

Putative Fusion 1

September 26, 2012

1 Fasta Sequences

These are the unfused sequences identified by fdfBLAST belonging to the putative gene fusion in FASTA format. Accessions may be shortened, but belong to either the taxons individual genome project or NCBI's accession numbering.

```
>lcl|SPBC29A302c unnamed protein product
MALLPFFDLTNFESDASEELGWLKYVGRVQTRVFPQHFKDNLEVKRISSETIDVIVDTTA
ELGPEACVNLLNAGALAILVNEEMLNELADISPRLVLKTDTTDIGKIEKLSQVAGSIQW
IGSAENYPPDFFERASKIIHKAVMPEGGGRTLYLEFPEQPSMEVLKSFSVHSVVPVLSSS
FLTVKPAEPPKKLSSLADLILISANTDREDGLFSTLVNELGIALGLVYSSKESVAESLKT
GTGVYQSRKRGWYKGASSGAVQHLIHIDVDCDEDCLRFVVYQTGKGFCHLDTLHCFGQA
SGLCQLEKTLIDRKNNAAPEGSYTARLFSDPKLLRAKIMEEAELCDATTKENVIWEMADL
MYFAITRCVGSGVSLNDISRHLDLKHRKVTRRKGDAKVAWQEKLKDGGVANTSYTA
>lcl|SPBC171113 unnamed protein product
MPEYEIQVPSYRAAALTAEERTLLARPIQNTQKIRTIVQPIIEDVKSRGAEASLIDYASK
FEKVQLKSAVLKAPFDDLMKISPMIKEDIDIAFNNIFAFHSSQLRPTIAVQTMRGVVCQ
RMSRPINRVGLYIPGGTAVLPSTALMLGPVAKVAGCPHVVISTPVRKDGTVAPEIVYIAN
KIGAEAIILAGGAQAIAMAYGISGVPKVNKFPGPNQFVTAAKMHVQNDY GALVAIDLPA
AGPSEVLVIADETCNPESVALDLLSQAEHGLDSQIILLTVSLSPEMFDRIQKAINDHALR
LSRSYIICKHAIKSVIVQVDNVDQAFEWSNLGYGPEHLVLHLKNASSYIPKIDNAGSVFVG
PWSPVSMGDYASGTNHTLPTYGYASSYSGVSTDLSFLKYITTQELTEEGIQRLGPTVIRLA
ELEGLTAAHADAVRVRGVRL
```

2 Annotated Phylogenograms

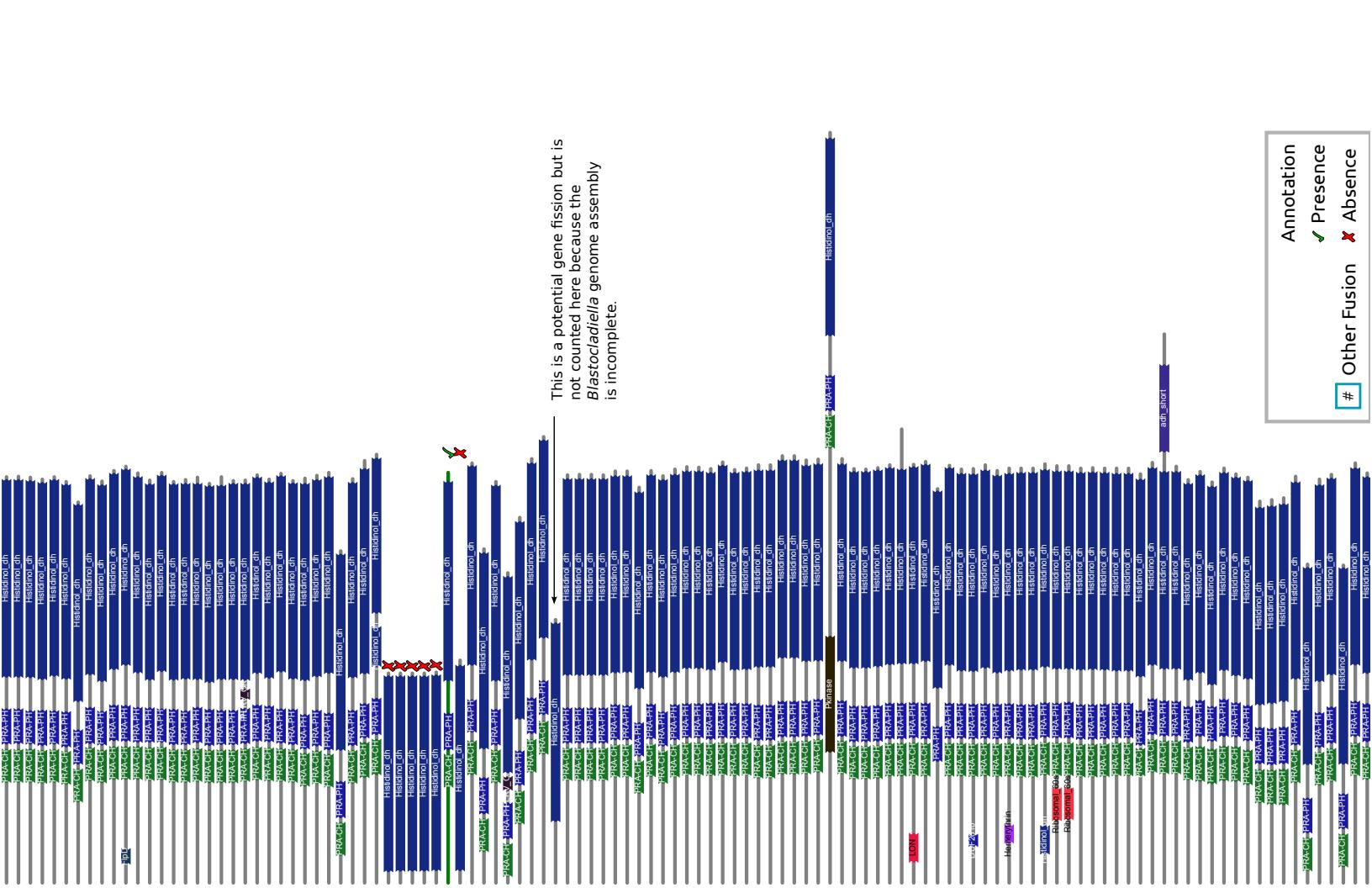
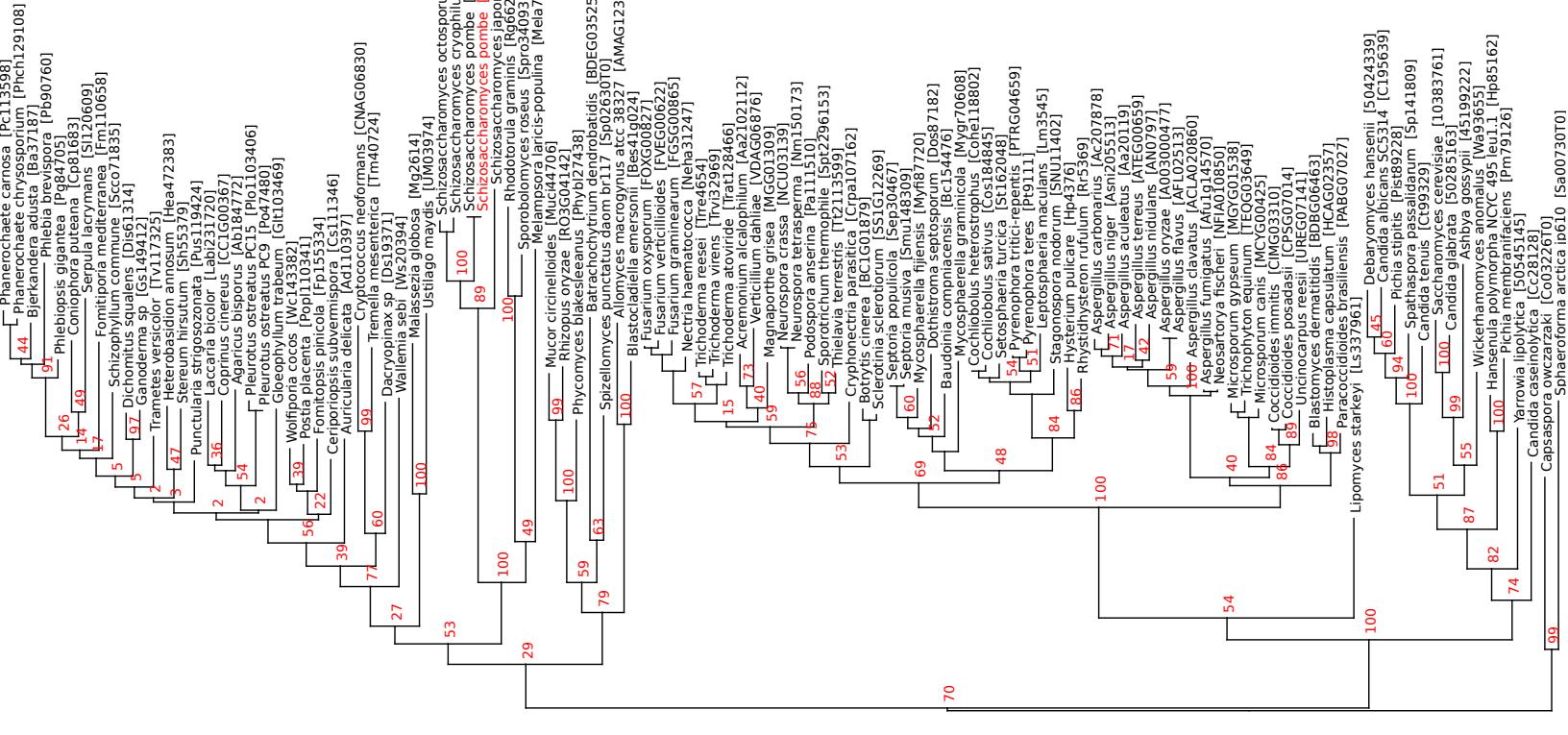
All trees were generated from an initial run of Darren's Orchard pipeline against 139 taxa (Table S1), using the above corresponding un-fused sequences as BLAST seeds. The alignments were then checked for any missing taxa, manually masked and then ProtTest3 was run, please see the Methods section for detail. The final trees were generated by the following command:

```
phyml -i alignment_file -d aa -b 100 -m model -c 8 -v invariant_sites -s BEST --quiet
-a gamma
```

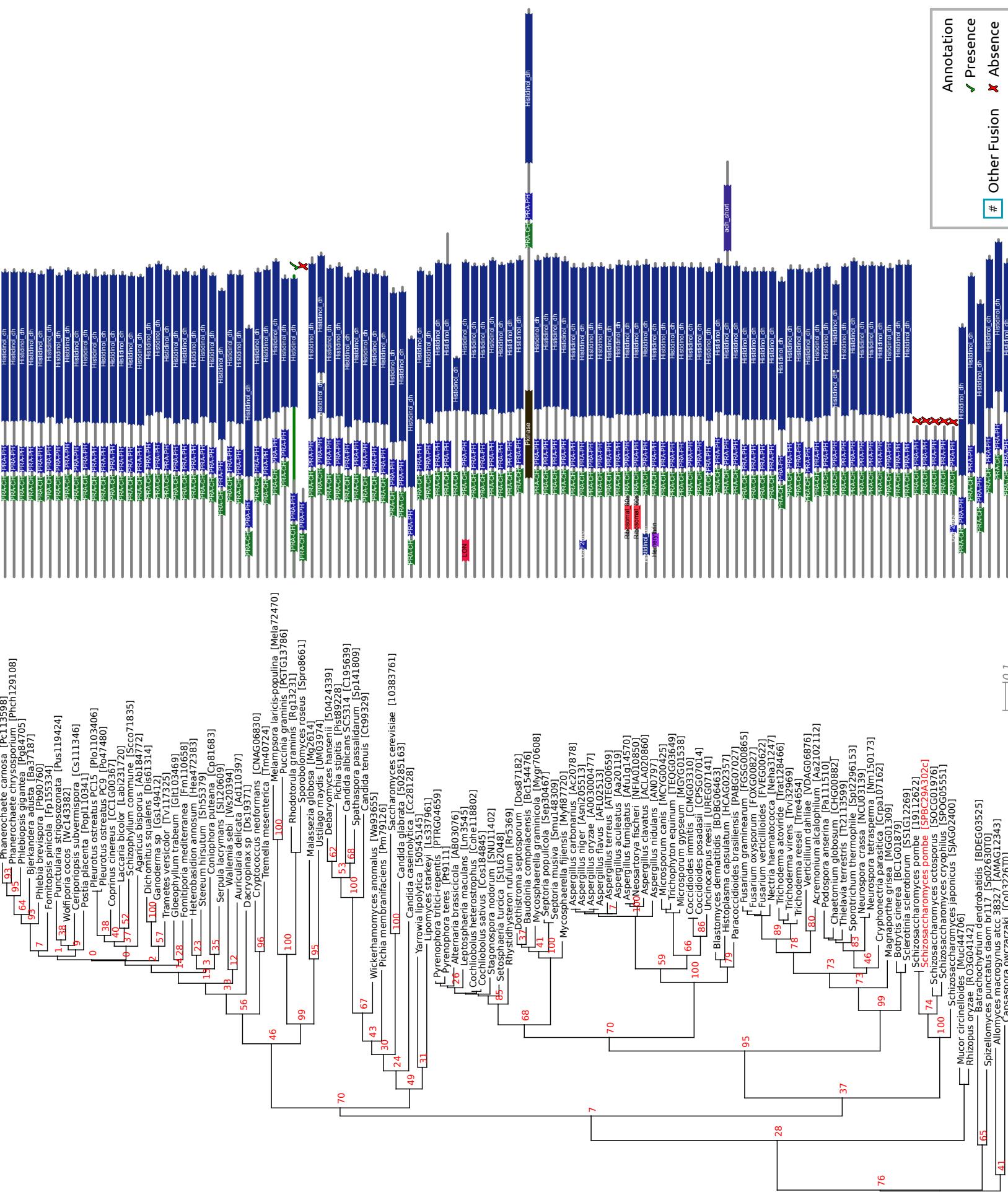
Styling and annotation was made possible by Dendroscope and Inkscape.

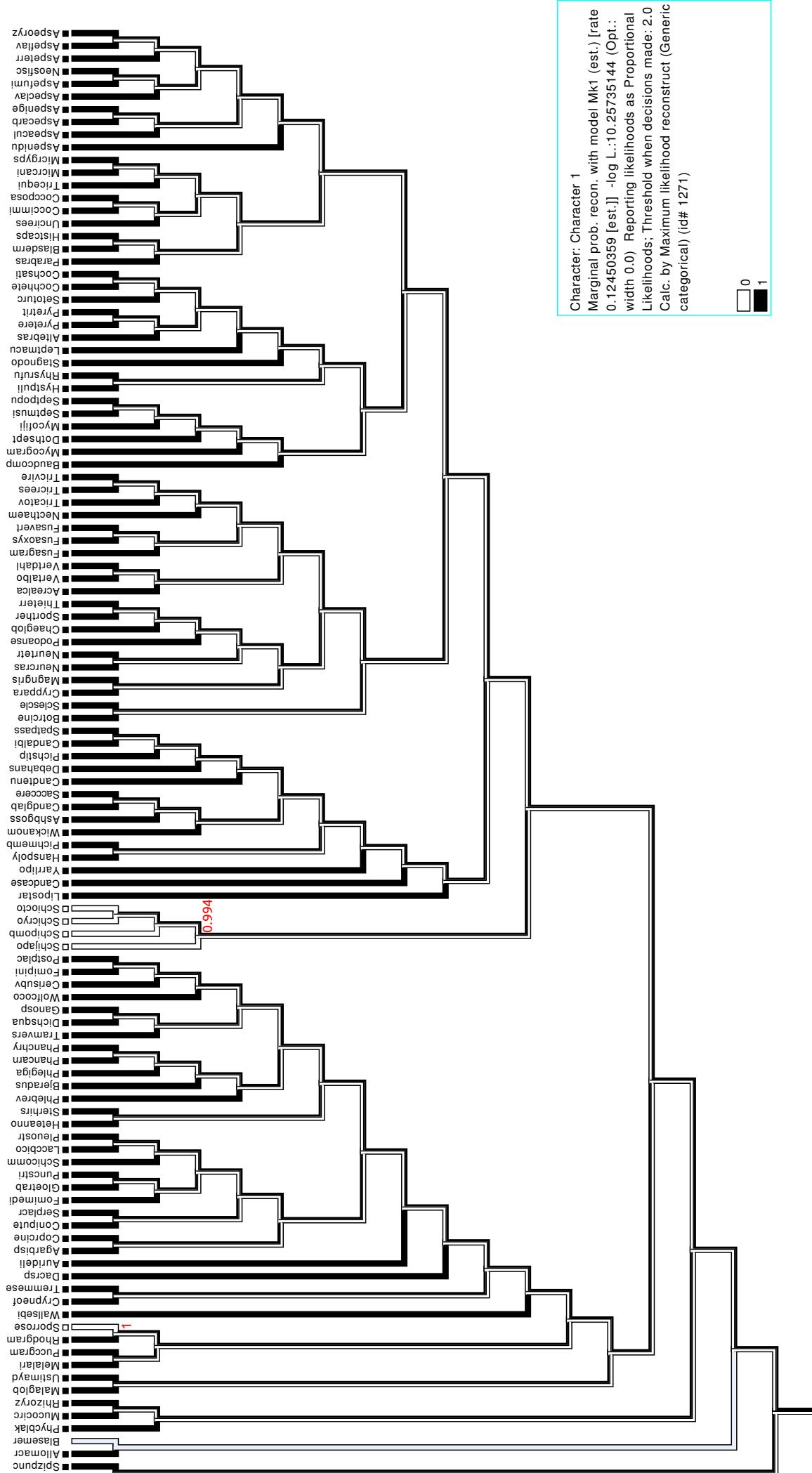
3 Mesquite Cladogram

This tree is the 68-gene concatenated phylogeny (Fig. 1), with the presence of a fusion (black), presence of a fission (white), and absent/undetermined (grey) status of gene fusion characters plotted on to it using a "1/0/-" nexus-style data matrix. We used the program 'Mesquite' to calculate proportional likelihoods based on either an "Mk1" or "Assym. 2 param model." (see Table S4) of character change across the fungal phylogeny (Fig. 1). This allowed for a proportional likelihood of the position of the fusion/fission to be calculated.



Annotation
Presence
Absence





Putative Fusion 2

September 26, 2012

1 Fasta Sequences

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```
>lcl|Mc157403 unnamed protein product
MVQKAVLVTGGAGYIGSHTVIELLNAGREVVIYDNLYNASYEAVRRIEQISGKKPHFYKADILDKKALLEVFSRHPIDS
IHFLAGLKAVGESTQIPLDYNNITGTIVLLQAMKEANVKNIVFSSSATVYGEPPVPIPETSPTDAKSPYGRTKLFVEH
IIRDLCTAEKDWNAAALLRYFNPAGAHPSGILGENPTGVPNNLMPYFSQVAIGKREYLSVFGNDYPTRDGTCIRDYIHVVD
LAEGHLAALKLEDNPGCVEYNLGTGVGSTVLEMVHAFQKAVGREL PYKIA PRRPGDVPDLTADPAKANKELGWKVKFSL
EDACASLWNWQSKNPEGLEGYPSEAPSECVINYL
>lcl|Mc156734 unnamed protein product
MPVTKLTIAPIGVDQYTLINKSKTLAVMVLTYGAVISHVLTPDKTGAVRDVVLGFDDFESYKNPANPYFGAVVGRYGNRIG
KGQFTVDGKDQLAINNGPNALHGLEFDKRIWTATVVSEEPASVRLELVSPDGDQGYPGTVTTQLTYTVTDNDELILE
YHATTDKDTVINLTNSYFNLSGVELNPNI LDHRVTMTDEVKAVLECDGDCPTGKVLSWSEPVWMNFSGENAGKPIGAR
LENLQGTRGYDH PYVIHSDYKTDTAGLPLRKA AVVYSPDTGIELEFSTTEPAFQFYTG WIASDKMTAKDQAGAKIGPA
SGFCLEASRNPDSPNKP DWRSATLLQDG VYSQKTVYAFHARLD
```

2 Annotated Phylogenograms

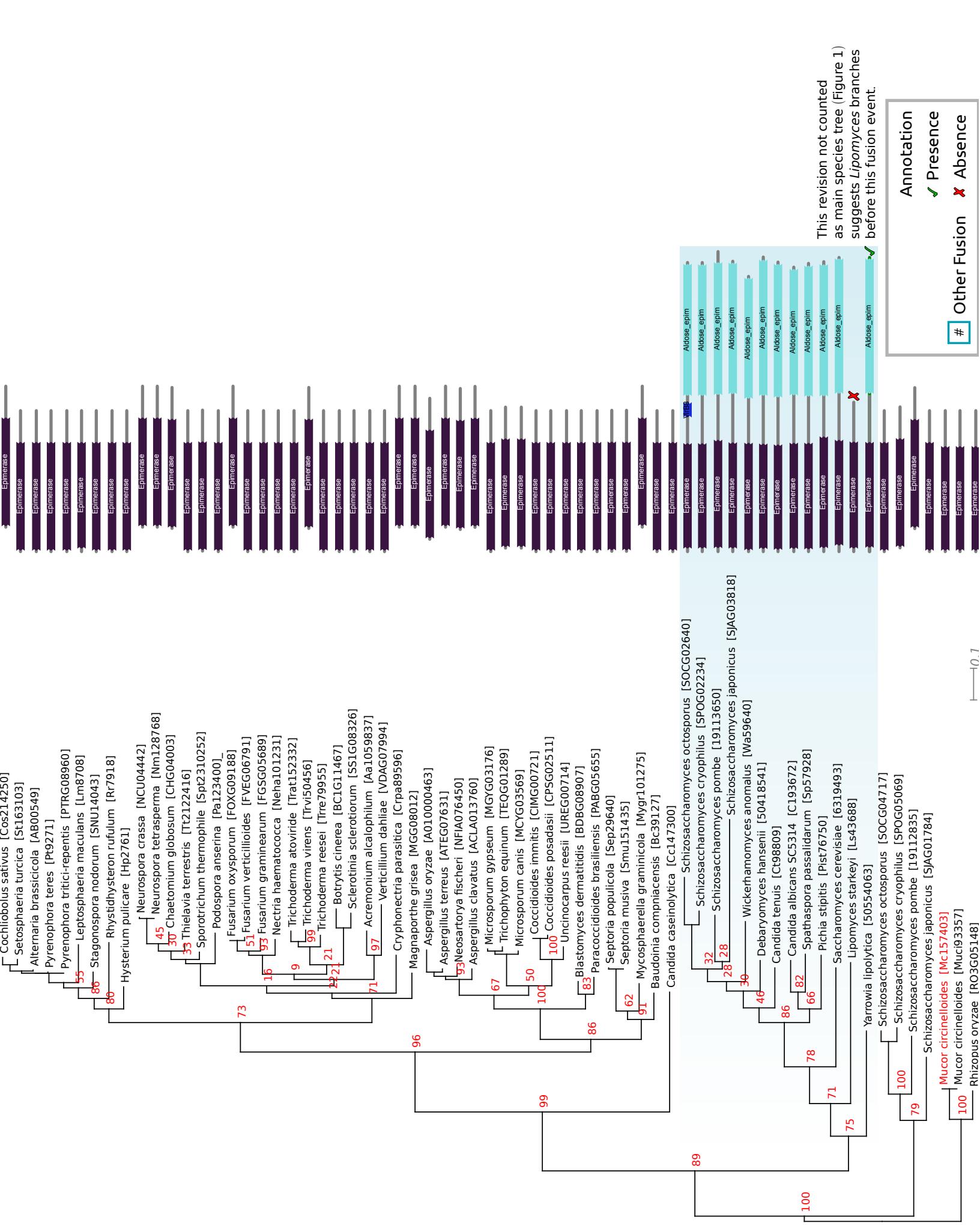
All trees were generated from an initial run of Darren's Orchard pipeline against 139 taxa (Table S1), using the above corresponding un-fused sequences as BLAST seeds. The alignments were then checked for any missing taxa, manually masked and then ProtTest3 was run, please see the Methods section for detail. The final trees were generated by the following command:

```
phyml -i alignment_file -d aa -b 100 -m model -c 8 -v invariant_sites -s BEST --quiet
-a gamma
```

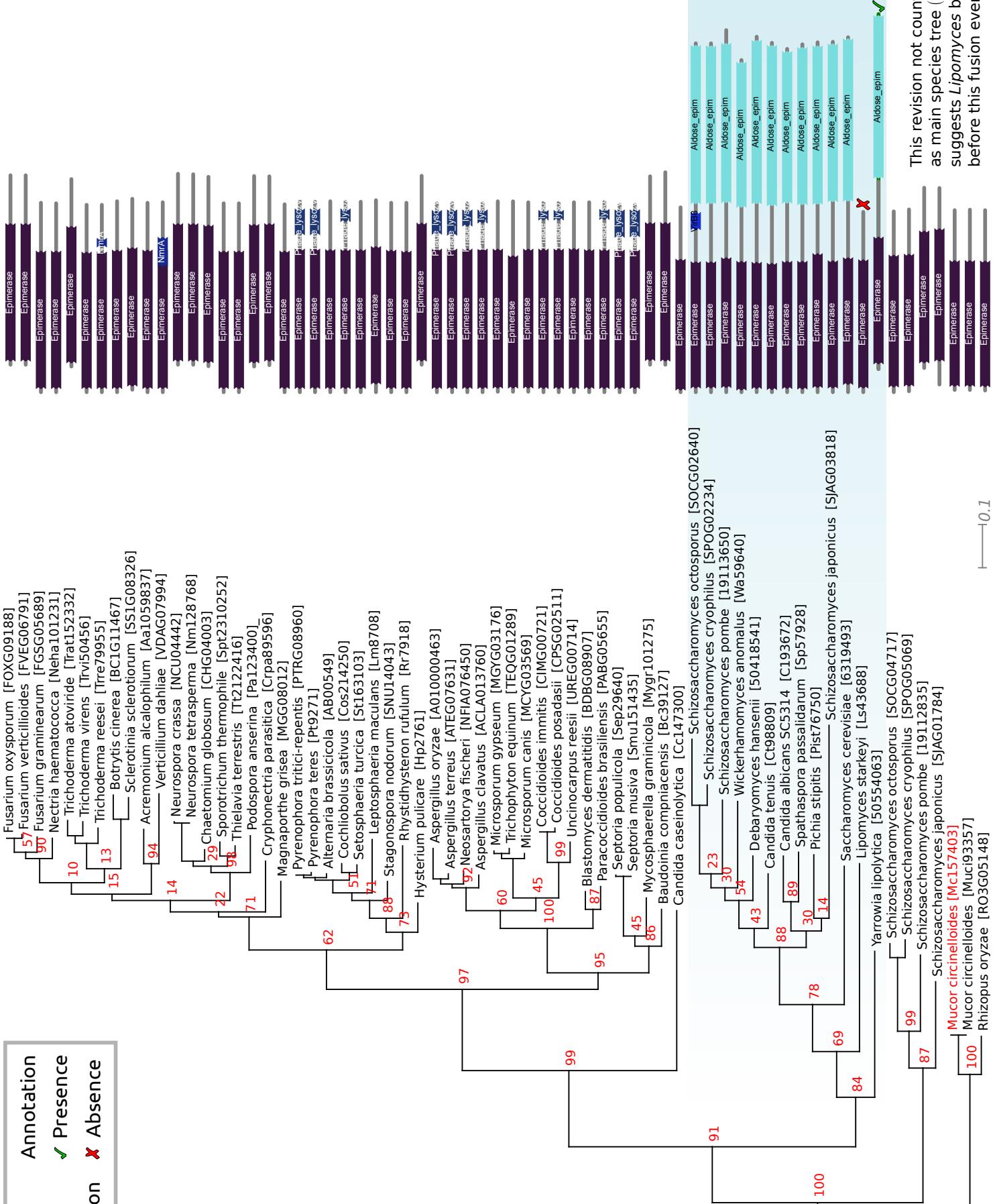
Styling and annotation was made possible by Dendroscope and Inkscape.

3 Mesquite Cladogram

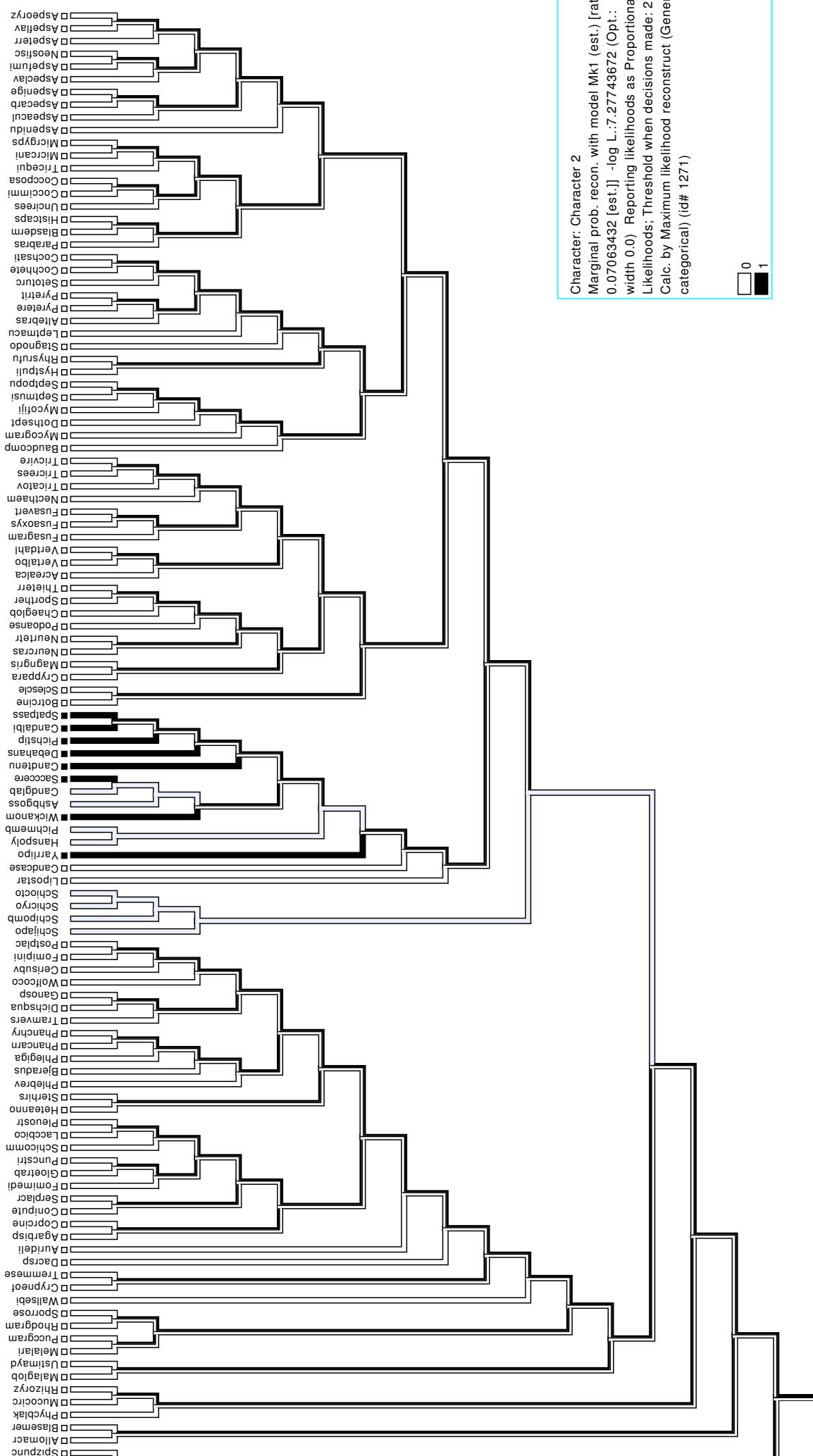
This tree is the 68-gene concatenated phylogeny (Fig. 1), with the presence of a fusion (black), presence of a fission (white), and absent/undetermined (grey) status of gene fusion characters plotted on to it using a "1/0/-" nexus-style data matrix. We used the program 'Mesquite' to calculate proportional likelihoods based on either an "Mk1" or "Assym. 2 param model." (see Table S4) of character change across the fungal phylogeny (Fig. 1). This allowed for a proportional likelihood of the position of the fusion/fission to be calculated.



#	Annotation
	Presence
	Absence
<input checked="" type="checkbox"/>	Other Fusion



This revision not counted
as main species tree (Figure 1)
suggests *Lipomyces* branches
before this fusion event.



Putative Fusion 3

September 26, 2012

1 Fasta Sequences

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```
>lcl|CC1G06724 unnamed protein product
MSISVPTILLTNDDGPPHPKESPYVLGLYRHLTERLGWNVKVVLPPSSQKSWIGRYFYPREDGNGEQSPKSRLKPGELAE
WILLDGTPATCANVALHNLYPGQIDLVSGPNLGRNTSAAFALSSGTIGAALSSSLSKVRSIALSEYGTV рHPTPTTYFEP
AHRIGCRIIQHLWHNWGSDDCGLRNGEVDLYSVNIPLIEDILSEEGLKVYWTMWRNSYGRLFKDVSRRKSIDGATVNP
AGPDAATSPQTAVKPIDEEGLLFKWAPEMRGLIQPLSDELPVGSDAYAIHTGSISVTALRACFAEPPTSVDPVLRQIKL
>lcl|CC1G03660 unnamed protein product
MASSSFSAVVVWPNAPLITDSLVKKALSQFHPKYLQFPEDDDAIVQWSSYDVIDHELLTRPSHVLOSSYIFRKALIRKHF
LSRIVHAYCIKNPDTILKTAFLTYELEISFADELDEMWTDELWELGERLDSDDTWILKPGMANRGMGIRLFDSKDQLQ
QIFEDFEEEDDDTDDDTKGNDTSVVTSQLRHFIIQEYIPDPLLFDPREVSQEKNLEINCLQGHKFHLRVYCVATGALKLY
LYDRILALFASLPYGPPTFEVIEPDEPPVINLQHLTNTSLQAEKGEENVRLLDELDGCQILSGDGEHGKFTSADIKFLI
NQMGEVLSETFKAALENPIHFQAIPNAFELYGVDFLVSHSPNSPFSVKLLEINAEPAIELTGPRLTWILEDLFKIAE
VSIKPFFAPNKENDWPVGETRHLLKCLDVSMRFD
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2 Annotated Phylogenograms

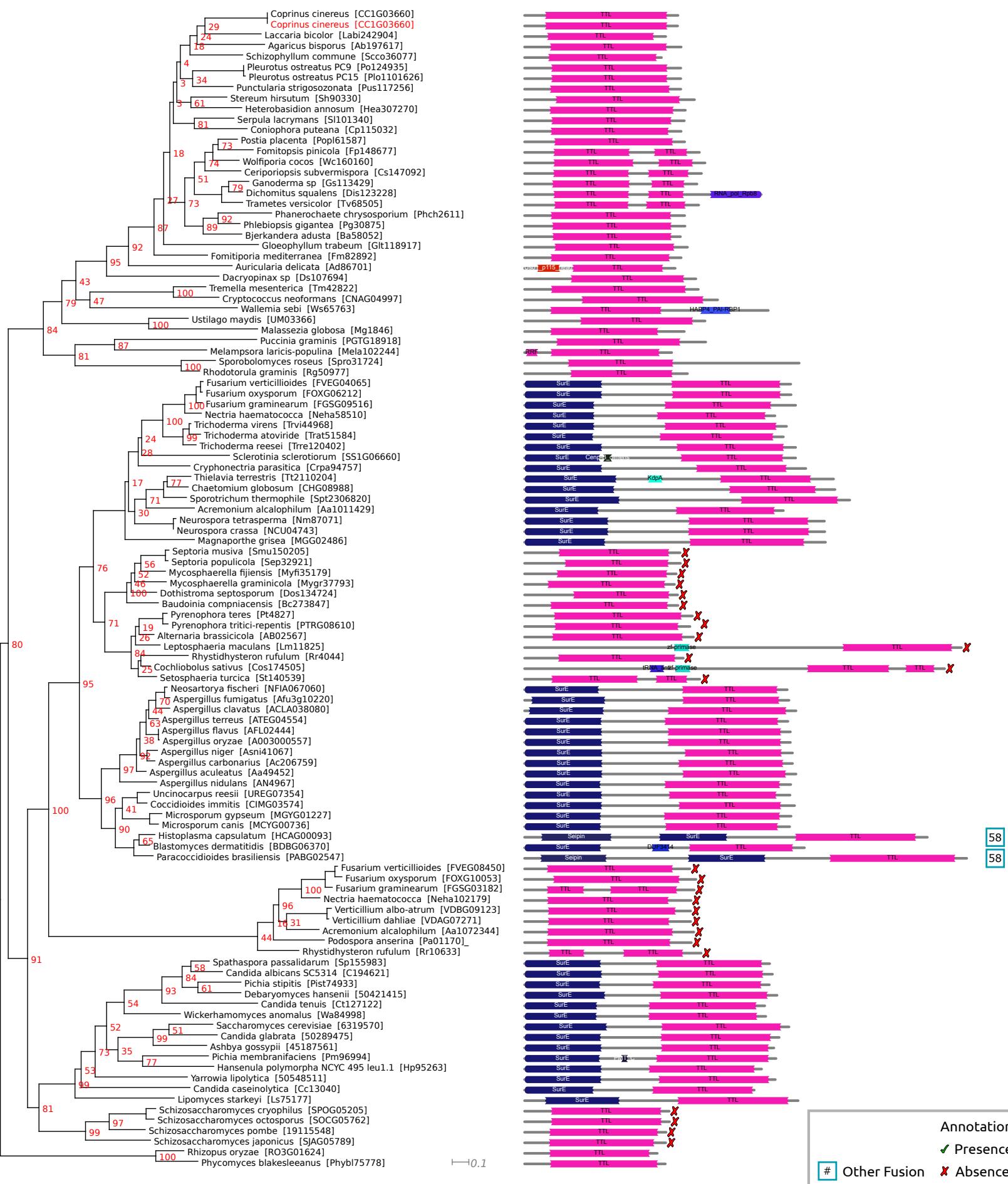
All trees were generated from an initial run of Darren's Orchard pipeline against 139 taxa (Table S1), using the above corresponding un-fused sequences as BLAST seeds. The alignments were then checked for any missing taxa, manually masked and then ProtTest3 was run, please see the Methods section for detail. The final trees were generated by the following command:

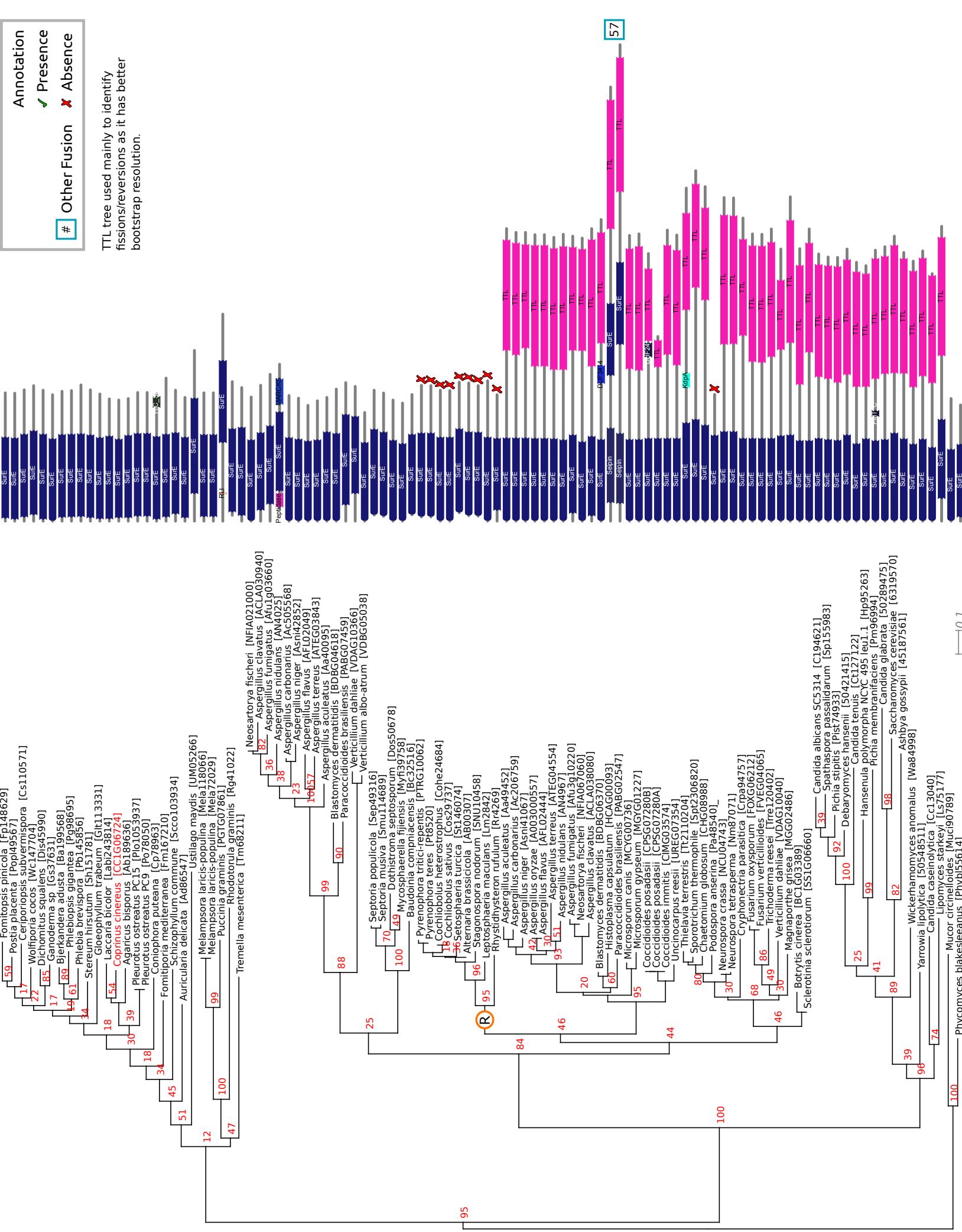
```
phyml -i alignment_file -d aa -b 100 -m model -c 8 -v invariant_sites -s BEST --quiet
-a gamma
```

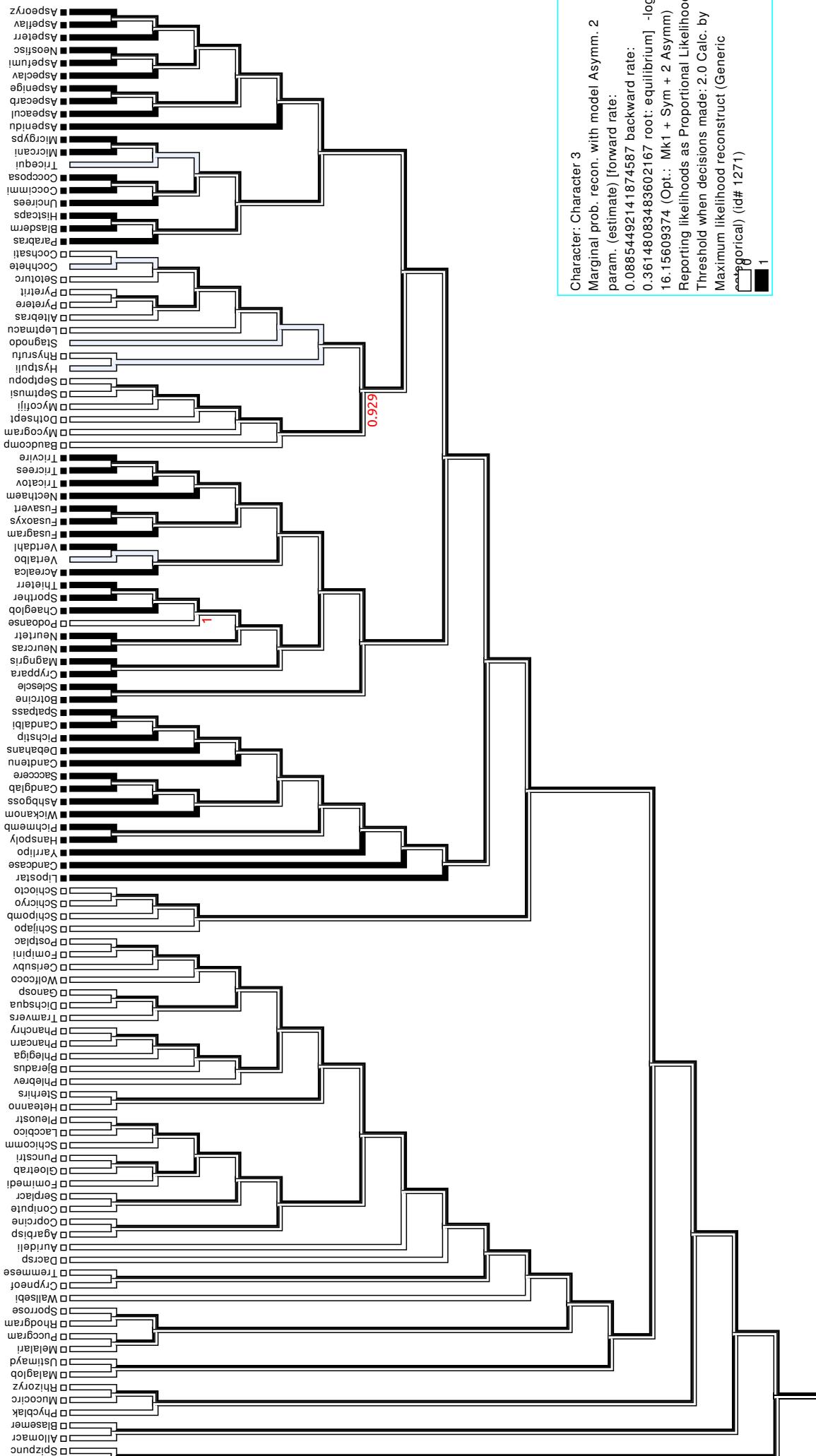
Styling and annotation was made possible by Dendroscope and Inkscape.

3 Mesquite Cladogram

This tree is the 68-gene concatenated phylogeny (Fig. 1), with the presence of a fusion (black), presence of a fission (white), and absent/undetermined (grey) status of gene fusion characters plotted on to it using a "1/0/-" nexus-style data matrix. We used the program 'Mesquite' to calculate proportional likelihoods based on either an "Mk1" or "Assym. 2 param model." (see Table S4) of character change across the fungal phylogeny (Fig. 1). This allowed for a proportional likelihood of the position of the fusion/fission to be calculated.







Putative Fusion 4

September 27, 2012

1 Fasta Sequences

These are the unfused sequences identified by fdfBLAST belonging to the putative gene fusion in FASTA format. Accessions may be shortened, but belong to either the taxons individual genome project or NCBI's accession numbering.

```
>lcl|AMAG_11004 unnamed protein product
MSWTKTPVRLTLSTVFGSLADCCLPQTGLRRVTPYYYLYKTHAKQRWLGSELLAVFDKEFQDRQPGYYVRAHCRHRRRFP
RSIPLALTIPTNPLQKKAIQVNHQSVPTTYLLKNNDLITHRNHRHEPPVTSAPITILARTPHFVVVNKPASIPVH
PSGRYRHNSVLHIVRRALGTSSTDLVGPPLYALHRLDRLTSGVLILCSDRARIGKLSKQFAAQVGKSYLCVVAGEFPAG
TTTVDAPIMVVSHKLGLNSVHPDGKPSTTHFDLLATDGTRSLVRARPVTGRTHQIRVHLRHLGFPIANDPLYNNPNHRHV
KAEREKAAAAAVAESNSGEDATTDSAGAEGTPGATDDETAAWVAAVAETASRDALTGTGQCTECGTDLYADPPHDHRLI
YLHAYEYAVRMSLGELDAPSEYITYDEATKTTVRTPLPEATDWPGFDPRVLDVVPSANVDEALQQS
>lcl|AMAG_02082 unnamed protein product
MSTTNAAADAADRYWLRHAITIAHRsapVPSAYCVGAVLVSRTSTILPRASDAITPPDAPTNQIVLATGFSRELPGNTHA
EEVCLLKLPVGTDLAGCTMYTTMEPCSTRLSGRPSCTGRVLDAKVPRVVMGIVEPADLFVKCTGADTLRERGVVVHIQG
LEEECWAPNRHLRERYDDGRNGAPRDSGAAADA
```

2 Annotated Phylogenograms

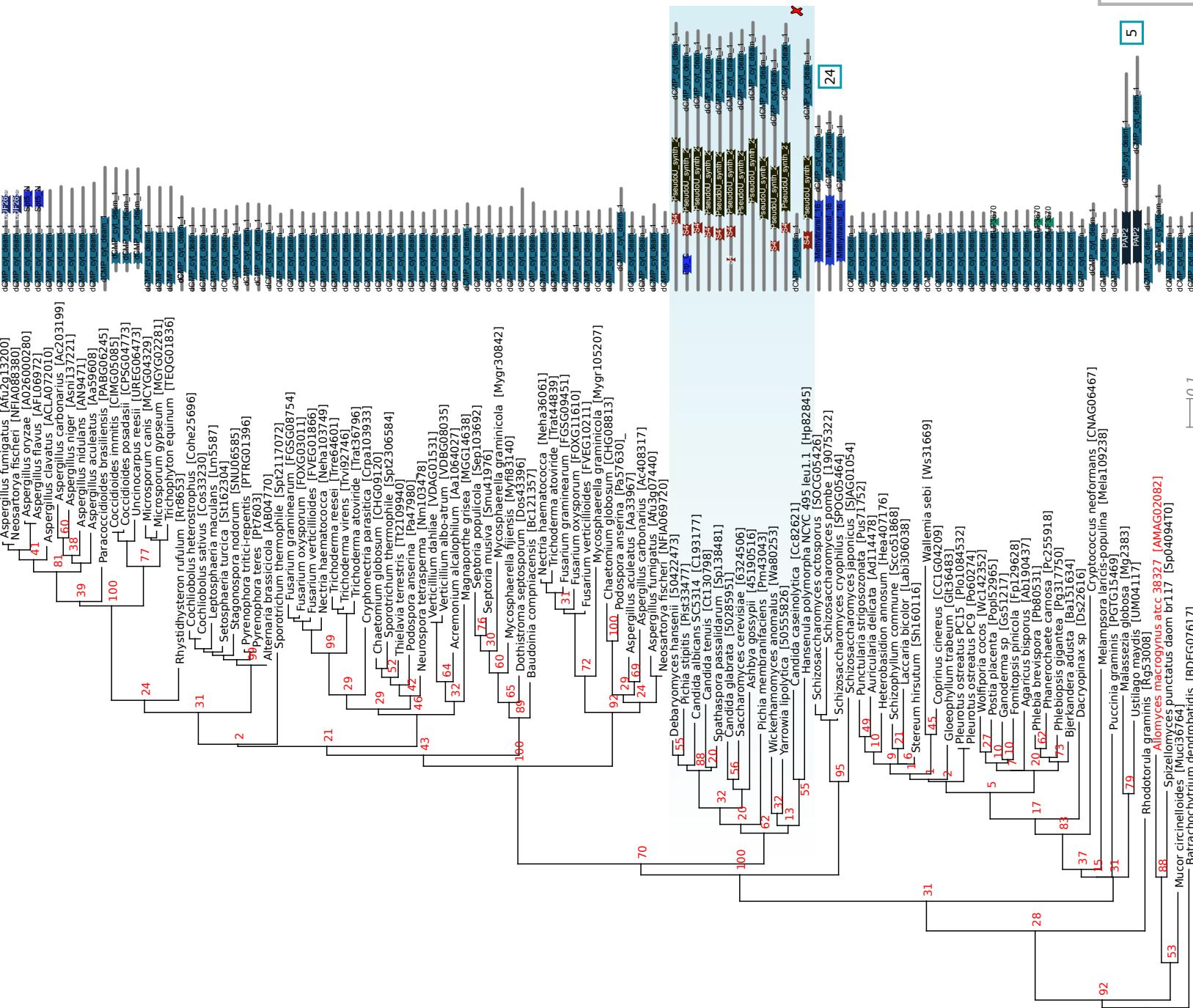
All trees were generated from an initial run of Darren's Orchard pipeline against 139 taxa (Table S1), using the above corresponding un-fused sequences as BLAST seeds. The alignments were then checked for any missing taxa, manually masked and then ProtTest3 was run, please see the Methods section for detail. The final trees were generated by the following command:

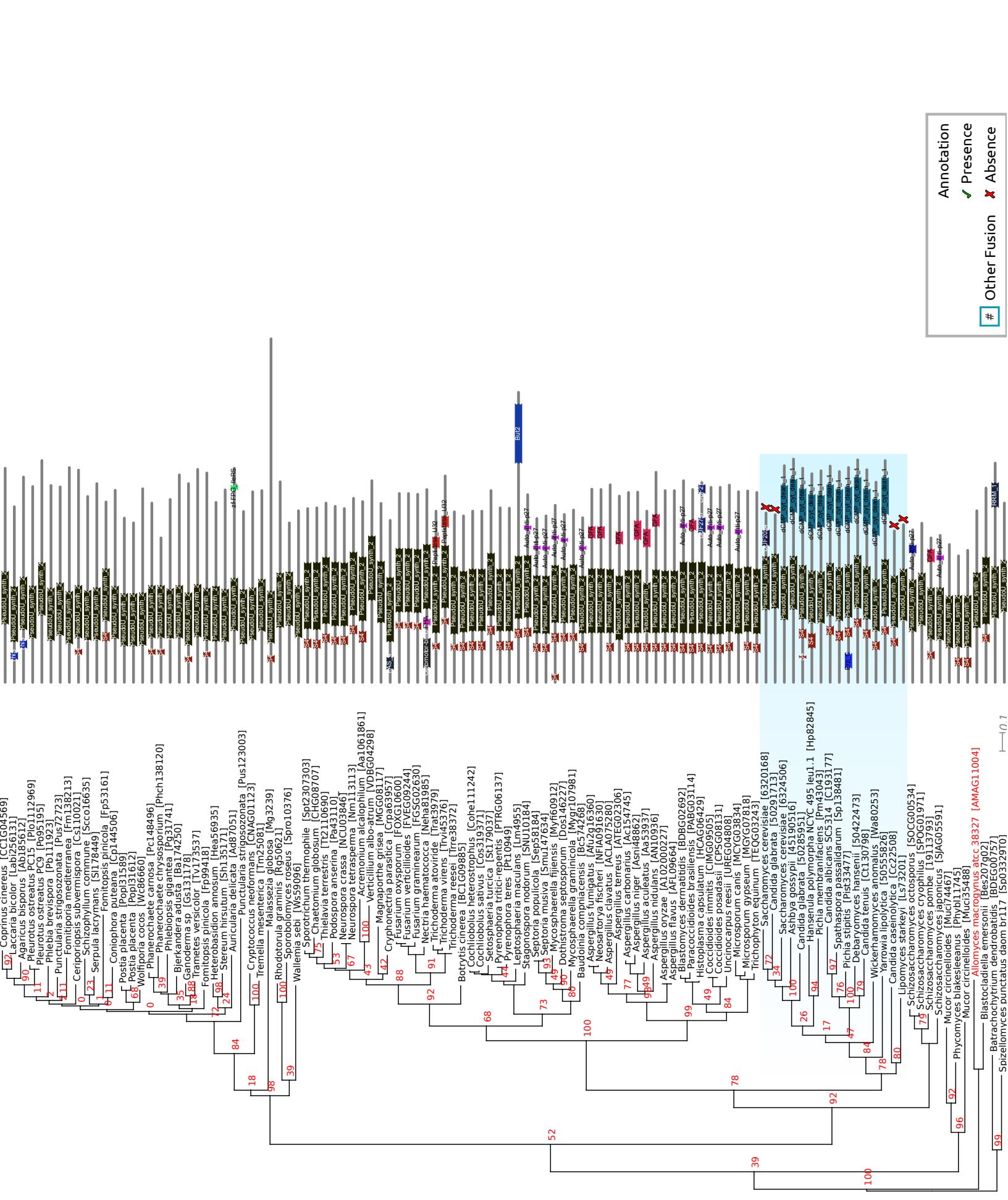
```
phym -i alignment_file -d aa -b 100 -m model -c 8 -v invariant_sites -s BEST --quiet -a gamma
```

Styling and annotation was made possible by Dendroscope and Inkscape.

3 Mesquite Cladogram

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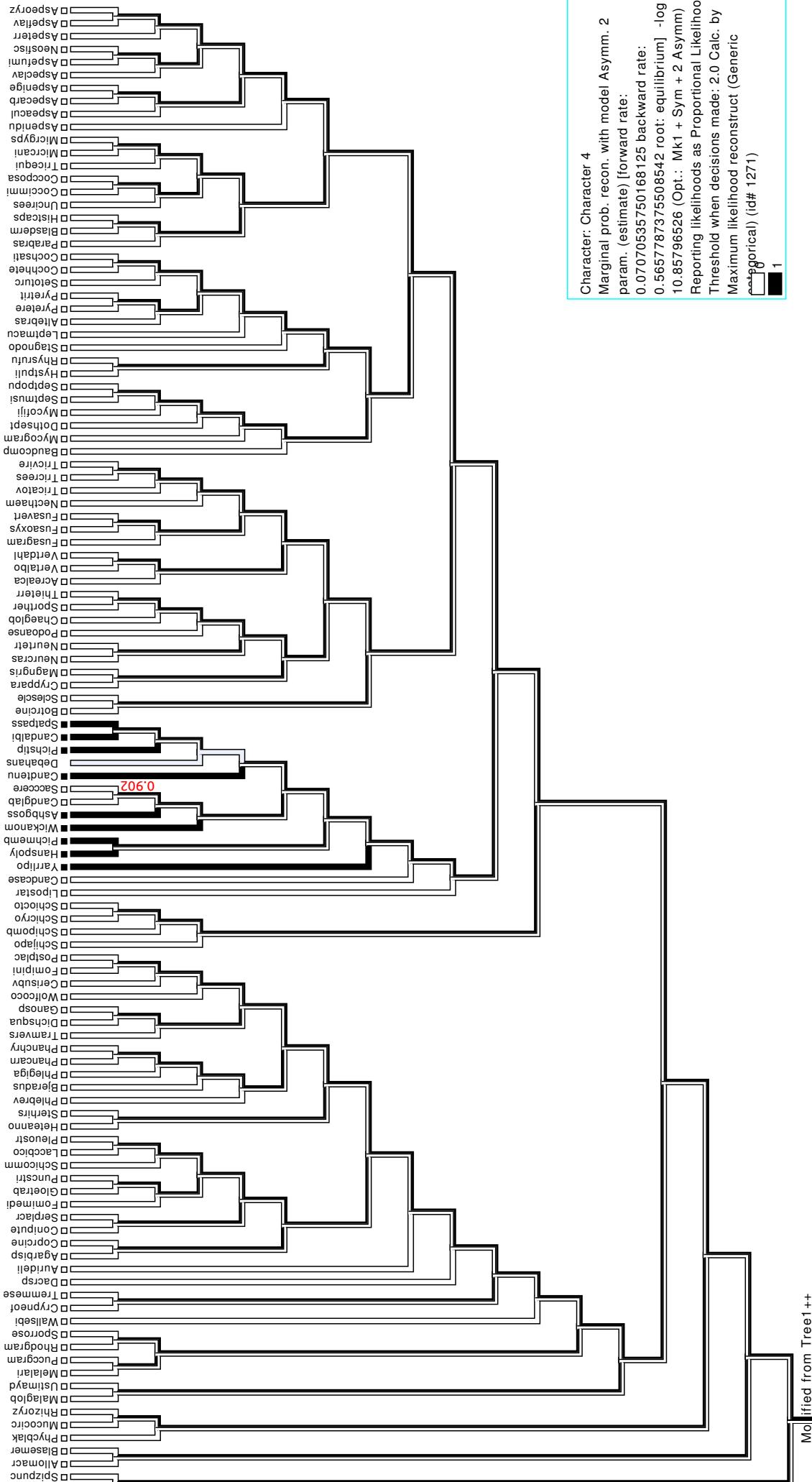




Annotation

- ✓ Presence
- ✗ Absence
- # Other Fusion

#



Putative Fusion 5

September 26, 2012

1 Fasta Sequences

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```
>lcl|AMAG_11801 unnamed protein product
MDQPVALAAPRGSLAACAHDPAAALTSLSLTHVMYHVDDALIGKALALITLLPLAMVSYATLAAARPREPLWLAMF
LGQLGNEGLNFVLKRWIAEHRPTPFLGKGYGMPSHQAQFMSYWICFVLLVHAERRRLPSWLGPLIQLAALAIAALVIYS
RVHLQYHTVAQVLAGTAIGTVVGAVWFALVHPRFPLLPSRPRPAEQHAKQE
>lcl|AMAG_02082 unnamed protein product
MSTTTNAADAADRYWLRAITIAHRSAPVPSAYCVGAVLVSRTSTILPRASDAITPPDAPTNQIVLATGFSRELPGNTHA
EEVCLLKLPVGTDLAGCTMYTTMEPCSTRLSGRPSCTGRVLDAKVPRVVMGIVEPADLFVKCTGADTLERGVVVHIQG
LEEECWAPNRHLRERYDDGRNGAPRDSGAAADA
```

2 Annotated Phylogenograms

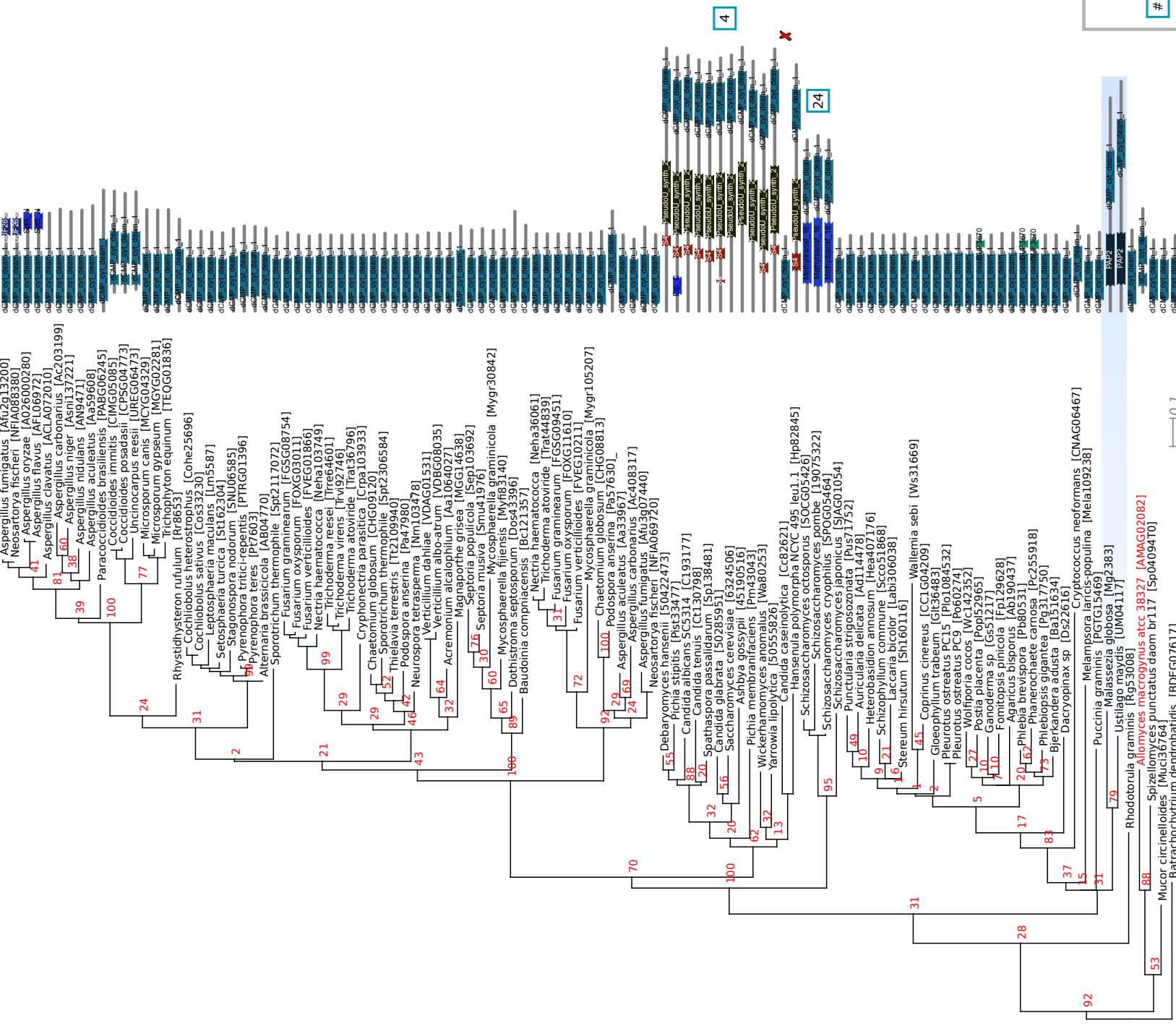
All trees were generated from an initial run of Darren's Orchard pipeline against 139 taxa (Table S1), using the above corresponding un-fused sequences as BLAST seeds. The alignments were then checked for any missing taxa, manually masked and then ProtTest3 was run, please see the Methods section for detail. The final trees were generated by the following command:

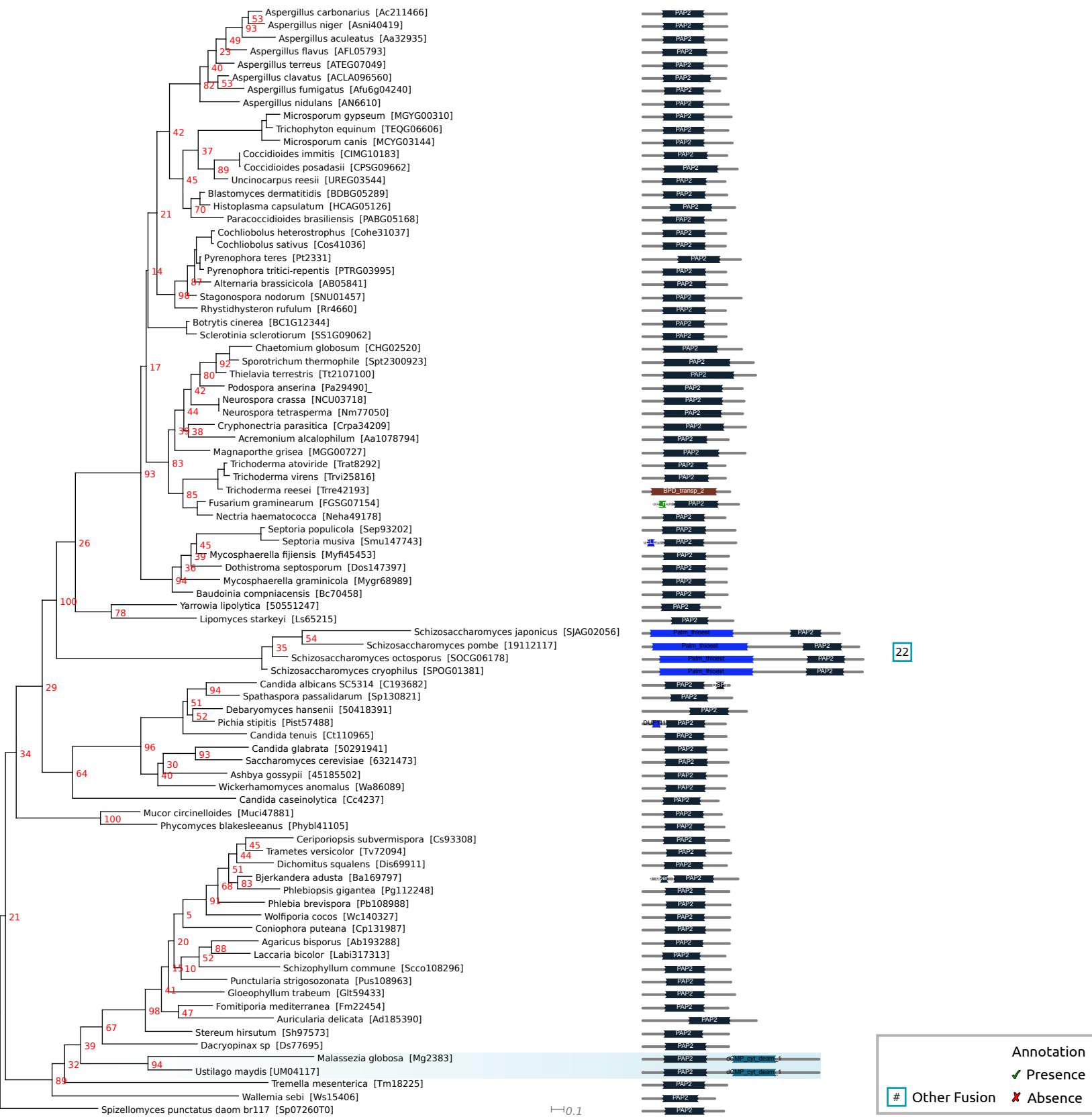
```
phyml -i alignment_file -d aa -b 100 -m model -c 8 -v invariant_sites -s BEST --quiet
-a gamma
```

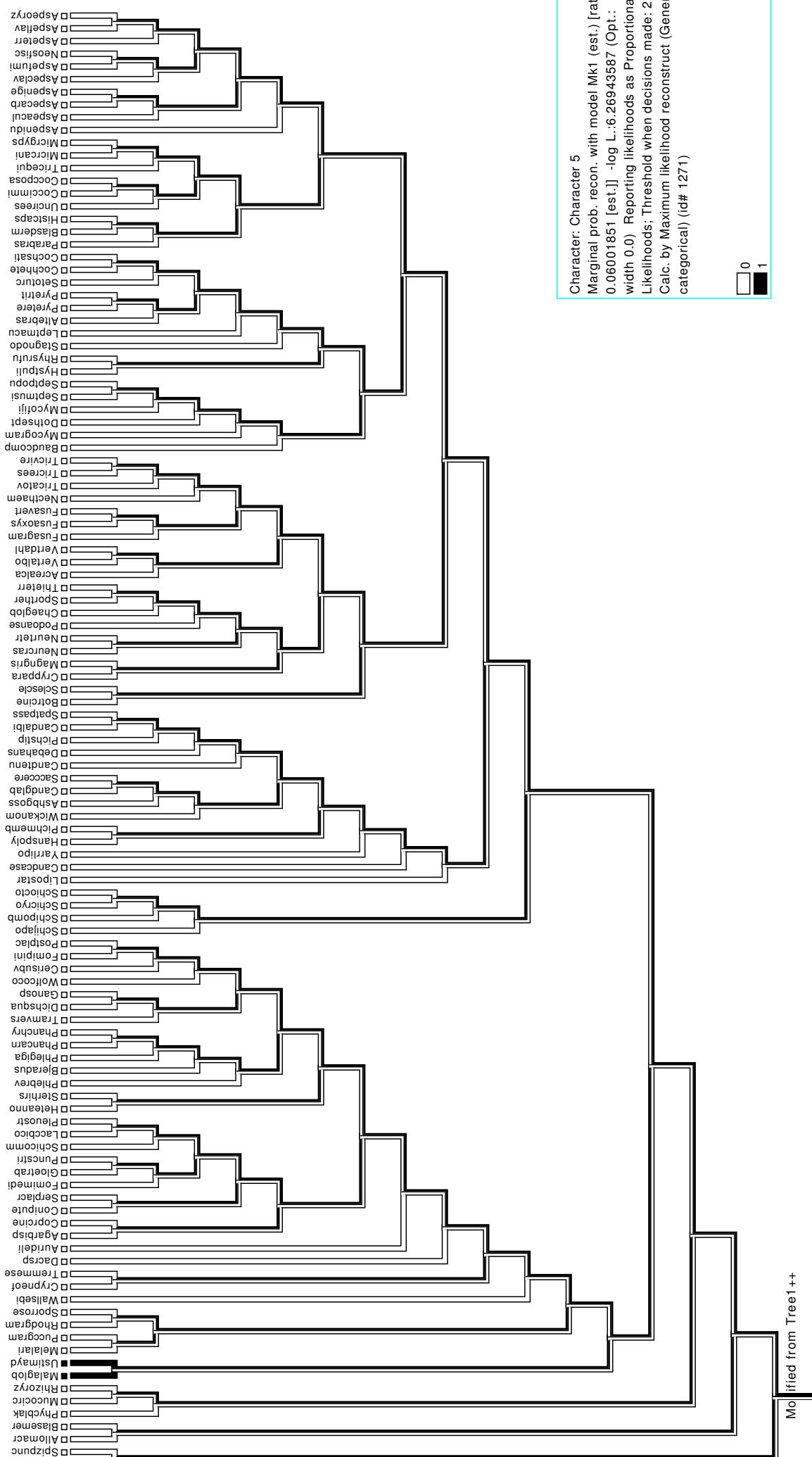
Styling and annotation was made possible by Dendroscope and Inkscape.

3 Mesquite Cladogram

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Putative Fusion 6

September 26, 2012

1 Fasta Sequences

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```
>lcl|CC1G01304 unnamed protein product
MTSTTEFPPLQNDLLLRAARGEKTERAPVWVMRQAGRYLPEFREVRKSHEFFEVCRTPDLAMEVTLQPIRRYKGLLDASI
IFSDILVVPQAMGMEVLNPGPSFPEPLDVPADVEKLKEVDVNKEVNLGYVFEAITQTRKGLEGVVPLIGFCGAPWTLFSY
MIEGGGSKTLQAKTWFKYPEESKALLHRIA VVCVDFLVGQVKAGAQLLQVFDSWAGELSPHDFDRFSFPTLQYIAKTV
RQR LAEAGLPDVPLTLFAKGANYALKLADES GYDVLGLDWCIDPAEAR RIVGDKVALQGNMDPNVLYGGREAIEQTVKR
MSAAFSGKGGWIANLGHGITPGVDPEDMRWFLECVHKYSSSG
>lcl|CC1G11378 unnamed protein product
MATETKQPRTFVVAARNSQLAQVQANSVLAQLEQLYASSDDPSKPFTSFNSTAGDKNQSQALYLMGGKALWTKELEVA
LKDKEVDMVLVHS LKDVP TTLPEGC LLGAILEREDPV DALVVKKGKEGVWKSLEDLPEGSVVG TSSVRRVAQLKRKF PGLR
FLDV RGNLNTRLAKLDAEDGPYAA ALILA KAGL VRLGWGD RITADLNPTLYHAVSQ GALAVEIR DDLLES LEI LQKLTHR
GTDWK CRAER ALLRVLEGGCSVPGVYTTLTKEGGDELLEITGCVTS LDGSEHVEESLKEKV TSVEEA AVGVKLAKVLM
EKGATRILDEINKDREHRIELAKVADAKGGP
```

2 Annotated Phylogenograms

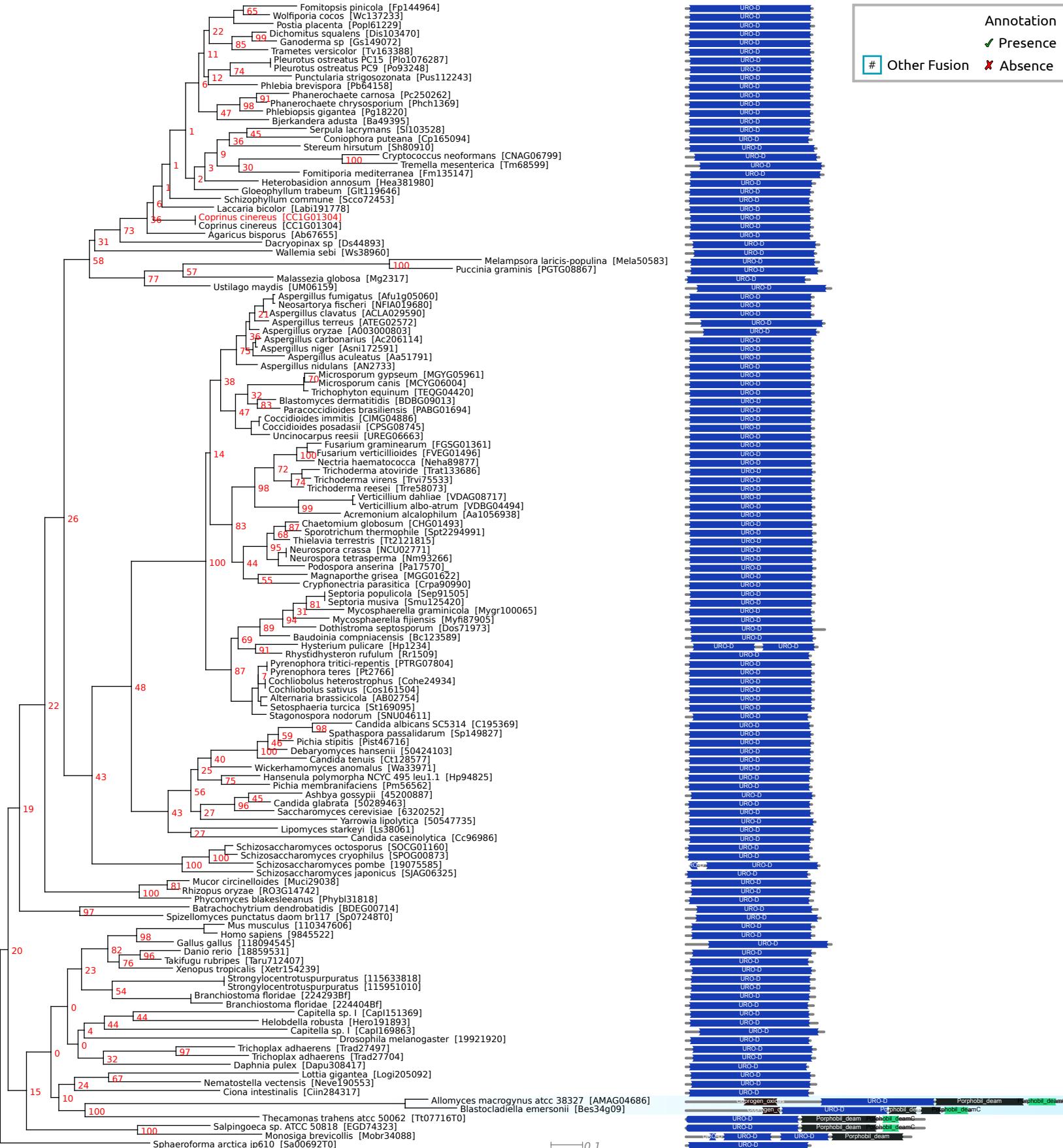
All trees were generated from an initial run of Darren's Orchard pipeline against 139 taxa (Table S1), using the above corresponding un-fused sequences as BLAST seeds. The alignments were then checked for any missing taxa, manually masked and then ProtTest3 was run, please see the Methods section for detail. The final trees were generated by the following command:

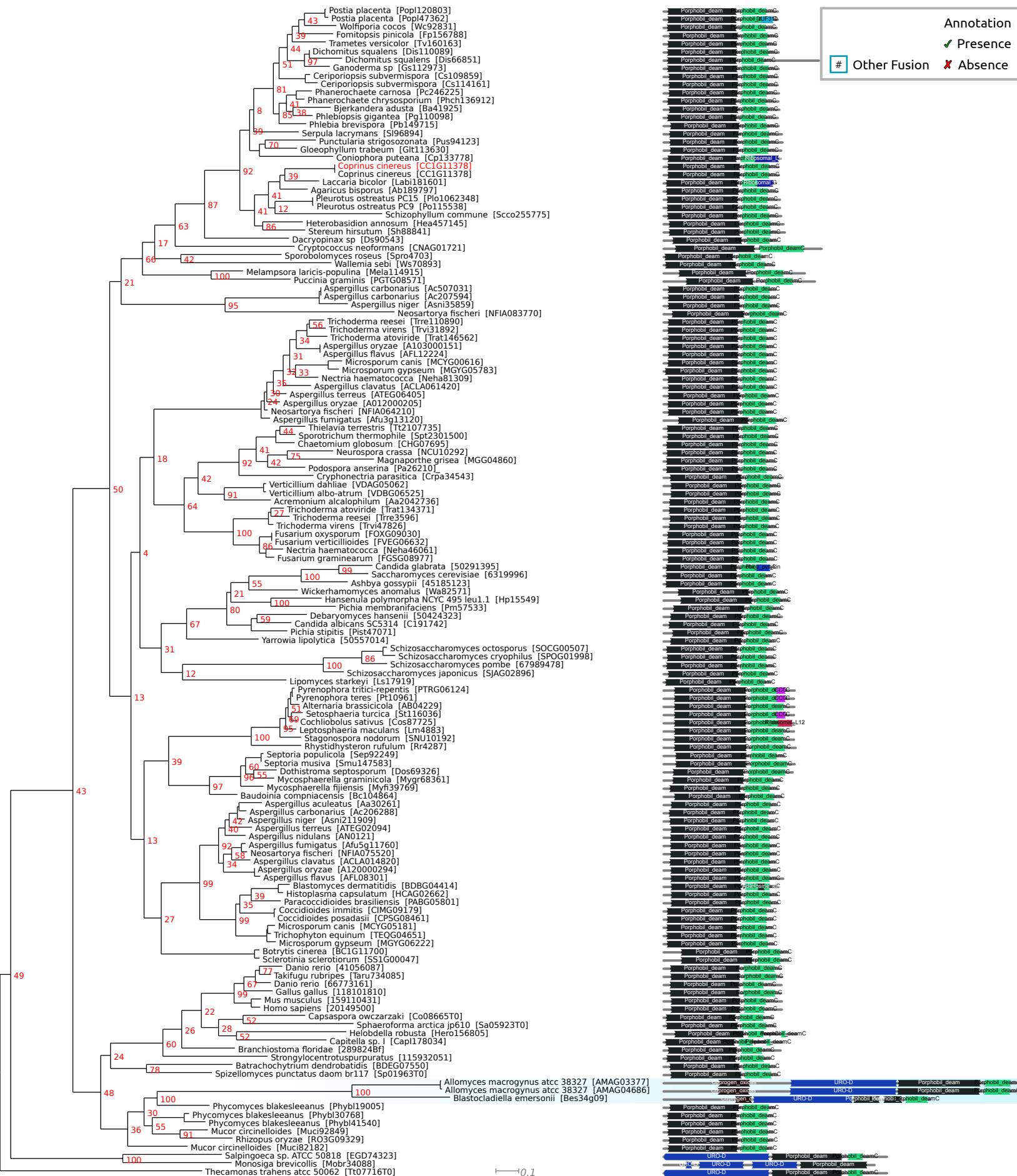
```
phyml -i alignment_file -d aa -b 100 -m model -c 8 -v invariant_sites -s BEST --quiet
-a gamma
```

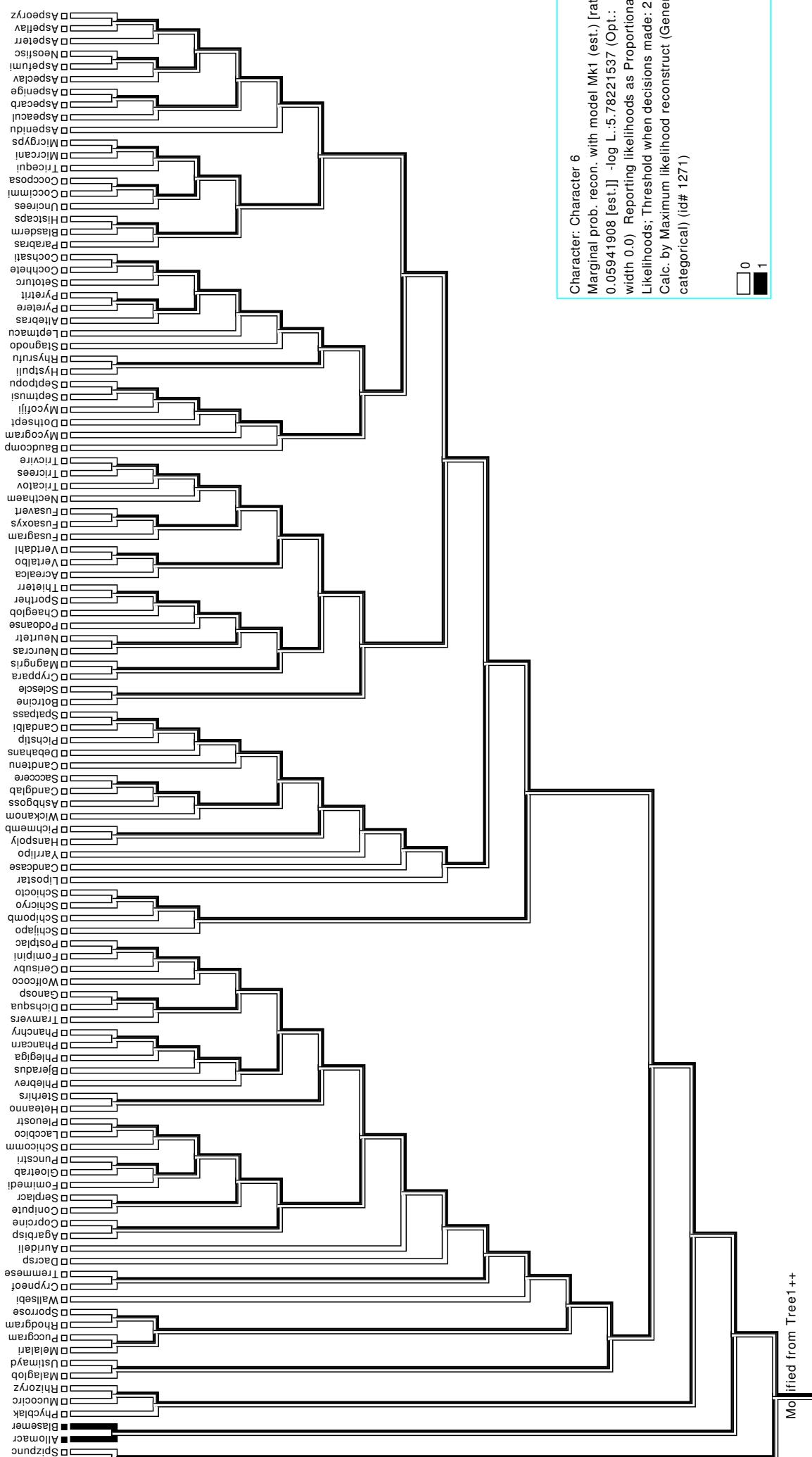
Styling and annotation was made possible by Dendroscope and Inkscape.

3 Mesquite Cladogram

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Putative Fusion 7

September 26, 2012

1 Fasta Sequences

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```
>lcl|R03T03066 unnamed protein product
MSPKKVSIVCLPGDGVGPEIVAEAVKLEIISKYRSAALGVEFEFKHELIGLAAMEKTGEPLPDSALDACKQADAIILLGA
VGGLPGAQIGSGPRAEQGLLKLRKELDLYANLRPVSFAAEKLLHLSPLKDHVVKGTNFVFVRELVGGIYFGDRKEAGEDG
KAYDTLPYSKPEVERVTRLAALLAKKQSPPGIHSVDKANVLATSRLWRKTVTETMEKEFPELGFDHQQLVDSCAMAMVQR
PTSLNGVVLTENMFGDILSDEASIVGSLGLLPSASLSGLPDGNGKCLGVYEPIHGSAPDIAGQGIANPVATILSVAMLL
RYSLGFSEAVAVEEAVRKVLDAGIYTRDLKGDKSTVEVGNAVCHEELVELLKSL
>lcl|R03T05663 unnamed protein product
MARTLYDKVLEDHIIDRQEDGTCLIYIDRHLVHEVTSPQAFEGLRNAGRVPVRPDCTLATVDHNIPTSRKNFKNIATFI
KEADSRTQCETLEQNIEAFGLTYFGMEDSRQGIVHVIQPEQGFTLPGTTVCGDSHTSTHGAFGALAFGIGTSEVEHVL
TQTLLQQKSKNMRIRVEGKPSAGVTSKDIALHIVGIVTAGGTGCVIEFCGEAIESLSMESRMSICNMSIEAGARAGMIA
PDDITFEYLRNKPLAPKGEEDRAVAYWKTLSADAQYDITVDIKASDIAPTVTWGTSPQDVAPITGKTPDLDIADPL
RRLAVQRALDYIGIAPNTPLEGVKIDKVFFIGSCTNSRIEDLRAAAIVKGKRVADWDAMVPGSLVKRQAEREGLDKI
FQEAGFDWREAGCSMCLGMNPDQLKPGERCCASTSNRFGRQGAGGRTHLLSPAMAAAAGIKGCLTDVRHMEVAEIALTG
NESPRQEVVASEYDGSAEVSESTDQDTTPAVKPPQPASDSSSSGGMPAFTTLKGYAAPLDISNIDTMIIPKQFLKTIKRT
GLGSALFYSLRFDPQTGAENPAFVLNQEPFRQARILVCTGPNFGCGSSREHAPWAFNDFGIRCIAPSFADIFFNNCFKN
GMLPIVLPQAQLEAIAAAEAKGVEVEVDLVQQIVRYPGGEVSDVEEFRKHCLVNGLDDIGLTMQKADKIAQFETKRTQT
WPWLDGKGYKGKATKIEINGGQQKKAKLDW
```

2 Annotated Phylogenograms

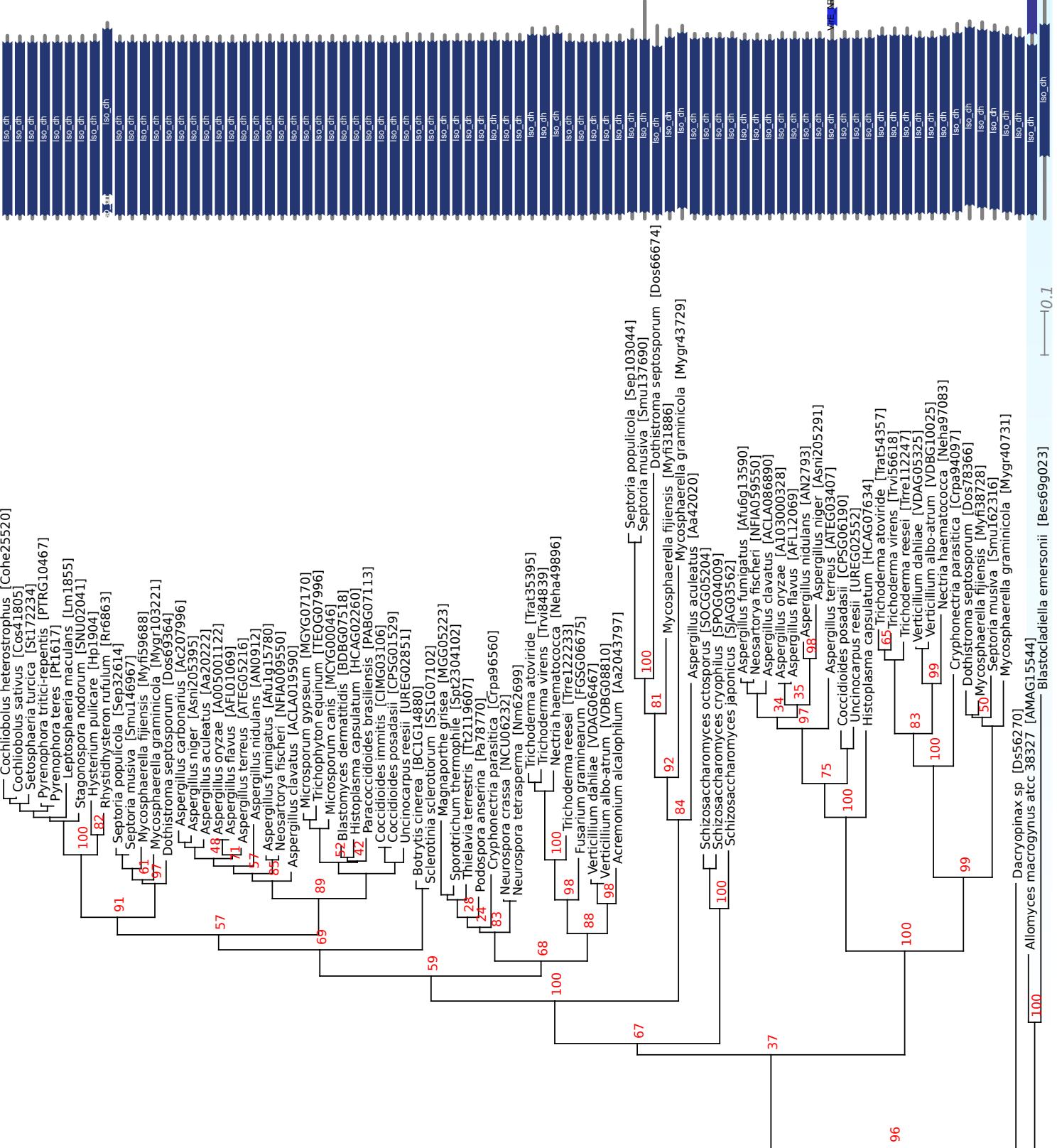
All trees were generated from an initial run of Darren's Orchard pipeline against 139 taxa (Table S1), using the above corresponding un-fused sequences as BLAST seeds. The alignments were then checked for any missing taxa, manually masked and then ProtTest3 was run, please see the Methods section for detail. The final trees were generated by the following command:

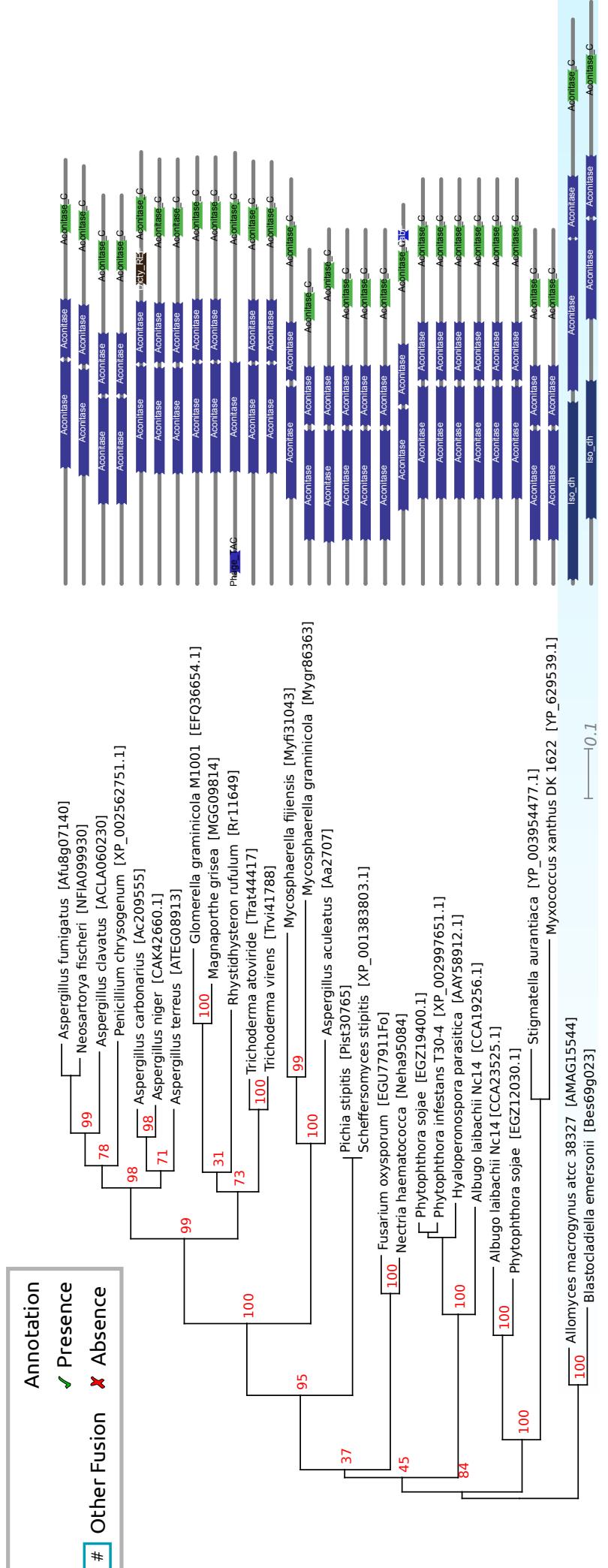
```
phyml -i alignment_file -d aa -b 100 -m model -c 8 -v invariant_sites -s BEST --quiet
-a gamma
```

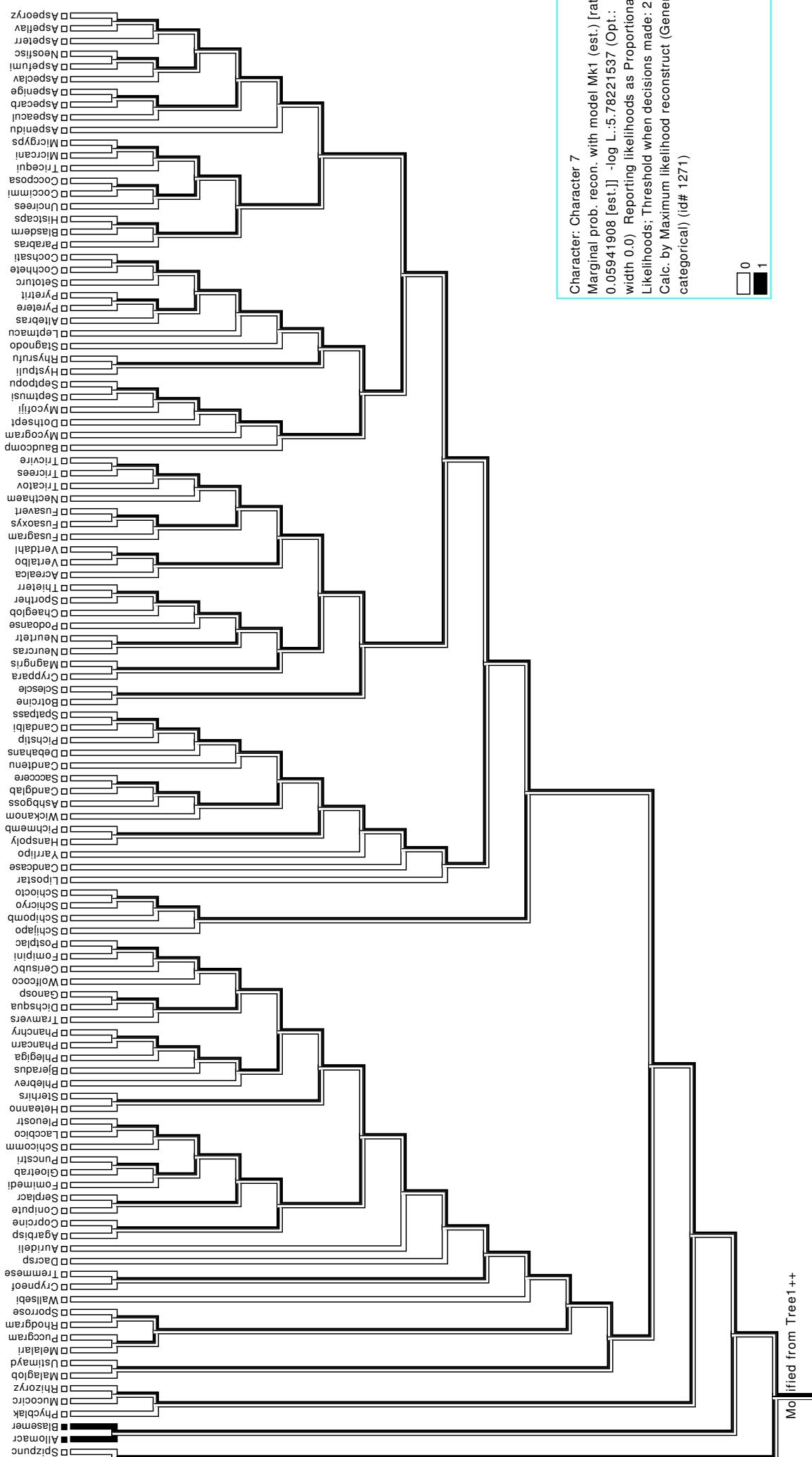
Styling and annotation was made possible by Dendroscope and Inkscape.

