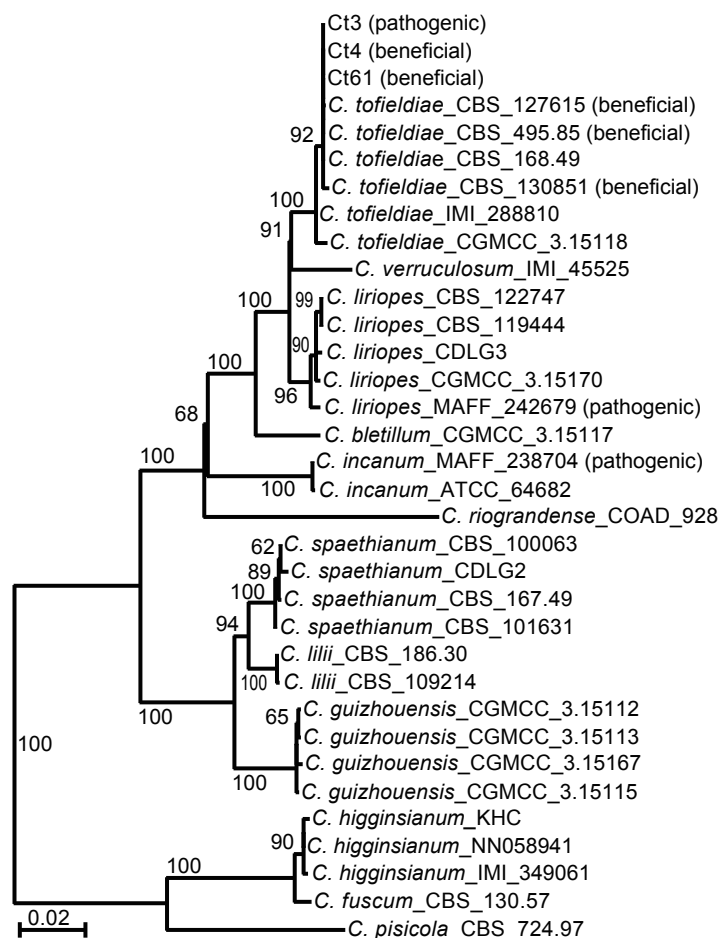
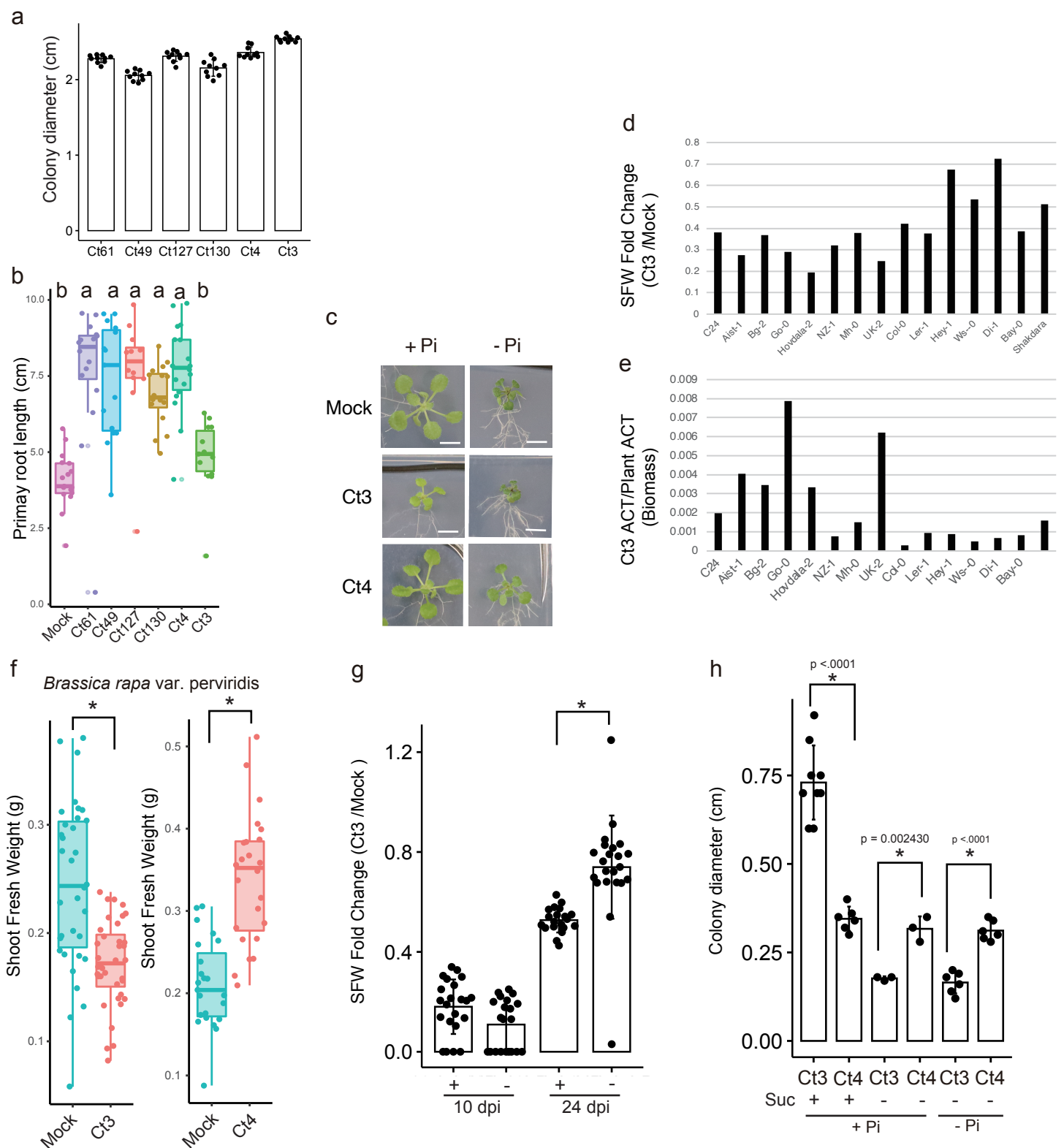


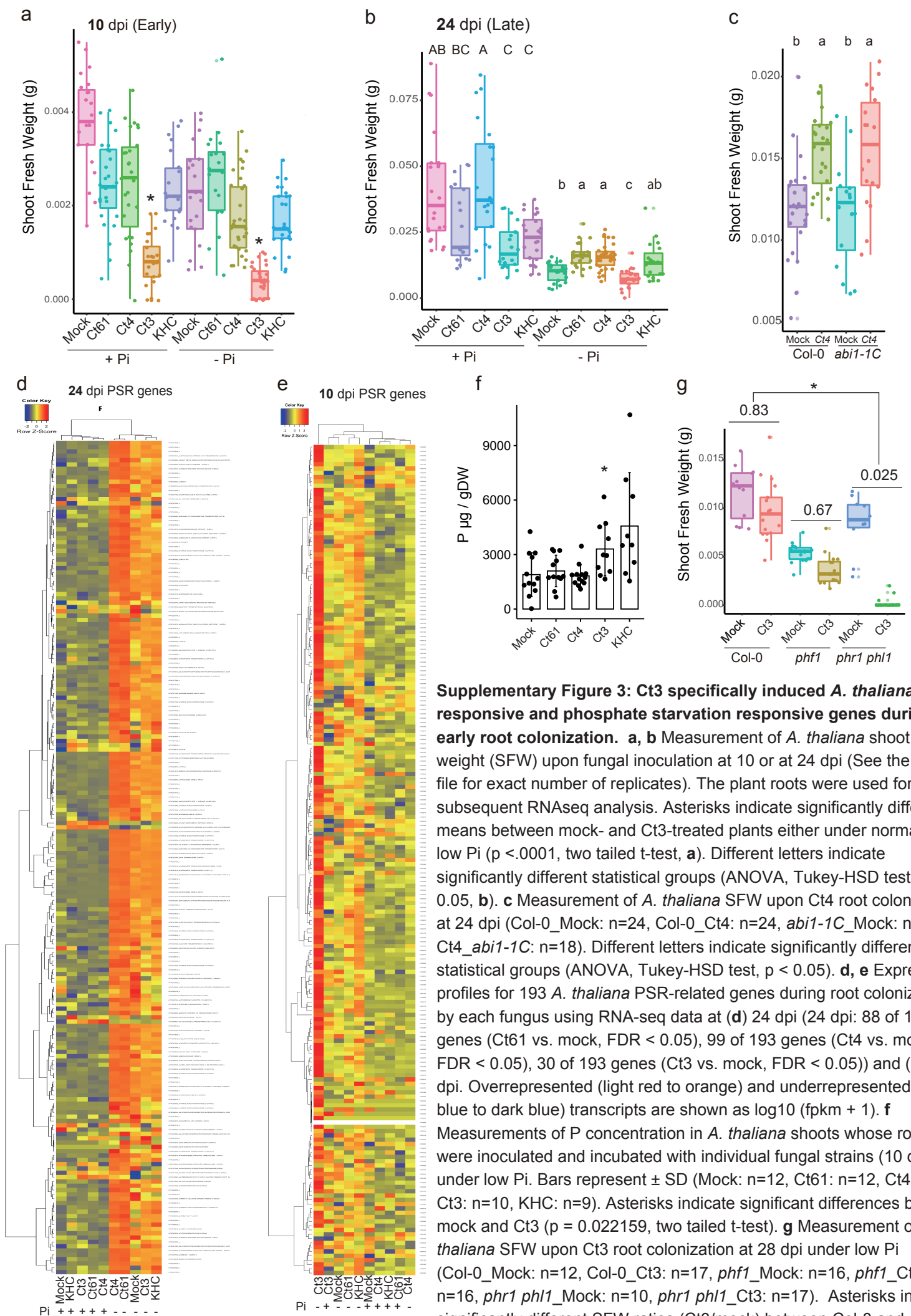


Supplementary Figure 1: Ct3 and Ct4 belong to *Colletotrichum tofieldiae* species.

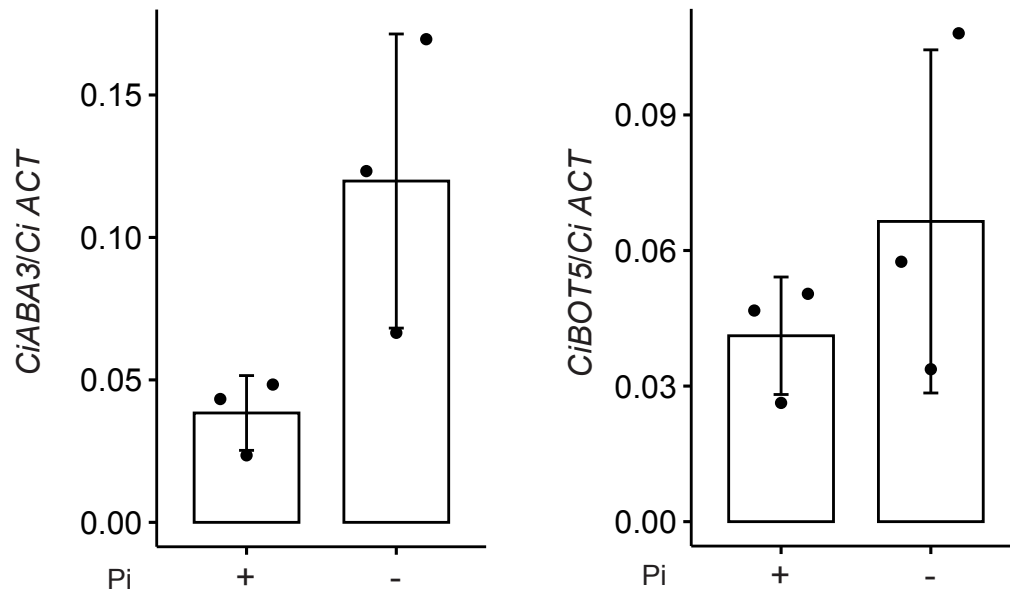
Maximum-likelihood phylogenetic tree of 34 strains in 12 species of the genus *Colletotrichum* based on a concatenated alignment of six fungal marker nucleotide sequences (ITS, TUB2, ACT, HIS3, CHS-1, and GAPDH). Ultrafast bootstrap values (1,000 replicates) are shown on the branches. The strains in the *C. destructivum* species complex are used as an outgroup. Lifestyles of some *Colletotrichum* fungi in *A. thaliana* roots under low Pi were indicated (beneficial or pathogenic). CBS_127615 = Ct127, CBS_495.85 = Ct49, CBS_130851 = Ct130.



Supplementary Figure 2: A Ct strain (Ct3) inhibits plant growth of *A. thaliana* and *B. rapa*. **a** Measurements of fungal colony diameters ($n = 10$). Bars = $\pm$ SD. **b** Measurements of *A. thaliana* primary root length upon fungal inoculation. Plants were incubated for 24 days under low-Pi ($50 \mu\text{M KH}_2\text{PO}_4$) from germination either with mock treatment, Ct61, Ct49, Ct127, Ct130, Ct4 or Ct3 (Mock: $n=17$, Ct61: $n=16$, Ct49: $n=15$, Ct127: $n=12$, Ct130: $n=16$, Ct4: $n=18$, Ct3: $n=14$). Each dot represents an individual plant sample. Different letters indicate significantly different statistical groups (ANOVA, Tukey-HSD test, $p < 0.05$). **c** Pictures of *A. thaliana* plants grown in normal or low Pi conditions with and without Ct3 or Ct4. The picture was taken after 24-day post inoculation (24 dpi) on the same scale. bars = 0.5 cm. **d, e** Inoculation of Ct3 against 15 different *A. thaliana* accessions under low Pi. The negative impacts on plant growth by Ct3 were estimated by SFW fold change (Ct3/Mock) at 24 dpi. At least four plants per accession and treatment were used to calculate SFW fold change. qRT-PCR analyses were used to measure fungal biomass as estimated by relative expression between CtACTIN and PlantACTIN (CtACTIN/PlantACTIN). **f** Measurement of *B. rapa* SFW either upon Ct3 (Left, Mock: $n=34$, Ct3: $n=36$) or Ct4 (Right, Mock: $n=23$, Ct4: $n=24$) inoculation under low nutrient soils. Asterisks indicate significantly different statistical groups ($p < .0001$, two tailed t-test). **g** Degree of Ct3-mediated plant growth inhibition under normal (+, $625 \mu\text{M KH}_2\text{PO}_4$) and low (-) Pi conditions. Asterisks indicate significantly different statistical groups ($p < .0001$, two tailed t-test, Bars = $\pm$ SD). **h** Fungal growth either on normal Pi + 0.8% sucrose, normal Pi without sucrose, or low Pi without sucrose media. The diameter of each fungal colony was measured after 3 days of incubation. Asterisks indicate significantly different values between Ct3 and Ct4 ($\pm$ SD, $n = 3\sim 9$, $p < 0.01$, two tailed t-test).

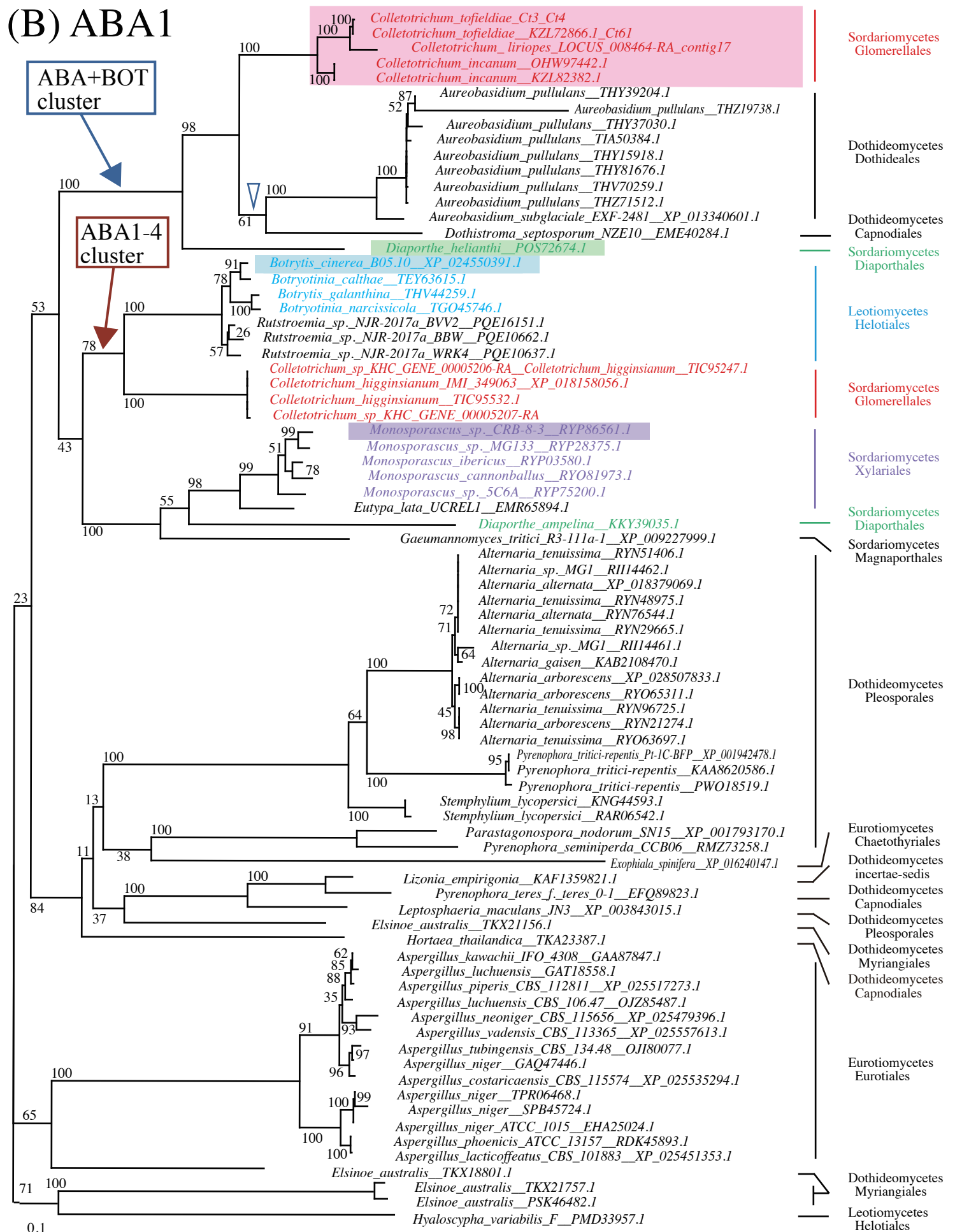


Supplementary Figure 3: Ct3 specifically induced *A. thaliana* ABA responsive and phosphate starvation responsive genes during early root colonization. **a, b** Measurement of *A. thaliana* shoot fresh weight (SFW) upon fungal inoculation at 10 or at 24 dpi (See the source file for exact number of replicates). The plant roots were used for the subsequent RNAseq analysis. Asterisks indicate significantly different means between mock- and Ct3-treated plants either under normal or low Pi ($p < 0.0001$, two tailed t-test, **a**). Different letters indicate significantly different statistical groups (ANOVA, Tukey-HSD test, $p < 0.05$, **b**). **c** Measurement of *A. thaliana* SFW upon Ct4 root colonization at 24 dpi (Col-0_Mock: $n=24$, Col-0_Ct4: $n=24$, *abi1-1C*_Mock: $n=16$, Ct4_*abi1-1C*: $n=18$). Different letters indicate significantly different statistical groups (ANOVA, Tukey-HSD test, $p < 0.05$). **d, e** Expression profiles for 193 *A. thaliana* PSR-related genes during root colonization by each fungus using RNA-seq data at (**d**) 24 dpi (24 dpi: 88 of 193 genes (Ct61 vs. mock, FDR < 0.05), 99 of 193 genes (Ct4 vs. mock, FDR < 0.05), 30 of 193 genes (Ct3 vs. mock, FDR < 0.05)) and (**e**) 10 dpi. Overrepresented (light red to orange) and underrepresented (light blue to dark blue) transcripts are shown as $\log_{10}(\text{fpkm} + 1)$. **f** Measurements of P concentration in *A. thaliana* shoots whose roots were inoculated and incubated with individual fungal strains (10 dpi) under low Pi. Bars represent $\pm$ SD (Mock: $n=12$, Ct61: $n=12$, Ct4: $n=13$, Ct3: $n=10$, KHC: $n=9$). Asterisks indicate significant differences between mock and Ct3 ($p = 0.022159$, two tailed t-test). **g** Measurement of *A. thaliana* SFW upon Ct3 root colonization at 28 dpi under low Pi (Col-0_Mock: $n=12$, Col-0_Ct3: $n=17$, *phf1*_Mock: $n=16$, *phf1*_Ct3: $n=16$, *phr1 phl1*_Mock: $n=10$, *phr1 phl1*_Ct3: $n=17$). Asterisks indicate significantly different SFW ratios (Ct3/mock) between Col-0 and *phr1 phl1* ($p < 0.05$, two tailed t-test).



