

**The recombination-cold region as an epidemiological marker of recombinogenic opportunistic pathogen *Mycobacterium avium***

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**Contents of additional file 3**

**Phylogenetic trees based on codon alignments of marker gene candidates and the *hsp65* gene.**

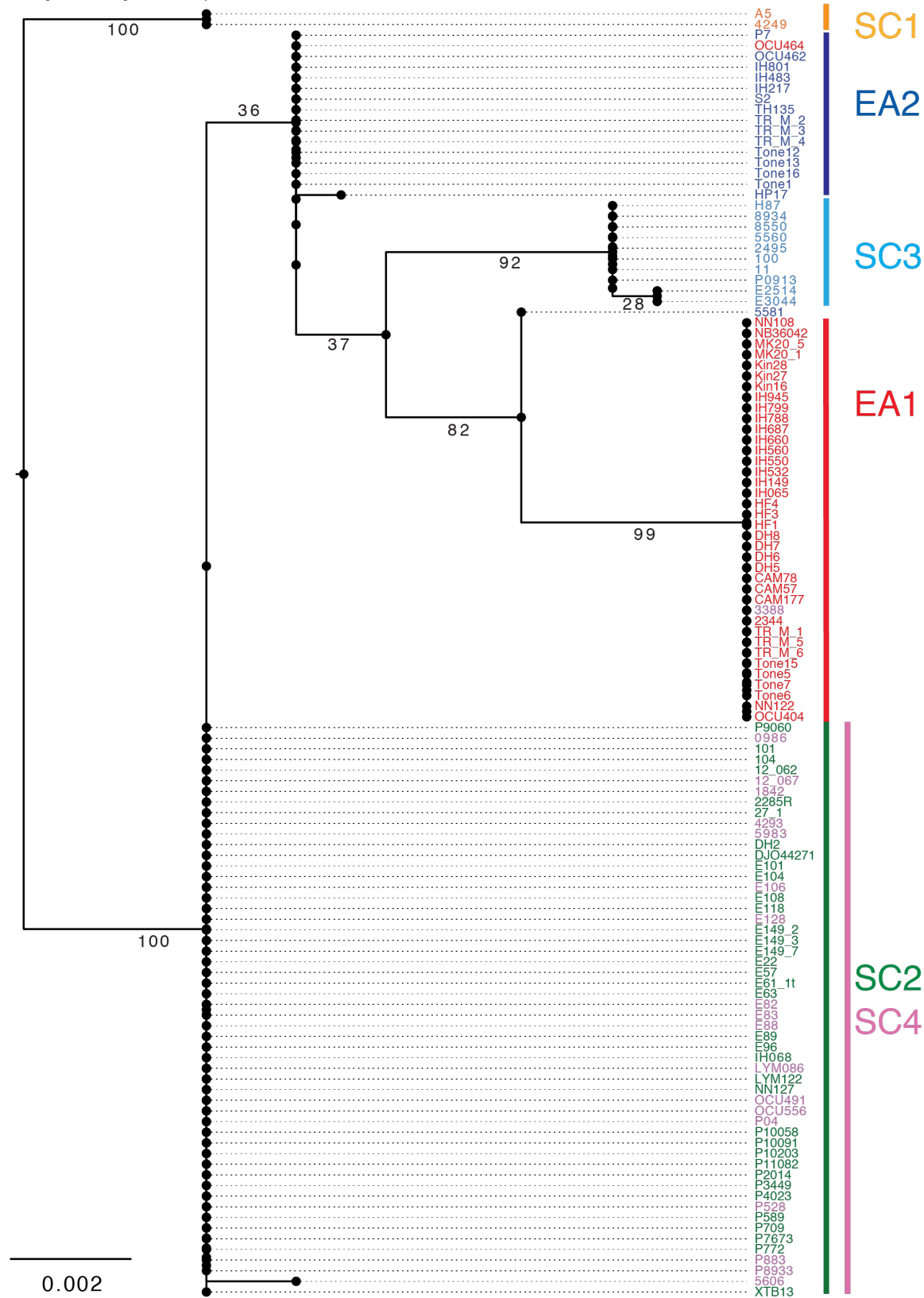
- (i) MAH\_0788/MAV\_0940 ortholog,
- (ii) MAH\_0771/MAV\_0930 ortholog,
- (iii) MAH\_0766/MAV\_0925 ortholog
- (iv) MAH\_0809/MAV\_0960 ortholog,
- (v) MAH\_2714/ MAV\_2410 ortholog (inadequate marker gene),
- (vi) *hsp65* ortholog,
- (vii) MAV\_1375 ortholog,
- (viii) MAV\_2820 ortholog

Trees were constructed using GTR+G model in PhyML with 100 times bootstrapping run. Values by the branch indicate the number of bootstrap support. Allele of strain A5 is used as out group for the analysis in panels i-vi. Out group was not used for tree construction of panels vii and viii. Alignment information is also shown by the tree as follows: n.allele, number of alleles in the alignment (population); nuc.diversity, average pairwise nucleotide diversity (number of site differences) in the alignment; hap.diversity, probability of haplotype (allele) differences in the alignment; alignment length, length of alignment without gaps.