3 Mesquite Cladogram

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Putative Fusion 8

September 26, 2012

1 Fasta Sequences

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```
>lcl|173045Sc unnamed protein product
MSVHAATNPINKHVLIDNYDSFTWNVYELYCQEGAKVSYRNDAITVPEIAALNPDTLLISPAGPCKTDGKISRDCIR
YFTGKIPVFGICMGQQCMFDVFGEVAYAGEIVHGKTSPISHDNCIFRNVVPQGIAVTRYHSLAGTESSLPSCLKVTAST
ENGIIMGVRHKKYTVEGVQFHPESILTEEGHLMIRNILNVSGGTWEENKSSPSNSILDRIYARRKIDVNEQSKIPGFTFQ
DLQSNYDLGLAPPLQDFYTVLSSHKRAVVLAEVKRASPSKGPICLKAVALAEQALKYAEAGASAISVLTEPHWFHGSLQD
LVNVRKILDLKFPKPERPCVLRKEFISKYQILEARLAGADTVLLIVKMLSQPLLKELYSYSKDLNMEPLVEVNSKEELQ
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ELCE
>lcl|136348Sc unnamed protein product
MSVINFTGSSGPLVKVCLQSTEAAECALDSDADLLGIICVPNRKRTIDPVIARKISTLVKAYKNSSGTPKYLGVFRNQ
PKEDVLAJVNDYGDIVQLHGDESWQEYQEFGLPVIKRLVFPKDCNILLSAASQKPHSFIPLFDSEAGGTGELLDWNSI
SDWVGRQESPESLHFMLAGGLTPENVGDALRLNGVIGVDVSGGVETNGVKDSNKIANFVKNAKK
```

2 Annotated Phylogenograms

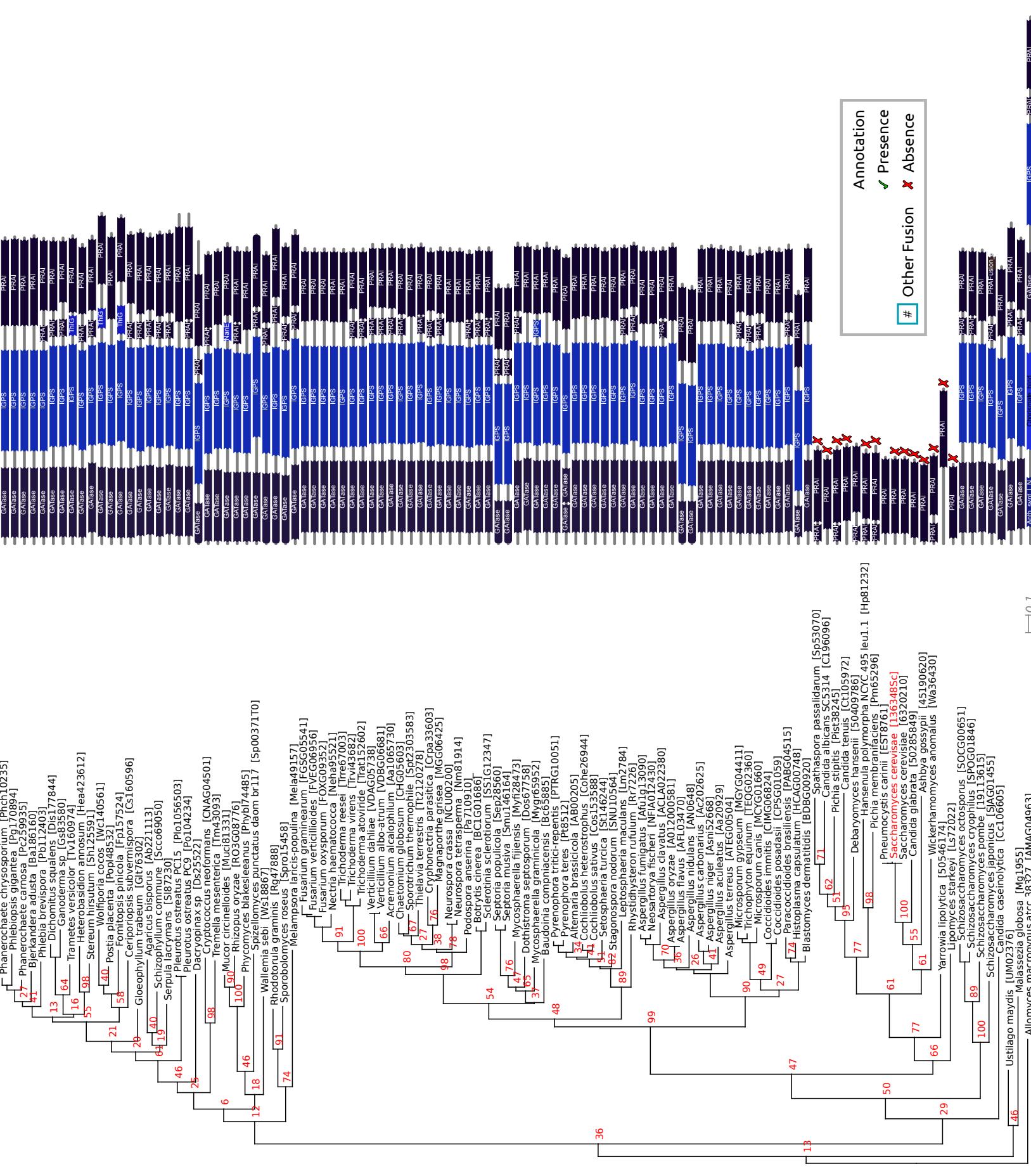
All trees were generated from an initial run of Darren's Orchard pipeline against 139 taxa (Table S1), using the above corresponding un-fused sequences as BLAST seeds. The alignments were then checked for any missing taxa, manually masked and then ProtTest3 was run, please see the Methods section for detail. The final trees were generated by the following command:

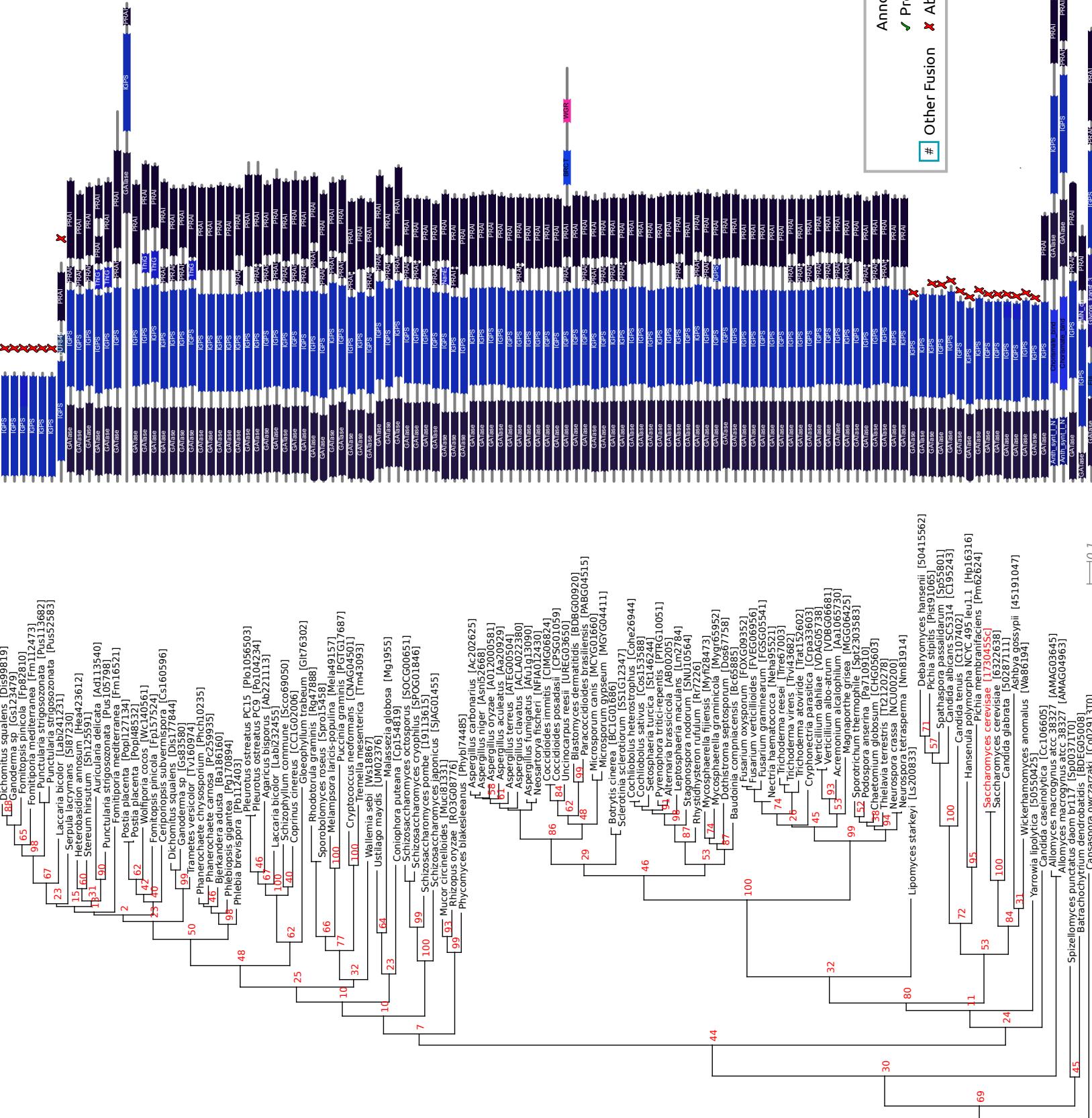
```
phyml -i alignment_file -d aa -b 100 -m model -c 8 -v invariant_sites -s BEST --quiet
-a gamma
```

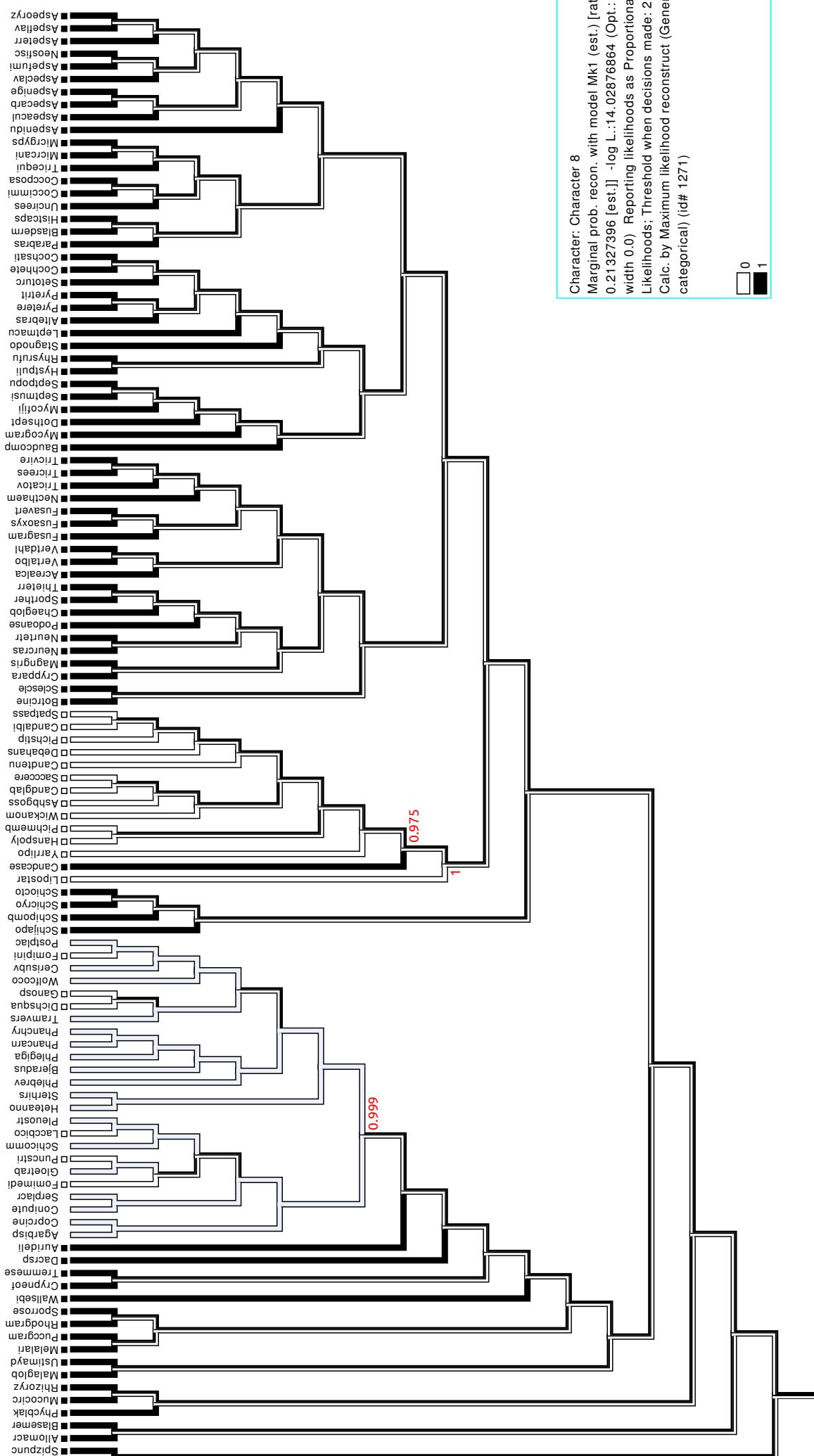
Styling and annotation was made possible by Dendroscope and Inkscape.

3 Mesquite Cladogram

This tree is the 68-gene concatenated phylogeny (Fig. 1), with the presence of a fusion (black), presence of a fission (white), and absent/undetermined (grey) status of gene fusion characters plotted on to it using a "1/0/-" nexus-style data matrix. We used the program 'Mesquite' to calculate proportional likelihoods based on either an "Mk1" or "Assym. 2 param model." (see Table S4) of character change across the fungal phylogeny (Fig. 1). This allowed for a proportional likelihood of the position of the fusion/fission to be calculated.







Putative Fusion 9

September 26, 2012

1 Fasta Sequences

These are the unfused sequences identified by fdfBLAST belonging to the putative gene fusion in FASTA format. Accessions may be shortened, but belong to either the taxons individual genome project or NCBI's accession numbering.

```
>lcl|Mc109954 unnamed protein product
MLLTASRVFTISKRSFHYAPIAKKFVITPEIKAIAIERKGPVVALESTIISHGMPYPQNVTAKAVENIIREQGAIPATIA
LLDGKVHIGLTDETLEHLGKIGPKAQKTSRRDLSVVLSQLNKAGATTVASTMILARAAGIPVFTGGIGGVHRGAEQSFDI
SADLTELGRTPVAVVCAGVKSILDIPKTLEVLETQGVTVTTIGKNNQFPAYTPDSGFKSPYHVEDPLDAAKSIHANHEL
EMNSGMVFAVPIPSASAADAASIQHAIDTAIAEARANNVHGKEETPFLLKRIAELTKGESLAANIALVKNNAKIGGQIAV
HLSQLKNRV
>lcl|Mc168016 unnamed protein product
MSGKPLLVIGGIALDITATVGKSGASILHTSTPGHVQSLGGVGRNVAEEAWRTGARVKLVSVVGDDLAGESVKQGLKS
ISMNTEYIQTLANQPTAVYNALHSEDGQLIAAVADMNIFDAMDTTKIISILQHEKPSFVCFDGNITAQMMSIATMCQAL
AIPALFEPTSVPKSLKLFQHAETMMAQAVKYTSPNQFELEAMCDTIRSNPVFSDDKAAKQQNAPTLAHLALPNACFLSQF
IPNVITKLGEEGCLYVSKNAGAEYFAPESIEPNEIVNVTGAGDCFVGTLIANLQKHANANMLSSNVRSIIIRNAQTASI
RTLKSNRASDEISPDLQL
```

2 Annotated Phylogenograms

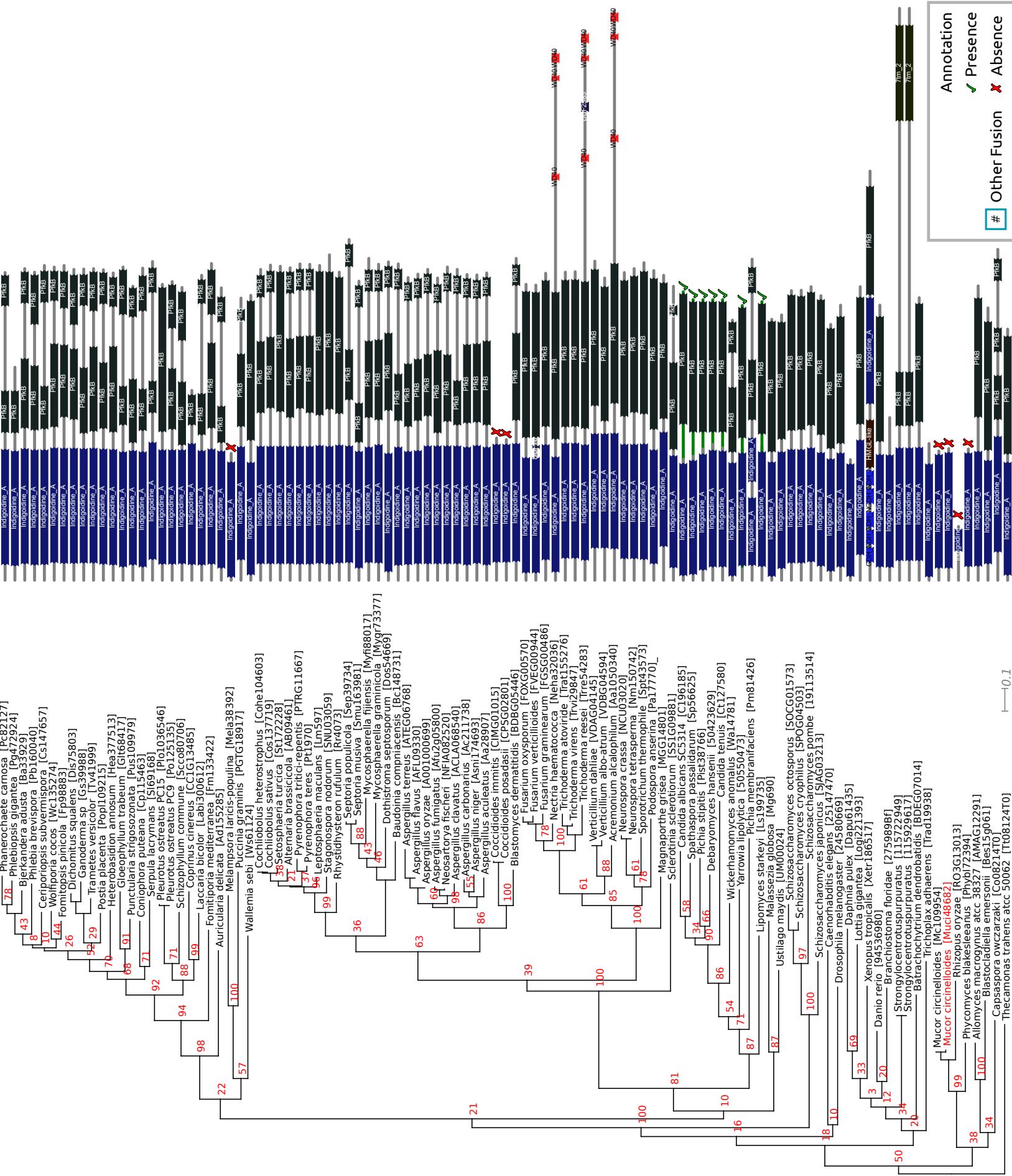
All trees were generated from an initial run of Darren's Orchard pipeline against 139 taxa (Table S1), using the above corresponding un-fused sequences as BLAST seeds. The alignments were then checked for any missing taxa, manually masked and then ProtTest3 was run, please see the Methods section for detail. The final trees were generated by the following command:

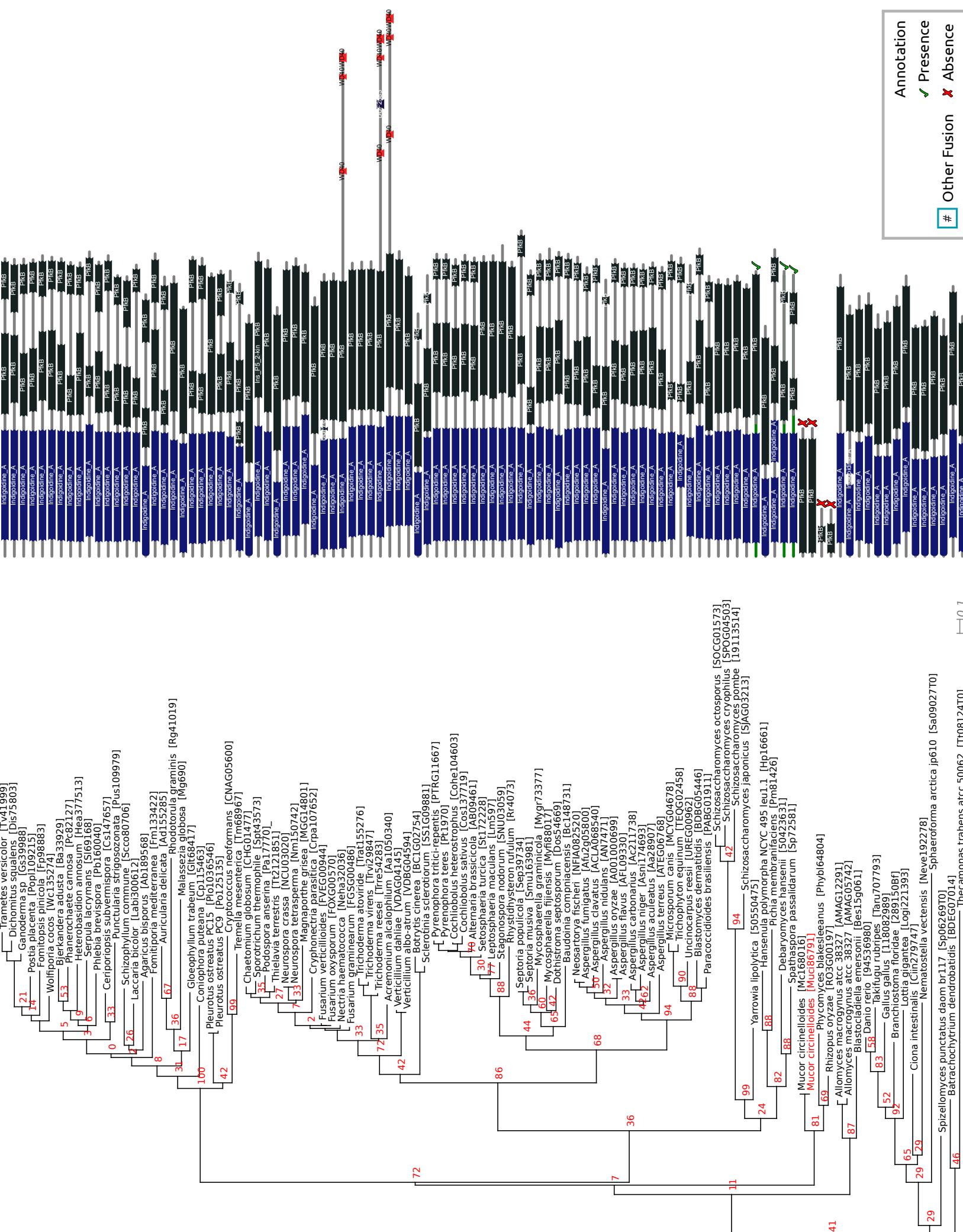
```
phyml -i alignment_file -d aa -b 100 -m model -c 8 -v invariant_sites -s BEST --quiet
-a gamma
```

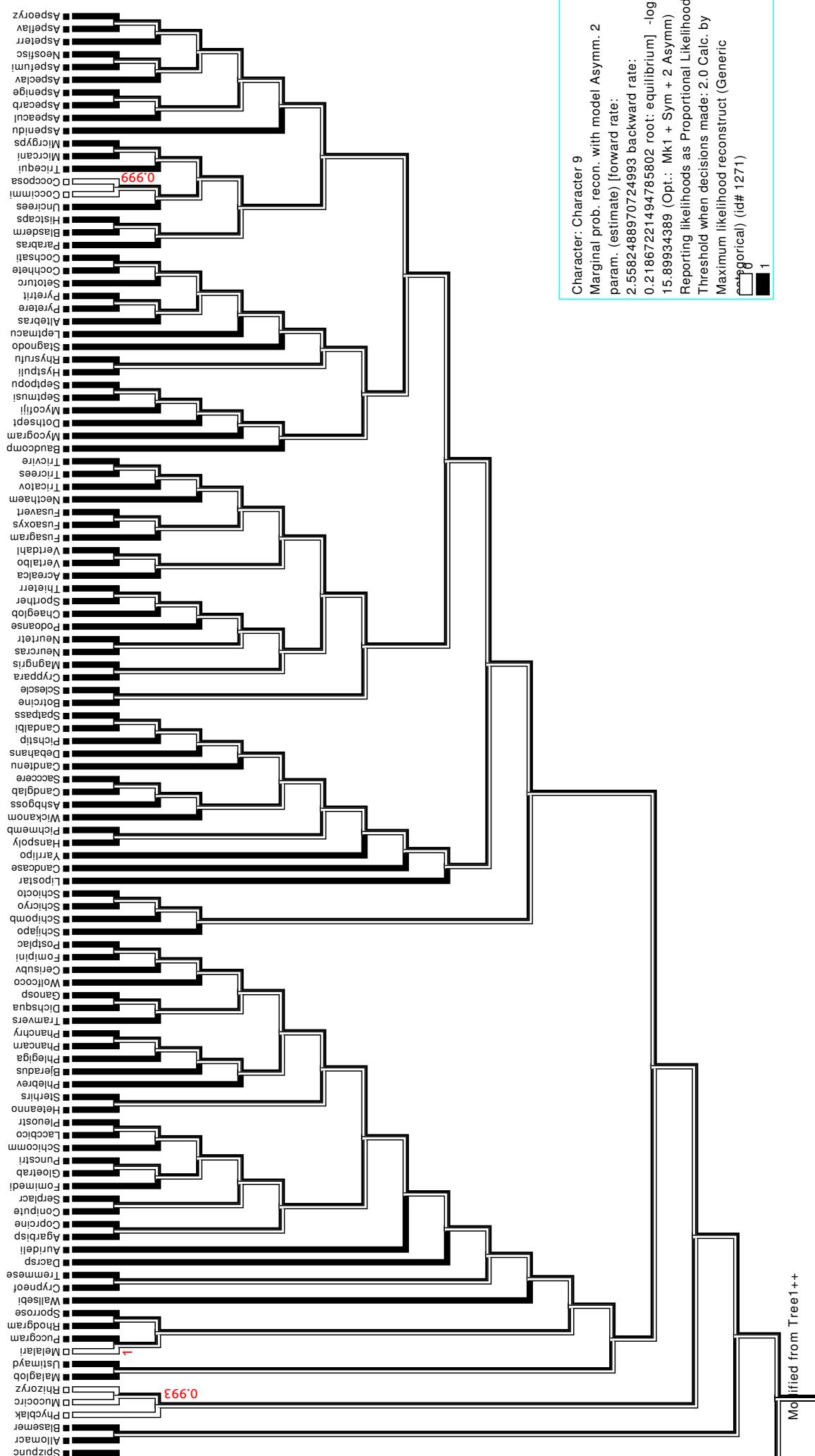
Styling and annotation was made possible by Dendroscope and Inkscape.

3 Mesquite Cladogram

This tree is the 68-gene concatenated phylogeny (Fig. 1), with the presence of a fusion (black), presence of a fission (white), and absent/undetermined (grey) status of gene fusion characters plotted on to it using a "1/0/-" nexus-style data matrix. We used the program 'Mesquite' to calculate proportional likelihoods based on either an "Mk1" or "Assym. 2 param model." (see Table S4) of character change across the fungal phylogeny (Fig. 1). This allowed for a proportional likelihood of the position of the fusion/fission to be calculated.







Putative Fusion 10

September 26, 2012

1 Fasta Sequences

These are the unfused sequences identified by fdfBLAST belonging to the putative gene fusion in FASTA format. Accessions may be shortened, but belong to either the taxons individual genome project or NCBI's accession numbering.

```
>lcl|CC1G01201 unnamed protein product
MLDQTWLVAIFQVLTQTVGYRWPSPQYDALEGLLYEGRRDGNSLASIQHPCKNRPGSRASIGAEWRLAYHDVATH
NIETGTGGLDASIAFELDRAENFGNGMHESIEDFETFPSKYISRADVIAIGTILGVASCGGPIIPFRGGGRIDALSADVAG
VPEPHQDLETHTEIFRRQGFSQEEMIGLVACGHTMGGVRSSDFPDIVPPQDDSERFADFDDTHEFDNDVVVKYIDGTTQN
PLVVHANMTLNSDLRIFESDGNATMRRLASPEDFSSTCGTLLEKMLNVVPSNVVLTTEEITMLPVKVTDAHLTIENEQLVF
KASLRIAQPISAPNKNRLVKIFWCDRYGANKDCENRTGKTAGVASSPRIDDQPVSPLTFRAGFQFVHYDFIVPIDTEESL
SKFWFEVDEKDGTKPKRHDNDGEGYVLQQDNVIYVPRLSSISFNREDRTQKTYYITAGVKSGASPSRVYMSAFDSATDAF
STIIDEDVDMALNETLPSAAGYTFYSASIESPGTQLTVDLHAVIDGETYTEDYMQTFFVAG RTPSTKPTNVTIVDIVPPT
KLDLSSATANILSLDIIGLLALSAFIF
>lcl|CC1G00884 unnamed protein product
MKHRHTSGNSSSTAGEKAKANGTAGGMGGEKREYTQEQLSVVKVRACKVTEYYEILSVKRDCEDAEIKKAYRKLALALH
PDKNAGPADEAFKLVSKAFQVLSDPQKRAIYDSSGADPESRGGMSSSSPSFSTASPFAAGGHAGFGDEISPEELFMNFF
GGPGFSAGFGPGTATFSFGPGMTFTSNGGFARRRAAAPNANANMEPRSLLIQLLPLILLFAFSILSALPSIFSEPPV
PDPRFSFTNTRQYNAQLETGKLGVPYYVNPTEFTAHPVIGPELA KAGVKIGKQGEELKSGKESDSVKGKRGPA
KFEDNVEGIYTHDLRVQCHRGRE RLERLDAEIGIFGIGTDWEKVKKIESEVIPSCEELKRLGVL
```

2 Annotated Phylogenograms

All trees were generated from an initial run of Darren's Orchard pipeline against 139 taxa (Table S1), using the above corresponding un-fused sequences as BLAST seeds. The alignments were then checked for any missing taxa, manually masked and then ProtTest3 was run, please see the Methods section for detail. The final trees were generated by the following command:

```
phym -i alignment_file -d aa -b 100 -m model -c 8 -v invariant_sites -s BEST --quiet
-a gamma
```

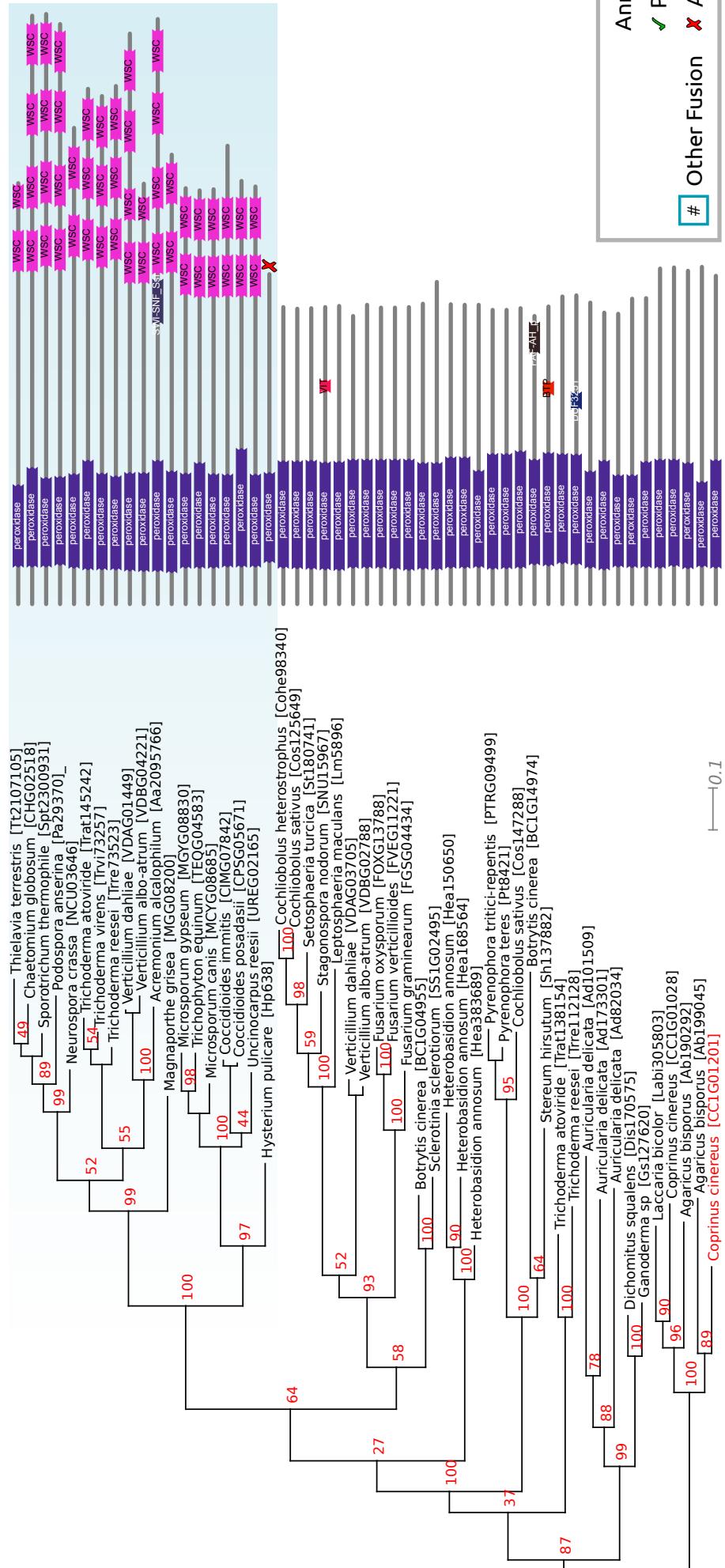
Styling and annotation was made possible by Dendroscope and Inkscape.

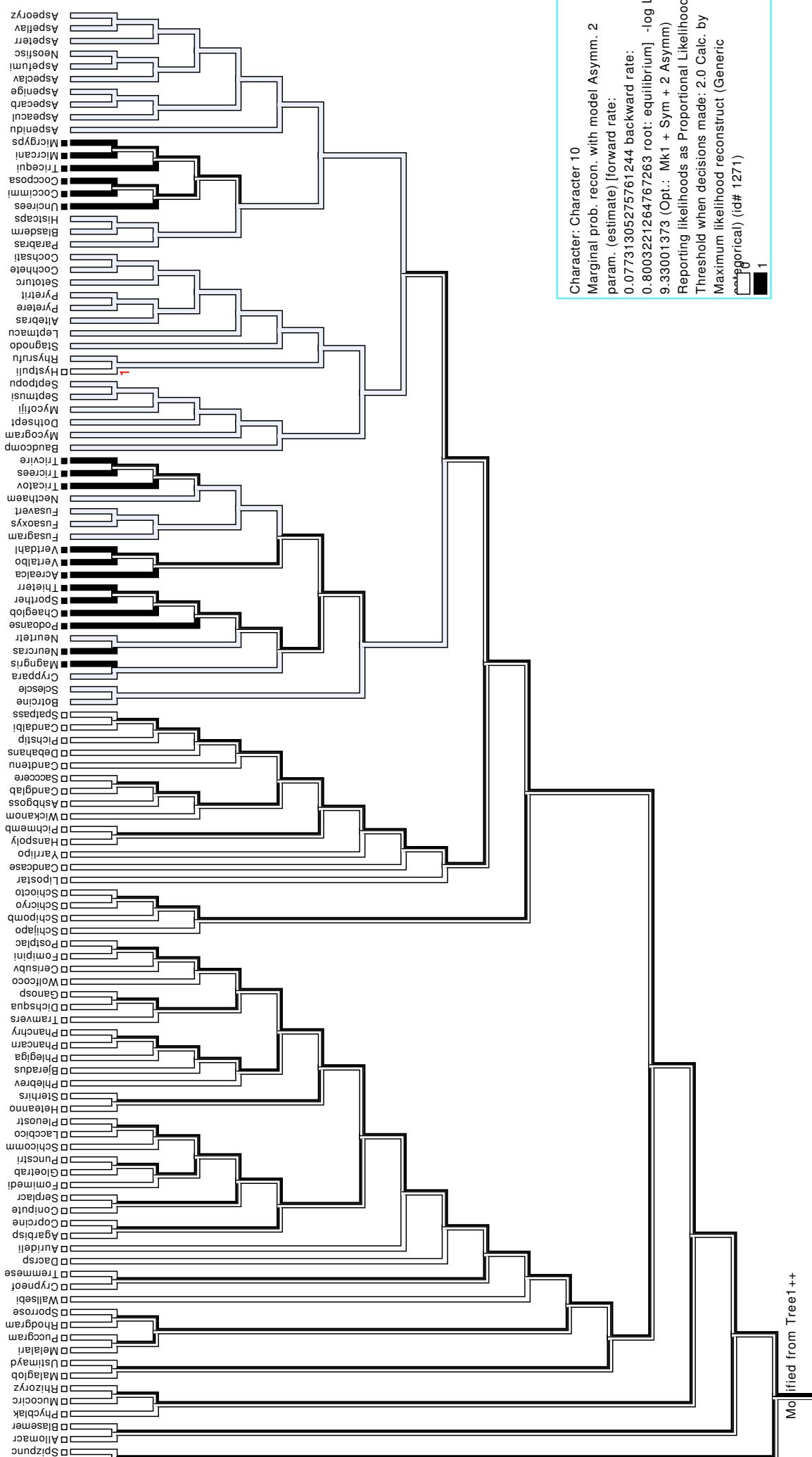
2.1 Important Notes

There is only one phylogeny here as one domain consists of a series of repeats and so an alignment would not be possible as the resulting phylogeny would likely be unresolved.

3 Mesquite Cladogram

This tree is the 68-gene concatenated phylogeny (Fig. 1), with the presence of a fusion (black), presence of a fission (white), and absent/undetermined (grey) status of gene fusion characters plotted on to it using a "1/0/-" nexus-style data matrix. We used the program 'Mesquite' to calculate proportional likelihoods based on either an "Mk1" or "Assym. 2 param model." (see Table S4) of character change across the fungal phylogeny (Fig. 1). This allowed for a proportional likelihood of the position of the fusion/fission to be calculated.





Putative Fusion 11

September 26, 2012

1 Fasta Sequences

These are the unfused sequences identified by fdfBLAST belonging to the putative gene fusion in FASTA format. Accessions may be shortened, but belong to either the taxons individual genome project or NCBI's accession numbering.

```
>lcl|6322220Sc unnamed protein product
MKFFSLADEAEFKSIIISKNKAVDViGSKLGQVVSFSDEWFASAENLIQPTAPIRDPTRFVHSGAWYDGWETRRHNEME
YDWVIIKMGVAAAHIIGGEIDTAFFNGNHAPFVSIEALYDEGEEGNIVEEDDSRWVEIVEKFECGPSQRHLFVRGNGLTKE
RFTHIKLKMYPDGGIARFRLYGRVVPELKTKDHIIDLAYVCNGAVALKYSDQHFGSVDNLLPGRGHDMSDGWETKRSR
QPQHTDWAVIQLGRESSFIEKIIIVDTAHFRGNFPQFITVEGCLKESESENTGEGTWVELVGKSKTGPDKEHVYEIRKSI
RVSHVKLTIIIPDGGVKRIRVWGY
>lcl|6322223Sc unnamed protein product
MVTVVAETLTKESFEYGTIISPDEEISRMQNLEKGANQGTAIKLLQVSQVENKSTSKVPNWNLFRCFPQPHLNRVFTQG
SNQAISHSIKVLEKHPCSTQTFVPMGRTSAEVAYLVVVAKEIGNKPDLSTLRAFTCLGNQAVTYGLGTWHAPMIVLGKEE
HLDHSVLIYESLDPDRPEKDCVEEHYSDGDVCIII
```

2 Annotated Phylogenograms

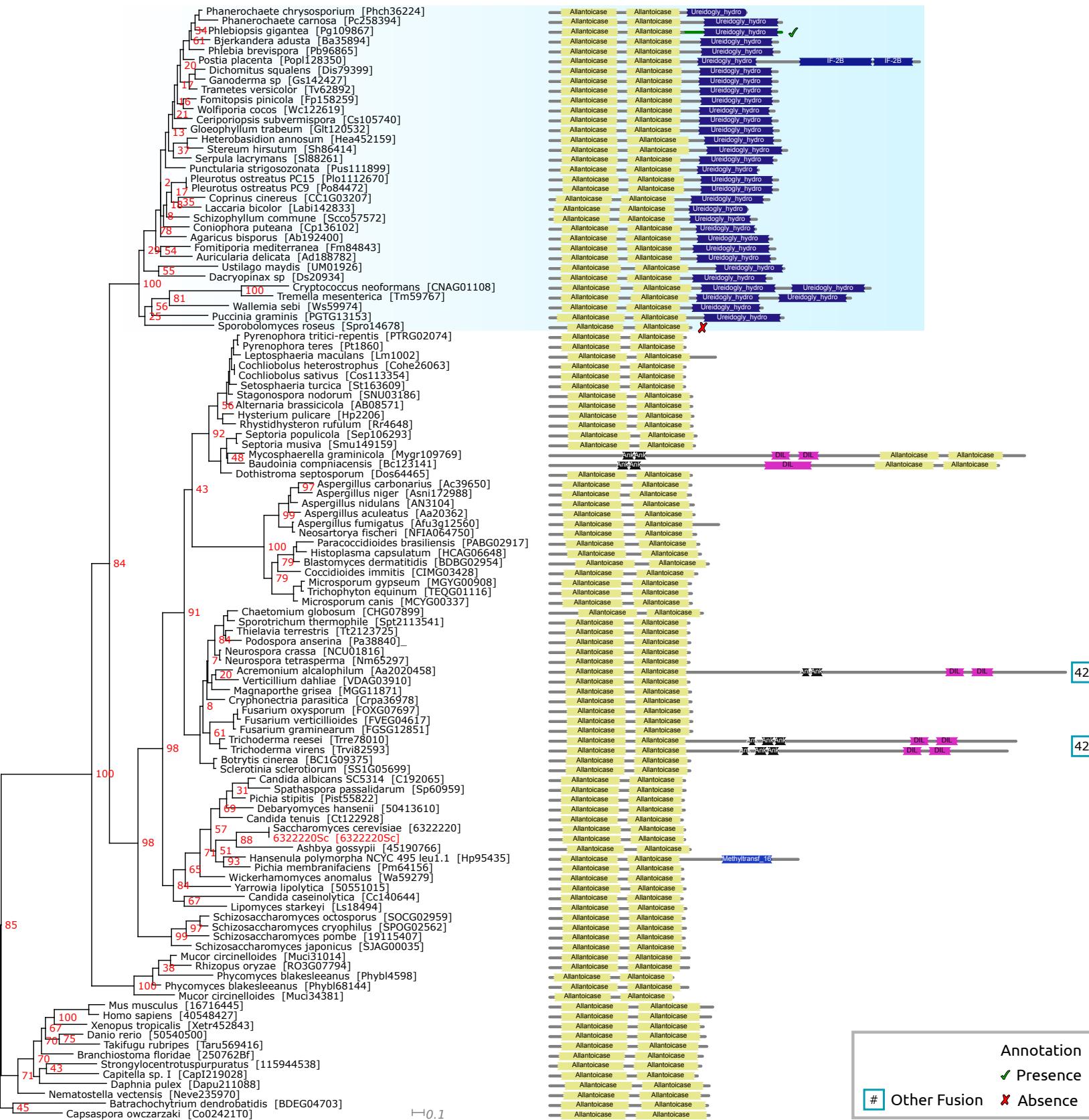
All trees were generated from an initial run of Darren's Orchard pipeline against 139 taxa (Table S1), using the above corresponding un-fused sequences as BLAST seeds. The alignments were then checked for any missing taxa, manually masked and then ProtTest3 was run, please see the Methods section for detail. The final trees were generated by the following command:

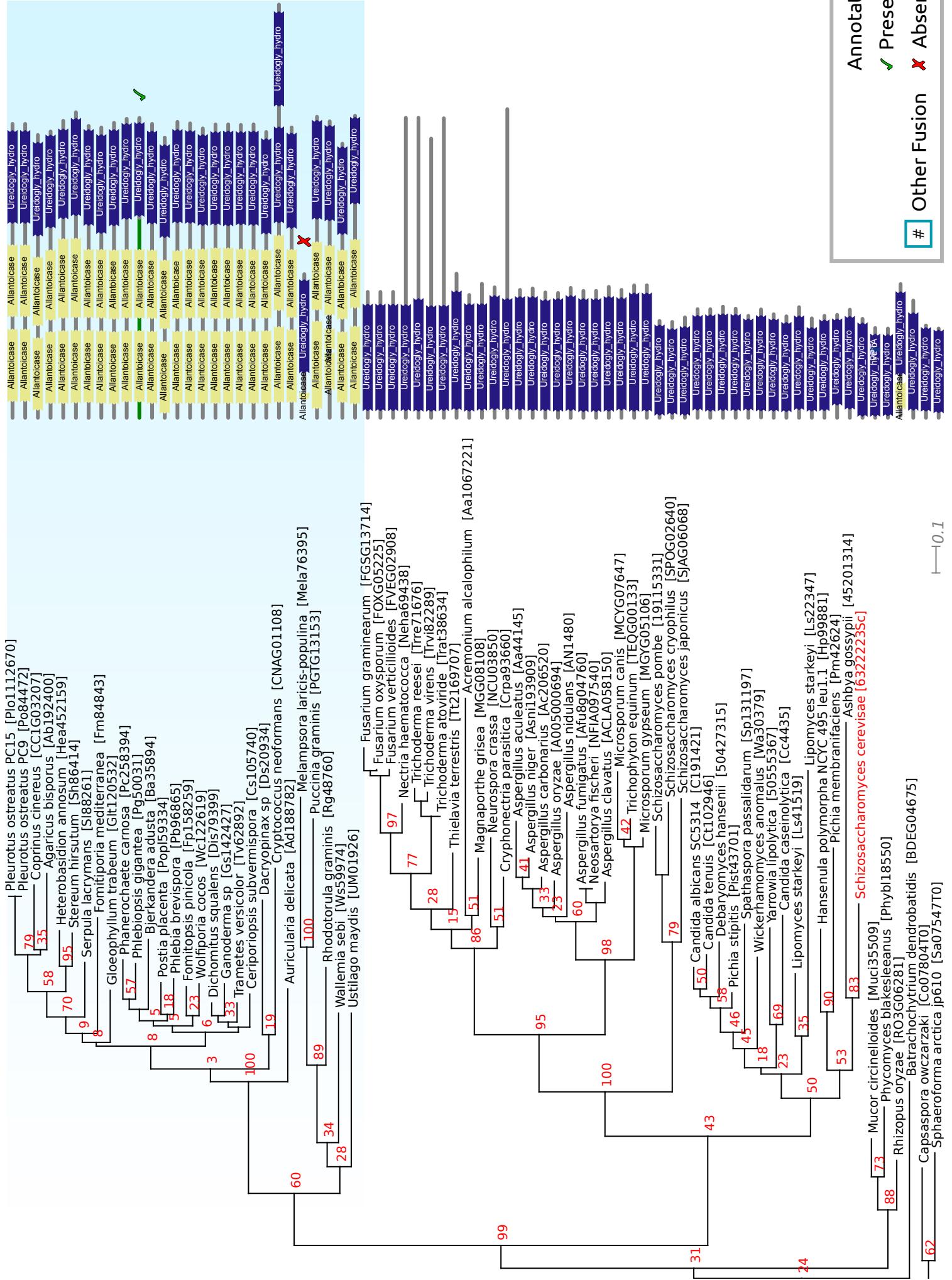
```
phylml -i alignment_file -d aa -b 100 -m model -c 8 -v invariant_sites -s BEST --quiet
-a gamma
```

Styling and annotation was made possible by Dendroscope and Inkscape.

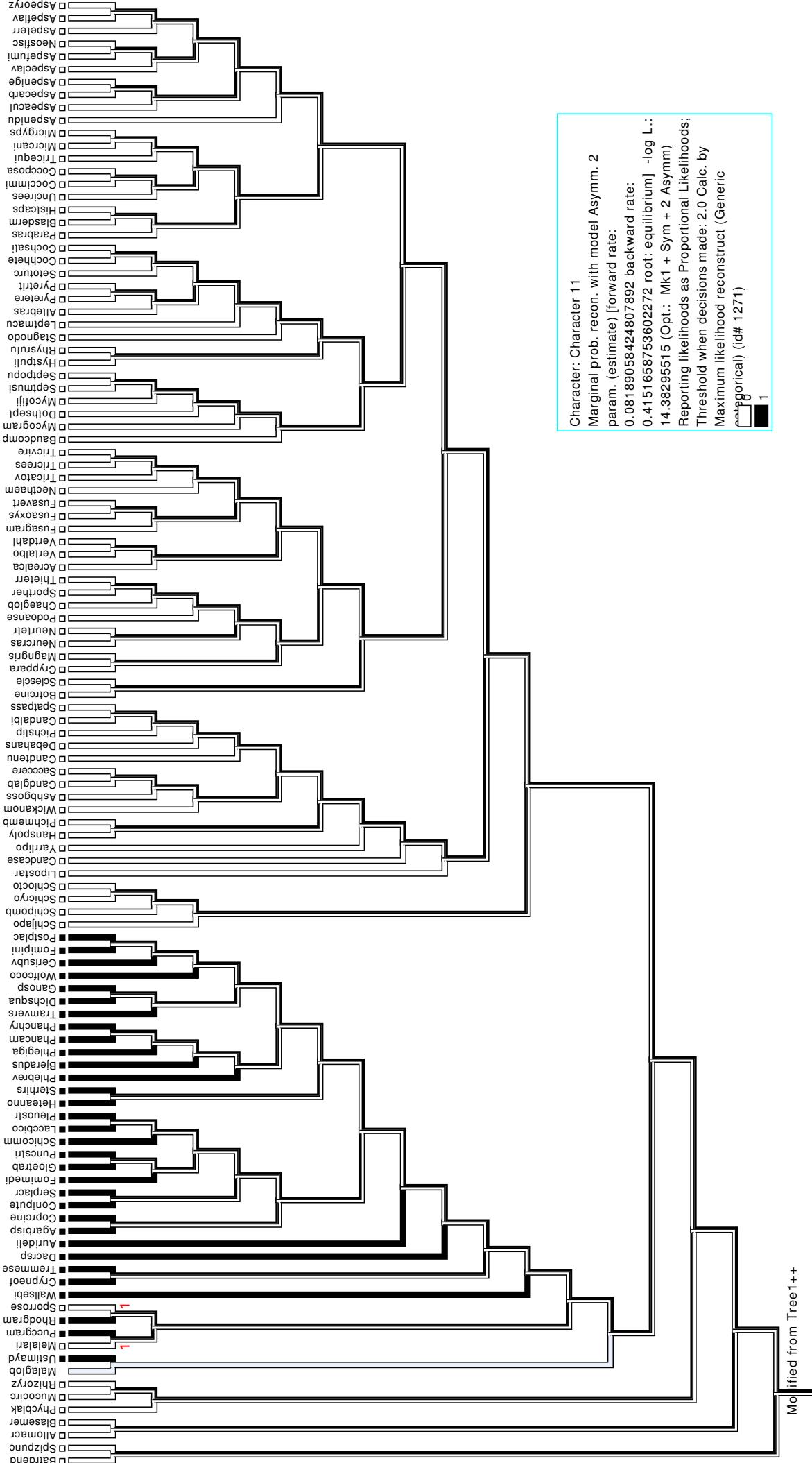
3 Mesquite Cladogram

This tree is the 68-gene concatenated phylogeny (Fig. 1), with the presence of a fusion (black), presence of a fission (white), and absent/undetermined (grey) status of gene fusion characters plotted on to it using a "1/0/-" nexus-style data matrix. We used the program 'Mesquite' to calculate proportional likelihoods based on either an "Mk1" or "Assym. 2 param model." (see Table S4) of character change across the fungal phylogeny (Fig. 1). This allowed for a proportional likelihood of the position of the fusion/fission to be calculated.





—|—0.1



Putative Fusion 12

September 26, 2012

1 Fasta Sequences

These are the unfused sequences identified by fdfBLAST belonging to the putative gene fusion in FASTA format. Accessions may be shortened, but belong to either the taxons individual genome project or NCBI's accession numbering.

```
>lcl|AMAG_02423 unnamed protein product
MDLFSTLHPSQASTPSVFEVAQEQLHNLLSPALRSVLASYAIRYPRYLLRVLQFHDELFALLMLVVQRHYLRTSKASFA
ESFYGLKRARTVVVPYLKQQLHEHLREWSTELGTDVLDGESDGSITESVELPATPATAAARRRTKLKRLFLKIYPLV
HFVYTGTTHLVYQLLYMFWDWTRYSPPLLHVLGVEVKRVTSADMRAQMRIAASAPPRTGLAAAGHVALEALKVGLPVAIFFS
KFLDWFAATTDYARQERRRVPIPPPPrVQPPDPKGVPPLKDPTCPLCCRAVTNAAALPTGVVYCYPVCFRAVQDNGVCPV
TRKPVVVGDIRRVFQSQ
>lcl|AMAG_14666 unnamed protein product
MKFGKQIQNQAITEWSQYYINYKALKVINSLEKSQQLHDGTPNGGSASATSAHSITIAASPVLLDSEPPSFADAHTDPI
QAHKAFFYKLERELEDRVNAYLTKEFDLKVRSLSLKKRLAQGSQAVRGTHAAKNHGANLRTIQEALWHLQQDLTKLQ
QFVALNAEGFRKILKKWDKRSKSSTKELYLSRQVEIQPCFNRTDTTELTDIVSTHAAELSMDLAAVASPAPGPVLGAGA
TTALARSDSLLDDLESDELAHVVKAGATDRLRDTLARLRTASPAQATTAVSVRLVRACRQGGAKAADAVAVLVESGFADVH
YRDEINDRTALHAATLAGDVAIVRTLLTAGADGAARDVYGRTPHYAAMHGFTEVAVLVGGLDRIKVDAEGANEEDDDR
SVCVAPDHDFGSPLIYAIIGGFTDIVAKLLDQHPQLLQTTVPHVLSLAQYGHVDIATLLLAKGAPIAPEEGLHPLHIT
AKQGHVTLLCDHMASVDTSDKYYNWTPLFYAASEGHQDCVEVLLEYGASTNLVDETGWTVLHTLYRGHIAAVVLW
EHMQRYKAMHPPSATASPALFLAANATPAVIQPIAPSGLLRPRTNTAPAVPAAADDADGDPMDFDAIPSLALPPPIPFR
IYGHTYLESKYQVQIAVPVAPVLYAQKLASLRVLAAPDPGAVPHTLILPADDEREAVAFQAANLDVFSLHIDVFPTY
TRPIARAABLVLVRARHGETLGADPSSHAPTHGRVVVPLFDAMNVVGELTLDYALIAPFNHPKLAvggpiatywkttq
VVSAVAAAGAATAAAAGTRPTGLLAHPGVSSLMPSPTLPSGGPTTPSGIIPAAHGTVASLITASSLAQKYVHVVVQLTV
DLVPVLYPTWHVTVPGLPGGGVGIQVPAQLTHAQFQAVGRADPRLVDSLAPSSATLAHALRHAYLSLGEALDALPS
DTALFVELKYPTALDAARHRLPCTASVDFVFDKVLTAVYDRAAPRALVFASFSPLACNAVWKQPNNYPVFFNTWAGYPPE
AADASTALLGIDAPPAAVVDADAVPDARCASIKEAIRFTKHNNLLGVCFARPLIQVPALIQAVKEAGLILATFGAENAVP
QHVLQAQEKGVDGVYSDGVVRFTSAAGVI
```

2 Annotated Phylogenograms

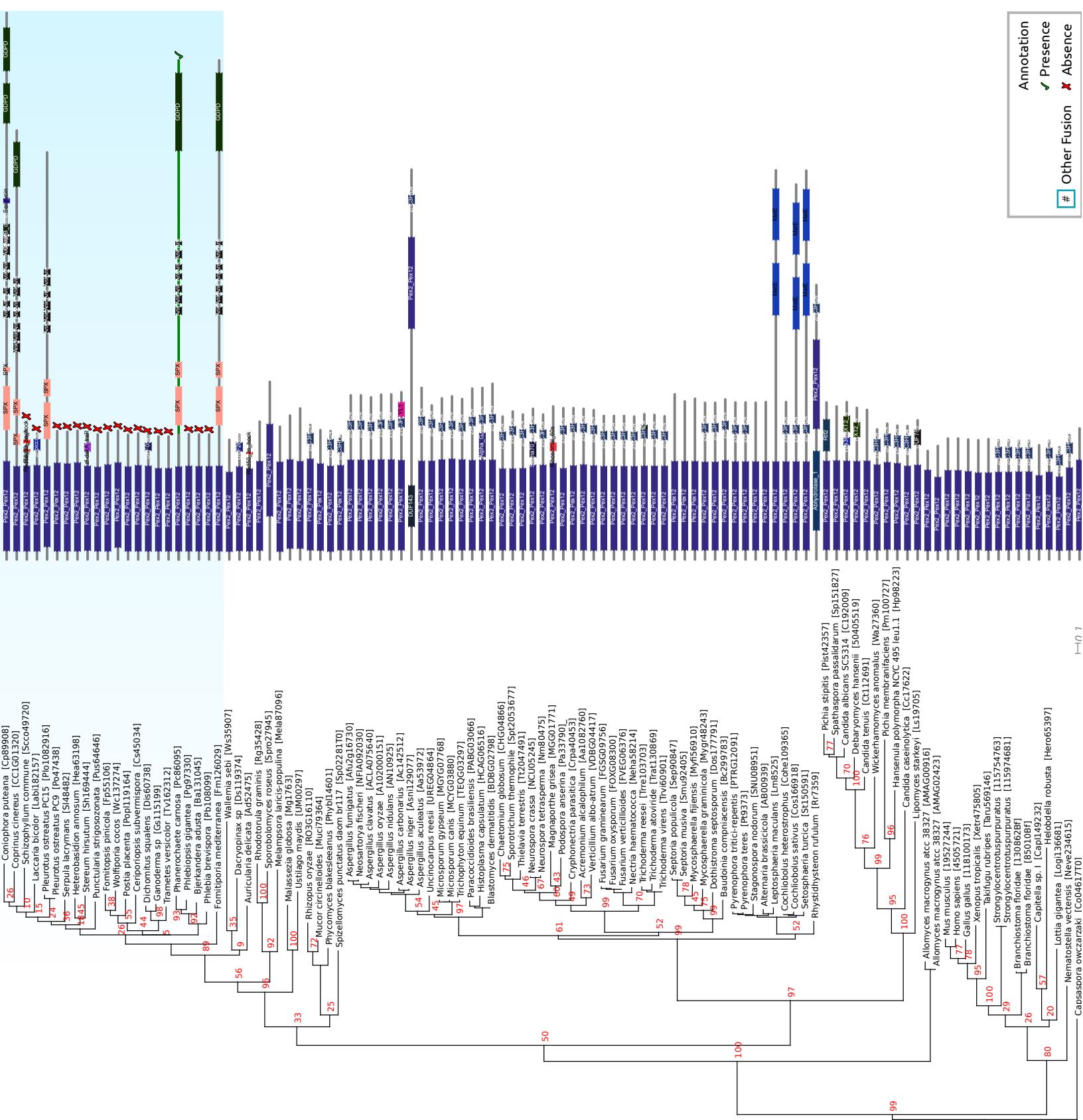
All trees were generated from an initial run of Darren's Orchard pipeline against 139 taxa (Table S1), using the above corresponding un-fused sequences as BLAST seeds. The alignments were then checked for any missing taxa, manually masked and then ProtTest3 was run, please see the Methods section for detail. The final trees were generated by the following command:

```
phyml -i alignment_file -d aa -b 100 -m model -c 8 -v invariant_sites -s BEST --quiet
-a gamma
```

Styling and annotation was made possible by Dendroscope and Inkscape.

3 Mesquite Cladogram

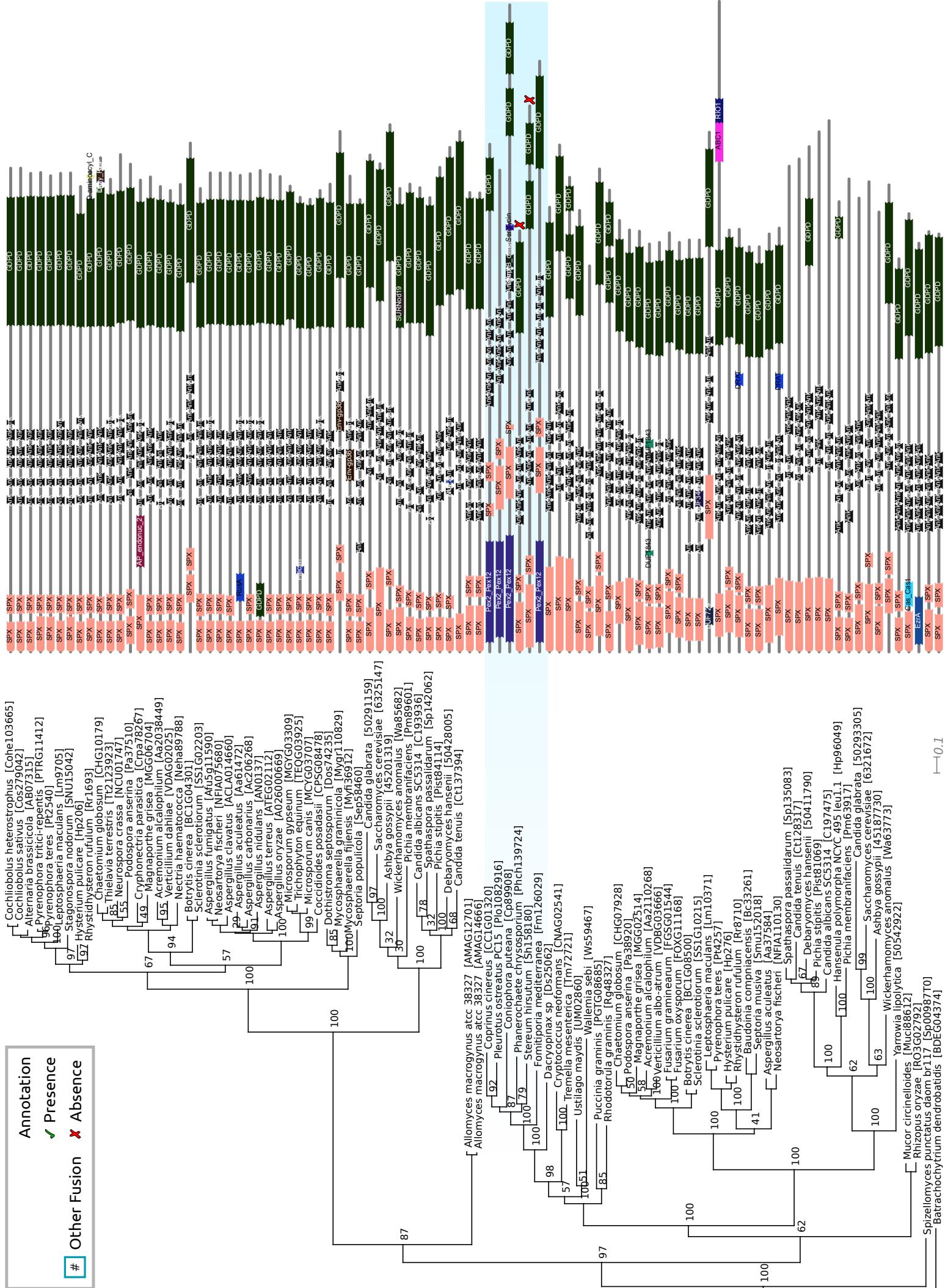
This tree is the 68-gene concatenated phylogeny (Fig. 1), with the presence of a fusion (black), presence of a fission (white), and absent/undetermined (grey) status of gene fusion characters plotted on to it using a "1/0/-" nexus-style data matrix. We used the program 'Mesquite' to calculate proportional likelihoods based on either an "Mk1" or "Assym. 2 param model." (see Table S4) of character change across the fungal phylogeny (Fig. 1). This allowed for a proportional likelihood of the position of the fusion/fission to be calculated.

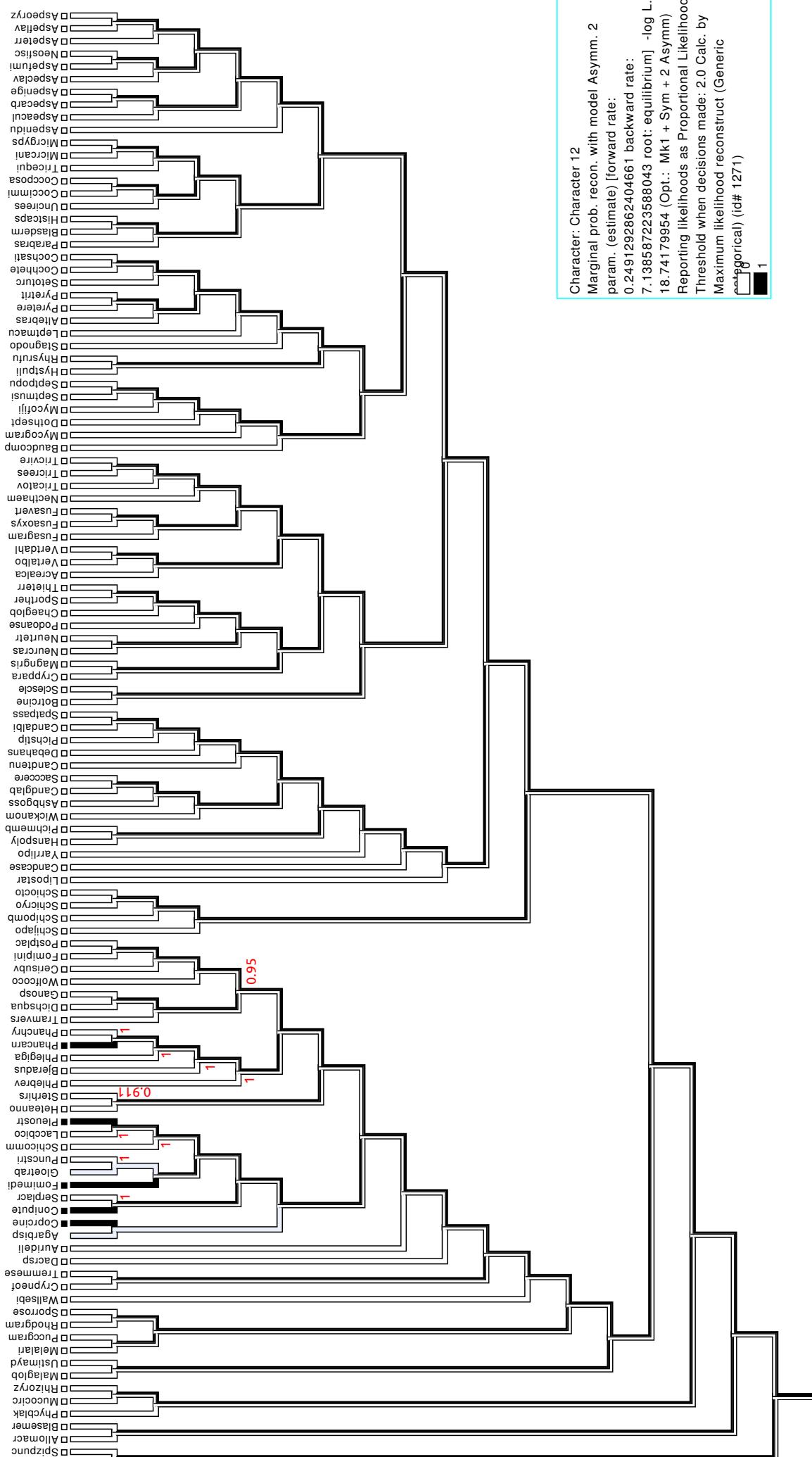


Annotation
✓ Presence
✗ Absence

Other Fusion

—|—|—





Putative Fusion 13

September 26, 2012

1 Fasta Sequences

These are the unfused sequences identified by fdfBLAST belonging to the putative gene fusion in FASTA format. Accessions may be shortened, but belong to either the taxons individual genome project or NCBI's accession numbering.

```
>lcl|6325326Sc unnamed protein product
MAQEITHPTIVDGWFREISDTMWPQAMTLKVEKVLHHEKS KYQDVLIFKSTTYGNVLVLDNVIQATERDEFAYQEMIAH
LALNSHPNPKVKVLVIGGGDGGVLREVVKHDSVEEAWLCDIDEAVIRLSKEYLPPEMAASYSHPKVKTHIGDGFQFLRDYQN
TFDVIITDSSDPEGPAETLFQKEYFQLLN SALTEKG VITTQAESMWIHLPIIKDLKKACSEVFVVAEYSFVTIPTYPTGT
IGFMVCSKDKTCNVKKPLREISDEKEAELYRYYNKKIHEASFVLPWAAKELN
>lcl|6324378Sc unnamed protein product
MGKNVLLGSGFVAQPVIDT LAANDINVTVACRT LANAQALAKPSGSKAISLDVTDDSALDKVLADNDVVISLIPYTFH
PNVVKS AIRTKTDVVTSYISPALRELEPEIVKAGITVMNEIGLDPGIDHLYAVKTIDEVHRAGGKLKSFLSYCGGLPAP
EDSDNPLGYKFSSRGVLLALRNSAKYWDGKIETVSSEDLMATAKP YFIYPGYAFVCYPNRDSTLFKDLYHIPEAETV
IRGTLRYQGFPEFVKALVDMGMLKDDANEIFS KPIAWNEALKQYLGA KSTSKE DLIASIDS KATWKDDEDRERILSGFAW
LGLFSDAKITPRGNALDTLCARLEELM QYEDNERDMVVLQHKFGIEWADGTETRTSTLV DYGVGGYSSMAATVGYPVA
IATKFVLDGT IKGPGLLAPYSPEINDPIMKELKDYGIYLKEKTVA
```

2 Annotated Phylogenograms

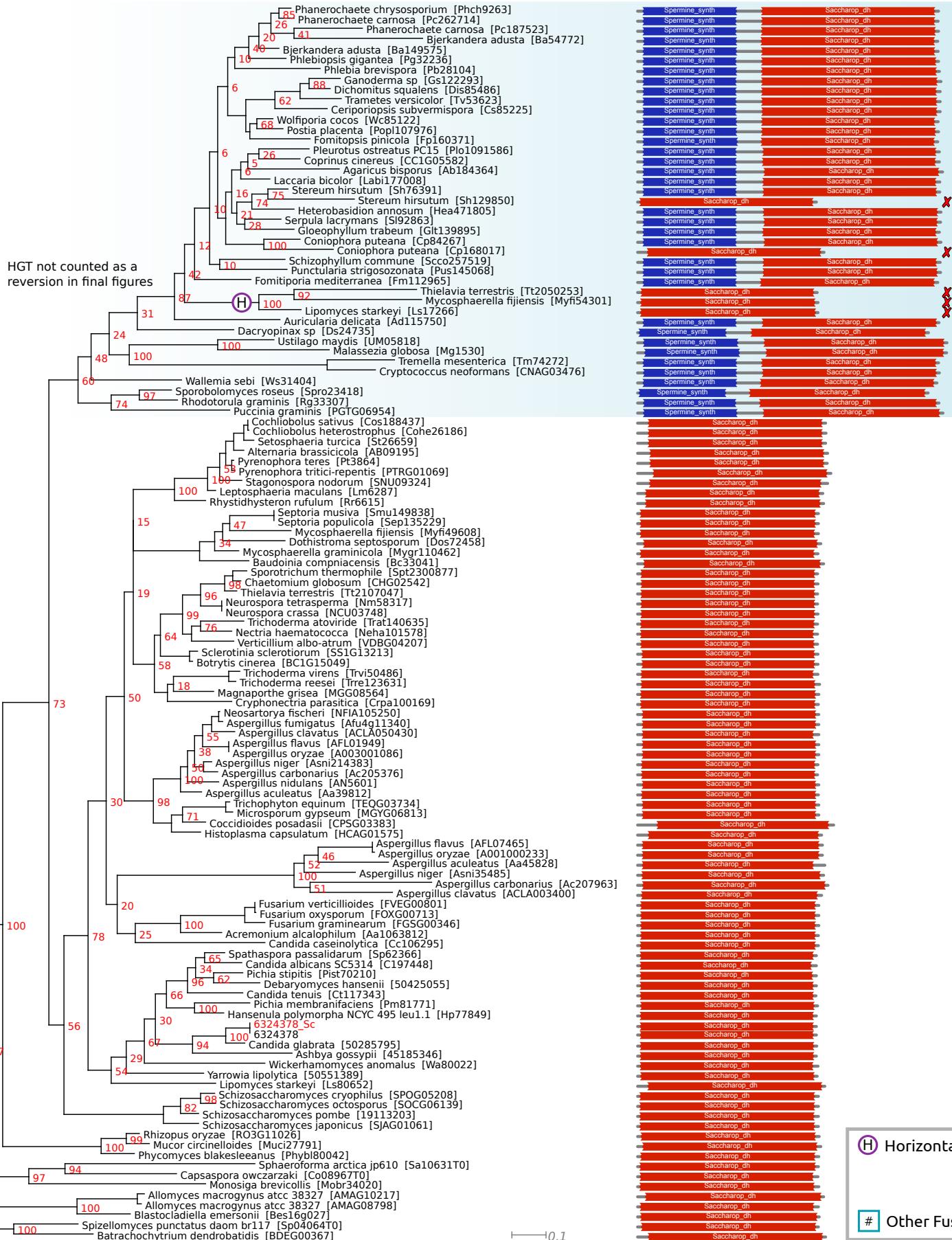
All trees were generated from an initial run of Darren's Orchard pipeline against 139 taxa (Table S1), using the above corresponding un-fused sequences as BLAST seeds. The alignments were then checked for any missing taxa, manually masked and then ProtTest3 was run, please see the Methods section for detail. The final trees were generated by the following command:

```
phyml -i alignment_file -d aa -b 100 -m model -c 8 -v invariant_sites -s BEST --quiet
-a gamma
```

Styling and annotation was made possible by Dendroscope and Inkscape.

3 Mesquite Cladogram

This tree is the 68-gene concatenated phylogeny (Fig. 1), with the presence of a fusion (black), presence of a fission (white), and absent/undetermined (grey) status of gene fusion characters plotted on to it using a "1/0/-" nexus-style data matrix. We used the program 'Mesquite' to calculate proportional likelihoods based on either an "Mk1" or "Assym. 2 param model." (see Table S4) of character change across the fungal phylogeny (Fig. 1). This allowed for a proportional likelihood of the position of the fusion/fission to be calculated.



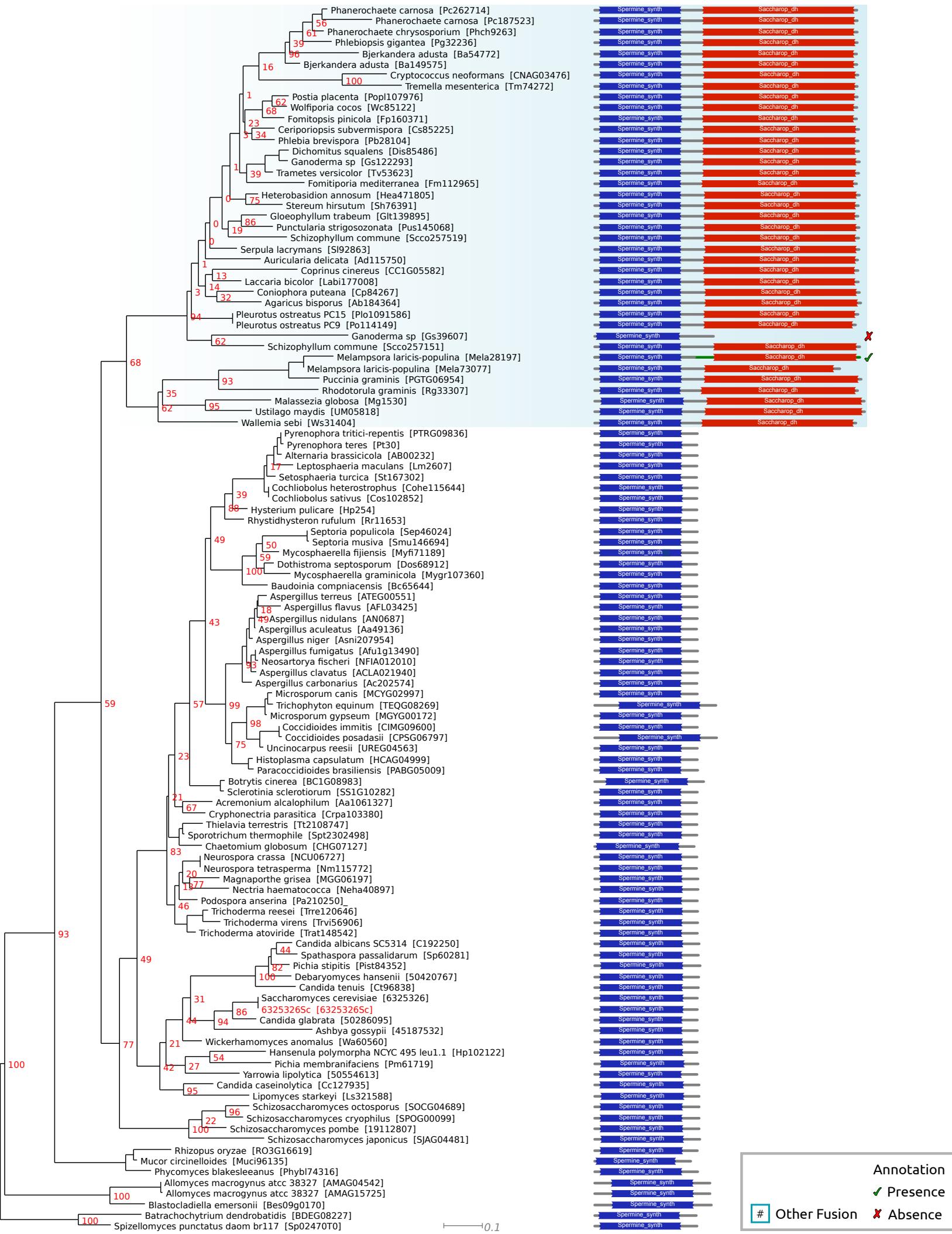
(H) Horizontal Gene Transfer?

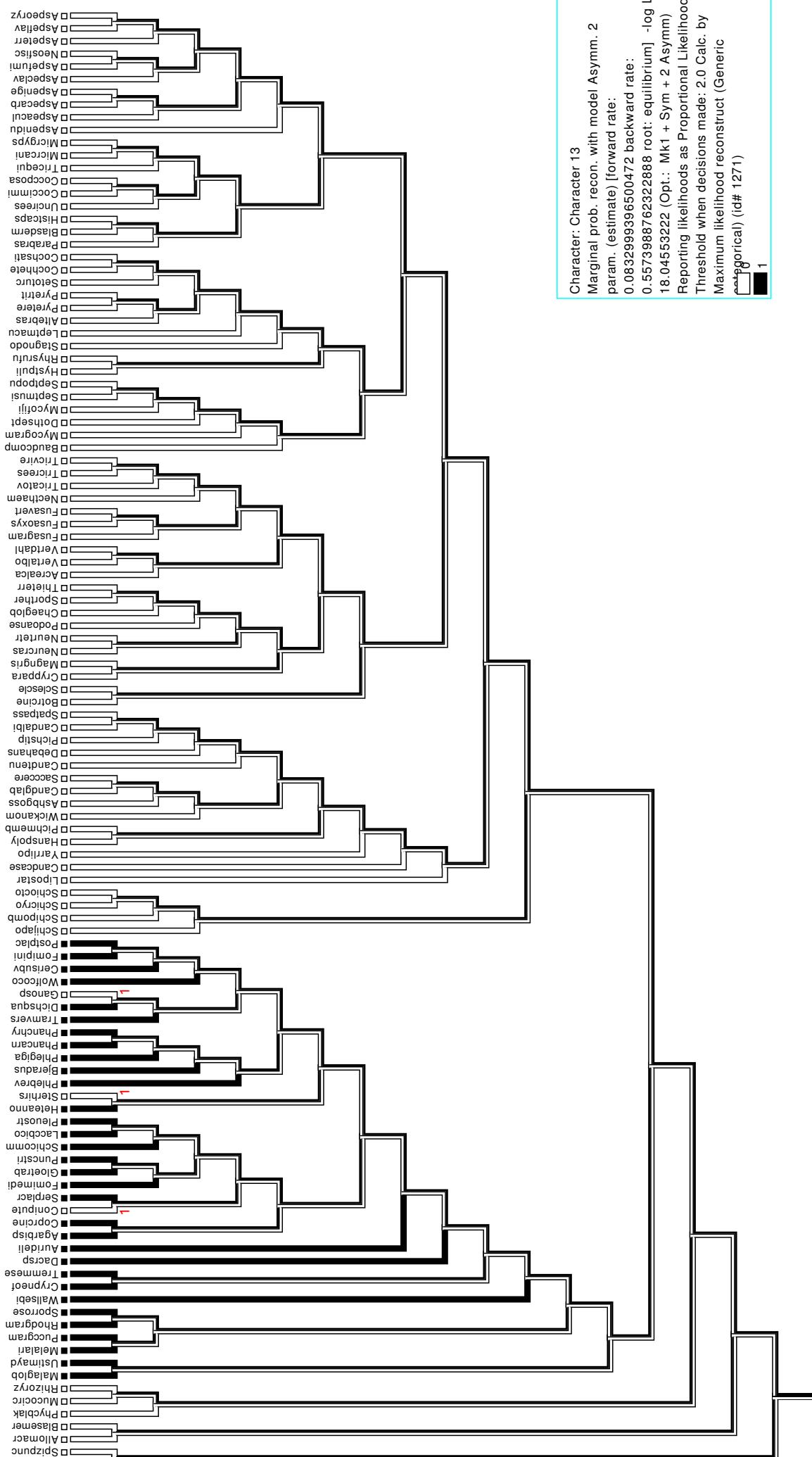
Annotation

✓ Presence

Other Fusion

X Absence





Putative Fusion 14

September 26, 2012

1 Fasta Sequences

These are the unfused sequences identified by fdfBLAST belonging to the putative gene fusion in FASTA format. Accessions may be shortened, but belong to either the taxons individual genome project or NCBI's accession numbering.

```
>lcl|6321254Sc unnamed protein product
MPIKRLDTVNTGSQNDQHSASVPPVYLSTTFKVDLNNEDAQNYYDYSRSGNPTRSVLQHQIGKLYRVPQENVLAVSSGM
TALDVLIRGLVLLNGTDNHTPTIAGDDLYGGTQRLLNFFKQQSHAVSVHVDTSDFEKFKTVFQSLDKVDCVLLESPTNP
LCKVVDIPRILRFVKCISPDTVVVDNTMMSGLNCNPLQLNPGCDVVYESATKYLNGHHDLMGGVIISKTPEIASKLYFV
INSTGAGLSPMDSWLLVRGLKTLGVRLYQQQRNAMILAHWLENSCGFKPTRTNKATKTRFVGLRSNPDFKLHKSFNNPGP
AVLSFETGSFEHSKRLVSSKKLSIWAVTVSGCVNSLLSMPCKMSHASIDPELRKERDFPEDLVRLLCGIENIVDLKKDL
LAAMVDADIIEVRENGKYLNFNKNLNAVNTTIDDLHKPLSIYEEFYQNQDLIRKDSELNIKSSKL
>lcl|6323864Sc unnamed protein product
MSLPFLTSAPGKVIIFGEHSAVYNKPAVAASVSALRTYLLISESSAPDTIELDFPDISFNHKWSINDFNAITEDQVNSQK
LAQAQQATDGLSQELVSLLDPLLAQLSESFHYHAFCFLYMFVCLCPHAKNIKFSLKSTLPIGAGLGSSASISVSLALAM
AYLGGLIGSNDLEKLSENDKHIVNQWAFIGEKCIHGTPSGIDNAVATYGNALLFEKDSHNGTINTNNFKFLDDFPAIPMI
LTYTRIPRSTKDLVARVRVLVTEKFPEVMKPILDAMGECALQGLEIMTKLSKCKGTDEAVETNNELYEQLLELIRINHG
LLVSIGVSHPGLELIKNLSDLRIGSTKLTGAGGGCSLTLLRRDITQEIQIDSFKKKLQDDFSYETFETDLGGTGCCLLS
AKNLNKDLKIKSLVFQLFENKTTKQQIDDLLPGNTNLPWTS
```

2 Annotated Phylogenograms

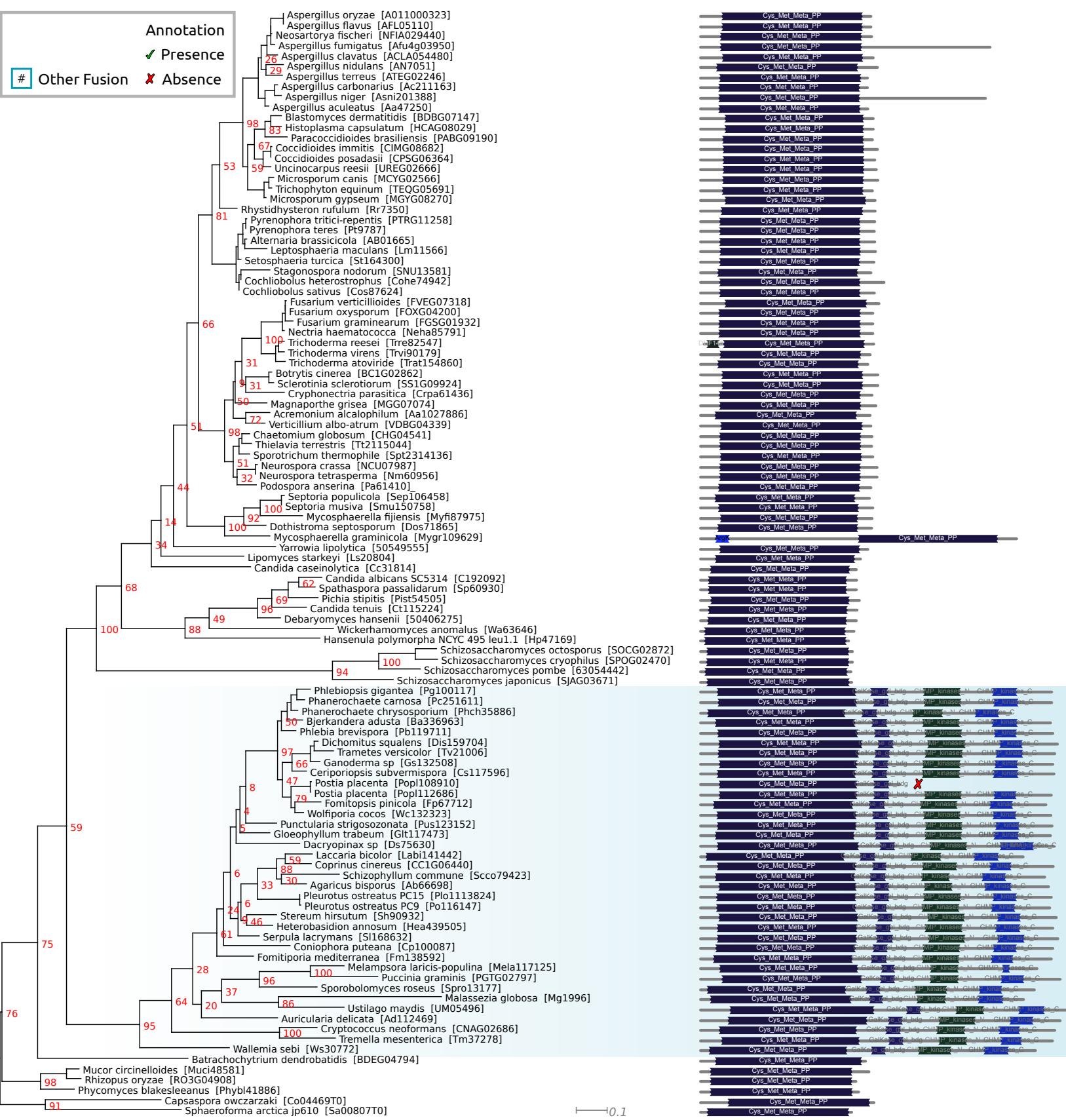
All trees were generated from an initial run of Darren's Orchard pipeline against 139 taxa (Table S1), using the above corresponding un-fused sequences as BLAST seeds. The alignments were then checked for any missing taxa, manually masked and then ProtTest3 was run, please see the Methods section for detail. The final trees were generated by the following command:

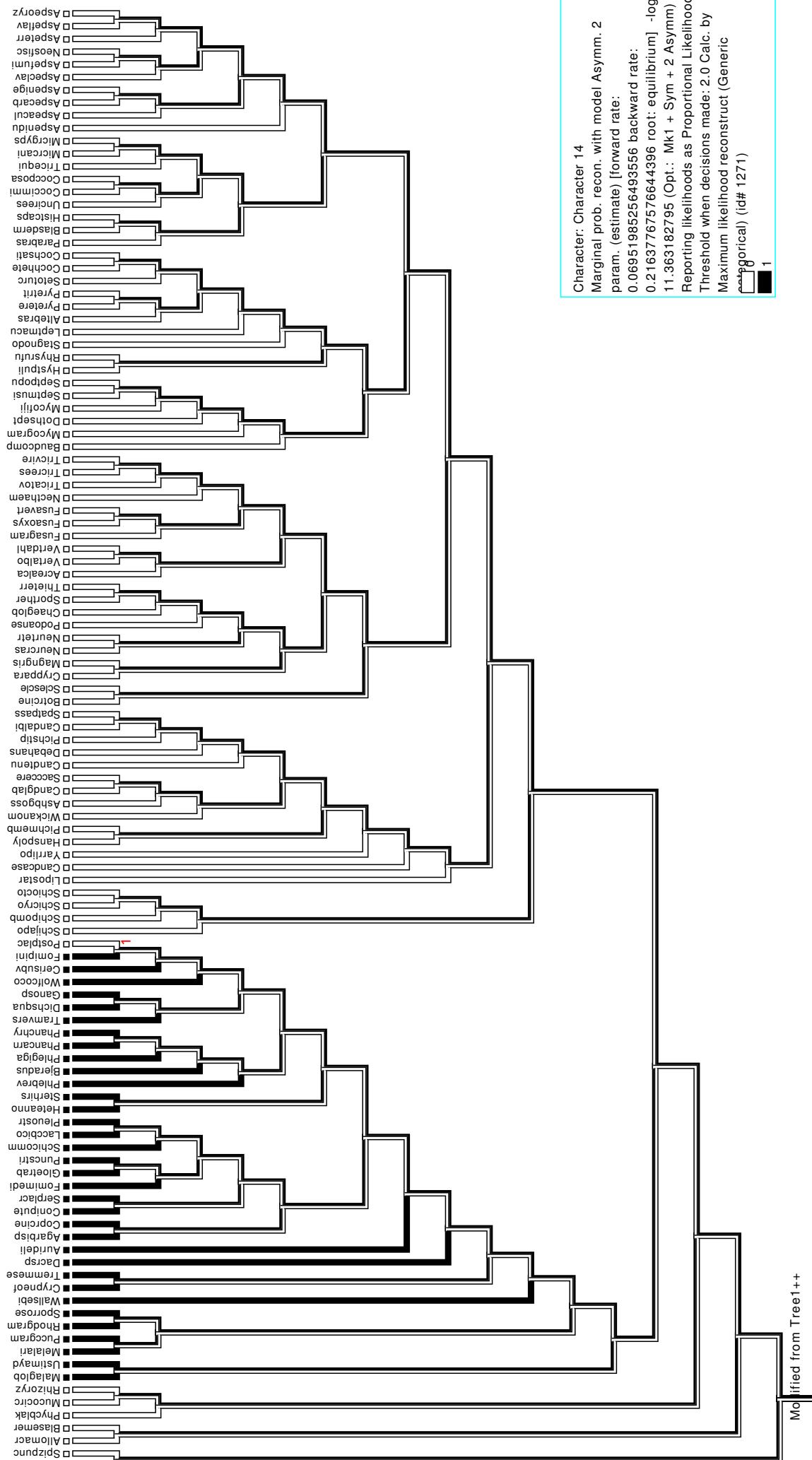
```
phyml -i alignment_file -d aa -b 100 -m model -c 8 -v invariant_sites -s BEST --quiet
-a gamma
```

Styling and annotation was made possible by Dendroscope and Inkscape.

3 Mesquite Cladogram

This tree is the 68-gene concatenated phylogeny (Fig. 1), with the presence of a fusion (black), presence of a fission (white), and absent/undetermined (grey) status of gene fusion characters plotted on to it using a "1/0/-" nexus-style data matrix. We used the program 'Mesquite' to calculate proportional likelihoods based on either an "Mk1" or "Assym. 2 param model." (see Table S4) of character change across the fungal phylogeny (Fig. 1). This allowed for a proportional likelihood of the position of the fusion/fission to be calculated.





Putative Fusion 15

September 26, 2012

1 Fasta Sequences

These are the unfused sequences identified by fdfBLAST belonging to the putative gene fusion in FASTA format. Accessions may be shortened, but belong to either the taxons individual genome project or NCBI's accession numbering.

```
>lcl|Mc113296 unnamed protein product
MSNHSSSQHNNDATDDGTIPLTQHRLALELKSHPVRGRGVFTKEPLDRNVLVEISPILLFNAEYDTYGKHTVLDQYTY
CWQGGFALALGLGSMFNHNSTPNVGFIIRDIPNKLIRYVTLLRRIEKDEELCISYGNHLWFEDESNTAAAASDSEDEPFPF
QDSSEDEQAYL
>lcl|Mc106337 unnamed protein product
MLYSLLMENKQENSGTRSKQAKSQQEASIPREEWPFEEVLSDEYERHLETIDVYTAHVEPKQTNSILKFAQKKLPSLEGL
EHCKKIRRIAKPETESGFELEVILCKADALDQDKLVDMlkeHQFEDCRISTPVSKHAPLNRRQQFDAWRHVWPMSYREDT
RLDPKFTQQDIDIHSHMQAILANQQHSVVCRVVDPSTNEIMAEKSDTRAEHPLHAAVMNSIDHVAQNESKLYGGCGRMK
RTASQMTAVDDDAEAAAACKAAYLCTGYDIYITHEPCAMCAMALVHSRVSRYFYSIPSKTGSLGTNYKIHAHASLNNHYRV
FRHVLKDAAFTLDSSLQDQEL
```

2 Annotated Phylogenograms

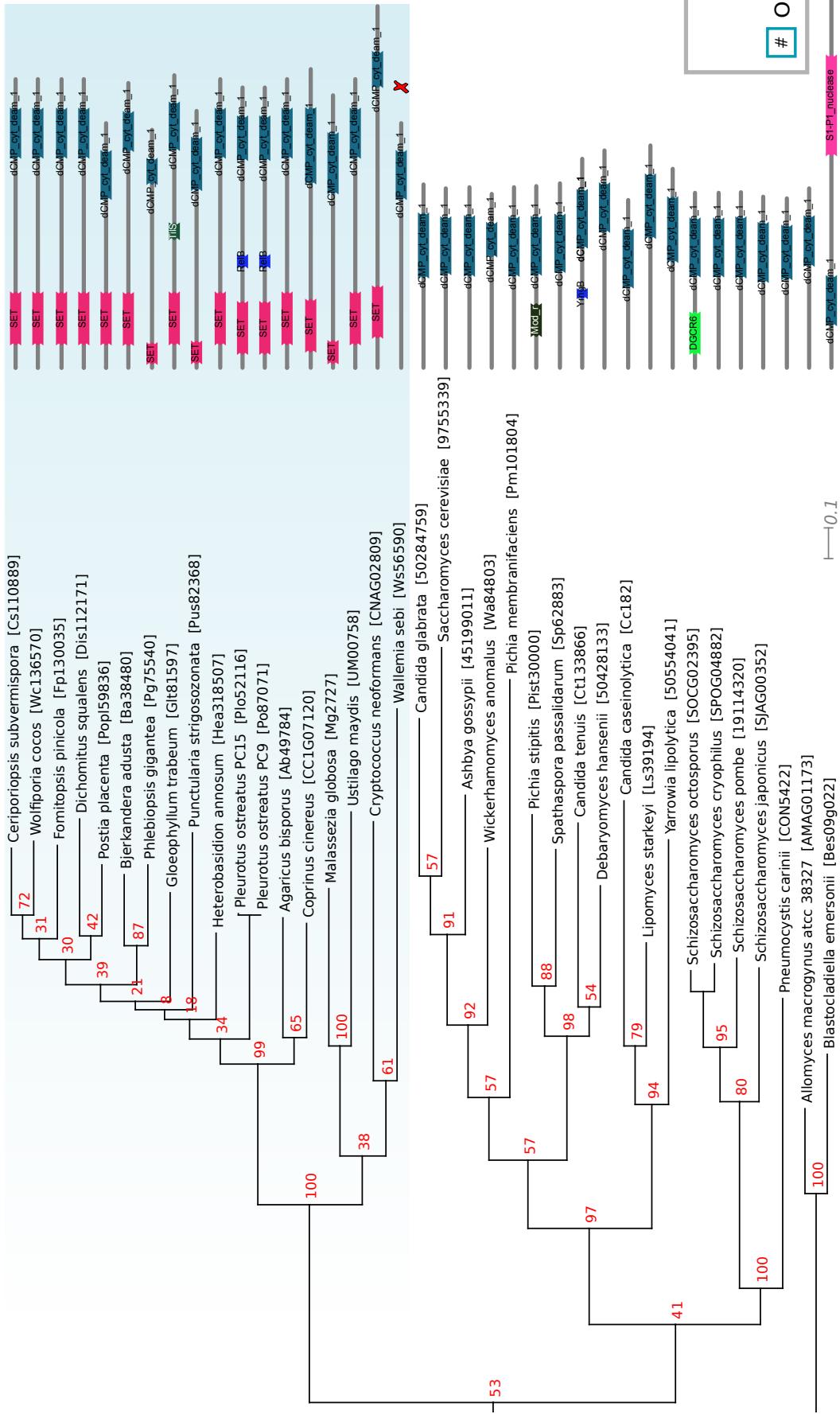
All trees were generated from an initial run of Darren's Orchard pipeline against 139 taxa (Table S1), using the above corresponding un-fused sequences as BLAST seeds. The alignments were then checked for any missing taxa, manually masked and then ProtTest3 was run, please see the Methods section for detail. The final trees were generated by the following command:

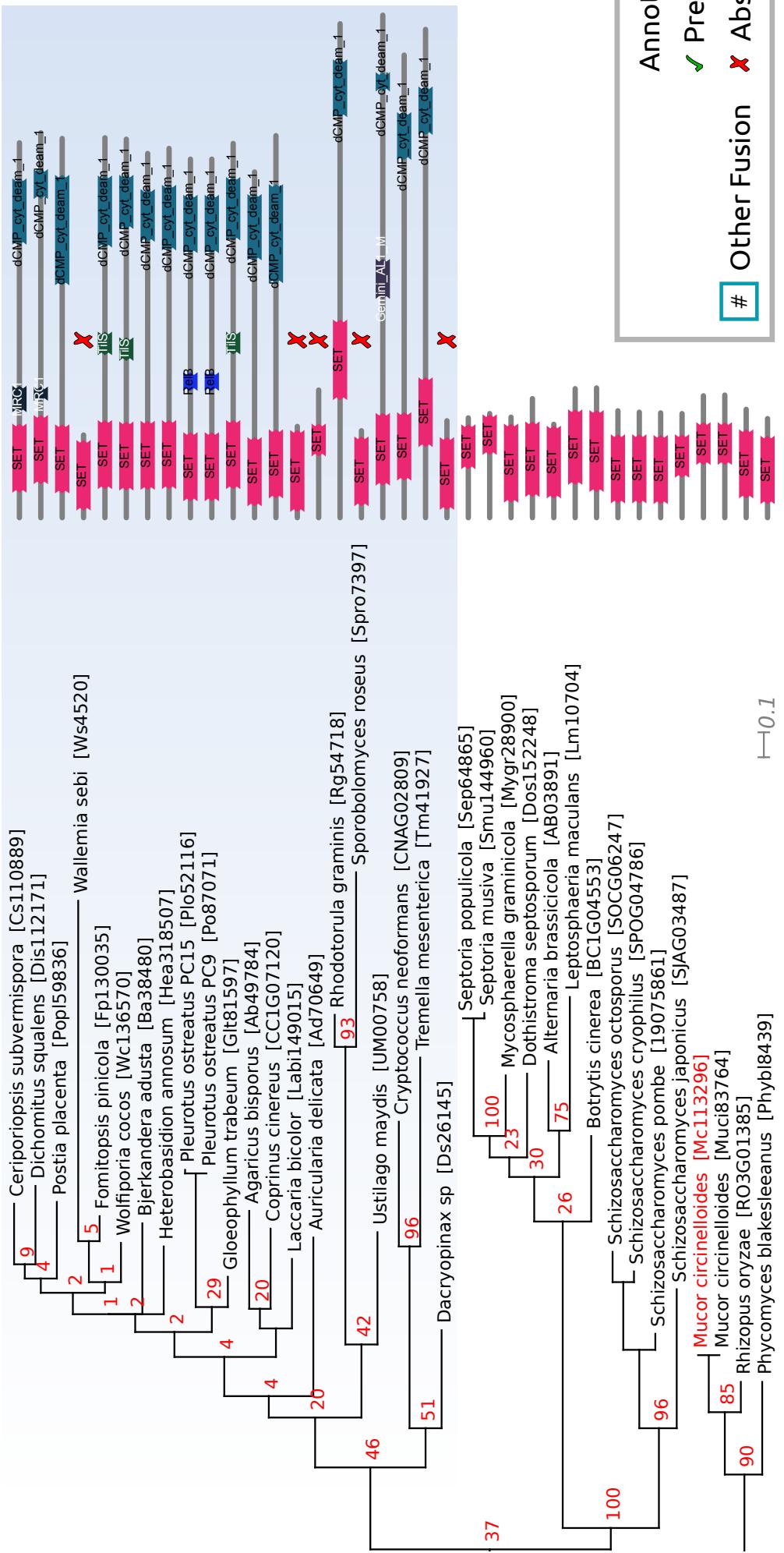
```
phylml -i alignment_file -d aa -b 100 -m model -c 8 -v invariant_sites -s BEST --quiet
-a gamma
```

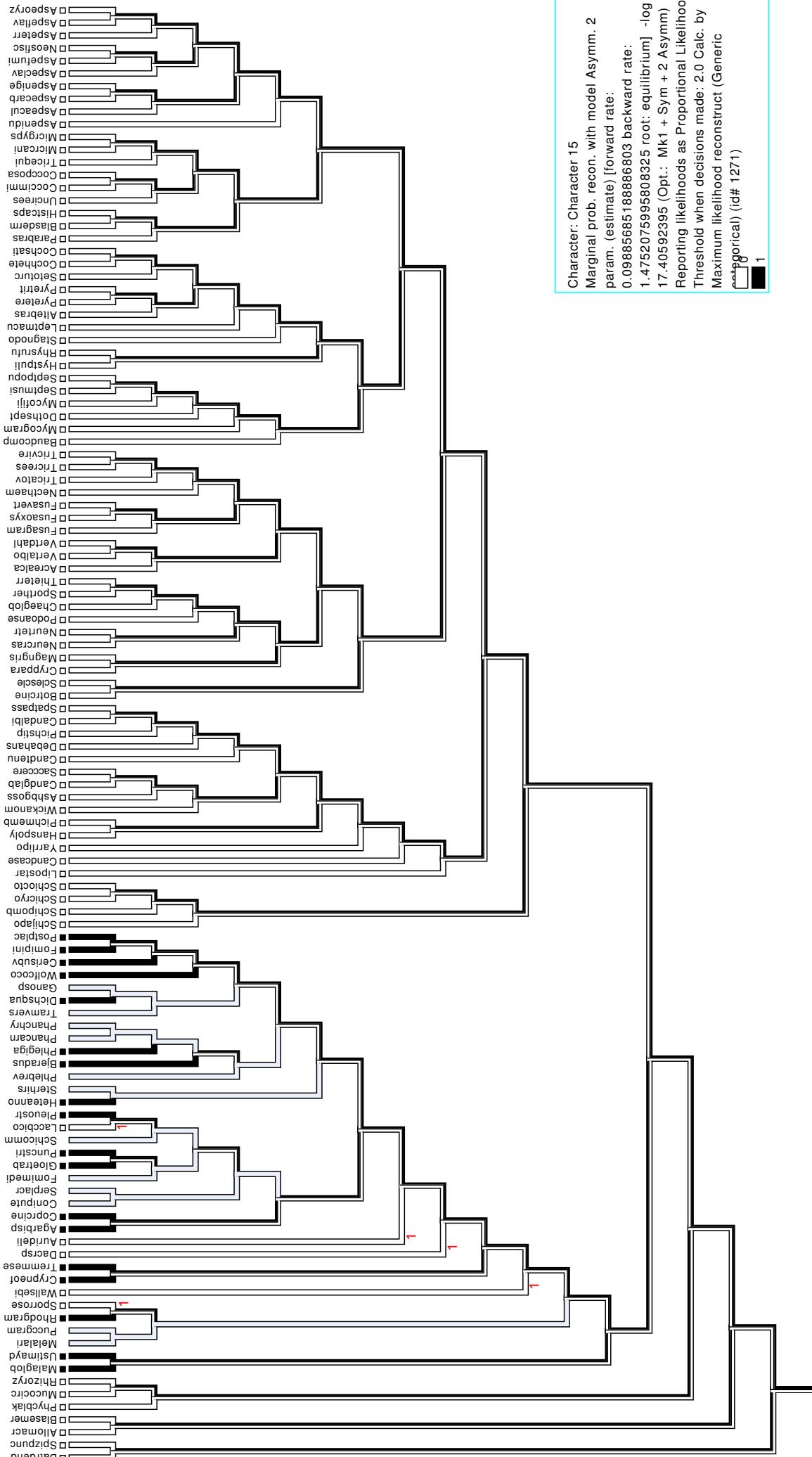
Styling and annotation was made possible by Dendroscope and Inkscape.

3 Mesquite Cladogram

This tree is the 68-gene concatenated phylogeny (Fig. 1), with the presence of a fusion (black), presence of a fission (white), and absent/undetermined (grey) status of gene fusion characters plotted on to it using a "1/0/-" nexus-style data matrix. We used the program 'Mesquite' to calculate proportional likelihoods based on either an "Mk1" or "Assym. 2 param model." (see Table S4) of character change across the fungal phylogeny (Fig. 1). This allowed for a proportional likelihood of the position of the fusion/fission to be calculated.







Putative Fusion 16

September 26, 2012

1 Fasta Sequences

These are the unfused sequences identified by fdfBLAST belonging to the putative gene fusion in FASTA format. Accessions may be shortened, but belong to either the taxons individual genome project or NCBI's accession numbering.

