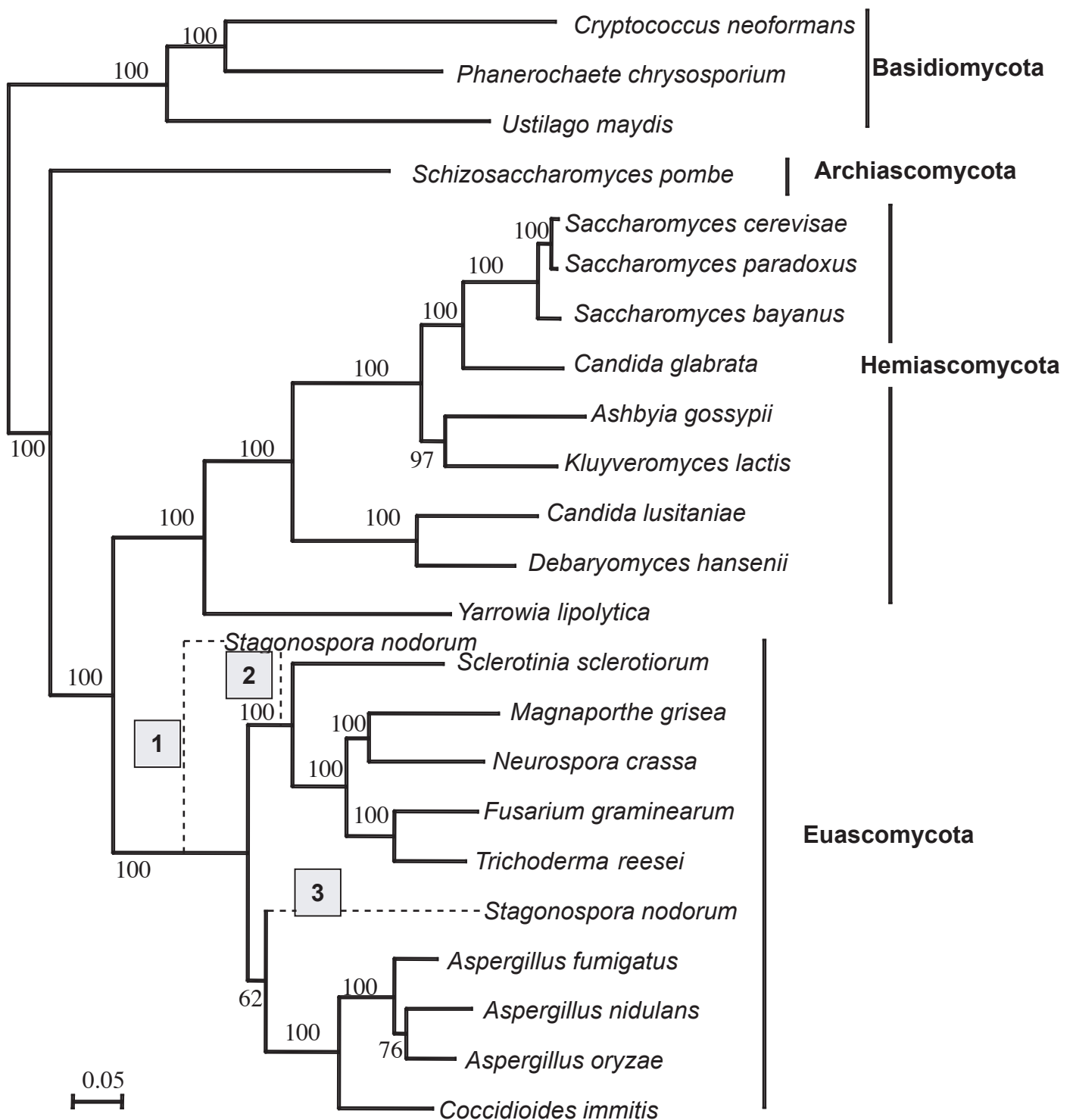


ONLINE APPENDIX 1. Unrooted phylogeny of the concatenated dataset with the 23 genomes from Table 1 (219 single-copy orthologs). The three placements most often recovered in single-gene phylogenies for *Stagnospora nodorum* are indicated with numbers 1-3. Indicated supports are percentages over 250 bootstraps.

