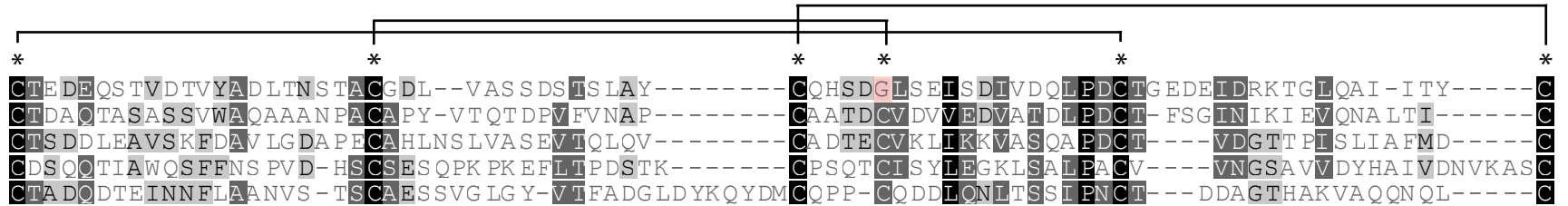


- 1. ACHHYP_00687*
- 2. ACHHYP_00689*
- 3. ACHHYP_03599*
- 4. ACHHYP_04414
- 5. ACHHYP_06115
- 6. ACHHYP_07959
- 7. THRCLA_11203
- 8. THRCLA_11204
- 9. THRCLA_01689*
- 10. THRCLA_05061*
- 11. SPRG_04384T0
- 12. SPRG_04168T0
- 13. SPRG_04167T0
- 14. SPRG_13072T0
- 15. SPRG_15859T0
- 16. ACHHYP_12792
- 17. ACHHYP_14321*
- 18. THRCLA_11549
- 19. SPRG_14023T0
- 20. SPRG_03101T0
- 21. PYU1_T012502
- 22. PYU1_T011089
- 23. PYU1_T009879
- 24. PYU1_T009797
- 25. PYU1_T009222
- 26. PYU1_T009895
- 27. PYU1_T009894
- 28. PYU1_T009821
- 29. PYU1_T008920
- 30. PYU1_T008919
- 31. PYU1_T008918
- 32. PYU1_T008907
- 33. PYU1_T008435
- 34. PYU1_T008434
- 35. PYU1_T008432
- 36. PYU1_T005237
- 37. PYU1_T002858
- 38. PITG_23095
- 39. PITG_22847
- 40. PITG_22846
- 41. PITG_22845
- 42. PITG_22741
- 43. PITG_21410
- 44. PITG_16907
- 45. PITG_16873
- 46. PITG_16872
- 47. PITG_12562
- 48. PITG_12561
- 49. PITG_12556
- 50. PITG_12551
- 51. PITG_08143
- 52. AC2VRR_s00136g103
- 53. AC2VRR_s00008g273

Sequence alignment showing amino acid residues for each entry. The alignment is color-coded to highlight conserved regions. Asterisks (*) above the alignment indicate specific clades or nodes. The sequences are aligned in a way that shows their evolutionary relationships, with closely related sequences grouped together.

