

Table S1: Information of 91 fungal genomes investigated in this study

Species name	Subphylum	Source
<i>Agaricus bisporus bisporus H97</i>	Agaricomycotina	JGI
<i>Agaricus bisporus burnettii JB137-s8</i>	Agaricomycotina	JGI
<i>Amanita muscaria</i>	Agaricomycotina	JGI
<i>Amanita thiersii</i>	Agaricomycotina	JGI
<i>Auricularia subglabra</i>	Agaricomycotina	JGI
<i>Bjerkandera adusta</i>	Agaricomycotina	JGI
<i>Boletus edulis</i>	Agaricomycotina	JGI
<i>Botryobasidium botryosum</i>	Agaricomycotina	JGI
<i>Ceriporiopsis subvermispora</i>	Agaricomycotina	JGI
<i>Cerrena unicolor</i>	Agaricomycotina	JGI
<i>Coniophora puteana</i>	Agaricomycotina	JGI
<i>Coprinopsis cinerea</i>	Agaricomycotina	JGI
<i>cryptococcus gattii r265</i>	Agaricomycotina	Broad Institute
<i>cryptococcus gattii wm276</i>	Agaricomycotina	Broad Institute
<i>Cryptococcus neoformans var neoformans JEC21</i>	Agaricomycotina	JGI
<i>Cryptococcus neoformans var. grubii H99</i>	Agaricomycotina	JGI
<i>Cryptococcus vishniacii</i>	Agaricomycotina	JGI
<i>Dacryopinax sp. DJM 731 SSP1</i>	Agaricomycotina	JGI
<i>Daedalea quercina</i>	Agaricomycotina	JGI
<i>Dichomitus squalens</i>	Agaricomycotina	JGI
<i>Dioszegia cryoxerica</i>	Agaricomycotina	JGI
<i>Fistulina hepatica</i>	Agaricomycotina	JGI
<i>Fomitiporia mediterranea</i>	Agaricomycotina	JGI
<i>Fomitopsis pinicola</i>	Agaricomycotina	JGI
<i>Galerina marginata</i>	Agaricomycotina	JGI
<i>Ganoderma sp. 10597 SS1</i>	Agaricomycotina	JGI
<i>Gloeophyllum trabeum</i>	Agaricomycotina	JGI
<i>Gymnopus luxurians</i>	Agaricomycotina	JGI
<i>Hebeloma cylindrosporum</i>	Agaricomycotina	JGI
<i>Heterobasidion irregulare</i>	Agaricomycotina	JGI
<i>Hydnomerulius pinastri</i>	Agaricomycotina	JGI
<i>Hypholoma sublateritium</i>	Agaricomycotina	JGI
<i>Jaapia argillacea</i>	Agaricomycotina	JGI
<i>Laccaria amethystina</i>	Agaricomycotina	JGI
<i>Laccaria bicolor</i>	Agaricomycotina	JGI

<i>Laetiporus sulphureus</i>	Agaricomycotina	JGI
<i>Neolentinus lepideus</i>	Agaricomycotina	JGI
<i>Paxillus involutus</i>	Agaricomycotina	JGI
<i>Paxillus rubicundulus</i>	Agaricomycotina	JGI
<i>Phanerochaete carnosa</i>	Agaricomycotina	JGI
<i>Phanerochaete chrysosporium</i>	Agaricomycotina	JGI
<i>Phlebia brevispora</i>	Agaricomycotina	JGI
<i>Phlebiopsis gigantea</i>	Agaricomycotina	JGI
<i>Piloderma croceum</i>	Agaricomycotina	JGI
<i>Piriformospora indica</i>	Agaricomycotina	JGI
<i>Pisolithus microcarpus</i>	Agaricomycotina	JGI
<i>Pisolithus tinctorius</i>	Agaricomycotina	JGI
<i>Pleurotus ostreatus PC15</i>	Agaricomycotina	JGI
<i>Pleurotus ostreatus PC9</i>	Agaricomycotina	JGI
<i>Plicaturopsis crispa</i>	Agaricomycotina	JGI
<i>Polyporus arcularius</i>	Agaricomycotina	JGI
<i>Postia placenta MAD-698-R-SB12</i>	Agaricomycotina	JGI
<i>Punctularia strigosozonata</i>	Agaricomycotina	JGI
<i>Schizophyllum commune</i>	Agaricomycotina	JGI
<i>Scleroderma citrinum</i>	Agaricomycotina	JGI
<i>Sebacina vermifera</i>	Agaricomycotina	JGI
<i>Serpula lacrymans S7.3</i>	Agaricomycotina	JGI
<i>Serpula lacrymans S7.9</i>	Agaricomycotina	JGI
<i>Serpula lacrymans-shastensis</i>	Agaricomycotina	JGI
<i>Sphaerobolus stellatus</i>	Agaricomycotina	JGI
<i>Stereum hirsutum</i>	Agaricomycotina	JGI
<i>Suillus luteus</i>	Agaricomycotina	JGI
<i>Trametes versicolor</i>	Agaricomycotina	JGI
<i>Tremella mesenterica</i>	Agaricomycotina	JGI
<i>Tulasnella calospora</i>	Agaricomycotina	JGI
<i>Wolfiporia cocos</i>	Agaricomycotina	JGI
<i>Agaricostilbum hyphaenes</i>	Pucciniomycotina	JGI
<i>Atractiellales sp</i>	Pucciniomycotina	JGI
<i>Cronartium quercuum</i>	Pucciniomycotina	JGI
<i>Heterogastridium pycnidioideum</i>	Pucciniomycotina	JGI
<i>Melampsora laricis-populina</i>	Pucciniomycotina	JGI
<i>Mixia osmundae</i>	Pucciniomycotina	JGI

<i>Naiadella fluitans</i>	Pucciniomycotina	JGI
<i>Puccinia graminis</i>	Pucciniomycotina	JGI
<i>Puccinia striiformis</i>	Pucciniomycotina	JGI
<i>Rhodotorula graminis</i>	Pucciniomycotina	JGI
<i>Rhodotorula minuta</i>	Pucciniomycotina	JGI
<i>Sporobolomyces linderæ</i>	Pucciniomycotina	JGI
<i>Sporobolomyces roseus</i>	Pucciniomycotina	JGI
<i>Tritirachium sp. CBS 265.96</i>	Pucciniomycotina	JGI
<i>Exobasidium vaccinii</i>	Ustilaginomycotina	JGI
<i>Malassezia globosa</i>	Ustilaginomycotina	JGI
<i>Malassezia sympodialis</i>	Ustilaginomycotina	JGI
<i>Pseudozyma antarctica</i>	Ustilaginomycotina	JGI
<i>Pseudozyma hubeiensis</i>	Ustilaginomycotina	JGI
<i>Sporisorium reilianum</i>	Ustilaginomycotina	JGI
<i>Tilletiaria anomala</i>	Ustilaginomycotina	JGI
<i>Ustilago maydis</i>	Ustilaginomycotina	JGI
<i>Aplosporella prunicola</i>	Ascomycota	JGI
<i>Pyrenophora tritici-repentis</i>	Ascomycota	JGI
<i>Saitoella complicata</i>	Ascomycota	JGI