ONLINE APPENDIX 3. Distribution of the number of occurrences for given Robinson-Foulds distances on 10 subsets of 15 species for the 246 individual gene phylogenies (A), and for the two genes yielding a 100% topological score: MS456 (B) and MS277 (C).

ONLINE APPENDIX 4. Distribution of the number of occurrences for given Kuhner-Felsenstein distances on 10 subsets of 15 species for the 246 individual gene phylogenies (A), and for the two genes yielding a 100% topological score: MS456 (B) and MS277 (C).

ONLINE APPENDIX 5. Phylogeny based on MS456 of the 35 fungal species for which a putative ortholog of this gene could be identified. *Homo sapiens* was used as outgroup. Indicated supports are percentages over 250 bootstrap.



ONLINE APPENDIX 2. Ortholog clusters whose corresponding topologies are closest to that of the concatenated dataset. Clusters are ranked by their topological score, the number of nodes in the trees with bootstrap values lower than 70%, and their annotation as in *Saccharomyces cerevisiae*.

Cluster	Topology Score	Nodes with bootstrap<70	Annotation
MS277	100.0	6	Protein required for processing of 20S pre-rRNA in the cytoplasm associates with pre-40S ribosomal particles
MS456	100.0	3	Component of the hexameric MCM complex which is important for priming origins of DNA replication in G1 and becomes an active ATP-dependent helicase that promotes DNA melting and elongation when activated by Cdc7p-Dbf4p in S-phase
FG805	96.3	7	Catalytic subunit of the NatB N-terminal acetyltransferase which catalyzes acetylation of the amino-terminal methionine residues of all proteins beginning with Met-Asp or Met-Glu and of some proteins beginning with Met-Asn or Met-Met
FG832	96.3	5	Translation initiation factor eIF-5; N-terminal domain functions as a GTPase-activating protein to mediate hydrolysis of ribosome-bound GTP; C-terminal domain is the core of ribosomal preinitiation complex formation
MS413	96.3	6	Component of the holoenzyme form of RNA polymerase transcription factor TFIIH has DNA-dependent ATPase/helicase activity and is required with Rad3p for unwinding promoter DNA; involved in DNA repair; homolog of human ERCC3
MS444	96.3	5	Cytoplasmic isoleucine-tRNA synthetase target of the G1-specific inhibitor reveromycin A
FG570	96.0	3	NAD <sup>+</sup> -dependent glutamate dehydrogenase degrades glutamate to ammonia and alpha-ketoglutarate; expression sensitive to nitrogen catabolite repression and intracellular ammonia levels
FG533	95.8	4	Histone acetyltransferase subunit of the Elongator complex which is a component of the RNA polymerase II holoenzyme; activity is directed specifically towards histones H3 and H4; disruption confers resistance to <i>K. lactis</i> zymotoxin
FG595	95.8	3	Acetolactate synthase catalyses the first common step in isoleucine and valine biosynthesis and is the target of several classes of inhibitors localizes to the mitochondria; expression of the gene is under general amino acid control
MS378	95.7	3	Subunit of TORC1 a rapamycin-sensitive complex involved in growth control that contains Tor1p or Tor2p Lst8p and Tco89p; contains four HEAT repeats and seven WD-40 repeats; may act as a scaffold protein to couple TOR and its effectors

