Wickerhamomyces canadensis	NRRL Y-1888	GCA 003707015.2	97.90%	97.50%	0.40%	0.50%	1.60%
Wickerhamomyces chambardii	NRRL Y-2378	GCA 030574595.1	91.70%	84.00%	7.70%	4.00%	4.30%
Wickerhamomyces chaumierensis	CBS 8565	GCA 030566875.1	93.00%	92.70%	0.30%	0.70%	6.30%
Wickerhamomyces ciferrii	NRRL Y-1031	GCA 000313485.1	96.70%	96.70%	0.00%	0.80%	2.50%
Wickerhamomyces hampshirensis	NRRL YB-4128	GCA 003706765.2	98.40%	98.30%	0.10%	0.50%	1.10%
Wickerhamomyces kurtzmanii	CBS 15418	GCA 030572875.1	95.40%	95.00%	0.40%	2.60%	2.00%
Wickerhamomyces lynferdii	NRRL Y-7723	GCA 030582155.1	97.10%	4.50%	92.60%	1.20%	1.70%
Wickerhamomyces mucosus	CBS 6341	GCA 020536175.1	95.80%	95.50%	0.30%	0.50%	3.70%
Wickerhamomyces onychis	NRRL Y-7123	GCA 030582435.1	96.90%	96.60%	0.30%	1.50%	1.60%
Wickerhamomyces pijperi	CBS 2887	GCA 020536225.1	92.20%	92.10%	0.10%	0.90%	6.90%
Wickerhamomyces queroliae	NRRL Y-48478	GCA 030674255.1	98.40%	98.00%	0.40%	0.40%	1.20%
Wickerhamomyces rabaulensis	NRRL Y-7945	GCA 030574855.1	97.80%	97.50%	0.30%	0.70%	1.50%
Wickerhamomyces silvicola	NRRL Y-1678	GCA 030570795.1	91.50%	91.40%	0.10%	2.40%	6.10%

Table S1. List of yeast strains and genomes used in this study (Continue)

Taxa	Strain	Assembly	Complete BUSCOs (C)	Complete and single-copy BUSCOs (S)	Complete and duplicated BUSCOs (D)	Fragmented BUSCOs (F)	Missing BUSCOs (M)
Wickerhamomyces sp.	yHMH451	GCA 030571095.1	98.70%	98.40%	0.30%	0.50%	0.80%
Wickerhamomyces sp.	yHQL14	GCA 030561705.1	93.10%	47.80%	45.30%	1.30%	5.60%
Wickerhamomyces sp.	NRRL Y-7574	GCA 030580075.1	97.90%	97.80%	0.10%	0.40%	1.70%
Wickerhamomyces sp.	NRRL YB-2243	GCA 003706815.2	97.80%	97.40%	0.40%	0.40%	1.80%
Wickerhamomyces sp.	NRRL YB-3031	GCA 030564165.1	98.00%	97.50%	0.50%	0.30%	1.70%
Wickerhamomyces sp.	yHMH26	GCA 030571235.1	96.90%	96.60%	0.30%	0.30%	2.80%
Wickerhamomyces sp.	yHMH617	GCA 030571115.1	98.30%	97.90%	0.40%	0.10%	1.60%
Wickerhamomyces sp.	NRRL Y-17067	GCA 030581995.1	97.80%	97.40%	0.40%	0.40%	1.80%
Wickerhamomyces sp.	NRRL Y-48258	GCA 030557145.1	93.00%	91.20%	1.80%	0.70%	6.30%
Wickerhamomyces strasburgensis	NRRL Y-2383	GCA 030574715.1	96.10%	94.50%	1.60%	0.80%	3.10%
Wickerhamomyces subpelliculosus	NRRL Y-1683	GCA 030582255.1	97.20%	97.10%	0.10%	1.30%	1.50%
Wickerhamomyces sydowiorum	NRRL Y-7130	GCA 030574735.1	95.60%	95.50%	0.10%	2.90%	1.50%
Wickerhamomyces tratensis	CBS 12176	GCA 030564005.1	92.70%	92.60%	0.10%	2.20%	5.10%
Wickerhamomyces xylosica	NBRC 108869	GCA 030581495.1	94.50%	94.10%	0.40%	0.30%	5.20%

Table S1. List of yeast strains and genomes used in this study (Continue)

Taxa	Strain	Assembly	Complete BUSCOs (C)	Complete and single-copy BUSCOs (S)	Complete and duplicated BUSCOs (D)	Fragmented BUSCOs (F)	Missing BUSCOs (M)
Trigonopsidomycetes							
Tortispora ganteri	NRRL Y-17035	GCA 003707115.1	92.50%	92.00%	0.50%	1.80%	5.70%
Trigonopsis variabilis	NRRL Y-1579	GCA 003707065.2	97.50%	97.40%	0.10%	0.40%	2.10%

Table S2. List of yeasts and GenBank numbers used for the rDNA phylogenetic analysis

Taxa	Basionym or important synonym	Strain (T=type)	D1/D2	ITS
Dipodascomycetes				
Dipodascales				
Dipodascaceae				
Middelhovenomyces				
M. petrohuensis		NRRL Y-17663^T = CBS 8173	JQ689061	KY104263
M. tepae		NRRL Y-17670^T = CBS 5115	JQ689063	KY104265
Trichomonascaceae				
Blastobotrys				
B. adeninivorans		NRRL Y-17692^T = CBS 8244	NG_055336	NR_165943
B. allociferrii		IFO 10194^T = CBS 5166	NG_055298	KY101922
B. americana		NRRL Y-6844^T = CBS 10337	NG_055338	NR_153635
B. arbuscula		NRRL Y-17585^T = CBS 227.83	U40108	OL772655
B. aristatus		NRRL Y-17579^T = CBS 521.75	U40109	OP221981
B. attinorum		CBS 9734^T	NG_058625	NR_153636
B. baotianmanensis		CBS16024^T = NYNU 1581	KU128725	KU128710
B. bombycis		CBS 15274^T = PYCC 8105 = MCC 1427	MG018987	MG018986
B. buckinghamii		CBS 13900^T = NRRL Y-63727	OL772654	OL772658
B. capitulata		NRRL Y-17573^T = CBS 287.82	U40104	OL772659
B. chiropterorum		NRRL Y-17071^T = CBS 6064	NG_055412	NR_153637
B. davincii		CBS 16861^T	MW367634	MW367648
B. elegans		NRRL Y-17572^T = CBS 530.83	U40095	OL772660
B. farinosus		CBS 140.71^T	U40132	OL772661
B. illinoisensis		NRRL Y-1343^T = CBS 10339	NG_042438	NR_165957
B. indianensis		NRRL YB-1950^T = CBS 9600	NG_055333	KY101752
B. malaysiensis		NRRL Y-6417^T = CBS 10336	NG_042437	NR_165958
B. meliponae		URM7224^T = CBS 14100	NG_055399	KT448721
B. mokoenaii		NRRL Y-27120^T = CBS 8435	NG_055335	NR_073348
B. mucifera		CBS 7409^T	KY106587	KY102217
B. muscicola		NRRL Y-7993^T = CBS 10338	NG_055329	KY101755

Table S2. List of yeasts and GenBank numbers used for the rDNA phylogenetic analysis (Continue)

Taxa	Basionym or important synonym	Strain (T=type)	D1/D2	ITS
B. niveus		NRRL Y-17581^{T} = CBS 163.67	U40110	NR_077180
B. parvus	*Sympodiomyces parvus*	NRRL Y-10004^{T} = CBS 6147	NG_055334	NR_153639
B. peoriensis		NRRL YB-2290^{T} = CBS 10340	NG_055339	NR_153640
B. persicus		IBRC-M 30238^{T} = CBS 14259	KU659141	OL772663
B. proliferans		NRRL Y-17577^{T} = CBS 522.75	U40098	NR_077193
B. raffinosifermentans		NRRL Y-27150^{T} = CBS 6800	NG_055337	NR_165959
B. robertii		NRRL Y-27775^{T} = CBS 10106	NG_055356	KY101760
B. terrestris	*Arxula terrestris*	NRRL Y-17704^{T} = JCM 16832 = CBS 278.86	U40103	AB565767
B. serpentis		NRRL Y-48249^{T} = CBS 10541	AM410667	AM410670
B. xishuangbannaensis		CBS 16044^{T} = NYNU 181024	MK682809	MK682811
Uncultured *Stephanoascus* clone		F9-K27	\	KC535144
Uncultured *Stephanoascus* clone		CI-K20	\	KP828159
***Casaregolazyma* gen. nov.** (*Candida lundiana* clade)				
C. lundiana comb. nov.	*Candida lundiana*	JCM 16823^{T} = CBS 12271	AB565752	NR_137645
C. patagonica sp. nov.	*Candida patagonica*	CECT 12029^{T} = CBS 10443	DQ841165	NR_159550
C. suthepensis comb. nov.	*Candida suthepensis*	CBS 12270^{T} = JCM 16822	AB565751	\
Crinitomyces				
C. flavificans		CBS 760.79^{T}	OK298462	NR_182465
C. ghanaensis		NRRL YB-1486^{T} = CBS 8798	KY106464	KY102101
C. reliqui		DMKU FW23-23^{T}	NG_153944	NR_182708
***Daia gen. nov.* (*Zygoascus tannicola clade*)**				
D. ofunaensis comb. nov.	*Zygoascus ofunaensis*	NRRL Y-10998^{T}	U45829	genome
D. tannicola comb. nov.	*Zygoascus tannicola*	CBS 6065^{T}	U45803	KY106018
Deakozyma gen. nov.				
D. indianensis sp. nov.	*Deakozyma indianensis*	NRRL YB-1937^{T} = CBS 12903	NG_064315	KJ476205
D. yunnanensis sp. nov.	*Deakozyma yunnanensis*	NYNU 16742^{T} = CICC 33160 = CBS 14688	KY284160	KY284161
Diddensiella				
D. caesifluorescens		NCAIM Y.01949^{T} = CBS 12613 = NRRL Y-48781	GU195654	JF895509
D. luoyangensis		NYNU 201062^{T}	MW374264	MW374289
D. parasantjacobensis		NCAIM Y.02121 = CBS 17819	KJ186105	MZ331535

Table S2. List of yeasts and GenBank numbers used for the rDNA phylogenetic analysis (Continue)

Taxa	Basionym or important synonym	Strain (T=type)	D1/D2	ITS
D. santjacobensis		NRRL Y-17667^{T} = CBS 8183	JQ689062	NR_151808
D. transvaalensis		NRRL Y-27140^{T}	DQ442702	OP689516
Entelexis (*Starmerella* clade 1)				
E. apis comb. nov.	*Starmerella apis*	CBS 2674^{T} = JCM 8256 = NRRL Y-2482	NG_060800	OW987779
E. geochares comb. nov.	*Starmerella geochares*	CBS 6870^{T} = NRRL Y-17073	KY106462	KY102099
E. gropengiesseri comb. nov.	*Starmerella gropengiesseri*	NRRL Y-17142^{T} = JCM 8255 = CBS 156	U45721	KY106485
E. litoralis comb. nov.	*Starmerella litoralis*	UFMG-CM-Y603^{T} = CBS 14104	KU724083	MG272263
E. paramagnoliae comb. nov.	*Starmerella magnoliae*	PYCC 2903^{T} = CBS 166^{T}	NG_060814	KF181964
E. magnoliae		CBS 2798^{T}	AY521568	\
E. potacharoeniae comb. nov.	*Starmerella potacharoeniae*	CBS 11674^{T} = NBRC 106439	AB537430	\
E. sorbosivorans comb. nov.	*Starmerella sorbosivorans*	CBS 8768^{T}	NG_060827	KJ630500
E. spenceri comb. nov.	*Candida spenceri*	CBS 11673^{T} =NBRC 106445	AB537437	MW544063
E. stigmatis sp. nov.	*Starmerella stigmatis*	CBS 11464^{T}	KY106782	GQ184143
E. syriaca sp. nov.	*Starmerella syriaca*	CBS 13909^{T}	JX515986	JX515987
E. tilneyi sp. nov.	*Starmerella tilneyi*	CBS 8794^{T}	KY106810	KJ630493
E. vaccinii comb. nov.	*Starmerella vaccinii*	CBS 7318^{T} = JCM 9446 = NRRL Y-17684	KY106857	KJ630498
E. xylocopis comb. nov.	*Starmerella xylocopis*	CBS 5659^{T}	AY521569	KF181968
Starmerella sp.		D91W	JQ026356	\
Starmerella sp.		CBS 6425	KF501396	\
Starmerella sp.		UASWS2977 SBI-E01	ON454162	\
Starmerella sp.		D91WR	KF850165	\
Starmerella sp.		11-1755	MW899350	\
Grinbergsozyma gen. nov. (single-species lineage *Candida bentonensis*)				
G. bentonensis comb. nov.	*Candida bentonensis*	CBS 9994^{T} = NRRL YB-2364	NG_058978	KY101956
G. bentonensis		Y1M	MG478466	\
G. bentonensis		MEA1981	MT123750	\
G. bentonensis		AUMC10764	\	KY495732
Candida sp.		UWO(PS)00-168.1	AF530620	\
Candida sp.		UFMG-CM-Y6917	OM321692	\
Candida sp.		UFMG-CM-Y2876	MG694211	\

Table S2. List of yeasts and GenBank numbers used for the rDNA phylogenetic analysis (Continue)

Taxa	Basionym or important synonym	Strain (T=type)	D1/D2	ITS
Candida sp.		UWO(PS)91-151	AF530617	\
Groenewaldozyma				
G. auringiensis	*Candida auringiensis*	NRRL Y-17674^T = CBS 6913	DQ438225	KY103491
G. salmanticensis	*Torulopsis salmanticensis*	CBS 5121^T = NRRL Y-17090	KY107773	NR_111299
G. tartarivorans	*Candida tartarivorans*	CBS 7955^T = NRRL Y-27291	KY107774	KY103493
Limtongella gen. nov.				
L. siamensis sp. nov.	*Limtongella siamensis*	DMKU-JMGT1-45^T = CBS 11022	NG_075300	\
L. incommunis comb. nov.	*Candida incommunis*	NRRL Y-17085^T = CBS 5604 = MUCL29843	U62303	NR_077184
Candida cf. incommunis		UWO(PS)01-669.2	AF530616	\
Candida sp.		YWW5-1	LC387304	\
Candida sp.		DMKU-FW29-11	OL679539	\
Spencermartinsiella				
S. cellulosicola	*Candida cellulosicola*	CBS 11952^T	NG_055207	NR_151783
S. europaea		NRRL Y-48265^T = CBS 11730	NG_042528	KY105460
S. henanensis		NYUN 211162^T	OM017166	OM017167
S. japonica		JCM 35526^T	LC709264	LC709262
S. ligniputridi		CBS 12585^T	KY109692	KY105462
S. nicolii		CBS 14238^T	KT377038	KT377038
S. silvicola		UFMG-CM-Y274^T = CBS 13490	KC906243	KT222943
Spencermartinsiella sp.		W379	JN544060	JN581122
Candida sp.		NCAIM Y.01957	GU195663	KT222945
Candida sp.		NCAIM Y.01937	GQ340914	KT222944
Candida sp.		GY44S02	FJ527143	FJ873418
Candida sp.		GYA1S04	FJ527142	FJ873417
Starmerella sensu stricto				
S. batistae		CBS 8550^T	NG_060801	NR_155813
S. bombicola		NRRL Y-17069^T = CBS 6009 = JCM 9596	JQ689065	KY105542
S. caucasica		CBS 12650^T	NG_058407	NR_155849
S. floricola		CBS 7289^T = NRRL Y-17676	KY106448	NR_155819
S. ilheusensis		UFMG-CM-Y596^T = CBS 14131	KR232374	KR232375

Table S2. List of yeasts and GenBank numbers used for the rDNA phylogenetic analysis (Continue)

Taxa	Basionym or important synonym	Strain (T=type)	D1/D2	ITS
S. kuoi		CBS 7267^T = NRRL Y-27208	NG_073590	NR_164377
S. monicapupoae		PYCC 8897^T	MG737688	MW289921
S. orientalis sp. nov.	*Starmerella orientalis*	IBRC-M 30204^T = CBS 14142	KM269180	KM269181
S. powellii sp. nov.	*Starmerella powellii*	CBS 8795^T	KY106697	KY102339
S. riodocensis		CBS 10087^T = NRRL Y-27859	KY106726	NR_137870
Starmerella cf. bombicola		UWOPS 00-227.2	HQ111057	HQ111057
Starmerella cf. bombicola		UWOPS 00-531	HQ111056	HQ111056
Candida cf. floricola		UWO(PS)95-408.3	AF313349	\
Candida cf. powellii		UWO(PS)00-195.2	AF313355	\
***Starmerella apicola* clade**				
S. aceti		CBS 13086^T	KF247224	NR_160317
S. anomalae		NYNU 15745^T = CBS 14178	KU128732	KU128715
S. apicola		NRRL Y-2481^T = JCM 9592=CBS 2868	U45703	KY101940
S. asiatica		NYNU 15782^T = CBS 14173	KU128728	KU128719
S. bombi		NRRL Y-17081^T = CBS 5836	U45706	MW074167
S. cerana		HSB-15^T	OR475317	OR470602
S. gilliamiae		CBS 16166^T	MG737679	MW289920
S. henanensis		NYNU 15766^T = CBS 14172	KU128730	KU128716
S. jinningensis		CBS 11864^T	NG_058408	NR_155850
S. kisarazuensis		NBRC 115909^T	LC775089	LC775092
S. neotropicalis		CBS 12811^T	KC776265	NR_160316
S. opuntiae		UFMG-CM-Y286^T = CBS 13466	MG564473	MG066593
S. reginensis		CLIB 1634^T = CBS 15247	LN870357	LN870338
S. scarabaei		NYNU 15821^T = CBS 14174	KU128729	KU128718
S. vitae		UWOPS 00-107.2^T = CBS 15147	KX418642	KX418642
Starmerella sp.		\	MG980067	MG980067
***Starmerella cellae* clade**				
S. camargoi		UFMG-CM-Y595^T = CBS 14130	KR232373	KU710345
S. cellae		CBS 10086^T = NRRL Y-27860	KY106391	KY102026
S. etchellsii		JCM 8066^T = NRRL Y-17084 = CBS 1750	U45723	KY102077

Table S2. List of yeasts and GenBank numbers used for the rDNA phylogenetic analysis (Continue)

Taxa	Basionym or important synonym	Strain (T=type)	D1/D2	ITS
S. floris		CBS 10593^{T} = NRRL Y-48255	KY106449	NR_155820
S. khaoyaiensis		CBS 10839^{T} = NBRC 104213	NG_060812	NR_155821
S. kourouensis		CLIB 1707^{T}	LN909483	LN909469
S. meliponinorum		UWO(PS)00-227.1^{T} = CBS 9117	AF313354	KY105547
S. ratchasimensis		CBS 10611^{T}	KY106719	KY102359
S. roubikii		UWOPS 01-191^{T} = CBS 15148	AY257050	MF668211
***Starmerella stellata* clade**				
S. bacillaris		PYCC 3044^{T} = CBS 834	KY106894	KY102524
S. bacillaris	*Candida zemplinina*	CBS 9494^{T}	HE657235	\
S. davenportii		CBS 9069^{T}	KY106407	NR_155815
S. lactis-condensi		NRRL Y-1515^{T} = CBS 52^{T} = JCM 9472	U45724	KY102179
S. stellata		CBS 157^{T} = NRRL Y-1446	NG_060828	NR_155771
S. vitis		CBS 16418^{T}	KC992848	MN317383
Starmerella sirachaensis		CBS 12094^{T} = NBRC 108605	KY106758	KY102396
Candida sp.		CBS 4353	AY574387	\
Candida sp.		R-55246	LT631806	\
Candida sp.		AS2.4033	FJ613525	FJ61352
Starmerella sp.		2-1361	JX515983	JX515984
Starmerella sp.		UFMG-CM-Y6313	MG732918	\
Starmerella sp.		ST1-01	AB294245	\
Sugiyamaella				
S. amazoniana		UFMG-CM-Y6922^{T}	MZ254647	MZ261923
S. americana		NRRL YB-2067^{T} = ATCC MYA-4662 = CBS 10352	NG_055322	NR_137759
S. ayubii		UFMG CM-Y607^{T} = CBS 14108	KR184132	NR_155796
S. bahiana		UFMG CM-Y304^{T} = CBS 13474	NG_059957	NR_155810
S. bielyi		UFMG CM-Y607^{T} = CBS 14108	MZ254646	MZ261922
S. bonitensis		UFMG CM-Y304^{T} = CBS 13474	KT006004	NR_155798
S. boreocaroliniensis		NRRL YB-1835^{T} = CBS 10344	KY106370	NR_165963
S. bullrunensis		UFMGCMY6921^{T}	NG_055380	NR_111543

Table S2. List of yeasts and GenBank numbers used for the rDNA phylogenetic analysis (Continue)

Taxa	Basionym or important synonym	Strain (T=type)	D1/D2	ITS
S. carassensis		UFMG CM-Y608^T = CBS 14270	KX550111	NR_155808
S. castrensis		NRRL Y-17329^T = CBS 8172	NG_042425	NR_111229
S. chiloensis		NRRL Y-17646^T = JCM 9583 = CBS 8168	NG_055306	NR_156607
S. chuxiongensis		NYNU 181038^T = CBS 16006 = CICC 33361	MK682795	MK682800
S. cylindrica		NYNU 201067^T	MW368731	MW368732
S. floridensis		NRRL YB-3827^T = CBS 10350	NG_042435	NR_111230
S. grinbergsii		NRRL Y-27117^T = CBS 5924	KY106484	NR_165964
S. japonica		NRRL YB-2798^T = CBS 10354	NG_042432	NR_111239
S. ligni		NRRL YB-1835^T = CBS 10344	KX550112	KX550112
S. lignohabitans		NRRL YB-1473^T = CBS 10342	DQ438198	DQ911444
S. marilandica		NRRL YB-1847^T = CBS 10346	KY106556	NR_165965
S. marionensis		NRRL YB-1336^T = CBS 10341	NG_042427	NR_111237
S. mastotermitis		CBS 14182^T	NG_058230	NR_156606
S. neomexicana		NRRL YB-2450^T = CBS 10349	KY106598	NR_165966
S. novakii		NRRL Y-27346^T = CBS 8402	KY106607	NR_111235
S. paludigena		NRRL Y-12697^T = CBS 8005	NG_042424	NR_111236
S. pinicola		NRRL YB-2263^T	DQ438200	NR_155810
S. qingdaonensis		CBS 11390^T = AS2.4031	FJ613527	KY102352
S. robnettiae		NYNU 201066^T	MW368701	MW368730
S. smithiae		NRRL Y-17850^T = CBS 7522	DQ438218	KY105568
S. trypani		WA 67193^T	MK387312	MK388412
S. valenteae		UFMG CM-Y609^T = CBS 14109	KT005999	NR_155797
S. valdiviana		NRRL Y-7791^T = CBS 5721	KY106859	NR_111544
S. xiaguanensis		NYNU 161041^T = CBS 14696	KY213817	KY213802
S. xylanicola		UFMG-CA-32^T = CBS 12683	JX487183	KC493642
S. xylolytica		UFMG-CM-Y348^T = CBS 13493	KF889433	KU214874
S. yunnanensis		NYNU 161059^T = CBS 14701	MT257257	MT257259
Sugiyamaella sp.		UFMG-CM-Y6964	MZ264216	MZ264217
Sugiyamaella sp.		BG090816.9.10.1A.3.19	JN805467	\
Candida sp.		CBS 10848	EU570112	\

Table S2. List of yeasts and GenBank numbers used for the rDNA phylogenetic analysis (Continue)

Taxa	Basionym or important synonym	Strain (T=type)	D1/D2	ITS
Candida sp.		GA3M12	FJ873524	FJ873593
Candida sp.		SD4S01	EF653948	\
Candida sp.		CBS 10852	EU570106	EU570107
Candida sp.		CBS 10851	EU570114	EU570115
Candida sp.		BG02-3-7-5-1-2	AY390774	\
Candida sp.		GY43S04	FJ527154	FJ873425
Candida sp.		NCAIM Y.01893	GQ258822	\
Tardiomyces gen. nov.				
T. blankii comb. nov.	*Tardiomyces blankii*	NRRL Y-17068^{T} = CBS 1898	NG_055179	NR_111312
T. depauwii sp. nov.	*Tardiomyces depauwii*	CBS 18495^{T}	genome	genome
T. digboiensis comb. nov.	*Tardiomyces digboiensis*	CBS 9800^{T}	KY106417	KY102051
Trichomonascus				
Trichomonascus apis		CBS 10922^{T} = NRRL Y-48475	KY109911	KY105699
Trichomonascus ciferrii	*Stephanoascus ciferrii*	CBS 4856^{T}	KY109914	KY105703
Trichomonascus petasosporus		NRRL YB-2092^{T} = CBS 9602	JQ689064	KY105704
Trichomonascus vanleenenianus		CBS 14902^{T}	MG986492	MG986487
Westerdijkia gen. nov. (single-species lineage *Candida sungouii*)				
W. sungouii sp. nov.	*Candida sungouii*	CBS 13907^{T}	NG_055228	KM384539
Candida sp.		BG02-7-18-018A-2-2	AY520408	\
Zygoascus				
Z. biomembranicola		JCM 31007^{T} = CBS 14158 = CBS 14157	LC060997	NR_156007
Z. bituminiphila		NRRL Y-27974^{T} = CBS 8813	NG_055308	NR_137545
Z. detingensis		NYNU 201087^{T}	MW368733	MW374088
Z. flipseniorum		CBS 14876^{T}	MF695078	MF695077
Z. hellenicus		NRRL Y-7136^{T} = CBS 5839	NG_055323	NR_111258
Z. meyerae		CBS 4099^{T} = NRRL Y-17319	KY110225	KY106013
Z. polysorbophila		NRRL Y-27161^{T}	NG_064312	NR_160311
incertae sedis* in *Dipodascomycetes				
Dengshuqunia gen. nov. (single-species lineage *Candida hispaniensis*)				
D. hispaniensis comb. nov.	*Candida hispaniensis*	CBS 9996^{T} = NRRL Y-5580	KY106499	KY102133

Table S2. List of yeasts and GenBank numbers used for the rDNA phylogenetic analysis (Continue)

Taxa	Basionym or important synonym	Strain (T=type)	D1/D2	ITS
Yarrowia' sp.		VR571	KU570469	\
Yarrowia' sp.		VR572	KU570470	OM837194
Yarrowia' sp.		VR546	KU570466	\
Yarrowia' sp.		VR547	KU570467	\
Nadsonia				
N. commutata		NRRL Y-7950^T = CBS 6640	U73598	NR_154249
N. fulvescens var. elongata		NRRL Y-1568^T = CBS 2594	U94942	KY104309
N. fulvescens var. fulvescens		NRRL Y-12810^T = CBS 2596	JQ689059	KY104312
N. starkeyi-henricii		CBS 2159^T = NRRL YB-3963	NG_055214	KY105364
the single-species lineage *Candida tunisiensis*				
Candida tunisiensis		CBS 12513^T	KY106854	KY102485
Yarrowia				
Y. alimentaria		NRRL Y-48253^T = CBS 10151	NG_058277	NR_151793
Y. brassicae sp. nov.	*Yarrowia brassicae*	NYNU17218^T = CBS 15225	MF136065	MF136067
Y. bubula		NCAIM Y.01998^T = CBS 12934	NG_059943	NR_155999
Y. deformans		CBS 2071^T	KY110177	NR_161005
Y. divulgata sp. nov.	*Yarrowia divulgata*	CBS 11013^T	NG_058444	NR_156000
Y. galli		CBS 9722^T	KY106459	NR_077078
Y. hollandica		CBS 4855^T	NG_058982	NR_151802
Y. keelungensis sp. nov.	*Yarrowia keelungensis*	CBS 11062^T	NG_064314	NR_160312
Y. lipolytica		NRRL YB-423^T = CBS 6124	JQ689067	KY105973
Y. osloensis		CBS 10146^T	NG_058984	NR_151804
Y. parophoni		CBS 12427^T	NG_075176	NR_173711
Y. phangngaensis sp. nov.	*Yarrowia phangngaensis*	CBS 10407^T = ATCC MYA-4467	FJ196734	NR_111357
Y. porcina		NCAIM Y.02100^T = CBS 12935	NG_066361	NR_164526
Y. yakushimensis		CBS 10254^T	AM268474	AM279262
Yarrowia sp.		KBP:Y-7314	OR582607	\
Uncultured *Yarrowia*		clone Nves *B08	KF419465	\
Uncultured *Yarrowia*		clone Name *25	KF419434	\
Uncultured *Yarrowia*		clone Name *40	KF419445	\

Table S2. List of yeasts and GenBank numbers used for the rDNA phylogenetic analysis (Continue)

Taxa	Basionym or important synonym	Strain (T=type)	D1/D2	ITS
Pichiomycetes				
Pichiales				
Cephaloascaceae				
Cephaloascus				
C. albidus		CBS 389.77^{T}	MH872847	MH861079
C. fragrans		CBS 121.29^{T} = NRRL Y-6742	NG_063972	NR_159763
Pichiaceae				
Allodekkera				
A. sacchari		JCM 18455^{T} = CBS 14167	KY432360	NR_153584
Ambrosiozyma				
A. ambrosiae		NRRL Y-7524^{T} = CBS 6003	U73605	NR_153563
A. angophorae		NRRL Y-7118^{T} = CBS 5823	NG_055197	NR_153564
A. cicatricosa		NRRL Y-17594^{T} = CBS 6157	U40128	NR_153565
A. kamigamensis		NRRL Y-63629^{T} = JCM 15019 = CBS 10899	NG_055216	KY101638
A. kashinagacola		NRRL Y-63631^{T} = CBS 10903	KF061197	KY101639
A. llanquihuensis		NRRL Y-17657^{T} = CBS 8128	NG_055194	NR_153567
A. maleeae		NRRL Y-63635^{T} = CBS 11900	KF061198	KY101641
A. monospora		NRRL Y-1484^{T} = CBS 2554	EU011590	NR_153569
A. neoplatypodis		NRRL Y-63630^{T} = CBS 10900	NG_055217	KY101645
A. oregonensis		NRRL Y-6106^{T} = CBS 5560	NG_056814	NR_153571
A. philentoma		NRRL Y-7523^{T} = CBS 6276	NG_055200	NR_153572
A. platypodis		NRRL Y-6732^{T} = CBS 4111	U40083	NR_153573
A. pseudovanderkliftii		NR_R Y-63632^{T} = CBS 10904	NG_055220	NR_153574
A. vanderkliftii		NRRL Y-63633^{T} = CBS 10905	NG_055221	NR_153575
Ambrosiozyma sp.		Lym1-4	LC586258	LC718469
Ambrosiozyma sp.		NRRL Y-6106	EU011596	\
Ambrosiozyma sp.		UWOPS 01-647.2	OQ676562	\
Ambrosiozyma sp.		HD1-5-1	LC718445	LC718458
Ambrosiozyma sp.		Lym1-7	LC586259	LC718470
Candida wuzhishanensis	*Candida wuzhishanensis*	CBS 10850^{T}	EU570110	EU570111

Table S2. List of yeasts and GenBank numbers used for the rDNA phylogenetic analysis (Continue)

