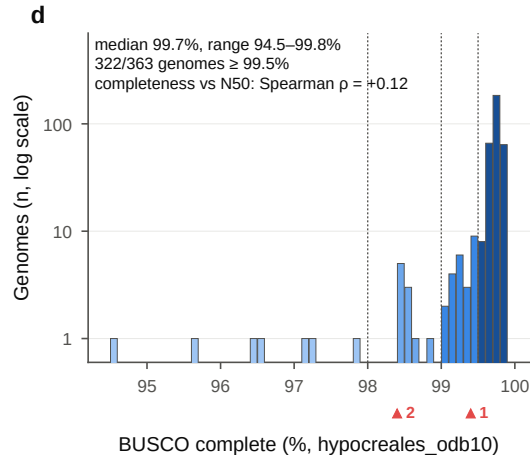
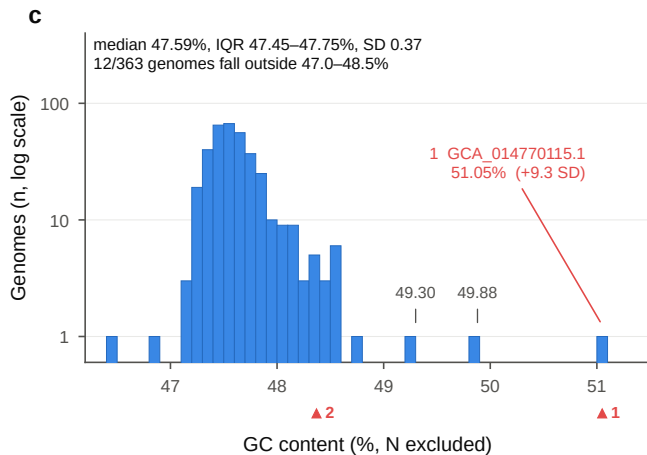
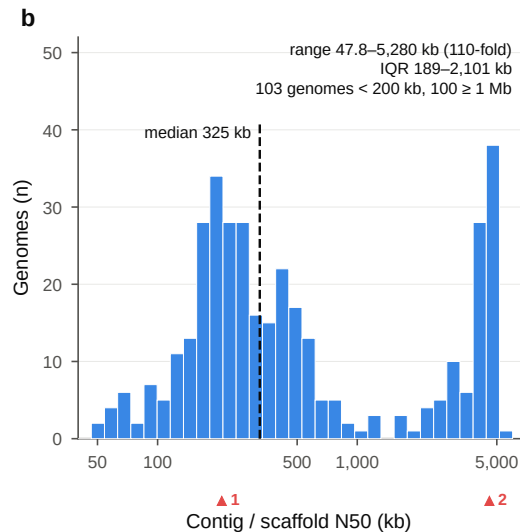
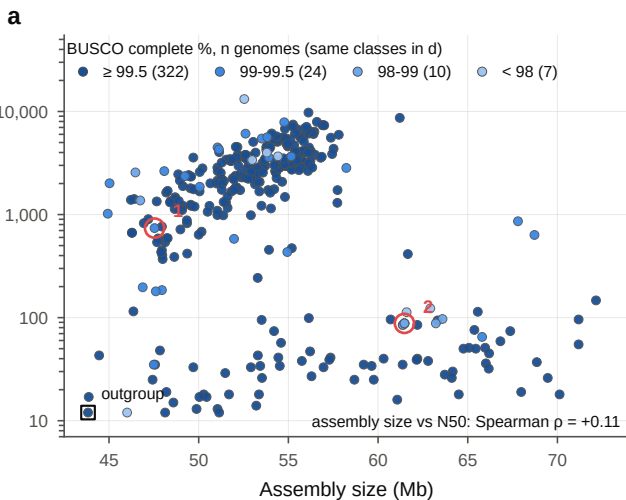




