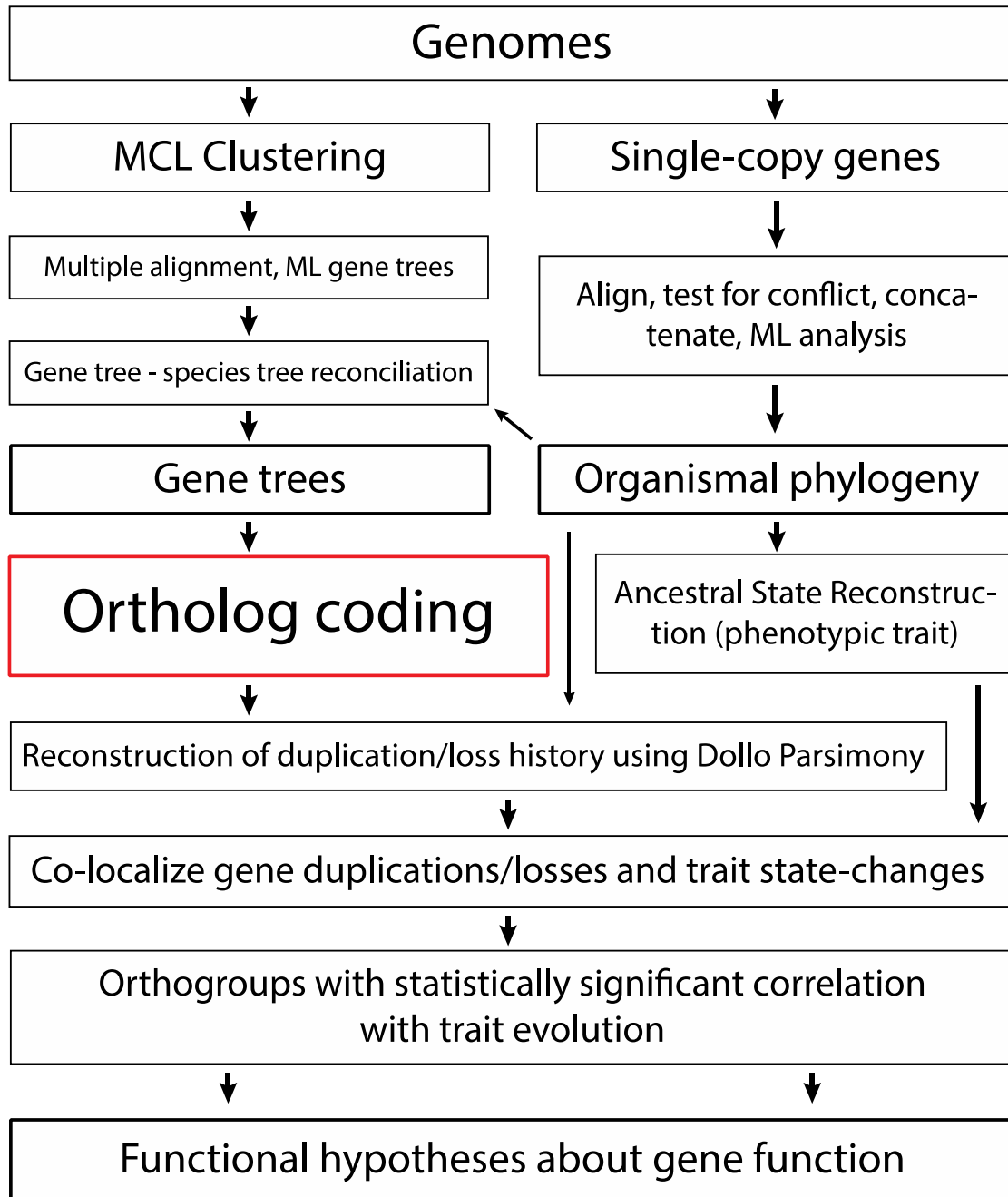
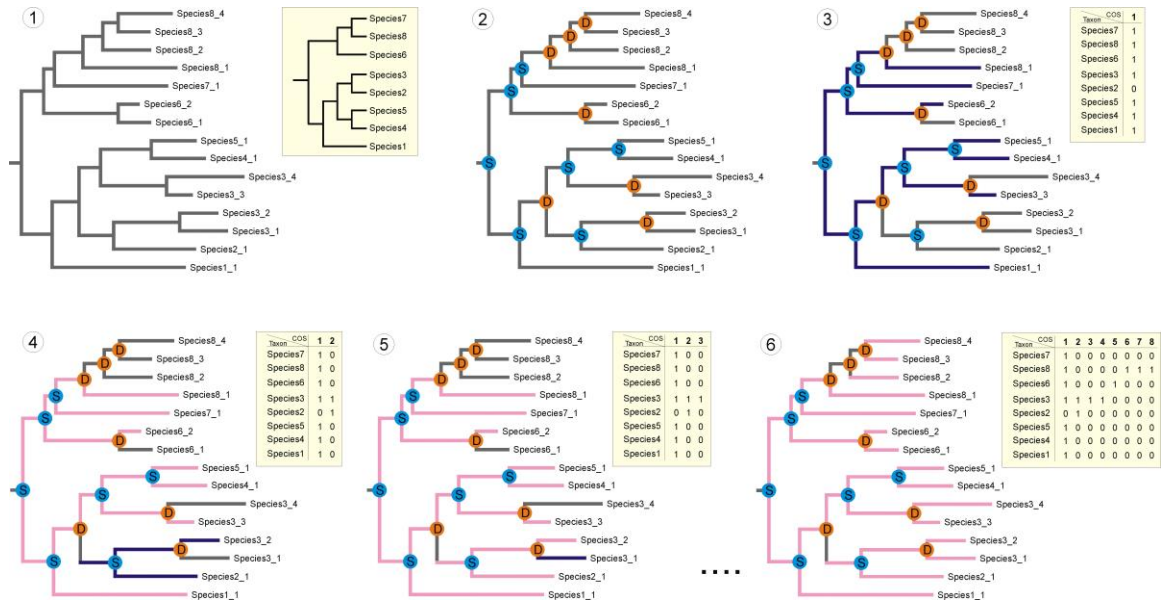