Supplementary Figure 4a: Fungal ABA and BOT biosynthesis genes were induced during root colonization by *C. incanum*. The expression of *CiABA3* or *CiBOT5* genes during root colonization by *C. incanum*. Plants were incubated with *C. incanum* for 23 dpi under normal (+) or low (-) Pi ($\pm$ SD, n =3).

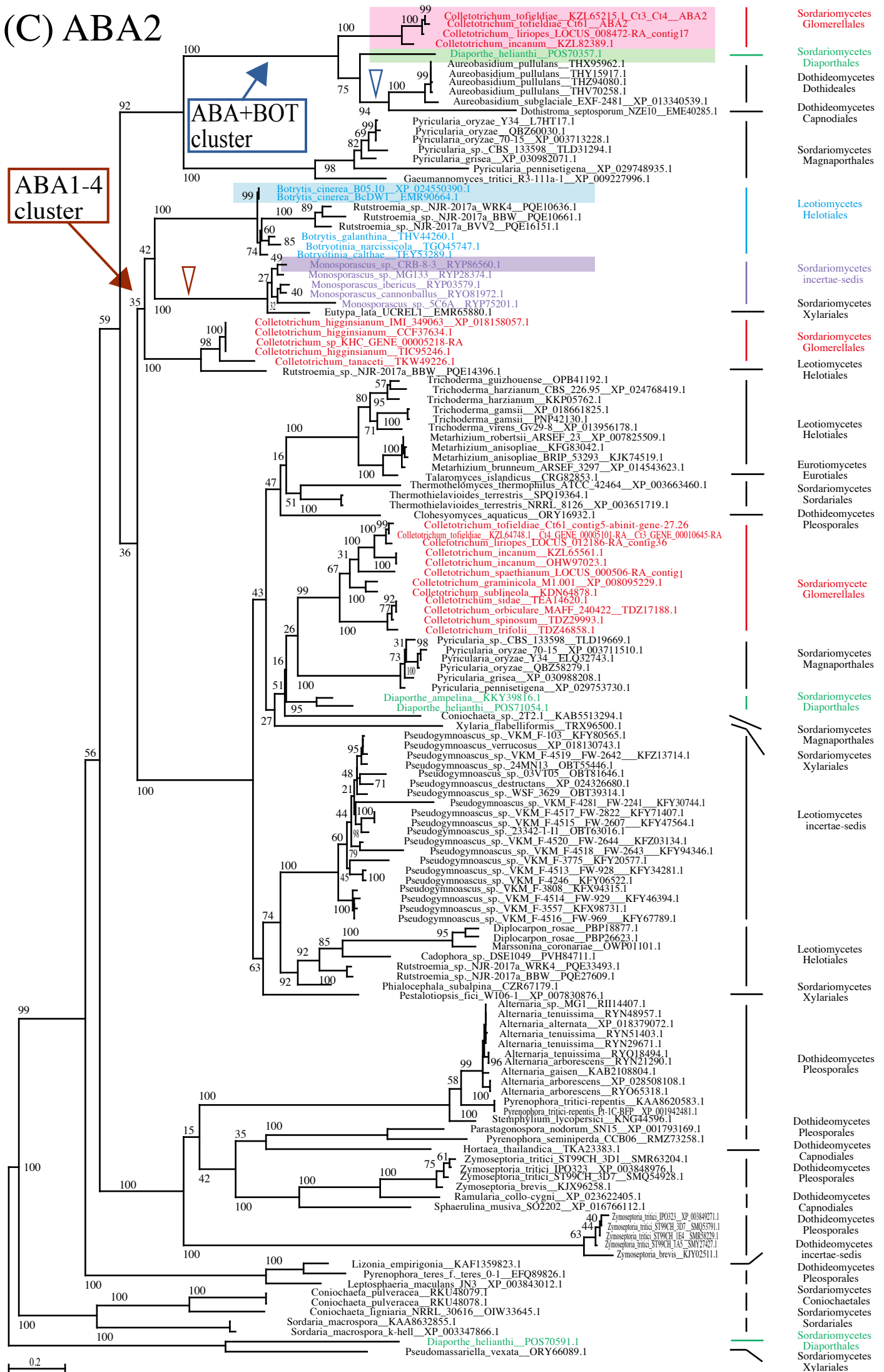
(B) ABA1



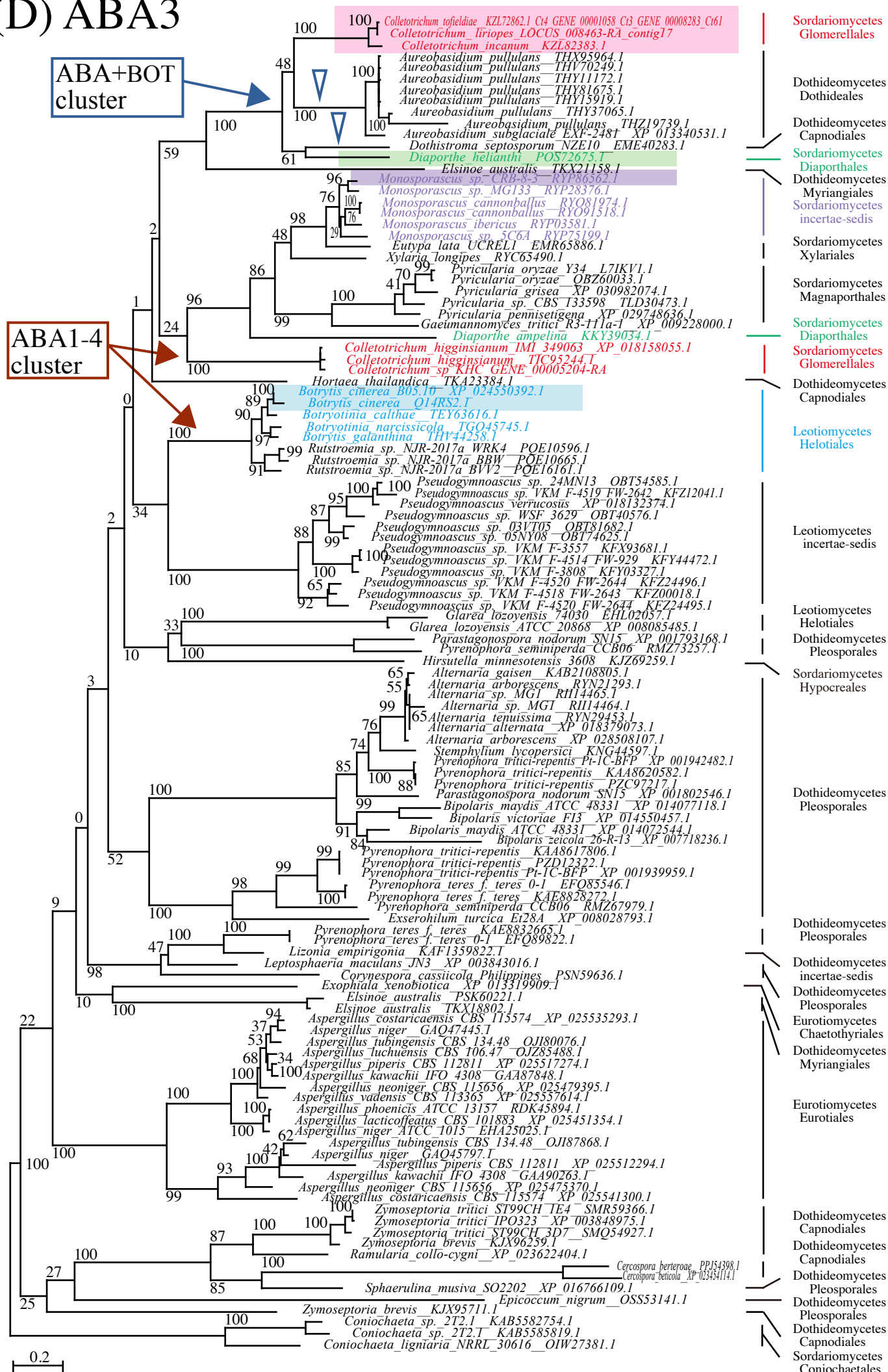
b-l. Phylogenies of ABA and BOT genes using IQ-TREE version 1.6.11. Arrow indicates origins of various gene clusters. Triangles with the same color as the arrows show deletion of the clusters. Genes of *Colletotrichum*, *Botrytis*, *Diaporthe*, and *Monosporascus* are indicated with the colors of red, blue, green, and purple, respectively. Organism strains that have both ABA and BOT gene clusters in their genome are labeled with the same color background as the letters. The bootstrap probability is shown on the branches. The scale bar represents substitutions per site.

b-e ABA1-4 genes. **f-l** BOT1-7 genes.