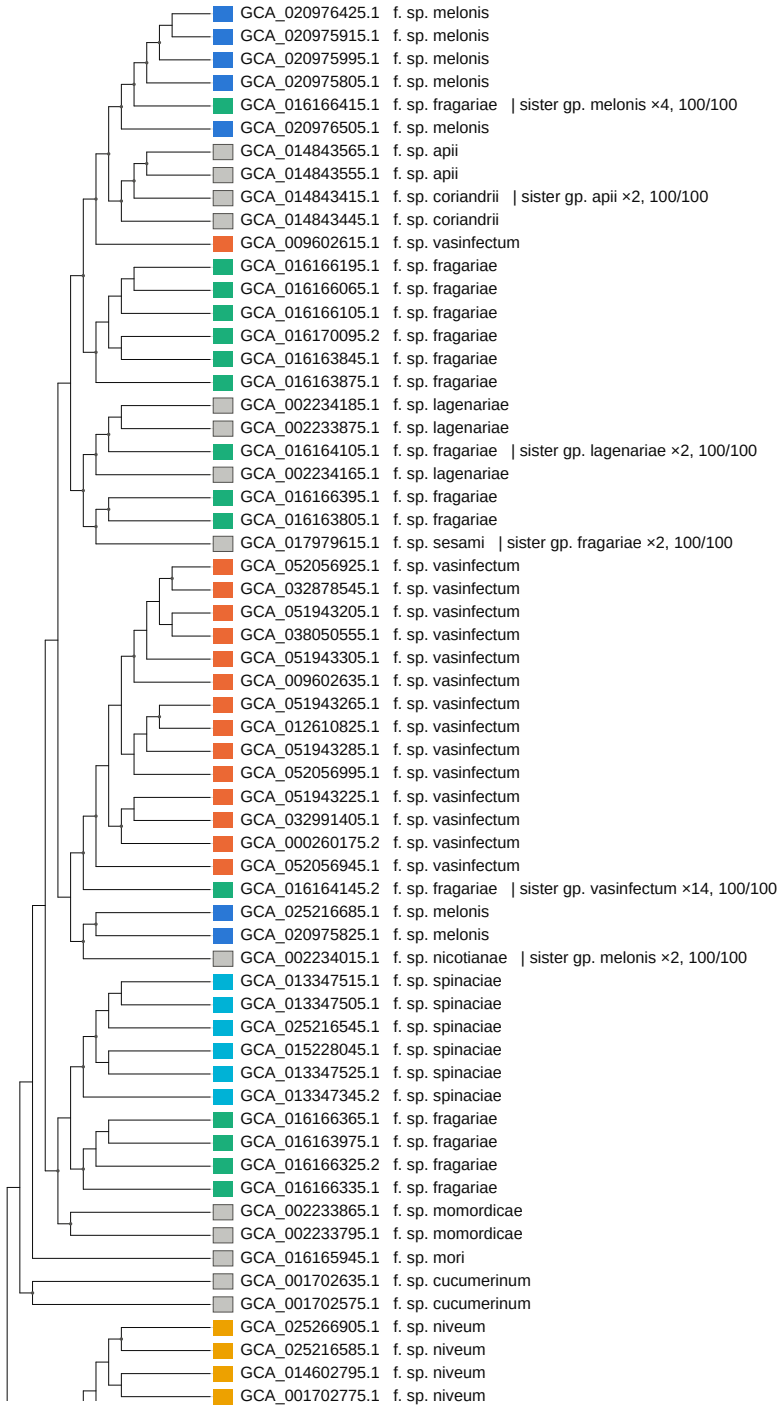
▲ 1, ▲ 2 the two genomes Section 3.7 flags for follow-up. 1 = GCA\_014770115.1 (f. sp. capsici), the 0.2708 subs/site terminal branch.  
2 = GCA\_000149955.2 (Fol4287); GCA\_011316005.3 and GCA\_016802225.1, both deposited as f. sp. cubense, have identical values for every statistic shown here, so all three genomes plot as one point in (a).

Figure S1

Fully labelled maximum-likelihood tree of 363 genomes from 1,455 strict-core BUSCO loci — page 1 of 6, tips 1–61 in plotted order. Same topology, rooting, tip order and colours as Figure 1.

Branch lengths are not drawn to scale here. The tree is too shallow for a phylogram to show its topology at any page size — 355 of its 362 internal nodes lie between 0.020 and 0.0287 substitutions per site from the root — so nodes are placed by nesting level and tips are aligned. Branch lengths are in Figure 1, Table 5 and the source-data table.

'Sister gp.' names the forma specialis shared by every member of a tip's sister group, that group's size and its SH-aLRT/UFBoot support (Table 3). 'Off scale' gives the root-to-tip distance of a branch truncated in Figure 1, with its terminal branch length in parentheses.



## Figure S1

Fully labelled maximum-likelihood tree of 363 genomes from 1,455 strict-core BUSCO loci — page 2 of 6, tips 62–122 in plotted order. Same topology, rooting, tip order and colours as Figure 1.

Branch lengths are not drawn to scale here. The tree is too shallow for a phylogram to show its topology at any page size — 355 of its 362 internal nodes lie between 0.020 and 0.0287 substitutions per site from the root — so nodes are placed by nesting level and tips are aligned. Branch lengths are in Figure 1, Table 5 and the source-data table.

