

## Supplemental Materials

**Figure S1.** Maximum likelihood analyses of protein alignments in this study. A = *hyp1*, B = *hyp2*, C = *hppD*, D = *hmgX*, E = *hmgA*, F = *fahA*, G = *hmgR*, H = *maiA*, I = *tspH*, J = *aspH*, K = *mfsG*, L = *fphG*, M = *sdoG*, N = *ctfG*, O = *gdoG*, P = *sahG*, Q = *adhG*, R = *mfsH*, S = *mfsBX*, T = *iclBX*, U = species tree.

**Figure S2.** Paralogous gentisate catabolism clusters.

**Figure S3.** Mauve alignments of gentisate catabolism (GC) cluster loci. A. *A. fumigatus* GC cluster and flanking sequences aligned with the *A. fischerianus* homologous locus. B. *A. niger* GC cluster and flanking sequences aligned with the *A. carbonarius* homologous locus. Matching colored histograms correspond to aligned sequence and direction is indicated by position of histograms above or below the horizontal axis.

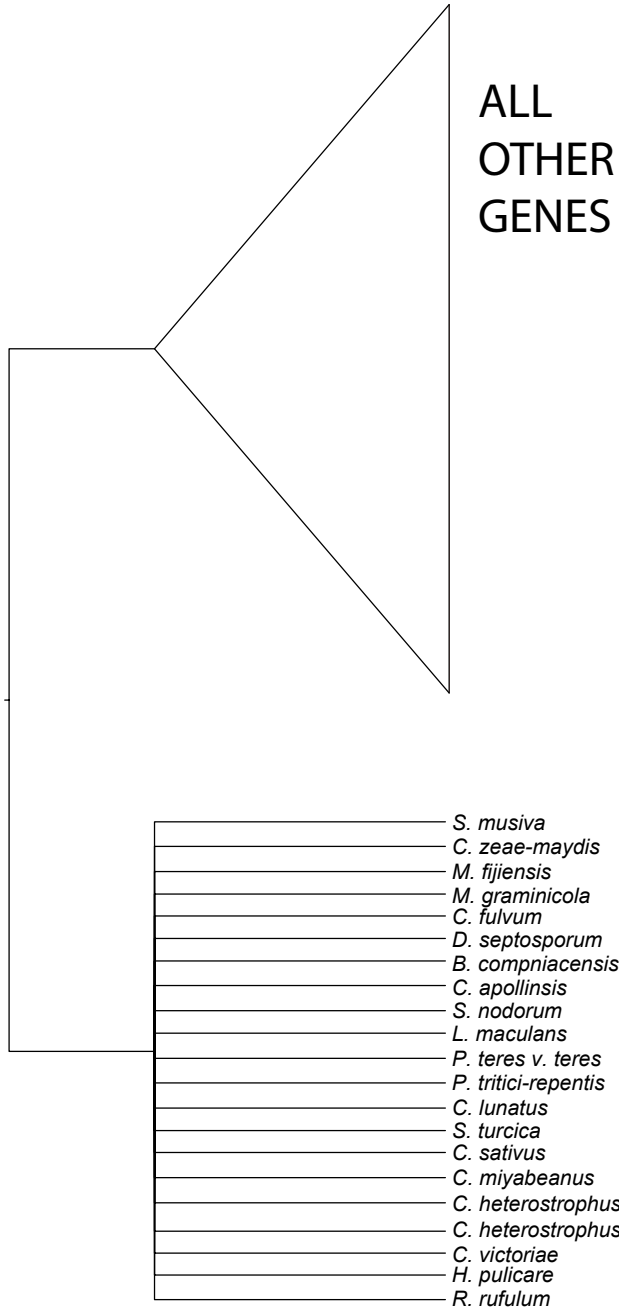
**Figure S4.** Distribution and clustering of phenolic metabolism genes in Pezizomycotina fungi. Taxa on y-axis are ordered as in Figure 2 and abbreviated as in Table S1. Cell colors in the matrix indicate the following states: Black = no detected homologs, light blue = single homolog unclustered, dark blue = multiple homologs unclustered, pink = a single homolog, which is clustered, and red = multiple homologs with at least 1 clustered.

**Figure S5.** Alignment logos of A. bacterial, and B. fungal gentisate 1,2-dioxygenase amino acid sequences. Stack height at each position indicates residue conservation, and relative residue height within each position corresponds to the frequency it is encountered. Known functional positions (see table S2) indicate the corresponding residue in salicylate 1,2 dioxygenase in *Psuedaminobacter salicylatoxidans*.

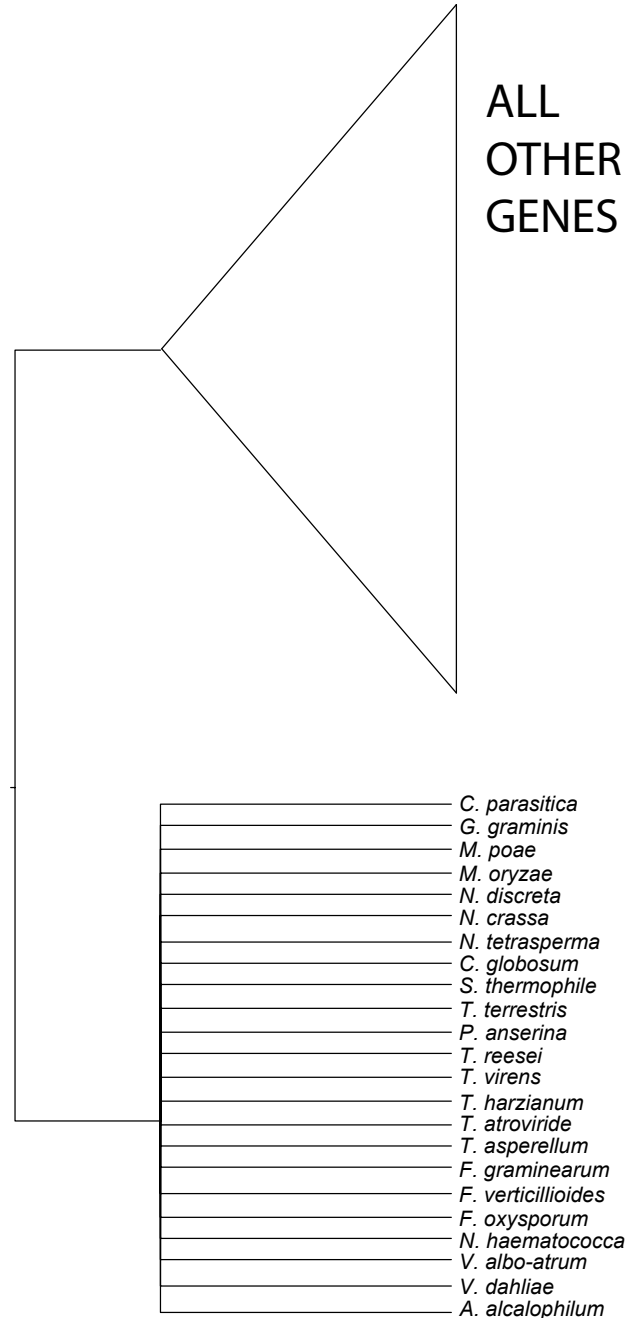
**Table S1.** Genomes analyzed in this study.

**Table S2.** Comparison of function-related residues among gentisate 1,2 dioxygenase homologs in fungi and bacteria.

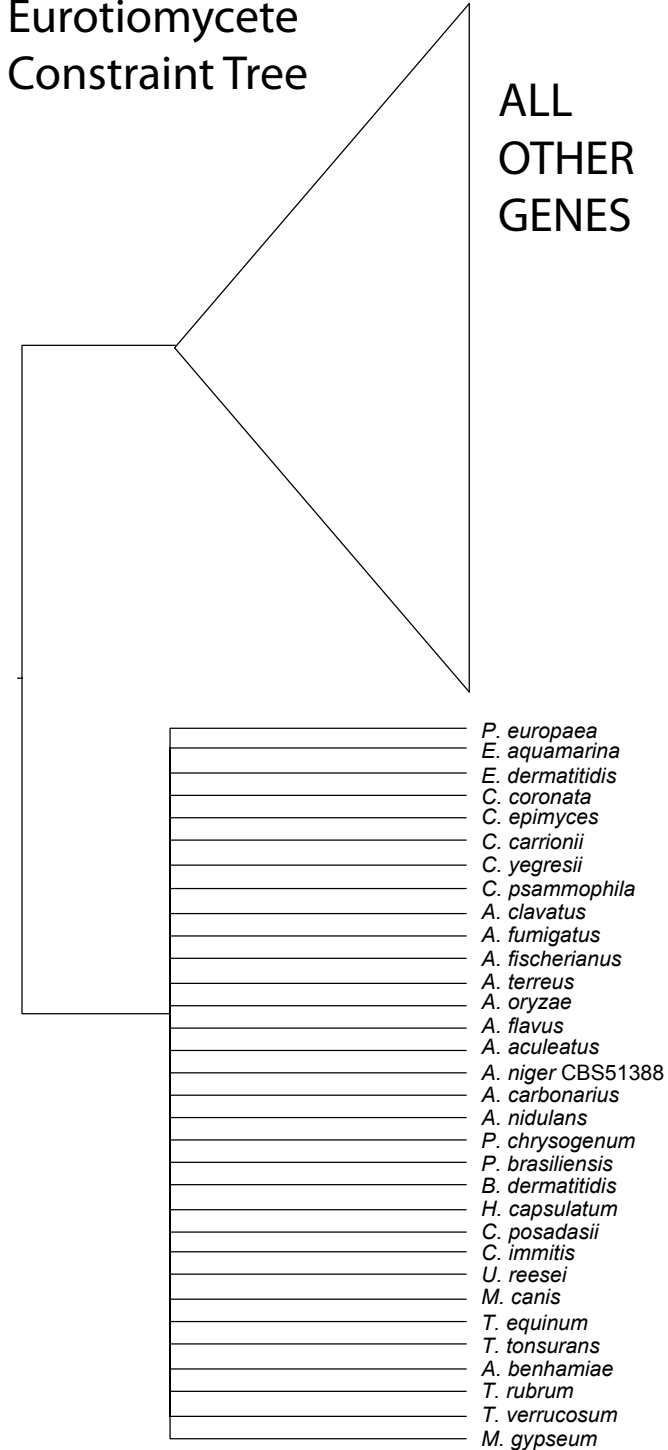
Monophyletic  
Dothidiomycete  
Constraint Tree



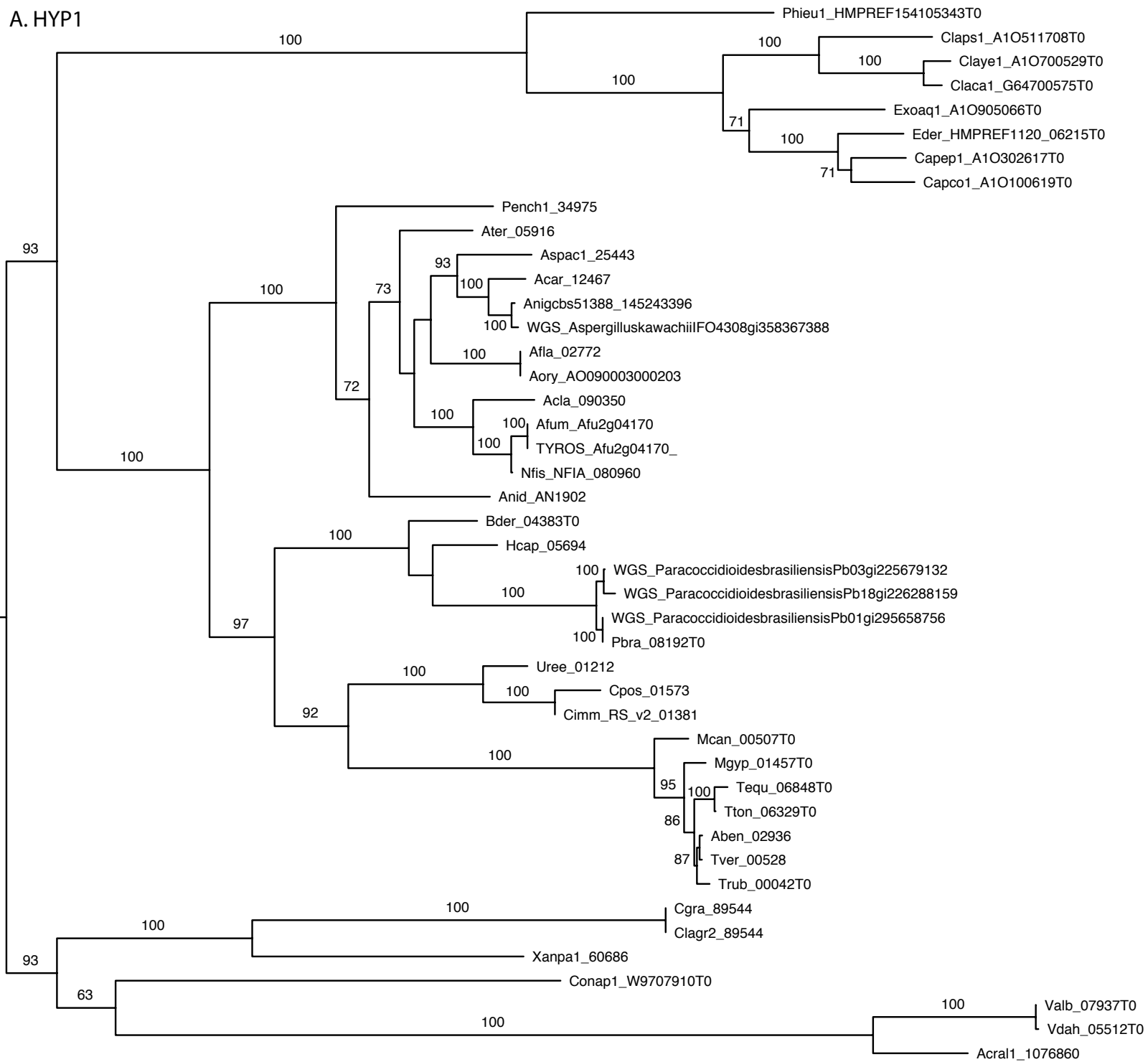
Monophyletic  
Sordariomycete  
Constraint Tree