Taxa	Basionym or important synonym	Strain (T=type)	D1/D2	ITS
Candida sp.		JW01-7-11-1-4-y2	AY242326	\
Candida sp.		ST-246	DQ404487	\
Candida sp.		JCM 15018	AB291684	\
Candida sp.		JCM 16747	AB552927	\
Brettanomyces				
B. acidodurans		NCAIM Y.02178^T = CBS 14519	NG_055168	KX792141
B. anomalus		NRRL Y-17522^T = CBS 8139	U84244	NR_138183
B. custersianus		NRRL Y-6653^T = CBS 4805	U76199	NR_165960
B. bruxellensis		NRRL Y-12961^T = CBS 74	JQ689028	NR_165974
B. naardenensis		NRRL Y-17526^T = CBS 6042	U76200	NR_165961
B. nana		NRRL Y-17527^T = CBS 1945	U76197	NR_153642
Citeromyces				
C. cibodasensis		NBRC 110244^T = InaCC Y703	LC015650	LC060677
C. hawaiiensi		NRRL Y-11581^T	NG_055053	JN016711
C. matritensis		IFO 0954^T	KY106924	KY102552
C. nyonsensis		CLIB 1303^T	NG_055051	NR_154768
C. siamensis		IFO 11052^T	NG_055012	JN016715
Komagataella				
K. kurtzmanii		VKPM Y-727^T	NG_060295	NR_164523
K. mondaviorum		CBS 15017^T	MF276795	MF276791
K. pastoris		ATCC 28485^T	JQ689069	NR_164380
K. phaffii		NRRL Y-7556^T	EF550256	NR_164378
K. populi		NRRL YB-455^T	JN234404	JQ398744
K. pseudopastoris		NRRL Y-27603^T	EF550255	NR_163279
K. ulmi		CBS 12361^T	JN234403	JQ398746
Kregervanrija				
K. delftensis		NRRL Y-7119^T = CBS 2614	KY108168	KY103893
K. fluxuum		NRRL YB-4273^T = CBS 2287	EF550268	KY103903
K. pseudodelftensis		NRRL Y-5494^T = CBS 10105	KY108177	KY103905
Kuraishia				

Table S2. List of yeasts and GenBank numbers used for the rDNA phylogenetic analysis (Continue)

Taxa	Basionym or important synonym	Strain (T=type)	D1/D2	ITS
K. borneana		CBS 12507^T	JQ001938	JQ038035
K. capsulata		NRRL Y-1842^T = CBS 1993	EF550270	KY103911
K. cidri		NRRL Y-27078^T = CBS 4241	AF245402	KY103912
K. floccosa		NRRL Y-27951^T = CBS 10307	KM065899	KY103913
K. hungarica		NRRL Y-27594^T	NG_055192	EU722410
K. mediterranea		CBS 15107^T	HE799687	HE799687
K. molischiana		NRRL Y-27899^T = CBS 9993	NG_058325	NR_164409
K. ogatae		NRRL Y-48474^T = CBS 10924	KM065903	NR_155244
K. piskuri		NRRL YB-2544^T = CBS 13714	NG_055227	NR_155218
Martiniozyma				
M. abiesophila		NRRL Y-11514^T = CBS 5366	NG_066352	NR_161000
M. asiatica		CBS 10863^T = NRRL Y-63747	NG_055167	NR_154199
Candida sp.		BG02-7-17-007A-1-1	AY520359	\
***Nothofagozyma* gen. nov.** (single-species lineage *Candida chilensis*)				
N. chilensis comb. nov.	*Candida chilensis*	NRRL Y-7790^T = CBS 5719	U45821	KY102029
Candida cf. chilensis		CBS 11766	FN824503	\
Ogataea sensu stricto				
O. allantospora		CBS 10576^T = NRRL Y-48267	KY108668	KY104390
O. angusta		NRRL Y-2214^T = CBS 7073	EF550269	KY104391
O. chonburiensis sp. nov.	*Ogataea chonburiensis*	CBS 10363^T	KY108671	KY104393
O. chumphonensis sp. nov.	*Candida chumphonensis*	CBS 12096^T	NG_060803	NR_155569
O. deakii sp. nov.	*Ogataea deakii*	NCAIM Y.01896^T = CBS 12735	NG_060259	NR_156550
O. dorogensis		NRRL Y-27599^T = CBS 9260	NG_055143	NR_155586
O. haglerorum		VKPM Y-2583^T = CBS 14645	NG_058451	NR_155603
O. histrianica sp. nov.	*Ogataea histrianica*	ZIM2463^T = NRRL Y-63658 = CBS 12779	HE799677	NR_155556
O. kodamae		NRRL Y-17234^T = CBS 7081	KY108676	KY104400
O. kolombanensis sp. nov.	*Ogataea kolombanensis*	NRRL Y-63657^T = ZIM2322 = CBS 12778	NG_055164	NR_155557
O. mangiferae		UFMG-CM-Y253^T = CBS 13492	KF585022	KF585022
O. mattraensis sp. nov.	*Candida mattraensis*	CBS 12097^T	NG_060815	NR_155572
O. minuta		NRRL Y-411^T = CBS 1708	U75515	genome

Table S2. List of yeasts and GenBank numbers used for the rDNA phylogenetic analysis (Continue)

Taxa	Basionym or important synonym	Strain (T=type)	D1/D2	ITS
O. nakhonphanomensis sp. nov.	*Ogataea nakhonphanomensis*	ATCC MYA-4463^T = CBS 10362	NG_042512	NR_111420
O. nonfermentans		NRRL YB-2203^T = CBS 5764	KY108687	KY104413
O. paradorogensis		NBRC100261^T = CBS 10978	NG_055082	NR_137524
O. parapolymorpha		CBS 12304^T = ATCC 26012	NG_058360	NR_165981
O. philodendri		NRRL Y-7210^T = CBS 6075	NG_058361	NR_155594
O. phyllophila sp. nov.	*Ogataea phyllophila*	CBS 12095^T	NG_058362	NR_155595
O. polymorpha		NRRL Y-5445^T = CBS 4732	KY108707	KY104435
O. siamensis sp. nov.	*Ogataea siamensis*	CBS 10095^T	KY108716	NR_111421
O. thermomethanolica sp. nov.	*Ogataea thermomethanolica*	CBS 10098^T = NRRL Y-27981	KY108717	KY104445
O. thermophila sp. nov.	*Candida thermophila*	NRRL Y-27863^T = CBS 11284	DQ402185	KY102443
O. uvarum		CBS 12829^T	KY971684	HE965024
O. xyloterini comb. nov.	*Candida xyloterini*	CBS 11547^T = ATCC 62898	KY106891	KY102251
***Ogataea saltuana* subclade**				
O. corticis		NBRC 1794^T	NG_055087	NR_137525
O. ganodermae sp. nov.	*Ogataea ganodermae*	CBS 10646^T	NG_058359	NR_138174
O. glucozyma		NRRL YB-2185^T = CBS 5766	EU011626	KY104398
O. henricii		NRRL YB-2194^T = CBS 5765	KY108675	KY104399
O. krabiensis sp. nov.	*Candida krabiensis*	CBS 10097^T = NRRL Y-27965	KY106540	KY102173
O. nemodendra comb. nov.	*Candida nemodendra*	NRRL Y-7779^T = CBS 6280	U70246	KY102228
O. neopini		ATCC 28781^T = CBS 5435	NG_055085	NR_137643
O. ortonii sp. nov.	*Candida ortonii*	CBS 8843^T = NRRL Y-48038	KY106637	KY102275
O. pini		NRRL Y-11528^T = JCM 3655 = CBS 744	KY108701	KY104429
O. saltuana		NCAIM Y.01833^T = CBS10795 = NRRL Y-48448	NG_055162	NR_137064
O. zsoltii		NRRL Y-27601^T =CBS 9262	KY108723	NR_138176
Ogataea sp.		NRRL YB-2437	genome	genome
***Ogataea pilisensis* subclade**				
O. arabinofermentans comb. nov.	*Candida arabinofermentans*	NRRL YB-2248^T = CBS 8468	NG_055150	NR_155568
O. cecidiorum		CBS 11522^T	NG_058358	NR_155585
O. degrootiae		CBS 15033^T	NG_068257	NR_168172
O. methanolica		NRRL Y-7685^T = CBS 6515 = JCM 10240	JQ689008	KY104403

Table S2. List of yeasts and GenBank numbers used for the rDNA phylogenetic analysis (Continue)

Taxa	Basionym or important synonym	Strain (T=type)	D1/D2	ITS
O. nitratoaversa		NRRL Y-48449^T = CBS 10796	KY108686	KY104412
O. ovalis comb. nov.	*Candida ovalis*	NRRL Y-17662^T = CBS 7298	U70248	KY102280
O. paraovalis		NYNU167106^T = CBS 14697	KY213806	KY213805
O. piceae comb. nov.	*Candida piceae*	NRRL YB-2107^T = CBS 8701	KY106691	KY102332
O. pignaliae		NRRL Y-17664^T = JCM 9836 = CBS 6071	KY108695	KY104422
O. pilisensis		NRRL Y-27598^T = CBS 9259	KY108696	KY104423
O. pinus comb. nov.	*Candida pinus*	NRRL Y-2023^T = JCM 9826 = CBS 970	NG_055153	KY102335
O. rishirensis comb. nov.	*Candida rishirensis*	CBS 11662^T	KY106727	KY102366
O. salicorniae		NRRL Y-12834^T = CBS 8071	KY108715	KY104443
O. sithepensis sp. nov.	*Candida sithepensis*	CBS 10096^T = JCM 12265	KY106759	KY102397
O. sonorensis comb. nov.	*Candida sonorensis*	NRRL Y-7800^T = CBS 6792	U70185	KY102404
O. trehalophila		NRRL Y-6781^T = CBS 5361	KY108719	KY104447
***Ogataea wickerhamii* subclade**				
O. kanchanaburiensis sp. nov.	*Ogataea kanchanaburiensis*	CBS 12673^T	AB734090	NR_138178
O. maris comb. nov.	*Candida maris*	NRRL Y-6696^T = CBS 5151	U70181	KY102191
O. populialbae		CBS 11363^T = NRRL Y-48632	NG_058363	NR_155597
O. trehaloabstinens		NRRL Y-27595^T = CBS 9256	KY108718	genome
O. wickerhamii		NRRL YB-4943^T = CBS 4307	KY108721	KY104449
Ogataea sp.		NRRL YB-2442	genome	genome
Pichia				
P. awuae sp. nov.	*Candida awuae*	CBS 11011^T	KY106314	NR_151796
P. barkeri		NRRL Y-17350^T = CBS 7256	U75735	NR_153283
P. bovicola		DMKU-MP6-4^T = TBRC 15616	MZ322503	MZ841616
P. bruneiensis sp. nov.	*Pichia bruneiensis*	CBS 12611^T	JQ692181	JX112045
P. cactophila		NRRL Y-10963^T = CBS 6926	U75731	KY104514
P. californica		CBS 989^T	KY106378	KY102011
P. cecembensis		NRRL Y-27985^T = CBS 10445	KY108786	NR_164078
P. cephalocereana		NRRL Y-17225^T = CBS 7273	U75737	NR_153285
P. chibodasensis sp. nov.	*Pichia chibodasensis*	NBRC 111569^T	NG_055170	NR_153305
P. deserticola		NRRL Y-12918^T = CBS 7119	U75734	NR_077085

Table S2. List of yeasts and GenBank numbers used for the rDNA phylogenetic analysis (Continue)

Taxa	Basionym or important synonym	Strain (T=type)	D1/D2	ITS
P. dushanensis sp. nov.	*Pichia dushanensis*	CBS 13912^T	NG_064367	NR_160321
P. eremophila		NRRL Y-17224^T = CBS 7272	NG_055120	NR_153287
P. ethanolica		NRRL Y-12615^T = CBS 8041	U71073	KY102081
P. exigua		NRRL Y-10920^T = CBS 6836	KY108791	KY104525
P. fermentans		NRRL Y-1619^T = CBS 187	U75726	KY104545
P. galeolata		NRRL Y-64187^T = CBS 16864	OL583873	OL583853
P. garciniae		CBS 10758^T	NG_058374	NR_153289
P. gijzeniarum		CBS 15024^T	NG_068258	NR_168173
P. heedii		NRRL Y-10967^T = CBS 6930	U75733	KY104553
P. inconspicua		NRRL Y-2029^T = CBS 180	U71062	KY102148
P. insulana sp. nov.	*Pichia insulana*	CBS 11169^T	NG_055166	KM252834
P. kluyveri		NRRL Y-11519^T = CBS 188	U75727	NR_138210
P. kurtzmaniana		CGMCC 2.7213^T	OR258060	OR258060
P. kudriavzevii		NRRL Y-7551^T = CBS 5147	KY108833	KY104577
P. mandshurica		CBS 209^T	KY108860	KY104597
P. membranifaciens		NRRL Y-2026^T = CBS 107	EF550227	NR_111195
P. nakasei		NRRL Y-7686^T = CBS 5141	U75728	KY104634
P. nanzhaoensis		NYNU178136^T = CBS 15346	MG255700	MG255719
P. norvegensis		NRRL Y-7687^T = CBS 6564	U75730	KY104635
P. occidentalis		NRRL Y-7552^T = CBS 5459	NG_055110	genome
P. paraexigua		NYNU178135^T = CBS 15237	MG255712	MG255726
P. phayaonensis sp.nov.	*Pichia phayaonensis*	NBRC 108868^T	AB557865	AB704714
P. pseudocactophila		NRRL Y-17239^T = CBS 6929	U75732	genome
P. pseudolambica		NRRL Y-17318^T = CBS 2063	U71063	KY102346
P. rugopelliculosa		NRRL Y-17079^T = CBS 6377	U71069	KY102367
P. scutulata		NRRL Y-7663^T = CBS 6670	KY108916	KY104645
P. sporocuriosa		NRRL Y-27347^T = CBS 8806	NG_055107	KY104647
P. thaimueangensis		NRRL Y-27416^T = CBS 10360	KY106806	KY102439
***Pichia terricola* clade**				
P. cabralensis		CBS 11679^T	NG_055163	NR_153279

Table S2. List of yeasts and GenBank numbers used for the rDNA phylogenetic analysis (Continue)

Taxa	Basionym or important synonym	Strain (T=type)	D1/D2	ITS
P. terricola		NRRL YB-4310^{T} = CBS 2617	KY108920	NR_153295
P. sorboxylosa comb. nov.	*Candida sorboxylosa*	NRRL Y-17669^{T} = CBS 6378	EF550253	genome
Ramirezia gen. nov.				
R. boidinii comb. nov.	*Candida boidinii*	NRRL Y-2332^{T} = CBS 2428	JQ689009	NR_164406
Candida boidinii		ATCC 62809	\	FJ914929
Candida boidinii		392a	\	PQ865360
Candida boidinii		392b	\	PQ865361
Candida boidinii		392e	\	PQ865362
Candida boidinii		3Y79	\	MT131300
Candida boidinii		4035	\	KJ794107
Candida boidinii		ATCC MYA-4485	\	FJ196791
Candida boidinii		AUMC10756	\	KY445950
Candida boidinii		B4M1030AL6F	\	PV240593
Candida boidinii		B4S1030BL4F	\	PV240610
Candida boidinii		B4S1030CL3F	\	PV240617
Candida boidinii		CB15	\	KP281424
Candida boidinii		CB3	\	KP281427
Candida boidinii		CB6	\	KP281426
Candida boidinii		CBS 2429	\	KY101976
Candida boidinii		CBS 3092	\	KY101986
Candida boidinii		CBS 5777	\	KY101983
Candida boidinii		CBS 6056	\	KY101981
Candida boidinii		CBS 6202	\	KY101993
Candida boidinii		CBS 6368	\	KY101988
Candida boidinii		CBS 6510	\	KY101973
Candida boidinii		CBS 6774	\	KY101980
Candida boidinii		CBS 6990	\	KY101987
Candida boidinii		CBS 7063	\	KY101977
Candida boidinii		CBS 7299	\	KY101991
Candida boidinii		CBS 7447	\	KY101989

Table S2. List of yeasts and GenBank numbers used for the rDNA phylogenetic analysis (Continue)

Taxa	Basionym or important synonym	Strain (T=type)	D1/D2	ITS
Candida boidinii		CBS 7778	\	KY101975
Candida boidinii		CBS 8030	\	KY101995
Candida boidinii		CBS 8051	\	KY101978
Candida boidinii		CBS 8052	\	KY101974
Candida boidinii		CBS 8106	\	KY101985
Candida boidinii		CBS 8251	\	KY101979
Candida boidinii		CBS 8567	\	KY101984
Candida boidinii		CBS 8568	\	KY101992
Candida boidinii		CBS 8569	\	KY101994
Candida boidinii		cl/MP/12	\	PV670455
Candida boidinii		cl/MP/2K	\	PV670452
Candida boidinii		cl/MP/3M	\	PV670453
Candida boidinii		cl/MP/6K	\	PV670454
Candida boidinii		clone ADR12	\	PV590121
Candida boidinii		CM65	\	MG817595
Candida boidinii		CM67	\	MG817594
Candida boidinii		DBMY178	\	KJ706396
Candida boidinii		DBMY338	\	KJ706555
Candida boidinii		DBMY497	\	KJ706714
Candida boidinii		DBMY656	\	KJ706873
Candida boidinii		DF130	\	MW895348
Candida boidinii		DF139B	\	MW895349
Candida boidinii		DF149	\	MW895351
Candida boidinii		EJ28	\	MW895259
Candida boidinii		fo/BM/03	\	PV686764
Candida boidinii		fo/MP/01	\	PV686765
Candida boidinii		fo/MP/03	\	PV686766
Candida boidinii		G1AL001	\	ON077142
Candida boidinii		IST 473	\	OQ092419
Candida boidinii		IST 509	\	OQ092420

Table S2. List of yeasts and GenBank numbers used for the rDNA phylogenetic analysis (Continue)

Taxa	Basionym or important synonym	Strain (T=type)	D1/D2	ITS
Candida boidinii		IST 592	\	OQ092421
Candida boidinii		IST 599	\	OQ092422
Candida boidinii		IST 600	\	OQ092423
Candida boidinii		IST 605	\	OQ092424
Candida boidinii		J4 e	\	PV471499
Candida boidinii		K65	\	MT889808
Candida boidinii		KL-1	\	KF699345
Candida boidinii		KLG-036	\	PQ055828
Candida boidinii		L21	\	ON038416
Candida boidinii		LL11 101	\	KF057593
Candida boidinii		LL11 121	\	KF057615
Candida boidinii		LL11 142	\	KF057723
Candida boidinii		LR20	\	ON716452
Candida boidinii		MV44	\	MW895261
Candida boidinii		NTOU 4959	\	MZ422941
Candida boidinii		P35-1B	\	MW895883
Candida boidinii		PH13	\	MW895262
Candida boidinii		PH29	\	MW895263
Candida boidinii		PMM10-1634L	\	KP132263
Candida boidinii		PYCC 4993	\	OL415600
Candida boidinii		S60 ITI	\	MT875270
Candida boidinii		ST18	\	MW895265
Candida boidinii		ST6	\	MW895260
Candida boidinii		UCDFST 09-399	\	MH595392
Candida boidinii		UCDFST 11-630	\	MH595368
Candida boidinii		UCDFST 70-104	\	MH595275
Candida boidinii		UCDFST 78-95	\	MH595233
Candida boidinii		WC91-1	\	EF197945
Candida boidinii		yHKS467	\	KM384039
Candida boidinii		yHRVM68	\	OK052465

Table S2. List of yeasts and GenBank numbers used for the rDNA phylogenetic analysis (Continue)

Taxa	Basionym or important synonym	Strain (T=type)	D1/D2	ITS
Candida sp.		MYf128	\	KX079903
Candida sp.		MYf155	\	KX079901
Candida sp.		MYf157	\	KX079899
Fungal *sp.*		MNFU072	\	OQ331085
Fungal *sp.*		MNFU073	\	OQ331084
Saccharomycetales sp.		LM233	\	EF060568
Saccharomycetales sp.		LM580	\	EF060866
Saccharomycetales sp.		LM621	\	EF060905
Saccharomycetales sp.		LM641	\	EF060925
Saturnispora				
S. ahearnii		NRRL Y-7555^T = CBS 6121	U94935	NR_155830
S. besseyi		NRRL YB-4711^T = CBS 6343	KY109540	NR_155831
S. bothae		CBS 13484^T	NG_064347	NR_160328
S. diversa		NRRL Y-5713^T = JCM 1848 = CBS 4074	KY109545	NR_119732
S. dispora		NRRL Y-1447^T = CBS 794	JQ689027	NR_155832
S. galanensis		NYNU 1797^T = CBS 15223	MG255699	MG255730
S. gosingensis		NRRL Y-48718^T = CBS 11755	GU952248	NR_155833
S. hagleri		NRRL Y-27828^T	NG_058400	KY105319
S. halmiae		CBS 11009^T	DQ466525	genome
S. kantuleensis		DMKU PPS4-5^T = CBS 15217	NG_064447	NR_164565
S. mangrovi		CBS 15874^T	MH559121	MH559120
S. mendoncae		NRRL Y-11515^T = CBS 5620	KY109547	NR_155834
S. quitensis		NCYC3744^T = CBS 12184	FN908197	FN985101
S. saitoi		NRRL Y-6671^T = CBS 4910	U94932	NR_155835
S. sanitii		CBS 10864^T	NG_055080	NR_155836
S. sekii		CBS 10931^T	NG_055094	NR_164410
S. serradocipensis		UFMG DC-198^T	GU952247	NR_155777
S. siamensis		CBS 11022^T = NBRC 104878	NG_055084	\
S. silvae		NRRL Y-6725^T = CBS 5498	KY109554	NR_155837
S. suwanaritii		CBS 11021^T	NG_055083	\

Table S2. List of yeasts and GenBank numbers used for the rDNA phylogenetic analysis (Continue)

Taxa	Basionym or important synonym	Strain (T=type)	D1/D2	ITS
S. zaruensis		NRRL Y-7008^T = CBS 5799	U94933	NR_155838
Wenyingozyma gen. nov.				
W. cellulolytica comb. nov.	*Candida cellulolytica*	JCM 9397^T = NRRL Y-17856	U94928	KY102420
W. methanosorbosa comb. nov.	*Candida methanosorbosa*	NRRL Y-17320^T = CBS 7029	U70186	KY102211
W. methylovora comb. nov.	*Ogataea methylovora*	NRRL Y-17250^T = CBS 7300	KY108683	KY104408
W. naganishii comb. nov.	*Ogataea naganishii*	NRRL Y-7654^T = CBS 6429	KY108685	KY104410
W. nanaspora comb. nov.	*Candida nanaspora*	NRRL Y-17679^T = CBS 7200	U70187	KY102225
W. neixiangensis comb. nov.	*Ogataea neixiangensis*	NYNU16951^T = CBS 14695	KY213811	KY213810
W. nitratophila comb. nov.	*Candida nitratophila*	NRRL YB-3654^T = CBS 2027	U70180	KY102230
W. ramenticola comb. nov.	*Ogataea ramenticola*	NRRL YB-1985^T = CBS 8699	KY108713	KY104442
W. succiphila comb. nov.	*Candida succiphila*	NRRL Y-11998^T = JCM 9445 = CBS 8003	U70189	KY102421
W. suzukii comb. nov.	*Candida suzukii*	NRRL Y-27593^T = CBS 9253	KY106788	KY102423
W. wangdongensis sp. nov.	*Ogataea wangdongensis*	CBS 12674^T = KM 15	AB734092	NR_138179
Ogataea sp.		NRRL YB-1238	genome	genome
Ogataea sp.		NRRL Y-27166	genome	genome
Ogataea sp.		yHMJ1	genome	genome
Ogataea sp.		NRRL Y-27170	genome	genome
Xiuguozyma gen. nov. (*Candida insectalens* clade)				
X. insectalens comb. nov.	*Candida insectalens*	NRRL Y-7778^T = JCM 9610 = CBS 6036	U62304	EU364562
X. silvatica comb. nov.	*Candida silvatica*	NRRL Y-7777^T = JCM 9828 = CBS 6277	U76201	KY102393
Candida sp.		JCM 15000 = CBS 10902	AB291677	\
Serinales				
Debaryomycetaceae				
Aciculoconidium				
A. aculeatum		NRRL YB-4298^T = CBS 5578	JQ689029	OW983919
Candida sensu stricto				
C. albicans		CBS 562^T = NRRL Y-12983N	U45776	NR_125332
C. albicans		CEC4854	AY342214	AY342214
C. aquae-textoris		DBVPG6732^T = CBS 7923	GU142862	KJ651205
C. baotianmanensis sp. nov.	*Candida baotianmanensis*	NYNU 14719^T = CBS 13915	KM586733	KM586734

Table S2. List of yeasts and GenBank numbers used for the rDNA phylogenetic analysis (Continue)

Taxa	Basionym or important synonym	Strain (T=type)	D1/D2	ITS
C. buenavistaensis		CBS 9895^{T} = NRRL Y-27734	KY106374	KY102007
C. dubliniensis		NRRL Y-17841^{T} = CBS 7987	U57685	NR_119386
C. frijolesensis		NRRL Y-48060^{T} = CBS 10377	NG_054802	NR_136989
C. gigantensis		CBS 9896^{T} = NRRL Y-27736	KY106465	KY102102
C. kantuleensis		CBS 15219^{T}	NG_066388	NR_164020
C. labiduridarum		CBS 10452^{T} = NRRL Y-27940	KY106543	KY102176
C. maltosa		NRRL Y-17677^{T} = CBS 5611	U45745	NR_138346
C. neerlandica		CBS 434^{T} = NRRL Y-27057	KY106596	KY102226
C. pellucidi		CBS 16171^{T}	MN908679	MN908679
C. prachuapensis		CBS 11024^{T}	NG_054767	\
C. pseudoviswanathii sp. nov.	*Candida pseudoviswanathii*	NYNU 14772^{T} =^{T}CBS 13916	KM586735	KM586736
C. sanyaensis sp. nov.	*Candida sanyaensis*	CBS 12637	NG_054829	NR_138302
C. saraburiensis sp. nov.	*Candida saraburiensis*	CBS 11696^{T}	KY106752	KY102390
C. sojae		NRRL Y-17909^{T} = JCM 1644 = CBS 7871	U71070	KY102400
C. tetrigidarum		ATCC MYA-4369^{T}	NG_042507	NR_111411
C. tetrigidarum		CBS 10457^{T}	KY106803	genome
C. tropicalis	*Candida vulgaris*	NRRL Y-12968^{T} = CBS 94	U45749	KY102470
C. viswanathii		NRRL Y-6660^{T} = JCM 9567 = CBS 4024	U45752	KY102515
C. yunnanensis		NYNU 17948^{T} = CBS 15276	MG255709	MG255721
Candida sp.		LN1	genome	genome
Candida sp.		LDI48194	genome	genome
Debaryomyces				
D. apis		CBS 16297^{T}	MN585723	MN585723
D. castellii		NRRL Y-7423^{T} = JCM 6177 = CBS 2923	NG_054864	NR_111306
D. coudertii		NRRL Y-7425^{T} = JCM 2387 = CBS 5167	U45846	KY103186
D. fabryi		NRRL Y-17914^{T} = JCM 2104 = CB S789	U94927	KY103198
D. hansenii		NRRL Y-7426^{T} = JCM 1990 = CBS 767	JQ689041	KY103230
D. macquariensis		CBS 5572^{T}	KY107564	KY103270
D. maramus		CBS 1958^{T} = JCM 1528 = NRRL Y-2171	KY107572	KY103271
D. mycophilus		CBS 8300^{T}	KY107573	KY103280

Table S2. List of yeasts and GenBank numbers used for the rDNA phylogenetic analysis (Continue)

Taxa	Basionym or important synonym	Strain (T=type)	D1/D2	ITS
D. nepalensis		NRRL Y-7108^T = JCM 2095 = CBS 5921	U45839	KY103281
D. prosopidis		CBS 8450^T = JCM 9913 = NRRL Y-27369	KY107579	KY103284
D. psychrophila comb. nov.	*Candida psychrophila*	NRRL Y-17665^T = JCM 2388 = CBS 5956	U45813	KY102350
D. psychrosporus		CBS 11845^T = NRRL Y-48723	KY107580	KY103285
D. renaianus sp. nov.	*Debaryomyces renaii*	CBS 10891^T	KY107581	KY103286
D. robertsiae		NRRL Y-6670^T = CBS 2934	U45805	KY103288
D. singareniensis		CBS 10405^T	KY107585	KY103290
D. subglobosus		CBS 792^T = JCM 1989 = NRRL Y-6666	KY107586	KY103291
D. udenii		NRRL Y-17354^T = JCM 7855 = CBS 7056	U45844	KY103296
D. vietnamensis		CBS 10535^T	NG_055689	NR_152497
D. vindobonensis sp. nov.	*Debaryomyces vindobonensis*	CBS 11666^T	KY107591	KY103298
the single-species lineage *Candida anutae*				
Candida anutae		CBS 8787^T = NRRL Y-27374	NG_058974	NR_151794
the single-species lineage *Candida argentea*				
Candida argentea		CBS 12358^T	NG_058975	JF682350
Diutina				
D. bernalii		NCAIM Y.02230^T = DEBM179	MN219652	MN219642
D. catenulata		NRRL Y-1508^T = CBS 565	U45714	KY103376
D. mesorugosa		CBS 12656^T	KT336716	NR_131299
D. neorugosa		UTHSC 10-2054^T = CBS 12627	NG_067521	NR_138360
D. pseudorugosa		CBS 10433^T	NG_059159	NR_137599
D. ranongensis		CBS 10861^T	NG_059160	NR_138361
D. rugosa		NRRL Y-1496^T = CBS 613	FJ768915	KY103379
D. scorzettiae		CBS 10107^T	NG_059161	NR_164090
D. siamensis		DMKU RE43^T = CBS 13388	KT336715	NR_155042
D. sipiczkii		NCAIM Y.02232^T	MN219654	MN219645
Fermentozyma gen. nov.				
F. sake comb. nov.	*Candida sake*	NRRL Y-1622^T = CBS 159	NG_055231	KY102379
F. vespimorsuum comb. nov.	*Candida vespimorsuum*	ICMP 22109^T	NG_059018	NR_151814
Candida sp.		KBP Y-6292	OP941477	OP941477

Table S2. List of yeasts and GenBank numbers used for the rDNA phylogenetic analysis (Continue)

Taxa	Basionym or important synonym	Strain (T=type)	D1/D2	ITS
Hemisphaericaspora gen. nov.				
H. elongata comb. nov.	*Spathaspora elongata*	NYNU 18115^{T}	MK682796	MK682770
H. gorwiae comb. nov.	*Spathaspora gorwiae*	UFMG CM-Y312^{T} = CBS 13472	NG_059956	NR_155784
H. hagerdaliae comb. nov.	*Spathaspora hagerdaliae*	UFMG CM-Y303^{T} = CBS 13475	KU556168	NR_155800
H. insectamans comb. nov.	*Hemisphaericaspora insectamans*	NRRL Y-7786^{T} = JCM 9611 = CBS 6033	U45753	MK394129
H. jiuxiensis comb. nov.	*Spathaspora jiuxiensis*	NYNU 17416^{T}	MG255705	MG255728
H. lyxosophila comb. nov.	*Candida lyxosophila*	NRRL Y-17539^{T} = CBS 8194	U76204	genome
H. mengyangensis comb. nov.	*Spathaspora mengyangensis*	NYNU 17741^{T}	MG255706	MG255718
H. nanyangensis sp. nov.	*Hemisphaericaspora nanyangensis*	NYNU13717^{T} = CBS 13020	KF690375	KF690366
H. parajiuxiensis comb. nov.	*Spathaspora parajiuxiensis*	NYNU 16747^{T}	KY213819	KY213816
H. roraimensis comb. nov.	*Spathaspora roraimensis*	UFMG-XMD23.3^{T} = CBS12681	JN099269	JN099269
H. rosae comb. nov.	*Spathaspora rosae*	NYNU 17934^{T}	NG_081458	NR_175617
H. subhashii comb. nov.	*Candida subhashii*	CBS 10753^{T}	EU836708	NR_073356
H. xylanilytica sp. nov.	*Candida xylanilytica*	CBS 11761^{T} = NBRC 106499	AB523752	MN904886
H. xylofermentans comb. nov.	*Spathaspora xylofermentans*	UFMG-HMD23.3^{T}=CBS 12682	JN099268	JN099268
Intestinozyma gen. nov. (single-species lineage *Candida alai*)				
I. alai comb. nov.	*Candida alai*	ATCC MYA-4364^{T} = CBS 9899 = NRRL Y-27739	NG_042504	NR_111408
Candida sp.	*Candida* sp.	B53C		MW165503
Insectozyma gen. nov. (*Candida corydali* clade)				
I. bohioensis comb. nov.	*Candida bohioensis*	CBS 9897^{T} = NRRL Y-27737	KY106329	KY101972
I. chauliodis comb. nov.	*Candida chauliodis*	CBS 10157^{T} = NRRL Y-27909	KY106392	KY102027
I. coleopterorum comb. nov.	*Candida coleopterorum*	CBS 14180^{T}	NG_064395	NR_159749
I. corydali comb. nov.	*Candida corydali*	CBS 10158^{T} = NRRL Y-27910	KY106400	KY102035
I. morakotiae comb. nov.	*Candida morakotiae*	BCC 7718^{T} = CBS 12091	NG_054768	KY102216
I. parachauliodis comb. nov.	*Candida parachauliodes*	CBS 13928^{T}	NG_064384	NR_159747
I. prachuapensis sp. nov.	*Candida prachuapensis*	CBS 11024^{T}	NG_054767	\
I. sakaeoensis sp. nov.	*Candida sakaeoensis*	CBS 12318^{T}	KY106731	KY102369
I. verbasci sp. nov.	*Candida verbasci*	CBS 12699^{T}	KY106867	KY102495
I. xiaguanensis comb. nov.	*Candida xiaguanensis*	CBS 13923^{T}	NG_064372	NR_159746
Kodamaea				

