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Phylogenomic Analysis of a 55.1-kb 19-Gene Dataset Resolves a Monophyletic Fusarium that Includes the Fusarium solani Species Complex.

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1 Phylogenomic analysis of a 55.1 kb 19-gene dataset resolves a monophyletic *Fusarium* that includes the  
2 *Fusarium solani* Species Complex

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**144 Abstract**

145 Scientific communication is facilitated by a data-driven, scientifically sound taxonomy that considers the  
146 end-user's needs and established successful practice. Previously (Geiser et al. 2013; *Phytopathology*  
147 103:400-408. 2013), the *Fusarium* community voiced near unanimous support for a concept of *Fusarium*  
148 that represented a clade comprising all agriculturally and clinically important *Fusarium* species, including  
149 the *F. solani* Species Complex (FSSC). Subsequently, this concept was challenged by one research group  
150 (Lombard et al. 2015 *Studies in Mycology* 80: 189-245) who proposed dividing *Fusarium* into seven  
151 genera, including the FSSC as the genus *Neocosmospora*, with subsequent justification based on claims  
152 that the Geiser et al. (2013) concept of *Fusarium* is polyphyletic (Sandoval-Denis et al. 2018; *Persoonia*  
153 41:109-129). Here we test this claim, and provide a phylogeny based on exonic nucleotide sequences of  
154 19 orthologous protein-coding genes that strongly support the monophyly of *Fusarium* including the  
155 FSSC. We reassert the practical and scientific argument in support of a *Fusarium* that includes the FSSC  
156 and several other basal lineages, consistent with the longstanding use of this name among plant  
157 pathologists, medical mycologists, quarantine officials, regulatory agencies, students and researchers  
158 with a stake in its taxonomy. In recognition of this monophyly, 40 species recently described as  
159 *Neocosmospora* were recombined in *Fusarium*, and nine others were renamed *Fusarium*. Here the  
160 global *Fusarium* community voices strong support for the inclusion of the FSSC in *Fusarium*, as it remains  
161 the best scientific, nomenclatural and practical taxonomic option available.

162

**163 Introduction**

164 Scientific advances and new fungal nomenclatural rules have forced necessary changes in fungal  
165 names in recent years, many of which are inconvenient. But unlike other fungal genera where  
166 phylogenetics and nomenclatural conflicts forced very difficult taxonomic decisions (e.g.,  
167 *Magnaporthe/Pyricularia*; Zhang et al. 2016), there is a clear path to define *Fusarium* phylogenetically,  
168 eliminate confusing dual nomenclature/taxonomy, and maintain a generic circumscription that has been  
169 widely used for over a century (Bilal 1955; Booth 1971; Gams and Nirenberg 1989; Gerlach and  
170 Nirenberg 1982; Joffe 1974; Leslie and Summerell 2006a; Matuo 1972; Nelson et al. 1983; Raillo 1950;  
171 Snyder and Hansen 1941; Summerell 2019; Wollenweber 1913; Wollenweber and Reinking 1935). The  
172 highest impact taxonomic outcome at stake is the segregation of *F. solani* and the *F. solani* Species  
173 Complex (FSSC) out of *Fusarium* into the relatively obscure taxon *Neocosmospora*, the type of which  
174 represents a morphologically aberrant lineage within the FSSC. Here we argue that this move is

175 scientifically unnecessary and impractical, and refute phylogenetic arguments that have been presented  
176 to support it (Sandoval-Denis and Crous 2018).

177 The scientific argument for a monophyletic *Fusarium* in Geiser et al. (2013) was strongly  
178 supported by 66 authors from 17 countries representing the *Fusarium* community. The goal was to  
179 promote a generic concept of *Fusarium* that is scientifically (i.e., monophyletic) and nomenclaturally  
180 sound, and at the same time minimizes disruption by protecting scientifically valid, longstanding use.  
181 *Fusarium* is one of the most commonly used ascomycete generic names in the scientific literature  
182 (Geiser et al. 2013), so this practical consideration is essential due to the negative impact of  
183 disconnecting past, current and future uses of the name.

184 The Geiser et al. (2013) phylogenetic circumscription of *Fusarium* precisely corresponds to a  
185 monophyletic group that encompassed all economically important *Fusarium* species, originally termed  
186 the Terminal *Fusarium* Clade (herein abbreviated TFC; Gräfenhan et al. 2011). Members of this clade  
187 almost always produce spores and colonies with a recognizable *Fusarium* morphology. The TFC included  
188 the type species of *Fusarium*, *F. sambucinum*, the same species in which the competing teleomorph  
189 genus *Gibberella* is typified: *G. pulicaris*. This overlap made it straightforward to propose unitary use of  
190 the name *Fusarium* over *Gibberella* (Rossman et al. 2013). That proposal, however, did not address the  
191 many *Fusarium* species within the TFC with connections to teleomorph genera other than *Gibberella*,  
192 comprising the FSSC and all other Species Complexes in Figure 1 that resolve basally with respect to the  
193 *F. buharicum* Species Complex.

194 Geiser et al. (2013) proposed that all members of the TFC be included in *Fusarium*, not just  
195 those associated with *Gibberella*, and synonymized competing genera in the TFC under that name.  
196 Based on portions of two loci (the second-largest RNA polymerase II B-subunit (*rpb2*) and larger ATP  
197 citrate lyase (*acl1*) genes), the Gräfenhan et al. (2011) phylogenetic analysis provided only weak  
198 statistical support for the node associated with the TFC. The proposal in Geiser et al. (2013) was based  
199 on a phylogenetic analysis of a much larger set of species in the TFC that utilized more informative loci  
200 (*rpb2*, as well as the largest RNA Polymerase II B-subunit gene *rpb1*; O'Donnell et al. 2013). This analysis  
201 also resolved the TFC as monophyletic ("node F1"), with improved but still weak statistical support  
202 (<70% maximum parsimony bootstrap (MP-BS) and maximum likelihood bootstrap (ML-BS); 1.0 Bayesian  
203 posterior probability (BPP). Recognizing this uncertainty, a second node ("F2"), which received much  
204 stronger statistical support (87% MP-BS; 100% ML-BS; 1.0 BPP), was offered as an alternative to F1,  
205 should more rigorous analyses reject the monophyly of F1. F2 comprises all of F1 except its two basal-

206 most clades (the *F. ventricosum* and *F. dimerum* Species Complexes; FVSC and FDSC respectively).  
207 Notably, both the F1 and the F2 hypotheses include the FSSC within *Fusarium*.

208         Based on a phylogenetic analysis of nine concatenated loci and a rich sampling of nectriaceous  
209 taxa, Lombard et al. (2015) also resolved the same TFC node, but again with weak statistical support.  
210 Although the aforementioned studies all resolved the same node, with different levels of support,  
211 Sandoval-Denis and Crous (2018) claimed with no new phylogenetic evidence that the concept of  
212 *Fusarium* proposed by Geiser et al. (2013) is polyphyletic. However, as carefully accounted for in Geiser  
213 et al. (2013) and O'Donnell et al. (2013), statistical support for that node based on analyses of *RPB1* and  
214 *RPB2* was in need of a more rigorously tested phylogeny using additional genes. In this paper, we  
215 address this with a phylogenetic inference based on complete exonic nucleotide sequences of 19  
216 protein-coding genes, derived from whole-genome sequences of 89 taxa, 47 of which were generated in  
217 the present study (Supp. Table 1). The resulting analysis provides 100% ML-BS/1.0 BPP for the  
218 monophyly of *Fusarium* as delimited by Geiser et al. (2013; i.e., the F1 node in Fig. 1), reaffirming the  
219 taxonomic hypothesis that *Fusarium* has nomenclatural priority over all names typified in that clade,  
220 including *Neocosmospora*.

221         We also present a phylogeny of 77 FSSC species based on three-loci: portions of *rpb2* and *tef1*  
222 (translation elongation factor 1- $\alpha$ ), and rDNA (a contiguous portion of the nuclear ribosomal RNA gene  
223 repeat comprising the internal transcribed spacer (ITS) and D1-D2 regions of the nuclear large subunit).  
224 Sandoval-Denis and Crous (2018) and Sandoval-Denis et al. (2019) typified and named many of the  
225 previously unnamed species within the FSSC. This is an extremely important advance in the taxonomy of  
226 this group, an effort and will greatly facilitate scientific communication about these fungi. However, we  
227 disagree with their placement in *Neocosmospora*, for reasons we outline here and in O'Donnell et al.  
228 (2020). Accordingly, we list the combinations of these taxa in *Fusarium* (Aoki et al. 2020), along with  
229 other FSSC species typified or previously combined in *Neocosmospora*.

230

## 231 **Materials and Methods**

232 ***Selection and extraction of marker loci.*** Exonic nucleotide sequences of the 19 housekeeping genes  
233 (Table 1) used to infer the *Fusarium* phylogeny in this study were selected based on (i) their use in  
234 previous studies for inferring phylogenetic relationships within this genus and across the Kingdom *Fungi*  
235 (Floudas et al. 2012; O'Donnell et al. 2013; Sarver et al. 2011; Villani et al. 2019; Watanabe et al. 2011);  
236 (ii) their utility in previous studies of the distribution and evolution of secondary metabolite genes/gene  
237 clusters in *Fusarium* (Brown and Proctor 2016; Brown et al. 2019; Busman et al. 2012; Kim et al. 2020;

238 Proctor et al. 2009, 2010, 2013, 2018) and (iii) their relative lengths. Full-length exonic sequences of  
239 each gene were obtained from whole-genome sequences of 89 taxa, generated in-house at the USDA-  
240 ARS-NCAUR (n=65), or by the Beijing Genome Institute (BGI; n=4), or downloaded from the GenBank  
241 database at the National Center for Biotechnology Information (n=20; Suppl. Table 1).

242 Genomic DNA for sequencing was extracted from mycelia grown in liquid GYP medium (2%  
243 glucose, 1% peptone, and 0.3% yeast extract) for 2 – 3 days, harvested by filtration, lyophilized, and  
244 ground to a powder. Genomic DNA was then extracted using a ZR Fungal/Bacterial DNA MiniPrep kit  
245 (Zymo Research, Irvine, CA), the Qiagen Genomic-Tip 20/G protocol, or a previously described  
246 chloroform-phenol-based method (Raeder and Broda 1985). For data generated in-house, sequence  
247 reads were generated using the MiSeq systems (Illumina) and processed using CLC Genomics  
248 Workbench (CLC) versions 8 – 20 (Qiagen) as previously described (Laraba et al. 2020a, b; Proctor et al.  
249 2018). Sequence reads were imported into CLC and then screened against genome sequences of 84  
250 bacterial species to remove contaminating DNA introduced during library preparation and/or the  
251 sequencing process. Reads were trimmed to remove low-quality data and assembled using the following  
252 parameter settings in CLC: word size = 20; bubble size = 50; minimum contig length = 500; auto-detect  
253 paired distances = checked; and perform scaffolding = checked.

254 Protein coding genes were predicted with the program AUGUSTUS (Stanke and Morgenstern  
255 2005) using *F. graminearum* genes as a reference and the fgenesh algorithm (Solovyev et al. 2006)  
256 implemented online in Softberry (<http://www.softberry.com>). Gene sequences were retrieved from  
257 coding region databases of each strain using the BLASTn function in CLC Genomics Workbench and  
258 query sequences from *F. fujikuroi*, *F. graminearum* and *F. vanettenii* (formerly reported as *Nectria*  
259 *haematococca* mating population MPVI; Coleman et al. 2009). Sequences of each gene were aligned  
260 with the query sequences using MUSCLE (Edgar 2004) as implemented in MEGA7 (Kumar et al. 2016),  
261 and the resulting alignments were examined for differences between predicted coding regions and the  
262 query sequences. When necessary, genes were manually annotated using genome sequence data to  
263 correct errors introduced by the automated annotation, particularly with respect to predicted intron-  
264 splicing sites. The three loci utilized for phylogenetic analysis of the FSSC were those utilized in previous  
265 studies (O'Donnell et al. 2008; Sandoval-Denis and Crous 2019).

266 **Molecular phylogenetics.** Two multilocus datasets were assembled and analyzed using partitioned  
267 maximum likelihood bootstrapping (ML-BS, 5000 replicates) with IQ-TREE 1.6.12 for MacOS (Nguyen et  
268 al. 2015; <http://www.iqtree.org/>) and Bayesian inference with MrBayes v.3.2.7 (Ronquist et al. 2019). A  
269 partitioned 19-gene 55.1 kb dataset was assembled to assess *Fusarium* monophyly (Table 1). It



270 contained complete exonic nucleotide sequences for 84 fusaria, a putative sister group comprising three  
271 *Neonectria* species, and sequences of two non-nectriaceous hypocrealean taxa, *Beauveria bassiana*  
272 (Cordycipitaceae) and *Trichoderma brevicompactum* (Hypocreaceae), which were used to root the  
273 phylogeny. A partitioned 3-locus 3.2 kb dataset was constructed to infer evolutionary relationships  
274 among 77 species within the FSSC, derived from previous studies (O'Donnell et al. 2008; Sandoval-Denis  
275 and Crous 2019). Sequences were aligned with MUSCLE and then manually edited using TextPad 8  
276 (<https://www.textpad.com>) to improve the alignment. ModelFinder (Kalyaanamoorthy et al. 2017) was  
277 used to identify the best-fit model of molecular evolution for each partition based on the Bayesian  
278 information criterion (BIC) scores (Chernomor et al. 2016). Bayesian inference was conducted using  
279 1,000,000 generations in four chains (3 cold, and one hot, with 25% burnin), using the GTR+Γ+I  
280 evolutionary model. To assess compatibility of individual loci in the phylogenetic inference, gene  
281 compatibility factors (gCF) were calculated using IQ-TREE v.2.1.2 (Minh et al. 2020a,b); gCF values,  
282 representing the proportion of gene partitions that resolve a particular node, were translated into  
283 numerals representing the number of supporting loci out of 19. In addition, Internode Certainty (IC), IC-  
284 All (ICA), Tree Certainty (TC) and relative TC values (Salichos and Rokas 2013; Salichos et al. 2014) were  
285 calculated for the IQ-TREE partitioned ML tree in RAxML v.8.2.12 (Stamakis 2014; Kobert et al. 2016).  
286 Aligned 19- and 3-locus datasets and best ML trees in NEXUS format, with genes partitioned as charsets,  
287 are included as Supplemental Materials, and also deposited in TreeBASE (Study S27101;  
288 <http://purl.org/phylo/treebase/phyloids/study/TB2:S27101>).

289

## 290 Results

291 **Fusarium phylogenetics.**— The 19-gene nucleotide alignment of full-length exons totalled 55,140 sites,  
292 23,668 of which were parsimony informative (Table 1). Individual genes provided a range of 0.5% (*cal1*)  
293 to 12.7% (*dpe1*) of the total parsimony informative sites in the concatenated character set. In the best  
294 ML phylogeny (Fig. 1), 72/86 inferred nodes were supported at the 100% level by ML bootstrapping (BS)  
295 as well as 1.0 Bayesian Posterior Probability (BPP), with only two nodes receiving <80% BS/<0.99 BPP  
296 support (highlighted in magenta in Fig. 1). The F1/TFC node, upon which the Geiser et al. (2013)  
297 circumscription was based (O'Donnell et al. 2013), received 100% BS/1.0 BPP, as did the previously  
298 proposed alternate node F2. The ML and Bayesian (Suppl. Fig. 1) trees were topologically identical  
299 except for placement of *F. ventricosum* within node F1 (see discussion below), which neither method  
300 resolved with statistical confidence (BS <50%; 0.88 BPP for an alternative topology; see Fig. 1 and Suppl.  
301 Fig. 1).

302 Based on gCF values, 53/86 internodes in the ML tree were supported by at least 16/19 loci in  
303 the dataset, while 71/86 were supported by at least half (Suppl. Fig. 3). Nodes F1 and F2 were  
304 supported by 12 and 14 individual loci. The most poorly supported node in the ML tree (unresolved in  
305 the majority-rule bootstrap consensus tree and by Bayesian analysis) placed *F. ventricosum* as a sister to  
306 the *F. dimerum* Species Complex, within the F1 node. In 7/19 individual gene trees (*act1*, *cal1*, *dpe1*,  
307 *ku70*, *pgk1*, *tef1*, *tub2*; Suppl. Fig. 2), ingroup taxa (usually *F. ventricosum*) resolved among outgroup  
308 taxa. These genes tend to be shorter and have lower PIC/bp values than those that resolve F1 (Table 1).  
309 However, the F1/TFC, inclusive of *F. ventricosum* was supported in each of the remaining 12 individual  
310 gene trees, with bootstrap values between 78-100%. Three loci, *fas1*, *fas2*, and *ku70*, representing  
311 24.6% of the parsimony-informative characters in the matrix, are co-located within ~30kb on the same  
312 contig (FFUJ\_scaffold03) of the *F. fujikuroi* genome sequence. Removal of these linked loci and  
313 reanalysis using IQ-TREE resolved the F1/TFC node with 100% ML bootstrap support (result not shown).  
314 The IC and ICA values for the F1 node were 0.19 and 0.33, respectively (Suppl. Fig. 3), indicating that  
315 roughly 70% of the genes support the bipartition (see Fig. 2 in Salichos et al., 2014). This value is similar  
316 to the proportion of 12/19 (~63%) indicated by gCF, and evident by visual inspection of individual gene  
317 trees (Suppl. Figs. 2 and 3). TC, representing the sum of IC values across trees, was 48.41, and relative  
318 TC, representing TC normalized to the maximum TC for the phylogeny, was 0.563.

319 Three additional Species Complexes recognized within *Fusarium* since the publication of the  
320 *rpb1 + rpb2* phylogeny (O'Donnell et al. 2013) are represented in the dataset: the *F. torreyae* Species  
321 Complex (FtorSC; Zhou et al. 2018), the *F. newnesense* Species Complex (FnewSC; Laurence et al. 2016)  
322 and *F. burgessii* Species Complex (FburSC, here represented by *F. beomiforme*; Laraba et al. 2018;  
323 Laurence et al. 2011; Nelson and Toussoun 1987), bringing the total to 23 Species Complexes recognized  
324 within the genus. Each of these Species Complexes received at least 95% ML-BS, except for the *F.*  
325 *concolor* Species Complex (FconSC), which received 69% ML-BS/0.98 BPP support. This lack of resolution  
326 appears to be due to FconSC's sister taxon, the *F. babinda* Species Complex, being represented by a  
327 single taxon in the dataset. When *F. babinda* was removed, FconSC received 100% BS support (result not  
328 shown). Similarly, the *F. ventricosum* Species Complex (FVSC) is represented by a single taxon on a long  
329 branch, which likely explains the failure to resolve its placement (Felsenstein 1978). However, it does  
330 resolve within the FTC/F1 node with 100% ML-BS and 1.0 BPP support, as it did with weaker support in  
331 previous studies (Gräfenhan et al. 2011; Lombard et al. 2015; O'Donnell et al. 2013).

332 **FSSC phylogenetics.** The 3-locus DNA alignment for the FSSC comprised 3209 sites (665 for *TEF1*, 956 for  
333 rDNA, 1588 for *RPB2*), 655 of which were parsimony-informative (164 for *TEF1*, 131 for rDNA, 360 for

334 *RPB2*). In the best ML cladogram, the previously identified major clades 1, 2 and 3 (O'Donnell 2000)  
335 were resolved with 100% bootstrap support. Three clades with unique morphologies and host  
336 associations were also resolved within the FSSC: (i) the subclade within Clade 3 that is morphologically  
337 associated with *Neocosmospora*'s type (Smith 1899); (ii) the Ambrosia *Fusarium* Clade (AFC; Kasson et  
338 al. 2013; O'Donnell et al. 2015); and (iii) the Soybean Sudden Death Syndrome (SDS) and Bean Root Rot  
339 (BRR) pathogen clade nested in Clade 2 (Aoki et al. 2012).

340 **Taxonomy.** Recognizing that *Neocosmospora sensu* Lombard et al. (2015), Sandoval-Denis and Crous  
341 (2018) and Sandoval-Denis et al. (2018, 2019) represents a later synonym of *Fusarium* under this  
342 taxonomic hypothesis, species combinations (Aoki et al. 2020) are listed in Appendix A.