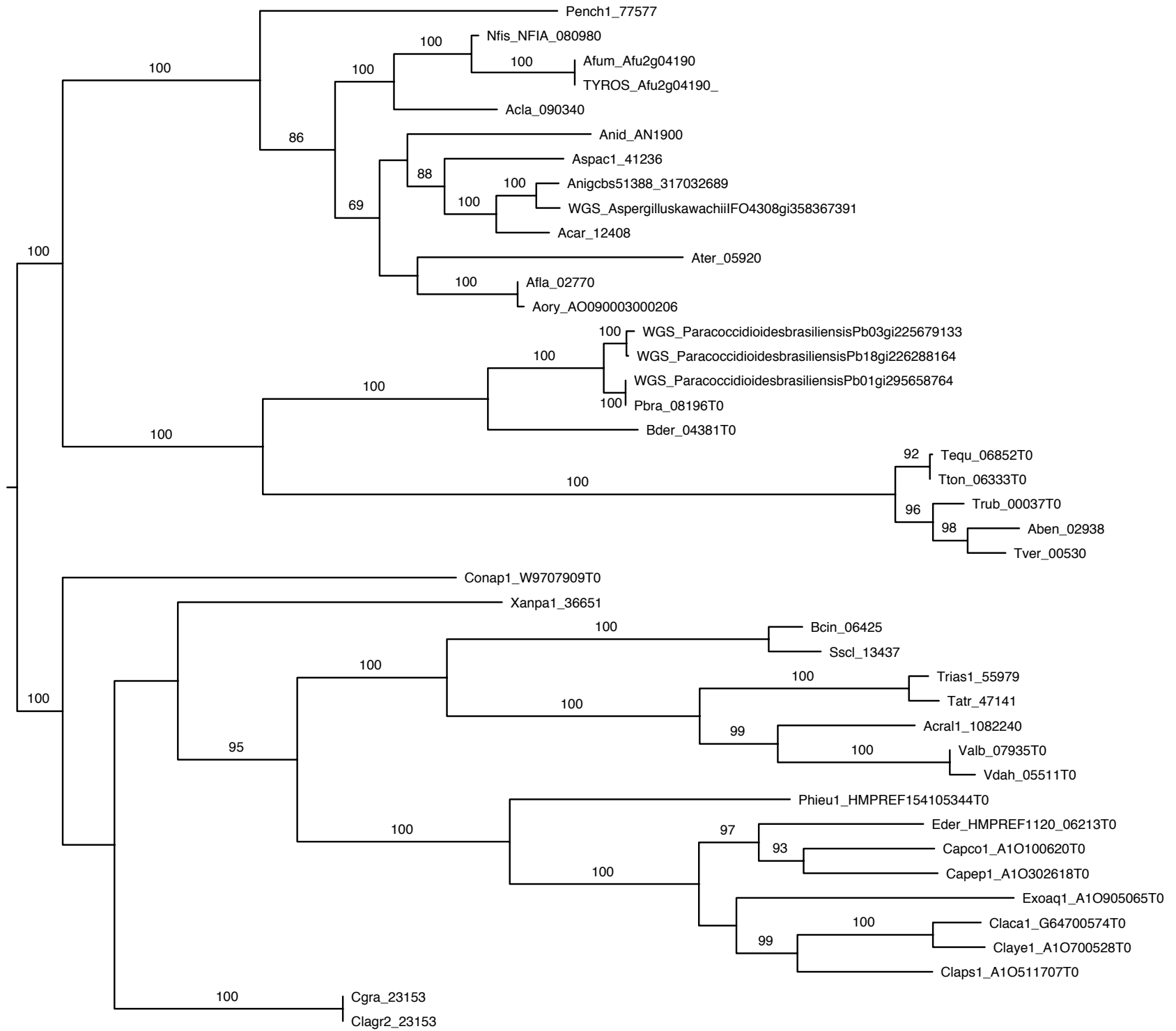
Monophyletic  
Eurotiomycete  
Constraint Tree