```
>lcl|Mc139598 unnamed protein product
MEHEEDEDCTVQDSTEIIQLEHHIVYSTSYQVPVIYFKATFSDGTPLSHNEIFQYIIPDTYQDAVVSQNDHPILGIPCWY
IHPCDTRSLMNTMTFDPVDYIKVWLSAYGPIVKCSIPTSMFTRS
>lcl|Mc72864 unnamed protein product
MLASSRQFIPSLRTDVVIASAV RTPVGCFNGSLKSLRAIELGGIAAKSAIEKAGIKPEDVEEAYFGNVLQANLGQSPARQ
AILNAGCPETTEATTINKVCASGMKAVMLAAQTICKAGDRNVMVAGGMESMSNAPYYAPRGAAYGHQQLSDAIIKDGLWDA
YNNIHMGSCHAENTAANYNITREDQDNHAIIESYKRAAKAWENGAFDAEIAPVTIKSKKGETVIKDEEYKNVKFDKITSRL
AVFKKDGTVTAANASTLNDGASALVLMSRAKEELGVKPLARIVSYADAATAPIDFTIAPAKALPVALEKAGLTVDISK
FELNEAFSVVARVNEQLMKLDPSKVNVNGGAVALGHPIGSSGSRIIVTLTHLLKSGEFGAAAVCNGGAASSIVIQRE
```

2 Annotated Phylogenograms

All trees were generated from an initial run of Darren's Orchard pipeline against 139 taxa (Table S1), using the above corresponding un-fused sequences as BLAST seeds. The alignments were then checked for any missing taxa, manually masked and then ProtTest3 was run, please see the Methods section for detail. The final trees were generated by the following command:

```
phylml -i alignment_file -d aa -b 100 -m model -c 8 -v invariant_sites -s BEST --quiet
-a gamma
```

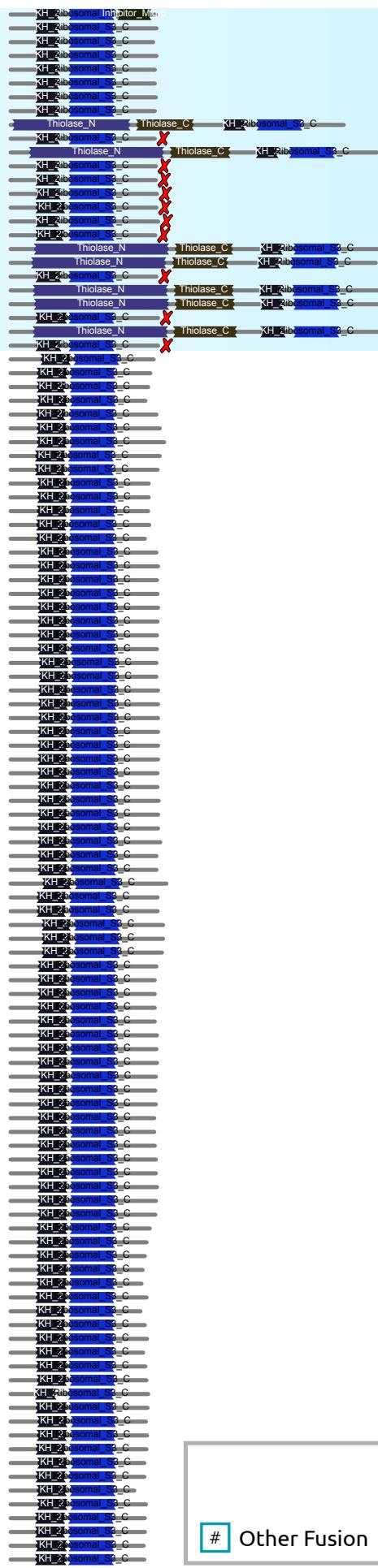
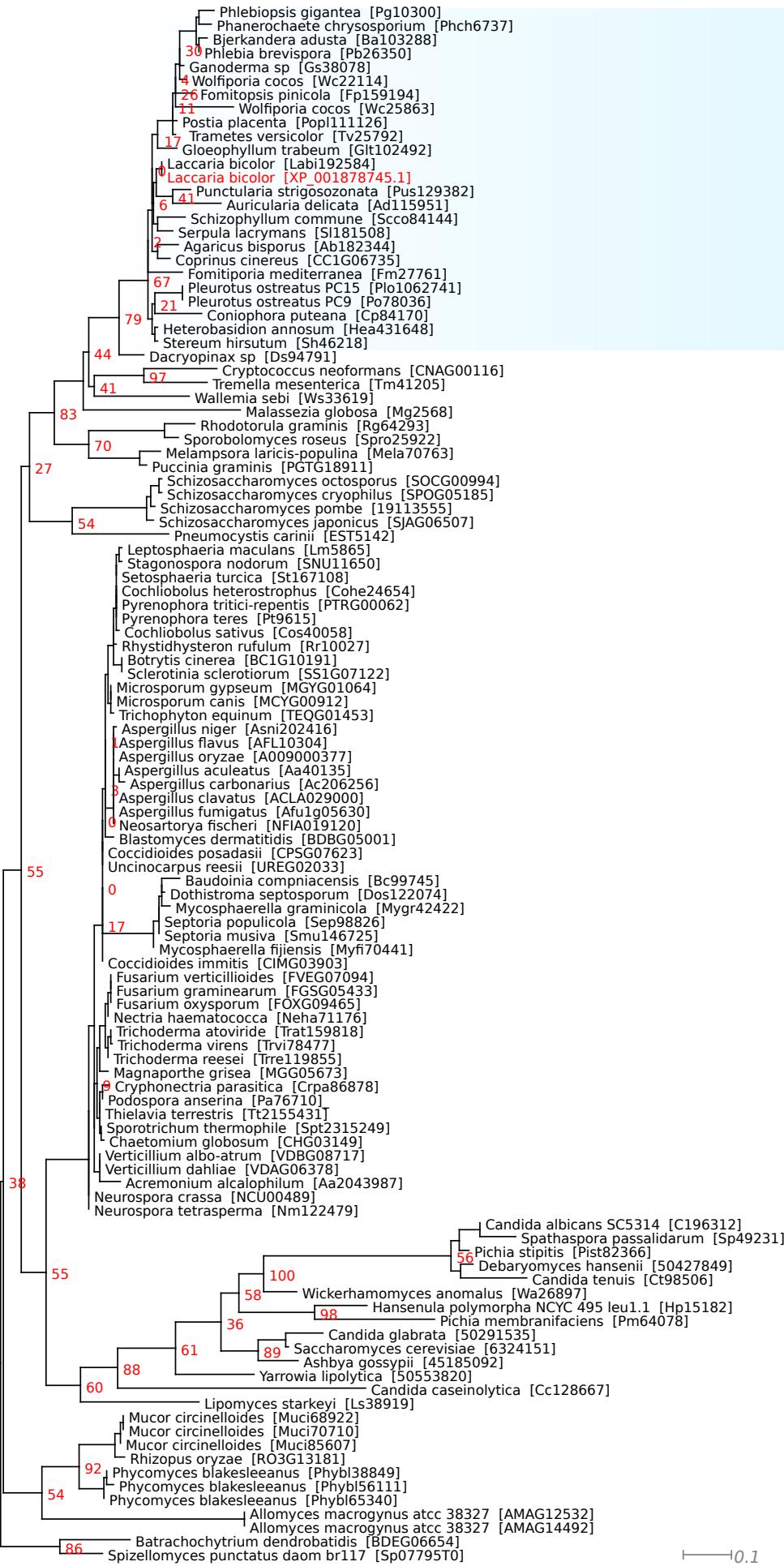
Styling and annotation was made possible by Dendroscope and Inkscape.

2.1 Important Notes

First domain phylogeny showed low resolution, so this result was not included here.

3 Mesquite Cladogram

This tree is the 68-gene concatenated phylogeny (Fig. 1), with the presence of a fusion (black), presence of a fission (white), and absent/undetermined (grey) status of gene fusion characters plotted on to it using a "1/0/-" nexus-style data matrix. We used the program 'Mesquite' to calculate proportional likelihoods based on either an "Mk1" or "Assym. 2 param model." (see Table S4) of character change across the fungal phylogeny (Fig. 1). This allowed for a proportional likelihood of the position of the fusion/fission to be calculated.

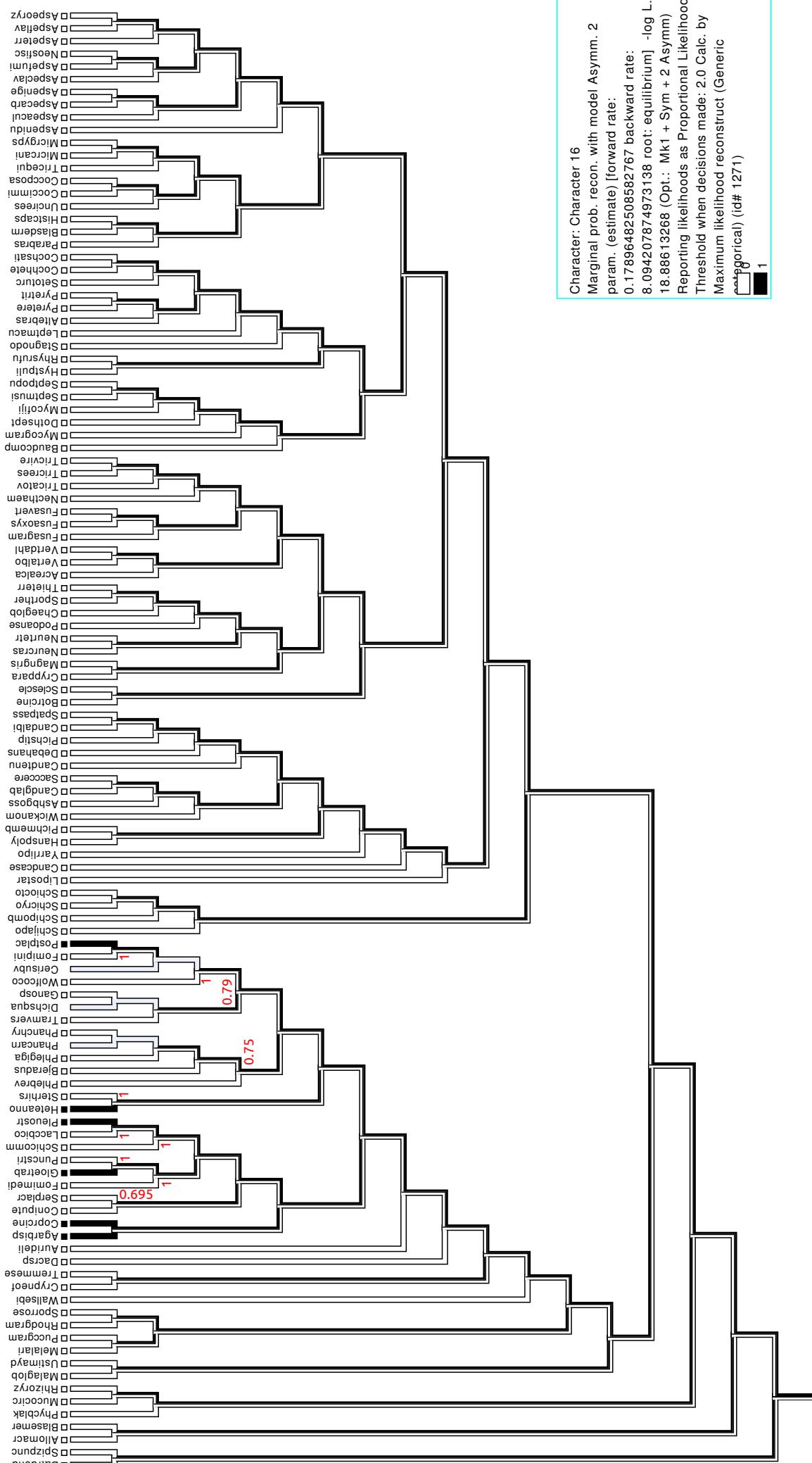


Annotation

✓ Presence

Other Fusion

Other Fusion ✗ Absence



Character: Character 16
Marginal prob. recon. with model Asymm. 2
param. (estimate) [forward rate]:
0.17896488508882767 backward rate:
8.0894207874973138 root: equilibrium -log
18.88613268 (Opt.: Mk1 + Sym + 2 Asym)
Reporting likelihoods as Posterior Likelihood
Threshold when decisions made: 2.0 Calc. b
Maximum likelihood reconstruct (Generic
Empirical) (id# 1271)

Putative Fusion 17

September 26, 2012

1 Fasta Sequences

These are the unfused sequences identified by fdfBLAST belonging to the putative gene fusion in FASTA format. Accessions may be shortened, but belong to either the taxons individual genome project or NCBI's accession numbering.

```
>lcl|NCU02798T0 unnamed protein product
MADTFVSDFQVRSLAGEPCA AVSVRN LSTTL YASDAWGRKCTVAPQPCLISAEVHFKQPF GTAAANDQLGADTVHYGNL
SKA ILERMKRFTVPREQE QEQE QEQKQSGSGNGN GDHSVQETNNNNNNNNFTLAYVIHDLWVGLTGWAHFGSVKEEEK
PFLDISSIRFLS LT VLPKASLLGDGVSM TCSQFFKNGPGEKMREN LISA SLKI HNLKVPTLVGVNP HERRAKQFVVTSV
NVERYFRMDDYYSELEG VVVKA LEES YYETLEALGAHLAEKILEPDHRKDHTKWQVH IRMEKPTAVPLADCP IVE VRAGY
GFPAPGRPAAS
>lcl|NCU09930T0 unnamed protein product
MTDAIDLPASSKPAAPTV RTAYIALGSNLGDRIGWIEKACKEMDARGIKVKRTSCLWETEPMYVLDQDRFVNGACEVETT
LEPLEL LDALQDIENSLGRKKI IDKGPRN IDLDILLYENLKVDHERLKIPHIGIPEREFVLRPLAELIPDKPLDHTRPWT
LTRD LLDALPPS STPI TT MTP LSSHGH PPIQ ALNPSRK THVM AILN MTP DSFDGGQ HASAGLESTIQSF LDAGATMIDV
GGQ STAP RTPQ VSAEE EIGRVV PAIKMIREKF SHRDVL ISV DTYRASVA EAA VAGADIVNDVSGGSM DPMLPTV ARLG
STICLMHM RGT PANM SSLNEYPEAEGGLIGGI AKELV GRVAAA EAGIR RWI VLD PGLGFA KVGPQ NVDV RLH LEE LRS
WPGLQGLPW LVGSSR KSFIG QVTGV PTPKERI WGT AATV AAAVQGGAD VVRV HDV KEMA QVVA MADAI WRY
```

2 Annotated Phylogenograms

All trees were generated from an initial run of Darren's Orchard pipeline against 139 taxa (Table S1), using the above corresponding un-fused sequences as BLAST seeds. The alignments were then checked for any missing taxa, manually masked and then ProtTest3 was run, please see the Methods section for detail. The final trees were generated by the following command:

```
phyml -i alignment_file -d aa -b 100 -m model -c 8 -v invariant_sites -s BEST --quiet
-a gamma
```

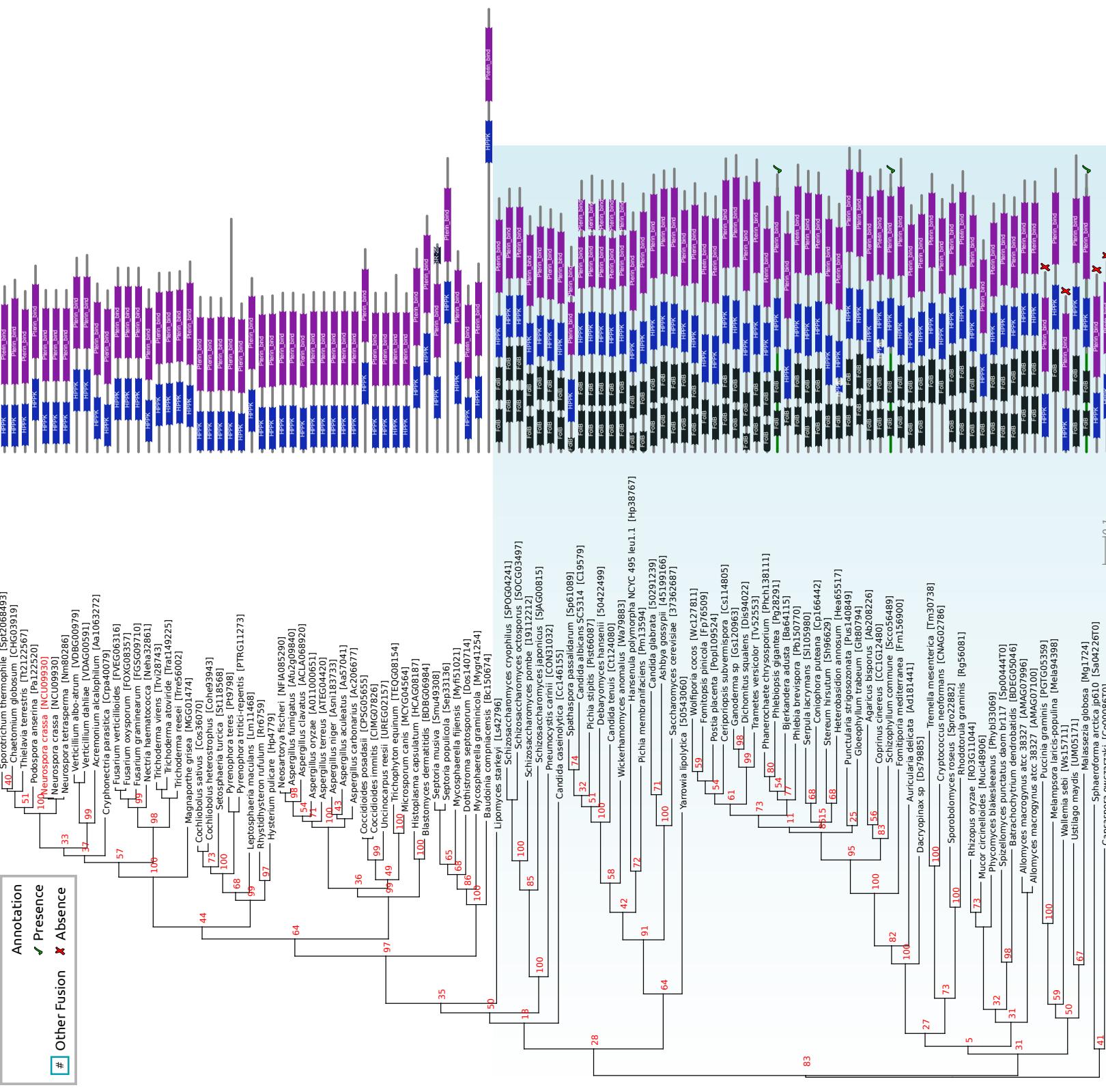
Styling and annotation was made possible by Dendroscope and Inkscape.

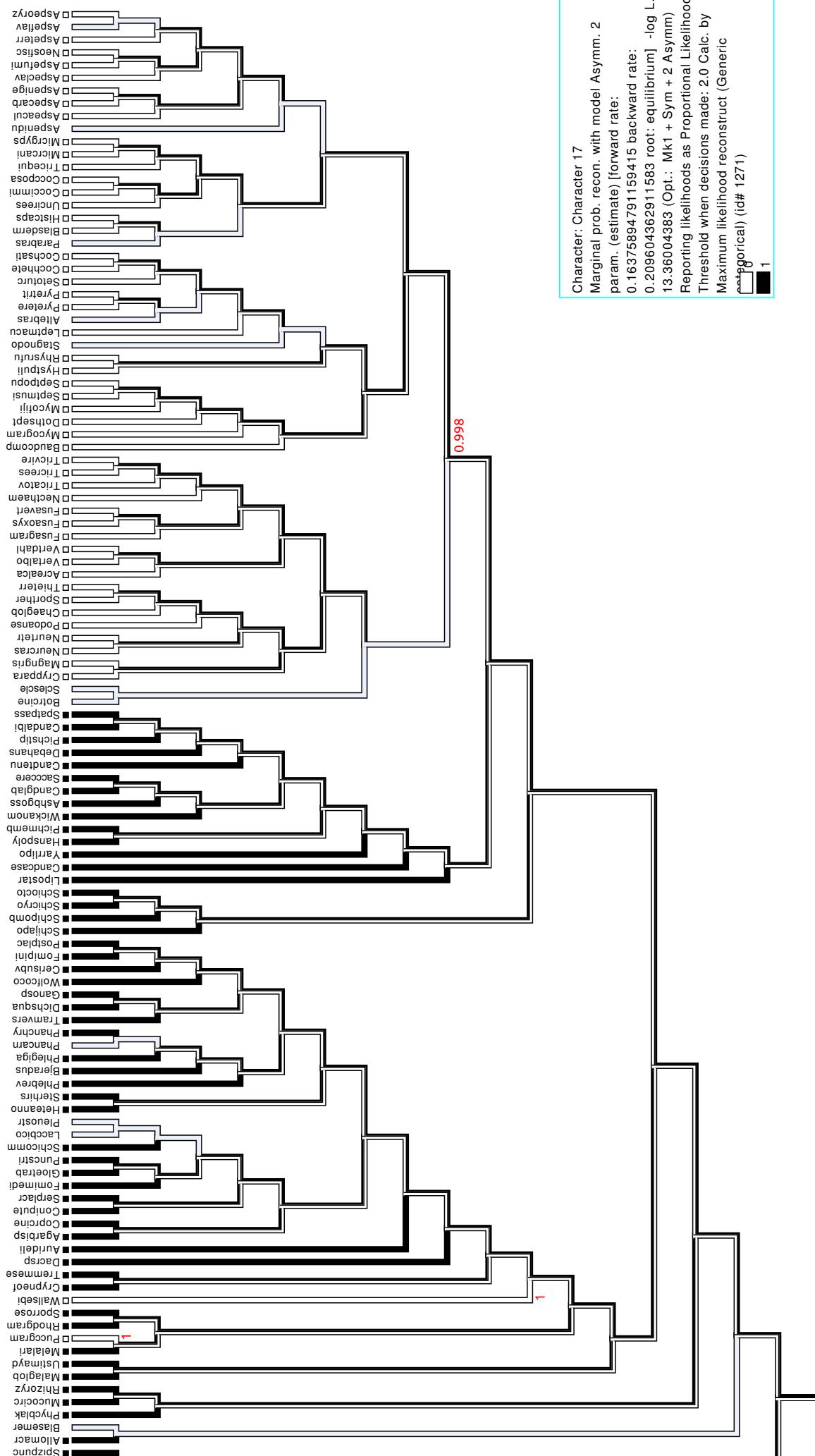
2.1 Important Notes

FolB phylogney showed low resolution, so this result was not included here.

3 Mesquite Cladogram

This tree is the 68-gene concatenated phylogeny (Fig. 1), with the presence of a fusion (black), presence of a fission (white), and absent/undetermined (grey) status of gene fusion characters plotted on to it using a "1/0/-" nexus-style data matrix. We used the program 'Mesquite' to calculate proportional likelihoods based on either an "Mk1" or "Assym. 2 param model." (see Table S4) of character change across the fungal phylogeny (Fig. 1). This allowed for a proportional likelihood of the position of the fusion/fission to be calculated.





Putative Fusion 18

September 26, 2012

1 Fasta Sequences

These are the unfused sequences identified by fdfBLAST belonging to the putative gene fusion in FASTA format. Accessions may be shortened, but belong to either the taxons individual genome project or NCBI's accession numbering.

```
>lcl|NCU08029T0 unnamed protein product
MTPRLSTLDLVAKVDAFPYADRPEAYAQIMKSFYTFWEDQQGQVPIGYVKLDVVDALNKAPATLKGQLGLHIDVSNRT
VVLFRDAPDKTYEERTRLVGKLTALWREQEAFAILKSWRNELWPVYGRNKEVLFSIERAAMGLFGTTRYGVHMNAFIRRQ
DASSSKYDLRIWPKRSATKSTYPSMLDNAVAGGLMTNEDPFECVIREADEEASLSEHIVRNNNAKEVCTITYIYITDERAG
GEAGLIYPECQWIYDLELPADGSVVPEPKDGEVESFSLCTVEEIQKQLAQGMWKPNCAVVMLDFFVRHGIYTPENEPHYD
AFRDRAHRHIAFPGPHQA
>lcl|NCU04944T0 unnamed protein product
MLGFGSKFIPTKLPSISRIFISFHVSPCRTVTALPDLTFTTRGTQLFQLNNYKGRAIHSNETMGTTNGTTQSTGALDEGQ
IFEWYPLDLVRDYEQQQKQHDHNDQLQNGSNGTTHKPEPFALVVNLQPLTHLGLVKRLWKNASIRVAADGGANCLYDVAGK
NGDHDFDDLTAAIGDLDSSLTTETRTYFTTHSSSPTASQTAIIHEPSQYSTDFAKSVDYLRGPSCSKPDAPPDIVAIGGL
GGRVDQGLSQLHHLYLFQSSPTYADGRMYLFGESLTFLLKSGTHRIRVREPGQANQPEKDVFAKWVGILPVKEPSRIWT
KGLEWDVEDWPTEFGGQVSTS NHVPETEVVEVRATKDVLFTIALRDL
```

2 Annotated Phylogenograms

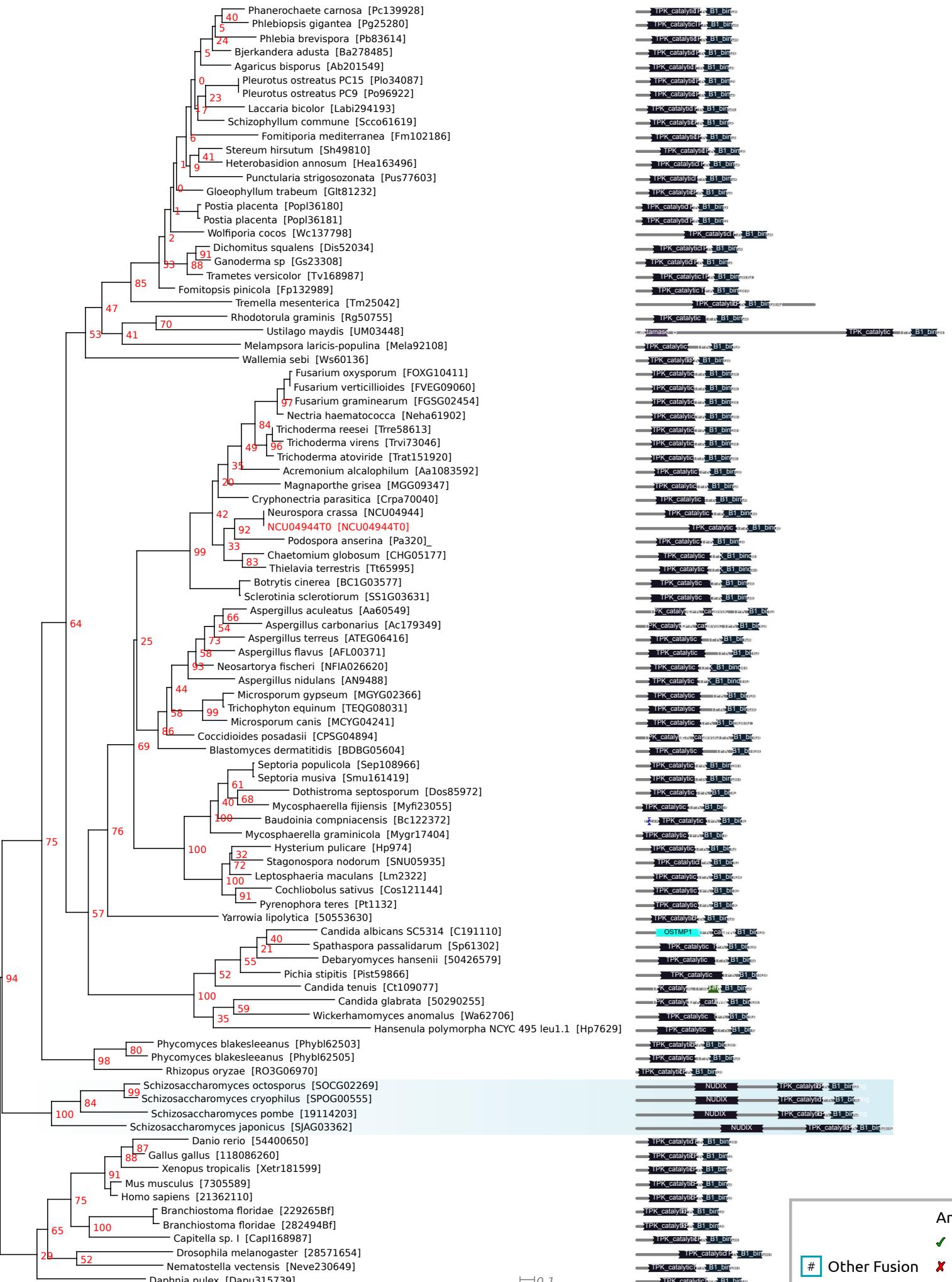
All trees were generated from an initial run of Darren's Orchard pipeline against 139 taxa (Table S1), using the above corresponding un-fused sequences as BLAST seeds. The alignments were then checked for any missing taxa, manually masked and then ProtTest3 was run, please see the Methods section for detail. The final trees were generated by the following command:

```
phyml -i alignment_file -d aa -b 100 -m model -c 8 -v invariant_sites -s BEST --quiet
-a gamma
```

Styling and annotation was made possible by Dendroscope and Inkscape.

3 Mesquite Cladogram

This tree is the 68-gene concatenated phylogeny (Fig. 1), with the presence of a fusion (black), presence of a fission (white), and absent/undetermined (grey) status of gene fusion characters plotted on to it using a "1/0/-" nexus-style data matrix. We used the program 'Mesquite' to calculate proportional likelihoods based on either an "Mk1" or "Assym. 2 param model." (see Table S4) of character change across the fungal phylogeny (Fig. 1). This allowed for a proportional likelihood of the position of the fusion/fission to be calculated.



Annotation

✓ Presence

✗ Absence

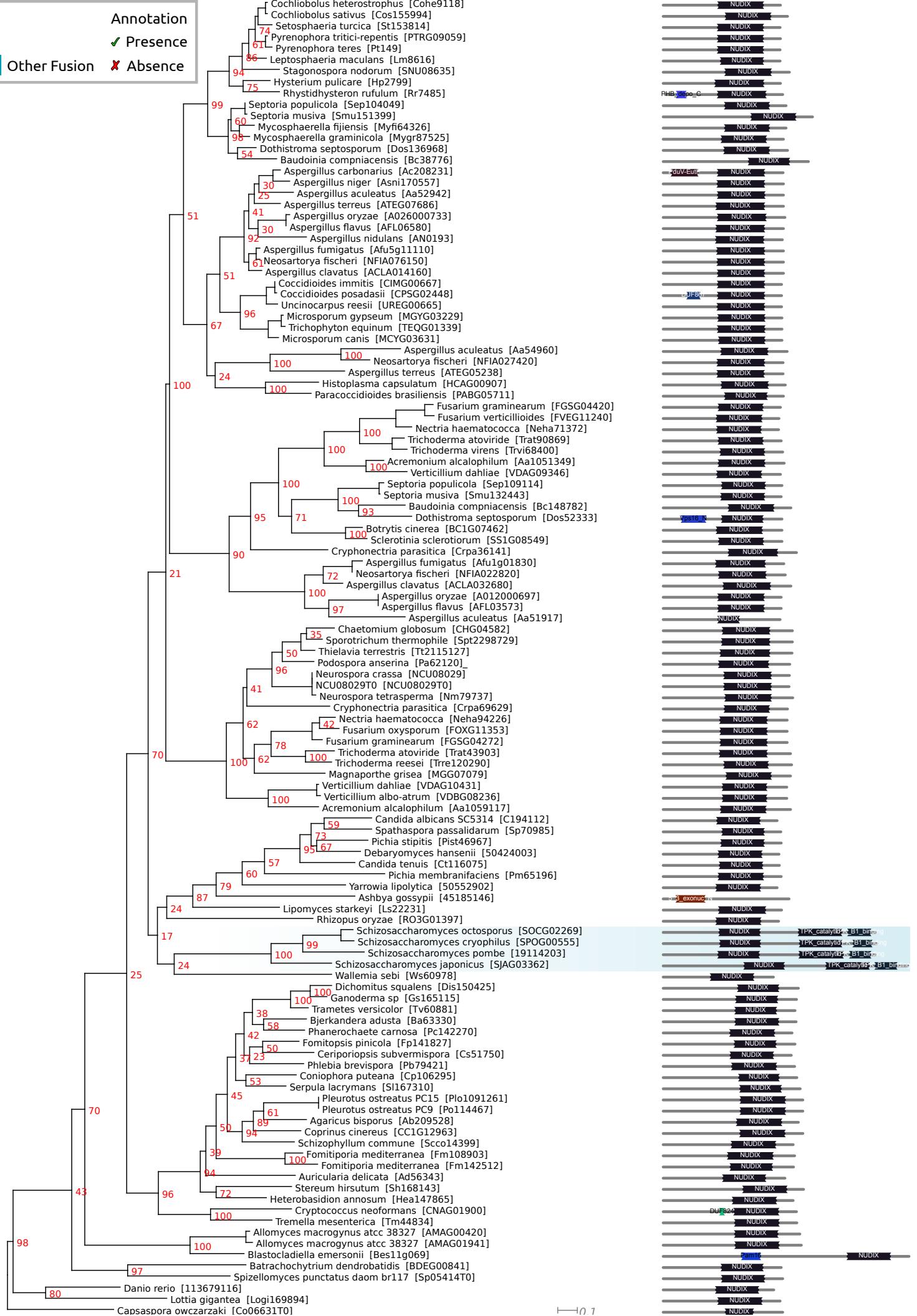
Other Fusion

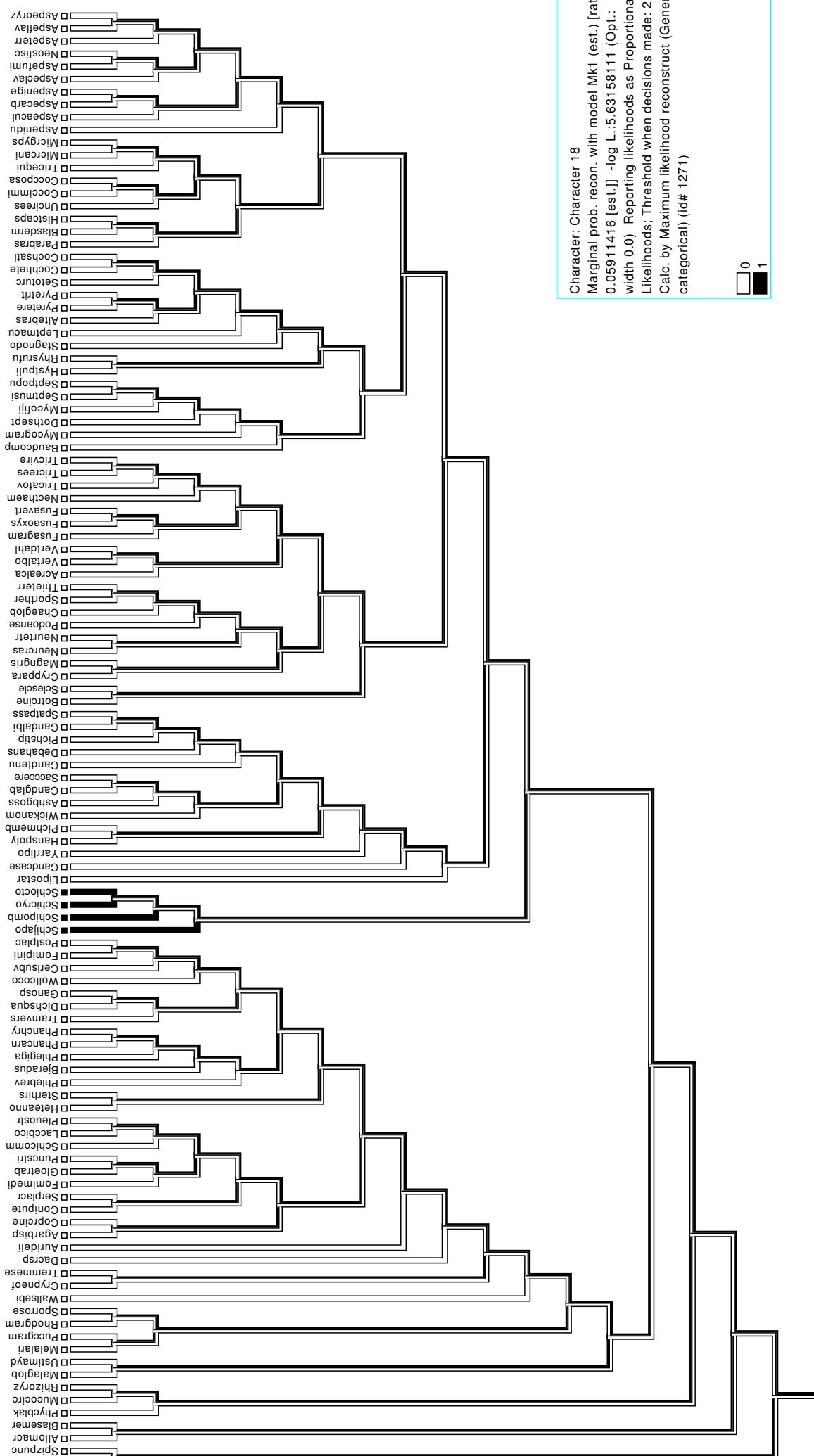
Annotation

✓ Presence

Other Fusion

✗ Absence





Character: Character 18
Marginal prob. Recon. with model Mk1 (est.) [rate 0.0591146 [est.]] - log L. 5.6315811 (Opt.: width 0.0). Reporting likelihoods as Proportional Likelihoods; Threshold when decisions made: 2.0
Calc. by Maximum likelihood reconstruct (Generic categorical) (id# 1271)

Putative Fusion 19

September 26, 2012

1 Fasta Sequences

These are the unfused sequences identified by fdfBLAST belonging to the putative gene fusion in FASTA format. Accessions may be shortened, but belong to either the taxons individual genome project or NCBI's accession numbering.

```
>lcl|CC1G00485 unnamed protein product
MQALLKDVDMAFANHNPALQPKHRELTAEPVAEAEALEEVYESFESPEDTLDRKSPAALFGSQKIGQVVVPQQLQDAIV
ALIDESDKGLLHSDAKRLFGGLHNPGVDSGLVQLDTKYRSRKQGERHADRDAIAFAAVVLPAHYAAVAVLEHVKHRLG
SSWEVERVIDWGAGAGTGLWASLFSFQSAGASHEPEGVDASQSTLRSYLGIDKRQAMVALAERIQNNITPPEGFSLQFKK
TFSEEDNVPREEGTKTVALSAFTLSSLPTPLARKALVKEMWESGAHTLVLMDHNTKEGFESIAQAREYLLRQGRKEVEKS
EAESPSSLEGAYVVAAPCPHDSACPLLNNSGSNRLVCGFNQRLQRPSFVRLTKHSGIGHEDIGTYVVIQRGSRGKVESQL
GRVGLVGRWEQEAKLTKVVKELQLFDQASPEVPGLASKSAVPAEEPSEAEVHETLRQEAYHWPRLVFPFMKKSGHVILDS
CTSEGKIVRMTIPKSQGKQPYYDARKSAWGDLFPHPKNPPQERVVIRDVEGKALSVERDHIGKNSSTRPAKKADKKYSE
HLASTIREAKKAKRRWERNVKSSVIWDKDD
>lcl|CC1G06294 unnamed protein product
MSFLRGIGIQSARQFAFASRQTYYQQAWRMSCRRHASTTPAPRPTTTSTPPPLTGNAPPRPKFKTREQVYRERNQAL
FMYTSAVILFAVGASYAAVPLYRMFCATGFAGTPKVTGRFEPELRVPVENARRIKVHFNADKSEQLPWKFTPQQKFVN
VLPGESSLAFYTAKNDSEQDIIGIATYNVTPDRVAPYFSKVECFCFEEQKLLAGEEIDMPLLFFIDKDILEDPACRVNQD
VVLSYTFFRARRNKFGHLEPDATDDAVQSSLGFDKFEHGSSSSSEKSS
```

2 Annotated Phylogenograms

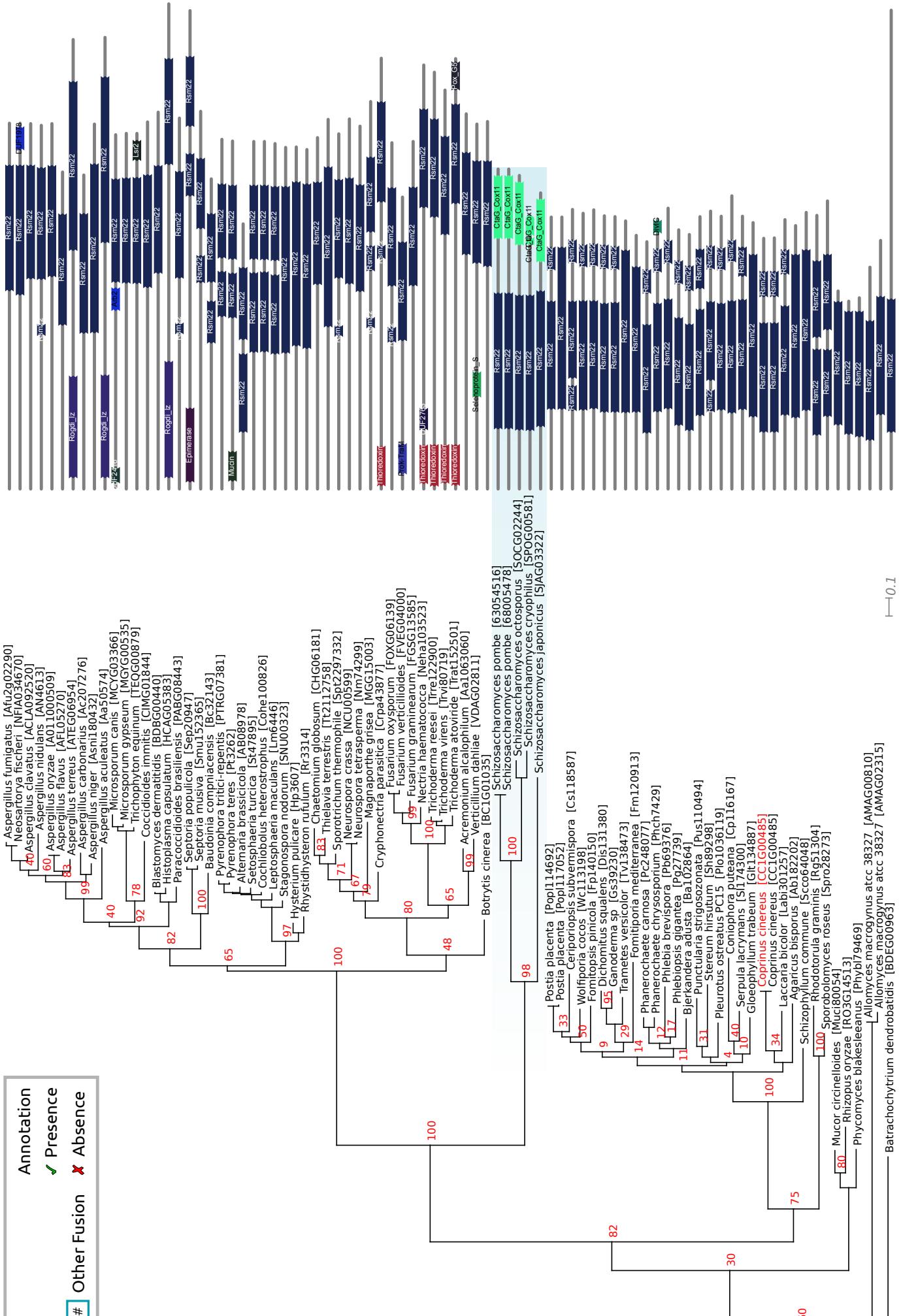
All trees were generated from an initial run of Darren's Orchard pipeline against 139 taxa (Table S1), using the above corresponding un-fused sequences as BLAST seeds. The alignments were then checked for any missing taxa, manually masked and then ProtTest3 was run, please see the Methods section for detail. The final trees were generated by the following command:

```
phyml -i alignment_file -d aa -b 100 -m model -c 8 -v invariant_sites -s BEST --quiet
-a gamma
```

Styling and annotation was made possible by Dendroscope and Inkscape.

3 Mesquite Cladogram

This tree is the 68-gene concatenated phylogeny (Fig. 1), with the presence of a fusion (black), presence of a fission (white), and absent/undetermined (grey) status of gene fusion characters plotted on to it using a "1/0/-" nexus-style data matrix. We used the program 'Mesquite' to calculate proportional likelihoods based on either an "Mk1" or "Assym. 2 param model." (see Table S4) of character change across the fungal phylogeny (Fig. 1). This allowed for a proportional likelihood of the position of the fusion/fission to be calculated.

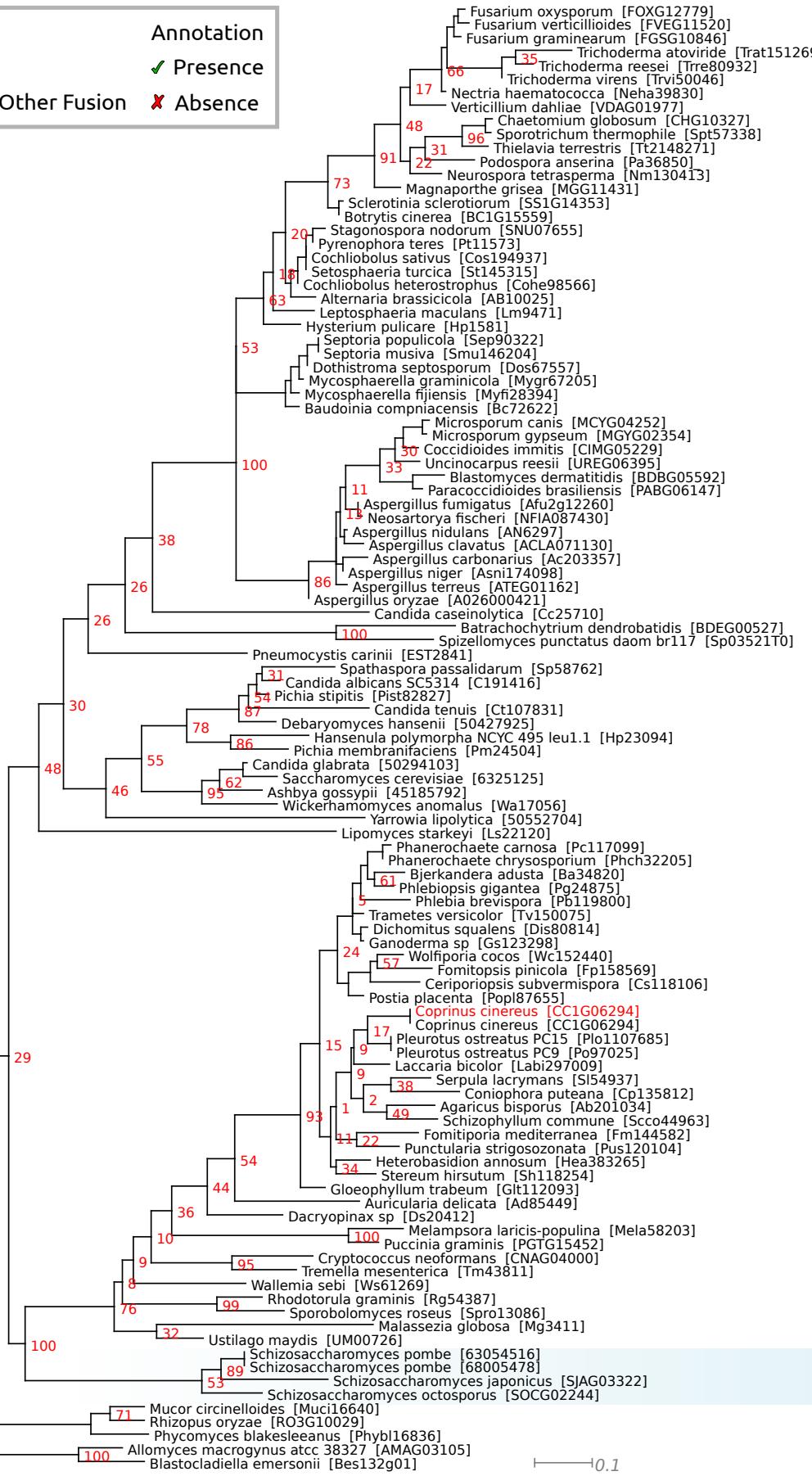


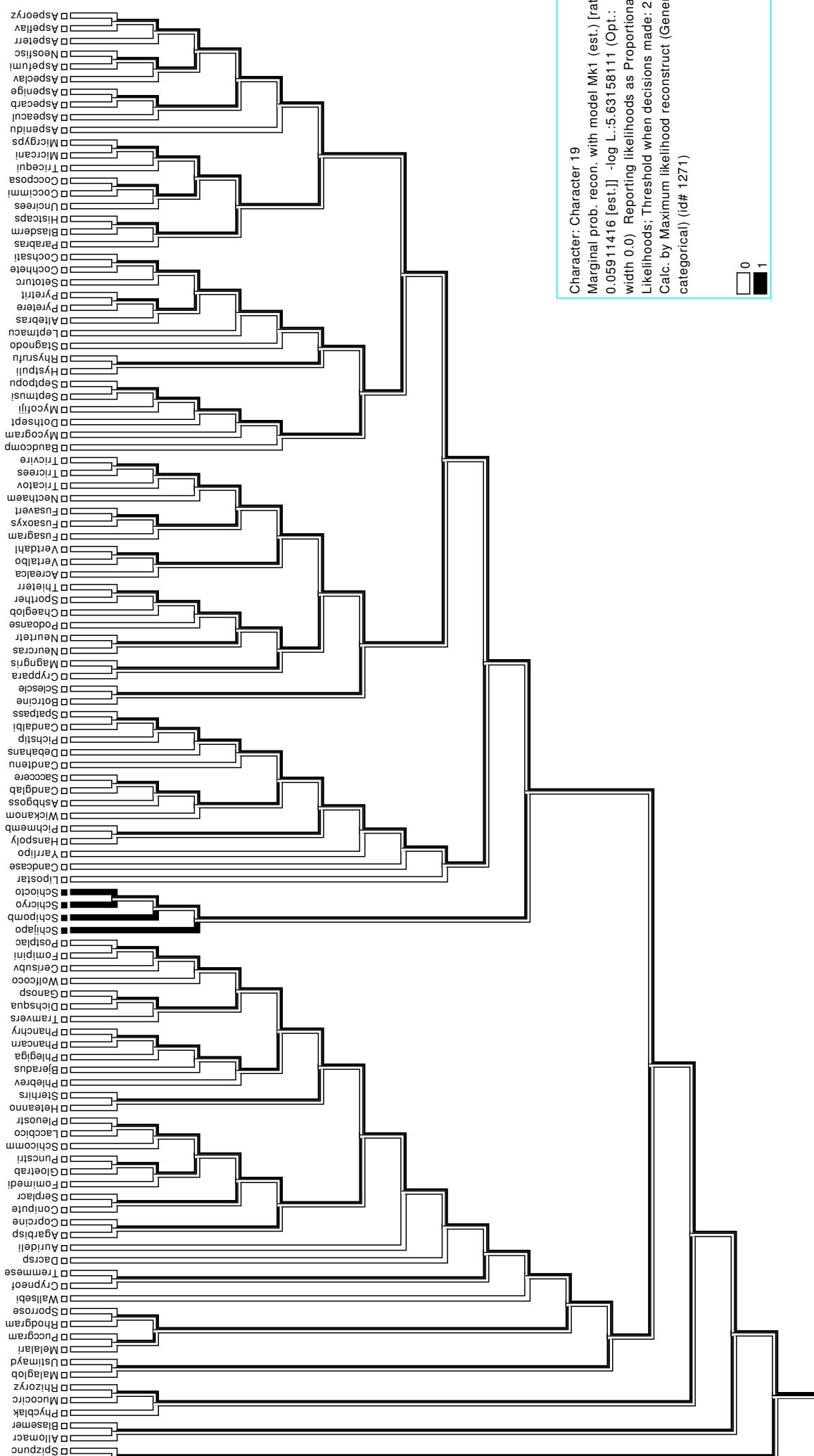
Annotation

✓ Presence

Other Fusion

✗ Absence





Character: Character 19
Marginal prob. recon. with model Mkt1 (est.) [rate 0.05911416 [est.]] - log L: -5.63158111 (Opt.: width 0.0). Reporting likelihoods as Proportional Likelihoods; Threshold when decisions made: 2.0 Caic. by Maximum likelihood reconstruct (Generic categorical) (id# 1271)

Putative Fusion 20

September 26, 2012

1 Fasta Sequences

These are the unfused sequences identified by fdfBLAST belonging to the putative gene fusion in FASTA format. Accessions may be shortened, but belong to either the taxons individual genome project or NCBI's accession numbering.

```
>lcl|Mc138671 unnamed protein product
MTSILNRAAFAVYGRKTAFSGIARSISTIQKPNYAFAFDIDGVLIKGRRIPEATRALKLLNGDNAHNRRNIPFVLLTNGG
GVTEEKARQISELVGVKIDPKQVILSHPMQNLATKYNDKRVLIIGGKGRNCYDVAKKYGFKEAVTPHDIMHWNSSSWP
HSTPTSDLSMLTSTFSNLPIHAVMVFHDTYDWGRDLQIMLDALCSQDGIIIGTRKSDYTIQDVPLYWSNNDLIWSTDFPAP
RLGQGAFKIALDSLYKTLTGHDLKSTSFGKPHGATYQFAEQVLASLEPGSQQPNSRRVYAVGDNPASDIRGANDYGWTS
MLVRTGIFTGNGNASDFPADIVCENVEEAVESIIAREEKHQ
>lcl|Mc161540 unnamed protein product
MASSRIKPMPSKAHWIKLATFKPVVRINTWRPLQRCFNSNLKQASSPPPHKEDKDKKSFKEELKEDIYTIPNLLTFGRL
AAAPCVGYMILQQNYDGALVLFALAGFTDLLDGHIARKYNMKTLLGTIIDPLADKVLMVTMVTLAMEGTLPVPLAAIIL
GRDAGLVLSAFYYRYISLPEPKTVARYFDGSIPS AEVKPTQISKINTALQLLMGFSLTTVSMGMPSEAMTALQWVVG
TTVWSGASYVFSKDAVRILK
```

2 Annotated Phylogenograms

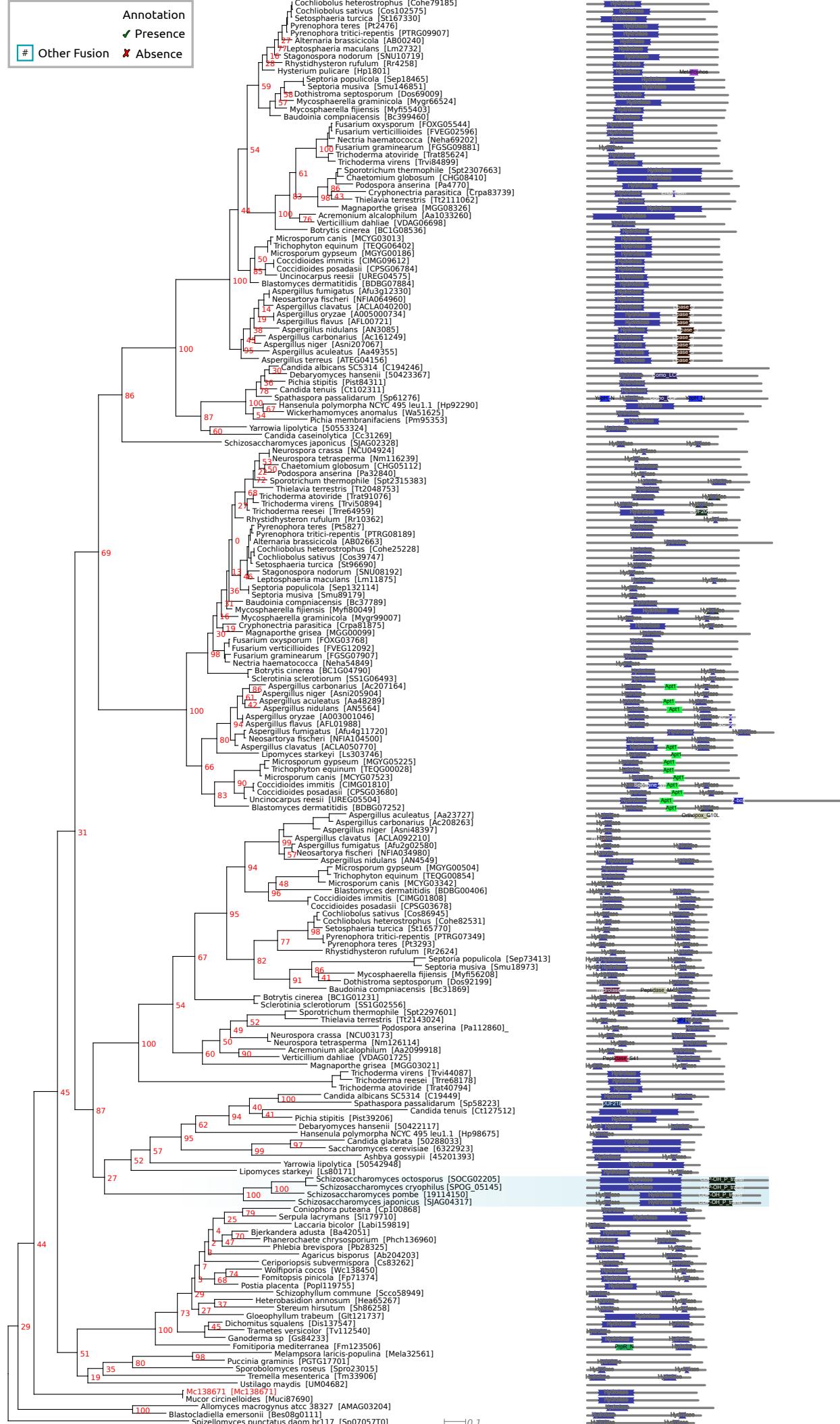
All trees were generated from an initial run of Darren's Orchard pipeline against 139 taxa (Table S1), using the above corresponding un-fused sequences as BLAST seeds. The alignments were then checked for any missing taxa, manually masked and then ProtTest3 was run, please see the Methods section for detail. The final trees were generated by the following command:

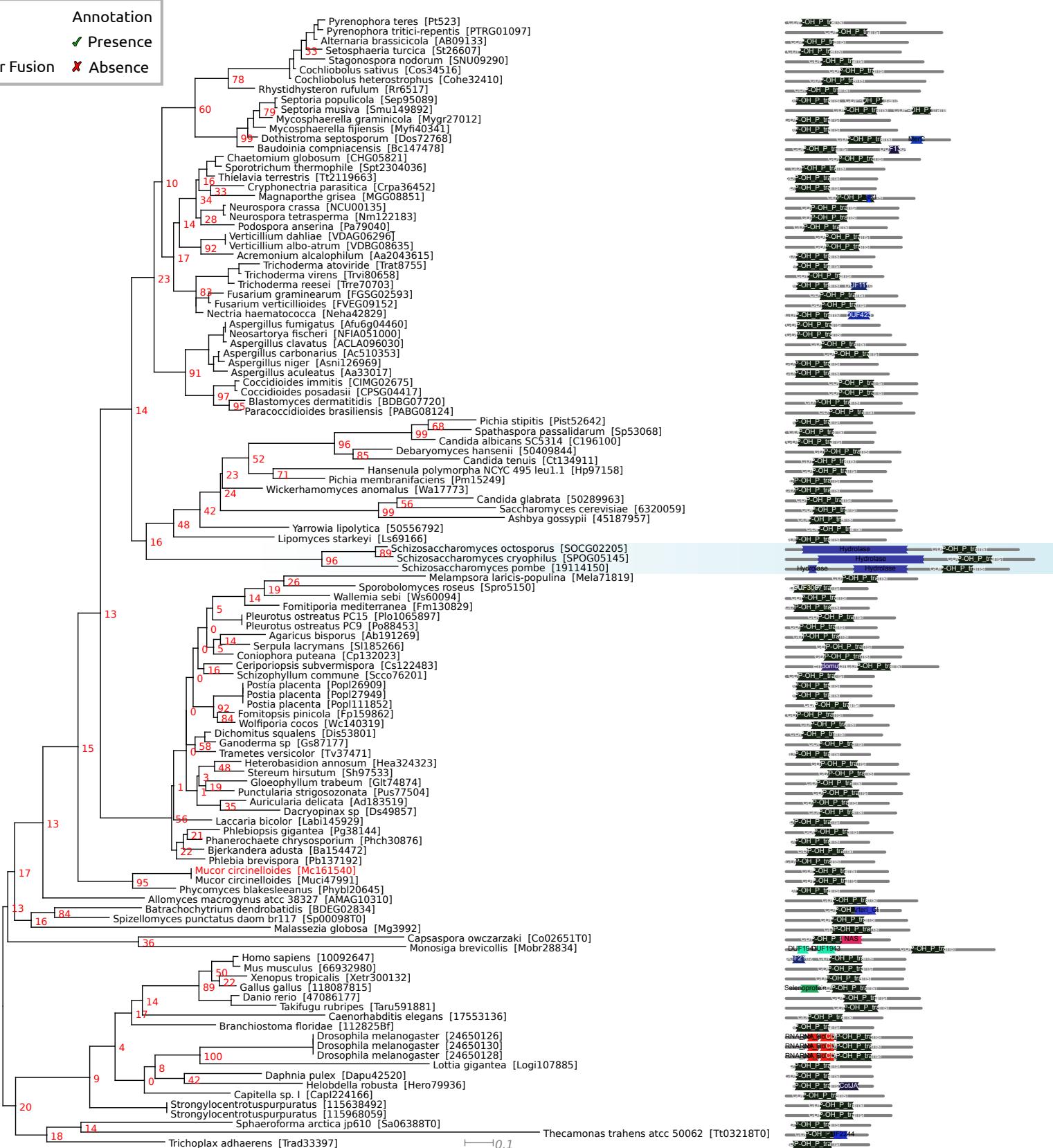
```
phyml -i alignment_file -d aa -b 100 -m model -c 8 -v invariant_sites -s BEST --quiet
-a gamma
```

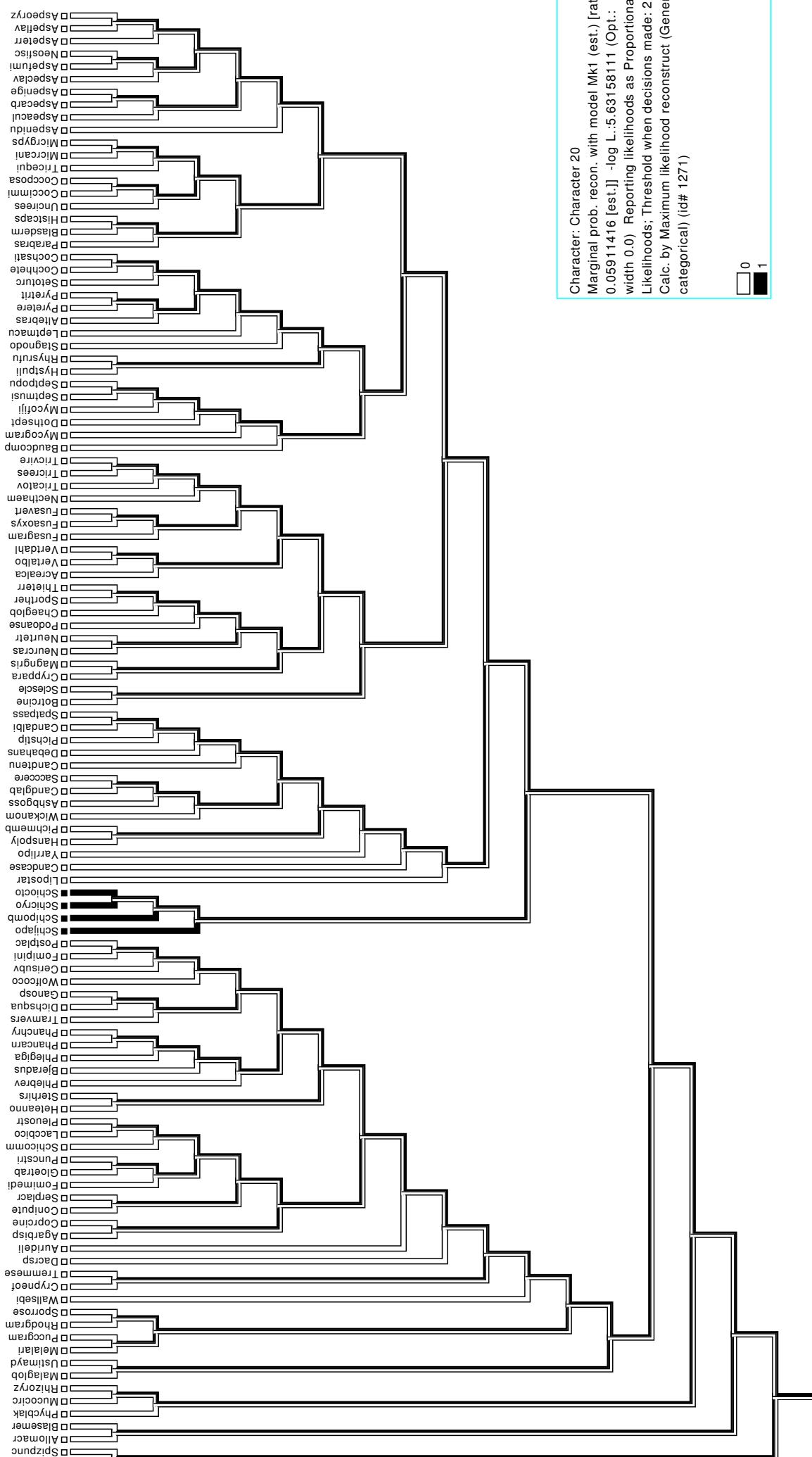
Styling and annotation was made possible by Dendroscope and Inkscape.

3 Mesquite Cladogram

This tree is the 68-gene concatenated phylogeny (Fig. 1), with the presence of a fusion (black), presence of a fission (white), and absent/undetermined (grey) status of gene fusion characters plotted on to it using a "1/0/-" nexus-style data matrix. We used the program 'Mesquite' to calculate proportional likelihoods based on either an "Mk1" or "Assym. 2 param model." (see Table S4) of character change across the fungal phylogeny (Fig. 1). This allowed for a proportional likelihood of the position of the fusion/fission to be calculated.







Putative Fusion 21

September 26, 2012

1 Fasta Sequences

These are the unfused sequences identified by fdfBLAST belonging to the putative gene fusion in FASTA format. Accessions may be shortened, but belong to either the taxons individual genome project or NCBI's accession numbering.

```
>lcl|6320989Sc unnamed protein product
MLFRNIEVGRQAAKLLTRTSSRLAWQSIGASRNISTIRQQIRKTQLYNFKKTVSIRPFSLSSPVFKPHVASESNPIESRL
KTSKNVAYWLIGTSGLVFGIVVLLGLTRLTESGLSITEWKPVGTLPMMNQKEWEEFIKYKESPEFKLLNSHIDLDEFK
FIFFMEWIHRLWGRAIGAVFILPAVFYFAVSKKTSGHVNKRLFGLAGLLGLQGFVGWWMVKSGLDQEQLDARKSKPTVSQY
RLTTHLGTAFFLYMGMLWTGLEILRECKWIKNPVQAISLFKKLDNPAIGPMRKISLALLAVSFLTAMSGGMVAGLDAGWV
YNTWPKMGERWFPSRELMDENFCRREDKKDLWWRNLLNPVTVQLVHRTCAYVAFTSVLAAHMYAIKKKAVIPRNAMTS
LHVMMGVVTLQATLGILTILYLVPISLASIHQAGALALLTSSLVFASQLRKPAPMRNVIITLPHSSKVTSKILSEASK
LASKPL
>lcl|73530106Sc unnamed protein product
EELKITFILKDGSQKTYEVCEGETILDIAQGHNLDMEGACGGSCACSTCHVIVDPDYYDALPEPEDDENMDLAYERGLTE
TSRLGCQIKMSKDIDGIRVALPQMTRNVNNNDFS
```

2 Annotated Phylogenograms

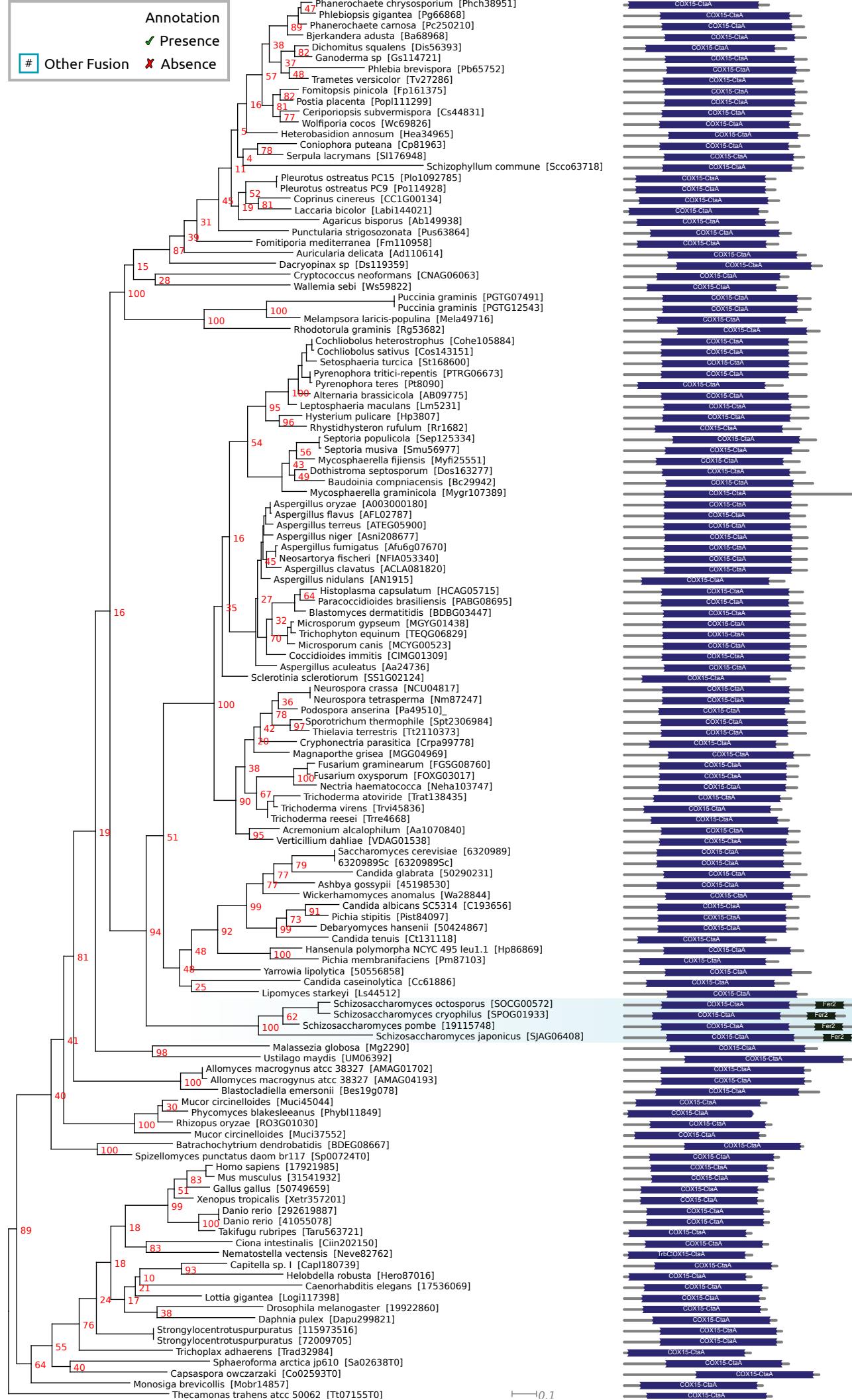
All trees were generated from an initial run of Darren's Orchard pipeline against 139 taxa (Table S1), using the above corresponding un-fused sequences as BLAST seeds. The alignments were then checked for any missing taxa, manually masked and then ProtTest3 was run, please see the Methods section for detail. The final trees were generated by the following command:

```
phyml -i alignment_file -d aa -b 100 -m model -c 8 -v invariant_sites -s BEST --quiet
-a gamma
```

Styling and annotation was made possible by Dendroscope and Inkscape.

3 Mesquite Cladogram

This tree is the 68-gene concatenated phylogeny (Fig. 1), with the presence of a fusion (black), presence of a fission (white), and absent/undetermined (grey) status of gene fusion characters plotted on to it using a "1/0/-" nexus-style data matrix. We used the program 'Mesquite' to calculate proportional likelihoods based on either an "Mk1" or "Assym. 2 param model." (see Table S4) of character change across the fungal phylogeny (Fig. 1). This allowed for a proportional likelihood of the position of the fusion/fission to be calculated.

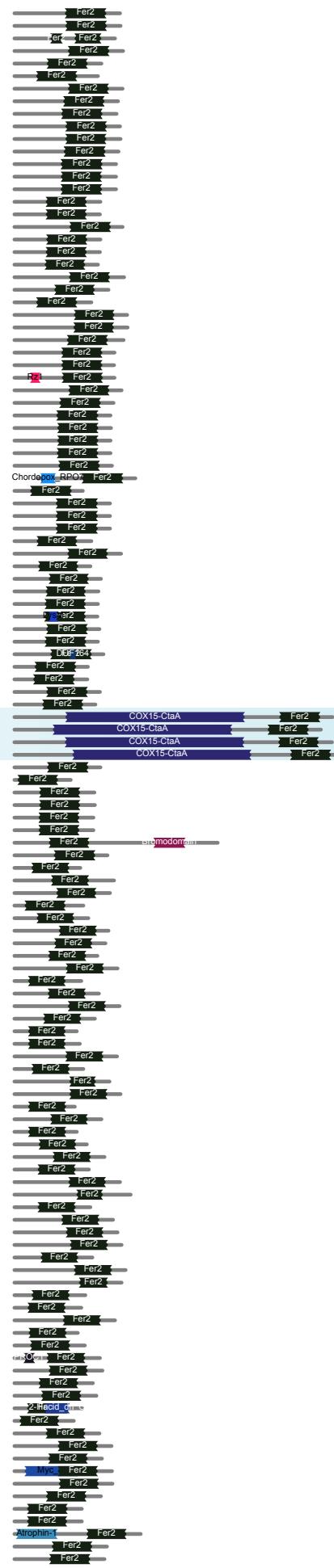
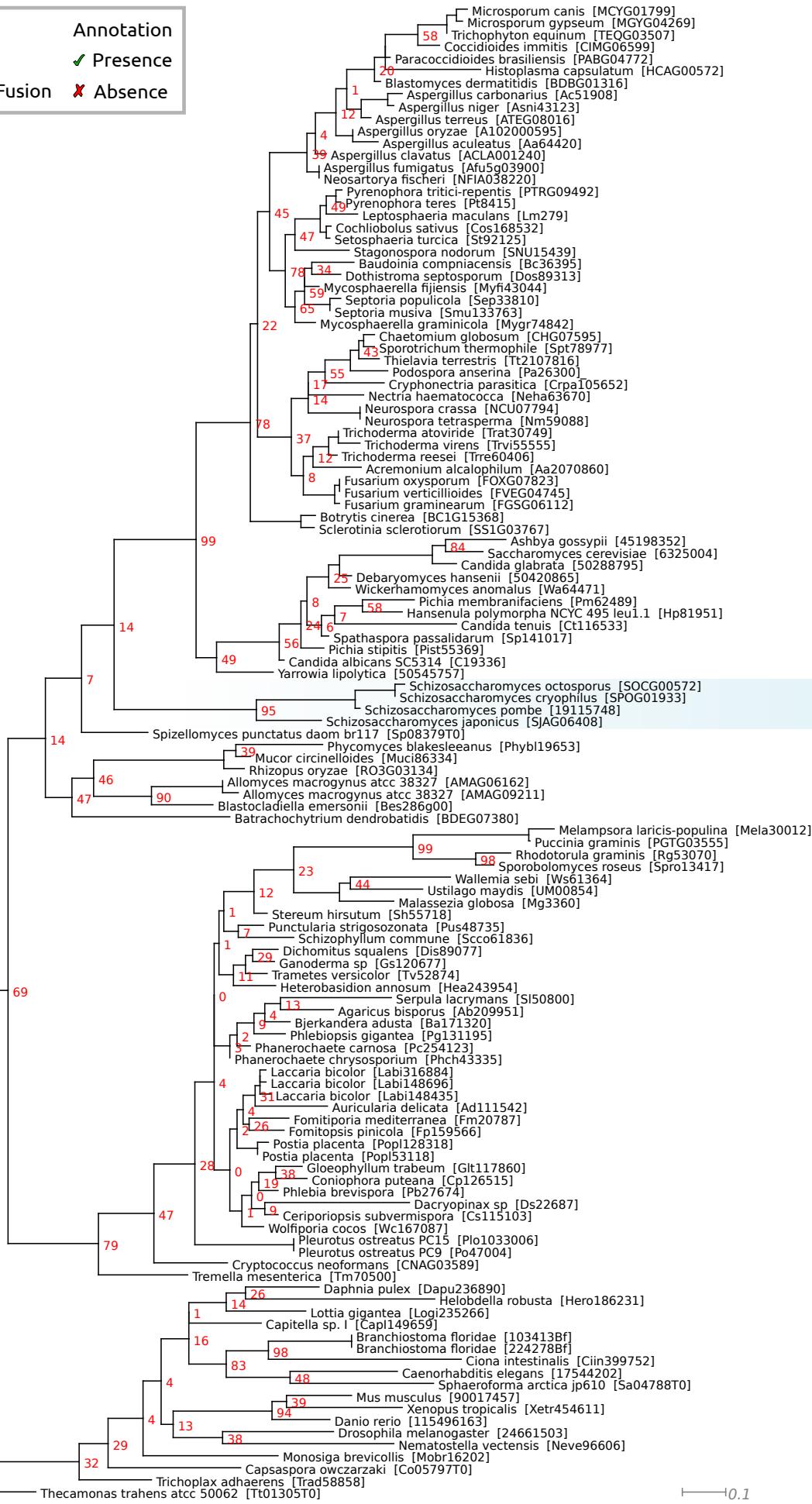


Annotation

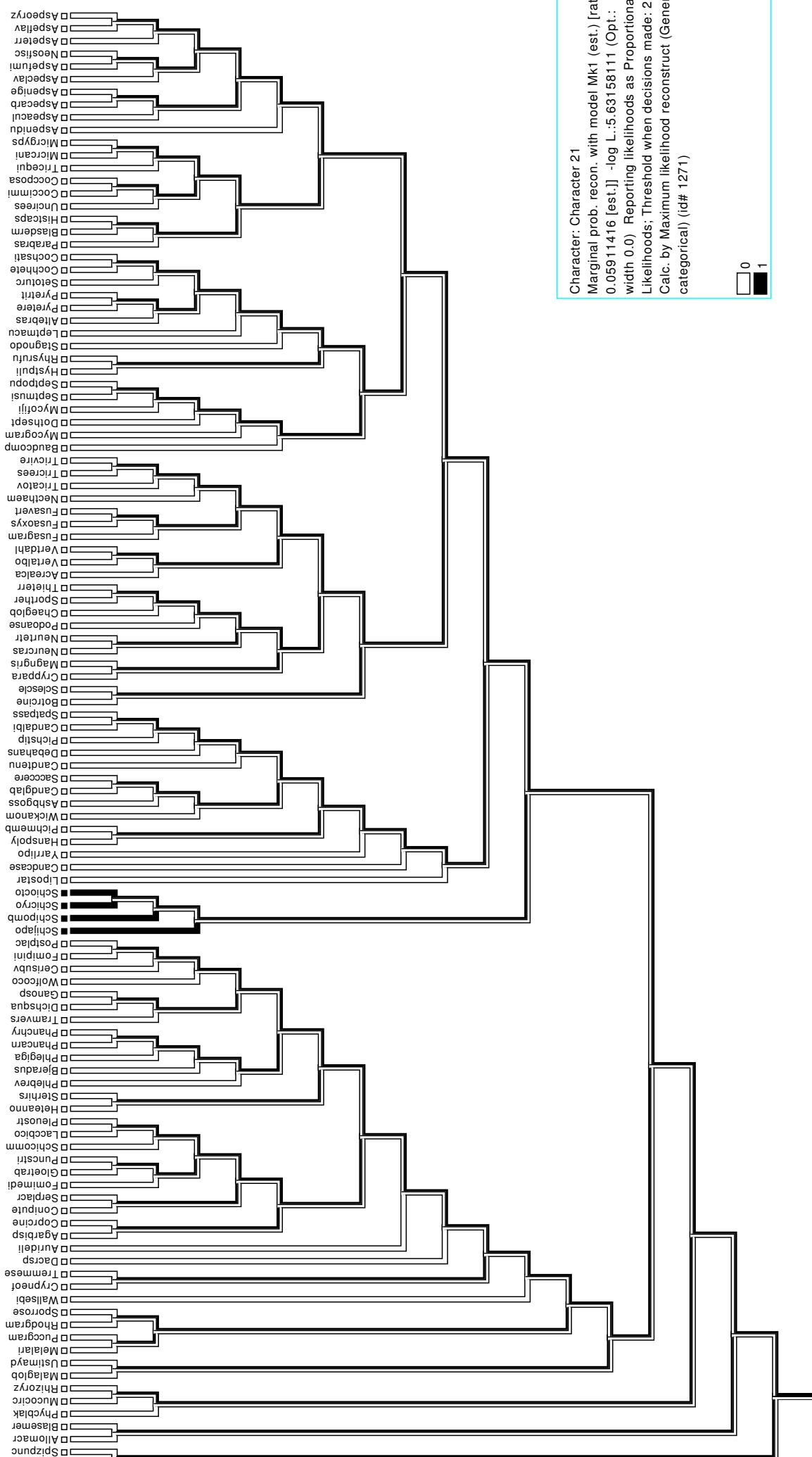
✓ Presence

✗ Absence

Other Fusion



0.1



Character: Character 21
 Marginal prob. recon. with 0.05911416 [est.] - log width 0.0 Reporting like Likelihoods: Threshold w Calc. by Maximum likelihood categorical) (#d 1271)

Putative Fusion 22

September 26, 2012

1 Fasta Sequences

These are the unfused sequences identified by fdfBLAST belonging to the putative gene fusion in FASTA format. Accessions may be shortened, but belong to either the taxons individual genome project or NCBI's accession numbering.

```
>lcl|AMAG_05362 unnamed protein product
MTRTIHLLLLAALVLAAPRPSHGASIGAVILDQQQADEVQAWPARRDKTPLPVVLWHGMGDSCCGQGMSDIKAALEHEV
PGVFVHSIRVGGRDANEDETMRGFLDDNVQTQVCALKSMEKLKRGFHFFIGFSQGGLFARSLVERCEGLKVETLITFAAP
HQGIKDVPESWCDSPVFCMARMTIRYGAYSPPLVQGKVVQAAYIKTPWNHNAYLRGNRFLPDINNENNPKAYKERMTT
LKALVLVRHEDDTVLSLRDSAWFYEDLMSGPVPFNETALYKDDVIGLRKLHKKGKVAFTLPGDHMQFSIASFLAVVLPY
LRDASTAVMHANEHVDAVAVRLHARQLAHTNPAWLDRVPFARSTL
>lcl|AMAG_11801 unnamed protein product
MDQPVALAAPRGSLAAMCAAHPDPAALTSLSLTHVMYHVDDALIGKALALITLLPLAMVVSYATLAAARPREPLWLAMF
LGQLGNEGLNFVLKRWIAEHRPTPFLGKGYGMPSHQAQFMSYWICFVLLVHAERRRLPSWLGPLIQLAALAIAALVIYS
RVHLQYHTVAQVLAGTAIGTVVGAVWFALVHPRFPLLPSRPRPAEQHAKQE
```

2 Annotated Phylogenograms

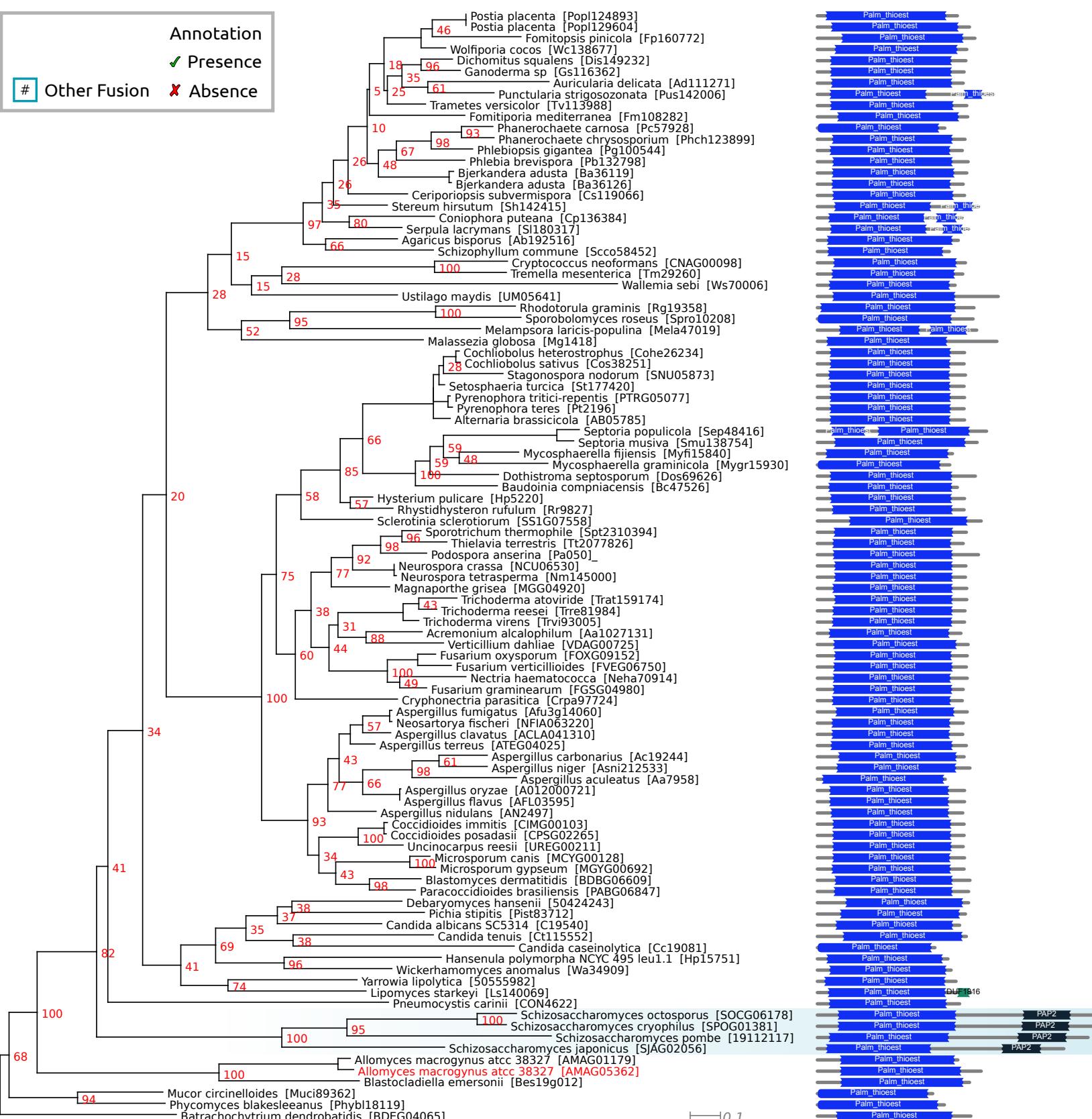
All trees were generated from an initial run of Darren's Orchard pipeline against 139 taxa (Table S1), using the above corresponding un-fused sequences as BLAST seeds. The alignments were then checked for any missing taxa, manually masked and then ProtTest3 was run, please see the Methods section for detail. The final trees were generated by the following command:

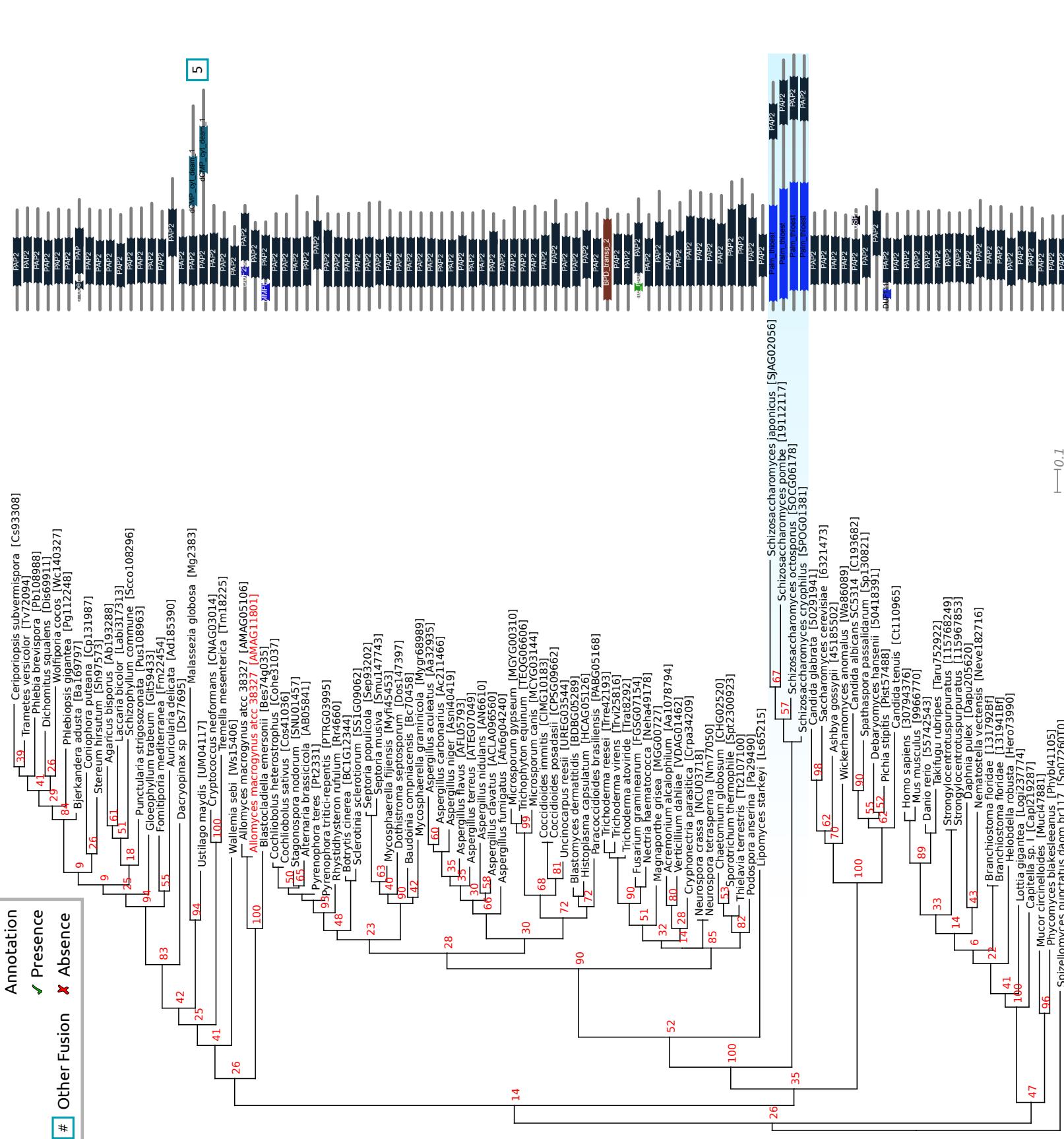
```
phylml -i alignment_file -d aa -b 100 -m model -c 8 -v invariant_sites -s BEST --quiet
-a gamma
```

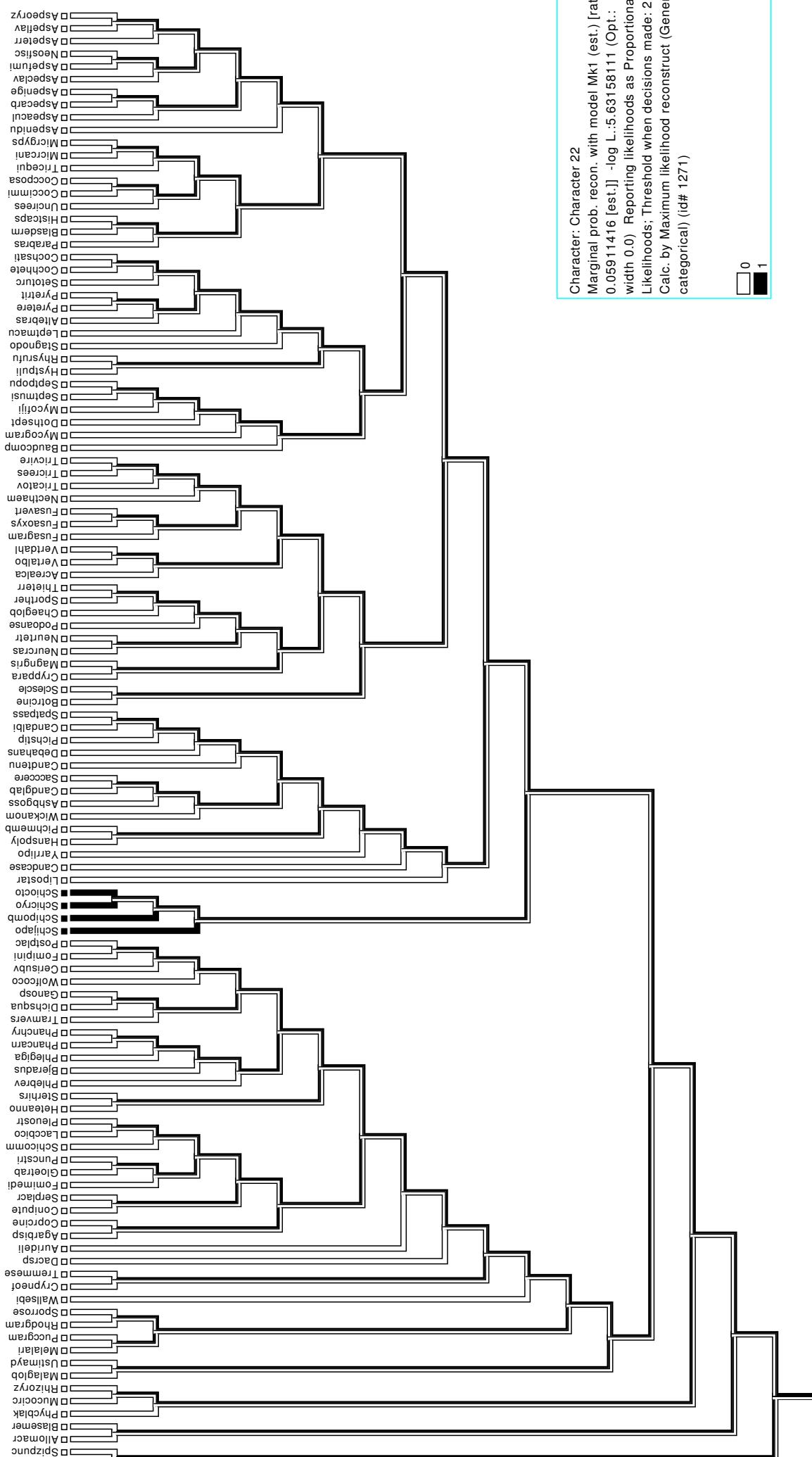
Styling and annotation was made possible by Dendroscope and Inkscape.

3 Mesquite Cladogram

This tree is the 68-gene concatenated phylogeny (Fig. 1), with the presence of a fusion (black), presence of a fission (white), and absent/undetermined (grey) status of gene fusion characters plotted on to it using a "1/0/-" nexus-style data matrix. We used the program 'Mesquite' to calculate proportional likelihoods based on either an "Mk1" or "Assym. 2 param model." (see Table S4) of character change across the fungal phylogeny (Fig. 1). This allowed for a proportional likelihood of the position of the fusion/fission to be calculated.







Putative Fusion 23

September 26, 2012

1 Fasta Sequences

These are the unfused sequences identified by fdfBLAST belonging to the putative gene fusion in FASTA format. Accessions may be shortened, but belong to either the taxons individual genome project or NCBI's accession numbering.

```
>lcl|6322261Sc unnamed protein product
MLSSANRFYIKRHLATHANMFPSVSKNFQTKVPPYAKLLTNLDKIKQITNNAPLTAAEKILYSHLCDPEESITSSDLSTI
RGNKYLKLNPDRVAMQDASAQMALLQFMTTGLNQTSPASIHCDSHTPNAGGLGAIAGVGGADAVDALTGTPWELKAPKILGVKLTGKLNWST
QFWGPGSGIIHQIVLENFSAPGLMMLGTDSTSCTGMATICNMGAIEGATTSTFPYQEAHKRYLQATNRRAEVAEAADVAL
PKDVITKLAGLLTVRGGTGYIVEYFGEGVSTLSCTGMATICNMGAIEGATTSTFPYQEAHKRYLQATNRRAEVAEAADVAL
NKFNFLRADKDAQYDKVIEIDLSAIEPHVNGPFTPDLSTPISQYAEKSLKENWPQKVSAGLIGSCTNSSYQDMMSRVVDLV
KQASKAGLKPRIPFFVTPGSEQIRATLERDGIIDIFQENGAKVLANACGPCIGQWNREDVSCTSKEFTNTIFSFRNRFRA
RNDGMRNTMNFLTSPEIVTAMSYSGDAQFNPLTDSIKLPNGKDFKFQPPKGDELPKRGFEHGRDKFYPEMDPKPDSNVEI
KVDPNSDRLQLLEPFKPWNKGELKTNVLLKVEGKCTTDHISAAGVWLKYKGHENISYNTLIGAQNKETGEVNKAYDLDG
TEYDIPGLMMWKSDGRPWTVAEHNNGEGSAREHAALSPRFLGGEILLVKSFARIHETNLKKQGVPLTFANESDYDKI
SSGDVLETLNLVDMIAKDGNNNGGEIDVKITKPGESFTIKAKHTMSKDQIDFFKAGSAINYIGNIRRNE
>lcl|37362666Sc unnamed protein product
MLQLKFIWPVARITPIYRPFTSHPFRNLATSSSISSTKAKKTTKDTTPLKLSNELYAIFKIHNRPYLVTEGDRVILPFKL
KQAEVGDIILNMTDVTLGSRNYKLVGHPINTSLYTLKATVVGKTKRAFQTREVTKRRNRRVRHAKSKGDLTILRISELSM
N
```

2 Annotated Phylogenograms

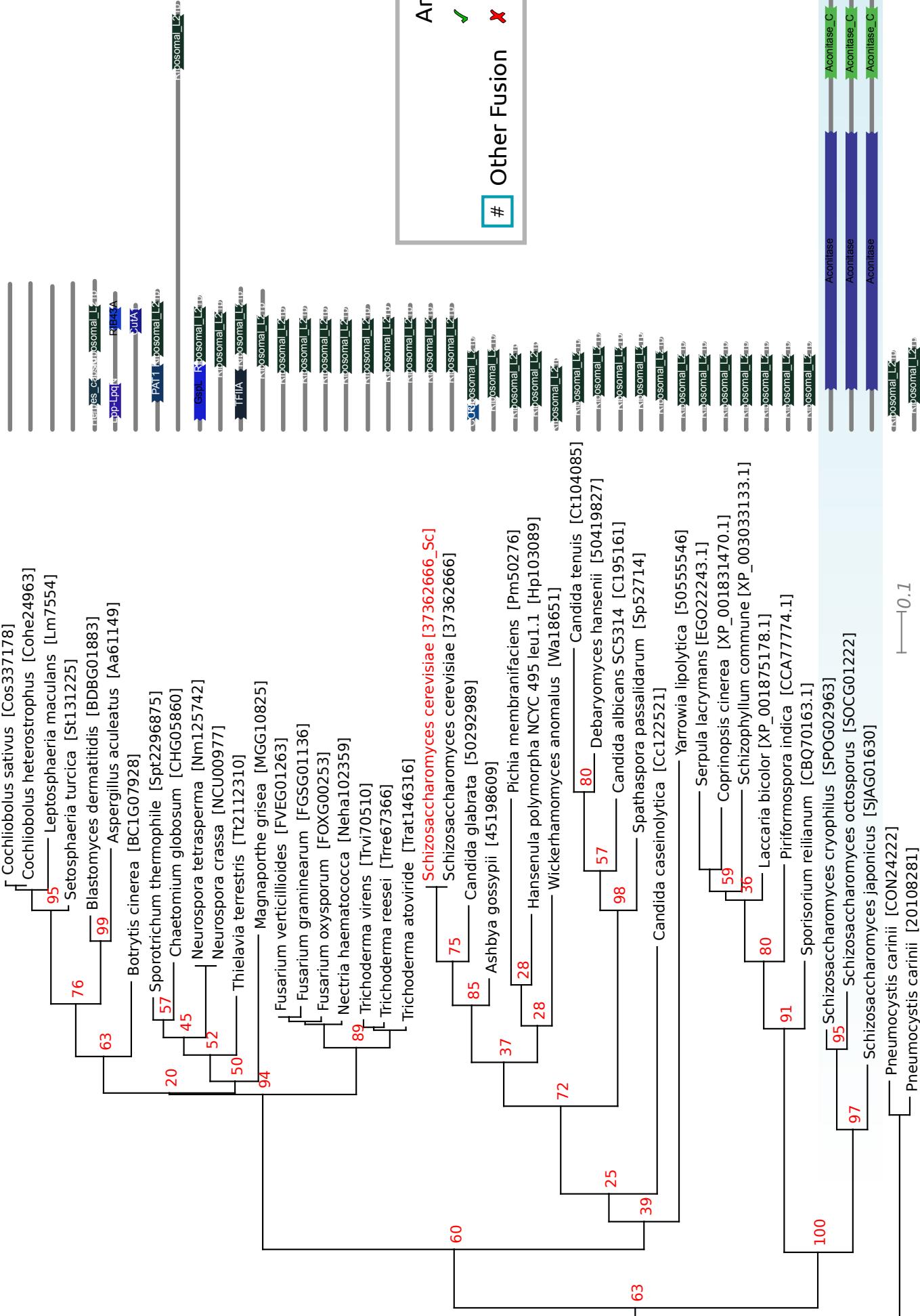
All trees were generated from an initial run of Darren's Orchard pipeline against 139 taxa (Table S1), using the above corresponding un-fused sequences as BLAST seeds. The alignments were then checked for any missing taxa, manually masked and then ProtTest3 was run, please see the Methods section for detail. The final trees were generated by the following command:

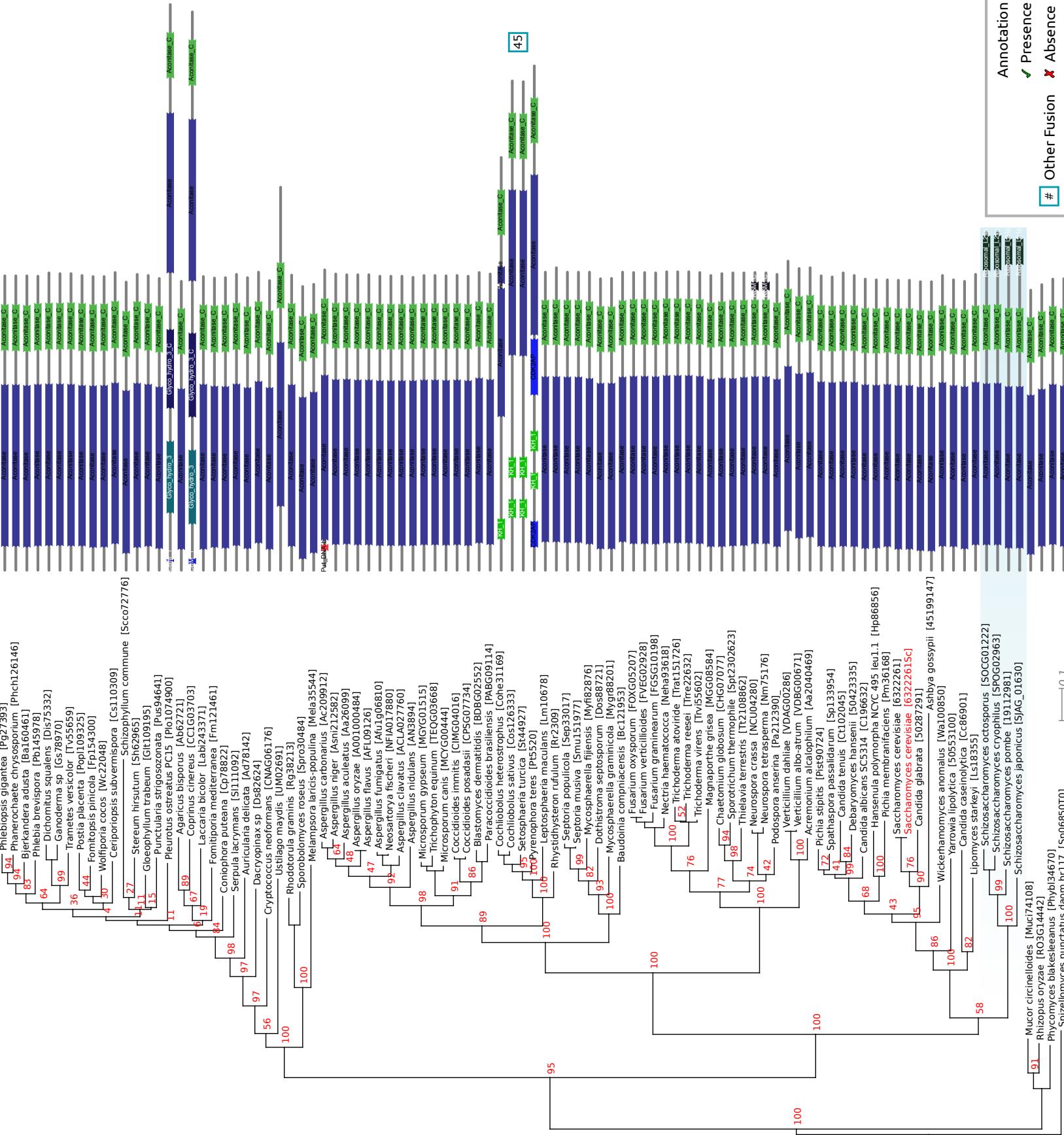
```
phym -i alignment_file -d aa -b 100 -m model -c 8 -v invariant_sites -s BEST --quiet
-a gamma
```

Styling and annotation was made possible by Dendroscope and Inkscape.

3 Mesquite Cladogram

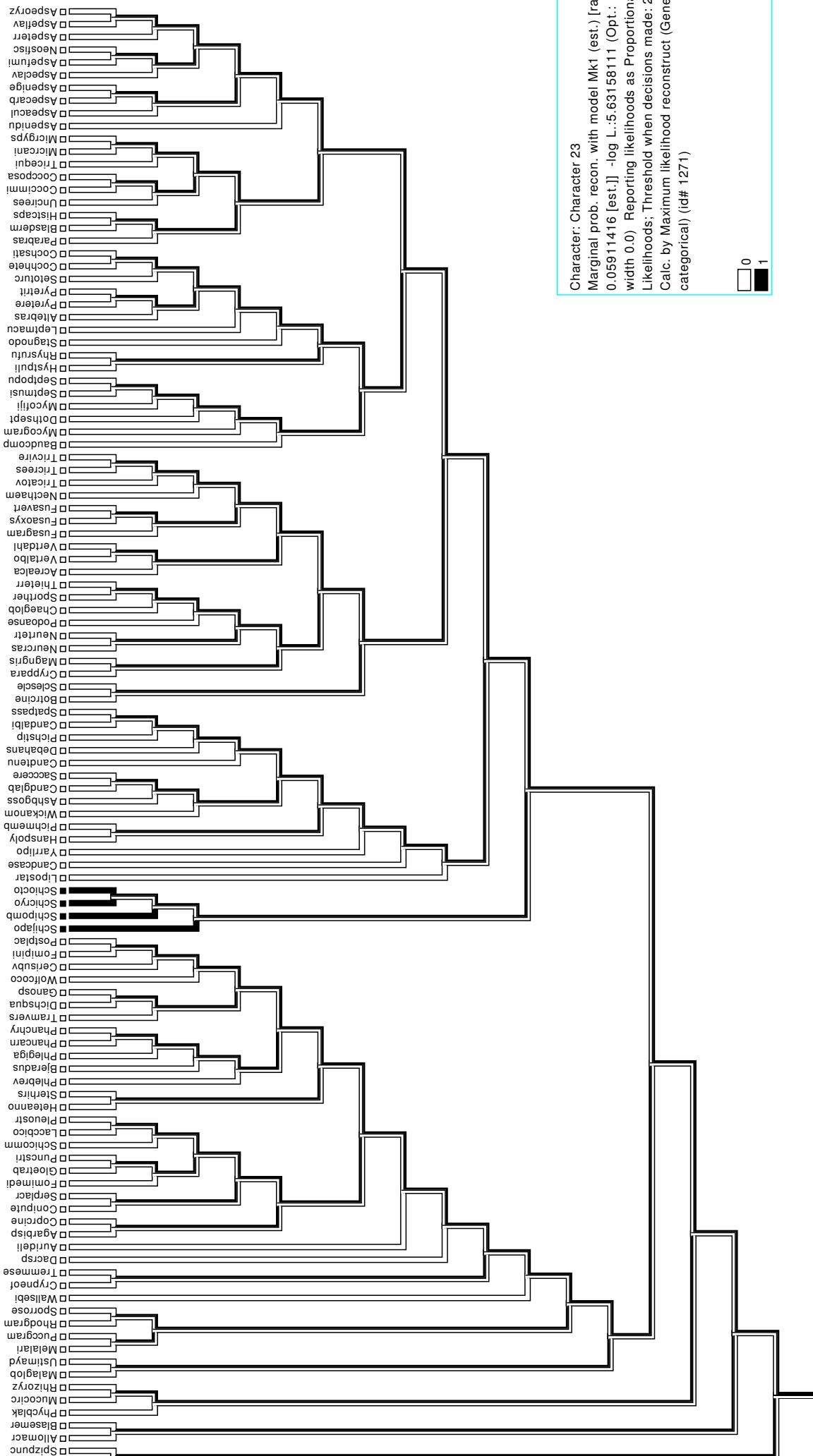
This tree is the 68-gene concatenated phylogeny (Fig. 1), with the presence of a fusion (black), presence of a fission (white), and absent/undetermined (grey) status of gene fusion characters plotted on to it using a "1/0/-" nexus-style data matrix. We used the program 'Mesquite' to calculate proportional likelihoods based on either an "Mk1" or "Assym. 2 param model." (see Table S4) of character change across the fungal phylogeny (Fig. 1). This allowed for a proportional likelihood of the position of the fusion/fission to be calculated.





Character: Character 23
 Marginal prob. recon. with model Mk1 (est.) [rate
 0.05911416 [est.]] -log L.: 5.63158111 (Opt.:
 width 0.0) Reporting likelihoods as Proportional
 Likelihoods: Threshold when decisions made: 2.0
 Calc. by Maximum likelihood reconstruct (Generic
 categorical) (id# 1271)

0
1



Putative Fusion 24

September 26, 2012

1 Fasta Sequences

These are the unfused sequences identified by fdfBLAST belonging to the putative gene fusion in FASTA format. Accessions may be shortened, but belong to either the taxons individual genome project or NCBI's accession numbering.