Table S2. List of yeasts and GenBank numbers used for the rDNA phylogenetic analysis (Continue)

Taxa	Basionym or important synonym	Strain (T=type)	D1/D2	ITS
K. alishanica		CBS 11429^T	NG_063941	NR_159556
K. anthophila		CBS 8494^T	KY108132	KY103864
K. arcana		NRRL Y-27712^T = CBS 9883	AY242347	genome
K. derodonti		CBS 9882^T	NG_060804	KY102047
K. fukazawae		JCM 1641^T = CBS 9137	NG_059419	AB028033
K. fungicola		CBS 9138^T	KY106457	AB028031
K. hsintzibuensis		CBS 11427^T	EF653944	NR_160557
K. jinghongensis		NYNU 167162^T = CBS 14700	KY213807	KY213814
K. kakaduensis		CBS 8611^T	NG_058321	NR_155240
K. kaohsiungensis		CBS 11435^T	KY106535	KY102167
K. laetipori		NRRL Y-27713^T	AY520398	genome
K. leandrae		CBS 9735^T	NG_060374	NR_155222
K. lidongshanica		CBS 11426^T	EF653949	GU126451
K. loeiensis		CBS 11899^T	AB602835	KY102182
K. meredithae		CBS 13899^T = NRRL Y-63729	KM408123	KM384057
K. mesenterica		NRRL Y-1494^T = CBS 602	NG_060816	NR_111297
K. neixiangensis		NYNU 167139^T = CBS 14699	KY213820	KY213808
K. nitidulidarum		CBS 8491^T	KY108137	KY103867
K. ohmeri		NRRL Y-1932^T = CBS 5367	GU597323	KY103872
K. plutei		ATCC MYA-4329^T = CBS 9885	NG_066357	NR_111389
K. restingae		CBS 8493^T	KY106720	KY102360
K. sagamina		JCM 10144^T	AY313959	AB028032
K. samutsakhonensis		TBRC 16043^T	LC706545	LC706547
K. smagusa		ATCC MYA-4755^T =^{T}CBS 11430	NG_063943	NR_111611
K. suecica		NRRL Y-12943^T = JCM 7530 = CBS 5724	U45732	genome
K. transpacifica		CBS 12823^T	KF002564	NR_173358
Kodamaea sp.		yHQL449	genome	genome
Lizanozyma gen. nov. (*Scheffersomyces gosingicus* clade)				
L. gosingicus sp. nov.	*Scheffersomyces gosingicus*	CBS 11433^T	KY109563	KY105339
L. spartinae comb. nov.	*Scheffersomyces spartinae*	NRRL Y-7322^T = CBS 6059	JQ689045	NR_111290

Table S2. List of yeasts and GenBank numbers used for the rDNA phylogenetic analysis (Continue)

Taxa	Basionym or important synonym	Strain (T=type)	D1/D2	ITS
L. thasaensis sp. nov.	*Candida thasaensis*	CBS 12529^T	NG_055174	NR_111028
Lodderomyces				
L. beijingensis		CBS 14171^T = NYNU 15764	NG_064393	NR_160326
L. cetoniae comb. nov.	*Candida cetoniae*	IMB1R2^T = CBS 12463	KC118128	NR_132875
L. elongisporus		NRRL YB-4239^T = CBS 2605 = ATCC 11503	JQ689035	KY104078
L. hyderabadensis comb. nov.	*Candida hyderabadensis*	CBS 10444^T = NRRL Y-27953	NG_064308	NR_159741
L. jiufengensis comb. nov.	*Candida jiufengensis*	CGMCC 2.3688^T = CBS 10846	EU402935	EU402936
L. margitis comb. nov.	*Candida margitis*	CICC 33091^T = NYNU 15857 = CBS 14175	NG_064394	NR_159750
L. metapsilosis comb. nov.	*Candida metapsilosis*	ATCC 96144^T = CBS 10907	KY106577	KY102203
L. orthopsilosis comb. nov.	*Candida orthopsilosis*	ATCC 96139^T = CBS 10906	NG_054816	NR_130661
L. oxycetoniae comb. nov.	*Candida oxycetoniae*	CGMCC 2.3656^T = CBS 10844	KY106643	KY102281
L. parapsilosis comb. nov.	*Candida parapsilosis*	NRRL Y-12969^T = CBS 604 = ATCC 22019	U45754	KY102290
L. pseudojiufengensis comb. nov.	*Candida pseudojiufengensis*	CGMCC 2.3693^T = CBS 10847	KY106704	KY102345
L. theae sp. nov.	*Candida theae*	CBS 12239^T	KY106808	KY102442
Millerozyma				
M. acaciae		NRRL Y-7117^T = JCM 10732 = CBS 5656	KY108556	KY104268
M. farinosa		NRRL Y-7553^T = JCM 10734 = CBS 185	JQ689046	KY104273
M. koratensis		BCC 11769^T = JCM 12576 = CBS 12092	NG_054797	NR_138173
M. miso		CBS 2004^T	KY108801	FR668056
M. phetchabunensis		CBS 11682^T	AB371638	AB371639
M. porticicola comb. nov.	*Pichia porticicola*	NBRC 100302^T = CBS 11715	KY108913	KY104643
M. pseudofarinosa comb. nov.	*Candida pseudofarinosa*	NCYC 386^T = CLIB 1231	FN565484	genome
Nematodospora				
N. anomalae		NYNU 14914^T = CBS 13927	KP054269	NR_173254
N. valgi		CBS 12562^T	HM627112	NR_132909
Priceomyces				
P. carsonii		NRRL YB-4275^T = JCM 8121 = CBS 2285	KY108936	NR_111117
P. castillae		NRRL Y-7501^T = JCM 10733 = CBS 6053	JQ689040	KY104670
P. haplophilus		NRRL Y-7860^T = CBS 2028	JQ689039	NR_111020
P. medius		NRRL Y-7122^T = JCM 10737 = CBS 5521	KY108942	NR_155683

Table S2. List of yeasts and GenBank numbers used for the rDNA phylogenetic analysis (Continue)

Taxa	Basionym or important synonym	Strain (T=type)	D1/D2	ITS
P. melissophilus		NRRL Y-7585^T = JCM 1707 = CBS 6344	KY108946	KY104677
P. fermenticarens		JCM 9589^T = CBS 7040 = NRRL Y-17321	NG_054845	NR_077182
P. northwykensis		CBS 11370^T	NG_054817	NR_157459
P. vitoshaensis		CBS 12457^T	NG_054820	NR_155623
Scheffersomyces				
S. anoplophorae		NYNU 15730^T	KU128724	KU128714
S. broadrunensis comb. nov.	*Candida broadrunensis*	ATCC MYA-4650^T = CBS 11838	KY106372	KY102006
S. coipomoensis		CBS 8178^T	KY109557	NR_111424
S. cryptocercus		NRRL Y-48824^T = CBS 12658	NG_055704	NR_120091
S. ergatensis		CBS 6248^T	KY109560	KY105336
S. illinoinensis		NRRL Y-48827^T = CBS 12624	NG_042773	NR_111865
S. insectosa		ATCC 66611^T = CBS 4286	KY109565	KY105341
S. jinghongensis		NYNU 17926^T	MG255714	MG255722
S. lignicola sp. nov.	*Scheffersomyces lignicola*	NBRC 102564^T = CBS 10612	KY109567	KY105344
S. lignosus		NRRL Y-12856^T = CBS 4705 = ATCC58779	KY109568	NR_120020
S. paraergatensis		NYNU 16782^T	KY213826	KY213803
S. parashehatae		ATCC MYA-4653^T = CBS 12535	NG_055697	NR_138230
S. quercinus		NRRL Y-48825^T = CBS 12625	NG_055703	NR_120019
S. shehatae		NRRL Y-12858^T = CBS 5813	NG_055706	NR_120021
S. stambukii		CBS 14217^T	NG_064529	KT033721
S. stipitis		NRRL Y-7124^T = CBS 5773 = ATCC58376	JQ689044	NR_165947
S. titani		NYNU14712^T = CBS 13926	KP054262	NR_173253
S. virginianus		NRRL Y-48822^T = CBS 12625	KY109571	KY105348
S. xylosifermentans		CBS 12540^T	KY109586	KY105362
Schwanniomyces				
S. capriottii		NRRL Y-7423^T = CBS 2923	KY109604	KY105380
S. etchellsii		JCM 3656^T = NRRL Y-7121 = CBS 2011	JQ689043	NR_111017
S. occidentalis var. occidentalis		NRRL Y-10^T = CBS 819	JQ689042	KY105389
S. occidentalis var. persoonii		NRRL Y-7400^T = CBS 2169	NG_054863	KY105391
S. polymorphus		NRRL Y-2022^T = CBS 186	U45836	KY105399

Table S2. List of yeasts and GenBank numbers used for the rDNA phylogenetic analysis (Continue)

Taxa	Basionym or important synonym	Strain (T=type)	D1/D2	ITS
S. pseudopolymorphus		NRRL YB-4229^T = CBS 2008	KY109636	KY105403
S. vanrijiae var. vanrijiae		NRRL Y-7430^T = CBS 3024	NG_054865	KY105408
S. vanrijiae var. yarrowii		NRRL Y-7535^T = CBS 6246	NG_054866	KY105410
S. yamadae		NRRL Y-11714^T = CBS 7035	NG_054862	KY105413
Spathaspora sensu stricto				
S. allomyrinae		CCIC 33057^T = CBS 13924 = NYNU 1495	KP054267	KP054268
S. arborariae		CBS 11463^T = ATCC MYA-4684	NG_042574	NR_111592
S. brasiliensis sp. nov.	*Spathaspora brasiliensis*	UFMG-HMD19.3^T = CBS 12679	JN099271	JN099271
S. girioi		UFMG CM-Y302^T = CBS 13476	NG_059955	NR_155783
S. jeffriesii		CBS 9898^T = ATCC MYA-4346	KY106532	KY102164
S. materiae		CBS 10975^T	FJ154790	FJ154790
S. passalidarum		NRRL Y-27907^T = CBS 10155	NG_042631	NR_111397
S. piracicabensis		UFMG CM-Y5867^T = CBS 15054	KR864906	KR864907
S. suhii sp. nov.	*Spathaspora suhii*	UFMG-XMD16.2^T = CBS 12680	JN099270	JN099270
Suhomyces				
S. ambrosiae		NRRL YB-1316^T = CBS 8844	NG_054780	NR_155812
S. anneliseae		NRRL Y-27563^T = CBS 9837	KY106295	KY101930
S. atakaporum		NRRL Y-27570^T = CBS 9833	KY106307	KY101946
S. bokatorum		NRRL Y-27571^T = CBS 9824	KY106349	KY101996
S. bolitotheri		CBS 9832^T	KY106356	KY102003
S. bribrorum		NRRL Y-27572^T = CBS 9835	NG_054789	NR_155814
S. canberraensis		NRRL YB-2417^T = CBS 8846	NG_054781	NR_077195
S. caryicola comb. nov.	*Candida caryicola*	CBS 8847^T = NRRL YB-1499	KY106388	NR_077194
S. caryicola	*Candida caryicola*	EXF-12358	MW049167	MW031228
S. chickasaworum		NRRL Y-27566^T = CBS 9830	NG_054784	KY102028
S. choctaworum		CBS 9831^T	KY106395	KY102030
S. coccinellae		CLIB1706^T = CBS 14298	LN875195	LN875172
S. emberorum		NRRL Y-27606^T = CBS 9827	NG_054785	NR_155817
S. faveliae		CLIB1725^T = CBS 14299	LN875204	LN875182
S. guaymorum		NRRL Y-27568^T = CBS 9823	KY106486	KT823680

Table S2. List of yeasts and GenBank numbers used for the rDNA phylogenetic analysis (Continue)

Taxa	Basionym or important synonym	Strain (T=type)	D1/D2	ITS
S. kilbournensis		NRRL Y-17864^T = CBS 14276	KU751780	KU751781
S. kunorum		NRRL Y-27580^T = CBS 9825	KY106542	KY102175
S. maxii		NRRL Y-27588^T = CBS 9836	KY106566	KY102199
S. panamericanus		NRRL Y-27567^T = CBS 9834	KY106648	KY102287
S. prunicola		NRRL YB-869^T = CBS 8848	KY106698	NR_111288
S. pyralidae		NRRL Y-27085^T = CBS 5035	NG_054779	NR_164391
S. rongomai-pounamu comb. nov.	*Candida rongomai-pounamu*	ICMP 22125^T	NG_059019	NR_151813
S. taliae		NRRL Y-27589^T = CBS 9838	KY106790	KY102425
S. tanzawaensis		NRRL Y-17324^T = CBS 7422	KY106794	KY102429
S. terraborum		NRRL Y-27573^T = CBS 9826	KY106802	KY102437
S. tibetensis comb. nov.	*Candida tibetensis*	CGMCC 2.3072^T = CBS 10298	KY106809	KY102444
S. vadensis		NRRL Y-27778^T = CBS 9454	NG_054801	NR_155826
S. wounanorum		NRRL Y-27574^T = CBS 9828	KY106890	KY102520
S. xylopsoci		NRRL Y-27066^T = CBS 6037	NG_054782	FR819718
S. yuchorum		NRRL Y-27569^T = CBS 9829	NG_054786	NR_155827
S. drosophilae		CBS 16329^T	MN963956	MN963955
S. rilaensis		NBIMCC 8929^T = CBS 12443	HM627061	HM627147
Suzukiozyma gen. nov. (*Candida glaebosa* clade)				
S. fluviatilis comb. nov.	*Candida fluviatilis*	NRRL Y-7711^T = CBS 6776	U45717	NR_111589
S. glaebosa comb. nov.	*Candida glaebosa*	NRRL Y-6949^T = CBS 5691	U45757	NR_077183
S. manassasensis comb. nov.	*Candida manassasensis*	ATCC MYA-4652^T = CBS 12534	KY106555	KY102189
S. palmioleophila comb. nov.	*Candida palmioleophila*	JCM 5218^T = NRRL Y-17323 = CBS 7418	U45758	KY102283
S. pseudoglaebosa comb. nov.	*Candida pseudoglaebosa*	JCM 2168^T = NRRL Y-17911 = CBS 6715	U71072	KY102342
S. saitoana comb. nov.	*Torulopsis candida, Candida saitoana*	NRRL Y-17316^T = CBS 940	U45762	KY102368
S. sphagnicola comb. nov.	*Candida sphagnicola*	CBS 11774^T	KY106778	FN868154
Teunomyces				
T. aglyptinius		NRRL Y-27935^T = CBS 10311	NG_054798	NR_165962
T. atbi		NRRL Y-27651^T = CBS 9852	KY106309	KY101947
T. barrocoloradensis		NRRL Y-27934^T = CBS 10310	NG_054799	NR_155888
T. basidiocarpi		BCRC 23475^T	HM461612	HM461641

Table S2. List of yeasts and GenBank numbers used for the rDNA phylogenetic analysis (Continue)

Taxa	Basionym or important synonym	Strain (T=type)	D1/D2	ITS
T. cretensis		CBS 9453^T	KY106401	KY102036
T. funiuensis		CBS 13911^T	NG_064366	NR_160320
T. gatunensis		NRRL Y-48064^T = CBS 10379	KY106460	KY102098
T. kruisii		NRRL Y-17087^T = CBS 6451	KY106541	KY102174
T. luguensis		BCRC 23476^T	HM461614	HM461644
T. lycoperdinae		CBS 9850^T	KY106549	KY102183
T. pallodes		NRRL Y-27653^T = CBS 9845	NG_054795	NR_137667
T. panamensis		NRRL Y-27657^T = CBS 9849	NG_058280	NR_137668
T. stri		NRRL Y-48063^T = CBS 10378	NG_054800	NR_155925
T. tritomae		CBS 9843^T	KY106815	KY102447
Teunomyces sp.		UFMG-CM-Y6362	MG857092	OQ029643
Wickerhamia				
W. fluorescens		NRRL YB-4819^T = CBS 4565	JQ689034	KY105850
W. europaea		CBS 18675^T	OR582606	OR582606
the single-species lineage *Candida glucosophila*				
Candida glucosophila		CBS 7349^T = JCM 9440 = NRRL Y-17781	U45849	MF314336
Zhuliangozyma gen. nov. (*Candida blackwelliae* clade)				
Z. blackwellae comb. nov.	*Candida blackwellae*	CGMCC 2.3639^T = CBS 10843	KY106321	NR_111470
Z. boniae comb. nov.	*Spathaspora boniae*	UFMG CM-Y306^T = CBS 13262	KT276332	NR_158910
Z. parablackwelliae comb. nov.	*Candida parablackwelliae*	NYNU17763^T = CBS 15228	MG255702	MG255731
Metschnikowiaceae				
Metschnikowia				
***M. agaves* clade**				
Candida wancherniae		CBS 12090^T	KY106888	KY102518
***M. arizonensis* clade**				
Candida hawaiiana		NRRL Y-27473T = CBS 9146	KY106497	KY102130
***M. bicuspidata* clade**				
Candida golubevii		NBRC105679^T = CBS 11362 = NRRL Y-48707	DQ404455	
C. hydropsyches		NRRL Y-27752^T = CBS 9906	KY106510	KY102144
C. magnifica		NRRL Y-5717^T	U44821	

Table S2. List of yeasts and GenBank numbers used for the rDNA phylogenetic analysis (Continue)

Taxa	Basionym or important synonym	Strain (T=type)	D1/D2	ITS
***M. caudata* clade**				
Candida hainanensis		NRRL Y-48715^T = CBS 10696	EU284103	EU284099.1
the single-species lineage *Candida danieliae*				
Candida danieliae		CBS 8533^T	NG_058979	HM156530
Incertae sedis* in *Metschnikowiaceae				
Candida citri		CBS 11858^T	KY106398	KY102033
Candida xylosifermentans		TBRC 10387^T	AB525240	LC440109
***Incertae sedis* in Serinales**				
the single-species lineage *Candida ascalaphidarum*				
Candida ascalaphidarum		CBS 10156^T = NRRL Y-27908	NG_042502	NR_111405
Chernovozyma gen. nov. (*Candida aurita* clade)				
C. aurita	*Candida aurita*	CBS 9724^T	NG_058976	KY101953
C. palmyrensis	*Candida palmyrensis*	ATCC 62899^T = CBS 11546	KY106646	KY102285
C. sophiae-reginae	*Candida sophiae-reginae*	NRRL Y-17668^T = CBS 8175	U45817	KY102409
Dujonia gen. nov. (*Candida railenensis* clade)				
D. anglica comb. nov.	*Candida anglica*	CBS 4262^T = NRRL Y-27079	NG_054775	NR_163770
D. boleticola comb. nov.	*Candida boleticola*	NRRL Y-17080^T = CBS 6420	U45777	NR_077166
D. oleophila comb. nov.	*Candida oleophila*	NRRL Y-2317^T = CBS 2219	U45793	KY102254
D. railenensis comb. nov.	*Candida railenensis*	NRRL Y-17762^T = CBS 8164	U45800	KY102355
D. santamariae comb. nov.	*Candida santamariae var. membranifaciens*	NRRL Y-17647^T = CBS 5838	U45785	KY102386
D. santamariae comb. nov.	*Candida santamariae var. santamariae*	NRRL Y-6656^T = CBS 4515	U45794	KY102387
D. santamariae comb. nov.	*Candida santamariae*	CECT 11165^T	U45798	AJ539373
D. schatavii comb. nov.	*Candida schatavii*	NRRL Y-17078^T = JCM 1778 = CBS 6452	U45795	NR_155214
D. zeylanoides comb. nov.	*Candida zeylanoides*	NRRL Y-1774^T = CBS 619	U45832	KY102539
Glucitozyma gen. nov.				
G. multigemmis comb. nov.	*Candida multigemmis*	NRRL Y-17659^T = CBS 6524	JQ689037	KY102218
Keqinozyma gen. nov. (*Candida sinolaborantium* clade)				
K. heliconiae comb. nov.	*Candida heliconiae*	CBS 10000^T = NRRL Y-27813	KM065900	KY102131
K. nonsorbophila comb. nov.	*Candida nonsorbophila*	CBS 10862^T	KY106601	KY102232

Table S2. List of yeasts and GenBank numbers used for the rDNA phylogenetic analysis (Continue)

Taxa	Basionym or important synonym	Strain (T=type)	D1/D2	ITS
K. sinolaborantium comb. nov.	*Candida sinolaborantium*	NRRL Y-27765^T = CBS 9940	KM065905	KY102395
K. temnochilae comb. nov.	*Candida temnochilae*	NRRL Y-27763^T = CBS 9938	KM065906	KY102432
Kurtzmaniella				
K. cleridarum		NRRL Y-48386^T = CBS 8793	JQ689038	NR_111153
K. fragi		NRRL Y-17910^T = JCM 1791 = CBS 7702	U71071	KY102089
K. hittingeri		CBS 13469^T	KF582609	KF582611
K. natalensis		NRRL Y-17680^T = JCM 1445	NG_055225	KC542314
K. quercitrusa		NRRL Y-5392 = CBS 4412	NG_055226	NR_163508
Meyerozyma				
M. amylolytica		CBS 15272^T = DSM 27310	KY673531	NR_154976
M. athensensis		CBS 9840^T = NRRL Y-27644	NG_054793	KY101949
M. caribbica		NRRL Y-27274^T = CBS 9966	KY108516	KY104222
M. caribbica	*Candida fermentati*	NRRL Y-27401^T	AY187283	AF022718
M. carpophila		JCM 9396^T = CBS 5256	MK394110	NR_152984
M. elateridarum		CBS 9842^T	NG_042465	NR_111350
M. guilliermondii		NRRL Y-2075^T = CBS 2030	JQ689047	KY104252
M. neustonensis		CBS 11061^T	NG_054803	NR_152946
M. smithsonii		CBS 9839^T	NG_054792	NR_111339
***Yamadazyma sensu stricto* clade**				
Y. aaseri		NRRL YB-3897^T = CBS 1913	U45802	NR_077069
Y. akitaensis		NRRL Y-7904^T = CBS 6701	NG_054847	NR_138229
Y. andamanensis sp. nov.	*Candida andamanensis*	CBS 10859^T	NG_055688	NR_155982
Y. atlantica	*Candida atlantica*	NRRL Y-17759^T = JCM 9548 = CBS 5263	U45799	NR_155983
Y. atmosphaerica	*Candida atmosphaerica*	NRRL Y-17642^T = JCM 9549 = CBS 4547	U45779	AJ539369
Y. barbieri		CBS 14301^T	NG_064450	NR_160336
Y. cocois		VCIM 4241^T	KM248523	NR_173296
Y. conglobata	*Candida conglobata*	NRRL1504^T = JCM 2373 = CBS 2018	U45789	AJ539370
Y. dendronema		NRRL Y-7781^T = CBS 6270	U45751	NR_155957
Y. diddensiae	*Candida diddensiae*	CBS 2214^T = NRRL Y-7589	KY106414	KY102049
Y. dushanensis sp. nov.	*Yamadazyma dushanensis*	CBS 13914^T	NG_064369	NR_160323

Table S2. List of yeasts and GenBank numbers used for the rDNA phylogenetic analysis (Continue)

Taxa	Basionym or important synonym	Strain (T=type)	D1/D2	ITS
Y. germanica		CBS 4105^{T} = NRRL Y-27064	KY106463	KY102100
Y. insectorum		NRRL Y-7787^{T} = JCM 9457 = CBS 6213	U45791	KY102150
Y. kanchanaburiensis		CBS 11266^{T}	KY106534	KY102166
Y. laniorum		NRRL Y-63967^{T} = CBS 14780	KY588136	KY588337
Y. luoyangensis		NYNU 201035^{T}	MZ318422	MZ318445
Y. mexicana		NRRL Y-11818^{T} = CBS 7066	NG_058439	NR_138213
Y. naeodendra		NRRL Y-10942^{T} = CBS 6032	U45759	KY102222
Y. nakazawae		NRRL Y-7903^{T} = CBS 6700	NG_054843	NR_119733
Y. oceani sp. nov.	*Candida oceani*	CBS 11857^{T} = DSM 23777	KY106609	KY102240
Y. ovata		NYUN 19130^{T}	MZ318425	MZ318424
Y. paraaseri		NYNU 181033^{T}	MZ318460	MZ318421
Y. paraphyllophila sp. nov.	*Yamadazyma paraphyllophila*	CBS 9928^{T}	AY562397	NR_111164
Y. philogaea		NRRL Y-7813^{T} = CBS 6696	JQ689048	NR_119915
Y. phyllophila sp. nov.	*Yamadazyma phyllophila*	CBS 12572^{T}	KY110162	NR_119421
Y. pseudoaaseri		CBS 11170^{T}	KY106699	KY102340
Y. riverae		UFMG CM-Y444^{T} = CBS 14121	NG_059986	NR_155968
Y. scolyti		NRRL Y-5512^{T} = CBS 4802	JQ689050	NR_111287
Y. siamensis sp. nov.	*Yamadazyma siamensis*	CBS 12573^{T}	NG_058440	NR_119420
Y. spencermartinsiae	*Candida spencermartinsiae*	CBS 10894^{T} = NRRL Y-48663	KY106777	KY102414
Y. taylorii	*Candida taylorii*	CBS 8508^{T} = NRRL Y-27213	KY106796	KY102431
Y. tenuis		NRRL Y-1498^{T} = JCM 9827 = CBS 615	U45774	KY102434
Y. terventina		CBS 12510^{T}	JQ247717	NR_160050
Y. trypodendri		NRRL Y-6488^{T} = CBS 8505	KY106852	KY102483
Y. ubonensis sp. nov.	*Yamadazyma ubonensis*	CBS 12859^{T}	NG_058443	NR_155998
Y. vaughaniae		CBS 8583^{T}	KY106866	KY102494
***Yamadazyma epiphylla* clade**				
Yamadazyma endophytica		DMKU-CE23^{T} = CBS 14163	KT307981	genome
Y. epiphylla		NBRC110423^{T} = CBS 13384	LC006026	LC006082
***Yamadazyma triangularis* clade**				
Yamadazyma insecticola		NBRC110421^{T} = CBS 13382	DQ400379	NR_138248

Table S2. List of yeasts and GenBank numbers used for the rDNA phylogenetic analysis (Continue)

Taxa	Basionym or important synonym	Strain (T=type)	D1/D2	ITS
Y. triangularis		NRRL Y-5714^{T} = CBS 4094	JQ689051	NR_111309
Yamadazyma sp.		13Y203	LC060701	LC060702
Yamadazyma sp.		14Y266	LC060707	LC060708
Yamadazyma sp.		SK21-421	OM802623	OM920822
Metschnikowia hawaiiana'		DBMY342	\	KJ706559
Metschnikowia hawaiiana'		DBMY501	\	KJ706718
***Yamadazyma olivae* clade**				
Yamadazyma amphicis	*Candida amphicis*	NRRL Y-27704^{T} = CBS 9877	KY106290	KY101926
Y. blattariae	*Candida blattariae*	CBS 9876^{T}	KY106328	KY101971
Y. buinensis	*Candida buinensis*	NRRL Y-11706^{T} = CBS 6796	U45778	KY102008
Y. cerambycidarum	*Candida cerambycidarum*	CBS 9879^{T} = NRRL Y-27706	AY520299	AY964669
Y. diospyri	*Candida diospyri*	CBS 9769^{T}	KY106418	NR_137665
Y. endomychidarum	*Candida endomychidarum*	CBS 9881^{T} = NRRL Y-27708	KY106430	KY102069
Y. friedrichii	*Candida friedrichii*	NRRL Y-17653^{T} = JCM 9553 = CBS 4114	U45781	KY102092
Y. gorgasii	*Candida gorgasii*	CBS 9880^{T} = NRRL Y-27707	KY106481	KY102113
Y. jaroonii sp. nov.	*Candida jaroonii*	CBS 10790^{T}	KY106531	KY102163
Y. keroseneae	*Candida keroseneae*	CECT 1305^{T} = IMI 395605	FJ357698	NR_137563
Y. khao-thaluensis	*Candida khao-thaluensis*	CBS 8535^{T}	KY106536	KY102168
Y. kitorensis		JCM31005^{T} = CBS 14158	LC060995	NR_156006
Y. lessepsii	*Candida lessepsii*	CBS 9941^{T} = NRRL Y-27766	KY106548	KY102181
Y. membranifaciens	*Candida membranifaciens*	NRRL Y-2089^{T} = CBS 1952	U45792	KY102202
Y. michaelii	*Candida michaelii*	CBS 9502^{T}	KY106583	NR_111391
Y. olivae	*Candida olivae*	CBS 11171^{T}	KY110160	KY105946
Y. olivae	*Candida olivae*	ATCC MYA-4568^{T}	NG_042526	NR_111477
Y. songkhlaensis sp. nov.	*Candida songkhlaensis*	CBS 10791^{T} = NBRC 103214	KY106765	KY102403
Y. tallmaniae	*Candida tallmaniae*	CBS 8575^{T}	KY106791	KY102426
Y. tammaniensis	*Candida tammaniensis*	CBS 8504^{T} = NRRL Y-8257	KY106792	KY102427
Y. takamatsuzukensis		CBS 10916^{T} = JCM 28201 = NBRC 104391	NG_058441	NR_144770
Y. tumulicola		CBS 10917^{T} = JCM 28226 = NBRC 104392	NG_058442	NR_144769
Y. vrieseae sp. nov.	*Candida vrieseae*	CBS 10829^{T}	NG_060833	NR_155991

Table S2. List of yeasts and GenBank numbers used for the rDNA phylogenetic analysis (Continue)