Table S2: Domain structure and conservation of 171 gene clusters

Cluster ID	# of Domain detected	GeneID in original genome annotations	Domain Structure		Best BLAST hit in NR	Occur in plants or animals
			Profile IDs from N' to C'	Domain Names from N' to C'		
group_1	1	jgi Rhoba1_1 3746 gw1.3.293.1	PF00466.15	Ribosomal_L10	mRNA turnover protein 4	TRUE
group_2	1	jgi Spoli1 204666 fgenes1_pm.3_#_201	PF06068.8	TIP49	RuvB-like protein 2	TRUE
group_3	1	jgi Cryne_H99_1 2024 CNAG_02236T0	PF00149.23	Metallophos	serine/threonine-protein phosphatase	TRUE
group_4	2	jgi Malsy1_1 3204 MSY001_1846m.01	PF04194.8;PF02219.12	PDCD2_C;MTHFR	MET12-methylenetetrahydrofolate reductase	FALSE
group_5	1	jgi Fishe1 54650 e_gw1.574.92.1	PF00004.24	AAA	26S subunit, ATPase, 1	TRUE
group_6	2	PTRG_00048	PF01602.15;PF13646.1	Adaptin_N;HEAT_2	protein phosphatase PP2A regulatory subunit A	TRUE
group_7	1	jgi SerlaS7_3_2 175548 estExt_fgenes1_kg.C_21_024	PF00677.12	Lum_binding	riboflavin synthase alpha chain	FALSE
group_8	3	jgi Jaaar1 79123 estExt_fgenes1_pg.C_130037	PF04669.8;PF04821.9;PF05029.8;	Polysacc_synt_4;TIMELESS;TIMELESS_C;	duf757 domain-containing protein	FALSE
group_9	2	jgi Schco3 2624702 fgenes1_kg.5_#_4142_#_Locus899v1rpkm215.08	PF00226.26;PF02889.11;	DnaJ;Sec63;	Null ¹	FALSE
group_10	2	jgi Pucgr1 22361 PGTT_01827	PF03483.12;PF03484.10;	B3_4;B5;	phenylalanyl-tRNA synthetase beta subunit	FALSE
group_11	1	jgi Psehu1 2208 PHSY_002881m.01	PF09139.6	Mmp37	mmp37-domain-containing protein	FALSE
group_12	3	jgi Phlbr1 30713 fgenes1_kg.34_#_4_#_isotig08860	PF00483.18;PF00132.19;PF02020.13;	NTP_transferase;Hexapep;W2;	translation initiation factor eif-2b subunit epsilon	FALSE
group_13	2	jgi Phlbr1 30713 fgenes1_kg.34_#_4_#_isotig08860	PF10584.4;PF00227.21	Proteasome_A_N;Proteasome;	PSMA7 protein	TRUE
group_14	1	jgi Hypsu1 944453 CE723447_12297	PF01189.12	Nol1_Nop2_Fmu	tRNA (cytosine-5-)-methyltransferase NCL1	FALSE
group_15	1	jgi Travel1 174957 estExt_Genewise1Plus.C_13_t2_0147	PF00735.13	Septin	cell division control protein 12	FALSE
group_16	2	jgi Hebcy2 439117 fgenes1_kg.2_#_59_#_Locus612v1rpkm112.82	PF01012.16;PF00766.14;	ETF;ETF_alpha;	electron transfer flavoprotein subunit alpha	FALSE
group_17	1	jgi Treme1 41792 estExt_Genewise1Plus.C_10962	PF00153.22	Mito_carr	calcium-binding mitochondrial carrier protein Aralar1	FALSE
group_18	2	jgi Aplpr1 305724 fgenes1_pg.4_#_376	PF00270.24;PF00271.26;	DEAD;Helicase_C;	DEAD/DEAH box RNA helicase	FALSE

group_19	1	jgi Cryne_H99_1 4184 CNAG_04651T0	PF02077.10	SURF4	SURF4 family protein	FALSE
group_20	1	jgi SerlaS7_3_2 99496 estExt_Genewise1.C_360012	PF04280.10	Tim44	related to TIM44-mitochondrial inner membrane import receptor subunit	FALSE
group_21	1	jgi Cryne_JEC21_1 4487 CNE03090.t01	PF10609.4	ParA	cytosolic Fe-S cluster assembly factor nbp35	TRUE
group_22	1	jgi Glotr1_1 119689 estExt_fgenesh1_pg.C_00002_t20141	PF00400.27	WD40	set1 complex component swd1	FALSE
group_23	3	jgi Mixos1 77705 estExt_Genewise1Plus.C_9_t10153	PF13774.1;PF00957.16;PF01553.16;	Longin;Synaptobrevin;Acyltransferase;	transport protein sec22	FALSE
group_24	1	jgi Hebcy2 440383 fgenesh1_kg.3_#_157_#_Locus5798v1rpkm8.46	PF01926.18	MMR_HSR1	mitochondrial gtpase	FALSE
group_25	2	jgi Aplpr1 262865 estExt_Genewise1Plus.C_2_t20225	PF04045.9;PF00565.12;	P34-Arc;Snase;	ARP2/3 complex 34 kDa subunit	FALSE
group_26	2	jgi Pucst1 493332 maker-PST130_20759-snap-gene-0.12-mRNA-1	PF01172.13;PF09377.5;	SBDS;SBDS_C;	null	FALSE
group_27	6	jgi Ustma1 3490 UM03490	PF00069.20;PF01237.13;PF00160.16;PF00076.17;PF00654.15;PF00571.23;	Pkinase;Oxysterol_BP;Pro_isomerase;RRM_1;Voltage_CLC;CBS;	CLC voltage-gated chloride channel	FALSE
group_28	3	jgi Saico1 79558 estExt_Genewise1.C_100050	PF13207.1;PF08142.7;PF04950.7;	AAA_17;AARP2CN;DUF663;	ribosome biogenesis protein BMS1	FALSE
group_29	1	jgi Fompi3 1162809 estExt_Genewise1Plus.C_260253	PF00400.27	WD40	U4/U6 small nuclear ribonucleoprotein Prp4	FALSE
group_30	3	jgi Rhomi1 112433 CE112432_5887	PF03105.14;PF09359.5;PF02656.10;	SPX;VTC;DUF202;	vacuolar transporter chaperone 4	FALSE
group_31	1	jgi Sporo1 27320 fgenesh1_pg.C_scaffold_5000209	PF00022.14	Actin	actin-related protein 8	FALSE
group_32	1	jgi Gansp1 121666 fgenesh1_kg.10_#_446_#_isotig12297	PF02466.14	Tim17	mitochondrial import inner membrane translocase subunit tim22	FALSE
group_33	2	jgi Aplpr1 218091 e_gw1.1.156.1	PF03901.12;PF11927.3;	Glyco_transf_22;DUF3445;	alpha-1,2-mannosyltransferase	FALSE
group_34	2	jgi Fompi3 1148592 estExt_Genewise1.C_430037	PF01137.16;PF05189.8;	RTC;RTC_insert;	RNA 3'-terminal phosphate cyclase	FALSE
group_35	2	jgi Mixos1 47766 e_gw1.4.54.1	PF00428.14;PF13489.1;	Ribosomal_60s;Methyltransf_23;	hexaprenyldihydroxybenzoate methyltransferase	FALSE
group_36	1	jgi Aplpr1 226223 e_gw1.10.2.1	PF10354.4	DUF2431	null	FALSE
group_37	1	jgi Sporo1 3876 gw1.6.318.1	PF03152.9	UFD1	ubiquitin fusion degradation protein	FALSE
group_38	2	jgi SerlaS7_3_2 170214 estExt_fgenesh1_pm.C_100249	PF00400.27;PF10294.4;	WD40;Methyltransf_16;	WD40 repeat-like protein	FALSE