```
>lcl|CC1G05752 unnamed protein product
MTTQMATKRQEADIFLYTDLQGVHASPEDGNRYRGLGYIDSTKDVL EIALELLPEDPPKEPTSTEWPSAMNVECEAPK
SKQRRRRTRPTATSAQNKGPEKVEIELLQDITSLSRSRKGDTGSVVKASIDFARYVLQRHFPSEQSLFNYERLKECHVL
ELGSGTGILSILLSPPLVAKYTVDIEALVPLIQKNINKNFPSEDTSRPNISAEP LDWIALHSSTPAQRAKLFSNDPPVDLI
LVVDCIYHP SLIPPLLSTIDHVTIPDR TTVLV LSEL RSEEVLREFLLSWLDIPGWKIWHVGGDLLQNKRYVMWTGWPST
KGRES
>lcl|CC1G04209 unnamed protein product
MAPHDDHIVYMKMALEEEAEKAVPVPGAF CGVGC VLVARLLHKS VVLSTGYSRELPGNTHAEANALAKVAEISPKEWSALSE
SYEASSDLSKILECTDVYTTLEPC SIR TSGLSPCADALIKAKVRRCIIGVNEPPDFVKCEGADR LKAAGIEVIWLSGMEE
DCLRVAR KGH
```

2 Annotated Phylogenograms

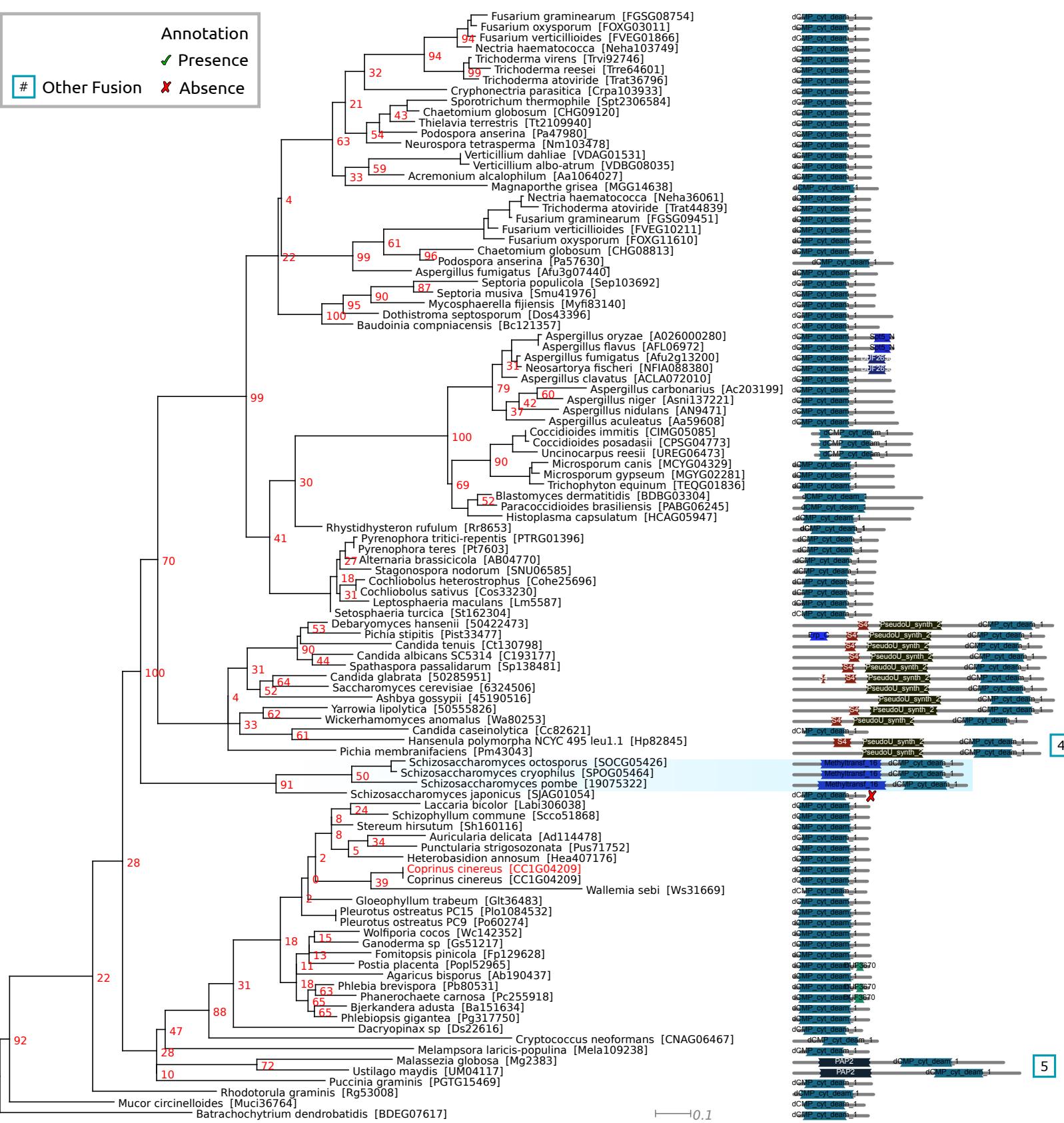
All trees were generated from an initial run of Darren's Orchard pipeline against 139 taxa (Table S1), using the above corresponding un-fused sequences as BLAST seeds. The alignments were then checked for any missing taxa, manually masked and then ProtTest3 was run, please see the Methods section for detail. The final trees were generated by the following command:

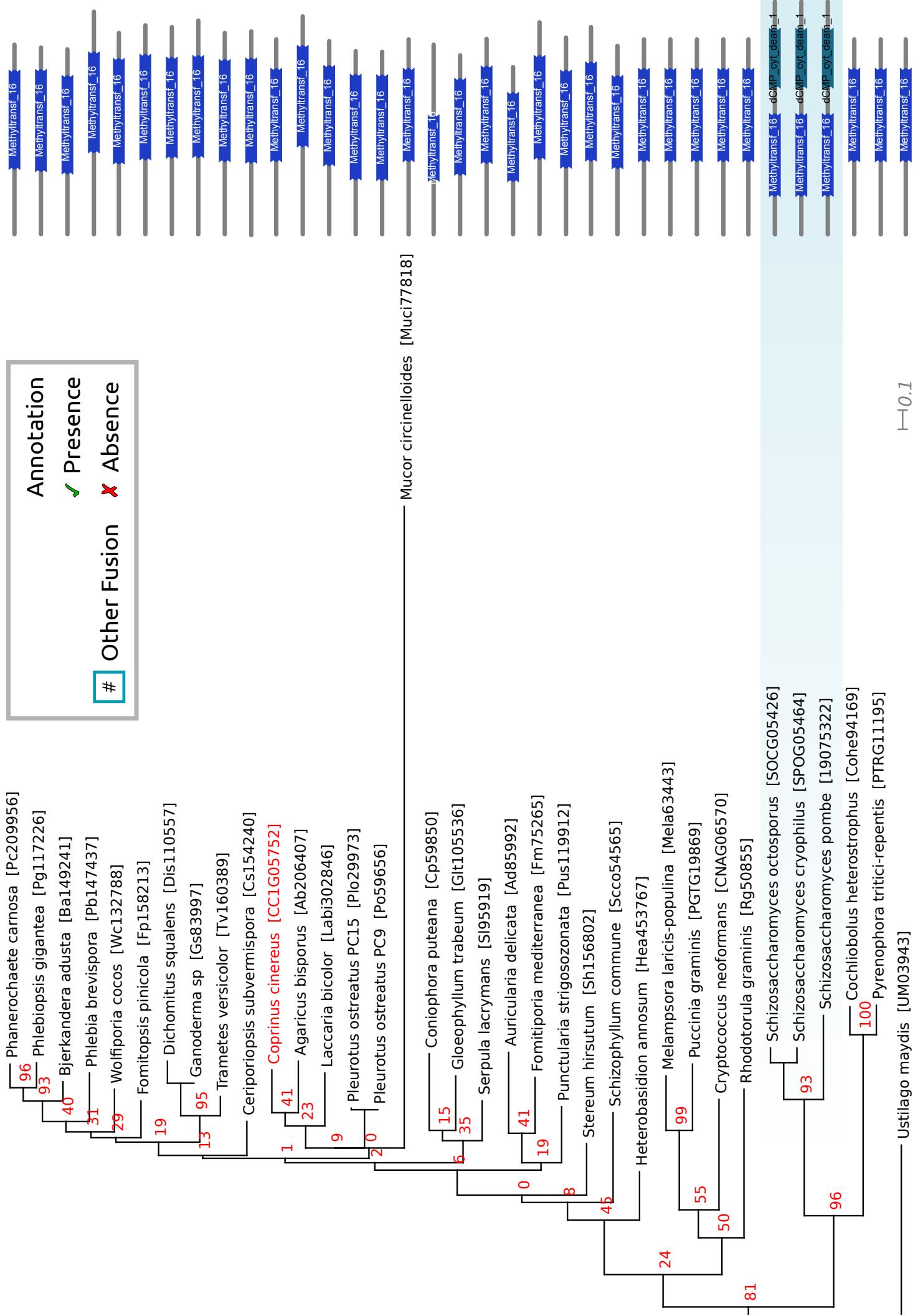
```
phylml -i alignment_file -d aa -b 100 -m model -c 8 -v invariant_sites -s BEST --quiet
-a gamma
```

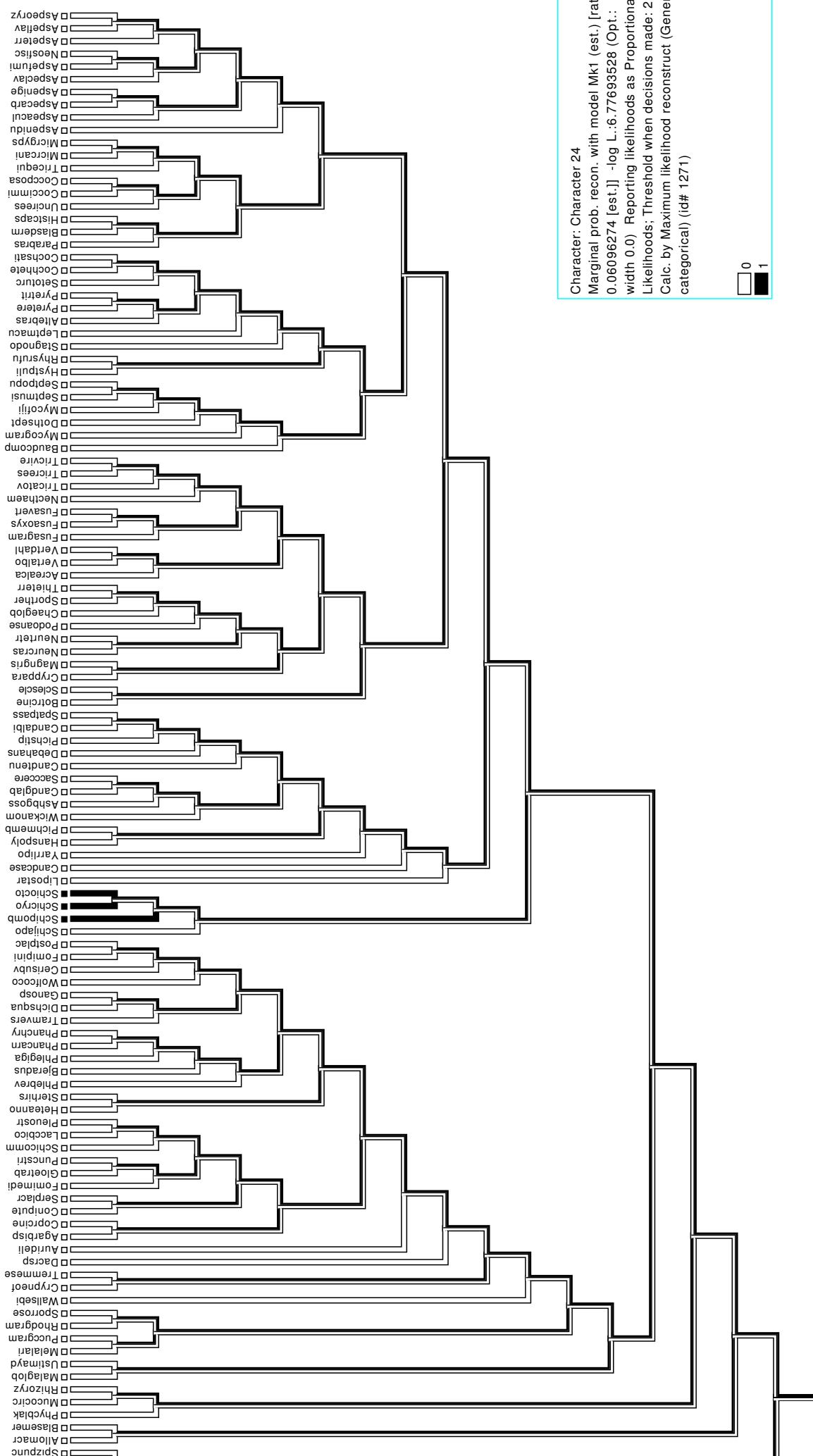
Styling and annotation was made possible by Dendroscope and Inkscape.

3 Mesquite Cladogram

This tree is the 68-gene concatenated phylogeny (Fig. 1), with the presence of a fusion (black), presence of a fission (white), and absent/undetermined (grey) status of gene fusion characters plotted on to it using a "1/0/-" nexus-style data matrix. We used the program 'Mesquite' to calculate proportional likelihoods based on either an "Mk1" or "Assym. 2 param model." (see Table S4) of character change across the fungal phylogeny (Fig. 1). This allowed for a proportional likelihood of the position of the fusion/fission to be calculated.







Character: Character 24
 Marginal prob. recon. with
 0.06096274 [est.] - log
 width 0.0 Reporting like
 Likelihoods: Threshold w
 Calc. by Maximum likelihood
 categorical) (#d 1271)

Putative Fusion 25

September 26, 2012

1 Fasta Sequences

These are the unfused sequences identified by fdfBLAST belonging to the putative gene fusion in FASTA format. Accessions may be shortened, but belong to either the taxons individual genome project or NCBI's accession numbering.

```
>lcl|6324854Sc unnamed protein product
MSEKKVVMLHGTVQSDKIFSAKTGLRKNLKLGVDLYYPCAPHSIDKKALFQSESEKGRDAAKEFNTSATSDEVYGWF
FRNPESFNSFQIDQKVFNLYRNYLENGPDFGVIGFSQGAGLGGYLVTDFNRILNLTDEQQPALKFFISFSGFKLEDQSY
QKEYHRIIQVPSLHVRGELDEVVAESRIMALYESWPDNKRTLLVHPGAHFVPNSKPFVSQVCNWIQGITSKEGQEHNNAQP
EVDRKQFDKPQLEDDLLDMIDSLGKL
>lcl|6324810Sc unnamed protein product
MAGGKIPIVGIVACLQPEMGIGFRGGLPWRLPSEMKYFRQVTSLTKDPNKKNALIMGRKTWESIPPKFRPLPNRMNVIIS
RSFKDDFVHDKERSIVQSNSLANAIMLESNFKEHLERIYVIGGEVYSQIFSITDHWLITKINPLDKNATPAMDTFLDA
KKLEEVFSEQDPAQLKEFLPPKVELPETDCDQRYSLEEKGYCFEFTLYNRK
```

2 Annotated Phylogenograms

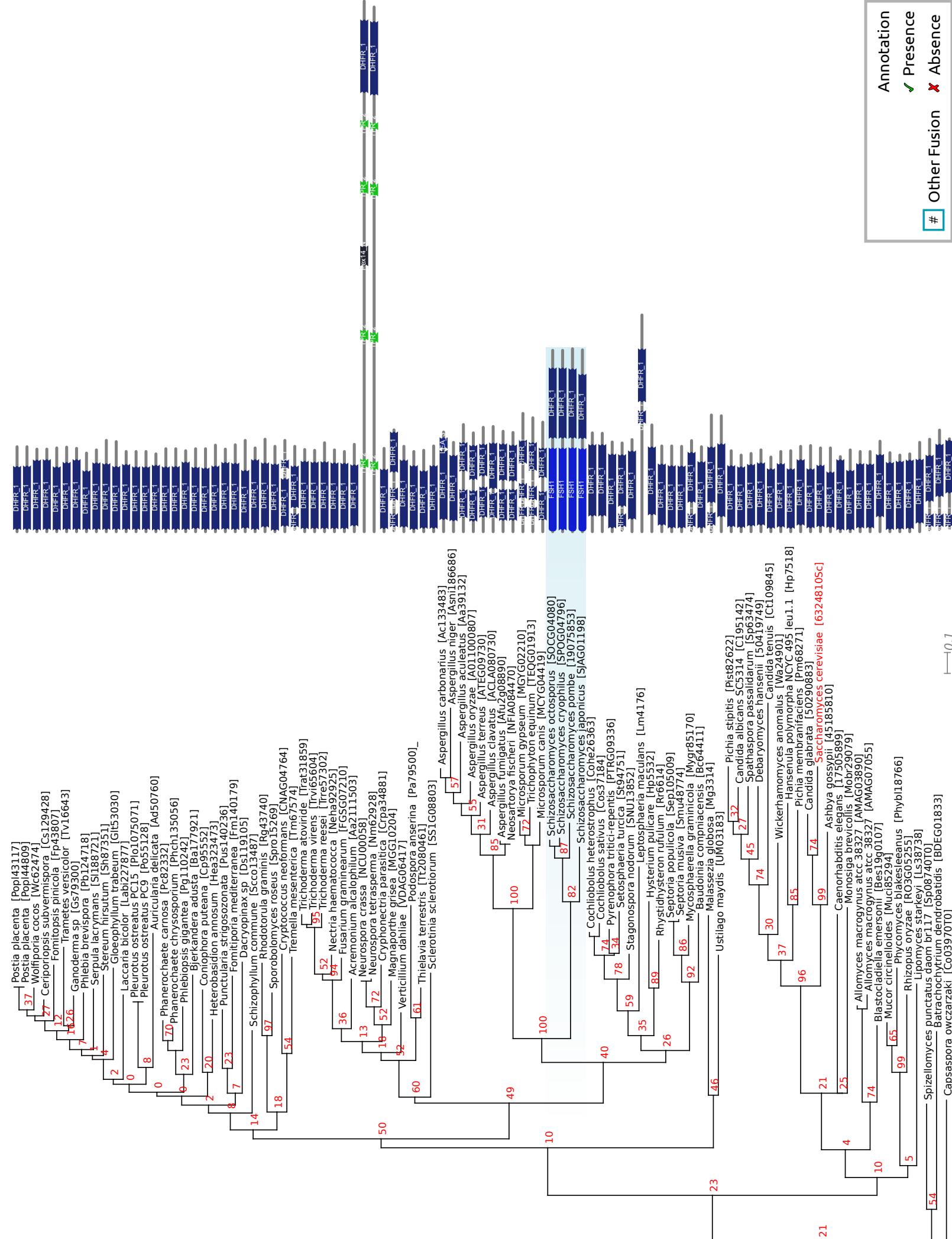
All trees were generated from an initial run of Darren's Orchard pipeline against 139 taxa (Table S1), using the above corresponding un-fused sequences as BLAST seeds. The alignments were then checked for any missing taxa, manually masked and then ProtTest3 was run, please see the Methods section for detail. The final trees were generated by the following command:

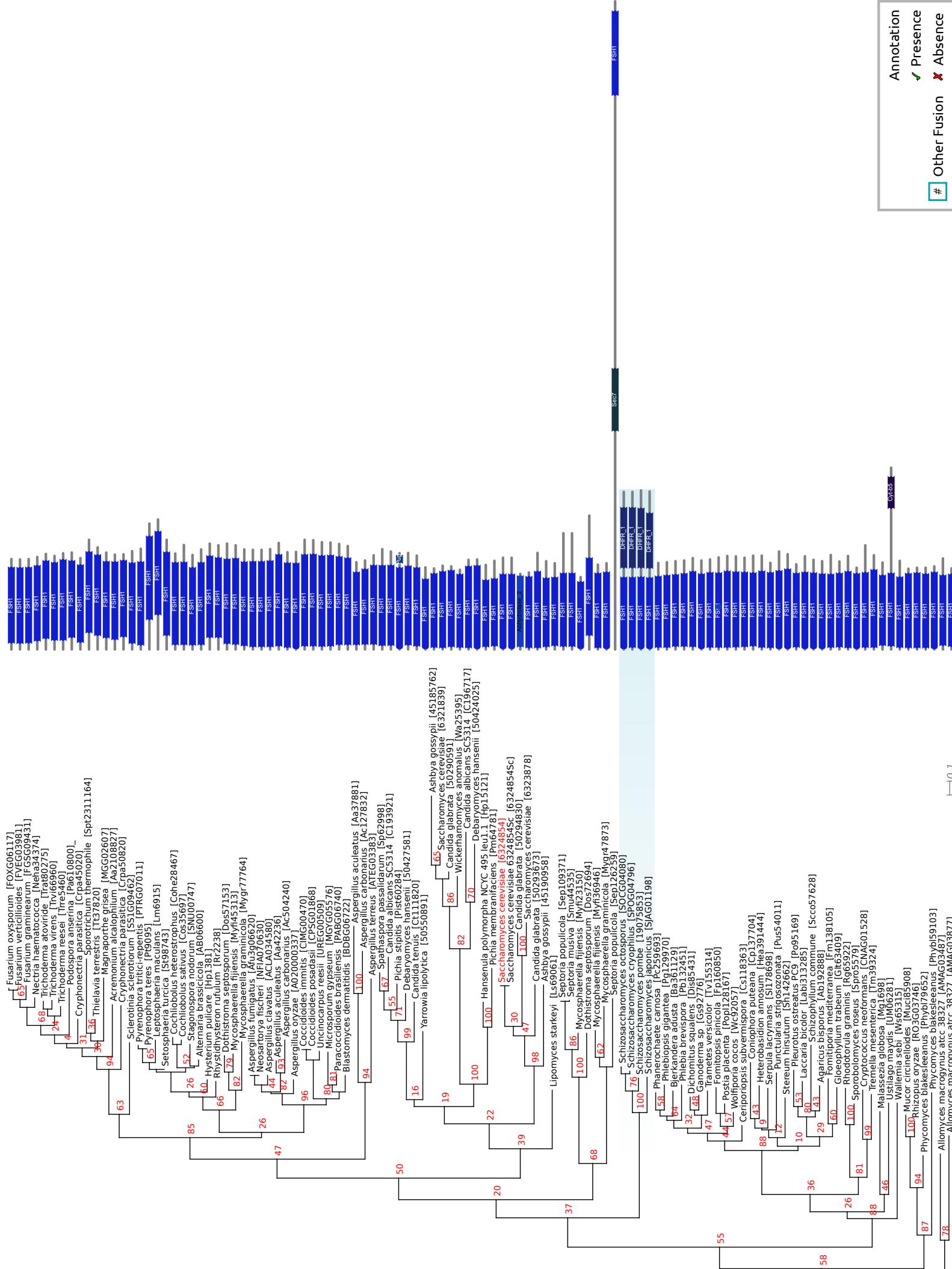
```
phylml -i alignment_file -d aa -b 100 -m model -c 8 -v invariant_sites -s BEST --quiet
-a gamma
```

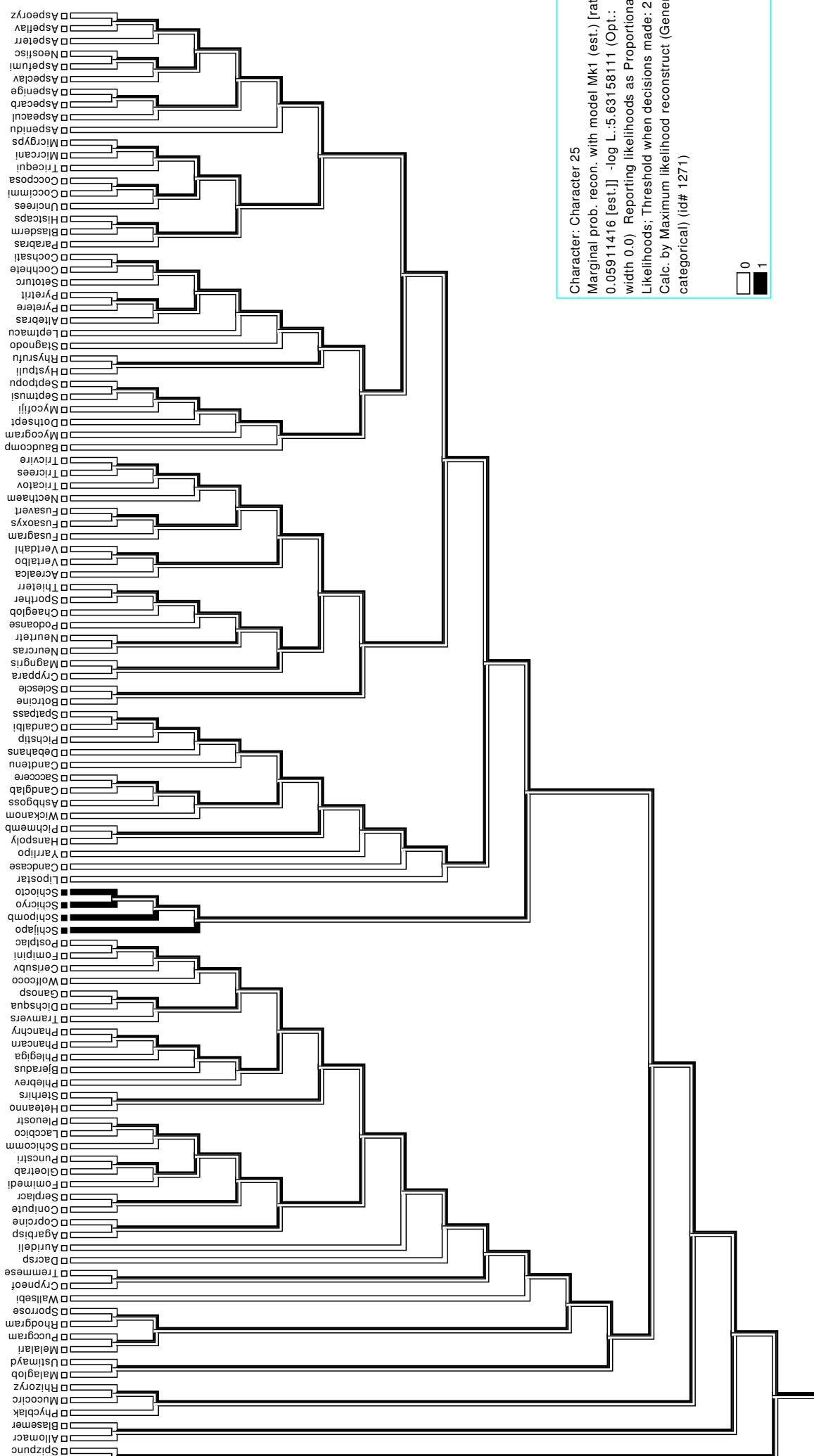
Styling and annotation was made possible by Dendroscope and Inkscape.

3 Mesquite Cladogram

This tree is the 68-gene concatenated phylogeny (Fig. 1), with the presence of a fusion (black), presence of a fission (white), and absent/undetermined (grey) status of gene fusion characters plotted on to it using a "1/0/-" nexus-style data matrix. We used the program 'Mesquite' to calculate proportional likelihoods based on either an "Mk1" or "Assym. 2 param model." (see Table S4) of character change across the fungal phylogeny (Fig. 1). This allowed for a proportional likelihood of the position of the fusion/fission to be calculated.







Character: Character 25
 Marginal prob. recon. with model Mk1 (est.) [rate : 0.05911416 [est.]] -log L.: 563158111 (Opt. : width 0.0). Report likelihoods as Proportional Likelihoods; Threshold when decisions made: 2.0 Calc. by Maximum likelihood reconstruct (Generic categorical) (id# 1271)

Putative Fusion 26

September 26, 2012

1 Fasta Sequences

These are the unfused sequences identified by fdfBLAST belonging to the putative gene fusion in FASTA format. Accessions may be shortened, but belong to either the taxons individual genome project or NCBI's accession numbering.

```
>lcl|Mc151744 unnamed protein product
MGFPSWASVIVALGAATVLAIAGDFIYSKLTTRVPFKAAGKHCFITGGSTGLGKSLAVQLVKEGADVCIVARRVSELEAAV
EEIKASCLNENQKVIYISADVTNQKDVVRAFDEAKVKMGRNPDFVCACAGASYPKFFLDHTMEDFEKLTLNYLGQAYVA
HQAAQRMRDSNIKDGKIVFVSSLLGMISFAGWATYSPTKYAVRGLADTLRNELKRYNIGVHIFFPGGIESPGFETENLTK
PEVTKIIEGANTPQTGAECAKSLMKGLHQGQYMIVTDALSEVLRCCVVRGVGPTNNLVLDYILAAIGQPLGSAFALYADYV
VKSAKYDK
>lcl|Mc112741 unnamed protein product
MKPFGTELVIGLLAIGLNYGATFKLPATSLLKDPVQTLSTTVPLFVGHIILVLFAHILRGTTNKALKSVGYSILATATA
TGVLHVLTVLFGAPLIEKIPNTFLFAAYLSILTVMPCYESFQETAWIKVFLQHSPTTSEIYAYAQCALSGAWIGAIV
LPLWDREWQAWPISCVISTYVGHSGVLAFFVWASLKLMLFGKKSE
```

2 Annotated Phylogenograms

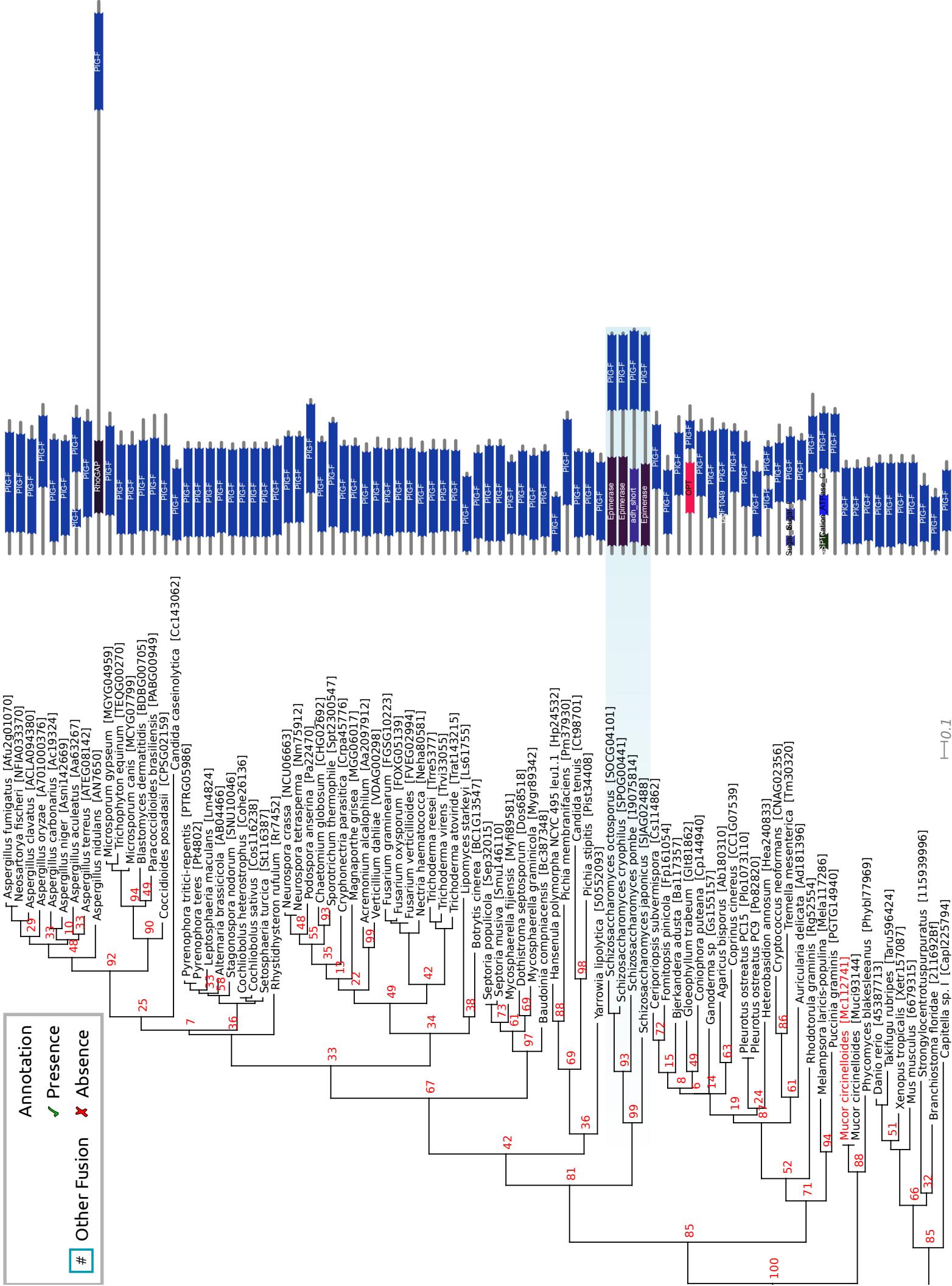
All trees were generated from an initial run of Darren's Orchard pipeline against 139 taxa (Table S1), using the above corresponding un-fused sequences as BLAST seeds. The alignments were then checked for any missing taxa, manually masked and then ProtTest3 was run, please see the Methods section for detail. The final trees were generated by the following command:

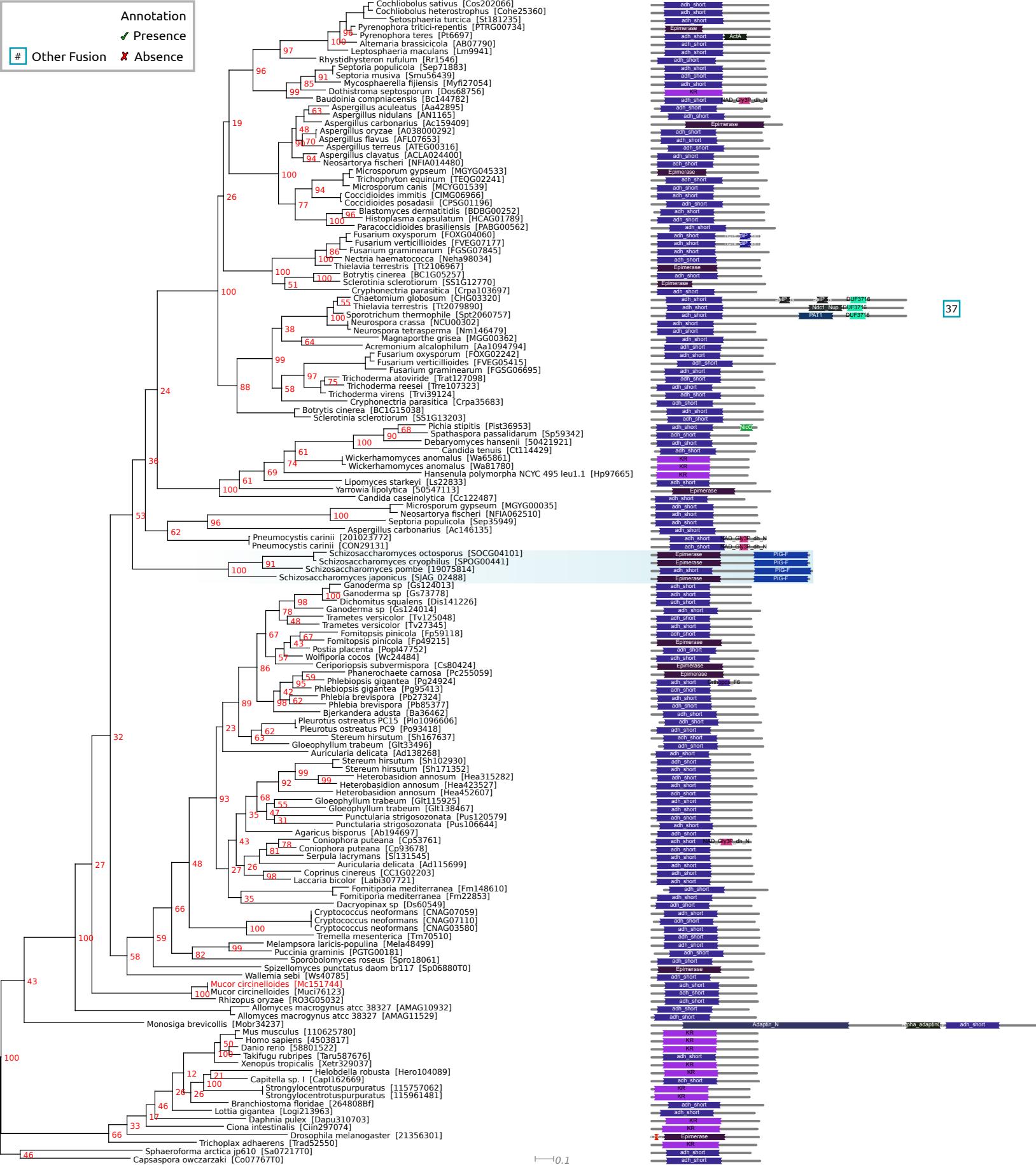
```
phylml -i alignment_file -d aa -b 100 -m model -c 8 -v invariant_sites -s BEST --quiet
-a gamma
```

Styling and annotation was made possible by Dendroscope and Inkscape.

3 Mesquite Cladogram

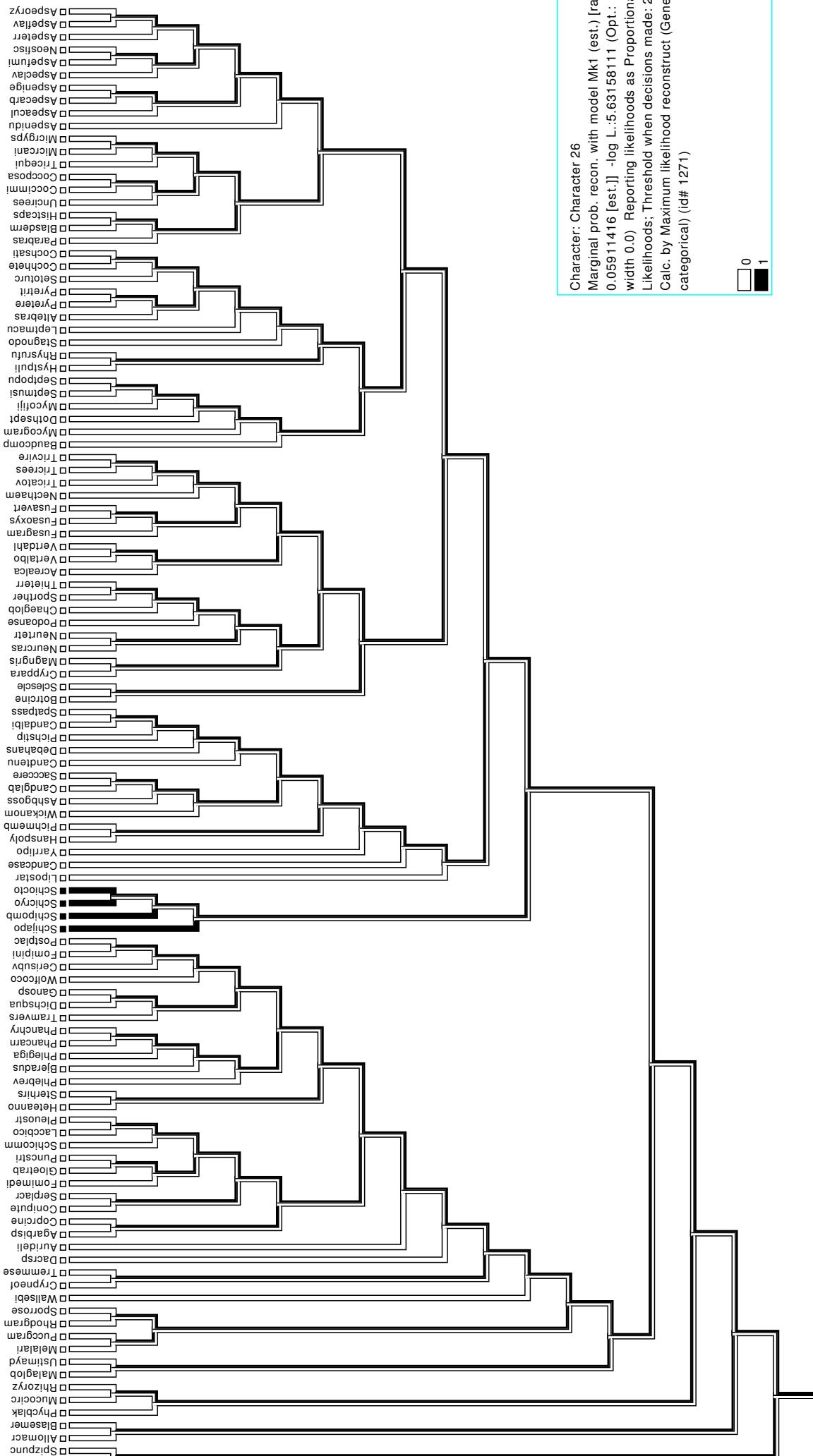
This tree is the 68-gene concatenated phylogeny (Fig. 1), with the presence of a fusion (black), presence of a fission (white), and absent/undetermined (grey) status of gene fusion characters plotted on to it using a "1/0/-" nexus-style data matrix. We used the program 'Mesquite' to calculate proportional likelihoods based on either an "Mk1" or "Assym. 2 param model." (see Table S4) of character change across the fungal phylogeny (Fig. 1). This allowed for a proportional likelihood of the position of the fusion/fission to be calculated.





Character: Character 26
 Marginal prob. recon. with model Mk1 (est.) [rate
 0.05911416 [est.]] -log L.: 5.63158111 (Opt.:
 width 0.0) Reporting likelihoods as Proportional
 Likelihoods: Threshold when decisions made: 2.0
 Calc. by Maximum likelihood reconstruct (Generic
 categorical) (id# 1271)

0
1



Putative Fusion 27

September 26, 2012

1 Fasta Sequences

These are the unfused sequences identified by fdfBLAST belonging to the putative gene fusion in FASTA format. Accessions may be shortened, but belong to either the taxons individual genome project or NCBI's accession numbering.

```
>lcl|6324283Sc unnamed protein product
MFLLPFVIRHSSSIYLPTLFRGLLTIVSRNIHISTPHKMLPLSIEQRRPSRSPEYDQSTLSNYKDFAVLHTDLNLSVSF
EKAISGSVTFQLKKLHEGKNKSDELHLDTSYLDVQEVIDGSKADFQIEQRKEPLGSRLVINNASCNDNFTLNQIYFRTT
DKCTALQWLNSKQTGGKPYVFSQLEAIHARSLFPCFDTPSVKSTFTASIESPLPVVFSGIRIEDTSKDTNIYRFEQKVP
IPAYLIGIASGDLSSAPIGPRSTVYTEPFRLKDCQWEFENDVEKFIQTAEKIIIFEYEWGTYDILVNVDSPYGGMESPNM
TFATPTLIAHRSNIDVIAHELAHSWGNLVTNCWSNHFWLNEGWTYLERRIIGAIHGEPTRHFSALIGWSDLQNSIDS
MKDPERFSTLVQNLNDNTDPDDAFSTVYEPYEGFNLFFLETILGGKAEFDPFIRHYFKKFAKSLDTFQFLDTLYEFYPE
KKEILDSDVETWLYKPGMPPRPHFITALADNVYQLADKWVEMAQHLKTTEDFRSEFNADIKDFNSNQLVLFLETLTQN
GHSNKKPKDFDWAKFPVASRALLDIYQDNIVKSQNAEVVFKMFKFQIFAKLQEEYKHLADWLGTVGRMKFVRPGYRLLNS
VDRRLALATFDKFKDTHYPICKALVKQDLGL
>lcl|6324848Sc unnamed protein product
MLKGPLKGCLMSKKVIVIAGTTGVGKSQLSIQLAQKFNGEVINSDSMQVYKDIPIITNKHPLQEREGIPHVMNHVDWS
EEYYSHRFETECMNAIEDIHRRGKIPIVVGTHYQLQTLFNKRVDTKSSERKLTRKQLDILESTDPAVIYNTLVKCDPDI
ATKYHPNDYRRVQRMLEIYYKTGKPKSETFNEQKITLKFDTLFLWLYSKPEPLFQRLDDRVDMLERGALQEIKQLYEYY
SQNKFTPEQCEENGWQVIGFKEFLPWLTGKTDNTVKLEDCIERMKTRTRQYAKRQVWKIKMLIPDIKGDYLLDATDL
SQWDTNASQRAIAISNDFISNRPIKQERAPKALEELLSKGETTMKKLDDWTHYTCNVCRNADGKNVVAIGEKYWKIHGS
RRHKSNLKRNTRQADFEKWKINKKETVE
```

2 Annotated Phylogenograms

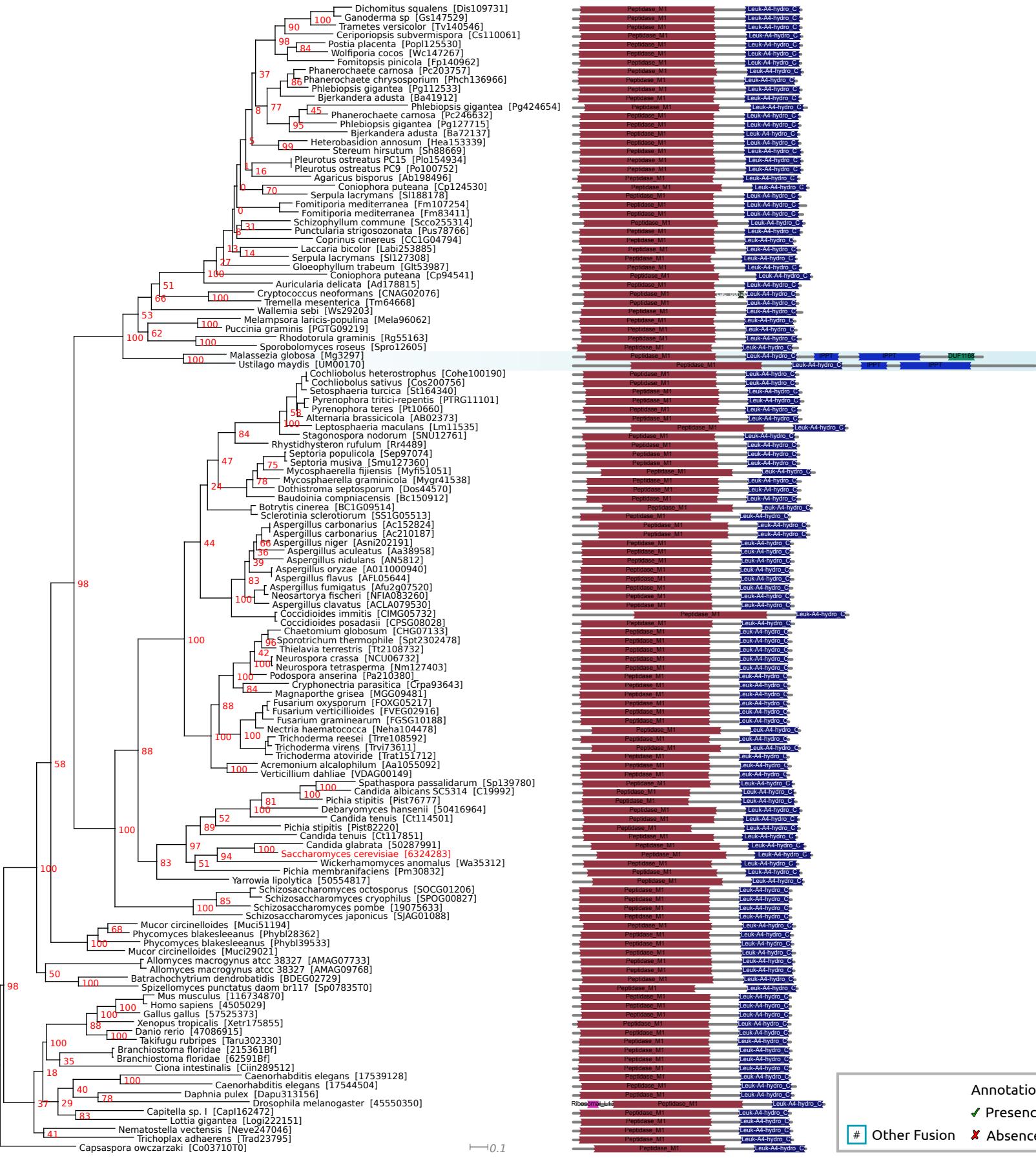
All trees were generated from an initial run of Darren's Orchard pipeline against 139 taxa (Table S1), using the above corresponding un-fused sequences as BLAST seeds. The alignments were then checked for any missing taxa, manually masked and then ProtTest3 was run, please see the Methods section for detail. The final trees were generated by the following command:

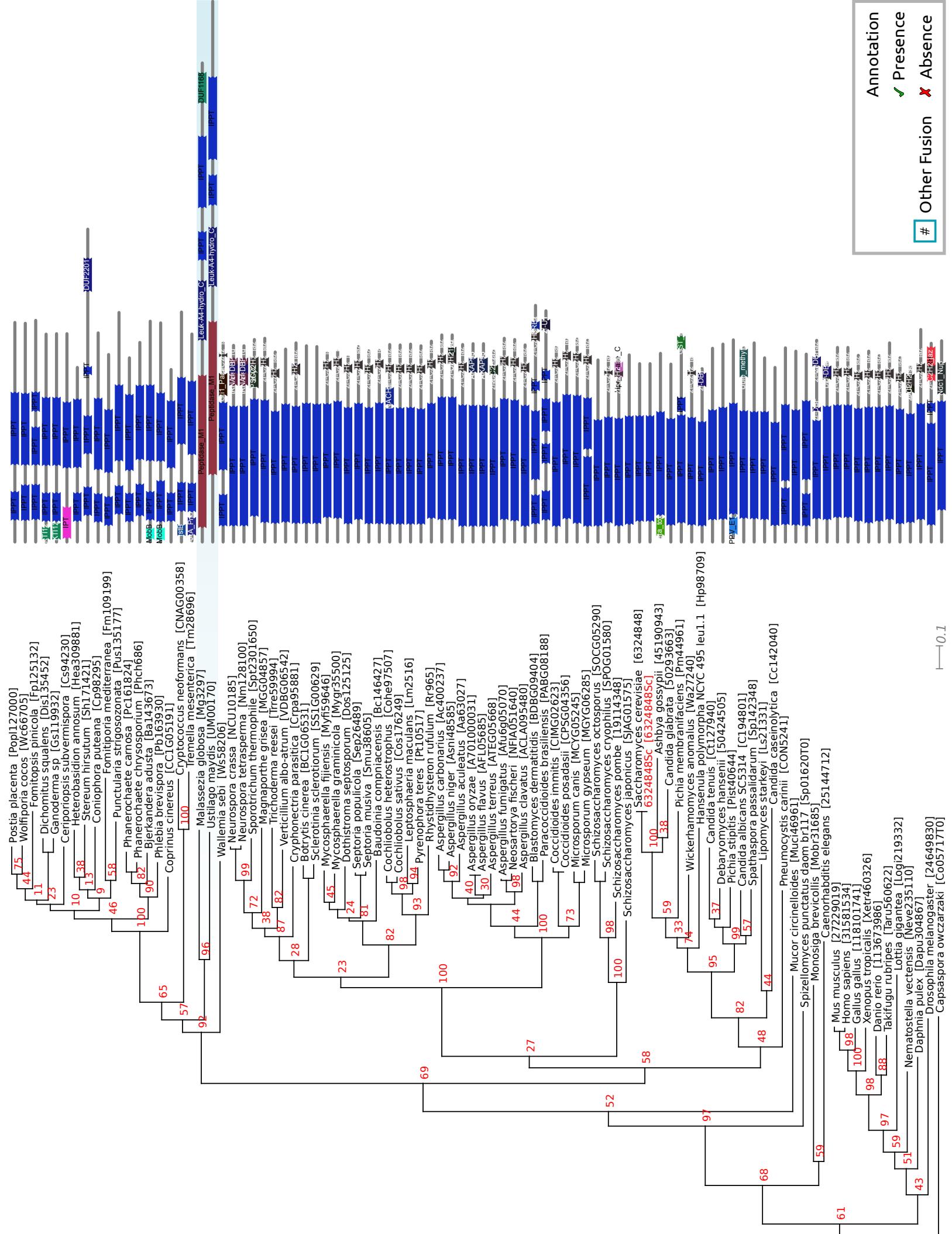
```
phyml -i alignment_file -d aa -b 100 -m model -c 8 -v invariant_sites -s BEST --quiet
-a gamma
```

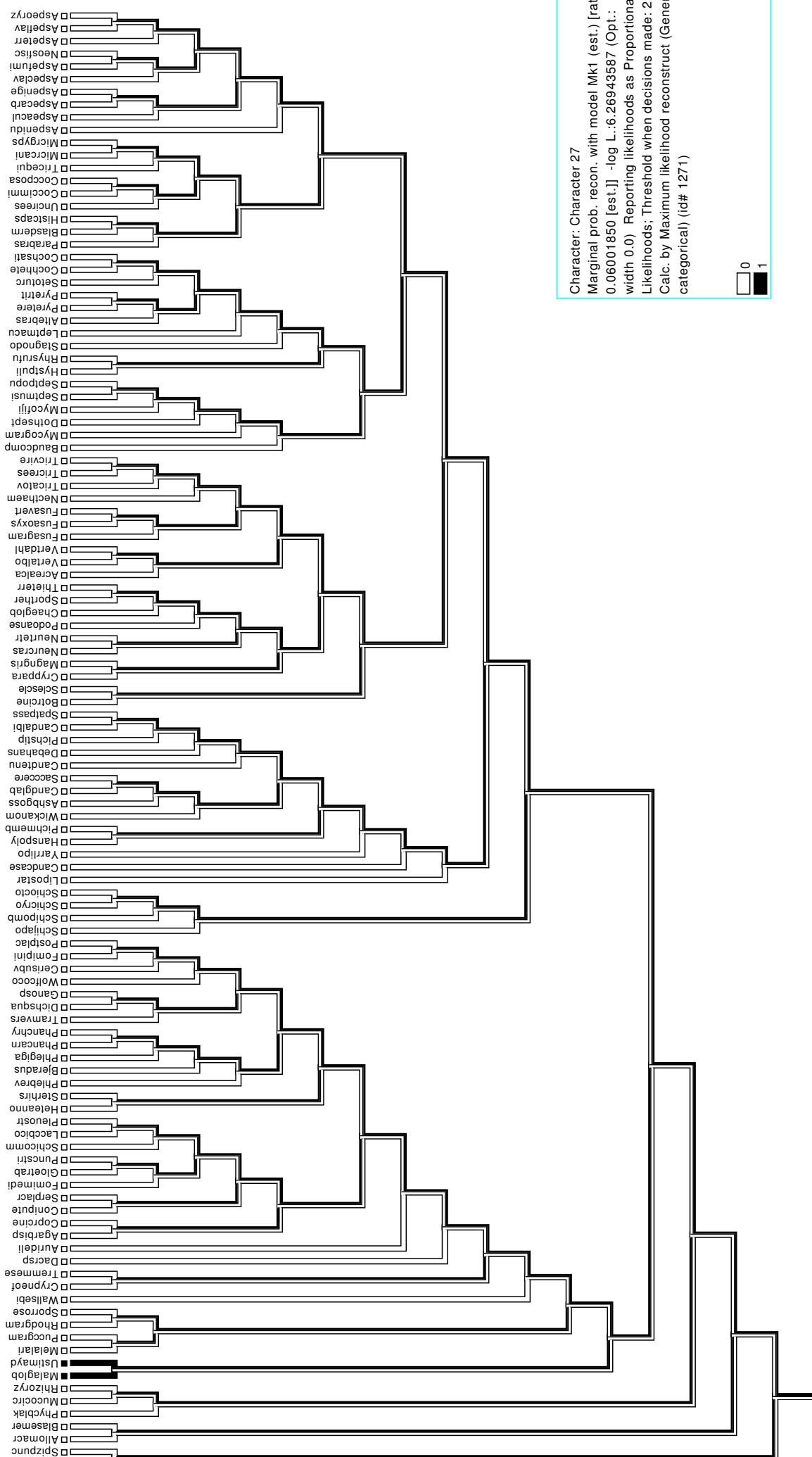
Styling and annotation was made possible by Dendroscope and Inkscape.

3 Mesquite Cladogram

This tree is the 68-gene concatenated phylogeny (Fig. 1), with the presence of a fusion (black), presence of a fission (white), and absent/undetermined (grey) status of gene fusion characters plotted on to it using a "1/0/-" nexus-style data matrix. We used the program 'Mesquite' to calculate proportional likelihoods based on either an "Mk1" or "Assym. 2 param model." (see Table S4) of character change across the fungal phylogeny (Fig. 1). This allowed for a proportional likelihood of the position of the fusion/fission to be calculated.







Character: Character 27
Marginal prob. recon. with model Mk1 (est.) [rate 0.06001850 [est.]] - log L: -6.28943557 (Opt.: width 0.0). Reporting likelihoods as Proportional Likelihoods; Threshold when decisions made: 2.0 Calc. by Maximum likelihood reconstruct (Generic categorical) (id# 1271)

Putative Fusion 28

September 26, 2012

1 Fasta Sequences

These are the unfused sequences identified by fdfBLAST belonging to the putative gene fusion in FASTA format. Accessions may be shortened, but belong to either the taxons individual genome project or NCBI's accession numbering.

```
>lcl|6322896Sc unnamed protein product
MPSLTPRCIIVRHGQTEWSKSGQYTGLTDPLTPLTYGEGQMLRTGESVFRNNQFLNPDNITYIFTSPRLRARQTVDLVLKP
LSDEQRRAKIRVVVDDDLREWEYGDYEGMLTREIIIELRKSRGDKERPWNIWRDGCENGETTQQIGLRLSRAIAARIQNLHR
KHQSEGRASDIMVFAHGHALRYFAAIWFGLGVQKKCETIEEIQNVKSYDDDTVPYVKLESYRHLVDNPCFLLDAGGIGVL
SYAHHNIDEPALELAGPFVSPPEESQHGDV
>lcl|83578104Sc unnamed protein product
MTMDGKNKEEQYLDLCKRIIDEGEFRPDRTGTGTLSLFAPPQLRFSLRDDTFPLLTGVFTRGIIILELLWFLAGDTA
NLLSEQGVKIWDGNGSREYLDKMGFKDRKVGLGPVYGFQWRHFGAKYKTCDDDYTGQGIDQLKQVIHKLKTNPYDRRII
MSAWNPNADFDKMLPPCHIFSQFYVSFPKEGEKGSKPRLSCLLYQRSCDMGLGVPFNIASYALLTRMIAKVVDMEPGEFI
HTLGDAHVYKDHDALKEQITRNPRFPKLIKRDVKDIDDFKLTDFEIEDYNPHPRIQMKMSV
```

2 Annotated Phylogenograms

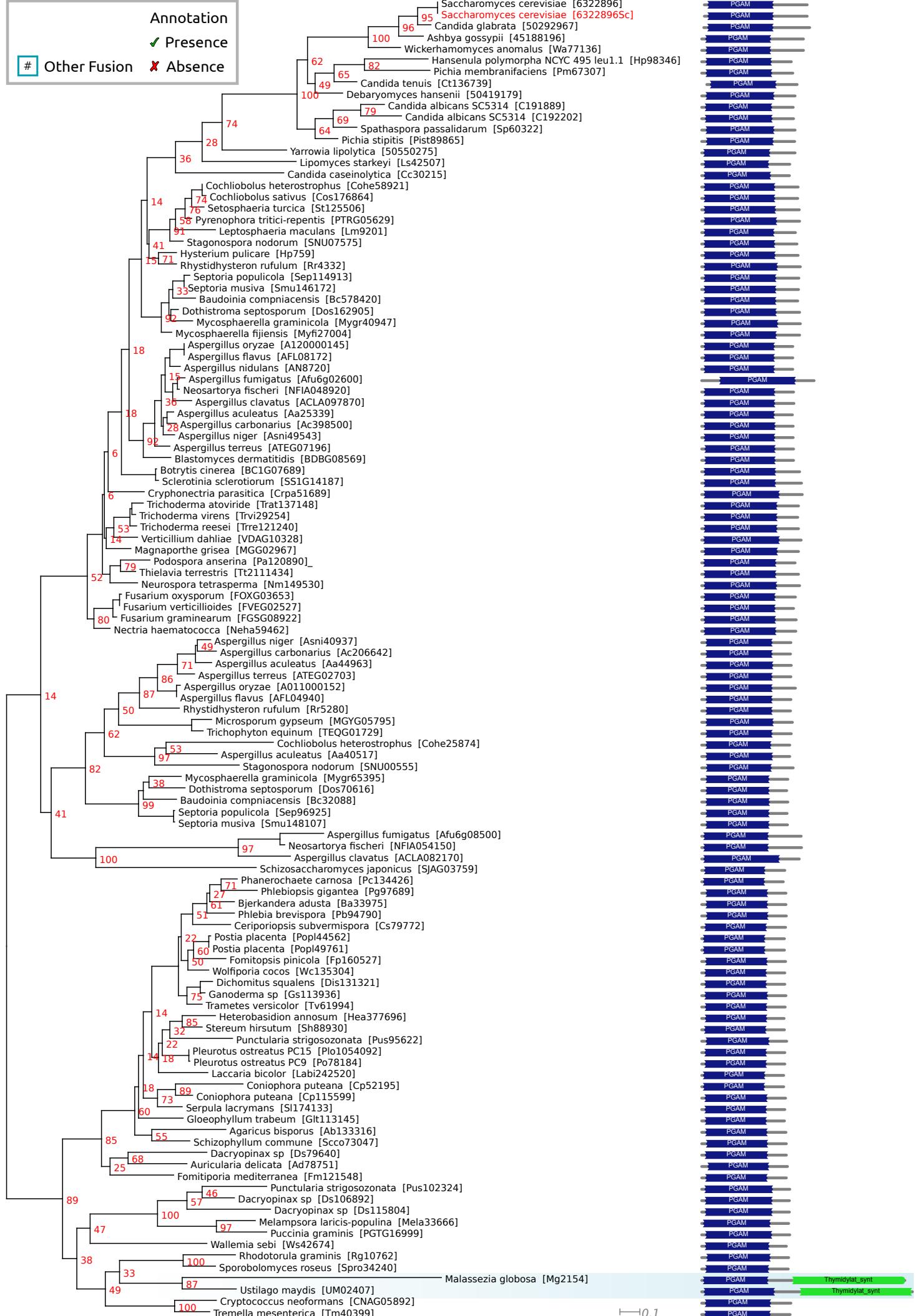
All trees were generated from an initial run of Darren's Orchard pipeline against 139 taxa (Table S1), using the above corresponding un-fused sequences as BLAST seeds. The alignments were then checked for any missing taxa, manually masked and then ProtTest3 was run, please see the Methods section for detail. The final trees were generated by the following command:

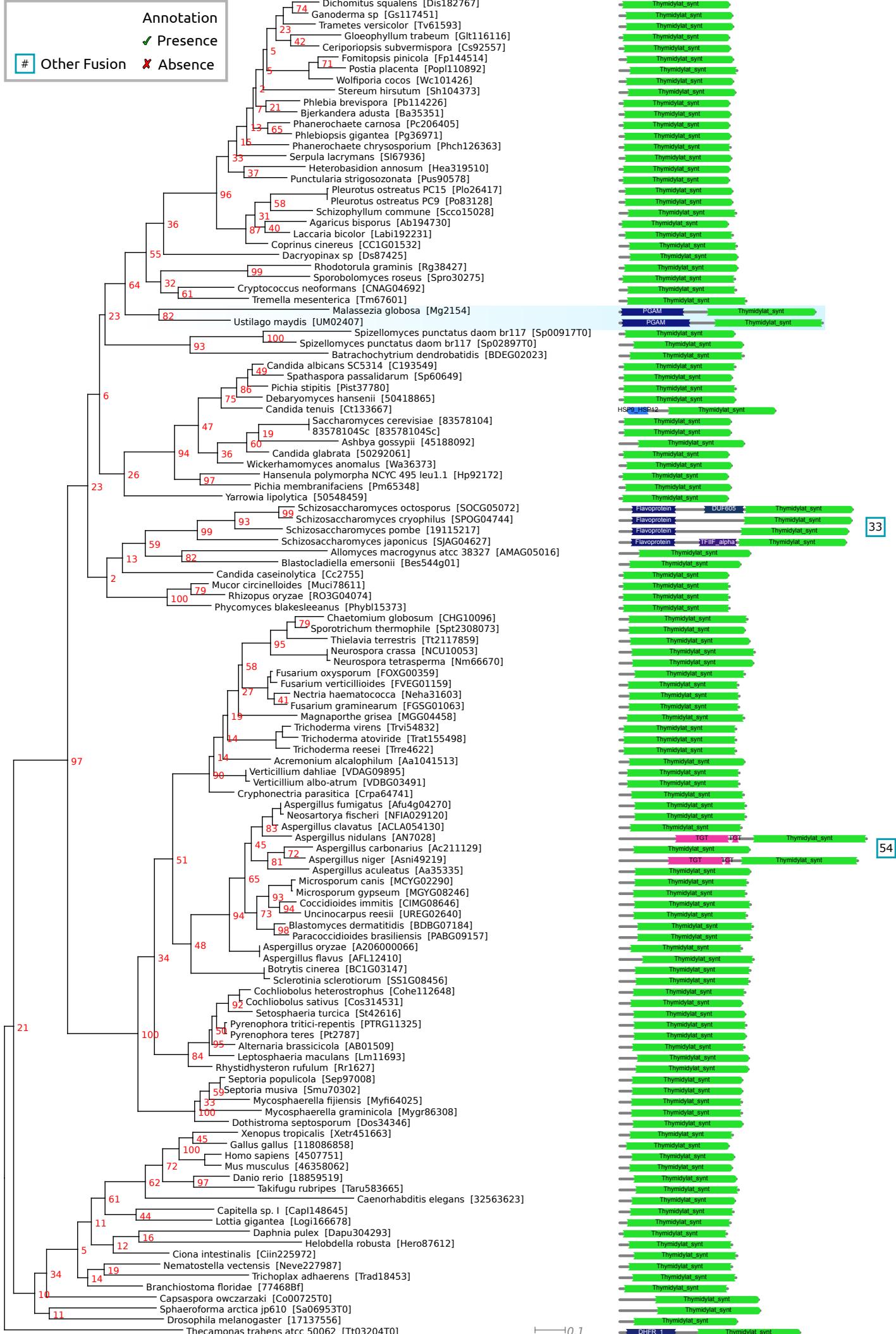
```
phylml -i alignment_file -d aa -b 100 -m model -c 8 -v invariant_sites -s BEST --quiet
-a gamma
```

Styling and annotation was made possible by Dendroscope and Inkscape.

3 Mesquite Cladogram

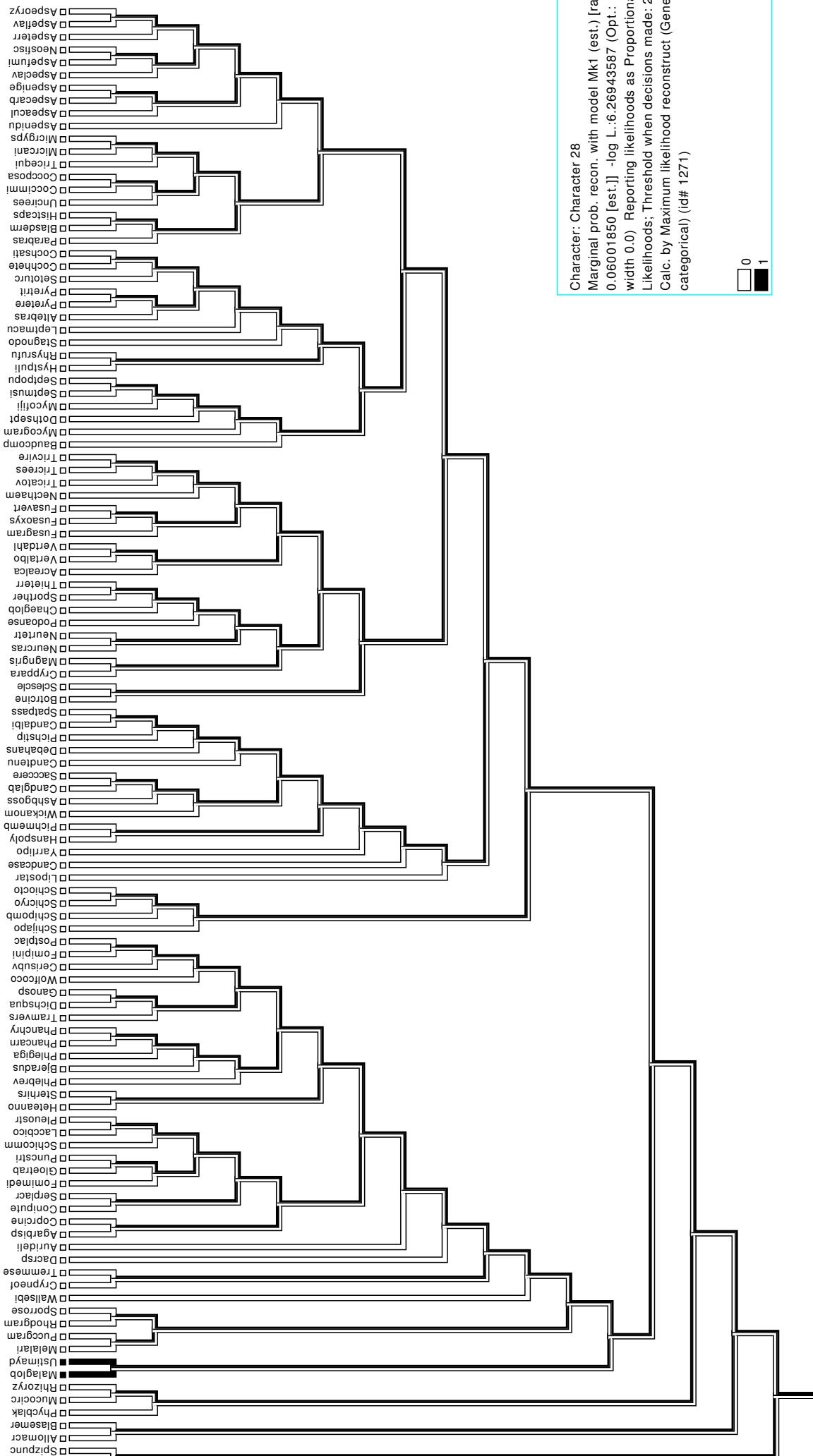
This tree is the 68-gene concatenated phylogeny (Fig. 1), with the presence of a fusion (black), presence of a fission (white), and absent/undetermined (grey) status of gene fusion characters plotted on to it using a "1/0/-" nexus-style data matrix. We used the program 'Mesquite' to calculate proportional likelihoods based on either an "Mk1" or "Assym. 2 param model." (see Table S4) of character change across the fungal phylogeny (Fig. 1). This allowed for a proportional likelihood of the position of the fusion/fission to be calculated.





Character: Character 28
 Marginal prob. recon. with model Mk1 (est.) [rate
 0.06001850 [est.]] -log L.: 6.26943587 (Opt.:
 width 0.0) Reporting likelihoods as Proportional
 Likelihoods: Threshold when decisions made: 2.0
 Calc. by Maximum likelihood reconstruct (Generic
 categorical) (id# 1271)

0
1



Putative Fusion 29

September 26, 2012

1 Fasta Sequences

These are the unfused sequences identified by fdfBLAST belonging to the putative gene fusion in FASTA format. Accessions may be shortened, but belong to either the taxons individual genome project or NCBI's accession numbering.

```
>lcl|AMAG_01942 unnamed protein product
MSLAIDTRVKVLVTGASGLGPVGAAFSRAEPPPLVKVDLTSKESVVAFDHLAPQGTEPVIHCAAERRPEVAEKDKDATT
KLNVDSTRLLAELCAARGIFLVYISTDYVFDGLKPSAYDVDDVPNPLNGYQSKRAGEIAVTEVMTAAGPNAKYAIMRVP
VLYGEVSPTVGNKESAVNILVDVARNASADRPQAQDDVMPRYPTHVGDVARVLADTLRAAVKGELVHGIFHYSAAEQWT
KFDMTALFVELLGTTLDHIERVTPSTDVTRPKHVKLSTKRLRDGMGVDVTARSFRGWWTANL
>lcl|AMAG_06610 unnamed protein product
MDSYATSAATRATGFHAFGDDDPLANPFADMPGAGRTTPPSAQQIDQDAAAEESDDEDNVTLGQYSSARILFTSDRVTDGS
HDTSTEPVVDHDHDHAEHTHLTASPHHPADASAPLSAALFDVSLHAPLPASPARAYIEPLTSTATPPPVLPPSGPPSR
MSSTASFTGTPLRARSGLASPRLQSLSSVAHDPLVHPLAALVAPSAAAPLAPTTAPAQTVPAVQAPAPLLLPAADMHPGS
PDAASSVVGIPPRSTVSTPTPFPPLAAVASPIATNGGADRSLPAVPASPAPPSSALQVDKRPLSYSKIQLQVPAVAASP
FKVSVSEPTKIGDAMSPFTAYKVVTKTQPGFRSESVSRRYSEFLWLYQRLVTQHPGIVVPGTPEKQAIGRFSEGFVEH
RRVGLQVFLRKVAAHPVLRDPAFQMFVEAESLKDEIQADKNVTLPPKAKMNEIDPWFEKRRQVDQFEAQIKALNKSLD
LLATRQRETATAHYELAETLAMLAEVELPHPFGRRVEMLAETHKVRDLLFAMATIDLGAMQTALDDQLRTVAIRVATQ
LRANAYVHWQALETAVLKKEAAVKSRVQMPALEAEVYELTQQRRAAKNLFETTSMLRQELEVDQDKVHELSAAIKCV
AESLWGHQQETVNLWDELIKARPAMPV
```

2 Annotated Phylogenograms

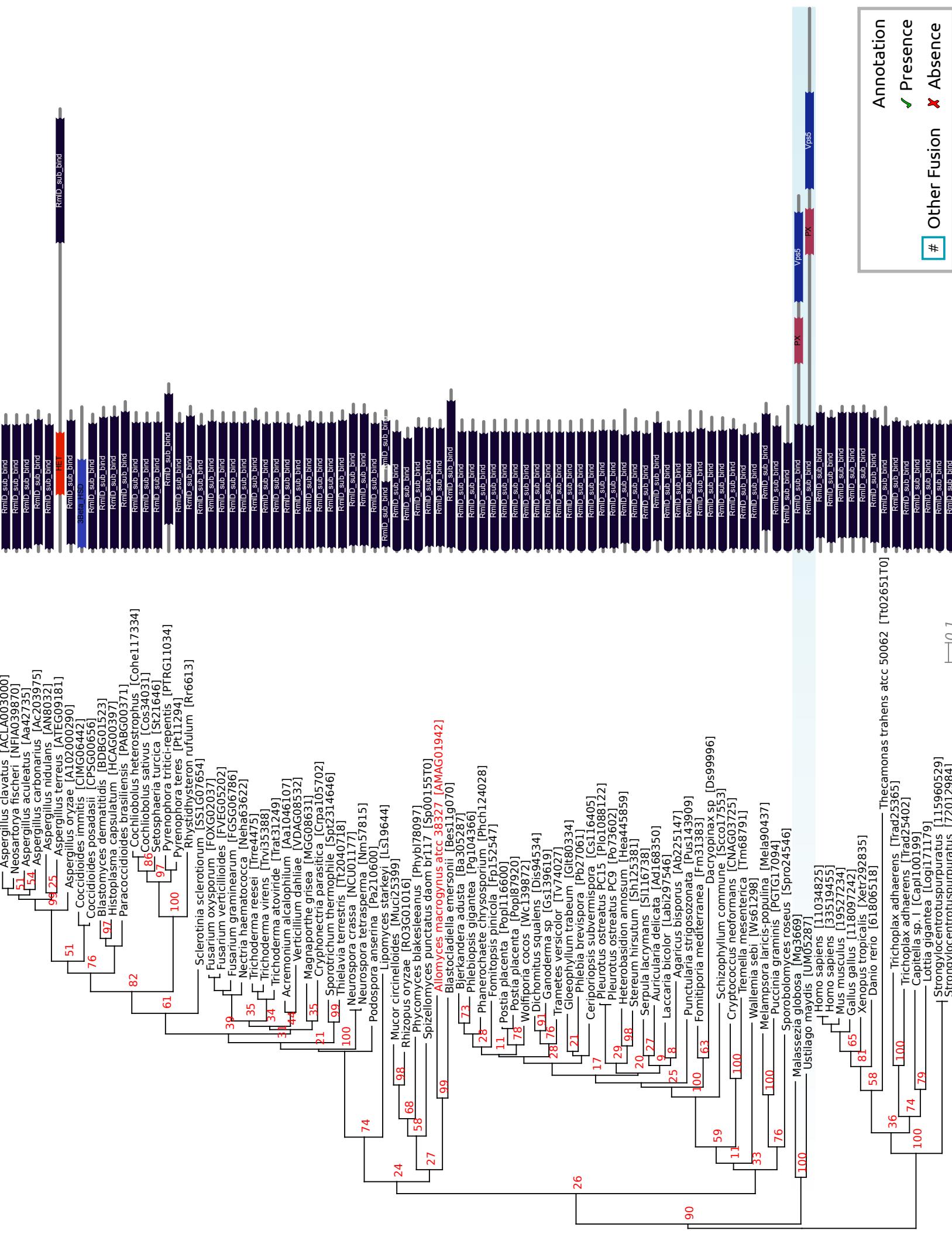
All trees were generated from an initial run of Darren's Orchard pipeline against 139 taxa (Table S1), using the above corresponding un-fused sequences as BLAST seeds. The alignments were then checked for any missing taxa, manually masked and then ProtTest3 was run, please see the Methods section for detail. The final trees were generated by the following command:

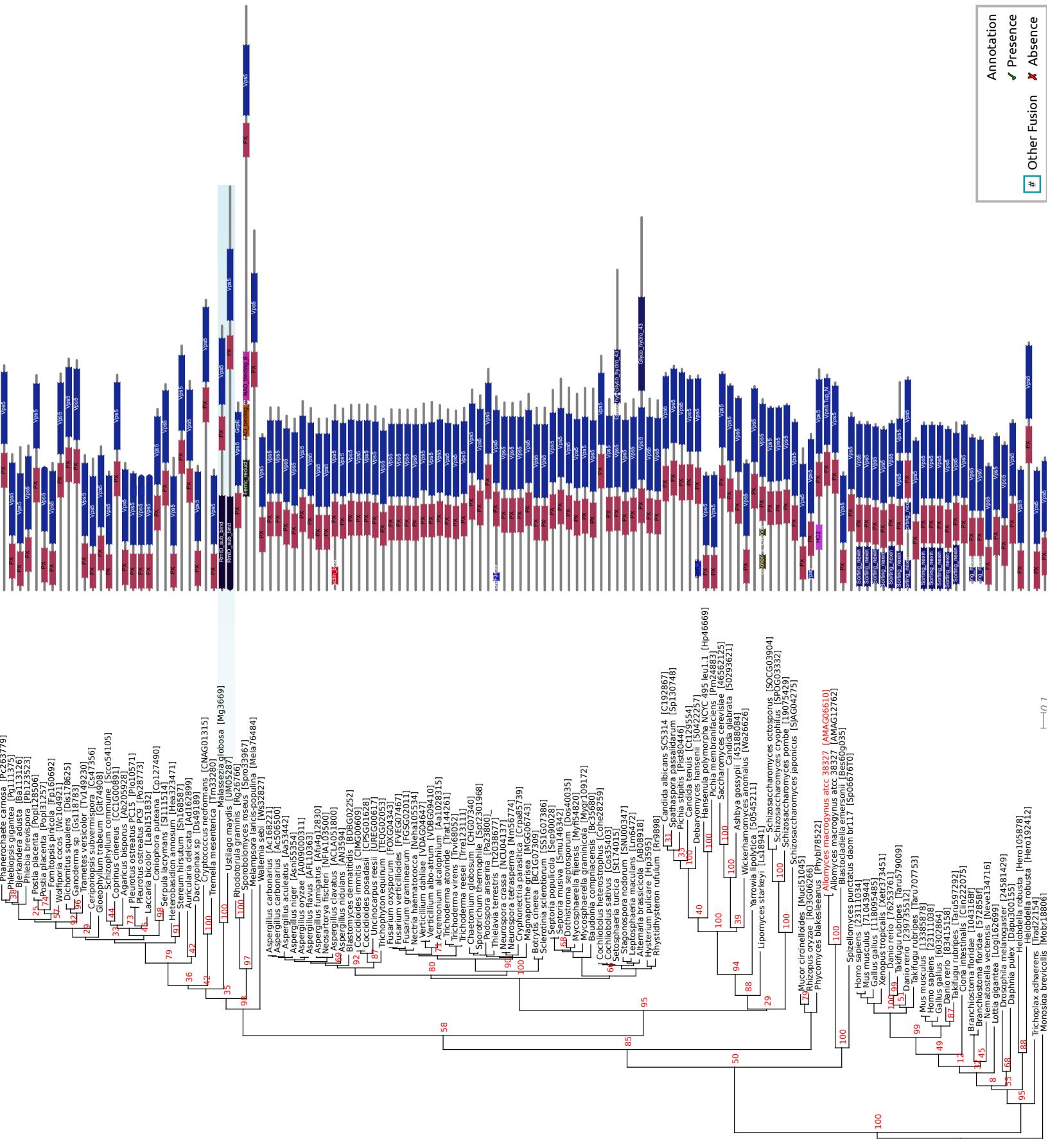
```
phym -i alignment_file -d aa -b 100 -m model -c 8 -v invariant_sites -s BEST --quiet
-a gamma
```

Styling and annotation was made possible by Dendroscope and Inkscape.

3 Mesquite Cladogram

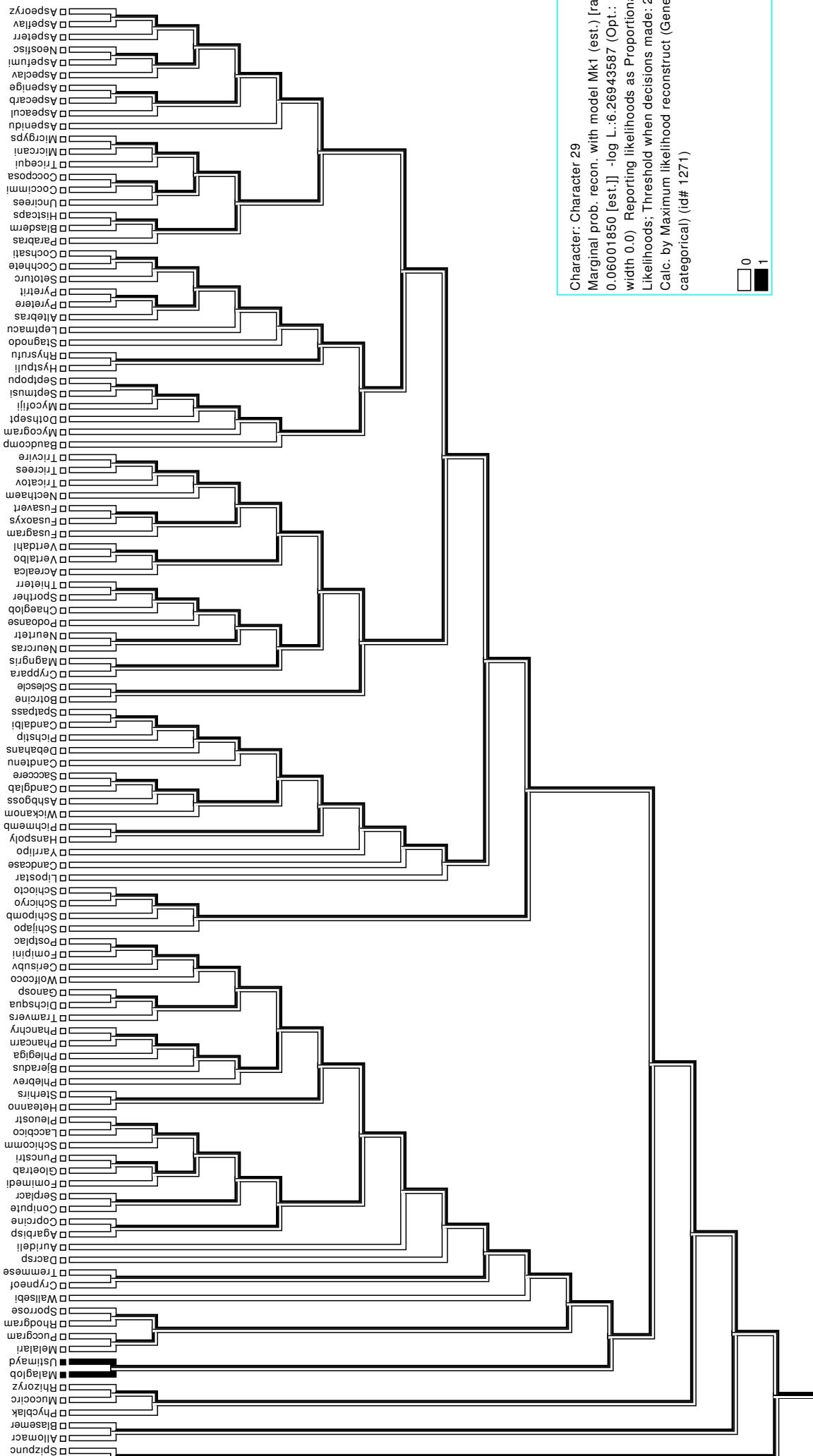
This tree is the 68-gene concatenated phylogeny (Fig. 1), with the presence of a fusion (black), presence of a fission (white), and absent/undetermined (grey) status of gene fusion characters plotted on to it using a "1/0/-" nexus-style data matrix. We used the program 'Mesquite' to calculate proportional likelihoods based on either an "Mk1" or "Assym. 2 param model." (see Table S4) of character change across the fungal phylogeny (Fig. 1). This allowed for a proportional likelihood of the position of the fusion/fission to be calculated.





Character: Character 29
 Marginal prob. recon. with model Mk1 (est.) [rate
 0.06001850 [est.]] -log L.: 6.26943587 (Opt.:
 width 0.0) Reporting likelihoods as Proportional
 Likelihoods: Threshold when decisions made: 2.0
 Calc. by Maximum likelihood reconstruct (Generic
 categorical) (id# 1271)

0
1



Putative Fusion 30

September 26, 2012

1 Fasta Sequences

These are the unfused sequences identified by fdfBLAST belonging to the putative gene fusion in FASTA format. Accessions may be shortened, but belong to either the taxons individual genome project or NCBI's accession numbering.

```
>NCU04237
MLQайдниHDRQFLAAELASSATLAAELAQPEIKNILLAASGSVATIHKSSYQYGTTWALARHGDKIRI
RIILTHFAKHFLGGQSKEQPVYSSLLDYPHVEAIYDDADEWGPEPWQRGASILHIELRRWADILVVAPLS
ANTLAKIVNGMSDNLLTSVIRAWTDSSIDNKKVIMVAPAMNSAMWRHPITAKQIRVLQEEWGVRDPEP
SEGDTAGVAVANGWFQVIMDSCMW
>NCU10053
MTVTTSEPVAPAQSQSQTSSRTNPTSKRHEEYQYLDLVRQILDEGELREDRTGTGTYSIFAPTPLKFALS
RPSSSSPSSSSSDPSSPDYTYPILPLLTCKRVFTKAVLLELLWFISASTSSTTLAQGVKIWDGNGSR
AFLDMLGLSHRKEDGLGPVYGFQWRHFGAEYVDCETDYTGQGVDQLQRIIDTLRNNPYDRRLILSAWNPK
DMSQMVLPPCHMFAQFYVSYPGSRTRGGATQTQNKEGELDTPPKEKKPRGHLHCQLYQRSCDMGLGVPFN
IASYALLTHMLAHVCDLPGSLTHVMGDAHVYLNHVDALKTQLEREPEFPTLEIQREKGGSIDGWKAED
FVIKGYEPHKTIAMEMSV
```

2 Annotated Phylogenograms

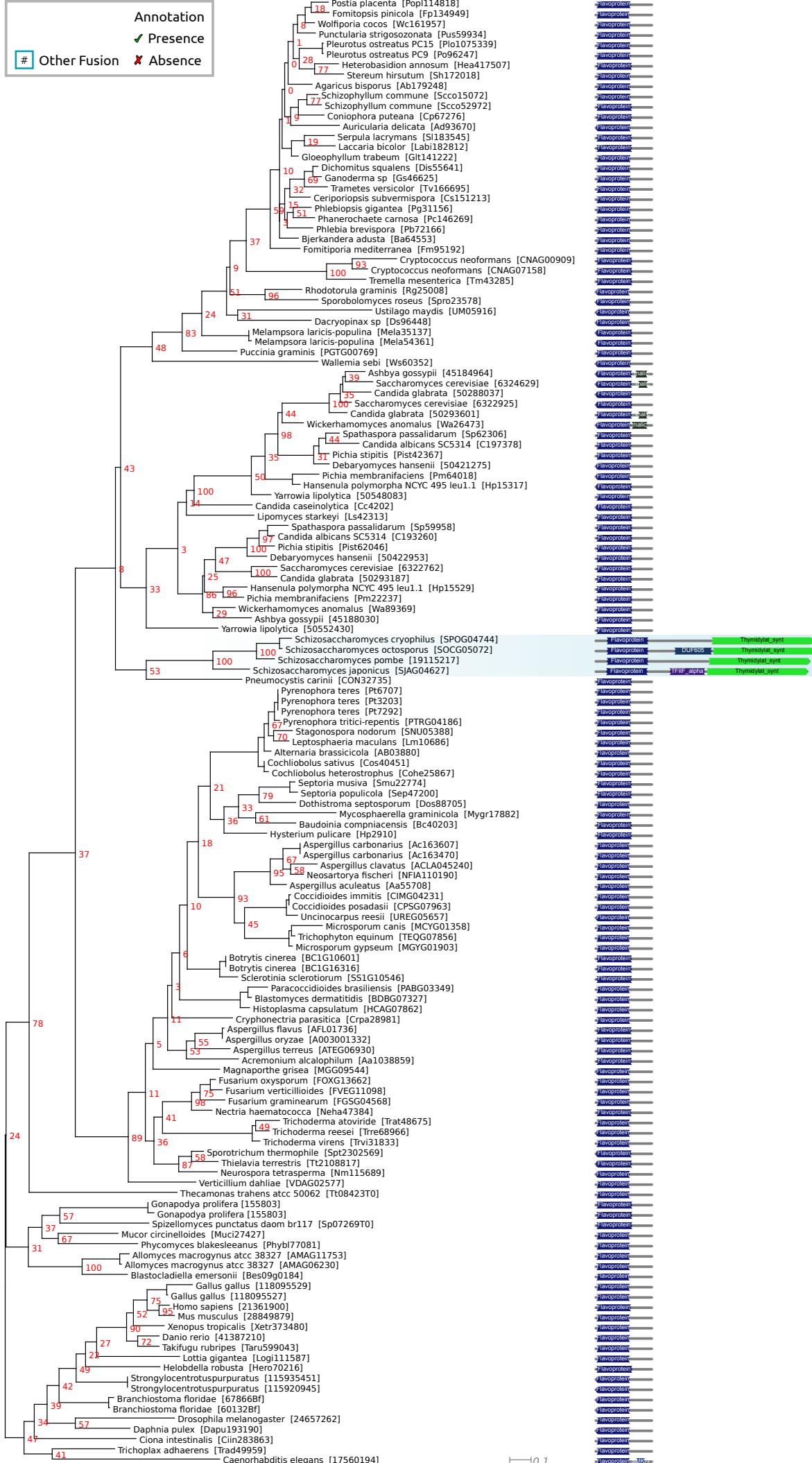
All trees were generated from an initial run of Darren's Orchard pipeline against 139 taxa (Table S1), using the above corresponding un-fused sequences as BLAST seeds. The alignments were then checked for any missing taxa, manually masked and then ProtTest3 was run, please see the Methods section for detail. The final trees were generated by the following command:

```
phyml -i alignment_file -d aa -b 100 -m model -c 8 -v invariant_sites -s BEST --quiet
-a gamma
```

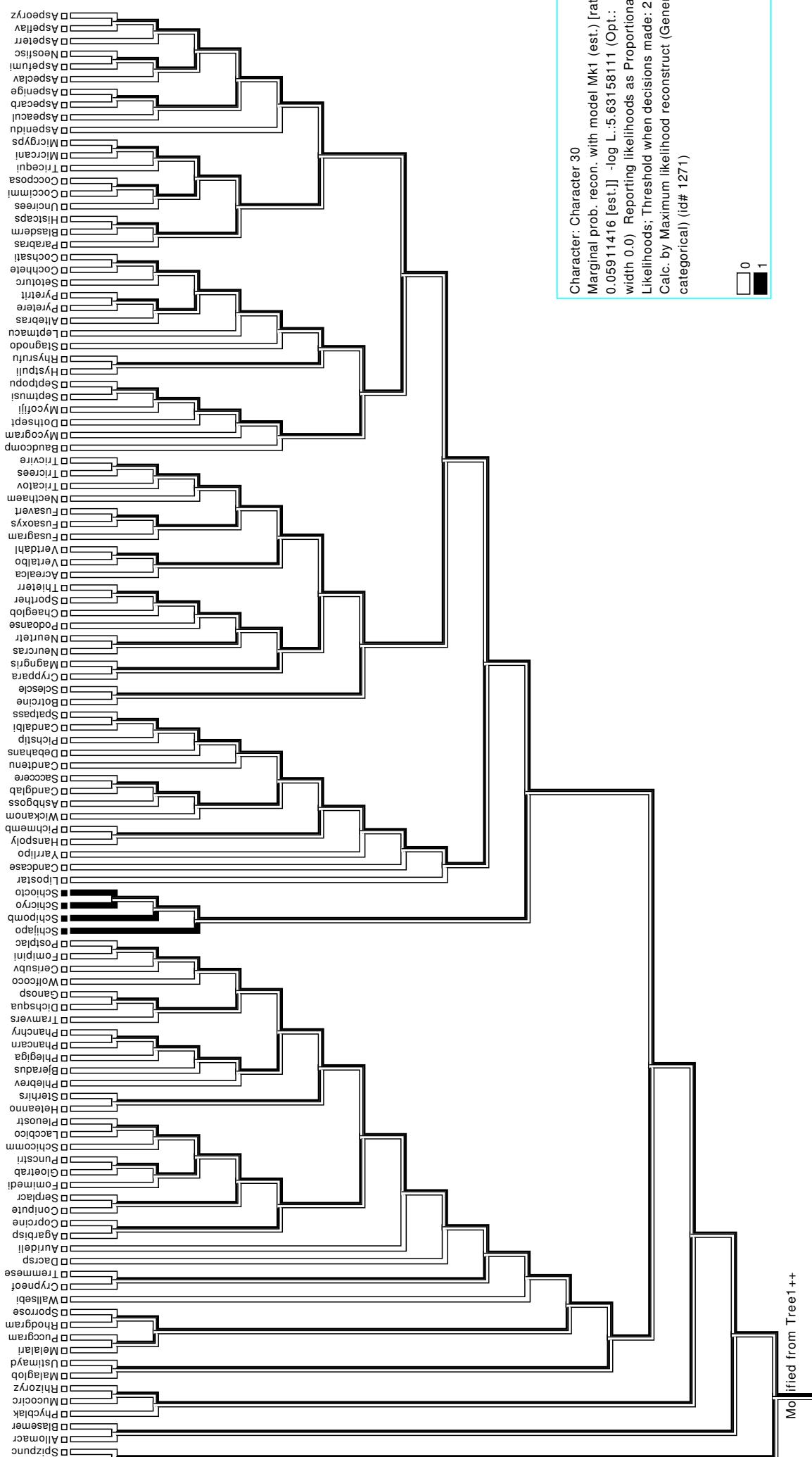
Styling and annotation was made possible by Dendroscope and Inkscape.

3 Mesquite Cladogram

This tree is the 68-gene concatenated phylogeny (Fig. 1), with the presence of a fusion (black), presence of a fission (white), and absent/undetermined (grey) status of gene fusion characters plotted on to it using a "1/0/-" nexus-style data matrix. We used the program 'Mesquite' to calculate proportional likelihoods based on either an "Mk1" or "Assym. 2 param model." (see Table S4) of character change across the fungal phylogeny (Fig. 1). This allowed for a proportional likelihood of the position of the fusion/fission to be calculated.







Putative Fusion 31

September 26, 2012

1 Fasta Sequences

These are the unfused sequences identified by fdfBLAST belonging to the putative gene fusion in FASTA format. Accessions may be shortened, but belong to either the taxons individual genome project or NCBI's accession numbering.

```
>lcl|6319631Sc unnamed protein product
MSSVNANGGYTKPQKYVPGPGDPELPPQLSEFKDKTSDEILKEMNRMPFFMTKLDETDGAGGENVEALKALAYEGEPH
EIAENFKKQGNELYKAKRKFKDARELYSKGLAVECEDKSINESLYANRAACELELKNYRRCIEDCSKALTINPKNVKCYYR
TSKAFFQLNKLREAKSAATFANQRIDPENKSILNMLSVIDRKEQELKAKEEKQQREAQERENKKIMLESAMTLRNITNIK
THSPVELLNEGKIRLEDPMDFESQLIYPALIMYPTQDEFDFVGEVSELTTVQELVDLVLEGPQERFKKEGKENFTPKKVL
VFMETKAGGLIKAGKKLTFHDLKKESPDVPLFDNALKIQIVPKVESEGWISKWDKQKALERRSV
>lcl|6324670Sc unnamed protein product
MSAPQAKILSQAPTELELQVAQAFVELENSSPELKAELRPLQFKSIREIDVAGGKKALAIFVPVPSLAGFHKVQTKLTRE
LEKKFQDRHVIFLAERRILPKPSRTSRQVQKRPRSRTLTAVHDKILEDLVFPTEIVGKRVRYLVGGNKIQKVLLDSKDVQ
QIDYKLESFQAVYNKLTGKQIVFEIPSETH
```

2 Annotated Phylogenograms

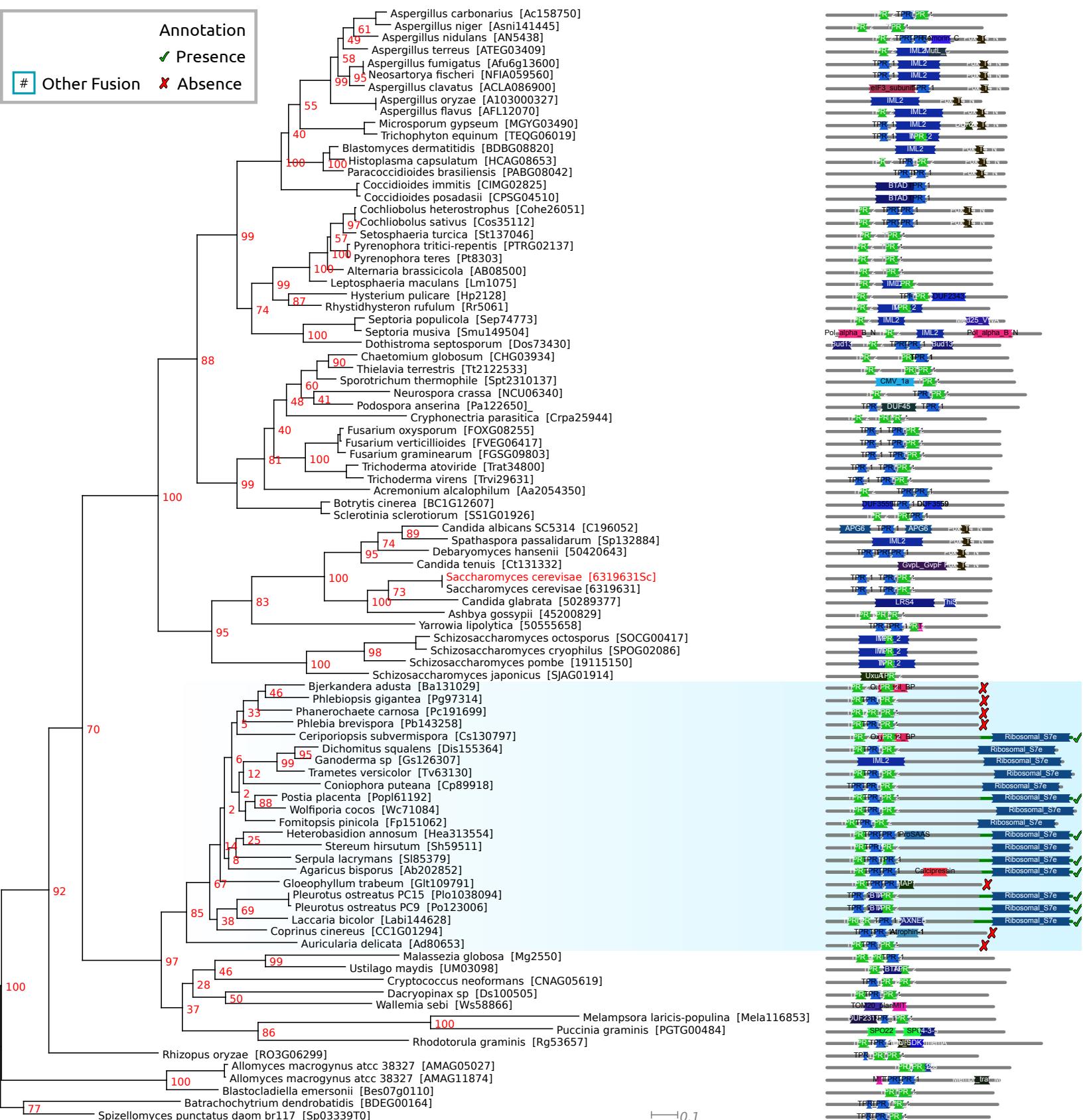
All trees were generated from an initial run of Darren's Orchard pipeline against 139 taxa (Table S1), using the above corresponding un-fused sequences as BLAST seeds. The alignments were then checked for any missing taxa, manually masked and then ProtTest3 was run, please see the Methods section for detail. The final trees were generated by the following command:

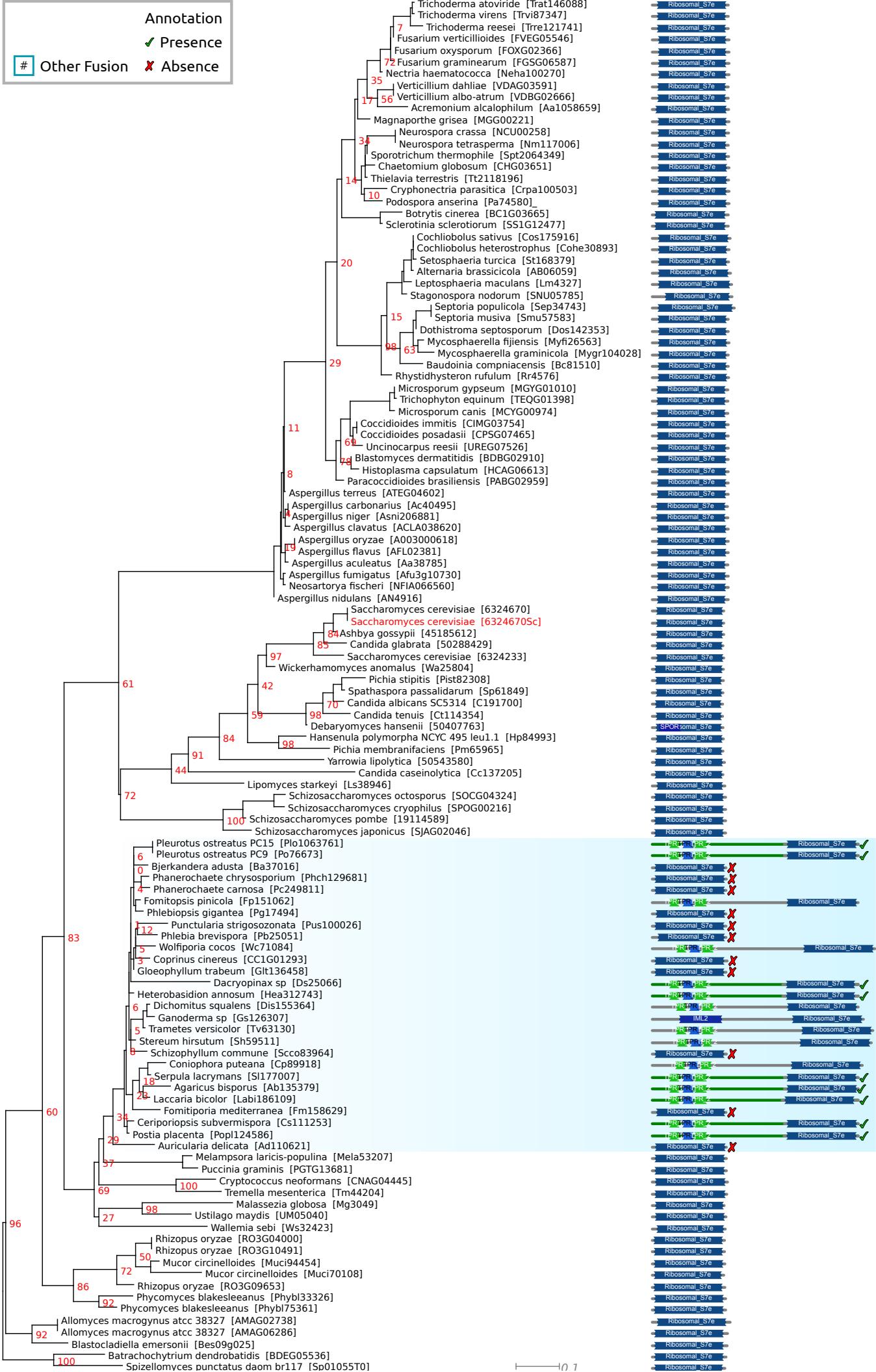
```
phylml -i alignment_file -d aa -b 100 -m model -c 8 -v invariant_sites -s BEST --quiet
-a gamma
```

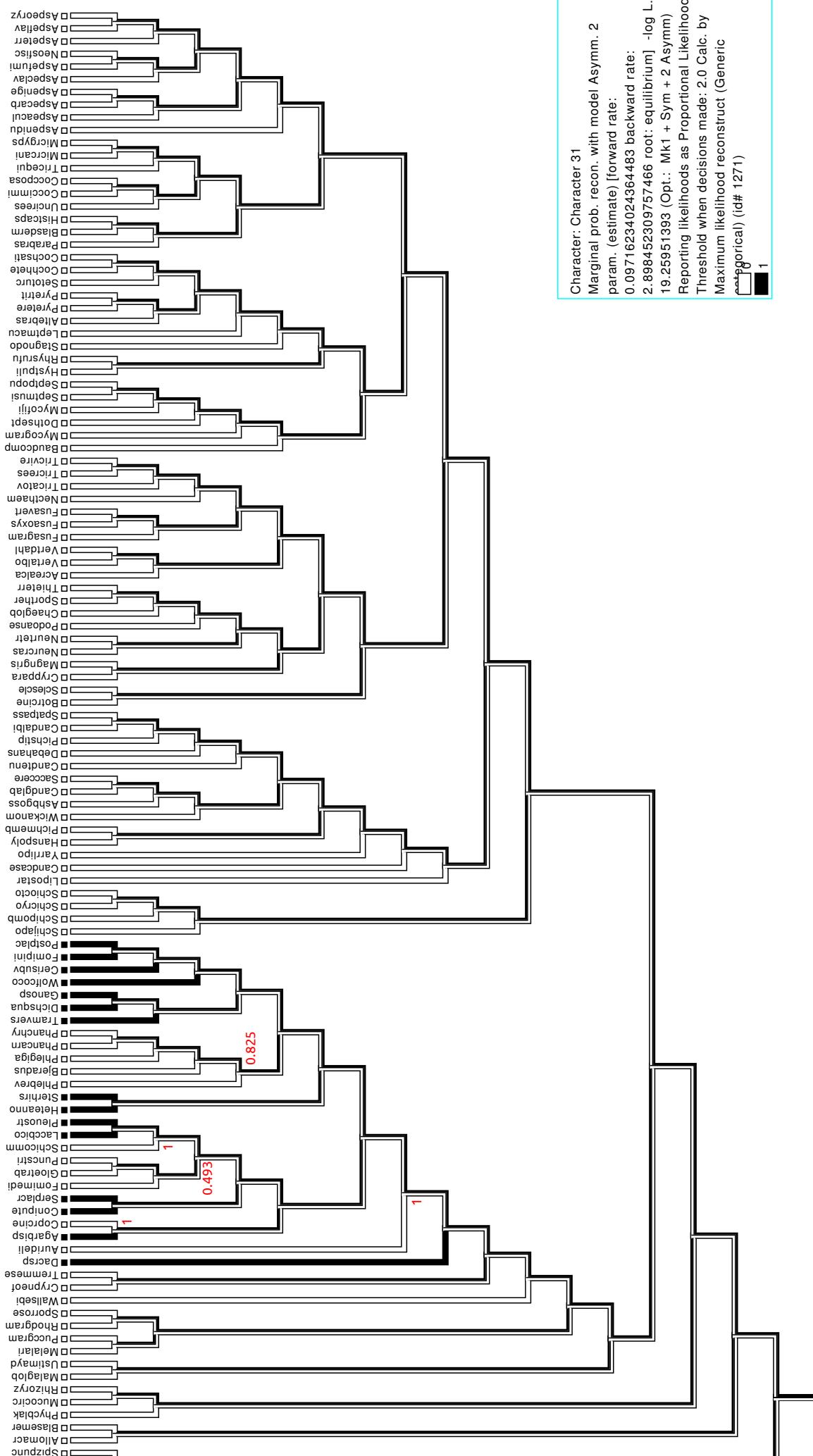
Styling and annotation was made possible by Dendroscope and Inkscape.

3 Mesquite Cladogram

This tree is the 68-gene concatenated phylogeny (Fig. 1), with the presence of a fusion (black), presence of a fission (white), and absent/undetermined (grey) status of gene fusion characters plotted on to it using a "1/0/-" nexus-style data matrix. We used the program 'Mesquite' to calculate proportional likelihoods based on either an "Mk1" or "Assym. 2 param model." (see Table S4) of character change across the fungal phylogeny (Fig. 1). This allowed for a proportional likelihood of the position of the fusion/fission to be calculated.







Putative Fusion 32

September 26, 2012

1 Fasta Sequences

These are the unfused sequences identified by fdFBLAST belonging to the putative gene fusion in FASTA format. Accessions may be shortened, but belong to either the taxons individual genome project or NCBI's accession numbering.