MS431	95.7	2	Mismatch repair protein forms dimers with MSh2p that mediate repair of insertion or deletion mutations and removal of nonhomologous DNA ends contains a PCNA Pol30p binding motif required for genome stability
FG1024	95.4	3	Conserved 90S pre-ribosomal component essential for proper endonucleolytic cleavage of the 35 S rRNA precursor at A0 A1 and A2 sites; contains eight WD-repeats; PWP2 deletion leads to defects in cell cycle and bud morphogenesis
FG610	95.4	2	Subunit of the cytosolic chaperonin Cct ring complex related to Tcp1p required for the assembly of actin and tubulins in vivo
FG657	95.4	3	Protein required for maturation of the 25S and 5.8S ribosomal RNAs; constituent of 66S pre-ribosomal particles; homologous to mammalian Bop1
FG692	95.4	2	Catalytic subunit of the DNA polymerase alpha-primase complex required for the initiation of DNA replication during mitotic DNA synthesis and premeiotic DNA synthesis
FG848	95.4	0	Ubiquitin activating enzyme involved in ubiquitin-mediated protein degradation and essential for viability
FG916	95.4	10	Subunit E of the eight-subunit V1 peripheral membrane domain of the vacuolar H <sup>+</sup> -ATPase V-ATPase an electrogenic proton pump found throughout the endomembrane system; required for the V1 domain to assemble onto the vacuolar membrane
MS351	95.4	3	Metallopeptidase localized to the mitochondrial matrix
MS407	95.4	2	Essential protein involved in transcription regulation; component of chromatin remodeling complexes; required for assembly and function of the INO80 complex; member of the RUVB-like protein family
MS442	95.4	3	Major karyopherin involved in export of proteins RNAs and ribosomal subunits from the nucleus
FG542	95.2	5	Essential protein involved in transcription regulation; component of chromatin remodeling complexes; required for assembly and function of the INO80 complex; member of the RUVB-like protein family
MS485	95.2	2	Endosomal Na <sup>+</sup> /H <sup>+</sup> exchanger required for intracellular sequestration of Na <sup>+</sup> ; required for osmotolerance to acute hypertonic shock
FG535	95.1	9	Subunit of the 26S proteasome substrate of the N-acetyltransferase Nat1p
FG702	93.1	9	Essential protein of the mitochondrial inner membrane component of the mitochondrial import system
FG638	93.0	2	Cytosolic leucyl tRNA synthetase ligates leucine to the appropriate tRNA
MS484	92.6	1	Phosphatidylinositol 3-kinase responsible for the synthesis of phosphatidylinositol 3-phosphate; forms membrane-associated signal transduction complex with Vps15p to regulate protein sorting; similar to p110 subunit of mammalian PI 3-kinase
FG718	92.3	5	Subunit of DNA primase which is required for DNA synthesis and double-strand break repair
MS397	92.3	2	Acyltransferase that catalyzes diacylglycerol esterification; one of several acyltransferases that contribute to

FG559	92.1	5	triglyceride synthesis; putative homolog of human lecithin cholesterol acyltransferase
FG598	92.1	3	Putative endonuclease subunit of the mRNA cleavage and polyadenylation specificity complex required for 3' processing of mRNAs
FG730	92.1	5	Subunit of the core complex of translation initiation factor 3eIF3 which is essential for translation
MS379	92.1	5	Protein that forms a heterotrimeric complex with Erp1 Erp2p and Emp24 member of the p24 family involved in endoplasmic reticulum to Golgi transport
MS398	92.1	2	Metalloprotease subunit of the 19S regulatory particle of the 26S proteasome lid; couples the deubiquitination and degradation of proteasome substrates
MS401	92.0	3	Alpha subunit of COPI vesicle coatamer complex which surrounds transport vesicles in the early secretory pathway
MS462	91.8	2	Possible U3 snoRNP protein involved in maturation of pre-18S rRNA based on computational analysis of large-scale protein-protein interaction data
MS501	91.8	1	Subunit of the multiprotein cohesin complex required for sister chromatid cohesion in mitotic cells; also required with Rec8p for cohesion and recombination during meiosis; phylogenetically conserved SMC chromosomal ATPase family member
FG465	91.7	1	Nuclear import receptor mediates the nuclear localization of proteins involved in mRNA-nucleus export
FG534	91.7	3	Protein component of the small 40S subunit essential for control of translational accuracy; has similarity to E. coli S5 and rat S2 ribosomal proteins
MS358	91.7	4	Aspartate kinase L-aspartate 4-P-transferase; cytoplasmic enzyme that catalyzes the first step in the common pathway for methionine and threonine biosynthesis; expression regulated by Gcn4p and the general control of amino acid synthesis
MS394	91.7	6	Cytoplasmic alanyl-tRNA synthetase required for protein synthesis; point mutation cdc64-1 allele causes cell cycle arrest at G1; lethality of null mutation is functionally complemented by human homolog
FG898	91.5	5	Nuclear 5' to 3' single-stranded RNA exonuclease involved in RNA metabolism including rRNA and snRNA processing as well as mRNA transcription termination
MS467	91.4	7	Chorismate mutase catalyzes the conversion of chorismate to prephenate to initiate the tyrosine/phenylalanine-specific branch of aromatic amino acid biosynthesis
FG821	91.3	3	Mitochondrial inner membrane protein exposed to the mitochondrial matrix associates with mitochondrial ribosomes NOT required for respiratory growth; homolog of human Letm1 a protein implicated in Wolf-Hirschhorn syndrome
			ER membrane glycoprotein subunit of the glycosylphosphatidylinositol transamidase complex that adds glycosylphosphatidylinositol GPI anchors to newly synthesized proteins; human PIG-K protein is a