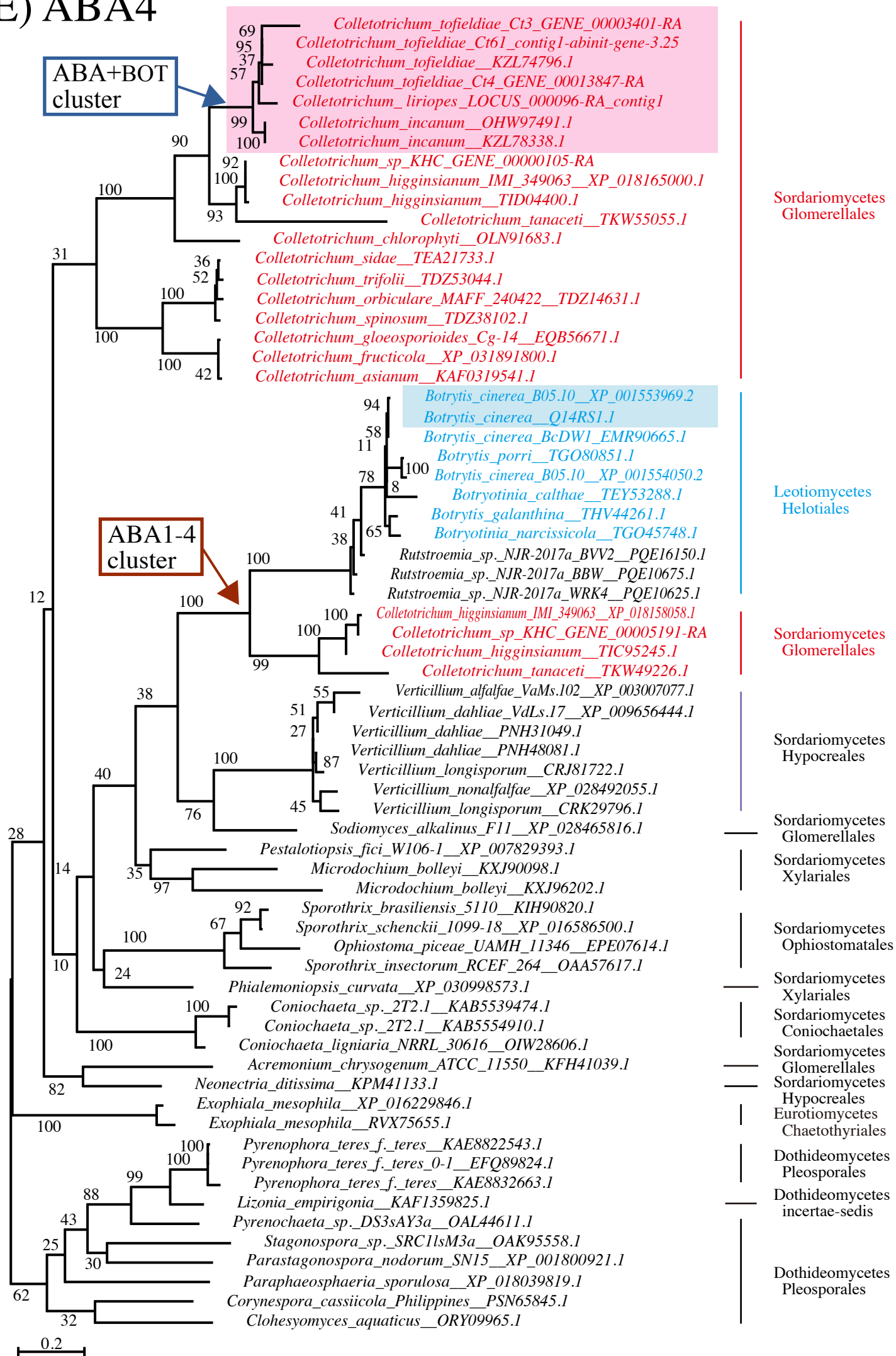
(C) ABA2



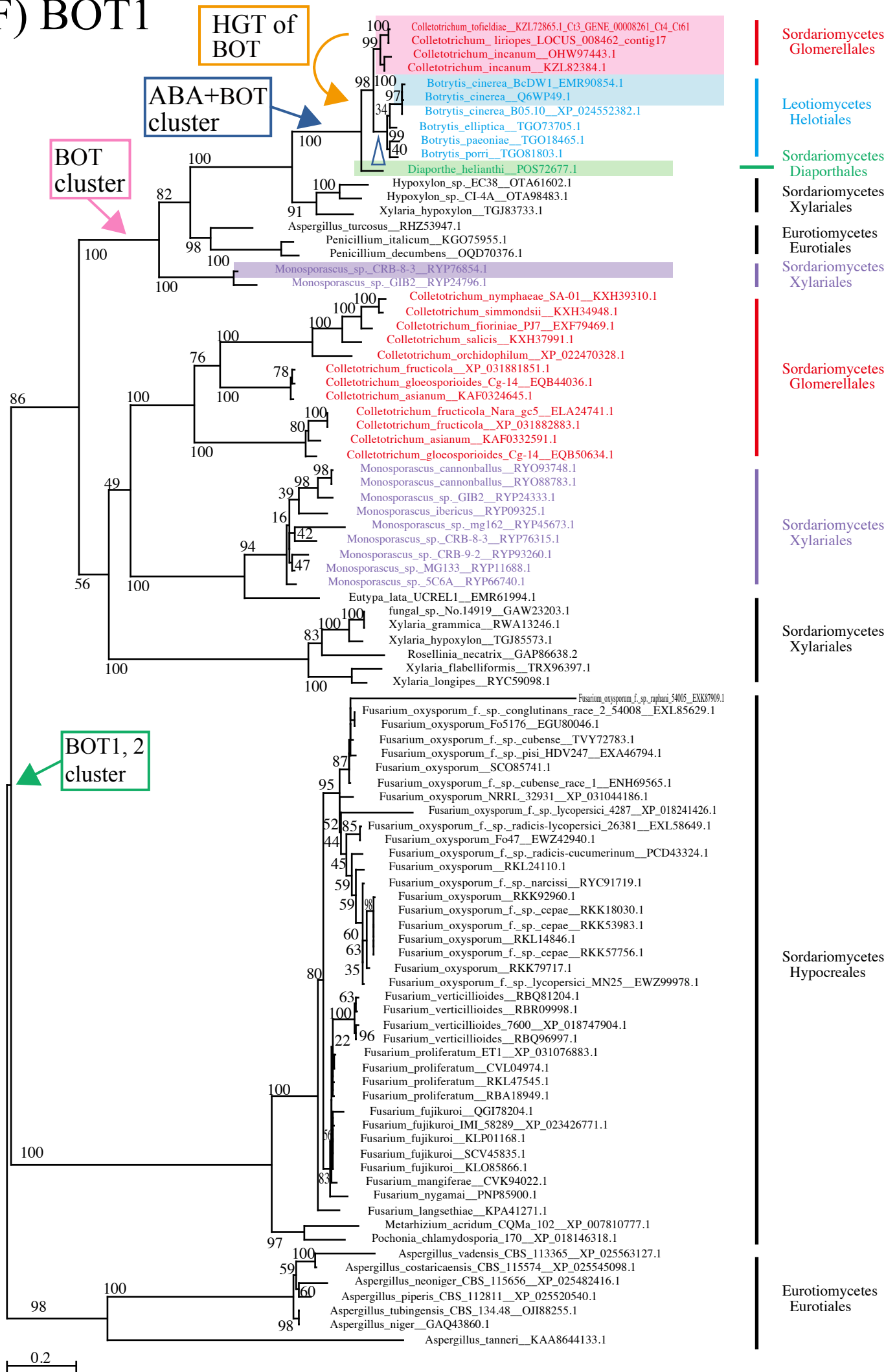
(D) ABA3



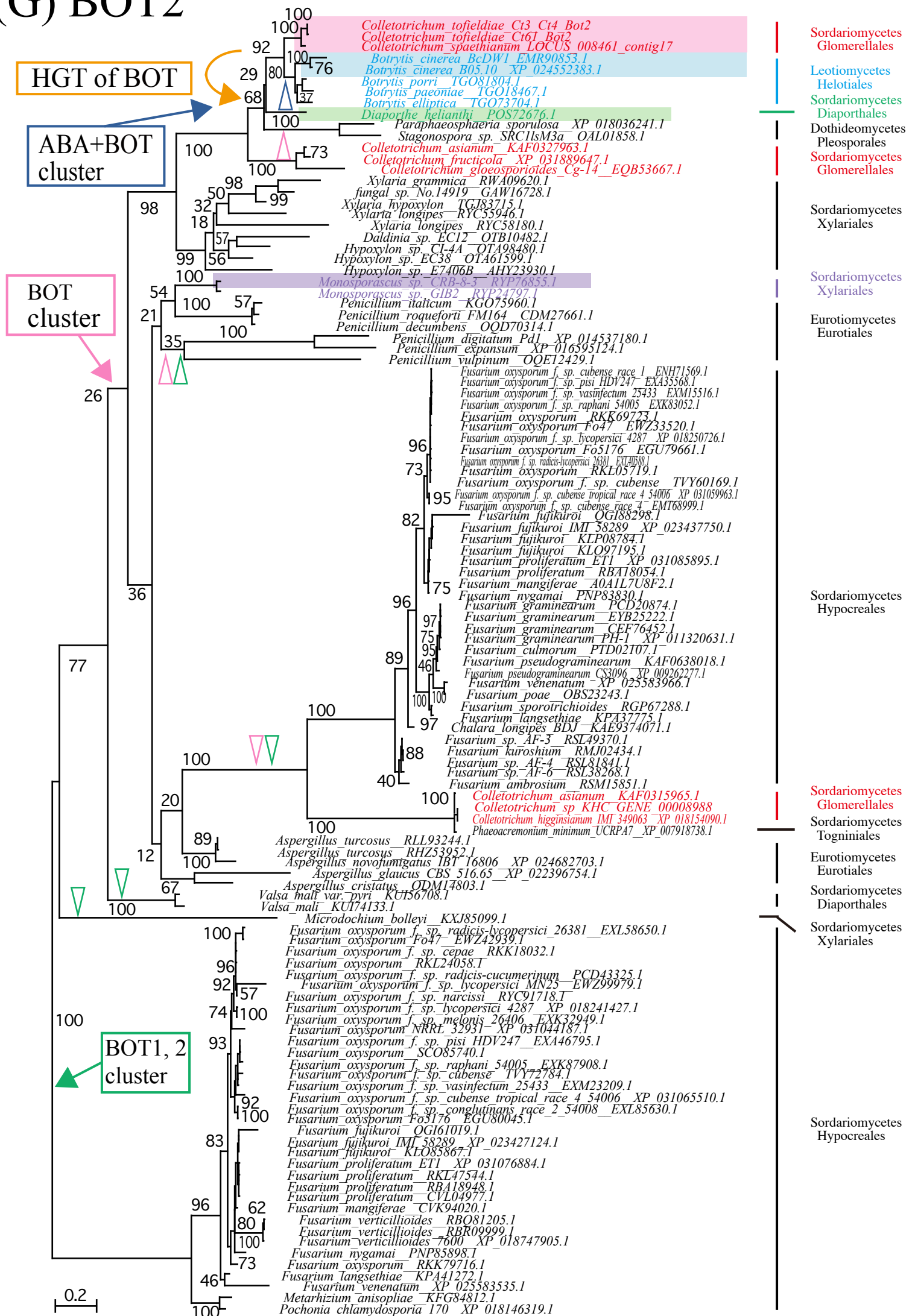
(E) ABA4



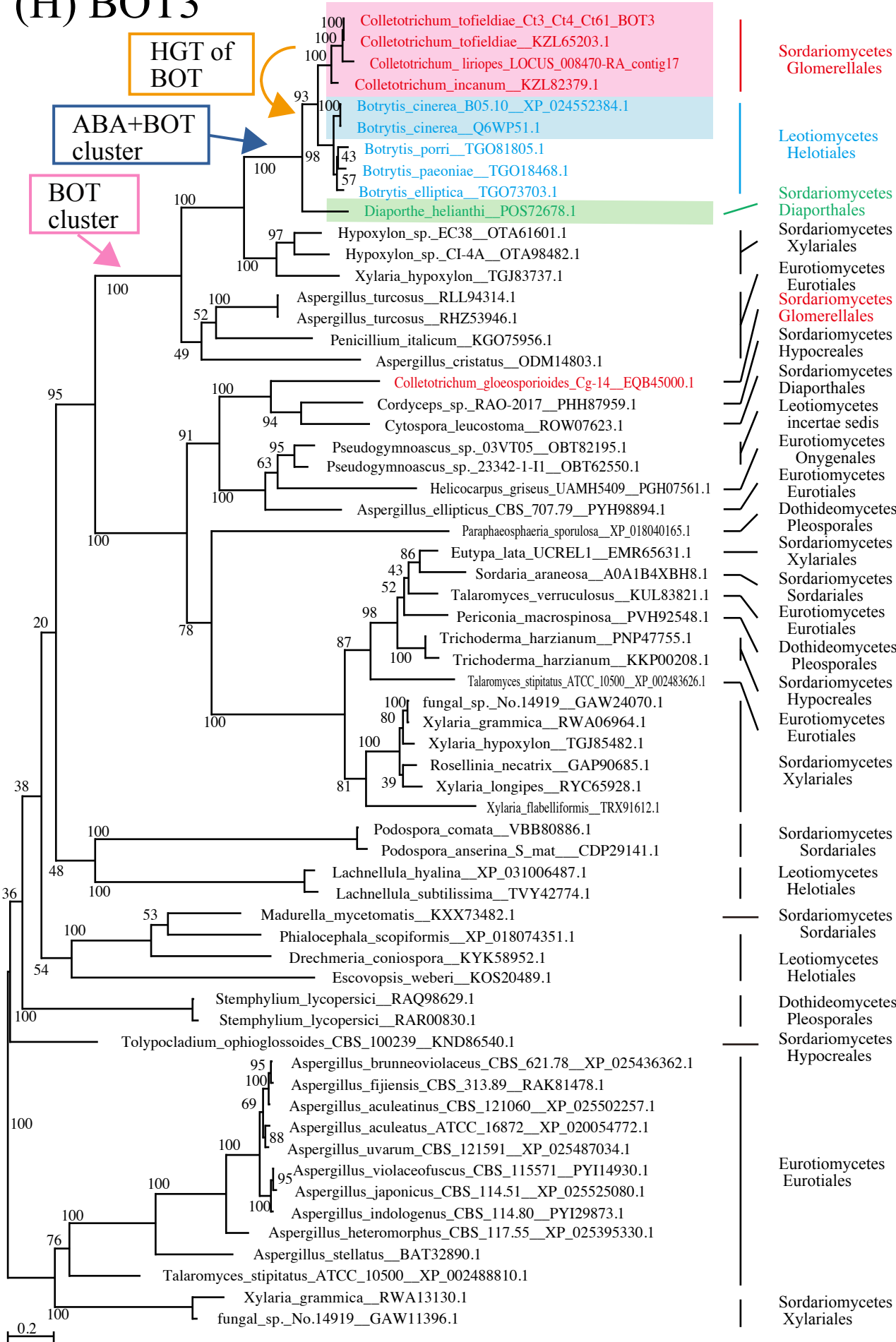
(F) BOT1



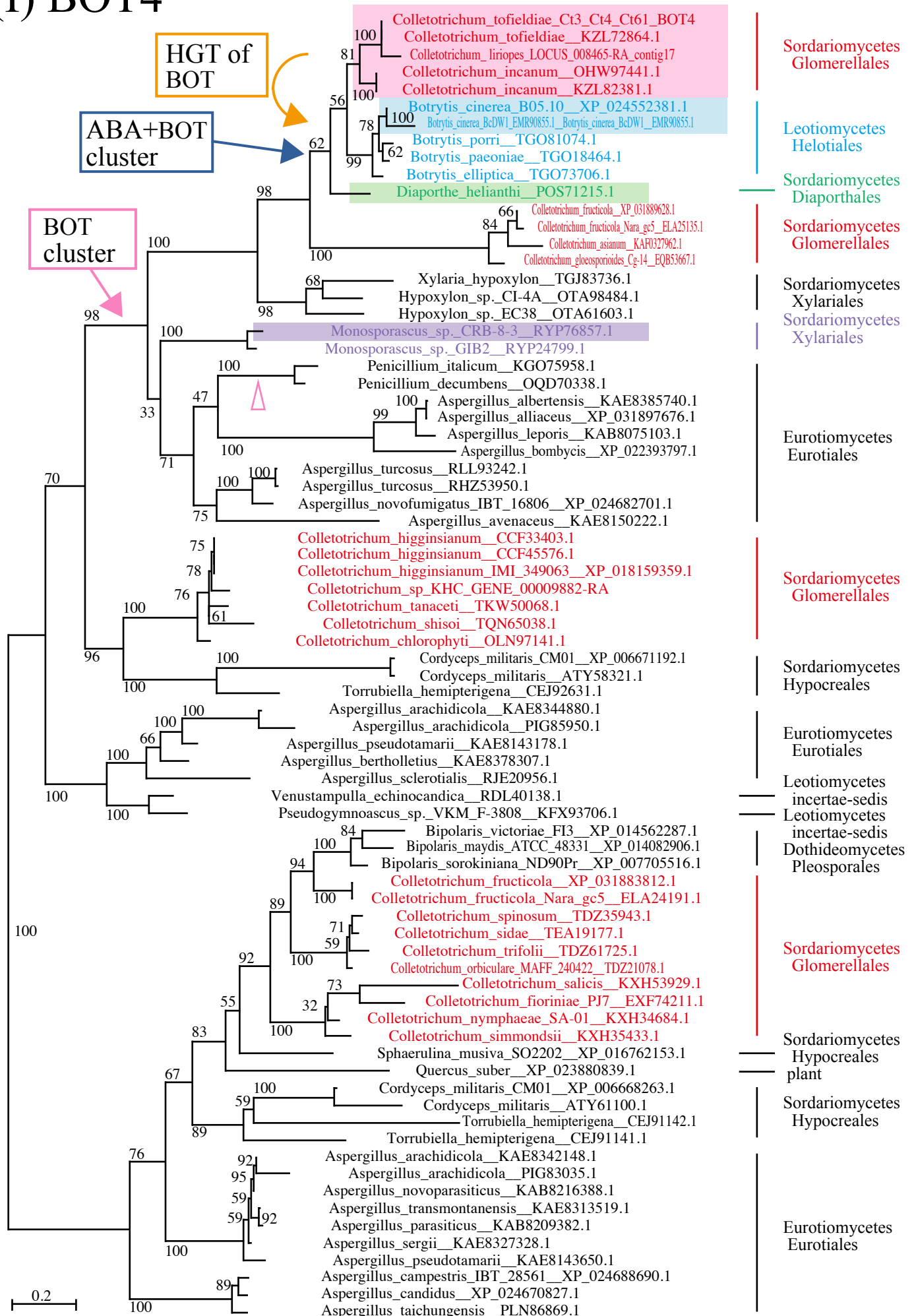
(G) BOT2



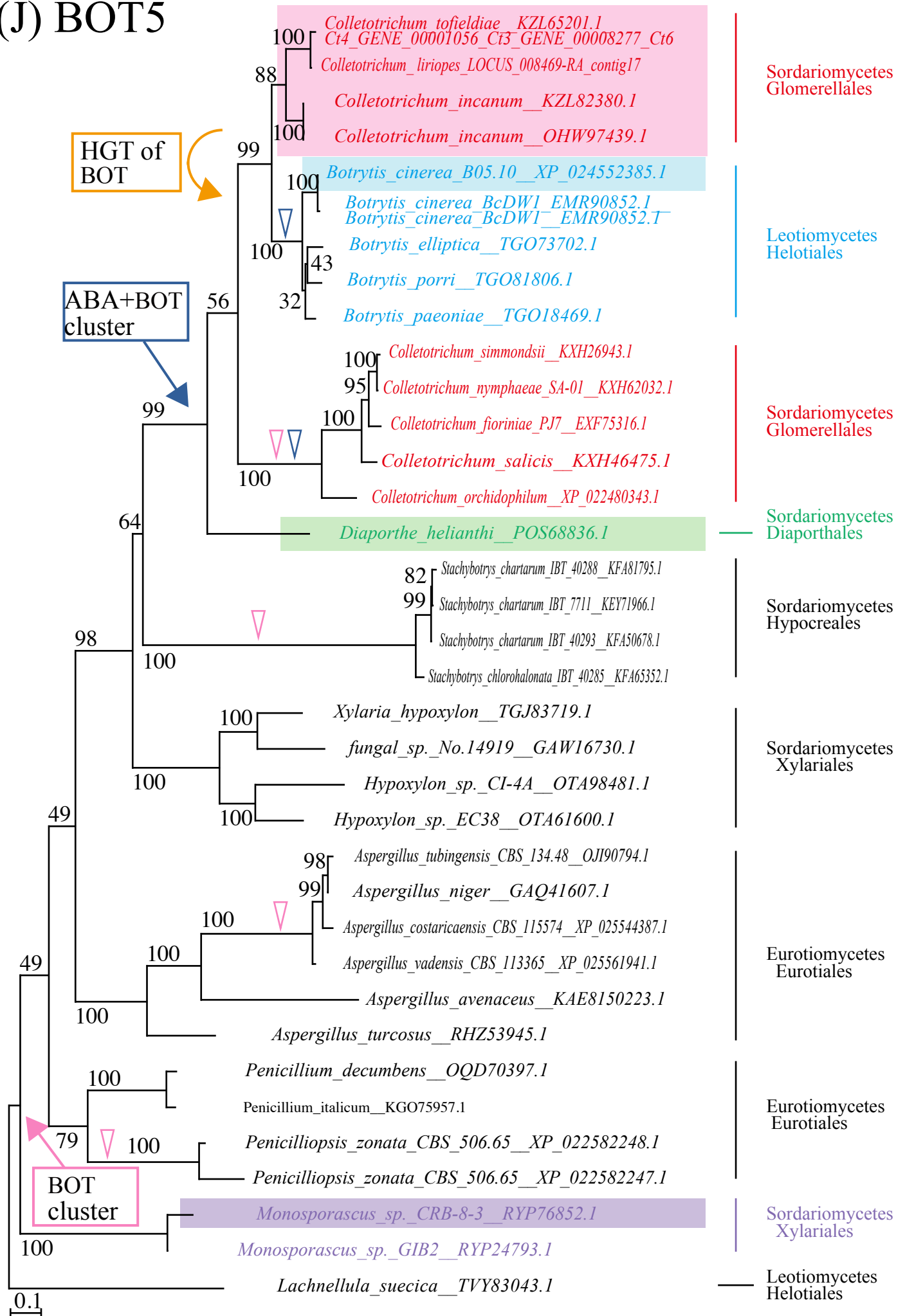
(H) BOT3



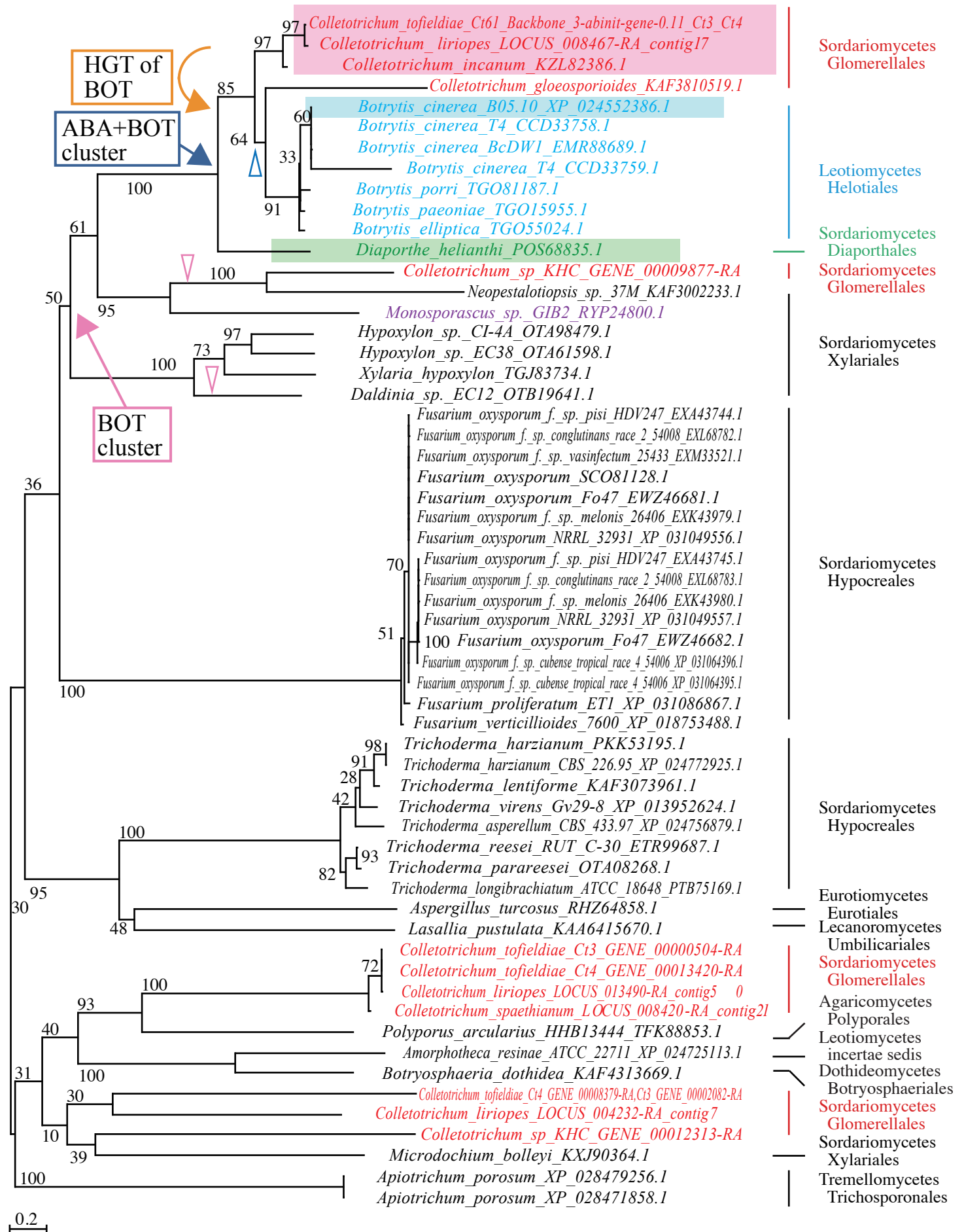
(I) BOT4



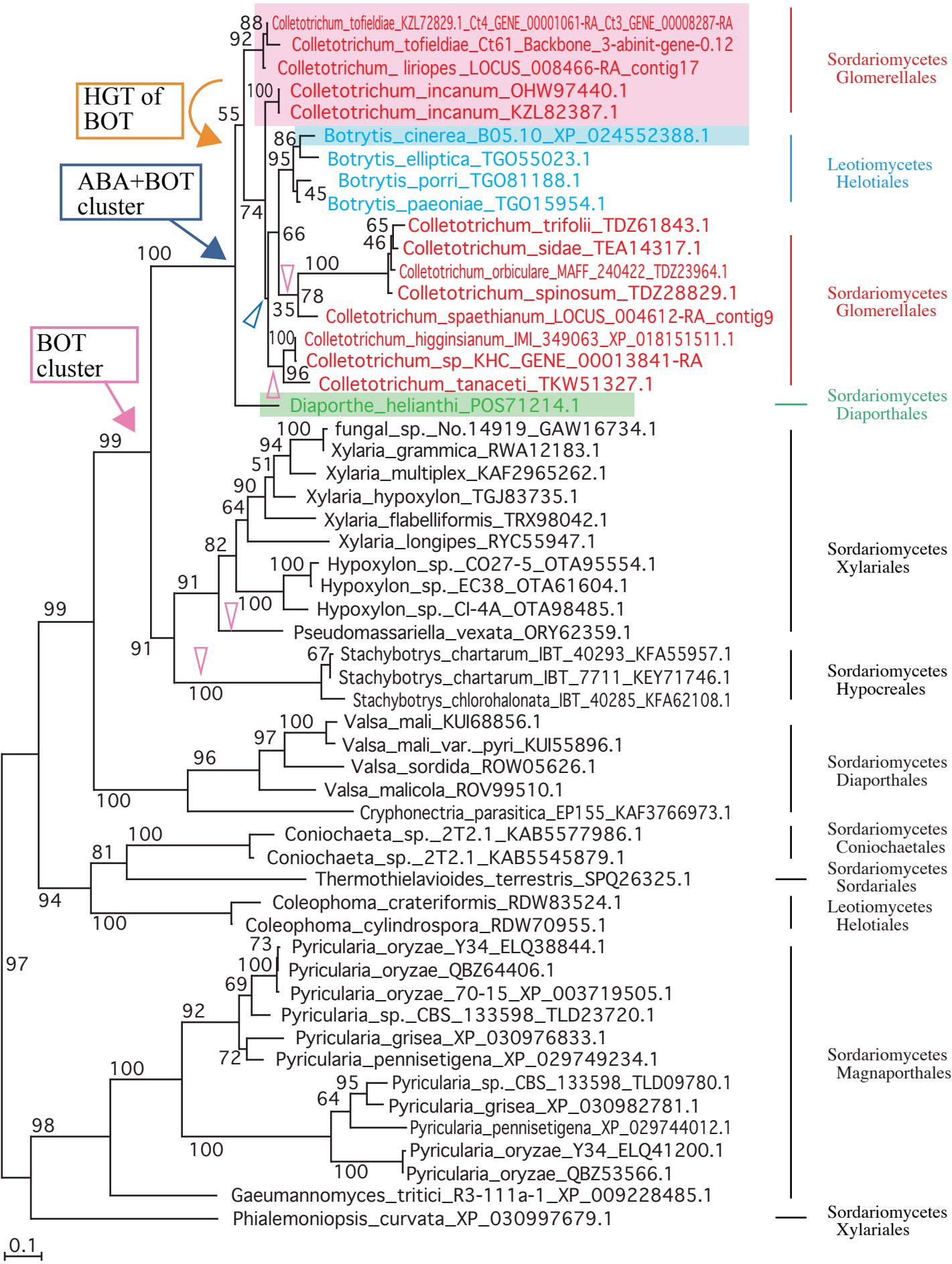
(J) BOT5

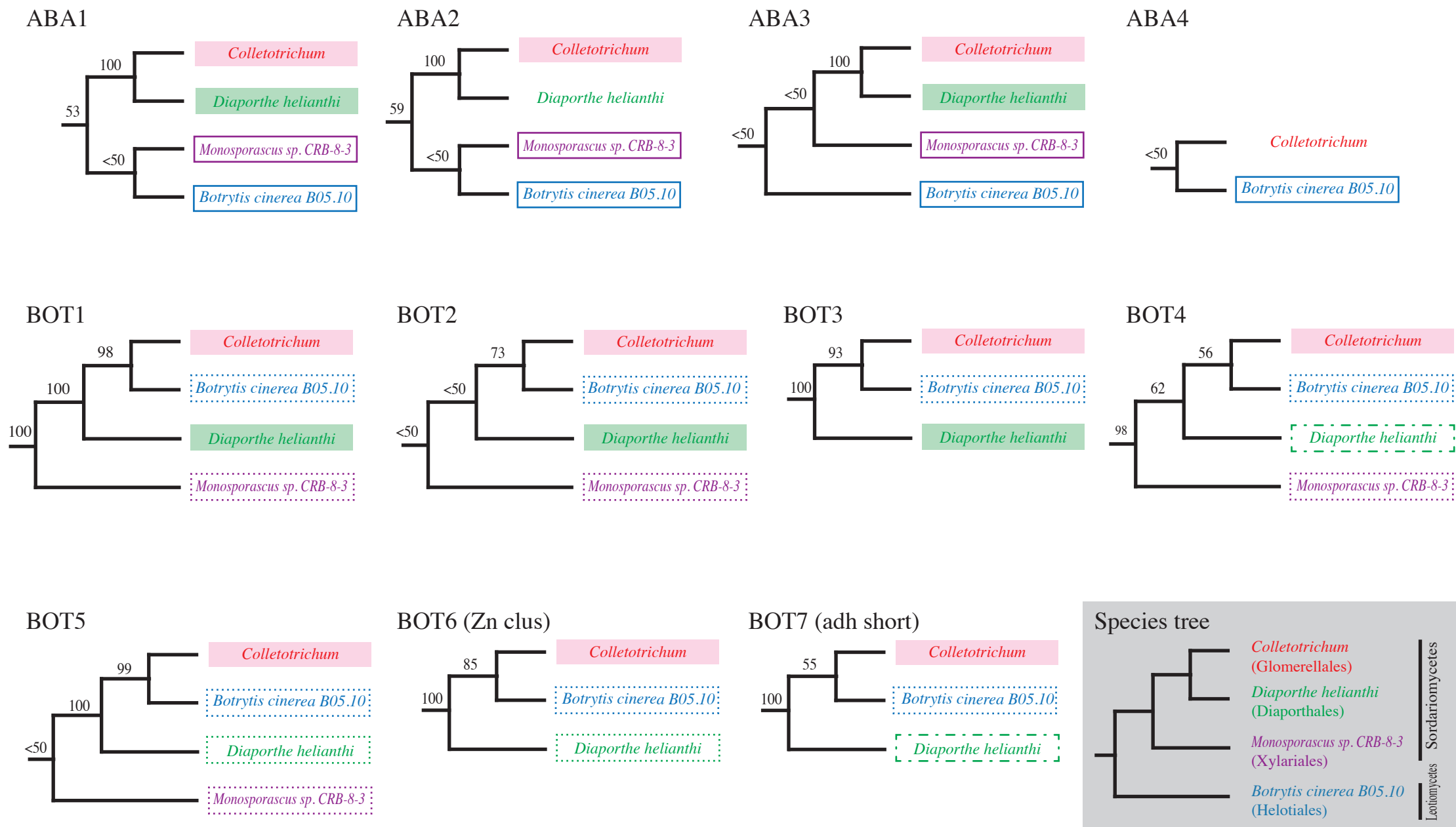


(K) BOT6 (Zn_clus)



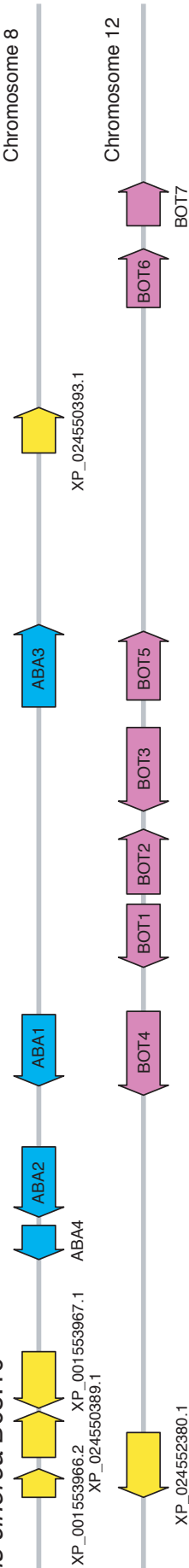
(L) BOT7 (Adh_short)



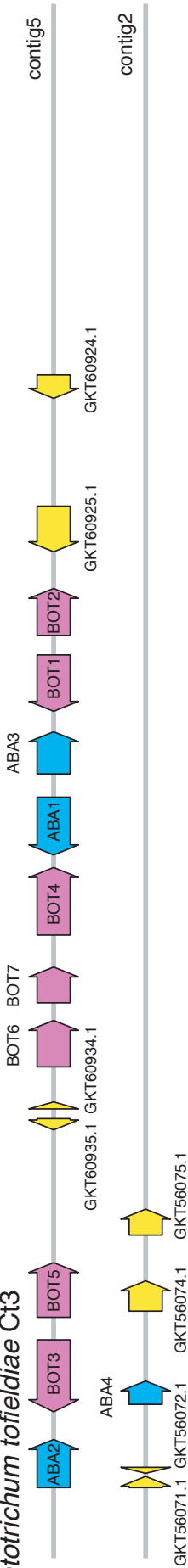


m. Phylogenetic relationship of ABA and BOT genes in the four organisms that have both ABA and BOT clusters in their genome. The relationship and branch support are based on Supplementary Figure 4b-1. The bootstrap probability is shown on the branches. The species tree of the four organisms is shown in the rectangle with a gray background. Organisms that have ABA-BOT cluster are labeled with red or green backgrounds. Organism names of each gene that is on the same molecule (contig), but not on ABA-BOT cluster, are boxed with the same solid or dotted line.

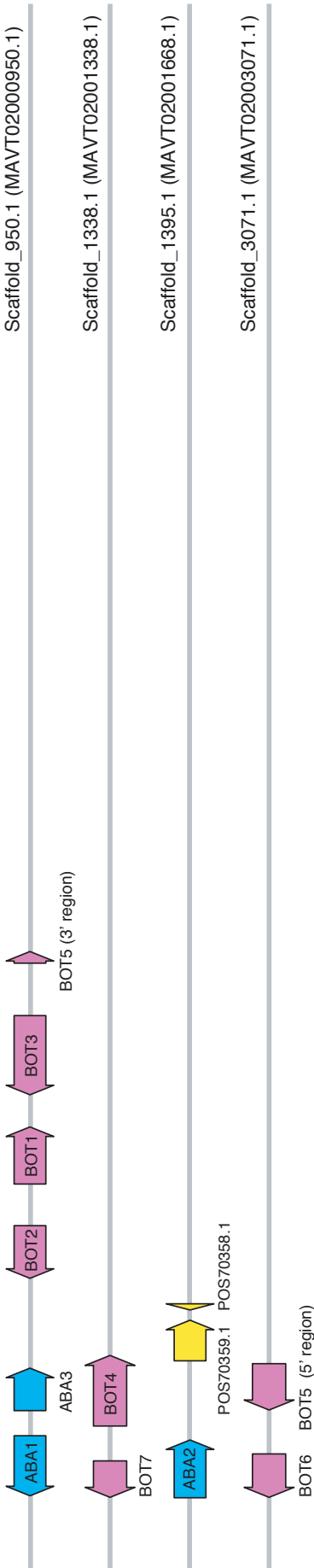
Botrytis cinerea B05.10



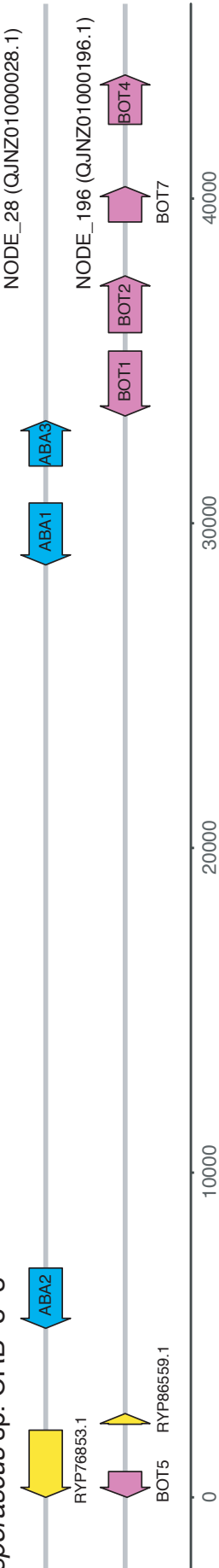
Colletotrichum tofieldiae Ct3



Diaporthe helianthi strain 7/96



Monosporascus sp. CRB-8-3



n. Schematic drawing of genetic structures of ABA and BOT gene clusters. Genes on the same molecule (chromosome or scaffold) are drawn on a line side by side. Color coding; blue: ABA genes, red: BOT genes, yellow: other genes. Bar indicates base pairs.

Supplementary Figure 4o: Amino acids alignments of Ct ABA and BOT genes.

CLUSTAL format alignment by MAFFT (v7.511)

ABA1

Ct3 MSSFLITASYTSLLGAGAGILVFCYLLSALYSWNRLGAVPAASWTAHFSYLWLAKTTYSG
Ct4 MSSFLITASYTSLLGAGAGILVFCYLLSALYSWNRLGAVPAASWTAHFSYLWLAKTTYSG
Ct61 MSSFLITASYTSLLGAGAGILVFCYLLSALYSWNRLGAVPAASWTAHFSYLWLAKTTYSG

Ct3 RQYWVHRSLHKDKGPLVRVGPNEVVTNDPKLVRKISGTDERWARDPFYITGKFNPYHDNM
Ct4 RQYWVHRSLHKDKGPLVRVGPNEVVTNDPKLVRKISGTDERWARDPFYITGKFNPYHDNM
Ct61 RQYWVHRSLHKDKGPLVRVGPNEVVTNDPKLVRKISGTDERWARDPFYITGKFNPYHDNM

Ct3 FSILNPREHQLAKSRRLAAYSGRETPDLEIGMDTLVKTLIDMIETRYTSPVQDSRPVPLL
Ct4 FSILNPREHQLAKSRRLAAYSGRETPDLEIGMDTLVKTLIDMIETRYTSPVQDSRPVPLL
Ct61 FSILNPREHQLAKSRRLAAYSGRETPDLEIGMDTLVKTLIDMIETRYTSPVQDSRPVPLL