Taxa	Basionym or important synonym	Strain (T=type)	D1/D2	ITS
Candida koratica'		BCC 7743^{T} = NBRC 103208	AB354232	AB360443
Saccharomycetes				
Phaffomycetales				
Phaffomycetaceae				
Barnettozyma				
B. californica		NRRL Y-17395^{T} = CBS 252	EF550276	NR_138212
B. hawaiiensis		NRRL Y-27270^{T} = CBS 8760	NG_058701	NR_153631
B. menglunensis		NYNU 1811121^{T}	MK682804	MK682797
B. populi		NRRL Y-12728^{T} = CBS 8094	NG_058630	NR_153632
Candida sanyiensis	*Candida sanyiensis*	CBS 10592^{T}	NG_060378	NR_154871
B. sucrosica sp. nov.	*Barnettozyma sucrosica*	CBS 11512^{T}	KY106187	KY101734
B. vustinii		CBS 11554^{T}	NG_058702	NR_137724
B. xylosica sp. nov.	*Barnettozyma xylosica*	NBRC 111558^{T}	LC202861	NR_154882
B. xylosiphila sp. nov.	*Barnettozyma xylosiphila*	NBRC 110202^{T}	NG_058713	NR_174638
Pichia sp.		KY-328	\	AB428337
Barnettozyma sp.		NYNU 1811121	MK682804	\
Gotozyma gen. nov. (*Barnettozyma siamensis* clade)				
G. botsteinii sp. nov.	*Barnettozyma botsteinii*	CBS 16679^{T}	MN509221	MN509222
G. montana comb. nov.	*Candida montana*	NRRL Y-17326^{T} = CBS 8057	U62305	KY102215
G. siamensis comb. nov.	*Barnettozyma siamensis*	CBS 13392^{T}	AB741519	KJ413945
Komagataea (*Barnettozyma wickerhamii* clade)				
K. norvegica comb. nov.	*Candida norvegica*	NRRL Y-17660^{T} = CBS 4239	U62299	KY102237
K. pratensis	*Barnettozyma pratensis*	NRRL Y-12696^{T} = CBS 7079	NG_058629	NR_153633
K. qinlingensis comb. nov.	*Candida qinlingensis*	CBS 9768^{T}	KY106712	KY102353
K. salicaria comb. nov.	*Barnettozyma salicaria*	NRRL Y-6780^{T} = CBS 5456	NG_058628	genome
K. salicaria		0H7	KM103058	\
K. salicaria		0H4	KM103057	\
K. wickerhamii comb. nov.	*Barnettozyma wickerhamii*	NRRL Y-2435^{T} = CBS 4107	U75419	genome
Millerago				

Table S2. List of yeasts and GenBank numbers used for the rDNA phylogenetic analysis (Continue)

Taxa	Basionym or important synonym	Strain (T=type)	D1/D2	ITS
M. galiae		CBS 8842^{T}	KY106458	KY102096
M. ficus sp. nov.	*Candida ficus*	CBS 12638^{T}	JQ713956	JQ713957
M. phaffii		CBS 18021^{T}	ON264698	ON311286
Phaffomyces				
P. antillensis		NRRL Y-12881^{T} = CBS 7111	NG_060074	genome
P. coquimbonensis sp. nov.	*Candida coquimbonensis*	CBS 12348^{T}	JF733717	genome
P. opuntiae		NRRL Y-11707^{T} = CBS 7010	NG_060075	genome
P. orba comb. nov.	*Candida orba*	CBS 8782^{T} = NRRL Y-27336	EF550265	NR_154354
P. thermotolerans		NRRL Y-11709^{T} = CBS 7012	KY108772	KY104502
P. usticensis		CBS 12958^{T}	KF719195	\
Wickerhamomycetaceae				
Buckleya gen. nov. (single-species lineage *Candida freyschussii*)				
B. freyschussii comb. nov.	*Candida freyschussii*	CBS 2162^{T} = JCM 9850	NG_055229	KY102090
Candida sp.		NIAH-01	AB703242	\
Uncultured fungus isolate		5671_38	\	OR982231
Uncultured fungus clone		5426_384	\	OM614845
Uncultured fungus clone		5426_524	\	OM614856
Hansenula (*Hansenula* clade)				
H. anomala	*Wickerhamomyces anomalus*	NRRL Y-366^{T} = CBS 5759	U74592	KY105894
H. arboraria	*Wickerhamomyces arborarius*	CBS 12941^{T}	NG_057179	NR_155000
H. ciferrii	*Wickerhamomyces ciferrii*	NRRL Y-1031^{T} = CBS 111	U74587	FJ153218
H. edaphica	*Wickerhamomyces edaphicus*	CBS 10408^{T}	KY110120	KY105904
H. lynferdii	*Wickerhamomyces lynferdii*	NRRL Y-7723^{T} = CBS 6695 = BCRC 22676	NG_057175	NR_111798
H. myanmarensis	*Pichia myanmarensis*	CBS 9786^{T}	KY108896	KY104632
H. queroliae comb. nov.	*Wickerhamomyces queroliae*	UFMG-T05-200.1^{T} = NRRL Y-48478	EU580140	genome
H. siamensis	*Wickerhamomyces siamensis*	DMKU RK359^{T} = CBS 12570	NG_042337	NR_111029
H. silvicultrix comb. nov.	*Candida silvicultrix*	NRRL Y-7789^{T} = CBS 6269	U69879	KY102394
H. spegazzinii sp. nov.	*Wickerhamomyces spegazzinii*	CBS 12756^{T}	NG_063933	NR_160053
H. subpelliculosa	*Wickerhamomyces subpelliculosus*	NRRL Y-1683^{T} = CBS 5767	KY110142	NR_111336
H. sydowiorum	*Wickerhamomyces sydowiorum*	NRRL Y-7130^{T} = CBS 5995	KY110146	NR_138219

Table S2. List of yeasts and GenBank numbers used for the rDNA phylogenetic analysis (Continue)

Taxa	Basionym or important synonym	Strain (T=type)	D1/D2	ITS
H. sylviae sp. nov.	*Wickerhamomyces sylviae*	PYCC 6345^{T} = CBS 12888	KF240728	genome
***Liangdongia* gen. nov.** (*Starmera dryadoides* clade)				
L. berthetii comb. nov.	*Candida berthetii*	NRRL Y-17644^{T} = NBRC10266 = CBS 5452	U62298	NR_077118
L. dendrica comb. nov.	*Candida dendrica*	NRRL Y-7775^{T} = CBS 6151	U62301	NR_155816
L. dryadoides comb. nov.	*Starmera dryadoides*	NRRL Y-10990^{T} = CBS 6154	NG_058406	NR_155848
L. ilhagrandensis comb. nov.	*Starmera ilhagrandensis*	CBS 16316^{T}	MH279972	MH279972
L. laemsonensis sp. nov.	*Candida laemsonensis*	CBS 11419^{T}	AB438205	AB534173
L. nongkratonensis comb. nov.	*Pichia nongkratonensis*	BCC 11772^{T}	NG_055079	\
L. quercuum comb. nov.	*Starmera quercuum*	NRRL YB-4281^{T} = CBS 2283	U75416	genome
Petasospora (*Cyberlindnera sensu stricto* clade)				
P. adriatica comb. nov.	*Candida adriatica*	CBS 12504^{T} = ZIM2334	NG_060386	NR_152453
P. americana	*Cyberlindnera americana*	CBS 5645^{T} = NRRL Y-2156	EF550328	KY103038
P. amylophila	*Cyberlindnera amylophila*	CBS 7020^{T} = NRRL YB-1287	EF550319	NR_152480
P. bimundalis	*Cyberlindnera bimundalis*	NRRL Y-5343^{T} = CBS 5642	NG_069004	KY103040
P. dasilvae	*Cyberlindnera dasilvae*	CBS 16129^{T} = UFMG-CM-Y519	MT311982	MT312230
P. easanensis sp. nov.	*Candida easanensis*	CBS 11708^{T} =JCM12474=JCM 12476	NG_059425	KY102065
P. euphorbiae	*Cyberlindnera euphorbiae*	NRRL Y-17232^{T} = CBS 8033	NG_058754	KY103041
P. euphorbiiphila	*Cyberlindnera euphorbiiphila*	NRRL Y-12742^{T}	EF550312	\
P. fabianii	*Cyberlindnera fabianii*	NRRL Y-1871^{T} = CBS 5640	U73573	KY103043
P. hungchunana sp. nov.	*Candida hungchunana*	CBS 12243^{T}	KY106509	KY102143
P. japonica	*Cyberlindnera japonica*	NRRL YB-2750^{T} = CBS 7209	KY107369	KY103061
P. maesae	*Cyberlindnera maesae*	ATCC MYA-4698^{T} = CBS 12240	NG_059473	NR_152454
P. maritima	*Cyberlindnera maritima*	JCM 9612^{T} = CBS 5107 = NRRL Y-17775	KY106562	NR_152474
P. meyerae	*Cyberlindnera meyerae*	NRRL Y-17236^{T} = CBS 7076	KY107374	KY103066
P. mississippiensis	*Cyberlindnera mississippiensis*	NRRL YB-1294^{T} = CBS 7023	KY107376	KY103068
P. mycetangii	*Cyberlindnera mycetangii*	NRRL Y-6843^{T} = CBS 8675	NG_060382	NR_152475
P. nakhonratchasimensis sp. nov.	*Cyberlindnera nakhonratchasimensis*	JCM 12474^{T} = CBS 11706	KY106593	KY102223
P. pattaniensis sp. nov.	*Candida pattaniensis*	JCM 12475^{T} = CBS 11707	AY634568	NR_144776
P. petersonii	*Cyberlindnera petersonii*	NRRL YB-3808^{T} = CBS 5555	KY107385	KY103077
P. rhizosphaerae	*Cyberlindnera rhizosphaerae*	CBS 11400^{T}	KY107386	KY103078

Table S2. List of yeasts and GenBank numbers used for the rDNA phylogenetic analysis (Continue)

Taxa	Basionym or important synonym	Strain (T=type)	D1/D2	ITS
P. rhodanensis		NRRL Y-7854^{T} = CBS 5518	U73571	KY103083
P. stauntonica sp. nov.	*Candida stauntonica*	CBS 12241^{T}	KY106779	KY102415
P. sylvatica	*Cyberlindnera sylvatica*	CBS 16335^{T}	MT316316	\
P. taoyuanica sp. nov.	*Candida taoyuanica*	CBS 12242^{T}	KY106795	KY102430
P. veronae	*Cyberlindnera veronae*	NRRL Y-7818^{T} = CBS 6591	KY107421	KY103115
P. wuzhiensis	*Cyberlindnera wuzhiensis*	AS 2.3480^{T}	FJ606825	FJ606824
P. xishuangbannaensis	*Cyberlindnera xishuangbannaensis*	NYNU 16752^{T} = CBS 14692	KY213813	KY213821
P. xylebori	*Cyberlindnera xylebori*	CBS 12187^{T}	KY107422	KY103116
P. xylebori		1106PJ03B	MF784950	MF964601
P. xylebori		1030PJ02F	\	MF964600
P. xylebori		1028HS02	MF784948	MF964599
P. xylosilytica	*Cyberlindnera xylosilytica*	NRRL YB-2097^{T} = CBS 13984	NG_064313	NR_172382
Ruyongia gen. nov. (*Wickerhamomyces chambardii* clade)				
R. chambardii comb. nov.	*Wickerhamomyces chambardii*	NRRL Y-2378^{T} = CBS 1900	U74590	NR_154969
R. mori comb. nov.	*Wickerhamomyces mori*	CBS 12678^{T}	NG_064343	NR_160438
R. namnaoensis comb. nov.	*Candida namnaoensis*	CBS 12175^{T}	KY106594	KY102224
R. patagonica comb. nov.	*Wickerhamomyces patagonicus*	CBS 11398^{T}	NG_057185	NR_137719
R. ponderosae comb. nov.	*Candida ponderosae*	NRRL YB-2307^{T} = CBS 8801	NG_057178	KY102338
R. rarassimilans comb. nov.	*Pichia rarassimilans*	CBS 10901^{T}	NG_055081	KY104644
R. tratensis comb. nov.	*Wickerhamomyces tratensis*	CBS 12176^{T}	KY110150	KY105935
Starmera sensu stricto				
S. amethionina		NRRL Y-10978^{T} = CBS 6940	NG_058405	genome
S. caribaea		NRRL Y-17468^{T} = CBS 7692	KY109776	KY105539
S. foglemanii		CBS 16113^{T} = UFMG-CM-Y6337	MG807013	MN990206
S. pachycereana		NRRL Y-10981^{T} = CBS 6943	NG_059915	genome
S. pilosocereana		CBS 13266^{T}	KF666636	KP036617
S. stellimalicola		NRRL Y-17912^{T} = CBS 7853	U84234	KY102417
Taiozyma gen. nov. (*Wickerhamomyces bovis* clade)				
T. bovis comb. nov.	*Wickerhamomyces bovis*	NRRL YB-4184^{T} = CBS 2616	KY110109	NR_154968

Table S2. List of yeasts and GenBank numbers used for the rDNA phylogenetic analysis (Continue)

Taxa	Basionym or important synonym	Strain (T=type)	D1/D2	ITS
T. dajiaensis sp. nov.	*Candida dajiaensis*	CBS 10590^T	NG_057181	NR_154959
T. odintsovae comb. nov.	*Candida odintsovae*	NRRL Y-17760^T = CBS 6026	U70182	NR_077084
T. onychis comb. nov.	*Wickerhamomyces onychis*	NRRL Y-7123^T = CBS 5587	U75421	KY105910
T. peoriensis comb. nov.	*Candida peoriensis*	CBS 8800^T = NRRL YB-1497	KY106687	KY102329
T. rabaulensis comb. nov.	*Wickerhamomyces rabaulensis*	NRRL Y-7945^T = CBS 6797	KY110128	NR_138207
T. yuanshanica sp. nov.	*Candida yuanshanica*	CBS 10589^T	KY106892	KY102522
Waltiozyma (*Wickerhamomyces mucosus+Wickerhamomyces pijperi* clade)				
W. chaumierensis comb. nov.	*Wickerhamomyces chaumierensis*	CBS 8565^T	NG_057180	HM156503
W. mucosa	*Wickerhamomyces mucosus*	NRRL YB-1344^T = CBS 6341	KY110124	NR_154970
W. pijperi comb. nov.	*Wickerhamomyces pijperi*	NRRL YB-4309^T = CBS 2887	KY110127	KY105912
W. solani comb. nov.	*Candida solani*	NRRL Y-2224^T = JCM 2339 = CBS 1908	U70179	KY102402
W. xylosica	*Wickerhamomyces xylosica*	CBS 12320^T	NG_064304	NR_160310
Wickerhamomyces sensu stricto				
W. alni		NRRL Y-11625^T = CBS 6986	KY110065	NR_154966
W. bisporus		NRRL Y-1482^T = CBS 1890	U74589	KY105897
W. canadensis		NRRL Y-1888^T = CBS 1992	EF550300	genome
W. corioli		CGMCC 2.6969^T	OQ179822	OQ179818
W. jianshihensis sp. nov.	*Candida jianshihensis*	CBS 10591^T	KY106533	KY102165
W. menglaensis		NYNU1673^T = CBS 14689	KY213812	KY213818
W. ochangensis		CBS 11843^T	HM485464	NR_154971
W. orientalis		CBS 13306^T	KF938676	KF938677
W. psychrolipolyticus		NBRC 113263^T	LC333101	\
W. quercuum comb. nov.	*Candida quercuum*	NRRL Y-12942^T = CBS 6422	U70184	KY102354
W. sinyiensis		EN27S07^T	MW755436	MF737103
W. ulmi comb. nov.	*Candida ulmi*	NRRL YB-2694^T = CBS 8670	NG_057160	genome
single-species lineage *Wickerhamomyces kurtzmanii*				
Wickerhamomyces kurtzmanii		CBS 15418^T	MK573939	NR_173823
single-species lineage *Wickerhamomyces silvicola*				
Wickerhamomyces silvicola		NRRL Y-1678^T = CBS 1705	U74588	NR_155012
Williopsis (*Williopsis* clade)				

Table S2. List of yeasts and GenBank numbers used for the rDNA phylogenetic analysis (Continue)

Taxa	Basionym or important synonym	Strain (T=type)	D1/D2	ITS
W. culbertsonii sp. nov.	*Cyberlindnera culbertsonii*	CBS 13898^{T}	NG_058894	KM384448
W. dauci comb. nov.	*Cyberlindnera dauci*	DSM 111207^{T} = CBS 16524	MT636878	MT636878
W. galapagoensis comb. nov.	*Cyberlindnera galapagoensis*	CBS 13997^{T} = CLQCA 24SC-025	KJ020281	NR_159816
W. jadinii comb. nov.	*Cyberlindnera jadinii*	NRRL Y-324^{T} = CBS 566	NG_056278	NR_111211
W. lachancei comb. nov.	*Cyberlindnera lachancei*	NRRL Y-27008^{T} = CBS 8557	KY107372	KY103063
W. maclurae comb. nov.	*Cyberlindnera maclurae*	NRRL Y-5377^{T} = CBS 8671	KY107373	KY103065
W. mengyuniae comb. nov.	*Candida mengyuniae*	CBS 10845^{T}	NG_064316	NR_159549
W. misumaiensis comb. nov.	*Cyberlindnera misumaiensis*	NRRL Y-17389^{T} = CBS 8062	KY107377	KY103070
W. mrakii	*Cyberlindnera mrakii*	NRRL Y-1364^{T} = CBS 1707	KY107382	KY103075
W. samutprakarnensis sp. nov.	*Cyberlindnera samutprakarnensis*	CBS 12528^{T}	KY107391	KY103084
W. sargentensis comb. nov.	*Cyberlindnera sargentensis*	CBS 6342^{T} = NRRL YB-4139	KY107392	NR_165970
W. saturnus	*Cyberlindnera saturnus*	NRRL Y-17396^{T} = CBS 254	U75958	KY103100
W. suaveolens	*Cyberlindnera suaveolens*	NRRL Y-17391^{T} = CBS 255	U94930	KY103113
W. subsufficiens	*Cyberlindnera subsufficiens*	NRRL Y-1657^{T} = CBS 5763	KY107420	KY103114
W. takata sp. nov.	*Candida takata*	CBS 12244^{T}	KY106789	KY102424
W. tropicalis comb. nov.	*Cyberlindnera tropicalis*	CBS 14558^{T} = TBRC 6562	KY010353	KY010353
W. vartiovaarae comb. nov.	*Candida vartiovaarae*	NRRL Y-6701^{T}	U69875	KY102493
Xingzhongia gen. nov. (*Wickerhamomyces hampshirensis* clade)				
X. hampshirensis comb. nov.	*Wickerhamomyces hampshirensis*	NRRL YB-4128^{T} = CBS 7208	KY110121	KY105905
X. scolytoplatypi comb. nov.	*Wickerhamomyces scolytoplatypi*	CBS 12186^{T}	KY110130	KY105915
X. strasburgensis comb. nov.	*Wickerhamomyces strasburgensis*	NRRL Y-2383^{T} = CBS 2939	U74591	NR_154973
Candida sp.		KBP:Y-5949	OP740285	OP740285
Cyberlindnera sp.		Y-82	OR651375	OR651375

Table S3. The phenotypic characteristics of newly reclassified *Candida* and related taxa in *Saccharomycotina*

Taxa	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43
Dipodascomycetes																																											
Casaregolazyma	-	-	-	-	-	-	-	-	+	-	-	+	+	+	v	v	v	+	v	v	-	-	v	v	+	v	v	-	v	v	+,n	v	-	-	+,n	v	v	+,n	-,n	-,n	n	41.58-45.31	11-12M
Daia	+	+	-	-	-	-	+	-	v	v	+	+	+	v	v	v	-	v	+	-	v	-	+	+	v	+	+	v	+	v	+	-	v	n	n	n	n	v	v	v	n	40.91-43.72	11-13M
Deakozyma	v	-	-	v	-	-	-	v	+	v	-	+	+	+	+	+	-	+	v	+	-	-	+	+	-	v	v	v	v	+,n	+,n	-,n	+	+,n	v	+,n	-,n	-	+,n	v	n	47.81-47.81	12-12M
Dengshuqunia	-	-	-	-	-	-	-	-	-	-	-	-	+	-	-	-	-	w	-	-	-	-	v	+	-	+	+	-	-	n	-	+	-	n	+	n	n	-	+	+	n	41.69-41.69	11-11M
Diddensiella	v	v	-	-	-	-	v	v	+	+	+	+	+	+	+	+	v	+	+	v	+	-	+	+	+	+	+	+	+	+,n	+,n	-,n	-	-,n	v	+,n	v	v	+,n	+	Q-9	44.66-45.14	12-13M
Entelexis	v	-	v	-,n	-,n	v	v	v	v	v	-	v	v	v	v	-,n	-,n	v	v	v	v	-	v	+	-	+	v	-	v	v	-,n	v	v	v	v	v	v	v	v	v	Q-9	46.18-58.67	9.3-11M
Grinbergsozyma	-	-	-	-	-	-	-	-	+	-	-	w	+	+	+	+	-	+	+	-	-	-	+	+	-	+	+	+	+	n	+	+	+	n	+	n	n	+	+	+	n	51.61-51.61	12-12M
Limtongella	v	-	v	-	-	-	-	v	+	v	v	+	+	+	+,n	+	-,n	+	+	v	v	v	+	+	+,n	+	+	+	+,n	+,n	+	+,n	+	+	+	+	+	-	v	v	Q-8	46.88-46.88	12-12M
Nadsonia	v	v	v	v	-	-	-	-	v	-	-	v	v	v	-	v	-	v	-	-	v	-	v	v	-	v	v	-	-	-	n	v	-	v	v	v	v	n	-	n	Q-6	38.18-40.72	14-15M
Spencermartinsiella	v	-,n	-,n	-,n	-,n	-,n	-,n	v	+	v	v	+,w	+	+	+	v	v	v	+	v	v	-	+	+	+	+	+	v	v	+,n	+,n	v	v	v	v	v	v	-,n	+,n	+,n	n	44.70-46.29	14-15M
Starmerella apicola clade	v	-,n	v	v	-,n	v	v	v	v	v	v	v	v	v	-,n	-,n	-,n	v	v	v	v	-,n	v	v	-,n	v	v	-,n	v	v	-,n	-,n	v	v	v	v	v	v	v	-,n	Q-9	45.23-52.42	7.9-11M
Starmerella cellae clade	v	-,n	v	v	-,n	v	-,n	v	v	v	-	v	v	v	v	-,n	-,n	v	v	-,n	v	-,n	v	+	-	+	+,n	-	v	v	-,n	-,n	+,n	+,n	v	v	v	v	v	v	Q-9	40.96-54.89	8.3-16M
Starmerella sensu stricto clade	v	v	v	v	-,n	v	-,n	v	v	v	v	v	v	v	v	v	v	v	v	-	v	-	v	+	v	v	+	-	v	v	-,n	-,n	v	v	v	+	v	v	v	v	Q-9	44.67-58.16	9.3-10M

Table S3. The phenotypic characteristics of newly reclassified *Candida* and related taxa in *Saccharomycotina* (Continue)

Taxa	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43
Starmerella stellata clade	v	v	v	-,n	-,n	v	-,n	-	v	v	-	-	-	-	-	-	-	-	-	-	v	-	-	-	-	-	-	-	-	-	-,n	-,n	v	v	-	+	-	v	v	-,n	Q-8	39.46-57.21	7-9.3M
Tardiomyces	v	v	v	v	-,n	-	v	v	+,n	v	v	+	+,n	+,n	v	v	+,n	+	+	v	+,n	-,n	v	+,n	+	+,n	+,n	+,n	v	+	+,n	+,n	-	-,n	+,n	+,n	+,n	v	v	+,n	Q-9	48.74-57.59	14-15M
the single-species lineage *Starmerella sirachaensis*	v	-	-	-	-	-	-	-	+	v	-	+	-	+	-	-	-	+	-	-	+	-	-	+	-	+	+	-	+	v	-	n	+	+	+	+	+	+	-	-	Q-9	52.21-52.21	9.5-9.5M
Westerdijkia	+	w	-	-	-	-	n	n	+	l	-	+	n	+	n	n	n	l	l	-	l	+	-	l	n	n	n	-	l	n	n	n	-	-	n	+	n	n	n	n	n	n	n
Yarrowia	-,n	-,n	-,n	-,n	-,n	-,n	-,n	v	-,n	-	-,n	v	v	v	-,n	-,n	-,n	v	v	v	v	-,n	+,n	v	v	v	v	-,n	v	v	v	+,n	-,n	v	v	+,n	v	v	+,n	+,n	Q-9	43.46-50.89	16-30M
Zygoascus sensu stricto clade	v	v	v	v	-,n	v	v	-,n	v	v	-	+	+	v	v	v	+,n	+	+	v	v	-,n	+,n	v	v	v	+,n	v	v	v	+,n	v	v	v	v	v	v	v	+	+,n	Q-9	43.09-48.39	11-12M
the single-species lineage *Zygoascus detingensis*	-	-	-	-	-	-	-	+	+	+	+	+	+	+	+	+	-	-	+	+	w	-	+	+	+	+	+	+	-	w	n	n	-	-	-	+	+	-	n	+	n	n	n
Pichiomycetes																																											
Pichiales																																											
Brettanomyces	v	v	v	v	v	v	v	v	v	-,w	-	v	v	v	v	v	v	-	v	-	-,w	-	+,w	v	-	v	v	-	-	v	n	n	v	v	v	v	v	n	+,w	v	n	39.59-44.53	9.9-22M
Candida methanosorbosa subclade	+	v	-	-	-	-	+	-	-	-	-	+	+	-	-	-	-	+,w	+	-	+	+	+	+	-	+	+	-	+	+	+	w	+	+	+	+	+	-	v	d	Q-7	35.69-36.25	11-13M
Kuraishia clade 1	v	-	-	v	-	-	v	-	-,w	-	-	-	+	v	v	-,w	v	v	+	+,w	+	+,w	+	+	+	+	+	-	v	+	n	n	+	v	v	+	v	v	v	v	n	45.18-51.63	8.6-13M
Ogataea naganishii subclade	+	v	-	-	-	-	+	v	v	-	-	v	+	v	v	-	-	v	+	v	+	+	+	+	+	+	+	-	v	+	+,n	-	-	-	v	v	+	v	+	v	Q-7	41.12-44.87	12-12M
Ogataea pilisensis subclade	v	-,n	-,n	-,n	-,n	-,n	v	-,n	v	-	-,n	v	v	v	-	v	v	v	v	v	v	v	+,n	v	v	v	+,n	v	v	+,n	v	v	v	v	v	+,n	+,n	v	+,n	v	Q-7	30.70-42.98	12-16M
Ogataea ramenticola subclade	v	v	-	-	-	-	v	v	-	-	-	+	v	-	-	-	-,n	v	+	v	v	+	+	v	v	v	+,n	-	-	+,n	+,n	v	+	v	v	+	v	v	v	v	Q-7	27.29-37.08	12-13M

Table S3. The phenotypic characteristics of newly reclassified *Candida* and related taxa in *Saccharomycotina* (Continue)

Taxa	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43
Ogataea saltuana subclade	v	-	-	-	-	-	v	-	v	v	v	v	v	v	-	v	v	v	v	v	v	v	+,n	v	v	v	v	v	v	v	-,n	v	v	v	v	v	v	v	v	+,n	Q-7	38.77-49.30	11-14M
Ogataea sensu stricto subclade	v	-,n	v	v	-,n	-,n	v	-	v	v	v	v	v	v	v	v	v	v	v	v	v	+	+	v	v	v	v	-,w	v	v	v	-,n	v	v	+,n	v	v	v	v	v	Q-7	39.31-49.45	8.4-11M
Ogataea wickerhamii subclade	-	-	-	-	-	-	-	-	-	-	-	v	v	v	-	-	-	v	v	v	v	+	v	v	v	v	v	-	-	v	-	-,n	v	v	+	+	+	-	v	v	Q-7	40.53-48.87	9.9-12M
Ramirezia	v	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-,w	+	-,w	+	+	+	+,w	+	+,w	+	-	-	+	+	-	v	+	+	+	+	-	v	+	Q-7	30.84-30.84	19-19M
the single-species lineage *Allodekkera sacchari*	-	n	n	n	n	n	n	-	+	-	-	-	+,w	+	+,w	+,w	-	-	-	-	-	-	+	+,w	-	+	+,w	-	+	-,w	+	-	+	+,w	+	+	+	-	-	n	Q-9	43.24-43.24	13-13M
the single-species lineage *Ogataea methylovora*	v	-	v	-	-	v	v	-	+	+	-	-	+	-	-	-	-	+,w	+	+,w	+	+	+	+	+	+	+	-	+	+	+	-	+	+	+	+	+	-	+	-	Q-7	33.66-33.66	13-13M
Wenyingozyma	v	v	v	-	-	v	v	v	v	v	-	v	v	v	v	-	-,n	v	+	v	v	+	+	v	v	v	+,n	-	v	+,n	-	v	v	v	v	v	v	v	v	v	Q-7	27.29-44.87	11-13M
Xiuguozyma	-	-	-	-	-	-	-	-	-	-	-	v	+	-	-	-	-	-	-	v	-	-	+	v	-	+	+	-	-	-	+	-	-	-	+	+	+	-	-	n	n	43.29-55.34	9-9.8M
Serinales																																											
Candida sensu stricto clade	v	v	v	v	-	v	v	v	v	v	v	v	v	v	v	v	v	v	v	v	v	-,n	+	v	v	v	+,n	v	v	v	v	v	v	v	v	v	v	v	v	v	Q-9	31.46-44.80	12-23M
Candida tibetensis clade	+	-	-	-	-	-	-,n	v	+	-	-	+	+	+	+	+	-,n	-	+	+	+	-	v	+	-,n	+	+	-	+	-,n	+,n	v	-	-	+	+	+	w,n	-,n	-,n	Q-9	39.34-54.07	12-12M
Cephaloascus	v	v	-	-	-	-	-	-	-	v	v	+	v	-	-	-	v	v	+	v	-	-	+	+	-	+	+	-	+	n	v	-	-	-	+	+	+	v	n	n	Q-9	34.64-36.9	14-15M
Chernovozyma	+	v	-	-	-	-	v	-	v	-	-	+	+	v	v	v	-	v	-	-	v	-	+	v	v	+	+	-	v	v	+,n	-,n	-	-	+	+,n	+,n	-	v	-	Q-9	35.43-51.92	12-20M
Debaryomyces sensu stricto clade	v	v	v	v	v	v	v	v	v	v	v	v	v	v	v	v	v	v	+	v	v	-,n	v	v	v	v	+	-	v	+,n	v	v	v	v	v	v	v	v	v	v	Q-9	35.42-41.42	11-13M

Table S3. The phenotypic characteristics of newly reclassified *Candida* and related taxa in *Saccharomycotina* (Continue)