A. HYP1

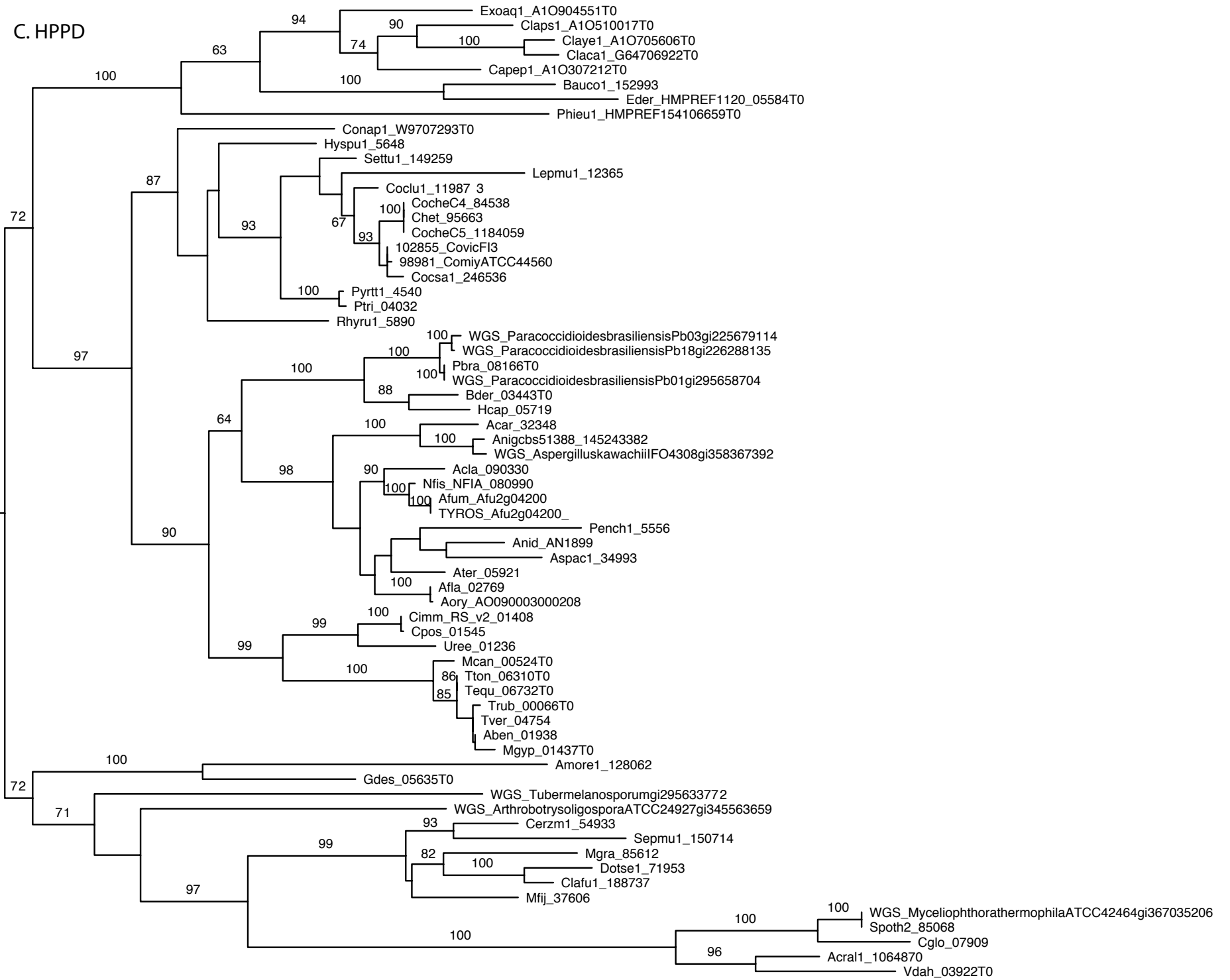


B. HYP2



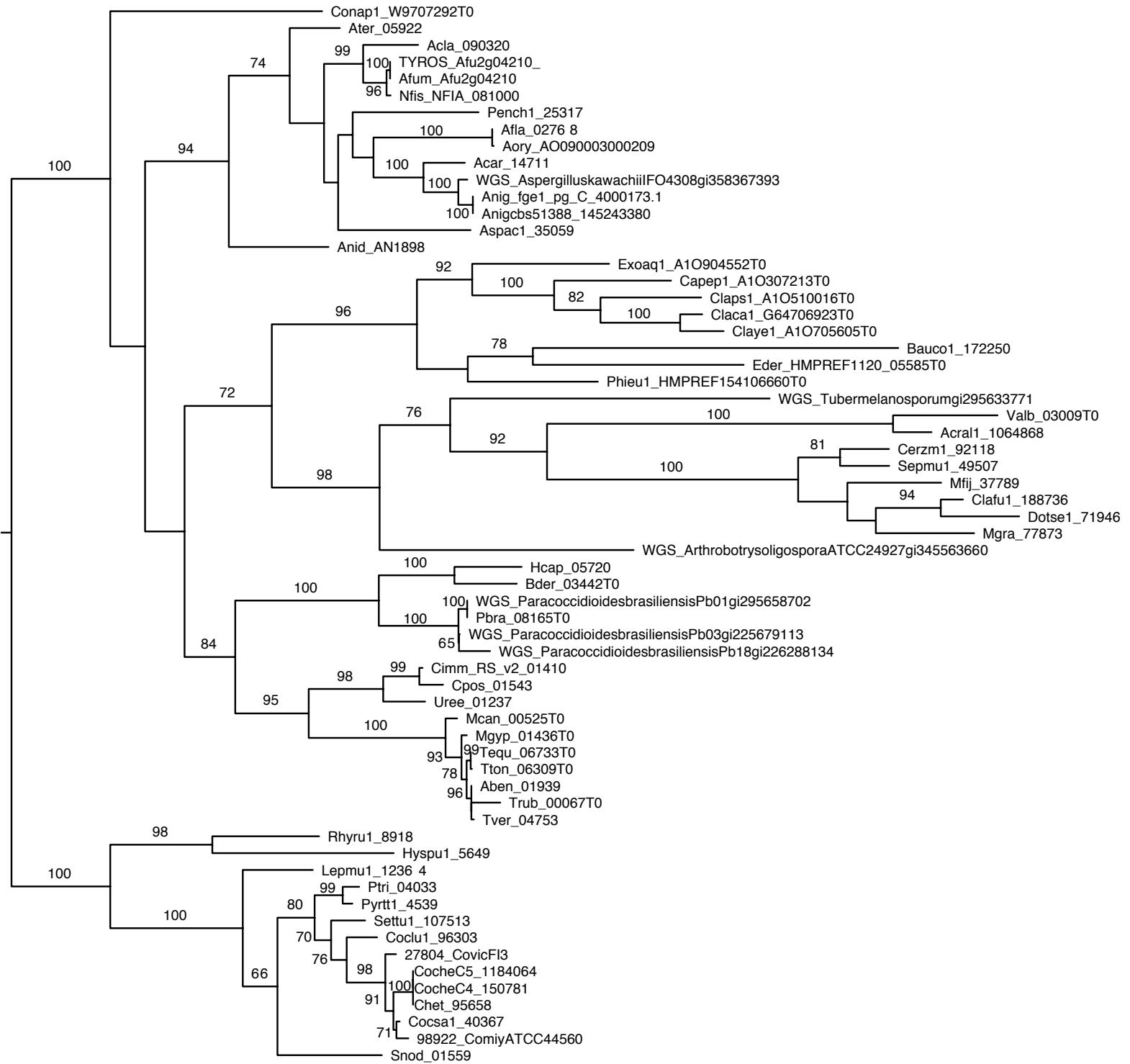
0.4

C. HPPD

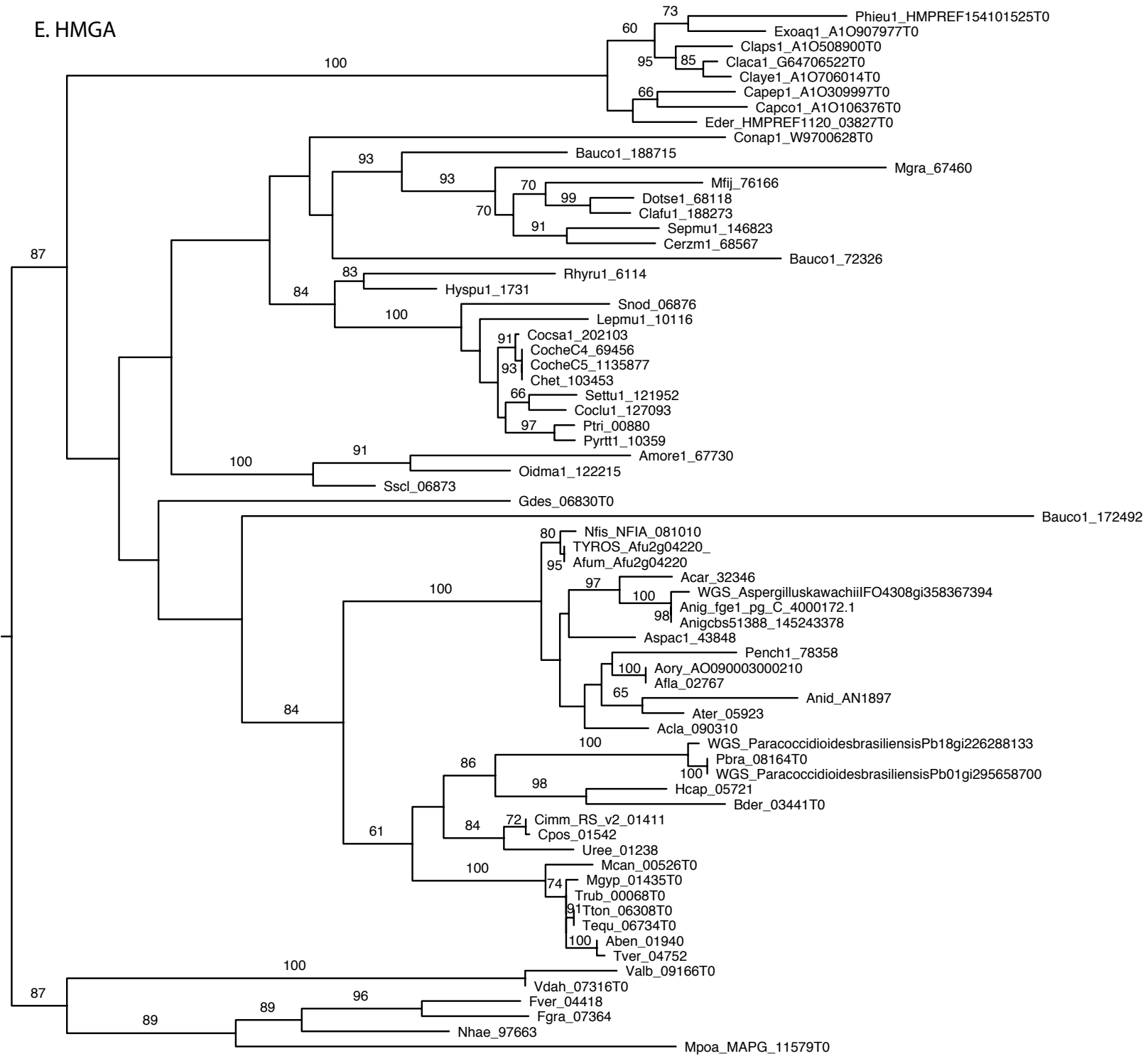


0.2

D. HMGX

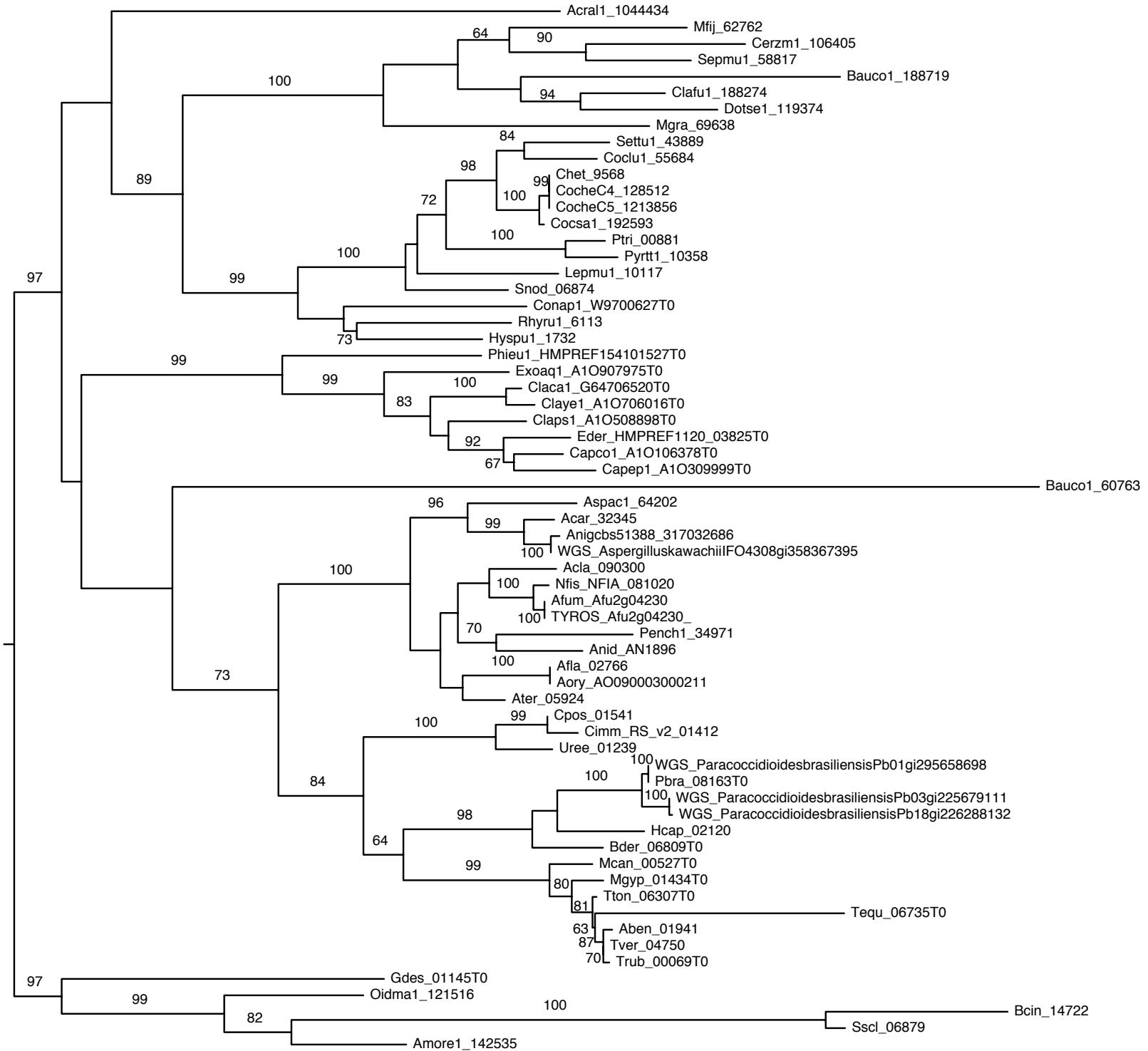


E. HMGA



0.1

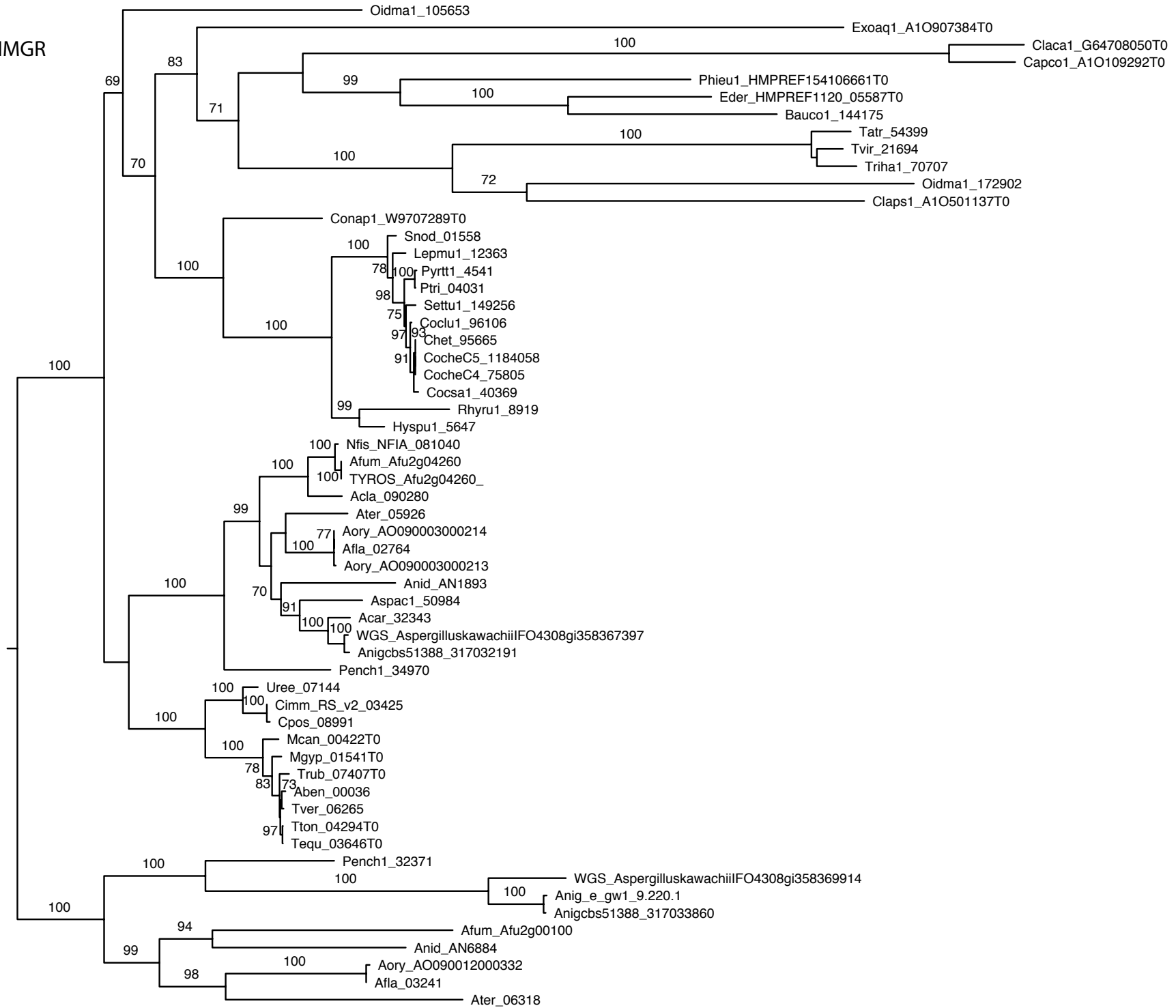
F. FAHA



0.2

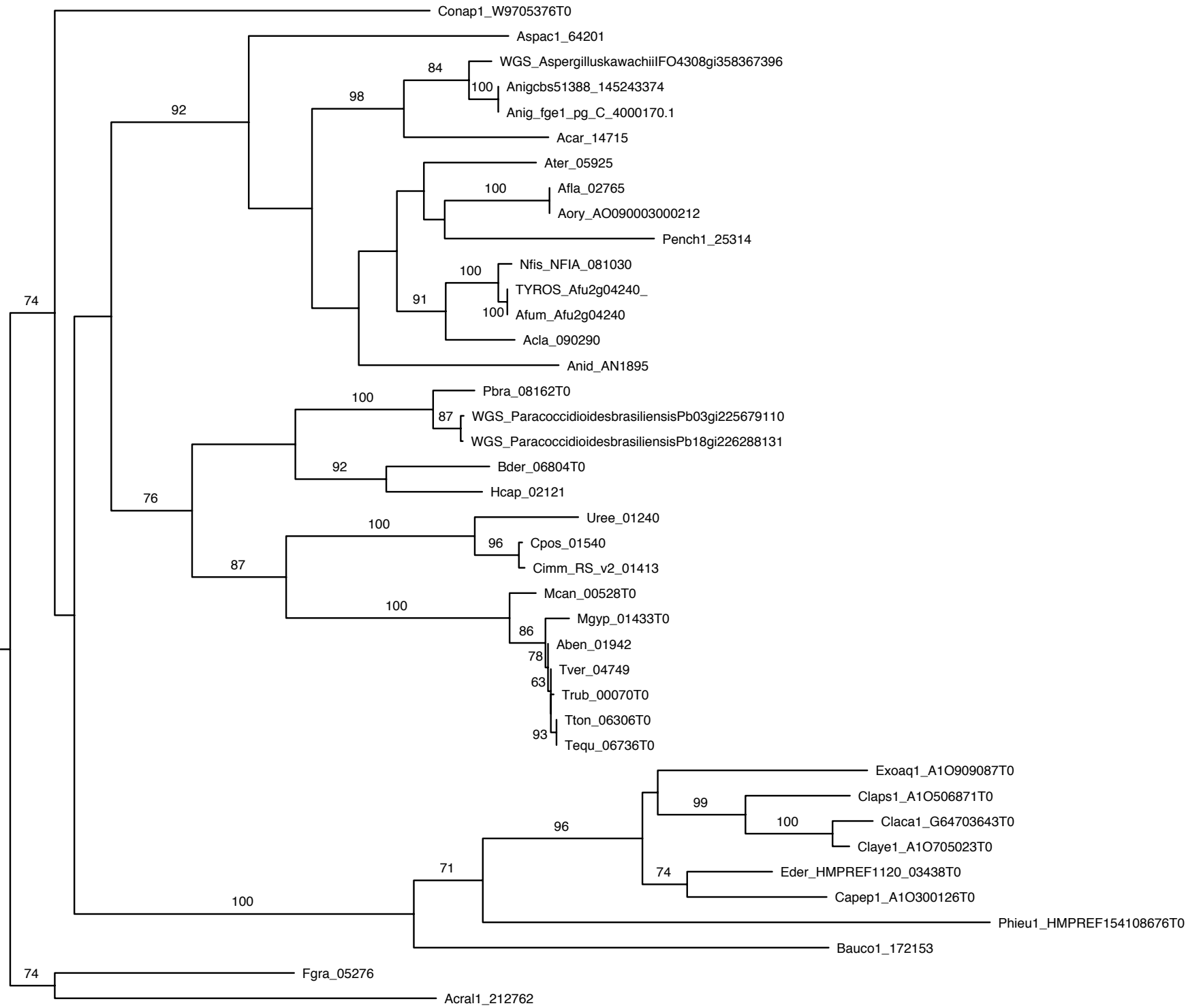


G. HMGR



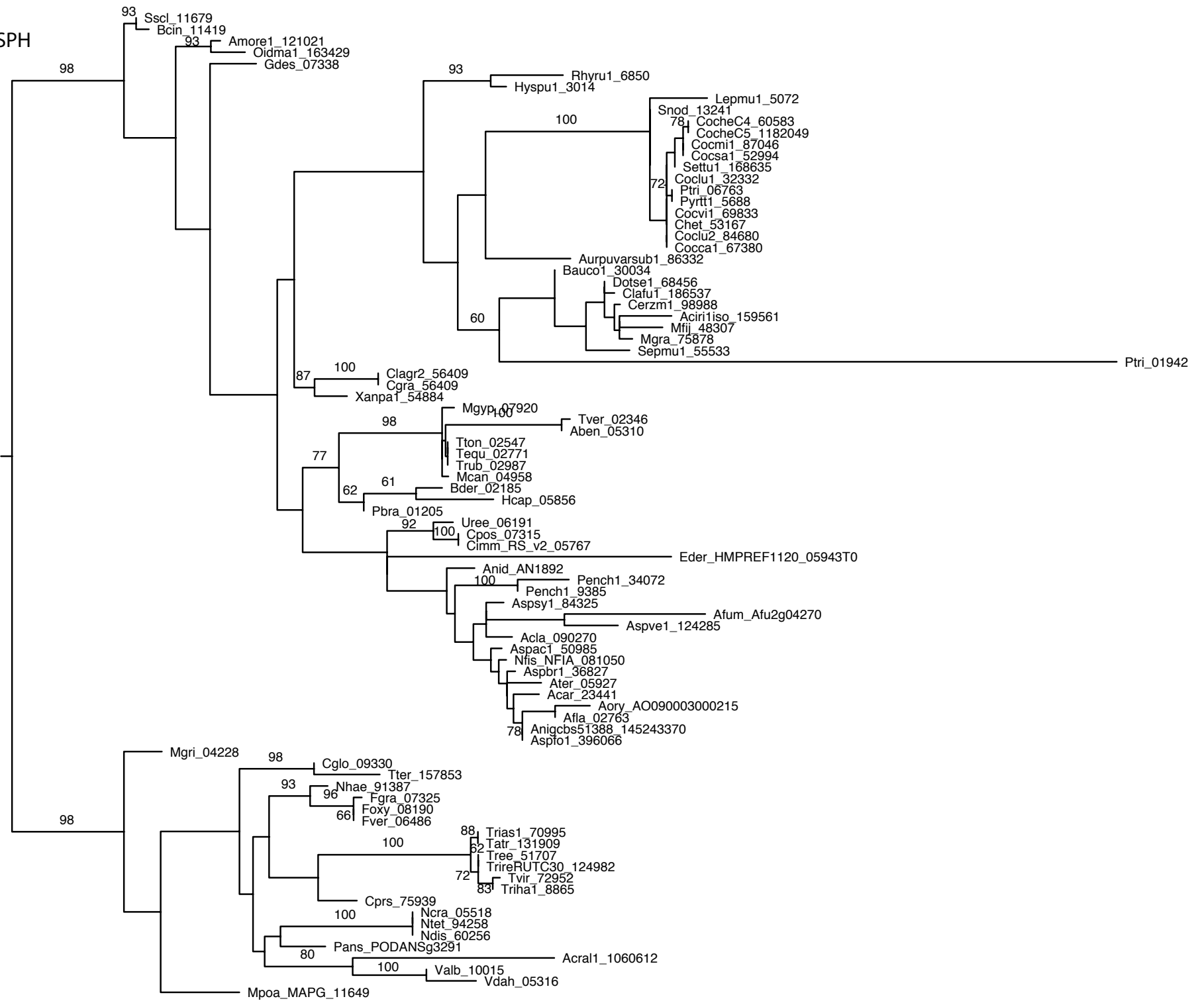
0.5

H. MAIA



0.2

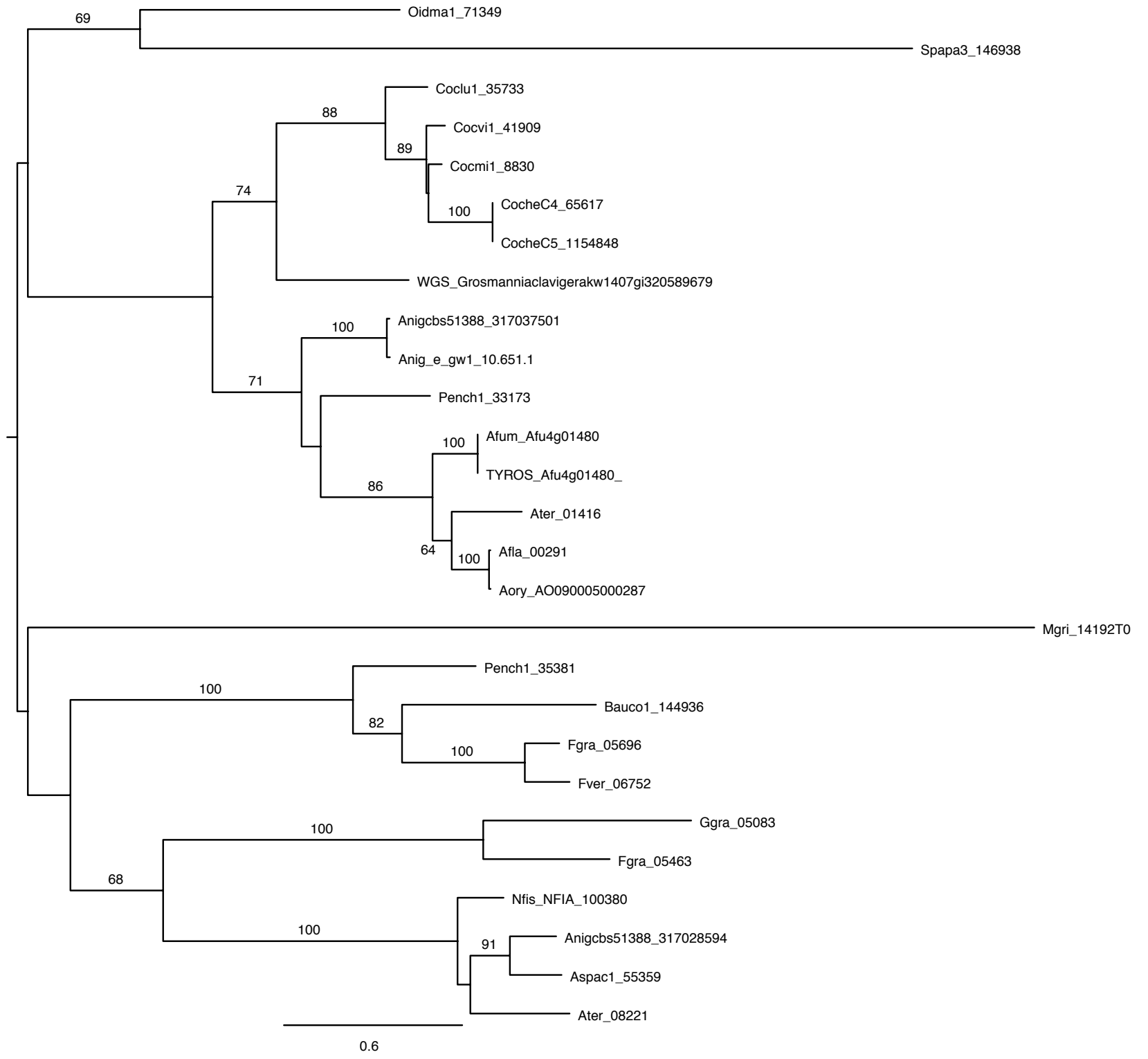
I. TSPH



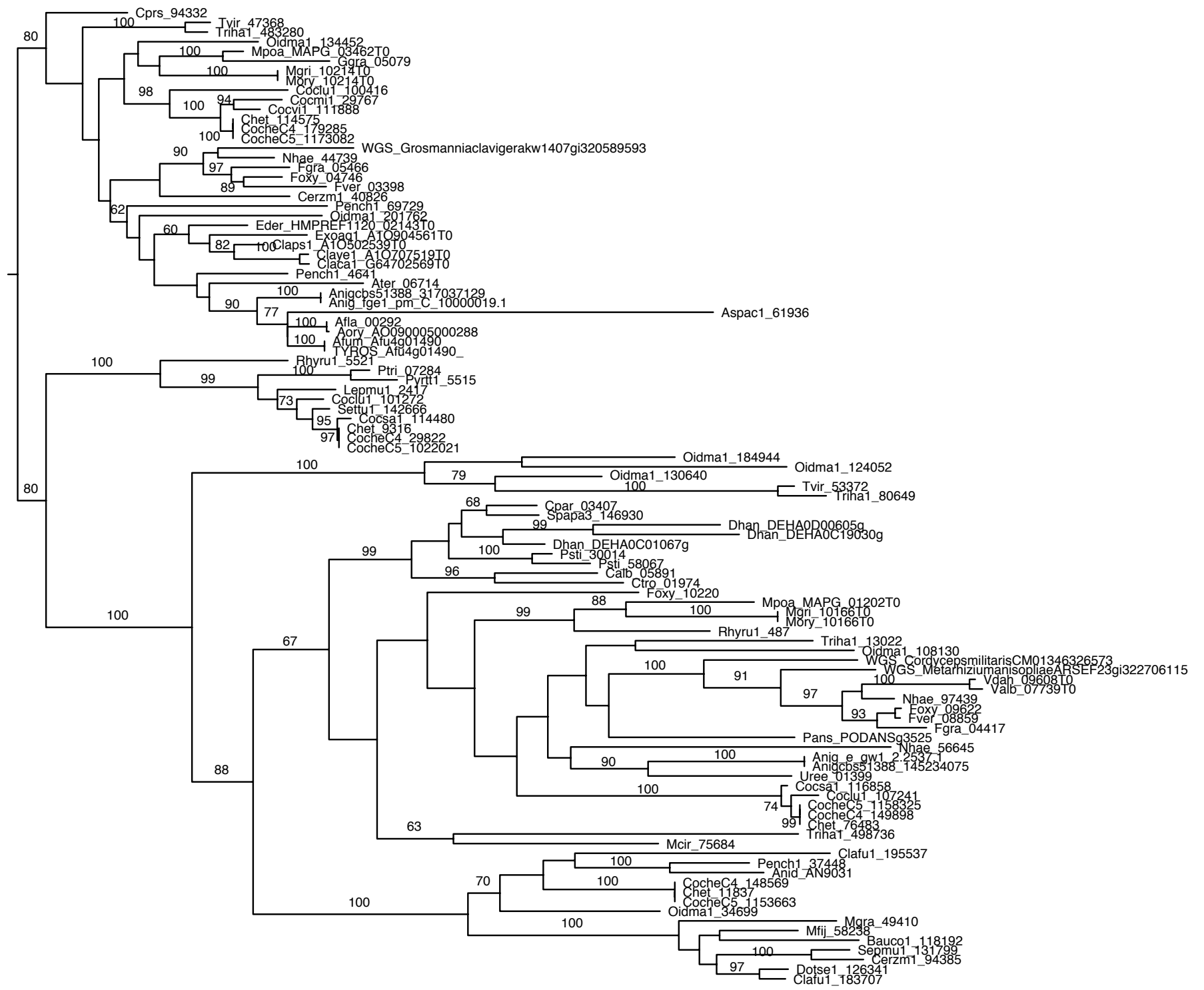
0.3



K. MFSG

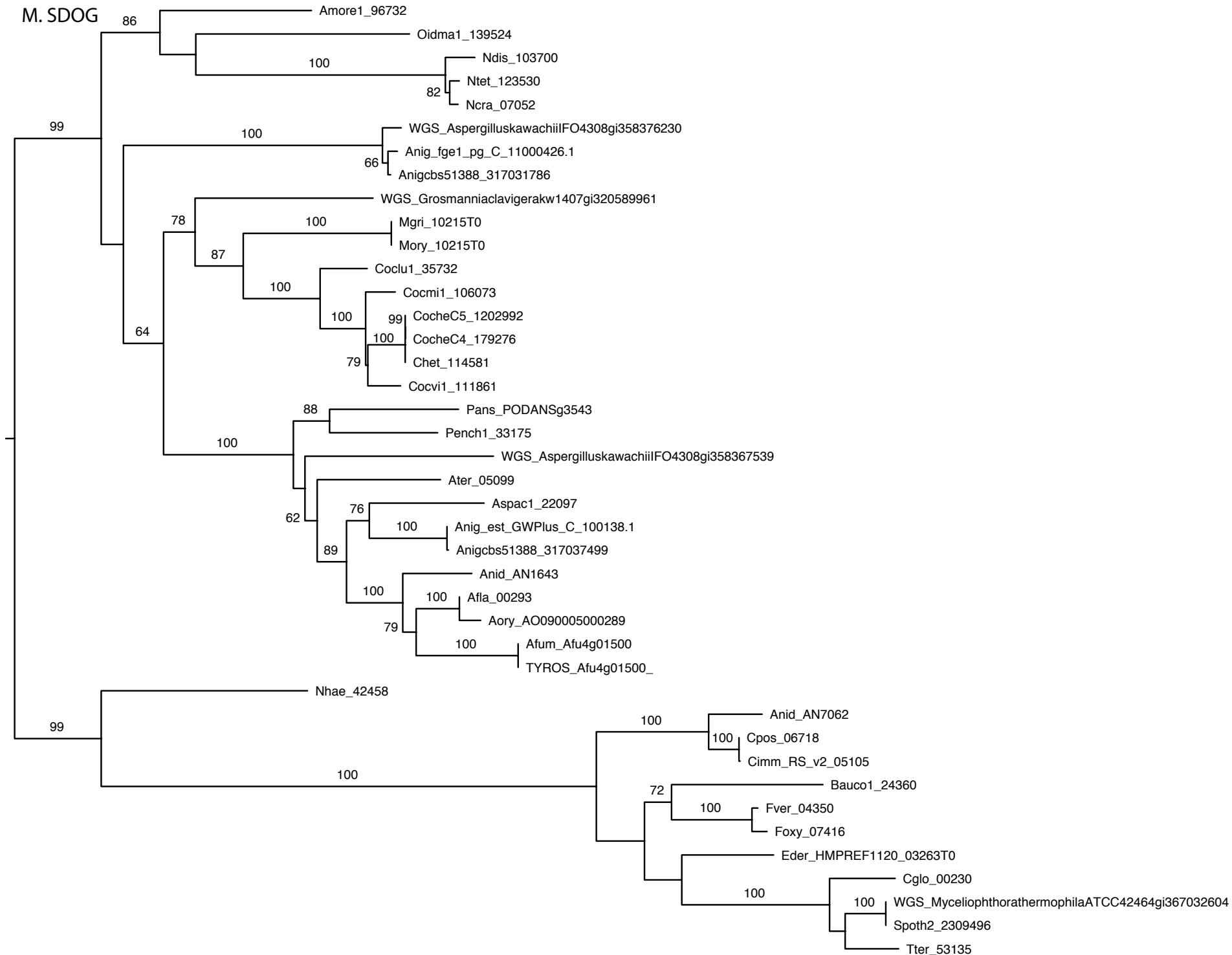


L. FPHG



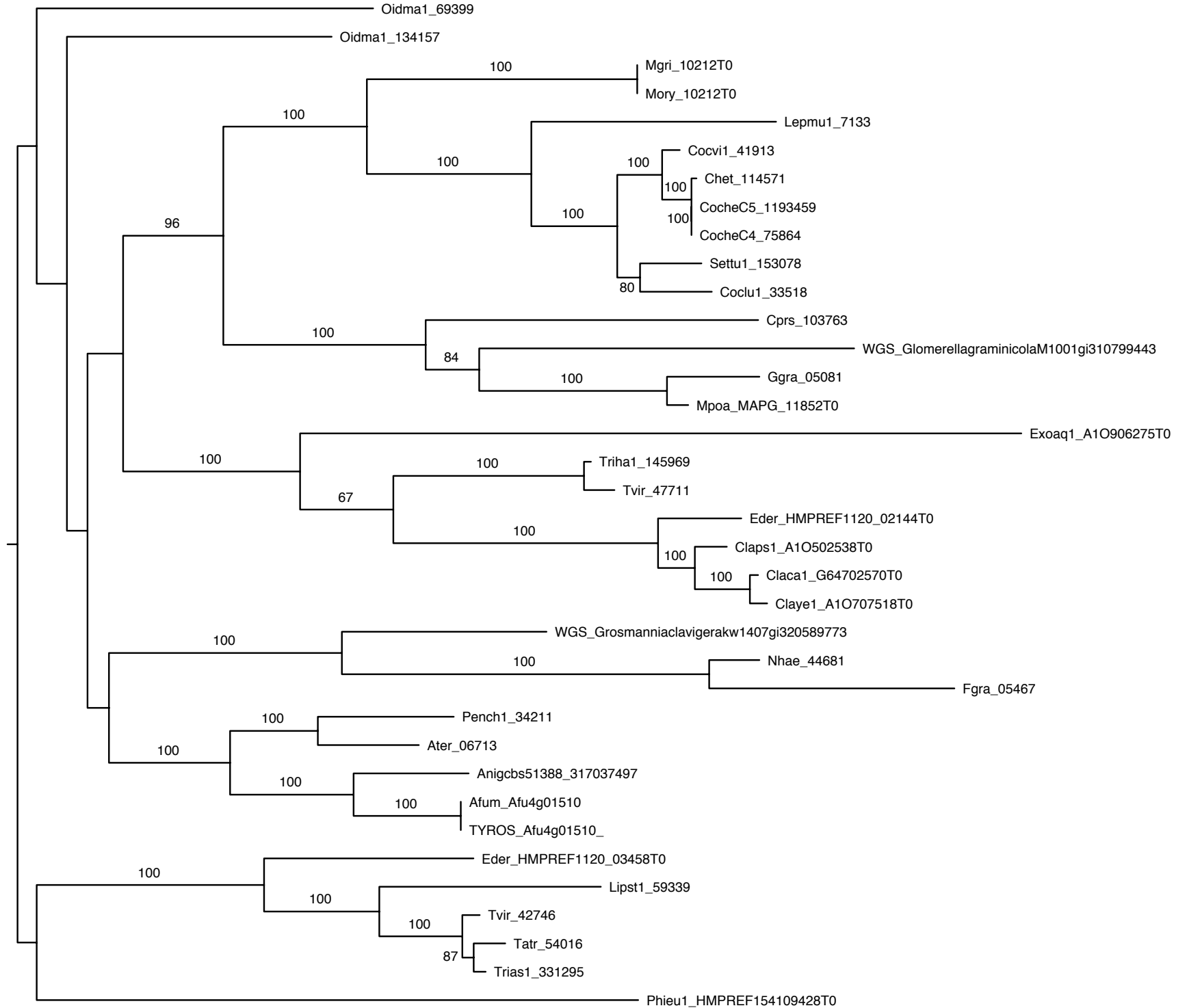
0.2

M. SDOG



0.3

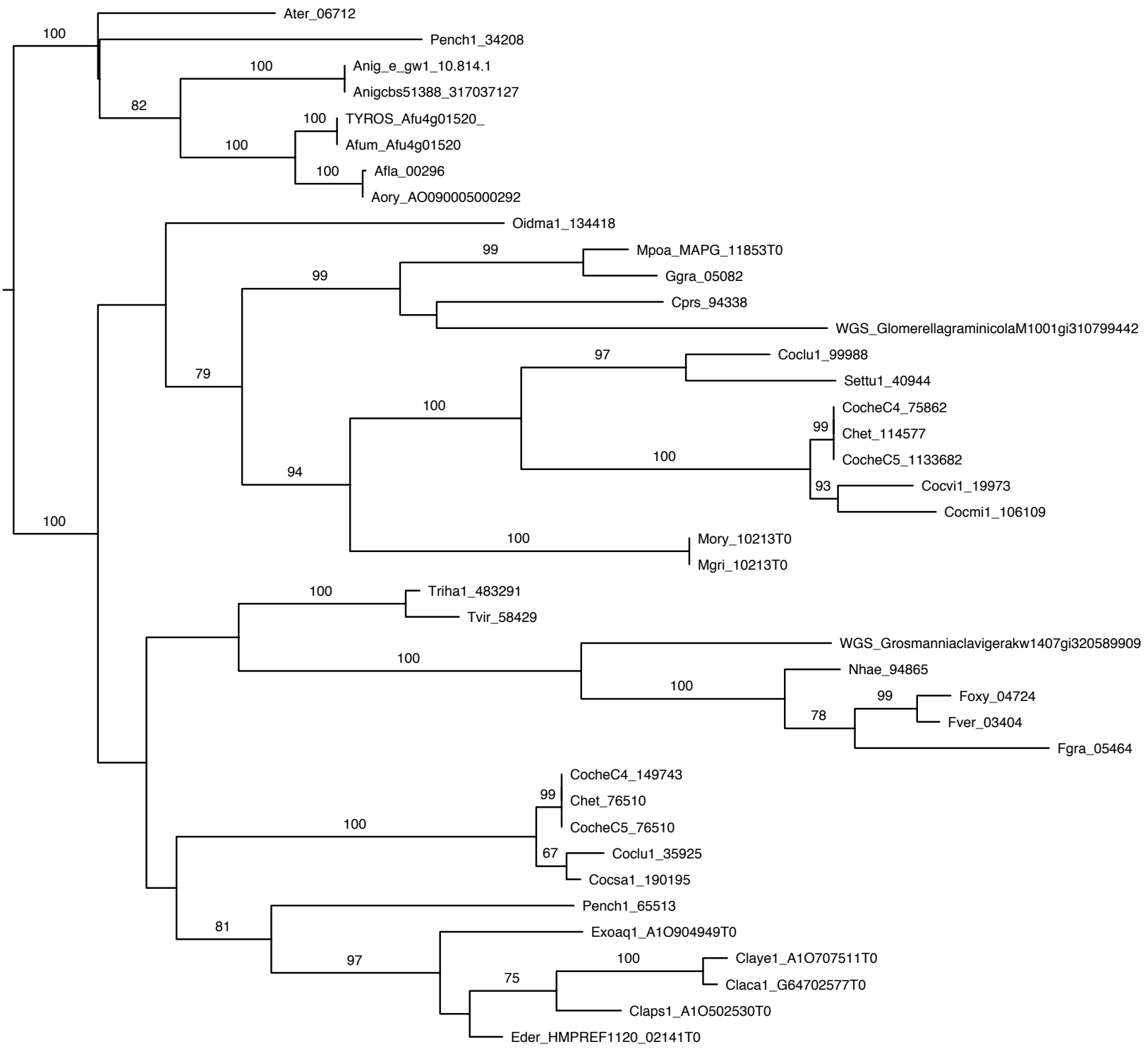
N. CTFG



0.4



O. GDOG



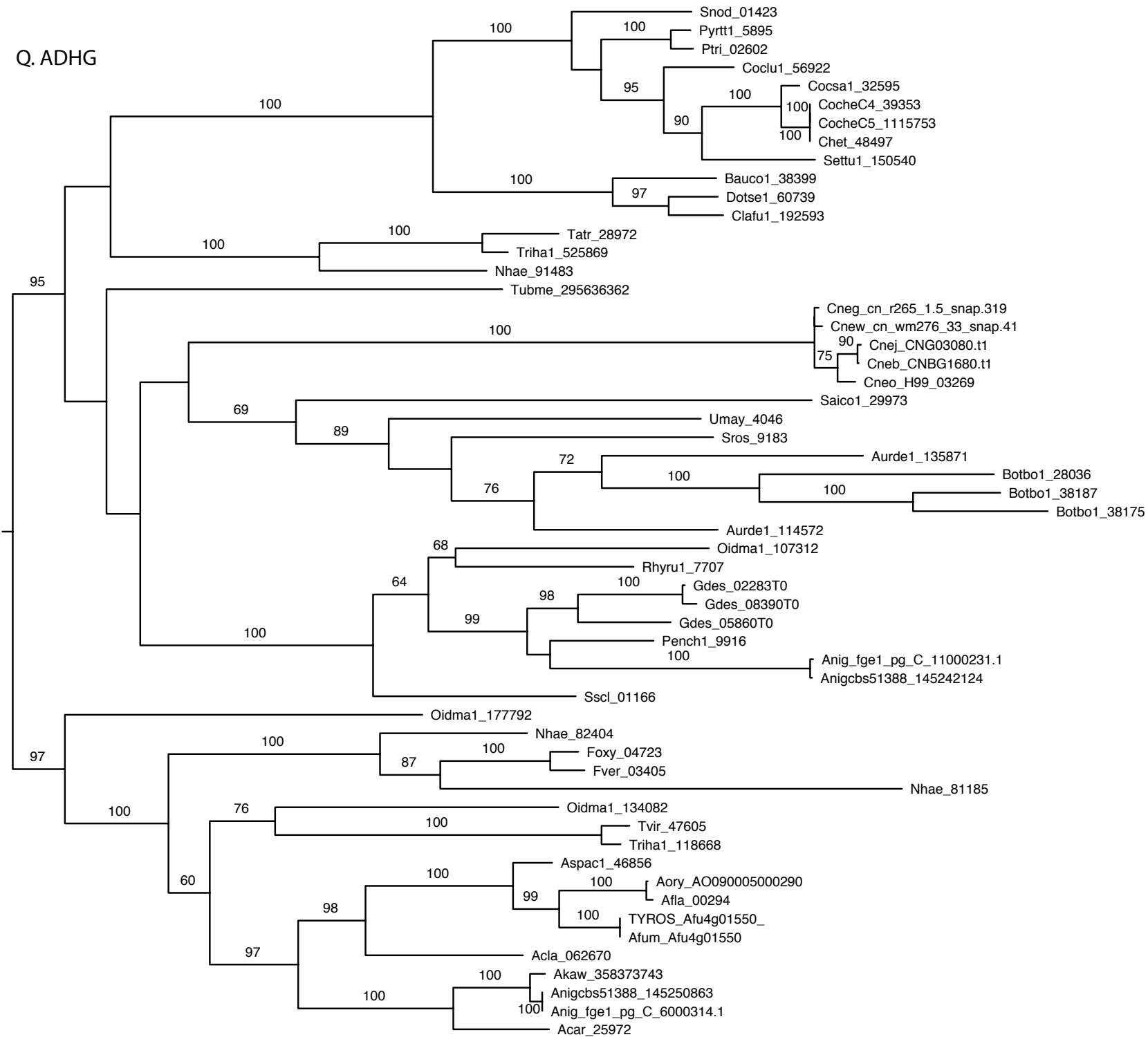
0.2

P. SAHG



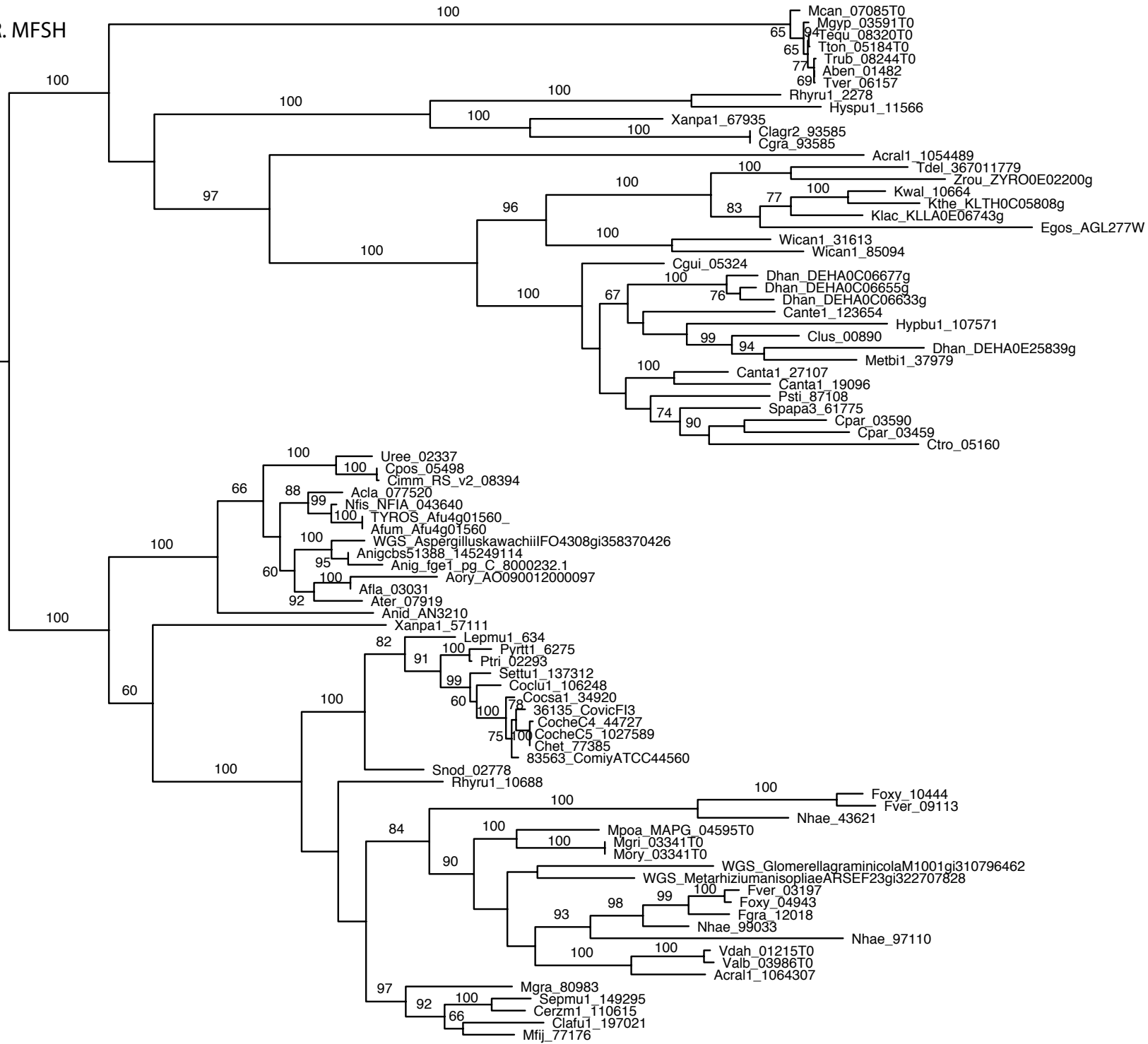
0.4

Q. ADHG