group_39	3	jgi Glotr1_1 71297 estExt_Genewise1Plus.C_00002_t40499	PF08156.8;PF08060.8;PF01798.13;	NOP5NT;NOSIC;Nop;	NOP58 protein	TRUE
group_40	2	jgi Mixos1 619488 MIX15280_34319_52	PF00153.22; PF08449.6;	Mito_carr;UAA;	null	FALSE
group_41	1	jgi Malsy1_1 2393 MSY001_1044m.01	PF01920.15	Prefoldin_2	Gim complex component GIM4	FALSE
group_42	1	jgi Pilcr1 813691 fgenes1_kg.00007_#_228_#_Locus2724v1rpkm76.72	PF00071.17	Ras	small GTP binding protein RAB5	TRUE
group_43	3	jgi Plicr1 40112 fgenes1_kg.6_#_398_#_Locus3522v1rpkm49.31	PF13855.1;PF14580.1;PF12799.2;	LRR_8;LRR_9;LRR_4;	protein phosphatases PP1 regulatory subunit sds22	FALSE
group_44	1	jgi Laesu1 738167 fgenes1_pm.38_#_25	PF00071.17	Ras	protein-L-isoaspartate O-methyltransferase	FALSE
group_45	2	jgi Ustma1 2848 UM02848	PF00179.21;PF01135.14;	UQ_con;PCMT;	NEDD8-conjugating enzyme UBC12	FALSE
group_46	1	jgi Lacbi2 448332 gm1.12776_g	PF00810.13	ER_lumen_recept	ER lumen protein retaining receptor	FALSE
group_47	1	jgi Cryne_H99_1 1465 CNAG_01638T0	PF02301.13	HORMA	mitotic spindle checkpoint protein	FALSE
group_48	2	jgi Pilcr1 5570 gm1.5570_g	PF00270.24;PF00271.26	DEAD;Helicase_C;	DEAD-box ATP-dependent RNA helicase	TRUE
group_49	1	jgi Lacbi2 581744 e_gw1.2.4868.1	PF01269.12	Fibrillarin	rRNA 2'-O-methyltransferase fibrillarin	TRUE
group_51	1	jgi Cryne_H99_1 4293 CNAG_04765T0	PF04062.9	P21-Arc	ARP2/3 complex 21 kDa subunit	FALSE
group_52	1	jgi Agabi_varbur_1 55377 estExt_Genewise1.C_31323	PF12171.3	zf-C2H2_jaz	zinc finger protein	FALSE
group_53	2	jgi Phlbr1 142945 gm1.631_g	PF00248.16;PF00542.14;	Aldo_ket_red;Ribosomal_L12;	50S ribosomal protein L12	FALSE
group_54	1	jgi SerlaS7_3_2 53296 e_gw1.6.1819.1	PF03850.9	Tfb4	rna polymerase ii transcription factor b subunit 4	FALSE
group_55	2	jgi Psehu1 1058 PHSY_001757m.01	PF00076.17;PF13499.1;	RRM_1;EF-hand_7;	SSP120-secretory protein	FALSE
group_56	1	jgi Sphst1 46786 fgenes1_pg.36_#_250	PF14580.1	LRR_9	U2 small nuclear ribonucleoprotein A'	FALSE
group_57	1	jgi Cryne_H99_1 4718 CNAG_05241T0	PF01423.17	LSM	U6 snRNA-associated Sm-like protein LSM7	TRUE
group_58	2	jgi Treme1 32917 e_gw1.9.265.1	PF14259.1;PF13893.1;	RRM_6;RRM_5;	Splicing factor U2AF-associated protein 2	FALSE
group_59	5	jgi Sebve1 20807 gm1.2079_g	PF01423.17;PF08839.6;PF00270.24;PF00271.26;PF09369.5	LSM;CDT1;DEAD;Helicase_C;DUF1998;	P-loop nucleoside triphosphate hydrolase	FALSE
group_60	2	jgi Psehu1 4814 PHSY_005286m.01	PF00226.26;PF07743.8;	DnaJ;HSCB_C;	co-chaperone Hsc20	FALSE

group_61	1	jgi Hebcy2 439853 fgenes1_kg.2_#_795_#_Locus7028v7rpkm0.40_PRE	PF01398.16	JAB	translation initiation factor 3 subunit 3	FALSE
group_62	1	jgi Tulca1 243742 fgenes1_kg.84_#_4_#_Locus405v1rpkm965.62	PF00179.21	UQ_con	Protein UBC-14	FALSE
group_63	1	jgi Dacsp1 72045 estExt_Genewise1.C_220369	PF00025.16	Arf	ADP-ribosylation factor A1E	TRUE
group_64	2	jgi Malsy1_1 513 MSY001_2345m.01	PF00400.27;PF09325.5;	WD40;Vps5;	null	FALSE
group_65	1	jgi PosplRSB12_1 1143524 e_gw1.7.1189.1	PF08265.6	YL1_C	Ino eighty subunit 6	FALSE
group_66	1	jgi Dacsp1 22365 fgenes1_kg.9_#_236_#_isotig09731	PF03657.8	UPF0113	60S ribosome subunit biogenesis protein NIP7 homolog	TRUE
group_67	2	jgi Ustma1 175 UM00175	PF01398.16;PF13012.1;	JAB;MitMem_reg;	translation initiation factor 3, subunit f	FALSE
group_68	2	jgi Exova1 291539 estExt_fgenes1_pg.C_2_t10484	PF10785.4PF12853.2;	NADH-u_ox-rdase;NADH_u_ox_C;	NADH-ubiquinone oxidoreductase complex i, 21 kDa subunit	FALSE
group_69	1	jgi Lacbi2 480626 fgenes1_pm.LG_2_#_764	PF04410.9	Gar1	H/ACA ribonucleoprotein complex subunit 1	FALSE
group_70	1	jgi Cryvi1 295086 estExt_Genewise1Plus.C_150161	PF03232.8	COQ7	null	FALSE
group_71	1	jgi Spore1 2004 sr15833m.01	PF11708.3	Slu7	RNA splicing factor - Slu7p	FALSE
group_72	1	jgi Gansp1 113266 fgenes1_kg.1_#_384_#_isotig12156	PF01217.15	Clat_adaptor_s	Protein APS-3	TRUE
group_73	2	jgi Spore1 4326 sr12571m.01	PF01281.14;PF01722.13;	Ribosomal_L9_N;Bola;	bola-like protein	FALSE
group_74	1	jgi Spoli1 197984 gm1.2880_g	PF08241.7	Methyltransf_11	S-adenosyl-L-methionine-dependent methyltransferase	FALSE
group_75	1	jgi Hydpi2 179735 estExt_fgenes1_pm.C_30352	PF01990.12	ATP-synt_F	vacuolar ATP synthase subunit F	FALSE
group_76	1	jgi Phlbr1 25049 fgenes1_kg.1_#_593_#_isotig11603	PF01423.17	LSM	small nuclear ribonucleoprotein G	TRUE
group_77	2	jgi Cryne_H99_1 3582 CNAG_03989T0	PF07792.7;PF08616.5;	Afi1;SPA;	spindle pole body interacting protein	FALSE
group_78	2	jgi Tulca1 66641 e_gw1.13.61.1	PF10607.4;PF13445.1;	CLTH;zf-RING_UBOX;	null	FALSE
group_79	2	jgi Conpu1 81807 fgenes1_kg.5_#_354_#_isotig03693	PF06212.7	GRIM-19	NADH-ubiquinone oxidoreductase subunit GRIM-20	FALSE
group_80	1	jgi Dacsp1 94841 estExt_fgenes1_pm.C_90083	PF13185.1	GAF_2	null	FALSE
group_81	2	jgi Paxru1 144401 e_gw1.338.20.1	PF00168.25;PF00616.14;	C2;RasGAP;	null	FALSE