Taxa	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43
Diutina	v	v	-,n	v	-,n	-,n	-,n	-,w	v	v	v	+	v	v	v	v	v	v	v	-,n	v	-,n	+	v	v	v	+,n	v	v	v	+,n	v	v	v	+	+	v	v	v	v	Q-9	41.23-53.05	12-16M
Dujonia	v	v	v	v	-	-	v	-,w	v	-	-	v	+,w	v	v	v	-	v	v	v	v	-	+	+,w	v	+	+,w	-	+,w	v	+	v	-	v	v	+,w	+,w	v	+	+	Q-9	35.72-55.69	11-15M
Fermentozyma	v	v	v	v	-,n	-	v	v	v	v	v	v	+	v	v	v	v	v	v	v	v	-,n	v	+	v	v	v	-,n	v	v	v	v	v	-	v	v	v	v	-,n	-,n	Q-9	38.76-38.76	14-14M
Glucitozyma	v	-	-	-	-	-	v	-	+	-	-	+	+	+	+	-	-	+	+	-	-,w	-	-	+	-	-	+	-	+	+	+	+	-	-	+	+	+	v	-	n	Q-9	32.36-32.36	10-10M
Hemisphaericaspora	v	v	v	v	-,n	-,n	v	v	v	v	-	v	v	+	v	+,n	v	v	+	v	v	v	v	v	v	v	v	-	v	v	v	v	-	-	v	+	v	-,n	v	-,n	Q-9	33.86-37.53	14-18M
Insectozyma	+	v	v	v	-,n	-	v	v	v	v	v	v	v	v	v	v	v	v	v	-	v	v	+	v	-	v	+,n	v	v	v	+,n	+,n	-	-	v	v	v	v	v	v	n	23.91-36.04	11-16M
Intestinozyma	+	+	-	-	-	-	-	-	+	-	-	+	+	+	+	+	-	-	+	-	d	-	w	w	-	+	+	-	+	-	-	n	-	-	+	+	+	-	-	n	n	45.46-45.46	14-14M
Keqinozyma	v	v	v	-,n	-,n	-,n	v	-	+	-	-	+	v	+	v	+	-	v	+	v	v	-	+	+	v	+	+	-	v	v	+,n	v	-	-	+	+	+	v	v	+,n	Q-9	41.31-48.77	10-11M
Kurtzmaniella	+	v	v	v	-,n	-,n	-	-,w	+	v	-	+	v	+	+	v	-	+	v	-	v	-	+	+	-,n	+	+	-	+	+	+	v	v	v	+,n	+,n	+,n	v	v	-,n	Q-9	33.02-45.16	12-15M
Lizanozyma	+	-	v	v	-	-	-,n	-	+	-	-	-	+	+	+	+	v	v	-	-	-	-	+	v	-	+	+	-	v	+	-	+,n	-	-	+	+	+	v	v	v	Q-9	38.39-40.85	12-14M
Lodderomyces	v	v	v	v	-,n	-,n	v	v	v	v	v	v	v	v	v	v	v	v	v	v	v	-,n	v	v	-,n	v	+	v	v	v	+,n	v	v	v	+,n	v	v	v	v	v	Q-9	27.21-45.28	13-15M
Meyerozyma	v	v	v	v	-	v	v	v	+	v	v	v	+	+,w	v	+	v	v	+	v	+	-	v	v	v	v	v	v	v	v	v	n	-	v	n	+	n	v	v	v	Q-9	42.40-49.79	9.4-11M
Millerozyma	v	v	v	v	v	-,n	v	-,n	v	-	-	+,n	v	v	v	v	v	v	v	-,n	v	-,n	+,n	v	v	+,n	+,n	-	+,n	v	+,n	+,n	v	-,n	+	v	v	+	v	-,n	Q-9	40.16-41.43	11-11M
Nematodospora	v	v	-	v	-,n	-,n	+,n	-	v	-	-	+	+	+	v	v	+	v	+	-	-	-	+	+	-	+	+	-	v	v	n	n	-	-	w	+	+,n	-	-	n	n	35.44-35.46	12-13M

Table S3. The phenotypic characteristics of newly reclassified *Candida* and related taxa in *Saccharomycotina* (Continue)

Taxa	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43
Nothofagozyma	+	-	-	-	-	-	v	-	+	-	-	+	+	+	+	+	-	+	+	+	+	-	+	+	+	+	+	-	+	+	v	+	+	+	+	+	+	-	+	+	Q-7	41.45-41.45	14-14M
Priceomyces	v	-	-	-	-	-	-,n	-	v	v	v	+	v	v	v	v	v	v	v	v	v	-	v	+,w	v	+	+	-	v	v	v	v	-	v	+,n	+	+	v	v	v	Q-9	36.80-41.14	11-12M
Scheffersomyces sensu stricto clade	v	v	-,n	v	-,n	-,n	v	v	+	v	v	+	+	+	v	v	v	v	+	v	v	v	v	v	v	v	v	v	v	v	v	+,n	v	v	v	v	v	v	v	v	Q-9	28.15-45.65	13-17M
Schwanniomyces sensu stricto clade	v	v	v	v	-	v	v	v	+	v	v	v	v	+	v	v	v	v	v	v	v	-	+	d	v	v	+	-	v	v	+,n	v	-	v	v	+	+	v	v	v	Q-9	30.16-34.91	12-13M
Spathaspora sensu stricto clade	+	+,n	-,n	v	-,n	-,n	v	-	+	-	-	+	+	+	+	+,n	v	v	+	v	v	-	v	v	+,n	+	v	-	v	v	+,n	v	-,n	-,n	+,n	+,n	+,n	v	-,n	-,n	n	31.73-37.40	13-20M
Suhomyces	v	v	v	v	v	v	v	v	v	v	v	+,n	+	v	v	v	v	v	v	v	v	-,n	v	v	v	v	+,n	-,n	v	v	v	v	v	v	v	v	v	v	v	v	Q-9	36.92-47.23	12-15M
Suzukiozyma	v	v	v	v	-,n	-	v	v	+	v	v	+	+	+	v	v	v	v	+	v	v	-,n	+	+	-	+	+,n	-	+	+,n	+,n	v	-	v	+,n	+,n	v	v	v	v	Q-9	31.16-41.24	12-25M
Teunomyces	v	v	v	v	v	v	+,n	-,w	v	v	v	v	+	v	v	+	v	v	v	v	v	v	v	v	v	v	v	-,n	v	v	+,n	+,n	v	v	+	+,n	v	v	v	v	Q-9	41.03-46.16	10-13M
the single-species lineage *Candida anglica*	+	-,+	-	-	-	-	+	-	-	-	-	+	+	-	-	-	-	+	-	-	-	-	+	+	-	+	+	-	+	d	+	-	-	-	+	+	+	+	-	-	n	38.63-38.63	13-13M
the single-species lineage *Candida anutae*	-	-	-	-	-	-	-	-	+,w	-	-	-	+	-	-	-	-	-	-	-	-	-	-	+	-	+	d	-	+	-	+	d	-	-	-,w	-,w	-,w	+	+	v	n	47.87-47.87	11-11M
the single-species lineage *Debaryomyces singareniensis*	+	+	-	-	-	-	-	-	-	-	-	+	-	-	-	-	n	+	-	-	+	-	+	+	+	+	+	-	-	+	n	n	-	-	+	+	-	n	-	-	n	36.07-36.07	9.7-9.7M
the single-species lineage *Schwanniomyces etchellsii*	v	-	v	v	-	-	-	-	+	-	-	+	+,w	+	+	+	-	+	+	-,w	+,w	-	+	+	-	+	+	-	v	+	+	w,d	-	-	+	+	+	+	-	n	Q-9	38.54-38.54	11-11M
Wickerhamia	+	v	+	-	-	+	-	-	+	+	-	+	-	-	-	-	-	-	-	-	-	-	+	+	-	+	+	-	+	-	n	+	-	-	+	+	+	w	+	+	Q-9	37.80-37.80	14-14M
Yamadazyma epiphylla clade	+	-,n	-,n	-,n	-,n	-,n	-,n	-	+	v	v	+	+	+	+	+	v	+	+	+	+	-,n	+	+	+	+	+	-	v	+	+,n	v	-	-	+	+	+	+	-	-	Q-9	34.93-40.97	11-11M

Table S3. The phenotypic characteristics of newly reclassified *Candida* and related taxa in *Saccharomycotina* (Continue)

Taxa	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43
Yamadazyma olivae clade	v	v	v	v	v	v	v	v	+,n	v	v	v	v	+	v	v	v	v	v	v	v	v	v	v	v	v	v	-	v	v	v	v	v	v	+,n	+	v	v	v	v	Q-9	28.16-43.49	9.1-13M
Yamadazyma sensu stricto clade	v	v	v	v	v	v	v	v	v	v	v	+,n	+,n	v	v	v	v	v	+	v	v	-,n	+,n	+,n	v	+,n	+,n	-,n	v	v	v	v	v	v	v	v	v	v	v	v	Q-9	33.64-44.62	9.7-13M
Yamadazyma triangularis clade	v	v	-	-	-	-	-	-	+	-	-	+	+	+	+	+	v	v	+	v	+	-,n	+	+	+	+	+	-	+,w	v	+,n	-	-	-	+	+	+	+	v	+,n	Q-9	30.90-33.83	11-21M
Zhuliangozyma	+	v	-,n	v	-,n	-,n	v	v	v	-	v	+	+	+	v	+,n	-,n	v	+	-	v	-	+	-	-	+	v	-	+	-,n	+,n	v	v	v	v	+	v	v	v	+,n	n	49.78-53.88	12-14M
Saccharomycetes																																											
Phaffomycetales																																											
Barnettozyma sensu stricto clade	v	-,n	-,n	-,n	-,n	-,n	-,n	v	v	v	v	v	v	v	v	v	v	v	+,n	v	v	-,n	v	+	v	v	v	v	v	v	-,n	-,n	v	+,n	v	v	v	-,n	-,n	-,n	Q-7	41.60-48.44	11-12M
Barnettozyma wickerhamii clade	v	v	v	v	-	-	-,n	v	v	v	v	v	v	v	v	v	v	v	+	v	v	-	+	v	v	v	v	v	v	v	v	-	v	v	v	v	v	v	-	-,n	Q-7	38.09-44.32	11-13M
Buckleya	v	-	v	-	-	-	-	-	+	-	-	-	d	+	+	+	-	-	+	-	-	-	+	+	-	+	+	-	+	+	-	-	-	-	+	+	+	-	-	n	Q-7	42.53-42.53	11-11M
Gotozyma	v	-,n	-	v	-,n	-,n	-,n	-,n	-	v	-,n	-,n	-,n	v	-,n	-,n	-,n	-,n	v	-,n	v	-,n	+,n	+	-,n	+,n	-,n	-,n	+	-,n	-,n	-,n	-,n	-,n	+,n	+,n	+,n	-,n	-,n	-,n	Q-7	34.85-37.83	11-13M
Hansenula clade	v	v	v	v	-,n	v	v	v	v	v	v	v	+,n	v	v	v	v	v	v	v	v	v	v	v	v	v	v	-	v	v	v	v	v	v	v	v	v	v	v	v	Q-7	30.39-39.70	13-25M
Komagataea	v	v	v	v	-	-	-,n	v	v	v	v	v	v	v	v	v	v	v	+	v	v	-	+	v	v	v	v	v	v	v	v	-	v	v	v	v	v	v	-	-,n	Q-7	38.09-44.32	11-13M
Lacusozyma	-	-	-	-	-	-	-	-	+	-	w	-	-	-	-	-	-	-	-	n	-	n	n	+	-	w	-	n	-	n	n	n	+	+	+	+	+	-	n	n	n	34.47-34.47	12-12M
Liangdongia	v	-,n	-,n	-,n	-,n	-,n	-,n	-	-	-	-	-	-	-	-	n	-	-,n	-	-	-	-	+	+	-	v	v	-,n	v	v	v	-,n	v	v	v	v	+,n	-,n	+,n	+,n	Q-7	29.76-40.63	12-16M
Millerago	-	n	n	n	n	n	n	v	+	v	v	v	v	-	v	n	v	v	v	v	v	n	n	+	v	v	v	v	v	v	n	n	-	-	n	v	n	n	-	n	n	30.83-31.77	9.8-13M

Table S3. The phenotypic characteristics of newly reclassified *Candida* and related taxa in *Saccharomycotina* (Continue)

Taxa	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43
Petasospora	v	v	v	v	-, n	v	v	v	+	v	v	v	v	+	v	v	v	v	+	v	v	-	v	+	-	v	v	-	v	v	v	-, n	v	v	v	+	v	v	v	-, n	Q-7	39.64-51.79	11-15M
Phaffomyces	-	-, n	-, n	-, n	-, n	-, n	-, n	-	v	-	-	-	v	v	-	-	-	-	v	-	v	-	v	+	-	v	v	-	v	v	-	-, n	-	-, n	+, n	+, n	+, n	-	-, n	-, n	Q-7	31.11-32.30	12-13M
Ruyongia	v	-, n	v	-, n	-, n	-, n	-, n	-, w	v	v	-	v	-	v	v	v	v	v	v	v	-	-	v	+	-	v	v	-	v	v	v	-, n	-, n	v	v	v	v	-, n	-, n	-, n	Q-7	26.18-35.55	12-15M
Starmera sensu stricto clade	v	-, n	-, n	-, n	-, n	-, n	-, n	-	-	v	-	-	-	-	-, n	-, n	-	-	v	v	-	-	+	+	-	v	v	-	v	v	v	-	-	-	v	v	v	-, n	-	-, n	Q-7	31.44-43.07	10-13M
Taiozyma	+	v	v	v	-	v	v	v	+	v	v	v	v	+	+	+	v	v	v	v	v	-	v	+	v	+	v	-	v	v	v	v	v	v	v	+	v	v	v	-, n	Q-7	34.46-42.63	12-20M
the single-species lineage *Barnettozyma botsteinii*	+	n	-	+	n	n	n	n	-	n	n	n	n	+	n	n	n	n	+	n	+	n	n	+	n	n	n	n	+	n	n	n	n	n	n	n	n	n	n	n	n	34.85-34.85	11-11M
the single-species lineage *Barnettozyma salicaria*	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	-	-	-	+	+	-	+, w	+	-	+	-, w	-	-	-	-, w	+, w	+	+	-	-	n	Q-7	38.42-38.42	11-11M
the single-species lineage *Wickerhamomyces mucosus*	+	-	-	-	-	-	-	-	+	-	-	-, w	+	+	+, w	+	-, w	+	+, w	+, w	-	-	+	v	-	-, w	+, w	-	-, w	+	n	-	-	-	-, w	-	+, w	v	-	-	Q-7	30.68-30.68	13-13M
Waltiozyma	+	-	-	-	-	-	-, n	-	v	-	-	v	v	v	v	v	v	+, n	+	v	-	-	+	v	-	v	v	-, n	v	+ ,n	-, n	-, n	-	-	v	v	+, n	v	-	-, n	Q-7	30.68-41.36	13-17M
Wickerhamomyces pijperi clade	+	-	-	-	-	-	-, n	-	v	-	-	-	v	v	v	v	-, n	+, n	+	-	-	-	+	+	-	v	v	-, n	v	+ ,n	-, n	-, n	-	-	+, n	+, n	+, n	-, n	-	-, n	Q-7	34.56-41.36	13-17M
Wickerhamomyces sensu stricto clade	v	v	-, n	-, n	-, n	-, n	-, n	v	v	v	v	v	v	v	v	v	v	v	+	v	v	-	v	v	v	v	+, n	v	v	v	-, n	-, n	v	v	v	v	v	v	-, n	-, n	Q-7	31.52-39.49	11-15M
Williopsis clade	v	v	v	v	-, n	v	v	v	v	v	v	v	v	v	v	v	v	v	v	v	v	-, n	v	v	v	v	v	v	v	v	v	v	v	v	v	v	v	v	v	v	Q-7	37.84-49.03	9.9-15M
Xingzhongia	+	v	v	-	-	v	v	-	+	v	-	v	+	+	v	+	v	-	+	-	v	-	+	+	-	+	+	-	v	v	-, n	-, n	v	-	+	+	+	v	-	n	Q-7	36.81-39.18	12-13M

1: Fermentation of glucose; 2: fermentation of galactose; 3: fermentation of sucrose; 4: fermentation of maltose; 5: fermentation of lactose; 6.fermentation of raffinose; 7: fermentation of a,a-trehalose; 8: inulin; 9: sucrose; 10: raffinose; 11: melibiose; 12: galactose; 13: trehalose; 14: maltose; 15: melezitose; 16: methyl-α-D-glucoside; 17: soluble starch; 18: L-sorbose; 19: D-xylose; 20: D-arabinose; 21: D-ribose; 22: methanol; 23: ethanol; 24: glycerol; 25: erythritol; 26: D-mannitol; 27: D-glucitol; 28: myo-inositol; 29: citrate; 30: xylitol; 31: N-acetyl-D-glucosamine; 32: hexadecane; 33: nitrate; 34: nitrite; 35: cadaverine; 36: L-lysine; 37: ethylamine; 38: 10% NaCl/5% glucose; 39: 0.01 % cycloheximide; 40: 0.1 % cycloheximide; 41: CoQ (Main component); 42: Mol % G+C (Ave.)；43：Genome size

Abbreviations: + = positive; – = negative; v = variable; w = weak; d = delay; n = not available.

Table S4. The antifungal resistance profiles of *Candida* species assigned to the newly created genera in this study

Taxa	Strains	Azole resistance-associated gene								Polyene resistance-associated gene	Echinocandin resistance-associated gene		Nucleoside analog resistance-associated gene
		ERG11								ERG2	FKS1		FUR1
		F126L	Y132F	K143R	F145L	G448E	F449V	G450E	G464S	F105SfsX23	S645P/Y/F	F641Y	F211I
Dipodascomycetes													
Casaregolazyma	*Candida lundiana* CBS 12271	F	Y	K	F	G	F	G	G	F	S	F	F
	Candida patagonica CBS 10443	F	Y	K	F	G	F	G	G	F	S	F	F
	Candida suthepensis CBS 12270	F	Y	K	F	G	F	G	G	F	S	F	F
Dengshuqunia	*Candida hispaniensis* NRRL Y-5580	F	Y	K	F	G	F	G	G	F	S	F	F
Grinbergsozyma	*Candida bentonensis* NRRL YB-2364	F	Y	K	F	G	F	G	G	F	S	F	-
Pichiomycetes													
Pichiales													
Ramirezia	*Candida boidinii* NRRL Y-2332	F	Y	K	F	G	F	G	G	F	S	F	F
Wenyingozyma	*Candida methanosorbosa* NRRL Y-17320	F	Y	K	F	G	F	G	G	F	S	F	F

Table S4. The antifungal resistance profiles of *Candida* species assigned to the newly created genera in this study (Continue)

Taxa	Strains	Azole resistance-associated gene								Polyene resistance-associated gene	Echinocandin resistance-associated gene		Nucleoside analog resistance-associated gene
		ERG11								ERG2	FKS1		FUR1
		F126L	Y132F	K143R	F145L	G448E	F449V	G450E	G464S	F105SfsX23	S645P/Y/F	F641Y	F211I
	Candida nanaspora NRRL Y-17679	F	Y	K	F	G	F	G	G	F	S	F	F
	Candida nitratophila NRRL YB-3654	F	Y	K	F	G	F	G	G	F	S	F	F
	Candida succiphila JCM 9445	F	Y	K	F	G	F	G	G	F	S	F	F
	Candida suzukii NRRL Y-27593	F	Y	K	F	G	F	G	G	F	S	F	F
Xiuguozyma	*Candida insectalens* NRRL Y-7778	F	Y	K	F	G	F	G	G	F	S	F	F
	Candida silvatica NRRL Y-7777	F	Y	K	F	G	F	G	G	F	-	-	F
Serinales													
Candida	*Candida albicans* SC5314	F	Y	K	F	G	F	G	G	F	S	F	F
	Candida buenavistaensis NRRL Y-27734	F	Y	K	F	G	F	G	G	F	S	F	-

Table S4. The antifungal resistance profiles of *Candida* species assigned to the newly created genera in this study (Continue)

Taxa	Strains	Azole resistance-associated gene								Polyene resistance-associated gene	Echinocandin resistance-associated gene		Nucleoside analog resistance-associated gene
		ERG11								ERG2	FKS1		FUR1
		F126L	Y132F	K143R	F145L	G448E	F449V	G450E	G464S	F105SfsX23	S645P/Y/F	F641Y	F211I
	Candida dubliniensis CD36	F	Y	K	F	G	F	G	G	F	S	F	F
	Candida frijolesensis NRRL Y-48060	F	Y	K	F	G	F	G	G	F	S	F	F
	Candida gigantensis NRRL Y-27736	F	Y	K	F	G	F	G	G	F	S	F	F
	Candida labiduridarum NRRL Y-27940	F	Y	K	F	G	F	G	G	F	S	F	F
	Candida maltosa Xu316	F	Y	K	F	G	F	G	G	F	S	F	F
	Candida neerlandica NRRL Y-27057	F	Y	K	F	G	F	G	G	F	S	F	F
	Candida pseudoviswanathii CBS 13916	F	Y	K	F	G	F	G	G	F	S	F	F
	Candida sanyaensis CBS 12637	F	Y	K	F	-	-	-	-	F	S	F	F

Table S4. The antifungal resistance profiles of *Candida* species assigned to the newly created genera in this study (Continue)

Taxa	Strains	Azole resistance-associated gene								Polyene resistance-associated gene	Echinocandin resistance-associated gene		Nucleoside analog resistance-associated gene
		ERG11								ERG2	FKS1		FUR1
		F126L	Y132F	K143R	F145L	G448E	F449V	G450E	G464S	F105SfsX23	S645P/Y/F	F641Y	F211I
	Candida sojae GF41	F	Y	K	F	G	F	G	G	F	S	F	F
	Candida tetrigidarum NRRL Y-48142	F	Y	K	F	G	F	G	G	F	S	F	F
	Candida tropicalis MYA-3404	F	Y	K	F	G	F	G	G	F	S	F	F
	Candida viswanathii NRRL Y-6660	F	Y	K	F	G	F	G	G	F	S	F	F
Chernovozyma	*Candida aurita* CBS 9724	F	Y	K	F	G	F	G	G	F	S	F	F
	Candida palmyrensis CBS 11546	F	Y	K	F	G	F	G	G	F	S	F	F
	Candida sophiae-reginae NRRL Y-17668	F	Y	K	F	G	F	G	G	F	S	F	F
Dujonia	*Candida boleticola* NRRL Y-17080	F	Y	K	F	G	F	G	G	F	S	F	F
	Candida oleophila NRRL Y-2317	F	Y	K	F	G	F	G	G	F	S	F	F

Table S4. The antifungal resistance profiles of *Candida* species assigned to the newly created genera in this study (Continue)

Taxa	Strains	Azole resistance-associated gene								Polyene resistance-associated gene	Echinocandin resistance-associated gene		Nucleoside analog resistance-associated gene
		ERG11								ERG2	FKS1		FUR1
		F126L	Y132F	K143R	F145L	G448E	F449V	G450E	G464S	F105SfsX23	S645P/Y/F	F641Y	F211I
	Candida railenensis CLIB 1423	F	Y	K	F	G	F	G	G	F	S	F	F
	Candida santamariae NRRL Y-6656	F	Y	K	F	G	F	G	G	F	S	F	F
	Candida schatavii NRRL Y-17078	F	Y	K	F	G	F	G	G	F	S	F	F
	Candida zeylanoides NRRL Y-1774	F	Y	K	F	G	F	G	G	F	S	F	F
Fermentozyma	*Candida sake* NRRL Y-1622	F	Y	K	F	G	F	G	G	F	A	F	F
Glucitozyma	*Candida multigemmis* NRRL Y-17659	F	Y	K	F	G	F	G	G	F	A	F	F
Hemisphaericaspora	*Candida lyxosophila* NRRL Y-17539	F	Y	K	F	G	F	G	G	F	S	F	F
	Candida subhashii CBS 10753	F	Y	K	F	G	F	G	G	F	S	F	F

Table S4. The antifungal resistance profiles of *Candida* species assigned to the newly created genera in this study (Continue)

Taxa	Strains	Azole resistance-associated gene								Polyene resistance-associated gene	Echinocandin resistance-associated gene		Nucleoside analog resistance-associated gene
		ERG11								ERG2	FKS1		FUR1
		F126L	Y132F	K143R	F145L	G448E	F449V	G450E	G464S	F105SfsX23	S645P/Y/F	F641Y	F211I
Insectozyma	*Candida xylanilytica* NBRC 106499	F	Y	K	F	G	F	G	G	F	S	F	F
	Candida bohioensis NRRL Y-27737	F	Y	K	F	G	F	G	G	F	S	F	F
	Candida chauliodis NRRL Y-27909	F	Y	K	F	G	F	G	G	F	S	F	F
	Candida coleopterorum CBS 14180	F	Y	K	F	G	F	G	G	F	S	F	F
	Candida corydali NRRL Y-27910	F	Y	K	F	G	F	G	G	F	S	F	F
	Candida morakotiae NRRL Y-48708	F	Y	K	F	G	F	G	G	F	S	F	F
	Candida parachauliodis CBS 13928	F	Y	K	F	G	F	G	G	F	S	F	F
	Candida sakaeoensis CBS 12318	F	Y	K	F	G	F	G	G	F	S	F	F

Table S4. The antifungal resistance profiles of *Candida* species assigned to the newly created genera in this study (Continue)

Taxa	Strains	Azole resistance-associated gene								Polyene resistance-associated gene	Echinocandin resistance-associated gene		Nucleoside analog resistance-associated gene
		ERG11								ERG2	FKS1		FUR1
		F126L	Y132F	K143R	F145L	G448E	F449V	G450E	G464S	F105SfsX23	S645P/Y/F	F641Y	F211I
	Candida verbasci CBS 12699	F	Y	K	F	G	F	G	G	F	S	F	F
	Candida xiaguanensis CBS 13923	F	Y	K	F	G	F	G	G	F	S	F	-
Intestinozyma	*Candida alai* NRRL Y-27739	F	Y	K	F	G	F	G	G	F	S	F	F
Keqinozyma	*Candida nonsorbophila* CBS 10862	F	Y	K	F	G	F	G	G	F	S	F	-
	Candida sinolaborantium LESF1467	F	Y	K	F	G	F	G	G	F	S	F	F
Lodderomyces	*Candida jiufengensis* CBS 10846	F	Y	K	F	G	F	G	G	F	S	F	F
	Candida margitis CBS 14175	F	Y	K	F	G	F	G	G	F	S	F	F
	Candida metapsilosis ATCC 96143	F	Y	K	F	G	F	G	G	F	S	F	F

Table S4. The antifungal resistance profiles of *Candida* species assigned to the newly created genera in this study (Continue)

Taxa	Strains	Azole resistance-associated gene								Polyene resistance-associated gene	Echinocandin resistance-associated gene		Nucleoside analog resistance-associated gene
		ERG11								ERG2	FKS1		FUR1
		F126L	Y132F	K143R	F145L	G448E	F449V	G450E	G464S	F105SfsX23	S645P/Y/F	F641Y	F211I
	Candida orthopsilosis Co 90-125	F	Y	K	F	G	F	G	G	F	S	F	F
	Candida oxycetoniae CBS 10844	F	Y	K	F	G	F	G	G	F	S	F	F
	Candida parapsilosis ATCC 22019	F	Y	K	F	G	F	G	G	F	S	F	F
	Candida pseudojiufengensis CBS 10847	F	Y	K	F	G	F	G	G	F	S	F	F
	Candida theae CBS 12239	F	Y	K	F	G	F	G	G	F	S	F	F
Nothofagozyma	*Candida chilensis* NRRL Y-17141	F	Y	K	F	G	F	G	G	F	S	F	F
Suzukiozyma	*Candida fluviatilis* NRRL Y-7711	F	Y	K	F	G	F	G	G	F	S	F	F
	Candida glaebosa NRRL Y-6949	F	Y	K	F	G	F	G	G	F	S	F	F

Table S4. The antifungal resistance profiles of *Candida* species assigned to the newly created genera in this study (Continue)

Taxa	Strains	Azole resistance-associated gene								Polyene resistance-associated gene	Echinocandin resistance-associated gene		Nucleoside analog resistance-associated gene
		ERG11								ERG2	FKS1		FUR1
		F126L	Y132F	K143R	F145L	G448E	F449V	G450E	G464S	F105SfsX23	S645P/Y/F	F641Y	F211I
	Candida manassasensis CBS 12534	F	Y	K	F	G	F	G	G	F	S	F	F
	Candida pseudoglaebosa NRRL Y-17911	F	Y	K	F	G	F	G	G	F	S	F	F
	Candida palmioleophila NRRL Y-17323	F	Y	K	F	G	F	G	G	F	S	F	F
	Candida sphagnicola CBS 11774	F	Y	K	F	G	F	G	G	F	S	F	F
Zhuliangozyma	*Candida blackwelliae* CBS 10843	F	Y	K	F	G	F	G	G	F	S	F	F
	Candida parablackwelliae CBS 15228	F	Y	K	F	G	F	G	G	F	S	F	F
	Candida tibetensis CBS 10298	F	Y	K	F	G	F	G	G	F	A	F	F
Saccharomycetes													
Phaffomycetales													

Table S4. The antifungal resistance profiles of *Candida* species assigned to the newly created genera in this study (Continue)

Taxa	Strains	Azole resistance-associated gene								Polyene resistance-associated gene	Echinocandin resistance-associated gene		Nucleoside analog resistance-associated gene
		ERG11								ERG2	FKS1		FUR1
		F126L	Y132F	K143R	F145L	G448E	F449V	G450E	G464S	F105SfsX23	S645P/Y/F	F641Y	F211I
Buckleya	*Candida freyschussii* NRRL Y-7957A	F	Y	K	F	G	F	G	G	F	S	F	F
Gotozyma	*Candida montana* NRRL Y-17326	F	Y	K	F	G	F	G	G	F	S	F	F
Liangdongia	*Candida berthetii* NRRL Y-17644	-	-	-	-	G	F	G	G	F	S	F	F
	Candida dendrica NRRL Y-7775	F	Y	K	F	G	F	G	G	F	S	F	F
Ruyongia	*Candida namnaoensis* CBS 12175	F	Y	K	F	G	F	G	G	F	S	F	F
	Candida ponderosae NRRL YB-2307	F	Y	K	F	G	F	G	G	F	S	F	F
Taiozyma	*Candida dajiaensis* CBS 10590	F	Y	K	F	G	F	G	G	F	S	F	F
	Candida odintsovae NRRL Y-17760	F	Y	K	F	G	F	G	G	F	S	F	F

Table S4. The antifungal resistance profiles of *Candida* species assigned to the newly created genera in this study (Continue)

Taxa	Strains	Azole resistance-associated gene								Polyene resistance-associated gene	Echinocandin resistance-associated gene		Nucleoside analog resistance-associated gene
		ERG11								ERG2	FKS1		FUR1
		F126L	Y132F	K143R	F145L	G448E	F449V	G450E	G464S	F105SfsX23	S645P/Y/F	F641Y	F211I
	Candida peoriensis NRRL YB-1497	F	Y	K	F	G	F	G	G	F	S	F	F
	Candida yuanshanica CBS 10589	F	Y	K	F	G	F	G	G	F	S	F	F

The bold and italics indicate a mutation in the antifungal resistance gene locus.

