Supplementary Table ST2: Single-copy, orthologous, housekeeping genes chosen for species tree reconstruction on basis of topological score over 90% (as reported in FUNYBASE (Aguileta et al. 2008; Marthey et al. 2008)).

Gene name	**Over 95%**	***Saccharomyces cerevisiae* S288c GI** **(for reference protein sequence)**	***Saccharomyces cerevisiae* S288c accession** **(for reference protein sequence)**	**Optimal model** **(according to BIC)**	**Description**
Cct8p	Y	6322452	NP_012526	LG+I+G	T-complex protein 1 subunit theta; molecular chaperone
Crm1p	Y	398366207	NP_011734	LG+I+G	chromosome region maintenance protein 1; exportin 1; acts as receptor for the leucine-rich nuclear export signal
Elp3p	Y	6325171	NP_015239	LG+I+G	elongator complex protein 3; acts during transcription, as catalytic subunit of the RNA polymerase II elongator complex
Erb1p	Y	6323693	NP_013764	LG+I+G	eukaryotic ribosome biogenesis protein 1; component of NOP7 complex required for rRNA maturation and formation of 60S subunit
Gdh2p	Y	6319986	NP_010066	LG+I+G	NAD-specific glutamate dehydrogenase; involved in glutamate degradation
Hsh49p	Y	6324895	NP_014964	LG+I+G	protein HSH49; possible SF-B3 like factor
Icp55p	Y	6320922	NP_011001	LG+I+G	intermediate cleaving peptidase 55; involved in stabilisation of mitochondrial proteome
Ils1p	Y	6319395	NP_009477	LG+I+G	isoleucine--tRNA ligase, cytoplasmic
Ilv2p	Y	6323755	NP_013826	LG+I+G	acetolactate synthase catalytic subunit, mitochondrial; involved in amino acid biosynthesis (valine and isoleucine)
Kog1p	Y	6321980	NP_012056	LG+I+G+F	target of rapamycin complex 1 subunit KOG1; kontroller of growth

					protein 1; part of TORC1 complex 1 involved in control of cellular growth in response to environmental stimuli
Mcm7p	Y	398365471	NP_009761	LG+I+G	DNA replication licensing factor MCM7; minichromosome maintenance protein 7
Msh3p	Y	157285763	NP_010016	LG+I+G	DNA mismatch repair protein MSH3; part of post-replicative DNA mismatch repair system
Nat3p	Y	31126970	NP_015456	LG+I+G	N-terminal acetyltransferase B complex catalytic subunit NAT3; involved in amino terminal acetylation of methionines
Nhx1p	Y	398366611	NP_010744	LG+I+G+F	endosomal/prevacuolar sodium/hydrogen exchanger; vacuolar protein sorting-associated protein 44
Pol1p	Y	398364843	NP_014297	LG+I+G	DNA polymerase I subunit A
Pwp2p	Y	6319903	NP_009984	LG+I+G+F	periodic tryptophan protein 2; U3 snoRNA-associated protein 1; required for bud site selection and cell separation, involved in nucleolar preprocessing of pre-18S RNA
Rvb1p	Y	6320396	NP_010476	LG+I+G	RuvB family ATP-dependent DNA helicase pontin; involved in chromatin remodelling complexes
Rvb2p	Y	6325021	NP_015089	LG+I+G	RuvB family ATP-dependent DNA helicase reptin; involved in chromatin remodelling complexes
Ssl2p	Y	6322048	NP_012123	LG+I+G	DNA repair helicase RAD25; supressor of stem loop mutation 2
Tif5p	Y	6325298	NP_015366	LG+I+G	eukaryotic translation initiation factor 5 (eIF5); GTP hydrolase
Tsr1p	Y	6320143	NP_010223	LG+I+G	ribosome biogenesis protein TSR1; required for transport of pre-40S molecules from the nucleus to cytoplasm
Uba1p	Y	6322639	NP_012712	LG+I+G+F	ubiquitin activating enzyme E1
Vma4p	Y	398366277	NP_014977	LG+I+G	vacuolar proton ATPase subunit E

					(V-ATPase component)

Aguileta G, Marthey S, Chiapello H, Lebrun M-H, Rodolphe F, Fournier E, Gendrault-Jacquemard A, Giraud T. 2008. Assessing the performance of single-copy genes for recovering robust phylogenies. Syst. Biol. 57:613–627.

Marthey S, Aguileta G, Rodolphe F, Gendrault A, Giraud T, Fournier E, Lopez-Villavicencio M, Gautier A, Lebrun M-H, Chiapello H. 2008. FUNYBASE: a FUNgal phYlogenomic dataBASE. BMC Bioinformatics 9:456.