```
>lcl|2624654Sc unnamed protein product
MASETFEFQAEITQLMSLIINTVYSNKEIFLRELISNASDALDKIRYKSLSDPKQLETEPDLFIRITPKPEQKVLEIRD
GIGMTKAELINNLGTTIAGSGTKAFMEALSAGADVSMIGQFGVGFYSLFLVADRVQVISKSNDDEQYIWESNAGGSFTVTL
DEVNERIGRGTILRLFLKDQLEYLEEKRIKEVIKRHSEFVAYPIQLVVTKVEVEKEVPIP
>lcl|42543758Sc unnamed protein product
GTKPLWTRNPSDTQEEYNAYKSISNDWEDPLYVKHFSVEGQLEFRAILFIPKRAPFDLFESKKKNNIKLYVRRVFI
TDEAEDLIPEWLSFVKGVDSEDLPLNLSREMLQQNKIMKVKRKNIVKKLIEAFNEIAEDSEQFEKFYSAFSKNIKLGVH
EDTQNRAALAKLLRYNSTKSVDLTS LTDYVTRMPEHQKNIYYITGESLKAVEKSPFLDALKAKNFEVLFLTDPIDEYAF
TQLKEFEGKTLVDITKDFEL
```

2 Annotated Phylogenograms

All trees were generated from an initial run of Darren's Orchard pipeline against 139 taxa (Table S1), using the above corresponding un-fused sequences as BLAST seeds. The alignments were then checked for any missing taxa, manually masked and then ProtTest3 was run, please see the Methods section for detail. The final trees were generated by the following command:

```
phym -i alignment_file -d aa -b 100 -m model -c 8 -v invariant_sites -s BEST --quiet
-a gamma
```

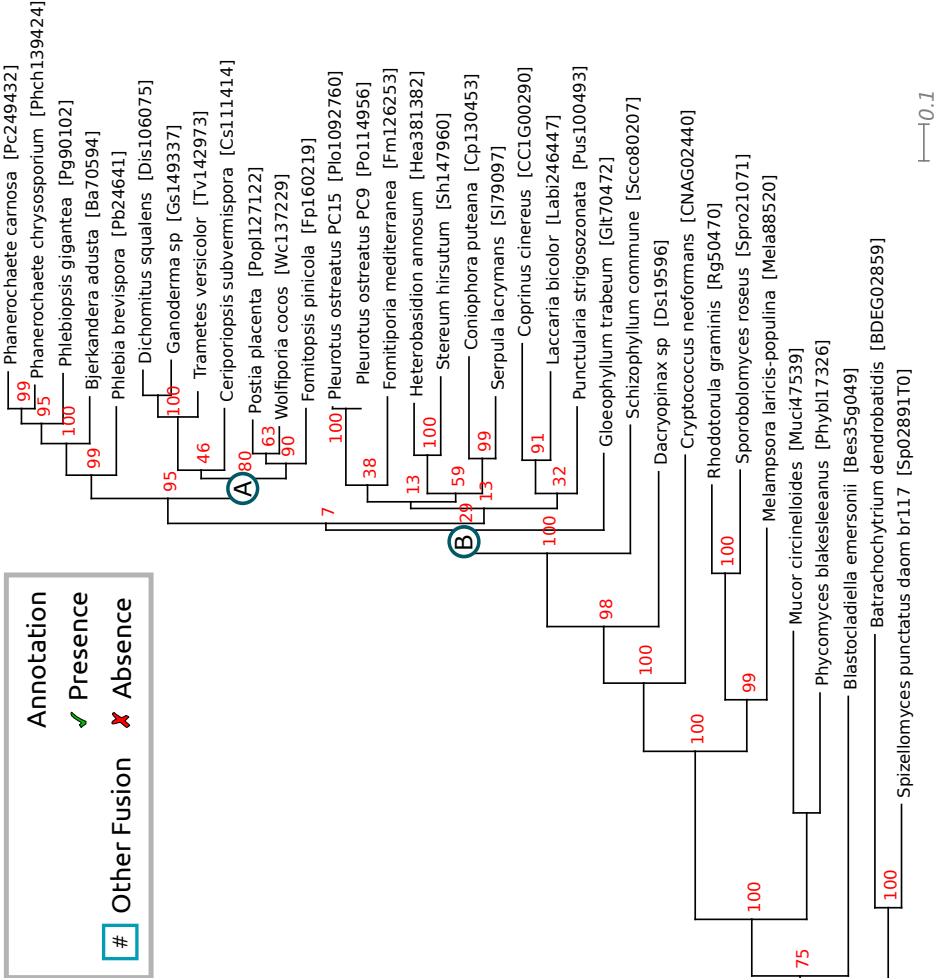
Styling and annotation was made possible by Dendroscope and Inkscape.

2.1 Important Notes

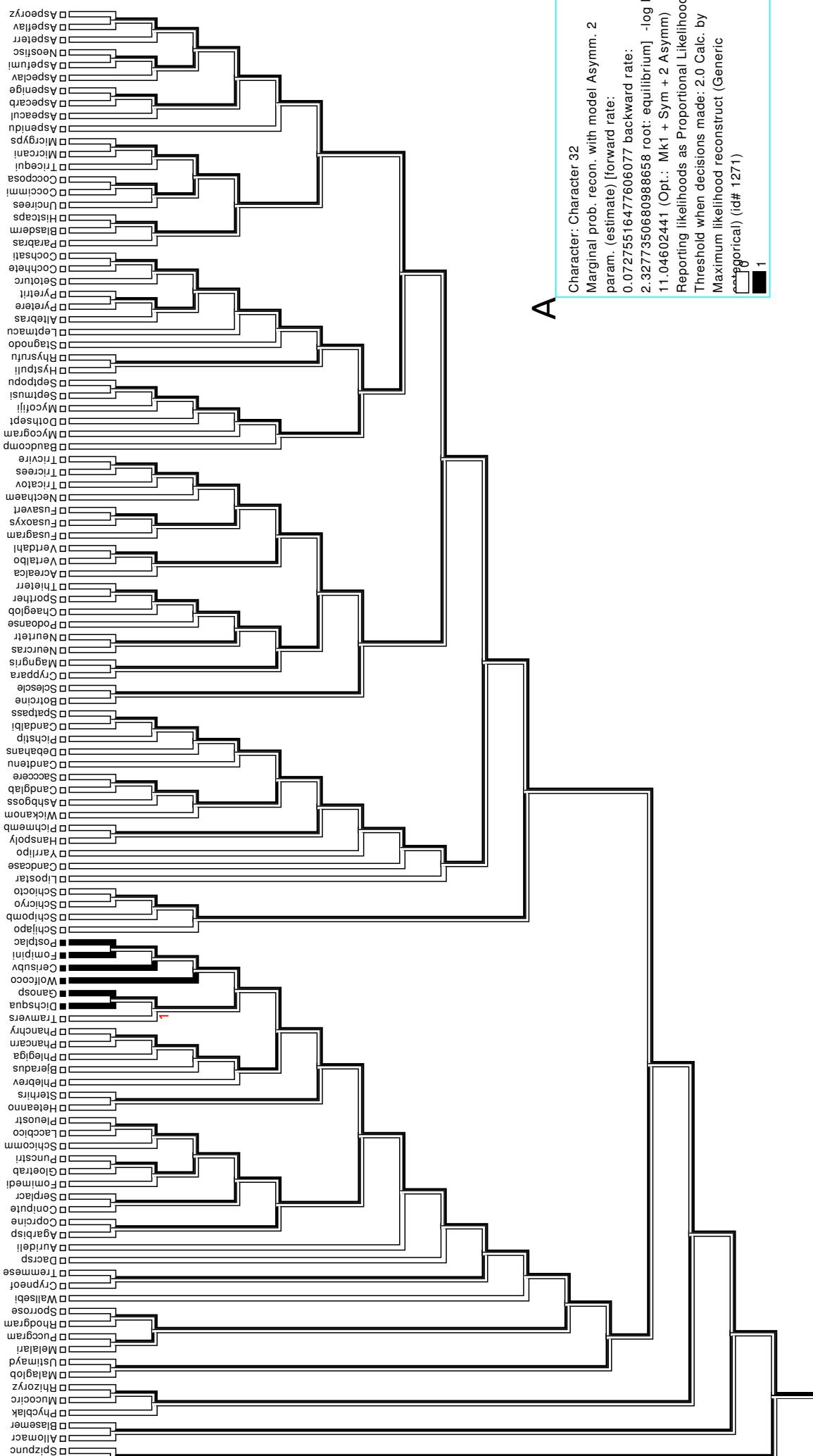
The original prediction made by fdFBLAST, on closer inspection (from the first round of phylogenies), indicated that there was not a gene fusion present between the above two domains but there was potentially a gene fusion with a third other domain. There is only one phylogeny here as the third domain consists of a series of repeats and so an alignment would not be possible as the resulting phylogeny would then be unresolved.

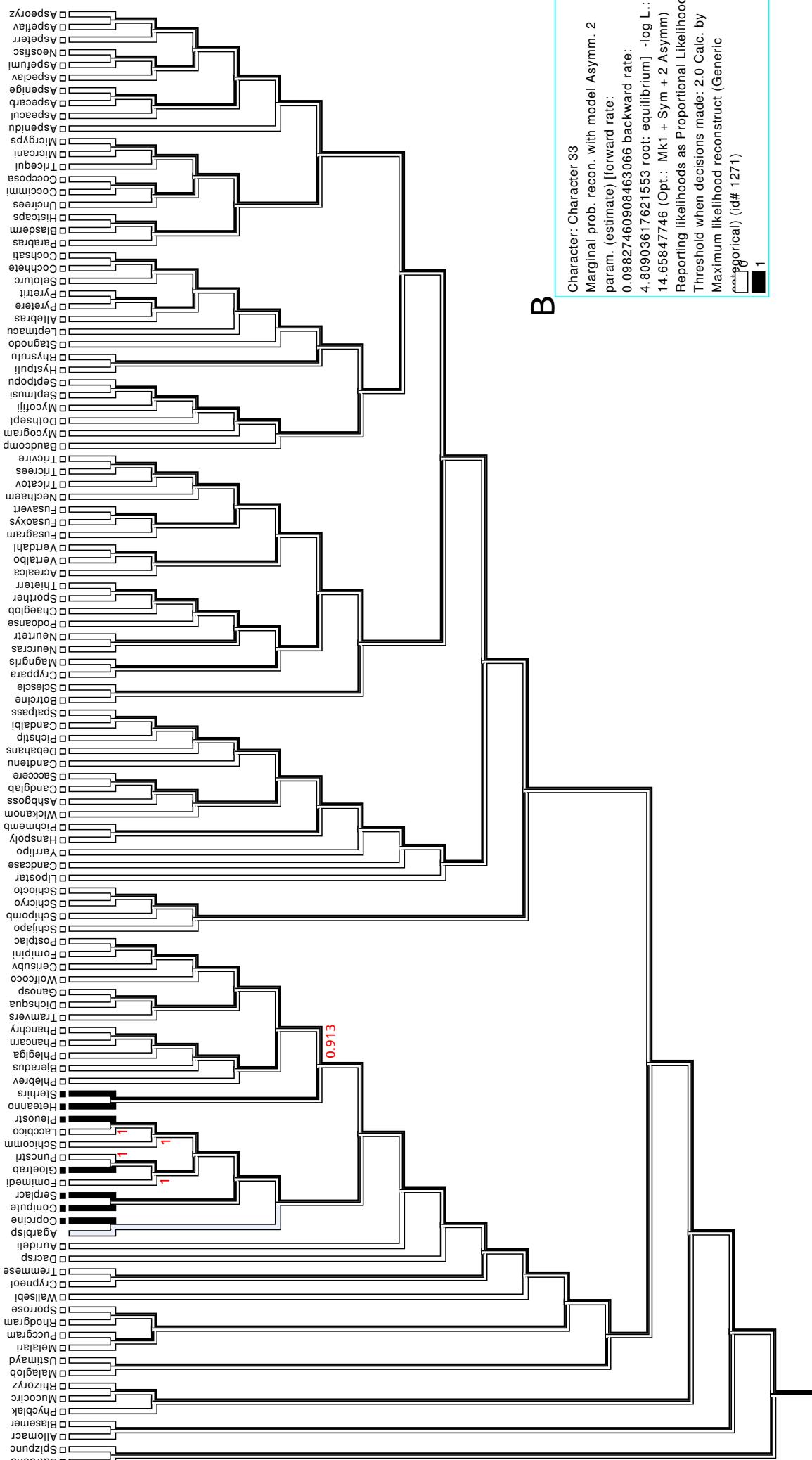
3 Mesquite Cladogram

This tree is the 68-gene concatenated phylogeny (Fig. 1), with the presence of a fusion (black), presence of a fission (white), and absent/undetermined (grey) status of gene fusion characters plotted on to it using a "1/0/-" nexus-style data matrix. We used the program 'Mesquite' to calculate proportional likelihoods based on either an "Mk1" or "Assym. 2 param model." (see Table S4) of character change across the fungal phylogeny (Fig. 1). This allowed for a proportional likelihood of the position of the fusion/fission to be calculated.



11





Putative Fusion 33

September 26, 2012

1 Fasta Sequences

These are the unfused sequences identified by fdFBLAST belonging to the putative gene fusion in FASTA format. Accessions may be shortened, but belong to either the taxons individual genome project or NCBI's accession numbering.

```
>lcl|Mc157300 unnamed protein product
MKLSLSIFLCVAACSHPLAVSVAAQSSPFYYQDYETSFHSEHAKQGSMVQQGRTGVAAMHAVLLNERSILIIDKAEENE
AKLDGVSAFSSLYDIETNTYRTLLETNTFC SAGGFLANGTFISTGGAESRGAWKAGR GHQSIRHFQPCSDDSCSWVEY
PTGKMYSNRWYPTVEQLPEGDLIIIGGSVAGTKYNTKEKNVPSYEFWPPRTEEPIQLDLLLHTLPY
>lcl|Mc157301 unnamed protein product
MLPLDPNDYNVEILICGGSSSPKATSAADDTGRINLGDEDPQWEMDTFVHKRVMPDGYKDANHDPTFDPLIYNHKKPL
GKRWTQGLASTDIARMYHSVALALPDGRLWIAGSNSVDPPDIHAKYPTEYRVEYYTPPHLYKRPEETRPRISHVPRVVTY
GQEFEILLHLQDNVKDAKKLVAVMRPGFSTHSMHSQRYVYLRYQVDPAFETLKIMAPPNANIYPPGSAYLVVTYDGVP
CKGTEFFIEKDVNLDQI
```

2 Annotated Phylogenograms

All trees were generated from an initial run of Darren's Orchard pipeline against 139 taxa (Table S1), using the above corresponding un-fused sequences as BLAST seeds. The alignments were then checked for any missing taxa, manually masked and then ProtTest3 was run, please see the Methods section for detail. The final trees were generated by the following command:

```
phyml -i alignment_file -d aa -b 100 -m model -c 8 -v invariant_sites -s BEST --quiet
-a gamma
```

Styling and annotation was made possible by Dendroscope and Inkscape.

2.1 Important Notes

The original prediction made by fdFBLAST, on closer inspection (from the first round of phylogenies), indicated that there was not a gene fusion present between the above two domains but there was potentially a gene fusion with a third other domain. There is only one phylogeny included here as the first domain *Chitin_bind* consists of a series of small noisy repeats and so an alignment would not be possible as the resulting phylogeny would appear to be unresolved.

3 Mesquite Cladogram

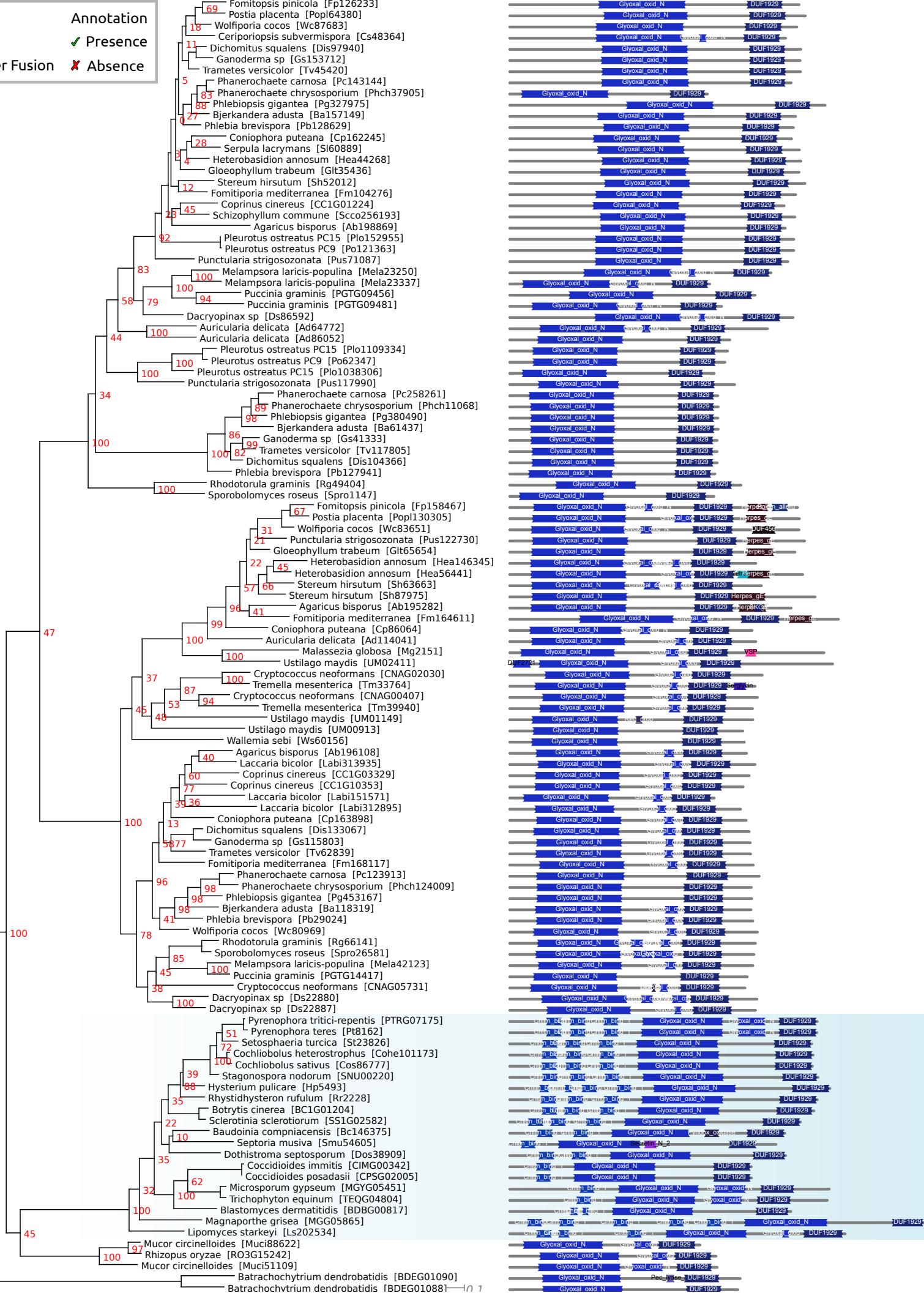
This tree is the 68-gene concatenated phylogeny (Fig. 1), with the presence of a fusion (black), presence of a fission (white), and absent/undetermined (grey) status of gene fusion characters plotted on to it using a "1/0/-" nexus-style data matrix. We used the program 'Mesquite' to calculate proportional likelihoods based on either an "Mk1" or "Assym. 2 param model." (see Table S4) of character change across the fungal phylogeny (Fig. 1). This allowed for a proportional likelihood of the position of the fusion/fission to be calculated.

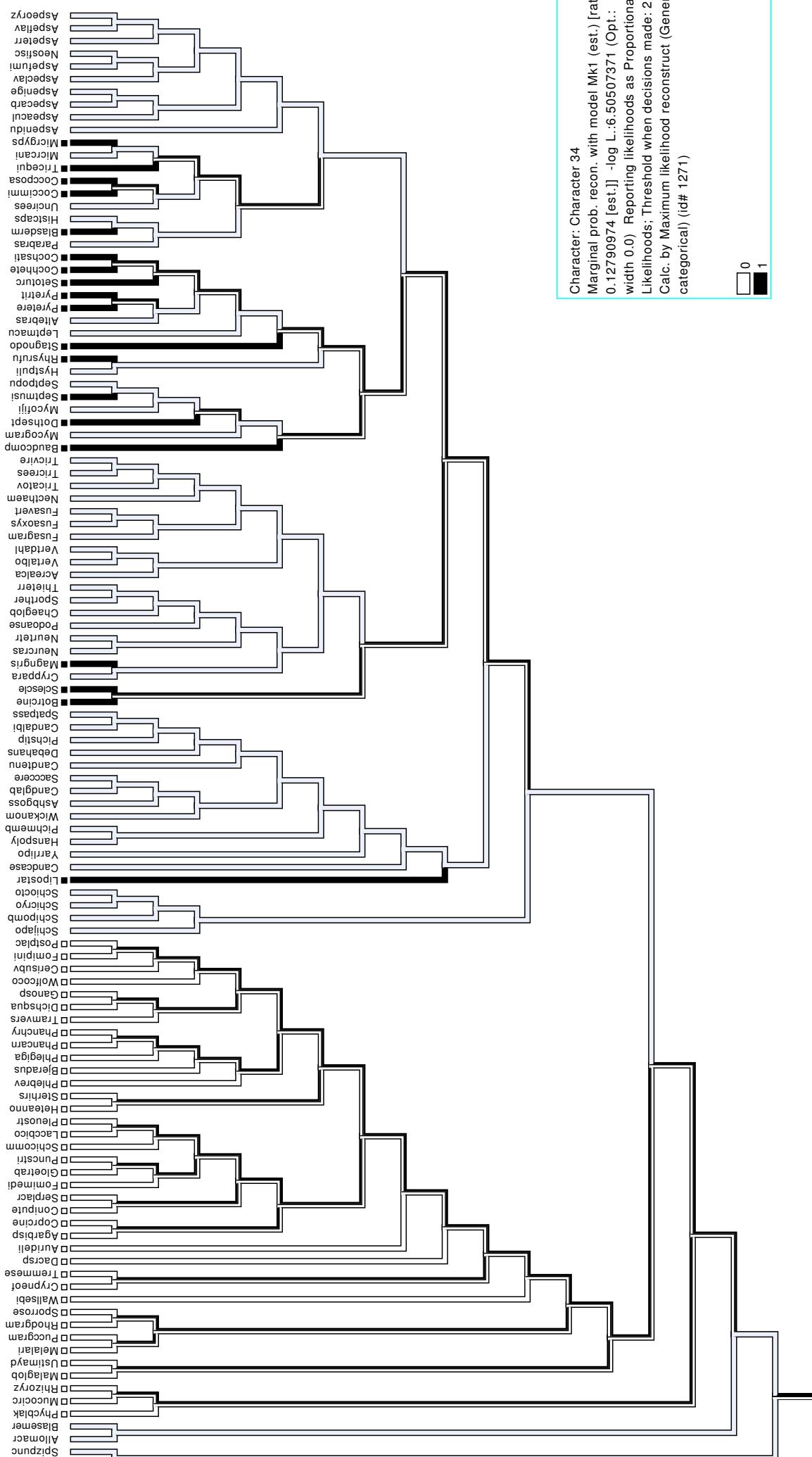
Annotation

✓ Presence

✗ Absence

Other Fusion





Character: Character 34
Marginal prob. recon. with
0.12790974 [test.] - log
width 0.0) Reporting likelihoods;
Threshold w/ Calcs. by Maximum likelihood
categorical) (id# 1271)

Putative Fusion 34

September 26, 2012

1 Fasta Sequences

These are the unfused sequences identified by fdfBLAST belonging to the putative gene fusion in FASTA format. Accessions may be shortened, but belong to either the taxons individual genome project or NCBI's accession numbering.

```
>NP_013239_F34_dom1
MAIWEQLEVSKAHVAYACVGVFSSIFSLVSLYVKEKLYIGESTVAGIFGLIVGPVCLNWF
NPLKWGNSDSITLEITRIVLCLQIFAVAVELPRKYMLKHWWVSVTMLLPVMTAGWLIIGL
FVWILIPGLNFSAALLISACITATDPILAQS VSGKFAQRVPGHLRNLLSAESGCNDGMA
FPFLFLSMNLILHPGNGREIVKDWCIVTILYECLFGCLLGCFIGYVGRITIRFAEKKNII
DRESFLAFYVVLAFMCAGFGSILGVDDLLVSFAAGATFAWDGWFSQKTQESNVSTVIDLL
LNYAYFIYFGAII PWSQFNNGEIGTNVWRLLIILSIVVIFLRRIPAVMILRPLIPDIKSWR
EALFVGHFGPIGVGAIAFAILARGELESTFSDEPTPLNVVPSKEESHWQLIACIWPITC
>NP_013239_F34_dom2
FFIVTSIIVHGSSVAIITLGRHLNTITLTKFTTHTTNGDNGKSSWMQRRLPSLDKAGRSF
SLHRMDTQM TLSGDEGEAE EGGGRKGLAGGEDEEGLNNDQIGSVATSGIPARPA GGMPRR
RKLSRKEKRLNRRQKLRNKGREIFSSRSKNEMYDDDELNDLGRERLQKEKEARAATFALS
TAVNTQRNEEIGMGGDEEEDEYTPKEYSDNYNNTPSFESSERSSSLRGRTYVPRNRYDG
EETESEIESEDEMENESERSMASSEERRIRKMKEEEMKPGTAYLDGNRMIIENKQGEILN
QVDIEDRNEARDEVSDSTAHSLLTMTNLSSSSGGRLKRILTPTSLGKIHS LVDKGK
DKNKNSKYHAFKIDNLLIENEDGDVIKRYKINPHKSDDDKSKNRP RND SVS RALT AVG
LKS KANSGVPPPVDEEKAIEGPSRKPGMLKKR LTPAPP RGVQDSDL DEP SSEEDLG
DSY NMDDSE DYDDN AYESET EFER Q RRLN ALGEM TAPAD Q DDEEL PPLP VEA QT GND GPG
TAEGKKKQKSAAVKSALS KTLGLNK
```

2 Annotated Phylogenograms

All trees were generated from an initial run of Darren's Orchard pipeline against 139 taxa (Table S1), using the above corresponding un-fused sequences as BLAST seeds. The alignments were then checked for any missing taxa, manually masked and then ProtTest3 was run, please see the Methods section for detail. The final trees were generated by the following command:

```
phyml -i alignment_file -d aa -b 100 -m model -c 8 -v invariant_sites -s BEST --quiet -a gamma
```

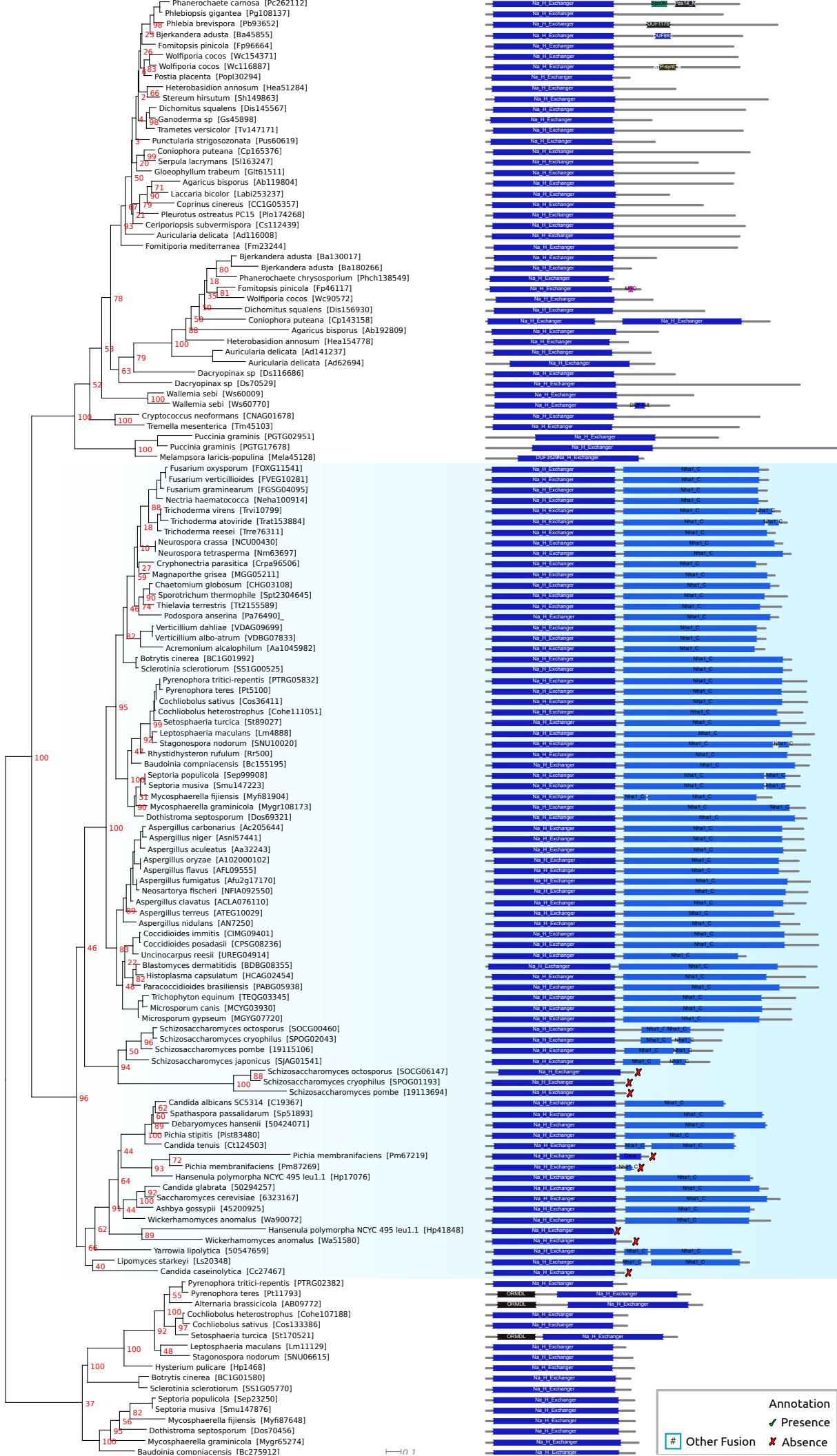
Styling and annotation was made possible by DendroScope and Inkscape.

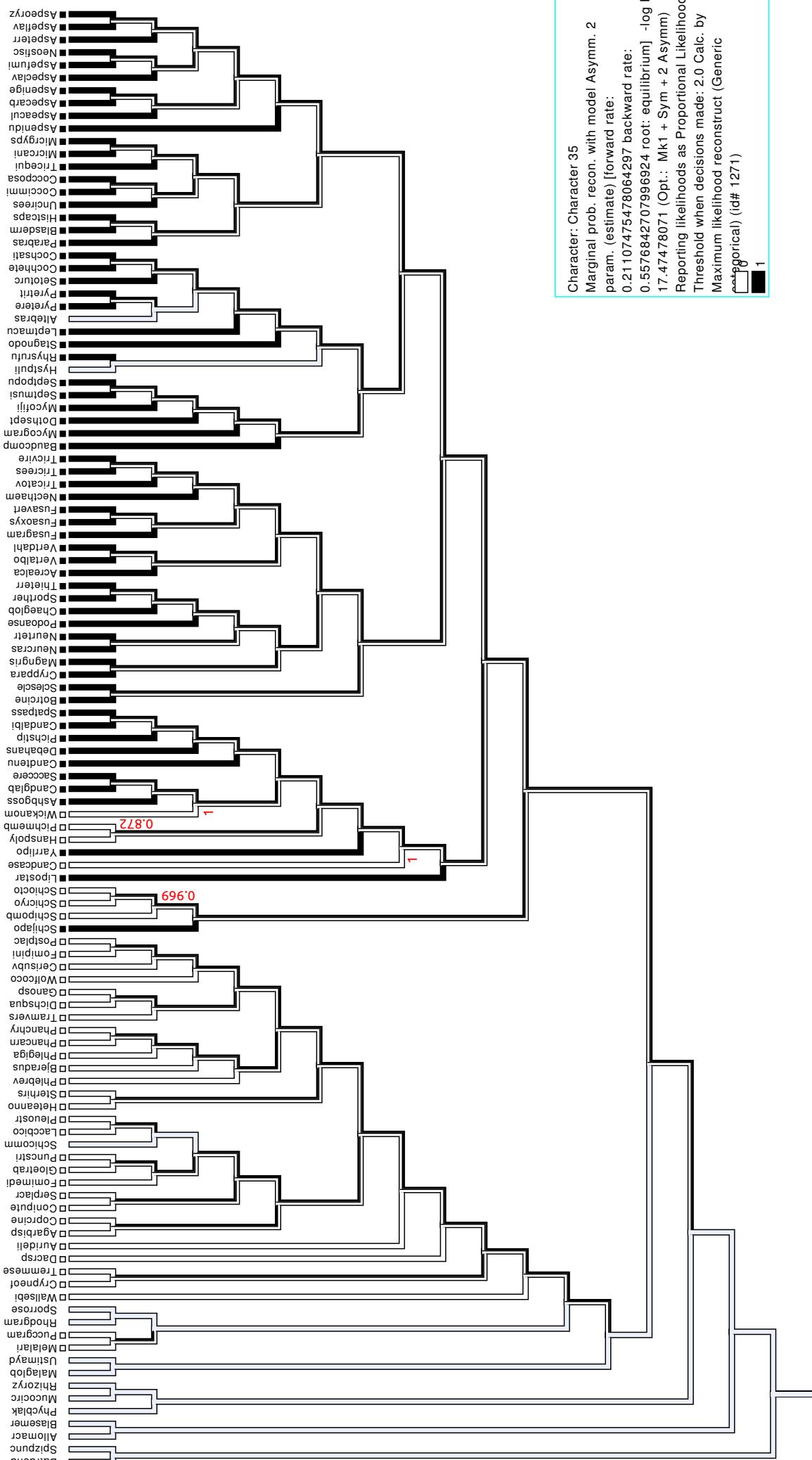
2.1 Important Notes

Sequences similar to Nha1_C domain are only present in ascomycete genomes so we did not conduct a phylogeny as this data would be uninformative for polarising ancestry of this gene fusion.

3 Mesquite Cladogram

This tree is the 68-gene concatenated phylogeny (Fig. 1), with the presence of a fusion (black), presence of a fission (white), and absent/undetermined (grey) status of gene fusion characters plotted on to it using a "1/0/-" nexus-style data matrix. We used the program 'Mesquite' to calculate proportional likelihoods based on either an "Mk1" or "Assym. 2 param model." (see Table S4) of character change across the fungal phylogeny (Fig. 1). This allowed for a proportional likelihood of the position of the fusion/fission to be calculated.





Putative Fusion 35

September 26, 2012

1 Fasta Sequences

These are the unfused sequences identified by fdfBLAST belonging to the putative gene fusion in FASTA format. Accessions may be shortened, but belong to either the taxons individual genome project or NCBI's accession numbering.

```
>gi|302414152|ref|XP_003004908.1| WSC domain-containing protein [Verticillium albo-atrum]
MTNEVCATFCASRGFAYAGTEWYQECYCGNALAVGGVIANELDCNTPCAGDTTQPCGGPNRLTLFFTEEA
NGPSVNPVGVGGWVSEGCYTDGAGGRTLSNGIGSIPASEMTVAKCLAACRAGNYKLGGEYGGECYCDNSL
KNGGAPAVDGCNMLCNGNTTEYCGGPNRLNLYNYKEVVDSSTTTPEPTGTASVIETVLPTSTITPTG
PSHPETVGPYSWVGCRTEATGARALGAKELANDQMTLETQTFCTGYKYFGTEYGRECFCGNTFAAGSQT
APESDCSMRCSGSPQQYCGAGNRLSVYMLDEGGSPASSAVTSGAATSDAGVASAVSTSTSARPVATGY
PSGWSEQGCWVDGAGGRILTHQVPDDNALTQKCAKKCFDLGYTVAGAEYYQQCFCGNAIINNGVKASSD
SQCNTPCAGDSTQMCGGGDRMTIISDGPPRVRGPPSPQLSGFNGDWTYQGCLQSFVGTTRFWQNFFPG
TMTANECLDRCGEGYMAAGLEYGEECYCGDPANIDTIGTVFRPESECNILCAGNDSSICGGGNRMSTYF
WTGTPPLYAWTFPQDVARAGSYELLIGGVCIPLMTMESITGKVTFLEKGWTGPANSTGAYELDSLTPNRN
TAWREMNVKTIDIFCSSGLILPDKAGRQLTVGGWSDSTYGVRLYTPDGSPGVNGTNDEENVNQLSLQDG
RWYPITTMIMANGSIFVIGGEEGSNGAAVPTIEVLPYTGRAPLFMDWLERTDPNNLYPFCAVLPSENIFVA
YWNEARILDKTTFETLTILPTIPGTVNMPMGGRTYPLEGTGVLLPKAPYTAGLGIICGGSTEGVATAIDNCVTIYPEAPEPEWVIERMPSRRVMSCMAPLDGTYLINNGAQQGVAGFGLAEFPNLNALIYDPEKRVGARITVVANTTIARLYHSESITLLDGRVLVTGSDPQDGVNPQEYRVEVFNPYLTSGKPRPTFTLANRDWDYDESITFTLGSAPVNGAISVTLLGGVSSTHGNSMGTRTILPSVSCSLTCTVTAPPDAGICPPGFQFFFVLDGGIPAVGVYVVRIGGDPAELGNWPDKSSFSPPGL
```

2 Annotated Phylogenograms

All trees were generated from an initial run of Darren's Orchard pipeline against 139 taxa (Table S1), using the above corresponding un-fused sequences as BLAST seeds. The alignments were then checked for any missing taxa, manually masked and then ProtTest3 was run, please see the Methods section for detail. The final trees were generated by the following command:

```
phym -i alignment_file -d aa -b 100 -m model -c 8 -v invariant_sites -s BEST --quiet -a gamma
```

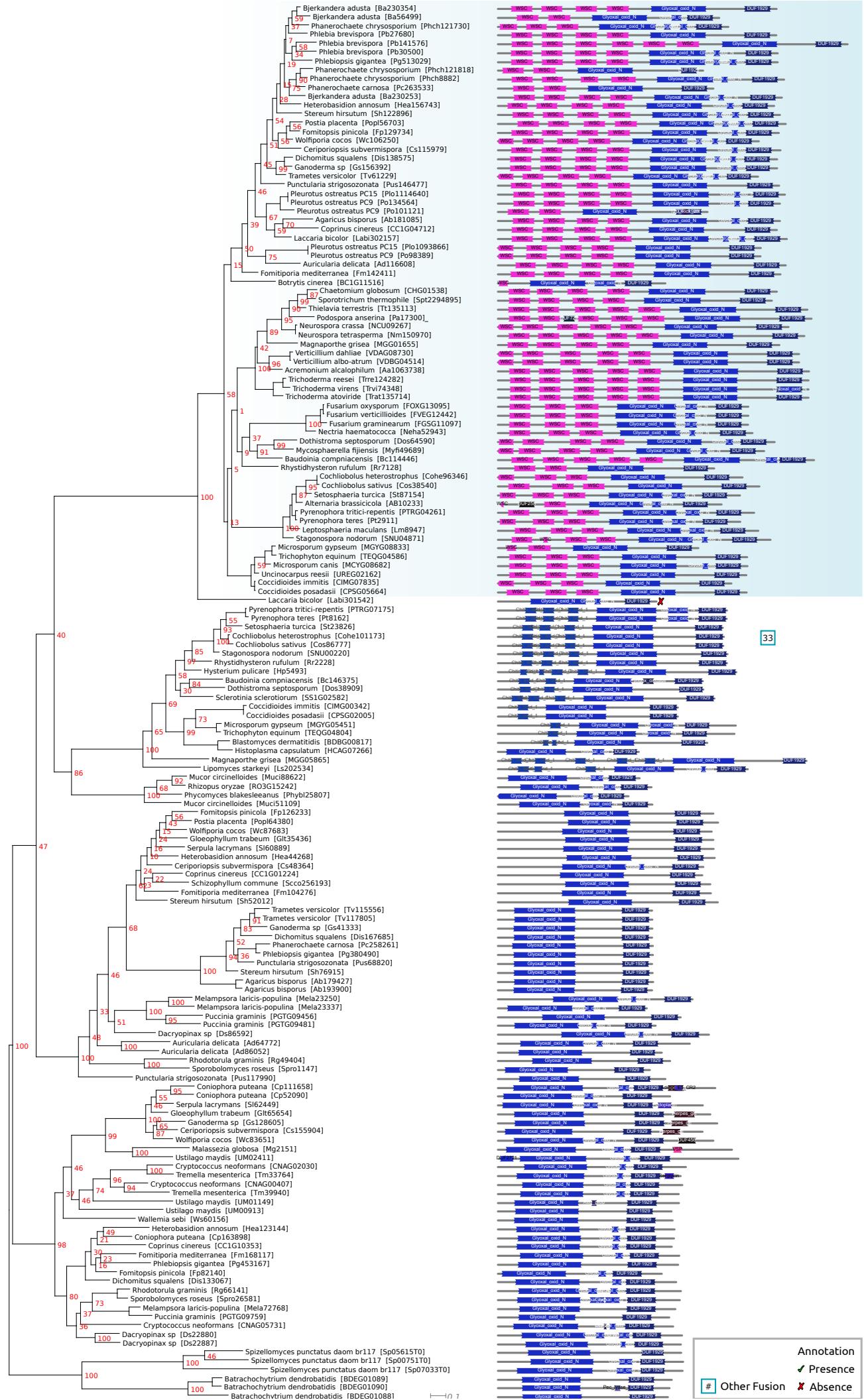
Styling and annotation was made possible by Dendroscope and Inkscape.

2.1 Important Notes

There is only one phylogeny here as one domain consists of a series of repeats and so an alignment would not be possible as the resulting phylogeny would then be unresolved.

3 Mesquite Cladogram

This tree is the 68-gene concatenated phylogeny (Fig. 1), with the presence of a fusion (black), presence of a fission (white), and absent/undetermined (grey) status of gene fusion characters plotted on to it using a "1/0/-" nexus-style data matrix. We used the program 'Mesquite' to calculate proportional likelihoods based on either an "Mk1" or "Assym. 2 param model." (see Table S4) of character change across the fungal phylogeny (Fig. 1). This allowed for a proportional likelihood of the position of the fusion/fission to be calculated.

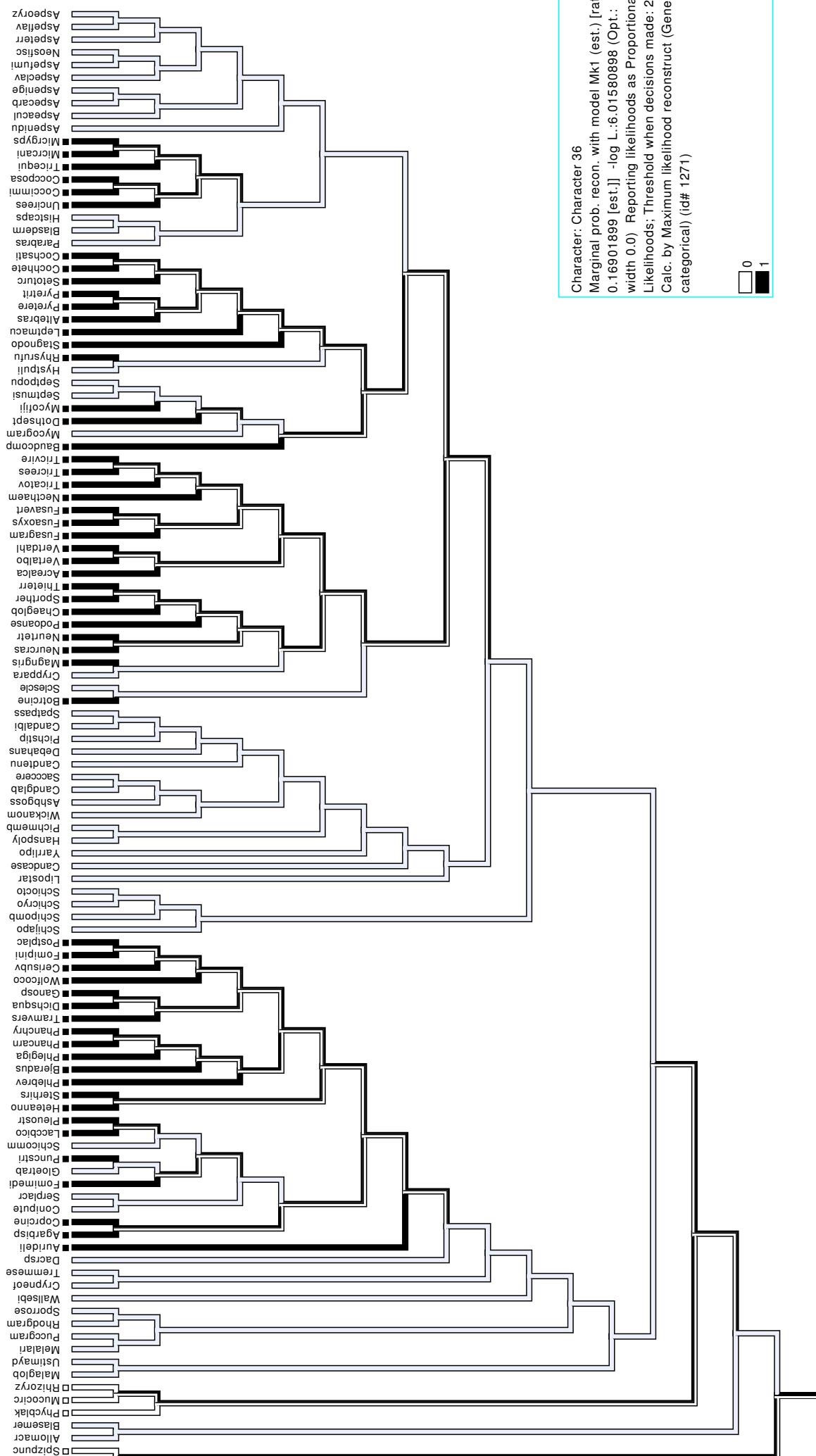


Annotation

✓ Presence

✗ Absence

Other Fusion



Character: Character 36
Marginal prob. recon. with model Mk1 (est.) [rate 0.16901899 [est.]] - log L: -6.01580888 (Opt.: width 0.0). Proportional likelihoods as Proportional Likelihoods; Threshold when decisions made: 2.0
Calc'd. by Maximum likelihood reconstruct (Generic categorical) (id# 1271)

Putative Fusion 36

September 26, 2012

1 Fasta Sequences

These are the unfused sequences identified by fdfBLAST belonging to the putative gene fusion in FASTA format. Accessions may be shortened, but belong to either the taxons individual genome project or NCBI's accession numbering.

```
>gi|242209591|ref|XP_002470642.1| predicted protein [Postia placenta Mad-698-R]
MAPKSDWEKWEKKADDKDEKEIKGTLIYPLSLLMLTEVQPSTTGQGPYAQKLKKIENDIKDAQKRVNEK
LGIKESDTGLAAPNLWDLAVDRQRMGEEHPLQVARCTKIIIPMNQEAAAARAVNPQGALQGQKGADEQDK
YVINIKQIAKFVVGLGDRVAPTDIEEGMRVGVDRNKYQIQIPLPPKIDASVTMMQVEEKPDVTYSVGGC
KEQIEKLREVETPLLSPERFVNLLGIDPPKGVLFFGPPGTGKTLCARAVANRTDATFIRVIGSELVQKYV
GEGARMVRELDEMRSKKACIIFFDEVDAIGGARFDDGAGGDNEVQRTMLELINQLDGFDPRGNIKVLMA
TNRPDTLDPAALLRPGRLLRRVEFSLPVEDGRASILRIHARMSCERDIRFDLIARLCPNTTGAELRSVAT
EAGMFAIRARRKVATERFLDAVEKVVVRQGTKSSTDYEDGGISAAELSRLMEEHAEQPPRPLTLSTLLS
LADPVTPESVLTsvryvtneiprrmamrarslealpyivgmnpfiartleayrksfrfltyppvqtled
NQRltaeldglvqshandiptmakgfqecaryltpeqistfldeairnriaavliaeqhiaisraleegg
DLKDHHGVVHLSCSPQDMIRMCGSWVSDLCEATLGAHPEIIIDGEVDAFAYVPVHLEYILTEILKNAFR
ATVERHARQPSIIRTSPVPPVRITISPPLTIPRPRFLSMRVRDQGGGVSPAHLAQIFSYSFTTAGRAT
TSPGGGVGWDDQETGGGPYAAQHVGGSAIIGGIDSMGGAGGLFAEMTGRGVQVMGTTAGLGYGLPMsRL
YTRYFGGSLDLMSLDGWGCDVFLKRLCLDDAGDVEI
```

2 Annotated Phylogenograms

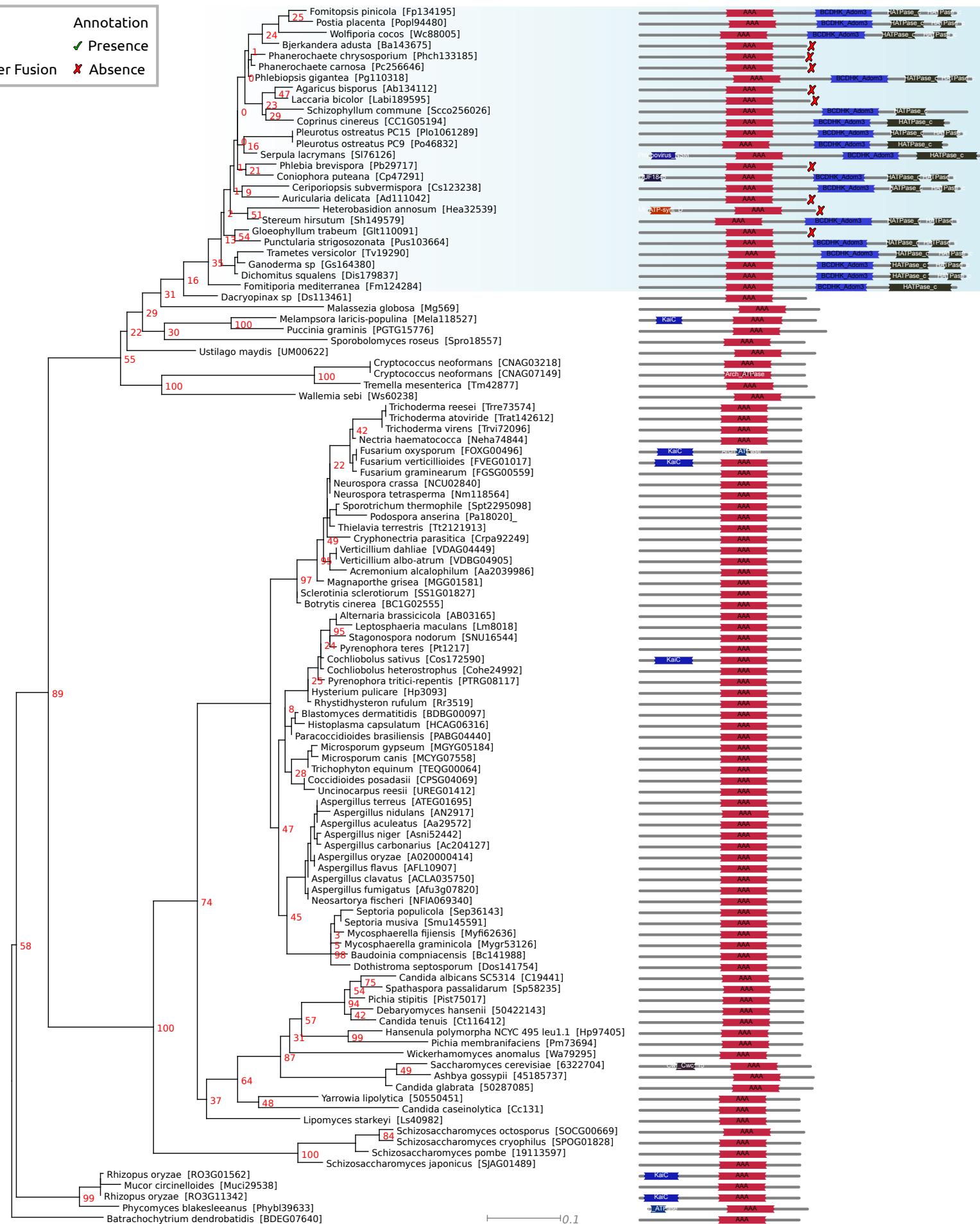
All trees were generated from an initial run of Darren's Orchard pipeline against 139 taxa (Table S1), using the above corresponding un-fused sequences as BLAST seeds. The alignments were then checked for any missing taxa, manually masked and then ProtTest3 was run, please see the Methods section for detail. The final trees were generated by the following command:

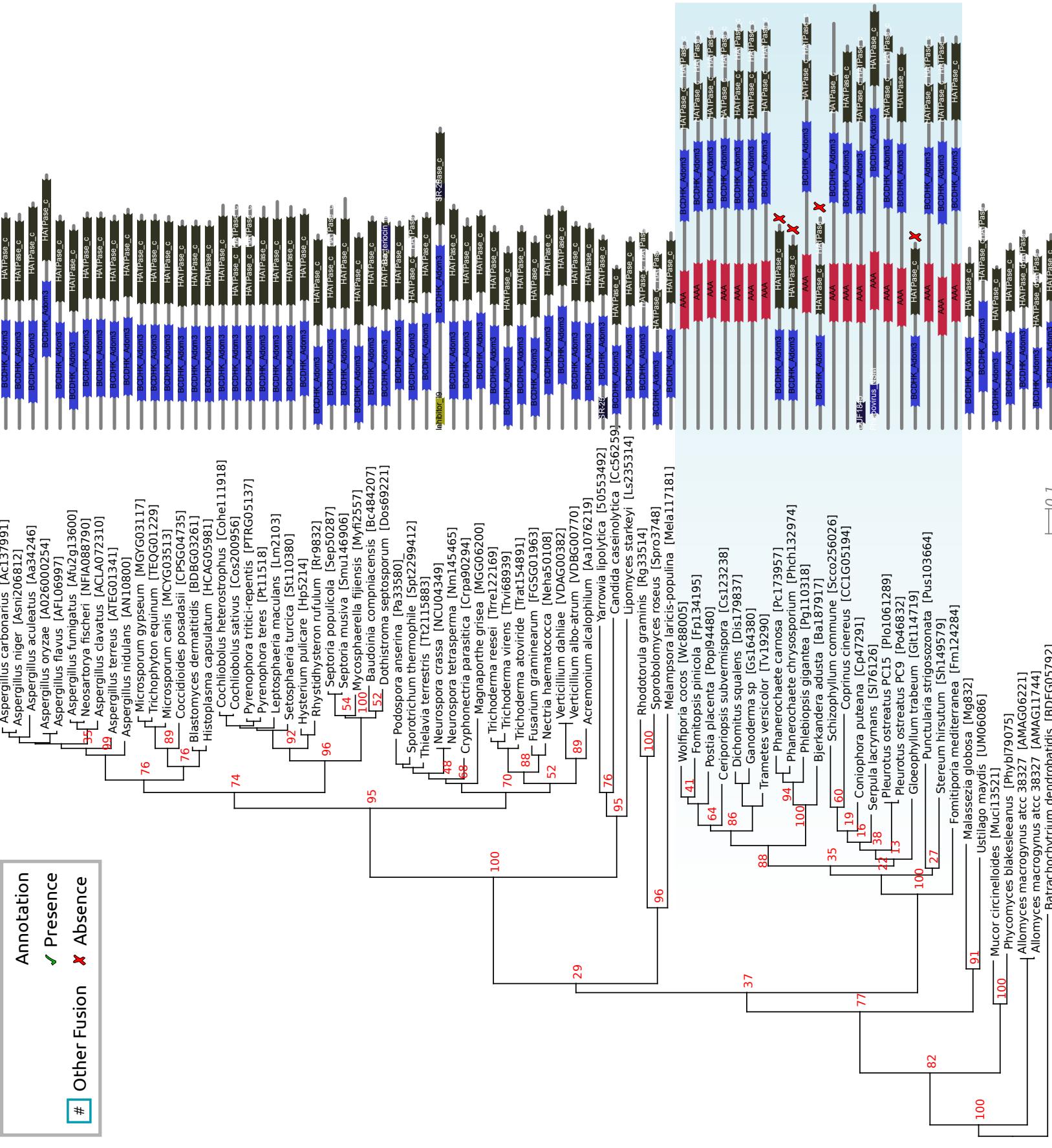
```
phyml -i alignment_file -d aa -b 100 -m model -c 8 -v invariant_sites -s BEST --quiet
-a gamma
```

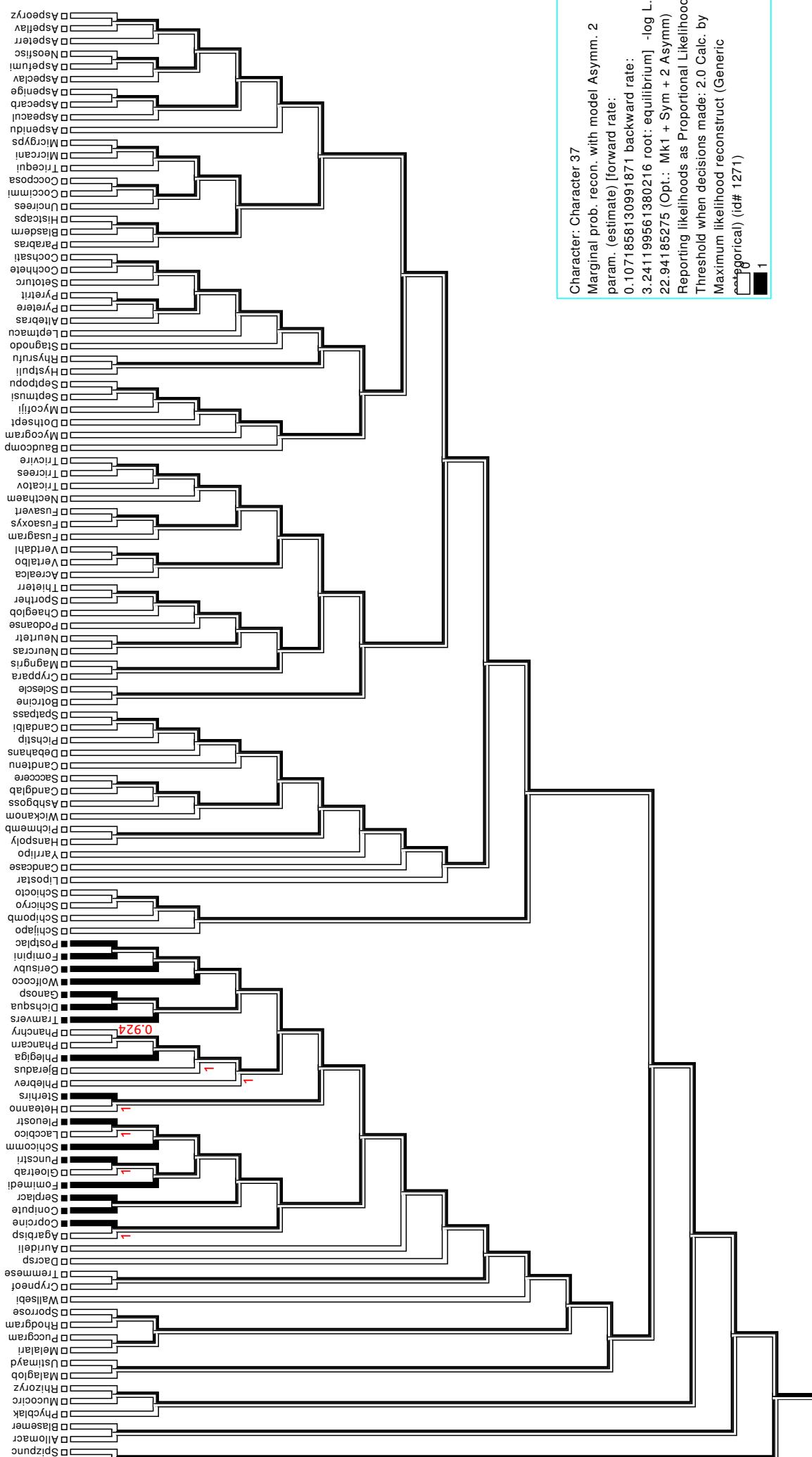
Styling and annotation was made possible by Dendroscope and Inkscape.

3 Mesquite Cladogram

This tree is the 68-gene concatenated phylogeny (Fig. 1), with the presence of a fusion (black), presence of a fission (white), and absent/undetermined (grey) status of gene fusion characters plotted on to it using a "1/0/-" nexus-style data matrix. We used the program 'Mesquite' to calculate proportional likelihoods based on either an "Mk1" or "Assym. 2 param model." (see Table S4) of character change across the fungal phylogeny (Fig. 1). This allowed for a proportional likelihood of the position of the fusion/fission to be calculated.







Putative Fusion 37

September 26, 2012

1 Fasta Sequences

These are the unfused sequences identified by fdfBLAST belonging to the putative gene fusion in FASTA format. Accessions may be shortened, but belong to either the taxons individual genome project or NCBI's accession numbering.

```
>gi|116208054|ref|XP_001229836.1| hypothetical protein CHGG_03320 [Chaetomium globosum]
MDILQRLGIPLPIATGALGLIVALIAGMGLFGRKNQMPVDGRTVLITGASEGMGRSAAIQLAAKGANIIL
VSRNVGRLEEALTDVKAASSPATQRFTYITADVSEPDYASAVIAEAIAWNGGRSPDIVWCIAGMSTPLL
WTDDNAMAAARRNMDVNYFGSAEMSRAILREWLNPNDNRDSTRPEPKHIVFTASVLALFAIVGYGPYTPSK
WALRGLADTLAMEVNLYPETPVKHVVFPATITSPGLERENKTPAITLEKDEPPTPDTVARRAIAG
LERGEYFVAVSFLGNLMRCGVMGGSRNNWLFDTLLGWLVPVIYFFVLRIMNGQLLNHNNPYRHQPSRTA
SGTILISRPGSTMKSSVIRSQRGPSKVTKSVPTPRGRTPRQVAAHLATQEDHSQVHNLGNQNHVHSHTH
GHGHDLSDLKTDPAVFDDVRMGAEDYAAAAAAAAMDLDLTAHGEAEAEADMDEDGGPSGLPHVD
LTAANILANGGAGPGNAMSQPVQEQLQEMQQNLAAHQHAHQHQQHHPHSHQHHQPPAQMGTPQQIQPG
HQGMDGSMVKTTEDLARDSGYGDLNVESALAKRLARDPGQRLAQQRRPEQVNLARRSNVEALFAHIAGE
PARIPCKNCHKHGWPWTSCVVVDGQMCANCWFNASGARCSFHETRNPQPVPQHPTILPAATTGMTND
PTYRFAAASHPLLQPHGPALGGVSHPGLLINNPVLQEMVNRAMVEVRQANKATRQLIQIEITAKQLALQ
IVECEEMVNNQEKGSGQQAMGDDSGA
```

2 Annotated Phylogenograms

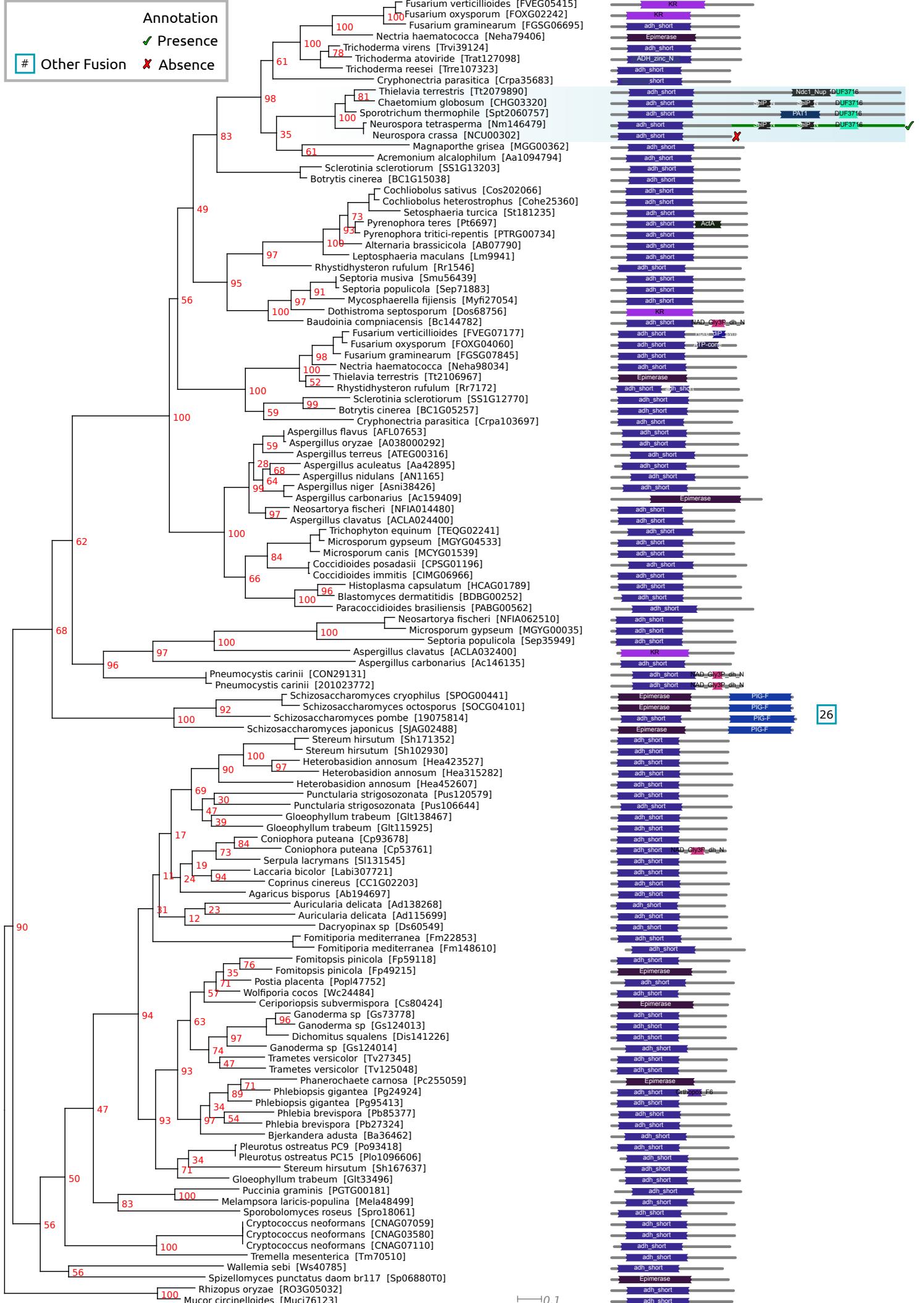
All trees were generated from an initial run of Darren's Orchard pipeline against 139 taxa (Table S1), using the above corresponding un-fused sequences as BLAST seeds. The alignments were then checked for any missing taxa, manually masked and then ProtTest3 was run, please see the Methods section for detail. The final trees were generated by the following command:

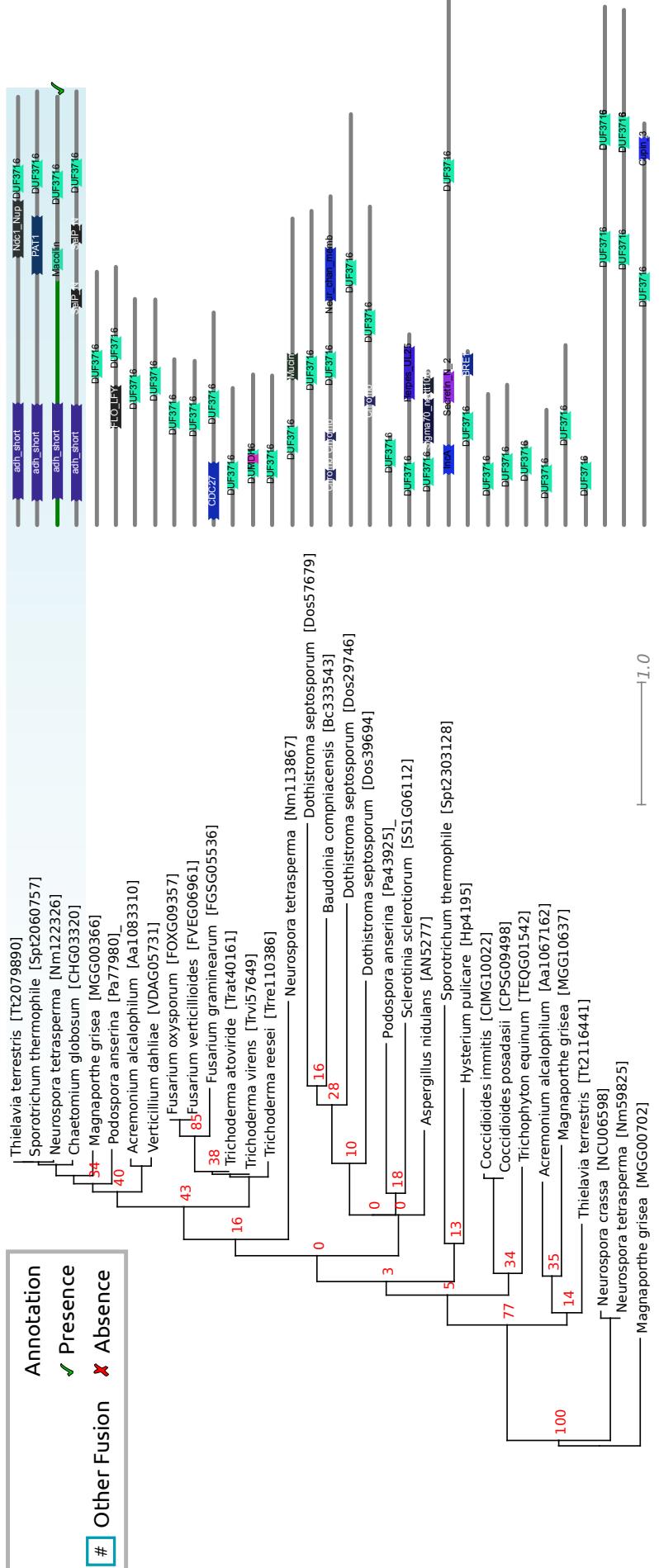
```
phym -i alignment_file -d aa -b 100 -m model -c 8 -v invariant_sites -s BEST --quiet
-a gamma
```

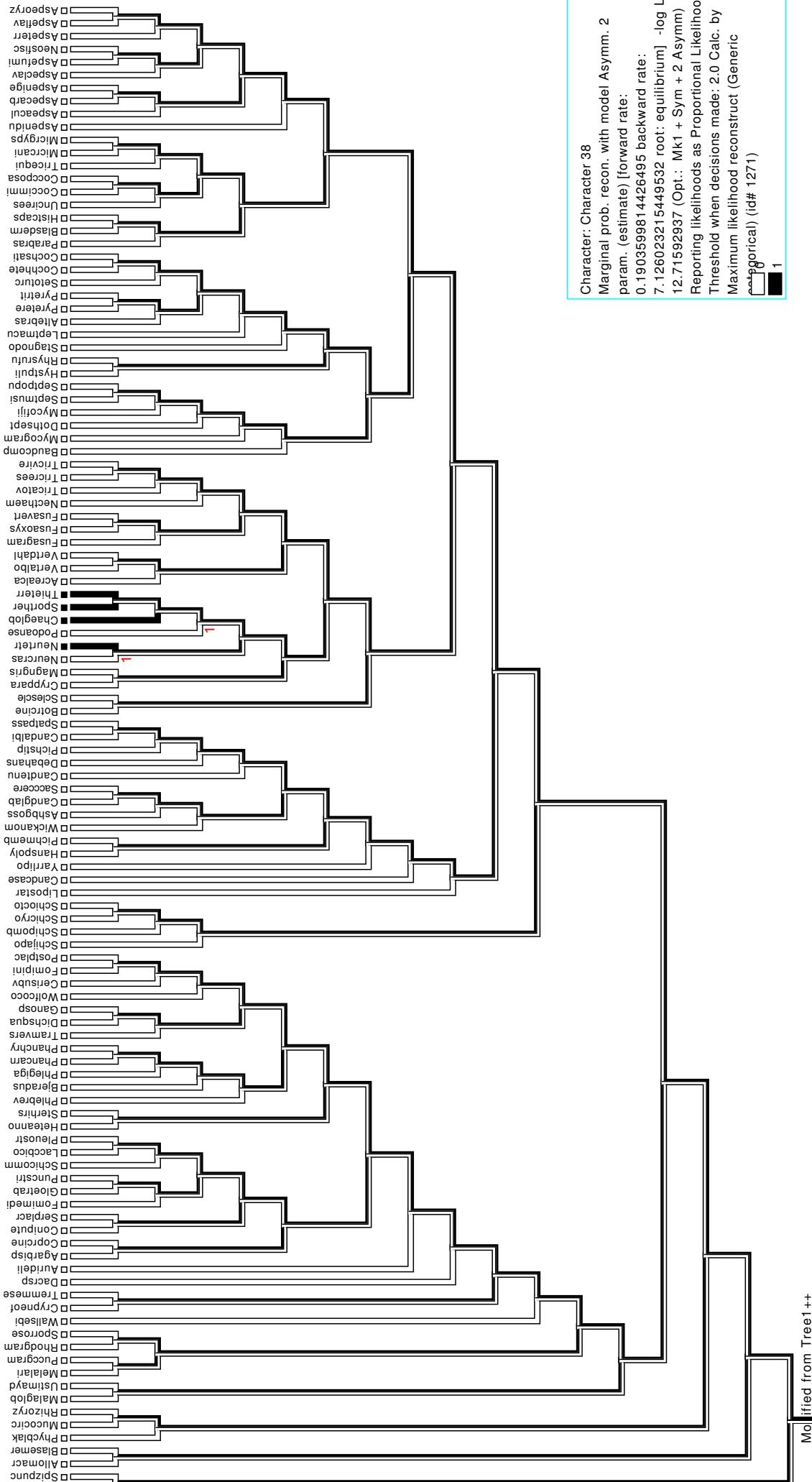
Styling and annotation was made possible by Dendroscope and Inkscape.

3 Mesquite Cladogram

This tree is the 68-gene concatenated phylogeny (Fig. 1), with the presence of a fusion (black), presence of a fission (white), and absent/undetermined (grey) status of gene fusion characters plotted on to it using a "1/0/-" nexus-style data matrix. We used the program 'Mesquite' to calculate proportional likelihoods based on either an "Mk1" or "Assym. 2 param model." (see Table S4) of character change across the fungal phylogeny (Fig. 1). This allowed for a proportional likelihood of the position of the fusion/fission to be calculated.







Putative Fusion 38

September 27, 2012

1 Fasta Sequences

These are the unfused sequences identified by fdfBLAST belonging to the putative gene fusion in FASTA format. Accessions may be shortened, but belong to either the taxons individual genome project or NCBI's accession numbering.

```
>Plo1073489_dom1
MISHFLRHPFQALCELLTNPRYFGAVAALVVVGDAVLTQLIVRFIPYTEIDWETYMAQIA
VIMKGETDYSRISGPTGPLVYPAGHVYIHQQLLYKITDAGRNMALSQQIYAGLYVSSLILT
CCIFYRKAGAPNWLLALPLSKRLHSIYVLRLFNDWSVTALAALAVLAYQFEMDDLAVLLY
STALSIKMSILLYLPGLLVLLYKRRGLTTFRQMITSFQAVIARTFIKADLSAYLNGA
FDLSRVFLFKWTVNWRILGEGLFLDRRAVGLLVGHVSVLVAFGYRWCRPDGGPLPTILR
GISRPSTPAGLVPVSPDYVATVLFTSNLIGIFFARSLHYQFYSWAQQLPFLVFKTRYAM
PVKLTIILVAVEFAWNVYPSTNVSSSILLAHSSLLAGIWRHNYTFPAIAPKDYLECRTLL
>Plo1073489_dom2
DDQILLIDNFLTAAECKQYIQFIDNLPLELTPPKKRGEAERVNYRFSIPSVDFAERLHSL
FQPYVLSLPTPSTWRTSESRRHSPVGCNSNIRLYKYNPGQHFGAHYDDSVRDPATGLKSEW
TILMYLSGIEDGVEGGETIFYLEQKGKAREPIAAPLTRGTALLHRHGSECLLHEGSPVRK
GTKYILRSDFMFKY
```

2 Annotated Phylogenograms

All trees were generated from an initial run of Darren's Orchard pipeline against 139 taxa (Table S1), using the above corresponding un-fused sequences as BLAST seeds. The alignments were then checked for any missing taxa, manually masked and then ProtTest3 was run, please see the Methods section for detail. The final trees were generated by the following command:

```
phylml -i alignment_file -d aa -b 100 -m model -c 8 -v invariant_sites -s BEST --quiet -a gamma
```

Styling and annotation was made possible by Dendroscope and Inkscape.

3 Mesquite Cladogram

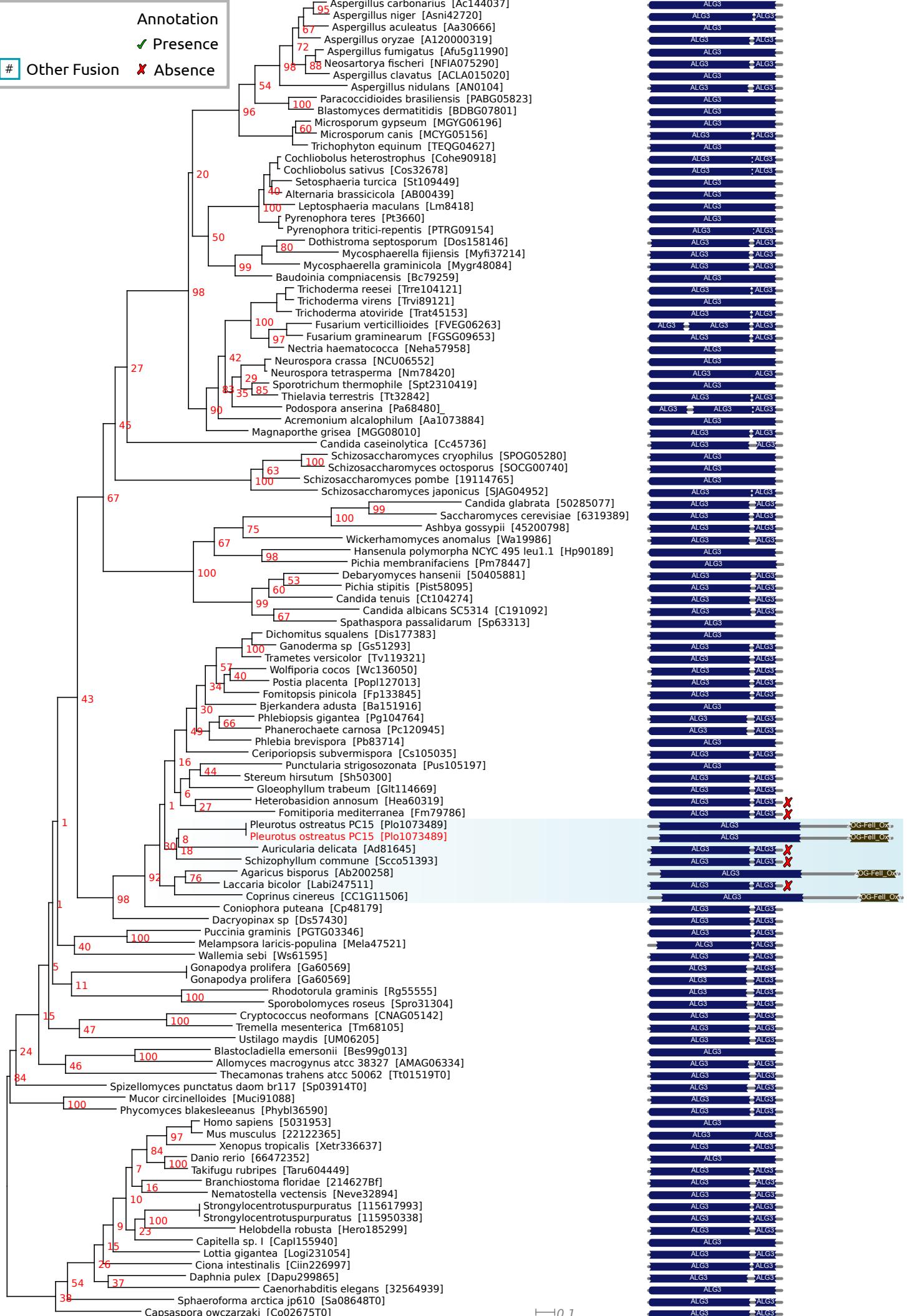
This tree is the 68-gene concatenated phylogeny (Fig. 1), with the presence of a fusion (black), presence of a fission (white), and absent/undetermined (grey) status of gene fusion characters plotted on to it using a "1/0/-" nexus-style data matrix. We used the program 'Mesquite' to calculate proportional likelihoods based on either an "Mk1" or "Assym. 2 param model." (see Table S4) of character change across the fungal phylogeny (Fig. 1). This allowed for a proportional likelihood of the position of the fusion/fission to be calculated.

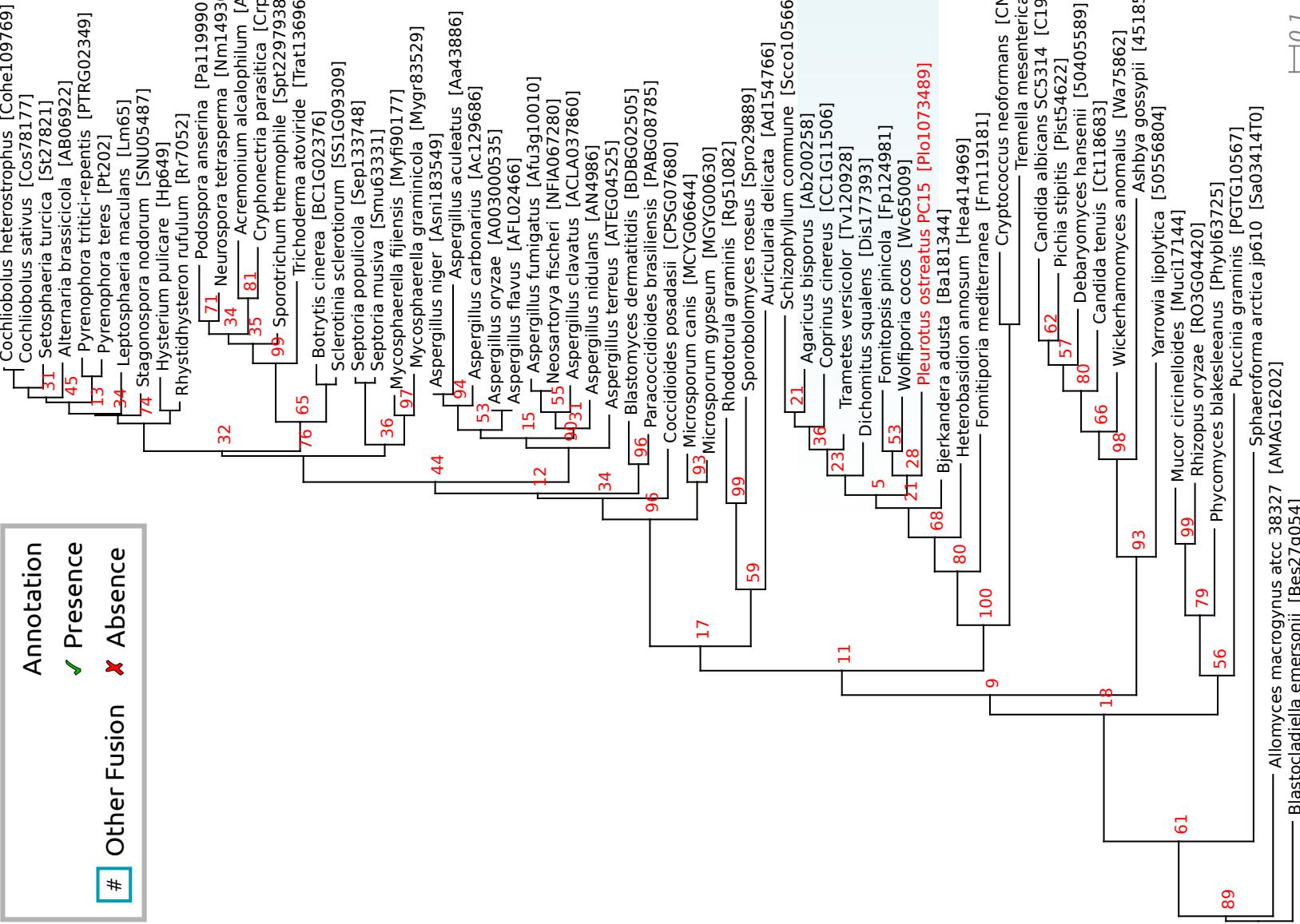
Annotation

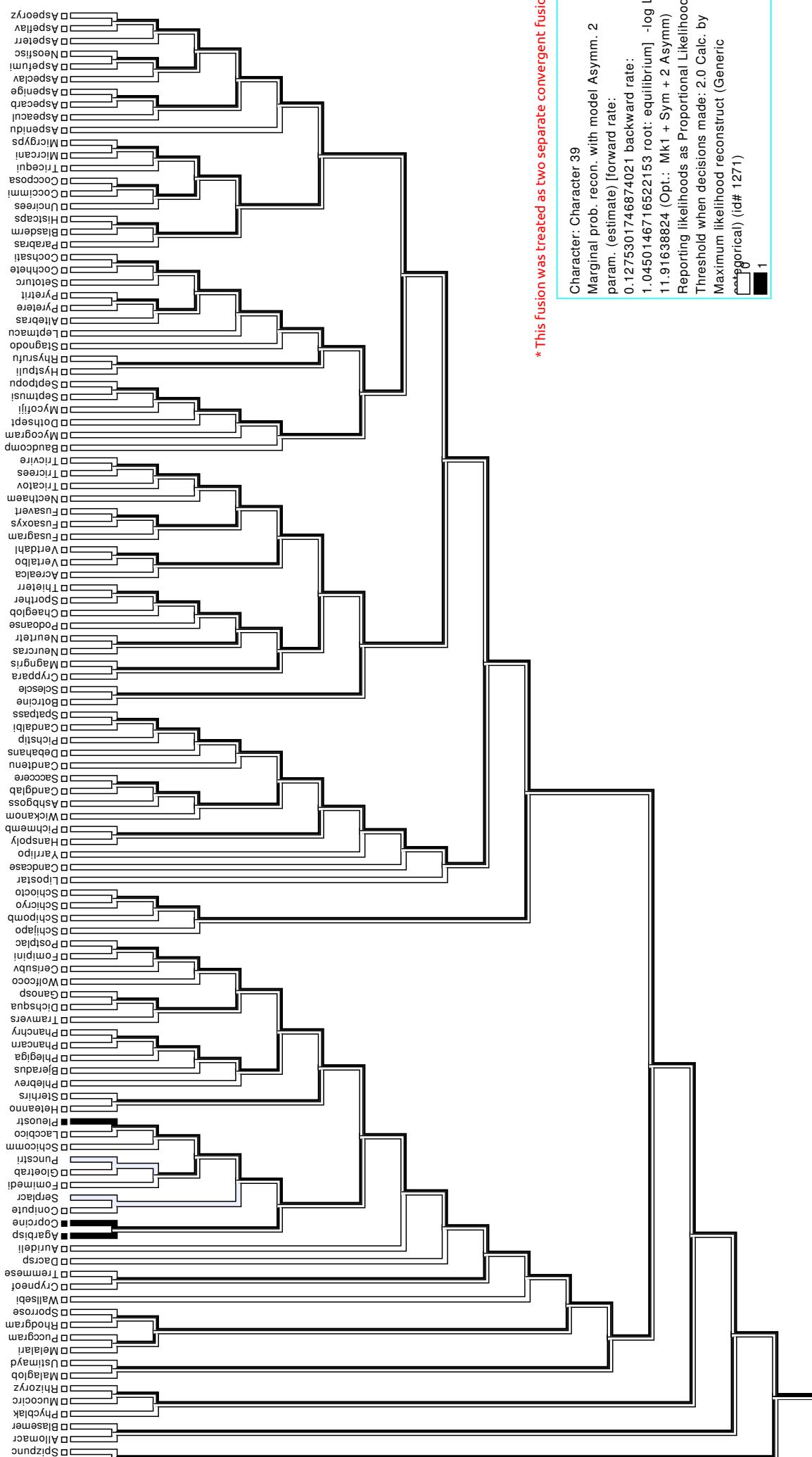
✓ Presence

✗ Absence

Other Fusion







* This fusion was treated as two separate convergent fusions

Putative Fusion 39

September 27, 2012

1 Fasta Sequences

These are the unfused sequences identified by fdFBLAST belonging to the putative gene fusion in FASTA format. Accessions may be shortened, but belong to either the taxons individual genome project or NCBI's accession numbering.

```
>XP_0030516041Neha_dom1
MTSIADEIEYKLDVTETQSAANDIDKTFRTTCIDLISALGGKVLGFSDQWFCEATNLL
NPKAPIRQQGKVMVFTGAWYDGWETRRHNSEPFDYVVIRLGVASGTIEGIEVDTAFFNGNH
APAISVEGCFSQDDEEVASWKGGRGKWETILGVQECGP SERFCWKLKPTQKQYTHVRLN
MYPDGGIARFRLFGHAVPVFPDDKDVF DLA AQQNGGLAVSCSDQHFGN KDNLLPGRGK
DMGDGWETARSRAKGHTDFAIKLGAPGYIERFGCEWTGHGDPVADAVAWREFVPPSKTG
PDQEHEFKSADGEKDRLVTHVKLIMIPDGGVVKRLRAFGKRAGQVGRLPSTTPRTISTQPQ
GISSQRPTTSPRPTVATRFKHAQTYSHTVCEIYPPKRLPPNSHEPSAASGSAPP SAMDL
>XP_0030516041Neha_dom2
GDSLGPGLPDNKPRALPSDPLPRS LDDRRHVPNEHLVTETEMYDGWQGQSQFLTTPALAK
PLNFGNLSLNDPDYDDNVTKGP KDSDTRLMEMLAQAQAHQSGSGFED EDEIVNDEKL PDS
EKKVKLQKALNMAASNGDVERIGKLLNGKAKEYIDINAEDEDGT PPLIYASCFGHEPVVQ
ALIGAGADV NKQDRNQWTALMWAMTNRHKGIAKLLLDNNASSDQK TSSGRTA FDFVPPDS
EMSYYLHDNGYNIGSAGTDDFYSPGFTQDRFEEMAENEMRRRLMMESARDLEV D LGNV
GMDDQPEP VDEFEEEQQEFDWNRCLHDQM FVQEHEDRILDIIITK MTPQRSPSQKP VP
ANMIFL SARYAHYHSRELLERLLVSAMD YINDVVERCQWDMTILA FWISNATLLLHYLK
KDAGLFHATAEFQ AQLAELINEIFILIVRDAERRLDKVLDVAML DHE TIPGF EDITF QNE
WKIFKRKAQVKEEPIEKFRPPSPKQRAK PAPRN VTSLLSSTLFVLDLYDIHSVISAQII
SQLLYWIGAELFN RIMS NRKYLARTKAMQIRMNISILEDWARTNNRQADHYEGSDMRSSG
ETTIDAARRH LAPVIQLLQWLQCFSSL DADDLEALVGTLQQLKRLSPQQLIHAANHYRPE
VGEKGLPKSAM KYLIAIQKEAALKRERRSGMASPQRSGQDSSPVT PVKNRSNGN HLETP
GSPPEDEWSDDDDA PEHLLDPALMLPFTLPSVT DMLVTY GAGFGGVN RERER KYIPTV
PPEFLEKLEVSGGTRKGPMFGEADWEEV
```

2 Annotated Phylogenograms

All trees were generated from an initial run of Darren's Orchard pipeline against 139 taxa (Table S1), using the above corresponding un-fused sequences as BLAST seeds. The alignments were then checked for any missing taxa, manually masked and then ProtTest3 was run, please see the Methods section for detail. The final trees were generated by the following command:

```
phylml -i alignment_file -d aa -b 100 -m model -c 8 -v invariant_sites -s BEST --quiet -a gamma
```

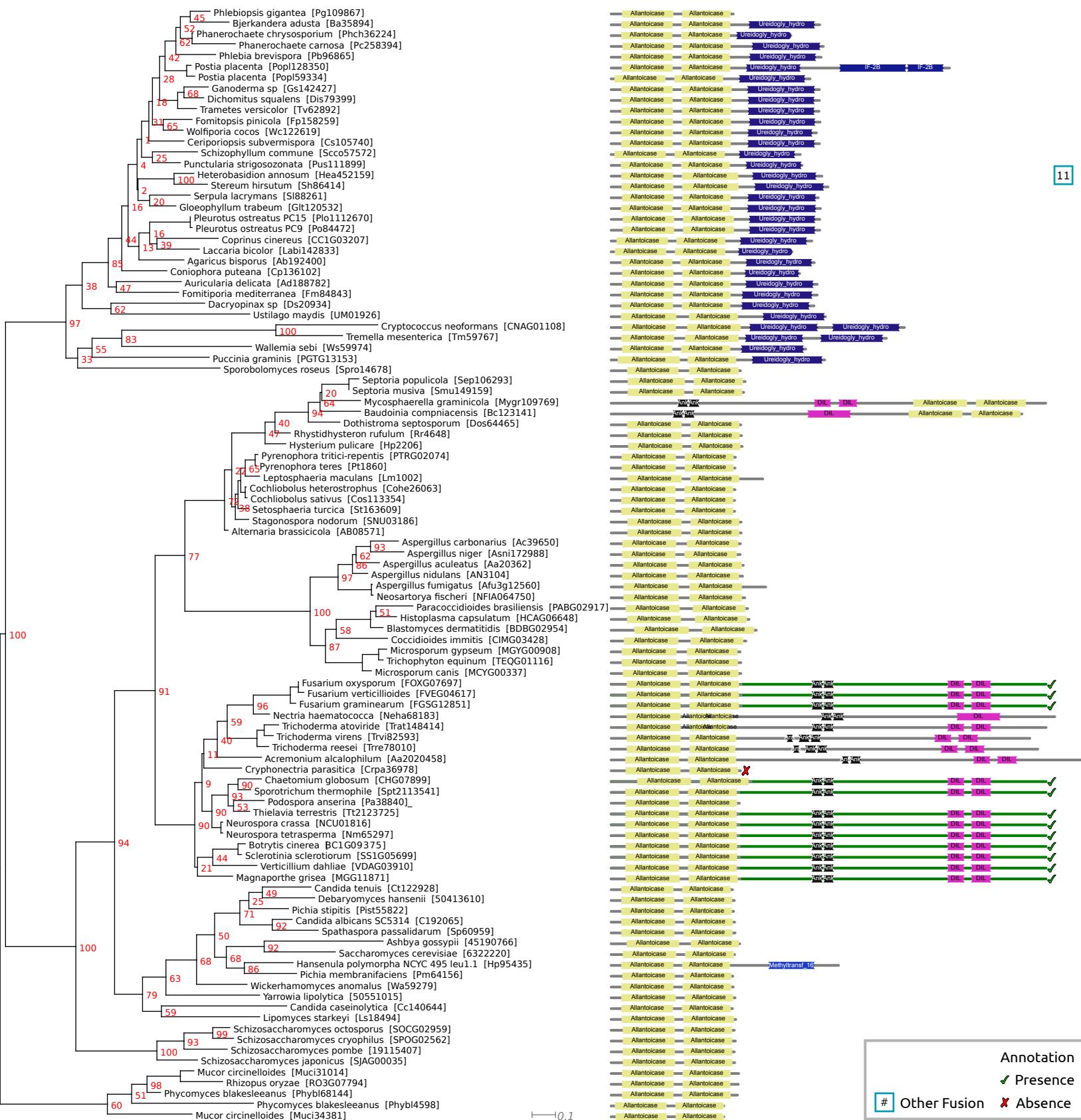
Styling and annotation was made possible by Dendroscope and Inkscape.

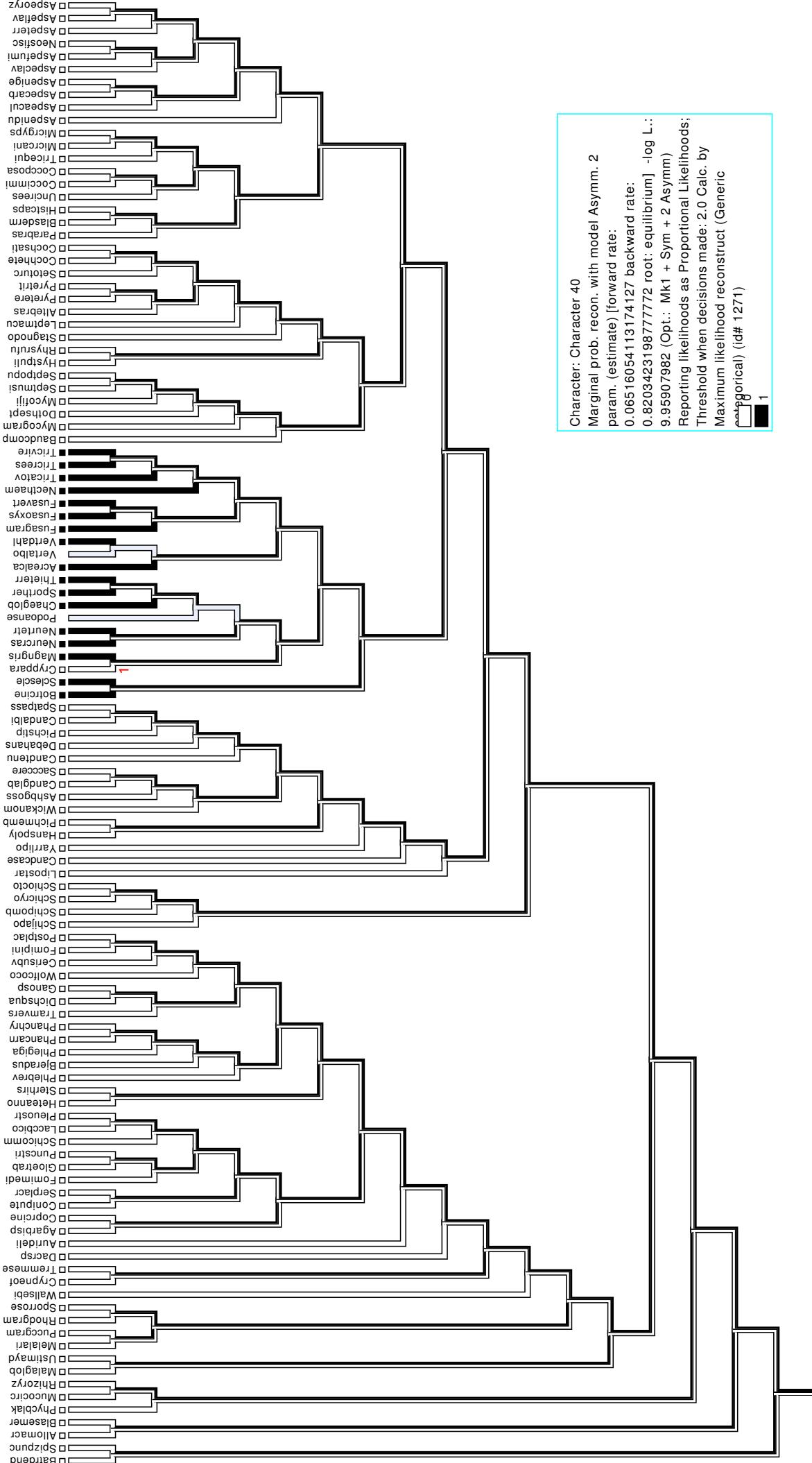
2.1 Important Notes

The original prediction made by fdFBLAST, on closer inspection (from the first round of phylogenies), indicated that there was not a gene fusion present between the above two domains but there was potentially a gene fusion with a third other domain. There is only one phylogeny here as the third domain consists of a series of repeats and so an alignment would not be possible as the resulting phylogeny would then be unresolved.

3 Mesquite Cladogram

This tree is the 68-gene concatenated phylogeny (Fig. 1), with the presence of a fusion (black), presence of a fission (white), and absent/undetermined (grey) status of gene fusion characters plotted on to it using a "1/0/-" nexus-style data matrix. We used the program 'Mesquite' to calculate proportional likelihoods based on either an "Mk1" or "Assym. 2 param model." (see Table S4) of character change across the fungal phylogeny (Fig. 1). This allowed for a proportional likelihood of the position of the fusion/fission to be calculated.





Putative Fusion 40

September 26, 2012

1 Fasta Sequences

These are the unfused sequences identified by fdfBLAST belonging to the putative gene fusion in FASTA format. Accessions may be shortened, but belong to either the taxons individual genome project or NCBI's accession numbering.