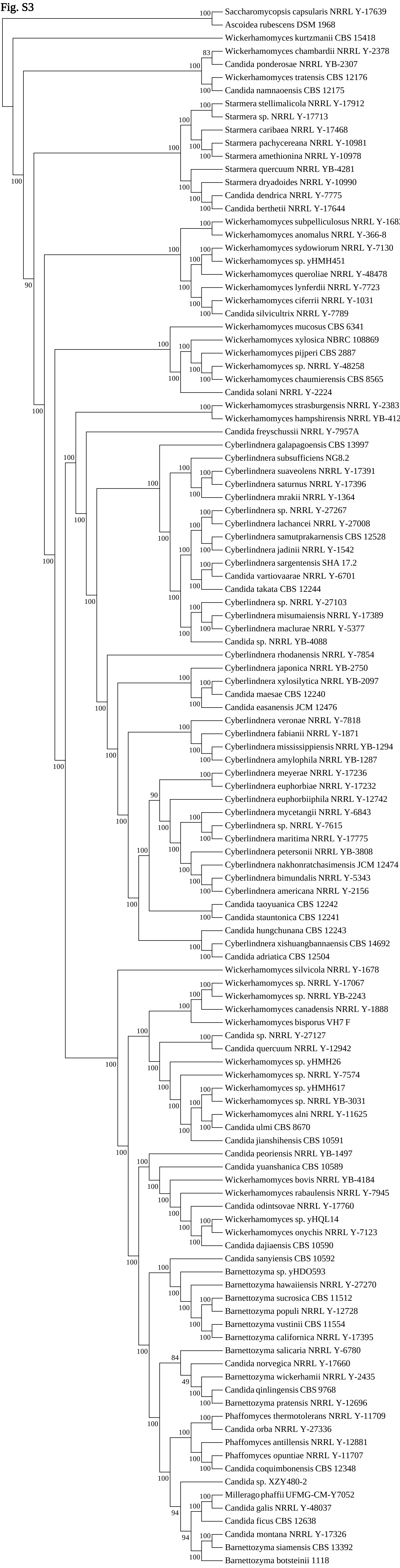
Fig. S1


Tortispora ganteri NRRL Y-17035
Trigonopsis variabilis NRRL Y-1579
Candida hispaniensis NRRL Y-5580
Yarrowia alimentaria CBS 10151
Yarrowia brassicae CBS 15225
Yarrowia deformans CBS 2071
Yarrowia galli CBS 9722
Yarrowia keelungensis CBS 11062
Yarrowia porcina CBS 12935
Yarrowia lipolytica CGMCC7326
Yarrowia osloensis CBS 10146
Yarrowia yakushimensis CBS 10253
Yarrowia hollandica CBS 4855
Yarrowia bubula NRRL Y-63668
Yarrowia phangngaensis CBS 10407
Nadsonia commutata NRRL Y-7950
Nadsonia fulvescens var. elongata DSM 6958
Nadsonia fulvescens var. fulvescens NRRL Y-1281
Nadsonia starkeyi-henricii UCD142
Candida tunisiensis CBS 12513
Dipodascus aggregatus NRRL Y-17564
Dipodascus restrictus CBS 111234
Dipodascus carabidarus NRRL Y-27727
Dipodascus histeridarus NRRL Y-27729
Dipodascus cucujoidarus NRRL Y-27731
Dipodascus fermentans NRRL Y-1492
Dipodascus armillariae NRRL Y-17580
Dipodascus macrosporus NRRL Y-17586
Dipodascus klebahnii NRRL Y-17568
Dipodascus albidus NRRL Y-12859
Dipodascus geniculatus NRRL Y-17628
Dipodascus ghanensis CBS 11010
Dipodascus siamensis CBS 10929
Dipodascus australiensis NRRL Y-17565
Galactomyces geotrichum NRRL Y-17569
Geotrichum europaeum CBS 866.68
Geotrichum phurueaensis CBS 11418
Geotrichum candidum CLIB 918
Galactomyces reessii NRRL Y-17566
Geotrichum citri-aurantii CBS 176.89
Magnusiomyces capitatus NRRL Y-17686
Magnusiomyces clavatus CNRMA 12.647
Magnusiomyces ingens NRRL Y-17630
Saprochaete ingens CBS 517.90
Magnusiomyces starmeri NRRL Y-17816
Magnusiomyces magnusii NRRL Y-17563
Saprochaete suaveolens
Magnusiomyces tetraspermus NRRL Y-7288
Saprochaete fungicola
Middelhovenomyces tepae NRRL Y-17670
Candida bentonensis NRRL YB-2364
Candida incommunis NRRL Y-17085
Deakozyma indianensis NRRL YB-1937
Tardiomyces blankii NRRL Y-17068
Tardiomyces depauwii NCPF13064
Tardiomyces digboiensis CBS 9800
Candida kazuoi JCM 12558
Wickerhamiella qilinensis CBS 13929
Wickerhamiella hasegawae JCM 12559
Wickerhamiella slavikovae CBS 12417
Wickerhamiella galacta NRRL Y-17645
Wickerhamiella alocasiicola PYCC 8427
Wickerhamiella vanderwaltii PYCC 3671
Wickerhamiella australiensis NRRL Y-27360
Wickerhamiella lipophila NRRL Y-27367
Wickerhamiella occidentalis NRRL Y-27364
Wickerhamiella cacticola NRRL Y-27362
Wickerhamiella azymoides CBS 10508
Wickerhamiella nectarea PYCC 8436
Wickerhamiella parazyma PYCC 8426
Wickerhamiella pararugosa NRRL Y-17089
Wickerhamiella shivajii CBS 15893
Wickerhamiella allomyrinae CBS 13167
Wickerhamiella brachini CBS 14176
Wickerhamiella sergipiensis CBS 9567
Wickerhamiella spandovensis PYCC 8431
Wickerhamiella musiphila CBS 10697
Wickerhamiella infanticola NRRL Y-17858
Wickerhamiella sorbophila DS02
Wickerhamiella siamensis CBS 13331
Starmerella apicola NRRL Y-50540
Starmerella bombi NRRL Y-17081
Starmerella vitae CBS 15147
Starmerella asiatica CBS 14173
Starmerella scarabaei CBS 14174
Starmerella bombicola NRRL Y-17069
Starmerella kuoi NRRL Y-27208
Starmerella riodocensis NRRL Y-27859
Starmerella floricola NRRL Y-17676
Starmerella powellii CBS 8795
Starmerella cellae NRRL Y-27860
Starmerella floris NRRL Y-48255
Starmerella etchellsii NRRL Y-17084
Starmerella roubikii CBS 15148
Starmerella ratchasimensis CBS 10611
Starmerella khaoyaiensis NBRC 104213
Starmerella bacillaris CBS 9494
Starmerella davenportii CBS 9069
Starmerella stellata NRRL Y-1446
Starmerella lactis-condensi NRRL Y-1515
Starmerella sirachaensis NBRC 108605
Starmerella apis NRRL Y-2482
Starmerella geochares NRRL Y-17073
Starmerella magnoliae PYCC 2903
Starmerella sorbosivorans CBS 8768
Starmerella potacharoeniae NBRC 106439
Starmerella vaccinii NRRL Y-17684
Starmerella stigmatis CBS 11464
Starmerella tilneyi CBS 8794
Starmerella gropengiesseri NRRL Y-17142
Wickerhamiella bombiphila NRRL Y-27640
Wickerhamiella domercqiae NRRL Y-6692
Wickerhamiella dianesei PYCC 8330
Wickerhamiella kurtzmanii PYCC 8437
Wickerhamiella versatilis NRRL Y-6652
Crinitomyces ghanaensis NRRL YB-1486
Sugiyamaella americana NRRL YB-2067
Sugiyamaella grinbergsii NRRL Y-27117
Sugiyamaella japonica NRRL YB-2798
Sugiyamaella neomexicana NRRL YB-2450
Sugiyamaella pinicola NRRL YB-2263
Sugiyamaella novakii NRRL Y-27346
Sugiyamaella lignohabitans CBS 10342
Sugiyamaella xylanicola CBS 12683
Sugiyamaella marionensis NRRL YB-1336
Sugiyamaella sp. yHKS617
Sugiyamaella castrensis NRRL Y-17329
Sugiyamaella paludigena NRRL Y-12697
Sugiyamaella chiloensis NRRL Y-17643
Sugiyamaella marilandica NRRL YB-1847
Sugiyamaella qingdaonensis CBS 11390
Sugiyamaella smithiae NRRL Y-17850
Sugiyamaella mastotermitis CBS 14182
Sugiyamaella boreocaroliniensis NRRL YB-1835
Sugiyamaella floridensis NRRL YB-3827
Sugiyamaella valdiviana NRRL Y-7791
Candida lundiana CBS 12271
Candida patagonica CBS 10443
Candida suthepensis CBS 12270
Zygoascus biomembranicola CBS 14157
Zygoascus flipseniorum CBS 14876
Zygoascus polysorbophila NRRL Y-27161
Zygoascus bituminiphia CBS 8813
Zygoascus hellenicus NRRL Y-7136
Zygoascus meyerae NRRL Y-17319
Zygoascus ofunaensis NRRL Y-10998
Zygoascus tannicola NRRL Y-17392
Groenewaldozyma auringiensis NRRL Y-17674
Groenewaldozyma tartarivorans NRRL Y-27291
Groenewaldozyma salmanticensis NRRL Y-17090
Groenewaldozyma sp. yHMH443
Diddensiella caesifluorescens NRRL Y-48781
Diddensiella santjacobensis NRRL Y-17667
Diddensiella transvaalensis NRRL Y-27140
Spencermartinsiella europaea NRRL Y-48265
Spencermartinsiella ligniputridi NRRL Y-48818
Blastobotrys muscicola NRRL Y-7993
Blastobotrys robertii NRRL Y-27775
Blastobotrys arbuscula NRRL Y-17585
Blastobotrys buckinghamii NRRL Y-63727
Blastobotrys capitulata NRRL Y-17573
Blastobotrys elegans NRRL Y-17572
Blastobotrys niveus NRRL Y-17581
Blastobotrys proliferans NRRL Y-17577
Blastobotrys attinorum NRRL Y-27639
Trichomonascus apis NRRL Y-48475
Blastobotrys parvus NRRL Y-1004
Blastobotrys indianensis NRRL YB-1950
Trichomonascus petasosporus NRRL YB-2092
Blastobotrys illinoisensis NRRL YB-1343
Blastobotrys mokoenaii NRRL Y-27120
Blastobotrys malaysiensis NRRL Y-6417
Trichomonascus vanleenenianus CBS 14902
Blastobotrys chiropterorum NRRL Y-17071
Blastobotrys terrestris NRRL Y-17704
Blastobotrys serpentis NRRL Y-48249
Blastobotrys persicus CBS 14259
Trichomonascus ciferrii NRRL Y-10943
Blastobotrys americana NRRL Y-6844
Blastobotrys peoriensis NRRL YB-2290
Blastobotrys adeninivorans TMCC 70007
Blastobotrys raffinosifermentans NRRL Y-27150

Fig. S2


Nakazawaea holstii NRRL Y-2155
Pachysolen tannophilus NRRL Y-2460
Citeromyces hawaiiensis NRRL Y-11581
Citeromyces nyonsensis CBS 12700
Citeromyces matritensis NRRL Y-2407
Citeromyces siamensis NRRL Y-27975
Komagataella kurtzmanii VKPM Y-727
Komagataella phaffii CBS 7435
Komagataella pastoris ATCC 28485
Komagataella ulmi CBS 12361
Komagataella mondaviorum CBS 15017
Komagataella populi NRRL YB-455
Komagataella pseudopastoris NRRL Y-27603
Kuraishia floccosa NRRL Y-27951
Kuraishia hungarica NRRL Y-27594
Kuraishia ogatae NRRL Y-48474
Kuraishia piskuri NRRL YB-2544
Kuraishia borneana CBS 12507
Kuraishia capsulata CBS 1993
Kuraishia molischiana NRRL Y-27899
Kuraishia cidri NRRL Y-27078
Candida boidinii NRRL Y-2332
Candida methanosorbosa NRRL Y-17320
Ogataea sp. NRRL Y-27170
Candida succiphila JCM 9445
Ogataea naganishii NRRL Y-7654
Candida nanaspora NRRL Y-17679
Ogataea sp. NRRL Y-27166
Candida sp. NRRL Y-12764
Ogataea sp. yHMJ1
Candida nitratophila NRRL YB-3654
Ogataea sp. NRRL YB-1238
Ogataea ramenticola NRRL YB-1985
Candida suzukii NRRL Y-27593
Ogataea methylovora NRRL Y-17250
Candida arabinofermentans NRRL YB-2248
Candida ovalis NRRL Y-17662
Candida sithepensis JCM 12265
Ogataea paraovalis CBS 14697
Ogataea degrootiae UCD465
Ogataea methanolica JCM 10240
Ogataea salicorniae NRRL Y-12834
Ogataea trehalophila NRRL Y-6781
Candida piceae NRRL YB-2107
Ogataea nitratoaversa NRRL Y-48449
Ogataea pilisensis NRRL Y-27598
Candida sonorensis NRRL Y-7800
Candida pignaliae NRRL Y-17664
Candida rishiriensis NBRC 105027
Candida pini NRRL Y-2023
Candida krabiensis NRRL Y-27965
Candida nemodendra NRRL Y-7779
Candida ortonii NRRL Y-48038
Ogataea corticis NBRC 1794
Ogataea zsoltii NRRL Y-27601
Ogataea saltuana NRRL Y-48448
Ogataea sp. NRRL YB-2437
Ogataea ganodermae CBS 10646
Ogataea henricii NRRL YB-2194
Ogataea neopini AB440274
Ogataea pini NRRL Y-11528
Ogataea glucozyma NRRL YB-2185
Candida mattraensis CBS 12097
Candida xyloterini CBS 11547
Ogataea paradorogensis CBS 10978
Ogataea allantospora NRRL Y-48267
Ogataea chonburiensis CBS 10363
Ogataea dorogensis NRRL Y-27599
Ogataea kodamae NRRL Y-17234
Ogataea angusta CBS 2575
Ogataea haglerorum 83-474-2
Ogataea parapolymorpha CBS 12304
Ogataea polymorpha NCYC 495 leu1.1
Ogataea thermophila NCAIM Y.01608
Ogataea siamensis NRRL Y-27963
Ogataea nakhonphanomensis CBS 10362
Ogataea thermomethanolica NRRL Y-27981
Ogataea philodendri NRRL Y-7210
Ogataea minuta NRRL Y-411
Ogataea nonfermentans NRRL YB-2203
Candida maris NRRL Y-6696
Ogataea sp. NRRL YB-2442
Ogataea trehaloabstinens NRRL Y-27595
Ogataea wickerhamii NRRL YB-4943
Ogataea populialbae NRRL Y-48632
Ambrosiozyma ambrosiae NRRL Y-7524
Ambrosiozyma platypodis NRRL Y-7524
Ambrosiozyma philentoma NRRL Y-7523
Ambrosiozyma oregonensis NRRL Y-6106
Ambrosiozyma kamigamensis NRRL Y-63629
Ambrosiozyma neoplatypodis NRRL Y-63630
Ambrosiozyma angophorae NRRL Y-7118
Ambrosiozyma cicatricosa NRRL Y-17594
Ambrosiozyma monospora JCM 7599
Ambrosiozyma kashinagicola JCM 15019
Ambrosiozyma pseudovanderkliftii NRRL Y-6363
Ambrosiozyma vanderkliftii NRRL Y-63633
Ambrosiozyma llanquihuensis NRRL Y-17657
Ambrosiozyma maleeae NRRL Y-63635
Candida awuae CBS 11011
Candida inconspicua CBS 180
Pichia cactophila NRRL Y-10963
Pichia insulana CBS 11169
Pichia pseudocactophila NRRL Y-17239
Pichia norvegensis NRRL Y-7687
Pichia sp. yHMH446
Pichia occidentalis NRRL Y-7552
Candida phayaonensis NBRC 108868
Pichia exigua NRRL Y-10920
Pichia paraexigua CBS 15237
Pichia scutulata NRRL Y-7663
Pichia sp. NRRL Y-12830
Pichia sp. NRRL Y-12827
Candida rugopelliculosa NRRL Y-17079
Candida pseudolambica NRRL Y-17318
Pichia sp. yHKS168
Pichia kudriavzevii NRRL Y-5396
Pichia sp. NRRL Y-12824
Pichia cephalocereana NRRL Y-17225
Pichia kluyveri B7036
Pichia eremophila NRRL Y-17224
Pichia nakasei NRRL Y-7686
Pichia heedii NRRL Y-10967
Pichia fermentans fo-MP-02
Candida californica Olga-1
Pichia sp. NRRL Y-27261
Candida ethanolica NRRL Y-12615
Pichia deserticola NRRL Y-12918
Candida thaimueangensis NBRC 101967
Pichia mandshurica NRRL Y-27978T
Pichia sp. NRRL YB-4149
Pichia membranifaciens KS47-1
Pichia sp. NRRL Y-27259
Pichia gijzenarium CBS 15024
Pichia nanzhaoensis CBS 15346
Pichia sporocuriosa NRRL Y-27347
Candida cabralensis CBS 11679
Pichia terricola NRRL YB-4310
Candida sorboxylosa NRRL Y-17669
Martiniozyma abietophila NRRL Y-11514
Martiniozyma asiatica NRRL Y-63747
Saturnispora ahearnii NRRL Y-7555
Saturnispora besseyi NRRL Y-63574
Saturnispora saitoi NRRL Y-6671
Saturnispora dispora NRRL Y-1447
Saturnispora gosingensis NRRL Y-48718
Saturnispora hagleri NRRL Y-27828
Saturnispora quitensis CBS 12184
Saturnispora serradocipensis NRRL Y-48717
Saturnispora zaruensis NRRL Y-7008
Saturnispora bothae yHDO578
Saturnispora sanitii CBS 10864
Saturnispora silvae NRRL Y-6725
Saturnispora halmiae CBS 11009
Saturnispora mendoncae NRRL Y-11515
Saturnispora galanensis CBS 15223
Saturnispora kantuleensis CBS 15217
Saturnispora sekii CBS 10931
Saturnispora diversa NRRL Y-5713
Kregervanrija delftensis NRRL Y-7119
Kregervanrija fluxuum NRRL YB-4273
Kregervanrija pseudodelftensis NRRL Y-5494
Allodekkera sacchari CBS 14167
Brettanomyces anomalus NRRL Y-17522
Brettanomyces bruxellensis NRRL Y-12961
Brettanomyces sp. kh3
Brettanomyces custersianus NRRL Y-6653
Brettanomyces naardenensis NRRL Y-17526
Brettanomyces nanus CBS 1945
Candida insectalens NRRL Y-7778
Candida silvatica NRRL Y-7777
100
98
96
75

Fig. S3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Saccharomycopsis capsularis NRRL Y-17639
Ascoidea rubescens DSM 1968
Wickerhamomyces kurtzmanii CBS 15418
83
Wickerhamomyces chambardii NRRL Y-2378
100
Candida ponderosae NRRL YB-2307
Wickerhamomyces tratensis CBS 12176
100
Candida namnaoensis CBS 12175
100
Starmera stellimalicola NRRL Y-17912
100
Starmera sp. NRRL Y-17713
Starmera caribaea NRRL Y-17468
100
100
Starmera pachycereana NRRL Y-10981
100
Starmera amethionina NRRL Y-10978
Starmera quercuum NRRL YB-4281
100
100
Starmera dryadoides NRRL Y-10990
100
Candida dendrica NRRL Y-7775
100
Candida berthetii NRRL Y-17644
100
Wickerhamomyces subpelliculosus NRRL Y-1683
100
Wickerhamomyces anomalus NRRL Y-366-8
100
Wickerhamomyces sydowiorum NRRL Y-7130
100
Wickerhamomyces sp. yHMH451
90
Wickerhamomyces queroliae NRRL Y-48478
100
Wickerhamomyces lynferdii NRRL Y-7723
100
Wickerhamomyces ciferrii NRRL Y-1031
100
Candida silvicultrix NRRL Y-7789
Wickerhamomyces mucosus CBS 6341
100
Wickerhamomyces xylosica NBRC 108869
100
Wickerhamomyces pijperi CBS 2887
100
Wickerhamomyces sp. NRRL Y-48258
100
Wickerhamomyces chaumierensis CBS 8565
Candida solani NRRL Y-2224
100
100
Wickerhamomyces strasburgensis NRRL Y-2383
Wickerhamomyces hampshirensis NRRL YB-412
Candida freyschussii NRRL Y-7957A
100
Cyberlindnera galapagoensis CBS 13997
Cyberlindnera subsufficiens NG8.2
100
100
Cyberlindnera suaveolens NRRL Y-17391
100
Cyberlindnera saturnus NRRL Y-17396
Cyberlindnera mrakii NRRL Y-1364
100
Cyberlindnera sp. NRRL Y-27267
100
100
Cyberlindnera lachancei NRRL Y-27008
100
Cyberlindnera samutprakarnensis CBS 12528
100
Cyberlindnera jadinii NRRL Y-1542
100
Cyberlindnera sargentensis SHA 17.2
100
Candida vartiovaarae NRRL Y-6701
100
Candida takata CBS 12244
100
100
Cyberlindnera sp. NRRL Y-27103
100
Cyberlindnera misumaiensis NRRL Y-17389
100
Cyberlindnera maclurae NRRL Y-5377
100
Candida sp. NRRL YB-4088
Cyberlindnera rhodanensis NRRL Y-7854
100
Cyberlindnera japonica NRRL YB-2750
100
Cyberlindnera xylosilytica NRRL YB-2097
100
Candida maesae CBS 12240
100
Candida easanensis JCM 12476
Cyberlindnera veronae NRRL Y-7818
100
Cyberlindnera fabianii NRRL Y-1871
100
Cyberlindnera mississippiensis NRRL YB-1294
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Cyberlindnera amylophila NRRL YB-1287
Cyberlindnera meyerae NRRL Y-17236
100
Cyberlindnera euphorbiae NRRL Y-17232
90
Cyberlindnera euphorbiiphila NRRL Y-12742
100
Cyberlindnera mycetangii NRRL Y-6843
100
100
Cyberlindnera sp. NRRL Y-7615
100
Cyberlindnera maritima NRRL Y-17775
100
Cyberlindnera petersonii NRRL YB-3808
100
Cyberlindnera nakhonratchasimensis JCM 12474
100
100
Cyberlindnera bimundalis NRRL Y-5343
100
Cyberlindnera americana NRRL Y-2156
100
Candida taoyuanica CBS 12242
100
Candida stauntonica CBS 12241
Candida hungchunana CBS 12243
100
Cyberlindnera xishuangbannaensis CBS 14692
100
Candida adriatica CBS 12504
Wickerhamomyces silvicola NRRL Y-1678
100
Wickerhamomyces sp. NRRL Y-17067
100
Wickerhamomyces sp. NRRL YB-2243
100
Wickerhamomyces canadensis NRRL Y-1888
100
Wickerhamomyces bisporus VH7 F
100
Candida sp. NRRL Y-27127
100
Candida quercuum NRRL Y-12942
100
Wickerhamomyces sp. yHMH26
100
Wickerhamomyces sp. NRRL Y-7574
100
Wickerhamomyces sp. yHMH617
100
Wickerhamomyces sp. NRRL YB-3031
100
Wickerhamomyces alni NRRL Y-11625
100
Candida ulmi CBS 8670
100
Candida jianshihensis CBS 10591
100
Candida peoriensis NRRL YB-1497
100
Candida yuanshanica CBS 10589
100
Wickerhamomyces bovis NRRL YB-4184
100
Wickerhamomyces rabaulensis NRRL Y-7945
100
Candida odintsovae NRRL Y-17760
100
Wickerhamomyces sp. yHQL14
100
Wickerhamomyces onychis NRRL Y-7123
100
Candida dajiaensis CBS 10590
Candida sanyiensis CBS 10592
100
Barnettozyma sp. yHDO593
100
Barnettozyma hawaiiensis NRRL Y-27270
100
Barnettozyma sucrosica CBS 11512
100
Barnettozyma populi NRRL Y-12728
100
Barnettozyma vustinii CBS 11554
100
Barnettozyma californica NRRL Y-17395
100
84
Barnettozyma salicaria NRRL Y-6780
Candida norvegica NRRL Y-17660
49
Barnettozyma wickerhamii NRRL Y-2435
100
Candida qinlingensis CBS 9768
100
Barnettozyma pratensis NRRL Y-12696
100
100
Phaffomyces thermotolerans NRRL Y-11709
100
Candida orba NRRL Y-27336
100
Phaffomyces antillensis NRRL Y-12881
100
Phaffomyces opuntiae NRRL Y-11707
100
Candida coquimbonensis CBS 12348
100
Candida sp. XZY480-2
100
Millerago phaffii UFMG-CM-Y7052
100
Candida galis NRRL Y-48037
94
Candida ficus CBS 12638
100
Candida montana NRRL Y-17326
94
Barnettozyma siamensis CBS 13392
100
Barnettozyma botsteinii 1118