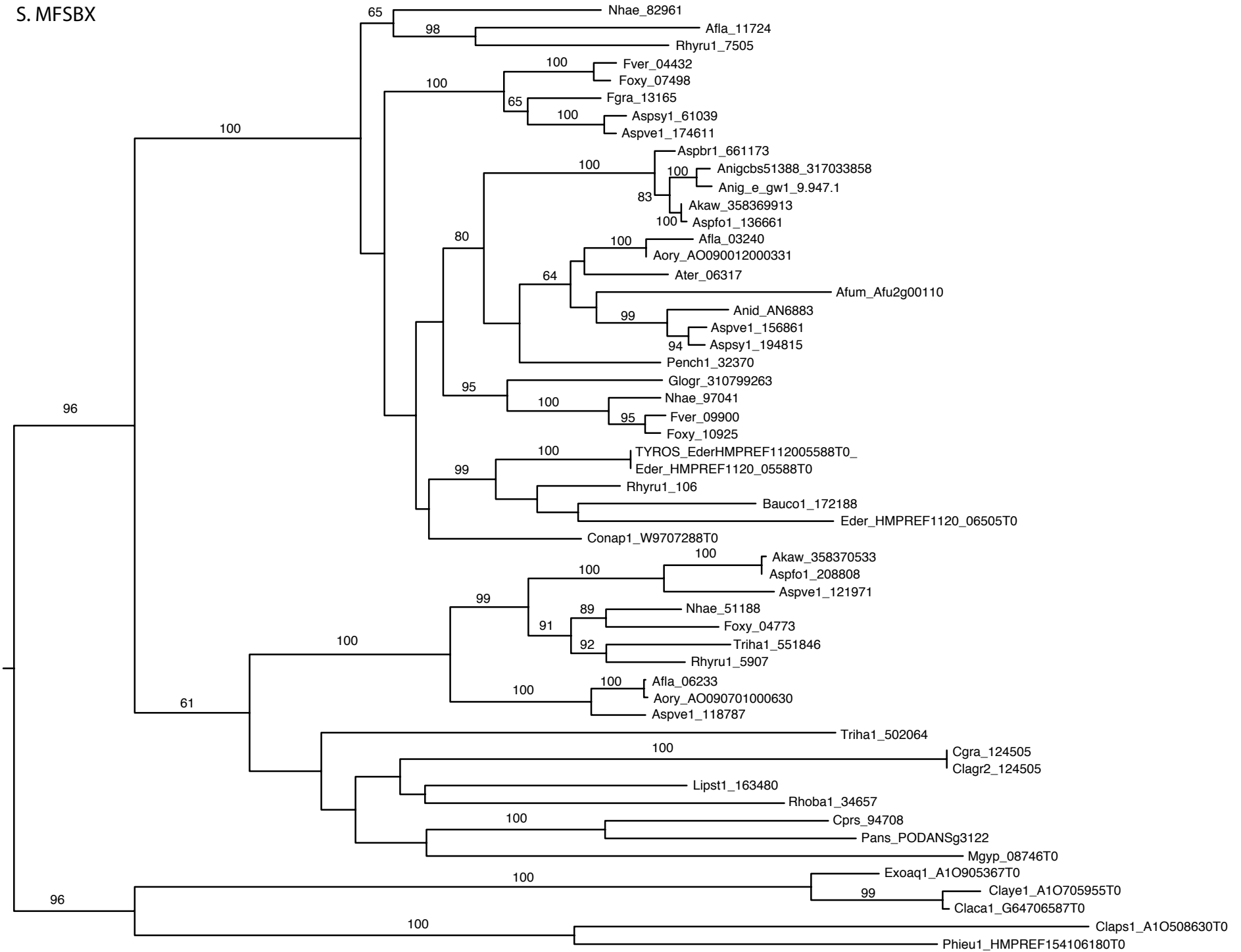
0.3

R. MFSH



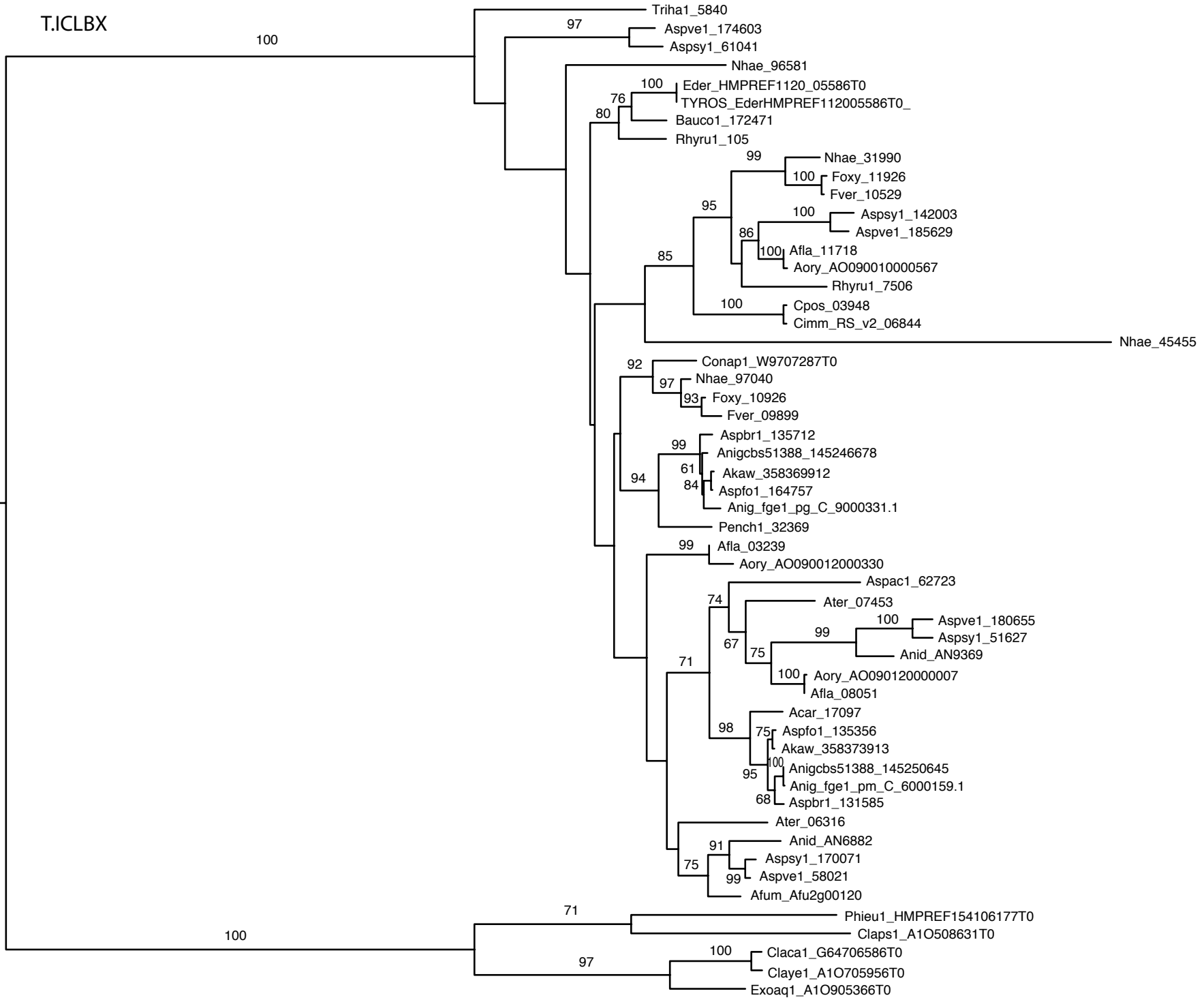
0.4

S. MFSBX



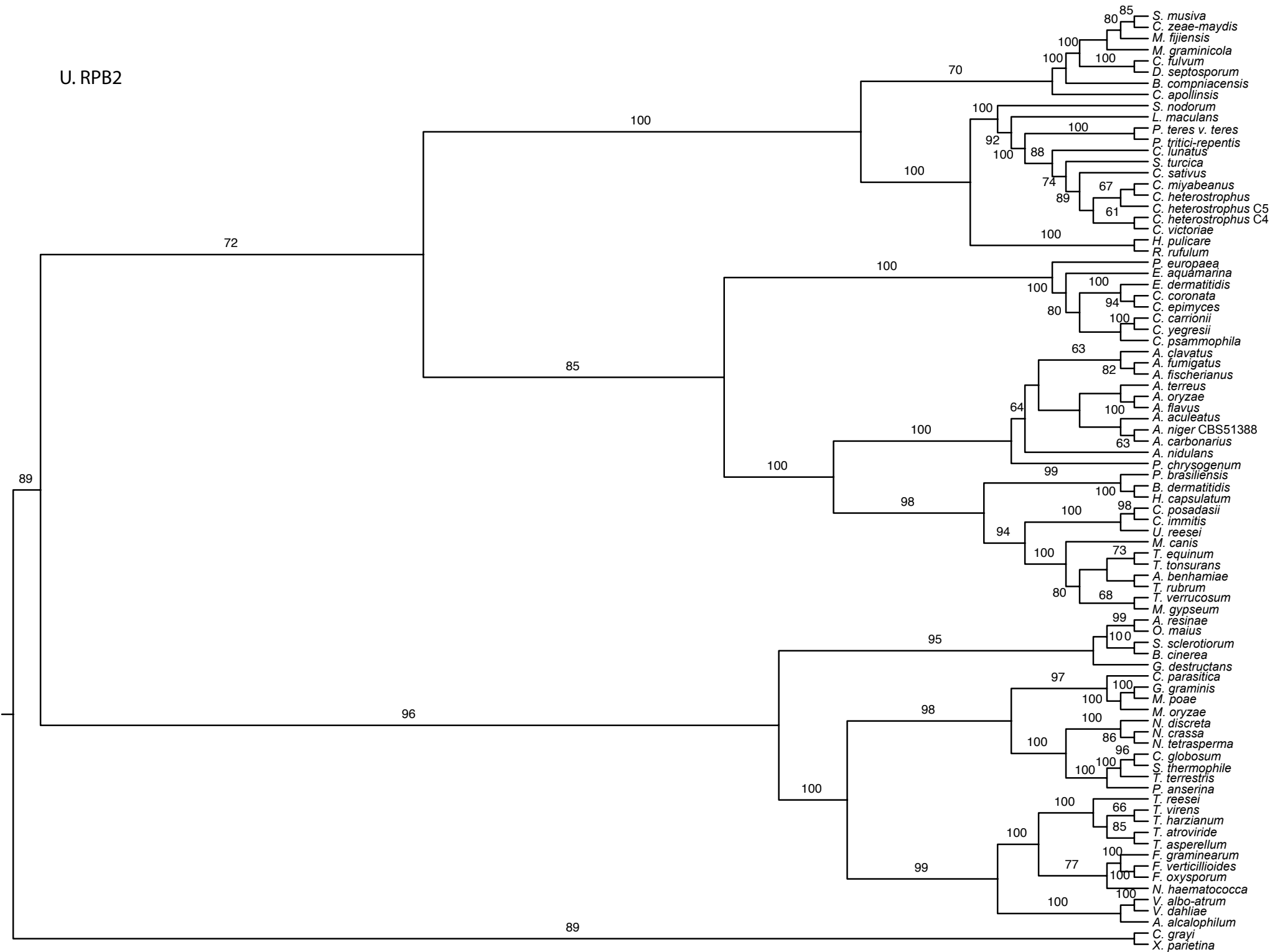
0.4

T.ICLBX



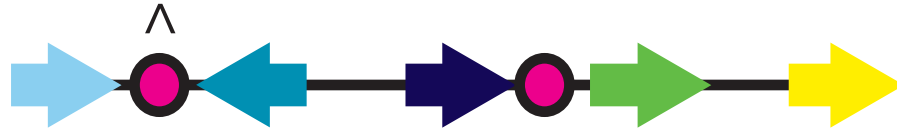
0.5

U. RPB2



## *O. maius*

Primary cluster



Scaffold 18: 884379-899328

Paralogous cluster



Scaffold 10: 892601-901355

## *E. dermatitidis*

Primary cluster



Supercontig 2: 1744551-1753834

Paralogous cluster 1



Supercontig 3: 1256091-1264197

Paralogous cluster 2



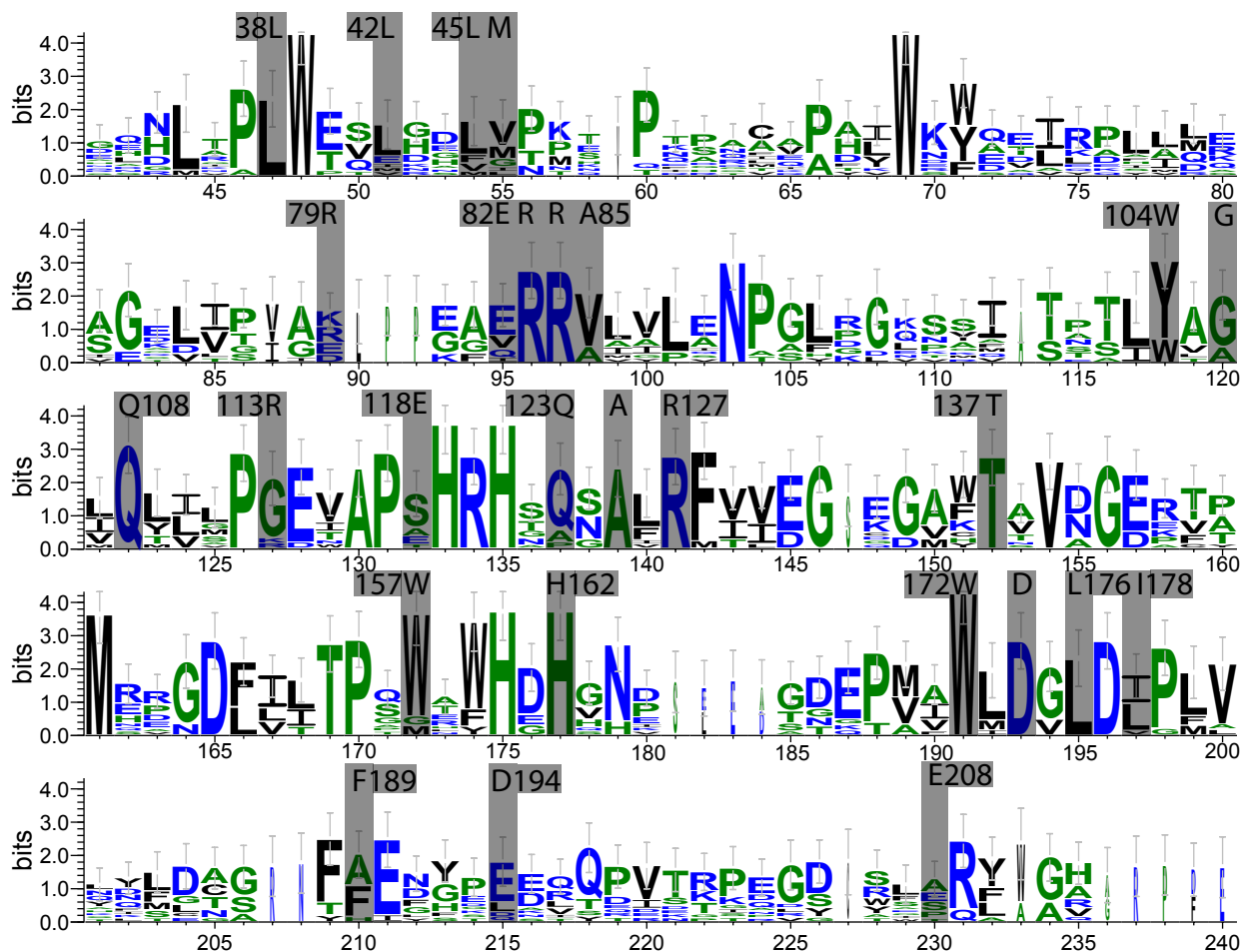
Supercontig 3: 727274-732304

### Gentisate Catabolism Clusters

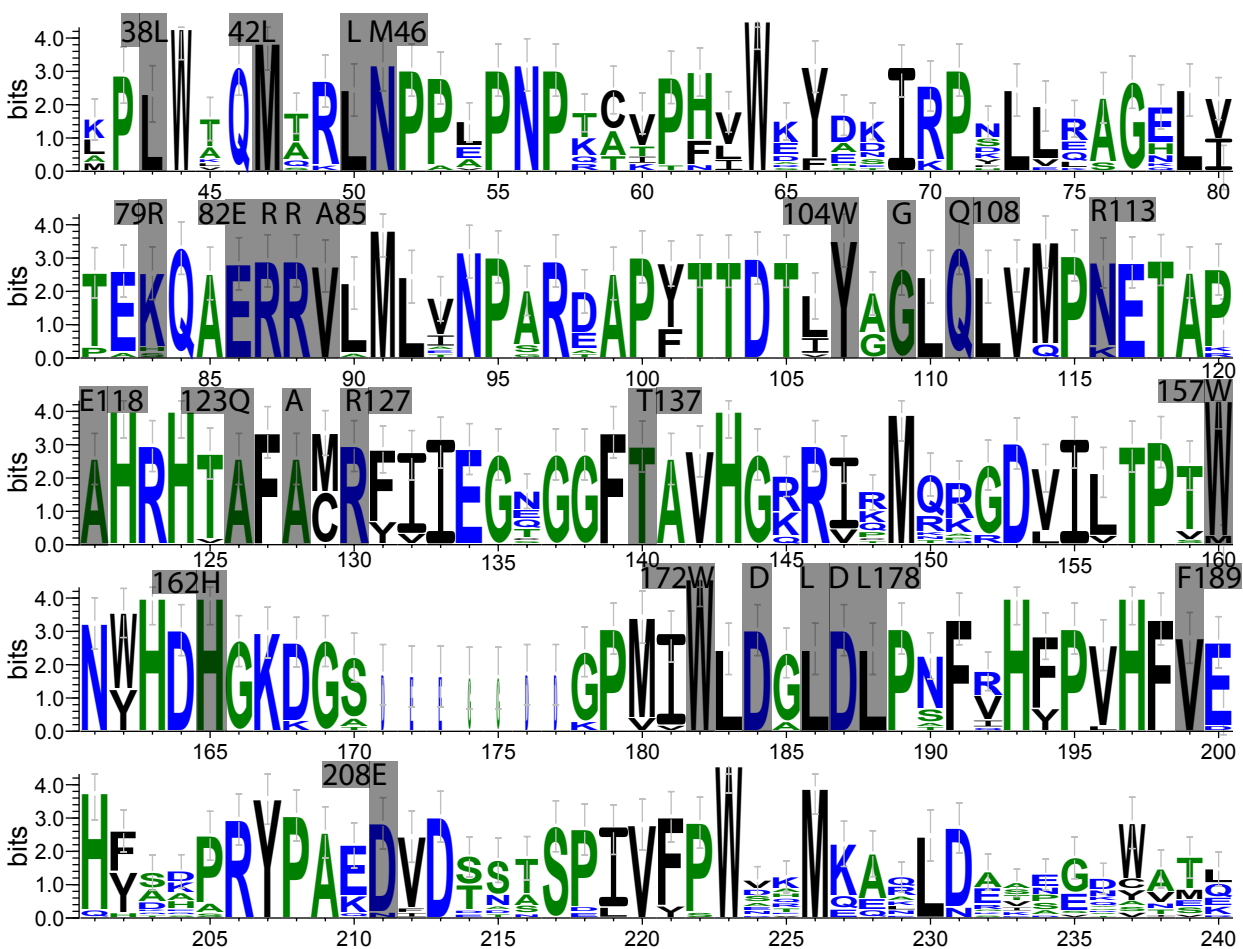
- MFS myo-inositol transporter, putative (*mfsh*)
- aldehyde dehydrogenase (*adhG*)
- salicylate hydroxylase (*sahG*)
- gentisate 1,2-dioxygenase oxidoreductase (*gdoG*)