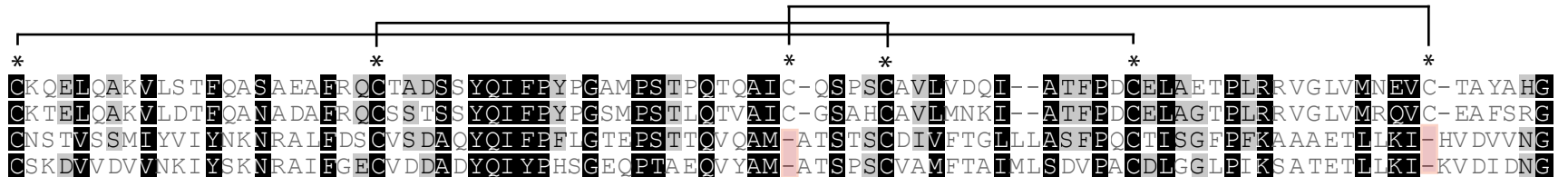
OG5_173373

1. PITG_20412
2. PITG_20413
3. PYU1_T010337
4. THRCLA_04403°
5. SPRG_16448T0



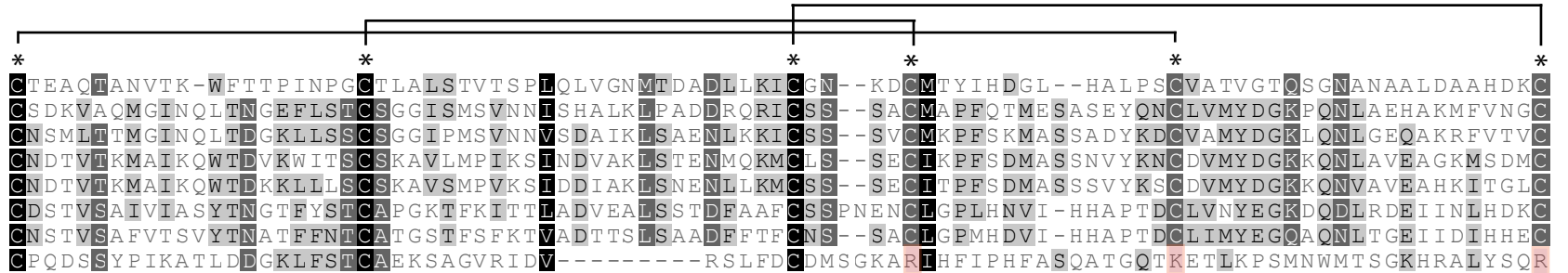
OG5_184829

1. ACHHYP_08659
2. SPRG_04087T0
3. PITG_01024
4. PYU1_T001844



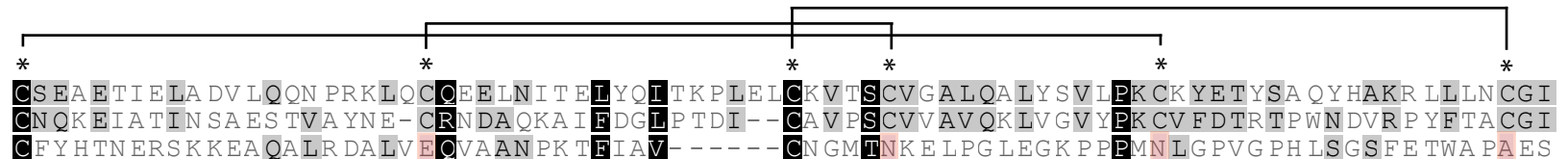
OG5_184830

1. ACHHYP_06054°
2. AC2VRR_s00023g85
3. AC2VRR_s00023g95
4. AC2VRR_s00023g107
5. AC2VRR_s00023g129
6. PYU1_T010721
7. PYU1_T010722
8. PITG_15497