Additional file 3

(i) MAH\_0788

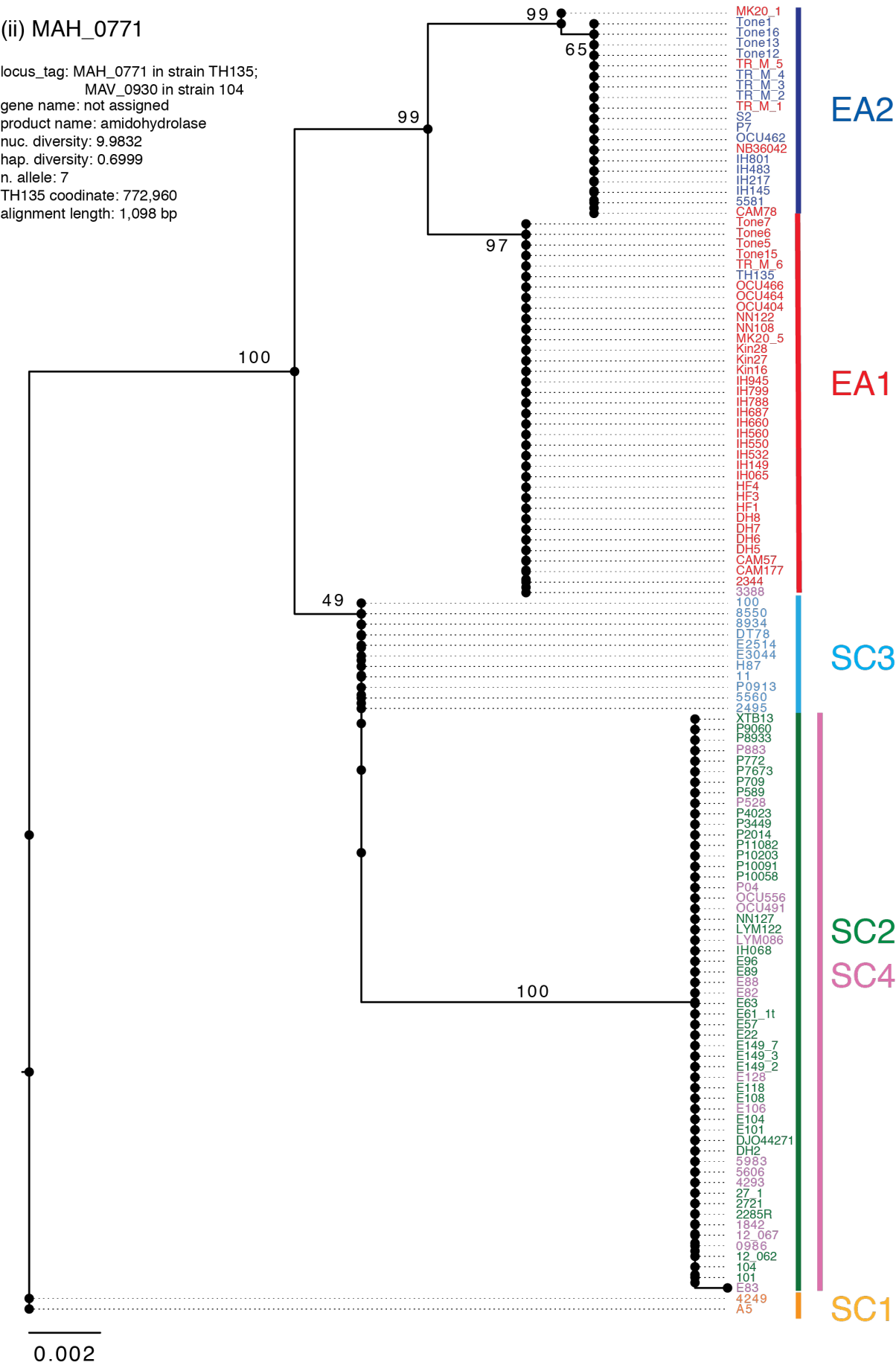
locus\_tag: MAH\_0788 in strain TH135, MAV\_0940 in strain 104  
gene name: cinA-1  
product name: 1,8-cineole 2-endo-monooxygenase (P-450)  
nuc. diversity: 5.7719  
hap. diversity: 0.6947  
n. allele: 9  
TH135 coordinate: 795,348  
alignment length: 1,362 bp