Fig. S4


Nakazawaea holstii NRRL Y-2155
Pachysolen tannophilus NRRL Y-2460
Babjeviella inositovora NRRL Y-12698
Candida pseudocylindracea CBS 10854
Limtongozyma cylindracea NRRL Y-17506
Candida chilensis NRRL Y-17141
Cephaloascus albidus NRRL Y-7343
Cephaloascus fragrans NRRL Y-6742
Candida anglica NRRL Y-27079
Kurtzmaniella cleridarum NRRL Y-48386
Kurtzmaniella fragi NRRL Y-17910
Kurtzmaniella natalensis NRRL Y-17680
Kurtzmaniella quercitrusa NRRL Y-5392
Kurtzmaniella quercitrusa var. filamentosus nom. nud. 1120
Kurtzmaniella quercitrusa var. comoensis nom. nud. 1112
Candida anglica VS III C KN 3
Candida santamariae NRRL Y-6656
Candida boleticola NRRL Y-17080
Candida schatavii NRRL Y-17078
Candida railenensis CLIB 1423
Candida oleophila NRRL Y-2317
Candida zeylanoides NRRL Y-1774
Candida aurita CBS 9724
Candida sophiae-reginae NRRL Y-17668
Candida palmyrensis CBS 11546
Candida sp. gmt3-3-4
Schwanniomyces sp. yHMH407
Candida glucosophila NRRL Y-17219
Debaryomyces singareniensis CBS 10405
Schwanniomyces etchellsii NRRL Y-7121
Candida pseudofarinosa NCYC 386
Millerozyma farinosa NRRL Y-7553
Millerozyma miso CBS 2004
Millerozyma acaciae JCM 10732
Candida psychrophila FYBW01
Debaryomyces coudertii NRRL Y-7425
Debaryomyces fabryi NRRL Y-17914
Debaryomyces prosopidis NRRL Y-27369
Debaryomyces subglobosus NRRL Y-6666
Debaryomyces hansenii NRRL Y-7426
Debaryomyces nepalensis NRRL Y-7108
Debaryomyces maramus NRRL Y-2171
Debaryomyces robertsiae NRRL Y-6670
Debaryomyces udenii NRRL Y-17354
Candida aaseri B8007
Candida andamanensis CBS 10859
Candida pseudoaaseri CBS 11170
Candida conglobata NRRL Y-1504
Candida trypodendroni NRRL Y-6488
Yamadazyma sp. yHKS699
Yamadazyma mexicana NRRL Y-11818
Yamadazyma sp. yHMH393
Yamadazyma dushanensis CBS 13914
Candida insectorum NRRL Y-7787
Candida dendronema NRRL Y-7781
Candida germanica NRRL Y-27064
Candida vaughaniae CBS 8583
Candida diddensiae NRRL Y-7589
Candida kanchanaburiensis NBRC 104475
Yamadazyma siamensis CBS 12573
Yamadazyma akitaensis NRRL Y-7904
Yamadazyma nakazawae NRRL Y-7903
Yamadazyma philogaea NRRL Y-7813
Yamadazyma paraphyllophila CBS 9928
Yamadazyma phyllophila CBS 12572
Yamadazyma ubonensis CBS 12859
Yamadazyma sp. yHMH685
Yamadazyma laniorum yHMH7
Yamadazyma tenuis ATCC 10573
Yamadazyma scolyti NRRL Y-5512
Candida atlantica NRRL Y-17759
Candida atmosphaerica NRRL Y-17642
Candida spencermartinsiae NRRL Y-48663
Candida oceani 2020i151
Candida taylorii NRRL Y-27213
Candida blattariae NRRL Y-27703
Candida buinensis NRRL Y-11706
Candida diospyri CBS 9769
Candida jaroonii CLIB 1444
Candida songkhlaensis NBRC 103214
Yamadazyma tumulicola NBRC 104392
Candida friedrichii NRRL Y-17653
Candida membranifaciens NRRL Y-2089
Candida membranifaciens subsp. flavinogenes IST 626
Candida tallmaniae CBS 8575
Yamadazyma olivae CBS 11171
Yamadazyma sp. yHKB15
Candida cerambycidarum NRRL Y-27706
Candida michaelii NRRL Y-27705
Candida gorgasii NRRL Y-27707
Candida endomychidarum NRRL Y-27708
Candida lessepsii NRRL Y-27766
Candida khao-thaluensis CBS 8535
Candida koratica NBRC 103208
Candida tammaniensis NRRL Y-8257
Yamadazyma kitorensis JCM 31005
Yamadazyma takamatsuzukensis NBRC 104391
Yamadazyma endophytica CBS 14163
Yamadazyma epiphylla CBS 13384
Yamadazyma insecticola CBS 13382
Yamadazyma triangularis NRRL Y-5714
Candida nonsorbophila CBS 10862
Candida sinolaborantium LESF1467
Candida ascalaphidarum NRRL Y-27908
Candida multigemmis NRRL Y-17659
Meyerozyma athensensis NRRL Y-27644
Meyerozyma caribbica NRRL Y-27274
Meyerozyma carpophila JCM 9396
Meyerozyma guilliermondii ATCC 6260
Meyerozyma smithsonii NRRL Y-27642
Meyerozyma elateridarum NRRL Y-27647
Hermanozyma aechmeae NRRL Y-48456
Hermanozyma ubatubensis NRRL Y-27812
Tanozyma kutaoensis CBS 11388
Clavispora asparagi CBS 9770
Clavispora fructus NRRL Y-17072
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Clavispora carvajalis NRRL Y-48694
Clavispora phyllophila CBS 12671
Clavispora vitiphila CBS 12672
Clavispora lusitaniae NRRL Y-11827
Clavispora opuntiae NRRL Y-11820
Sungouiella berkhoutiae CBS 11722
Sungouiella middelhoveniana CBS 12306
Sungouiella ezoensis CBS 11753
Sungouiella inulinophila CBS 11725
Sungouiella tsuchiyae NRRL Y-17840
Sungouiella intermedia NRRL Y-981
Sungouiella pseudointermedia NRRL Y-10939
Sungouiella blattae NRRL Y-27698
Sungouiella dosseyi NRRL Y-27950
Sungouiella ecuadorensis CBS 12653
Sungouiella suratensis CBS 10928
Sungouiella flosculorum NRRL Y-48731
Sungouiella pseudoflosculorum CBS 8584
Sungouiella sharkensis NRRL Y-48380
Sungouiella thailandica CBS 10610
Candida citri CBS 11858
Australozyma bambusicola CBS 11723
Australozyma touchengensis CBS 10585
Australozyma picinguabensis NRRL Y-27814
Australozyma saopauloensis NRRL Y-27815
Australozyma nongkhaiensis CBS 11724
Australozyma succicola CBS 11726
Australozyma saccharicola CBS 12575
Australozyma robnettiae CBS 8580
Candida danieliae CBS 8533
Candida golubevii NRRL Y-48707
Metschnikowia lunata NRRL Y-7131
Metschnikowia corniflorae NRRL Y-27750
Metschnikowia andauensis CBS 10809
Metschnikowia zizyphicola NRRL Y-48712
Metschnikowia shanxiensis NRRL Y-48710
Metschnikowia sinensis NRRL Y-48711
Metschnikowia fructicola NRRL Y-27328
Metschnikowia persimmonesis KIOM G15050
Metschnikowia pulcherrima NRRL Y-7111
Metschnikowia rubicola CBS 15344
Metschnikowia chrysoperlae NRRL Y-27615
Metschnikowia leonuri CBS 15341
Metschnikowia picachoensis NRRL Y-27607
Metschnikowia pimensis NRRL Y-27619
Metschnikowia kunwiensis NRRL Y-48698
Metschnikowia australis W7-5
Metschnikowia bicuspidata var. bicuspidata NRRL YB-4993
Metschnikowia bicuspidata var. californica NRRL Y-17916
Metschnikowia bicuspidata var. chathamia NRRL Y-17917
Metschnikowia krissii NRRL Y-5389
Metschnikowia zobellii CALNDW01
Metschnikowia henanensis CBS 12677
Metschnikowia kofuensis NRRL Y-27226
Metschnikowia viticola NRRL Y-48693
Metschnikowia noctiluminum NRRL Y-27753
Metschnikowia baotianmanensis CBS 15869
Metschnikowia koreensis CBS 8854
Metschnikowia peoriensis CBS 15345
Metschnikowia reukaufii MR1 2
Metschnikowia anglica CBS 15342
Metschnikowia gruessii NRRL Y-17809
Metschnikowia vanudenii NRRL Y-17036
Metschnikowia lachancei NRRL Y-27242
Metschnikowia chrysomelidarum NRRL Y-27749
Metschnikowia gelsemii NRRL Y-48212
Candida wancherniae NRRL Y-48709
Metschnikowia agaves UWOPS 92-210.1
Metschnikowia sp. yHJM9
Metschnikowia drosophilae UWOPS 83-1143.1
Metschnikowia torresii CBS 5152
Metschnikowia laotica CBS 12961
Metschnikowia sp. yHKB443
Candida hainanensis NRRL Y-48715
Metschnikowia lopburiensis CBS 12574
Metschnikowia caudata EBD-CdVSA57-2
Metschnikowia aberdeeniae SUB 05-213.1
Metschnikowia shivogae UWOPS 04-310.1
Metschnikowia hibisci UWOPS 95-797.2
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Metschnikowia colocasiae UWOPS 03-202.1
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Metschnikowia similis UWOPS 03-133.4
Metschnikowia borealis SUB 99-207.1
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Metschnikowia cerradonensis UFMG 03-T67.1
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Metschnikowia continentalis UWOPS 95-402.1
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Metschnikowia matae var. maris UFMG-CM-Y397
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Metschnikowia proteae EBD-T1Y1T
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Metschnikowia orientalis UWOPS 99-745.6
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Helenozyma melibiosica NRRL Y-17076
Helenozyma rhizophorensis NRRL Y-48382
Danielia oregonensis NRRL Y-5850
Danielia reshetovae CBS 11556
Candidozyma auris CBS 10913
Candidozyma chanthaburiensis CBS 10926
Candidozyma konsanensis CBS 12666
Candidozyma heveicola NRRL Y-48716
Candidozyma duobushaemuli NRRL Y-17802
Candidozyma vulturna CBS 14366
Candidozyma pseudohaemuli NRRL Y-48733
Candidozyma haemuli NRRL Y-6693
Candidozyma ruelliae NRRL Y-48703
Osmozyma mogii NRRL Y-17032
Osmozyma tolerans CBS 8613
Wilhelminamyces savonicus NRRL Y-17077
Wilhelminamyces tanticharoeniae CBS 11574
Gaillardinia entomophila NRRL Y-7783
Candida sp. UFMG-CM-Y605
Danielozyma ontarioensis NRRL YB-1246
Candida silvanorum NRRL Y-7782
Metschnikowia sp. yHQL527
Soucietia sequanensis NRRL Y-17682
Candida sp. XZY238F3
Isabelozyma gotoi NRRL Y-27225
Isabelozyma heimii NRRL Y-7502
Isabelozyma pseudorhagii NRRL YB-2076
Isabelozyma rhagii NRRL Y-2594
Hyphopichia burtonii NRRL Y-1933
Hyphopichia khmerensis CBS 9784
Hyphopichia fennica NRRL Y-7505
Hyphopichia pseudoburtonii makgeolli 2
Hyphopichia wangnamkhiaoensis CBS 11695
Hyphopichia buzzinii CBS 14300
Hyphopichia homilentoma JCM 1507
Priceomyces carsonii NRRL YB-4275
Priceomyces castillae NRRL Y-7501
Priceomyces haplophilus JCM 1635
Priceomyces medius NRRL Y-7122
Priceomyces fermenticarens NRRL Y-17321
Priceomyces melissophilus NRRL Y-7585
Schwanniomyces capriottii NRRL Y-7423
Schwanniomyces polymorphus var. africanus CBS 6741
Schwanniomyces polymorphus var. polymorphus NRRL Y-20
Schwanniomyces sp. NRRL Y-7430
Schwanniomyces vanrijiae var. vanrijiae NRRL Y-7535
Schwanniomyces vanrijiae var. yarrowii NRRL Y-11714
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Schwanniomyces occidentalis var. occidentalis NRRL Y-10
Schwanniomyces occidentalis var. persoonii NRRL Y-7400
Scheffersomyces gosingicus CBS 11433
Scheffersomyces spartinae ARV 011
Candida fluviatilis NRRL Y-7711
Candida sphagnicola CBS 11774
Candida manassasensis CBS 12534
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Candida glaebosa NRRL Y-6949
Candida saitoana NRRL Y-17316
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Diutina catenulata WY3-10-4
Diutina mesorugosa CBS 12656
Diutina neorugosa CBS 12627
Diutina pseudorugosa CBS 10433
Diutina rugosa CBS 613
Diutina ranongensis CBS 10861
Diutina siamensis CBS 13388
Diutina scorzettiae NRRL Y-27665
Candida africana CEC4854
Candida albicans SC5314
Candida dubliniensis CD36
Candida buenavistaensis NRRL Y-27734
Candida gigantensis NRRL Y-27736
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Candida neerlandica NRRL Y-27057
Candida pseudoviswanathii CBS 13916
Candida viswanathii NRRL Y-6660
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Candida tetrigidarum NRRL Y-48142
Candida sanyaensis CBS 12637
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Candida sp. LDI48194
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Candida tropicalis MYA-3404
Candida maltosa Xu316
Candida bohioensis NRRL Y-27737
Candida chauliodis NRRL Y-27909
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Candida parachauliodis CBS 13928
Candida coleopterorum CBS 14180
Candida verbasci CBS 12699
Candida corydali NRRL Y-27910
Candida morakotiae NRRL Y-48708
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Candida pseudojiufengensis CBS 10847
Candida margitis CBS 14175
Candida metapsilosis ATCC 96143
Candida theae CBS 12239
Candida orthopsilosis Co 90-125
Candida parapsilosis ATCC 22019
Candida oxycetoniae CBS 10844
Lodderomyces beijingensis CBS 14171
Lodderomyces elongisporus NRRL YB-4239
Nematodospora anomalae CBS 13927
Nematodospora valgi CBS 12562
Candida blackwelliae CBS 10843
Candida parablackwelliae CBS 15228
Spathaspora boniae UFMG-CM-Y306
Candida alai NRRL Y-27739
Spathaspora arborariae UFMG-HM19.1AT
Spathaspora girioi UFMG-CM-Y302
Spathaspora jeffriesii NRRL Y-27738
Spathaspora passalidarum NRRL Y-27907
Candida lyxosophila NRRL Y-17539
Spathaspora gorwiae UFMG-CM-Y312
Spathaspora hagerdaliae UFMG-CM-Y303
Candida subhashii CBS 10753
Candida xylanilytica NBRC 106499
Hemisphaericaspora nanyangensis CBS 13020
Hemisphaericaspora insectamans NRRL Y-7786
Spathaspora xylofermentans UFMG-HMD23.3
Scheffersomyces stambukii UFMG-CM-Y427
Candida broadrunensis CBS 11838
Scheffersomyces ergatensis NRRL Y-17652
Scheffersomyces coipomensis NRRL Y-17651
Scheffersomyces lignicola CBS 10612
Scheffersomyces cryptocercus NRRL Y-48824
Scheffersomyces parashehatae CBS 12535
Scheffersomyces quercinus NRRL Y-48825
Scheffersomyces virginianus NRRL Y-48822
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Scheffersomyces insectosa NRRL Y-12854
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Candida sake NRRL Y-1622
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Teunomyces barrocoloradensis NRRL Y-27934
Teunomyces gatunensis NRRL Y-48064
Teunomyces stri NRRL Y-48063
Teunomyces atbi NRRL Y-27651
Teunomyces lycoperdinae NRRL Y-27658
Teunomyces panamensis NRRL Y-27657
Teunomyces pallodes NRRL Y-27653
Teunomyces tritomae NRRL Y-27650
Teunomyces cretensis NRRL Y-27777
Teunomyces kruisii NRRL Y-17087
Teunomyces funiuensis CBS 13911
Candida caryicola NRRL YB-1499
Candida tibetensis CBS 10298
Kodamaea sp. yHQL451
Suhomyces sp. yHQL142
Suhomyces faveliae CBS 14299
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Suhomyces prunicola NRRL YB-869
Suhomyces sp. yHKS641
Suhomyces sp. yHMH580
Suhomyces vadensis NRRL Y-27778
Suhomyces ambrosiae NRRL YB-1316
Suhomyces atakaporum NRRL Y-27570
Suhomyces guaymorum NRRL Y-27568
Suhomyces tanzawaensis NRRL Y-17324
Suhomyces bokatorum NRRL Y-27571
Suhomyces panamericanus NRRL Y-27567
Suhomyces coccinellae CBS 14298
Suhomyces kunorum NRRL Y-27580
Suhomyces chickasaworum NRRL Y-27566
Suhomyces yuchorum NRRL Y-27569
Suhomyces emberorum NRRL Y-27606
Suhomyces wounanorum NRRL Y-27574
Suhomyces terraborum NRRL Y-27573
Suhomyces canberraensis NRRL YB-2417
Suhomyces bolitotheri NRRL Y-27587
Suhomyces choctaworum NRRL Y-27584
Suhomyces anneliseae NRRL Y-27563
Suhomyces taliae NRRL Y-27589
Suhomyces maxii NRRL Y-27588
Suhomyces bribrorum NRRL Y-27572
Kodamaea alishanica CBS 11429
Kodamaea sp. yHQL449
Candida loeiensis CBS 11899
Kodamaea nitidulidarum NRRL Y-27353
Kodamaea restingae NRRL Y-27358
Kodamaea ohmeri NRRL Y-1932
Kodamaea leandrae NRRL Y-27757
Kodamaea anthophila UWOPS 95-602.1
Kodamaea kakaduensis CBS 8611
Candida smagusa CBS 11430
Kodamaea fungicola JCM 10142
Kodamaea plutei NRRL Y-27715
Kodamaea lidongshanica CBS 11426
Kodamaea fukazawae JCM 1641
Kodamaea jinghongensis CBS 14700
Kodamaea hsintzibuensis CBS 11427
Kodamaea kaohsiungensis CBS 11435
Kodamaea neixiangensis CBS 14699
Kodamaea laetipori NRRL Y-27713
Kodamaea sagamina JCM 10144
Aciculoconidium aculeatum NRRL YB-4298
Candida mesenterica UWOPS 91-121.2
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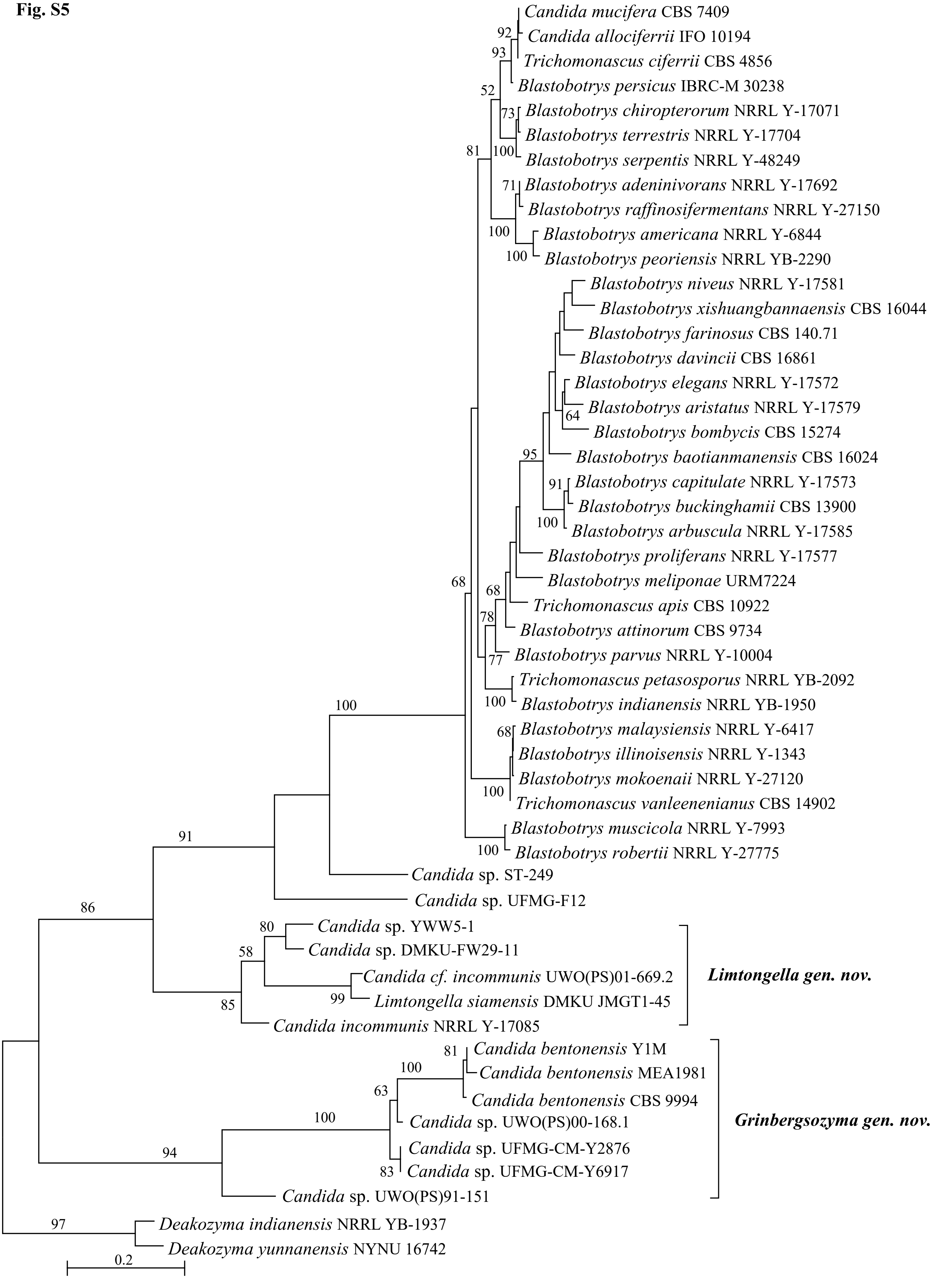
Kodamaea derodonti NRRL Y-27711

Fig. S5



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Candida allociferrii IFO 10194
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Trichomonascus ciferrii CBS 4856
Blastobotrys persicus IBRC-M 30238
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73
Blastobotrys chiropterorum NRRL Y-17071
Blastobotrys terrestris NRRL Y-17704
81
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Blastobotrys serpentis NRRL Y-48249
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Blastobotrys adeninivorans NRRL Y-17692
Blastobotrys raffinosifermentans NRRL Y-27150
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Blastobotrys americana NRRL Y-6844
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Blastobotrys peoriensis NRRL YB-2290
Blastobotrys niveus NRRL Y-17581
Blastobotrys xishuangbannaensis CBS 16044
Blastobotrys farinosus CBS 140.71
Blastobotrys davincii CBS 16861
Blastobotrys elegans NRRL Y-17572
Blastobotrys aristatus NRRL Y-17579
64
Blastobotrys bombycis CBS 15274
95
Blastobotrys baotianmanensis CBS 16024
91
Blastobotrys capitulate NRRL Y-17573
Blastobotrys buckinghamii CBS 13900
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Blastobotrys arbuscula NRRL Y-17585
Blastobotrys proliferans NRRL Y-17577
Blastobotrys meliponae URM7224
68
68
Trichomonascus apis CBS 10922
78
Blastobotrys attinorum CBS 9734
Blastobotrys parvus NRRL Y-10004
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Trichomonascus petasosporus NRRL YB-2092
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Blastobotrys malaysiensis NRRL Y-6417
Blastobotrys illinoisensis NRRL Y-1343
Blastobotrys mokoenaii NRRL Y-27120
100
Trichomonascus vanleenenianus CBS 14902
Blastobotrys muscicola NRRL Y-7993
91
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Blastobotrys robertii NRRL Y-27775
Candida sp. ST-249
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Candida sp. UFMG-F12
80
Candida sp. YWW5-1
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Limtongella gen. nov.
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Limtongella siamensis DMKU JMGT1-45
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Candida incommunis NRRL Y-17085
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Candida bentonensis CBS 9994
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Grinbergsozyma gen. nov.
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Candida sp. UFMG-CM-Y2876
83
Candida sp. UFMG-CM-Y6917
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Deakozyma yunnanensis NYNU 16742
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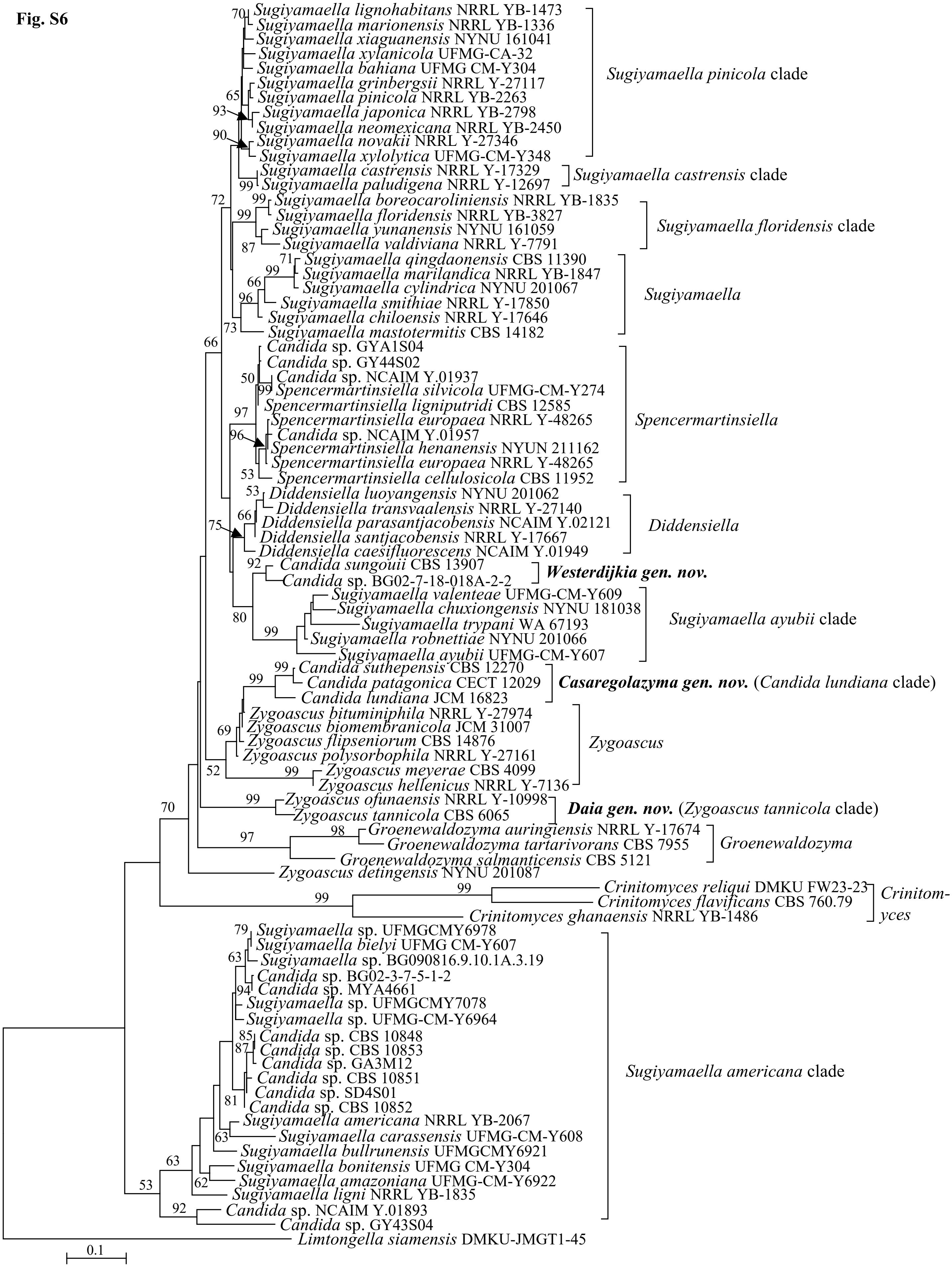
Fig. S6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Sugiyamaella lignohabitans NRRL YB-1473
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Sugiyamaella xylanicola UFMG-CA-32
Sugiyamaella bahiana UFMG CM-Y304
65
Sugiyamaella grinbergsii NRRL Y-27117
Sugiyamaella pinicola NRRL YB-2263
93
Sugiyamaella japonica NRRL YB-2798
Sugiyamaella neomexicana NRRL YB-2450
90
Sugiyamaella novakii NRRL Y-27346
Sugiyamaella xylolytica UFMG-CM-Y348
Sugiyamaella pinicola clade
Sugiyamaella castrensis NRRL Y-17329
99
Sugiyamaella paludigena NRRL Y-12697
Sugiyamaella castrensis clade
72
99
Sugiyamaella boreocaroliniensis NRRL YB-1835
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Sugiyamaella floridensis NRRL YB-3827
Sugiyamaella yunanensis NYNU 161059
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Sugiyamaella valdiviana NRRL Y-7791
Sugiyamaella floridensis clade
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Sugiyamaella qingdaonensis CBS 11390
99
Sugiyamaella marilandica NRRL YB-1847
66
Sugiyamaella cylindrica NYNU 201067
96
Sugiyamaella smithiae NRRL Y-17850
Sugiyamaella chiloensis NRRL Y-17646
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Sugiyamaella mastotermitis CBS 14182
Sugiyamaella
66
Candida sp. GYA1S04
Candida sp. GY44S02
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Candida sp. NCAIM Y.01937
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Spencermartinsiella silvicola UFMG-CM-Y274
97
Spencermartinsiella ligniputridi CBS 12585
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Candida sp. NCAIM Y.01957
Spencermartinsiella henanensis NYUN 211162
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Spencermartinsiella cellulosicola CBS 11952
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Diddensiella luoyangensis NYNU 201062
Diddensiella transvaalensis NRRL Y-27140
66
Diddensiella parasantjacobensis NCAIM Y.02121
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Diddensiella santjacobensis NRRL Y-17667
Diddensiella caesifluorescens NCAIM Y.01949
Diddensiella
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Candida sungouii CBS 13907
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Sugiyamaella trypani WA 67193
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Sugiyamaella robnettiae NYNU 201066
Sugiyamaella ayubii UFMG-CM-Y607
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Candida patagonica CECT 12029
Candida lundiana JCM 16823
Casaregolazyma gen. nov. (Candida lundiana clade)
Zygoascus bituminiphila NRRL Y-27974
Zygoascus biomembranicola JCM 31007
69
Zygoascus flipseniorum CBS 14876
Zygoascus polysorbophila NRRL Y-27161
99
Zygoascus meyerae CBS 4099
52
Zygoascus hellenicus NRRL Y-7136
Zygoascus
99
Zygoascus ofunaensis NRRL Y-10998
Zygoascus tannicola CBS 6065
Daia gen. nov. (Zygoascus tannicola clade)
70
98
Groenewaldozyma auringiensis NRRL Y-17674
97
Groenewaldozyma tartarivorans CBS 7955
Groenewaldozyma salmanticensis CBS 5121
Groenewaldozyma
Zygoascus detingensis NYNU 201087
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Crinitomyces reliqui DMKU FW23-23
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Crinitomyces flavificans CBS 760.79
Crinitomyces ghanaensis NRRL YB-1486
Crinitom-yces
79
Sugiyamaella sp. UFMGCMY6978
Sugiyamaella bielyi UFMG CM-Y607
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Candida sp. SD4S01
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Candida sp. CBS 10852
Sugiyamaella americana NRRL YB-2067
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Sugiyamaella carassensis UFMG-CM-Y608
Sugiyamaella bullrunensis UFMGCMY6921
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Sugiyamaella bonitensis UFMG CM-Y304
62
Sugiyamaella amazoniana UFMG-CM-Y6922
53
Sugiyamaella ligni NRRL YB-1835
92
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Candida sp. GY43S04
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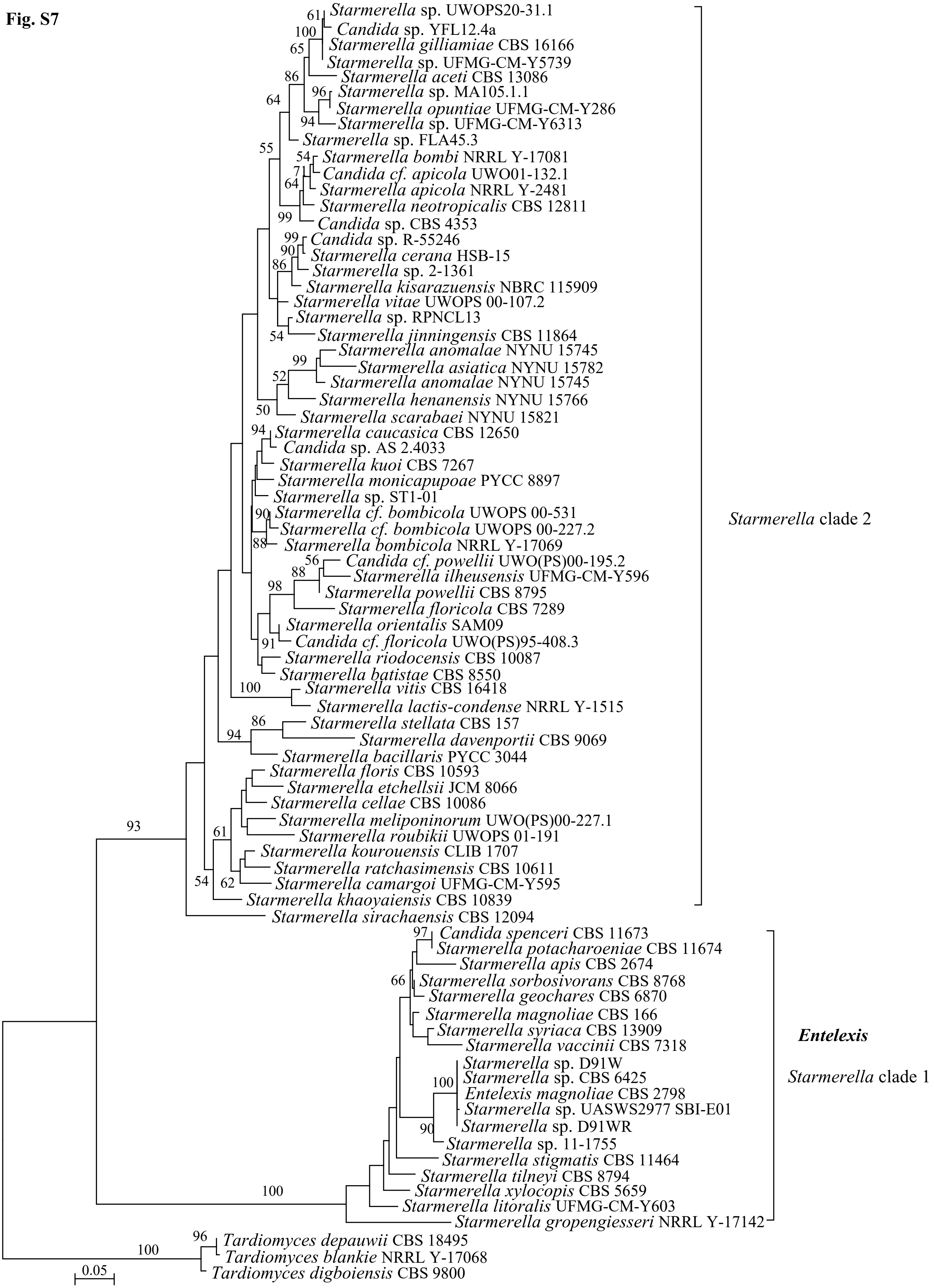
Fig. S7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Starmerella sp. UFMG-CM-Y5739
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96 Starmerella sp. MA105.1.1
Starmerella opuntiae UFMG-CM-Y286
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94 Starmerella sp. UFMG-CM-Y6313
Starmerella sp. FLA45.3
55
54 Starmerella bombi NRRL Y-17081
71 Candida cf. apicola UWO01-132.1
64 Starmerella apicola NRRL Y-2481
Starmerella neotropicalis CBS 12811
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Candida sp. CBS 4353
99 Candida sp. R-55246
90 Starmerella cerana HSB-15
86 Starmerella sp. 2-1361
Starmerella kisarazuensis NBRC 115909
Starmerella vitae UWOPS 00-107.2
Starmerella sp. RPNCL13
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Starmerella jinningensis CBS 11864
Starmerella anomalae NYNU 15745
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Starmerella asiatica NYNU 15782
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Starmerella anomalae NYNU 15745
Starmerella henanensis NYNU 15766
50
Starmerella scarabaei NYNU 15821
94 Starmerella caucasica CBS 12650
Candida sp. AS 2.4033
Starmerella kuoi CBS 7267
Starmerella monicapupoae PYCC 8897
Starmerella sp. ST1-01
Starmerella cf. bombicola UWOPS 00-531
90 Starmerella cf. bombicola UWOPS 00-227.2
88 Starmerella bombicola NRRL Y-17069
56 Candida cf. powellii UWO(PS)00-195.2
88 Starmerella ilheusensis UFMG-CM-Y596
98
Starmerella powellii CBS 8795
Starmerella floricola CBS 7289
Starmerella orientalis SAM09
91 Candida cf. floricola UWO(PS)95-408.3
Starmerella riodocensis CBS 10087
Starmerella batistae CBS 8550
100 Starmerella vitis CBS 16418
Starmerella lactis-condense NRRL Y-1515
86 Starmerella stellata CBS 157
94 Starmerella davenportii CBS 9069
Starmerella bacillaris PYCC 3044
Starmerella floris CBS 10593
Starmerella etchellsii JCM 8066
Starmerella cellae CBS 10086
Starmerella meliponinorum UWO(PS)00-227.1
93
61
Starmerella roubikii UWOPS 01-191
Starmerella kourouensis CLIB 1707
Starmerella ratchasimensis CBS 10611
54
62 Starmerella camargoi UFMG-CM-Y595
Starmerella khaoyaiensis CBS 10839
Starmerella sirachaensis CBS 12094
Starmerella clade 2
97 Candida spenceri CBS 11673
Starmerella potacharoeniae CBS 11674
Starmerella apis CBS 2674
66 Starmerella sorbosivorans CBS 8768
Starmerella geochares CBS 6870
Starmerella magnoliae CBS 166
Starmerella syriaca CBS 13909
Starmerella vaccinii CBS 7318
Entelexis
Starmerella sp. D91W
Starmerella sp. CBS 6425
100
Entelexis magnoliae CBS 2798
Starmerella sp. UASWS2977 SBI-E01
Starmerella sp. D91WR
90
Starmerella sp. 11-1755
Starmerella clade 1
Starmerella stigmatis CBS 11464
Starmerella tilneyi CBS 8794
100
Starmerella xylocopis CBS 5659
Starmerella litoralis UFMG-CM-Y603
Starmerella gropengiesseri NRRL Y-17142
96 Tardiomyces depauwii CBS 18495
100 Tardiomyces blankie NRRL Y-17068
Tardiomyces digboiensis CBS 9800
0.05