```
>XP_0012734091Ascl_dom1
MVASAVRMRVPSAMLSKGALCMRRPQVHRFKDAVQPQLPALAALSRFYASKSFPPTII
SMPALSPTMSAGNIGAWKKAGDSLVPGDVLVEIETDKAQMDFEFQEEGVLAKEVLKETGE
KDVAVGAPIAVLVEEGTDVSSFESFSLEAGGDKGAAAPAKETKEEPKADAAPAATPEPAP
EAYEPETSADKLQPSLDREPSISPAAKALALEKGVPVKALKGTGRGGQITKEDVEKYKPS
TSAAAAGPTYEDIPLTSMRKTIASRLQQSVRENPHFFVSTTLSVTKLKLRQALNASSEG
KYKLSVNDFLVKACAAALLKVPAVNSSWREENGQVVIRQHNAVDISVAVATPSGLITPVV
KDVQGLGLSSISNQIKDLGKRARENKLKPEEYQGGFTISNMGMNPAAVERFTAVINPPQA
GILAVGTTTRKVAVPVETEEGTSVEWDDQIVVTGSFDHKVVDGAIGAEWIKEKKVVENPL
ELLRAPNPTRTYLNETAESTASLDVDSPHVSVDSFLNQEVKTTQAERLEREAREE
>XP_0012734091Ascl_dom2
EERKERERAVEAEKAKAKAACRAGHVAKRNPVFVGNAIITYLVAALGYGAYRKHLEGRLS
WKLVGAWSGVVGAFGAVDYFVSNEVACHKSVLSPNENISASQIAASLASLSRTIDDYS
LSKKELIPAKQEKAFAERVKNFRAELADYRTHFDRLRKEREEAQSVTNRNELLGRRPHAA
TPENPYAQSSLQPSSPFANASSSRSGLSFGASPADFNRETHALREQSFFANTNTQLDEF
DRGRAVLADLGQQREVLKGTQRRLYSVANTLGISGDTIRRVERRAKQDKWIFWGGVLTFF
LFCWAVLHFLR
```

2 Annotated Phylogenograms

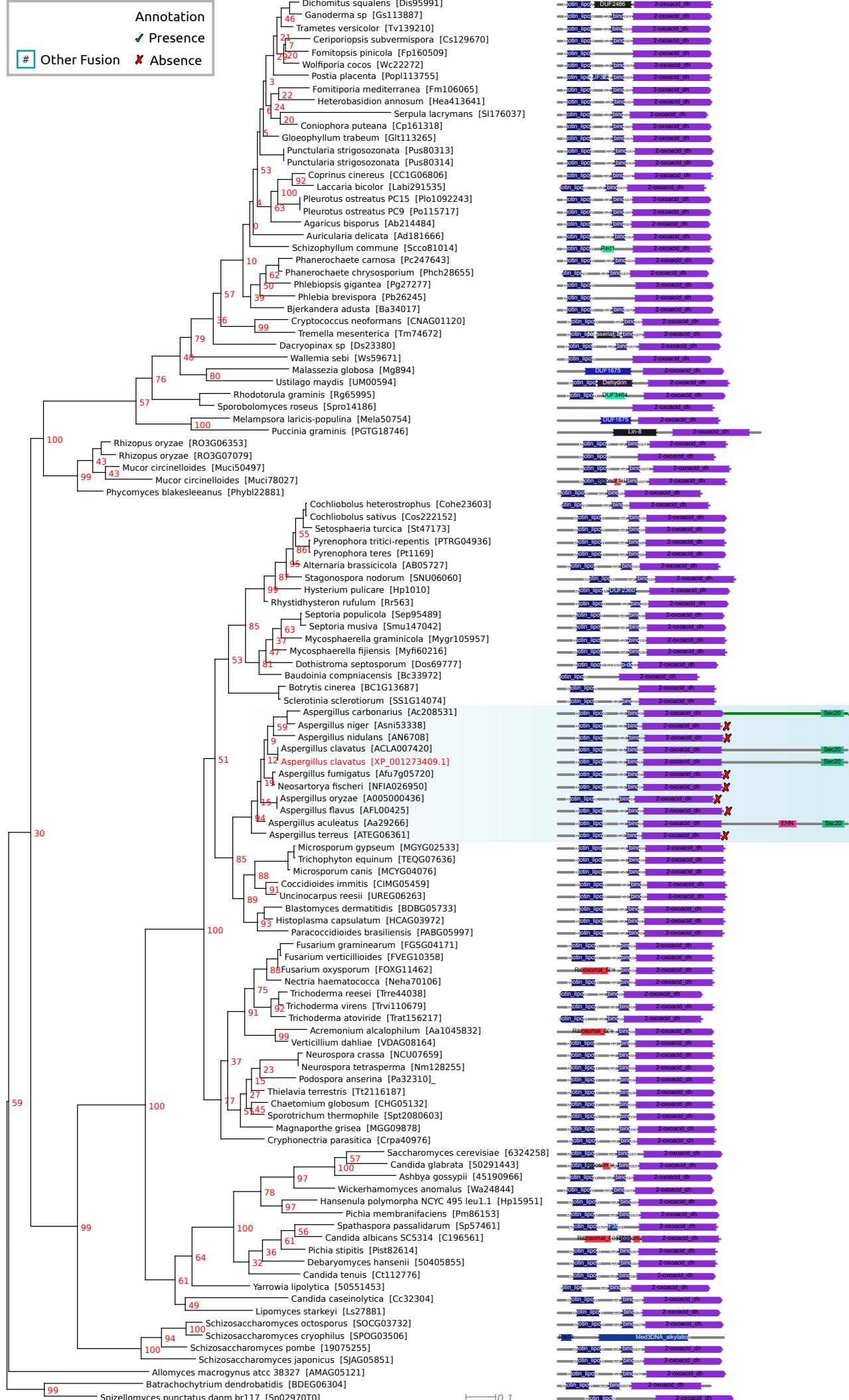
All trees were generated from an initial run of Darren's Orchard pipeline against 139 taxa (Table S1), using the above corresponding un-fused sequences as BLAST seeds. The alignments were then checked for any missing taxa, manually masked and then ProtTest3 was run, please see the Methods section for detail. The final trees were generated by the following command:

```
phyml -i alignment_file -d aa -b 100 -m model -c 8 -v invariant_sites -s BEST --quiet
-a gamma
```

Styling and annotation was made possible by Dendroscope and Inkscape.

3 Mesquite Cladogram

This tree is the 68-gene concatenated phylogeny (Fig. 1), with the presence of a fusion (black), presence of a fission (white), and absent/undetermined (grey) status of gene fusion characters plotted on to it using a "1/0/-" nexus-style data matrix. We used the program 'Mesquite' to calculate proportional likelihoods based on either an "Mk1" or "Assym. 2 param model." (see Table S4) of character change across the fungal phylogeny (Fig. 1). This allowed for a proportional likelihood of the position of the fusion/fission to be calculated.

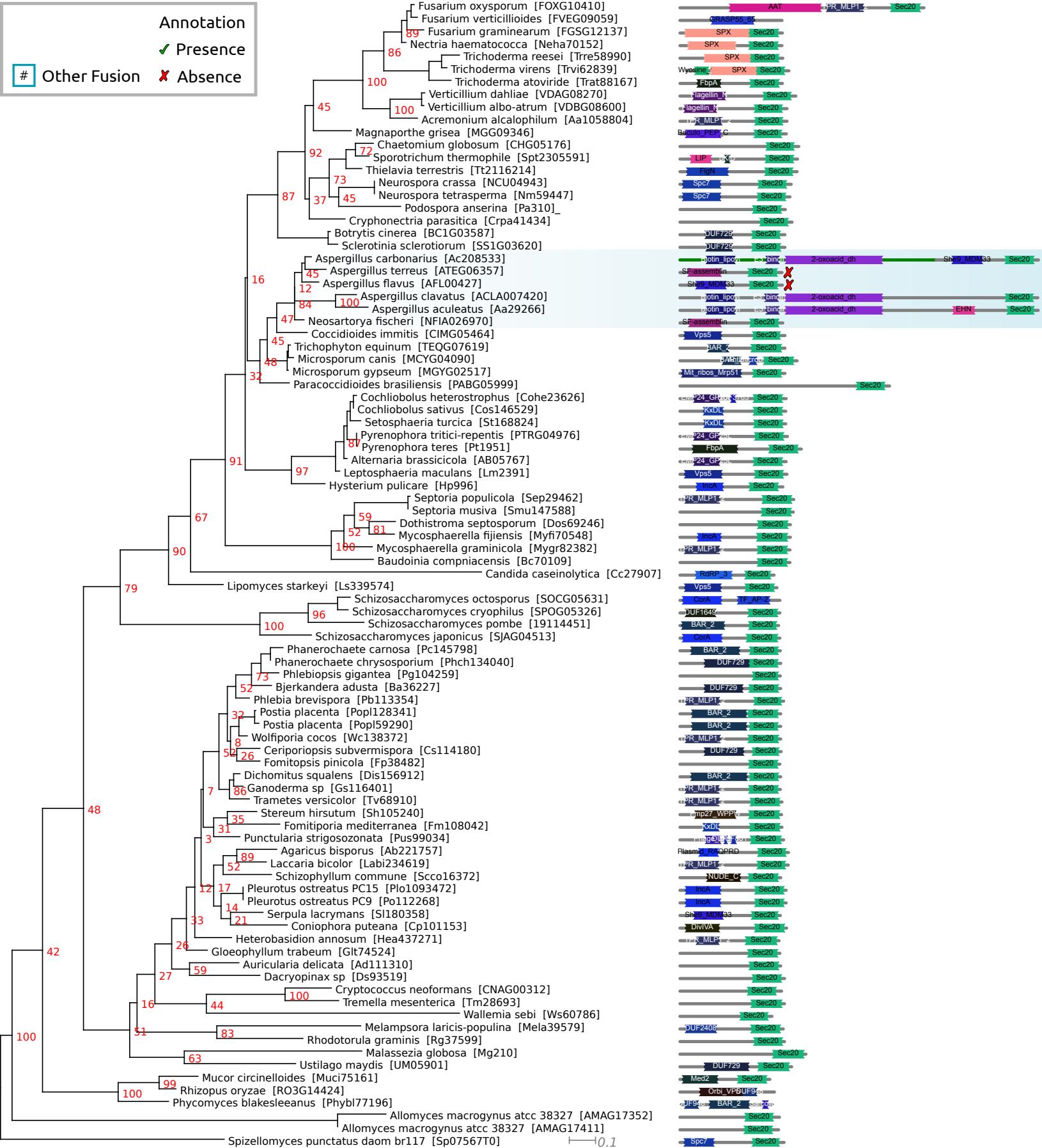


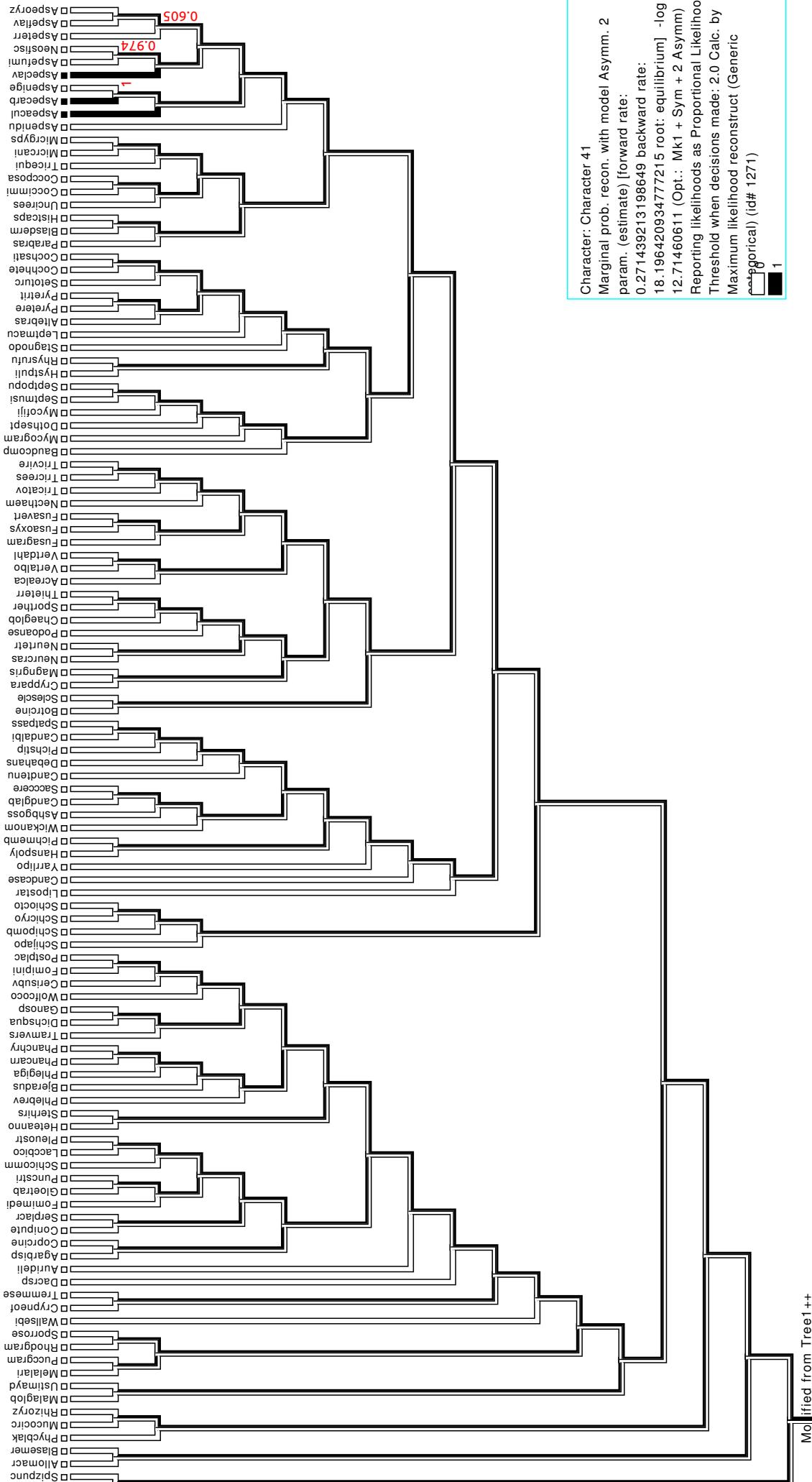
Annotation

✓ Presence

Other Fusion

✗ Absence





Putative Fusion 41

September 27, 2012

1 Fasta Sequences

These are the unfused sequences identified by fdfBLAST belonging to the putative gene fusion in FASTA format. Accessions may be shortened, but belong to either the taxons individual genome project or NCBI's accession numbering.

```
>EGZ73980_F41
MSASPTACQDLARSVLENISGINRALNVT PDDVNGVDSDPKINETHDGHNDKATTEAGNE
AAGTVEAVKQEASRSPVESFHEPPFSWLQPHALFVIIMVGPEGMPFGIQKDFLCAKSSYY
RRYFREKAANNESVEDVVELRDASVDVFGYTQHYLYTGHVYPDTPPDYEVЛИGWLGHС
LGIDGLCDATIDAMIEYRRITNSIPATALLVQVWDETPEGSSIRKLLSWAADYMRASED
RAEFAKALPQEVLSELVVAMSSL DATPAPAATPSSPVSQGVVNSAHQGWHDAVANC DGEQ
ARP AKRARYSDAGHTNGAKATPNGRKGPGRPSTTGPKTGQKRKYNVANGEVELTSKKLA
FCDDLLTRMLSGPGFWTRLVGPFRDPVNPE SDGVPDYFDKVAKPMDLQTMRACKMDRNEYA
DENEF LADMNQIFNNCYTYWAKKDPMWQACERLQKTFEDKYSQMSKWIAKMEGQEGSN
```

2 Annotated Phylogenograms

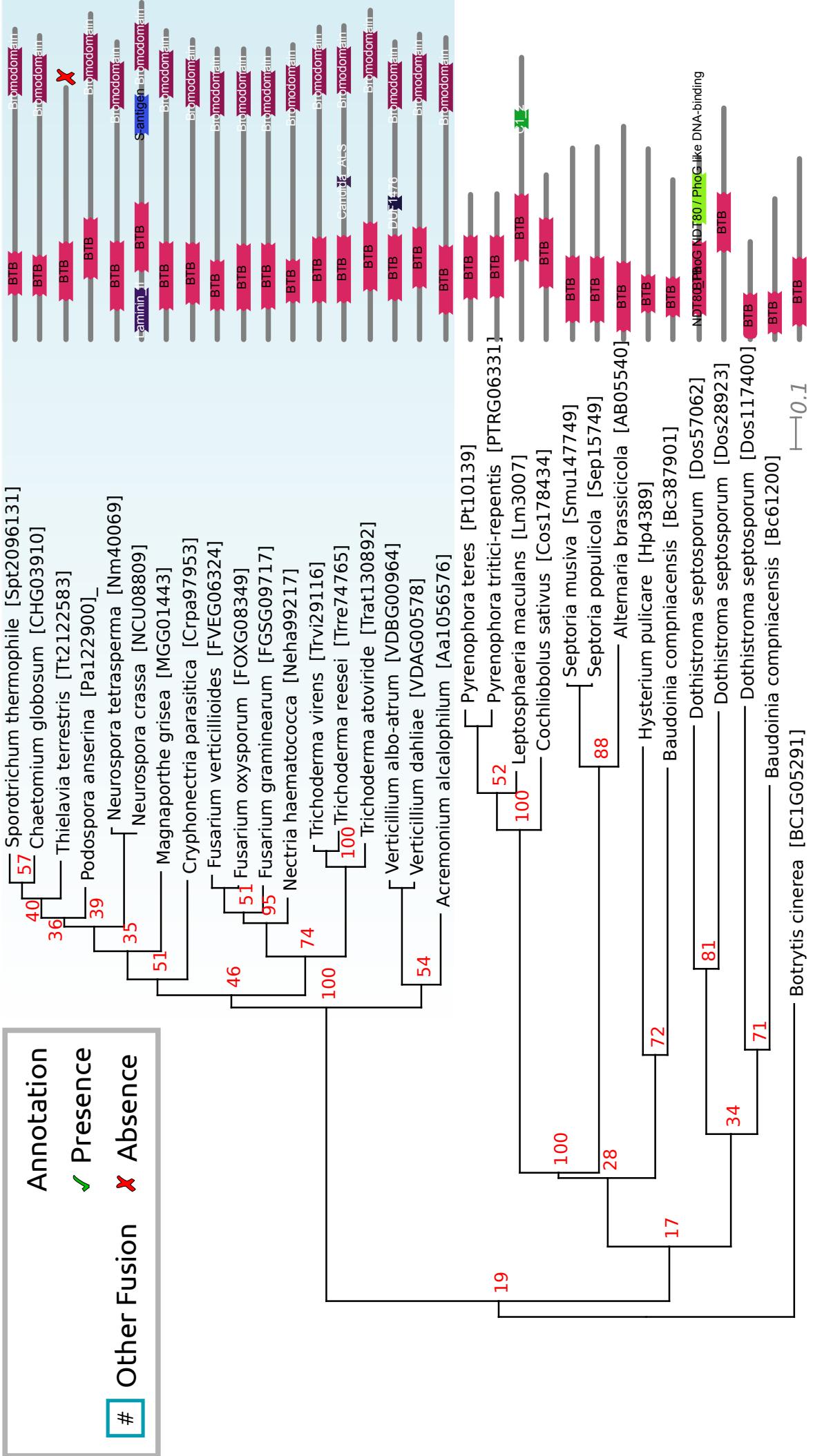
All trees were generated from an initial run of Darren's Orchard pipeline against 139 taxa (Table S1), using the above corresponding un-fused sequences as BLAST seeds. The alignments were then checked for any missing taxa, manually masked and then ProtTest3 was run, please see the Methods section for detail. The final trees were generated by the following command:

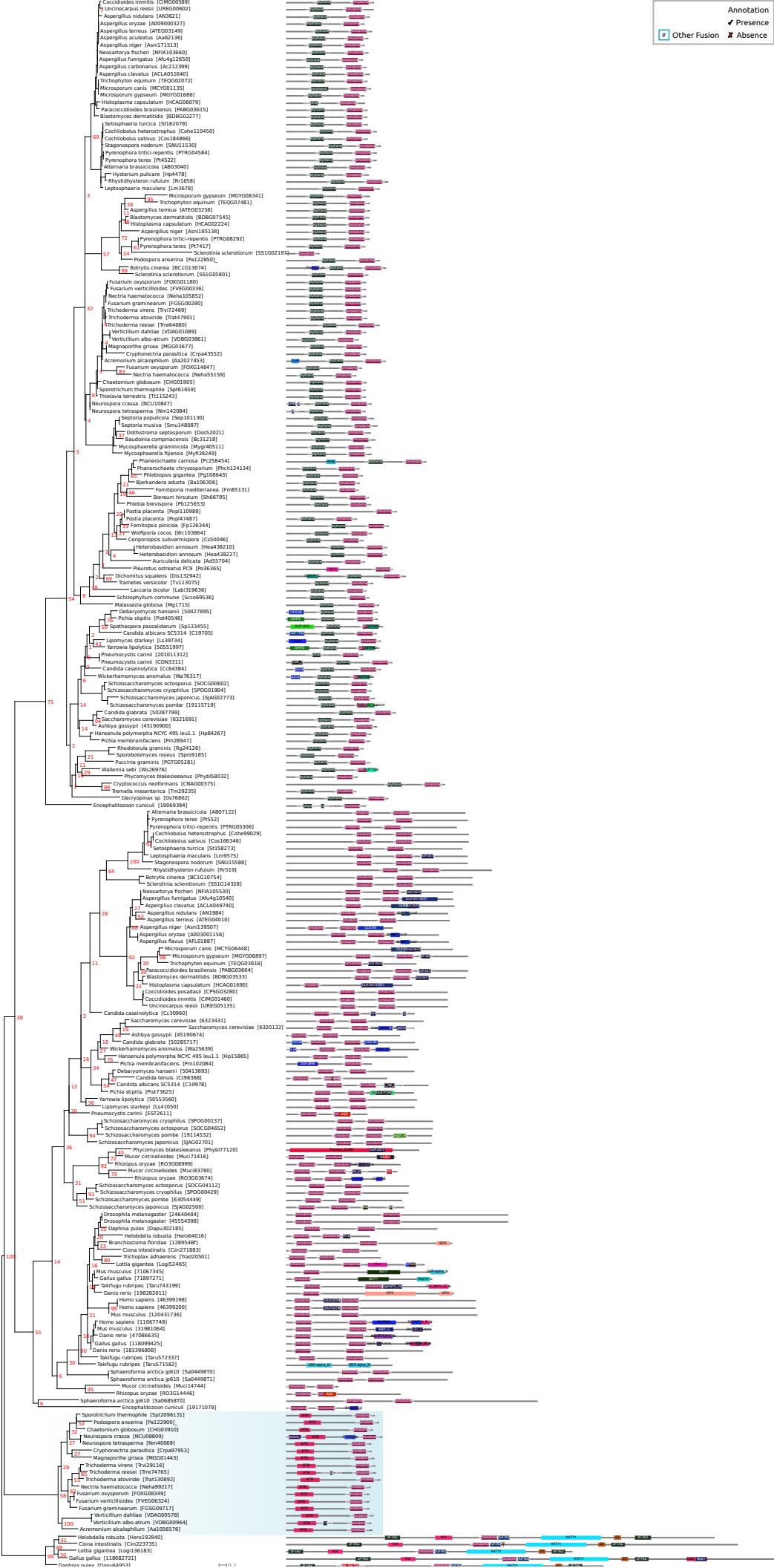
```
phyml -i alignment_file -d aa -b 100 -m model -c 8 -v invariant_sites -s BEST --quiet -a gamma
```

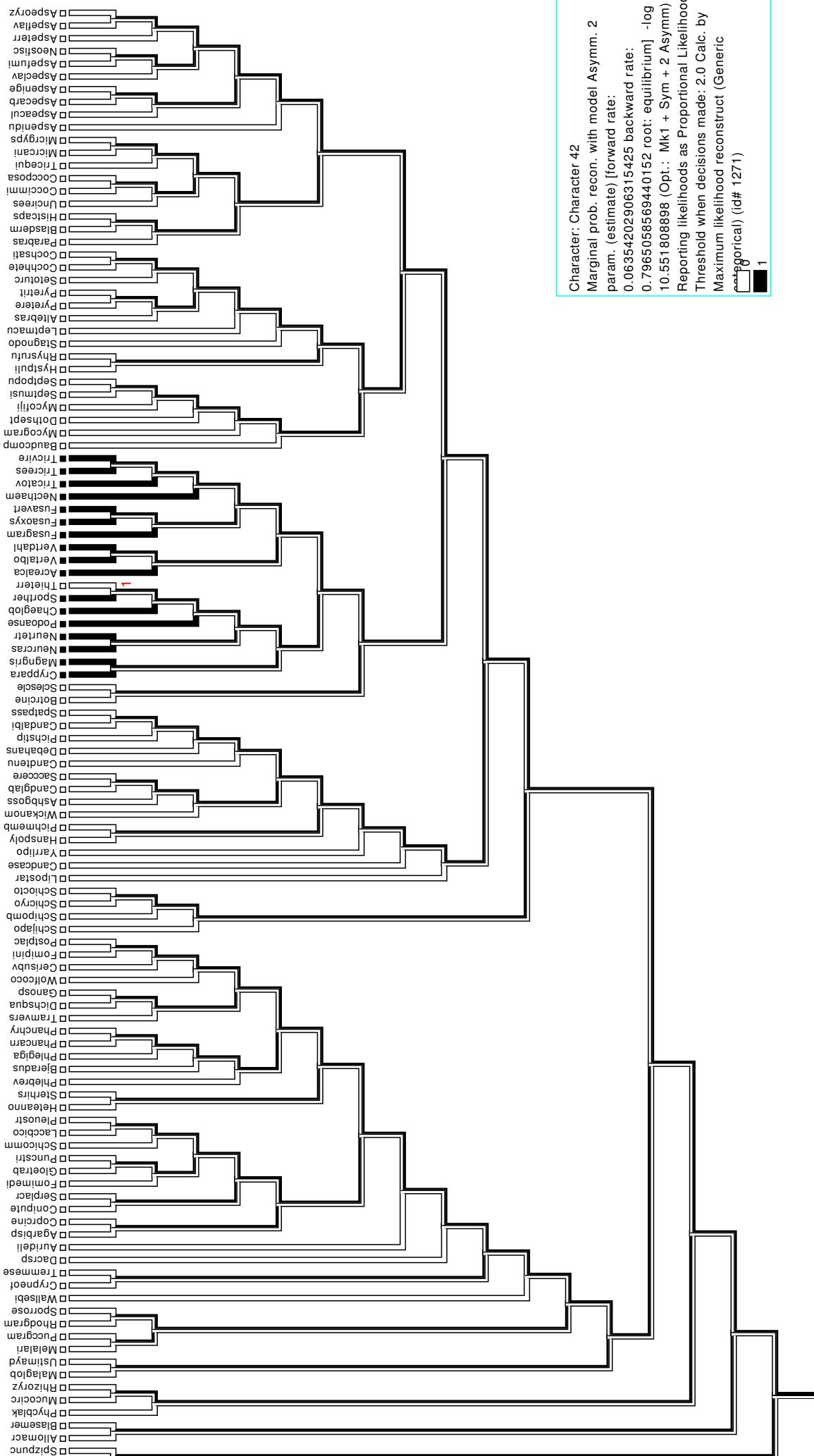
Styling and annotation was made possible by Dendroscope and Inkscape.

3 Mesquite Cladogram

This tree is the 68-gene concatenated phylogeny (Fig. 1), with the presence of a fusion (black), presence of a fission (white), and absent/undetermined (grey) status of gene fusion characters plotted on to it using a "1/0/-" nexus-style data matrix. We used the program 'Mesquite' to calculate proportional likelihoods based on either an "Mk1" or "Assym. 2 param model." (see Table S4) of character change across the fungal phylogeny (Fig. 1). This allowed for a proportional likelihood of the position of the fusion/fission to be calculated.







Putative Fusion 42

September 27, 2012

1 Fasta Sequences

These are the unfused sequences identified by fdfBLAST belonging to the putative gene fusion in FASTA format. Accessions may be shortened, but belong to either the taxons individual genome project or NCBI's accession numbering.

```
>XP_0033012721Pyte_dom1
MAGRLSDMSASPRTGKRNRGILPPANQPTRLCKLATPDTVRRESYNCNMSEERRPRSRF
DSDDNDRVPVRSRFDTDRRSRSPRKESESHARSPIAREGNESPAATSLKNKAAAAAAA
AARINAQIQAQKGIQHVVEVPPIRSAAPTAAVKSPSSNSAAISNETYQQDGFIFK DIEI
NDLRNRYTLTKGATQKRDHAFSGSAALPFIGVVELESDIKDETGADVTTRGEYPDKNM
ATATNPPLYLRITSTSKEGLDAIEEMMKEIDLPNLVDERFRREPENFERDEFGR
KWPEEKISVNLEPINGFNLRAQVVGRRGGDNVKYIQQETGCKVQIKGRGSGFMEPNSGQES
DEPMYLHIAGPRPEGVAYAKQLCEELKEVKTDYHAYKERPPPNNRYGDRDGYSGRPGY
DRGDRGDRERNNSYGYGGGGGGGGSGYGGGAGGGYGGQGGYGGHNGYAAQDTLMSPAAT
PTADANAQAYDANATQAAWAAYYAQNPEADPYAAYGGYQAYMQQYAAQSGYGTQSP
APAPGAGAAAPPPPSDGYGAPPPPPAASPPNYGATRLLSSLRQTSQRCLATSH
>XP_0033012721Pyte_dom2
NPPTARNVDIASRTPPYAKLLSRLLEVRRVLGSSRQLTLAEKILYSHLD SPEESLLSNTN
GGRDVRGQANLKLKPDRVMQDASAQM ALLQFMSCGLPSTA VPASIHC DHLIVGEKGADT
DLPQSITGNKEIFDFLESAAKKY GIEFWPPGAGIIHQSVLENYSAPGLMM LGTD SHSPNA
GGLGAIIVVGGA DAVALVDAPWELKAP KILGVKLTGE LSGWASP KDVILKLAGQLTVR
GGTGFII EYFGPGVQ TLSC TGMATIC NMGA EVGATT SLFP SPAH IPIYLQATH RGPI AEA
AAKIAQSPM QQNLLRPDPEAVYDKVIEINLSELEPHINGPFTPDLSKFKSVVEENG
WP KTFGAGLIGSCTN SSYQDMTRSEEIVKQASAAGLKPRADFFITPGSEQIRATLERDDT
LSTFTEAGGTRTDEVKKGESNAILTSYNRNFPG RNDGNR ATMNFLASPELITAMSYGST
TFNPMTDSIPTPSGEPKFAPPKGSDLPSAGFADGNPDFMPTPGVPDPSVEVVVSPSSR
LALLDPFAFPDSFTGLRVLYKVKGQCTTD TISAAGPWLK YKGHL PNISENTLIGAVNA
QTDEVNVAYDV DGKTSSIPELA KRWRDQGV EWL VVAEHN YGE GSARE HA ALQPRYLGRI
ILAKSFARIHETNLKKQGIIP LT FANE ADYDL FAAC DEVATRG LLDV LRSGGKGEVELVL
KKKD GSEKVIKT KHTL SHDC QCGF VL AGSALN LLARQGREI KEEV TRSA ELTD
```

2 Annotated Phylogenograms

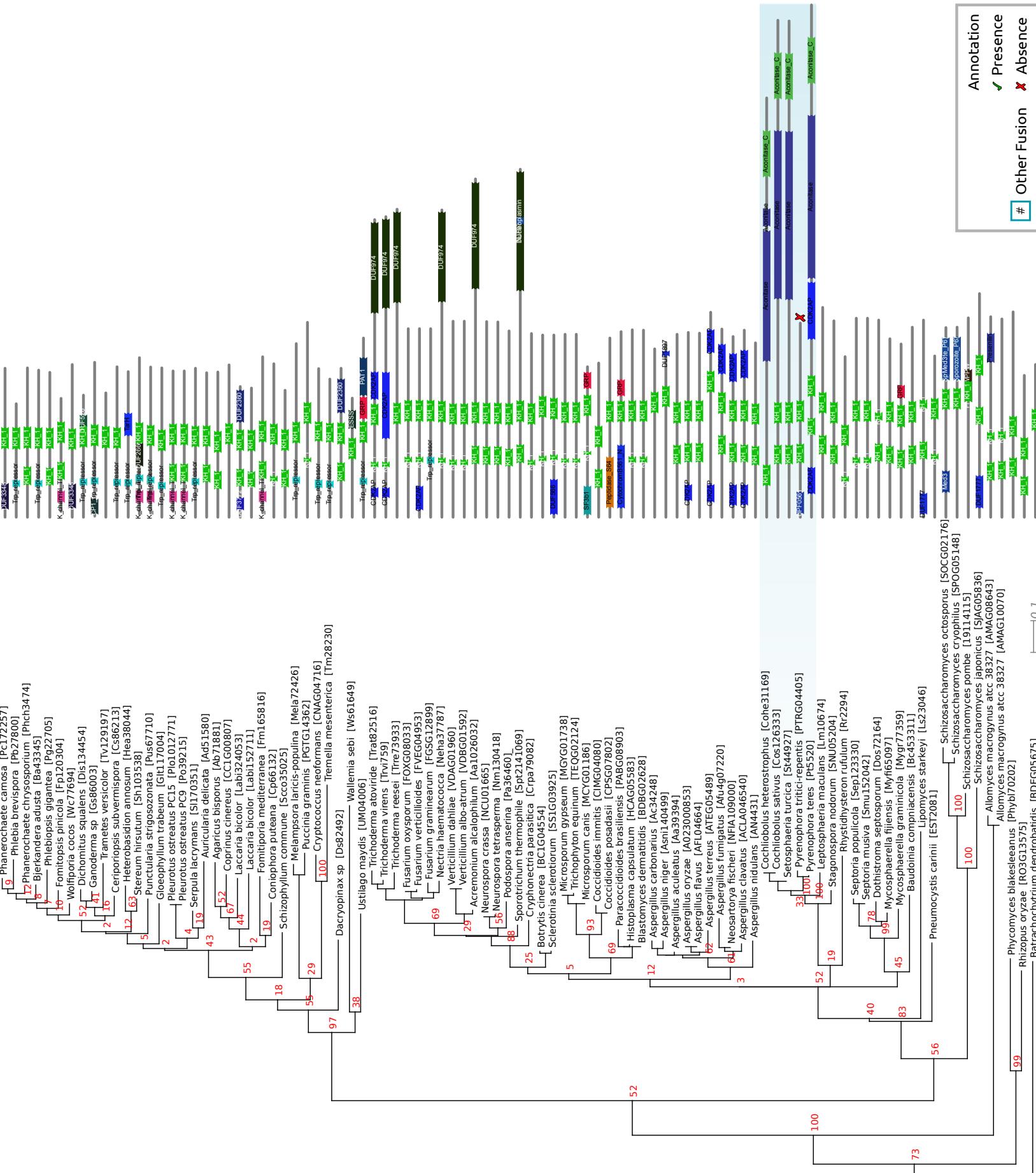
All trees were generated from an initial run of Darren's Orchard pipeline against 139 taxa (Table S1), using the above corresponding un-fused sequences as BLAST seeds. The alignments were then checked for any missing taxa, manually masked and then ProtTest3 was run, please see the Methods section for detail. The final trees were generated by the following command:

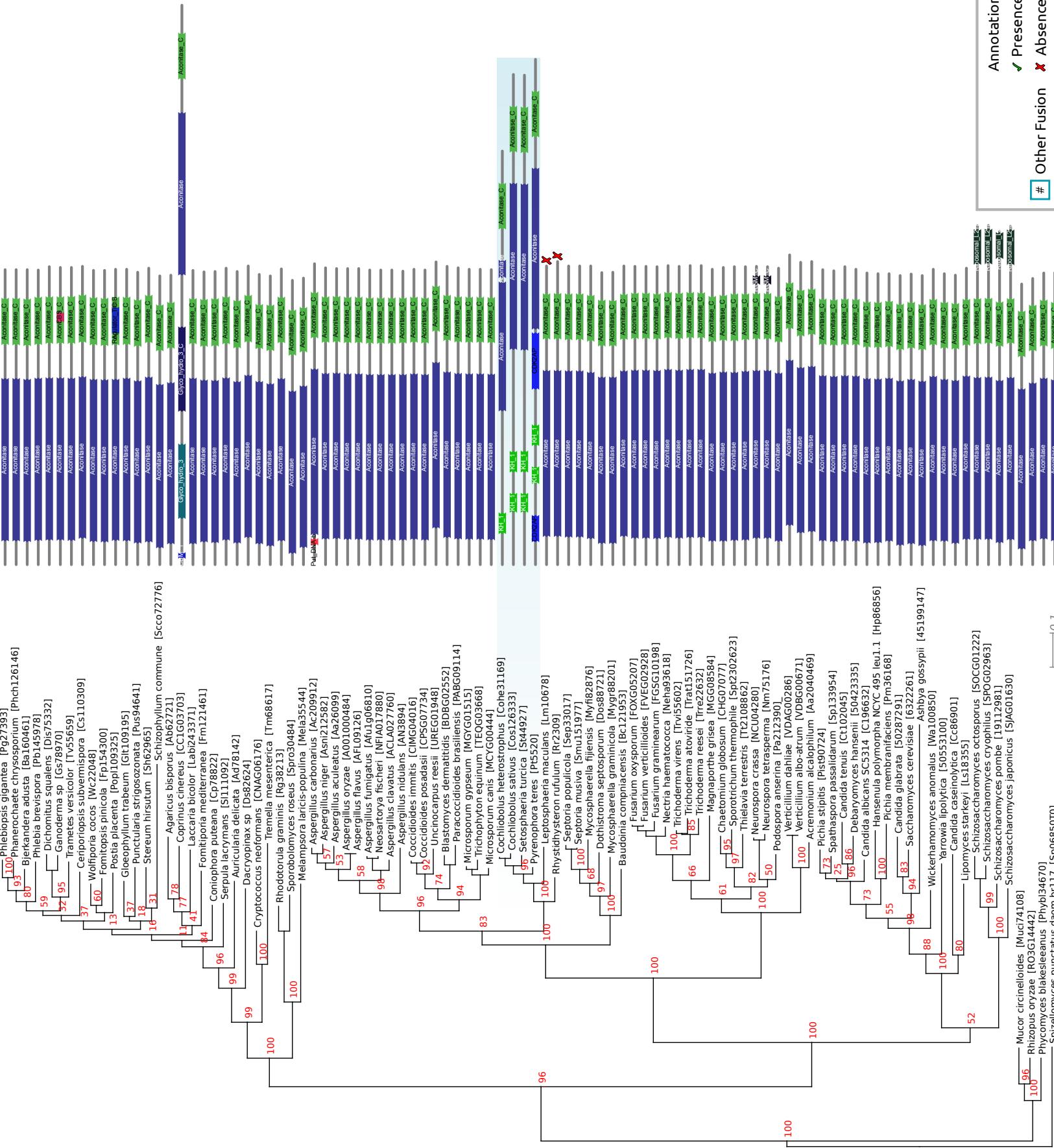
```
phylml -i alignment_file -d aa -b 100 -m model -c 8 -v invariant_sites -s BEST --quiet -a gamma
```

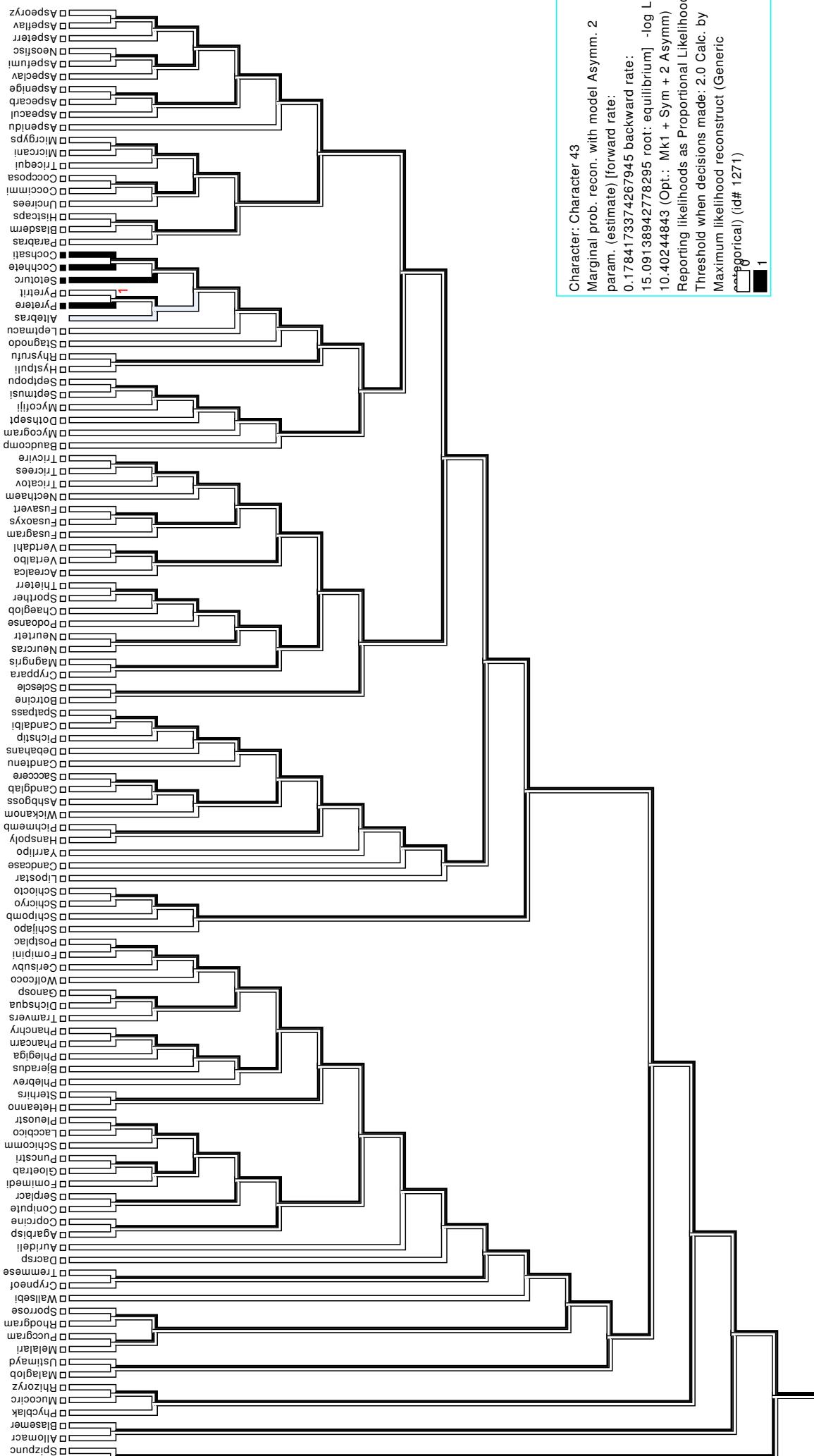
Styling and annotation was made possible by Dendroscope and Inkscape.

3 Mesquite Cladogram

This tree is the 68-gene concatenated phylogeny (Fig. 1), with the presence of a fusion (black), presence of a fission (white), and absent/undetermined (grey) status of gene fusion characters plotted on to it using a "1/0/-" nexus-style data matrix. We used the program 'Mesquite' to calculate proportional likelihoods based on either an "Mk1" or "Assym. 2 param model." (see Table S4) of character change across the fungal phylogeny (Fig. 1). This allowed for a proportional likelihood of the position of the fusion/fission to be calculated.







Putative Fusion 43

September 27, 2012

1 Fasta Sequences

These are the unfused sequences identified by fdfBLAST belonging to the putative gene fusion in FASTA format. Accessions may be shortened, but belong to either the taxons individual genome project or NCBI's accession numbering.

```
>XP_0033035321Pyte_dom1
MFGSSQDRARQLAGRNRERISSISSCSSLRSVSSSRAPPLRNRQSTLDSTIPSPSAVE
EHAACDESGTILGPHALEGQNQHAAEGPPVSALQLASGQGGSQVEQHRRQAEHLSQVLY
NGFALEPSVSPQSQFSLSHQTRHSTMGSQLDTALRLRNITASDPSSHLDPSLLKLLDS
FNATTGIRLASMPDHDPTSLTTVSLRGGEVDIPLPAPYFPNNRSDYGDYVAWKRHYYRL
MFRLDLDVSGAYHRTFSQQRQHFITPDFCAELQFLSQIPNSPNILVTSGYEYYGNVTGPN
PVASSSATKSTLNTLFNNYVEAGAQDKDIVGVEGTMQYFVEVDVDAEGLDALVALEIVQA
PTIGEMSREGFVNCGSERGCDTVDKQKRYIKTLKREMPGSKDLFTRVYRHTFPIAKTAGQ
KAVALDVALVYWELLFSSPLSAVKWSSPNTPWLTWWTEFLTSYKKSVNKDMWNETLKFA
>XP_0033035321Pyte_dom2
QLTLEDEAMSFWTEESSWPSVIDDFVDWVKKEKRGDVPEEMVAAKHVPIVKKHKRFNR
HQSDRFMCVDPSWRKPKGIDNRVRRFKGQAAMPKIGYGSNRKTRHMMPGKAFVVNNV
ADVDLLLHNSTFAAEIAHAVSARKRIDIIARAKQIGVKVTNGKARVKTES
```

2 Annotated Phylogenograms

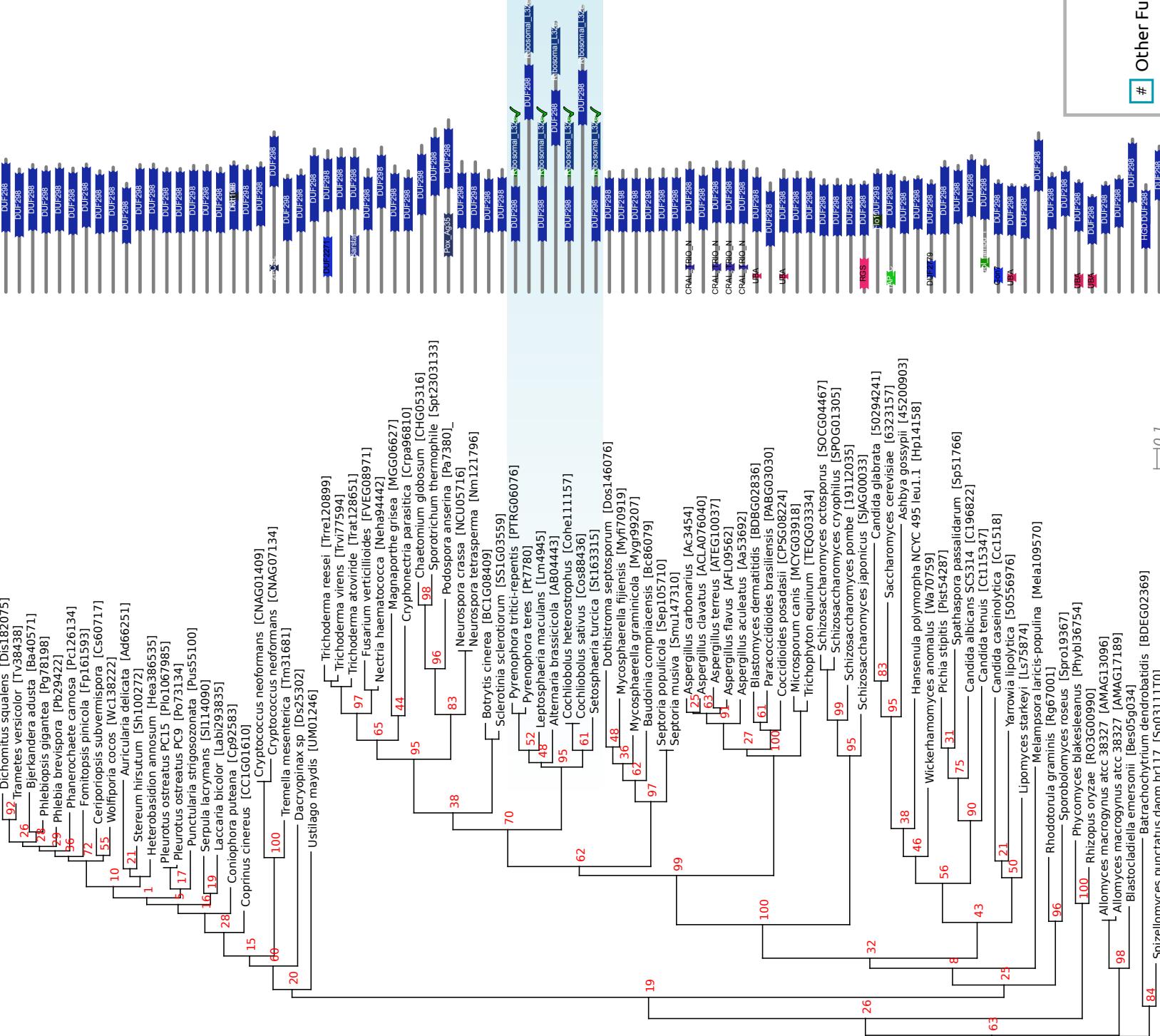
All trees were generated from an initial run of Darren's Orchard pipeline against 139 taxa (Table S1), using the above corresponding un-fused sequences as BLAST seeds. The alignments were then checked for any missing taxa, manually masked and then ProtTest3 was run, please see the Methods section for detail. The final trees were generated by the following command:

```
phylml -i alignment_file -d aa -b 100 -m model -c 8 -v invariant_sites -s BEST --quiet -a gamma
```

Styling and annotation was made possible by Dendroscope and Inkscape.

3 Mesquite Cladogram

This tree is the 68-gene concatenated phylogeny (Fig. 1), with the presence of a fusion (black), presence of a fission (white), and absent/undetermined (grey) status of gene fusion characters plotted on to it using a "1/0/-" nexus-style data matrix. We used the program 'Mesquite' to calculate proportional likelihoods based on either an "Mk1" or "Assym. 2 param model." (see Table S4) of character change across the fungal phylogeny (Fig. 1). This allowed for a proportional likelihood of the position of the fusion/fission to be calculated.

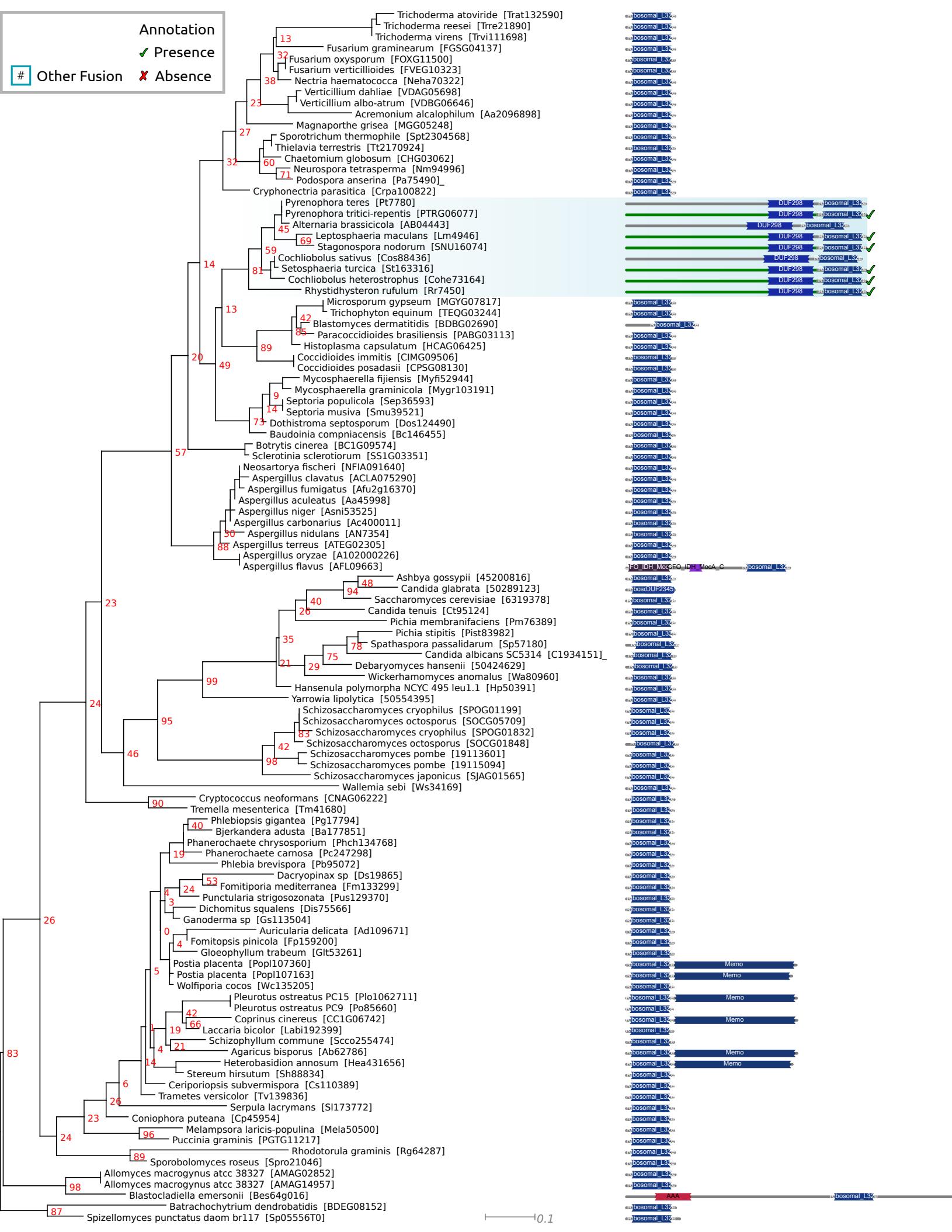


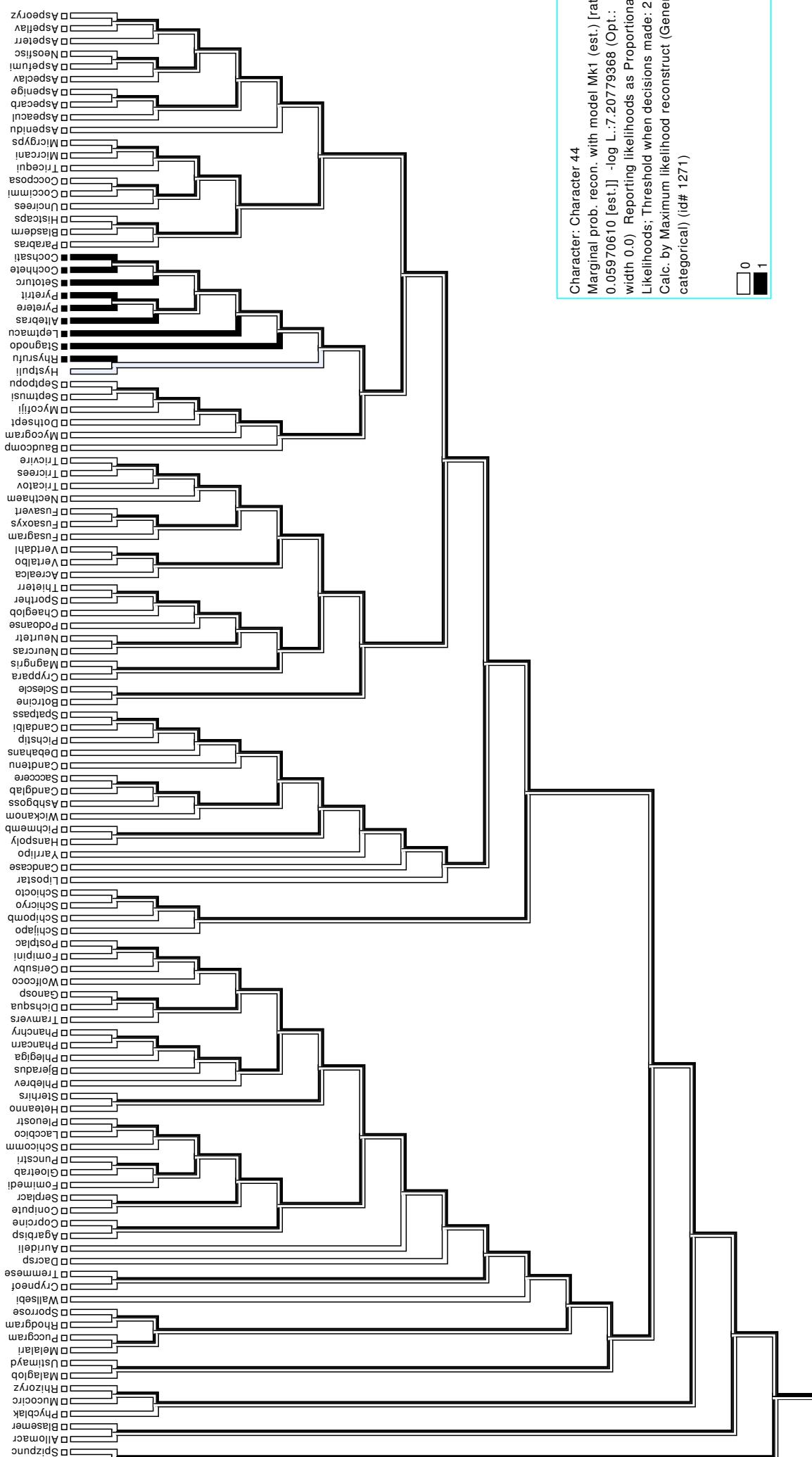
Other Fusion

Annotation

✓ Presence

✗ Absence





Character: Character 44
Marginal prob. recon. with
0.0597061 [est.] - log
width 0.0 Reporting like
Likelihoods; Threshold w
Calc. by Maximum likelih
categorical) (id# 1271)

Putative Fusion 44

September 27, 2012

1 Fasta Sequences

These are the unfused sequences identified by fdfBLAST belonging to the putative gene fusion in FASTA format. Accessions may be shortened, but belong to either the taxons individual genome project or NCBI's accession numbering.

```
>EHA223441Asni_dom1
MDGNPSTPPRSALVLYGSETGNSQEVAEELGALAERLHFHTHVGEMNEYRPEVLKSHTL
VIFVVATTGQGDFPANARSFWRSLLKRLPGDFLDGVQFASFGLGDSSYPKFNWAARKLH
KRLLQLGANEIYDAGEADQQHPEGWPIPDDVQLPPKWILKLQEGNAATAQEGHAVPGTHE
NLPAPEENPKLTRLHDLRPLPDTLTATLRENKRLTPQKHWDVRHVSLSVPEHTSYVPG
DMLCITPKNFSADVDALIQMMGWEDKADQLICLVPNSHIPADDLPLPIRGLDSYPQLTL
RALLTDYLDIQAIPRRSFFAEIAHYTNDEMHKERLEFTYTTSPEYLDLDELWDYTTPRRSI
LEVLFEDTVKVPWQHAIISVFPVLKGRQFSIASGGELKRGPEGTKFELMIAIVKYQTVI
KKIRQGVCTRYISALRPGSTLKVQLQRGGLNSSVNQLVGPTVLVGPGLAPLRSMLWEK
AAIIKAYQEENPGVELGIGPTLLLGYGRNREADFFFDEWEWQQLGQLTKLNVLTAFSRDQK
QKVYVQDVIRQNYALLFKLLHDMAGSVYICGSSGQMPKAVREALTEAFQHGAEVETDRFN
>EHA223441Asni_dom2
EQGAEQYLLGMKTGRAAAAPTDRCLSTLPSKRLLARLKIPPLHNIVIMSGLRILVPVKR
VIDYAVKPRVNKANTGVETAGVKHSLNPFDELSVEEAIRLERRGAKNQSPMKVENILALS
AGGAKCADTLRTAMAMGADRAFHVDVGESPDDGPEPLTIAKMLQGVVKSENIINLVLLGKQ
AIDGDQGQTGQMLLAGLLGPQATQASKVDIKDADGTVEVTHEVDGGVETLRAKLPMVITT
DLRLNEPRYATLPNIMKAKKKPLEKKTADFGVEDKKRLKTLVTEPPARQGGGKVEDVD
GLIGKLKELGAL
```

2 Annotated Phylogenograms

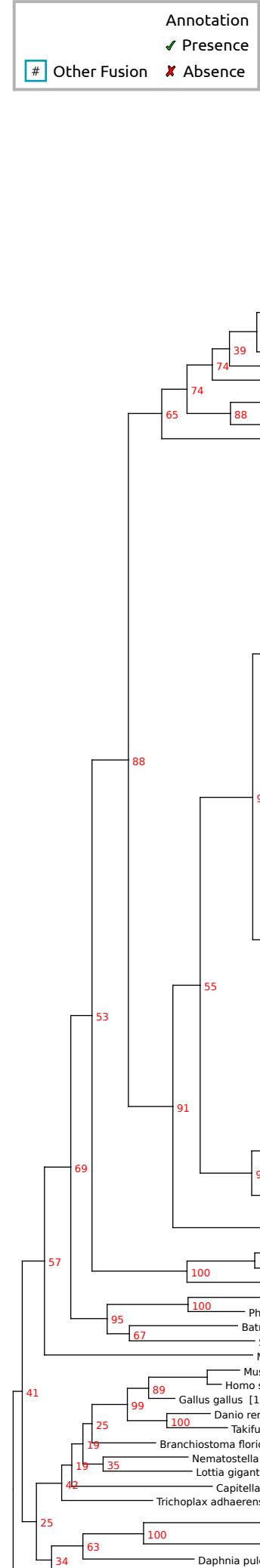
All trees were generated from an initial run of Darren's Orchard pipeline against 139 taxa (Table S1), using the above corresponding un-fused sequences as BLAST seeds. The alignments were then checked for any missing taxa, manually masked and then ProtTest3 was run, please see the Methods section for detail. The final trees were generated by the following command:

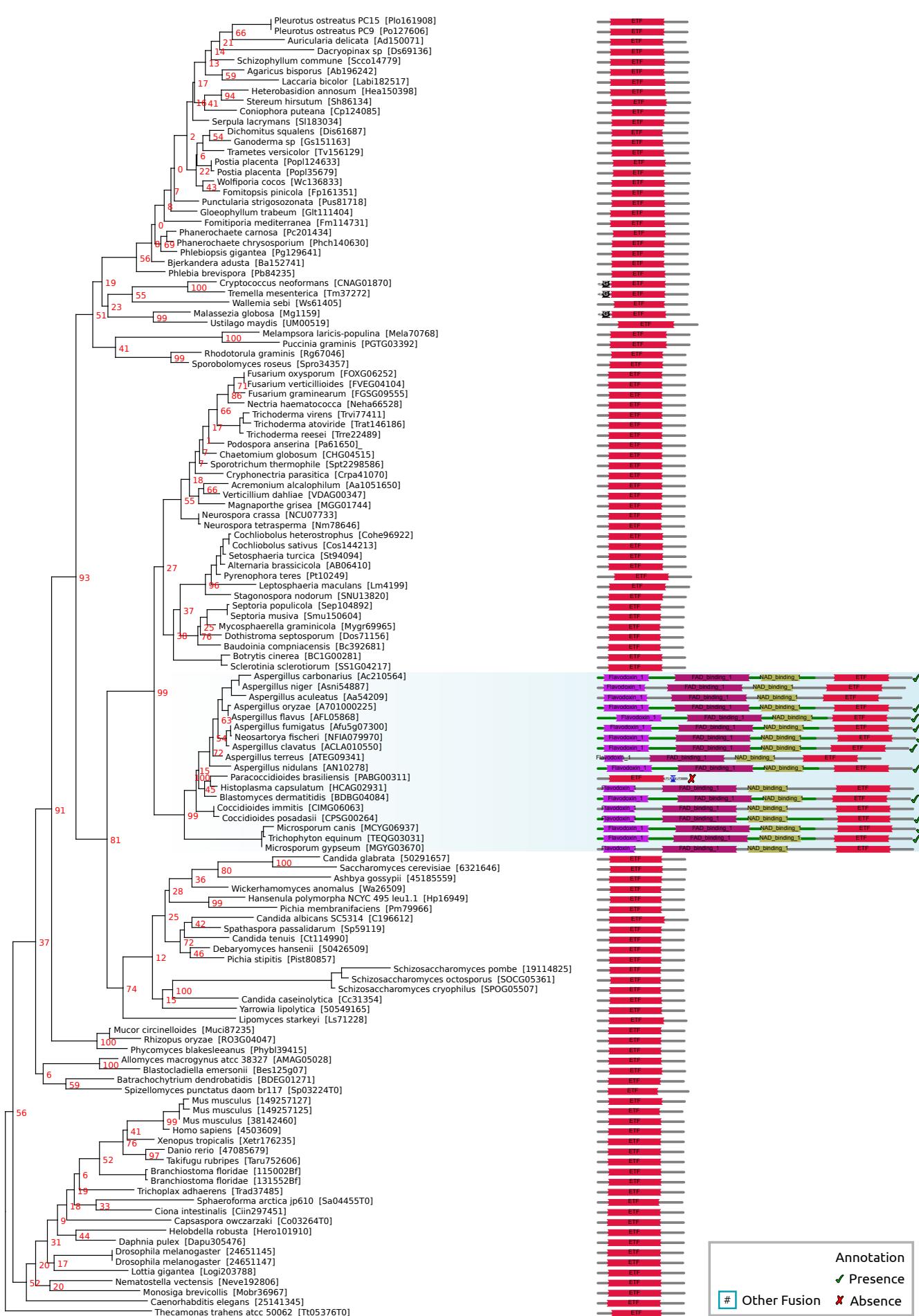
```
phyml -i alignment_file -d aa -b 100 -m model -c 8 -v invariant_sites -s BEST --quiet -a gamma
```

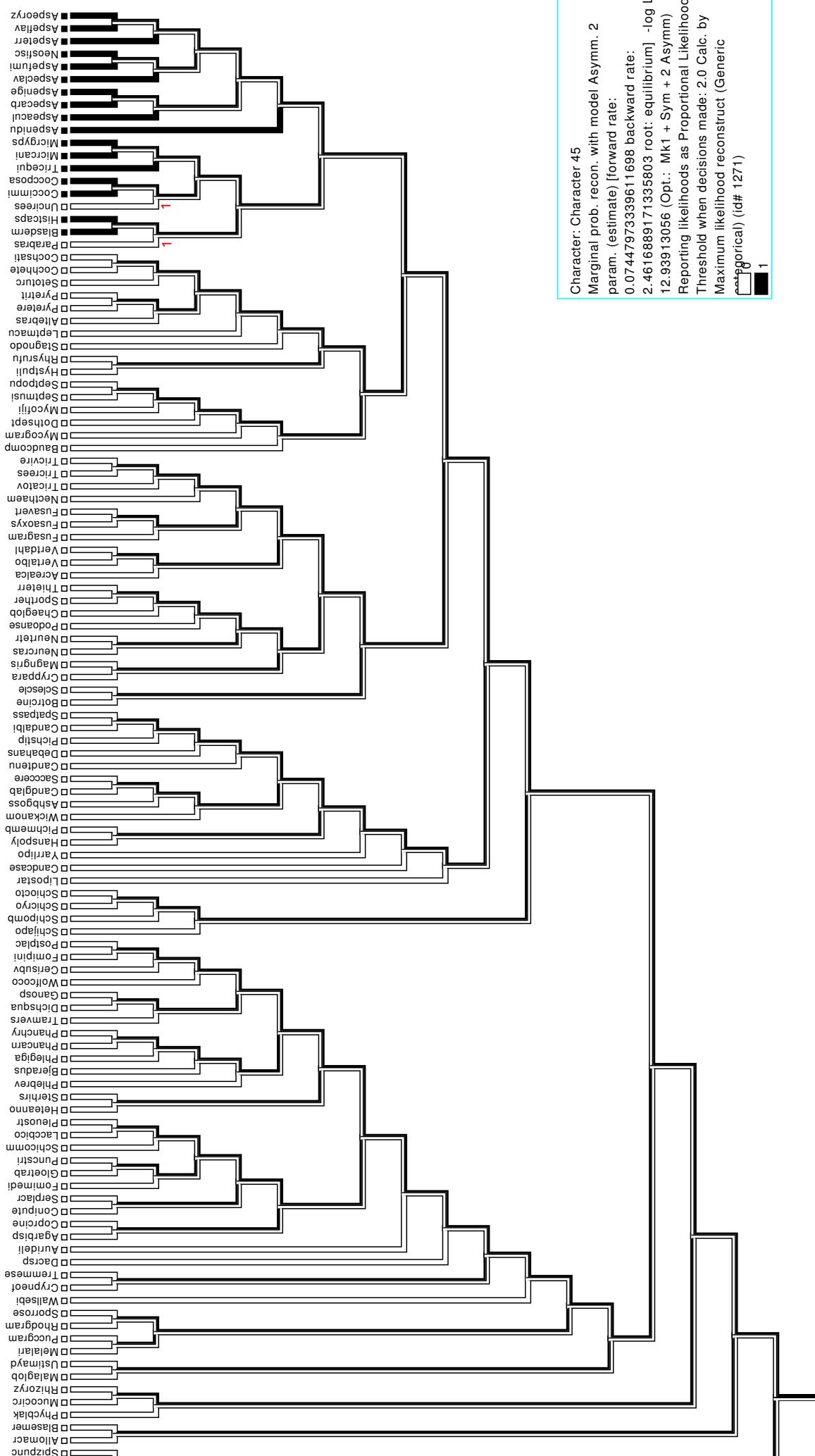
Styling and annotation was made possible by Dendroscope and Inkscape.

3 Mesquite Cladogram

This tree is the 68-gene concatenated phylogeny (Fig. 1), with the presence of a fusion (black), presence of a fission (white), and absent/undetermined (grey) status of gene fusion characters plotted on to it using a "1/0/-" nexus-style data matrix. We used the program 'Mesquite' to calculate proportional likelihoods based on either an "Mk1" or "Assym. 2 param model." (see Table S4) of character change across the fungal phylogeny (Fig. 1). This allowed for a proportional likelihood of the position of the fusion/fission to be calculated.







Putative Fusion 45

September 28, 2012

1 Fasta Sequences

These are the unfused sequences identified by fdfBLAST belonging to the putative gene fusion in FASTA format. Accessions may be shortened, but belong to either the taxons individual genome project or NCBI's accession numbering.

```
>EG0052791Sela_dom1
MASFEDYDEFGNYIGGDLASDEDDILQPDRPPVQEQQPATLEGYDDEPMGVQEDGALME
IDEPVHNAVVLHEDKQYYPSASDVYGADVETLVQEEADAQPLSEPIVAPIKVRKWTVEEKD
MPETRFDKGFLNMMSPDMIRNVAVVGHLLHGKTALVDMLVFETHKLIWDADQPTRYTD
THILSRERRISIKSSPMSLVLSTTSGKSHLVHLIDTPGHVNPFDEVASAMRLVDGIILVV
DVVEGMMINTEHIIRHAMQEGIKMTLVNKIDRLILELRIPADAYYKIKHTIEINTFI
SGIDDPDPLRLTPENGNAFASTDNNWCFTLRSFAQMYADTYGSLDVQSFADRLWGDIFF
NEETRKFRKQADPEQSRTFVHFIMDPLYKLYSHVLSQETDDLKQTLEGGLGIRLKPVMYK
MDVRPLLKAALDQFFGPSTGLVDMIAEHIPSPVEGASGKVERTYGPQTSVLVATMKACD
AEGPVMVQITKLYHTTDAQSFRSFGRVISGTIRKGMDIKVLGEGYSPEDEDMMKARVED
IWLSESRYFVPAEEAPAGNLVLLGGVDASISKTATLASVDIDDLHIFRPIKHMTESVLK
>EG0052791Sela_dom2
VAIEPIAPSELPKMLSGLRSINKSYPLAATKVEESEHVLIGTGELYLDCLHDLRKLFS
EIEIKVSDPVTKFCETVLETSALKCYADTPNKKNKITMIAEPLERGVAEDVERGRVTMRM
TPKERGSFFQEKYQWDLLASRSIWAQGPEESGPNIILDDTLPSQVDKMLGTVKEHIKQG
FQWGAREGPLCDEPMRVKFRILDASLAQEPIFRGQQIVPTARRVCYSSFLMATPRLME
PVYYVEVQAPADCISAVYTVLARRGHVTQDIPKAGSPLYTAKLIPVIDANGFETDLRT
ATQGQAFCLQVFDHWSIVPGDPTDTSIKLRPLEPASGQALARDLVLKTRRKGLGDQIAV
SKYLDEFVVTLSVLLAAAASASASDDAKPVFQATEITAPFLEQFTDDWSERWTPSEAT
KKTPVGETFSYVGKWEVEEPETVVVEGDKGLVAKTKAAHHAISAPFSEPISFKDKPLVV
QYEVKYQKGNCGGGVKLEDGFQTSGKEFSDNTPWWVMFGPDLCPTKLFIFRHKN
PITGEYEKHLVPPPKAPEKLTNLYTLIVNPDNTYDVLFNGESQKSGSLLEDFTPNAVNP
SKEIDDPEDTKPEDWVDTKRIADPDATKPADWDEDEPYQIVDEDAEKPEGWLDDEPDTP
DPDAEKPEEWDEEDGDWIAPTVSNPACEEAPGCGAWKAPMKANPAYKGKWWYAPMIDNPA
YIGEWAPRKIANPDFFEDLTPVQSLEKIGGIGIELWTMTEDILFNNIYIGHSAEDAKALA
AETFEVKRPLEVEAKVTLPPDDDEEVSAEDPVAFIRQKVFTFIDLAKLDPVLAFKTQPE
TGVALAGAVFTLFGMIGVLFGLVGAQQKPKITKSSKKTADPTADDKKDESAPVAPAGGEK
KDETPVKKRK
```

2 Annotated Phylogenograms

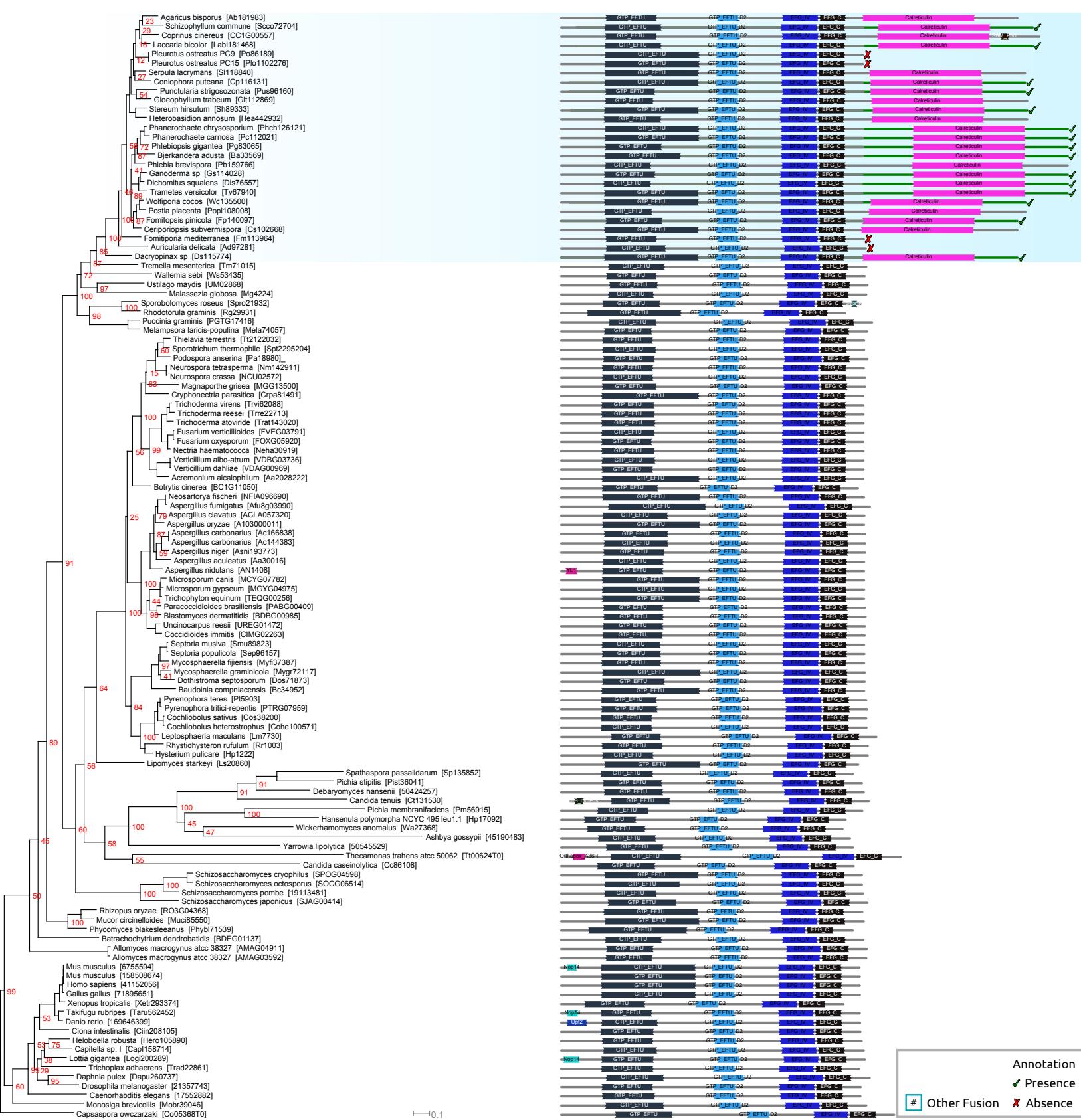
All trees were generated from an initial run of Darren's Orchard pipeline against 139 taxa (Table S1), using the above corresponding un-fused sequences as BLAST seeds. The alignments were then checked for any missing taxa, manually masked and then ProtTest3 was run, please see the Methods section for detail. The final trees were generated by the following command:

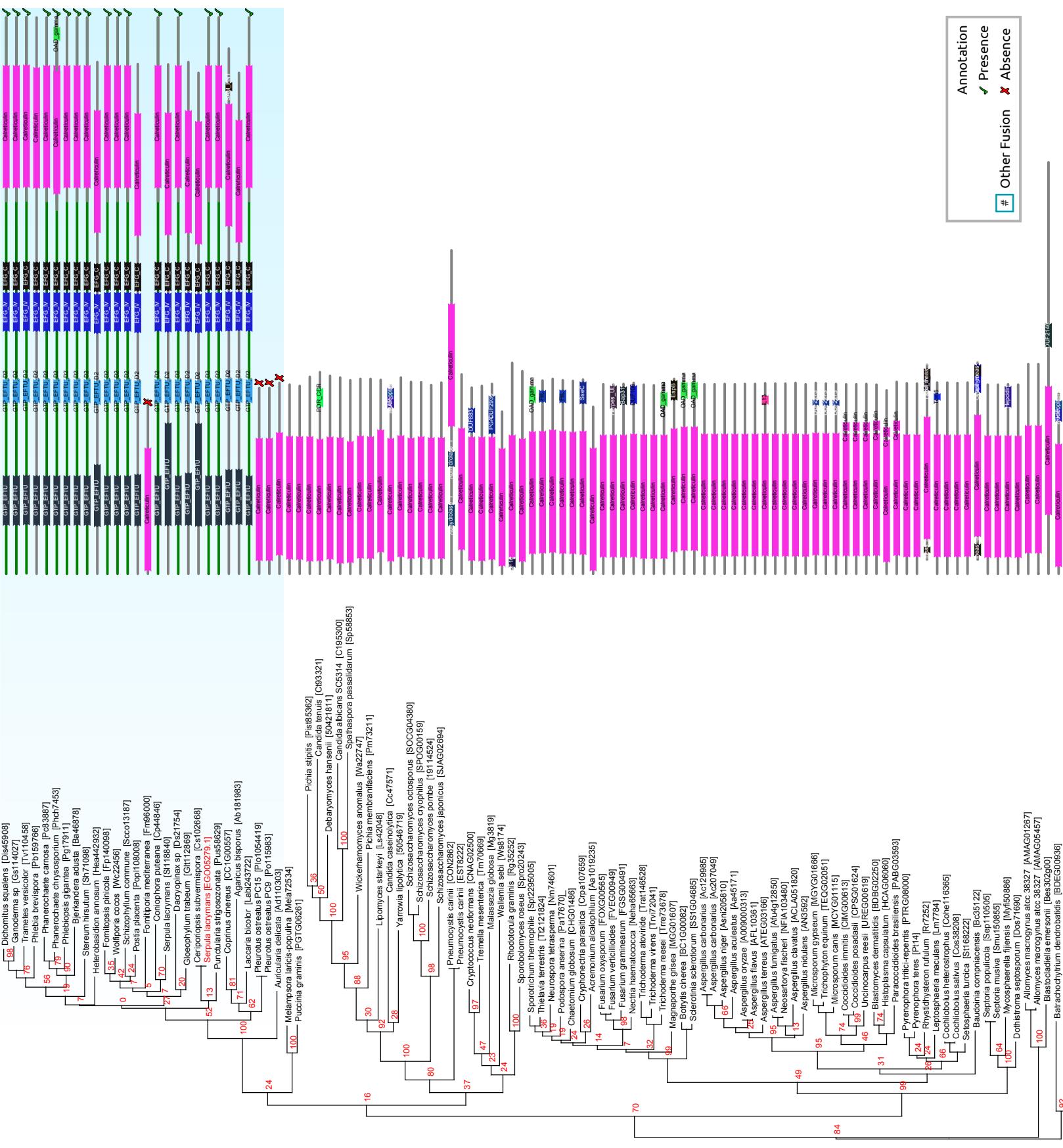
```
phyml -i alignment_file -d aa -b 100 -m model -c 8 -v invariant_sites -s BEST --quiet -a gamma
```

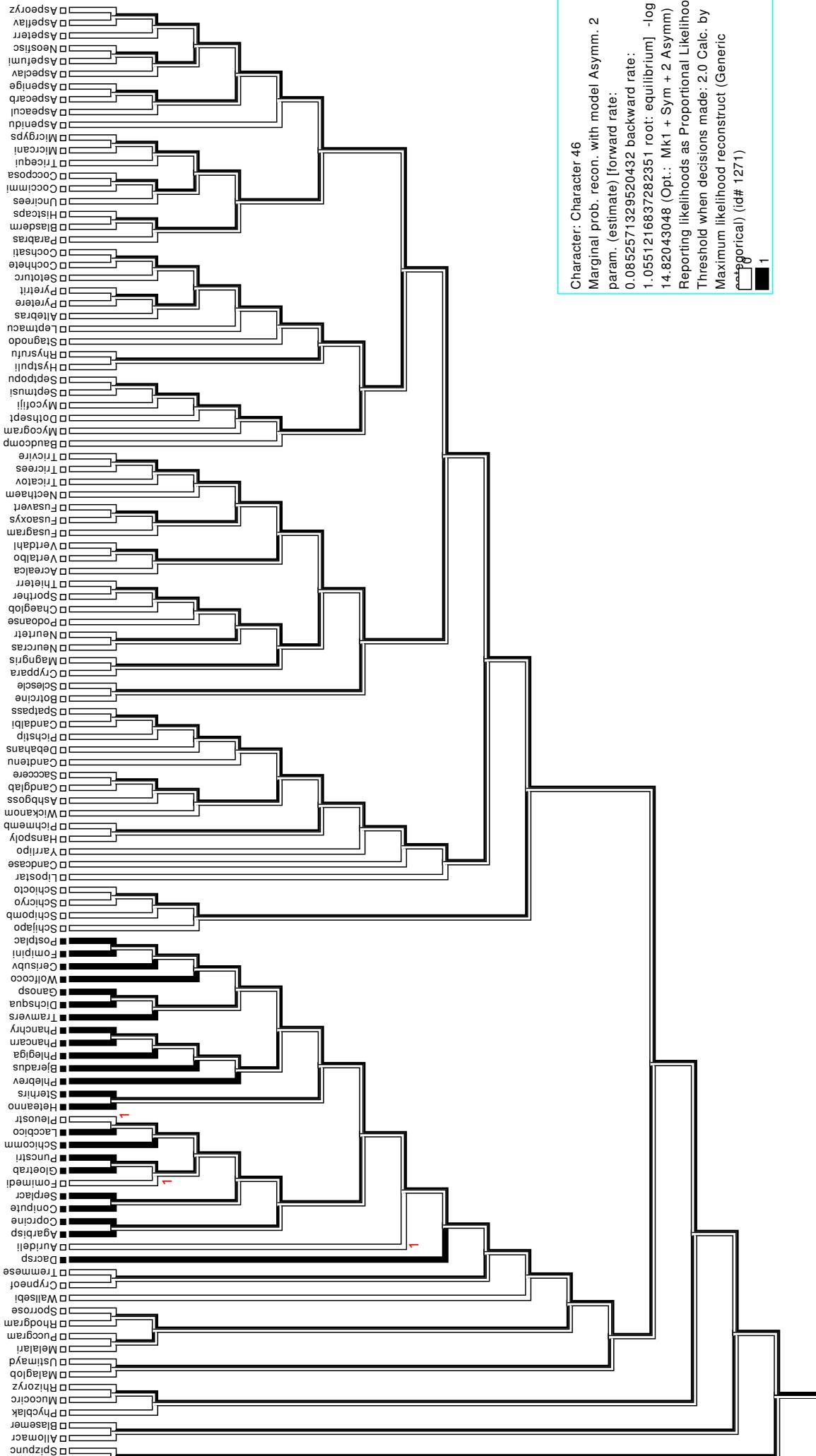
Styling and annotation was made possible by Dendroscope and Inkscape.

3 Mesquite Cladogram

This tree is the 68-gene concatenated phylogeny (Fig. 1), with the presence of a fusion (black), presence of a fission (white), and absent/undetermined (grey) status of gene fusion characters plotted on to it using a "1/0/-" nexus-style data matrix. We used the program 'Mesquite' to calculate proportional likelihoods based on either an "Mk1" or "Assym. 2 param model." (see Table S4) of character change across the fungal phylogeny (Fig. 1). This allowed for a proportional likelihood of the position of the fusion/fission to be calculated.







Putative Fusion 46

September 27, 2012

1 Fasta Sequences

These are the unfused sequences identified by fdfBLAST belonging to the putative gene fusion in FASTA format. Accessions may be shortened, but belong to either the taxons individual genome project or NCBI's accession numbering.

```
>EFY904791Meac_dom1
MEGDEAYGTGGLMDDPEDYYPPSPPPTKQIFGMQNGKQVTLHLVGHSPTEAHHLWNGAMF
ISDYFEQDPSRVEGKSVLELGAAGAGLPSLAVAGILGAKKVVMTDFPDPDLVANMQKNIDEC
NATVEPEGHIERTIDAAGFVWGADPEPLLARLAPGYQKGDRGDGMQQRFDVLVLADLLFR
HSEHGALVKTIKETMRASRDSAAYVFFTSYRPWKQDLDGMFFDVARNAGLEVEQVSERKL
EKPLFEGDPGDLDVQKTVGFIVRWRRVEDSLYIVLHQSKFAAKPPERMPPQTIAQGPLVA
>EFY904791Meac_dom2
VCCGGNSENYGVQRILESDLSGHMPAQKSTGHLAELERDGVVVRGIVTGQKLEELREAS
LKVEKLGSGQWPPIRTVGKQFPPWTSTEKGIGWVQHLMNPDLPGHEIFTRQYFSEEIL
SIVRELLQCDDNELVMELFNMLVRPDEHFELRWHRDDIPAEASAEEEMERLGRPAFHQAQY
NFALWEDESVLVIPGSHKRPRTETERNADPFEKVLPEQLVVKLGPVDIAFYNNNILHRGV
YDSKKDRVTLHGSGVHSGGSKLRARNVLQHGIGGYVDKVDLSDGERQRAEEMRARLV
KLGSESGDVGYSLG
```

2 Annotated Phylogenograms

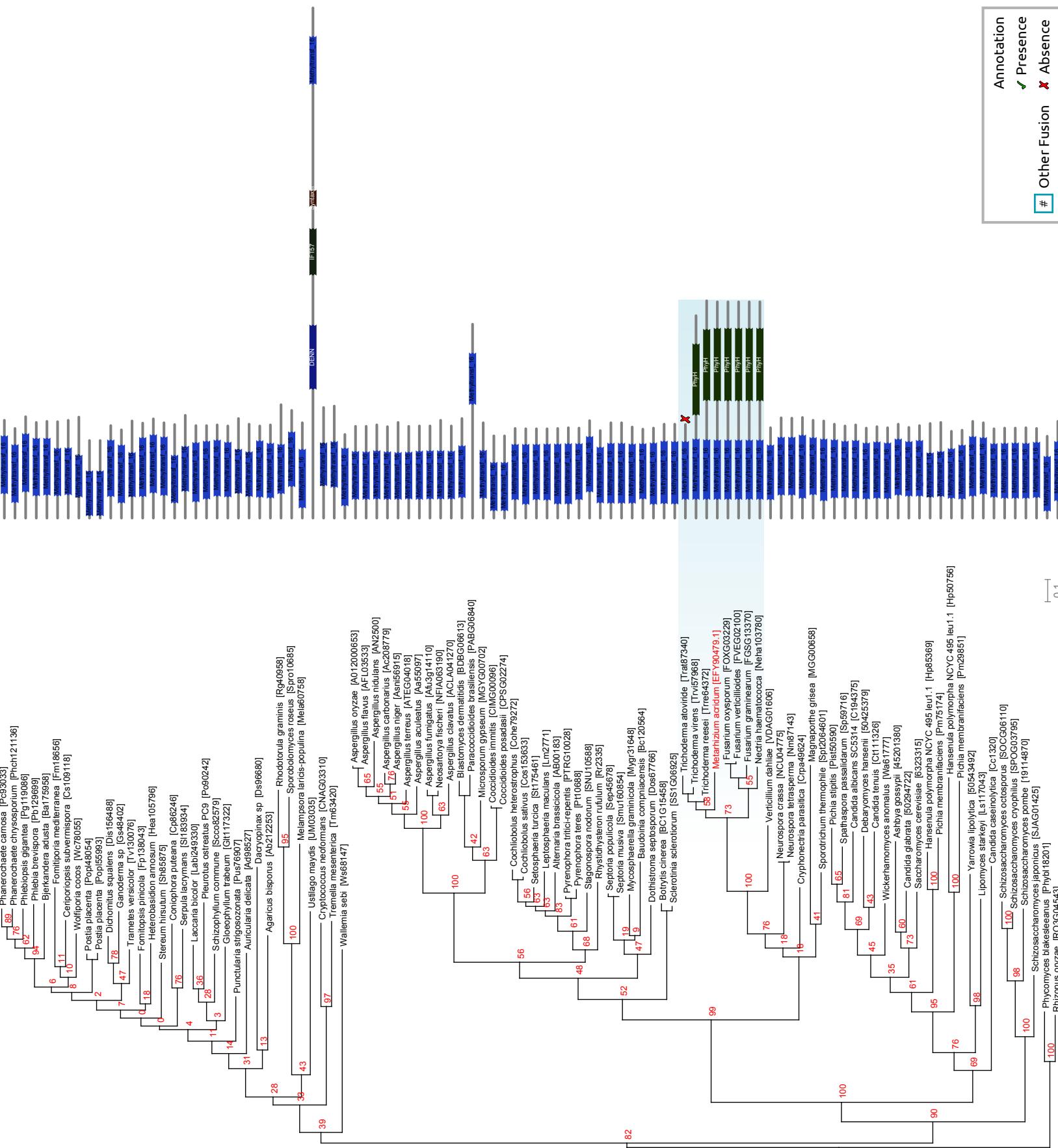
All trees were generated from an initial run of Darren's Orchard pipeline against 139 taxa (Table S1), using the above corresponding un-fused sequences as BLAST seeds. The alignments were then checked for any missing taxa, manually masked and then ProtTest3 was run, please see the Methods section for detail. The final trees were generated by the following command:

```
phylml -i alignment_file -d aa -b 100 -m model -c 8 -v invariant_sites -s BEST --quiet -a gamma
```

Styling and annotation was made possible by Dendroscope and Inkscape.

3 Mesquite Cladogram

This tree is the 68-gene concatenated phylogeny (Fig. 1), with the presence of a fusion (black), presence of a fission (white), and absent/undetermined (grey) status of gene fusion characters plotted on to it using a "1/0/-" nexus-style data matrix. We used the program 'Mesquite' to calculate proportional likelihoods based on either an "Mk1" or "Assym. 2 param model." (see Table S4) of character change across the fungal phylogeny (Fig. 1). This allowed for a proportional likelihood of the position of the fusion/fission to be calculated.

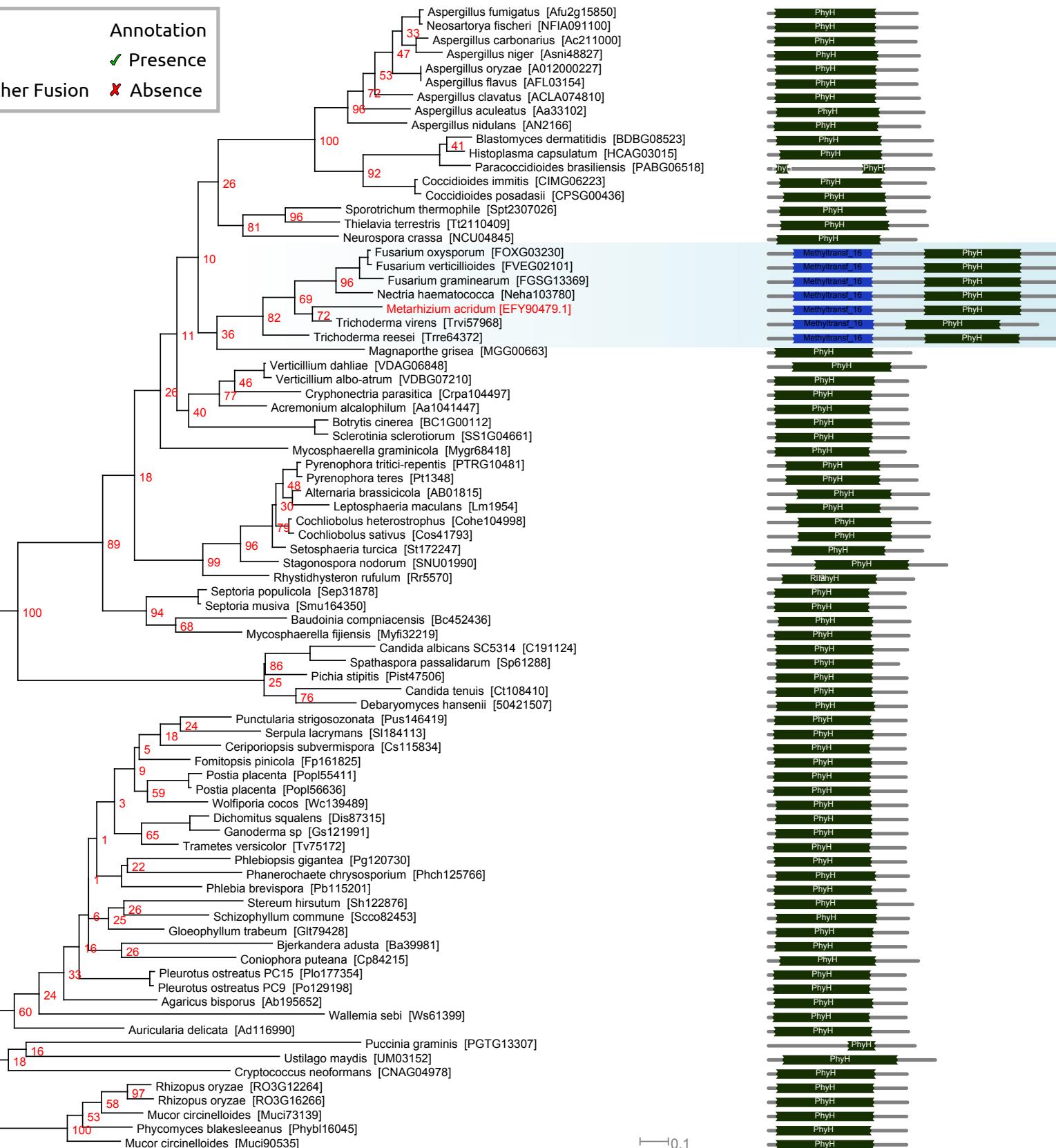


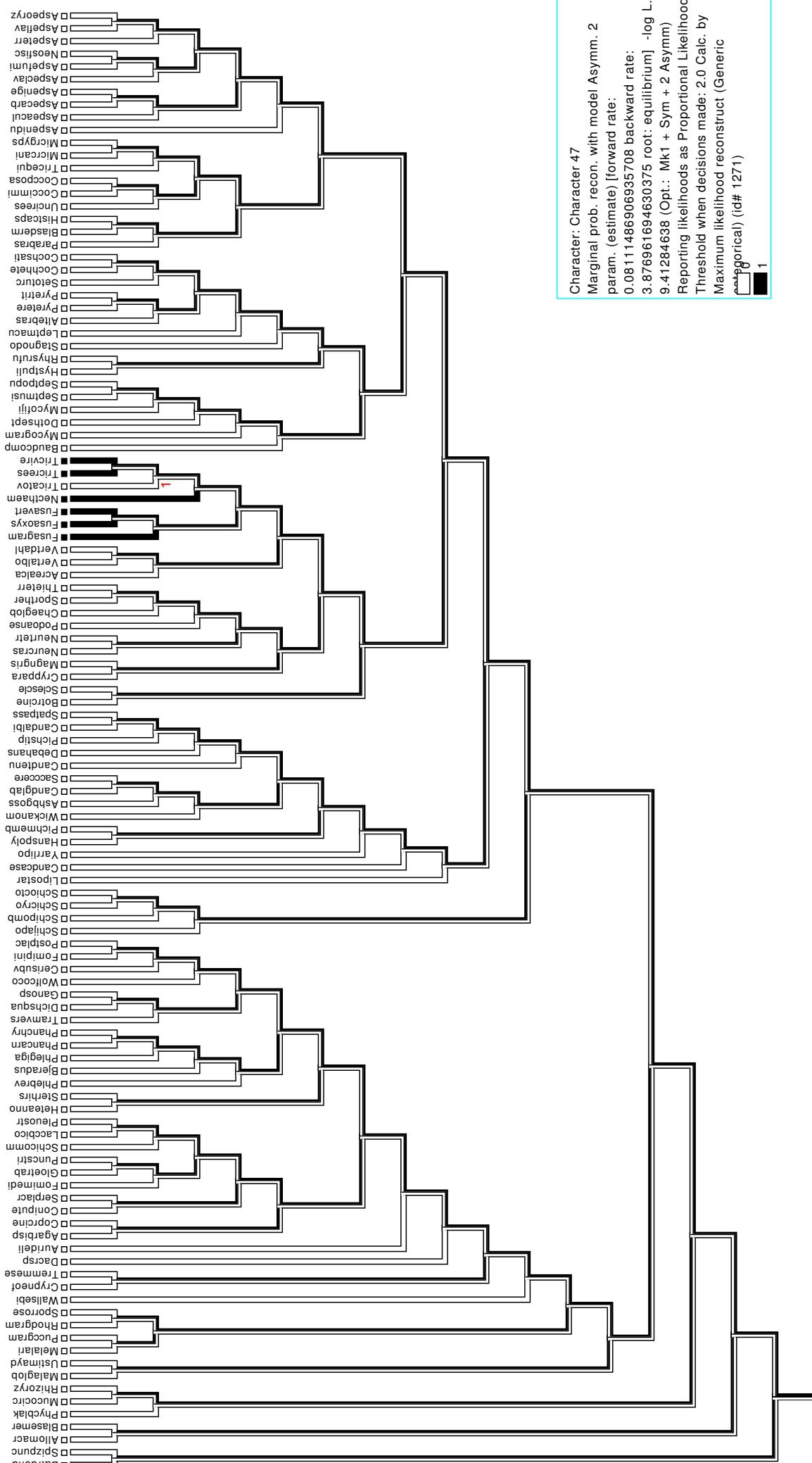
Annotation

✓ Presence

Other Fusion

✗ Absence





Character: Character 47

Marginal prob. recon. with model Asymm. 2 param. (estimate) [forward rate]:
0.0811486906935708 backward rate:
3.8798961694630375 root: equilibrium] -log
9.41284638 (Opt. Mk1 + Sym + 2. Asymm)

Reporting likelihoods as Posterior Likelihood Threshold when decisions made: 2.0 Calc. b

Maximum likelihood reconstruct (Generic Empirical) (id# 1271)

Putative Fusion 47

September 27, 2012

1 Fasta Sequences

These are the unfused sequences identified by fdfBLAST belonging to the putative gene fusion in FASTA format. Accessions may be shortened, but belong to either the taxons individual genome project or NCBI's accession numbering.

```
>CBY021751Lema_dom1
MRQVYGGPKLPVELRNQFDPSYGRSGRNGPATRKDKRKADRVKKKRQNQVRRPAPVR
PENGRGPAKRHGQGDEDDEDEAIDWDNVTEDGTPPPAPAKESLKKPKSILRKSSSQE
EDSEKPPSPVPRAIKEKLQNQDDAEIAALEKRLGVGKKSKGVEHDGLDDIFGDLGDFGSE
DEGLGQQPLKRKRNEDDNWLASKRQKALGAAPKDDTDDDKDSEAEESLDGEDYSDLDDL
GSDMEGFDSSEEDEENGESDEEPIQSVRVRENPYVAPIAPGASPAAKYVPPALRAPPSSDA
ETLSRLRRQIQGLFNRLSEANILTLKDIEGIYQNNPRGYVNTTLIDLITGMLSDPSALL
DTFLNLHAGFIAAIYKVIGPDFGAQMIERIVSEFDTHYQHNKEGTGQQTKNLISVVAELY
TFQVIGSNIVFDYIRFFLDELTEINTELLLRVVRAGPQLRQDDPTALKDIVVLLQKSLA
KVGQANLPVRTKFMETINDLKNMKMKTGIAASHMSREHTTRMKKQLGTLNSRNLKATEP
LRVGLKDIKDTDKKGKWWLVGASWRNEPGTEDPIQETKTIPRHTQTLENEDDDSEIDLVQ
LAREQQMNTDIRRAIYISIMSASDFKDAQIRLSKLNKRSQEVEIPRIVHCAGAEETYN
PYYTTLARKVCSDHKSRSQFALWDIFKSLGEKQDGADDSDDQDDTKNETNLRKIVSQ
GKLYGTLIGRKALPITSKLNLFPMQPKTKTTFEVILVTTILESLKGSKDKRNERAVRE
>CBY021751Lema_dom2
IFVEVDHAPEMIAGLQFFLKKTVRKTDIVEKADKETVRWACKSIMDIRIDQGGSRPSEFR
KKLNTSSRNEAPSIAACHLRHISHGFSWSPASLLSQFIMFRSLAPRALQRATRPVTQKSF
CASNLYFQNRLQRGYASEAAEKDLVIIGGGVAGYVAAIKAGQAGLSVACIEKRGSLGGTC
LNGCIPSKSLNNSHLYHQILHDTKGRGIEVGDVKLNLPMAMMKAQDTSVAGLTKGIEFL
FKKNNVEYIKGTGAFQDEHTIAVNLEGGETSVRGKNILIAATGSEATPPGLTIDEQKVI
TSTGAINLQEVPAKMTVIGGGIIGLEMASVWSRLGEVTVVEFLGQIGGPGMDNEIAKQS
QKILQKQGLKFKLNTKVTAGEVHDAGVKVSVEAAKGGKEETLDADVVLVAIGRRPYTAGL
GLDNISLETDERGRLIIDQEYRTKIPHRSIGDCTFGPMLAHKAEEEAVAIEYITKGHG
HVNYGAIPSVMYTHONPEVAWVGQNEQELKAAGIKYKTGNFPFSANSRAKTNLTDGFVKFL
SDAQTDRLGIHIIGANAGEMIAEGTLALEYGASSEDVARTCHAHPTLAEAFKEAAMATY
DKAVHY
```

2 Annotated Phylogenograms

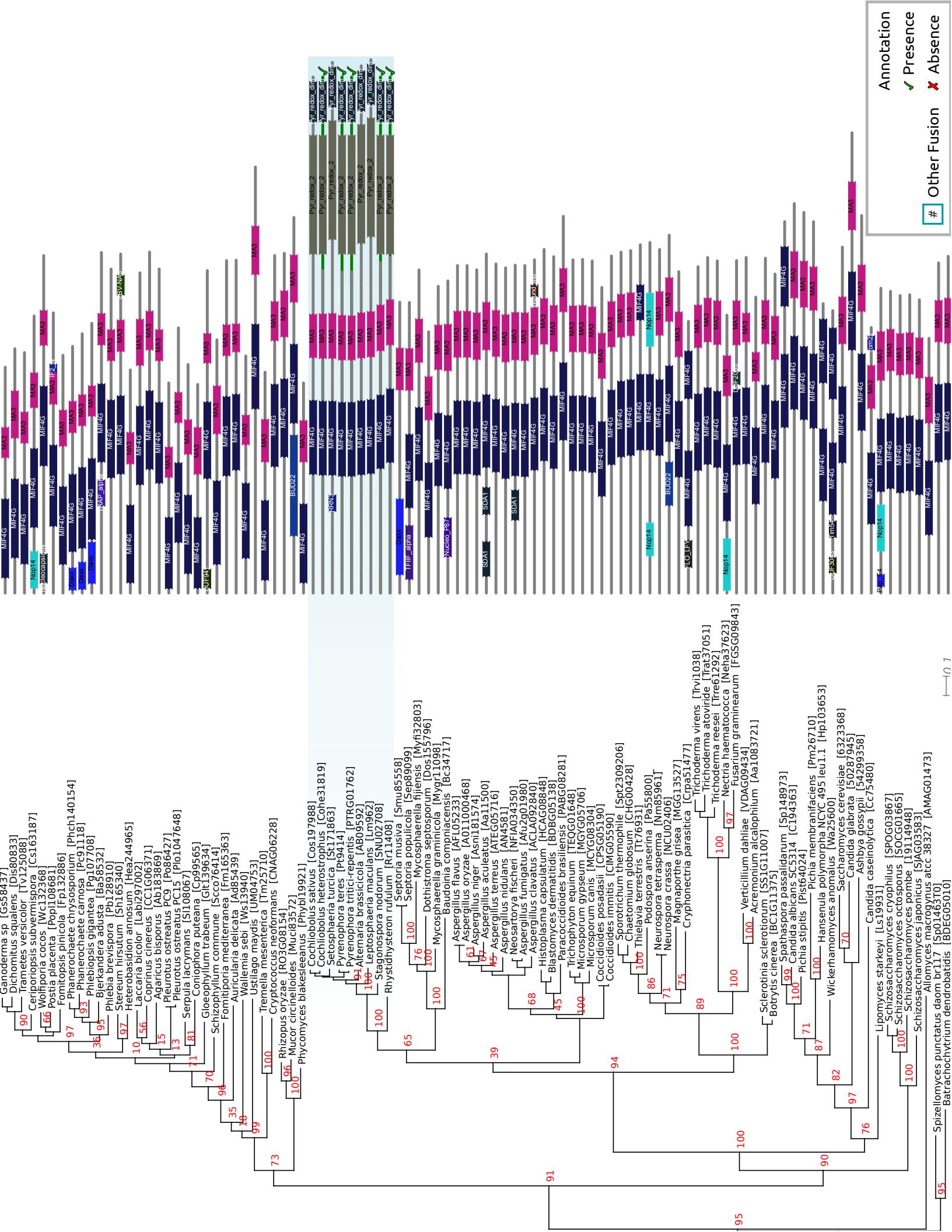
All trees were generated from an initial run of Darren's Orchard pipeline against 139 taxa (Table S1), using the above corresponding un-fused sequences as BLAST seeds. The alignments were then checked for any missing taxa, manually masked and then ProtTest3 was run, please see the Methods section for detail. The final trees were generated by the following command:

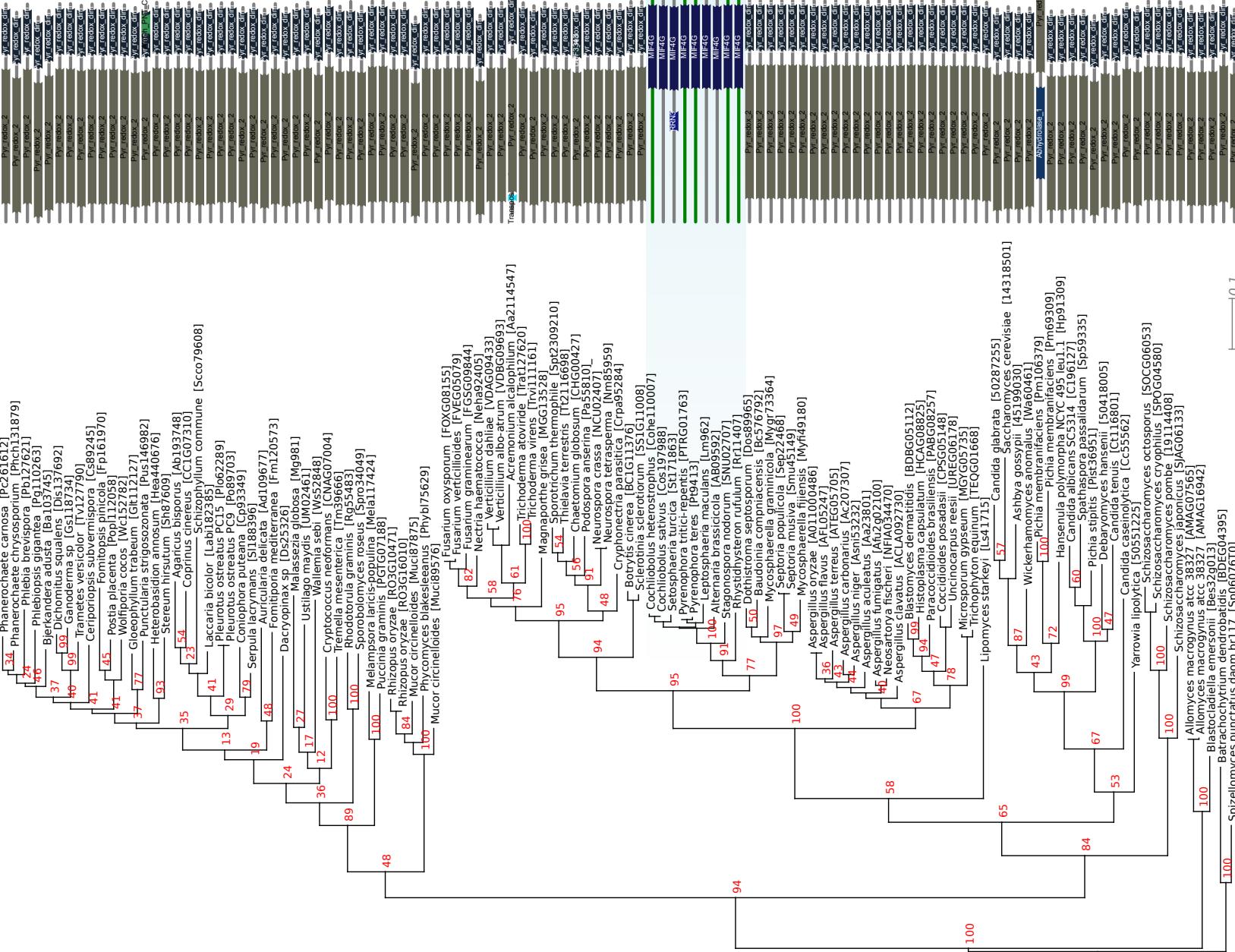
```
phym -i alignment_file -d aa -b 100 -m model -c 8 -v invariant_sites -s BEST --quiet -a gamma
```

Styling and annotation was made possible by Dendroscope and Inkscape.

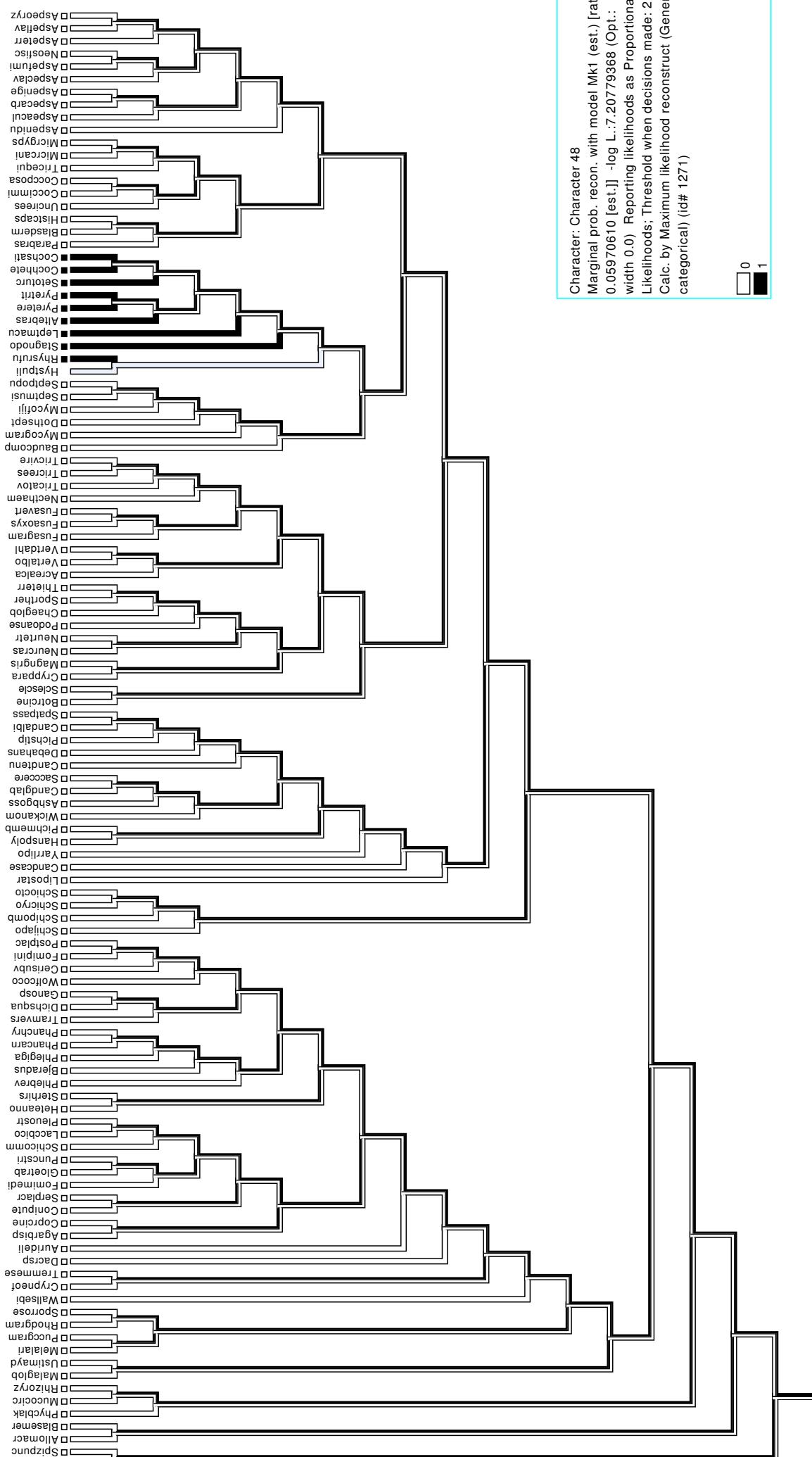
3 Mesquite Cladogram

This tree is the 68-gene concatenated phylogeny (Fig. 1), with the presence of a fusion (black), presence of a fission (white), and absent/undetermined (grey) status of gene fusion characters plotted on to it using a "1/0/-" nexus-style data matrix. We used the program 'Mesquite' to calculate proportional likelihoods based on either an "Mk1" or "Assym. 2 param model." (see Table S4) of character change across the fungal phylogeny (Fig. 1). This allowed for a proportional likelihood of the position of the fusion/fission to be calculated.





Annotation ✓ Presence ✗ Absence



Character: Character 48
Marginal prob. recon. with model Mk1 (est.) [rate 0.05970610 [est.]] - log L.: 7.20779368 (Opt.: width 0.0). Reporting likelihoods as Proportional Likelihoods; Threshold when decisions made: 2.0 Caic. by Maximum likelihood reconstruct (Generic categorical) (id# 1271)

Putative Fusion 48

October 5, 2012

1 Fasta Sequences

These are the unfused sequences identified by fdfBLAST belonging to the putative gene fusion in FASTA format. Accessions may be shortened, but belong to either the taxons individual genome project or NCBI's accession numbering.