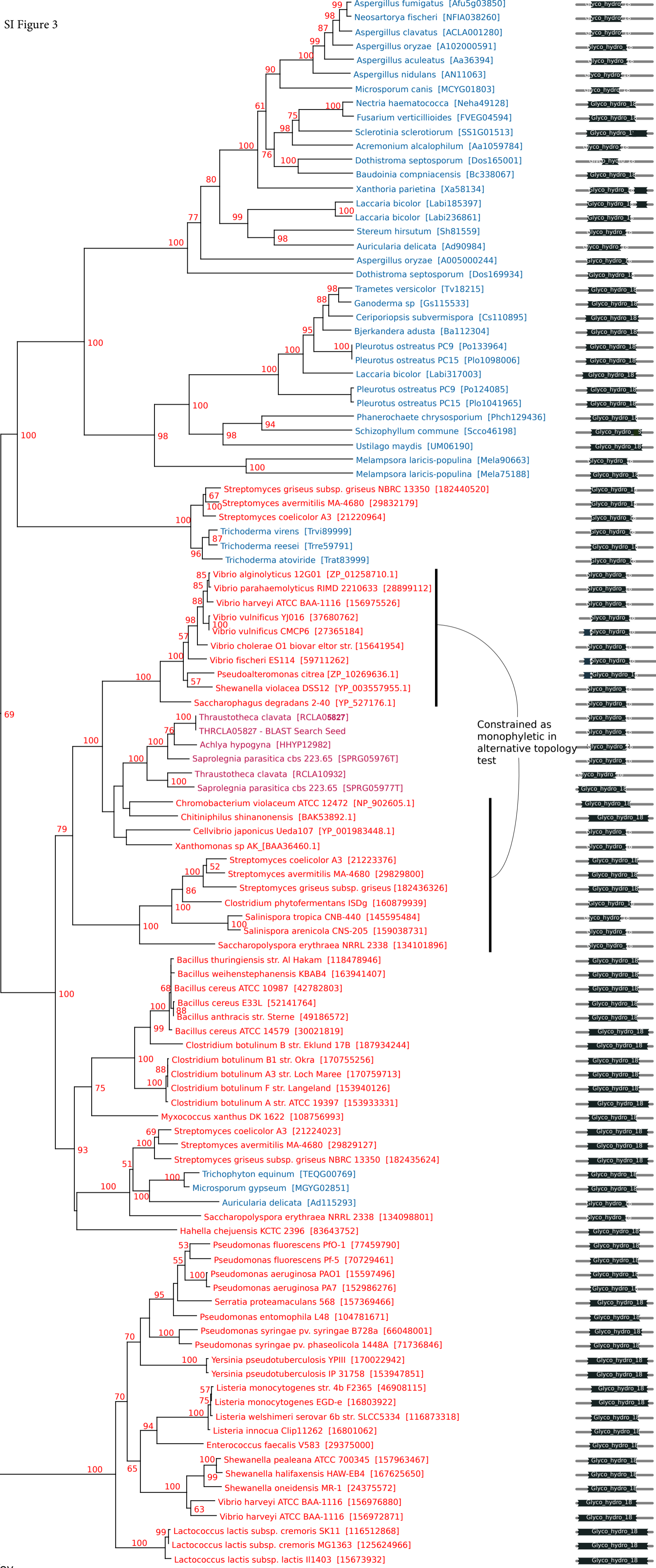


OG5_244191

1. AC2VRR_s00243g170
2. THRCLA_02002
3. PITG_03613



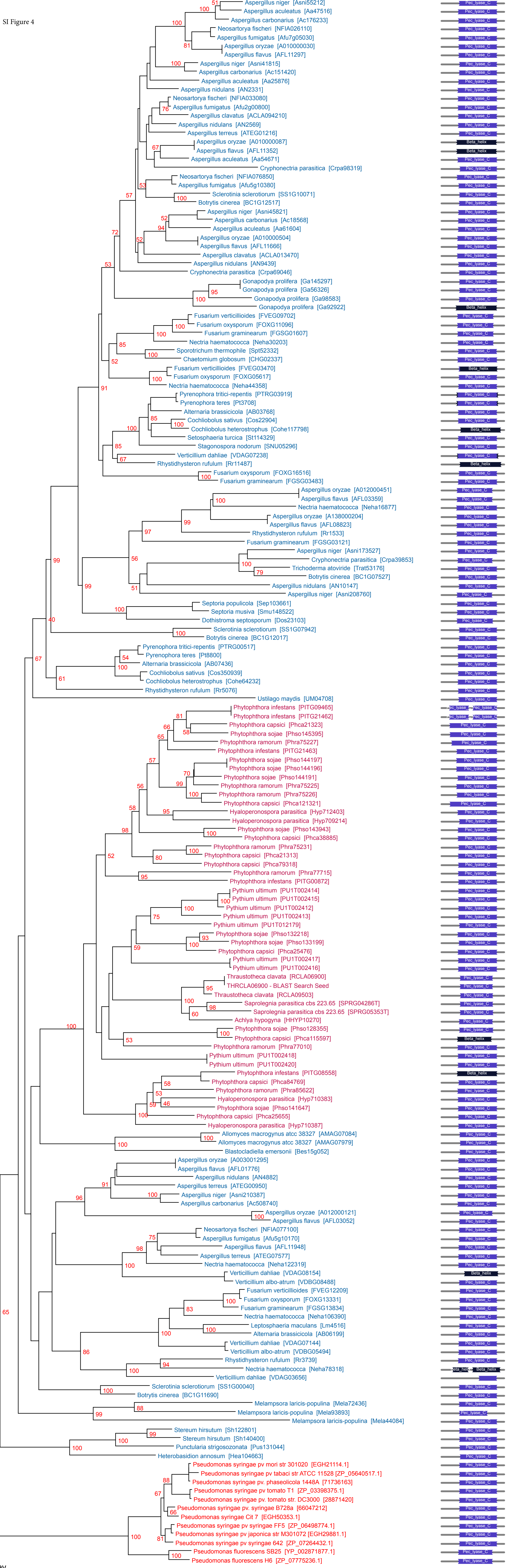
SI Figure 3



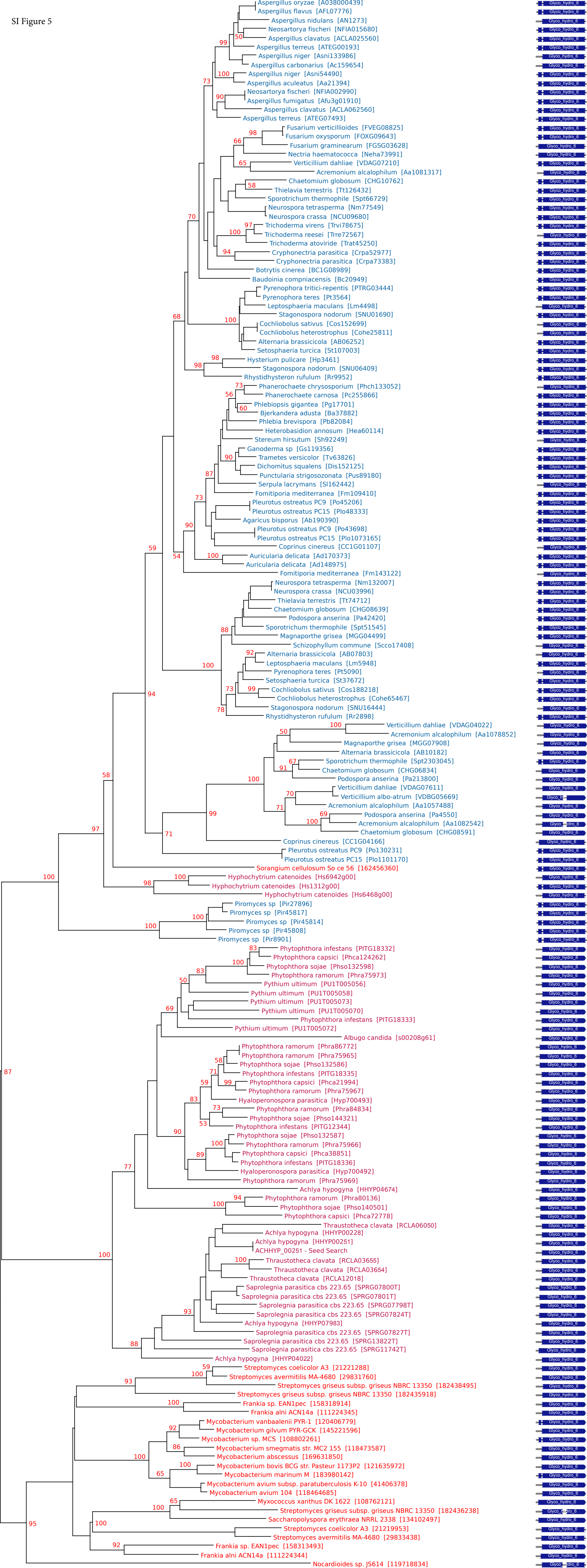
Key
 viridiplantae
 metazoa
 fungi
 microsporidia
 stramenopiles
 bacteria