group_82	1	jgi Galma1 91339 estExt_Genewise1Plus.C_5_t20004	PF04733.9	Coatomer_E	coatomer subunit	FALSE
group_83	2	jgi Malgl1 1661 MGL_1660	PF13855.1;PF00565.12;	LRR_8;SNase;	SNase-domain-containing protein	FALSE
group_84	1	jgi Hebcy2 63963 e_gw1.3.1137.1	PF01423.17	LSM	U6 snRNA-associated Sm-like protein LSM8	FALSE
group_85	2	PTRG_11391	PF00400.27;PF00106.20;	WD40;adh_short;	null	FALSE
group_86	1	jgi Lacbi2 677520 estExt_fgenes2_kg.C_LG_3_t10262	PF03604.8	DNA_RNApol_7kD	DNA-directed RNA polymerases I, II, and III subunit RPABC4	TRUE
group_87	1	jgi Amath1 71907 fgenes1_kg.498_#_3_#_isotig20761	PF00076.17	RRM_1	translation initiation factor 4B	FALSE
group_88	2	jgi Sphst1 33023 fgenes1_kg.81_#_78_#_Locus988v1rpkm215.86	PF02136.15;PF00076.17;	NTF2;RRM_1;	NTF2 and RRM domain-containing protein	FALSE
group_89	1	jgi Cryne_H99_1 2991 CNAG_03343T0	PF01997.11	Translin	null	FALSE
group_90	3	jgi Paxin1 179128 estExt_fgenes1_pg.C_50053	PF00009.22;PF03144.20;PF03144.21;	GTP_EFTU;GTP_EFTU_D2;GTP_EFTU_D3;	GTP-binding protein 1	TRUE
group_91	1	jgi PleosPC15_2 1031719 e_gw1.01.1306.1	PF00071.17	Ras	Small GTP binding protein Rab2	TRUE
group_92	1	jgi PleosPC15_2 1111361 estExt_Genemark1.C_030571	PF05700.6	BCAS2	Pre-mRNA-splicing factor SPF27	FALSE
group_93	2	jgi Saico1 27212 fgenes1_pg.23_#_49	PF13649.1;PF12937.2;	Methyltransf_25;F-box-like;	null	FALSE
group_94	2	jgi Sporo1 31819 estExt_fgenes1_pg.C_20324	PF09830.4;PF00134.18;	ATP_transf;Cyclin_N;	cyclin L1	FALSE
group_95	3	jgi Laesu1 695612 estExt_Genewise1Plus.C_7_t20348	PF02771.11;PF02770.14;PF00441.19;	Acyl-CoA_dh_N;Acyl-CoA_dh_M;Acyl-CoA_dh_1;	isovaleryl-CoA dehydrogenase	FALSE
group_96	1	jgi PleosPC15_2 1103189 gm1.4726_g	PF05653.9	Mg_trans_NIPA	duf803 domain membrane protein	FALSE
group_97	2	jgi Lacbi2 183429 Lacbi1.estExt_GeneWisePlus_human.C_50207	PF08240.7;PF00107.21;	ADH_N;ADH_zinc_N;	alcohol dehydrogenase	FALSE
group_98	2	jgi Suilu1 806651 fgenes1_kg.154_#_4_#_Locus3570v1rpkm46.42	PF00628.24;PF02373.17;	PHD;JmjC;	JmjC domain-containing histone demethylation protein	FALSE
group_99	2	jgi Malsy1_1 1529 MSY001_0503m.01	PF05347.10;PF00226.26;	Complex1_LYR;DnaJ;	PAB-dependent poly(A) ribonuclease, subunit PAN2	FALSE
group_100	1	jgi Cryne_H99_1 295 CNAG_00355T0	PF10159.4	MMtag	kinase phosphorylation protein	FALSE
group_101	1	jgi Lacam1 205024 CE69279_2165	PF01027.15	Bax1-I	bax Inhibitor family protein	FALSE
group_102	2	jgi Cryne_JEC21_1 6233 CNI02020.t01	PF08513.6;PF05022.7;	LisH;SRP40_C;	SRP40-serine-rich protein	FALSE

group_103	1	jgi Cerun2 169885 CE169884_61	PF05916.6	Sld5	DNA replication complex GINS protein PSF2	FALSE
group_104	1	jgi Hypsu1 108359 gw1.3.390.1	PF10153.4	DUF2361	rRNA-processing protein EFG1	FALSE
group_105	1	jgi Phchr1 4219 fgenesh1_pg.C_scaffold_7000032	PF08616.5;PF08219.6;	SPA;TOM13;	null	FALSE
group_106	1	jgi Hebcy2 221945 CE141685_1629	PF03372.18	Exo_endo_phos	ccr4 nocturin family endoribonuclease	FALSE
group_107	1	jgi Hebcy2 439887 fgenesh1_kg.2_#_829_#_Locus743v1rpkm90.53	PF04716.9	ETC_C1_NDUFA5	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 5	FALSE
group_108	1	jgi Glotr1_1 119002 estExt_fgenesh1_pg.C_00001_t20199	PF00642.19	zf-CCCH	zinc finger protein 36, C3H1 type-like 2-A	TRUE
group_109	1	jgi Diocr1 379101 gm1.3414_g	PF00400.27	WD40	null	FALSE
group_110	2	jgi Malsy1_1 623 MSY001_2455m.01	PF10791.4;PF03097.13;	F1F0-ATPsyn_F;BRO1;	ATP17-ATP synthase complex, subunit f	FALSE
group_111	2	jgi Hetpy1 192586 CE192585_3110	PF00043.20;PF01588.15;	GST_C;tRNA_bind;	nucleic acid-binding protein	FALSE
group_112	1	jgi Dacsp1 25025 fgenesh1_kg.22_#_122_#_isotig07348	null	Sedlin_N	Trafficking protein particle complex subunit 2	FALSE
group_113	3	jgi Mixos1 91293 fgenesh1_pm.1_#_21	PF10168.4;PF03476.11;PF03473.12;	Nup88;MOSC_N;MOSC;	null	FALSE
group_114	2	jgi Psehu1 4088 PHSY_004557m.01	PF00443.24;PF02970.11;	UCH;TBCA;	ubiquitin carboxyl-terminal hydrolase	FALSE
group_115	1	jgi Cryne_H99_1 5254 CNAG_05808T0	PF10496.4	Syntaxin-18_N	null	FALSE
group_116	1	jgi Dacsp1 20670 fgenesh1_kg.3_#_428_#_isotig09138	PF02656.10	DUF202	vacuole non-autophagic-related protein	FALSE
group_117	1	jgi Pismi1 30353 fgenesh1_pm.104_#_11	PF00134.18	Cyclin_N	cyclin ctk2	FALSE
group_118	2	jgi Ustma1 6250 UM06250	PF13041.1;PF08241.7	PPR_2;Methyltransf_11;	S-adenosyl-L-methionine-dependent methyltransferase	FALSE
group_119	0	jgi Diocr1 299433 estExt_Genewise1Plus.C_320052	null	null	null	FALSE
group_120	0	jgi Cryne_JEC21_1 1929 CNM01490.t01	null	null	null	FALSE
group_121	1	jgi Croqu1 52108 e_gw1.191.41.1	PF03908.8	Sec20	null	FALSE
group_122	1	jgi Lacbi2 478107 fgenesh1_pm.LG_1_#_824	PF07093.6	SGT1	null	FALSE
group_123	2	jgi Amath1 3432 gm1.3432_g	PF13432.1;PF13414.1;	TPR_16;TPR_11;	tpr repeat-containing protein	FALSE