Additional file 3

(ii) MAH\_0771

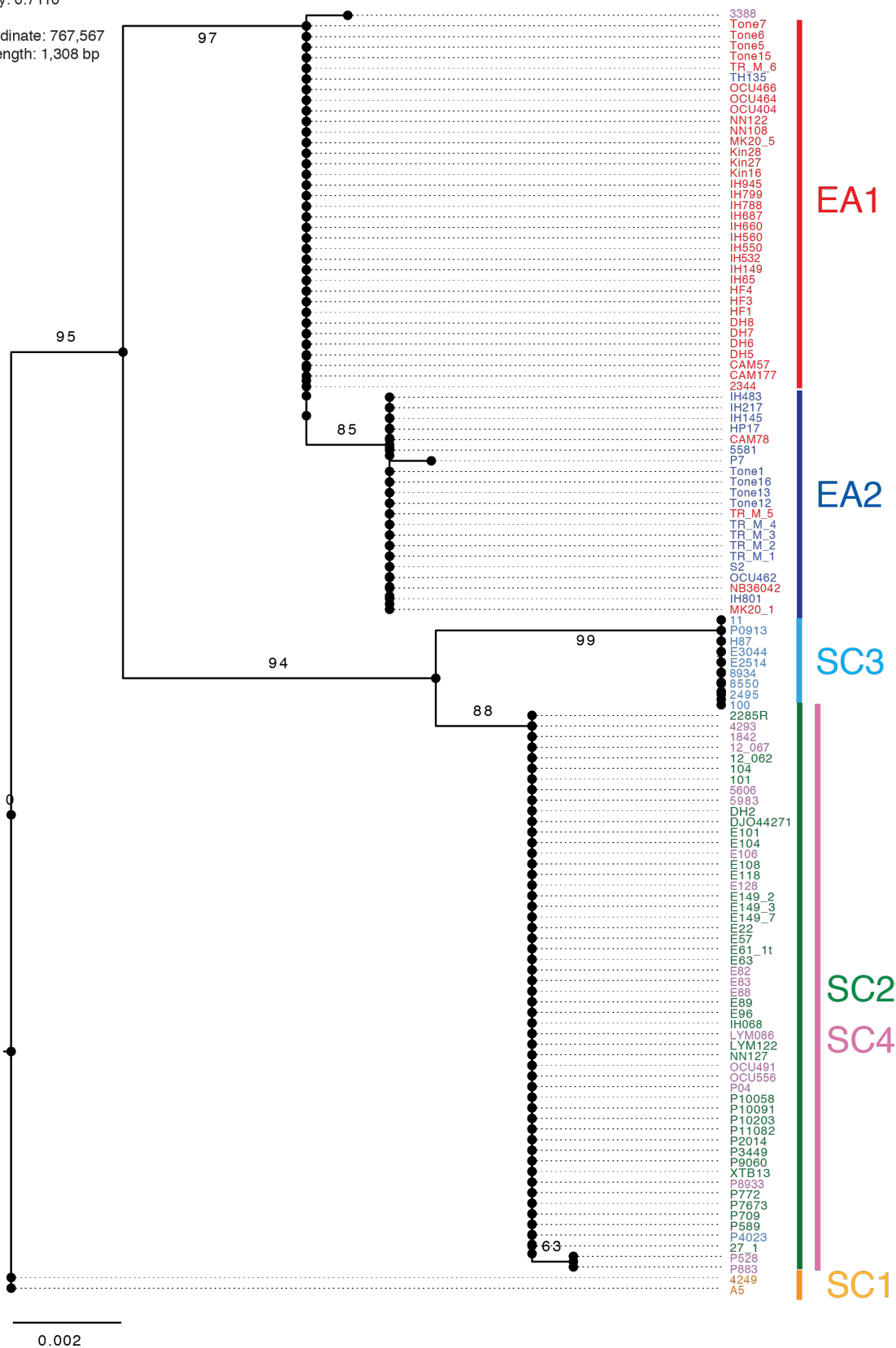
locus\_tag: MAH\_0771 in strain TH135;  
MAV\_0930 in strain 104  
gene name: not assigned  
product name: amidohydrolase  
nuc. diversity: 9.9832  
hap. diversity: 0.6999  
n. allele: 7  
TH135 coordinate: 772,960  
alignment length: 1,098 bp