Supplementary Figure 1. Complete duplication/loss mapping of orthogroups on the organismal phylogenetic tree inferred using Dollo parsimony. Yellow and grey boxes represent the number of inferred duplications and losses for each branch, respectively. Next to species names duplications for all genes and for inparalogs only are shown; the latter includes only proteins that are members of a gene family with more than one member. Note that 3383 orthogroups were inferred to have been present already in the root of the tree, followed by numerous expansions and contractions (e.g. in Microsporidia).

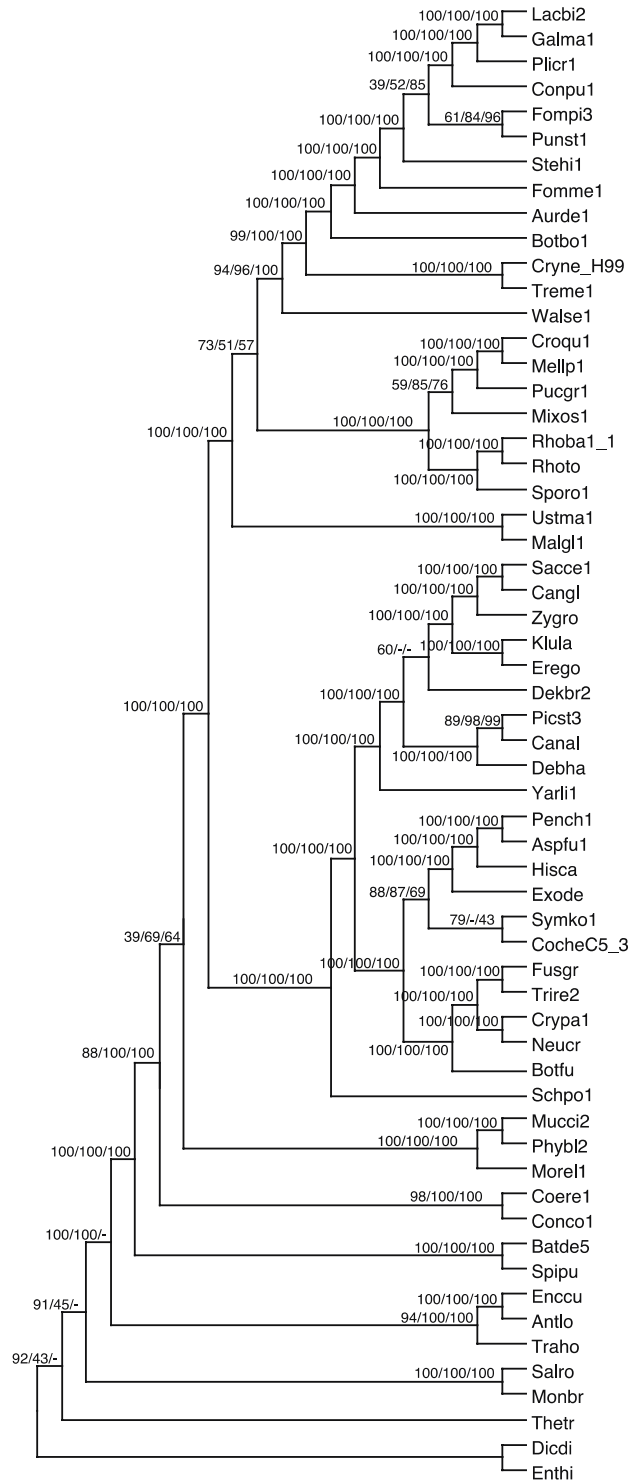


Supplementary Figure 2. The structure of the COMPARE pipeline. The analysis starts with predicted proteins of the input genomes, which are used