'Sister gp.' names the forma specialis shared by every member of a tip's sister group, that group's size and its SH-aLRT/UFBoot support (Table 3). 'Off scale' gives the root-to-tip distance of a branch truncated in Figure 1, with its terminal branch length in parentheses.

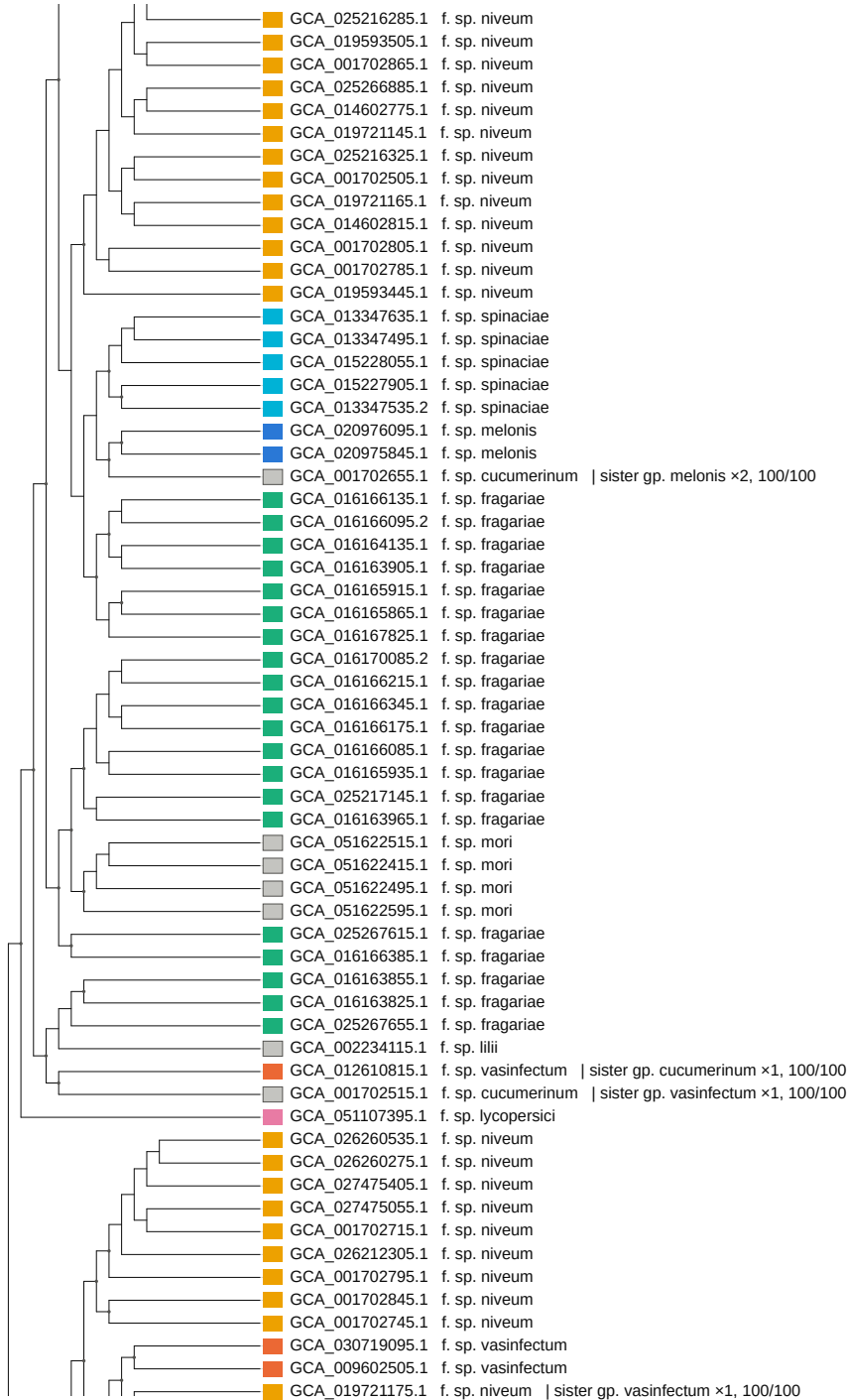
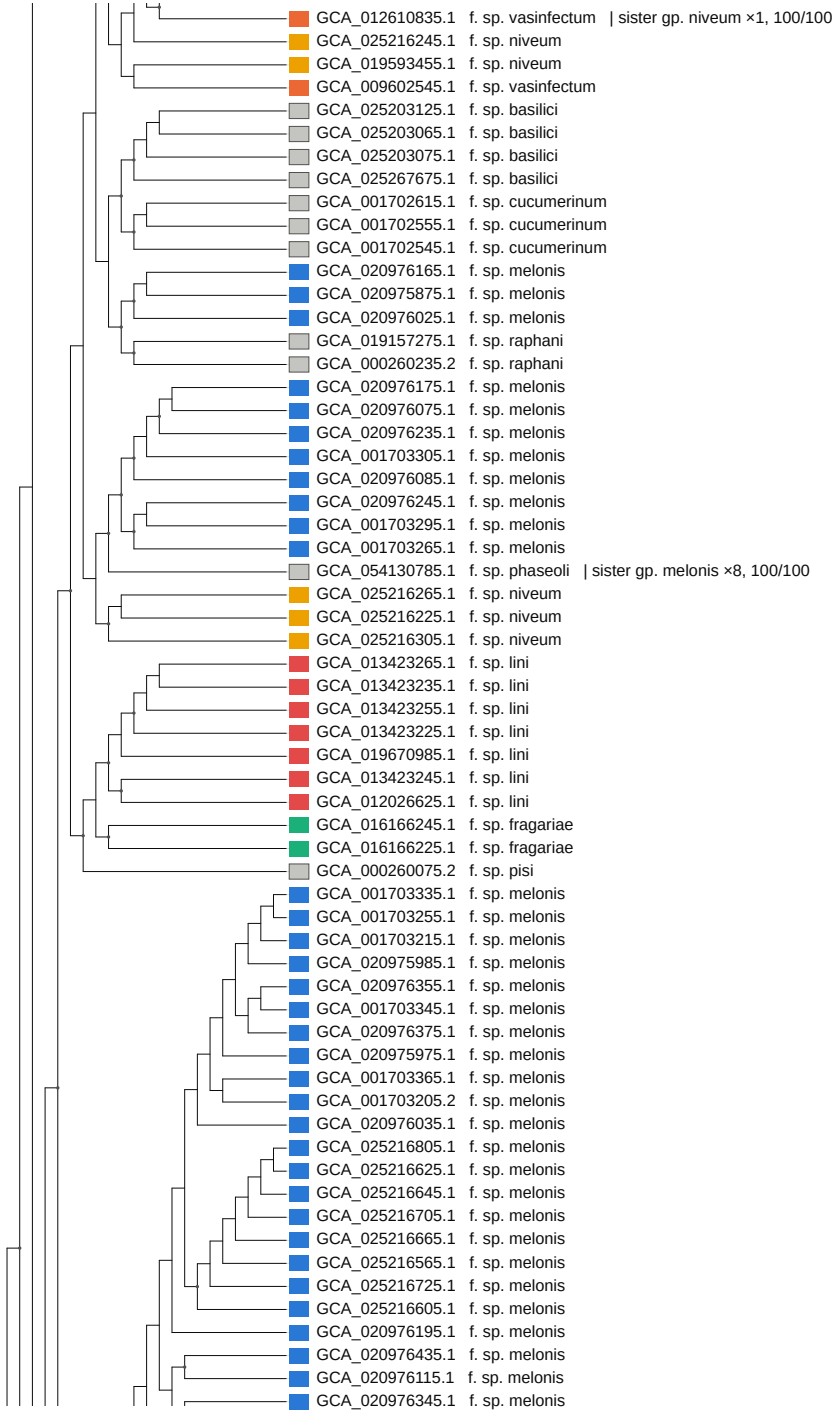