Additional file 3

(iii) MAH\_0766

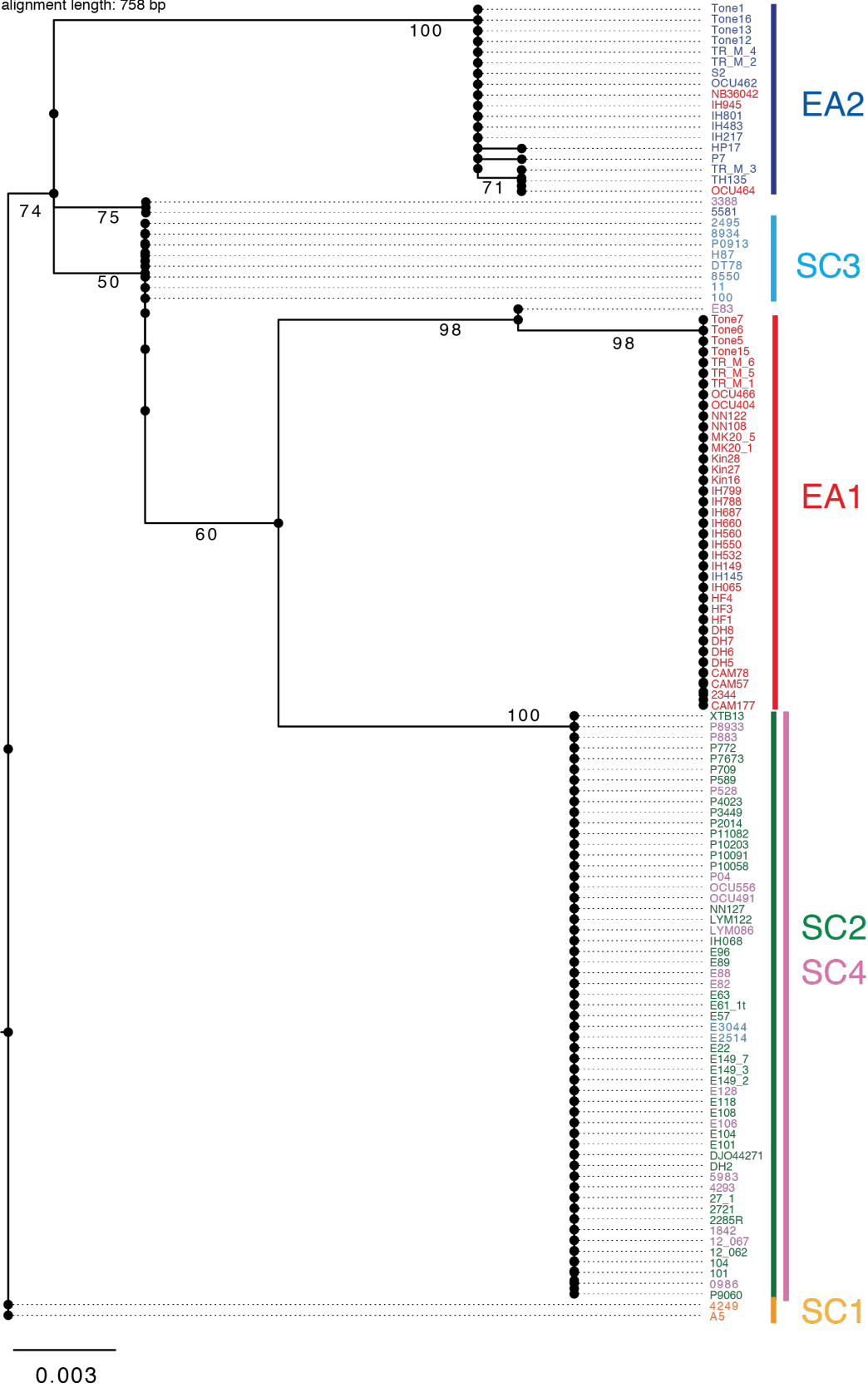
locus tag: MAH\_0766 in strain TH135; MAV\_0925 in strain 104  
gene name: *nuoF*  
product name: NADH dehydrogenase  
nuc.diversity: 7.9939  
hap.diversity: 0.7110  
n. allele: 8  
TH135 coordinate: 767,567  
alignment length: 1,308 bp