343         Importantly, we retained as distinct species the important soybean sudden death (SDS) and  
344 bean root rot (BRR) pathogens in the FSSC, *F. phaseoli*, *F. tucumaniae*, *F. virguliforme*, *F. brasiliense*, *F.*  
345 *cuneirostrum*, *F. crassistipitatum* and *F. azukicola*, which were synonymized under *F. phaseoli* by  
346 Sandoval-Denis et al. (2019). The latter authors performed a split graph analysis and interpreted  
347 reticulate patterns as evidence that these groups are conspecific. This is in contrast to previous work  
348 providing evidence that they were genealogically exclusive (Aoki et al. 2005, 2012). However, the split  
349 graph analysis was based on *tef1*, *rpb2* and *rDNA*, with only twelve parsimony informative sites among  
350 these taxa, and they did not analyze the more phylogenetically informative loci that indicated  
351 genealogical exclusivity among these species (Aoki et al. 2012). While the levels of sequence divergence  
352 among these species were very small, and scrutiny of the species boundaries based on information-rich  
353 phylogenomic datasets is encouraged, the reticulate pattern illustrating homoplasy could be due to  
354 processes other than intraspecific genetic exchange, including incomplete lineage sorting and  
355 convergence. The synonymization by Sandoval-Denis et al. (2019) also does not account for the  
356 morphological differences among these species, nor reported distinctions in their symptomology and  
357 host range (Aoki et al. 2005, 2012).

358

## 359 **Discussion**

360 The rationale for a phylogenetic delimitation of *Fusarium* outlined by Geiser et al. (2013), reaffirmed  
361 here, can be considered on its own merit. However, we emphasize that the 166 scientists from 30  
362 countries (aka core global *Fusarium* community) who co-authored the present publication  
363 enthusiastically support it as the best scientifically and nomenclaturally valid taxonomic option. We  
364 argue that the alternative posed by Lombard et al. (2015) is based on a taxonomic viewpoint that binds  
365 the concept of *Fusarium* to a teleomorph name, *Gibberella*. This approach was first hinted at (Gräfenhan

366 et al. 2011; Schroers et al. 2011), and later manifested in a proposal (Lombard et al. 2015) to split  
367 *Fusarium* into seven genera within the TFC: *Fusarium* (*Gibberella*'s de facto replacement), *Albonectria*,  
368 *Bisifusarium*, *Cyanonectria*, *Geejayessia*, *Neocosmospora*, and *Rectifusarium*. Although the generic  
369 concepts proposed by Lombard et al. (2015) are monophyletic and nomenclaturally valid, they fail on  
370 the practicality criterion because they exclude species with a longstanding place in *Fusarium*. We see no  
371 benefit in splitting *Fusarium* in favor of competing names that are largely tied to rarely observed sexual  
372 stages.

373 The most important exclusion by Lombard et al. (2015) is that of the FSSC, which was moved to  
374 the genus *Neocosmospora* in their taxonomic proposal. The type species, *Neocosmospora vasinfecta*,  
375 which was recombined in *Fusarium* as *F. neocosmosporiellum* (Geiser et al. 2013), represents an atypical  
376 morphological lineage derived within the FSSC (Figs. 1 and 2). *Fusarium neocosmosporiellum* and  
377 related species produce an asexual stage that, unlike most FSSC species, lacks the fusiform sporodochial  
378 macroconidia that are the hallmark of *Fusarium*, and a homothallic sexual stage consisting of smooth,  
379 thin-walled perithecia and ascospores that are mostly single-celled (Smith 1899; Wollenweber and  
380 Reinking 1935). However, *F. neocosmosporiellum* produces microconidiophores typical of the FSSC  
381 (Domsch et al. 1980). Viewed within a robust phylogenetic framework, *F. neocosmosporiellum* clearly  
382 represents a morphologically aberrant FSSC lineage whose species have lost the ability to produce the  
383 iconic multiseptate macroconidia and only occasionally produce two-celled ascospores (O'Donnell 2000;  
384 O'Donnell et al. 2013). Similarly, most of the 19 species in the Ambrosia *Fusarium* Clade are  
385 morphologically unique within the FSSC in that they produce club-shaped macroconidia that are  
386 hypothesized to be adaptive to roles associated with the ambrosia beetle symbiosis (Kasson et al. 2013).

387 While *Neocosmospora* works nomenclaturally as an available genus name typified within the  
388 FSSC, it would be unfortunate if its aberrant morphology were to replace *Fusarium*, which represents  
389 the dominant morphology of the group. Because *Neocosmospora* is the oldest teleomorph name  
390 associated with the FSSC, this awkward nomenclatural option seemed reasonable when it was applied  
391 under dual nomenclature (e.g., Nalim et al. 2011). However, the demise of dual nomenclature as of 01  
392 Jan 2013 opened the door to a much more practical and attractive option: *Fusarium*, an older name, and  
393 the dominant longstanding generic concept associated with the FSSC. Highlighting that status, '*Fusarium*  
394 *solani*' generated over 100 times more Google hits than '*Neocosmospora*' (3,000,000 to 27,600; search  
395 conducted on 09 July 2020). In summary, we argue that the practical and most scientifically attractive  
396 option is to combine *Neocosmospora* species under *Fusarium* (Geiser et al. 2013), not the other way  
397 around.

398           We refute the argument that inclusion of the FSSC in *Fusarium* “implies a denial of the current  
399 phenotypic ... evidence” (Sandoval-Denis et al. 2019), and, to the contrary, argue that the name  
400 ‘*Neocosmospora*’ is an atypical phenotypic fit for the FSSC. Sandoval-Denis et al. (2019) do not apply a  
401 rigorous test or accounting of phenotypic synapomorphies that invalidate the Geiser et al. (2013)  
402 circumscription. Iconic *Fusarium* multiseptate macroconidia are observed in a majority of FSSC species,  
403 as they are in members of every other *Fusarium* Species Complex. In addition to the aforementioned *F.*  
404 *neocosmosporiellum*, occasional isolates within multiple FSSC species appear to lack macroconidium  
405 production (Gams 1971; O’Donnell 2000; Short et al. 2013; Summerbell and Schroers 2002). However,  
406 the vast majority of isolates in the FSSC do produce these spores, and a lack of macroconidia is  
407 occasionally observed in *Fusarium sensu* Lombard et al. (2015) as well (*e.g.*, *F. xyrophilum*: Laraba et al.  
408 2020a). While the FSSC is morphologically distinguishable from other *Fusarium* Species Complexes, we  
409 do not accept that these differences are sufficiently significant to require recognition as a separate  
410 genus. To wit, the concept of *Fusarium* in existence for over a century has consistently accommodated  
411 this level of phenotypic diversity in the recognition of taxonomic subgroups within the genus  
412 (Wollenweber 1913; Wollenweber and Reinking 1935).

413           While there are indeed morphological and ecological trends associated with the phylogenetic  
414 structure within our circumscription of *Fusarium*, there are no convincing nomenclatural, scientific or  
415 practical criteria that obligate splitting it into multiple genera. Illustrating similarities between the FSSC  
416 and other *Fusarium* clades, FSSC species share many morphological, ecological and genomic  
417 characteristics with the *F. oxysporum* Species Complex (FOSC), which Lombard et al. (2015) retain in  
418 *Fusarium*. FSSC and FOSC often are co-isolated from the same soil and plant samples, and while they can  
419 be resolved morphologically, misidentification of one as the other is common. FSSC and the FOSC are  
420 cosmopolitan residents of soil and the rhizosphere, and of decaying and living plant material, where  
421 they may act as parasites and/or endophytes. Interestingly, their ecological similarities are reflected in  
422 their genomes, with both having significantly expanded accessory genomes that include supernumerary,  
423 conditionally dispensable chromosomes that harbor niche adaptive genes (Coleman et al. 2009; Ma et  
424 al. 2010; Waalwijk et al. 2018). While these two groups occupy different clades within *Fusarium*, and  
425 placing them in separate genera is a discretionary option, plant pathologists and medical mycologists  
426 have treated them as congeneric for the past century. International *Fusarium* Laboratory Workshops,  
427 which have been held regularly since the 1970s, (Leslie and Summerell 2006b) present the FSSC and the  
428 FOSC, which is retained in *Fusarium* by Lombard et al. (2015), together in lectures and the laboratory,  
429 reflecting the shared ecological, morphological and genomic characteristics that are relevant to

430 clinicians and researchers. In short, we argue that the individual lineages that comprise the  
431 monophyletic *Fusarium sensu* Geiser et al. (2013) share more in common than not.

432 In support of splitting *Fusarium* into seven genera and promoting the FSSC as *Neocosmospora*,  
433 additional claims were made about the status of the TFC as a monophyletic group (Sandoval-Denis and  
434 Crous 2018), including: (i) the Geiser et al. (2013) concept of *Fusarium* is “polyphyletic,” and (ii) moving  
435 it to *Neocosmospora* represents a “more natural classification.” To correct the record, there are no  
436 published phylogenies known to the authors of this paper with appropriate taxon sampling and  
437 resolving power showing the TFC to be anything but monophyletic, including the Lombard et al. (2015)  
438 phylogeny. Comparisons of the phylogeny in Lombard et al. (2015) with those in Geiser et al. (2013),  
439 O’Donnell et al. (2013) and Gräfenhan et al. (2011) reveal that a monophyletic TFC is resolved in **all** of  
440 them. Certainly, as has been shown in many publications, there is phylogenetic structure within  
441 *Fusarium*, but phylogenetic structure is not synonymous with polyphyly (i.e., having multiple distinct  
442 evolutionary origins (Farris 1990)); a strongly supported monophyletic genus can encompass strongly  
443 supported monophyletic subgroups. Nor would it be reasonable to argue that a genus can  
444 accommodate only a certain degree of phylogenetic structure, particularly when its well-studied  
445 taxonomy has unanimously accommodated substructure, in the form of Sections (Wollenweber 1913)  
446 and now phylogenetic lineages referred to as Species Complexes (O’Donnell et al. 2013).

447 We also reject the assertion that splitting the FSSC off as *Neocosmospora* represents a “more  
448 natural classification.” Given that *Neocosmospora sensu* Sandoval-Denis et al. (2019) and the  
449 circumscription of *Fusarium* in Geiser et al. (2013) are both monophyletic, the two concepts are of equal  
450 status regarding scientific support. In fact, Geiser et al. (2013) openly critiqued the phylogenetic  
451 evidence underlying their taxonomic hypothesis and presented an alternative circumscription of  
452 *Fusarium* in case additional data did not support this hypothesis. Although the concept proposed by  
453 Geiser et al. (2013) is based on phylogenetics, it is rooted in the first taxonomic synthesis of *Fusarium*  
454 (Wollenweber and Reinking, 1935), and subsequent modifications based on modern morphological (e.g.,  
455 moving ‘*F. nivale*’ into *Microdochium*; Samuels and Hallett 1983) and phylogenetic (Gräfenhan et al.  
456 2011; O’Donnell et al. 2013) information. It retains all agriculturally, medically and economically  
457 important species in *Fusarium*. In contrast to the claim that *Neocosmospora* is the more natural  
458 classification for the FSSC, we find its transfer to *Neocosmospora* unnatural in light of this historical and  
459 practical context. It is a morphologically counterintuitive, unnecessarily disruptive solution to a  
460 taxonomic problem that does not exist.

461 Our phylogenetic circumscription of *Fusarium* mirrors that of *Aspergillus* in several ways  
462 (Samson et al. 2014). *Aspergillus* is also one of the most commonly used generic names in *Fungi*, and it  
463 corresponds to a strongly supported clade (Kocsubé et al. 2016; Steenwyk et al. 2019). Both genera  
464 harbor great species diversity, with new species being discovered at high rates. However, the *Aspergillus*  
465 clade encompasses much greater morphological diversity than *Fusarium*, including sexual stages varying  
466 from asci enclosed within wefts of hyphal elements (*Neosartorya*, associated with *A. fumigatus*) to  
467 cleistothecia enclosed in sclerotial ascostromata (*Petromyces*, associated with *A. flavus*). While the  
468 familiar *Aspergillus* conidiophore morphology dominates, the clade also includes aberrant anamorph  
469 forms such as *Phialosimplex*. In the case of *Aspergillus*, it was decided that the broader circumscription  
470 was the most reasonable solution among nomenclaturally and scientifically valid options (Samson et al.  
471 2014), and all competing generic concepts have been subsumed under *Aspergillus*. While molecular  
472 phylogenetic studies over the past three decades have revealed *Aspergillus* and *Fusarium* are much  
473 larger than documented using morphology alone, it is important to note that both are monophyletic as  
474 presently circumscribed.

475 The strong statistical support presented in the 19-locus phylogeny solidifies the taxonomic  
476 hypothesis assigning the name *Fusarium* to all descendants of node F1 in Geiser et al. (2013) and  
477 O'Donnell et al. (2013), and the "Terminal *Fusarium* Clade" *sensu* Gräfenhan et al. (2011). This finding  
478 further negates the unsupported claim that *Fusarium sensu* Geiser et al. (2013) is polyphyletic, and it  
479 eliminates any remaining doubt regarding the robustness of the TFC/F1 node. As a result, all competing  
480 generic names typified in this clade, including *Albonectria*, *Bisifusarium*, *Cyanonectria*, *Geejayessia*,  
481 *Gibberella*, *Neocosmospora*, and *Rectifusarium*, are recognized as *Fusarium*. With taxon discovery and  
482 phylogenomic datasets rapidly accumulating, we will continue to scrutinize and refine our taxonomic  
483 hypothesis and promote a scientifically robust and practical, user-friendly generic concept. As shown  
484 here, consideration of additional data has significantly strengthened the inference that the present  
485 circumscription of *Fusarium* is monophyletic (Geiser et al. 2013).

486 Taxonomy's purpose is to foster clear scientific communication, and the job of taxonomists is to  
487 refine it with that in mind. In doing so, taxonomists must not only recommend improved communication  
488 going forward, but also weigh the costs of altering longstanding, effective communication (Booth 1978).  
489 This communication underlies international trade and agricultural biosecurity, pesticide and crop  
490 cultivar registration, and accurate identification and reporting of etiological agents essential for plant,  
491 animal and human disease management. In some cases, scientific evidence and practical merit require  
492 inconvenient disruptions of and changes in taxonomic usage to accommodate nomenclatural rules and

493 scientific rigor. As spelled out here and in Geiser et al. (2013), we assert that inclusion of the FSSC in  
 494 *Neocosmospora* rather than *Fusarium* is not such a case. In this age, when molecular phylogenetics is  
 495 informing a vastly improved taxonomy, the *Fusarium* community is fortunate that the genus-level  
 496 taxonomy is supported by a phylogenetically rigorous, nomenclaturally sound and user-friendly solution  
 497 allowing uninterrupted unitary use of the name *Fusarium*. In the interest of a robust taxonomy that  
 498 facilitates communication, we welcome cogent, data-driven alternative taxonomic hypotheses that fully  
 499 consider the scientific, nomenclatural and practical ramifications.

500

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502

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509

## 510 **DISCLAIMER**

511

512 The mention of company names or trade products does not imply that they are endorsed or  
 513 recommended by the US Department of Agriculture over other companies or similar products not  
 514 mentioned. USDA is an equal opportunity provider and employer.

515

## 516 **Appendix A**

517 A list of taxonomic changes follows (Aoki et al. 2020):

518 *Fusarium acutisporum* (Sand.-Den. & Crous) O'Donnell, Geiser, Kasson & T. Aoki, Index Fungorum 440: 1.  
 519 2020. [IF 557667]

520     ≡ *Neocosmospora acutispora* Sand.-Den. & Crous, Persoonia 43: 108. 2019. [MB 831170]

521

522 *Fusarium ambrosium* (Gadd & Loos) Agnihotr. & Nirenberg, Stud. Mycol. 32: 98. 1990. [MB 130225]

523     ≡ *Monacrosporium ambrosium* Gadd & Loos, Trans. Br. mycol. Soc. 30: 13. 1947. [MB 288427]

524     ≡ *Neocosmospora ambrosia* (Gadd & Loos) L. Lombard & Crous, Stud. Mycol. 80: 227. 2015.

525     [MB 810957]

526 Note: Also known as FSSC 19.

527



- 528 *Fusarium amplum* (Sand.-Den. & Crous) O'Donnell, Geiser, Kasson & T. Aoki, Index Fungorum 440: 1.  
 529 2020. [IF 557668]  
 530 ≡ *Neocosmospora ampla* Sand.-Den. & Crous, Persoonia 43: 110. 2019. [MB 831171]  
 531
- 532 *Fusarium bataticola* (Sand.-Den. & Crous) O'Donnell, Geiser, Kasson & T. Aoki, Index Fungorum 440: 1.  
 533 2020. [IF 557670]  
 534 ≡ *Neocosmospora bataticola* Sand.-Den. & Crous, Persoonia 43: 112 2019. [MB 831172]  
 535 Note: Also known as FSSC 23.  
 536
- 537 = *Neocosmospora striata* Udagawa & Y. Horie, Trans. Mycol. Soc. Japan 16: 340. 1975. [MB 318599]  
 538 (non *Fusarium striatum* Sherb. 1915 [MB240201])  
 539 = *Neocosmospora parva* Mahoney, Mycologia 68: 1111. 1976. [MB 318598]  
 540 = *Fusarium solani* f. *batatas* T.T. McClure, Phytopathology 41: 75. 1951. [MB 537090] (non *Fusarium*  
 541 *batatas* Wollenw. 1914. [MB 175963])  
 542 Note: Also known as *Nectria haematococca* Mating Population II (NhMP II).  
 543
- 544 *Fusarium bomiense* (Z.Q. Zeng & W.Y. Zhuang) O'Donnell, Geiser, Kasson & T. Aoki, Index Fungorum 440:  
 545 1. 2020. [IF 557671]  
 546 ≡ *Neocosmospora bomiensis* Z.Q. Zeng & W.Y. Zhuang, Phytotaxa 319(2): 177. 2017. [MB 570412]  
 547
- 548 *Fusarium borneense* (Petr.) O'Donnell, Geiser, Kasson & T. Aoki, Index Fungorum 440: 1. 2020. [IF  
 549 557672]  
 550 ≡ *Neocosmospora borneensis* (Petr.) Sand.-Den. & Crous, Persoonia 43: 115. 2019. [MB 831173]  
 551 ≡ *Nectria borneensis* Petr., Sydowia 8: 20. 1954. [MB 301755]  
 552 Note: Also known as FSSC 30.  
 553
- 554 *Fusarium bostrycoides* Wollenw. & Reinking, Phytopathology 15(3): 166. 1925. [MB 258714]  
 555 ≡ *Neocosmospora bostrycoides* (Wollenw. & Reinking) Sand.-Den. & Crous, Persoonia 43: 115.  
 556 2019. [MB 831174]  
 557 Note: Also known as FSSC 25.  
 558
- 559 *Fusarium breve* (Sand.-Den. & Crous) O'Donnell, Geiser, Kasson & T. Aoki, Index Fungorum 440: 1. 2020.  
 560 [IF 557673]  
 561 ≡ *Neocosmospora brevis* Sand.-Den. & Crous, Persoonia 43: 119. 2019. [MB 831176]  
 562 Note: Also known as FSSC 15.  
 563
- 564 *Fusarium breviconum* (Wollenw.) O'Donnell, Geiser, Kasson & T. Aoki, Index Fungorum 440: 1. 2020. [IF  
 565 557674]  
 566 ≡ *Hypomyces haematococcus* var. *breviconus* Wollenw., Fusaria autographice delineata 3: no. 828.  
 567 1930. [MB 373029]  
 568 ≡ *Neocosmospora brevicona* (Wollenw.) Sand.-Den. & Crous, Persoonia 43: 117. 2019. [MB 831175]  
 569 ≡ *Nectria haematococca* var. *breviconica* (Wollenw.) Gerlach, Fusarium: Disease, Biology, and  
 570 Taxonomy (State College), p. 422. 1981. [MB 117167]  
 571 = *Fusarium solani* var. *minus* Wollenw., Die Fusarien, ihre Beschreibung, Schadwirkung und  
 572 Bekämpfung (Berlin). p. 134. 1935. [MB 185066]  
 573