- C6 transcription factor (*ctfG*)
- stilbene-alpha-beta-dioxygenase (*sdoG*)
- fumarylpyruvate hydrolase (*fphG*)
- MFS sugar transporter, putative (*mfsg*)



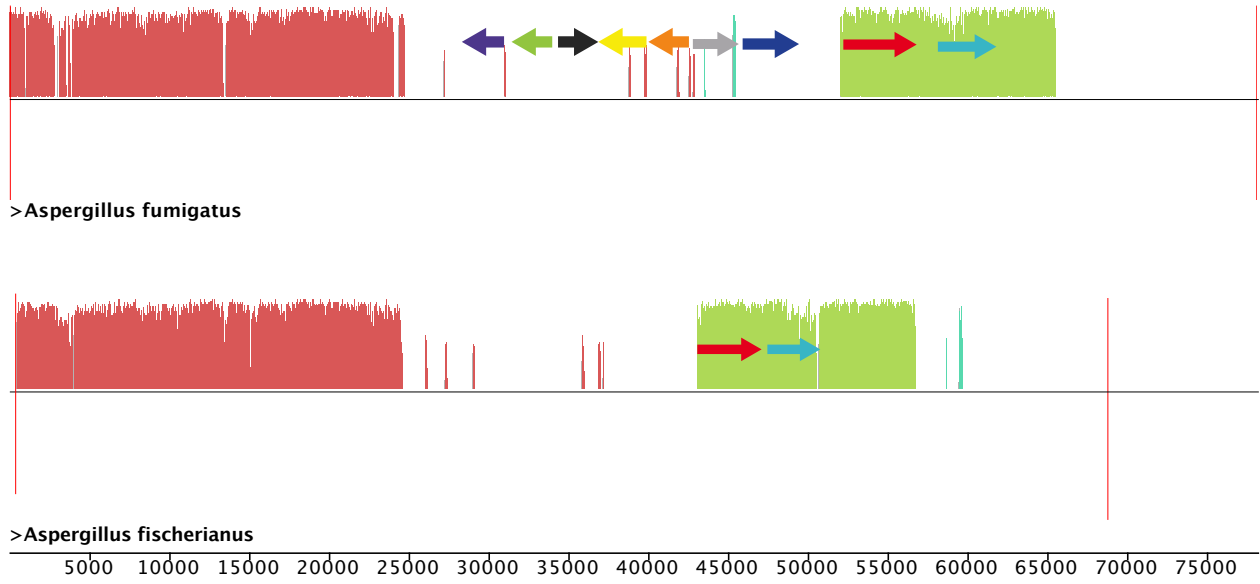
### A. Bacterial gentisate 1,2-dioxygenase alignment Logo



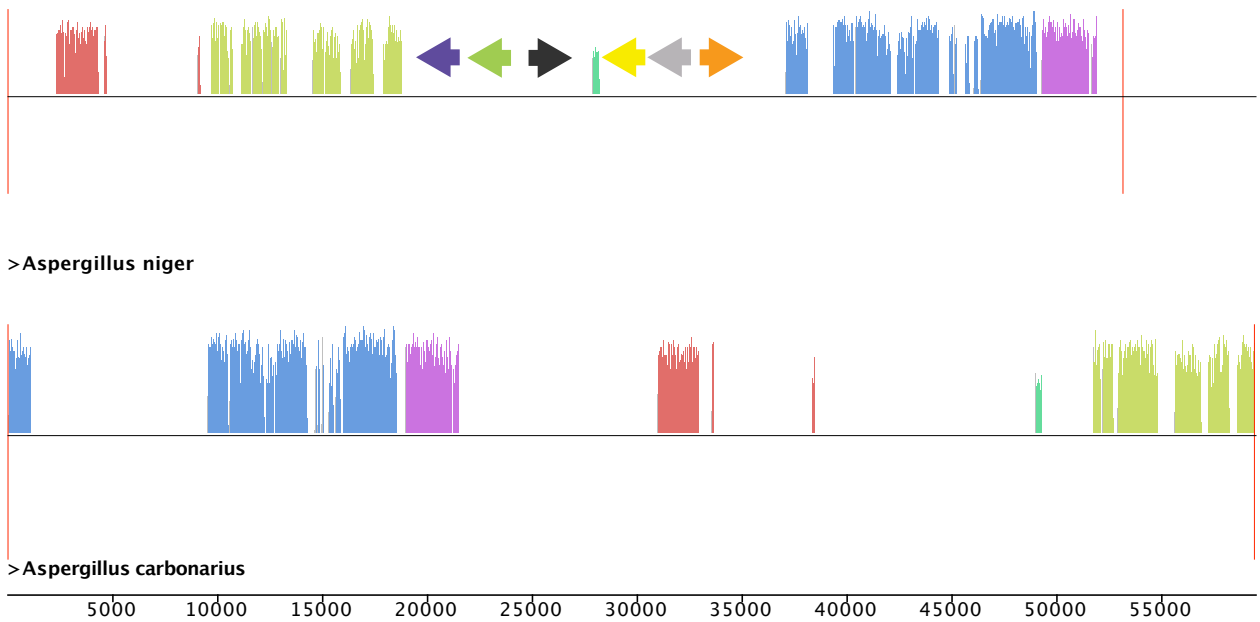
### B. Fungal gentisate 1,2-dioxygenase alignment Logo



A



B



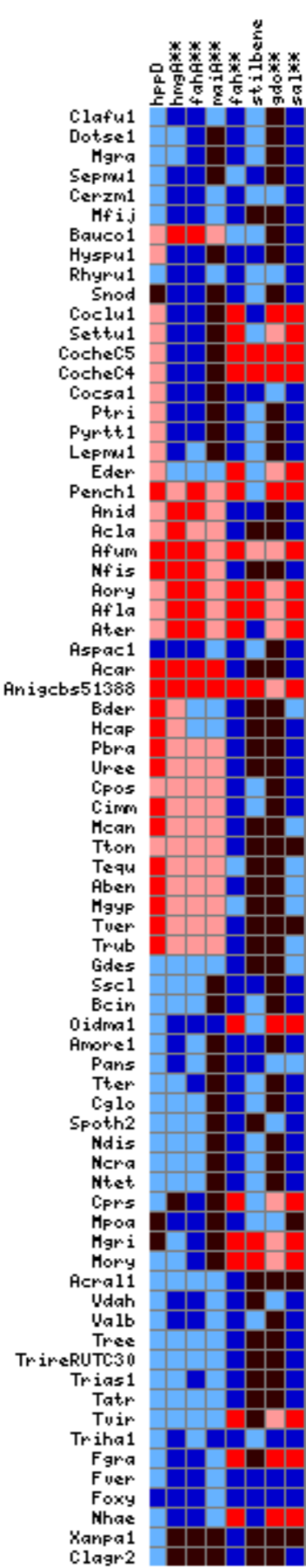


Table S1. Genomes analyzed in this study.

<b>Genome</b>	<b>Genome Code</b>	<b>Ecology</b>	<b>TD</b>	<b>GC +sdoG</b>	<b>GC -sdoG</b>
<b>Genomes in Figure 2</b>					
Acremonium alcalophilum	Acral1	sludge of pig manure compost	-	-	-
Amorphotheca resinae ATCC 22711	Amore1	jet fuel	-	-	-
Arthroderma benhamiae CBS 112371	Aben	human dermatophyte	+	-	-
Aspergillus aculeatus	Aspac1	soil, tomato, grape	+	-	-