in two paths. One (left panel) aims to infer gene trees on which orthogroups will be identified, the other uses single-copy genes to infer organismal phylogenies. Gene tree inference is preceded by clustering protein sequences into approximate gene families, inferring multiple sequence alignments and Maximum Likelihood gene trees for each cluster, which are then improved using gene tree – species tree reconciliations. Reconciled gene trees are subjected to ortholog-coding, which delimits orthogroups and creates an Ortholog x Species matrix. This is then used to reconstruct the duplication/loss history along the

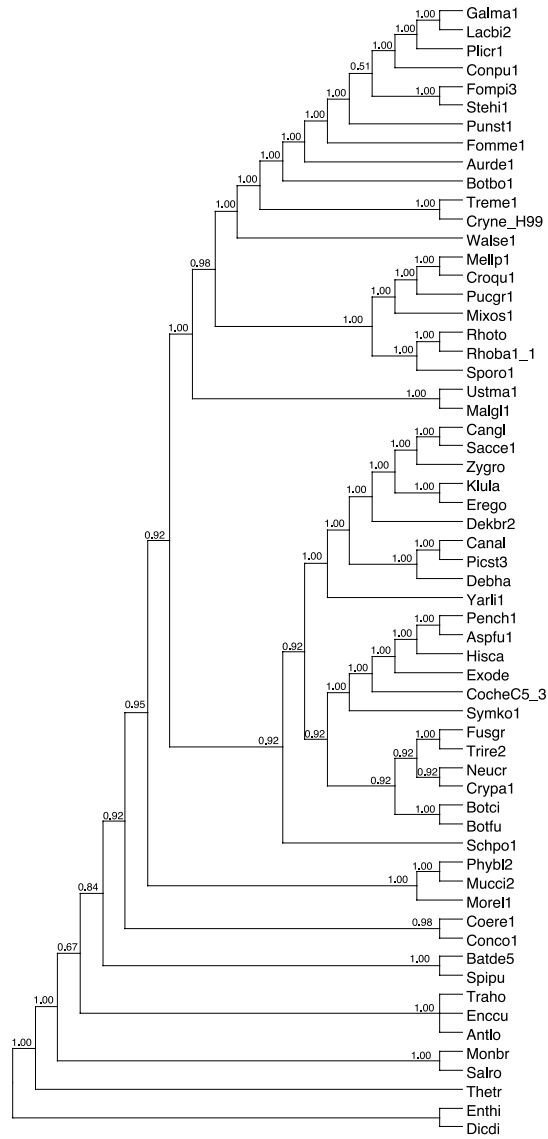
organismal phylogenetic tree and screen for correlated evolution of orthogroups with the phenotypic trait of interest.