- 574 *Fusarium catenatum* (Sand.-Den. & Crous) O'Donnell, Geiser & T. Aoki, Index Fungorum 440: 1. 2020. [IF  
575 557675]  
576 ≡ *Neocosmospora catenata* Sand.-Den. & Crous, Persoonia 41: 115. 2018. [MB 822898]  
577 Note: Also known as FSSC 43.  
578
- 579 *Fusarium crassum* (Sand.-Den. & Crous) O'Donnell, Geiser, Kasson & T. Aoki, Index Fungorum 440: 1.  
580 2020. [IF 557676]  
581 ≡ *Neocosmospora crassa* Sand.-Den. & Crous, Persoonia 43: 122. 2019. [MB 831177]  
582 Note: Also known as FSSC 34.  
583
- 584 *Fusarium croci* (Guarnaccia, Sand.-Den. & Crous) O'Donnell, Geiser & T. Aoki, Index Fungorum 440: 1.  
585 2020. [IF 557677]  
586 ≡ *Neocosmospora croci* Guarnaccia, Sand.-Den. & Crous, Persoonia 40: 17. 2017. [MB 820251]  
587
- 588 *Fusarium cryptoseptatum* (Sand.-Den. & Crous) O'Donnell, Geiser, Kasson & T. Aoki, Index Fungorum  
589 440: 1. 2020. [IF 557678]  
590 ≡ *Neocosmospora cryptoseptata* Sand.-Den. & Crous, Persoonia 43: 122. 2019. [MB 831178]  
591
- 592 *Fusarium cucurbiticola* O'Donnell, Geiser, Kasson & T. Aoki, Index Fungorum 440: 2. 2020. [IF 557679]  
593 ≡ *Neocosmospora cucurbitae* Sand.-Den., L. Lombard & Crous, Persoonia 43: 125. 2019. [MB  
594 831179] (non *Fusarium cucurbitae* Taubenh. 1920 [MB 509348])  
595 = *Fusarium solani* f. *cucurbitae* W.C. Snyder & H.N. Hansen, Amer. J. Bot. 28: 740. 1941. [MB 346145]  
596 = *Fusarium solani* f. sp. *cucurbitae* W.C. Snyder & H.N. Hansen, Root rots caused by Phycomycetes  
597 28: 740. 1941. [MB 434083]  
598 = *Hypomyces solani* f. *cucurbitae* W.C. Snyder & H.N. Hansen, Amer. J. Bot. 28: 741. 1941. [MB  
599 346179]  
600 ≡ *Nectria haematococca* var. *cucurbitae* (W.C. Snyder & H.N. Hansen) Dingley, New Zealand J. Agric.  
601 Res. 4: 337. 1961. [MB 349909]  
602 ≡ *Nectria solani* f. *cucurbitae* (W.C. Snyder & H.N. Hansen) G.R.W. Arnold, Z. Pilzk. 37: 193. 1972.  
603 [MB 348526]  
604 Note: Also known as *Nectria haematococca* Mating Population I (NhMPI) and FSSC 10.  
605
- 606 *Fusarium cyanescens* (G.A. de Vries, de Hoog & Bruyn) O'Donnell, Geiser & T. Aoki, Index Fungorum 440:  
607 2. 2020. [IF 557680]  
608 ≡ *Phialophora cyanescens* G.A. de Vries, de Hoog & Bruyn, Antonie van Leeuwenhoek 50(2): 150.  
609 1984. [MB 107121]  
610 ≡ *Neocosmospora cyanescens* (G.A. de Vries, de Hoog & Bruyn) Summerbell, Schroers & Scott,  
611 Biology of Microfungi (Cham) 183. 2016. [MB 813864]  
612 ≡ *Cylindrocarpon cyanescens* (G.A. de Vries, de Hoog & Bruyn) Sigler, J. Clin. Microbiol. 29: 1858.  
613 1991. [MB 499349]  
614 Note: Also known as FSSC 27.  
615
- 616 *Fusarium diminutum* (Sand.-Den. & Crous) O'Donnell, Geiser, Kasson & T. Aoki, Index Fungorum 440: 2.  
617 2020. [IF 557681]  
618 ≡ *Neocosmospora diminuta* Sand.-Den. & Crous, Persoonia 43: 127. 2019. [MB 831180]  
619 Note: Also known as FSSC 39.  
620

- 621 *Fusarium euwallaceae* S. Freeman, Z. Mendel, T. Aoki & O'Donnell, Mycologia 105(6): 1599. 2013. [MB  
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623 ≡ *Neocosmospora euwallaceae* (S. Freeman, Z. Mendel, T. Aoki & O'Donnell) Sand.-Den., L.  
624 Lombard & Crous, Persoonia 43: 129. 2019. [MB 831181]  
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- 626 *Fusarium falciforme* (Carrión) Summerb. & Schroers, J. Clin. Microbiol. 40(8): 2872. 2002. [MB 483950]  
627 ≡ *Cephalosporium falciforme* Carrión, Mycologia 43: 523. 1951. [MB 294124]  
628 ≡ *Acremonium falciforme* (Carrión) W. Gams, Cephalosporium-artige Schimmelpilze (Stuttgart):  
629 139. 1971. [MB 308145]  
630 ≡ *Neocosmospora falciformis* (Carrión) L. Lombard & Crous, Stud. Mycol. 80: 227. 2015. [MB  
631 810958]  
632 Note: Also known as FSSC 3+4.  
633
- 634 *Fusarium ferrugineum* (Sand.-Den. & Crous) O'Donnell, Geiser, Kasson & T. Aoki, Index Fungorum 440: 2.  
635 2020. [IF 557682]  
636 ≡ *Neocosmospora ferruginea* Sand.-Den. & Crous, Persoonia 43: 130. 2019. [MB 831182]  
637
- 638 *Fusarium haematococcum* Nalim, Samuels & Geiser, Mycologia 103(6): 1322. 2011. [MB 519837]  
639 = *Nectria haematococca* Berk. & Broome var. *haematococca*, J. Linn. Soc. Bot. 14: 116. 1875. [MB  
640 417425]  
641 ≡ *Neocosmospora haematococca* (Berk. & Broome) Nalim, Samuels & Geiser, Mycologia 103 (6):  
642 1322. 2011. [MB 519835]  
643 Note: Also known as FSSC 28.  
644
- 645 *Fusarium helgardnirenbergiae* O'Donnell, Geiser, Kasson & T. Aoki, Index Fungorum 440: 2. 2020. [IF  
646 557683]  
647 ≡ *Neocosmospora nirenbergiana* Sand.-Den. & Crous, Persoonia 43: 143. 2019. [MB 831189] (non  
648 *Fusarium nirenbergiae* L. Lombard & Crous 2018. [MB 826845])  
649 Etymology: In honor of Dr. Helgard Nirenberg.  
650
- 651 *Fusarium hengyangense* (Z.Q. Zeng & W.Y. Zhuang) O'Donnell, Geiser, Kasson & T. Aoki, Index Fungorum  
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653 ≡ *Neocosmospora hengyangensis* Z.Q. Zeng & W.Y. Zhuang, Phytotaxa 319: 179. 2017. [MB 570411]  
654
- 655 *Fusarium hypothenemi* (Sand.-Den. & Crous) O'Donnell, Geiser, Kasson & T. Aoki, Index Fungorum 440:  
656 2. 2020. [IF 557685]  
657 ≡ *Neocosmospora hypothenemi* Sand.-Den. & Crous, Persoonia 43: 132. 2019. [MB 831183]  
658 Note: Also known as FSSC 38.  
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- 660 *Fusarium illudens* C. Booth, The genus *Fusarium*: 54. 1971. [MB 314215]  
661 = *Neocosmospora illudens* (Berk.) L. Lombard & Crous, Stud. Mycol. 80: 227. 2015. [MB 810959]  
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- 665 *Fusarium kelerajum* Samuels, Nalim & Geiser, Mycologia 103(6): 1326. 2011. [MB 519856]  
666 = *Neocosmospora keleraja* Samuels, Nalim & Geiser, Mycologia 103(6): 1326. 2011. [MB 519854]  
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 670 ≡ *Neocosmospora keratoplastica* (Geiser, O'Donnell, D.P.G. Short & Ning Zhang) Sand.-Den. &  
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 672 Note: Also known as FSSC 2.  
 673
- 674 *Fusarium kuroshium* (F. Na, J.D. Carrillo & A. Eskalen ex Sand.-Denis & Crous) O'Donnell, Geiser, Kasson  
 675 & T. Aoki, Index Fungorum 440: 2. 2020. [IF 557669]  
 676 ≡ *Neocosmospora kuroshio* F. Na, J.D. Carrillo & A. Eskalen ex Sand.-Den. & Crous, Persoonia 41:  
 677 137. 2018. [MB 831184]  
 678 (≡ *Fusarium kuroshium* F. Na, J.D. Carrillo & A. Eskalen, Plant Disease 102: 1159. 2018. Nom. inval.,  
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 680
- 681 *Fusarium kurunegalense* Samuels, Nalim & Geiser, Mycologia 103(6): 1323. 2011. [MB 519848]  
 682 = *Neocosmospora kurunegalensis* Samuels, Nalim & Geiser, Mycologia 103(6): 1324. 2011. [MB  
 683 519847]  
 684
- 685 *Fusarium lichenicola* C. Massal., Annales Mycologici 1(3): 223. 1903. [MB 200576]  
 686 ≡ *Neocosmospora lichenicola* (C. Massal.) Sand.-Den. & Crous, Persoonia 41: 120. 2018. [MB  
 687 822901]  
 688 ≡ *Bactridium lichenicola* (C. Massal.) Wollenw. [as '*lichenicolum*'], Fusaria autographica delineata 1:  
 689 no. 456 (1916). [MB 101879]  
 690 ≡ *Cylindrocarpon lichenicola* (C. Massal.) D. Hawksw., Bull. Br. Mus. Nat. Hist., Bot. 6(3): 273. 1979.  
 691 [MB 312456]  
 692 Note: Also known as FSSC 16.  
 693
- 694 *Fusarium liriodendri* (Sand.-Den. & Crous) O'Donnell, Geiser, Kasson & T. Aoki, Index Fungorum 440: 2.  
 695 2020. [IF 557686]  
 696 ≡ *Neocosmospora liriodendri* Sand.-Den. & Crous, Persoonia 43: 139. 2019. [MB 831185]  
 697 Note: Also known as FSSC 24.  
 698
- 699 *Fusarium macrosporum* (Sand.-Den., Guarnaccia & Polizzi) O'Donnell, Geiser & T. Aoki, Index Fungorum  
 700 440: 2. 2020. [IF 557687]  
 701 ≡ *Neocosmospora macrospora* Sand.-Den., Guarnaccia & Polizzi, Persoonia 40: 21. 2017. [MB  
 702 820253]  
 703
- 704 *Fusarium mahasenii* Samuels, Nalim & Geiser, Mycologia 103(6): 1325. 2011. [MB 519853]  
 705 = *Neocosmospora mahasenii* Samuels, Nalim & Geiser, Mycologia 103(6): 1325. 2011. [MB 519852]  
 706
- 707 *Fusarium martii* Appel & Wollenw., Arbeiten Kaiserl. Biol. Anst. Land- u. Forstw. 8: 83. 1910. [MB  
 708 249096]  
 709 ≡ *Neocosmospora martii* (Appel & Wollenw.) Sand.-Den. & Crous, Persoonia 41: 121. 2018. [MB  
 710 831187]  
 711
- 712 *Fusarium metavorans* Al-Hatmi, S.A. Ahmed & de Hoog, Med. Mycol. 56: S147. 2018. [MB 821742]  
 713 ≡ *Neocosmospora metavorans* (Al-Hatmi, S.A. Ahmed & de Hoog) Sand.-Den. & Crous, Persoonia  
 714 41: 121. 2018. [MB 823687]

715 Note: Also known as FSSC 6.

716

717 *Fusarium mori* (Sand.-Den. & Crous) O'Donnell, Geiser, Kasson & T. Aoki, Index Fungorum 440: 2. 2020.  
718 [IF 557688]

719 ≡ *Neocosmospora mori* Sand.-Den. & Crous, Persoonia 43: 143. 2019. [MB 831188]

720 (= *Fusarium solani* f. *mori* Sawada, Special Publication College of Agriculture, National Taiwan  
721 University 8: 222. 1959. Nom. inval., Art. 39.1 [MB 353476])

722 (= *Hypomyces solani* f. *mori* Y. Sakurai & Matuo, Ann. Phytopathol. Soc. Japan 24: 222. 1959. Nom.  
723 inval., Art. 39.1 [MB 353542])

724 Note: Also known as *Nectria haematococca* Mating Population III (NhMPIII) and FSSC 17.

725

726 *Fusarium neocosmosporiellum* O'Donnell & Geiser, Phytopathology 103(5): 405. 2013. [MB 800615]

727 ≡ *Neocosmospora vasinfecta* E.F. Sm., Bulletin U.S. Dept. Agri. 17: 45. 1899. [MB 241907]

728 (non *Fusarium vasinfectum* G.F. Atk. 1892. [MB 225413])

729 *Typification* (for *N. vasinfecta*): Lectotype: USA: Pl. V, figs 1-2 as collected on 8 Oct. 1895 (Smith,  
730 Bull. U.S. Dept Agric. 17, 1899); Sandoval-Denis et al. 2019)[MBT 387252]; Neotype: USA, SOUTH

731 CAROLINA: Cameron, a dried specimen on cotton (*Gossypium hirsutum*), collected on Oct. 1902,

732 William A. Orton (BPI 630336, Cannon & Hawksworth 1984)[IF 596775]; Epitype: USA, ILLINOIS:

733 southern area, isolated from a cyst of *Heterodera glycines* in a soil sample from soybean field, 6 Apr.

734 1983, Lori M. Carris, CARRIS E-8-8 (BPI 910920, a dried culture of NRRL 22166, Aoki et al. 2020 [IF

735 557666]; Carris and Glawe 1989). Ex-epitype culture NRRL 22166 = ATCC 62199.

736 = *Neocosmospora vasinfecta* E.F. Sm. var. *africana* (Arx) P.F. Cannon & D. Hawksw. Trans. Br. Mycol.

737 Soc. 82(4): 676. 1984. [MB 116939]

738 ≡ *Neocosmospora africana* Arx, Antonie van Leeuwenhoek 21(2): 161. 1955. [MB 301806]

739 Note: Also known as FSSC 8.

740

741 *Fusarium ngaiotongaense* O'Donnell, Geiser, Kasson & T. Aoki, Index Fungorum 440: 3. 2020. [IF 557689]

742 ≡ *Neocosmospora longissima* Sand.-Den. & Crous, Persoonia 43: 141. 2019. [MB 831186] (non

743 *Fusarium longissimum* Sacc. & P. Syd. 1899. [MB 229470])

744 Etymology: *Ngaiotonga* + *-ensis* from the name of its type locality.

745

746 *Fusarium noneumartii* (Sand.-Den. & Crous) O'Donnell, Geiser, Kasson & T. Aoki, Index Fungorum 440: 3.

747 2020. [IF 557690]

748 ≡ *Neocosmospora noneumartii* Sand.-Den. & Crous, Persoonia 43: 145. 2019. [MB 831190]

749 Note: Also known as FSSC 42.

750

751 *Fusarium oblongum* (Sand.-Den. & Crous) O'Donnell, Geiser, Kasson & T. Aoki, Index Fungorum 440: 3.

752 2020. [IF 557691]

753 ≡ *Neocosmospora oblonga* Sand.-Den. & Crous, Persoonia 43: 148. 2019. [MB 831191]

754 Note: Also known as FSSC 29.

755

756 *Fusarium oligoseptatum* T. Aoki, M.T. Kasson, S. Freeman, D.M. Geiser & K. O'Donnell, Fungal

757 Systematics and Evolution 1: 29. 2018. [MB 822305]

758 ≡ *Neocosmospora oligoseptata* (T. Aoki et al.) Sand.-Den. & Crous, Persoonia 43: 149. 2019. [MB

759 831192]

760

- 761 *Fusarium ornamentatum* (M.A.F. Barbosa) O'Donnell, Geiser & T. Aoki, Index Fungorum 440: 3. 2020. [IF  
762 557692]  
763 ≡ *Neocosmospora ornamentata* M.A.F. Barbosa, Garcia de Orta, Revista da Junta de Investigações  
764 do Ultramar (Ministério de Ultramar, Lisboa), Série de Estudos Agrónomicos 13(1): 17. 1965. [MB  
765 335130]
- 766  
767 *Fusarium paraeumartii* (Sand.-Den. & Crous) O'Donnell, Geiser, Kasson & T. Aoki, Index Fungorum 440:  
768 3. 2020. [IF 557693]  
769 ≡ *Neocosmospora paraeumartii* Sand.-Den. & Crous, Persoonia 43: 149. 2019. [MB 831193]  
770
- 771 *Fusarium parceramosum* (Sand.-Den. & Crous) O'Donnell, Geiser, Kasson & T. Aoki, Index Fungorum 440:  
772 3. 2020. [IF 557694] ≡ *Neocosmospora parceramosa* Sand.-Den. & Crous, Persoonia 43: 151. 2019.  
773 [MB 831194]  
774 Note: Also known as FSSC 18.  
775
- 776 *Fusarium perseae* (Sand.-Den. & Guarnaccia) O'Donnell, Geiser & T. Aoki, Index Fungorum 440: 3. 2020.  
777 [IF 557695]  
778 ≡ *Neocosmospora perseae* Sand.-Den. & Guarnaccia, Fungal Syst. Evol. 1: 136. 2018. [MB 824587]  
779
- 780 *Fusarium petroliphilum* (Q.T. Chen & X.H. Fu) Geiser, O'Donnell, D.P.G. Short & N. Zhang, Fungal Genet.  
781 Biol. 53: 70. 2013. [MB 802539]  
782 ≡ *Fusarium solani* var. *petroliphilum* Q.T. Chen & X.H. Fu, Acta Mycol. Sinica, Suppl.: 330. 1987. [MB  
783 127720]  
784 ≡ *Neocosmospora petroliphila* (Q.T. Chen & X.H. Fu) Sand.-Den. & Crous, Persoonia 41: 121. 2018.  
785 [MB 822902]  
786 Note: Also known as *Nectria haematococca* Mating Population V (NhMPV) and FSSC 1  
787
- 788 *Fusarium phaseoli* (Burkh.) T. Aoki & O'Donnell, Mycologia 95(4): 671. 2003. [MB 488914]  
789 ≡ *Fusarium martii* f. *phaseoli* Burkh., Mem. Cornell U. Agr. Exp. Station 26: 1007. 1919. [MB  
790 489076]  
791 ≡ *Neocosmospora phaseoli* (Burkh.) L. Lombard & Crous, Stud. Mycol. 80: 227. 2015. [MB 810962]  
792
- 793 Also, we recognize the following valid existing species as distinct from *F. phaseoli*:  
794 *Fusarium tucumaniae* T. Aoki, O'Donnell, Yosh. Homma & Lattanzi, Mycologia 95(4): 664. 2003. [MB  
795 489463]  
796 ≡ *Neocosmospora tucumaniae* (T. Aoki et al.) L. Lombard & Crous, Stud. Mycol. 80: 228. 2015. [MB  
797 810966]  
798 *Fusarium virguliforme* O'Donnell & T. Aoki, Mycologia 95: 667. 2003. [MB 489315]  
799 ≡ *Neocosmospora virguliformis* (O'Donnell & T. Aoki) L. Lombard & Crous, Stud. Mycol. 80: 228.  
800 2015. [MB 810967]  
801 *Fusarium brasiliense* T. Aoki & O'Donnell, Mycoscience 46: 166. 2005. [MB 338753]  
802 *Fusarium cuneirostrum* O'Donnell & T. Aoki, Mycoscience 46: 170. 2005. [MB 341392]  
803 *Fusarium crassistipitatum* Scandiani et al., Mycoscience 53: 171. 2011. [MB 561257]  
804 *Fusarium azukicola* T. Aoki et al., Mycologia 104: 1075. 2012. [MB 563147]  
805
- 806 *Fusarium piperis* (F.C. Albuquerque) O'Donnell, Geiser, Kasson & T. Aoki, Index Fungorum 440: 3. 2020. [IF  
807 557696]