```
>XP_0032968951Pyte_dom1
MADARGEYWYFEDGVDPNKITVPELRSILLRHGATYPSSARKGTLVSLFVDVVLQPQPV
QRMLAQTKRSTRGIVDVPSSASTADTDETEDETLVAPTPATRRISRTTRGTTEDVDVP
APRAKTPSRAVPAKHSRALESEVDERPATRRTRKSVTPAVKEPSPDPVAWRNDAASPFT
QENPFQKGASSPAVPDTIARERRRTGYGRERRKSDALRRQTYQPSSELQDDGISVPTR
RTFDMDVDPRVKQEEDEEDEEDVVDAQEFTPEEQLELVRERAQTGEVDILPPRRQQKA
KATGRIKAGAGTILLTAAAVFAGVWRQEKIDVGFCGVGRDATALAGVDIPSAGQILPQC
EPCPPHAQCYRGLKIKCDPDFIEKDHPPLSLLGGLVPVPPCTEPDSEKTRKVNGIANRAEV
LRQRKAQYECGEPDSEGNPVESPEVKALKQHMASQKSKS LTDQEFSelfDRAFPEVIM
REEVVEETTNGTGGRRLASTSLAKSLVCSTRYLRQSFERHLLKIISVFLFAFLSLYGK
YSYTHNRSMEARAALASDAYDRLQDQAALSFLFEGAEGKISMTQLRDDILRTEFNASRR
QRLWTRVQAKVERNSNIRAGVRTTANGDVARMWEWIGPVKRLEDSKRESGRFSLGMGSSP
>XP_0032968951Pyte_dom2
PSGNRVAKEVNVPKTRRTYCKGKDCKKHTQHKVTQYKAGKASLFAQGKRRYDRKQSGYGG
QTKPVFHKRACKKKVVLRELECTACKTKAQLALKRCKHFELGGDKTKGAALVF
```

2 Annotated Phylogenograms

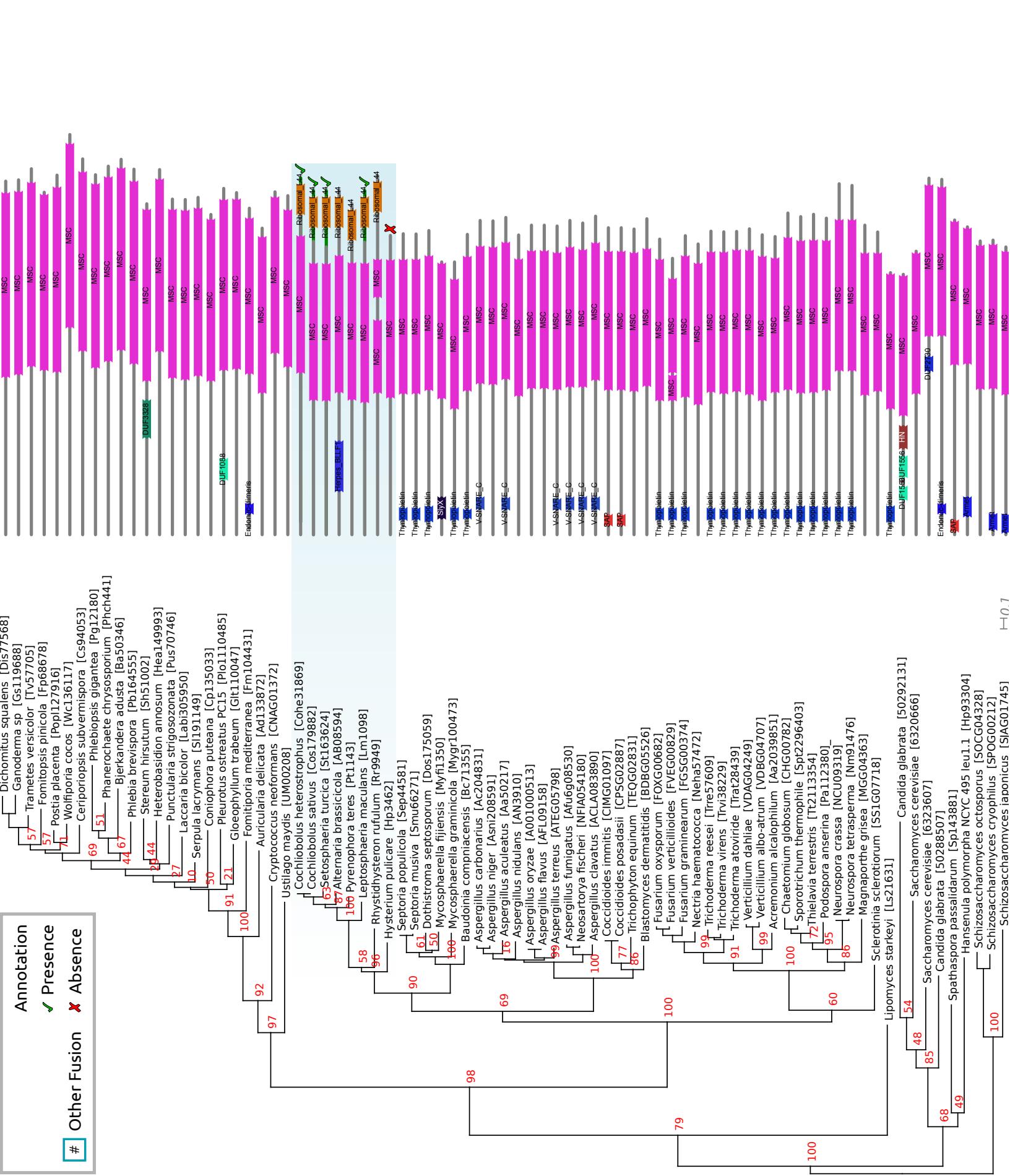
All trees were generated from an initial run of Darren's Orchard pipeline against 139 taxa (Table S1), using the above corresponding un-fused sequences as BLAST seeds. The alignments were then checked for any missing taxa, manually masked and then ProtTest3 was run, please see the Methods section for detail. The final trees were generated by the following command:

```
phylml -i alignment_file -d aa -b 100 -m model -c 8 -v invariant_sites -s BEST --quiet -a gamma
```

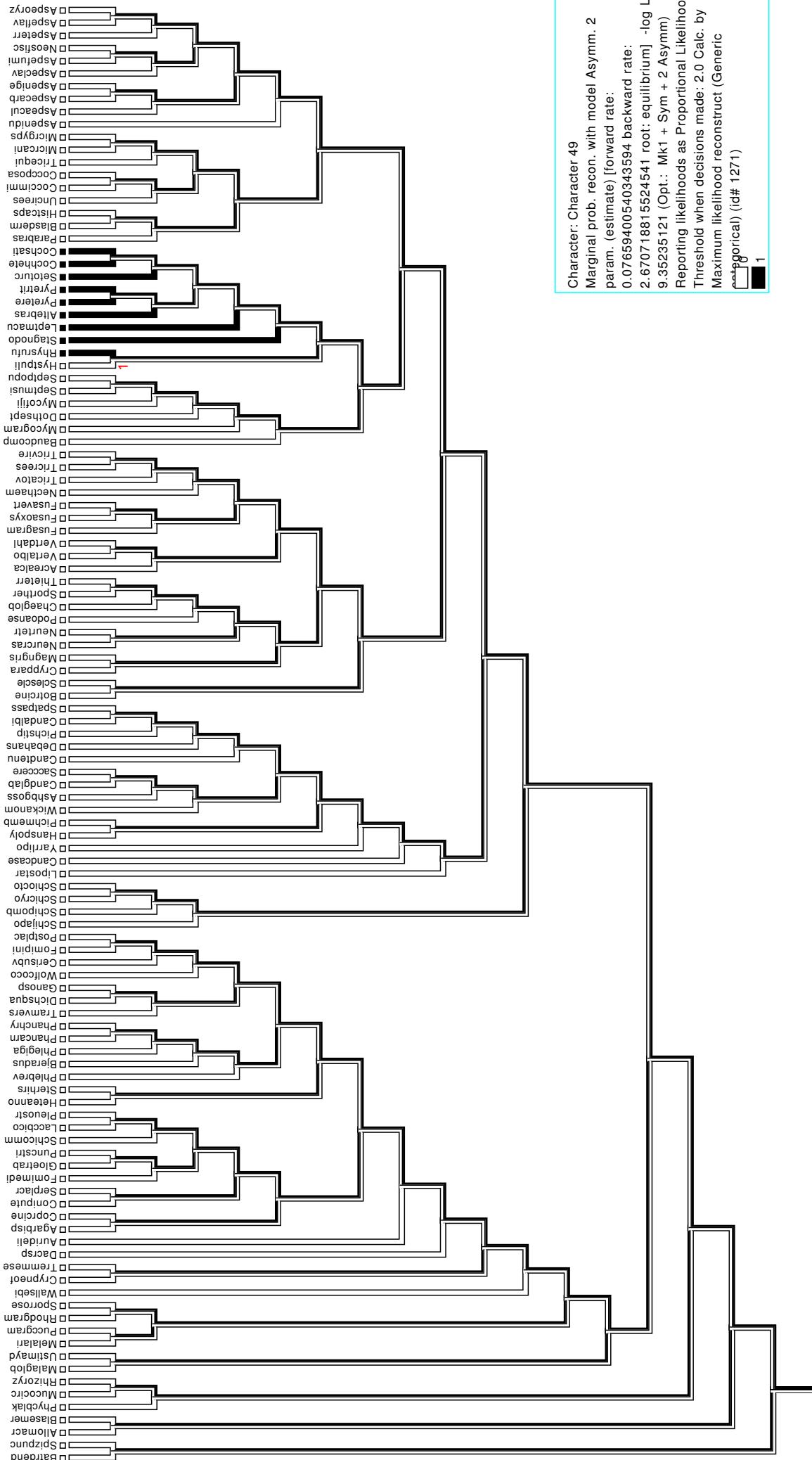
Styling and annotation was made possible by Dendroscope and Inkscape.

3 Mesquite Cladogram

This tree is the 68-gene concatenated phylogeny (Fig. 1), with the presence of a fusion (black), presence of a fission (white), and absent/undetermined (grey) status of gene fusion characters plotted on to it using a "1/0/-" nexus-style data matrix. We used the program 'Mesquite' to calculate proportional likelihoods based on either an "Mk1" or "Assym. 2 param model." (see Table S4) of character change across the fungal phylogeny (Fig. 1). This allowed for a proportional likelihood of the position of the fusion/fission to be calculated.







Putative Fusion 49

September 27, 2012

1 Fasta Sequences

These are the unfused sequences identified by fdfBLAST belonging to the putative gene fusion in FASTA format. Accessions may be shortened, but belong to either the taxons individual genome project or NCBI's accession numbering.

```
>Plo1062711_dom1
MAIKIICKRTKHFKRHQSDRYVSVKEAWRKPKGIDNRVRRRFKGQTMPKIGYGSNKTR
HLLPSGLKKFVVNNVREVDLLLHMNKSFAAEIAHNVSSRNRTVILERAKALGIKVTNAAA
>Plo1062711_dom2
RLRSEEKDVRASHAGSWYTDNRDELNEELEGWLEAVGPSEDFPVAGSKAIAPHAGYSY
SGPAAAWAYKSIGTTGIKRKFILGPSSHHFYLEGCALSRCKEYETPIGNLPLDIDTINELR
ATNEFEDLSLKADEAEHSLEMHLPYVRKIFEGQDISIVPIVVAISKSLEASYGKLLAPF
LSREDTFCVVSSDFCHWYAITSCLLQIHAYYQAGIRGTRFSYTYYPEPAPSDFPGINLT
RSVQPSTSHRIHKSIERLDREAMDLLAMPPSSAKDAHANFAEYLAQTHNTICGRHPIGVL
LGALAELESRKSTLKWWVRYEQSSACVNIADSSVSYASAWVRF
```

2 Annotated Phylogenograms

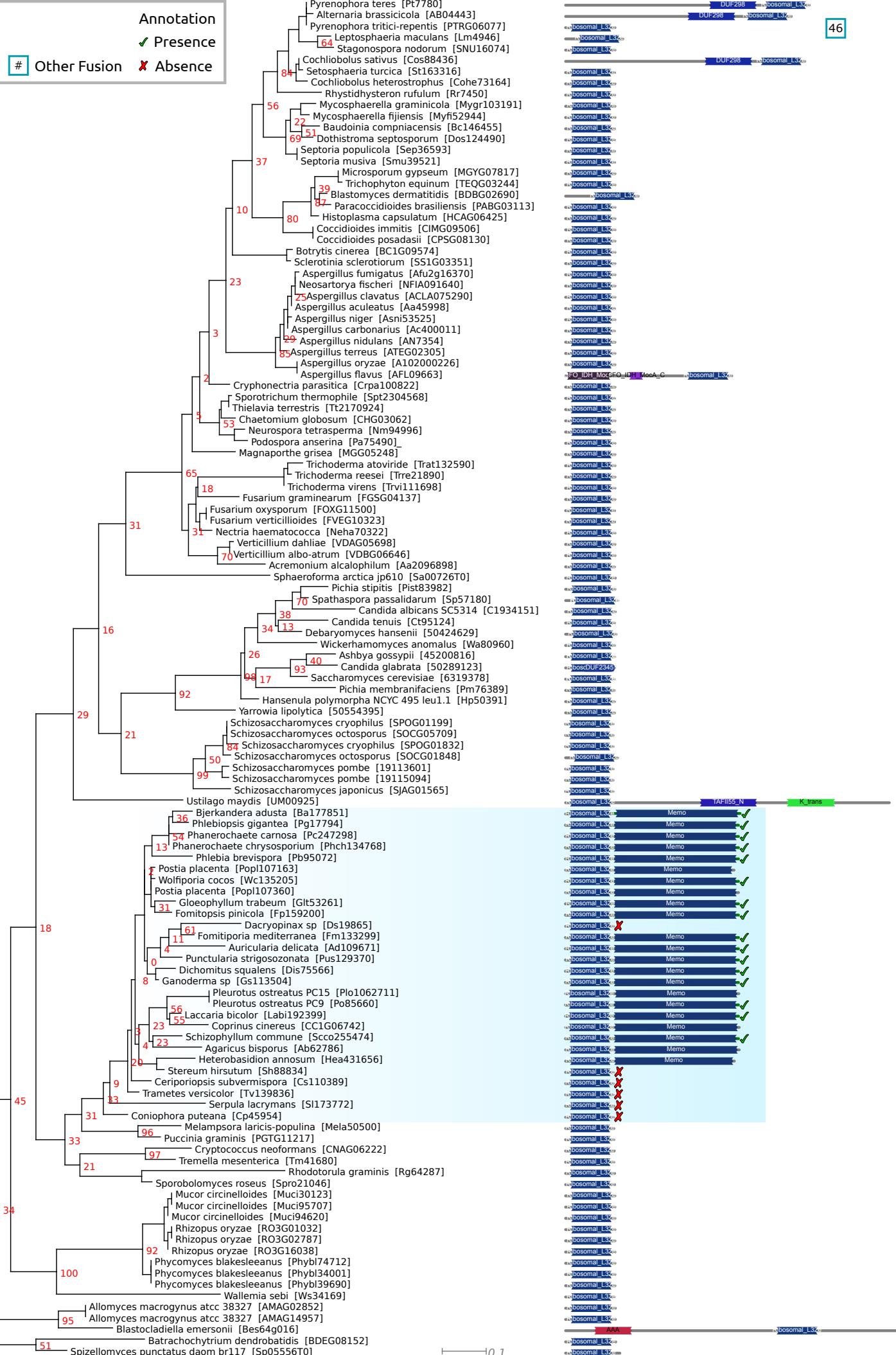
All trees were generated from an initial run of Darren's Orchard pipeline against 139 taxa (Table S1), using the above corresponding un-fused sequences as BLAST seeds. The alignments were then checked for any missing taxa, manually masked and then ProtTest3 was run, please see the Methods section for detail. The final trees were generated by the following command:

```
phym -i alignment_file -d aa -b 100 -m model -c 8 -v invariant_sites -s BEST --quiet -a gamma
```

Styling and annotation was made possible by Dendroscope and Inkscape.

3 Mesquite Cladogram

This tree is the 68-gene concatenated phylogeny (Fig. 1), with the presence of a fusion (black), presence of a fission (white), and absent/undetermined (grey) status of gene fusion characters plotted on to it using a "1/0/-" nexus-style data matrix. We used the program 'Mesquite' to calculate proportional likelihoods based on either an "Mk1" or "Assym. 2 param model." (see Table S4) of character change across the fungal phylogeny (Fig. 1). This allowed for a proportional likelihood of the position of the fusion/fission to be calculated.

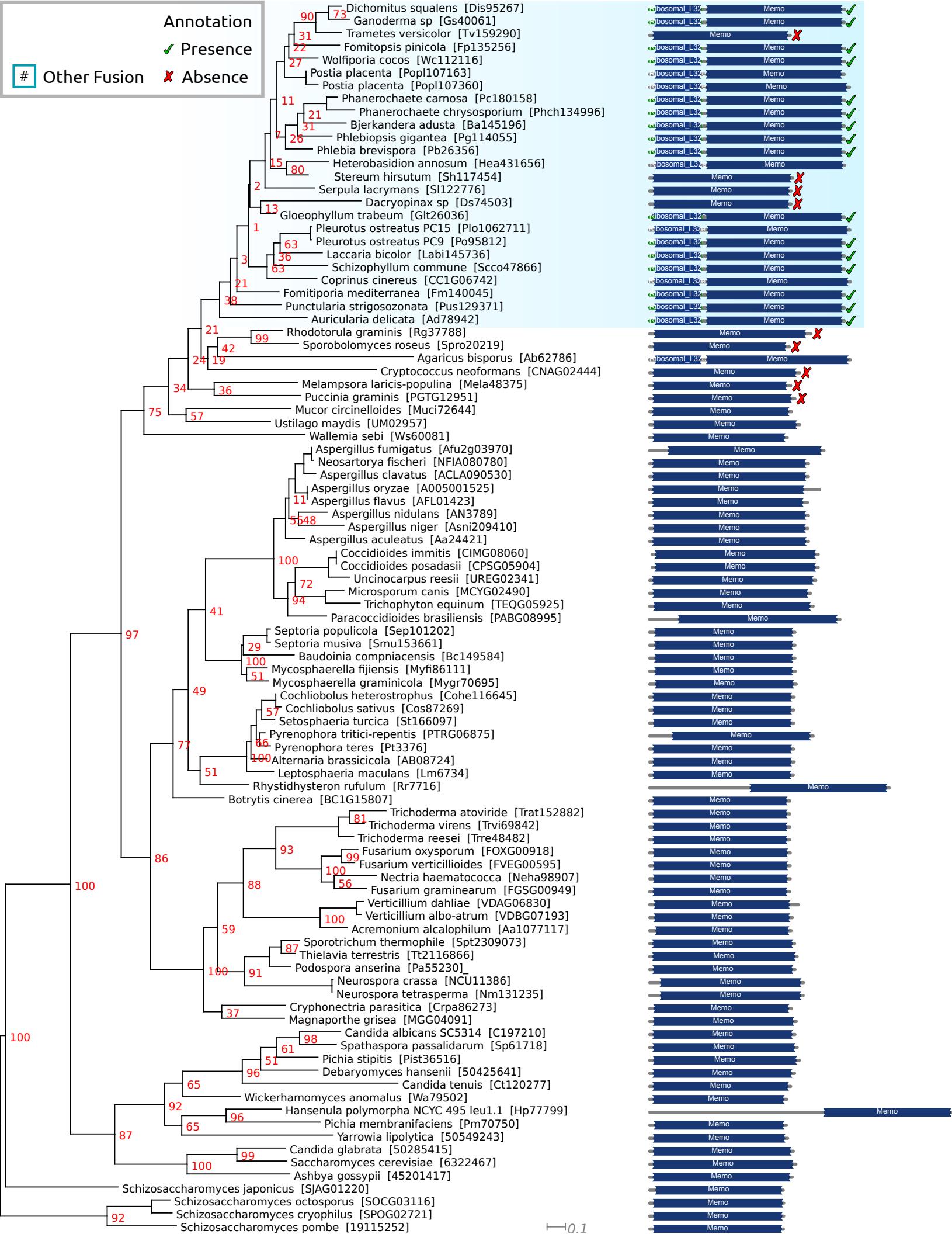


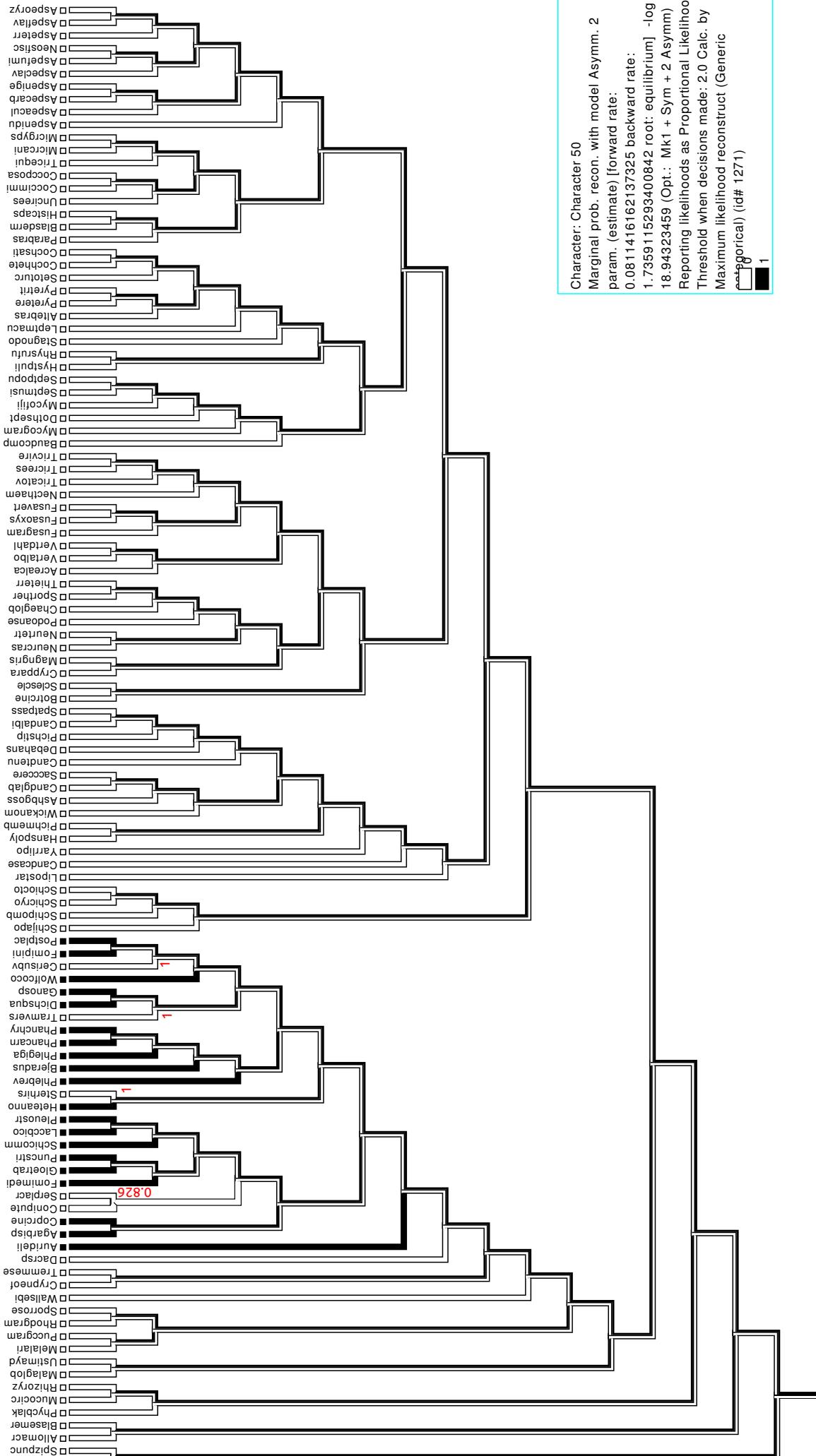
Annotation

✓ Presence

✗ Absence

Other Fusion





Putative Fusion 50

September 27, 2012

1 Fasta Sequences

These are the unfused sequences identified by fdfBLAST belonging to the putative gene fusion in FASTA format. Accessions may be shortened, but belong to either the taxons individual genome project or NCBI's accession numbering.

```
>XP_0012096401Aste_dom1
MATWAYPPLPAEHLDRREADSALARELEWLLRSLQDSLTSLREGLRECAVLLAPKEPGSTL
VLSSLRSEHVKGFTRVGKIVKGDIQLRLNSLASPRGSNTRLCLSSSPTAPELVLHQL
VSVRNLVNQSLDIVDVSATGDPLNANFISQLHLLHETISEARQLKGENDNTRGKWWDT
TSAEEMFDPPPLPPYLSFQLLIADSALVLYLRTLESATPTHTPTAFATDISLTGFNLRDR
LFGTRHRAHDEAGDVFTWKGEVKHQETGRWKLGRYYASSASSETADKHADRKAIFYVI
DKINENEVELAELMDELNLLDDYHGAINFDGPDYDDAVSQTIGQRDHQMLEARVRMARQQ
FGDVLPDGYLNATETELYTQLYGEPIIRHEEPEGALNIEETESTLREDGKGGWEVQY
>XP_0012096401Aste_dom2
ERFESDAEVPLVYDMEVGPLEDESAAMQRTREVAEQLGGEVMLEQFEDEANPDSTPRLHP
LTVEGKFSTDPTVFLPKDTVTGPISVILSDYSNKHIADVAHRVFGGTRVPYSTTPPPR
AQMPQLPIPLEASQRHMSEMEANAYIATLYPGMYASVLSVLTEVRKRLGSDWIRQLLTQE
GGPHVLDASAGGAGVLAWRDVLAERWELMVPDHPQSSPYPVGRSTVVGSETLRLRASLM
LENTSFLPRLPDYVHIREKPTLDDQRAPPKRKQYDVIIAPHSLLGIEEYMRKEHVENLW
NLLNPNGGVILLEGKQHGKQFEAIAGARDMLLKRHISSPGSVQYEDFLQSPGGGKYVNKE
AGMIIAPCTNHEKCPMFNVAGHSKGRKDYCHFEQRYIRPPFLQRLGIKDRNHEVDKFSY
VAVQRGVDRREKGDGIVQGAAATDAAFVGYEHLDSPAEQSEATEEPTTTAEGSERPSAE
GAEQFHALTLPRIVYPPMKRRGHVIFDLCTSAGKIERWTVPRSYSRRAFKDARKAQWGDL
WALGAKTRIPRSLRLGDKHGECKKERLARRAVERAEMNETEEMQLEEAGSAWPDLVPVKR
KKGQNIPSWKKHADKKKLRQATKKHAAAQLAHDDSLA
```

2 Annotated Phylogenograms

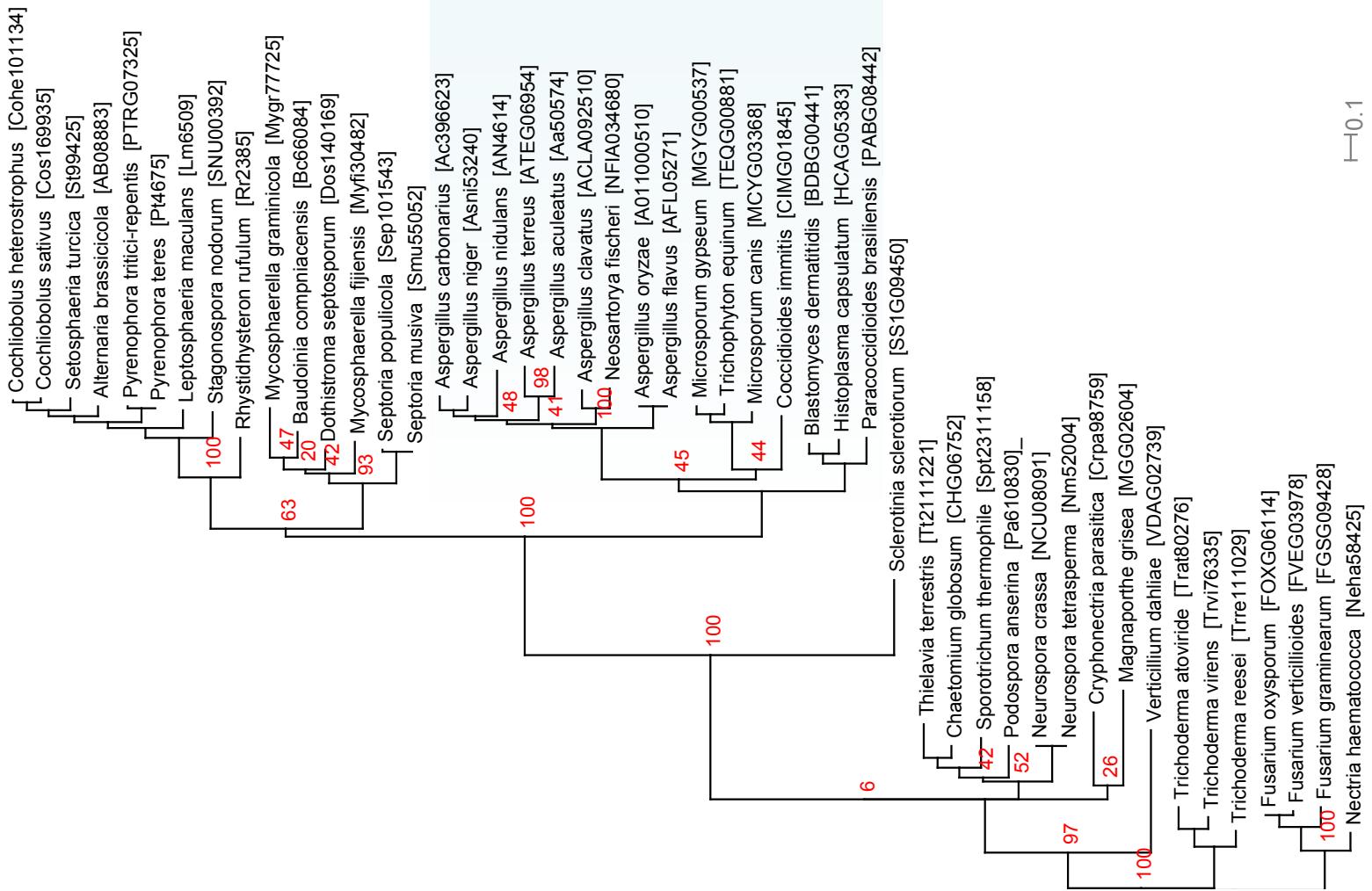
All trees were generated from an initial run of Darren's Orchard pipeline against 139 taxa (Table S1), using the above corresponding un-fused sequences as BLAST seeds. The alignments were then checked for any missing taxa, manually masked and then ProtTest3 was run, please see the Methods section for detail. The final trees were generated by the following command:

```
phyml -i alignment_file -d aa -b 100 -m model -c 8 -v invariant_sites -s BEST --quiet -a gamma
```

Styling and annotation was made possible by Dendroscope and Inkscape.

3 Mesquite Cladogram

This tree is the 68-gene concatenated phylogeny (Fig. 1), with the presence of a fusion (black), presence of a fission (white), and absent/undetermined (grey) status of gene fusion characters plotted on to it using a "1/0/-" nexus-style data matrix. We used the program 'Mesquite' to calculate proportional likelihoods based on either an "Mk1" or "Assym. 2 param model." (see Table S4) of character change across the fungal phylogeny (Fig. 1). This allowed for a proportional likelihood of the position of the fusion/fission to be calculated.



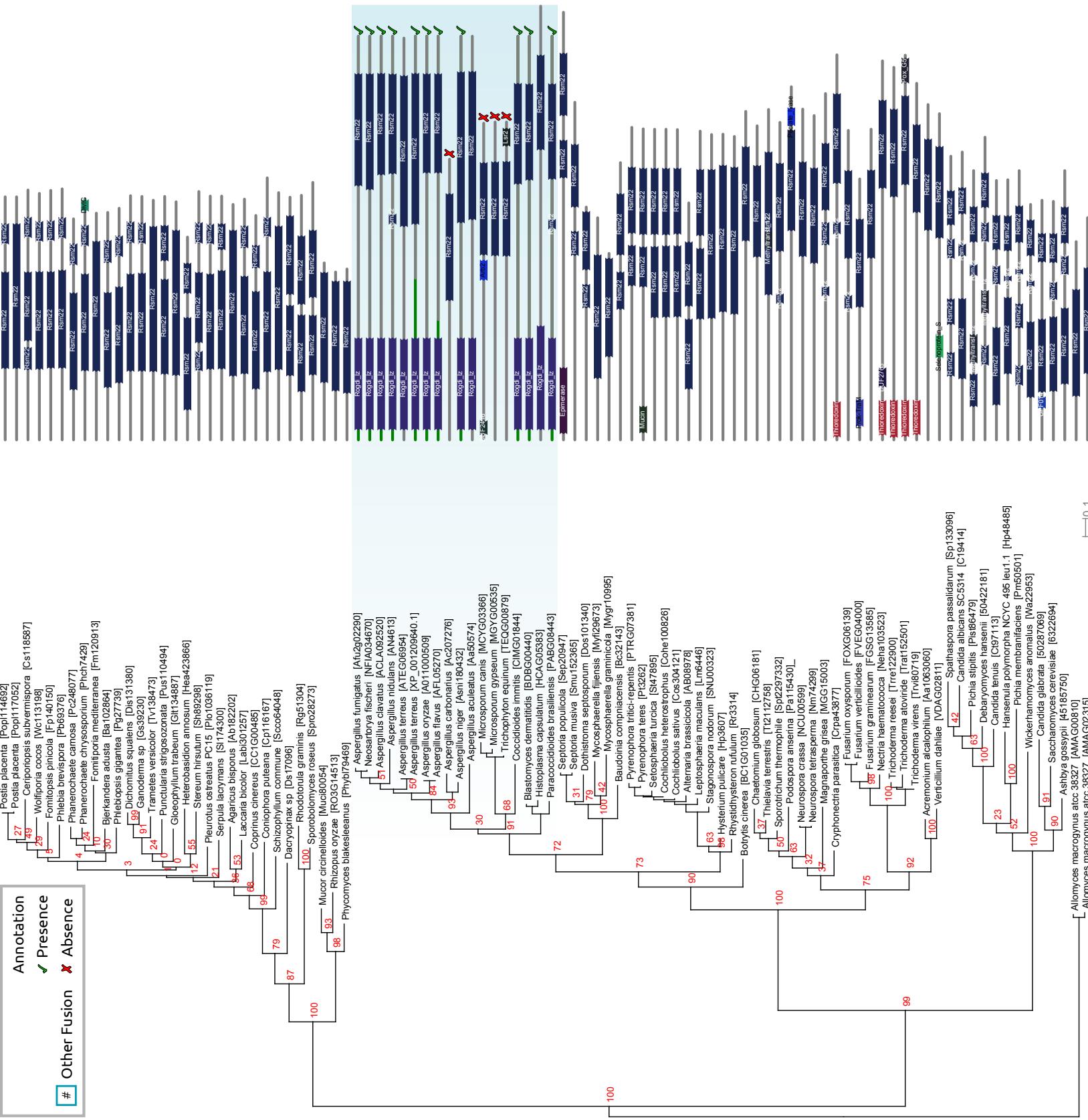
Annotation

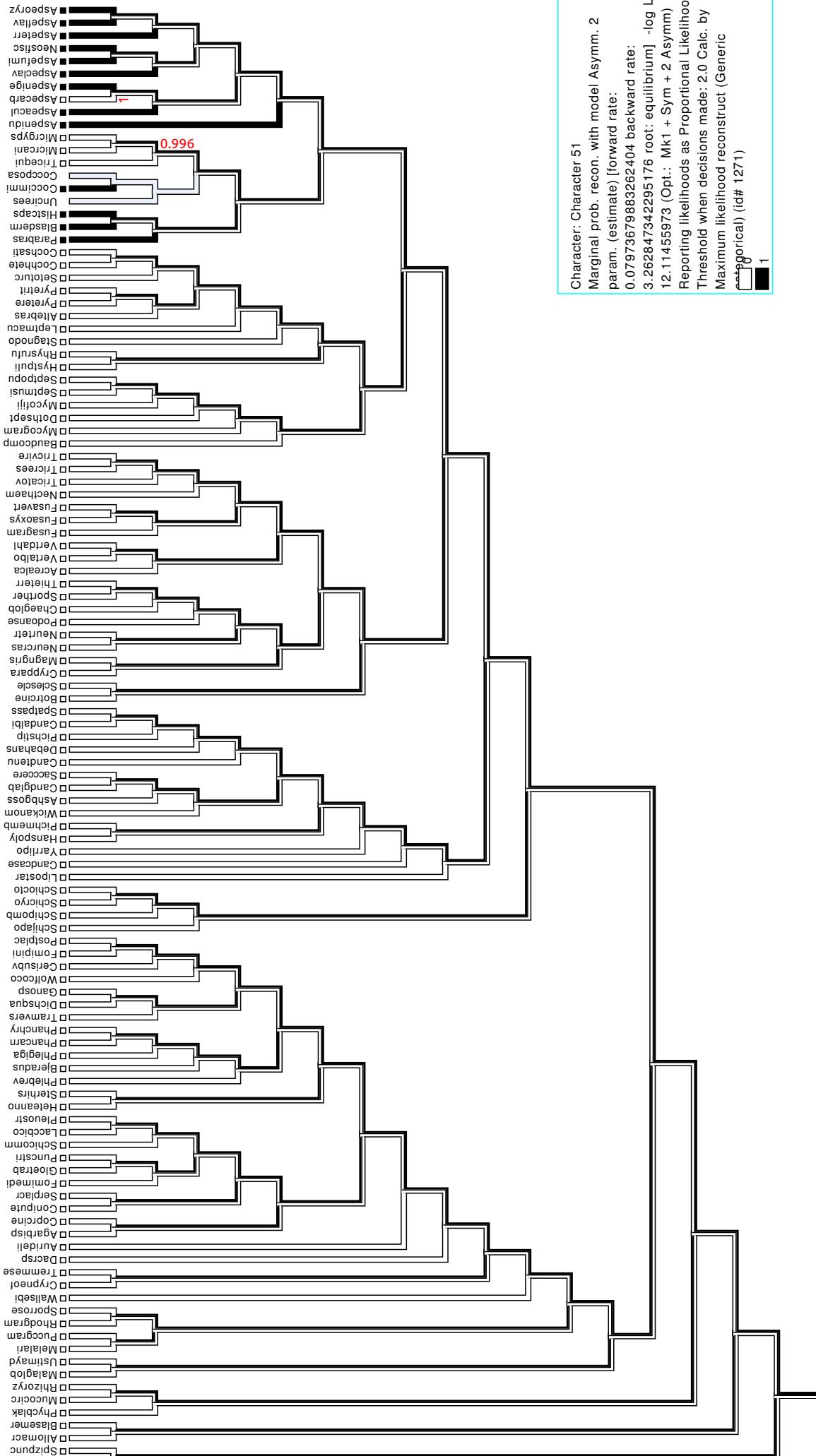
✓ Presence

✗ Absence

#

1-0.1





Putative Fusion 51

September 27, 2012

1 Fasta Sequences

These are the unfused sequences identified by fdfBLAST belonging to the putative gene fusion in FASTA format. Accessions may be shortened, but belong to either the taxons individual genome project or NCBI's accession numbering.

```
>XP_5672951Crne_dom1
MLPRAHRLVNQRPGIALRPHASHVSSAATSAVRRSVASQAAQVAQPPPIHPEIDGTFNDLIG
EGTMNMGMKPRGSDRTSLPYRNINEIELADHQPVVRHSGRKWSSLGLRIEQSDLVIDESPE
VYNSASEGEYHDFGREERRSPAALGSKRLGMVVLPEEMQRGIQRQIDLMDNPRDIRKSY
LALPNVPTPISATKSERRDKPFRTPEGEAKASAILPGEYGAJKNVLEELERRLGREWLT
SAKEGEILEFSSLGSGLWAIMDVMGGLLSSRRWQEGQDKLKQFVHSSRHGLDLVQRI
AEVPEEESADVQFNRRHVHSSTPSLILSTFHLTSFPTLPTRQLYLRQLELSSPYIVLIE
RSTPQGWAAISQARSYLLEKSTSENPLHVAPCPHDGKCPLVGTKDVCYGSQRLQRPSFL
RKTKHSSRGEEEKGYCYLVIAKGERPSVGTVAEDMKVAGRMGKVGREAAEKALIKSQGRS
IIQEVEGHEAVMEVVRLHEIEPGMENYFEETSPSVNSEELEENLRKEAYSWPRMVAPPMK
RKGHVTMDTCCADGNIQRLYTSHSKQSYHDARKSSWGDLFPHTSKGKPVIRTRGVRR
>XP_5672951Crne_dom2
AKSENNGDADAVISELLSASLEEMELEKAMEAVEVDELKELEMLGIKTPRAEVSKERQD
DDMLVWKSNKNGPFAASGQKRSYRTLTSTRSTSQPKTPPSIQTRSMSARPAPPIRPKATLS
SLLSLAKSGTPISVLTAYDYPTALLSESCLNDMLTVGDSLSQVALGHETTAITLDEMIH
HARTVVVRGAKTPFVADMPFGSFETSLEEGVRSVLRMVKEGGVDGVKIEGGREIVPLVRR
LSAIGIPVMPHLGLQPQRATSLSGYLVQGRTAQAAYEILQSARELANAGAFALLEAMPS
KVAKLVTEEVGKKGVFTIGIGAGNGTNGQVLVITDVLGIYAEDPPEDIATPNVTGETELV
STS RDFTKPLDAPRFVRQFGSLQEMRRRAVRAYVQAVKGRSFPDSKESYGMKKEEWETFL
EMVKREKDQH
```

2 Annotated Phylogenograms

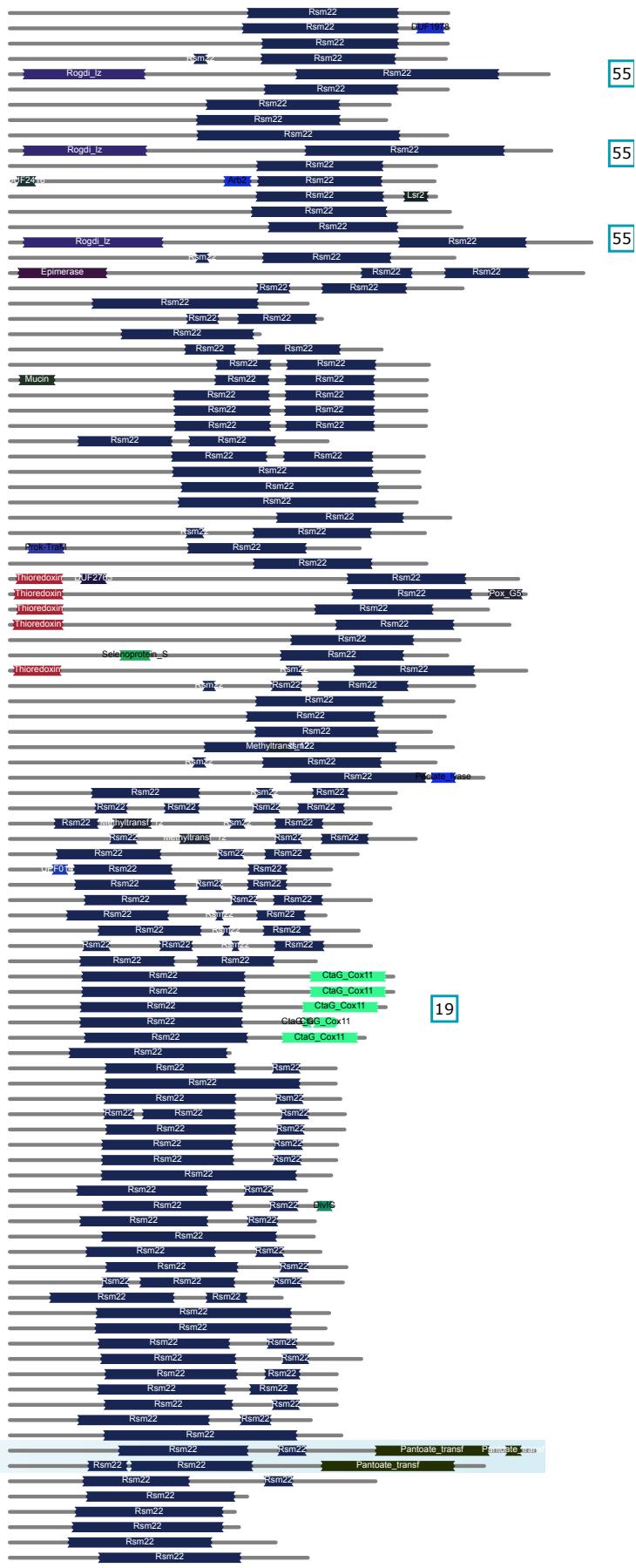
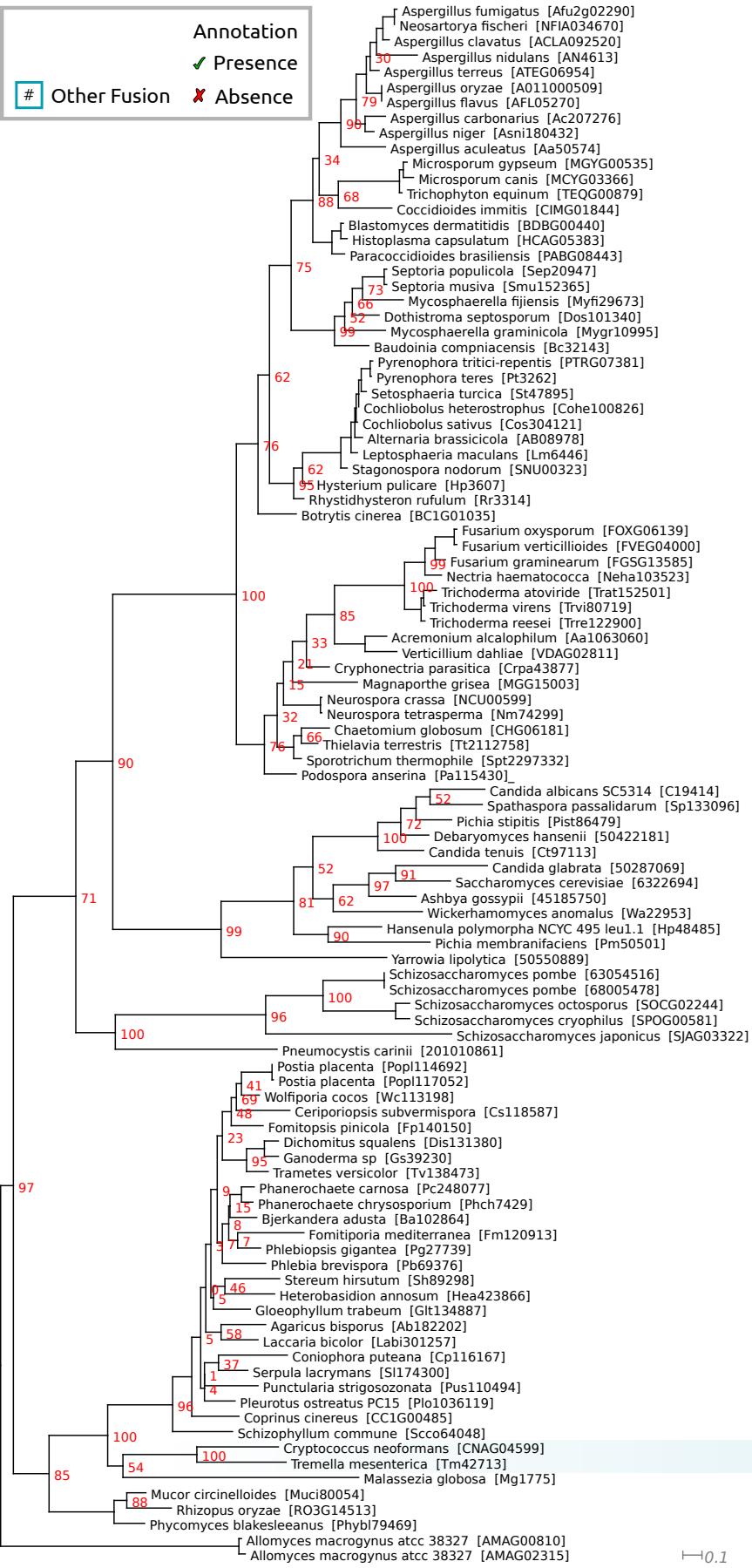
All trees were generated from an initial run of Darren's Orchard pipeline against 139 taxa (Table S1), using the above corresponding un-fused sequences as BLAST seeds. The alignments were then checked for any missing taxa, manually masked and then ProtTest3 was run, please see the Methods section for detail. The final trees were generated by the following command:

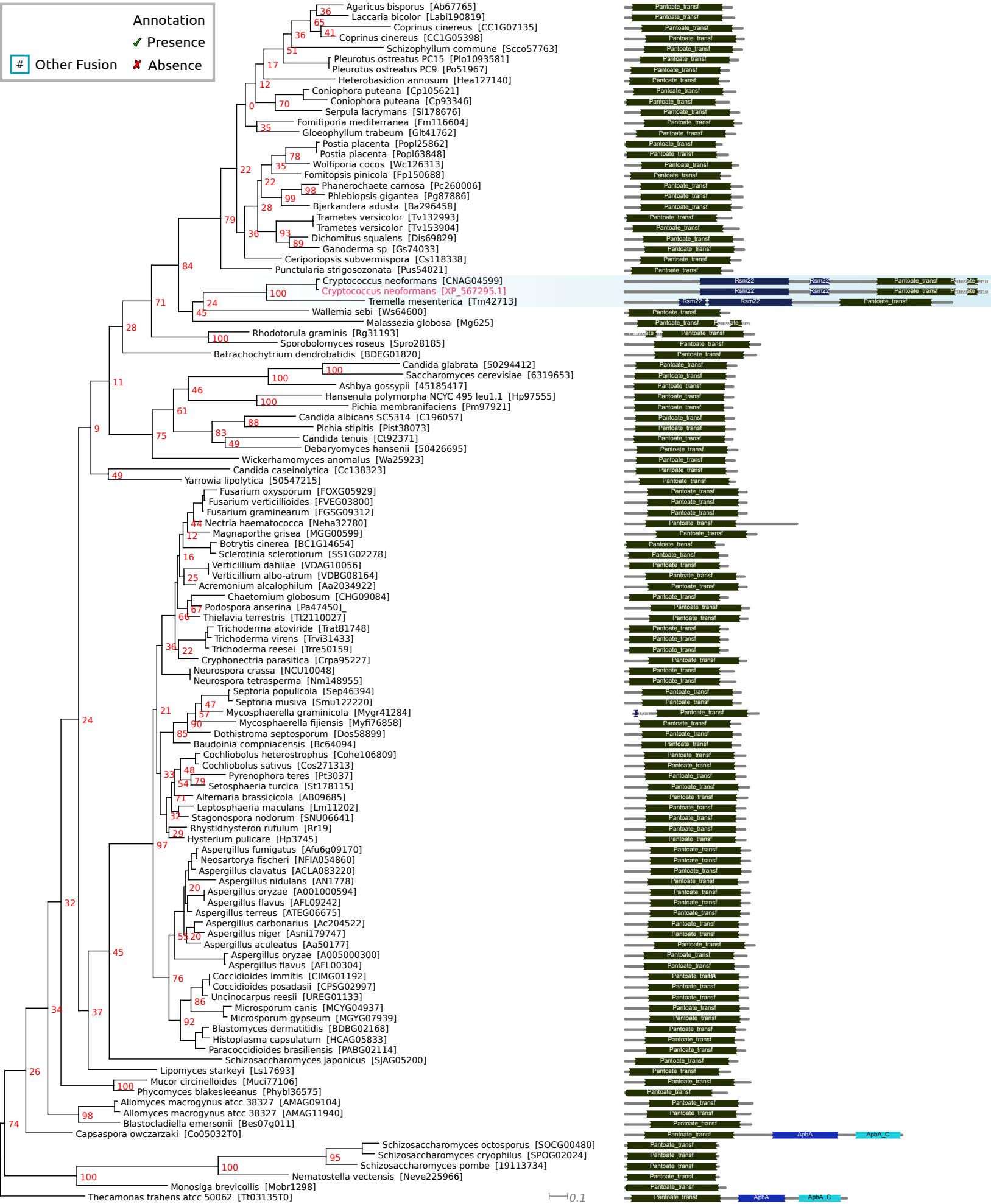
```
phyml -i alignment_file -d aa -b 100 -m model -c 8 -v invariant_sites -s BEST --quiet -a gamma
```

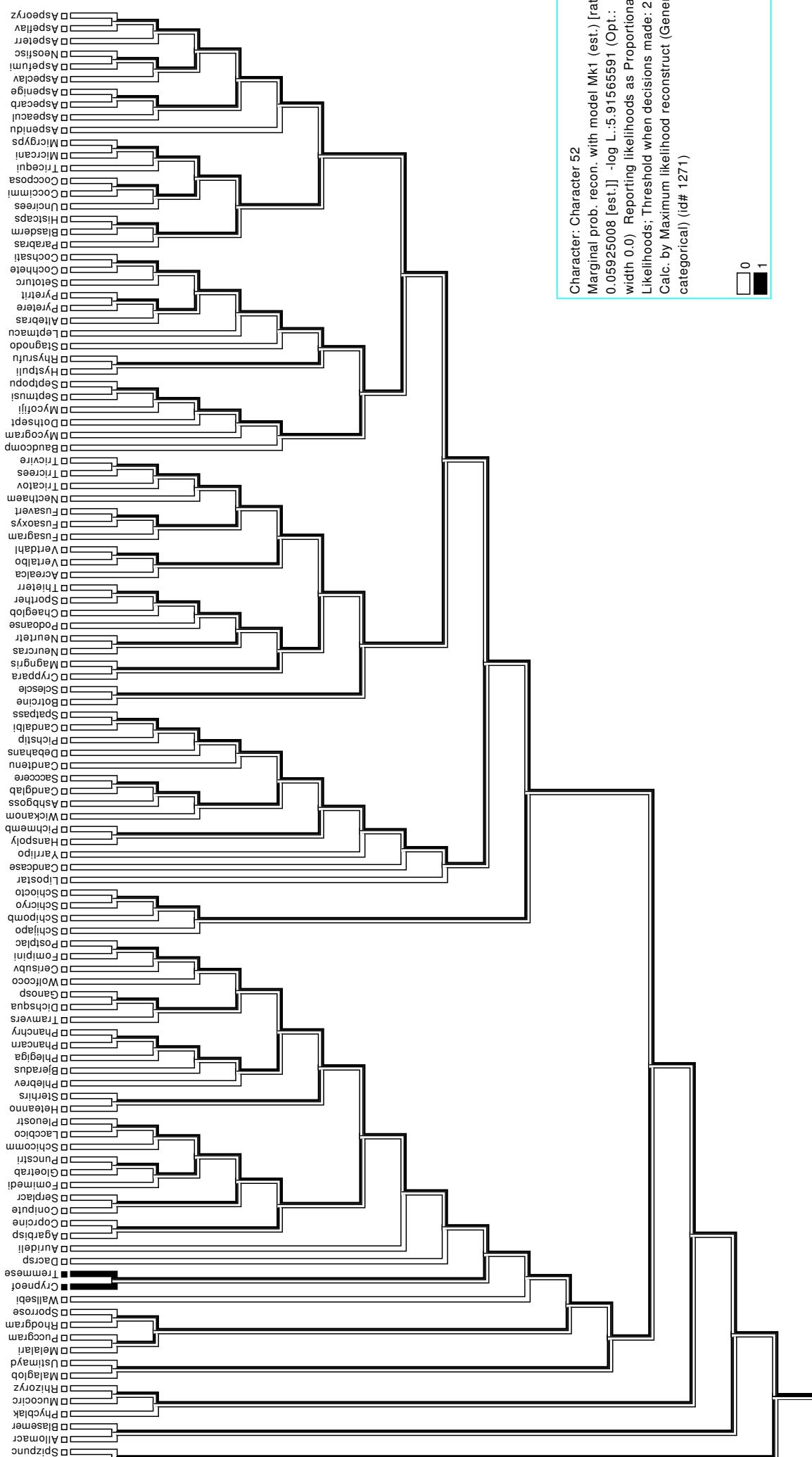
Styling and annotation was made possible by Dendroscope and Inkscape.

3 Mesquite Cladogram

This tree is the 68-gene concatenated phylogeny (Fig. 1), with the presence of a fusion (black), presence of a fission (white), and absent/undetermined (grey) status of gene fusion characters plotted on to it using a "1/0/-" nexus-style data matrix. We used the program 'Mesquite' to calculate proportional likelihoods based on either an "Mk1" or "Assym. 2 param model." (see Table S4) of character change across the fungal phylogeny (Fig. 1). This allowed for a proportional likelihood of the position of the fusion/fission to be calculated.







Putative Fusion 52

September 27, 2012

1 Fasta Sequences

These are the unfused sequences identified by fdfBLAST belonging to the putative gene fusion in FASTA format. Accessions may be shortened, but belong to either the taxons individual genome project or NCBI's accession numbering.

```
>EEH048921Ajca_dom1
MEDDTELSQSLYSMILAPFTEARRTIISKPARRYINTILFCLETSAAALLCISIVAYWIFY
YNYVPQISLERQVHLQFGDGHPYGTATLGTELIAAQYDVSVILYLPRSPPNLAAGNFMV
DLALFSSAKTNNTKIPTEASSIESRRPAIMTFTSPMVDTAKRVSKMPLYLLGWQREAE
GLKVNMMDRVEFGRKKGAMPKTLRLEIESEEKIQVYSAVVKFDAFKSGLRWIMYNWKIFS
ILTFTLTFWAVSMLFTSLVVVALASLAEPTVRTNPKLDEEEEENSSGISVKEEGSDG
EGASSKLTMPHERQMSDEPEKIKREENTEEYTVIQTLAGSDQPEAEAGAHPEVTSTSSQI
>EEH048921Ajca_dom2
TARDNSELVAQRRRGNWKIWKVGSLIKLAIYPVQYSIVFPPAVVNDGPPSNQSSPYVH
PLVHTLESAGHVVSVVLPHRQRSGKAHLVGATVKPTYFRPGTLHKDDGTIHHLPLGAE
GENDNMEPIVNEWILIDSTPASCVQIGLFHYFKDRGPIDLVISGPNYGRNSTAVFALSSG
TLGGALEAAVCGYRSIALSYAFSSRDHPVVIAEASRHSVRFLIGHLYKNWEEDVDFYSIN
VPLEAGVSEAKILYTNVLDNRWTSGSCFEAIDAAESGEGPDLQEQLRQAGEVDAGLGKG
TKPGTTTPGHRHMFKWAPKFSVDYKSVDLGPPGNDGWTVKEGMTSVTRLKANFMHSP
RPLGEIQLPFKTPIFYALVECQDSYVQPLVTQALRTRLHGIPYELIFSIRELPNPSSPLL
QYRVYEQCDFEHVLSHPATSLVNAYVIRKALIRKHYSNSVSNWAKHPDSILNAHVKP
VHFELDYAEFLDEALVEAYELQESFQANEGKEEAEKEWWILKPGMSDRGRGIRLFNSES
LREIFEGWEDDQPDSEDGEDSENGKVVANGNGKLNNDNRDDDHGIITSQLRFIAQPYI
HPPLLPSESNRKFHIRTYVLAVGSLQVYVYREMLALFAEKPYLSPWDSSGAGVDDLTRH
LTNTCLQTGRGGTAKQNSVRRFWALEDTAVPSLSSSSPPTSGEPNASTNWKESVYQKICA
VTGEVFEAAARGMLVHFQTLNAFEVFGVDFLVDSRGKVWLLELNAPFDFRQTGDELKD
VVGKLFEAVVEAVKPFVGIEKDIERAKARAQQLGLQLVRDLDGMKR
```

2 Annotated Phylogenograms

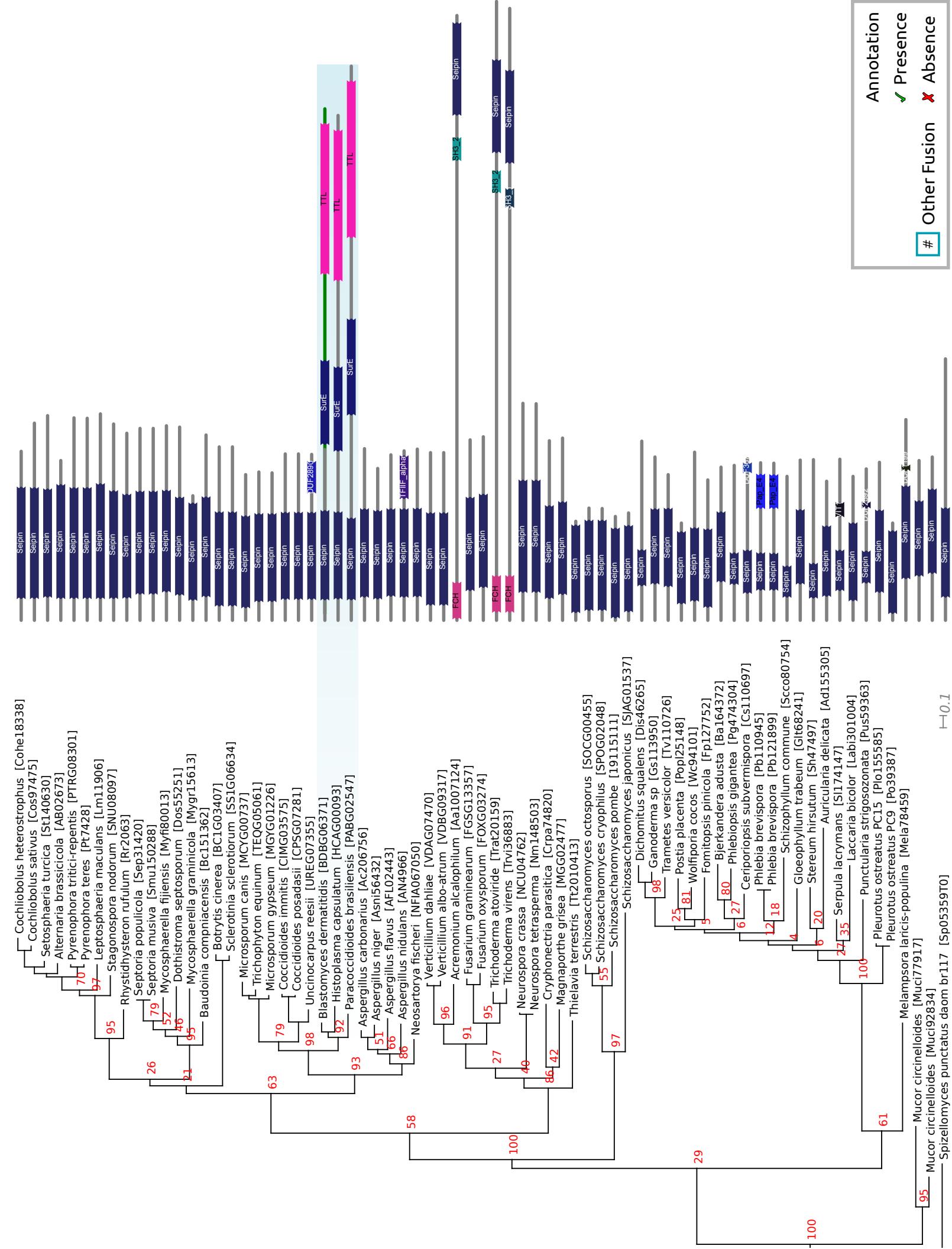
All trees were generated from an initial run of Darren's Orchard pipeline against 139 taxa (Table S1), using the above corresponding un-fused sequences as BLAST seeds. The alignments were then checked for any missing taxa, manually masked and then ProtTest3 was run, please see the Methods section for detail. The final trees were generated by the following command:

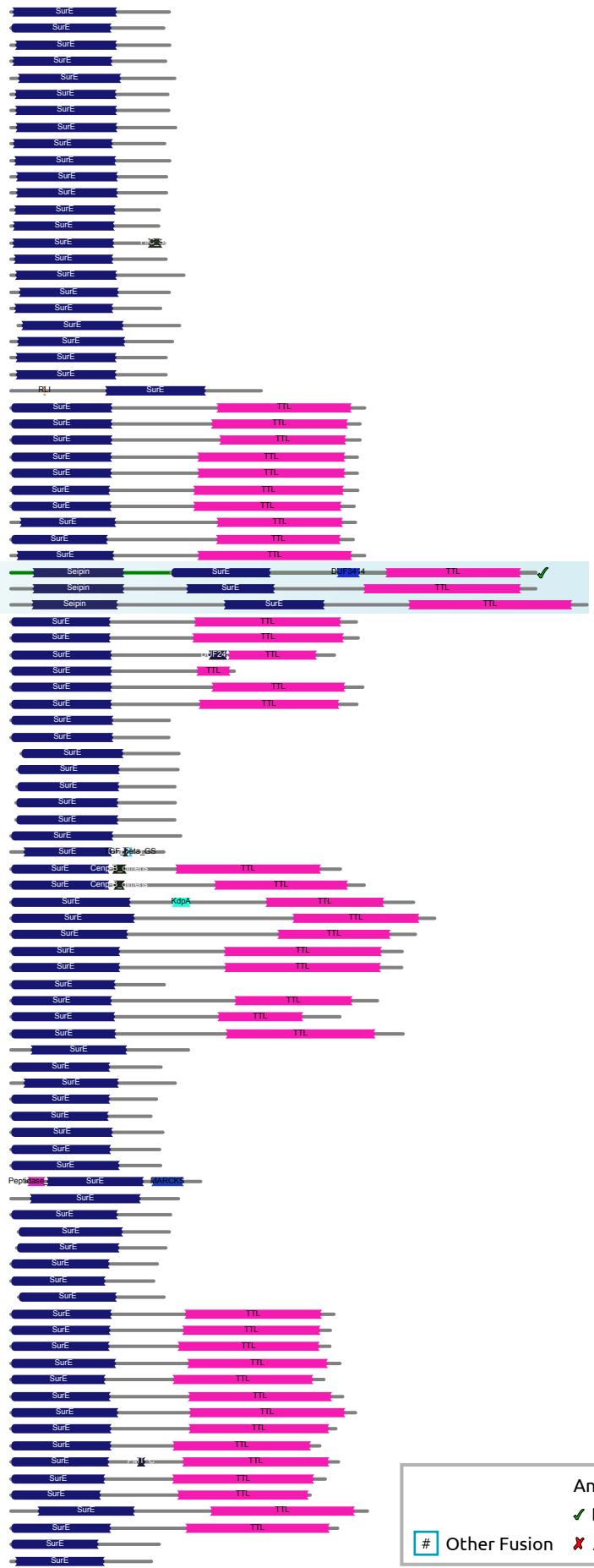
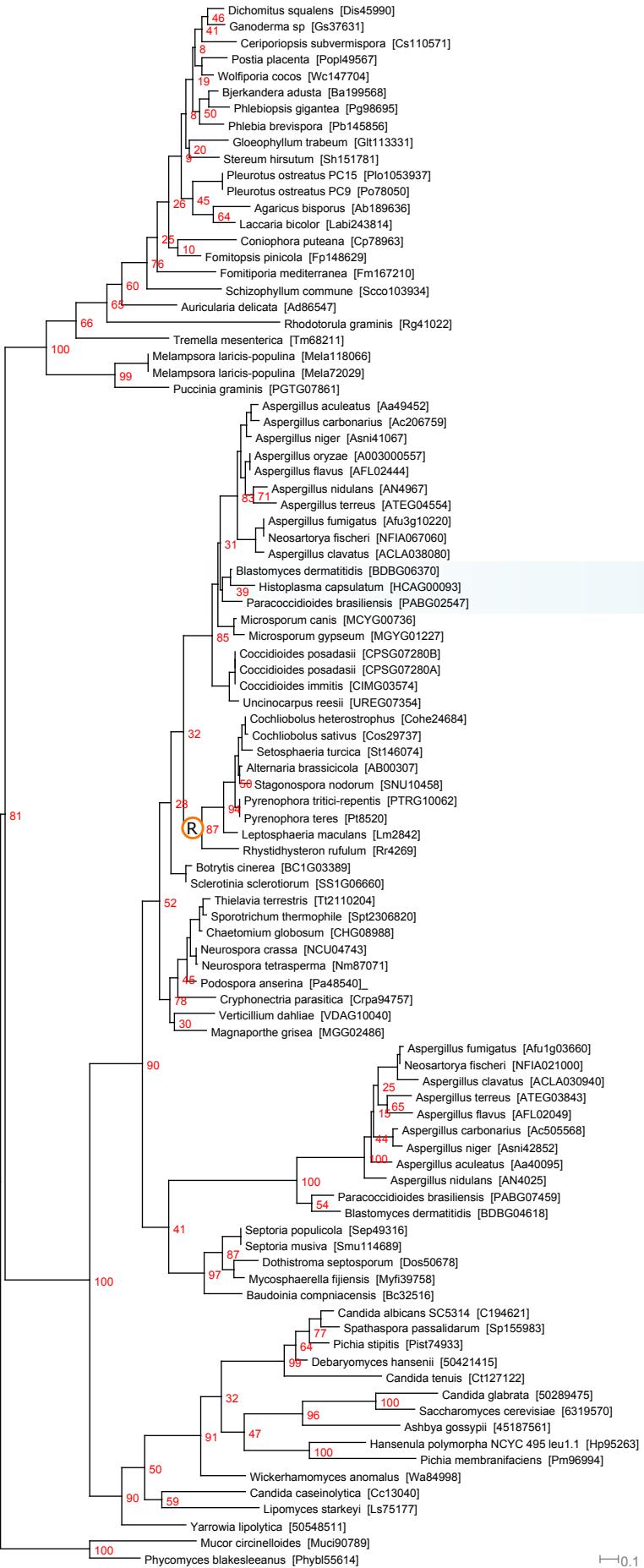
```
phyml -i alignment_file -d aa -b 100 -m model -c 8 -v invariant_sites -s BEST --quiet -a gamma
```

Styling and annotation was made possible by Dendroscope and Inkscape.

3 Mesquite Cladogram

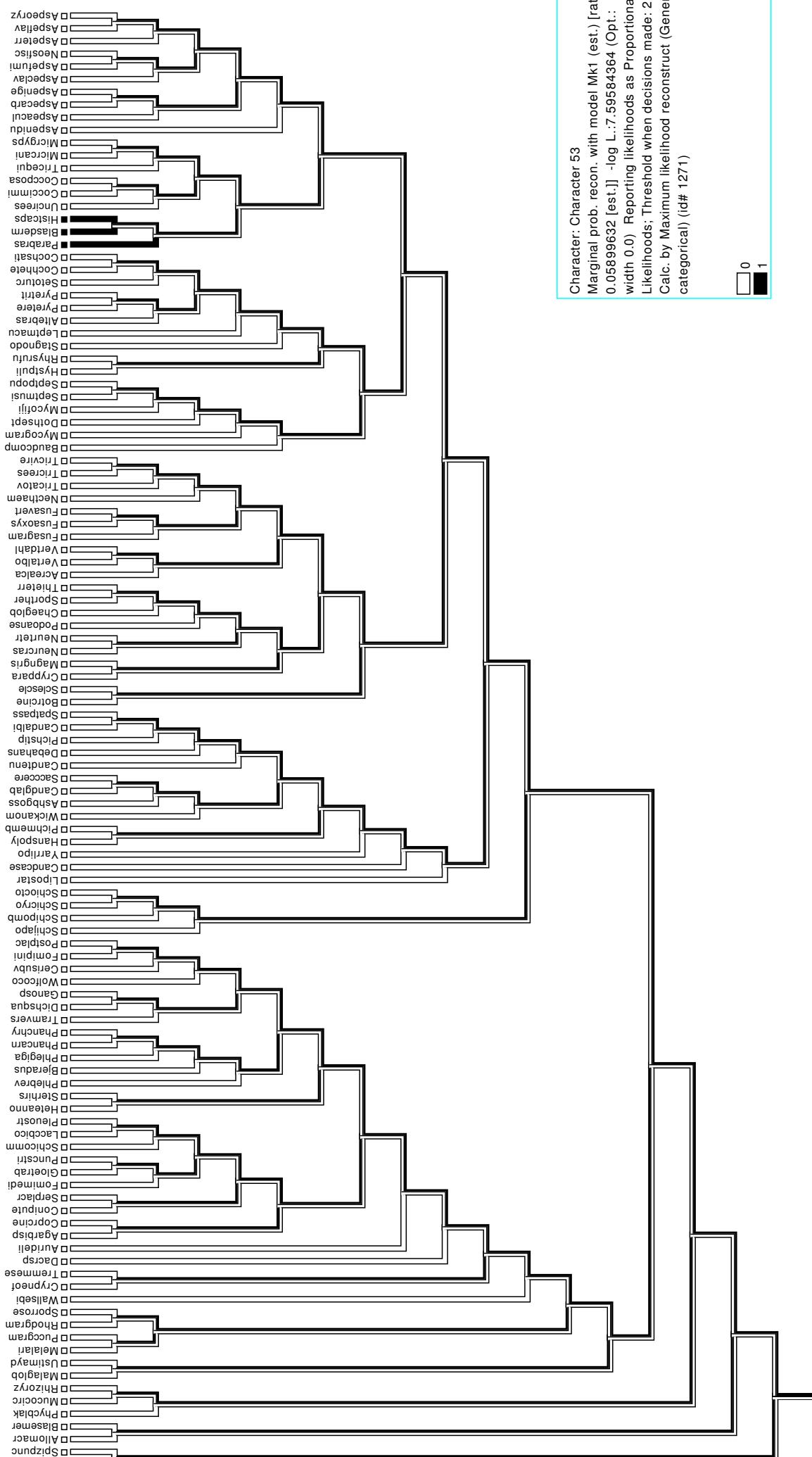
This tree is the 68-gene concatenated phylogeny (Fig. 1), with the presence of a fusion (black), presence of a fission (white), and absent/undetermined (grey) status of gene fusion characters plotted on to it using a "1/0/-" nexus-style data matrix. We used the program 'Mesquite' to calculate proportional likelihoods based on either an "Mk1" or "Assym. 2 param model." (see Table S4) of character change across the fungal phylogeny (Fig. 1). This allowed for a proportional likelihood of the position of the fusion/fission to be calculated.





10.1

Annotation
✓ Presence
Other Fusion
X Absence



Character: Character 53
Marginal prob. recon. with model Mk1 (est.) [rate 0.05899632 [est.]] - log L.: 7.59584364 (Opt.: width 0.0). Reporting likelihoods as Proportional Likelihoods; Threshold when decisions made: 2.0 Caic; by Maximum likelihood reconstruct (Generic categorical) (id# 1271)

September 27, 2012

1 Fasta Sequences

These are the unfused sequences identified by fdfBLAST belonging to the putative gene fusion in FASTA format. Accessions may be shortened, but belong to either the taxons individual genome project or NCBI's accession numbering.

```
>AE0673831Thte_dom1
MSSRPHPGHDAPAHPSGLRNTFTVSSASSTDEPSEPSEPGSPVSHAVSVPPHRHAAG
PSRPRPTEATALLDALDLREQAHEGPCSHGTFSPRPTSPTGSSLAADLASPSESEGECAA
DGPSDRPGSWRKRWAAKIRSKKMSATSALARRHGVKHSALMYLSYYLPVIAWAPEYSWSY
FKGDFVGALTAVAGMYVPMALSLADNLNAHVPLNGLYSFVFNPVLVALLGSCPAMVVGPEA
AGSLLVGTVVKTSVDRGRTTDDDATMHARLCGIVAGMSGAMVLIAGVARLGFLDNVLSRP
FLRGFISAIGVVVAVDQLVPELGLSGLADRAHLGHASSVDKLAFIFRHLDQVHTLTLAVA
ATSFAVIMVCREVKRRLQPRYPAVAYVPDRFIVVVLSAFLAYWYQWDRAFGAVVLGKVEAA
SGHPFTFRWPLQPANLPHMRDAMSTSFLIALLGFFESSVAAKSLGPDGFAQIQLSPNREL
VALGTANIVGACFMSLPAGGGYGRSKVNKATGGRTPVASILLSGLTLLCILVLLPYFYYL
PKPVSSLISVVAWSLIEECPHDVSSFFVRIRAWQELGLMTIVLATIFFSLSFGMAIGVG
LSVLQVIRHATTRPRIQILGRIPGTNRFENAEANLDRLEFIEGCLIVKIPEPLTFANTGEL
KARLRRLELYGTGLAHPALPRLRREDCNRIIIFDIHGVTSLDGSQTQVLEEIVRDYRQRG
VRIFSRGPGRDSPFGRLRRSGIVDLAGGEHHFVDDVHEALKTEAEEARLGAAADGQSG
>AE0673831Thte_dom2
LPPCGRHRCEGRRRQDTIQTTCWPSRYLSDRSWQTLTNGRQNGKAEQQAATTKQTVRP
APDPARTTTQPHHPILMSLSTVSRRERILGALLGVAGDALGATVEFAAWEDVQANYPD
GVRDIVGGGPGFWPPGHATDDTDLTRAVLLAYRDAAQLNPPPLPPSAPPYVVARAHHMV
DWYEGRWPGRTPGQQPRDVGLATVIGITFKKTGDPRSGAGEALLGNGSLMRCIPTALF
QPDAERAFAETIDISIAITHDDFHCTIACAAYNAVVRALVDGTSPEGAFQAGKDAVERAAA
VAAAEPТАNQRVKMARAAQKVGAAAMDAGKSLIRVRDLAENGPKGAANASKALLNKASGYV
LESLTAVAALFDPRPLEEVLIDVVRFQDADTNGAIAGGLLGARDGVDAIPARWREKLQ
FEKEFTEVADGLLARQDSGN
```

2 Annotated Phylogenograms

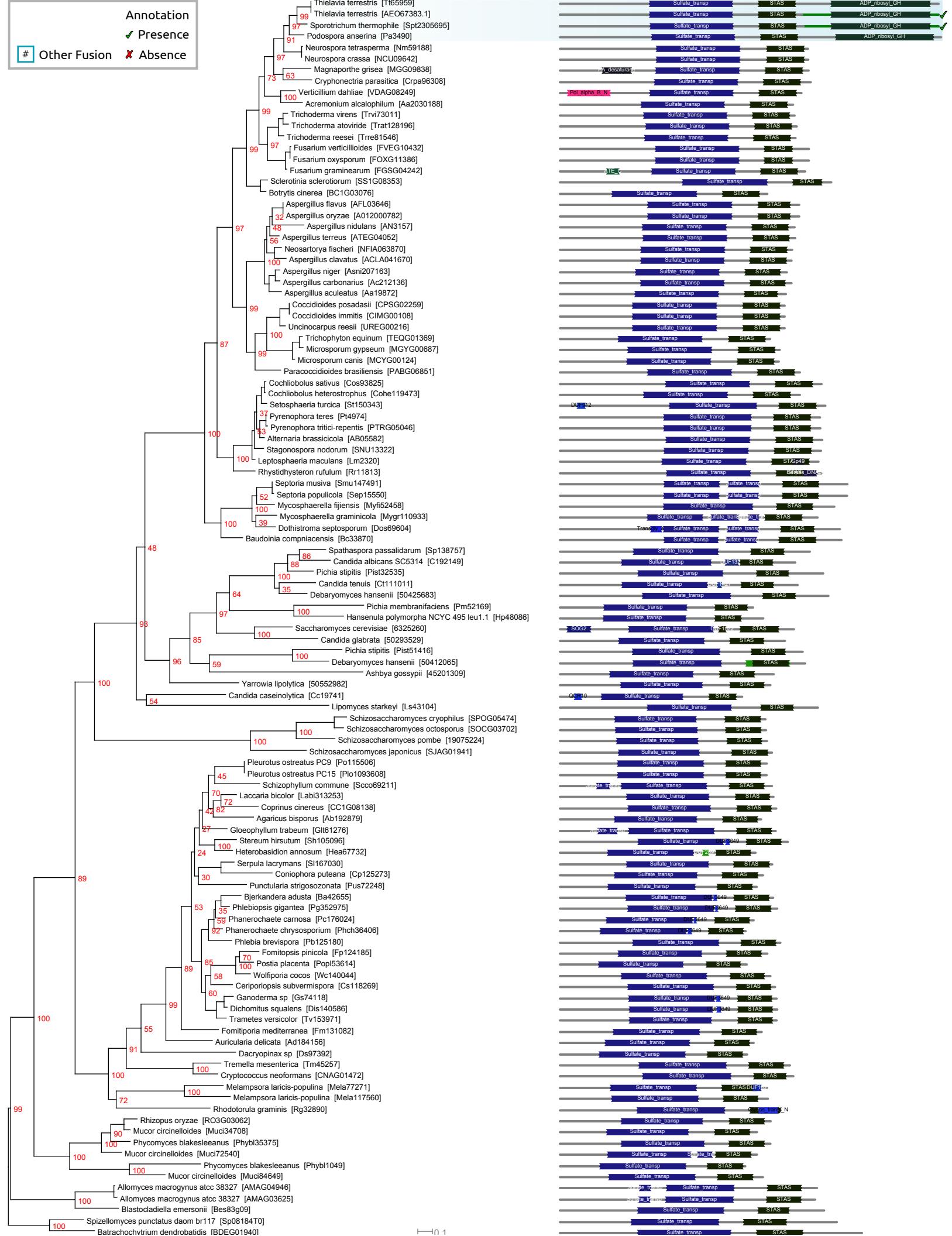
All trees were generated from an initial run of Darren's Orchard pipeline against 139 taxa (Table S1), using the above corresponding un-fused sequences as BLAST seeds. The alignments were then checked for any missing taxa, manually masked and then ProtTest3 was run, please see the Methods section for detail. The final trees were generated by the following command:

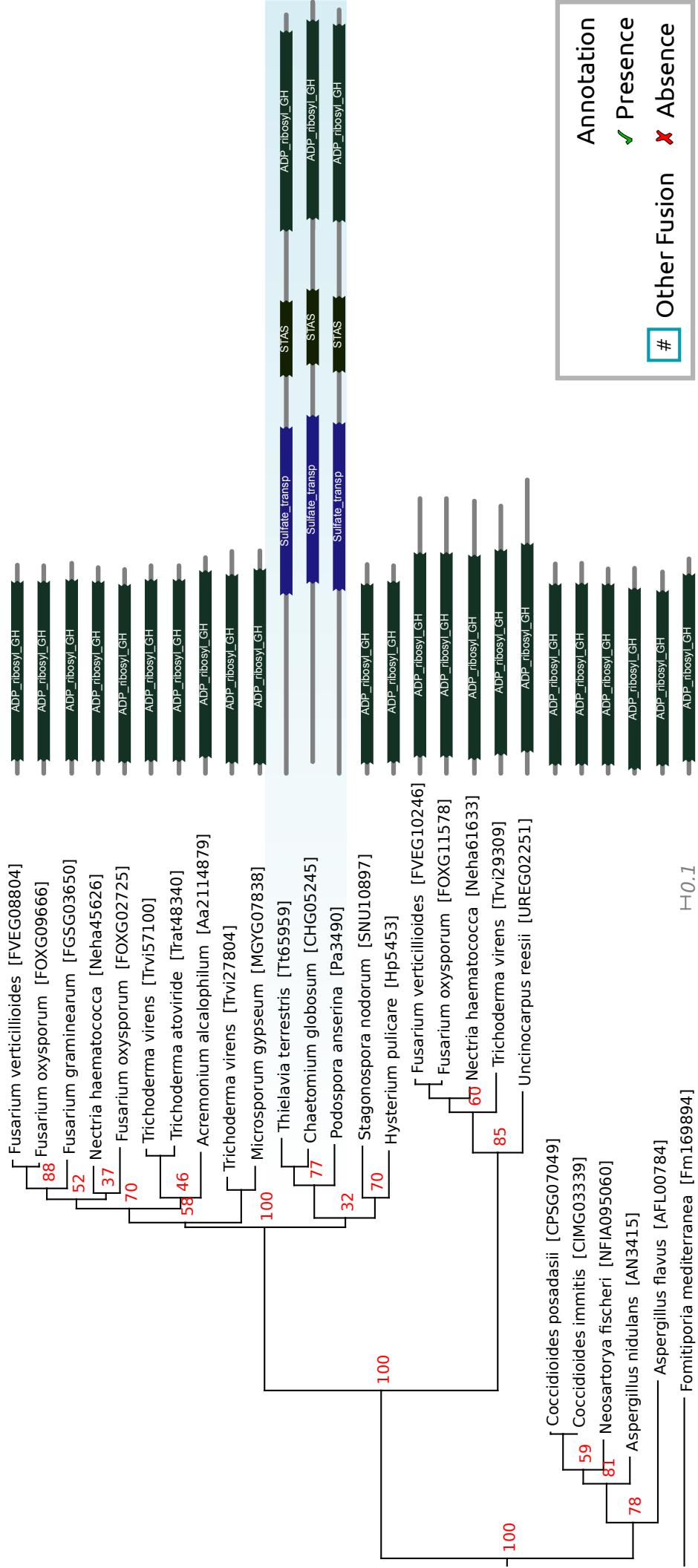
```
phyml -i alignment_file -d aa -b 100 -m model -c 8 -v invariant_sites -s BEST --quiet -a gamma
```

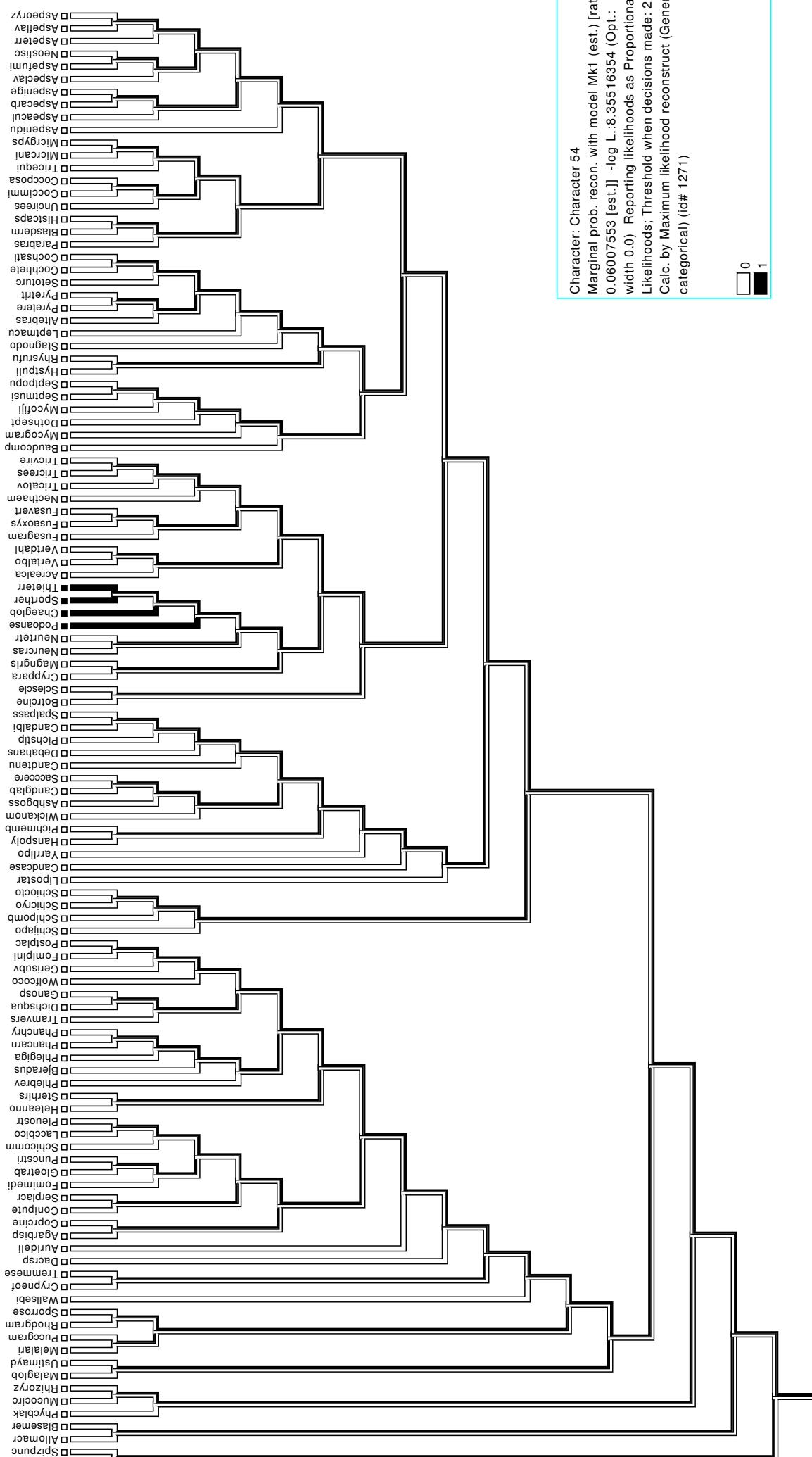
Styling and annotation was made possible by Dendroscope and Inkscape.

3 Mesquite Cladogram

This tree is the 68-gene concatenated phylogeny (Fig. 1), with the presence of a fusion (black), presence of a fission (white), and absent/undetermined (grey) status of gene fusion characters plotted on to it using a "1/0/-" nexus-style data matrix. We used the program 'Mesquite' to calculate proportional likelihoods based on either an "Mk1" or "Assym. 2 param model." (see Table S4) of character change across the fungal phylogeny (Fig. 1). This allowed for a proportional likelihood of the position of the fusion/fission to be calculated.







Character: Character 54
Marginal prob. recon. with
0.06007553 [est.] - log
width 0.0 Reporting like
Likelihoods: Threshold w
Calc. by Maximum likeli
categorical) (id# 1271)

Putative Fusion 54

September 27, 2012

1 Fasta Sequences

These are the unfused sequences identified by fdfBLAST belonging to the putative gene fusion in FASTA format. Accessions may be shortened, but belong to either the taxons individual genome project or NCBI's accession numbering.

```
>EHA275671Asni_dom1
MPSALTFDLHAKCSTTKARASTLRLPHGDVPLPIFMPVATQASLKGLTYDQLRQTGCQLC
LNNTYHLGLKPGQAVLDAVGGAHKLQGWDRNILTSGGFQMVSLLKLATVTEEGVRFLSP
HDGTPMLLTPEHSISLQN SIGSDIIMQLDDVIATTSPDQARIHEAMERSVRWLRCIDAH
KYPERQNLFCIIQGGLDLEMRKQCCEEMVARDTPGIAIGGLSGGEAKEDFCKERVDTCTG
LLPEKKPRYVMGVGYPEDLIMGVALGADMFDCCWPTRTAESTPQSTTTTTPQEPIP HD
PTHEEHQYLNL I
>EHA275671Asni_dom2
PTHEEHQYLNLIRRILSEGEHRPDRTGTGTRSIFAPPQMRFSLSKPSTNTTGKEYTPI
LPLLTTRKRVFLRAVLAELLWFISGTTSSLPLSEAGIKIWGDNGSREYLDKVGLSHREVGD
LGPVYGFQWRHFGAEYVDAKTDYSGQGV DQLAEVVKKLKENPFDRIIMSAWNPKDMRIM
ALPPCHMFAQFYVRFPDAKRDEEGVVRDGEWGRGHLDCLLYQRSADMGLGVPFNIA SYAL
LTHLLAHAVDMVPGLVHTLGDAHYLDHV DALKEQIEREPVAFPEVRIKREDRGSGVVD
GWKEEEFEVIGYKPHKAIKMKMSV
```

2 Annotated Phylogenograms

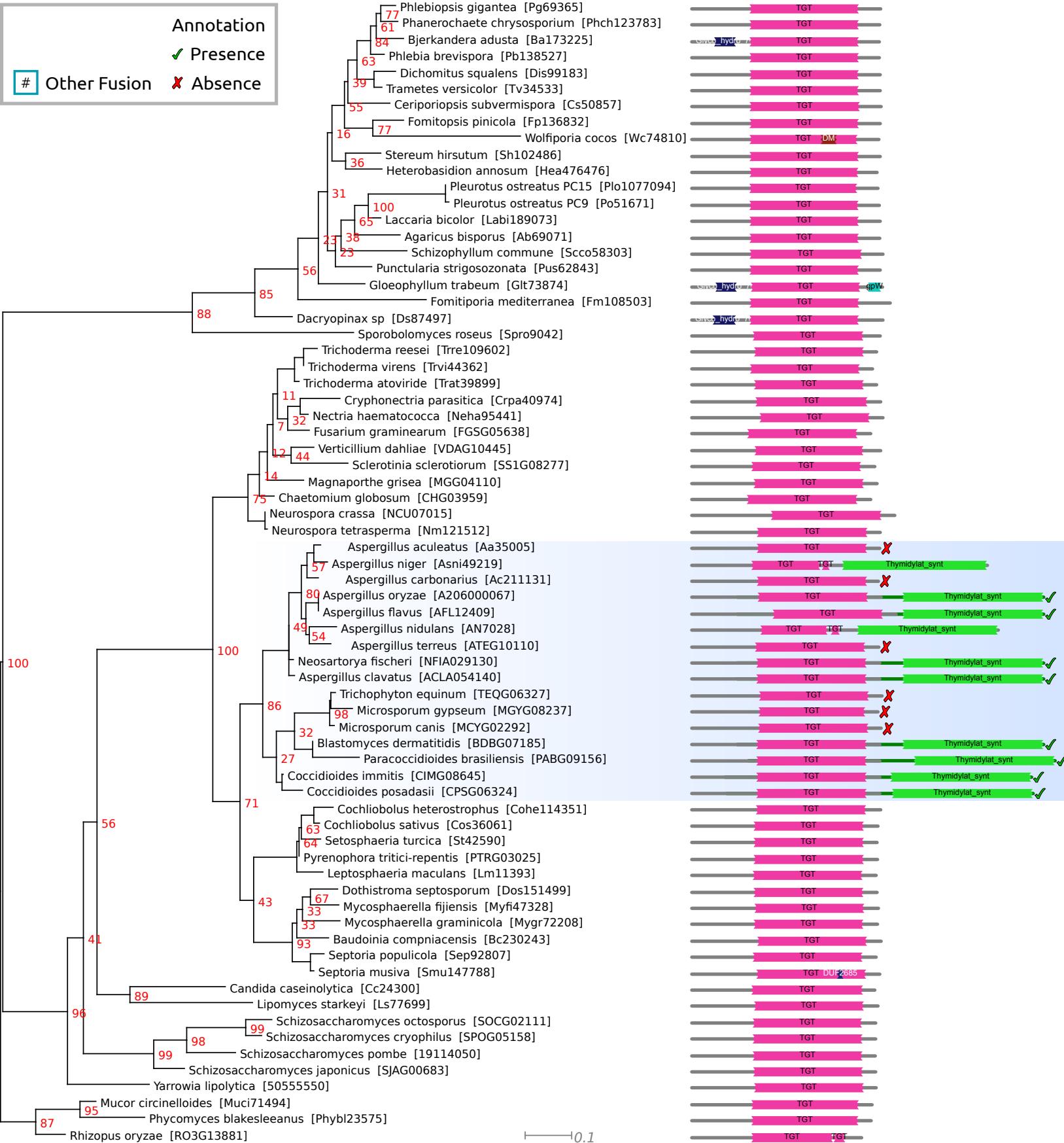
All trees were generated from an initial run of Darren's Orchard pipeline against 139 taxa (Table S1), using the above corresponding un-fused sequences as BLAST seeds. The alignments were then checked for any missing taxa, manually masked and then ProtTest3 was run, please see the Methods section for detail. The final trees were generated by the following command:

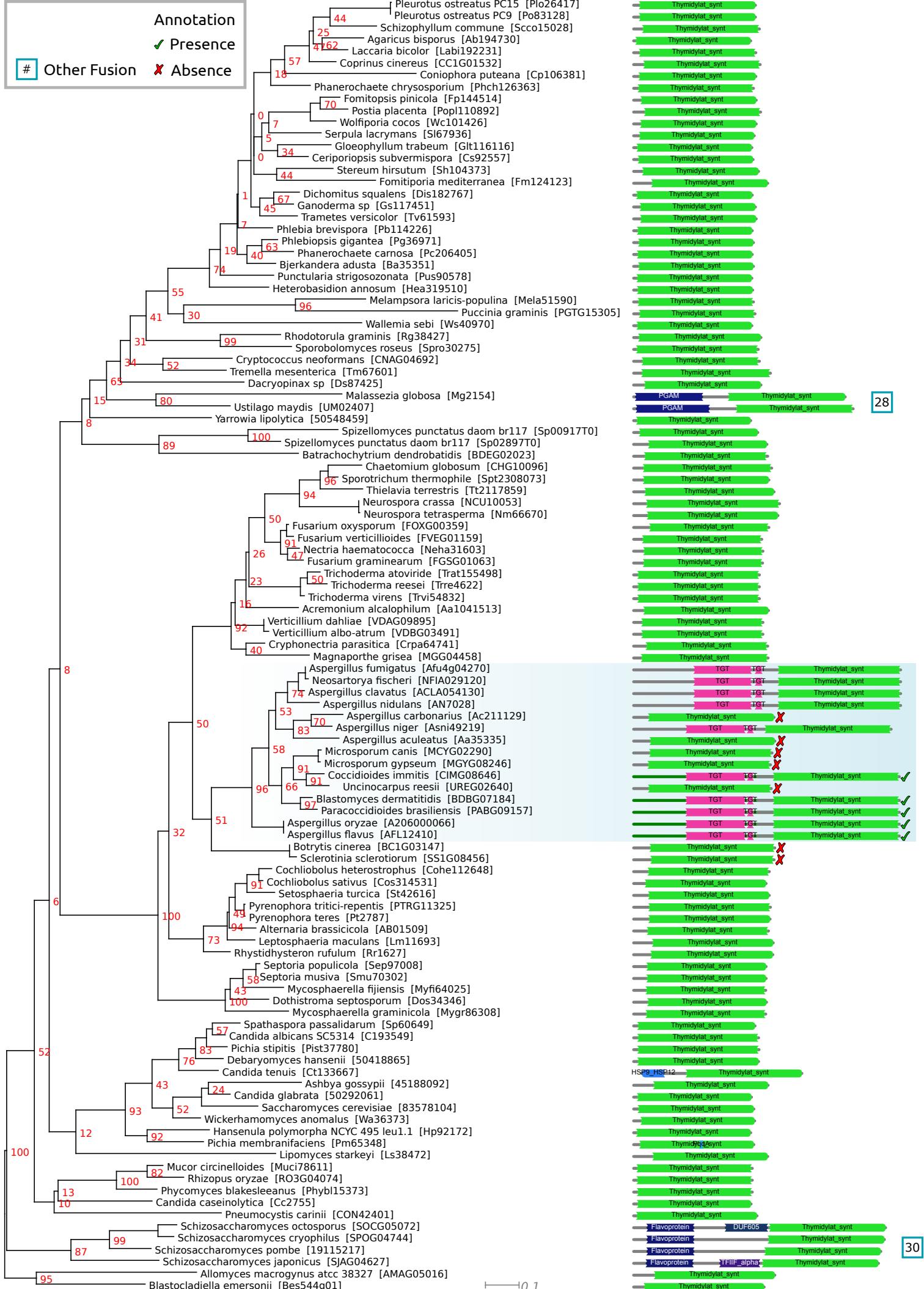
```
phylml -i alignment_file -d aa -b 100 -m model -c 8 -v invariant_sites -s BEST --quiet -a gamma
```

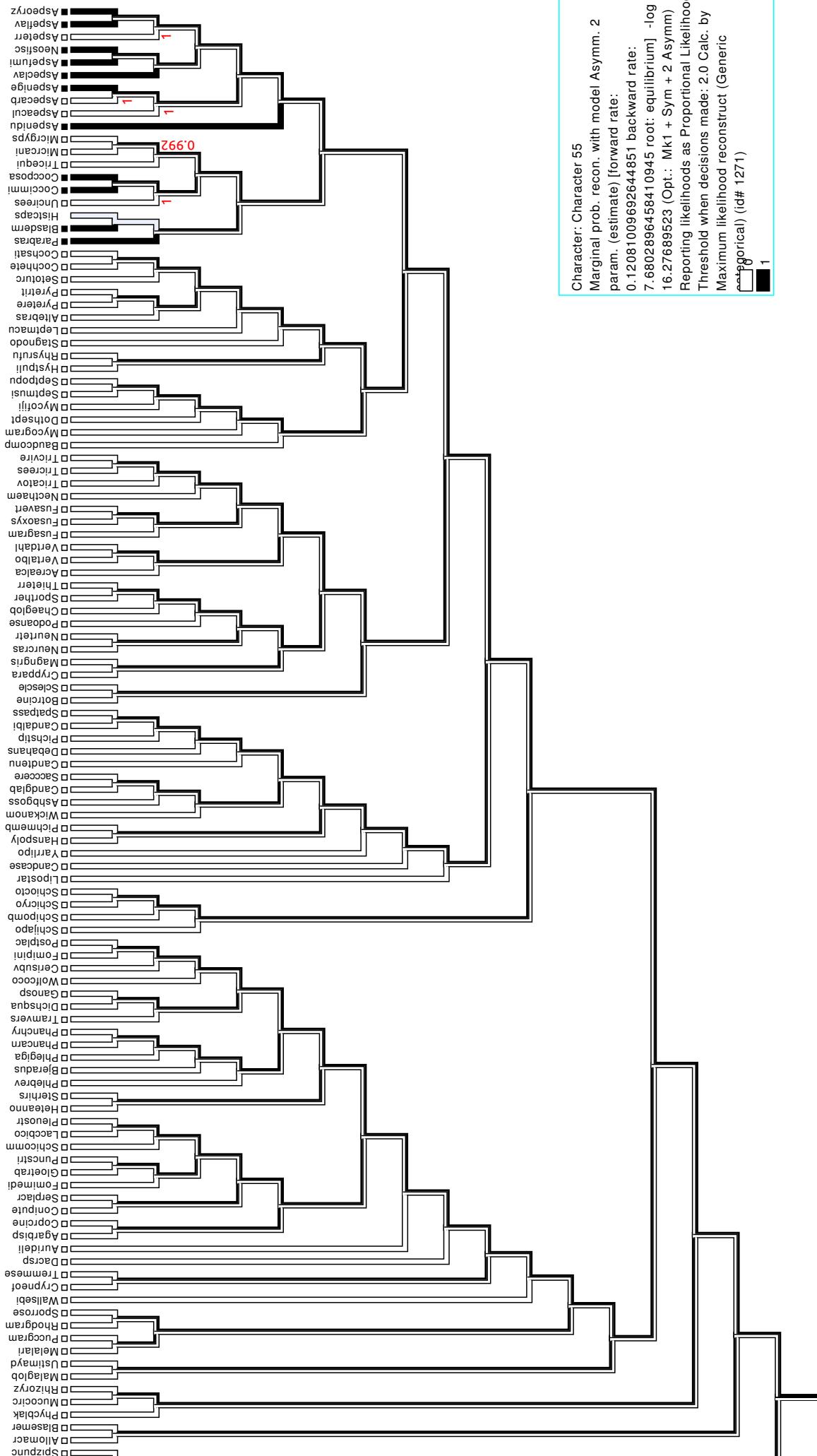
Styling and annotation was made possible by Dendroscope and Inkscape.

3 Mesquite Cladogram

This tree is the 68-gene concatenated phylogeny (Fig. 1), with the presence of a fusion (black), presence of a fission (white), and absent/undetermined (grey) status of gene fusion characters plotted on to it using a "1/0/-" nexus-style data matrix. We used the program 'Mesquite' to calculate proportional likelihoods based on either an "Mk1" or "Assym. 2 param model." (see Table S4) of character change across the fungal phylogeny (Fig. 1). This allowed for a proportional likelihood of the position of the fusion/fission to be calculated.







Putative Fusion 55

September 27, 2012

1 Fasta Sequences

These are the unfused sequences identified by fdfBLAST belonging to the putative gene fusion in FASTA format. Accessions may be shortened, but belong to either the taxons individual genome project or NCBI's accession numbering.