Supplementary Figure 3. Outline of the ortholog-coding algorithm. For explanation see Methods.



Supplementary Figure 4. Maximum Likelihood phylogram with support values from ML bootstrap analyses of the three datasets on branches. Numbers represent bootstrap percentages obtained using the datasets with exclusion threshold 0.95, 0.98 and 1.0, respectively.



Supplementary Figure 5. 50% Bayesian Majority Rule consensus tree obtained using the most stringent dataset (exclusion threshold 1.0). Numbers above branches represent Bayesian Posterior Probabilities.

Supplementary Table 1. Species, their abbreviations and source of whole genome sequences used in this study. Species marked by an asterisk (★) are unpublished and have been included in this study with permissions of the Principal Investigators of the genome projects.

TAXON NAME	ABBREVIATION	SOURCE
<i>Antonospora locustae</i>	Antlo	http://forest.mbl.edu/cgi-bin/site/antonospora01?page=download
<i>Aspergillus fumigatus</i>	Aspfu1	http://genome.jgi.doe.gov/Aspfu1/Aspfu1.home.html
<i>Auricularia delicata</i>	Aurde1	http://genome.jgi.doe.gov/Aurde1/Aurde1.home.html
<i>Batrachochytrium dendrobatidis</i>	Batde5	http://genome.jgi.doe.gov/Batde5/Batde5.home.html
<i>Botryobasidium botryosum</i>	Botbo1★	http://genome.jgi.doe.gov/Botbo1/Botbo1.home.html
<i>Botrytis cinerea</i>	Botci	http://www.broadinstitute.org/annotation/genome/botrytis_cinerea/MultiDownloads.html
<i>Candida albicans</i>	Canal	http://www.candidagenome.org/DownloadContents.shtml
<i>Candida glabrata</i>	Cangl	http://www.genolevures.org/download.html#klla
<i>Cochliobolus heterostrophus</i>	CocheC3	http://genome.jgi.doe.gov/CocheC5_3/CocheC5_3.home.html
<i>Coemansia reversa</i>	Coere1★	http://genome.jgi.doe.gov/Coere1/Coere1.home.html
<i>Conidiobolus coronatus</i>	Conco1★	http://genome.jgi.doe.gov/Conco1/Conco1.home.html
<i>Coniophora puteana</i>	Conpu1	http://genome.jgi.doe.gov/Conpu1/Conpu1.home.html
<i>Cronartium quercuum</i>	Croqu1★	http://genome.jgi.doe.gov/Croqu1/Croqu1.home.html
<i>Cryphonectria parasitica</i>	Crypa1	http://genome.jgi.doe.gov/Crypa2/Crypa2.home.html
<i>Cryptococcus neoformans</i>	CryneH1	http://genome.jgi.doe.gov/Cryne_JEC21_1/Cryne_JEC21_1.home.html
<i>Debaryomyces hanseni</i>	Debha	http://crdd.osdd.net/raghava/genomesrs/deb.php
<i>Dekkera bruxellensis</i>	Dekbr2	http://genome.jgi.doe.gov/Dekbr2/Dekbr2.home.html
<i>Dictyostelium discoideum</i>	Dicdi	http://dictybase.org/db/cgi-bin/dictyBase/download/blast_databases.pl
<i>Encephalitozoon cuniculi</i>	Enccu	http://www.broadinstitute.org/annotation/genome/microsporidia_comparative/MultiDownloads.html
<i>Entamoeba histolytica</i>	Enthi	ftp://ftp.sanger.ac.uk/pub/pathogens/Entamoeba/
<i>Eremothecium gossypii</i>	Eregog	http://www.genolevures.org/download.html#klla
<i>Exophiala dermatitidis</i>	Exode★	http://www.broadinstitute.org/annotation/genome/Black_Yeasts/MultiDownloads.html
<i>Fomitiporia mediterranea</i>	Fomme1	http://genome.jgi.doe.gov/Fomme1/Fomme1.home.html