Ct3 DLGKTSYCYFTLDVITRLAFGKEVGYLSEKDHFGFLGSLHDLWPQMSTCADIPMLRKFLF
Ct4 DLGKTSYCYFTLDVITRLAFGKEVGYLSEKDHFGFLGSLHDLWPQMSTCADIPMLRKFLF
Ct61 DLGKTSYCYFTLDVITRLAFGKEVGYLSEKDHFGFLGSLHDLWPQMSTCADIPMLRKFLF

Ct3 SSFFLKFMGPKTTDKVGFALMGVANHYVGNRFASTEKPQQDMLGSMIKHGLDQVECETE
Ct4 SSFFLKFMGPKTTDKVGFALMGVANHYVGNRFASTEKPQQDMLGSMIKHGLDQVECETE
Ct61 SSFFLKFMGPKTTDKVGFALMGVANHYVGNRFASTEKPQQDMLGSMIKHGLDQVECETE

Ct3 GLFMI IAGTESTASAIRSALVHAMTSPLVYQKLKDEIHTAVCEGKVSSPITFQEAKALPY
Ct4 GLFMI IAGTESTASAIRSALVHAMTSPLVYQKLKDEIHTAVCEGKVSSPITFQEAKALPY
Ct61 GLFMI IAGTESTASAIRSALVHAMTSPLVYQKLKDEIHTAVREGKVSSPITFQEAKALPY

Ct3 LQAVIYESIRMRPPLIGYFPKVPPGGETLLGYHLPAGTSIGTNMSAILSSTDIFGPDAG
Ct4 LQAVIYESIRMRPPLIGYFPKVPPGGETLLGYHLPAGTSIGTNMSAILSSTDIFGPDAG
Ct61 LQAVIYESIRMRPPLIGYFPKVPPGGETLLGYHLPAGTSIGTNMSAILSSTDIFGPDAG

Ct3 VFRPERFTELDEDSCKRMKRDVELAFSGQWCMGKTI AFMEINKSVFEI FRAFDIQLVE
Ct4 VFRPERFTELDEDSCKRMKRDVELAFSGQWCMGKTI AFMEINKSVFEI FRAFDIQLVE
Ct61 VFRPERFTELDEDSCKRMKRDVELAFSGQWCMGKTI AFMEINKSVFEI FRAFDIQLVE

Ct3 PFAPSTIATYGTFLSQMMAKVSKSDVS
Ct4 PFAPSTIATYGTFLSQMMAKVSKSDVS
Ct61 PFAPSTIATYGTFLSQMMAKVSKSDVS

ABA2

Ct3 MDTIVTSLAKSHSLLRDAKDALPKDSLLWVTSVAVTVFTLVILARI IKARFIHPLRKFPG
Ct4 MDTIVTSLAKSHSLLRDAKDALPKDSLLWVTSVAVTVFTLVILARI IKARFIHPLRKFPG
Ct61 MDTIVTSLAKSHSLLRDAKDALPKDSLLWVTSVAVTVFTLVILARI IKARFIHPLRKFPG

Ct3 PFLNSVSSLPAAYLVYRGNQPQSFKKLHEKYGPVVRTGPNELSF IGADAWEDIYGIQKVG
Ct4 PFLNSVSSLPAAYLVYRGNQPQSFKKLHEKYGPVVRTGPNELSF IGADAWEDIYGIQKVG
Ct61 PFLNSVSSLPAAYLVYRGNQPQSFKKLHEKYGPVVRTGPNELSF IGADAWEDIYGIQKVG

Ct3 LNFQKDPSWLAVVSPKDGQTGLSLAPPETHTRQRNALGATFLNEALLSQEHI IQGHVDKF
Ct4 LNFQKDPSWLAVVSPKDGQTGLSLAPPETHTRQRNALGATFLNEALLSQEHI IQGHVDKF
Ct61 LNFQKDPSWLAVVSPKDGQTGLSLAPPETHTRQRNALGATFLNEALLSQEHI IQGHVDKF

Ct3 MEVIKRHIAENKAIDL SHWYGYATFDVIGDVIFAEPFGCLDESEETQWMRAINDIFKSGA
Ct4 MEVIKRHIAENKAIDL SHWYGYATFDVIGDVIFAEPFGCLDESEETQWMRAINDIFKSGA

Ct61 MEVIKRHIAENKAIDLSHWYGYATFDVIGDVIFAEPFGCLDESEETQWMRAINDIFKSGA

Ct3 WEQAFGQLAGVGTLLHKL MVKFLIPNELKSWRLKHL SKATEKTRRRMATPNPAHPDMVAH
Ct4 WEQAFGQLAGVGTLLHKL MVKFLIPNELKSWRLKHL SKATEKTRRRMATPNPAHPDMVAH
Ct61 WEQAFGQLAGVGTLLHKL MVKFLIPNELKSWRLKHL SKATEKTRRRMATPNPAHPDMVAH

Ct3 ILKNNQTRKARLSDTEIILNMVQFISAGSETTASLLAGWTYFIVANPHVYKRVVAEVREA
Ct4 ILKNNQTRKARLSDTEIILNMVQFISAGSETTASLLAGWTYFIVANPHVYKRVVAEVREA
Ct61 ILKNNQTRKARLSDTEIILNMVQFISAGSETTASLLAGWTYFIVANPHVYKRVVAESLQC
***** :.