Figure S1

Fully labelled maximum-likelihood tree of 363 genomes from 1,455 strict-core BUSCO loci — page 3 of 6, tips 123–183 in plotted order. Same topology, rooting, tip order and colours as Figure 1.

Branch lengths are not drawn to scale here. The tree is too shallow for a phylogram to show its topology at any page size — 355 of its 362 internal nodes lie between 0.020 and 0.0287 substitutions per site from the root — so nodes are placed by nesting level and tips are aligned. Branch lengths are in Figure 1, Table 5 and the source-data table.

'Sister gp.' names the forma specialis shared by every member of a tip's sister group, that group's size and its SH-aLRT/UFBoot support (Table 3). 'Off scale' gives the root-to-tip distance of a branch truncated in Figure 1, with its terminal branch length in parentheses.

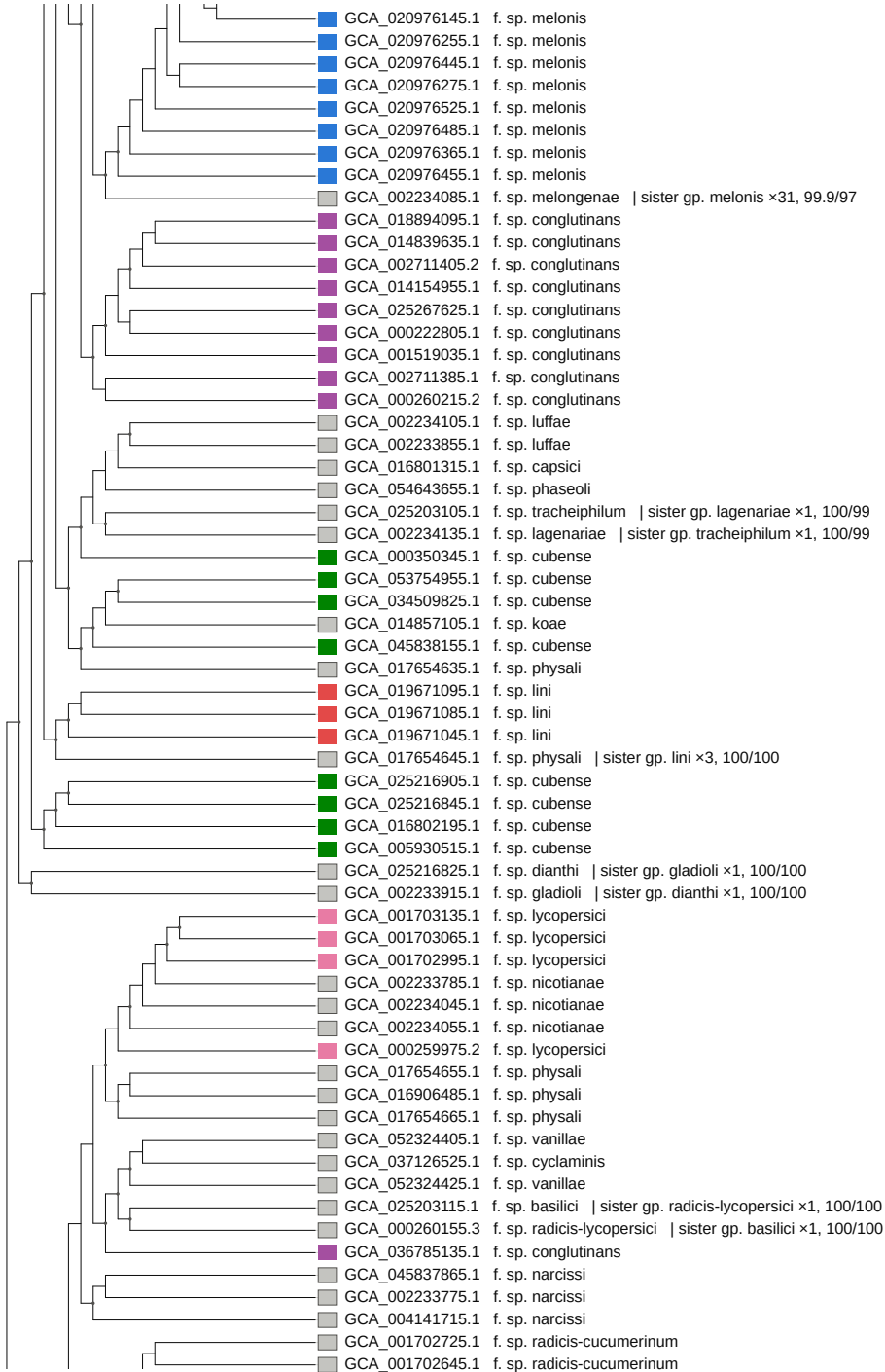


## Figure S1

Fully labelled maximum-likelihood tree of 363 genomes from 1,455 strict-core BUSCO loci — page 4 of 6, tips 184–244 in plotted order. Same topology, rooting, tip order and colours as Figure 1.

Branch lengths are not drawn to scale here. The tree is too shallow for a phylogram to show its topology at any page size — 355 of its 362 internal nodes lie between 0.020 and 0.0287 substitutions per site from the root — so nodes are placed by nesting level and tips are aligned. Branch lengths are in Figure 1, Table 5 and the source-data table.

'Sister gp.' names the forma specialis shared by every member of a tip's sister group, that group's size and its SH-aLRT/UFBoot support (Table 3). 'Off scale' gives the root-to-tip distance of a branch truncated in Figure 1, with its terminal branch length in parentheses.