<i>Fomitopsis pinicola</i>	Fompi3	http://genome.jgi.doe.gov/Fompi3/Fompi3.home.html
<i>Fusarium graminearum</i>	Fusgr	http://www.broadinstitute.org/annotation/genome/fusarium_group/MultiDownloads.html
<i>Galerina marginata</i>	Galma1★	http://genome.jgi.doe.gov/Galma1/Galma1.home.html
<i>Histoplasma capsulatum</i>	Hisca	http://www.broadinstitute.org/annotation/genome/histoplasma_capsulatum/MultiDownloads.html
<i>Kluyveromyces lactis</i>	Klula	http://www.genolevures.org/download.html#klla
<i>Laccaria bicolor</i>	Lacbi2	http://genome.jgi.doe.gov/Lacbi2/Lacbi2.home.html
<i>Malessezia globosa</i>	Malgl1	http://genome.jgi.doe.gov/Malgl1/Malgl1.home.html
<i>Melampsora laricis-populina</i>	Mellp1	http://genome.jgi.doe.gov/Mellp1/Mellp1.home.html
<i>Mixia osmundae</i>	Mixos1	http://genome.jgi.doe.gov/Mixos1/Mixos1.home.html
<i>Monosiga brevicollis</i>	Monbr★	http://www.broadinstitute.org/annotation/genome/multicellularity_project/MultiDownloads.html
<i>Mortierella elongata</i>	Morel1★	http://genome.jgi-psf.org/Morel1/Morel1.home.html
<i>Mucor circinelloides</i>	Mucci2	http://genome.jgi.doe.gov/Mucci2/Mucci2.home.html
<i>Neurospora crassa</i>	Neucr	http://www.broadinstitute.org/annotation/genome/neurospora/MultiDownloads.html
<i>Penicillium chrysogenum</i>	Pench1	http://genome.jgi.doe.gov/Pench1/Pench1.home.html
<i>Phycomyces blakesleeanus</i>	Phybl2	http://genome.jgi.doe.gov/Phybl2/Phybl2.home.html
<i>Pichia stipitis</i>	Picst3	http://genome.jgi.doe.gov/Picst3/Picst3.home.html
<i>Plicaturopsis crispa</i>	Plicr1★	http://genome.jgi.doe.gov/Plicr1/Plicr1.home.html
<i>Puccinia graminis</i>	Pucgr1	http://genome.jgi.doe.gov/Pucgr1/Pucgr1.home.html
<i>Punctularia strigosozonata</i>	Punst1	http://genome.jgi.doe.gov/Punst1/Punst1.home.html
<i>Rhodospidium toruloides</i> (=Rhodotorula glutinis)	Rhoba1★	http://crdd.osdd.net/raghava/genomesrs/rhodosp.php
<i>Rhodotorula graminis</i>	Rhoto	http://genome.jgi.doe.gov/Rhoba1_1/Rhoba1_1.home.html
<i>Saccharomyces cerevisiae</i>	Sacce1	http://genome.jgi.doe.gov/SacceYB210_1/SacceYB210_1.home.html
<i>Salpingoaea rosetta</i>	Salro★	http://www.broadinstitute.org/annotation/genome/multicellularity_project/MultiDownloads.html
<i>Schizosaccharomyces pombe</i>	Schpo1	http://genome.jgi.doe.gov/Schpo1/Schpo1.home.html
<i>Spizellomyces punctatus</i>	Spipu★	http://www.broadinstitute.org/annotation/genome/multicellularity_project/MultiDownloads.html
<i>Sporobolomyces roseus</i>	Sporo1★	http://genome.jgi.doe.gov/Sporo1/Sporo1.home.html
<i>Stereum hirsutum</i>	Stehi1	http://genome.jgi.doe.gov/Stehi1/Stehi1.home.html
<i>Symbiotaphrina kochii</i>	Symko1★	http://genome.jgi.doe.gov/Symko1/Symko1.home.html
<i>Thecamonas trahens</i>	Thetr★	http://www.broadinstitute.org/annotation/genome/multicellularity_project/MultiDownloads.html
<i>Trachipleistophora hominis</i>	Traho	http://www.ncbi.nlm.nih.gov/bioproject/84343
<i>Tremella mesenterica</i>	Treme1	http://genome.jgi.doe.gov/Treme1/Treme1.home.html
<i>Trichoderma reesei</i>	Trire2	http://genome.jgi.doe.gov/Trire2/Trire2.home.html