Ct3 FNAKEEITWTSVGKLYLEATLHEALRLTSPAPCNQHRVPPAGQGKVIDGHYVPPGTTV
Ct4 FNAKEEITWTSVGKLYLEATLHEALRLTSPAPCNQHRVPPAGQGKVIDGHYVPPGTTV
Ct61 -----TPGRVGLKLYLEATLHEALRLTSPAPCNQHRVPPAGQGKVIDGHYVPPGTTV
* *****

Ct3 AVAPWVAERHPDNFTDPETFEPERWLGAERYKNDKLHASQPFGLGVRACIGKNLSYFEAR
Ct4 AVAPWVAERHPDNFTDPETFEPERWLGAERYKNDKLHASQPFGLGVRACIGKNLSYFEAR
Ct61 AVAPWVAERHPDNFTDPETFEPERWLGAERYKNDKLHASQPFGLGVRACIGKNLSYFEAR

Ct3 LMMGHLLWHFDFAFEETKSAQAALRKWETADMLVWHVWDKPPLMVQFSEVHR
Ct4 LMMGHLLWHFDFAFEETKSAQAALRKWETADMLVWHVWDKPPLMVQFSEVHR
Ct61 LMMGHLLWHFDFAFEETKSAQAALRKWETADMLVWHVWDKPPLMVQFSEVHR

ABA3

Ct3 MQKTERAPRERDTWYFPPDIAHDLGIPLESVKGEILATAWEYTRTVIPNYTNWKRYV
Ct4 MQKTERAPRERDTWYFPPDIAHDLGIPLESVKGEILATAWEYTRTVIPNYTNWKRYV
Ct61 MQKTERAPRERDTWYFPPDIAHDLGIPLESVKGEILATAWEYTRTVIPNYTNWKRYV

Ct3 AFMRIVVMGIIAEFKGMDLDTLGDVSLNYSLDGVLSDLFGKTPGHTAMAREYKTFLLV
Ct4 AFMRIVVMGIIAEFKGMDLDTLGDVSLNYSLDGVLSDLFGKTPGHTAMAREYKTFLLV
Ct61 AFMRIVVMGIIAEFKGMDLDTLGDVSLNYSLDGVLSDLFGKTPGHTAMAREYKTFLLV

Ct3 GDKSSSRRTGEFFRYYVNLAHSPTRFFRLRDTDALCRFTIATALACNDLDDVWFTEEQF
Ct4 GDKSSSRRTGEFFRYYVNLAHSPTRFFRLRDTDALCRFTIATALACNDLDDVWFTEEQF
Ct61 GDKSSSRRTGEFFRYYVNLAHSPTRFFRLRDTDALCRFTIATALACNDLDDVWFTEEQF

Ct3 DLLAEMGDMYDAVSFFKHRSEGETNSTFAYMPADRLAAYRQCRELLWALDAAWCTRPE
Ct4 DLLAEMGDMYDAVSFFKHRSEGETNSTFAYMPADRLAAYRQCRELLWALDAAWCTRPE
Ct61 DLLAEMGDMYDAVSFFKHRSEGETNSTFAYMPADRLAAYRQCRELLWALDAAWCTRPE

Ct3 TACVTSFLRYFGGPLHLMRRYRFVEEGLTIGREEDAEVVNQTRNHYKLWNRIDANLRHA
Ct4 TACVTSFLRYFGGPLHLMRRYRFVEEGLTIGREEDAEVVNQTRNHYKLWNRIDANLRHA
Ct61 TACVTSFLRYFGGPLHLMRRYRFVEEGLTIGREEDAEVVNQTRNHYKLWNRIDANLRHA

Ct3 NEREKASLERYDAIVADSEKLLIPGLAGFLEAGGDGHCDSCRYQVSYGADGEYRFGGVEL
Ct4 NEREKASLERYDAIVADSEKLLIPGLAGFLEAGGDGHCDSCRYQVSYGADGEYRFGGVEL
Ct61 NEREKASLERYDAIVADSEKLLIPGLAGFLEAGGDGHCDSCRYQVSYGADGEYRFGGVEL

Ct3 CEDCRSKWRAFLLSFPERAAKVPELAGTYKIAITSSNKLESSGDGPLVLVPAA
Ct4 CEDCRSKWRAFLLSFPERAAKVPELAGTYKIAITSSNKLESSGDGPLVLVPAA
Ct61 CEDCRSKWRAFLLSFPERAAKVPELAGTYKIAITSSNKLESSGDGPLVLVPAA

ABA4

Ct3 MSTPHQFSDKVIAITGAASGIGLATAHLLASRGAKLSLTDNKEGLIEVQLNIQTQYPQV
Ct4 MSTPHQFSDKVIAITGAASGIGLATAHLLASRGAKLSLTDNKEGLIEVQLNIQTQYPQV
Ct61 MSTPHQFSDKVIAITGAASGIGLATAHLLASRGAKLSLTDNKEGLIEVQLNIQTQYPQV

Ct3 EVLISAADVTDYEQIEHWTVNTVDHFGKLDGAANLAGVIPKSVGKKGLIDQDFEEDWFVM
 Ct4 EVLISAADVTDYEQIEHWTVNTVDHFGKLDGAANLAGVIPKSVGKKGLIDQDFEEDWFVM
 Ct61 EVLISAADVTDYEQIEHWTVNTVDHFGKLDGAANLAGVIPKSVGKKGLIDQDFEEDWFVM

Ct3 GVNKKGVMHCLKAQLSVIQDHGSI VNASSIAGLQGRPYNGAYTAKHRRKLGYPTRLWDA
 Ct4 GVNKKGVMHCLKAQLSVIQDHGSI VNASSIAGLQGRPYNGAYTAKHAI VGLTRTAAKEV
 Ct61 GVNKKGVMHCLKAQLSVIQDHGSI VNASSIAGLQGRPYNGAYTAKHAI VGLTRTAAKEV
 ***** : : * . *

Ct3 -----QASPRK-----
 Ct4 GLRGIRVNAVCPGRIDTPMSRASAEGIQADAALGRSGKPEEVASLIAFLLSNESTYITG
 Ct61 GLRGIRVNAVCP-----
 . . *

Ct3 -----
 Ct4 NAVSIDGGWNC
 Ct61 -----

BOT1

Ct3 MGLLSDVVNVVDYLPQTPLAWAAFALGAFALYSIQLVVRRLYFHPLAKIPGPFLARTTY
 Ct4 MGLLSDVVNVVDYLPQTPLAWAAFALGAFALYSIQLVVRRLYFHPLAKIPGPFLARTTY
 Ct61 MGLLSDVVNVVDYLPQTPLAWAAFALGAFALYSIQLVVRRLYFHPLAKIPGPFLARTTY

Ct3 WYEFYQDIILGGMYVKNYAALHEKYGPVIRASPD RVHVS DPFFHEVYSSGSKYMKDPAF
 Ct4 WYEFYQDIILGGMYVKNYAALHEKYGPVIRASPD RVHVS DPFFHEVYSSGSKYMKDPAF
 Ct61 WYEFYQDIILGGMYVKNYAALHEKYGPVIRASPD RVHVS DPFFHEVYSSGSKYMKDPAF

Ct3 FQSSGGIPEALPAIVDVEYHKRRRKLINDLFSAKSMEALSHLVLVQNALRKANEHHDE
 Ct4 FQSSGGIPEALPAIVDVEYHKRRRKLINDLFSAKSMEALSHLVLVQNALRKANEHHDE
 Ct61 FQSSGGIPEALPAIVDVEYHKRRRKLINDLFSAKSMEALSHLVLVQNALRKANEHHDE

Ct3 NKVLDIQRLYTGITIDTIMQVLCDRTLNFIDAKEEPPFLATLRTFSENFFLLKHFPVLI
 Ct4 NKVLDIQRLYTGITIDTIMQVLCDRTLNFIDAKEEPPFLATLRTFSENFFLLKHFPVLI
 Ct61 NKVLDIQRLYTGITIDTIMQVLCDRTLNFIDAKEEPPFLATLRTFSENFFLLKHFPVLI

Ct3 WMALNIPKSI AAKLIPGEFEFRANINQWIRDRALEHELGV EKAEDGRKTVIDL L LRPEDG
 Ct4 WMALNIPKSI AAKLIPGEFEFRANINQWIRDRALEHELGV EKAEDGRKTVIDL L LRPEDG
 Ct61 WMALNIPKSI AAKLIPGEFEFRANINQWIRDRALEHELGV EKAEDGRKTVIDL L LRPEDG

Ct3 GRPLTHQAVEDETYSFAGTH TTSHTMSMGTYLLSNPSKLQKL RDELKTVPKNDQGLY
 Ct4 GRPLTHQAVEDETYSFAGTH TTSHTMSMGTYLLSNPSKLQKL RDELKTVPKNDQGLY
 Ct61 GRPLTHQAVEDETYSFAGTH TTSHTMSMGTYLLSNPSKLQKL RDELKTVPKNDQGLY

Ct3 EYKTVRALPYLNACIKESLRMSSPVPGILPRLVPVGGMTWQGHYLPAGTSVSSSIHCVHN
 Ct4 EYKTVRALPYLNACIKESLRMSSPVPGILPRLVPVGGMTWQGHYLPAGTSVSSSIHCVHN
 Ct61 EYKTVRALPYLNACIKESLRMSSPVPGILPRLVPVGGMTWQGHYLPAGTSVSSSIHCVHN

Ct3 DPSIFPNPEQFIPERWLANENLEHYLVVFGKGSRA CIGLNVAVWMETYLTF SNFFTSLDMS
 Ct4 DPSIFPNPEQFIPERWLANENLEHYLVVFGKGSRA CIGLNVAVWMETYLTF SNFFTSLDMS
 Ct61 DPSIFPNPEQFIPERWLANENLEHYLVVFGKGSRA CIGLNVAVWMETYLTF SNFFTSLDMS

Ct3 LFETNEQTTDWTDCGNSMIKKHVMVKVNSVAS
 Ct4 LFETNEQTTDWTDCGNSMIKKHVMVKVNSVAS
 Ct61 LFETNEQTTDWTDCGNSMIKKHVMVKVNSVAS

BOT2

Ct3	MATLAPALELHNADTASSDVSSNSTYSGYDTSYTTTPGEKLDTGGLQLQHDARPPFVRIP
Ct4	MATLAPALELHNADTASSDVSSNSTYSGYDTSYTTTPGEKLDTGGLQLQHDARPPFVRIP
Ct61	MATLAPALELHNADTASSDVSSNSTYSGYDTSYTTTPGEKLDTGGLQLQHDARPPFVRIP

Ct3	DLFGSIMATKPVVNPNYFAAKARGDRWIARVMNFDKVTAAARNAKVDLCFLASIWAPDASE
Ct4	DLFGSIMATKPVVNPNYFAAKARGDRWIARVMNFDKVTAAARNAKVDLCFLASIWAPDASE
Ct61	DLFGSIMATKPVVNPNYFAAKARGDRWIARVMNFDKVTAAARNAKVDLCFLASIWAPDASE

Ct3	DRLVMMLDWNHWVFLFDDQFDEGHLKEDPAAAAEEVRQTVAIMGGDAPVYTAESNPIRYV
Ct4	DRLVMMLDWNHWVFLFDDQFDEGHLKEDPAAAAEEVRQTVAIMGGDAPVYTAESNPIRYV
Ct61	DRLVMMLDWNHWVFLFDDQFDEGHLKEDPAAAAEEVRQTVAIMGGDAPVYTAESNPIRYV
***** : *****	
Ct3	FQECWERLSRVSSQEMQQRWIDQHKRYFAQLLVQVDQQVSGQNFVRDVEDAYMDLRRGTIG
Ct4	FQECWERLSRVSSQEMQQRWIDQHKRYFAQLLVQVDQQVSGQNFVRDVEDAYMDLRRGTIG
Ct61	FQECWERLSRVSSQEMQQRWIDQHKRYFAQLLVQVDQQVSGQNFVRDVEDAYMDLRRGTIG

Ct3	VYPAINLAEGADVRLPQYVYDHPSLQECMKISADLVTLVNDVLSYRKDELGVHDNLIS
Ct4	VYPAINLAEGADVRLPQYVYDHPSLQECMKISADLVTLVNDVLSYRKDELGVHDNLIS
Ct61	VYPAINLAEGADVRLPQYVYDHPSLQECMKISADLVTLVNDVLSYRKDELGVHDNLIS

Ct3	LLMERDSLISIQQAVDKIGDMVNDCYRRWYLALAEPSYGEKIDYKVMKFIEICRAVAQGN
Ct4	LLMERDSLISIQQAVDKIGDMVNDCYRRWYLALAEPSYGEKIDYKVMKFIEICRAVAQGN
Ct61	LLMERDSLISIQQAVDKIGDMVNDCYRRWYLALAEPSYGEKIDYKVMKFIEICRAVAQGN

Ct3	LYWSFQTGRYLGPEGHDVHETGIMHLPPIKALF
Ct4	LYWSFQTGRYLGPEGHDVHETGIMHLPPIKALF
Ct61	LYWSFQTGRYLGPEGHDVHETGIMHLPPIKALF

BOT3	
Ct3	MEKSSPALALASEKAWEFASKADAVLRTGVSRAAPHVLAANKKAWEGAHSIGTKLAQGNV
Ct4	MEKSSPALALASEKAWEFASKADAVLRTGVSRAAPHVLAANKKAWEGAHSIGTKLAQGNV
Ct61	MEKSSPALALASEKAWEFASKADAVLRTGVSRAAPHVLAANKKAWEGAHSIGTKLAQGNV

Ct3	GDIDRTEVTTILSVVLGLYFAYVFALVFYRLYLHPLAKFPGYKICAACEWYEFYCYIVKG
Ct4	GDIDRTEVTTILSVVLGLYFAYVFALVFYRLYLHPLAKFPGYKICAACEWYEFYCYIVKG
Ct61	GDIDRTEVTTILSVVLGLYFAYVFALVFYRLYLHPLAKFPGYKICAACEWYEFYCYIVKG

Ct3	GQWGNEIRKMHEKYGPIVRTSPWELSIRDPVFYDQLYVTAATRKTDMWPRGREGNGFDNS
Ct4	GQWGNEIRKMHEKYGPIVRTSPWELSIRDPVFYDQLYVTAATRKTDMWPRGREGNGFDNS
Ct61	GQWGNEIRKMHEKYGPIVRTSPWELSIRDPVFYDQLYVTAATRKTDMWPRGREGNGFDNS

Ct3	HHLVSHDLHRIRRKHLEPFFSRQGITRIEPRIAELVMKMDKRIVGLKGSGAVVPVDHLL
Ct4	HHLVSHDLHRIRRKHLEPFFSRQGITRIEPRIAELVMKMDKRIVGLKGSGAVVPVDHLL
Ct61	HHLVSHDLHRIRRKHLEPFFSRQGITRIEPRIAELVMKMDKRIVGLKGSGAVVPVDHLL

Ct3	CALTGDVIGQVSSGMQAGLLDDPDFTPAWKDLMIKSTTIAPLFRFCFPWINKFLQSLPTS
Ct4	CALTGDVIGQVSSGMQAGLLDDPDFTPAWKDLMIKSTTIAPLFRFCFPWINKFLQSLPTS
Ct61	CALTGDVIGQVSSGMQAGLLDDPDFTPAWKDLMIKSTTIAPLFRFCFPWINKFLQSLPTS

Ct3	MNSVYPKGISNMMLGKTGQRNIEKIKSDIATSKKDLSGVSVFHLLSSDVPESKSTDR
Ct4	MNSVYPKGISNMMLGKTGQRNIEKIKSDIATSKKDLSGVSVFHLLSSDVPESKSTDR
Ct61	MNSVYPKGISNMMLGKTGQRNIEKIKSDIATSKKDLSGVSVFHLLSSDVPESKSTDR

Ct3	RAESMILLLAGTLAGAHTLTFVVFYVLQNPQIEKRLRTELQPVFKGYPNKMPTWAELE
Ct4	RAESMILLLAGTLAGAHTLTFVVFYVLQNPQIEKRLRTELQPVFKGYPNKMPTWAELE
Ct61	RAESMILLLAGTLAGAHTLTFVVFYVLQNPQIEKRLRTELQPVFKGYPNKMPTWAELE

Ct3 PYLRGCIKEALRLNGLVGNLARCSPDEDIQFRQWVIPKKTTPVGMSIYAMHFDPSVFPEPE
Ct4 PYLRGCIKEALRLNGLVGNLARCSPDEDIQFRQWVIPKKTTPVGMSIYAMHFDPSVFPEPE
Ct61 PYLRGCIKEALRLNGLVGNLARCSPDEDIQFRQWVIPKKTTPVGMSIYAMHFDPSVFPEPE

Ct3 AFKPERWVGQYDRNMDRNFVPFTKGSRSCLGINLAWAELYLASAMLFPPGGPKLVHND
Ct4 AFKPERWVGQYDRNMDRNFVPFTKGSRSCLGINLAWAELYLASAMLFPPGGPKLVHND
Ct61 AFKPERWVGQYDRNMDRNFVPFTKGSRSCLGINLAWAELYLASAMLFPPGGPKLVHND

Ct3 ESDIKISRDYIMGFARADAKDIRIKVE
Ct4 ESDIKISRDYIMGFARADAKDIRIKVE
Ct61 ESDIKISRDYIMGFARADAKDIRIKVE

BOT4

Ct3 MDMAEYNVTTSTPEPKAGWPAVERLLGAYTTPETWSWQVAGCLATIIILCRFVAVWSYNL
Ct4 MDMAEYNVTTSTPEPKAGWPAVERLLGAYTTPETWSWQVAGCLATIIILCRFVAVWSYNL
Ct61 MDMAEYNVTTSTPEPKAGWPAVERLLGAYTTPETWSWQVAGCLATIIILCRFVAVWSYNL