group_124	3	jgi Sebve1 190836 CE107186_3945	PF10537.4;PF02791.12;PF15612.1;	WAC_Acf1_DNA_bd;DDT;WHIM1;	null	FALSE
group_125	1	jgi Galma1 124680 estExt_Genewise1.C_19_t10227	PF06229.7	FRG1	protein FRG1	FALSE
group_126	1	jgi Glotr1_1 57146 estExt_Genewise1.C_00003_t30332	PF03372.18	Exo_endo_phos	skeletal muscle/kidney enriched inositol 5-phosphatase	FALSE
group_127	4	jgi Pirin1 73311 mRNA:PIIN_02515	PF06148.6;PF12022.3;PF00288.21;PF08544.8;	COG2;DUF3510;GHMP_kinases_N;GHMP_kinases_C;	phosphomevalonate kinase	FALSE
group_128	1	jgi Hetpy1 271698 fgenes1_kg.2_#_1027_#_comp5857_c0_seq1	PF05093.8	CIAPIN1	null	FALSE
group_129	1	jgi Agabi_varbisH97_2 191860 estExt_fgenes2_kg.C_40278	PF00237.14	Ribosomal_L22	50S ribosomal protein L22	FALSE
group_130	2	jgi Rhoba1_1 50840 estExt_Genemark1.C_1_t10476	PF04129.7;PF01084.15;	Vps52;Ribosomal_S18;	37S ribosomal protein	FALSE
group_131	1	jgi Cersu1 80754 fgenes1_kg.2_#_823_#_isotig08497	PF00400.27	WD40	null	FALSE
group_132	2	jgi Phlgi1 29570 estExt_fgenes1_pm.C_430015	PF08567.6;PF03909.12;	TFIIH_BTF_p62_N;BSD;	transcription factor tfiih complex subunit tfb1	FALSE
group_133	2	jgi Wolco1 99699 estExt_Genewise1Plus.C_4_t20273	PF13191.1;PF14629.1;	AAA_16;ORC4_C;	null	FALSE
group_134	1	jgi Agahy1 269994 fgenes1_kg.8_#_22_#_comp3521_c0_seq13	PF12333.3	Ipi1_N	null	FALSE
group_135	2	jgi Psehu1 2819 PHSY_003495m.01	PF03770.11;PF15404.1;	IPK;PH_4;	ARG82-dual-specificity inositol polyphosphate kinase	FALSE
group_136	2	jgi Travel1 64856 estExt_fgenes1_pg.C_6_t10208	PF13639.1;PF15411.1;	zf-RING_2;PH_10;	von Willebrand RING finger domain-containing protein	FALSE
group_137	1	jgi Cryne_JEC21_1 1406 CNK02770.t01	PF09346.5	SMI1_KNR4	null	FALSE
group_138	3	jgi Hetan2 329913 e_gw1.12.1172.1	PF00270.24;PF00271.26;PF09382.5;	DEAD;Helicase_C;RQC;	ATP-dependent DNA helicase	FALSE
group_139	1	jgi Pisti1 138598 e_gw1.20.474.1	PF04930.10	FUN14	FUN14 domain-containing protein	FALSE
group_140	1	jgi Paxru1 130720 e_gw1.21.118.1	PF00621.15	RhoGEF	RhoGEF domain-containing protein	FALSE
group_141	1	jgi Dacsp1 21457 fgenes1_kg.6_#_132_#_isotig09307	PF05348.6	UMP1	UMP1 domain-containing protein	FALSE
group_142	1	jgi Psehu1 3450 PHSY_004128m.01	PF05502.8	Dynactin_p62	dynactin p62 family protein	FALSE
group_143	2	jgi Gymlu1 42552 fgenes1_kg.22_#_22_#_Locus5128v1rpkm32.55	PF00642.19;PF08590.5;	zf-CCCH;DUF1771;	ccch zinc finger and smr domain protein	FALSE
group_144	0	jgi Ustma1 3540 UM03540	null	null	null	FALSE

group_145	2	jgi Phlgi1 76254 e_gw1.144.52.1	PF13249.1;PF00432.16;	Prenyltrans_2;Prenyltrans;	Prenyltrans_2	FALSE
group_146	1	jgi Hydpi2 23380 gm1.535_g	PF02291.10	TFIID-31kDa	transcription initiation factor TFIID subunit 9	FALSE
group_147	1	jgi Sporo1 30937 estExt_fgenesh1_kg.C_50045	PF09724.4	DUF2036	null	FALSE
group_148	2	jgi Copci1 11368 CC1G_13817T0	PF04627.8;PF05729.7;	ATP-synt_Eps;NACHT;	null	FALSE
group_149	1	jgi Neole1 1176338 gm1.2563_g	PF00829.16	Ribosomal_L21p	ribosomal l21 domain-containing protein	FALSE
group_150	1	jgi Hypsu1 37761 fgenesh1_kg.15_#_65_#_Locus5356v1rpkm20.49	PF03467.10	Smg4_UPF3	Smg-4/UPF3 family protein	FALSE
group_151	2	jgi SerlaS7_9_2 1178773 estExt_Genewise1Plus.C_1_t40384	PF12739.2;PF08626.6;	TRAPPC-Trs85;TRAPPC9-Trs120;	null	FALSE
group_152	2	jgi Tulca1 16570 gm1.125_g	PF00069.20;PF13300.1;	Pkinase;DUF4078;	null	FALSE
group_153	1	jgi Dacsp1 109871 gm1.6989_g	PF03676.9	UPF0183	null	FALSE
group_154	3	jgi Phlbr1 17106 fgenesh1_pg.4_#_384	PF01423.17;PF01369.15;PF15410.1;	LSM;Sec7;PH_9;	small nuclear ribonucleoprotein sm d2	FALSE
group_155	1	jgi Suilu1 475367 CE363972_2385	PF10294.4	Methyltransf_16	null	FALSE
group_156	1	jgi Pilcr1 812622 fgenesh1_kg.00005_#_239_#_Locus2617v1rpkm79.79	PF05486.7	SRP9-21	signal recognition particle subunit SRP9	FALSE
group_157	1	jgi Lacam1 671684 fgenesh1_kg.4_#_110_#_Locus1707v1rpkm80.67	PF01250.12	Ribosomal_S6	37s ribosomal protein mrp17	FALSE
group_158	1	jgi Mixos1 94207 fgenesh1_pm.4_#_580	PF00249.26	Myb_DNA-binding	proteophosphoglycan ppg4	FALSE
group_159	2	jgi Spore1 6304 sr14314m.01	PF00069.20;PF00433.19;	Pkinase;Pkinase_C;	serine/threonine protein kinase B-related Ukb1	FALSE
group_160	0	jgi Schco3 2622721 fgenesh1_kg.5_#_2161_#_Locus5259v1rpkm23.65	Null	null	null	FALSE
group_161	1	jgi Stehi1 161869 gm1.10799_g	PF08495.5	FIST	null	FALSE
group_162	0	jgi Naifl1 237611 estExt_Genewise1Plus.C_950013	null	null	null	FALSE
group_163	1	jgi Glotr1_1 69997 estExt_Genewise1Plus.C_00002_t10315	PF09813.4	Coiled-coil_56	null	FALSE
group_164	1	jgi Neole1 1022940 gw1.76.16.1	PF06398.6	Pex24p	null	FALSE
group_165	1	jgi Galma1 233169 fgenesh1_kg.1_#_146_#_Locus1564v1rpkm84.28	PF12867.2	DinB_2	null	FALSE