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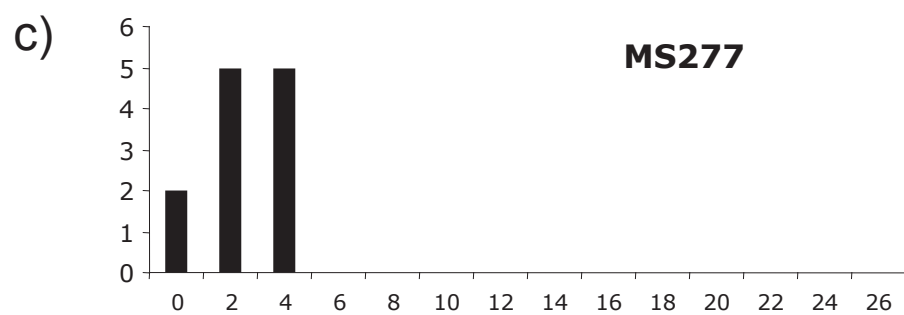
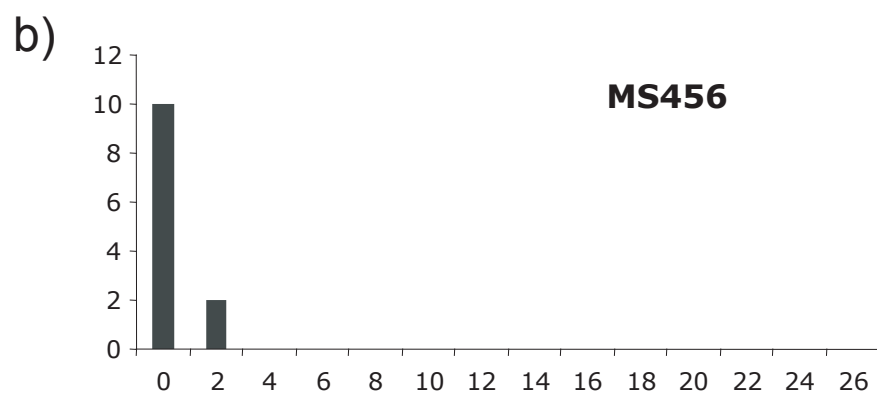
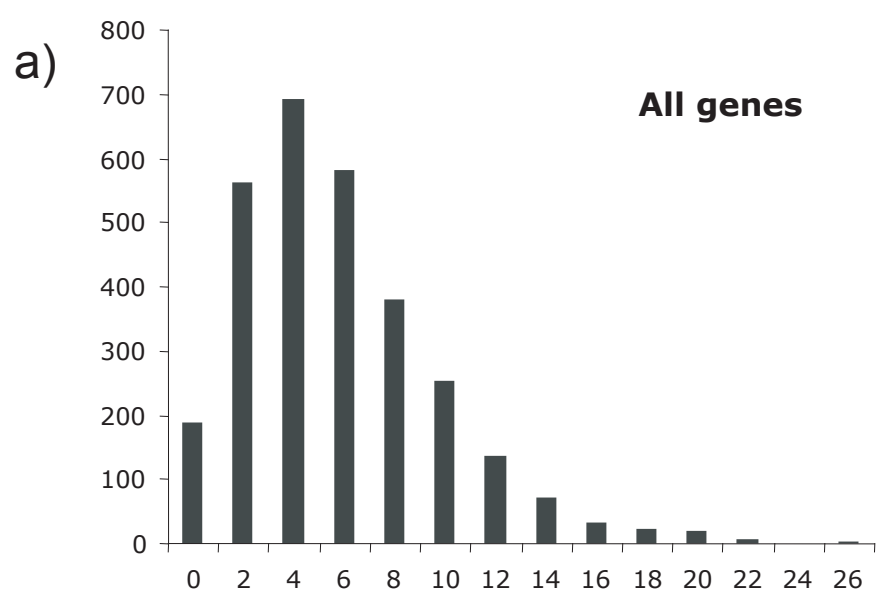
			functional homolog
FG1010	91.2	1	Subunit of the eukaryotic translation initiation factor 3 eIF3 involved in the assembly of preinitiation complex and start codon selection
FG651	91.2	4	Subunit of the cytosolic chaperonin Cct ring complex related to Tcp1p required for the assembly of actin and tubulins in vivo
FG668	91.2	2	Bifunctional enzyme exhibiting both indole-3-glycerol-phosphate synthase and anthranilate synthase activities forms multifunctional hetero-oligomeric anthranilate synthase:indole-3-glycerol phosphate synthase enzyme complex with Trp2p
FG855	91.2	7	E1 beta subunit of the pyruvate dehydrogenase PDH complex which is an evolutionarily-conserved multi-protein complex found in mitochondria
MS320	91.2	4	Gamma glutamylcysteine synthetase catalyzes the first step in the gamma-glutamyl cycle for glutathione GSH biosynthesis; expression induced by oxidants cadmium and mercury
MS329	91.2	1	Putative protein of unknown function; deletion mutant has decreased rapamycin resistance but normal wormannin resistance; green fluorescent protein GFP-fusion protein localizes to the vacuole