0.1

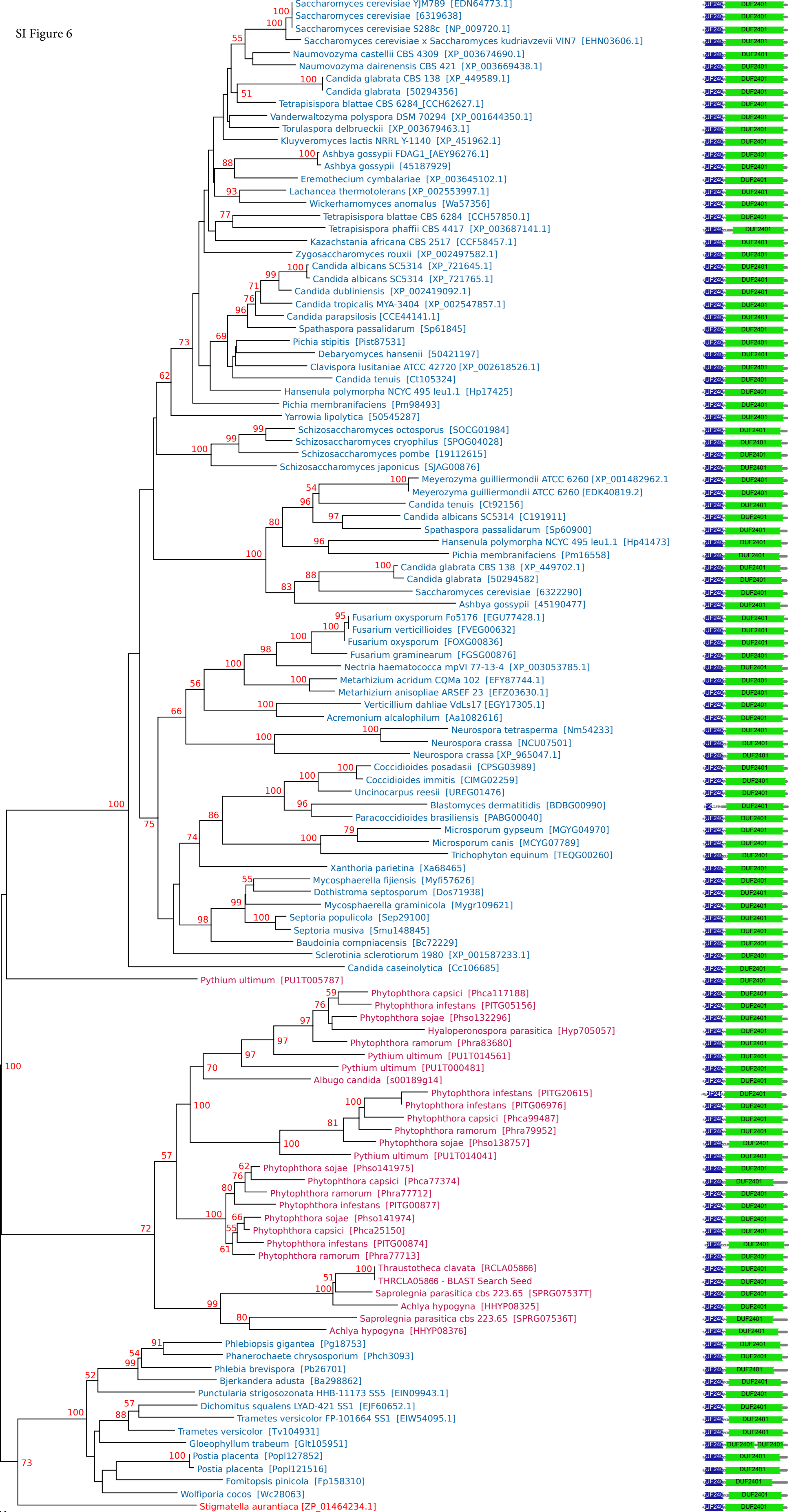
SI Figure 4



SI Figure 5



SI Figure 6

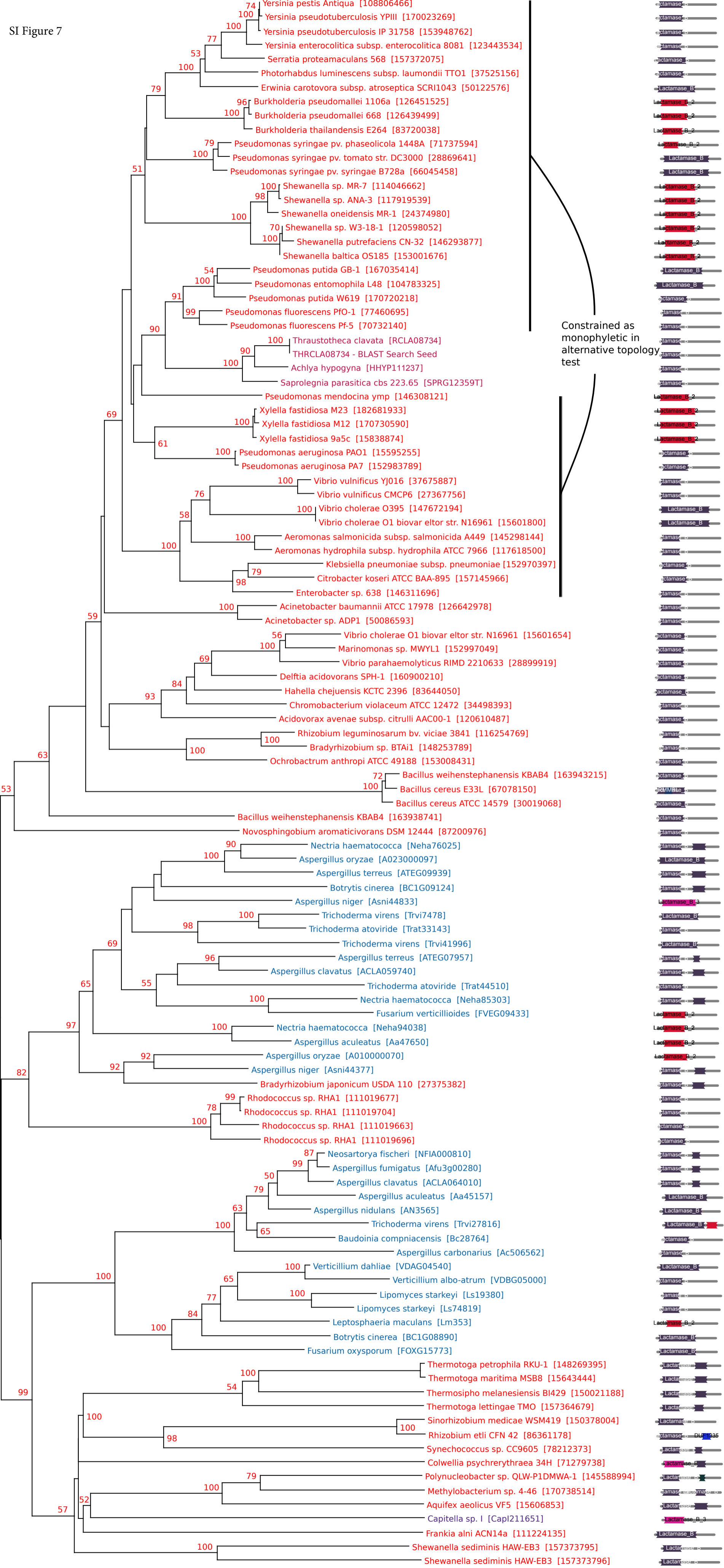


Key

fungi
stramenopiles