- 808       ≡ *Neocosmospora piperis* (F.C. Albuquerque) Sand.-Den. & Crous, *Persoonia* 43: 152. 2019. [MB 831195]  
 809       ≡ *Fusarium solani* f. *piperis* F.C. Albuquerque, *Circular do Instituto Agronómico do Norte* 5: 19. 1961. [MB  
 810       349447]  
 811       Note: Also known as FSSC 31.  
 812  
 813       *Fusarium plagianthi* (Dingley) O'Donnell & Geiser, *Phytopathology* 103(5): 404. 2013. [MB 800613]  
 814       ≡ *Nectria plagianthi* Dingley, *Trans. Proc. Royal Soc. New Zealand* 79: 196. 1951. [MB 301780]  
 815       ≡ *Neocosmospora plagianthi* (Dingley) L. Lombard & Crous, *Stud. Mycol.* 80: 227. 2015. [MB  
 816       810963]  
 817  
 818       *Fusarium protoensiforme* (Sand.-Den. & Crous) O'Donnell, Geiser, Kasson & T. Aoki, *Index Fungorum*  
 819       440: 3. 2020. [IF 557697]  
 820       ≡ *Neocosmospora protoensiformis* Sand.-Den. & Crous, *Persoonia* 43: 156. 2019. [MB 831197]  
 821       Note: Also known as FSSC 32.  
 822  
 823       *Fusarium pseudensiforme* Samuels, Nalim & Geiser, *Mycologia* 103(6): 1323. 2011. [MB 519839]  
 824       = *Neocosmospora pseudensiformis* Samuels, Nalim & Geiser, *Mycologia* 103(6): 1323. 2011. [MB  
 825       519838]  
 826       Note: Also known as FSSC 33.  
 827  
 828       *Fusarium pseudoradicicola* (Sand.-Den. & Crous) O'Donnell, Geiser, Kasson & T. Aoki, *Index Fungorum*  
 829       440: 3. 2020. [IF 557698]  
 830       ≡ *Neocosmospora pseudoradicicola* Sand.-Den. & Crous, *Persoonia* 43: 157. 2019. [MB 831198]  
 831       Note: Also known as FSSC 37.  
 832  
 833       *Fusarium pseudotonkinense* (Sand.-Den. & Crous) O'Donnell, Geiser, Kasson & T. Aoki, *Index Fungorum*  
 834       440: 3. 2020. [IF 557699]  
 835       ≡ *Neocosmospora pseudotonkinensis* Sand.-Den. & Crous, *Persoonia* 43: 159. 2019. [MB 831199]  
 836  
 837       *Fusarium quercinum* O'Donnell, Geiser, Kasson & T. Aoki, *Index Fungorum* 440: 4. 2020. [IF 557700]  
 838       ≡ *Neocosmospora quercicola* Sand.-Den. & Crous, *Persoonia* 43: 159. 2019. [MB 831200]  
 839       (non *Fusarium quercicola* Oudem. 1902 [MB 204737])  
 840       Etymology: *quercinus* (of oak), from the name of the original host plant, *Quercus cerris*.  
 841       Note: Also known as FSSC 14.  
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 952 Note: Also known as *Nectria haematococca* Mating Population VI (NhMPVI) and FSSC 11.  
 953 Etymology: In honor of the late Hans D. Van Etten, whose laboratory conducted extensive studies on this  
 954 species, making the first connection between plant pathogenicity and the fungal accessory genome.  
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 956 *Fusarium venezuelense* O'Donnell, Geiser, Kasson & T. Aoki, *Index Fungorum* 440: 5. 2020. [IF 557713]  
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 959 Etymology: *Venezuela* + *-ensis* from the name of its type locality.  
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 961 *Fusarium walteggamsii* O'Donnell, Geiser & T. Aoki, *Index Fungorum* 440: 5. 2020. [IF 557714]  
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 964 Etymology: In honor of the late Dr. Walter Gams.  
 965 Note: Also known as FSSC 7.  
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 977 Nom. inval., Art. 39.1 [MB 350974])  
 978 Note: Also known as *Nectria haematococca* Mating Population IV (NhMPIV) and FSSC 22.  
 979 Etymology: in honor of the late Dr. Wataro Yamamoto who originally found *Nectria elegans* and studied  
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1315 **Figure 1.** Partitioned maximum likelihood bootstrapped (ML-BS) phylogram of *Fusarium*, based on full-  
 1316 length exonic nucleotide (nt) sequences of 19 protein-coding genes (Table 1), inferred using IQ-TREE  
 1317 (Nguyen et al. 2015). Nodes supported by 100% ML bootstrap (5000 replicates; BS) and 1.0 Bayesian  
 1318 posterior probability (BPP), including F1 and F2, are indicated with asterisks; ML-BS/BPP values are  
 1319 shown for nodes receiving less than 100%/1.0 support. Two branches highlighted in magenta received  
 1320 BS <70 and BPP < 0.99. Two shades of blue highlight 23 species complexes within *Fusarium*. Numerals  
 1321 situated adjacent to nodes represent gene concordance factors (gCFs) calculated by IQ-TREE 2 for that  
 1322 node, expressed as the number of loci that resolve it out of 19. PIC = parsimony informative characters;  
 1323 TC = Tree credibility.

1324  
 1325 **Figure 2.** Partitioned maximum likelihood bootstrapped (ML-BS) cladogram of the *F. solani* Species  
 1326 Complex (FSSC) based on *tef1*, *rpb2* and rDNA, inferred using IQ-TREE (Nguyen et al. 2015). Clades 1, 2  
 1327 and 3 represent designations proposed in O'Donnell (2000). Numerical designations corresponding to an  
 1328 informal ad hoc nomenclature for phylogenetic species in the FSSC (e.g., FSSC 1) are provided in  
 1329 brackets. The Ambrosia *Fusarium* Clade (Kasson et al. 2013), the clade that encompasses species with  
 1330 typical *Neocosmospora* morphology, and the clade consisting of soybean sudden death syndrome (SDS)  
 1331 and bean root rot (BRR) pathogens, are indicated. ML-BS values, based on 5000 replicates, are shown for  
 1332 each node. + = medically important species, bp, base pairs; PIC = parsimony informative characters; ET =  
 1333 epitype isolate; IT = isotype isolate; T = type isolate. \*the type of *N. striata*, combined under *F.*  
 1334 *bataticola*. †the type of *N. boninensis*, combined under *F. tenuicristatum* (see Appendix A).

1335  
 1336 **Supplemental Figure 1.** Cladogram of *Fusarium* 19-locus dataset based on Bayesian inference. Numbers  
 1337 below nodes indicate Bayesian posterior probability on a 0-100 scale.

1338  
 1339 **Supplemental Figure 2.** Individual maximum likelihood bootstrap phylograms of 19 individual gene trees.  
 1340 Locus names and molecular evolutionary models used in IQ-TREE are as listed in Table 1. Numbers  
 1341 above or adjacent to nodes indicate bootstrap values (5000 replicates).

1342  
 1343 **Supplemental Figure 3.** Cladogram of *Fusarium* inferred using IQ-TREE, with Internode Credibility (IC)  
 1344 and Internode Credibility-All (ICA) values presented below nodes.

1345

**Table 1.** Phylogenetic data summary of 19 genes analyzed in the present study.

Locus	Protein encoded	Identifier <sup>1</sup>	Chr <sup>2</sup>	nt sites	AA <sup>3</sup>	PIC <sup>4</sup>	PIC/ site	% total PICs	Model <sup>5</sup>
<i>acl1</i>	ATP citrate lyase large subunit	FFUJ_13230	4	1473	490	505	0.34	2.13%	TN+F+I+G4
<i>act1*</i>	Actin	FFUJ_00687	1	1425	474	641	0.45	2.71%	TIM2+F+I+G4
<i>cal1*</i>	Calmodulin	FFUJ_12207	8	450	149	117	0.26	0.49%	TNe+I+G4
<i>cpr1</i>	Cytochrome P450 reductase	FFUJ_04716	2	2085	694	949	0.46	4.01%	TIM2+F+I+G4
<i>dpa1</i>	DNA polymerase alpha subunit	FFUJ_08551	7	4491	1498	2233	0.50	9.43%	GTR+F+I+G4
<i>dpe*1</i>	DNA polymerase epsilon subunit	FFUJ_13258	4	6699	2232	3005	0.45	12.70%	GTR+F+I+G4
<i>fas1</i>	Fatty acid synthase alpha subunit	FFUJ_04562	2	5622	1880	2191	0.39	9.26%	TIM2+F+I+G4
<i>fas2</i>	Fatty acid synthase beta subunit	FFUJ_04563	2	6330	2109	2608	0.41	11.02%	TN+F+I+G4
<i>ku70*</i>	ATP-dependent DNA helicase II	FFUJ_04557	2	1959	652	1020	0.52	4.31%	SYM+I+G4
<i>lcb2</i>	Sphinganine palmitoyl transferase subunit	FFUJ_09546	9	2121	706	910	0.42	3.84%	TIM2+F+I+G4
<i>mcm7</i>	DNA replication licensing factor	FFUJ_02741	3	2526	841	1211	0.48	5.12%	GTR+F+I+G4
<i>pgk1*</i>	Phosphoglycerate kinase	FFUJ_09403	9	1257	418	447	0.36	1.89%	TIM2+F+I+G4
<i>rpb1</i>	RNA polymerase largest subunit	FFUJ_00736	1	5382	1793	2348	0.44	9.92%	TIM2+F+I+G4
<i>rpb2</i>	RNA polymerase 2nd largest subunit	FFUJ_07996	5	3882	1293	1667	0.43	7.04%	TIM2e+F+I+G4
<i>tef1*</i>	Translation elongation factor 1-alpha	FFUJ_05795	6	1383	460	299	0.22	1.26%	GTR+F+I+G4
<i>top1</i>	Topoisomerase	FFUJ_02999	3	2859	952	1505	0.53	6.36%	TIM2+F+I+G4
<i>tsr1</i>	Ribosomal biogenesis protein	FFUJ_09872	9	2493	830	1261	0.51	5.33%	GTR+F+I+G4
<i>tub1</i>	Tubulin alpha subunit	FFUJ_00614	1	1350	449	383	0.28	1.62%	TIM+F+I+G4
<i>tub2*</i>	Tubulin beta subunit	FFUJ_04397	2	1353	450	368	0.27	1.55%	TN+F+I+G4
<b>TOTAL:</b>				55140	18370	23668		100.00%	

\*Individual gene tree does not resolve F1

<sup>1</sup>Gene identifier in the *Fusarium fujikuroi* genome (Wiemann et al. 2013)

<sup>2</sup>Chromosomal location as mapped to the *Fusarium fujikuroi* genome (Wiemann et al. 2013)

<sup>3</sup>Amino acid count, which does not account for in-frame insertions/deletions

<sup>4</sup>Parsimony-informative characters in the nucleotide alignment

<sup>5</sup>Best evolutionary model as determined by Bayesian Information Criterion estimated in IQ-Tree

**Supplemental Table 1.** GenBank accessions for genome sequences.

<b>Species</b>	<b>Isolate</b>	<b>GenBank Accession</b>
<i>F. albidum</i>	NRRL 22152	JABFEP000000000
<i>F. albosuccineum</i>	NRRL 20459	JAADYS000000000
<i>F. ambrosium</i>	NRRL 62606	NKCL00000000*
<i>F. anguioides</i>	NRRL 25385	JAALXK000000000**
<i>F. armeniacum</i>	NRRL 6227	JABFEC000000000
<i>F. asiaticum</i>	NRRL 26156	JABFEQ000000000
<i>F. avenaceum</i>	NRRL 54939 = Fa05001	JPYM00000000*
<i>F. aywerte</i>	NRRL 25410	JABCQV000000000**
<i>F. babinda</i>	NRRL 25539	JABCKA000000000
<i>F. buharicum</i>	NRRL 13371	JAATHB000000000
<i>F. beomiforme</i>	NRRL 25174	PVQB00000000*
<i>F. buxicola</i>	NRRL 36148	JAAVUK000000000
<i>F. chlamydosporum</i>	NRRL 13444	JAAVUD000000000
<i>F. circinatum</i>	NRRL 25331	JAAQPE000000000
<i>F. commune</i>	NRRL 28387	JABFES000000000
<i>F. compactum</i>	NRRL 13829	JABFET000000000
<i>F. concolor</i>	NRRL 13459	JABCJY000000000**
<i>F. continuum</i>	NRRL 66286	JABCKB000000000**
<i>F. culmorum</i>	NRRL 25475	JABFEU000000000
<i>F. cyanostoma</i>	NRRL 53998	JABCKW000000000
<i>F. decemcellulare</i>	NRRL 13412	JAAGWO000000000**
<i>F. dimerum</i>	NRRL 20691	JABGLY000000000
<i>F. domesticum</i>	NRRL 29976	JABFEV000000000
<i>F. equiseti</i>	NRRL 66338	QGEB00000000*
<i>F. falciforme</i>	NRRL 43529	JABEEK000000000**
<i>F. foetens</i>	NRRL 38302	JABFMM000000000
<i>F. fujikuroi</i>	NRRL 5538 = IMI 58289	GCF_900079805.1*
<i>F. gaditjirrii</i>	NRRL 45417	JABFAI000000000**
<i>F. graminearum</i>	NRRL 31084 = PH-1	GCA_900044135.1*
<i>F. graminum</i>	NRRL 20692	JAAGWP000000000**
<i>F. guttiforme</i>	NRRL 22945	JAAQRL000000000
<i>F. hainanense</i>	NRRL 66475	JABFEW000000000
<i>F. heterosporum</i>	NRRL 20693	JAAGWQ000000000**
<i>F. hostae</i>	NRRL 29888	JABCJX000000000**
<i>F. illudens</i>	NRRL 22090	JABFEX000000000
<i>F. irregulare</i>	NRRL 31160	QGEA00000000*
<i>F. langsethiae</i>	NRRL 53436 = FI201059	JXCE00000000.1*
<i>F. lateritium</i>	NRRL 13362	JAAVTZ000000000
<i>F. longipes – 4***</i>	NRRL 13317	JABFEY000000000
<i>F. longipes – 1***</i>	NRRL 13368	JABFEZ000000000



<i>F. lyarnte</i>	NRRL 54252	JAAVUB000000000
<i>F. mangiferae</i>	NRRL25226	FCQH00000000*
<i>F. miscanthi</i>	NRRL 26231	JAAVUA000000000
<i>F. nelsonii</i>	NRRL 13338	JAAVUC000000000
<i>F. nematophilum</i>	NRRL 54600	JABFFA000000000
<i>F. neocosmosporiellum</i>	NRRL 22166	SSHR00000000*
<i>F. newnesense</i>	NRRL 66241	JABCJW000000000**
<i>F. nisikadoi</i>	NRRL 25179	JABFFB000000000
<i>F. nurragi</i>	NRRL 36452	JAALXI000000000**
<i>F. oxysporum</i>	NRRL 32931	AFML00000000*
<i>F. oxysporum</i>	NRRL 34936 = Fo4827	AAXH00000000*
<i>F. penzigii</i>	NRRL 20711	JABFFC000000000
<i>F. poae</i>	NRRL 26941	JABFFD000000000
<i>F. praegraminearum</i>	NRRL 39664	LXHY00000000*
<i>F. pseudograminearum</i>	NRRL 28062	GCA_000974265.2*
<i>F. redolens</i>	NRRL 22901	JAAVUJ000000000
<i>F. rusci</i>	NRRL 22134	JADBHU000000000
<i>F. sacchari</i>	NRRL 66326	JABSTH000000000** †
<i>F. sambucinum</i>	NRRL 13708	JAAVUG000000000
<i>F. sarcochromum</i>	NRRL 20472	JABEXW000000000**
<i>F. scirpi</i>	NRRL 66328	QHHJ00000000*
<i>F. setosum</i>	NRRL 36526	JABFFE000000000
<i>F. sporotrichioides</i>	NRRL 3299	PXOF00000000*
<i>F. staphyleae</i>	NRRL 22316	JADDON000000000
<i>F. stilboides</i>	NRRL 20429	JAASAY000000000
<i>F. subglutinans</i>	NRRL 66333	JAAOAV000000000** †
<i>F. sublunatum</i>	NRRL 13384	JABFFF000000000
<i>F. thapsinum</i>	NRRL 22049	JAAOAX000000000** †
<i>F. torreyae</i>	NRRL 54149	JABEET000000000
<i>F. torulosum</i>	NRRL 22747	JABFMN000000000
<i>F. transvaalense</i>	NRRL 31008	JABFFG000000000
<i>F. tricinctum</i>	NRRL 25481	JAALXJ000000000**
<i>F. vanettenii</i>	NRRL 45880 = 77-13-4	ACJF00000000*
<i>F. venenatum</i>	NRRL 66329	JABFFH000000000
<i>F. ventricosum</i>	NRRL 25729	JABFFI000000000
<i>F. verrucosum</i>	NRRL 22566	JABFFJ000000000
<i>F. verticillioides</i>	NRRL 20956 = FGSC 7600	AAIM00000000*
<i>F. virguliforme</i>	NRRL 31041	JABEEP000000000**
<i>F. xylarioides</i>	NRRL 25486	JABFFK000000000
<i>F. zanthoxyli</i>	NRRL 66285	JABFFL000000000
<i>F. zealandicum</i>	NRRL 22465	JABEYC000000000**
<i>Fusarium</i> sp.	NRRL 25184	JABSSZ000000000
<i>Fusarium</i> sp.	NRRL 52700	JAAQPE000000000** †

<i>Fusarium</i> sp. [AF-6]	NRRL 62590	NKCJ00000000*
<i>Beauveria bassiana</i>	ARSEF 2860	GCA_000280675.1*
<i>Neonectria ditissima</i>	NRRL 20485	JABSTC000000000
<i>Neonectria</i> sp.	NRRL 22505	JABSTB000000000
<i>Neonectria coccinea</i>	NRRL 20487	JABSTD000000000
<i>Trichoderma brevicompactum</i>	IBT 40841	PXNZ00000000.1*

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<sup>1</sup> NRRL = USDA/ARS/NCAUR culture collection; IMI = CABI culture collection; FGSC = Fungal Genetics Stock Center; ARSEF = ARS Collection of Entomopathogenic Fungal Cultures; IBT = IBT Culture Collection of Fungi at Danish Technical University. All other strain numbers refer to published non-accession designations.