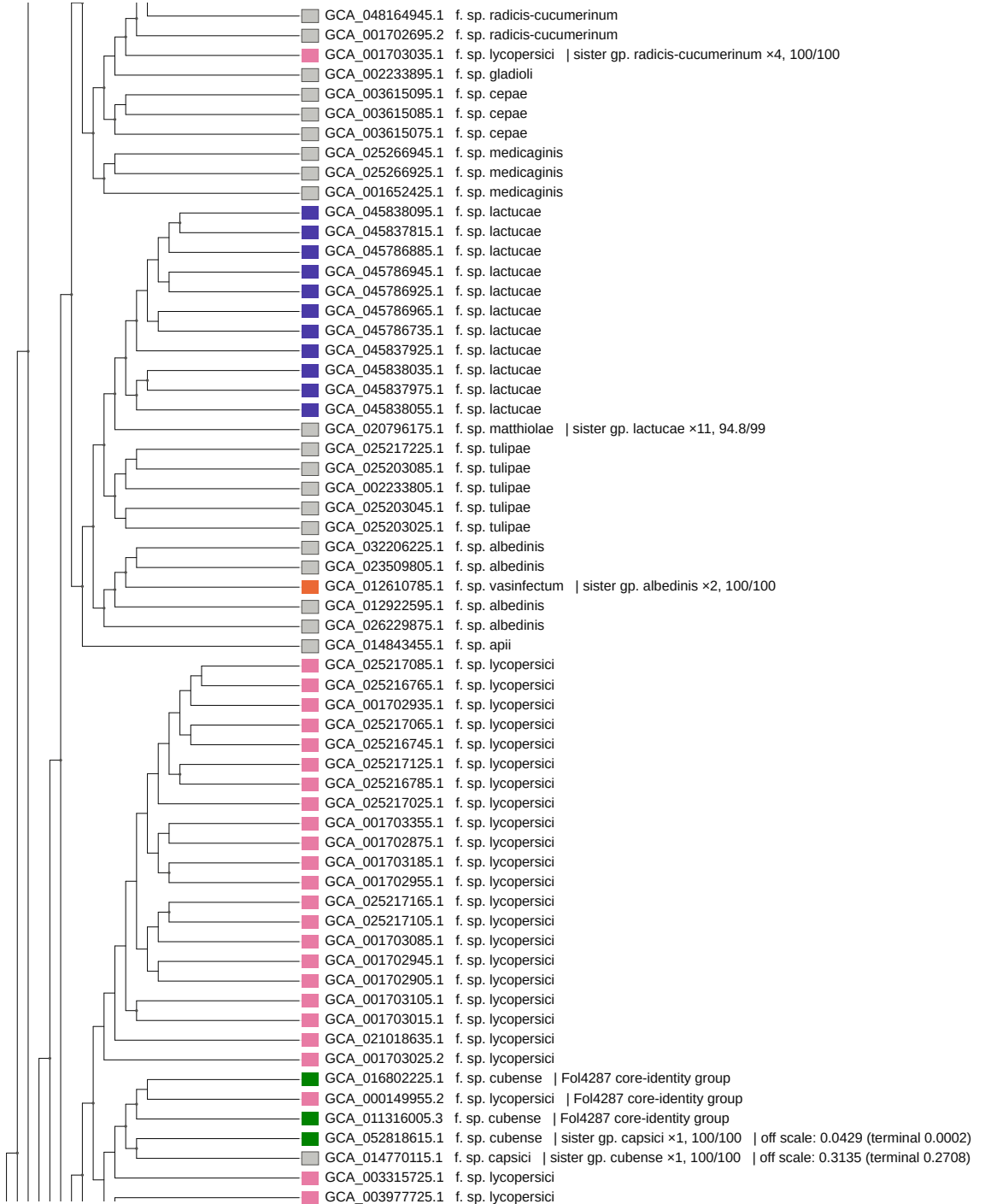


## Figure S1

Fully labelled maximum-likelihood tree of 363 genomes from 1,455 strict-core BUSCO loci — page 5 of 6, tips 245–305 in plotted order. Same topology, rooting, tip order and colours as Figure 1.

Branch lengths are not drawn to scale here. The tree is too shallow for a phylogram to show its topology at any page size — 355 of its 362 internal nodes lie between 0.020 and 0.0287 substitutions per site from the root — so nodes are placed by nesting level and tips are aligned. Branch lengths are in Figure 1, Table 5 and the source-data table.

'Sister gp.' names the forma specialis shared by every member of a tip's sister group, that group's size and its SH-aLRT/UFBoot support (Table 3). 'Off scale' gives the root-to-tip distance of a branch truncated in Figure 1, with its terminal branch length in parentheses.