Aspergillus carbonarius ITEM 5010	Acar	Grape berry, Brindis, Apulia, Italy. soil, manure, wheat,	+	-	-
Aspergillus clavatus NRRL 1	Acla	barley, maize	+	-	-
Aspergillus flavus NRRL 3357	Afla	corn, peanuts, cottonseed	+	+	-
Aspergillus fumigatus Af293	Afum	corn silage, lung tissue	+	+	-
Aspergillus nidulans FGSC A4	Anid	laboratory strain	+	-	-
Aspergillus niger	Anig	fruit, nuts, peanuts, cereal, meat, cheese	+	+	-
Aspergillus oryzae RIB40/ATCC 42149	Aory	cereal	+	+	-
Aspergillus terreus	Ater	soil, stored cereal	+	+	-
Baudonia compniacensis UAMH 10762	Bauco1	Exterior surfaces around distilleries	+	-	-
Blastomyces dermatitidis	Bder	soil, pathogen of mammals	+	-	-

Botrytis cinerea	Bcin	pathogen of plants: vegetables, fruits, shrubs, trees, flowers, weeds waterborne fungus associated with	-	-	-
Capronia coronata cbs 617.96	Capco1	plants hyperparasite associated with	-	-	-
Capronia epimyces cbs 606.96	Capep1	plants	+	-	-
Cercospora zea-maydis SCOH1-5	Cerzm1	pathogen of maize	-	-	-
Chaetomium globosum CBS 148.51	Cglo	decaying plant material	-	-	-
Cladonia grayi	Cgra	lichen	-	-	-
Cladophialophora psammophila cbs 110553	Claps1	hydrocarbon degrader	+	-	+
Cladophialophora yegresii cbs 114405	Claye1	epiphyte of cactus spines	+	-	+
Cladosporium fulvum	Clafu1	pathogen of tomato	-	-	-
Coccidioides immitis	Cimm	pathogen of humans	+	-	-
Coccidioides posadasii	Cpos	pathogen of humans	+	-	-
Cochliobolus heterostrophus C4	CocheC4	pathogen of maize	+	+	-
Cochliobolus heterostrophus C5	CocheC5	pathogen of sorghum; opportunistic	+	+	-
Cochliobolus lunatus m118	Coclu2	pathogen of humans	+	+	-
Cochliobolus sativus ND90Pr	Cocsa1	Tester for mating	+	-	-