group_166	1	jgi PleosPC9_1 123603 genemark.2921_g	PF00398.15	RrnaAD	null	FALSE
group_167	3	jgi Agahy1 285598 estExt_fgenesh1_pg.C_320033	PF14259.1;PF00076.17;PF00658.13;	RRM_6;RRM_1;PABP;	null	FALSE
group_168	2	jgi Rhomi1 210517 estExt_Genemark1.C_4_t10058	PF06159.8;PF01521.15;	DUF974;Fe-S_biosyn;	iron-sulfur cluster assembly accessory protein	FALSE
group_169	1	jgi Spore1 1331 sr14978m.01	PF00169.24	PH	zinc metalloprotease	FALSE
group_170	1	jgi Glotr1_1 100173 fgenesh1_kg.00008_#_32_#_Contig3603	PF09340.5	NuA4	NuA4 domain-containing protein	FALSE
group_171	1	jgi Boled1 910839 estExt_Genewise1Plus.C_6_t10298	PF13671.1	AAA_33	null	FALSE

1 "null" indicates that the best hit does not meet match criteria

Table S3: Enrichment analysis of functional categories of 78 gene clusters that have single-copy orthologs in yeast genome

Category	Term	Count	%	P-value	Gene ID ¹	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0006364~rRNA processing	14	17.94872	4.97E-05	S000001131, S000007608, S000005370, S000005091, S000002172, S000003931, S000001492, S000005837, S000006132, S000004898, S000004012, S000005005, S000006138, S000006156	75	239	4870	3.803626	0.025213	0.025213	0.071794
SP_PIR_KEYWORDS	ribosome biogenesis	10	12.82051	5.92E-05	S000006132, S000004012, S000001131, S000005005, S000005370, S000006138, S000002172, S000001492, S000003931, S000005837	78	148	6448	5.585586	0.007661	0.007661	0.06887
GOTERM_BP_FAT	GO:0016072~rRNA process metabolic	14	17.94872	7.30E-05	S000001131, S000007608, S000005370, S000005091, S000002172, S000003931, S000001492, S000005837, S000006132, S000004898, S000004012, S000005005, S000006138, S000006156	75	248	4870	3.665591	0.036808	0.018577	0.105422
GOTERM_BP_FAT	GO:0006396~RNA processing	20	25.64103	1.70E-04	S000006382, S000001131, S000003059, S000007608, S000005370, S000005091, S000002172, S000001492, S000003931, S000005837, S000006132, S000004898, S000004012, S000005005, S000006138, S000006156, S000005230, S000006134, S000002965, S000000441	75	515	4870	2.521683	0.083563	0.028669	0.245126
GOTERM_BP_FAT	GO:0042254~ribosome biogenesis	16	20.51282	1.96E-04	S000001131, S000004064, S000007608, S000005370, S000005091, S000002172, S000001492, S000003931, S000005837, S000006132, S000004898, S000004012, S000004703, S000005005, S000006138, S000006156	75	351	4870	2.959924	0.096007	0.024918	0.283474
GOTERM_BP_FAT	GO:0034660~ncRNA process metabolic	17	21.79487	2.04E-04	S000001131, S000003059, S000004050, S000007608,	75	393	4870	2.808821	0.099485	0.02074	0.294286

					S000005370, S000005091, S000002172, S000001492, S000003931, S000005837, S000006132, S000004898, S000004012, S000001053, S000005005, S000006138, S000006156								
GOTERM_BP_FAT	GO:0022613~ribonucleoprotein complex biogenesis	17	21.79487	2.29E-04	S000001131, S000004064, S000007608, S000005370, S000005091, S000002172, S000001492, S000003931, S000005837, S000006132, S000004898, S000004012, S000004703, S000005005, S000006138, S000006156, S000000441	75	397	4870	2.780521	0.111166	0.019449	0.330891	
GOTERM_BP_FAT	GO:0034470~ncRNA processing	15	19.23077	4.18E-04	S000003059, S000001131, S000007608, S000005370, S000005091, S000002172, S000003931, S000001492, S000005837, S000006132, S000004898, S000004012, S000005005, S000006138, S000006156	75	335	4870	2.907463	0.193351	0.030229	0.602493	
GOTERM_CC_FAT	GO:0005730~nucleolus	13	16.66667	4.19E-04	S000001131, S000007608, S000005370, S000005091, S000002172, S000001358, S000003931, S000001492, S000005837, S000006132, S000005005, S000006138, S000001185	68	269	4595	3.265635	0.084237	0.084237	0.528015	
GOTERM_CC_FAT	GO:0030684~preribosome	9	11.53846	4.77E-04	S000006132, S000004012, S000005005, S000005370, S000006138, S000002172, S000001492, S000003931, S000005837	68	128	4595	4.751264	0.095428	0.04891	0.601567	
SP_PIR_KEYWORDS	nucleus	34	43.58974	5.73E-04	S000003059, S000001131, S000005217, S000002172, S000003931, S000005837, S000000064, S000006132, S000004898, S000004012, S000003608, S000003567,	78	1636	6448	1.718011	0.071758	0.036547	0.664823	

					S000006156, S000006138, S000001185, S000006134, S000006382, S000005398, S000002699, S000004064, S000007608, S000005370, S000005091, S000001492, S000002165, S000001676, S000005005, S000000853, S000000770, S000005667, S000002965, S000005780, S000006260, S000000441								
GOTERM_CC_FAT	GO:0030687~preribosome, large subunit precursor	5	6.410256	0.002543	S000006132, S000004012, S000005005, S000001492, S000003931	68	40	4595	8.446691	0.414168	0.163259	3.16581	
GOTERM_CC_FAT	GO:0070013~intracellular organelle lumen	22	28.20513	0.002768	S000003036, S000001131, S000006208, S000007608, S000005370, S000005091, S000002172, S000001492, S000001358, S000003931, S000000064, S000005837, S000006132, S000003278, S000001053, S000003608, S000005005, S000006138, S000006156, S000002986, S000001185, S000006260	68	783	4595	1.898618	0.441257	0.135424	3.441229	
GOTERM_CC_FAT	GO:0043233~organelle lumen	22	28.20513	0.002768	S000003036, S000001131, S000006208, S000007608, S000005370, S000005091, S000002172, S000001492, S000001358, S000003931, S000000064, S000005837, S000006132, S000003278, S000001053, S000003608, S000005005, S000006138, S000006156, S000002986, S000001185, S000006260	68	783	4595	1.898618	0.441257	0.135424	3.441229	
GOTERM_CC_FAT	GO:0031981~nuclear lumen	17	21.79487	0.004207	S000001131, S000007608, S000005370, S000005091, S000002172, S000001492, S000001358, S000003931, S000000064, S000005837, S000006132, S000003608,	68	545	4595	2.107798	0.587442	0.162284	5.187252	