<i>Ustilago maydis</i>	Ustma1	http://genome.jgi.doe.gov/Ustma1/Ustma1.home.html
<i>Wallemia sebi</i>	Walse1	http://genome.jgi.doe.gov/Walse1/Walse1.home.html
<i>Yarrowia lipolytica</i>	Yarli1	http://genome.jgi.doe.gov/Yarli1/Yarli1.home.html
<i>Zygosaccharomyces rouxii</i>	Zygro	http://www.genolevures.org/download.html#klla

Supplementary Table 2. Classification and lifestyle (yeast, unicellular, filamentous or pseudohyphal) of the species included in the study.

TAXON	HIGHER CLASSIFICATION	LIFESTYLE ¹ (FI – FILAMENTOUS, YE – YEAST, PS – PSEUDOHYPHAL, UNI - UNICELLULAR)
<i>Antonospora locustae</i>	Microsporidia	UNI
<i>Aspergillus fumigatus</i>	Pezizomycotina	FI
<i>Auricularia delicata</i>	Agaricomycotina	FI
<i>Batrachochytrium dendrobatidis</i>	Chytridiomycota	UNI
<i>Botryobasidium botryosum</i>	Agaricomycotina	FI
<i>Botrytis cinerea</i>	Leotiomycetes	FI
<i>Candida albicans</i>	Saccharomycotina	YE,FI,PS
<i>Candida glabrata</i>	Saccharomycotina	YE,PS
<i>Cochliobolus heterostrophus</i>	Dothideomycetes	FI,YE
<i>Coemansia reversa</i>	Kickxellomycota	FI
<i>Conidiobolus coronatus</i>	Entomophthoromycotina	FI
<i>Coniophora puteana</i>	Agaricomycotina	FI
<i>Cronartium quercuum</i>	Pucciniomycotina	FI
<i>Cryphonectria parasitica</i>	Pezizomycotina	FI
<i>Cryptococcus neoformans</i>	Agaricomycotina	FI,YE
<i>Debaryomyces hansenii</i>	Saccharomycotina	YE,FI?,PS
<i>Dekkera bruxellensis</i>	Saccharomycotina	YE,FI,PS
<i>Dictyostelium discoideum</i>	Amoebozoa	UNI
<i>Encephalitozoon cuniculi</i>	Microsporidia	UNI
<i>Entamoeba histolytica</i>	Amoebozoa	UNI
<i>Eremothecium gossypii</i>	Saccharomycotina	FI
<i>Exophiala dermatitidis</i>	Pezizomycotina	FI,YE
<i>Fomitiporia mediterranea</i>	Agaricomycotina	FI
<i>Fomitopsis pinicola</i>	Agaricomycotina	FI
<i>Fusarium graminearum</i>	Pezizomycotina	FI
<i>Galerina marginata</i>	Agaricomycotina	FI
<i>Histoplasma capsulatum</i>	Pezizomycotina	FI,YE
<i>Kluyveromyces lactis</i>	Saccharomycotina	YE,PS
<i>Laccaria bicolor</i>	Agaricomycotina	FI
<i>Malessezia globosa</i>	Ustilaginomycotina	FI,YE