Ct3 WFHPLARFPGPLLGRCSLIFRFMHSSRGRIHSAIADAHKKYGDIVRIAPNELSFASVESW
Ct4 WFHPLARFPGPLLGRCSLIFRFMHSSRGRIHSAIADAHKKYGDIVRIAPNELSFASVESW
Ct61 WFHPLARFPGPLLGRCSLIFRFMHSSRGRIHSAIADAHKKYGDIVRIAPNELSFASVESW

Ct3 KAIYGHPTGGRPIAPKGPFEYVFAAGFSSKCVGSEDPKKHSAMRKMLNPAFSQRGLEEQ
Ct4 KAIYGHPTGGRPIAPKGPFEYVFAAGFSSKCVGSEDPKKHSAMRKMLNPAFSQRGLEEQ
Ct61 KAIYGHPTGGRPIAPKGPFEYVFAAGFSSKCVGSEDPKKHSAMRKMLNPAFSQRGLEEQ

Ct3 EEIISGIIIDKFVSILGEKAGPGTKGLNMTKWYEMNSFDILGEMAFGESFHS�DTGVPHF
Ct4 EEIISGIIIDKFVSILGEKAGPGTKGLNMTKWYEMNSFDILGEMAFGESFHS�DTGVPHF
Ct61 EEIISGIIIDKFVSILGEKAGPGTKGLNMTKWYEMNSFDILGEMAFGESFHS�DTGVPHF

Ct3 ADIVLEHLYVITLFDNLRRIGWLAKLAGLLVPASIVTSNQNSNYSRQQVEKRLKTQESRN
Ct4 ADIVLEHLYVITLFDNLRRIGWLAKLAGLLVPASIVTSNQNSNYSRQQVEKRLKTQESRN
Ct61 ADIVLEHLYVITLFDNLRRIGWLAKLAGLLVPASIVTSNQNSNYSRQQVEKRLKTQESRN

Ct3 DVFSLLDVKVRAGEVSKEEMTAHVSTLTIAGETVATTLSITFFLAQNPEKFERLTKEI
Ct4 DVFSLLDVKVRAGEVSKEEMTAHVSTLTIAGETVATTLSITFFLAQNPEKFERLTKEI
Ct61 DVFSLLDVKVRAGEVSKEEMTAHVSTLTIAGETVATTLSITFFLAQNPEKFERLTKEI

Ct3 RAAFSYKEINAVKAQQLPYLQAVINEGLRLFPASNGASRVSPGFSLHGKYIPEGTEIN
Ct4 RAAFSYKEINAVKAQQLPYLQAVINEGLRLFPASNGASRVSPGFSLHGKYIPEGTEIN
Ct61 RAAFSYKEINAVKAQQLPYLQAVINEGLRLFPASNGASRVSPGFSLHGKYIPEGTEIN

Ct3 VSPWSITHNPKYFSDPWDFKPERWLDPNSTDNRDANRPFLGPRDCLGRNFALMELNLVL
Ct4 VSPWSITHNPKYFSDPWDFKPERWLDPNSTDNRDANRPFLGPRDCLGRNFALMELNLVL
Ct61 VSPWSITHNPKYFSDPWDFKPERWLDPNSTDNRDANRPFLGPRDCLGRNFALMELNLVL

Ct3 AKLLWSYDMELVNKEVNFLEQSTVHVLWWKPAFVWRHPQSTSS
Ct4 AKLLWSYDMELVNKEVNFLEQSTVHVLWWKPAFVWRHPQSTSS
Ct61 AKLLWSYDMELVNKEVNFLEQSTVHVLWWKPAFVWRHPQSTSS

BOT5

Ct3 MATIPFFFSVLFLWHYFAYKLQKKQGGQGYIATEDAASKPDSPPQGDDEVLPVHFIDQAA
Ct4 MATIPFFFSVLFLWHYFAYKLQKKQGGQGYIATEDAASKPDSPPQGDDEVLPVHFIDQAA
Ct61 MATIPFFFSVLFLWHYFAYKLQKKQGGQGYIATEDAASKPDSPPQGDDEVLPVHFIDQAA

Ct3 IVRTSIIINYTFRYNDVLDASKLHRGLLHLLQIPGWNKLGGRLRATSGGKLEIHPKTFSR

Ct4 IVRTSI INYTFRYNDVLDASKLHRGLLHLLQIPGWNKLGRLRATSGGKLEIHVPKTF SR
Ct61 IVRTSI INYTFRYNDVLDASKLHRGLLHLLQIPGWNKLGRLRATSGGKLEIHVPKTF SR

Ct3 SRPAVKFSHVDLSDTRIEIHHLASQLPVSTGSLPSVQEGCHAFRTFALPADLPNNIDHYW
Ct4 SRPAVKFSHVDLSDTRIEIHHLASQLPVSTGSLPSVQEGCHAFRTFALPADLPNNIDHYW
Ct61 SRPAVKFSHVDLSDTRIEIHHLASQLPVSTGSLPSVQEGCHAFRTFALPADLPNNIDHYW

Ct3 KNDQPLLCLHVTSFANATLVGFTFPHSLSDAMGTSELLKAWSNV VAGKSCLVKPLHGTHV
Ct4 KNDQPLLCLHVTSFANATLVGFTFPHSLSDAMGTSELLKAWSNV VAGKSCLVKPLHGTHV
Ct61 KNDQPLLCLHVTSFANATLVGFTFPHSLSDAMGTSELLKAWSNV VAGKSCLVKPLHGTHV

Ct3 DVLGDVGTA FDKKASGGEFVLERQQTRAFSLLSFIVRYVWDVTTRRSIRTRHIYLPAYM
Ct4 DVLGDVGTA FDKKASGGEFVLERQQTRAFSLLSFIVRYVWDVTTRRSIRTRHIYLPAYM
Ct61 DVLGDVGTA FDKKASGGEFVLERQQTRAFSLLSFIVRYVWDVTTRRSIRTRHIYLPAYM

Ct3 RHLRHSVEEELRRKNRGVAPFVSDGDLITAWGSRMVISSSPWRNCSAVICNVFDLRGRLK
Ct4 RHLRHSVEEELRRKNRGVAPFVSDGDLITAWGSRMVISSSPWRNCSAVICNVFDLRGRLK
Ct61 RHLRHSVEEELRRKNRGVAPFVSDGDLITAWGSRMVISSSPWRNCSAVICNVFDLRGRLK

Ct3 NTFTPGGTYLQNLILPATTVL SRDETANATTAQIAWGLRKAILEQTEDVQARRLMRLARQ
Ct4 NTFTPGGTYLQNLILPATTVL SRDETANATTAQIAWGLRKAILEQTEDVQARRLMRLARQ
Ct61 NTFTPGGTYLQNLILPATTVL SRDETANATTAQIAWGLRKAILEQTEDVQARRLMRLARQ

Ct3 WFASMGMMPLFAGWDSRVI ACTNWTAKFLDAADF GPTALVSLGNHKPNGPTRKAVAEGA
Ct4 WFASMGMMPLFAGWDSRVI ACTNWTAKFLDAADF GPTALVSLGNHKPNGPTRKAVAEGA
Ct61 WFASMGMMPLFAGWDSRVI ACTNWTAKFLDAADF GPTALVSLGNHKPNGPTRKAVAEGA

Ct3 RPGRPVMYWGTTLSVTDSPRDTFVIYGKDAAGNYWIIHAYLREETWDLIQKELLSFR
Ct4 RPGRPVMYWGTTLSVTDSPRDTFVIYGKDAAGNYWIIHAYLREETWDLIQKELLSFR
Ct61 RPGRPVMYWGTTLSVTDSPRDTFVIYGKDAAGNYWIIHAYLREETWDLIQKELLSFR

BOT6 (Zn clus)
Ct3 MYGTLSFSKGNKKSSAEFHAFSEVHKRRLRQPACDECRIARVKCRGKSDGEKCARCQGTG
Ct4 MYGTLSFSKGNKKSSAEFHAFSEVHKRRLRQPACDECRIARVKCRGKSDGEKCARCQGTG
Ct61 MYGTLSFSKGNKKSSAEFHAFSEVHKRRLRQPACDECRIARVKCRGKSDGEKCARCQGTG

Ct3 RACTYNSTRRRSQASGKPAEPTHTTDDTDEDTGDKDGDGTPSAPSALEATASPQGPS
Ct4 RACTYNSTRRRSQASGKPAEPTHTTDDTDEDTGDKDGDGTPSAPSALEATASPQGPS
Ct61 RACTYNSTRRRSQASGKPAEPTHTTDDTDEDTGDKDGDGTPSAPSALEATASPQGPS

Ct3 SLPHDAHTKWWECRFEPFDLFVDPGADLAVDEAQAAPRKHVDGDSAAGSVNDGDGVHLHL
Ct4 SLPHDAHTKWWECRFEPFDLFVDPGADLAVDEAQAAPRKHVDGDSAAGSVNDGDGVHLHL
Ct61 SLPHDAHTKWWECRFEPFDLFVDPGADLAVDEAQAAPRKHVDGDSAAGSVNDGDGVHLHL

Ct3 ADLELASAVIGHHDAHGYGFI PCSDFAQIA PSTSSRSPPTPSLVWSTMSGHGEHQRP
Ct4 ADLELASAVIGHHDAHGYGFI PCSDFAQIA PSTSSRSPPTPSLVWSTMSGHGEHQRP
Ct61 ADLELASAVIGHHDAHGYGFI PCSDFAQIA PSTSSRSPPTPSLVWSTMSGHGEHQRP

Ct3 PSLSSDMLDHAASLPHNPDAQDDATHASTLAEFSDLIDVMQFAEGPSISGPATPASSSC
Ct4 PSLSSDMLDHAASLPHNPDAQDDATHASTLAEFSDLIDVMQFAEGPSISGPATPASSSC
Ct61 PSLSSDMLDHAASLPHNPDAQDDATHASTLAEFSDLIDVMQFAEGPSISGPATPASSSC

Ct3 TCLQDLTATLFSLSRSPDKTQVDHFLLLFKQVMQKWEAVETCARACRVSRSFALLVLMNV
Ct4 TCLQDLTATLFSLSRSPDKTQVDHFLLLFKQVMQKWEAVETCARACRVSRSFALLVLMNV
Ct61 TCLQDLTATLFSLSRSPDKTQVDHFLLLFKQVMQKWEAVETCARACRVSRSFALLVLMNV

Ct3 QELVTLLLEATSSANTSSGTAGRRESVLAISMGTFTVEDGADQRIIARMLLAVRMKELHS
 Ct4 QELVTLLLEATSSANTSSGTAGRRESVLAISMGTFTVEDGADQRIIARMLLAVRMKELHS
 Ct61 QELVTLLLEATSSANTSSGTAGRRESVLAISMGTFTVEDGADQRIIARMLLAVRMKELHS

Ct3 FITRISSQMKLGLDDIFTDFHHQIEMLRRAFTL
 Ct4 FITRISSQMKLGLDDIFTDFHHQIEMLRRAFTL
 Ct61 FITRISSQMKLGLDDIFTDFHHQIEMLRRAFTL

BOT7 (adh short)

Ct3 MPDAKPIYNLPEDAVWFI TGCSSGMGLALAQIVASKPTQRVVATARSVSKLAGKLPDSPR
 Ct4 MPDAKPIYNLPEDAVWFI TGCSSGMGLALAQIVASKPTQRVVATARSVSKLAGKLPDSPR
 Ct61 MPDAKPIYNLPEDAVWFI TGCSSGMGLALAQIVASKPTQRVVATARSVSKLAGKLPDSPR

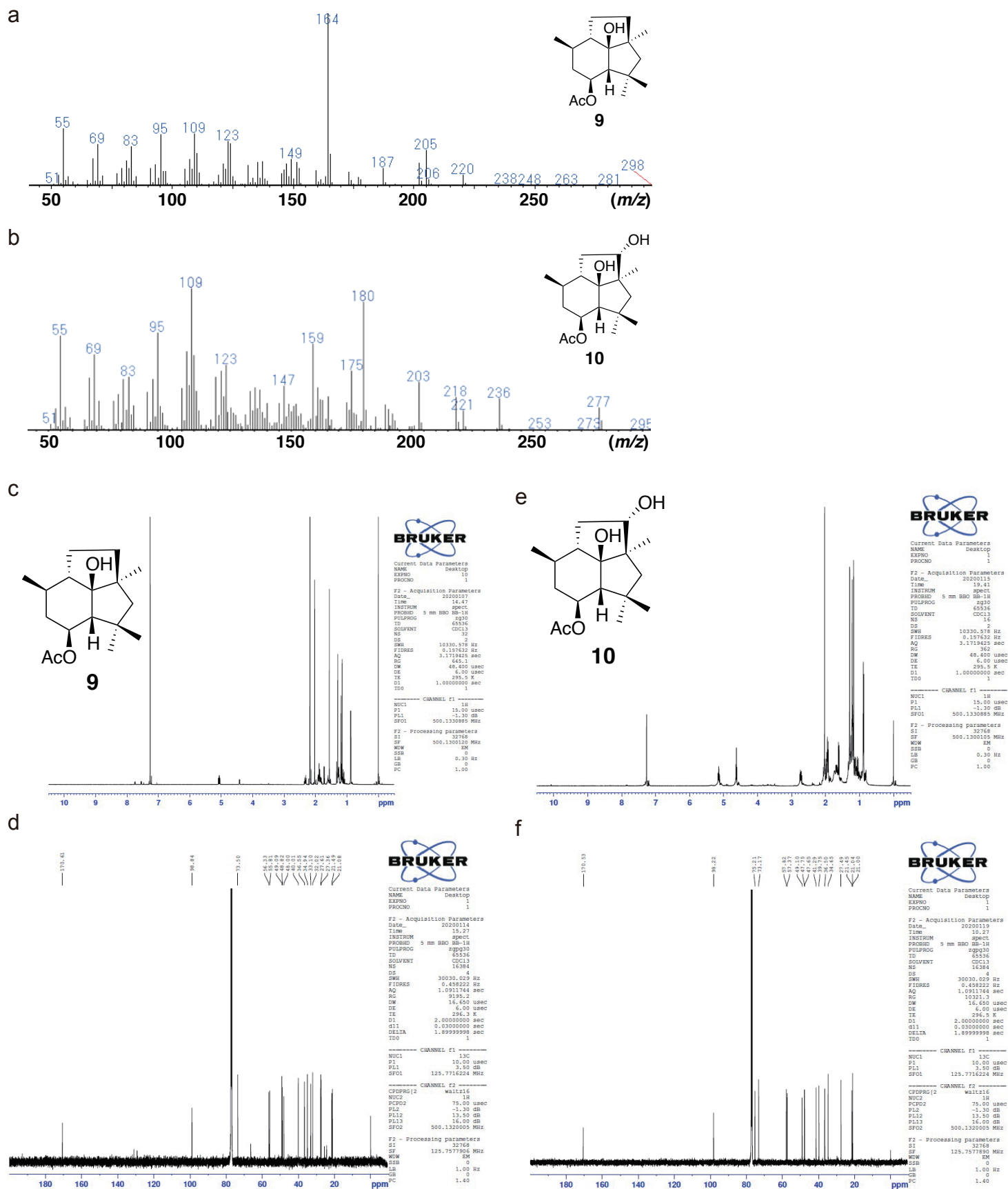
Ct3 VHLSLDVTSADSI TAAFDSAVAKFGRIDVVVNNAGYGLMGDTESFVINAEDHDKARKVV
 Ct4 VHLSLDVTSADSI TAAFDSAVAKFGRIDVVVNNAGYGLMGDTESFVINAEDHDKARKVV
 Ct61 VHLSLDVTSADSI TAAFDSAVAKFGRIDVVVNNAGYGLMGDTESFVINAEDHDKARKVV

Ct3 ETNFWGTAQVSAHAVRVFRDENPKSGQIGGVVLNVTSIGGFAGFPGSIFYHASKFAVEGY
 Ct4 ETNFWGTAQVSAHAVRVFRDENPKSGQIGGVVLNVTSIGGFAGFPGSIFYHASKFAVEGY
 Ct61 ETNFWGTAQVSAHAVRVFRDENPKSGQIGGVVLNVTSIGGFAGFPGSIFYHASKFAVEGY