MS384	91.2	6	Essential beta-coat protein of the COPI coatomer involved in ER-to-Golgi and Golgi-to-ER transport; contains WD40 domains that mediate cargo selective interactions; 45 sequence identity to mammalian beta-COP
MS463	91.2	2	Protein involved in DNA replication; component of the Mcm2-7 hexameric complex that binds chromatin as a part of the pre-replicative complex
MS470	91.2	3	Hypothetical protein
MS578	91.2	6	Subunit of DNA polymerase zeta which is involved in DNA repair; required for mutagenesis induced by DNA damage
MS561	91.1	6	Subunit of the oligosaccharyltransferase complex of the ER lumen which catalyzes asparagine-linked glycosylation of newly synthesized proteins; forms a subcomplex with Ost3p and Ost4p and is directly involved in catalysis
FG735	90.9	3	Subunit of the 26S proteasome substrate of the N-acetyltransferase Nat1p
FG659	90.7	6	Protein required for the transport of amino acid permease Gap1p from the Golgi to the cell surface; component of the TOR signaling pathway; associates with both Tor1p and Tor2p; contains a WD-repeat
FG901	90.7	6	Putative mitochondrial ribosomal protein of the small subunit has similarity to E. coli and human mitochondrial S12 ribosomal proteins
MS432	90.5	10	Protein of unknown function that associates with ribosomes and has a putative RNA binding domain; interacts with Tma20p; has homology to human protein DRP1 which interacts with human Tma20p