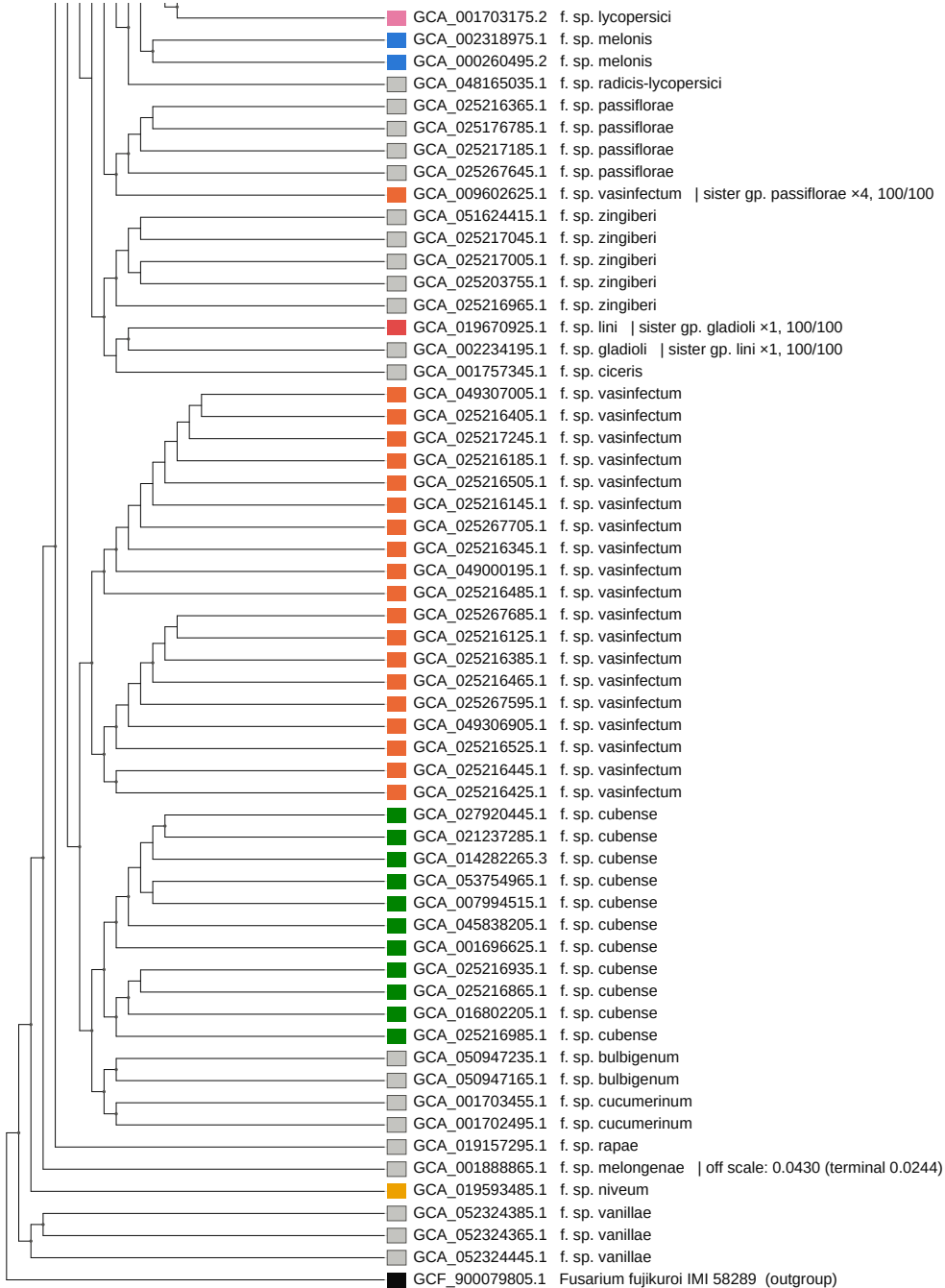


## Figure S1

Fully labelled maximum-likelihood tree of 363 genomes from 1,455 strict-core BUSCO loci — page 6 of 6, tips 306–363 in plotted order. Same topology, rooting, tip order and colours as Figure 1.

Branch lengths are not drawn to scale here. The tree is too shallow for a phylogram to show its topology at any page size — 355 of its 362 internal nodes lie between 0.020 and 0.0287 substitutions per site from the root — so nodes are placed by nesting level and tips are aligned. Branch lengths are in Figure 1, Table 5 and the source-data table.

'Sister gp.' names the forma specialis shared by every member of a tip's sister group, that group's size and its SH-aLRT/UFBoot support (Table 3). 'Off scale' gives the root-to-tip distance of a branch truncated in Figure 1, with its terminal branch length in parentheses.