```
>XP_0033016801Pyte_dom1
MVLALHVWGPAGLPSIEPECIATIAYCQRVIPRGQWTLVAEHDPTVGVTESLPILFDDD
VATASGFEDIVAYLRNYPAITNDLDASLSSRQRTDRTAFITFLQSTATPLIDLSLYVSAE
NYNTTSSAYTAILPWYANYTVPPKRRQLARTAHMGLSSLDMDTTAEDGFAPGRGTAS
SEYEAKRAAGIPTESKANTSLSNIGRSKGTLGLGGQMYAARFKLDALSADLLDPLSDL
GRHDYLLHGEQPSSLDCLAGYLSLLIYPPVPQAWLRETIKMKYPRIGAYIHKLHGDLFR
>XP_0033016801Pyte_dom2
NDEVNSAEVWSISSSSAKTPRTTLLPVARSETFASKALASAKEIAGSIPGISKFSGST
VVAVSKRSKSELPSPLLVSFSRAPTASQIQSPPPPASSTKSGRFFGKANIGHTFRHKSA
GAFGPDLAKKLSQLVKMEKNVMRSMELVSRRMEVAQQLSIWGEACDDDVSVDVTDKLGVL
IYEIGELEDQYVDRYDQYRVTIKSIRNIEASVQPSRDRKQKITDQIAQLKYKEPNSPKIV
VLEQELVRAEAESLVAEAQLSNITREKLKAAFNYQFDAMREHCEKLAIAGYGKHLLELV
DDTPVTPGETRQAYDGYEASKAIIQDCEDALTNWVSQLNASVAKLSQRSRTLSQRRRNRN
HSEGVDLSGQDQALDRESGLWIPASEHHGNGYEGEELDDDINSTIASEHQRGREDERIVA
A
```

2 Annotated Phylogenograms

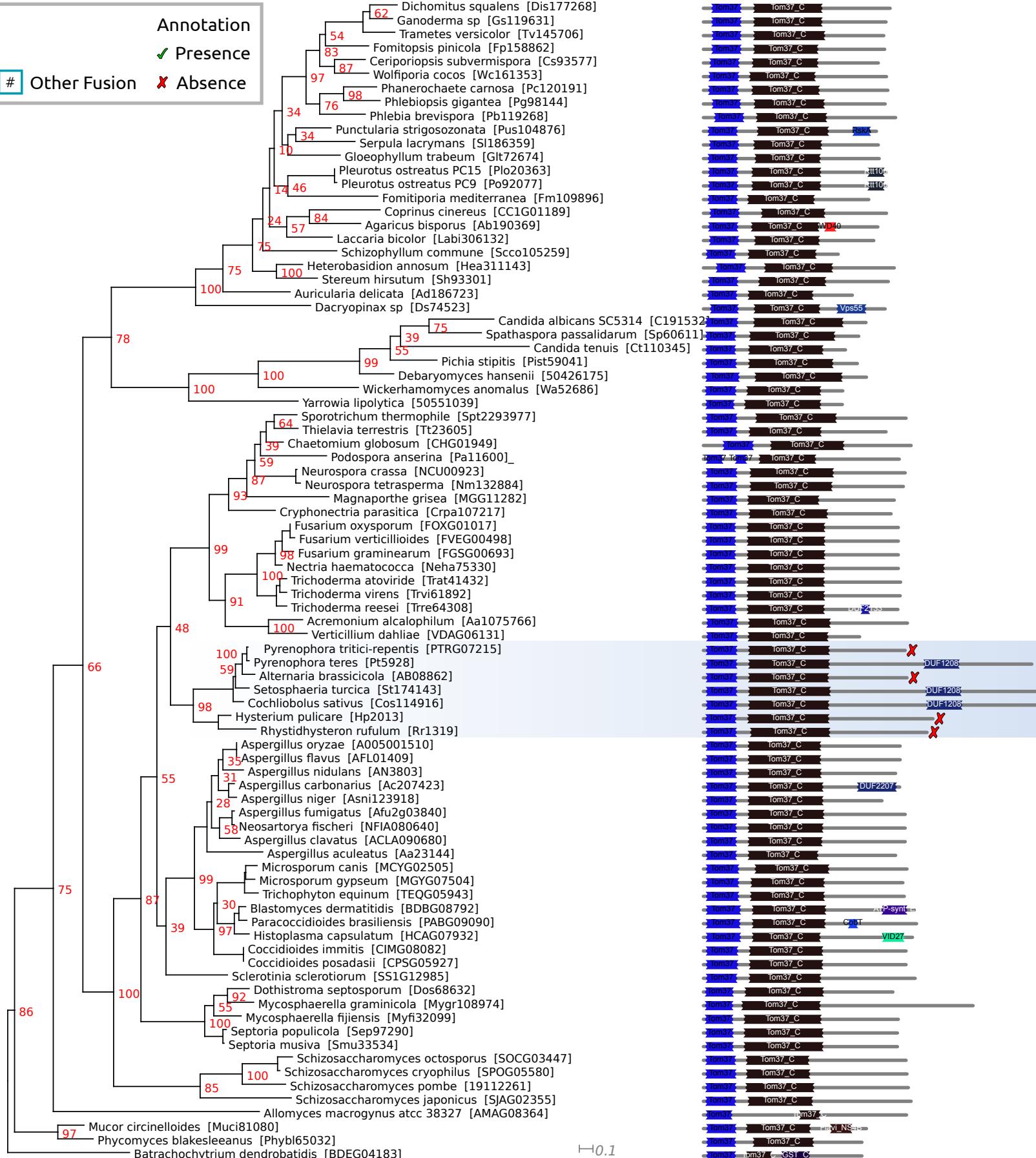
All trees were generated from an initial run of Darren's Orchard pipeline against 139 taxa (Table S1), using the above corresponding un-fused sequences as BLAST seeds. The alignments were then checked for any missing taxa, manually masked and then ProtTest3 was run, please see the Methods section for detail. The final trees were generated by the following command:

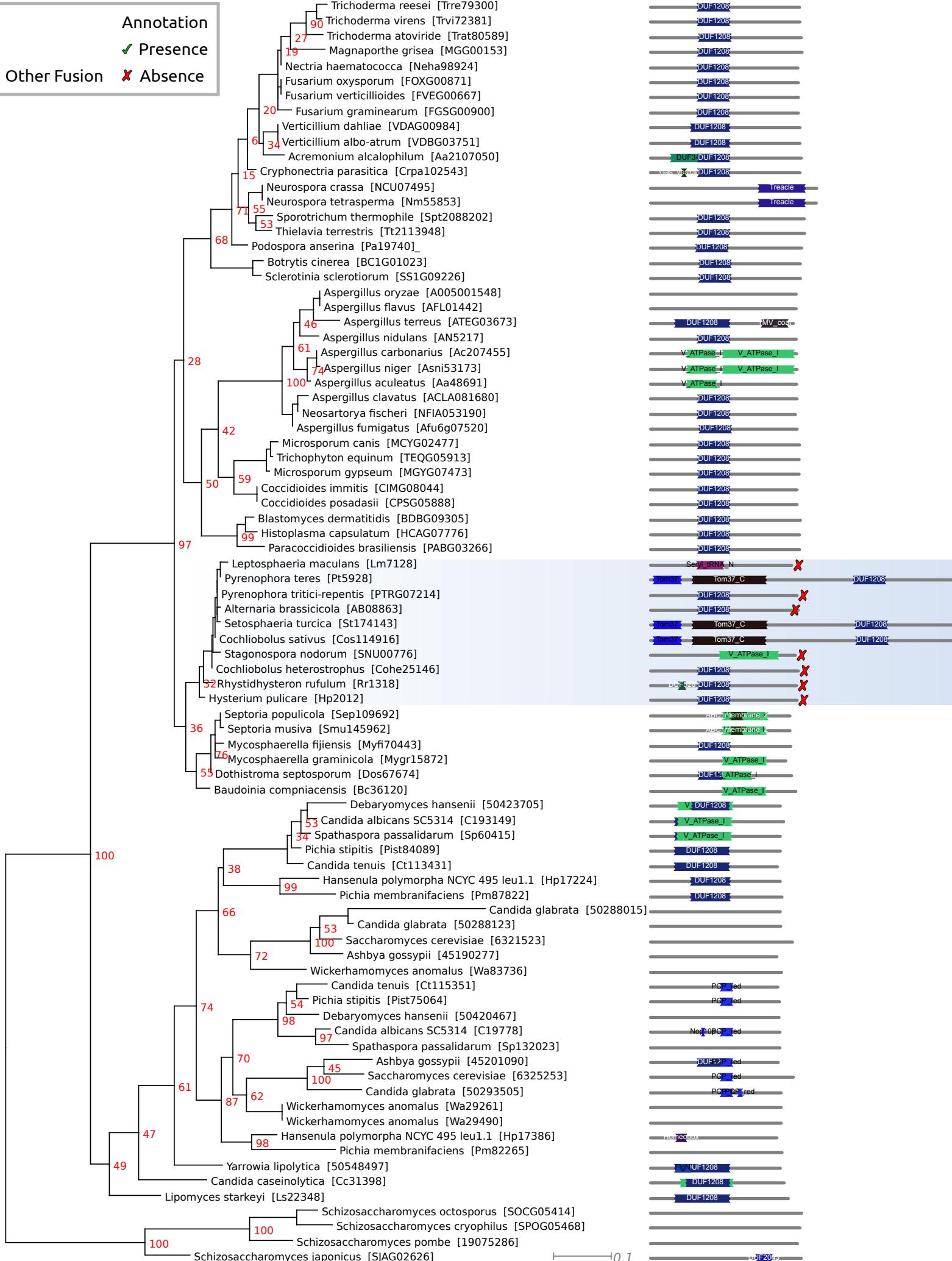
```
phylml -i alignment_file -d aa -b 100 -m model -c 8 -v invariant_sites -s BEST --quiet -a gamma
```

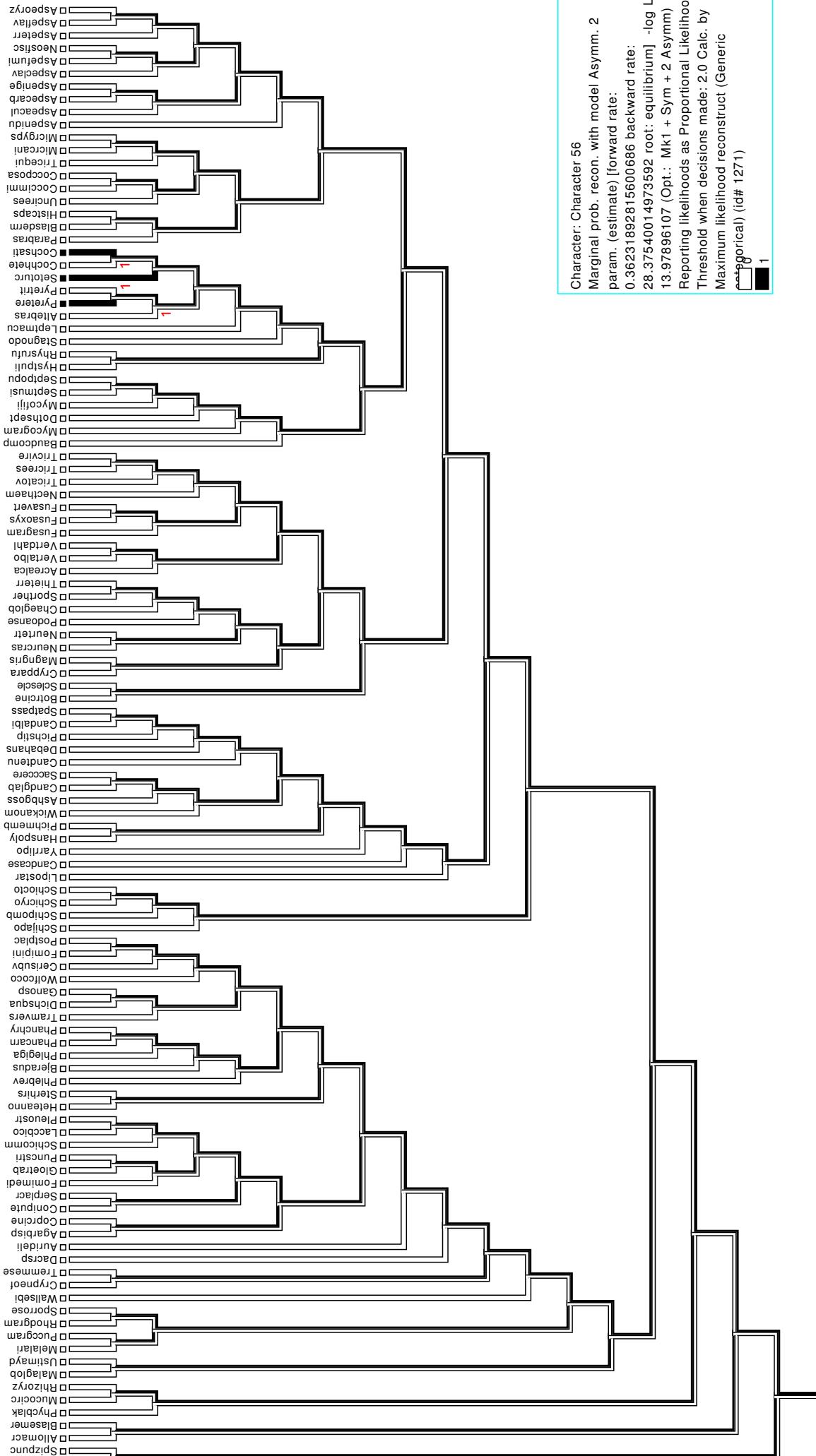
Styling and annotation was made possible by Dendroscope and Inkscape.

3 Mesquite Cladogram

This tree is the 68-gene concatenated phylogeny (Fig. 1), with the presence of a fusion (black), presence of a fission (white), and absent/undetermined (grey) status of gene fusion characters plotted on to it using a "1/0/-" nexus-style data matrix. We used the program 'Mesquite' to calculate proportional likelihoods based on either an "Mk1" or "Assym. 2 param model." (see Table S4) of character change across the fungal phylogeny (Fig. 1). This allowed for a proportional likelihood of the position of the fusion/fission to be calculated.







Putative Fusion 56

September 27, 2012

1 Fasta Sequences

These are the unfused sequences identified by fdfBLAST belonging to the putative gene fusion in FASTA format. Accessions may be shortened, but belong to either the taxons individual genome project or NCBI's accession numbering.

```
>XP_0029112401Coci_dom1
MDADLEKHIIEMARSQPAPVAGPRELSQEEIDAKLKALDDIPLFMKSLPDESENPVLAALQD
LAYEGTPDEIADNFKSRGNEYFKGKKYREAISFYTQGIEAKPTDPKIMTALLCNRAACN
LELQNYGSVLRDCSSALNDAHLSKAYYRSAQALLALDRLEEGLDCCDRKEAKEVQRERE
ERLKEQEAKRALAMAFRRERNLIDVPKPDGSSNPYEPRWDPEDPTNSTLVFPVFFLYP
QYATSDVIPDFVEDTIFGAHLMFPPAGTAPEWDKKGEYTVP SLVYAMTRRKRLFKV>XP_0029112401Coci_dom2
GKKMTLKDVFKAAPKKEGEPKDGLEVKDGCLTFVVVPKGDAEKKWVDEFKRSRDQISTES
SKRYNQKANLDQQKHTAVRRDQKGLSTANMSVTNKILRTANAPNTPPDEIETQVAQALID
LENNVPELKSELRLVLQISAAREVDVRGGKKAIIVIFVPVPQLKAFHKVQQRLTRELEKKFS
DRHVVFIAQRRLMLRKPTRTSRVKQKRPRSRTLSVHEKILEDLVFPTEIVGKRTRVAVDG
SKLLKVFLDSKDATSLEYKLDSSFSSVYRRLTGKDVVFEFPVVHGDKA
```

2 Annotated Phylogenograms

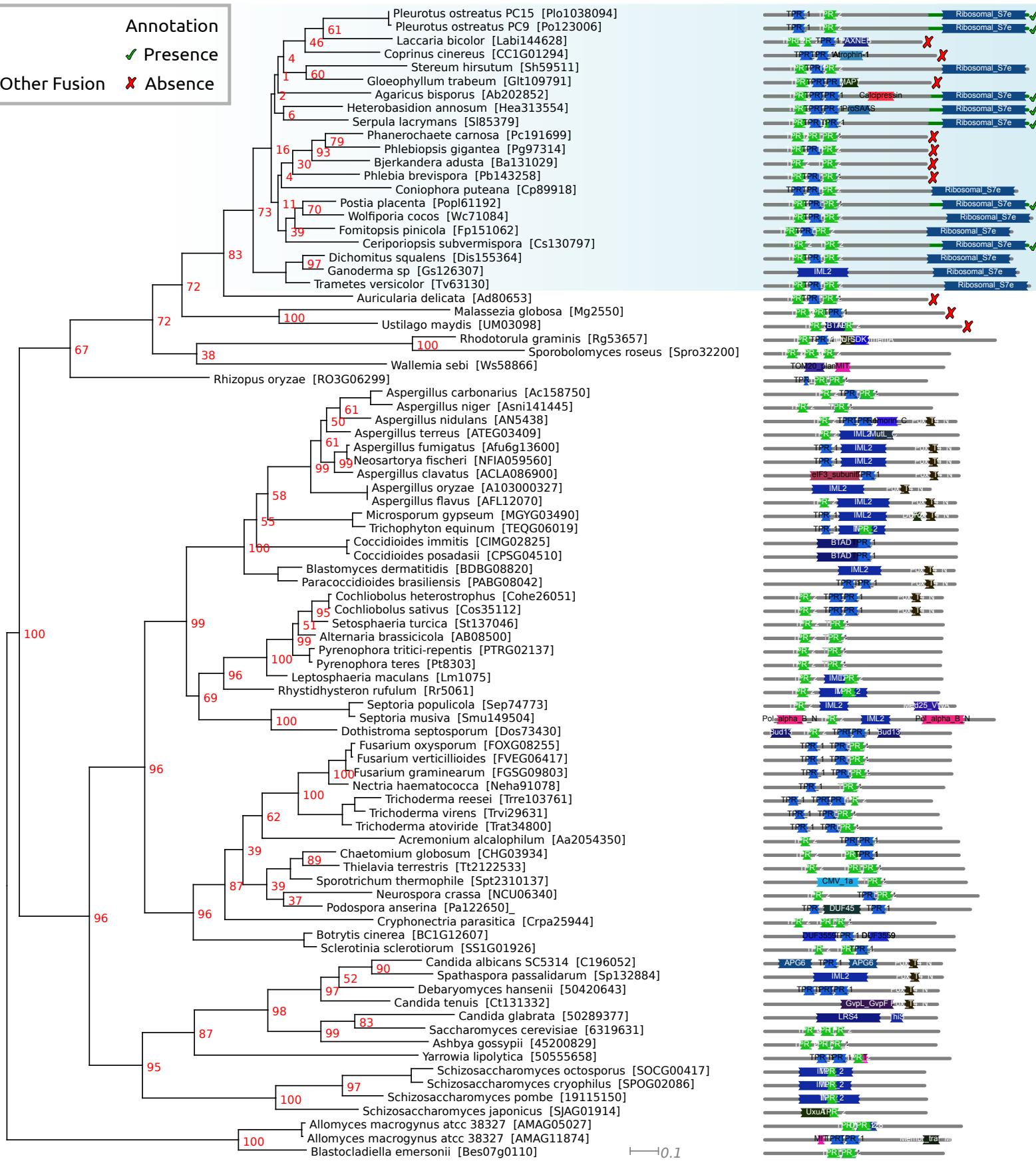
All trees were generated from an initial run of Darren's Orchard pipeline against 139 taxa (Table S1), using the above corresponding un-fused sequences as BLAST seeds. The alignments were then checked for any missing taxa, manually masked and then ProtTest3 was run, please see the Methods section for detail. The final trees were generated by the following command:

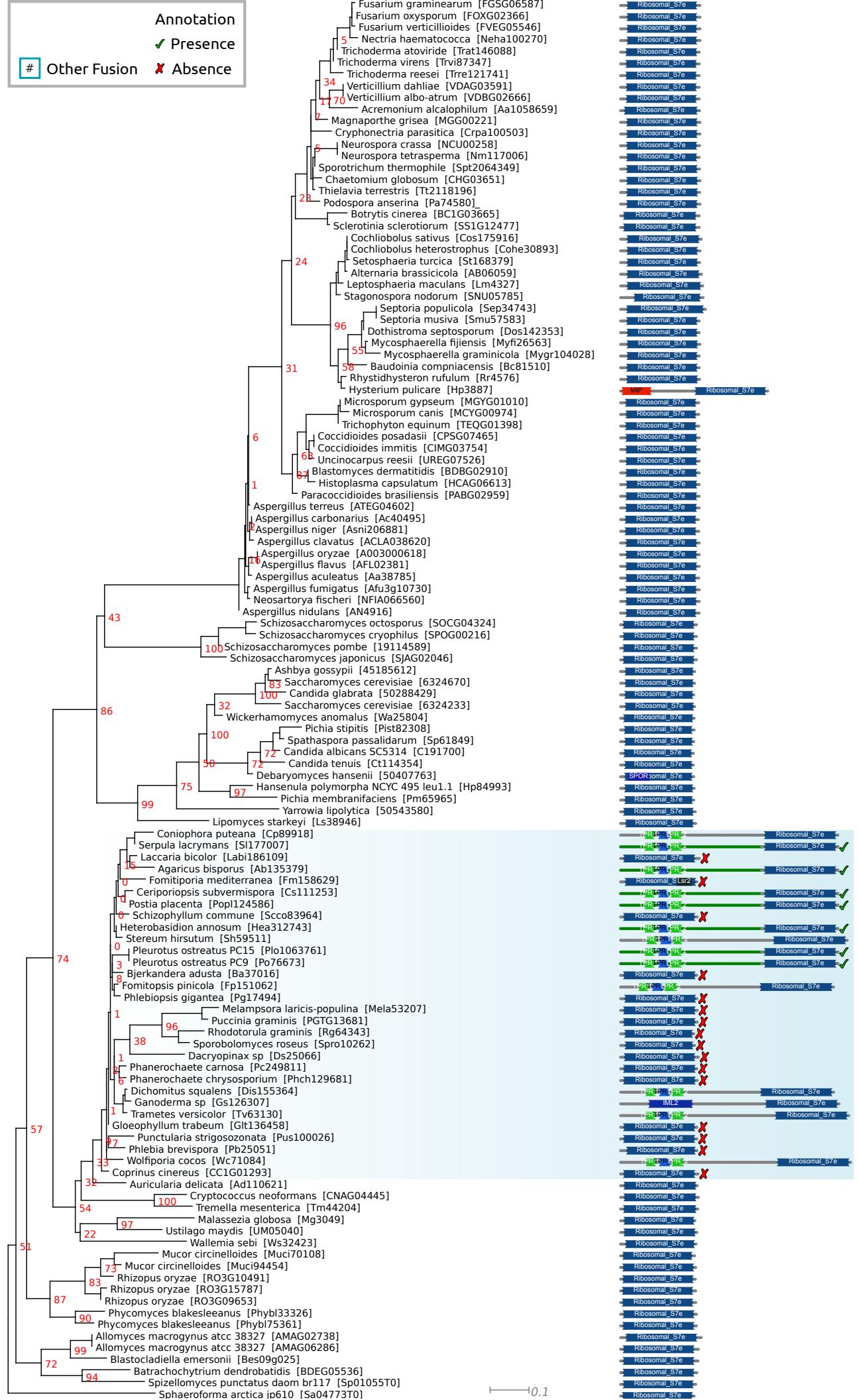
```
phylml -i alignment_file -d aa -b 100 -m model -c 8 -v invariant_sites -s BEST --quiet -a gamma
```

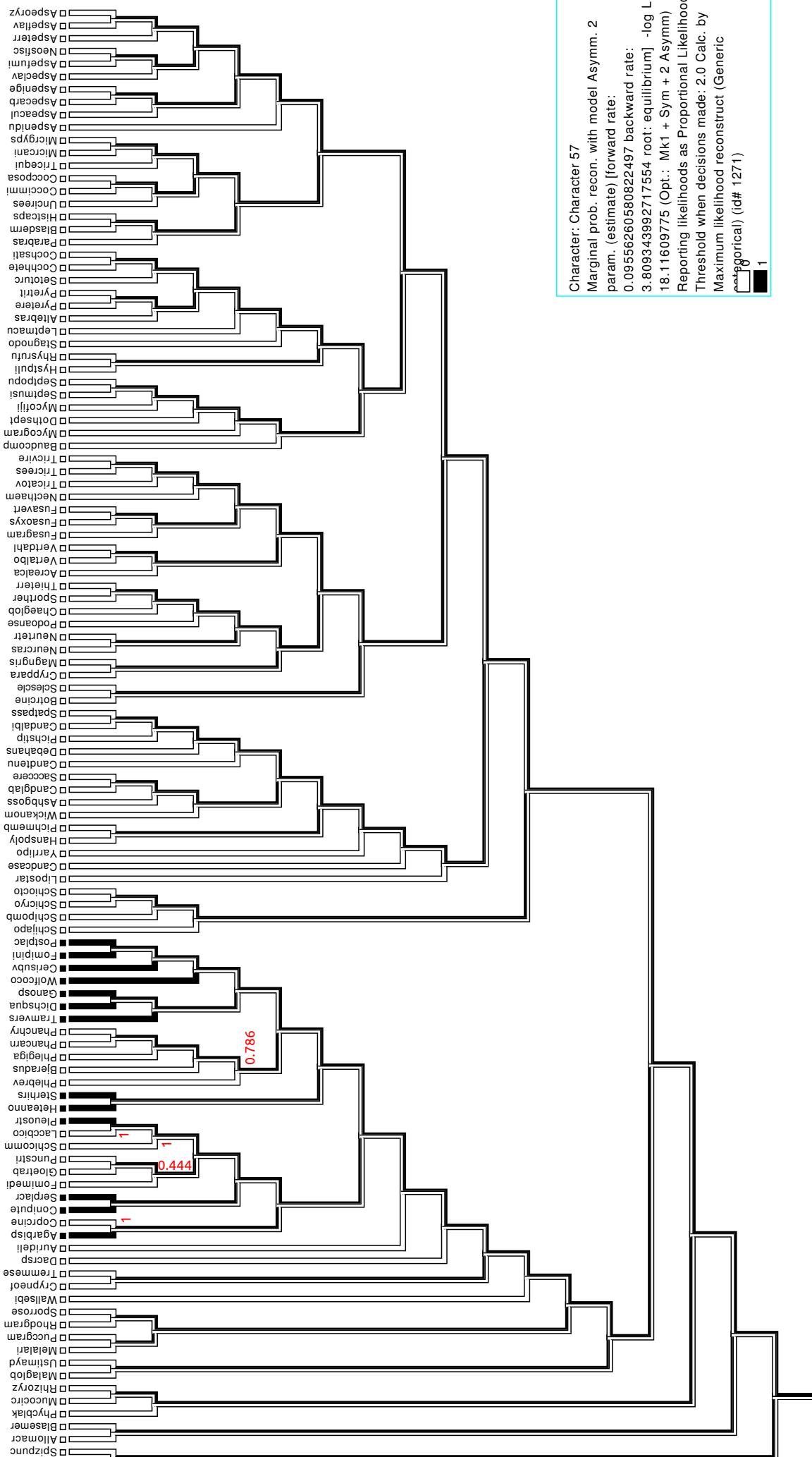
Styling and annotation was made possible by Dendroscope and Inkscape.

3 Mesquite Cladogram

This tree is the 68-gene concatenated phylogeny (Fig. 1), with the presence of a fusion (black), presence of a fission (white), and absent/undetermined (grey) status of gene fusion characters plotted on to it using a "1/0/-" nexus-style data matrix. We used the program 'Mesquite' to calculate proportional likelihoods based on either an "Mk1" or "Assym. 2 param model." (see Table S4) of character change across the fungal phylogeny (Fig. 1). This allowed for a proportional likelihood of the position of the fusion/fission to be calculated.







Putative Fusion 57

September 27, 2012

1 Fasta Sequences

These are the unfused sequences identified by fdfBLAST belonging to the putative gene fusion in FASTA format. Accessions may be shortened, but belong to either the taxons individual genome project or NCBI's accession numbering.

```
>XP_5665871Crne_dom1
MAAPSETTIQLSPEAEAQYERITRNLQEVTSGEVIRKVLSEGKVVKAYWGTAPTGRPHIA
YCVPLLKIADFLTAGVNVKVLLADLHAFLDASKSTLETVQYRVKYYSKLLITVFTVLGVP
TDKLEFITGSSYQLKPDYTLVDVYRFHALTSTREAEHAGADVVKESESPLMSSLYPGLQA
LDEQYLDVDFQFGGVQDRKIFMYAATFLPKLGYSKRAHLMNAMVPGLSGGKMSASDPKSK
IDFLDTAADIKSKIKAALCPPGEVENNGVIAFIKTVLIPIQALRIEQERRGEKAPVGEF
SFVKGPAPEGTIFSISRPEKFGGDIHFKSYEDLEKAYVAGDIHPGDLKTGVQEALIQFLG
PIRKSFDEDKEWQEVERTAYPSSSVAPTAEPKKAVSNKIVSLKKKDVRSKPPTEEERA
>XP_5665871Crne_dom2
LRAAKEKEKAAKAAKAVNEGTAAPPVPPVEDITASQLAQSSKEAVQITTSNATSSCVTST
NLSKLKLLAKGKVRDIYALPGKEDEDKLLFVATDRMSAFDVIMNNNGIPSKGITTTLSF
WFDKLKNIIPNHVLHPSPSACFSTPAQAWEQFPRSLDEYRDQLEGRSMIVKKCEVVKIEA
IVRGYITGSAWSEYKKSQTIHGIQMPAGLVESQKLPKALFTPSTKADQGEHDENIHPDKV
KDICGPELAAKIEKAIIQLYTEAAAYALERGLILADTKFEFGLLPDPPPSPNKTTLILIDE
VLTPDSSRYWAADYVVVGQPQPSFDKQYLRDWLIKEGLRGKEDVTLPEHVVSETRSKYEE
ARDRVMGLGEFGKHGQKGKIAQDEVALQTDQATDAIEEEARKQL
```

2 Annotated Phylogenograms

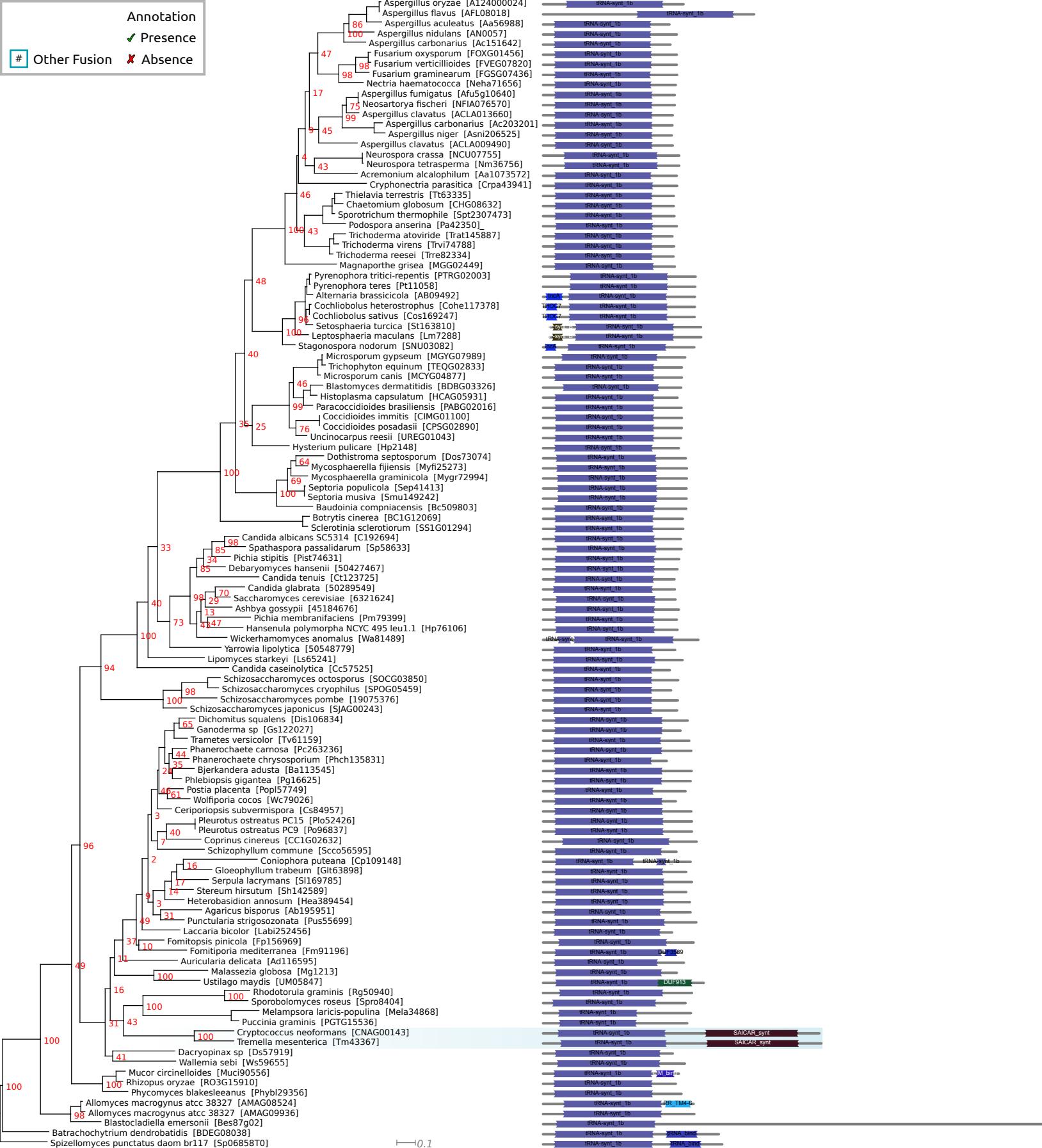
All trees were generated from an initial run of Darren's Orchard pipeline against 139 taxa (Table S1), using the above corresponding un-fused sequences as BLAST seeds. The alignments were then checked for any missing taxa, manually masked and then ProtTest3 was run, please see the Methods section for detail. The final trees were generated by the following command:

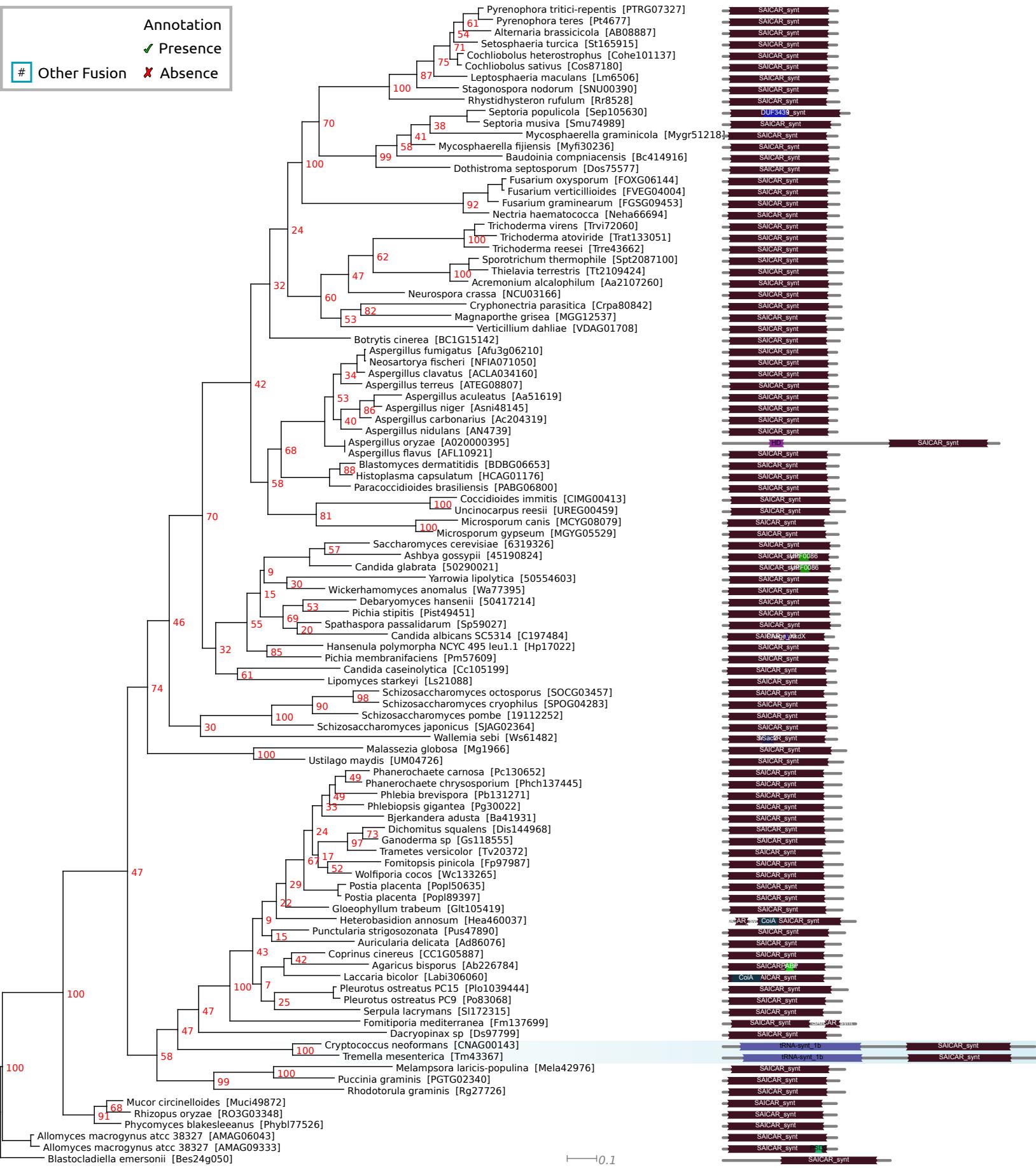
```
phyml -i alignment_file -d aa -b 100 -m model -c 8 -v invariant_sites -s BEST --quiet -a gamma
```

Styling and annotation was made possible by Dendroscope and Inkscape.

3 Mesquite Cladogram

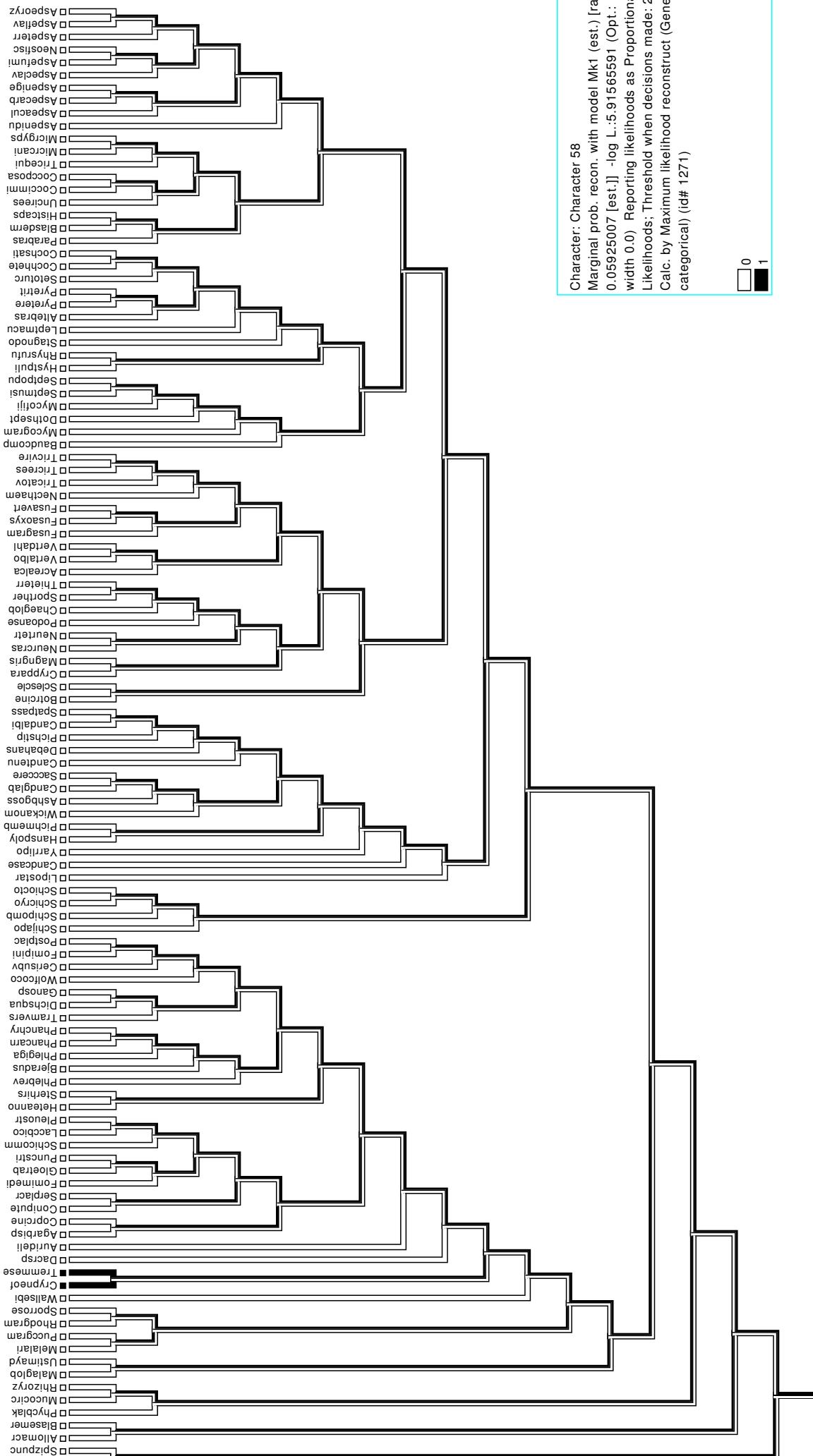
This tree is the 68-gene concatenated phylogeny (Fig. 1), with the presence of a fusion (black), presence of a fission (white), and absent/undetermined (grey) status of gene fusion characters plotted on to it using a "1/0/-" nexus-style data matrix. We used the program 'Mesquite' to calculate proportional likelihoods based on either an "Mk1" or "Assym. 2 param model." (see Table S4) of character change across the fungal phylogeny (Fig. 1). This allowed for a proportional likelihood of the position of the fusion/fission to be calculated.





Character: Character 58
 Marginal prob. recon. with model Mk1 (est.) [rate
 0.05925007 [est.]] -log L.: 5.91565591 (Opt.:
 width 0.0) Reporting likelihoods as Proportional
 Likelihoods: Threshold when decisions made: 2.0
 Calc. by Maximum likelihood reconstruct (Generic
 categorical) (id# 1271)

0
1



Putative Fusion 58

September 27, 2012

1 Fasta Sequences

These are the unfused sequences identified by fdfBLAST belonging to the putative gene fusion in FASTA format. Accessions may be shortened, but belong to either the taxons individual genome project or NCBI's accession numbering.

```
>XP_0012200951Chg1_dom1
MTSVYSPGSPILLPNGARIFNRLIDFLRQQYVRYGFQEVTPTIYKKALWAKSGHLENYS
DDMYTVTSTSPSRAEVTDRGEEAEYGLKPMNCPGHCLIFASQTRSYYRDLPIRYADFSPLH
RNEISGALSGLTRVRRFHQDDGHIFCRPSQIRDEIAKTLDFVRLTYGVGLGLGPYRLVLST
RPEQYIGSEEDWTQAESALREALVGSRQLQYTINPGDGAFYGPKIDIILKDSDGKEHQQTAT
IQLDFQLPKRFNLEYTAPAPEFEKRGAITTDAELLAEYGPVQPVLIHRAVLGSAERLMAL
LIEHYKGKWPFWLNPRQAIVITVNNEP VANWARQTRDILLGVSASTSTIEAASPTGLAI
DIDDSNRGVELKVREAKTKGYGLI1GVGPR
>XP_0012200951Chg1_dom2
DVETKTVGVNATSLAKPDATFHEIKKLKRIDMSPAKL RDYMLSSI KYNAMDLSNPSDPPP
DYITAARAHGIPLRQSAPIKKGPFPLELPILTHRSKRVILASASPRRKALLAQVSIHHS
PPCPFPLPSSQRTLLTPNPQIGLTNLEIIPSTEPEDLDKKTHTPEEYVAATARRKCLAV
YQTALTRQQATEHKQKQDVPNPVPDPRVLEDPAVVIADTVIATRGQFILEKPRSEADH
VRMLTHLRDTIRHRVLTAVCVLAPKADATHPGYEIASHVGETNVFFAGADDGLPDDVIES
YVRTREGADKAGGYALQGVGGMVLVDKVEGSVDNVIGLPVRKCLQLCERVVFRQGEEVEG
EDGEDEE
```

2 Annotated Phylogenograms

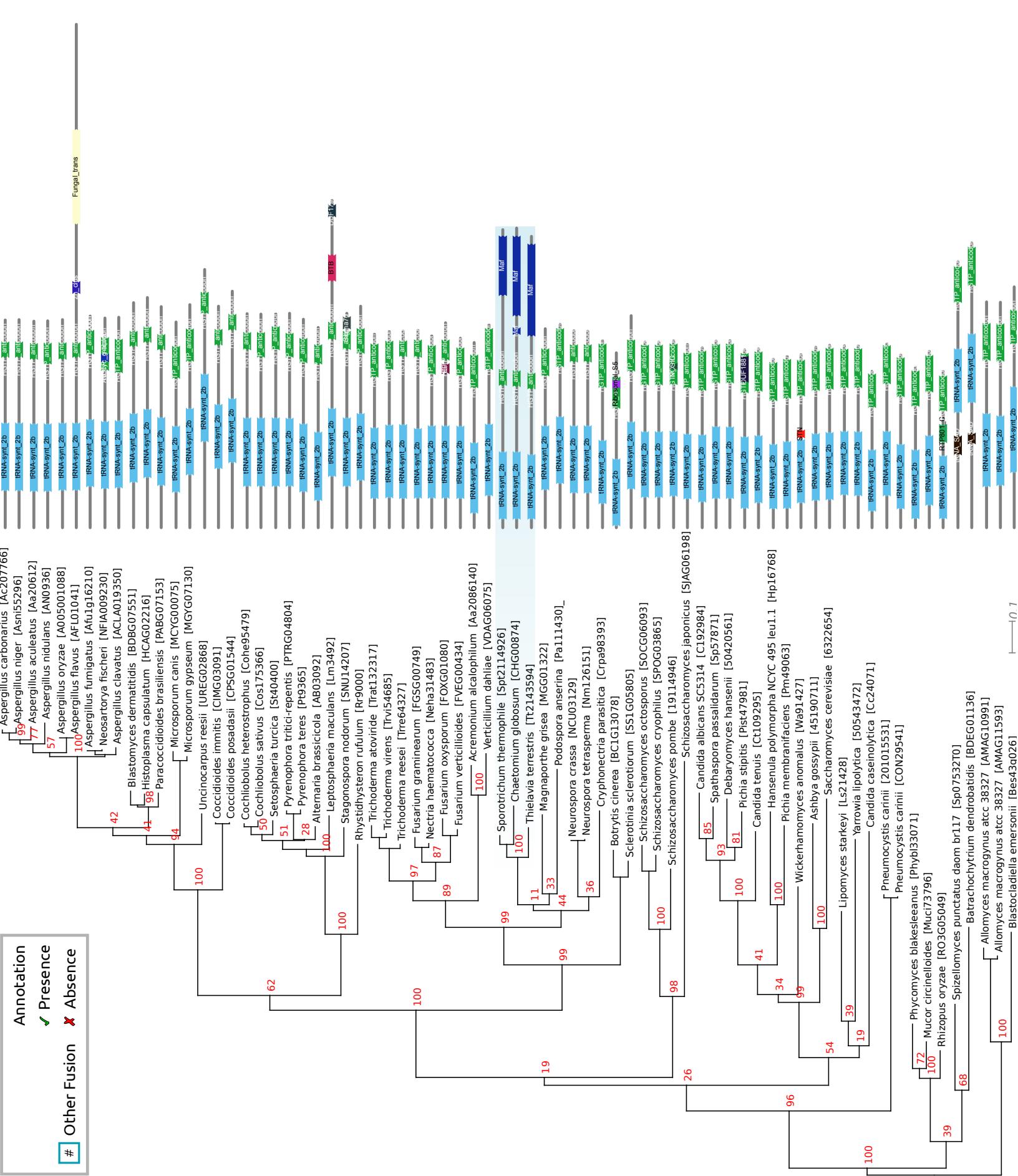
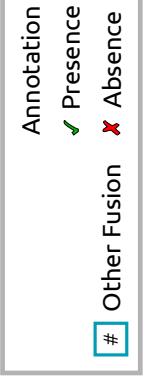
All trees were generated from an initial run of Darren's Orchard pipeline against 139 taxa (Table S1), using the above corresponding un-fused sequences as BLAST seeds. The alignments were then checked for any missing taxa, manually masked and then ProtTest3 was run, please see the Methods section for detail. The final trees were generated by the following command:

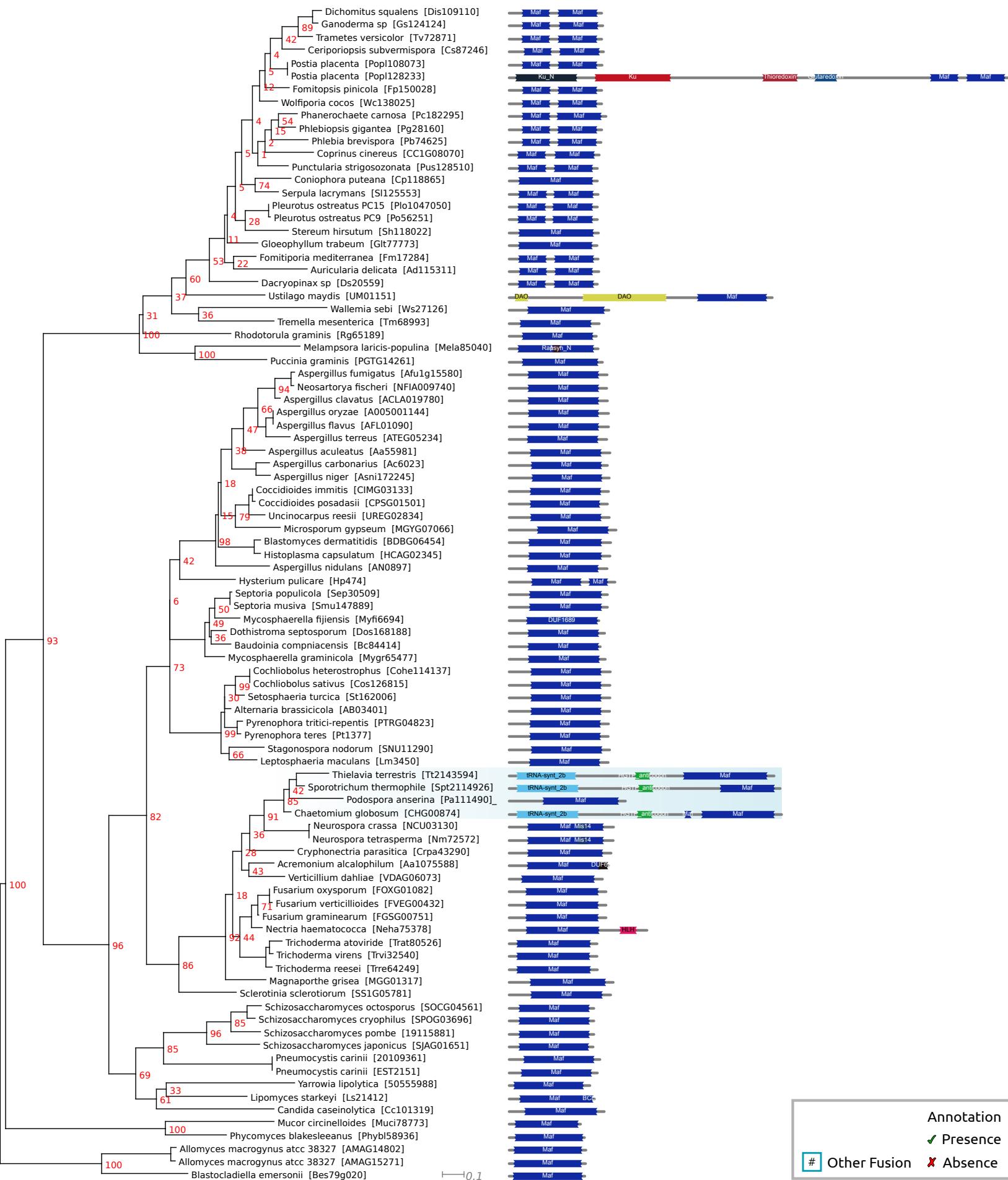
```
phyml -i alignment_file -d aa -b 100 -m model -c 8 -v invariant_sites -s BEST --quiet -a gamma
```

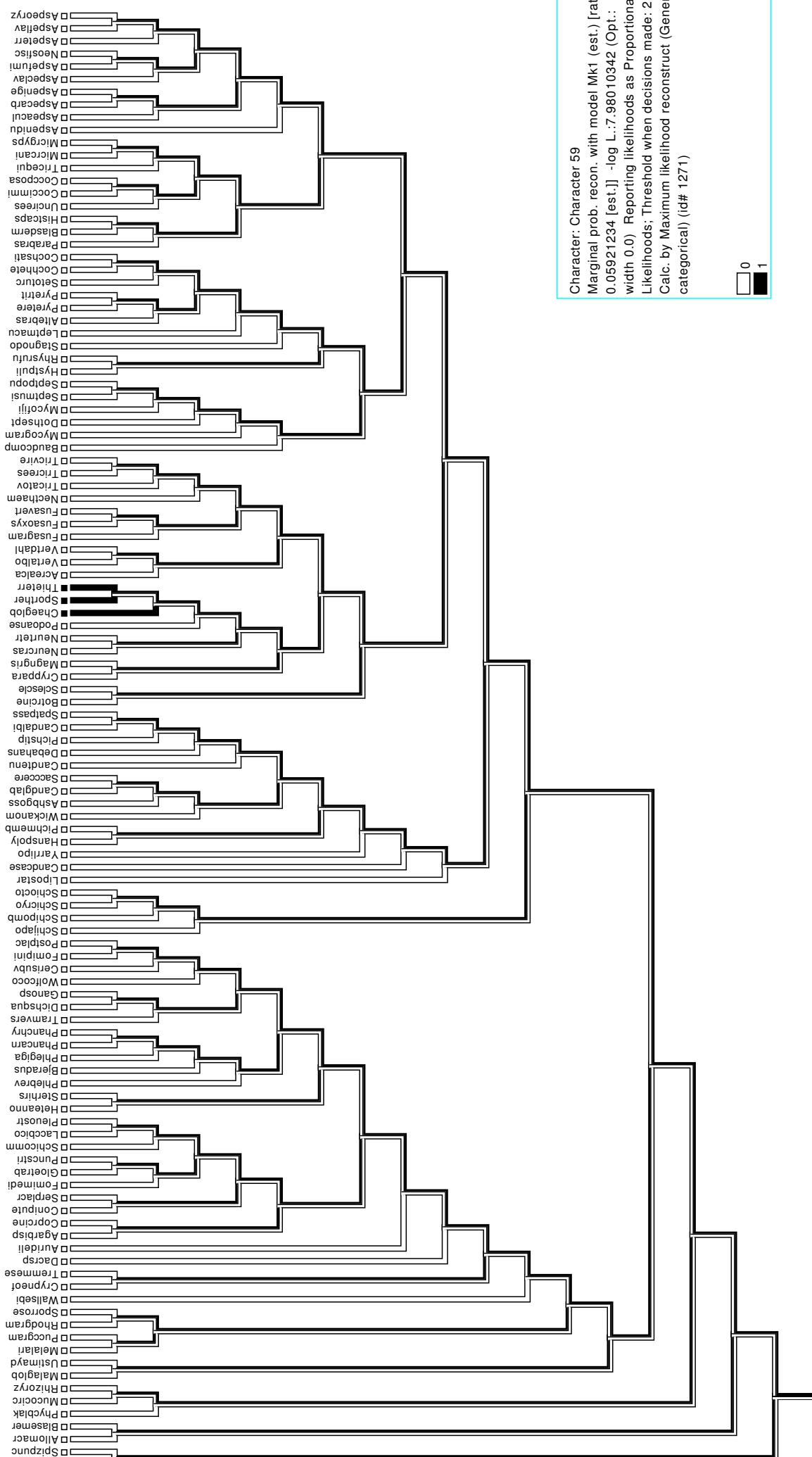
Styling and annotation was made possible by Dendroscope and Inkscape.

3 Mesquite Cladogram

This tree is the 68-gene concatenated phylogeny (Fig. 1), with the presence of a fusion (black), presence of a fission (white), and absent/undetermined (grey) status of gene fusion characters plotted on to it using a "1/0/-" nexus-style data matrix. We used the program 'Mesquite' to calculate proportional likelihoods based on either an "Mk1" or "Assym. 2 param model." (see Table S4) of character change across the fungal phylogeny (Fig. 1). This allowed for a proportional likelihood of the position of the fusion/fission to be calculated.







Character: Character 59
Marginal prob. recon. with model Mk1 (est.) [rate 0.0592/1234 [est.]] - log L.: 7.98010342 (Opt.): width 0.0). Reporting likelihoods as Proportional Likelihoods; Threshold when decisions made: 2.0 Caic. by Maximum likelihood reconstruct (Generic categorical) (id# 1271)

Putative Fusion 59

September 27, 2012

1 Fasta Sequences

These are the unfused sequences identified by fdfBLAST belonging to the putative gene fusion in FASTA format. Accessions may be shortened, but belong to either the taxons individual genome project or NCBI's accession numbering.

```
>XP_0032960621Pyte_dom1
MRVYGFPIALALVGAAQSAALQPRDVLKDLRNQAMKALEAAEAKSIHEKKAGCSLFQAP
GRQDWNVMSAEERKAYISAVQCMYSSPSKSDPALVPGARTRYDDFVAQHINQTRSIHGTG
NFLTWHRYFVHAYEKALRQECDGYTGYQPYWNWFTYQDDLRAPIFDGSDTSMGGDGTFVQ
HNGSTGGGTIYLPSGQGGGCISSGPFKGLQLNLGPISPTMDGQNKSVSELGYNPRCAKR
DLTTYASSTWLTIIDNLLNITSGAACSLNVGTFQNELQGRFPDGFLGLHAAGHFSINGDAGD
FYSSPNDPVFFLHHTMLDYAYWLWQAFHPDQAGTVMGTRTRFSPTAEKTLQDVISMNYL
>XP_0032960621Pyte_dom2
NVDDVTIEDLMDTYFHKHYFSSPKCPSHYLGMTKPIPIIGAGIAGLTLGRCLLHRGIPFV
LYEKASSKPRNSYAITLHSSAYRPLLSVLGIDEVTFKRRVAVDSETGGTGTIAQEVPPLN
HNGLYDTSSSFRANRAKFEQVLQQGIDIRWEHTLQSVEETPEGPKLQFHNGDSCSAKLA
AADGVHSNVRKLLPSAAVEILPYAVFNGKRKADYKSFGQVYGSAMEESNVIEKKQNDAI
LSASINDKKDDQIYINWIYSRPAREDPDPLYRPNRPLEGAQKIPDELFEVSSFDNLTTP
FSKVFDSETMRGDRMLHWLMRTTSAPLPSLQNVLTKSGVCVGDAIHAEPIVGGNGANAA
ILDGLTLAEAIERGGLGGISTWYAGRYATWTLGVEESQQAIAANMHPSKQLHGNL
```

2 Annotated Phylogenograms

All trees were generated from an initial run of Darren's Orchard pipeline against 139 taxa (Table S1), using the above corresponding un-fused sequences as BLAST seeds. The alignments were then checked for any missing taxa, manually masked and then ProtTest3 was run, please see the Methods section for detail. The final trees were generated by the following command:

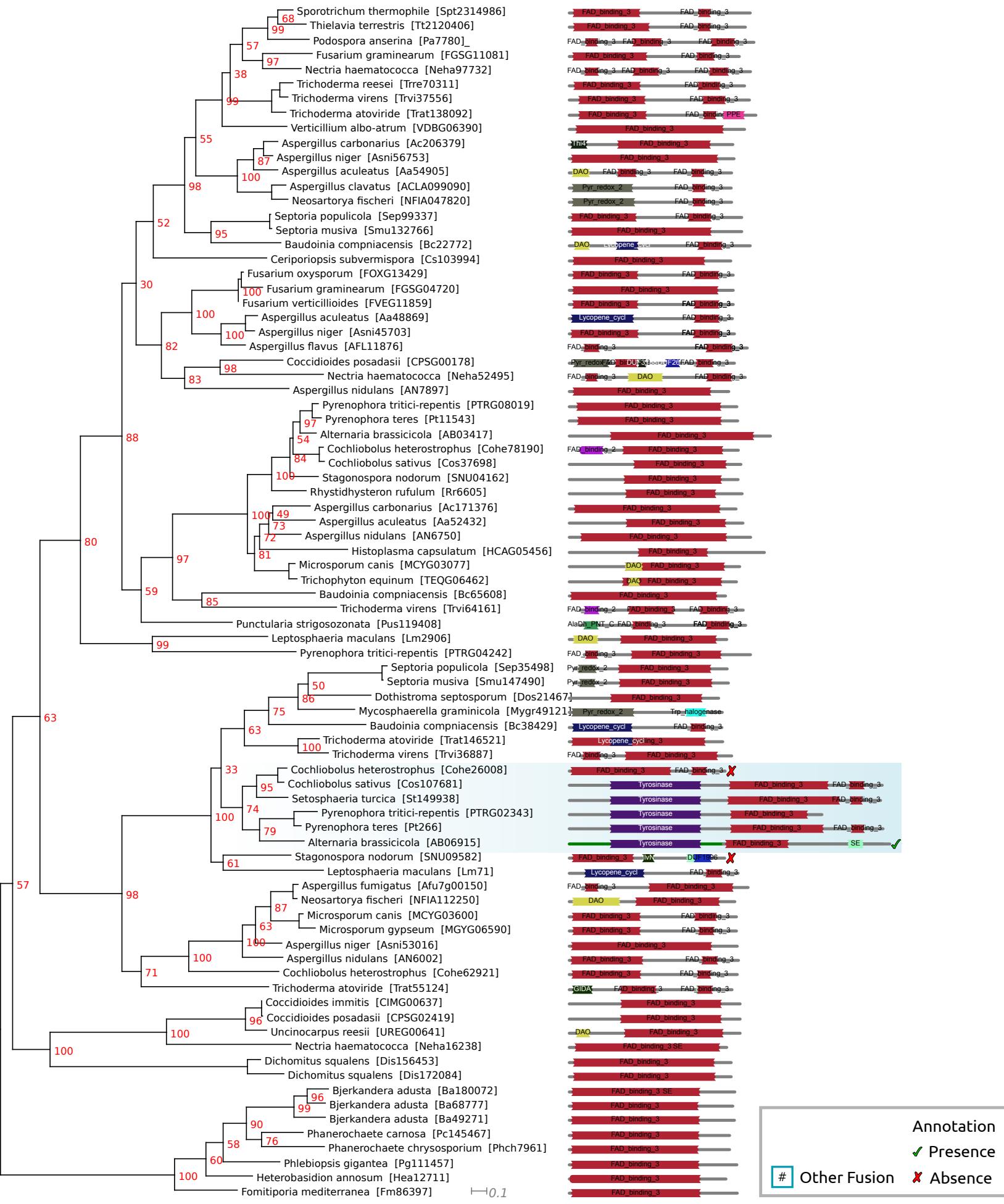
```
phylml -i alignment_file -d aa -b 100 -m model -c 8 -v invariant_sites -s BEST --quiet -a gamma
```

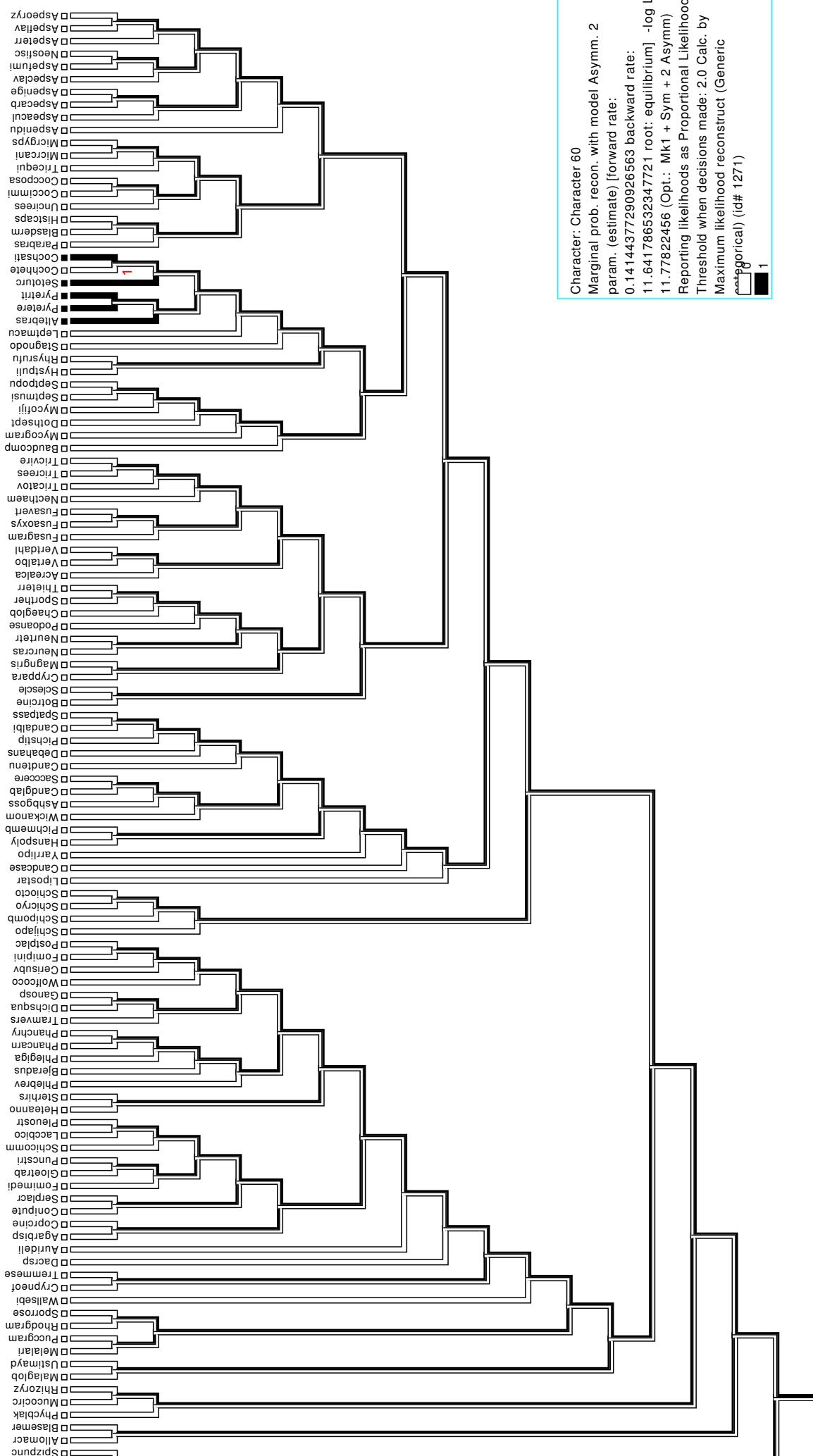
Styling and annotation was made possible by Dendroscope and Inkscape.

3 Mesquite Cladogram

This tree is the 68-gene concatenated phylogeny (Fig. 1), with the presence of a fusion (black), presence of a fission (white), and absent/undetermined (grey) status of gene fusion characters plotted on to it using a "1/0/-" nexus-style data matrix. We used the program 'Mesquite' to calculate proportional likelihoods based on either an "Mk1" or "Assym. 2 param model." (see Table S4) of character change across the fungal phylogeny (Fig. 1). This allowed for a proportional likelihood of the position of the fusion/fission to be calculated.







Putative Fusion 60

September 27, 2012

1 Fasta Sequences

These are the unfused sequences identified by fdfBLAST belonging to the putative gene fusion in FASTA format. Accessions may be shortened, but belong to either the taxons individual genome project or NCBI's accession numbering.

```
>XP_0018066581Phno_dom1
MAAIASIISFFSLIFGCCANVYCLEAIVKKEPDGGLLITLFQFVFTCLSTLHYQFDPNG
RYFLRSPVPFRKWCVSATLFTVTNMLNNWAFAFNISVPVHIIILRSFGSVTTMAAGWARG
KRYTRLQVFSAILTAVMVSAWADAQSKGKLANSKVDMTSGSFEAGLVILLIAQLLSA
WMGAYVEDIYRDHGKDQANLFYSHLLSIPMFAGFAPILYDQFTRLQSESFSVPVVA
QLPPSLNKALASTSQHVYIYTANAVTQLLCITGVNILSANTSAVTVTIVLNIRKLVSFML
SIWIFGNQMGGLMKGAGMVFGAGALYGWETSYRIPQQKKLESAKGKKGSKIESTMSSP
>XP_0018066581Phno_dom2
GGQVRQRATDKKRPTTPNPEALAEKVSEKVPVLEVKPKPAQQGEWDYKLAIAVMT
VLAFITRFWGIRHPDQVVFDEVHFGKFASYYLQRTYFFDVHPPFGKLLFAFAGWLGYKG
DFLFENIGDSYITNKVPPVAYRAMPASLGALTVPIVFMIMWESGYSLACVTAAGLMLLD
NAHIGQTRLILLDASLIFFMALSVLSYIRFYKLRHEPFGRKWWKWLLTGVNLSCVISIK
YVGVFTFFSFGVPVAIDLWDLMDVKKRQGALSLPEFGKHLAARVIGLIVVPFLLYLFWFQ
VHFSLSRSGPGDDFMTPEFQETLSDNMMTLQSVGIDYYDSITLRHKETKVYLHSHPDRY
PLRYDDGRVSSQQQVGTGYPHNNDTNNHWQILPATLPSKEANGSRFNDTLFEIKVDKGK
GDFKTMSTHFKLHVPTKVAMWHTSPLPDWAYKQAEINGKNIQQSSNVWYVDDIPS
AEDPRNKKEAKQVKRLSFLRKWVELQRAMFYHNNAALTSSH PYASQPISWPFLRGVSFWT
HNDTRQIYFLGNPIGWLASSLAVFAGIIGADQLALRRGMDALDDRTRSRLYNSTGFF
FLTWAHYIPFYIMGRQLFLHHYLPAHLASCLVTGALVEFIFCIEPMDVESPTIKGHRRT
QSRPVRERMATTSMGSWIATGVILAATLWSFLFFAPLTYGSPGLDVAQVQARKWLGYDL
HFAK
```

2 Annotated Phylogenograms

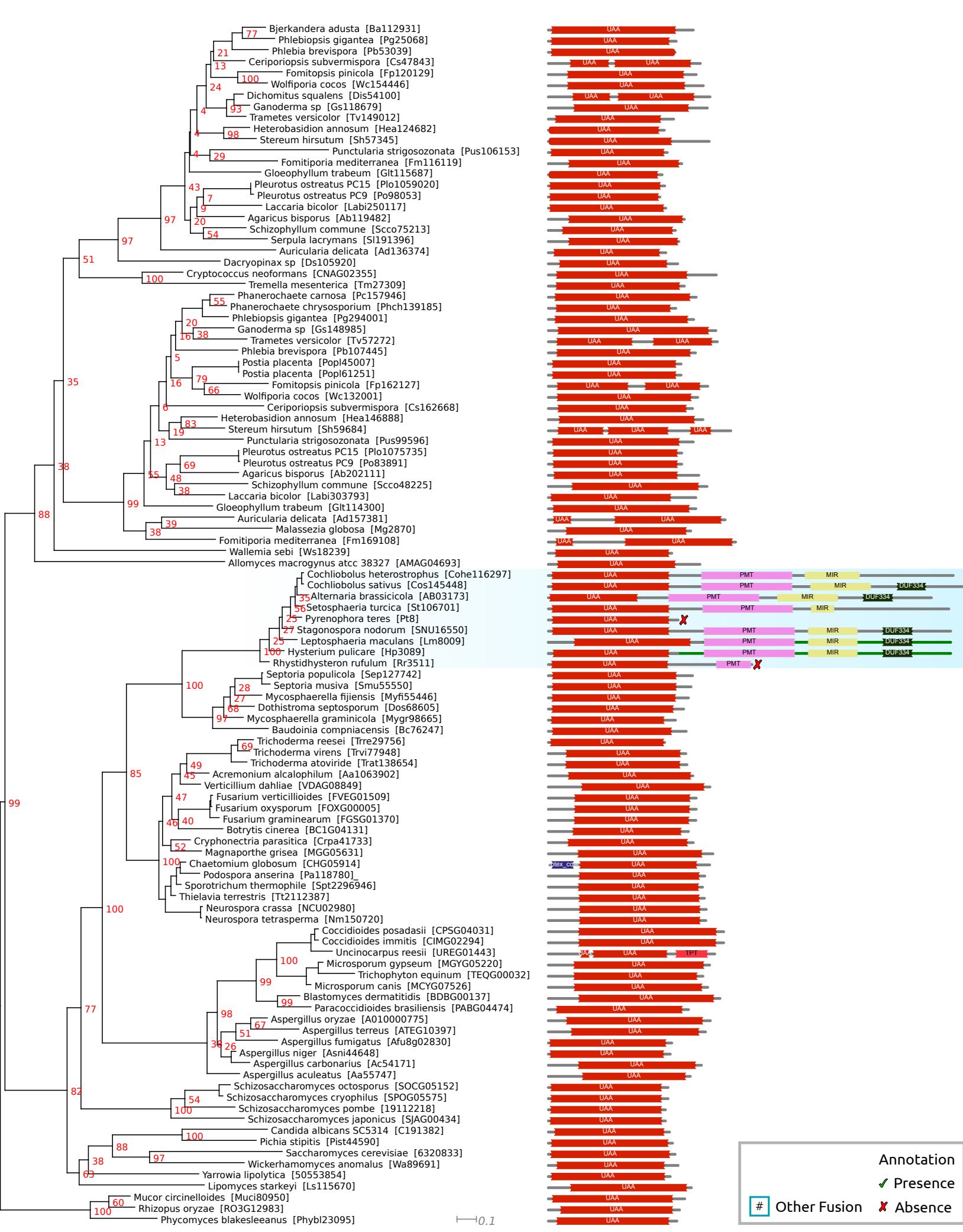
All trees were generated from an initial run of Darren's Orchard pipeline against 139 taxa (Table S1), using the above corresponding un-fused sequences as BLAST seeds. The alignments were then checked for any missing taxa, manually masked and then ProtTest3 was run, please see the Methods section for detail. The final trees were generated by the following command:

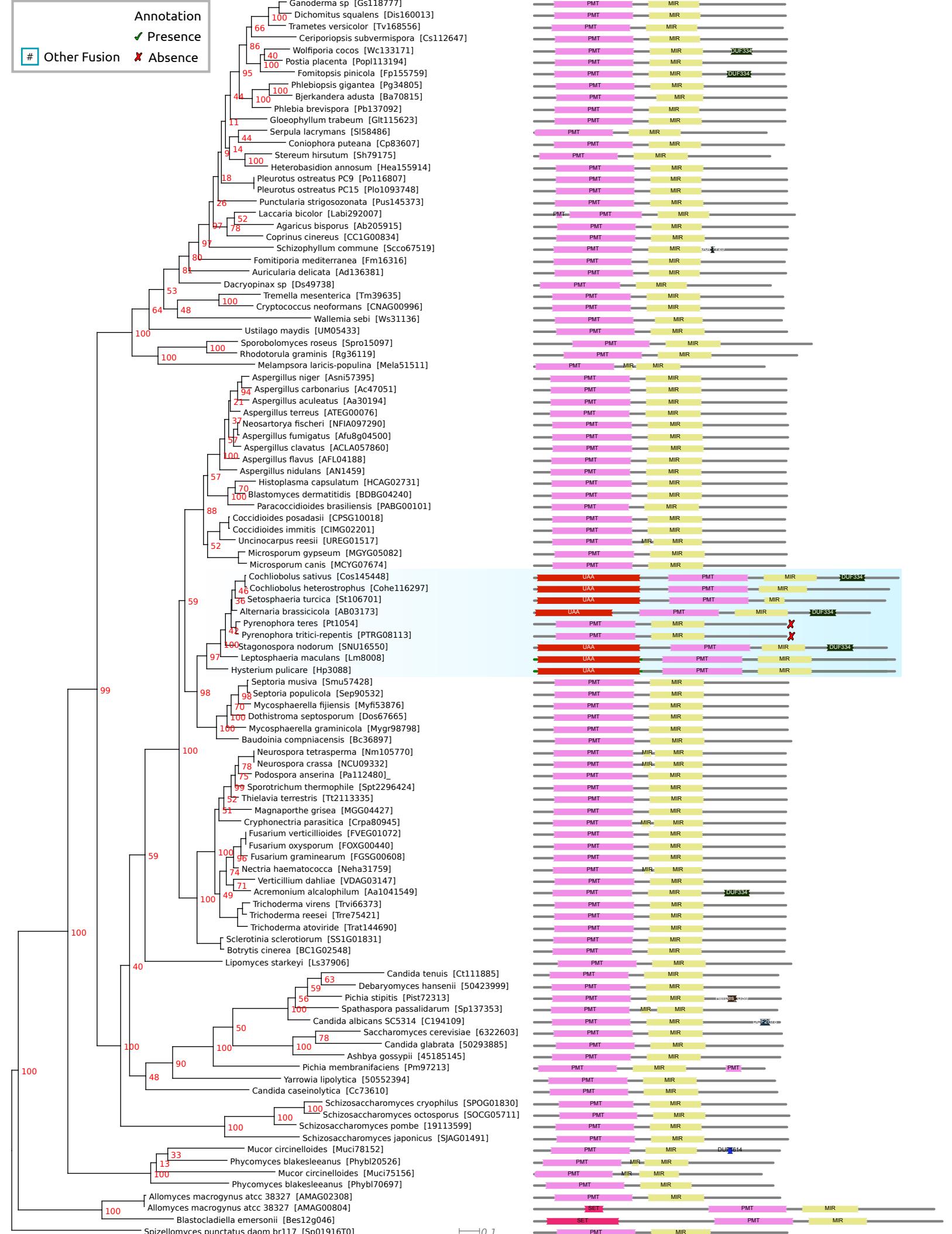
```
phyml -i alignment_file -d aa -b 100 -m model -c 8 -v invariant_sites -s BEST --quiet -a gamma
```

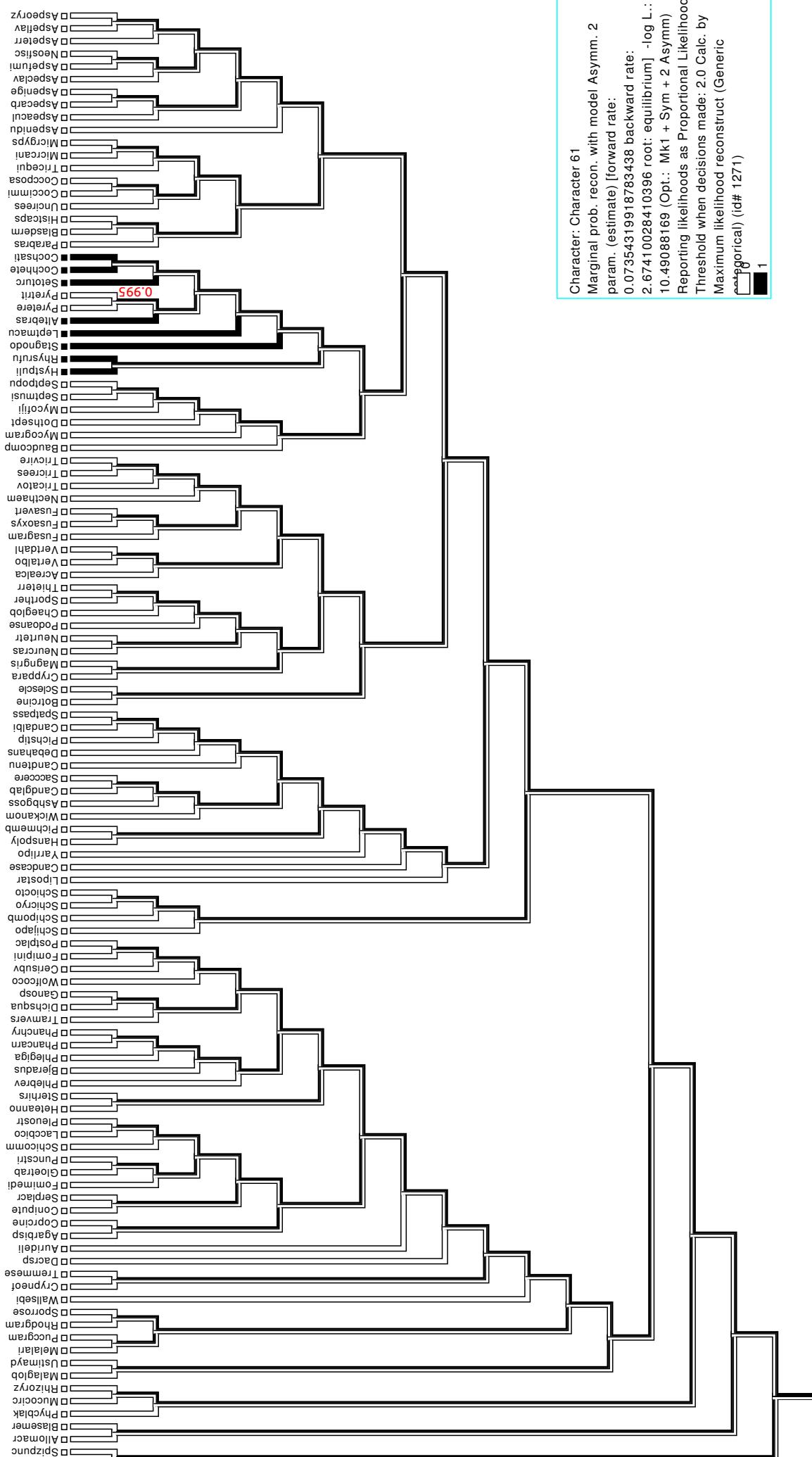
Styling and annotation was made possible by Dendroscope and Inkscape.

3 Mesquite Cladogram

This tree is the 68-gene concatenated phylogeny (Fig. 1), with the presence of a fusion (black), presence of a fission (white), and absent/undetermined (grey) status of gene fusion characters plotted on to it using a "1/0/-" nexus-style data matrix. We used the program 'Mesquite' to calculate proportional likelihoods based on either an "Mk1" or "Assym. 2 param model." (see Table S4) of character change across the fungal phylogeny (Fig. 1). This allowed for a proportional likelihood of the position of the fusion/fission to be calculated.







Putative Fusion 61

September 27, 2012

1 Fasta Sequences

These are the unfused sequences identified by fdfBLAST belonging to the putative gene fusion in FASTA format. Accessions may be shortened, but belong to either the taxons individual genome project or NCBI's accession numbering.

```
>XP_6815211Asni_N212
MKRLNRLLRHVHARAKPQQPSSSNDSQVLPLVHSQPPIAFAQDVPQTPIASSEPLSVFAHFLVGVAGSMS
PAEWEHNIIAAQEAHIDGFALNIAPQDDYTDQVLQTAYEAERIGDFSLFISFDYESGGAWPVDRVISTI
NRYKGRPAQYLYKGKPLVSTFEGSKSDDWPAIKQATGCVFVPSWTSPLSRLYTVHGTIDGAFSWDAWP
VGAQEKTSDKAWMNALSGKPYMMAVSPWFYTNLQPWNKWLWRGDDLWHYRWWQVIDLQPAMVQILSW
NDYGEAHYIGPIYEPEGIPEGASWFVKGCPHDRAWFLPHYIDAYRRRSAMFRERASNPATVTSFAPRRPL
SYTDKIVYWYRLNPSHSGSADGTTGNPNMGQPGDPEVSQDRVFVSVLVTEPSQVHIQIGPAASRVLI
AKESGVNHYSVPFDGHSGPVRIAIVRHGREVKATGPAAITEECTDGKILSDIHHHESNLAQRQYAQLPE
TLHLNYQPPTATATPAAHHTPIPEAINPDDYSQAYCDFMTEHPTIFHAVDGFSKQLESKGYKYLSERELW
TPQLKRGGKYYTTRNGSSLIAFSGVPEYKSGNGLAIIGHIDALTAKLKPVSKLPNKAGYIQMGVAPYAG
GLGKTWWDRDLSIGGKVLVRNASTGKVESKLVKLNWPIARIPTLAEHFGAPSQGPFNKETQMVPVIIGVDN
SDLFQSTTPAADEGIEPGTFASTQPPKLIKVISKELGITNYSSILSWELELYDSQPARIGGIDKDFIFAG
RIDDKLCCYAAQEAALMATSHTSPSSIKMVGYFDDEEIGSLLRQGARSNFMSSVIERIAQSFATSYGPDL
LAQTVAKSFLISSDVIAHVNPNFLNVYLENHAPRLNVGVSVSADSNHGHTTDSVSYGFIKRVAEKCGSQL
QVFQIRNDSRSGGTIGPMTSSRIGMRAIDVGIPQLSMHSIRATTGSRDPGLGVKLFKGFFDYFEEVDHNI
```

2 Annotated Phylogenograms

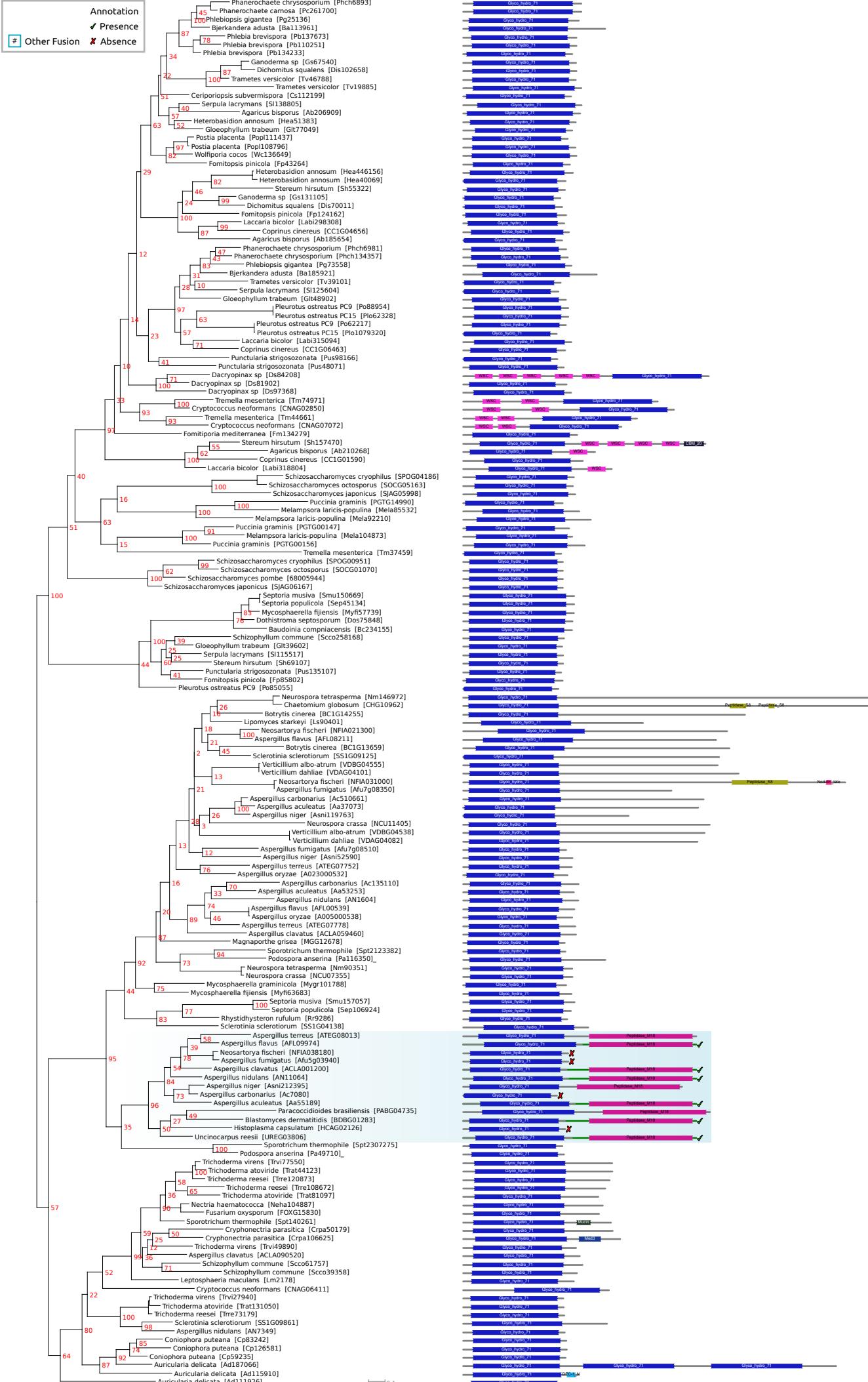
All trees were generated from an initial run of Darren's Orchard pipeline against 139 taxa (Table S1), using the above corresponding un-fused sequences as BLAST seeds. The alignments were then checked for any missing taxa, manually masked and then ProtTest3 was run, please see the Methods section for detail. The final trees were generated by the following command:

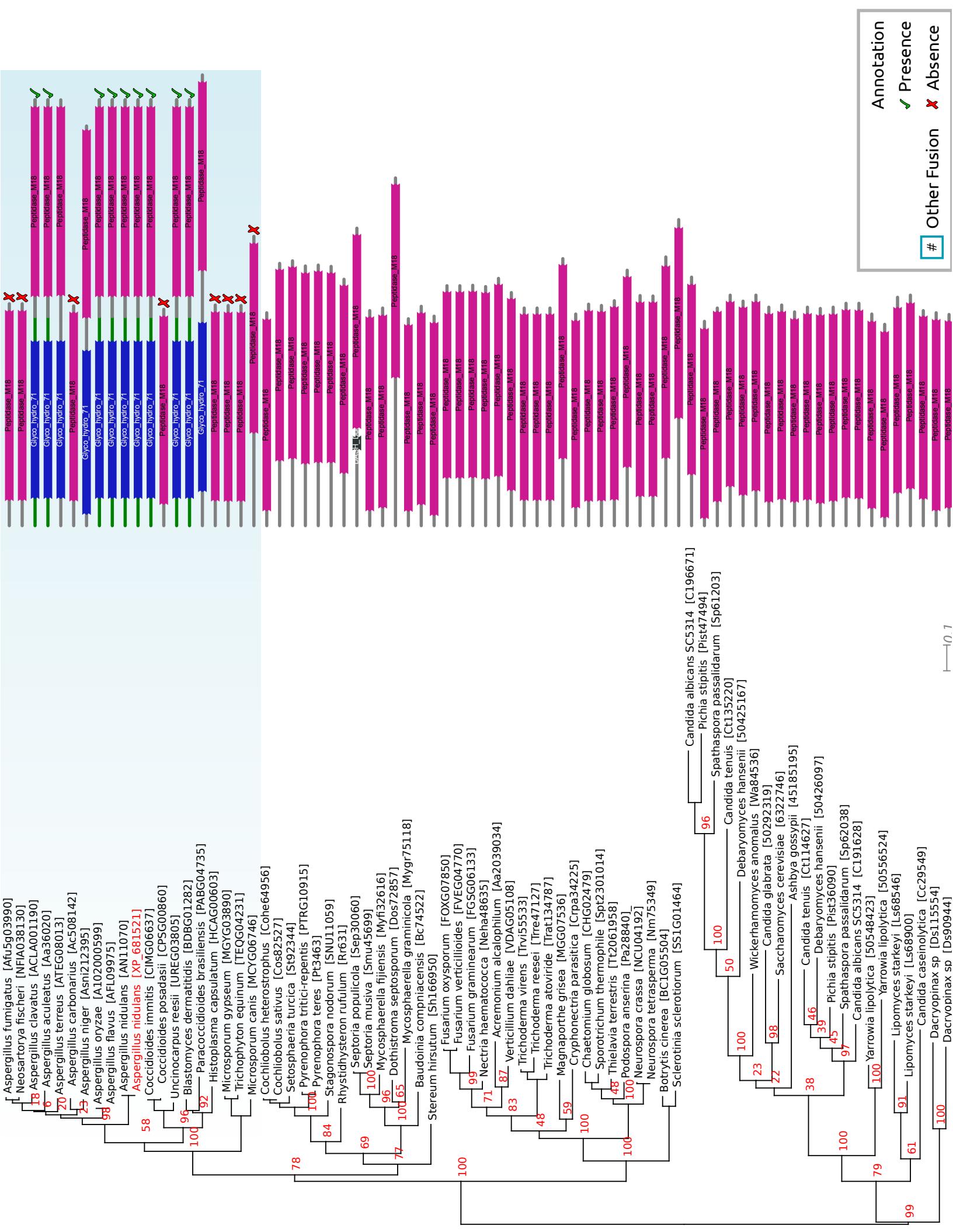
```
phylml -i alignment_file -d aa -b 100 -m model -c 8 -v invariant_sites -s BEST --quiet -a gamma
```

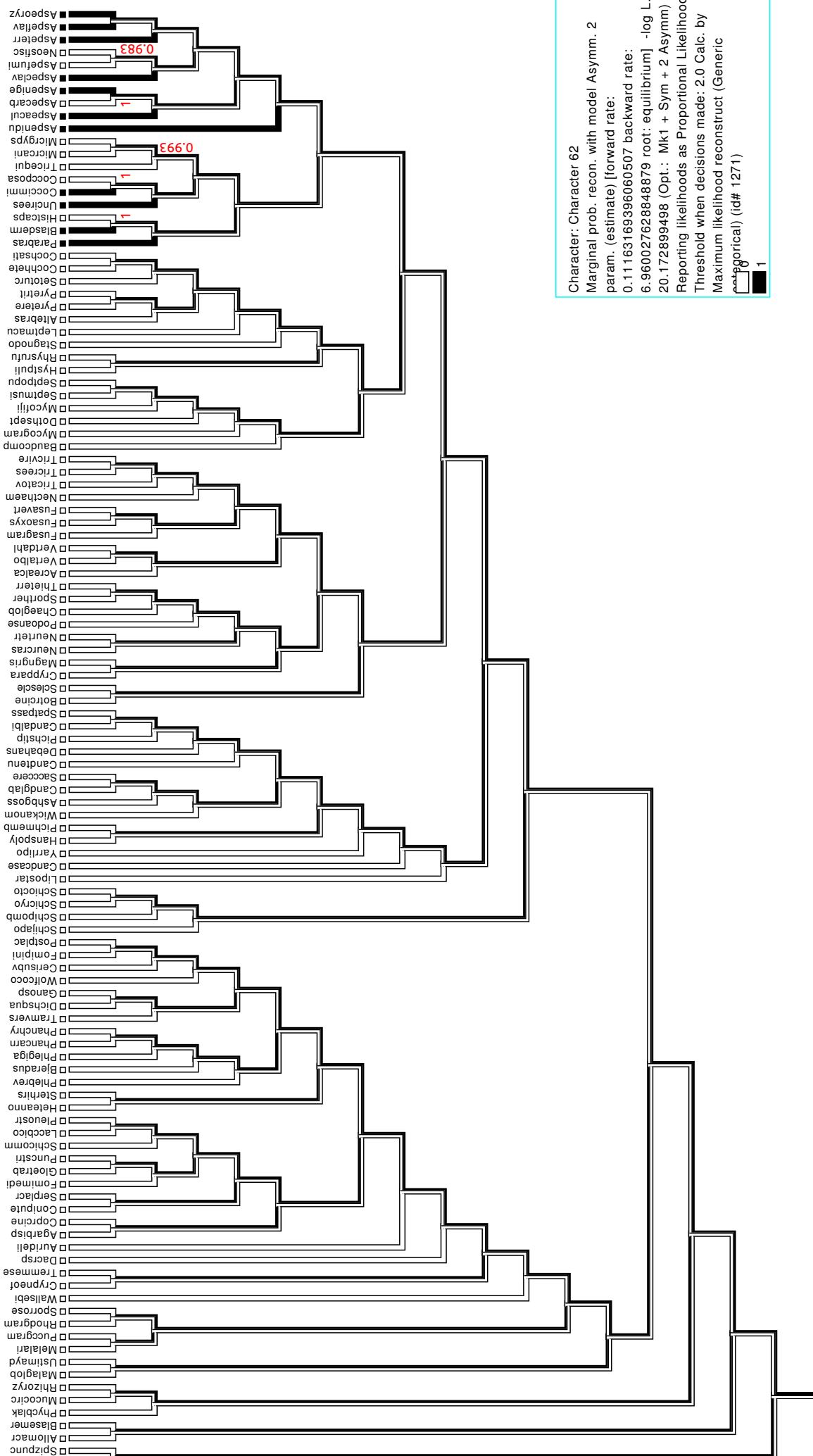
Styling and annotation was made possible by Dendroscope and Inkscape.

3 Mesquite Cladogram

This tree is the 68-gene concatenated phylogeny (Fig. 1), with the presence of a fusion (black), presence of a fission (white), and absent/undetermined (grey) status of gene fusion characters plotted on to it using a "1/0/-" nexus-style data matrix. We used the program 'Mesquite' to calculate proportional likelihoods based on either an "Mk1" or "Assym. 2 param model." (see Table S4) of character change across the fungal phylogeny (Fig. 1). This allowed for a proportional likelihood of the position of the fusion/fission to be calculated.







Putative Fusion 62

September 27, 2012

1 Fasta Sequences

These are the unfused sequences identified by fdfBLAST belonging to the putative gene fusion in FASTA format. Accessions may be shortened, but belong to either the taxons individual genome project or NCBI's accession numbering.

```
>BDEG_08038_dom_1
MTDSPFNCIQRFELITRNLQEHLGGDKIKEVLATRDLKVYWTGKPHIGYFVPMTKV
ADFLKAGCEVTILFADMHAFLDNQKAPWDLKLRTSYYEATIKSMLTSIGVPIEKLKFVV
GTSYQLSKEYSLDVYRLLSMTTEHAAKKAGAEVVKQVESPLLSGLVYPLLQALDEEYLGV
DAQFGGVDFQRKIFTFAEKFLPQLGYAKRAHLMNVGGLSGSKMSSDPDSKVDLLDEPD
SVVAKLKKAFCEEVNDDNPILAFIKAVVFPVNSLTNPSTFTIERPEKYGGNAEYSTYT
HLEEAFFREKLVHPGDLKSAAKAINSLEPIRANFHNSPELKQMAIDAYPTPKAKVEAEI
>BDEG_08038_dom_2
SRVDIRVGKVIETAHPERDNLVYKEKIDLGEATGPRTIVSGLAKYLTKEEFTGRVLVVA
NLKASKFAGVLSEGMVLAASNADKSVVELEPNEDSKIGEQVTFDGFTFSPDQTLPKHK
VFEKCAVDLTTTEECVATYKNIPFKTSQQVTVHSLRKATIS
```

2 Annotated Phylogenograms

All trees were generated from an initial run of Darren's Orchard pipeline against 139 taxa (Table S1), using the above corresponding un-fused sequences as BLAST seeds. The alignments were then checked for any missing taxa, manually masked and then ProtTest3 was run, please see the Methods section for detail. The final trees were generated by the following command:

```
phylml -i alignment_file -d aa -b 100 -m model -c 8 -v invariant_sites -s BEST --quiet -a gamma
```

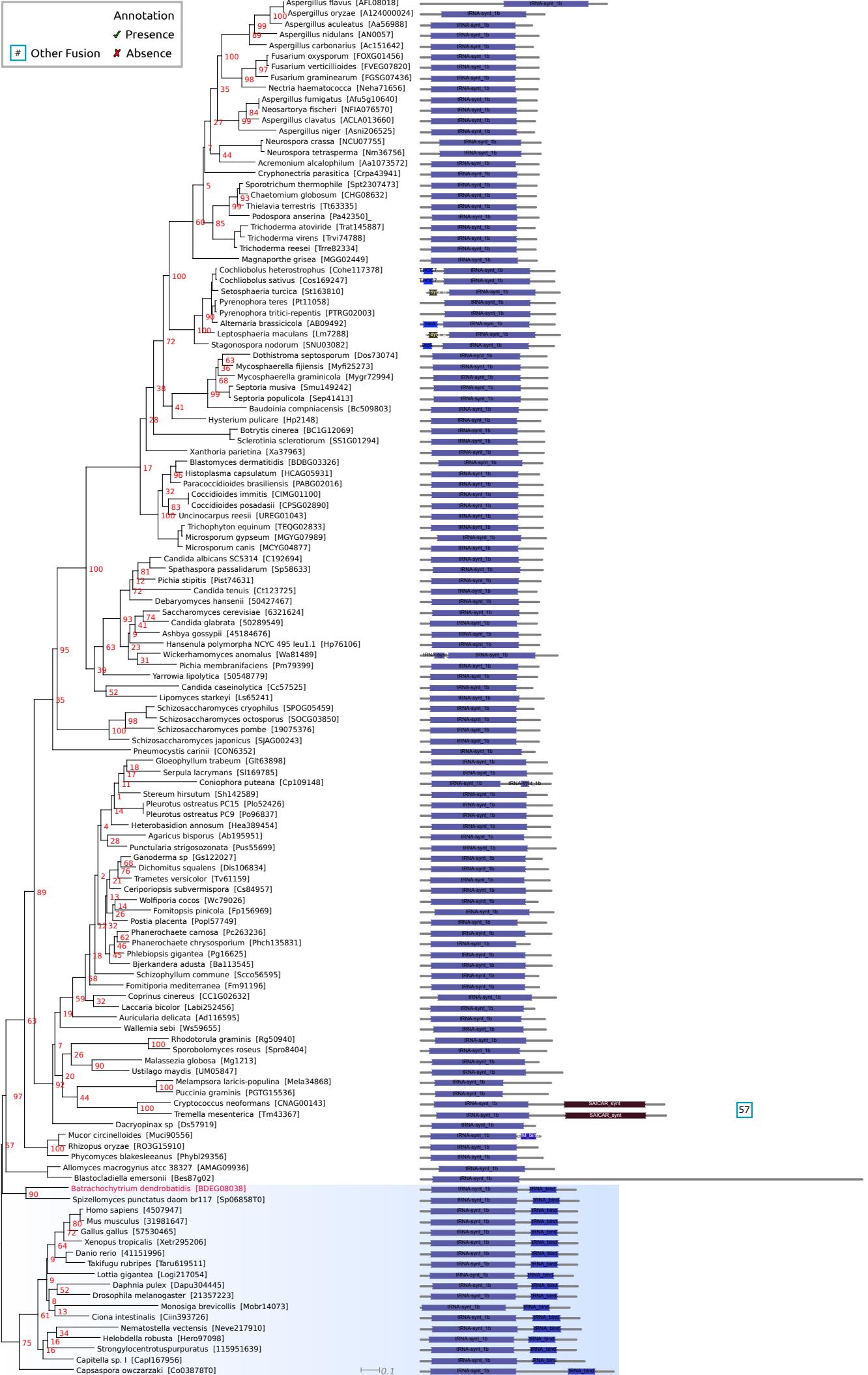
Styling and annotation was made possible by Dendroscope and Inkscape.

2.1 Important Notes

There is only one phylogeny shown here as the second domain is quite small and so the resulting alignment and phylogeny were mostly unresolved.

3 Mesquite Cladogram

This tree is the 68-gene concatenated phylogeny (Fig. 1), with the presence of a fusion (black), presence of a fission (white), and absent/undetermined (grey) status of gene fusion characters plotted on to it using a "1/0/-" nexus-style data matrix. We used the program 'Mesquite' to calculate proportional likelihoods based on either an "Mk1" or "Assym. 2 param model." (see Table S4) of character change across the fungal phylogeny (Fig. 1). This allowed for a proportional likelihood of the position of the fusion/fission to be calculated.



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