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FG948	90.4	12	homolog MCT-1 RNA polymerase III subunit C11; mediates pol III RNA cleavage activity and is important for termination of transcription
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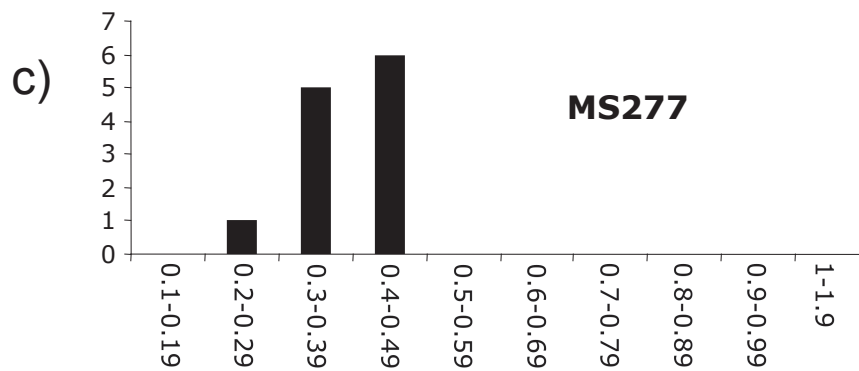
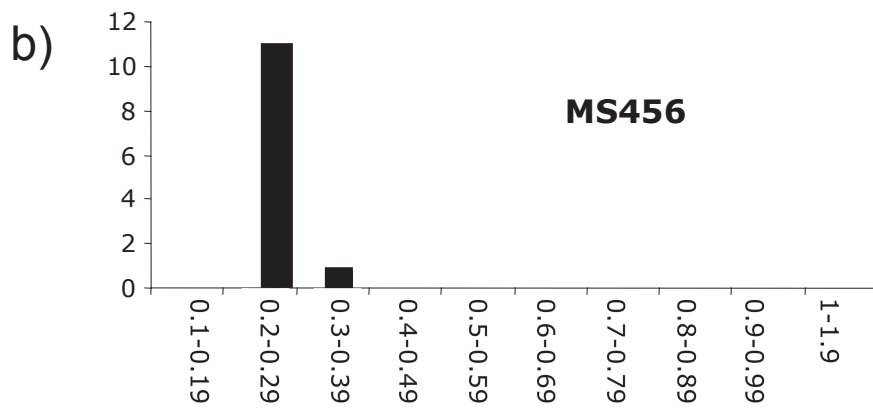
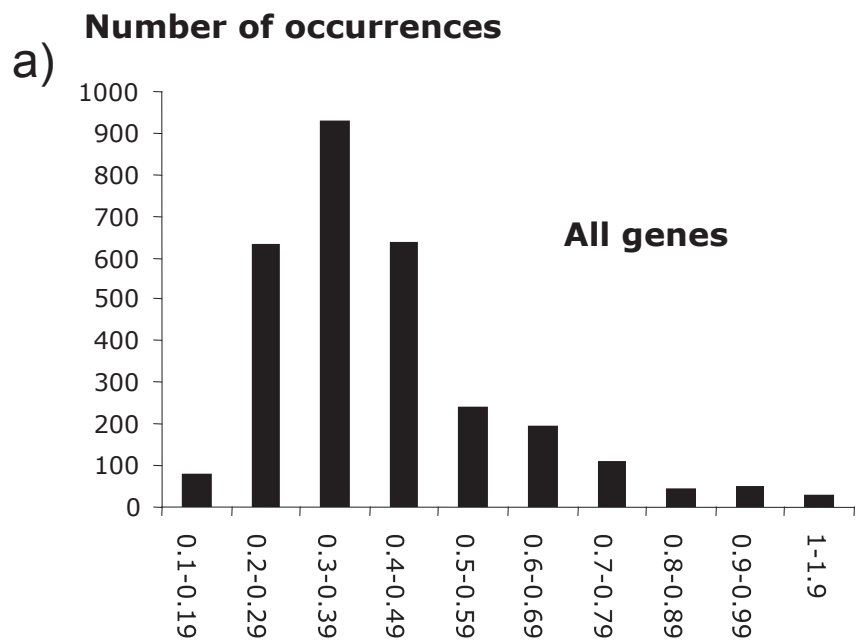
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## Number of occurrences



## Robinson-Foulds distance





**Kuhner-Felsenstein distance**