**a One-directional conflicts**  
14 genomes, each the sole differently-labelled sister of a uniformly labelled clade

| <i>labelled<br/>forma specialis</i> | <i>focal<br/>genome</i> | <i>SH-aLRT/<br/>UFBoot</i> | <i>sister-group<br/>size</i> | <i>is sister to →</i> | <i>sister-group<br/>forma specialis</i> |
|-------------------------------------|-------------------------|----------------------------|------------------------------|-----------------------|-----------------------------------------|
| f. sp. melongenae                   | <b>GCA_002234085.1</b>  | 99.9/97                    | 31                           | ●                     |                                         |
| f. sp. phaseoli                     | <b>GCA_054130785.1</b>  | 100/100                    | 8                            | ●                     |                                         |
| f. sp. fragariae                    | GCA_016166415.1         | 100/100                    | 4                            | ●                     |                                         |
| f. sp. nicotianae                   | GCA_002234015.1         | 100/100                    | 2                            | ●                     |                                         |
| f. sp. cucumerinum                  | GCA_001702655.1         | 100/100                    | 2                            | ●                     |                                         |
| f. sp. fragariae                    | <b>GCA_016164145.2</b>  | 100/100                    | 14                           | ●                     | f. sp. vasinfectum                      |
| f. sp. matthiolae                   | <b>GCA_020796175.1</b>  | 94.8/99                    | 11                           | ●                     | f. sp. lactucae                         |
| f. sp. lycopersici                  | <b>GCA_001703035.1</b>  | 100/100                    | 4                            | ●                     | f. sp. radicis-cucumerinum              |
| f. sp. vasinfectum                  | <b>GCA_009602625.1</b>  | 100/100                    | 4                            | ●                     | f. sp. passiflorae                      |
| f. sp. physali                      | GCA_017654645.1         | 100/100                    | 3                            | ●                     | f. sp. lini                             |
| f. sp. coriandrii                   | GCA_014843415.1         | 100/100                    | 2                            | ●                     | f. sp. apii                             |
| f. sp. sesami                       | GCA_017979615.1         | 100/100                    | 2                            | ●                     | f. sp. fragariae                        |
| f. sp. fragariae                    | GCA_016164105.1         | 100/100                    | 2                            | ●                     | f. sp. lagenariae                       |
| f. sp. vasinfectum                  | GCA_012610785.1         | 100/100                    | 2                            | ●                     | f. sp. albedinis                        |

**b Reciprocal pairs**  
7 pairs (14 genomes); each genome is the other's sole sister, so the pair is one edge of the tree

| <i>labelled<br/>forma specialis</i> | <i>genome A</i> | <i>SH-aLRT/<br/>UFBoot</i> | <i>sister-group<br/>size</i> | <i>← each is the other's sole sister →</i> | <i>genome B and its<br/>labelled forma specialis</i> |
|-------------------------------------|-----------------|----------------------------|------------------------------|--------------------------------------------|------------------------------------------------------|
| f. sp. tracheiphilum                | GCA_025203105.1 | 100/99                     | 1                            | ● ← → ●                                    | f. sp. lagenariae<br>GCA_002234135.1                 |
| f. sp. niveum                       | GCA_019721175.1 | 100/100                    | 1                            | ● ← → ●                                    | f. sp. vasinfectum<br>GCA_012610835.1                |
| f. sp. vasinfectum                  | GCA_012610815.1 | 100/100                    | 1                            | ● ← → ●                                    | f. sp. cucumerinum<br>GCA_001702515.1                |
| f. sp. dianthi                      | GCA_025216825.1 | 100/100                    | 1                            | ● ← → ●                                    | f. sp. gladioli<br>GCA_002233915.1                   |
| f. sp. cubense                      | GCA_052818615.1 | 100/100                    | 1                            | ● ← → ●                                    | f. sp. capsici<br>GCA_014770115.1†                   |
| f. sp. basilici                     | GCA_025203115.1 | 100/100                    | 1                            | ● ← → ●                                    | f. sp. radicis-lycopersici<br>GCA_000260155.3        |
| f. sp. lini                         | GCA_019670925.1 | 100/100                    | 1                            | ● ← → ●                                    | f. sp. gladioli<br>GCA_002234195.1                   |

Band width in (a) is proportional to sister-group size (0.28 pt per genome) and the size is printed alongside. A dot is one genome; a bar is a clade, drawn as tall as the bands it receives. The seven arrows in (b) share one fixed width because every sister group there is a single genome. Bands reaching the same bar lead to separate clades that happen to carry the same label: the five f. sp. melonis bands are five different clades. Tinted rows in (a) are the six cases named in Section 3.5; a third four-genome case (GCA\_016166415.1) ties with the last two of them. † longest terminal branch in the tree (0.2708 substitutions per site). The 28 genomes shown are 7.7% of the 363-genome panel.