Coniosporium apollinis cbs 100218	Conap1	type A rock-inhabiting fungus	-	-	-
Cryphonectria parasitica EP 155	Cprs	pathogen of chestnut trees	-	-	+
Dothistroma septosporum NZE10	Dotse1	pathogen of pine	-	-	-
Exophiala aquamarina cbs 119918	Exoaq1	marine animal pathogen	+	-	-
Exophiala dermatitidis UT8656	Eder	pathogen of humans	+	-	+
Fusarium graminearum	Fgra	pathogen of wheat and barley; endophyte	-	-	+
Fusarium oxysporum	Foxy	pathogen of fruit; endophyte	-	-	-
Fusarium verticillioides 7600	Fver	pathogen of maize; endophyte	-	-	-
Gaeumannomyces graminis var. tritici r3-111a-1	Gaegr1	pathogen of wheat and barley	-	-	+
Geomyces destructans 20631- 21	Gdes	brown bat bird/bat feces; pathogen of	-	-	-
Histoplasma capsulatum	Hcap	mammals	+	-	-
Hysterium pulicare	Hyspu1	Ascospore from Betula nigra	+	-	-
Leptosphaeria maculans	Lepmu1	pathogen of oilseed rape	+	-	-
Magnaporthe oryzae 70-	Mory	pathogen of rice	-	+	-

15(MG6)

Magnaporthe poae ATCC 64411	Mpoa	pathogen of rice	-	-	-
Microsporium canis CBS 113480	Mcan	Head of 3-year-old patient, Wurzburg, Germany.	+	-	-
Microsporium gypseum 118893	Mgyp	Skin of patient, Uganda.	+	-	-
Mycospharella fijiensis 10313	Mfij	pathogen of banana	-	-	-
Mycospharella graminicola 11395	Mgra	pathogen of wheat	-	-	-
Nectria haematococca MPV1	Nhae	plant pathogen, wide host range	-	-	+
Neosartorya fischeri NRRL 181	Nfis	soil, canned food	+	-	-
Neurospora crassa OR74A	Ncra	decaying plant material	-	-	-
Neurospora discreta FHSC 8579	Ndis	forest fire remains (trees)	-	-	-
Neurospora tetrasperma FGSC 2508 matA	Ntet	decaying plant material	-	-	-
Oidiodendron maius Zn	Oidma1	endophyte of ericaceous plants	-	-	+
Paracoccidioides brasiliensis Pb01	Pbra	human cervical lymph node, Belo Horizonte, Minas Gerais, Brazil	+	-	-
Penicillium chrysogenum Wis. 54-1255	Pench1	industrial strain	+	-	+
Podospora anserina	Pans	herbivore dung	-	-	-
Pyrenophora teres f. teres	Pyrtt1	pathogen of barley	+	-	-

<i>Pyrenophora tritici-repentis</i>	Ptri	Pathogen of grass saprobic with diverse habitats; wood of dicotyledonous plants	+	-	-
<i>Rhytidhysterium rufulum</i>	Rhyru1	moist soils, pathogen of wide variety of plants	+	-	-
<i>Sclerotinia sclerotiorum</i> ATCC 18683	Sscl	pathogen of poplars	-	-	-
<i>Septoria musiva</i> S02202	Sepmu1	pathogen of maize decaying plant	-	-	-
<i>Setosphaeria turcica</i> Et28A	Settu1	decaying plant material	+	+	-
<i>Sporotrichum thermophile</i>	Spoth2	pathogen of wheat	-	-	-
<i>Stagnospora nodorum</i> SN15	Snod	thermophile	+	-	-
<i>Thielavia terrestris</i> NRRL 8126	Tter	soil, endophyte, mycoparasite	-	-	-
<i>Trichoderma asperellum</i> CBS 433.97	Trias1	soil, endophyte, mycoparasite	-	-	-
<i>Trichoderma atroviride</i> IMI 206040	Tatr	soil, endophyte, mycoparasite soil, endophyte, mycoparasite, wood decay	-	-	-
<i>Trichoderma harzianum</i>	Triha1	soil, wood decay	-	-	-
<i>Trichoderma reesei</i>	Tree	soil, wood decay	-	-	-
<i>Trichoderma reesei</i> RUT C-30	TrireRUTC30	soil, wood decay soil, endophyte, mycoparasite	-	-	-
<i>Trichoderma virens</i> Gv29-8	Tvir	soil, endophyte, mycoparasite	-	-	+
<i>Trichophyton equinum</i> CBS 127.97	Tequ	horse	+	-	-
<i>Trichophyton rubrum</i> CBS	Trub	Patient with	+	-	-



118892		onychomycosis, Germany. cheek of man, Montreal, Quebec, Canada.			
Trichophyton tonsurans CBS 112818	Tton		+	-	-
Trichophyton verrucosum HKI0517	Tver	bovine	+	-	-
Uncinocarpus reesii 1704	Uree	soil	+	-	-
Verticillium albo-atrum	Valb	soil, pathogen of alfalfa, cotton, hops	-	-	-
Verticillium dahliae	Vdah	soil, pathogen of wide variety of plants	-	-	-
Xanthoria parietina 46-1	Xanpa1	lichen	-	-	-
<b>Other genomes investigated</b>					
Agaricus bisporus var. bisporus	Abibi				
Agaricus bisporus var. burnettii	Abibu				
Acidomyces richmondensis	Aciri1iso				
Allomyces macrogynus	Amac				
Aspergillus niger	Anigcbs51388				
Ascoidea rubescens NRRL Y17699	Ascru1				
Aspergillus brasiliensis	Aspbr1				
Aspergillus acidus	Aspfo1				
Aspergillus sydowii	Aspsy1				
Aspergillus versicolor	Aspve1				
Auricularia delicata SS-5	Aurde1				
Aureobasidium pullulans var. subglaciale EXF-2481	Aurpuvarsub1				

Babjeviella inositovora NRRL Y-12698	Babin1
Batrachochytrium dendrobatidis	Bden
Bjerkandera adusta	Bjead1
Botryobasidium botryosum	Botbo1
Candida albicans	Calb
Candida arabinof fermentans NRRL YB-2248	Canar1
Candida caseinolytica Y-17796	Canca1
Candida tanzawaensis NRRL Y-17324	Canta1
Candida tenuis NRRL Y-1498	Cante1
Catenaria anguillulae PL171	Catan1
Coprinopsis cinerea	Ccin
Candida glabrata	Cgla138
Candida guilliermondii	Cgui
Cochliobolus heterostrophus	Chet
Cladophialophora carrionii cbs 160.54	Claca1
Cladonia grayi(newer annotation)	Clagr2
Candida lusitaniae	Clus
Cryptococcus neoformans	Cneb
Cryptococcus gattii	Cneg
Cryptococcus neoformans	Cnej
Cryptococcus neoformans var. grubii	Cneo
Cryptococcus gattii	Cnew

Cochliobolus carbonum 26-R-13	Cocca1
Cochliobolus miyabeanus ATCC 44560	Cocmi1
Cochliobolus victoriae FI3	Cocvi1
Coemansia reversa NRRL 1564	Coere1
Conidiobolus coronatus NRRL28638	Conco1
Coniophora puteana	Conpu1
Candida parapsilosis	Cpar
Cronartium quercuum f. sp. fusiforme G11	Croqu1
Ceriporiopsis subvermispora	Csub
Candida tropicalis	Ctro
Dacryopinax sp. DJM 731 SSP1	Dacsp1
Dekkera bruxellensis CBS 2499	Dekbr2
Debaryomyces hansenii	Dhan
Dichomitus squalens	Dicsq1
Encephalitozoon cuniculi	Ecun
Eremothecium cymbalariae	Ecym
Eremothecium gossypii	Egos
Encephalitozoon intestinalis ATCC 50506	Eint
Fomitiporia mediterranea	Fomme1
Fomitopsis pinicola SS1	Fompi1
Galerina marginata	Galma1
Gonapodya prolifera	Ganpr1
Gloeophyllum trabeum	Glotr1
Gymnopus luxurians	Gymlu1

<i>Heterobasidion annosum</i>	Hann
<i>Hanseniaspora valbyensis</i> NRRL Y-1626	Hanva1
<i>Hebeloma cylindrosporum</i> h7	Hebcy1
<i>Hansenula polymorpha</i>	Hpol
<i>Hydnomerulius pinastri</i>	Hydpi1
<i>Hydnomerulius pinastri</i>	Hydpi2
<i>Hyphopichia burtonii</i> NRRL Y-1933	Hypbu1
<i>Hypholoma sublateritium</i>	Hypsu1
<i>Jaapia argillacea</i>	Jaaar1
<i>Kluyveromyces lactis</i>	Klac
<i>Kluyveromyces thermotolerans</i>	Kthe
<i>Kluyveromyces waltii</i>	Kwal
<i>Laccaria bicolor</i>	Lbic
<i>Lodderomyces elongisporus</i>	Lelo
<i>Lipomyces starkeyi</i> NRRL Y-11557	Lipst1
<i>Mucor circinelloides</i>	Mcir
<i>Metschnikowia bicuspidata</i> NRRL YB-4993	Metbi1
<i>Malassezia globosa</i>	Mglo
<i>Mixia osmundae</i> IAM 14324	Mixos1
<i>Melampsora laricis-populina</i>	Mlar
<i>Nadsonia fulvescens</i> var. <i>elongata</i> DSM 6958	Nadfu1
<i>Paxillus involutus</i> ATCC 200175	Paxin1
<i>Phycomyces blakesleeanus</i>	Pbla
<i>Phanerochaete chrysosporium</i>	Pchr

<i>Puccinia graminis</i> f. sp. <i>Tritici</i>	Pgra
<i>Phanerochaete carnosae</i> HHB-10118-Sp	Phaca1
<i>Phialophora europaea</i> cbs 101466	Phieu1
<i>Phlebiopsis gigantea</i>	Phlgi1
<i>Pichia membranifaciens</i>	Picme2
<i>Piloderma croceum</i> F 1598	Pilcr1
<i>Piromyces</i> sp. E2	PirE2
<i>Pisolithus microcarpus</i> 441	Pismi1
<i>Pisolithus tinctorius</i> Marx 270	Pisti1
<i>Plicaturopsis crispa</i>	Plicr1
<i>Postia placenta</i> MAD-698-R-SB12	PosplRSB12
<i>Pleurotus ostreatus</i>	Post
<i>Pichia pastoris</i> GS115	Ppas
<i>Postia placenta</i>	Ppla
<i>Pichia stipitis</i>	Psti
<i>Punctularia strigosozonata</i>	Punst1
<i>Puccinia triticina</i> 1-1BBBD Race 1	Putr
<i>Rhodotorula graminis</i> strain WP1	Rhoba1
<i>Rhizopus oryzae</i>	Rory
<i>Saitoella complicata</i> NRRL Y-17804	Saico1
<i>Saccharomyces bayanus</i>	Sbay
<i>Saccharomyces castellii</i>	Scas
<i>Saccharomyces cerevisiae</i>	Scer

<i>Scleroderma citrinum</i> Foug A	Sclici1
<i>Schizophyllum commune</i>	Scom
<i>Sebacina vermifera</i> MAFF 305830	Sebve1
<i>Serpula lacrymans</i> S7	SerlaS7
<i>Serpula lacrymans</i> var shastensis SHA21-2	Serlavarsha1
<i>Schizosaccharomyces japonicus</i>	Sjap
<i>Saccharomyces kluuyveri</i>	Sklu
<i>Saccharomyces kudriavzevii</i>	Skud
<i>Serpula lacrymans</i>	Slac
<i>Saccharomyces mikatae</i>	Smik
<i>Schizosaccharomyces</i> octosporus	Soct
<i>Schizosaccharomyces</i> cryophilus	Soyt
<i>Spathaspora passalidarum</i> NRRL Y-27907	Spapa3
<i>Saccharomyces paradoxus</i>	Spar
<i>Sphaerobolus stellatus</i>	Sphst1
<i>Schizosaccharomyces pombe</i>	Spom
<i>Spizellomyces punctatus</i>	Spun
<i>Sporobolomyces roseus</i>	Sros
<i>Stereum hirsutum</i> FP-91666 SS1	Stehi1
<i>Tremella mesenterica</i> Fries	Tmes
<i>Tetrapisispora phaffii</i> CBS 4417	Tpha
<i>Trametes versicolor</i>	Trave1
<i>Tulasnella calospora</i> AL13/4D	Tulca1
<i>Ustilago maydis</i>	Umay

Vanderwaltozyma_polyspora	Vpol
Wickerhamomyces anomalus	Wican1
Wolfiporia cocos MD-104 SS10	Wolco1
Yarrowia lipolytica	Ylip
Zygosaccharomyces rouxii	Zrou

Table S2. Comparison of function-related residues among gentisate 1,2 dioxygenase homologs in fungi and bacteria.

<b>function</b>	<b><i>P. salicylatoxidans</i></b>	<b>Bacteria</b>	<b><i>A. fumigatus</i></b>
Active site, conserved; stabilizes 4°	Leu(38)	Leu	Leu(31)
Closure of active site	Leu(42)	L/E/I/M/V	Met
Active site	Leu(45)	L/F/V/M	Leu(38)
Active site	Met(46)	V/M/G/I/L	Asn(39)
Closure of active site	Arg(79)	K/R/E/D	Lys
Active site	Glu(82)	E/V/Q/I	Glu(74)
Active site; closure of AS; stabilizes 4°	Arg(83)	Arg	Arg(75)
	Arg(84)	Arg	Arg(76)
Active site; stabilizes 4°	Ala(85)	Val>Ala	Val(77)
Active site	Trp(104)	Tyr>Trp	Tyr(95)
Substrate selection/binding	Gly(106)	Gly>>Ala	Gly(97)
Active site, conserved	Gln(108)	Gln	Gln(99)
	Arg(113)	Gly>K/R	Asn(104)
Active site closure	Glu(118)	S/A/E/T	Ala
Active site	Gln(123)	Q>A/P	Ala(114)
Active site; Coordination of metal ion/substrate	Ala(125)	Ala	Ala(116)
Active site, conserved	Arg(127)	Arg	Arg(118)
Active site	Thr(137)	Thr	Thr(128)
Hydrophobic shielding of active site	Trp(157)	Trp>G/M	Trp(148)
Active site, conserved	His(162)	His	His(153)
Active site, conserved	Trp(172)	Trp	Trp(163)
Active site, conserved	Asp(174)	Asp	Asp(165)
Active site, conserved	Leu(176)	Leu	Leu(167)
Active site	Ile(178)	I/L/V	Ile(169)
Stabilizes 4°	Phe*(189)	Y/G/H/F/S	Val(180)
Closure of active site	Asp(194)	E/L/D/Q	-
	Gln(208)	A/E/S/P/T	