<i>Melampsora laricis-populina</i>	Pucciniomycotina	FI
<i>Mixia osmundae</i>	Pucciniomycotina	FI,YE
<i>Monosiga brevicollis</i>	Choanoflagellata	UNI
<i>Mortierella elongata</i>	Zygomycota	FI
<i>Mucor circinelloides</i>	Zygomycota	FI,YE
<i>Neurospora crassa</i>	Pezizomycotina	FI
<i>Penicillium chrysogenum</i>	Pezizomycotina	FI,(YE) ²
<i>Phycomyces blakesleeanus</i>	Zygomycota	FI
<i>Pichia stipitis</i>	Saccharomycotina	YE,PS
<i>Plicaturopsis crispa</i>	Agaricomycotina	FI
<i>Puccinia graminis</i>	Pucciniomycotina	FI
<i>Punctularia strigosozonata</i>	Agaricomycotina	FI
<i>Rhodosporidium toruloides</i> (=Rhodotorula glutinis)	Pucciniomycotina	FI,YE
<i>Rhodotorula graminis</i>	Pucciniomycotina	FI,YE,PS
<i>Saccharomyces cerevisiae</i>	Saccharomycotina	YE,PS
<i>Salpingoaea rosetta</i>	Choanoflagellata	UNI
<i>Schizosaccharomyces pombe</i>	Taphrinomycotina	YE,PS
<i>Spizellomyces punctatus</i>	Chytridiomycota	UNI
<i>Sporobolomyces roseus</i>	Pucciniomycotina	FI,YE,PS
<i>Stereum hirsutum</i>	Agaricomycotina	FI
<i>Symbiotaphrina kochii</i>	Pezizomycotina	YE
<i>Thecamonas trahens</i>	Apusozoa	UNI
<i>Trachipleistophora hominis</i>	Microsporidia	UNI
<i>Tremella mesenterica</i>	Agaricomycotina	FI,YE
<i>Trichoderma reesei</i>	Pezizomycotina	FI
<i>Ustilago maydis</i>	Ustilaginomycotina	FI,YE
<i>Wallemia sebi</i>	Wallemiomycetes	FI
<i>Yarrowia lipolytica</i>	Saccharomycotina	FI,YE,PS
<i>Zygosaccharomyces rouxii</i>	Saccharomycotina	YE,PS

Supplementary Table 3. Datasets, data exclusion threshold, number of sites and loci of the three phylogenomic datasets.

EXCLUSION THRESHOLD	CONCATENATED LENGTH (AMINO ACIDS)	NUMBER OF LOCI	NUMBER OF MAXI MALLY SUPPORTED CLADES (ML)
0.95	172,073	594	47
0.98	117,517	567	45
1.0	51,789	371	41

Supplementary References

- 1 Kurtzman, C. P., Fell, J. V. & Boekhout, T. The yeasts - A taxonomic study. Fifth Edition. *Elsevier* (2011).
- 2 Boyce, K.J., Hynes, M.J., Andrianopoulos, A. The CDC42 homolog of the dimorphic fungus *Penicillium marneffei* is required for correct cell polarization during growth but not development. *J Bacteriol.* 183:3447-57. (2001)