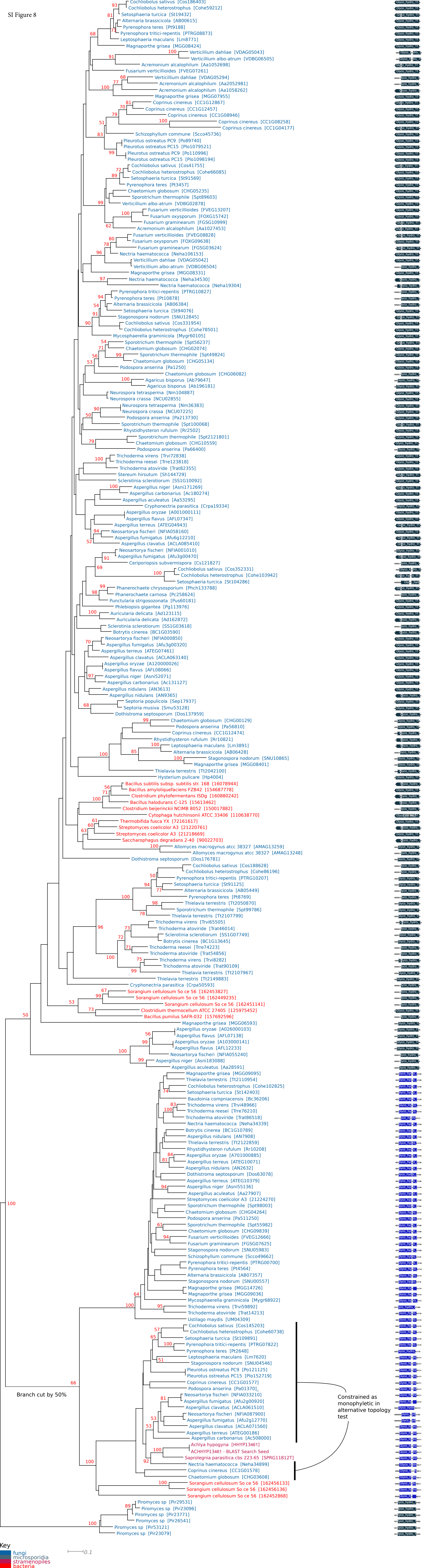
0.1

SI Figure 7

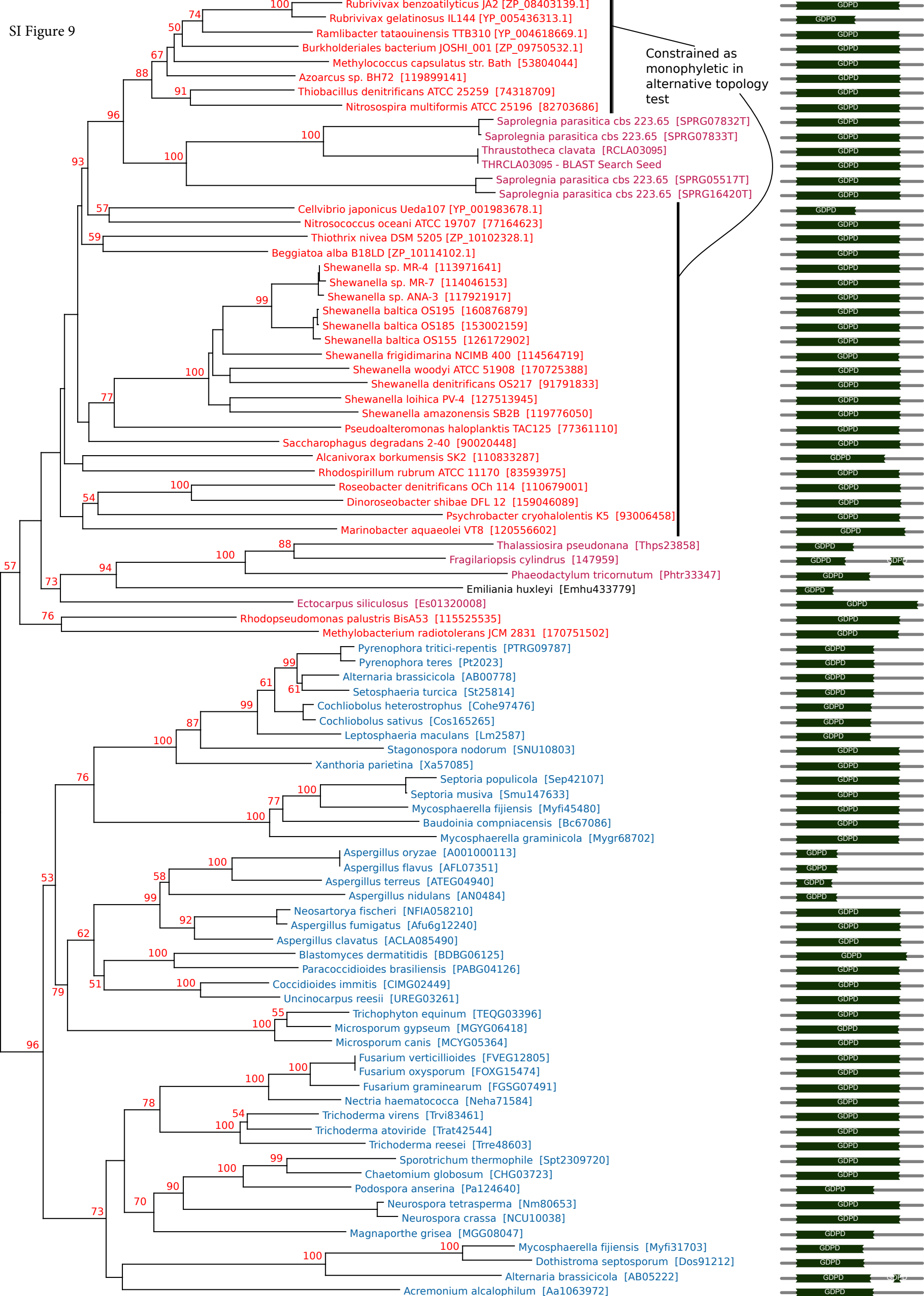


Constrained as monophyletic in alternative topology test