\* Genome sequence data previously reported and deposited in GenBank from other studies

\*\* Genome sequence data produced at USDA-ARS-NCAUR and reported in Kim et al. (2020)

\*\*\* Representing undescribed species 1 and 4 within the morphospecies *F. longipes*

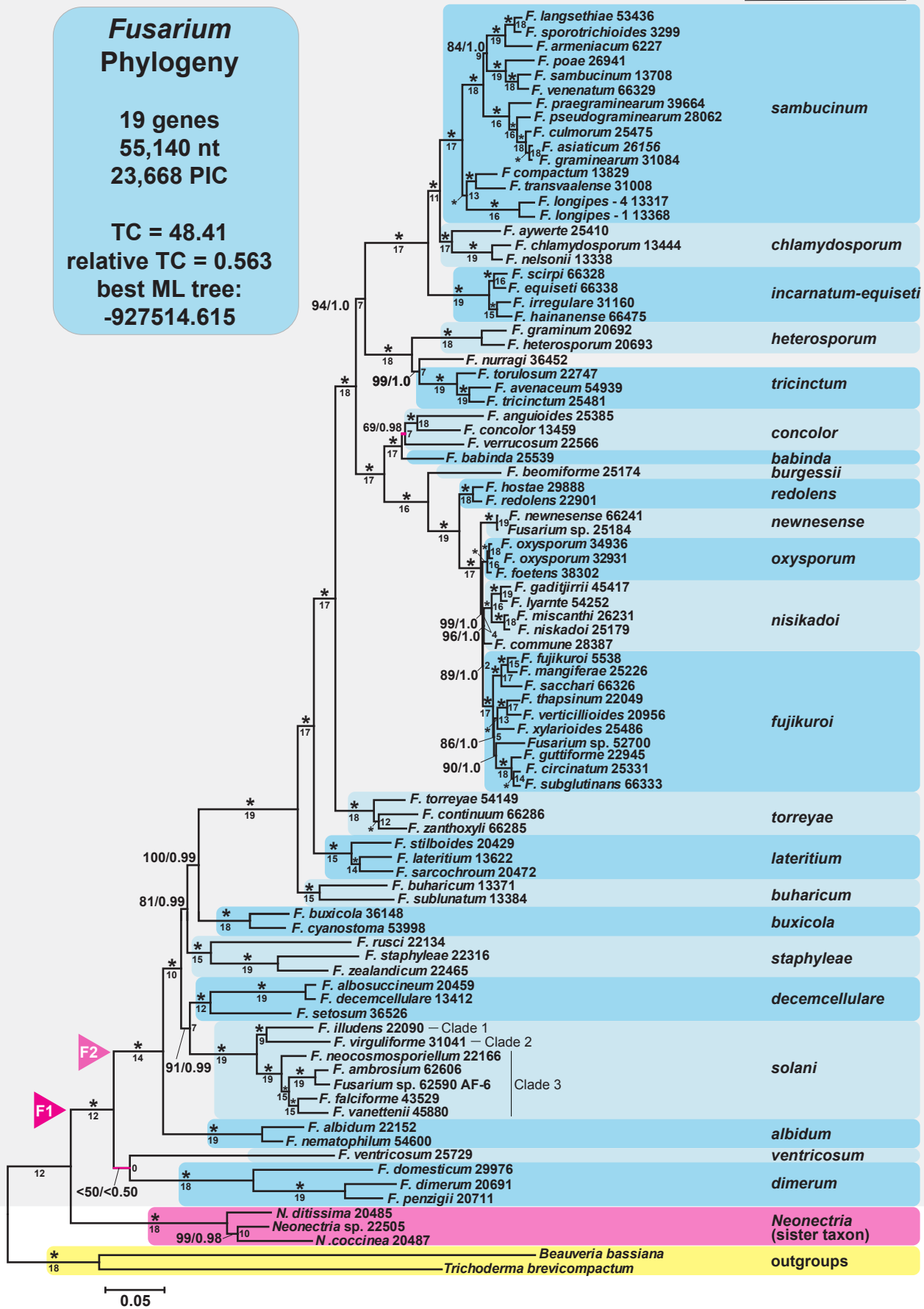
† Sequence data generated at the Beijing Genome Institute-Hong Kong for USDA-ARS-NCAUR and reported in Kim et al. (2020)

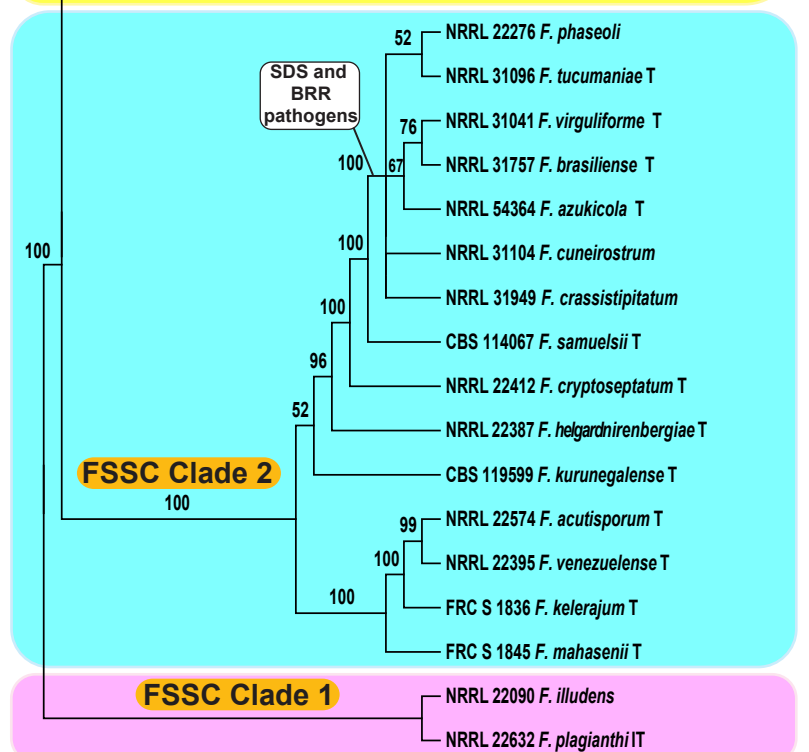
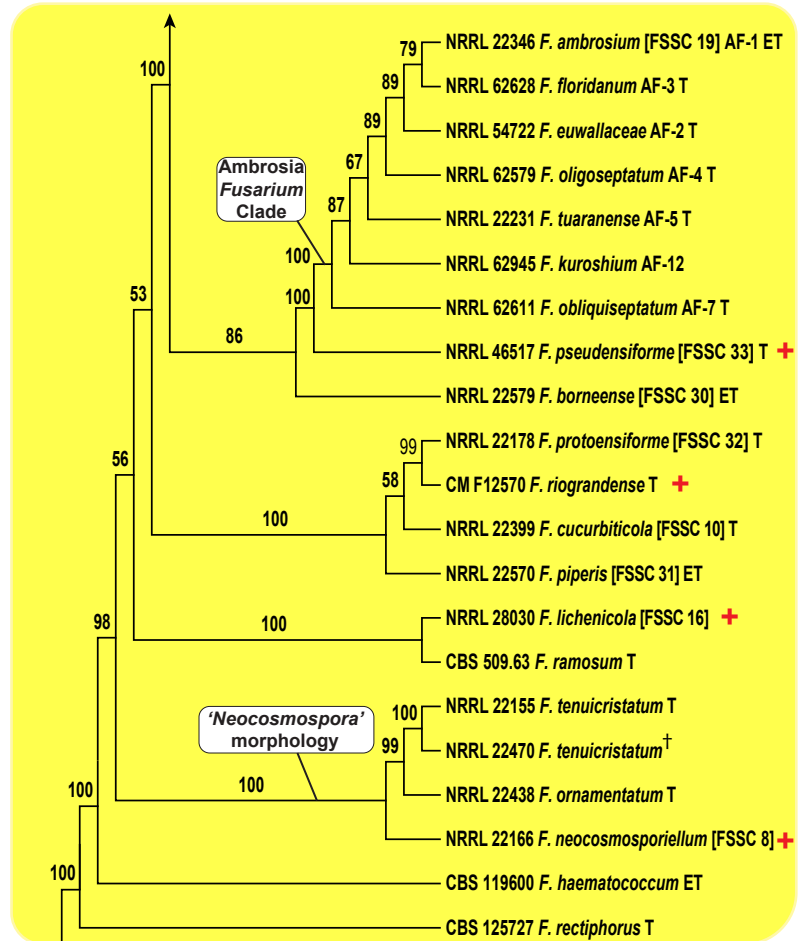
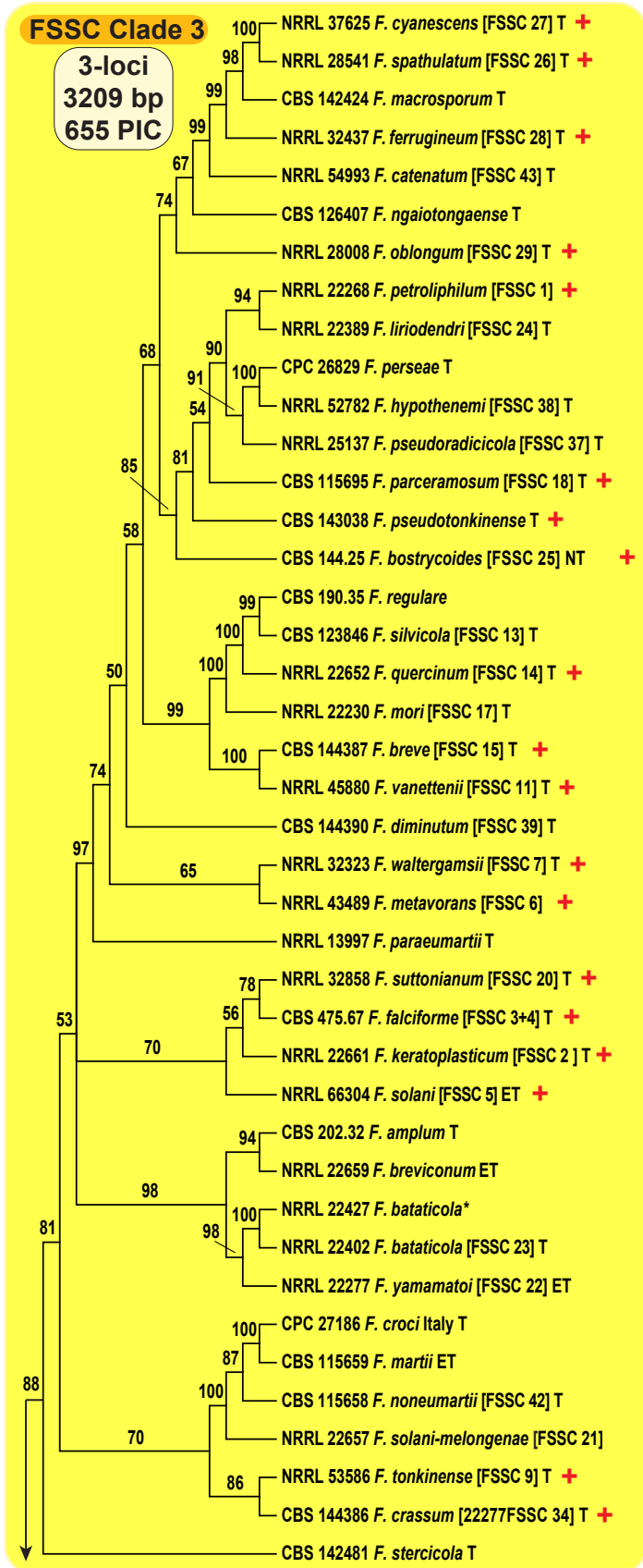
# Fusarium Phylogeny

19 genes  
55,140 nt  
23,668 PIC

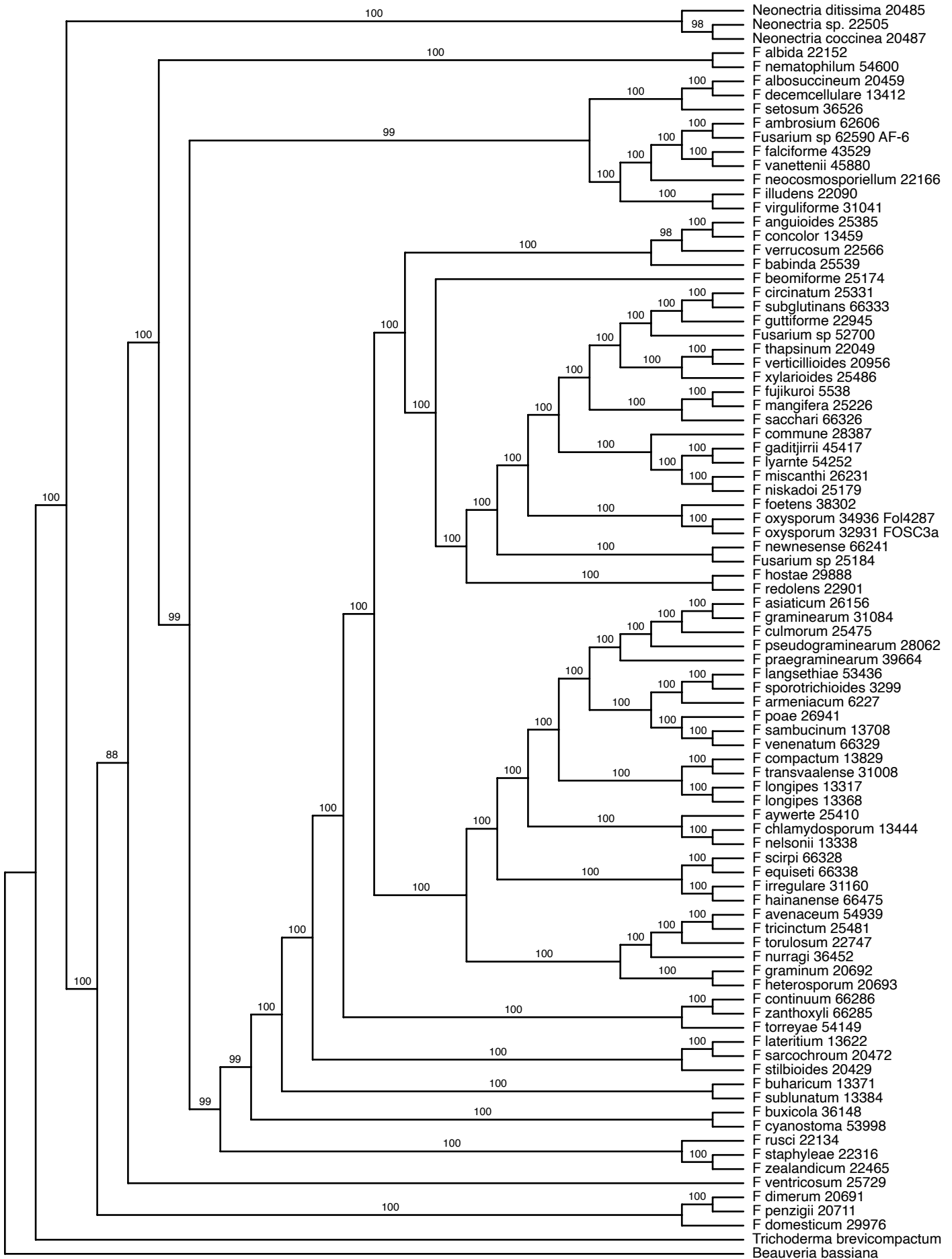
TC = 48.41  
relative TC = 0.563  
best ML tree:  
-927514.615