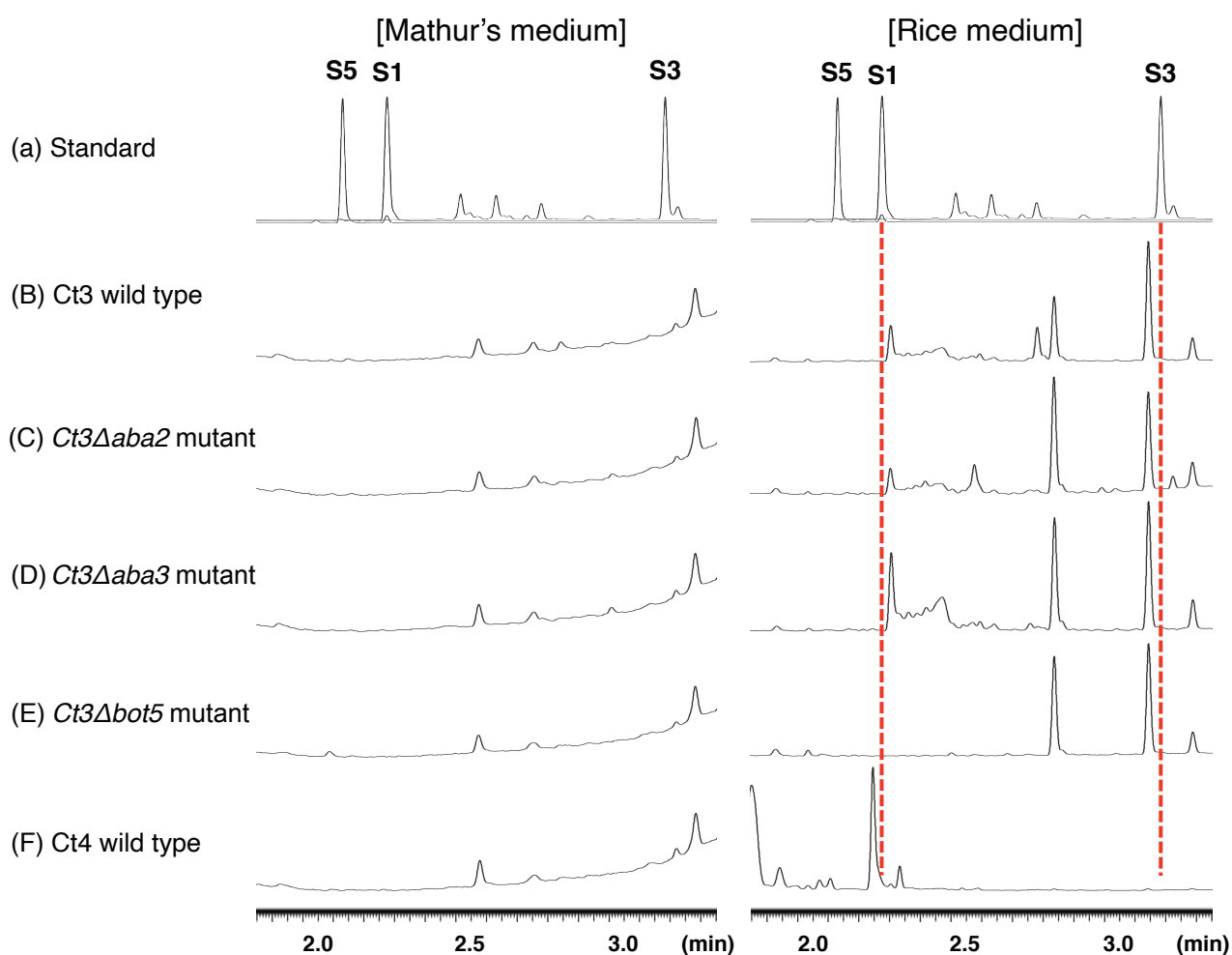
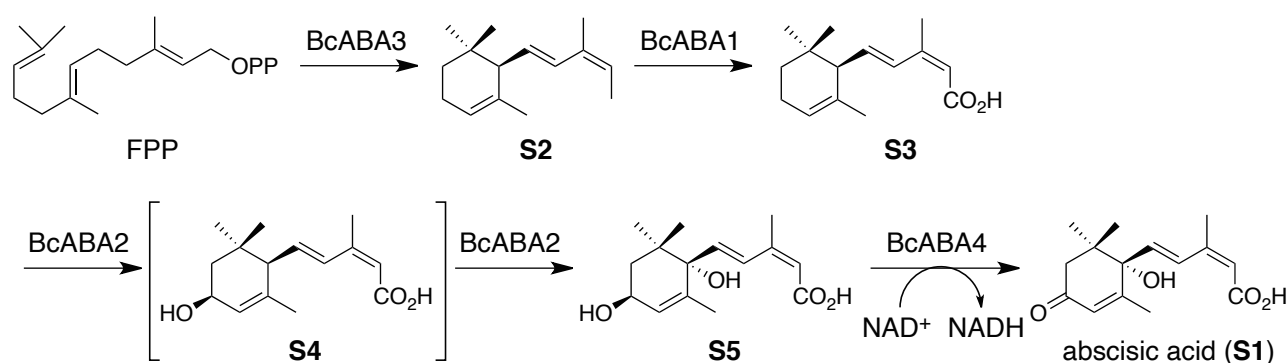
Ct3 TESLSKEVRSDWNIHFSI IEPGGTKTNFAGDSMAWFSAHPAYAAPDTPTRLLEGYVKSPD
 Ct4 TESLSKEVRSDWNIHFSI IEPGGTKTNFAGDSMAWFSAHPAYAAPDTPTRLLEGYVKSPD
 Ct61 TESLSKEVRSDWNIHFSI IEPGGTKTNFAGDSMAWFSAHPAYAAPDTPTRLLEGYVKSPD

Ct3 MQATWAPSENV-AAAMYEVVARKQAIPIRFPTGAPAWSVIKAEVEEVDKELLEIKELSF
 Ct4 MQATWAPSENV-AAAMYEVVARKQAIPIRFPTGAPAWSVIKAEVEEVDKELLEIKELSF
 Ct61 MQATWAPSENVAAAAMYEVVARKQAIPIRFPTGAPAWSVIKAEVEEVDKELLEIKELSF

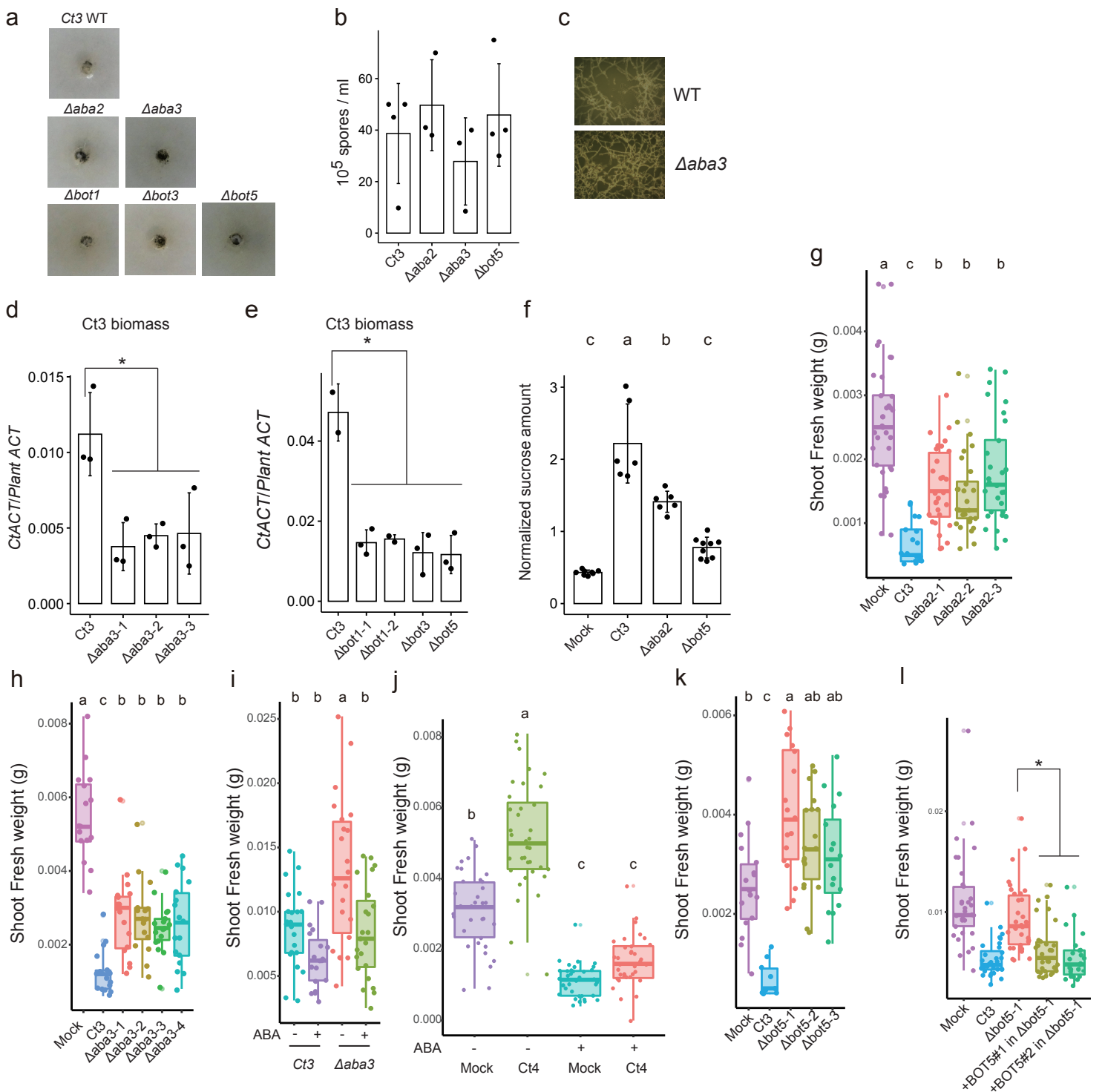
Ct3 VDDGSINKSGDFLKQKF
 Ct4 VDDGSINKSGDFLKQKF
 Ct61 VDDGSINKSGDFLKQKF



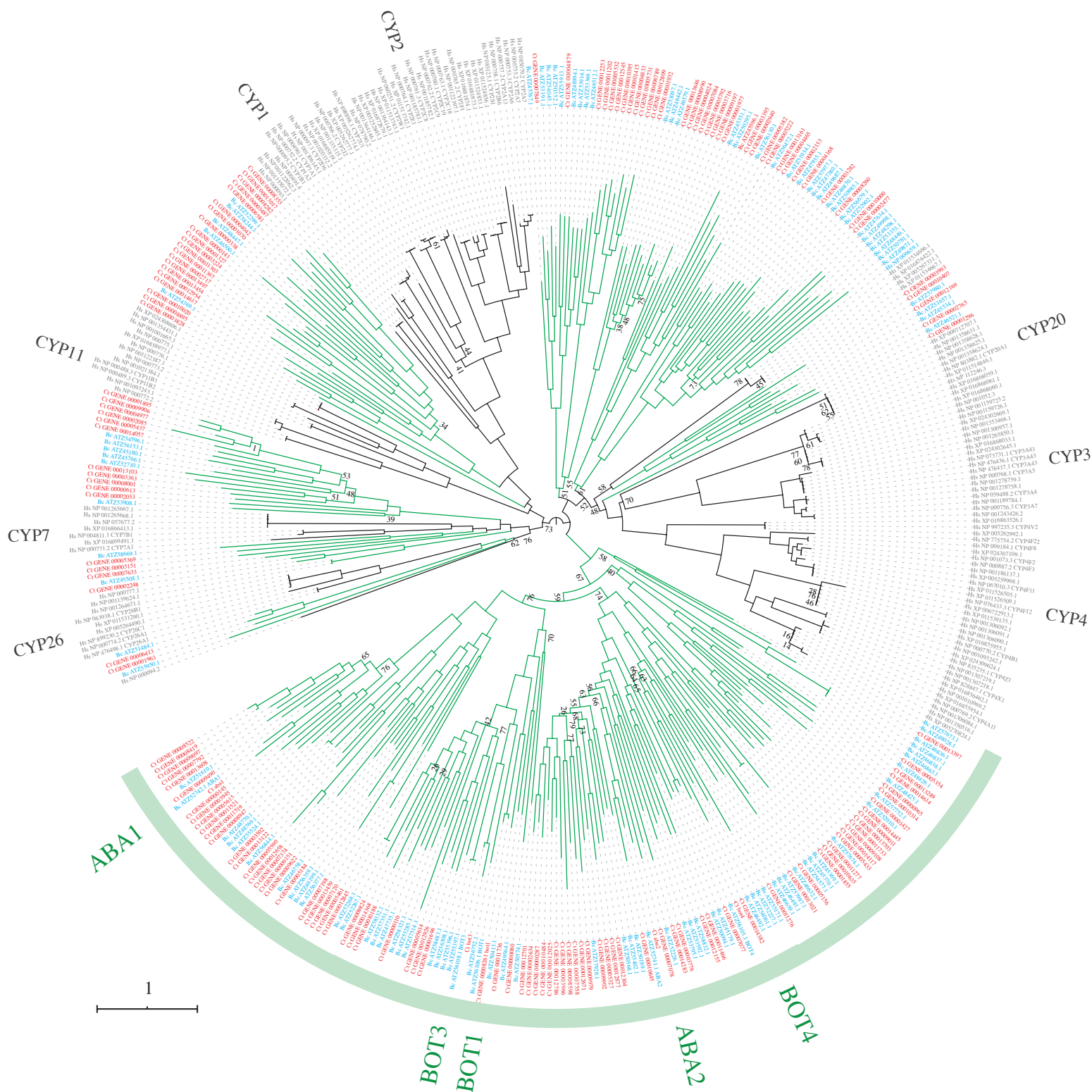
Supplementary Figure 5: Intermediate metabolites in BOT biosynthesis in Ct3. GC-MS spectra of 9 (a) and 10 (b). c 1H-NMR spectra of 9. d 13C-NMR spectra of 9. e 1H-NMR spectra of 10. f 13C-NMR spectra of 10.



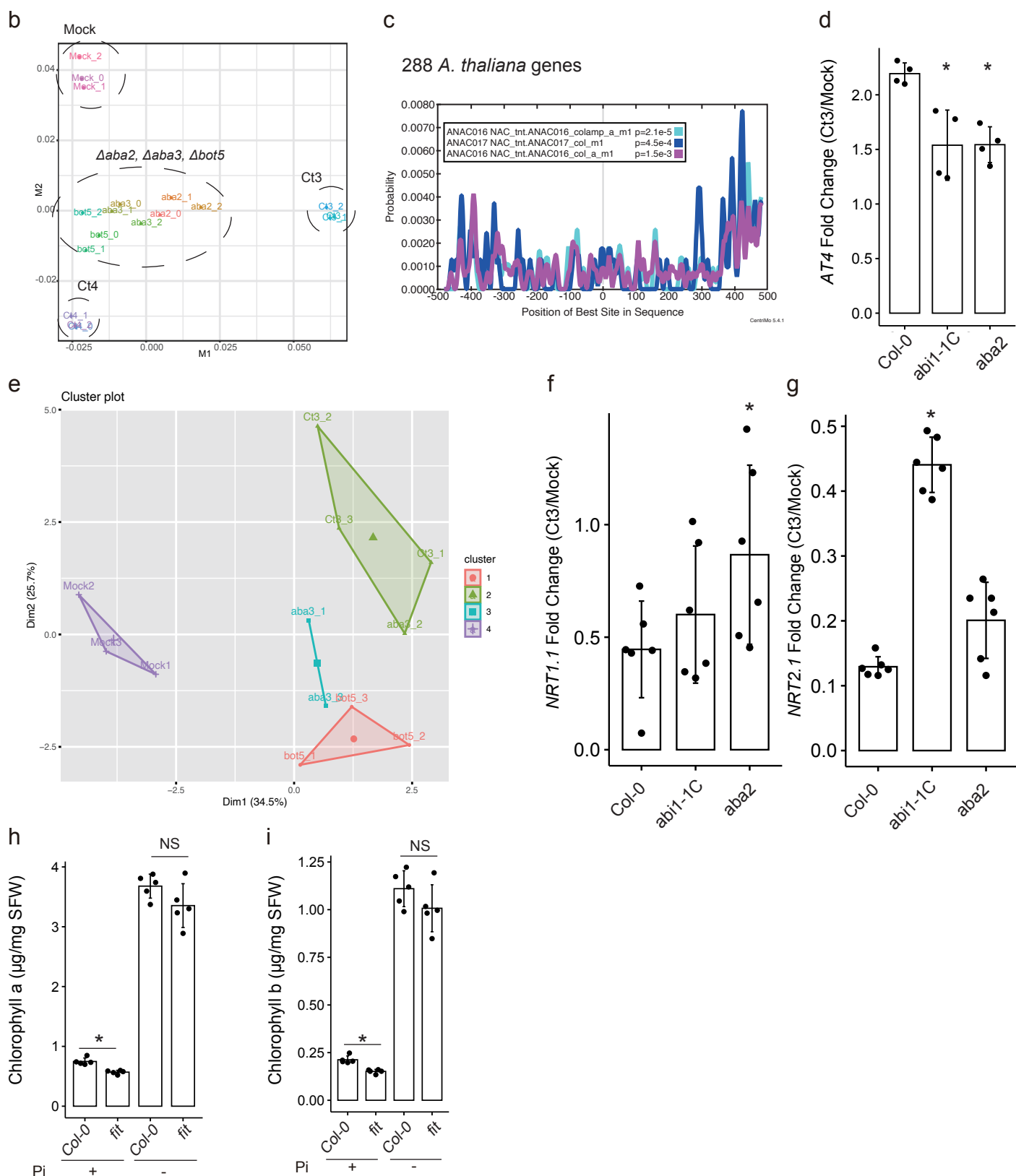
Supplementary Figure 6: Measurements of ABA and the intermediate metabolites in Mathurs media or Rice media. UPLC profiles (264 nm). (a) compounds, S1, S3, and S5, and metabolites from (b) Ct3 wild type strain, (c) *Ct3Δaba2* mutant, (d) *Ct3Δaba3* mutant, (e) *Ct3Δbot5* mutant, and (f) Ct4 wild type strain.



Supplementary Figure 7: Fungal ABA and BOT biosynthesis genes are required for root colonization by Ct3 and its virulence. **a** Fungal growth on low Pi media. Hyphae of Ct3WT, $\Delta aba2$, $\Delta aba3$, $\Delta bot1$, $\Delta bot3$, and $\Delta bot5$ were transferred to low Pi media (without sucrose) and incubated for three days. **b** Measurements of fungal spores generated from fungal strains grown in Mathurs nutrient media ($\pm$ SD, Ct3: n=4, $\Delta aba2$: n=3, $\Delta aba3$: n=3, $\Delta bot5$: n=4). **c** Spore germination and hyphal growth on glass slides. The same spore amount of Ct3WT or $\Delta aba3$ were placed on glass slides and incubated for 2 days, after which pictures were taken. **d, e** Fungal biomass measurements in *A. thaliana* roots under low Pi (24 dpi). qRT-PCR analyses were used to measure fungal biomass as estimated by relative expression between *CtACTIN* and *Plant ACTIN* (*CtACTIN/PlantACTIN*) ($\pm$ SD, n=3, p < 0.05, two tailed t-test, see also source Data File for exact p value). **f** LC/MS analyses for sucrose measurements for *A. thaliana* upon fungal colonization under low Pi (Log2 (normalized)). Different letters indicate significantly different statistical groups (ANOVA, Tukey-HSD test, p < 0.05, $\pm$ SD, Mock: n=8, Ct3: n=6, $\Delta aba2$: n=6, $\Delta bot5$: n=9). **g, h** Measurement of *A. thaliana* SFW upon Ct3 root colonization at 24 dpi under low Pi ((g) Mock: n=17, Ct3: n=9, $\Delta aba2$ -1: n=11, $\Delta aba2$ -2: n=16, $\Delta aba2$ -3: n=14, $\Delta aba2$ -4: n=14. (h) Mock: n=16, Ct3: n=17, $\Delta aba3$ -1: n=17, $\Delta aba3$ -2: n=16, $\Delta aba3$ -3: n=18, $\Delta aba3$ -4: n=17). Different letters indicate significantly different statistical groups (ANOVA, Tukey-HSD test, p < 0.05). **i** Quantitative measurement of *A. thaliana* SFW upon fungal root colonization at 24 dpi with and without ABA treatment (Ct3: n=23, Ct3_ABA: n=19, $\Delta aba3$ -1: n=22, $\Delta aba3$ -1_ABA: n=22). Ct3 or Ct3 $\Delta aba3$ were incubated with *A. thaliana* for 24 dpi on low Pi media with 10 μ M ABA. Different letters indicate significantly different statistical groups (ANOVA, Tukey-HSD test, p < 0.05). **j** Measurement of *A. thaliana* SFW upon fungal root colonization at 24 dpi with and without ABA treatment (Mock: n=34, Ct4: n=36, Mock_ABA: n=36, Ct4_ABA: n=36). Ct4 were incubated with *A. thaliana* for 24 dpi on low Pi media with 10 μ M ABA. **k** Measurement of *A. thaliana* SFW upon fungal root colonization under low Pi. Different letters indicate significantly different statistical groups (ANOVA, Tukey-HSD test, p < 0.05). **l** Quantitative measurement of *A. thaliana* SFW upon fungal root colonization at 24 dpi under normal Pi ($\Delta bot5$ -1 vs BOT5#1 in $\Delta bot5$ -1: p = 0.000118, $\Delta bot5$ -1 vs BOT5#2 in $\Delta bot5$ -1: p < 0.0001, two tailed t-test) (Mock: n=33, Ct3: n=32, $\Delta bot5$ -1: n=34, BOT5#1 in $\Delta bot5$ -1: n=30, BOT5#2 in $\Delta bot5$ -1: n=25).