					S000005005, S000006138, S000006156, S000001185, S000006260							
GOTERM_MF_FAT	GO:0003924~GTPase activity	6	7.692308	0.004878	S000004529, S000001722, S000004703, S000000368, S000001149, S000006138	68	70	4190	5.281513	0.603164	0.603164	5.891752
SP_PIR_KEYWORDS	mitochondrion inner membrane	8	10.25641	0.005289	S000001284, S000003489, S000005456, S000003278, S000004703, S000006225, S000005651, S000002376	78	179	6448	3.6946	0.498088	0.205289	5.988269
GOTERM_CC_FAT	GO:0031974~membrane-enclosed lumen	22	28.20513	0.005416	S000003036, S000001131, S000006208, S000007608, S000005370, S000005091, S000002172, S000001492, S000001358, S000003931, S000000064, S000005837, S000006132, S000003278, S000001053, S000003608, S000005005, S000006138, S000006156, S000002986, S000001185, S000006260	68	827	4595	1.797603	0.680343	0.173111	6.631425
GOTERM_CC_FAT	GO:0005732~small nucleolar ribonucleoprotein complex	4	5.128205	0.009081	S000001131, S000005091, S000002172, S000005837	68	30	4595	9.009804	0.852777	0.23943	10.88648
GOTERM_CC_FAT	GO:0030529~ribonucleoprotein complex	17	21.79487	0.009091	S000006382, S000003036, S000001131, S000005370, S000005091, S000002172, S000001492, S000003931, S000005837, S000006132, S000004012, S000005005, S000006138, S000005230, S000006134, S000002965, S000000441	68	590	4595	1.947034	0.853091	0.21317	10.89793
SP_PIR_KEYWORDS	nucleotide-binding	17	21.79487	0.011271	S000001284, S000004529, S000003059, S000004050, S000002699, S000004624, S000002165, S000003931, S000001053, S000001722, S000004703, S000000368, S000001149, S000006138, S000006156, S000004297, S000000441	78	731	6448	1.922481	0.770897	0.308157	12.3663
GOTERM_CC_FAT	GO:0043228~non-membrane-bounded	26	33.33333	0.011948	S000003036, S000004529,	68	1120	4595	1.568671	0.919873	0.244564	14.08897

	organelle				S000001131, S000005318, S000005217, S000002172, S000001358, S000003931, S000005837, S000000064, S000006132, S000003608, S000001149, S000006156, S000006138, S000003567, S000000014, S000001185, S000004362, S000007608, S000005370, S000005091, S000001492, S000005005, S000000770, S000005667								
GOTERM_CC_FAT	GO:0043232~intracellular non-membrane-bounded organelle	26	33.33333	0.011948	S000003036, S000004529, S000001131, S000005318, S000005217, S000002172, S000001358, S000003931, S000005837, S000000064, S000006132, S000003608, S000001149, S000006156, S000006138, S000003567, S000000014, S000001185, S000004362, S000007608, S000005370, S000005091, S000001492, S000005005, S000000770, S000005667	68	1120	4595	1.568671	0.919873	0.244564	14.08897	
GOTERM_CC_FAT	GO:0030532~small nuclear ribonucleoprotein complex	5	6.410256	0.01222	S000006382, S000005091, S000005230, S000002965, S000006134	68	62	4595	5.449478	0.924375	0.227556	14.38729	
GOTERM_BP_FAT	GO:0000398~nuclear mRNA splicing, via spliceosome	6	7.692308	0.017392	S000006382, S000005091, S000005230, S000002965, S000006134, S000000441	75	100	4870	3.896	0.999879	0.676081	22.40251	
GOTERM_BP_FAT	GO:0000377~RNA splicing, via transesterification reactions with bulged adenosine as nucleophile	6	7.692308	0.018798	S000006382, S000005091, S000005230, S000002965, S000006134, S000000441	75	102	4870	3.819608	0.999942	0.661696	23.9927	
UP_SEQ_FEATURE	nucleotide phosphate-binding region:GTP	5	6.410256	0.019091	S000004529, S000001722, S000004703, S000000368, S000001149	78	86	6448	4.806202	0.977132	0.977132	21.40008	
GOTERM_MF_FAT	GO:0032561~guanyl ribonucleotide binding	6	7.692308	0.020225	S000004529, S000001722, S000004703, S000000368, S000001149, S000006138	68	99	4190	3.734403	0.978968	0.854977	22.40954	
GOTERM_MF_FAT	GO:0005525~GTP binding	6	7.692308	0.020225	S000004529, S000001722, S000004703, S000000368,	68	99	4190	3.734403	0.978968	0.854977	22.40954	

					S000001149, S000006138								
GOTERM_MF_FAT	GO:0019001~guanyl nucleotide binding	6	7.692308	0.020225	S000004529, S000001722, S000004703, S000000368, S000001149, S000006138	68	99	4190	3.734403	0.978968	0.854977	22.40954	
GOTERM_BP_FAT	GO:0042273~ribosomal large subunit biogenesis	5	6.410256	0.02219	S000006132, S000004012, S000004064, S000001492, S000003931	75	71	4870	4.57277	0.99999	0.684449	27.70431	
SP_PIR_KEYWORDS	gtp-binding	5	6.410256	0.023817	S000004529, S000001722, S000004703, S000000368, S000001149	78	92	6448	4.492754	0.956442	0.465665	24.47566	
GOTERM_BP_FAT	GO:0000375~RNA splicing, via transesterification reactions	6	7.692308	0.024307	S000006382, S000005091, S000005230, S000002965, S000006134, S000000441	75	109	4870	3.574312	0.999997	0.683313	29.93409	
SP_PIR_KEYWORDS	rna-binding	9	11.53846	0.025919	S000006132, S000004898, S000001131, S000005005, S000005091, S000005230, S000002172, S000002965, S000003931	78	300	6448	2.48	0.967087	0.433898	26.34797	
GOTERM_MF_FAT	GO:0031202~RNA splicing factor activity, transesterification mechanism	5	6.410256	0.026037	S000006382, S000005091, S000002965, S000006134, S000000441	68	71	4190	4.339271	0.993169	0.810259	27.93575	
SP_PIR_KEYWORDS	protein transport	10	12.82051	0.028061	S000001284, S000003278, S000003561, S000002549, S000001722, S000000136, S000004258, S000000368, S000005780, S000002376	78	363	6448	2.277319	0.975277	0.410557	28.21193	
SP_PIR_KEYWORDS	mrna splicing	5	6.410256	0.035245	S000006382, S000005091, S000002965, S000006134, S000000441	78	104	6448	3.974359	0.990577	0.44182	34.1544	
SP_PIR_KEYWORDS	rrna processing	6	7.692308	0.037235	S000001131, S000007608, S000005091, S000006156, S000002172, S000005837	78	155	6448	3.2	0.992795	0.421961	35.71887	
GOTERM_CC_FAT	GO:0005743~mitochondrial inner membrane	8	10.25641	0.037306	S000001284, S000003489, S000005456, S000003278, S000004703, S000006225, S000005651, S000002376	68	217	4595	2.49119	0.999659	0.516081	38.14313	
GOTERM_MF_FAT	GO:0008026~ATP-dependent helicase activity	5	6.410256	0.044365	S000002699, S000006156, S000003931, S000005667, S000000441	68	84	4190	3.667717	0.999812	0.882837	43.07955	
GOTERM_MF_FAT	GO:0070035~purine NTP-dependent helicase activity	5	6.410256	0.044365	S000002699, S000006156, S000003931, S000005667,	68	84	4190	3.667717	0.999812	0.882837	43.07955	