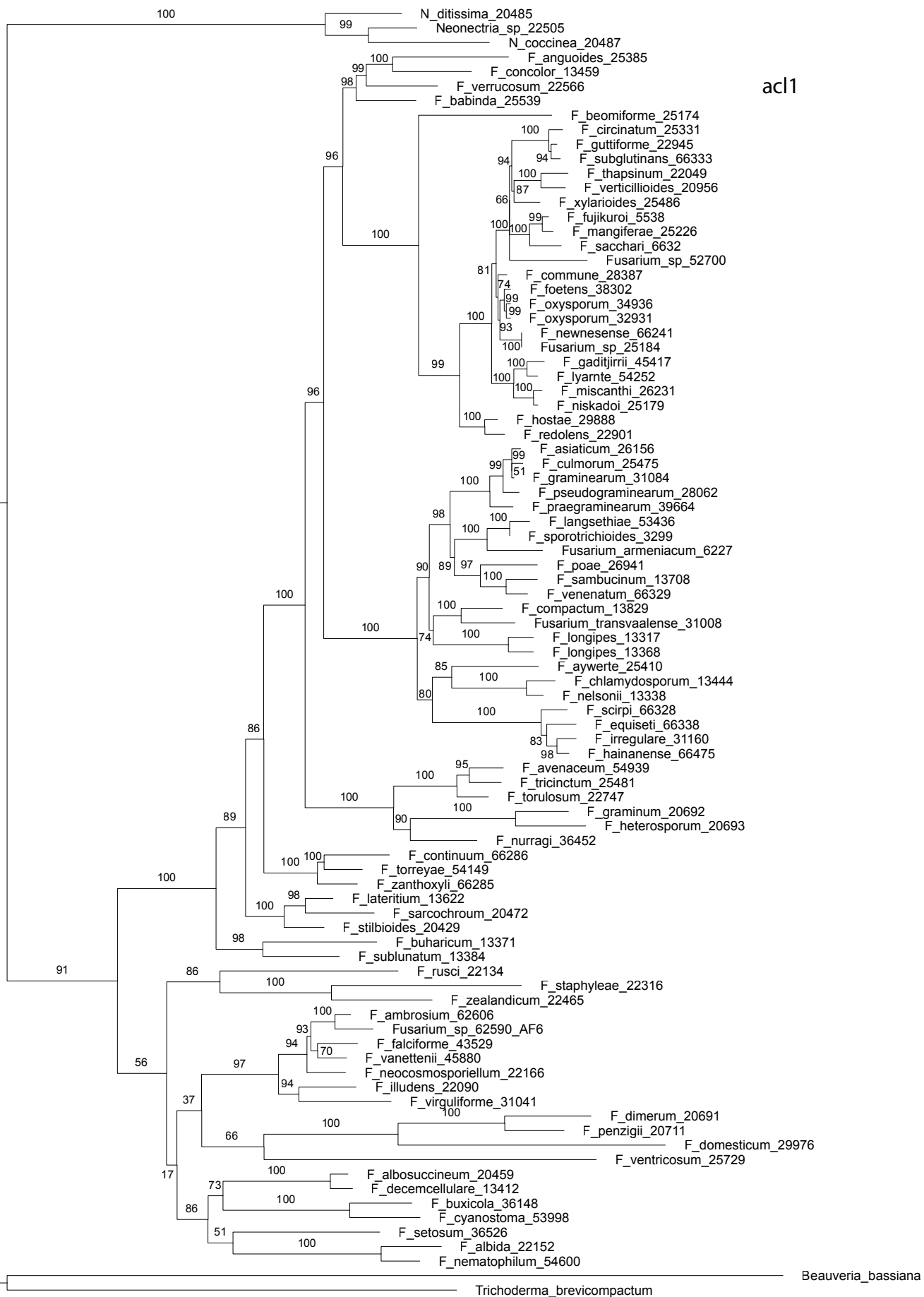
## Species Complex





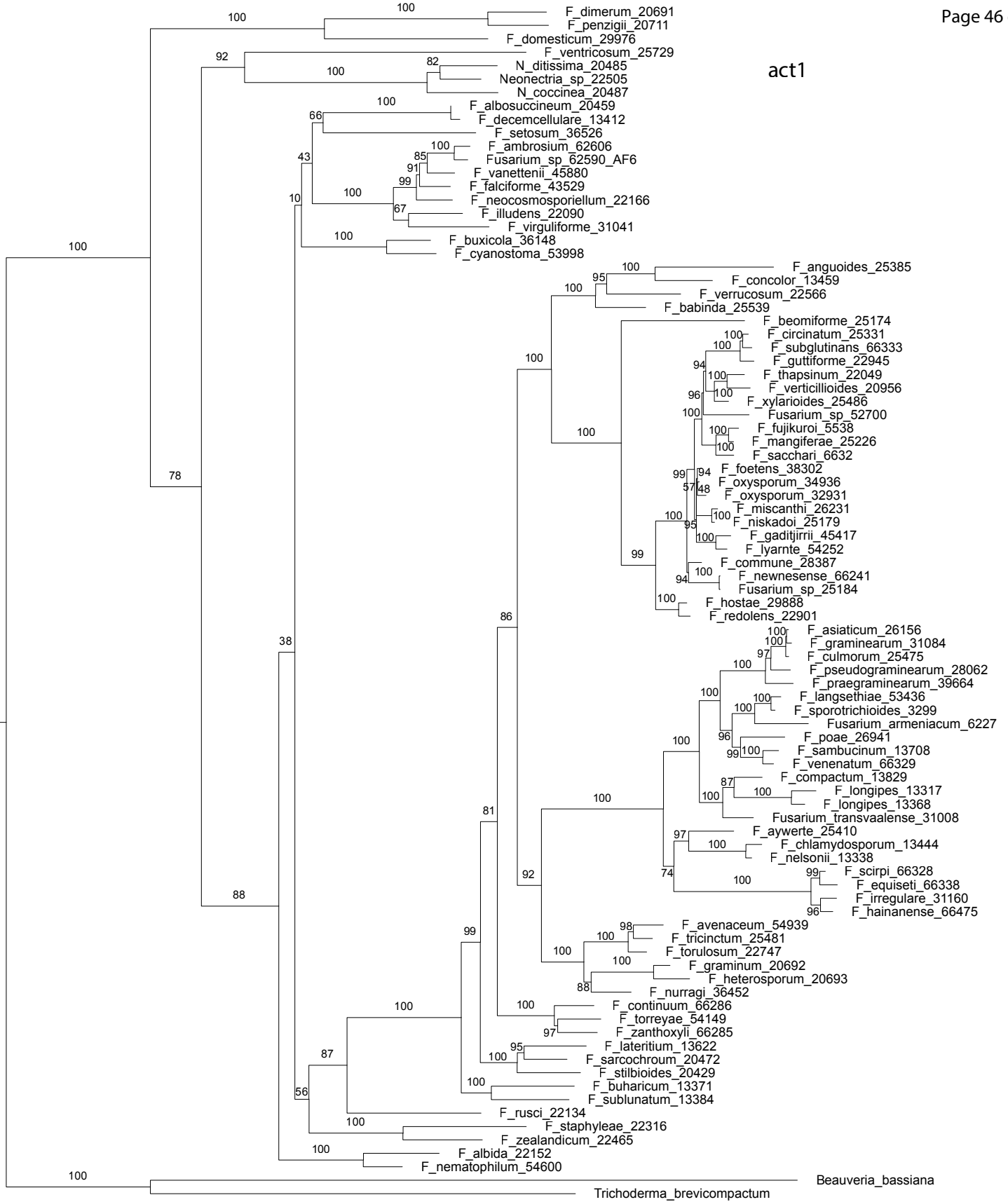
## MrBayes Consensus Cladogram



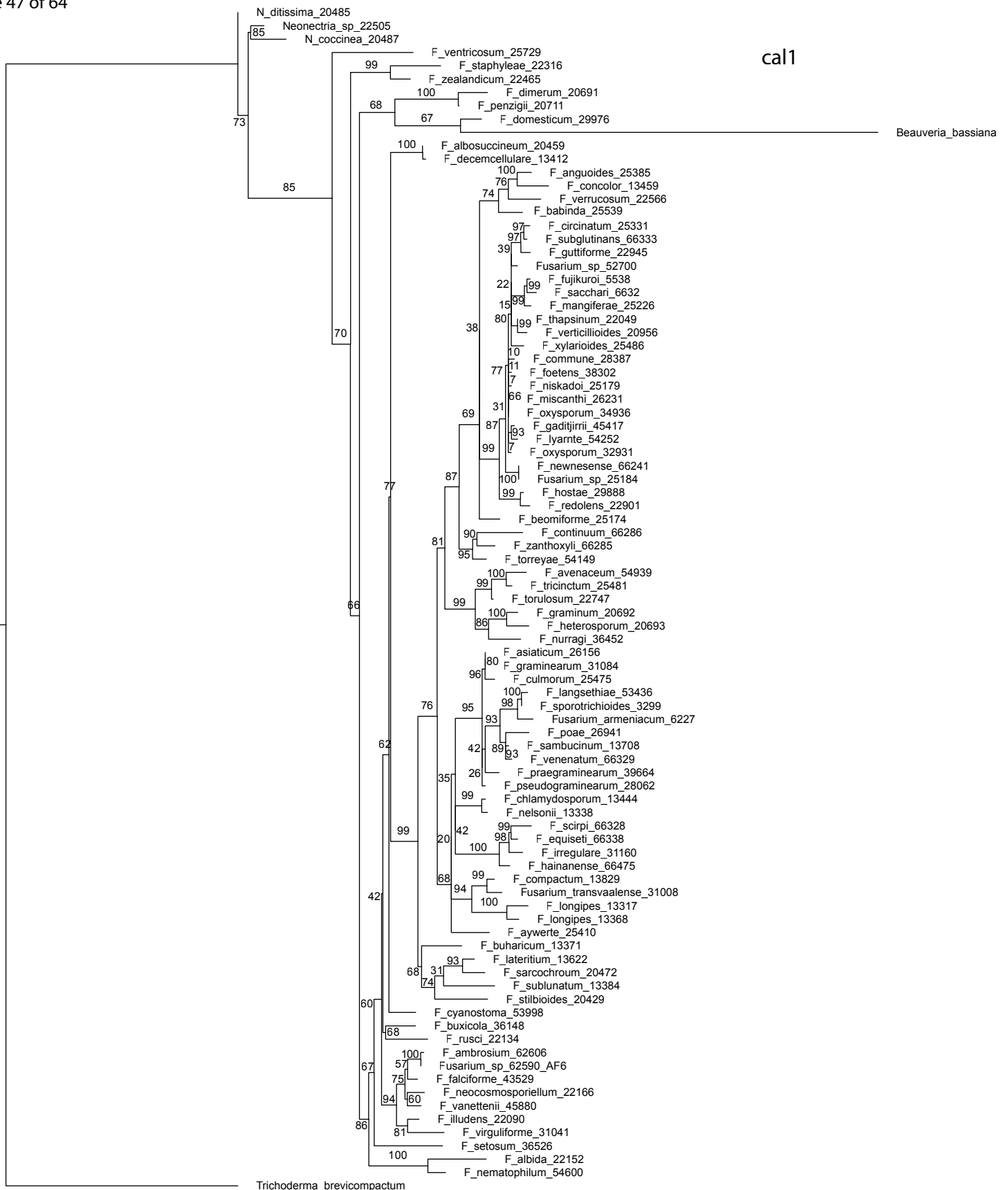


ac1

0.04

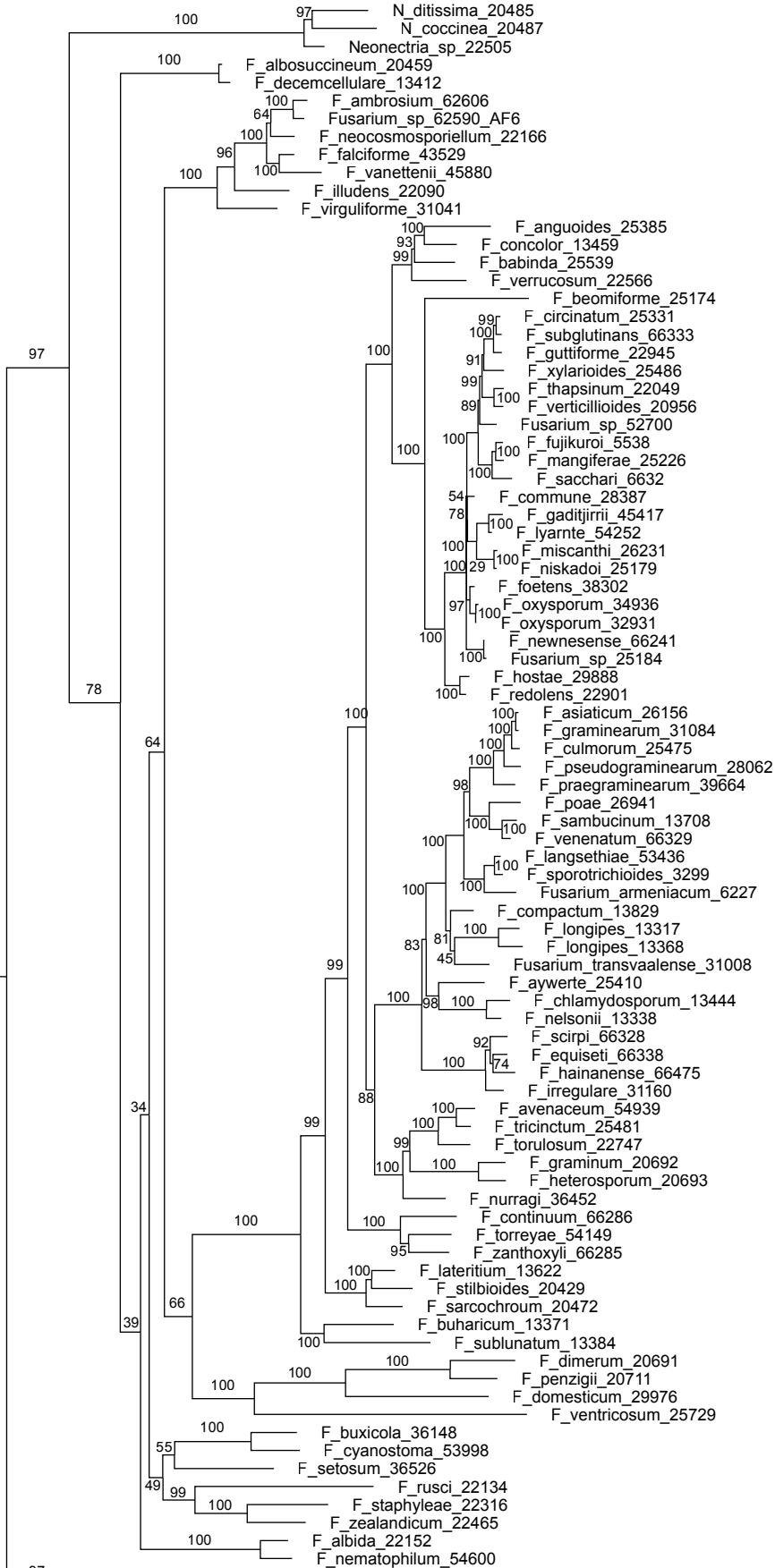


0.09





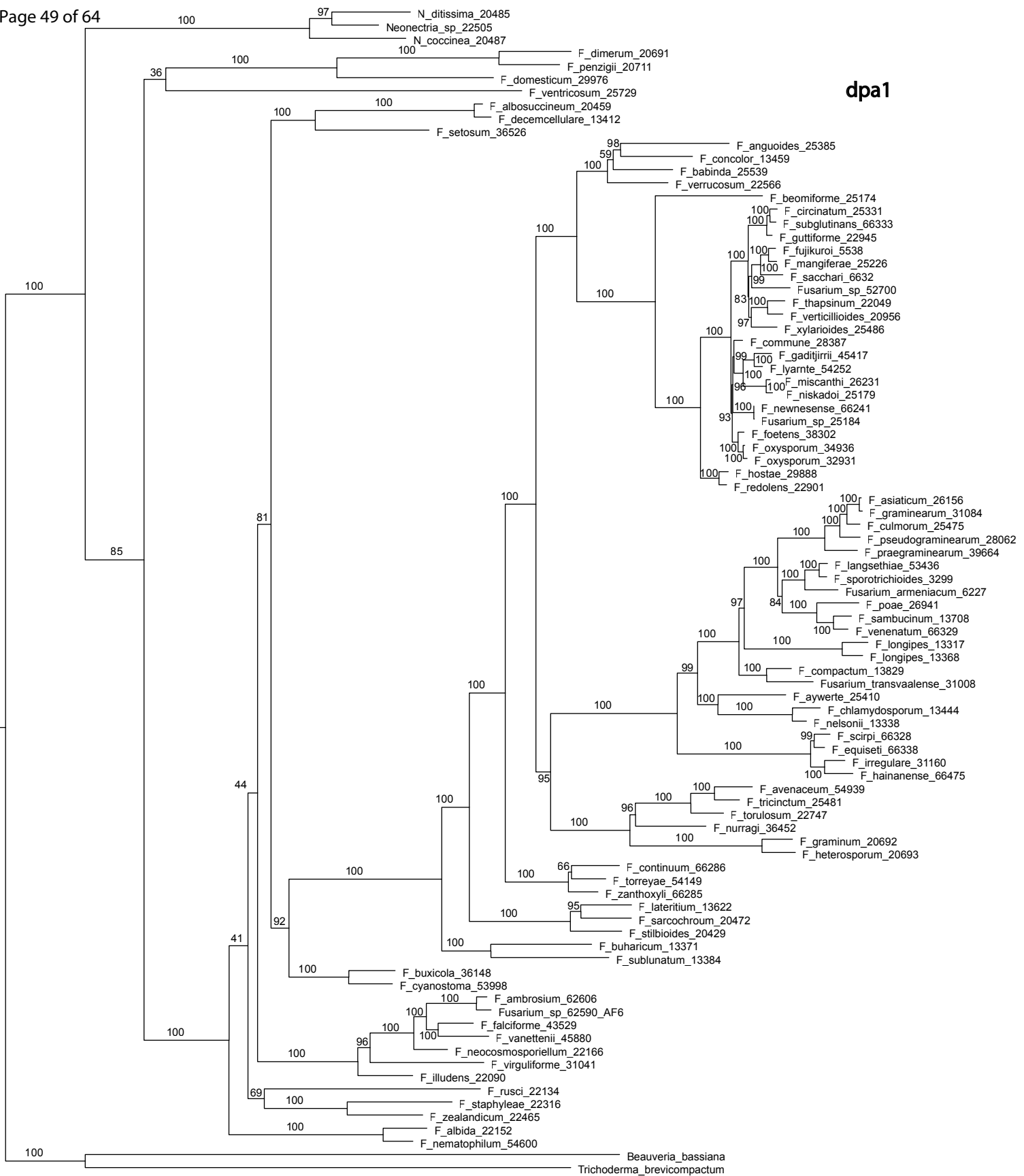
cpr1



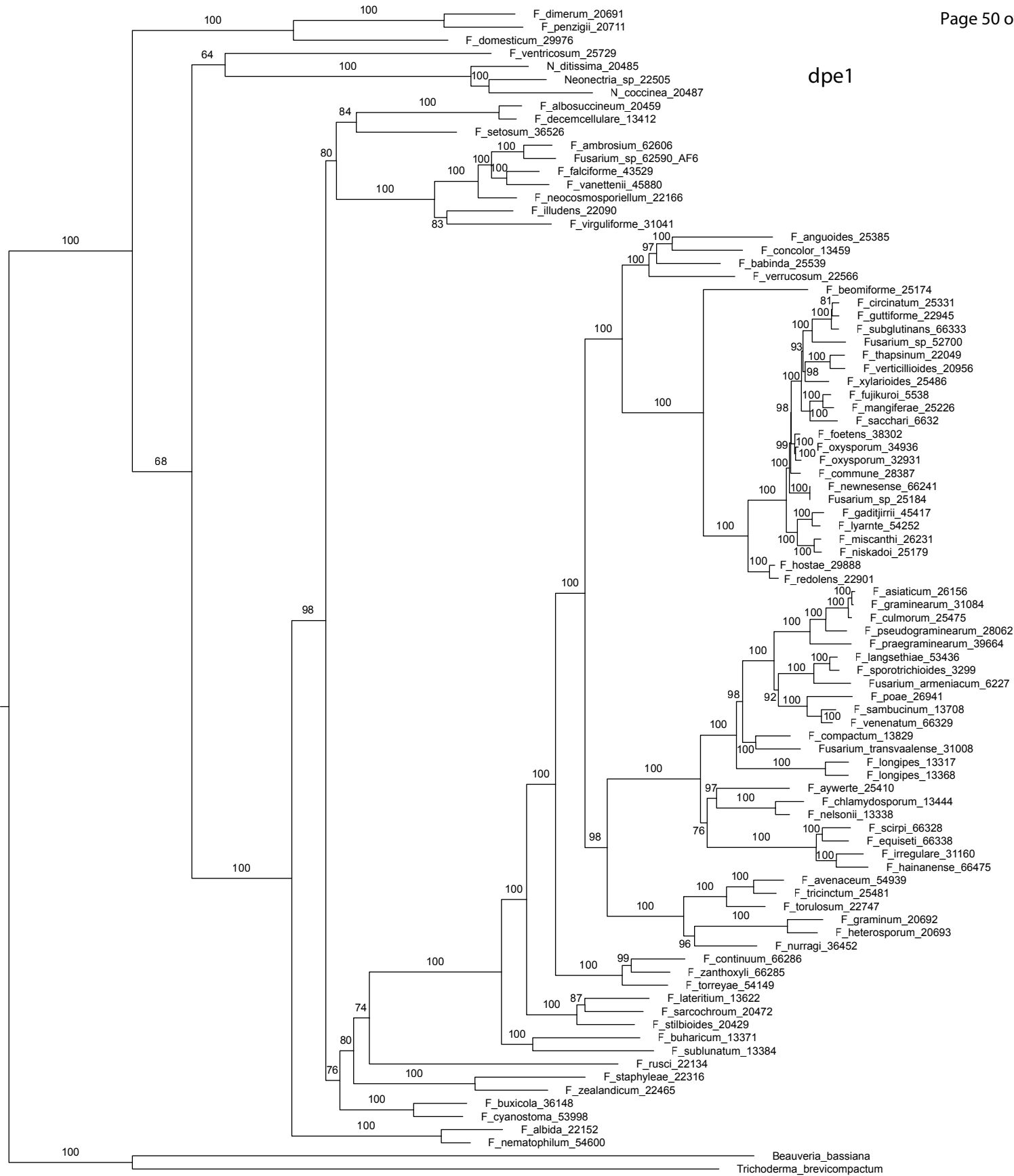
*Trichoderma\_brevicompectum*

*Beauveria\_bassiana*