Fig. S8

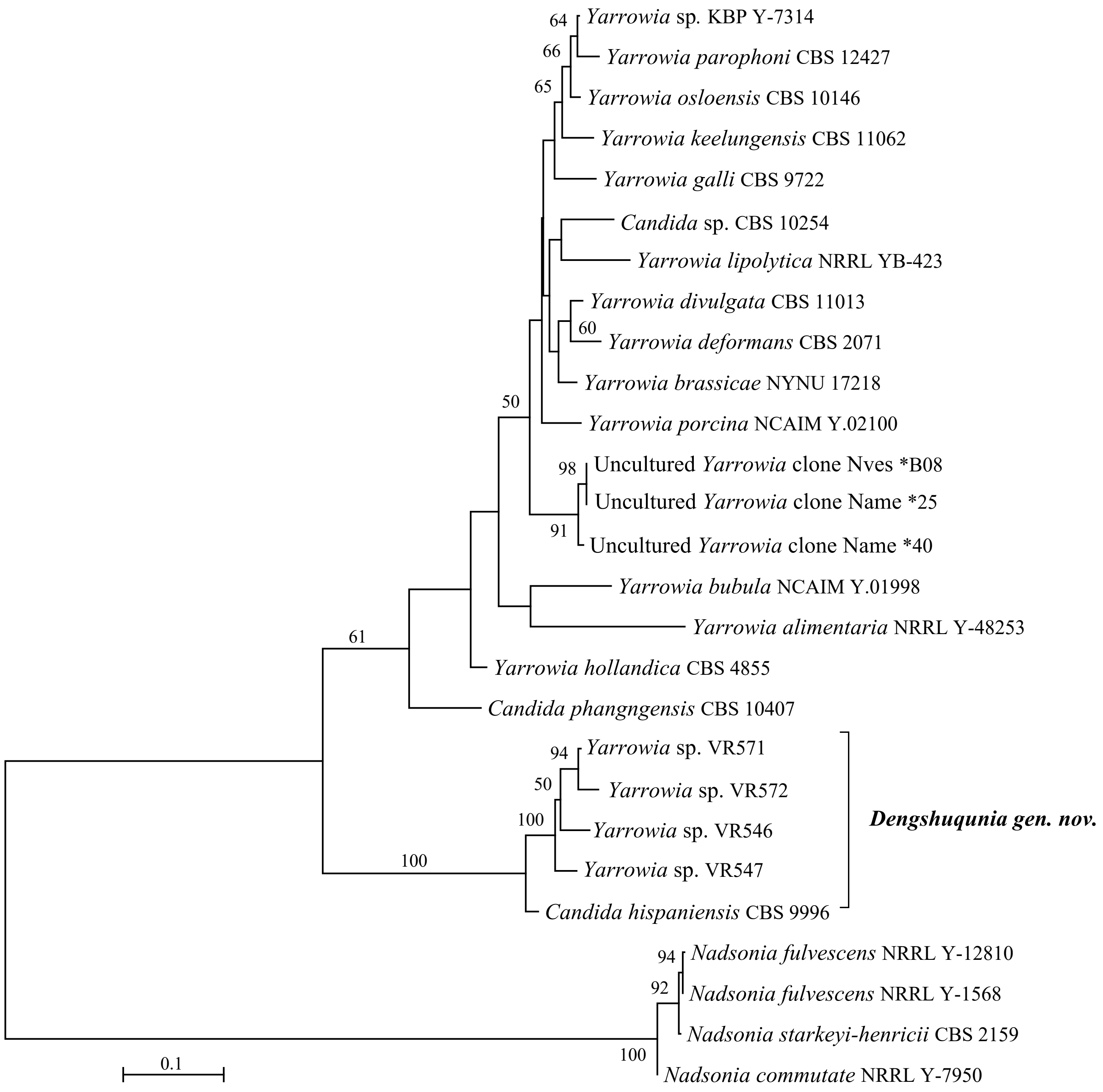
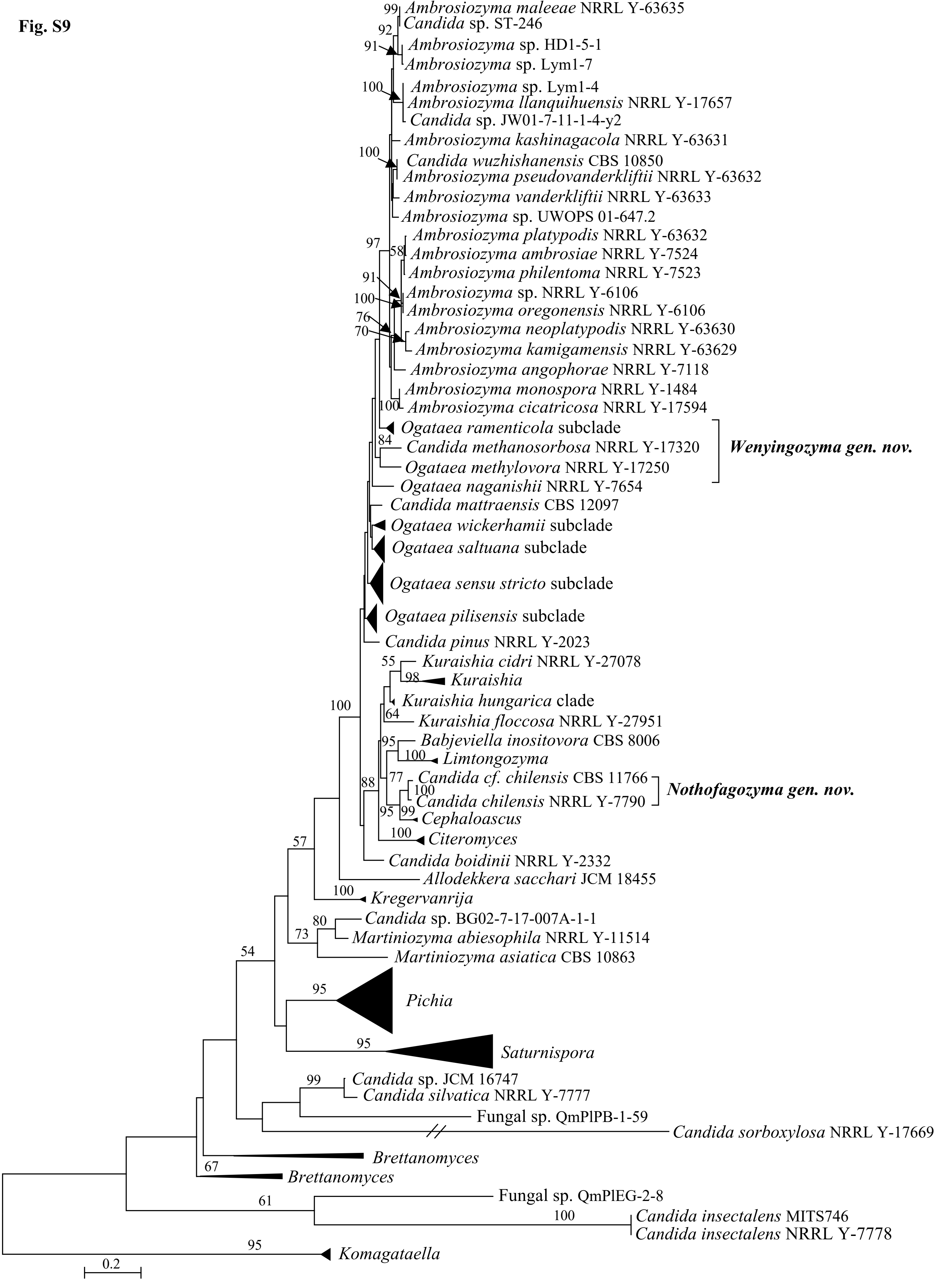

Yarrowia sp. KBP Y-7314
Yarrowia parophoni CBS 12427
Yarrowia osloensis CBS 10146
Yarrowia keelungensis CBS 11062
Yarrowia galli CBS 9722
Candida sp. CBS 10254
Yarrowia lipolytica NRRL YB-423
Yarrowia divulgata CBS 11013
Yarrowia deformans CBS 2071
Yarrowia brassicae NYNU 17218
Yarrowia porcina NCAIM Y.02100
Uncultured Yarrowia clone Nves *B08
Uncultured Yarrowia clone Name *25
Uncultured Yarrowia clone Name *40
Yarrowia bubula NCAIM Y.01998
Yarrowia alimentaria NRRL Y-48253
Yarrowia hollandica CBS 4855
Candida phangngensis CBS 10407
Yarrowia sp. VR571
Yarrowia sp. VR572
Yarrowia sp. VR546
Yarrowia sp. VR547
Candida hispaniensis CBS 9996
Dengshuqunia gen. nov.
Nadsonia fulvescens NRRL Y-12810
Nadsonia fulvescens NRRL Y-1568
Nadsonia starkeyi-henricii CBS 2159
Nadsonia commutate NRRL Y-7950
64
66
65
60
50
98
91
61
94
50
100
100
94
92
100
0.1

Fig. S9



99 Ambrosiozyma maleeae NRRL Y-63635
Candida sp. ST-246
92
91
Ambrosiozyma sp. HD1-5-1
Ambrosiozyma sp. Lym1-7
100
Ambrosiozyma sp. Lym1-4
Ambrosiozyma llanquihuensis NRRL Y-17657
Candida sp. JW01-7-11-1-4-y2
Ambrosiozyma kashinagacola NRRL Y-63631
100
Candida wuzhishanensis CBS 10850
Ambrosiozyma pseudovanderkliftii NRRL Y-63632
Ambrosiozyma vanderkliftii NRRL Y-63633
Ambrosiozyma sp. UWOPS 01-647.2
97
58
Ambrosiozyma platypodis NRRL Y-63632
Ambrosiozyma ambrosiae NRRL Y-7524
Ambrosiozyma philentoma NRRL Y-7523
91
Ambrosiozyma sp. NRRL Y-6106
100
Ambrosiozyma oregonensis NRRL Y-6106
76
70
Ambrosiozyma neoplatypodis NRRL Y-63630
Ambrosiozyma kamigamensis NRRL Y-63629
Ambrosiozyma angophorae NRRL Y-7118
Ambrosiozyma monospora NRRL Y-1484
100
Ambrosiozyma cicatricosa NRRL Y-17594
Ogataea ramenticola subclade
84
Candida methanosorbosa NRRL Y-17320
Ogataea methylovora NRRL Y-17250
Ogataea naganishii NRRL Y-7654
Wenyingozyma gen. nov.
Candida mattraensis CBS 12097
Ogataea wickerhamii subclade
Ogataea saltuana subclade
Ogataea sensu stricto subclade
Ogataea pilisensis subclade
Candida pinus NRRL Y-2023
55
Kuraishia cidri NRRL Y-27078
98
Kuraishia
Kuraishia hungarica clade
64
Kuraishia floccosa NRRL Y-27951
100
95
Babjeviella inositovora CBS 8006
100
Limtongozyma
77
Candida cf. chilensis CBS 11766
100
Candida chilensis NRRL Y-7790
Nothofagozyma gen. nov.
88
95
99
Cephaloascus
100
Citeromyces
Candida boidinii NRRL Y-2332
Allodekkera sacchari JCM 18455
57
100
Kregervanrija
80
Candida sp. BG02-7-17-007A-1-1
73
Martiniozyma abiesophila NRRL Y-11514
Martiniozyma asiatica CBS 10863
54
95
Pichia
95
Saturnispora
99
Candida sp. JCM 16747
Candida silvatica NRRL Y-7777
Fungal sp. QmPlPB-1-59
Candida sorboxylosa NRRL Y-17669
Brettanomyces
67
Brettanomyces
Fungal sp. QmPlEG-2-8
61
100
Candida insectalens MITS746
Candida insectalens NRRL Y-7778
95
Komagataella
0.2

Fig. S10

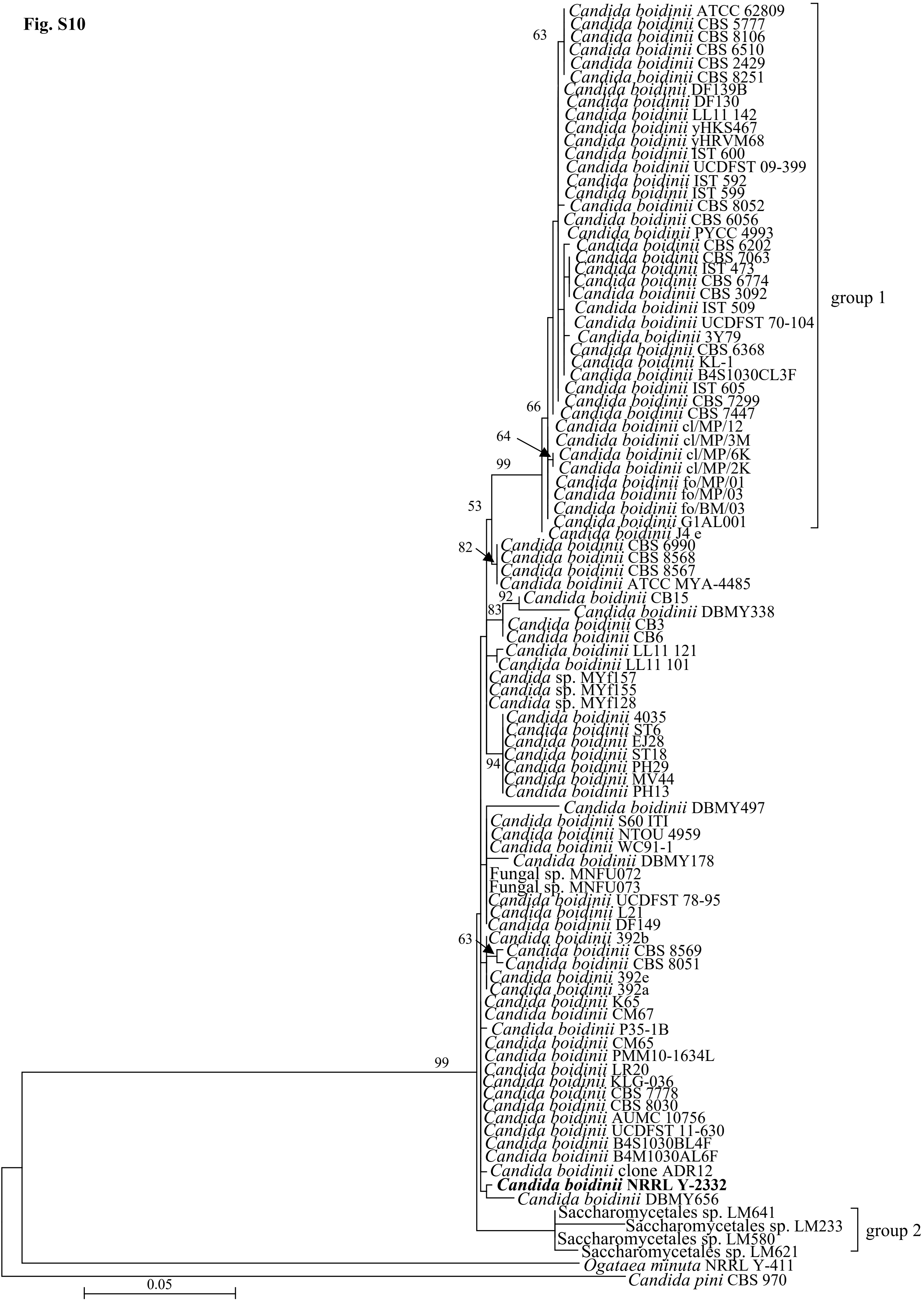

Candida boidinii ATCC 62809
Candida boidinii CBS 5777
Candida boidinii CBS 8106
Candida boidinii CBS 6510
Candida boidinii CBS 2429
Candida boidinii CBS 8251
Candida boidinii DF139B
Candida boidinii DF130
Candida boidinii LL11 142
Candida boidinii yHKS467
Candida boidinii yHRVM68
Candida boidinii IST 600
Candida boidinii UCDFST 09-399
Candida boidinii IST 592
Candida boidinii IST 599
Candida boidinii CBS 8052
Candida boidinii CBS 6056
Candida boidinii PYCC 4993
Candida boidinii CBS 6202
Candida boidinii CBS 7063
Candida boidinii IST 473
Candida boidinii CBS 6774
Candida boidinii CBS 3092
Candida boidinii IST 509
Candida boidinii UCDFST 70-104
Candida boidinii 3Y79
Candida boidinii CBS 6368
Candida boidinii KL-1
Candida boidinii B4S1030CL3F
Candida boidinii IST 605
Candida boidinii CBS 7299
Candida boidinii CBS 7447
Candida boidinii cl/MP/12
Candida boidinii cl/MP/3M
Candida boidinii cl/MP/6K
Candida boidinii cl/MP/2K
Candida boidinii fo/MP/01
Candida boidinii fo/MP/03
Candida boidinii fo/BM/03
Candida boidinii G1AL001
group 1
63
66
64
99
53
Candida boidinii J4 e
82
Candida boidinii CBS 6990
Candida boidinii CBS 8568
Candida boidinii CBS 8567
Candida boidinii ATCC MYA-4485
92
Candida boidinii CB15
Candida boidinii DBMY338
83
Candida boidinii CB3
Candida boidinii CB6
Candida boidinii LL11 121
Candida boidinii LL11 101
Candida sp. MYf157
Candida sp. MYf155
Candida sp. MYf128
Candida boidinii 4035
Candida boidinii ST6
Candida boidinii EJ28
Candida boidinii ST18
94
Candida boidinii PH29
Candida boidinii MV44
Candida boidinii PH13
Candida boidinii DBMY497
Candida boidinii S60 ITI
Candida boidinii NTOU 4959
Candida boidinii WC91-1
Candida boidinii DBMY178
Fungal sp. MNFU072
Fungal sp. MNFU073
Candida boidinii UCDFST 78-95
Candida boidinii L21
Candida boidinii DF149
Candida boidinii 392b
63
Candida boidinii CBS 8569
Candida boidinii CBS 8051
Candida boidinii 392e
Candida boidinii 392a
Candida boidinii K65
Candida boidinii CM67
Candida boidinii P35-1B
Candida boidinii CM65
Candida boidinii PMM10-1634L
99
Candida boidinii LR20
Candida boidinii KLG-036
Candida boidinii CBS 7778
Candida boidinii CBS 8030
Candida boidinii AUMC 10756
Candida boidinii UCDFST 11-630
Candida boidinii B4S1030BL4F
Candida boidinii B4M1030AL6F
Candida boidinii clone ADR12
Candida boidinii NRRL Y-2332
Candida boidinii DBMY656
Saccharomycetales sp. LM641
Saccharomycetales sp. LM233
Saccharomycetales sp. LM580
Saccharomycetales sp. LM621
group 2
Ogataea minuta NRRL Y-411
Candida pini CBS 970
0.05

Fig. S11

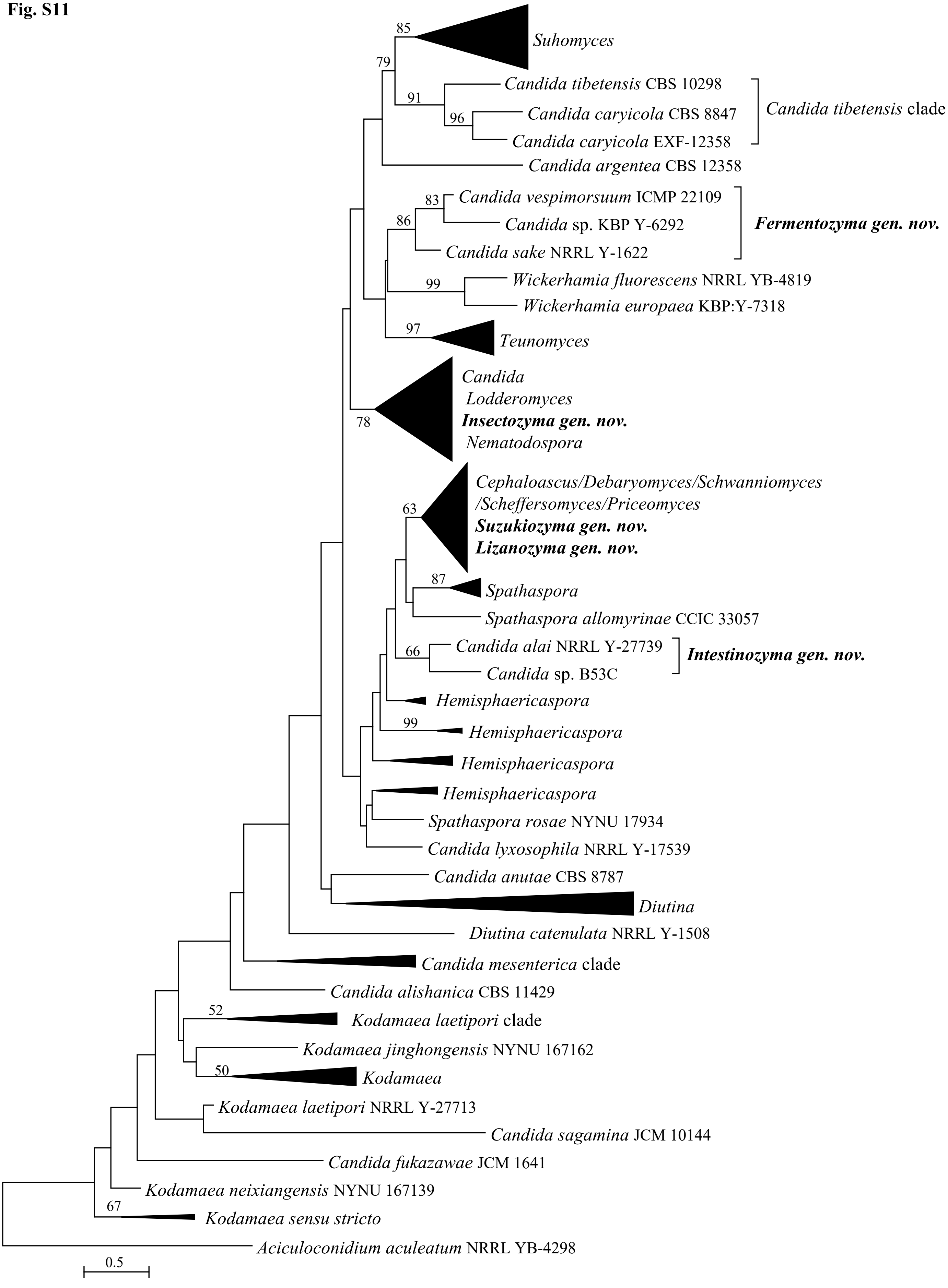

85
Suhomyces
79
Candida tibetensis CBS 10298
91
96
Candida caryicola CBS 8847
Candida caryicola EXF-12358
Candida tibetensis clade
Candida argentea CBS 12358
83
Candida vespimorsuum ICMP 22109
86
Candida sp. KBP Y-6292
Candida sake NRRL Y-1622
Fermentozyma gen. nov.
99
Wickerhamia fluorescens NRRL YB-4819
Wickerhamia europaea KBP:Y-7318
97
Teunomyces
Candida
Lodderomyces
78
Insectozyma gen. nov.
Nematodospora
Cephaloascus/Debaryomyces/Schwanniomyces
/Scheffersomyces/Priceomyces
63
Suzukiozyma gen. nov.
Lizanozyma gen. nov.
87
Spathaspora
Spathaspora allomyrinae CCIC 33057
66
Candida alai NRRL Y-27739
Candida sp. B53C
Intestinozyma gen. nov.
Hemisphaericaspora
99
Hemisphaericaspora
Hemisphaericaspora
Hemisphaericaspora
Spathaspora rosae NYNU 17934
Candida lyxosophila NRRL Y-17539
Candida anutae CBS 8787
Diutina
Diutina catenulata NRRL Y-1508
Candida mesenterica clade
Candida alishanica CBS 11429
52
Kodamaea laetipori clade
Kodamaea jinghongensis NYNU 167162
50
Kodamaea
Kodamaea laetipori NRRL Y-27713
Candida sagamina JCM 10144
Candida fukazawae JCM 1641
Kodamaea neixiangensis NYNU 167139
67
Kodamaea sensu stricto
Aciculoconidium aculeatum NRRL YB-4298
0.5

Fig. S12

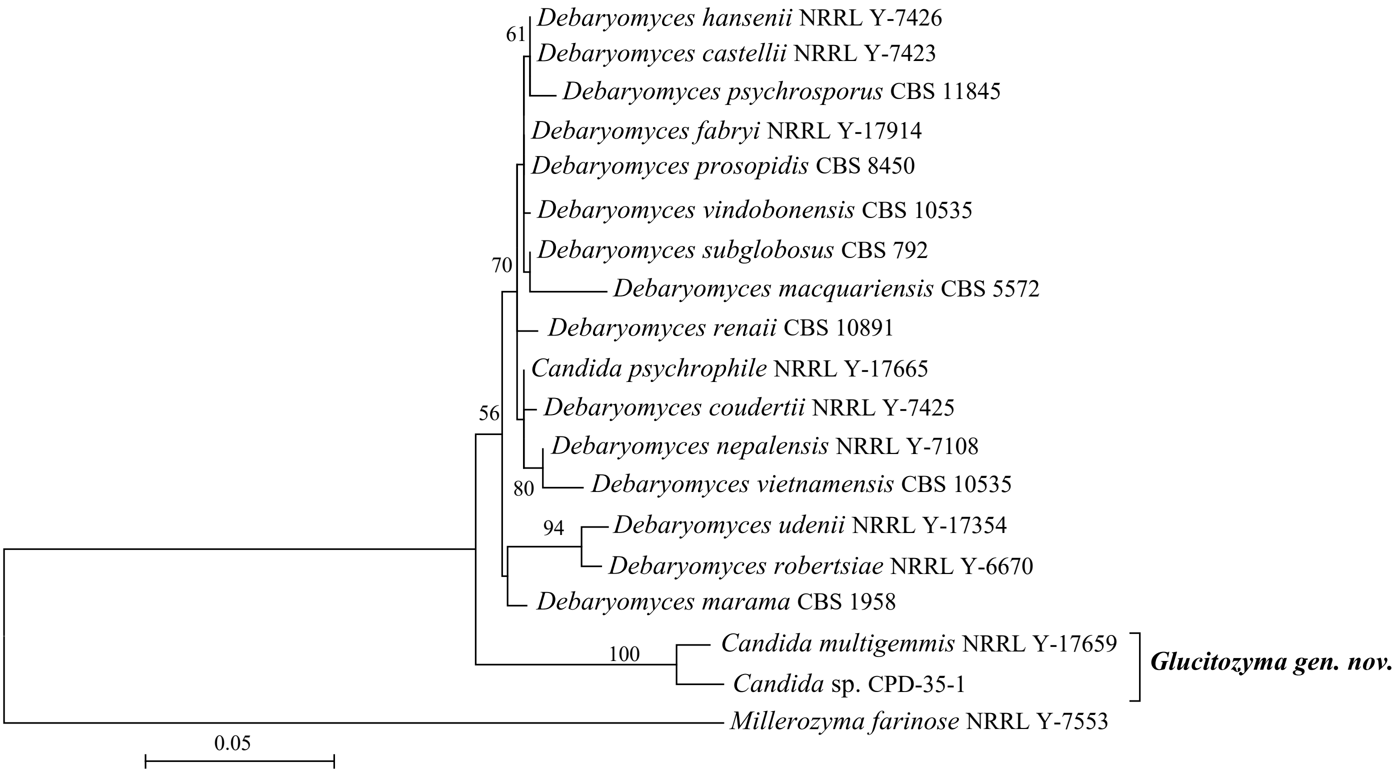
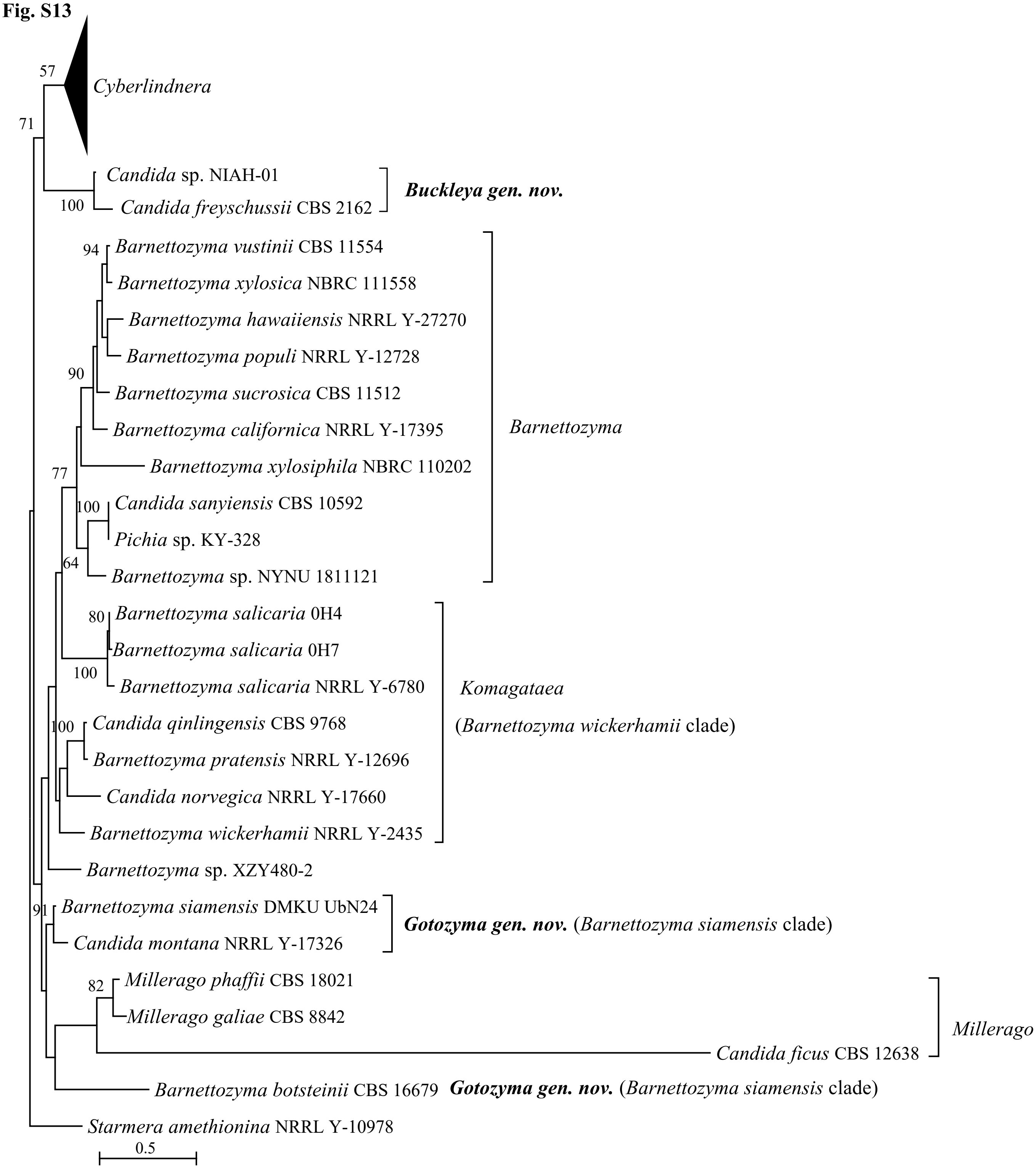

Debaryomyces hansenii NRRL Y-7426
61
Debaryomyces castellii NRRL Y-7423
Debaryomyces psychrosporus CBS 11845
Debaryomyces fabryi NRRL Y-17914
Debaryomyces prosopidis CBS 8450
Debaryomyces vindobonensis CBS 10535
Debaryomyces subglobosus CBS 792
70
Debaryomyces macquariensis CBS 5572
Debaryomyces renaii CBS 10891
Candida psychrophile NRRL Y-17665
56
Debaryomyces coudertii NRRL Y-7425
Debaryomyces nepalensis NRRL Y-7108
80
Debaryomyces vietnamensis CBS 10535
94
Debaryomyces udenii NRRL Y-17354
Debaryomyces robertsiae NRRL Y-6670
Debaryomyces marama CBS 1958
Candida multigemmis NRRL Y-17659
100
Candida sp. CPD-35-1
Glucitozyma gen. nov.
Millerozyma farinose NRRL Y-7553
0.05

Fig. S13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Cyberlindnera
71
Candida sp. NIAH-01
100
Candida freyschussii CBS 2162
Buckleya gen. nov.
94
Barnettozyma vustinii CBS 11554
Barnettozyma xylosica NBRC 111558
Barnettozyma hawaiiensis NRRL Y-27270
Barnettozyma populi NRRL Y-12728
90
Barnettozyma sucrosica CBS 11512
Barnettozyma californica NRRL Y-17395
Barnettozyma
Barnettozyma xylosiphila NBRC 110202
77
100
Candida sanyiensis CBS 10592
Pichia sp. KY-328
64
Barnettozyma sp. NYNU 1811121
80
Barnettozyma salicaria 0H4
Barnettozyma salicaria 0H7
100
Barnettozyma salicaria NRRL Y-6780
Komagataea
100
Candida qinlingensis CBS 9768
(*Barnettozyma wickerhamii* clade)
Barnettozyma pratensis NRRL Y-12696
Candida norvegica NRRL Y-17660
Barnettozyma wickerhamii NRRL Y-2435
Barnettozyma sp. XZY480-2
91
Barnettozyma siamensis DMKU UbN24
Gotozyma gen. nov. (*Barnettozyma siamensis* clade)
Candida montana NRRL Y-17326
82
Millerago phaffii CBS 18021
Millerago galiae CBS 8842
Millerago
Candida ficus CBS 12638
Barnettozyma botsteinii CBS 16679
Gotozyma gen. nov. (*Barnettozyma siamensis* clade)
Starmera amethionina NRRL Y-10978
0.5