					S000000441								
GOTERM_CC_FAT	GO:0019866~organelle inner membrane	8	10.25641	0.045841	S000001284, S000003489, S000005456, S000003278, S000004703, S000006225, S000005651, S000002376	68	227	4595	2.381446	0.999947	0.560088	44.7249	
KEGG_PATHWAY	sce03040:Spliceosome	4	5.128205	0.05147	S000006382, S000005091, S000002965, S000000441	21	62	1439	4.420891	0.592741	0.592741	31.7914	
GOTERM_BP_FAT	GO:0008380~RNA splicing	6	7.692308	0.063684	S000006382, S000005091, S000005230, S000002965, S000006134, S000000441	75	142	4870	2.743662	1	0.940305	61.37428	
KEGG_PATHWAY	sce00130:Ubiquinone and other terpenoid-quinone biosynthesis	2	2.564103	0.067679	S000005456, S000005651	21	5	1439	27.40952	0.696183	0.448804	39.79429	
GOTERM_BP_FAT	GO:0006605~protein targeting	8	10.25641	0.06937	S000001284, S000003278, S000002549, S000001722, S000000368, S000005780, S000002376, S000005837	75	239	4870	2.173501	1	0.941723	64.63018	
GOTERM_CC_FAT	GO:0031428~box C/D snoRNP complex	2	2.564103	0.07084	S000002172, S000005837	68	5	4595	27.02941	1	0.694832	60.47663	
GOTERM_CC_FAT	GO:0046540~U4/U6 x U5 tri-snRNP complex	3	3.846154	0.074298	S000006382, S000005091, S000002965	68	31	4595	6.539374	1	0.685901	62.29547	
GOTERM_MF_FAT	GO:0008565~protein transporter activity	4	5.128205	0.078762	S000001284, S000003561, S000005780, S000002376	68	63	4190	3.912232	1	0.954996	63.89436	
GOTERM_BP_FAT	GO:0033365~protein localization in organelle	6	7.692308	0.080181	S000001284, S000003278, S000005780, S000002376, S000005837, S000001676	75	152	4870	2.563158	1	0.95351	70.12767	
SP_PIR_KEYWORDS	transport	15	19.23077	0.081224	S000001284, S000003561, S000002549, S000000136, S000006208, S000004258, S000003801, S000003489, S000003278, S000001722, S000000368, S000006225, S000003252, S000005780, S000002376	78	788	6448	1.573604	0.999984	0.667553	62.71315	
GOTERM_BP_FAT	GO:0042255~ribosome assembly	4	5.128205	0.086686	S000006132, S000004703, S000006138, S000003931	75	69	4870	3.764251	1	0.955272	73.04067	
SP_PIR_KEYWORDS	helicase	4	5.128205	0.087509	S000002699, S000006156, S000003931, S000000441	78	88	6448	3.757576	0.999993	0.661177	65.57765	
GOTERM_MF_FAT	GO:0004386~helicase activity	5	6.410256	0.088344	S000002699, S000006156, S000003931, S000005667, S000000441	68	106	4190	2.906493	1	0.945715	68.29046	
UP_SEQ_FEATURE	nucleotide phosphate-binding	9	11.53846	0.089165	S000001284, S000001053,	78	387	6448	1.922481	1	0.999894	68.86134	

	region:ATP				S000003059, S000002699, S000006156, S000006138, S000002165, S000003931, S000000441							
SP_PIR_KEYWORDS	ubiquinone biosynthesis	2	2.564103	0.091682	S000005456, S000005651	78	8	6448	20.66667	0.999996	0.647161	67.36687
GOTERM_BP_FAT	GO:0034613~cellular localization protein	10	12.82051	0.095813	S000001284, S000003278, S000003561, S000002549, S000001722, S000000368, S000005780, S000002376, S000005837, S000001676	75	362	4870	1.793738	1	0.960664	76.68396
GOTERM_CC_FAT	GO:0044452~nucleolar part	4	5.128205	0.098358	S000001131, S000002172, S000001185, S000005837	68	76	4595	3.556502	1	0.765319	72.96675

1 Gene IDs are from DAIVD website *Saccharomyces cerevisiae* gene set

Table S4: Approximately Unbiased (AU) test of the three topologies

Topology	Log-likelihood of RAxML	Difference¹	<i>P</i>-value of AU test
(((Ag,Pu),Us),Out) ²	-2063178.2	(best)	0.790
(((Ag,Us),Pu),Out)	-2063207.1	28.9	0.219
((Ag,(Pu,Us)),Out)	-2063268.1	89.9	0.001

1 Difference between likelihood at this row and the best likelihood

2 Ag: Agaricomycotina; Pu: Pucciniomycotina; Us: Ustilaginomycotina; Out; Outgroup

Table S5: Other tests of the three topologies using CONSEL package

Topology	Log-likelihood of RAxML	Difference ¹	P-values					
			Bootstrap	Bayesian Posterior Probability	Kishino - Hasegawa Test	Shimodaira-Hasegawa Test	Weighted Kishino - Hasegawa Test	Weighted Shimodaira - Hasegawa Test
(((Ag,Pu),Us),Out) ²	-2063178.2	(best)	0.798	1.000	0.803	0.905	0.803	0.897
(((Ag,Us),Pu),Out)	-2063207.1	28.9	0.202	3e-13	0.197	0.286	0.197	0.310
((Ag,(Pu,Us)),Out)	-2063268.1	89.9	3e-04	9e-40	0.002	0.003	0.002	0.004

1 Difference between likelihood at this row and the best likelihood

2 Ag: Agaricomycotina; Pu: Pucciniomycotina; Us: Ustilaginomycotina; Out; Outgroup

Table S6: Gene cluster removal in the evaluation of potential sequence bias

Sequence bias type	Cases of gene cluster removal	# of gene clusters discarded
Long branch attraction	a	31
	b	8
	c	8
	d	10
Mutaional saturation	e	13
	f	4
	g	30
	h	13
	i	32
Long branch attraction + Mutaional saturation	j	55

a. Mean value of upper quartile of LB score > 60

b. Mean value of upper quartile of LB score > 70

c. Standard deviation of LB score > 50

d. Mean value of upper quartile of LB score > 70 or standard deviation of LB score > 50

e. Slope of the linear regression < 0.1

f. R^2 of the linear regression < 0.3

g. R^2 of the linear regression < 0.65

h. Slope of the linear regression < 0.1 or R^2 of the linear regression < 0.3

i. Slope of the linear regression < 0.1 or R^2 of the linear regression < 0.65

j. Mean value of upper quartile of LB score > 60 or Slope of the linear regression < 0.1 or R^2 of the linear regression < 0.65

Table S7: Stability analysis of CVTree

Percentage of gene retained in the random gene set	Topology of the three subphyla
60	(((Ag,Pu)90,Us)100),Out) ¹
65	(((Ag,Pu)94,Us)100),Out)
70	(((Ag,Pu)95,Us)100),Out)
75	(((Ag,Pu)100,Us)100),Out)
80	(((Ag,Pu)97,Us)100),Out)
85	(((Ag,Pu)99,Us)100),Out)
90	(((Ag,Pu)99,Us)100),Out)
95	(((Ag,Pu)100,Us)100),Out)

¹ Ag: Agaricomycotina; Pu: Pucciniomycotina; Us: Ustilaginomycotina; Out; Outgroup