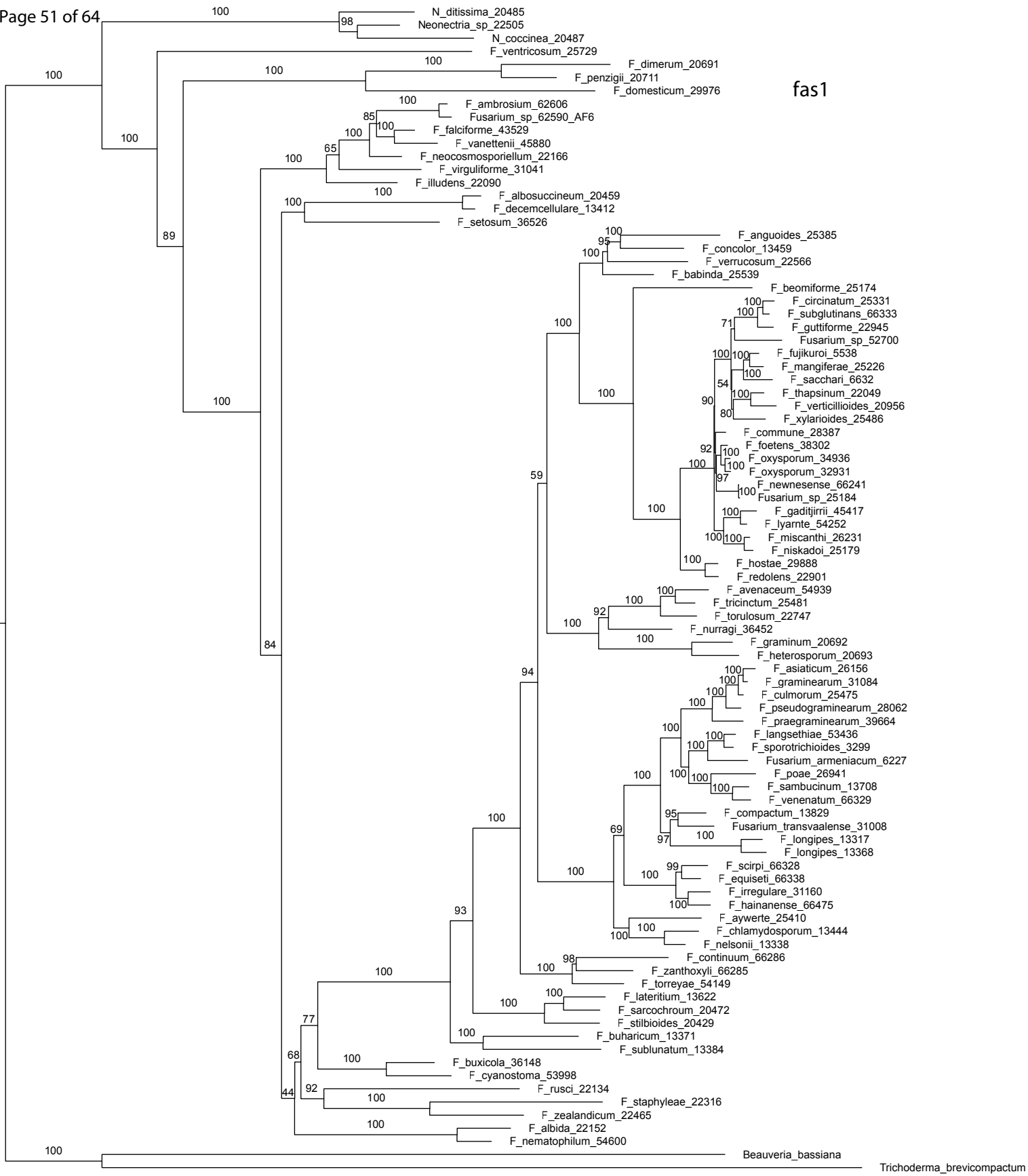
0.1



dpa1



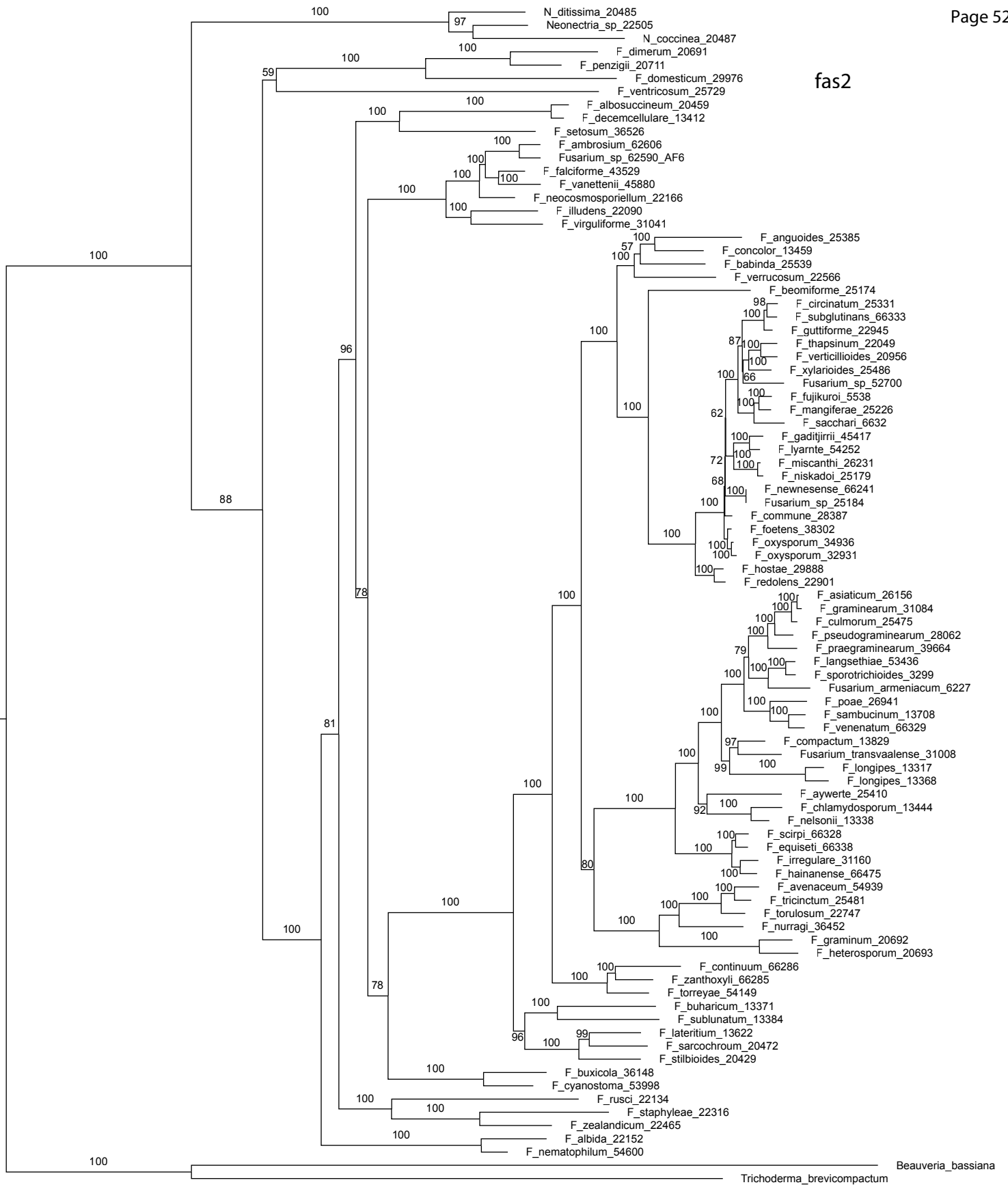
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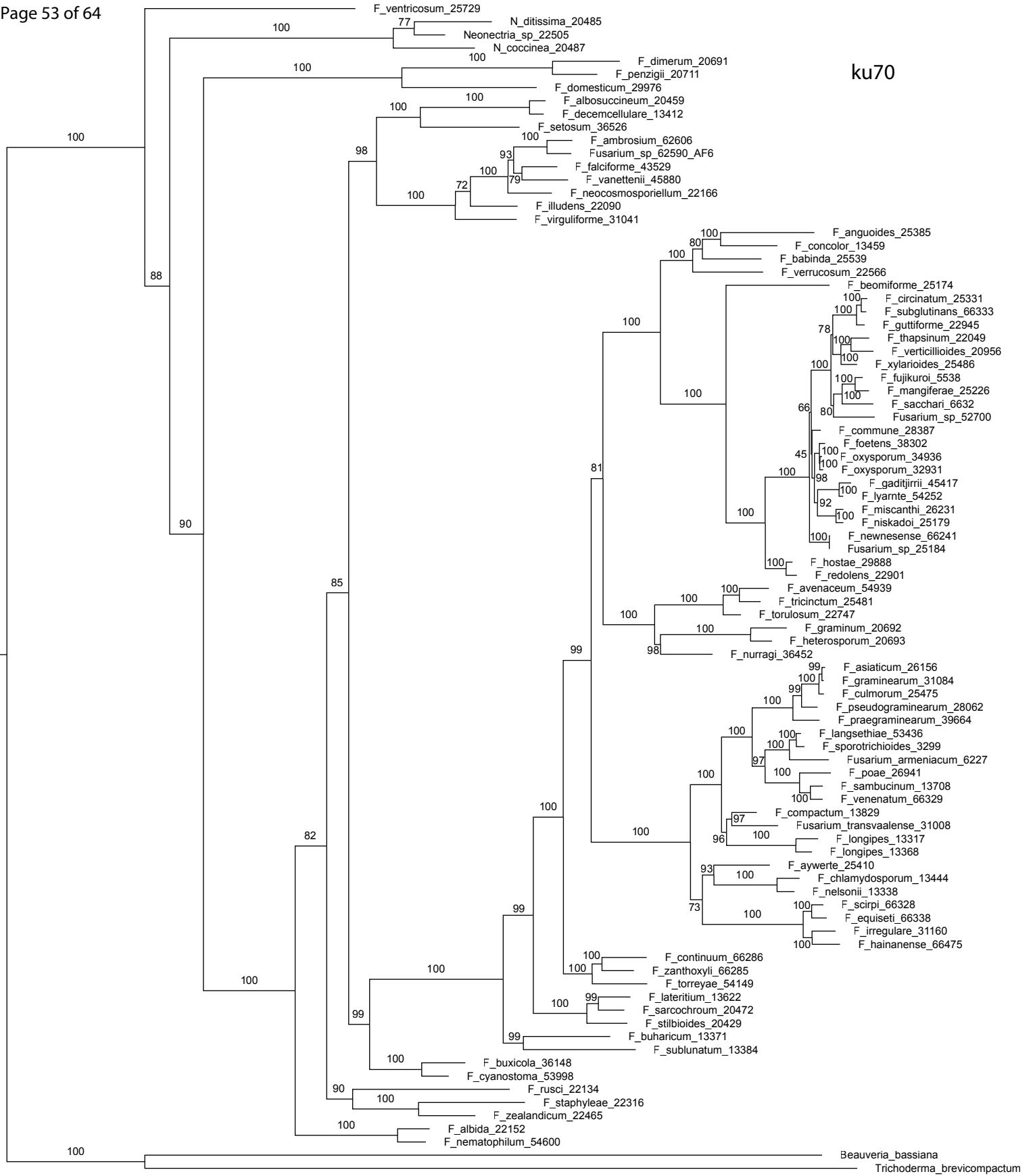


0.06

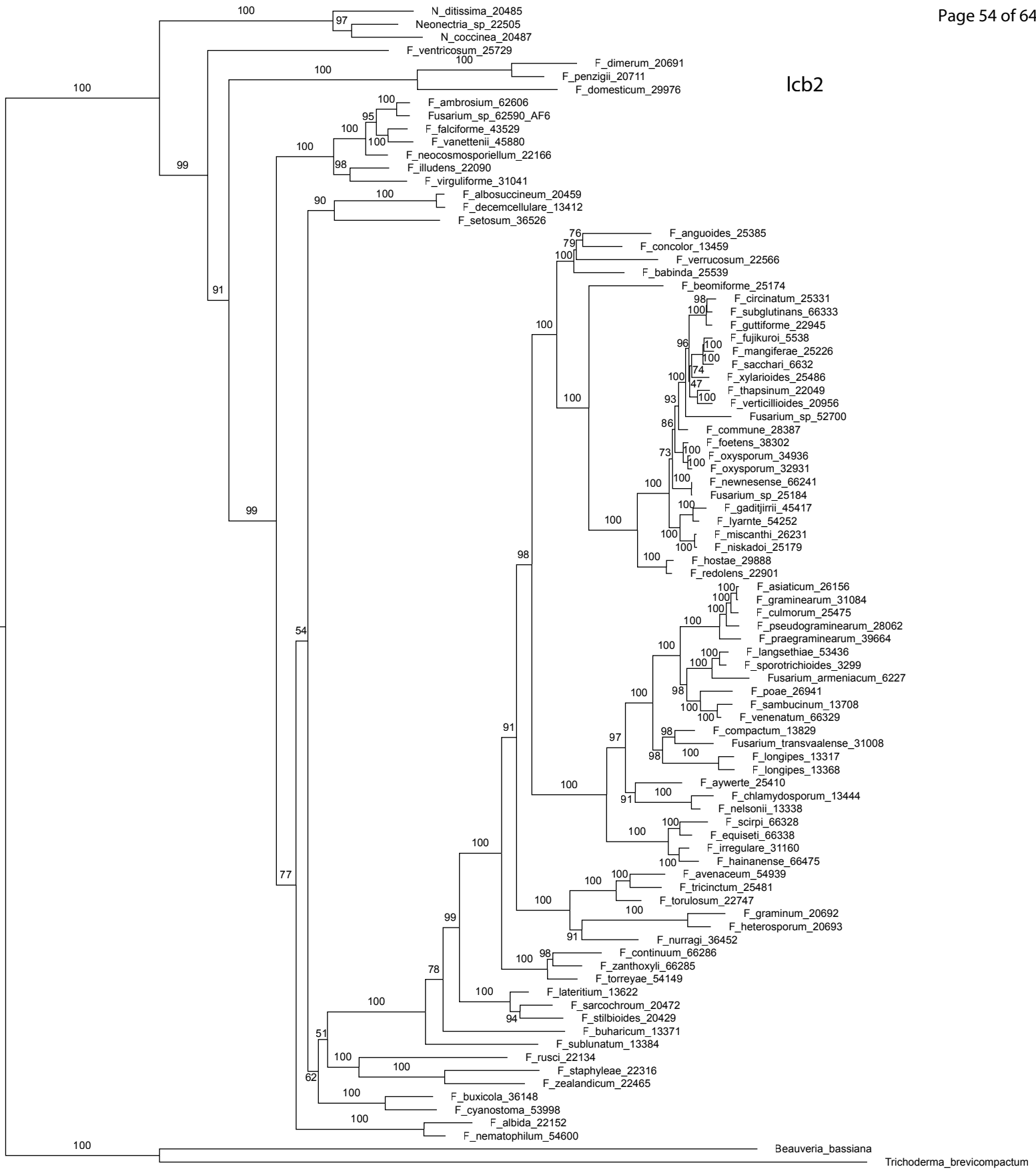
Beauveria\_bassiana

Trichoderma\_brevicomactum





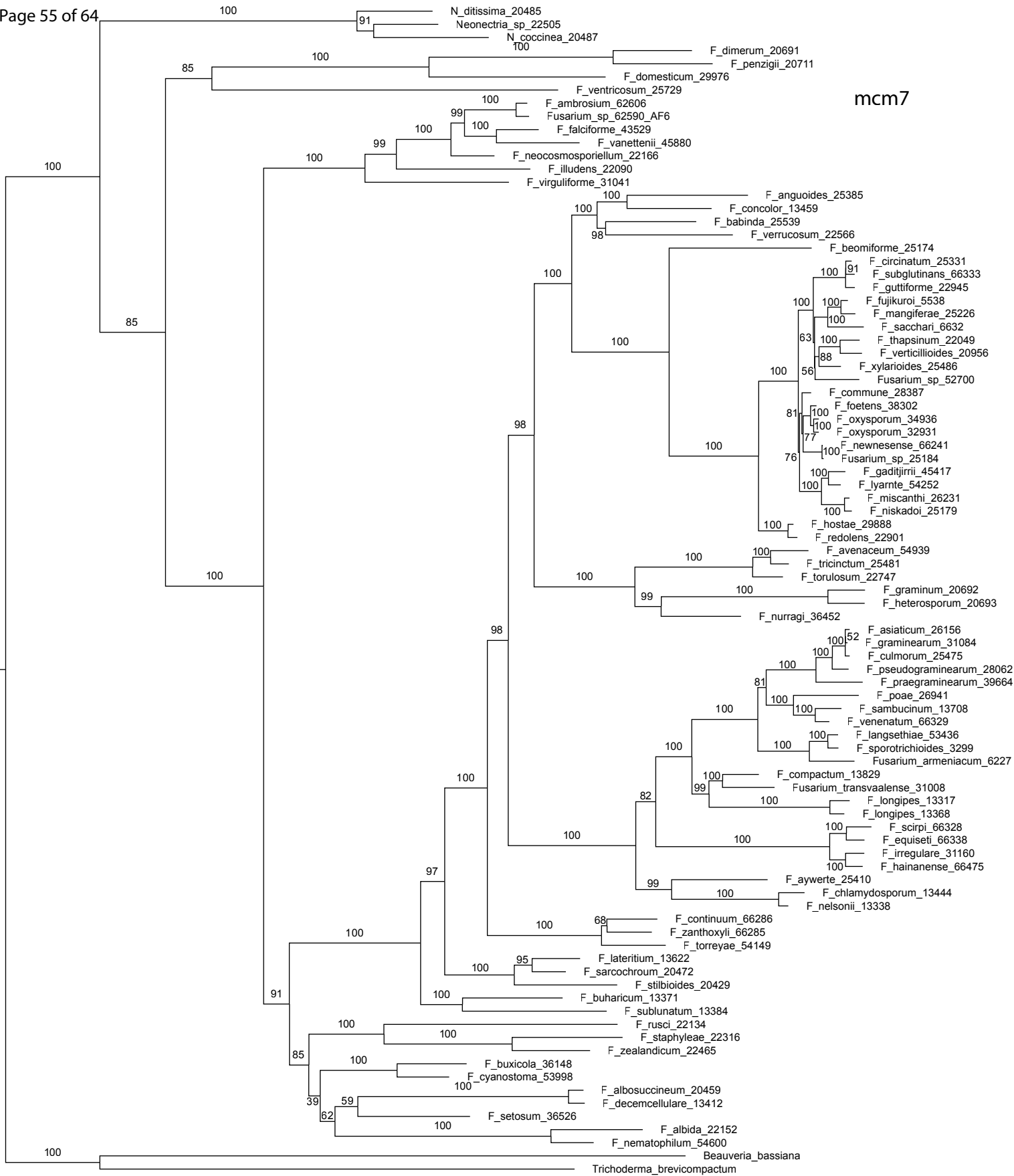
*Beauveria\_bassiana*  
*Trichoderma\_brevicomactum*