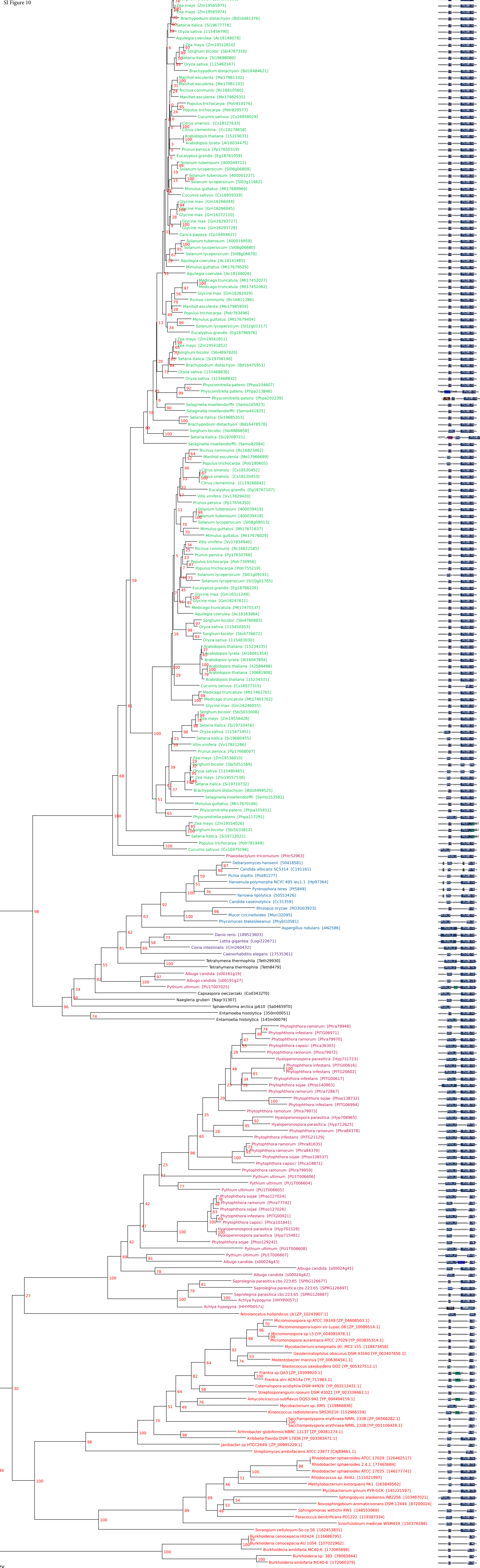




SI Figure 9



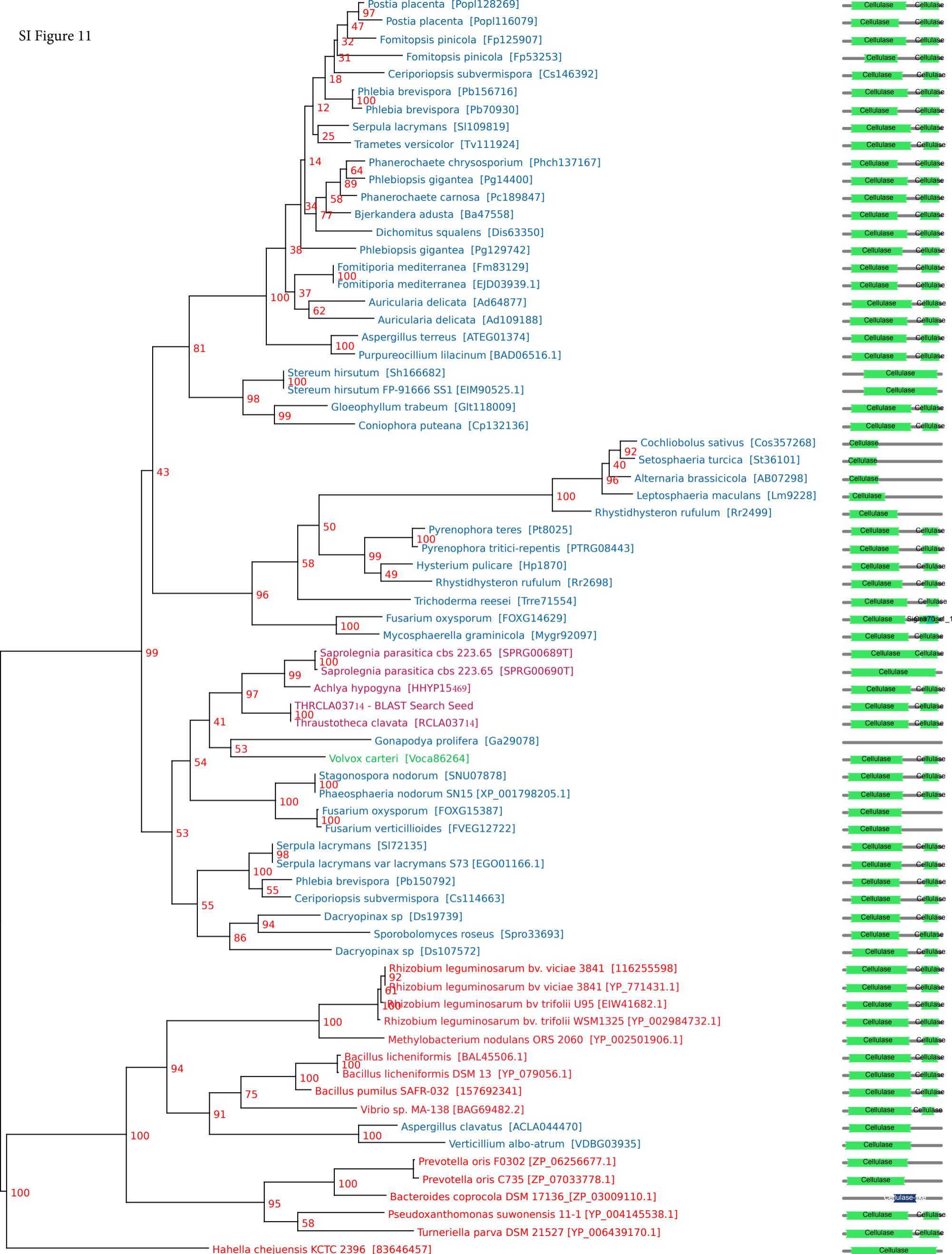
SI Figure 10



Key
 viridiplantae
 metazoa