Supplementary Figure 8a Phylogenetic tree of the genes in cytochrome C P450 families. 414 genes of *C. tofieldiae* Ct3, *B. cinerea* B05.10, and *H. sapiens* are used for the ML analysis with IQ-TREE version 1.6.11. Branches with green and black indicate the lineages of fungi and humans, respectively. Red letters indicate *C. tofieldiae* genes, blue indicates *B. cinerea*, and gray indicates *H. sapiens*. ABA, BOT, and CYP genes are shown notably. Note that all the ABA and BOT genes are included in a large monophyletic clade of fungi (green arc). The number at each node corresponds to the ultrafast bootstrap values support from the ML analysis using IQ-TREE (Only less than 80% were indicated). The scale bar represents substitutions per site. Root of the tree is based on the option of root mid-point of iTOL v5.6.



Supplementary Figure 8: Fungal ABA and BOT biosynthesis genes suppress the expression of nutrient uptake *A. thaliana* genes while activating PSR genes.

b MDS chart generated from plant transcriptome profile during association with mock (M), Ct3, $\Delta aba2$, $\Delta aba3$, $\Delta bot5$, and Ct4 under low Pi. The three independent biological replicates are shown. **c** Motif analysis against 1,000 bp upstream sequences of 288 up-regulated *A. thaliana* genes during root colonization by Ct3 compared to $\Delta aba2$, $\Delta aba3$, $\Delta bot5$, and Ct4. **d** *AtAT4* gene fold change under low Pi. The fold change Ct3/mock is calculated by relative expression of *AtAT4*. Asterisks indicate significantly different means between Col-0 and the corresponding mutants ($\pm$ SD, $n = 3$, $p < 0.05$, two tailed t-test). **e** PCA analysis of shoot mineral nutrient composition (ionome) in plants grown in normal Pi treated with either mock, Ct3, $\Delta aba2$, $\Delta aba3$, or $\Delta bot5$. The samples were separated into four different clusters. **f** *AtNRT1.1* gene fold change under low Pi. Asterisks indicate significantly different means between Col-0 and the corresponding mutants ($n = 3$, $p < 0.05$, two tailed t-test). **g** *AtNRT2.1* gene fold change under low Pi. Asterisks indicate significantly different means between Col-0 and the corresponding mutants ($\pm$ SD, $n = 3$, $p < 0.05$, two tailed t-test). **h, i** Data of plant shoot chlorophyll a or b in Col-0 and *fit* under normal and low Pi. Asterisks indicate significantly different means between Col-0 and *fit* plants ($\pm$ SD, $p < 0.01$, two-tailed t-test).

Supplementary Table 1: Background information regarding *Colletotrichum tofieldiae* and KHC (Originally named as KHC23) isolates and the Ct3 mutants used in this study.

Isolate ID	Species	Accession Number (a)	Location	Host plant	Publication
Ct61	<i>C. tofieldiae</i>	Ct0861	Spain	<i>A. thaliana</i>	3
Ct127	<i>C. tofieldiae</i>	CBS 127615	Portugal	<i>Agapanthus sp.</i>	21
Ct130	<i>C. tofieldiae</i>	CBS 130851	Germany	<i>Semele gayae</i>	21
Ct49	<i>C. tofieldiae</i>	CBS 495.85	Switzerland	<i>Tofieldia calyculata</i>	21
Ct3	<i>C. tofieldiae</i>	MAFF 712333	Japan	<i>Ornithogalum dubium</i>	24
Ct4	<i>C. tofieldiae</i>	MAFF 712334	Japan	<i>Ornithogalum dubium</i>	24
<i>Ct3 Δaba2-1</i>	<i>C. tofieldiae</i>	MAFF 712333	Japan	<i>Ornithogalum dubium</i>	this study
<i>Ct3 Δaba2-2</i>	<i>C. tofieldiae</i>	MAFF 712333	Japan	<i>Ornithogalum dubium</i>	this study
<i>Ct3 Δaba2-3</i>	<i>C. tofieldiae</i>	MAFF 712333	Japan	<i>Ornithogalum dubium</i>	this study
<i>Ct3 Δaba3-1</i>	<i>C. tofieldiae</i>	MAFF 712333	Japan	<i>Ornithogalum dubium</i>	this study
<i>Ct3 Δaba3-2</i>	<i>C. tofieldiae</i>	MAFF 712333	Japan	<i>Ornithogalum dubium</i>	this study
<i>Ct3 Δaba3-3</i>	<i>C. tofieldiae</i>	MAFF 712333	Japan	<i>Ornithogalum dubium</i>	this study
<i>Ct3 Δaba3-4</i>	<i>C. tofieldiae</i>	MAFF 712333	Japan	<i>Ornithogalum dubium</i>	this study
<i>Ct3 Δbot1-1</i>	<i>C. tofieldiae</i>	MAFF 712333	Japan	<i>Ornithogalum dubium</i>	this study
<i>Ct3 Δbot1-2</i>	<i>C. tofieldiae</i>	MAFF 712333	Japan	<i>Ornithogalum dubium</i>	this study
<i>Ct3 Δbot3</i>	<i>C. tofieldiae</i>	MAFF 712333	Japan	<i>Ornithogalum dubium</i>	this study

<i>Ct3 Δbot5-1</i>	<i>C. tofieldiae</i>	MAFF 712333	Japan	<i>Ornithogalum dubium</i>	this study
<i>Ct3 Δbot5-2</i>	<i>C. tofieldiae</i>	MAFF 712333	Japan	<i>Ornithogalum dubium</i>	this study
<i>Ct3 Δbot5-3</i>	<i>C. tofieldiae</i>	MAFF 712333	Japan	<i>Ornithogalum dubium</i>	this study
<i>Ct3BOT5#1 in Δ</i> <i>bot5-1</i>	<i>C. tofieldiae</i>	MAFF 712333	Japan	<i>Ornithogalum dubium</i>	this study
<i>Ct3BOT5#2 in Δ</i> <i>bot5-1</i>	<i>C. tofieldiae</i>	MAFF 712333	Japan	<i>Ornithogalum dubium</i>	this study
Ci	<i>C. incanum</i>	MAFF 238704	Japan	<i>Raphanus sativus</i>	21
KHC (KHC23) b)	<i>C. higginsianum</i>	MAFF 245053	Japan	<i>Scopolia japonica</i>	this study

a) CBS: Culture Collection of the Centraalbureau voor Schimmelcultures, Fungal Biodiversity Centre, Utrecht, The Netherlands.

MAFF: MAFF Genebank Project, Ministry of Agriculture, Forestry

b) *C. higginsianum* was originally identified as *C. tofieldiae*.

Supplementary Table 2: Genome sequencing and assembly statistics of *C. tofieldiae* isolates and KHC

Assembly Statistics	Illumina +454	Pacbio	Pacbio + Illumina	Pacbio	Pacbio
Isolate	Ct61 ^a	Ct61 (PacBio)	Ct4	Ct3	KHC
Genome (bp)	52836184	52991954	53983402	54252643	49069799
Number of Scaffolds	1048	28	27	19	27
Largest scaffold (bp)	861708	6294542	6028009	6503204	5997240
Smallest scaffold (bp)	201	19730	323670	8543	4021
Genome N50 (bp)	209340	4211846	3719715	6011218	4389193
GC content (%)	45.7	50.3	52.1	48.6	50.6
Number of CDS	12501	15617	14573	14916	14359
Number of tRNA	389	390	370	418	380
Number of rRNA	73	124	70	86	113
Candidate secreted proteins	1391	1397	1446	1481	1426
Candidate effector proteins	430	490	496	507	475
Carbohydrate-active enzymes	720	710	729	733	679
Candidate secondary metabolites	59	59	59	56	77
BUSCO genome mode	97.6	88.5	97.4	97.2	93.6
BUSCO protein mode	94.7	86	95	94.4	90.5

a) This genome assembly has been reported in Hacquard et al. 2016²¹.

Supplementary Table 3: The information of ABA and BOT genes based on *B. cinerea* (a) and the bit scores of BLASTP results between ABA and BOT genes of Ct3 and *B. cinerea* (b)

Supplementary Table 3a

Product	Gene (<i>B. cinerea</i>)	Gene (<i>C. tofieldiae</i>)	putative function	biosynthetic role
<i>abscisic acid</i>	<i>BcABA1</i>	<i>CtABA1</i>	cytochrome P450	tailoring enzyme
	<i>BcABA2</i>	<i>CtABA2</i>	cytochrome P450	tailoring enzyme
	<i>BcABA3</i>	<i>CtABA3</i>	alpha-ionylideneethane synthase	sesquiterpene core formation
	<i>BcABA4</i>	<i>CtABA4</i>	short-chain dehydrogenase/reductase	tailoring enzyme
<i>botrydial</i>	<i>BcBOT1</i>	<i>CtBOT1</i>	cytochrome P450	tailoring enzyme
	<i>BcBOT2</i>	<i>CtBOT2</i>	presilphiperfolan-8-beta-ol synthase	sesquiterpene core formation
	<i>BcBOT3</i>	<i>CtBOT3</i>	cytochrome P450	tailoring enzyme
	<i>BcBOT4</i>	<i>CtBOT4</i>	cytochrome P450	tailoring enzyme
	<i>BcBOT5</i>	<i>CtBOT5</i>	acetyltransferase	tailoring enzyme
	<i>BcBOT6</i>	<i>CtBOT6</i>	transcription factor	-
	<i>BcBOT7</i>	<i>CtBOT7</i>	dehydrogenase	tailoring enzyme

Supplementary Table 3b

Query	Database (<i>Botrytis cinerea</i> B05.10 proteome)										
	BcABA1	BcABA2	BcABA3	BcABA4	BcBOT1	BcBOT2	BcBOT3	BcBOT4	BcBOT5	BcBOT6	BcBOT7
Ct3ABA1	619	114			108		87.0	91.3			
Ct3ABA2	105	570			157		122	222			
Ct3ABA3			548								
Ct3ABA4				184							41.6
Ct3BOT1	107	159			976		196	147			
Ct3BOT2						674					
Ct3BOT3	98.6	126				199	1036	127			
Ct3BOT4	107	261			136		137	958			
Ct3BOT5									870		
Ct3BOT6										483	
Ct3BOT7				53.9							557

Supplementary Table 4: Expression of Ct3, Ct4, Ct61 or KHC ABA and BOT genes during the root colonization. The values represent fpkm. This value was calculated based on Ct3, Ct4, Ct61 or KHC draft genome assemblies.

Ct3

		<i>ABA1</i>	<i>ABA1</i>	<i>ABA2</i>	<i>ABA3</i>	<i>ABA4</i>	<i>BOT1</i>	<i>BOT2</i>	<i>BOT3</i>	<i>BOT4</i>	<i>BOT5</i>	<i>BOT6</i>	<i>BOT7</i>
	Normal Pi	125.251	91.7376	352.335	128.089	9.22808	412.383	385.366	135.292	295.088	237.207	473.298	2760.42
10 dpi	Low Pi	137.857	81.0386	422.115	128.999	0	302.254	338.355	105.574	243.581	185.434	472.06	2783.61
	Normal Pi	0	0	0	0	0	9.2847	0	0	0	0	8.11209	709.583
24 dpi	Low Pi	12.046	19.0386	0	0	0	0	6.19581	0	5.11354	0	16.4728	392.748

Ct4

		<i>ABA1</i>	<i>ABA2</i>	<i>ABA3</i>	<i>ABA4</i>	<i>BOT1</i>	<i>BOT2</i>	<i>BOT3</i>	<i>BOT4</i>	<i>BOT5</i>	<i>BOT6</i>	<i>BOT7</i>
	Normal Pi			0	0	0	1.1704	8.95731	1.38108	0	11.1849	220
10 dpi	Low Pi			0	0	0	0.4132	0	12.3495	0	6.69306	216.865
	Normal Pi			0	22	0	0	10.9126	0	0	33.5001	1240.51
24 dpi	Low Pi			5.54179	4	0	3.80622	12.2368	15.7535	3.07394	0	1058.05

Ct61

		<i>ABA1</i>	<i>ABA2</i>	<i>ABA2</i>	<i>ABA3</i>	<i>ABA4</i>	<i>BOT1</i>	<i>BOT2</i>	<i>BOT3</i>	<i>BOT4</i>	<i>BOT5</i>	<i>BOT6</i>	<i>BOT7</i>
	Normal Pi	1.85582	2.13089	5.47731	1.56631		9.38142	14.1809	9.71836	5.69527	12.8488		618.987
10 dpi	Low Pi	0	0.697352	0	2.72031		7.92429	7.38662	8.63708	12.6158	6.07758		558.398
	Normal Pi	0	0	0	0		0	9.14703	0	0	0		851.557
24 dpi	Low Pi	0	0	13.9356	8.96509		38.1794	63.3038	19.5615	42.5972	9.43841		1146.65

KHC

		<i>ABA1</i>	<i>ABA1</i>	<i>ABA2</i>	<i>ABA3</i>	<i>ABA4</i>	<i>BOT1</i>	<i>BOT2</i>	<i>BOT3</i>	<i>BOT4</i>	<i>BOT5</i>	<i>BOT6</i>	<i>BOT7</i>
	Normal Pi	0	0	0	0	11.0101							
10 dpi	Low Pi	0	0	4.49654	0	0							
	Normal Pi	0	0	0	0	28.8942							
24 dpi	Low Pi	0	0	2.15742	0	8.51124							

a) Note that automatically annotated *Ct3ABA1*, *Ct61ABA2* and *KHCABA1* genes were separated into two.

CtABA genes used in Fig. 4 and Supplementary Fig. 4 were re-predicted using RNAseq-derived reads. The reannotated amino acid sequences are available from Supplementary Fig. 4o.

Supplementary Table 5: Primers used in this study

Gene/Region	Gene_Name or Primer Name	Forward	Reverse	Use
AT3G18780	<i>ATACT2</i>	ACCTTGCTGGACGTGACCTTACTGAT	GTTGTCTCGTGGATTCCAGCAGCTT	qRT-PCR
AT5G52310	<i>RD29A</i>	CAAAGGTGTTTCCTGTCGTGTC	AATCGGTACATCTCTTTCTCTTCC	qRT-PCR
AT1G05100	<i>MAPKKK18</i>	AAGCGGC GCGTGAGAGAGA	GCTGTCCATCTCTCCGTCGC	qRT-PCR
AT5G03545	<i>AT4</i>	GTCTTTTGTATCCCTCGTTTGGG	ACCGGAAACAAAGTAAACACGG	qRT-PCR
CTACT	<i>CtACT</i>	GAGTCCTTCTGGCCCATAC	GAGTCCTTCTGGCCCATAC	qRT-PCR
CT3ABA3	<i>Ct3ABA3</i>	ACCTCGTGAGCGCGATACATGGTA	GTTGAGGACACTGTGCGCCAAT	qRT-PCR
CT3BOT5	<i>Ct3BOT5</i>	ACGAGGTGTTGCCCGTACACTT	GGAAAGTGCAGCTGGGAGAACTT	qRT-PCR
CiABA3	<i>CiABA3</i>	TCATGCGGCTGGTACCAACAA	CTTTTGATTCTGGGCTTGC	qRT-PCR
CiBOT5	<i>CiBOT5</i>	ACCACTTTTCTTCTCACTCGTG	TGATGATGGATGTGCGTACAATCG	qRT-PCR
Ct3ABA2	<i>Ct3ABA2_infu_5F</i>	TATCGATACCGTCGACTATGCAACTAGAGACCACGC	ACCAGTTAACGTCGACCGTCACAATTAACTAATTAGG	Knockout
Ct3ABA2	<i>Ct3ABA2_infu_3F</i>	ATCAGTTAACGTCGACATTCAACGGGTTATTTTCGAAG	CCCCCTCGAGGTGACACCAGAACCCTCAAATCGAGAAG	Knockout
Ct3ABA3	<i>Ct3ABA3_infu_5F</i>	TATCGATACCGTCGACCATTCGACCTGATCCAGCCCAT	ACCAGTTAACGTCGACCCCTGGCAGGTTCTTTGGCGTG	Knockout
Ct3ABA3	<i>Ct3ABA3_infu_3F</i>	ATCAGTTAACGTCGACGAGCCATGGGATAAAGATAACTG	CCCCCTCGAGGTGACACCCGCACGCTCAACTTCATCGA	Knockout
Ct3BOT1	<i>Ct3BOT1_infu_5F</i>	TATCGATACCGTCGACGAGAAGCTGTGCGAAGTAGCGCT	ACCAGTTAACGTCGACCGTAGGACGTGTGCTGCGGGCTTG	Knockout
Ct3BOT1	<i>Ct3BOT1_infu_3F</i>	ATCAGTTAACGTCGACTGGATGATGATTACGGACACAC	CCCCCTCGAGGTGACAGACGGACCGTGTAAGCAAGA	Knockout
Ct3BOT3	<i>Ct3BOT3_infu_5F</i>	TATCGATACCGTCGACAGTTCCTCCACGGGCTCGATGAT	ACCAGTTAACGTCGACGATAACGTCACCGACTGTAAAG	Knockout
Ct3BOT3	<i>Ct3BOT3_infu_3F</i>	ATCAGTTAACGTCGACAAACAGACTCCGGTTGGTATG	CCCCCTCGAGGTGACGCTGAGGTTGCGGAAGCCTTCAAT	Knockout
Ct3BOT5	<i>Ct3BOT5_infu_5F</i>	TATCGATACCGTCGACGCTTGCATACCGCTAGACACCT	ACCAGTTAACGTCGACGTTGTGTATGGGTAGCTGCTGCG	Knockout
Ct3BOT5	<i>Ct3BOT5_infu_3F</i>	ATCAGTTAACGTCGACTGTCGTGGTTGAGGCCTAGTCG	CCCCCTCGAGGTGACTCCATTACCTTTATCTCGGGTC	Knockout
Ct3BOT5	<i>Ct3BOT5_infu_Com</i>	CGGCCCATGGTCTAGAAACGCCGACAAGTCCTTCTT	GCTTGTTAACGAATTCAGGCGCTTTTACCCACCTCTA	Complementation