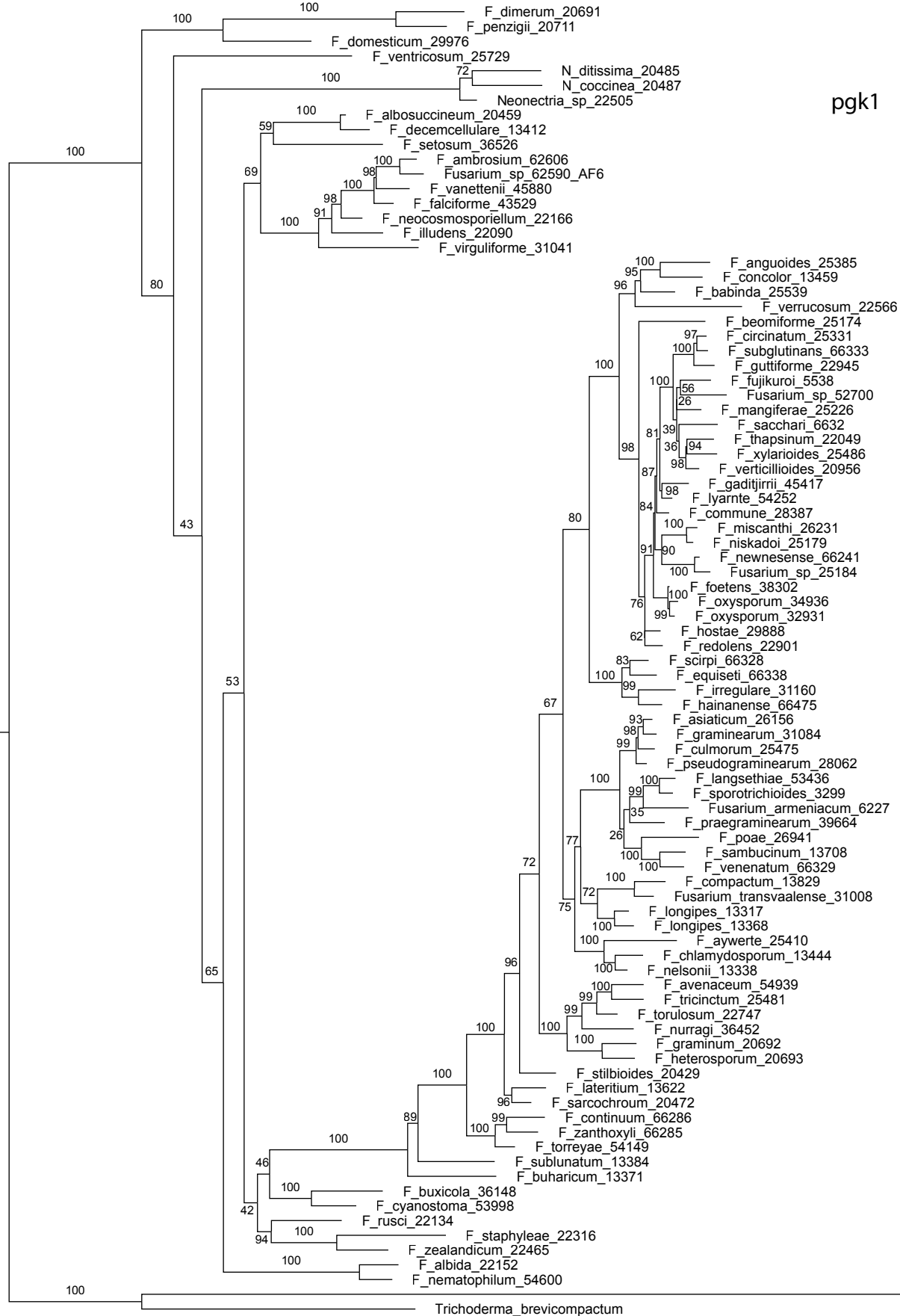
Icb2

Beauveria\_bassiana  
Trichoderma\_brevicomactum

0.1

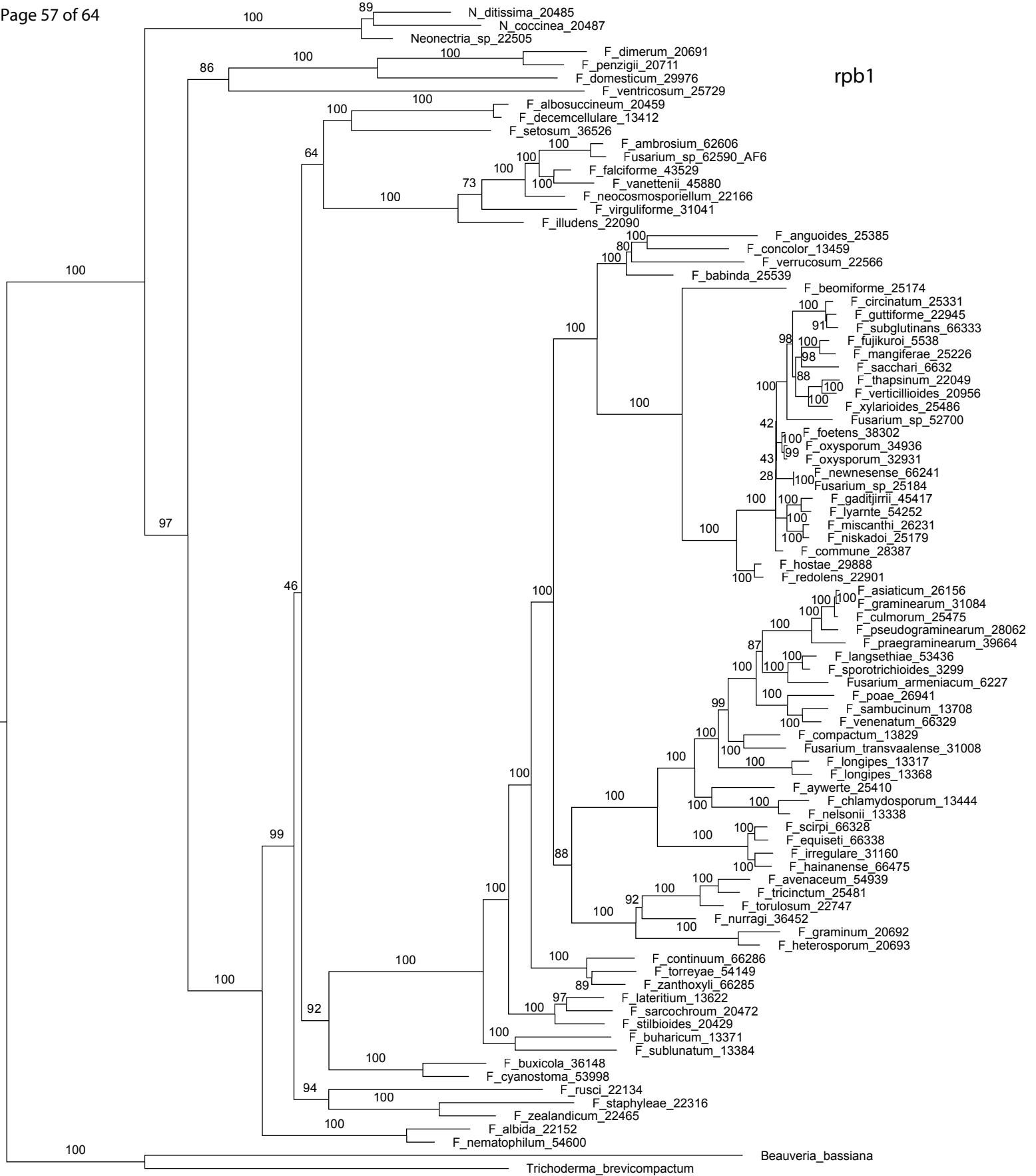




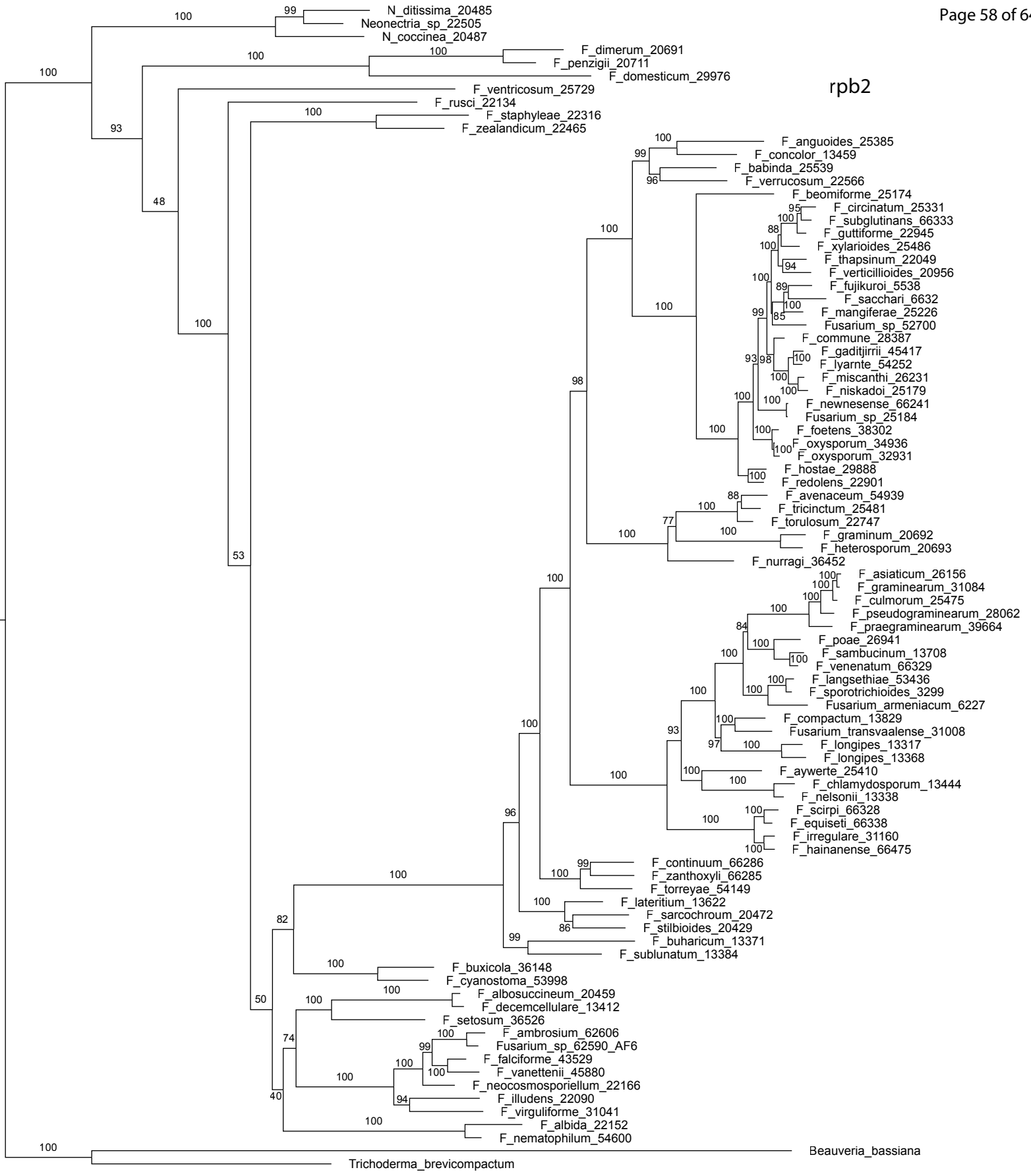


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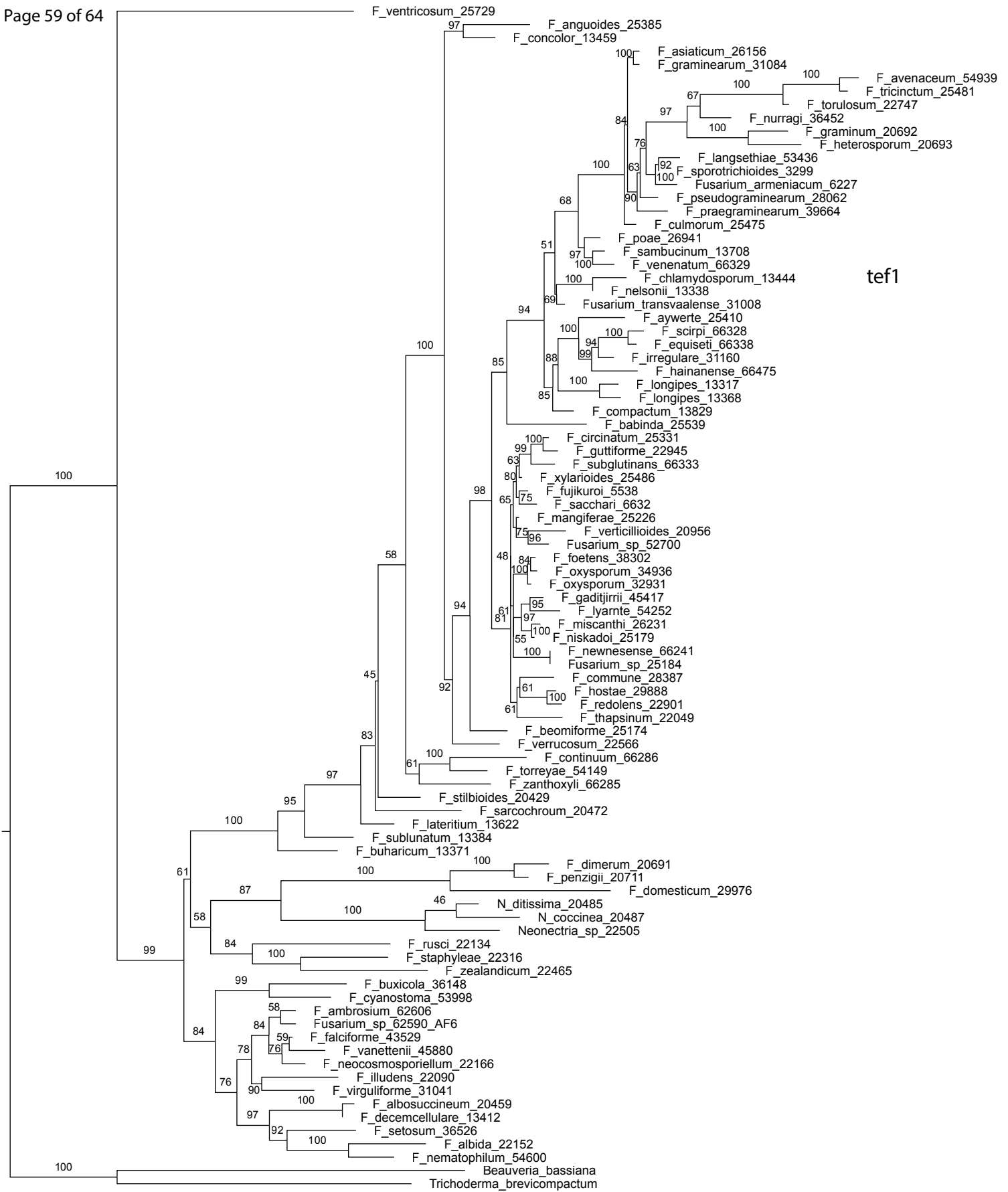
Beauveria\_bassiana



0.07

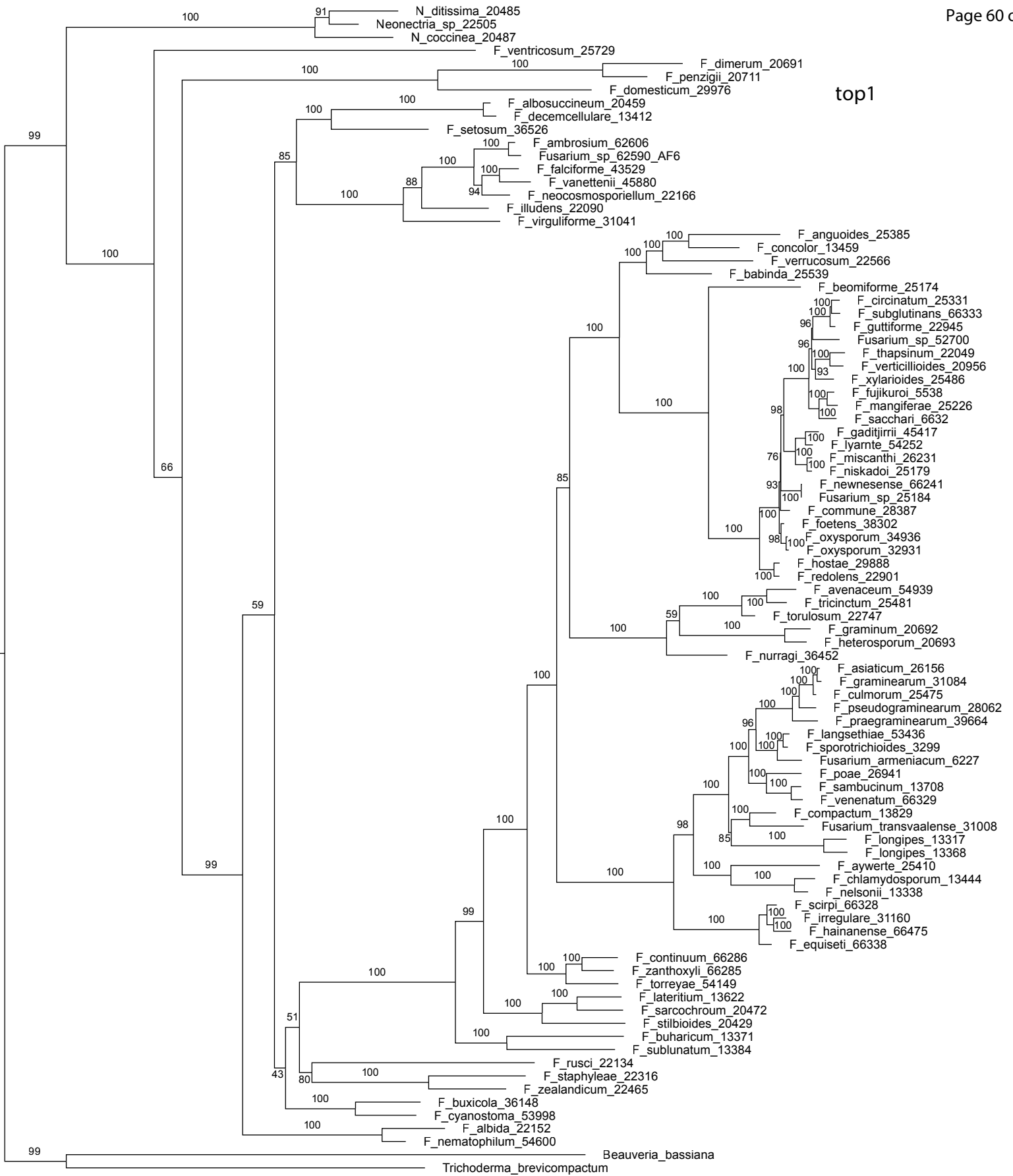


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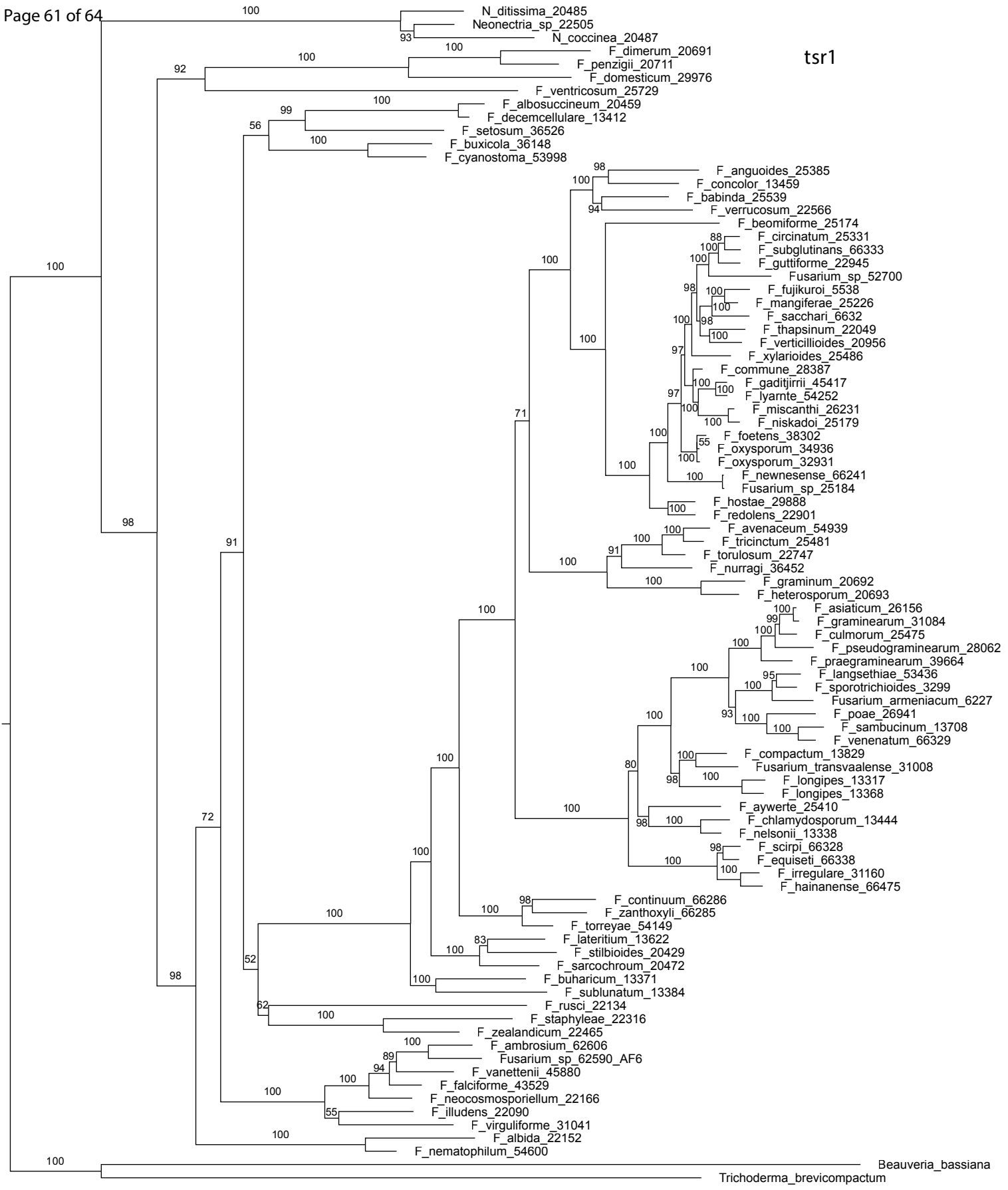


tef1

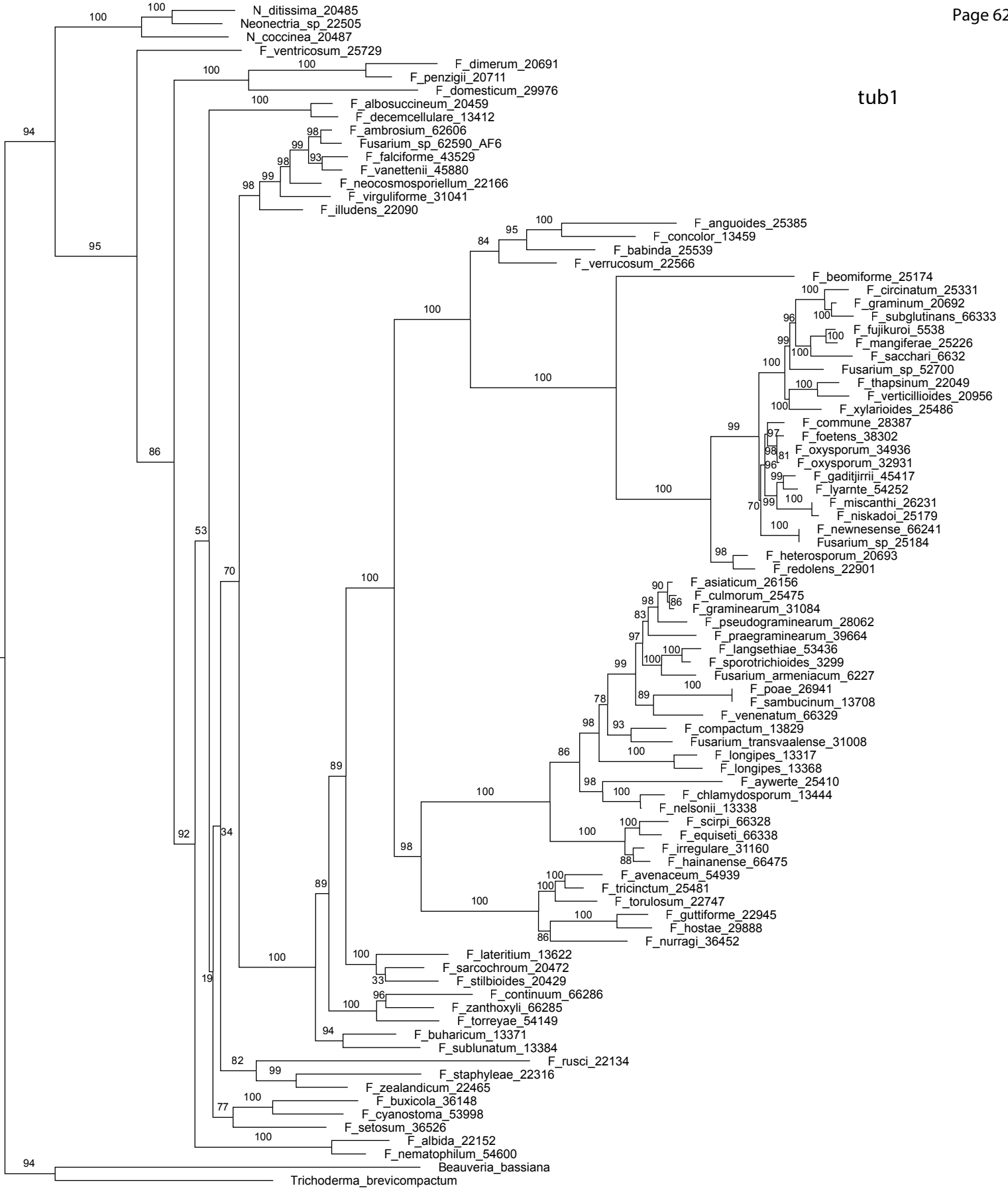
0.02



0.07



0.08



0.03