 fungi
 microsporidia
 stramenopiles
 bacteria

0.1

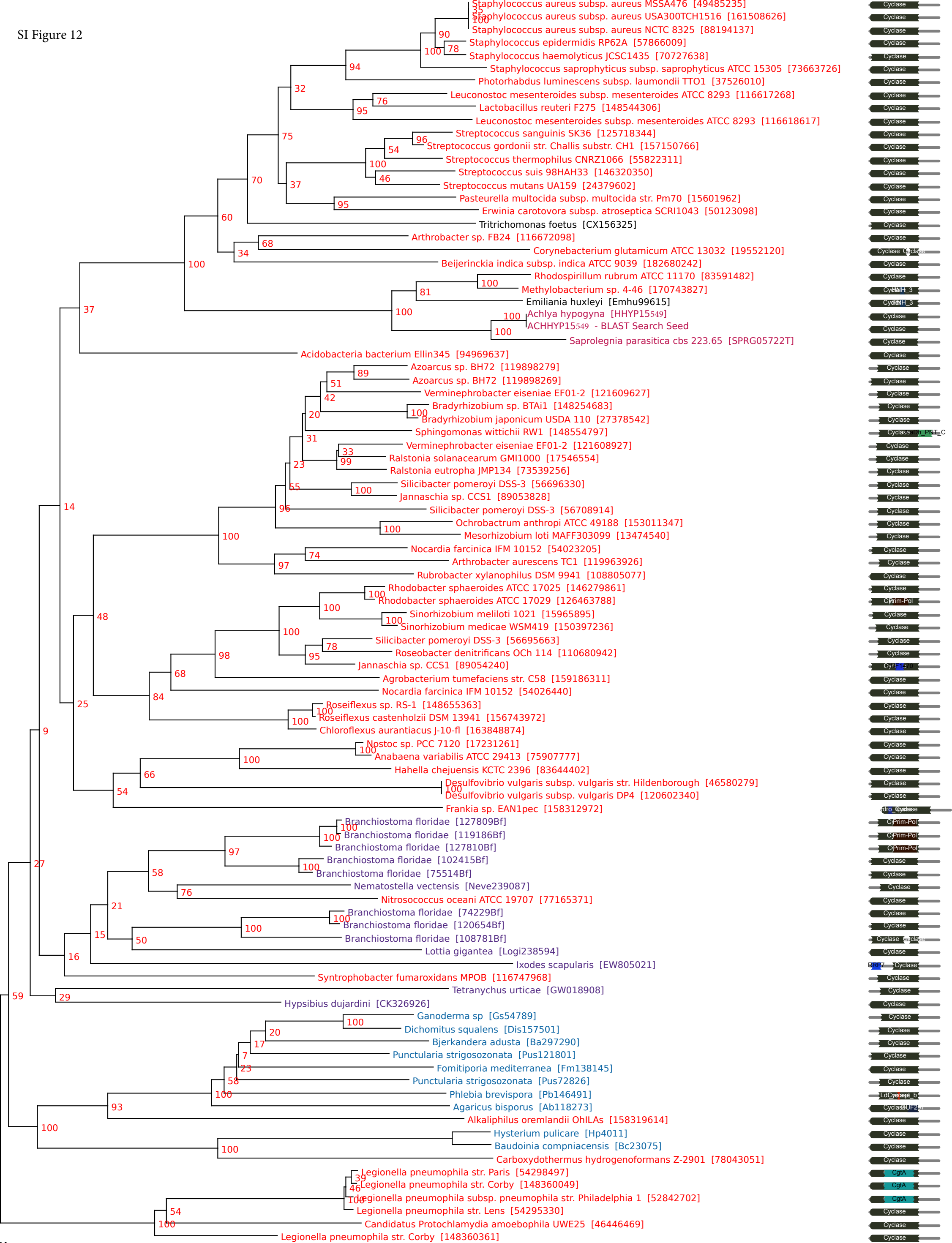
SI Figure 11



Key
 viridiplantae
 metazoa
 fungi
 microsporidia
 stramenopiles
 bacteria

0.1

SI Figure 12



Key

- ascormycota
- basidiomycota
- other fungi
- oomycetes
- other stramenopiles
- metazoa
- bacteria