Additional file 3

(iv) MAH\_0809

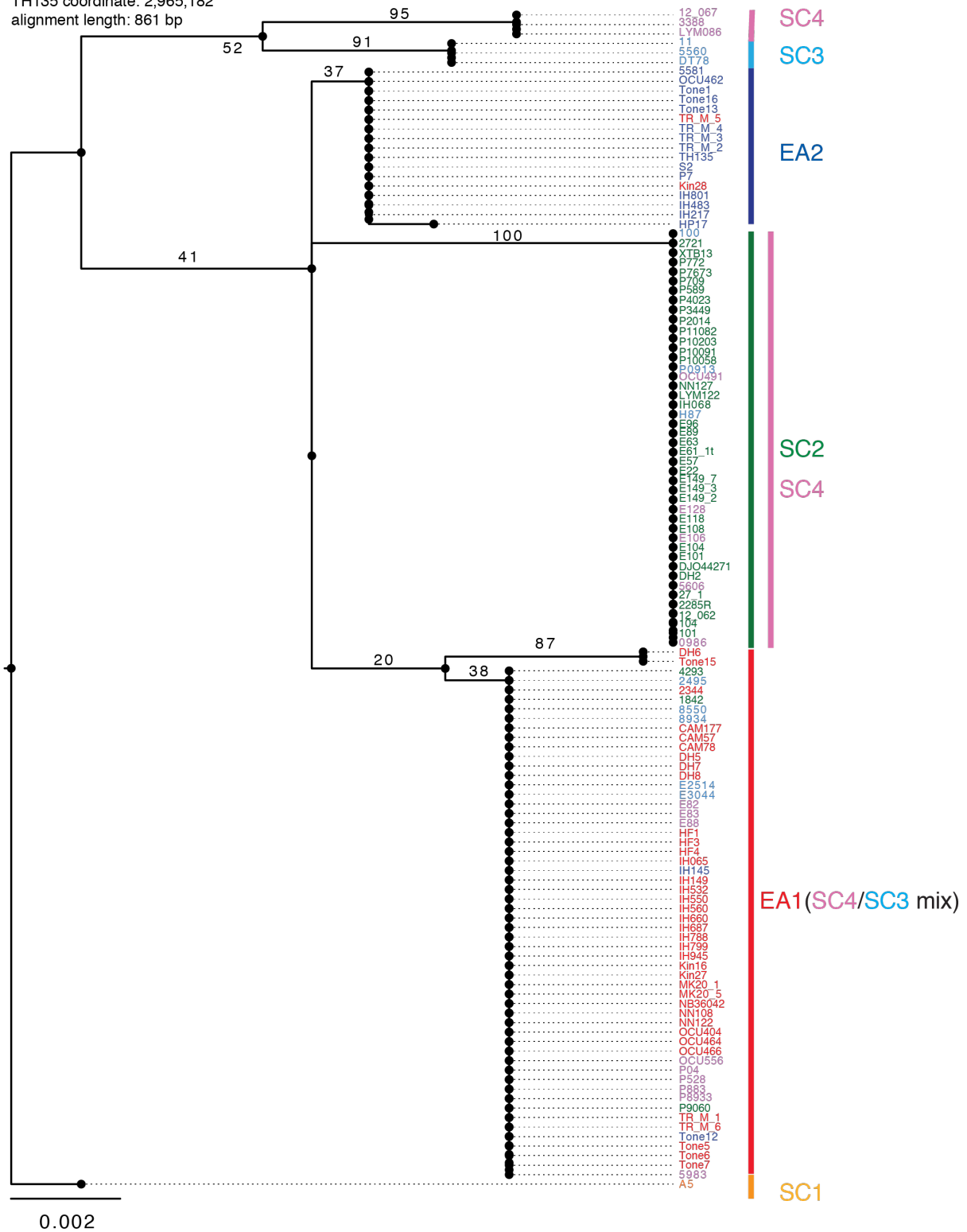
locus\_tag: MAH\_0809 in strain TH135; MAV\_0960 in strain 104  
gene name: not assigned  
product name: hypothetical protein or membrane protein  
nuc. diversity: 9.4242  
hap. diversity: 0.6985  
n.allele: 10  
TH135 coordinate: 813,897  
alignment length: 758 bp



Additional file 3

(v) MAH\_2714

locus\_tag: MAH\_2714 in TH135; MAV\_2410 in strain 104  
gene name: tatC  
product name: Sec-independent protein translocase protein TatC  
nuc. diversity: 5.3282  
hap. diversity: 0.6716  
n.allele: 8  
TH135 coordinate: 2,965,182  
alignment length: 861 bp



Additional file 3

(vi) *hsp65*

locus tag: MAH\_4120 in strain TH135; MAV\_4707 in strain 104

gene name: *groEL1*

product name: molecular cheperone GroEL

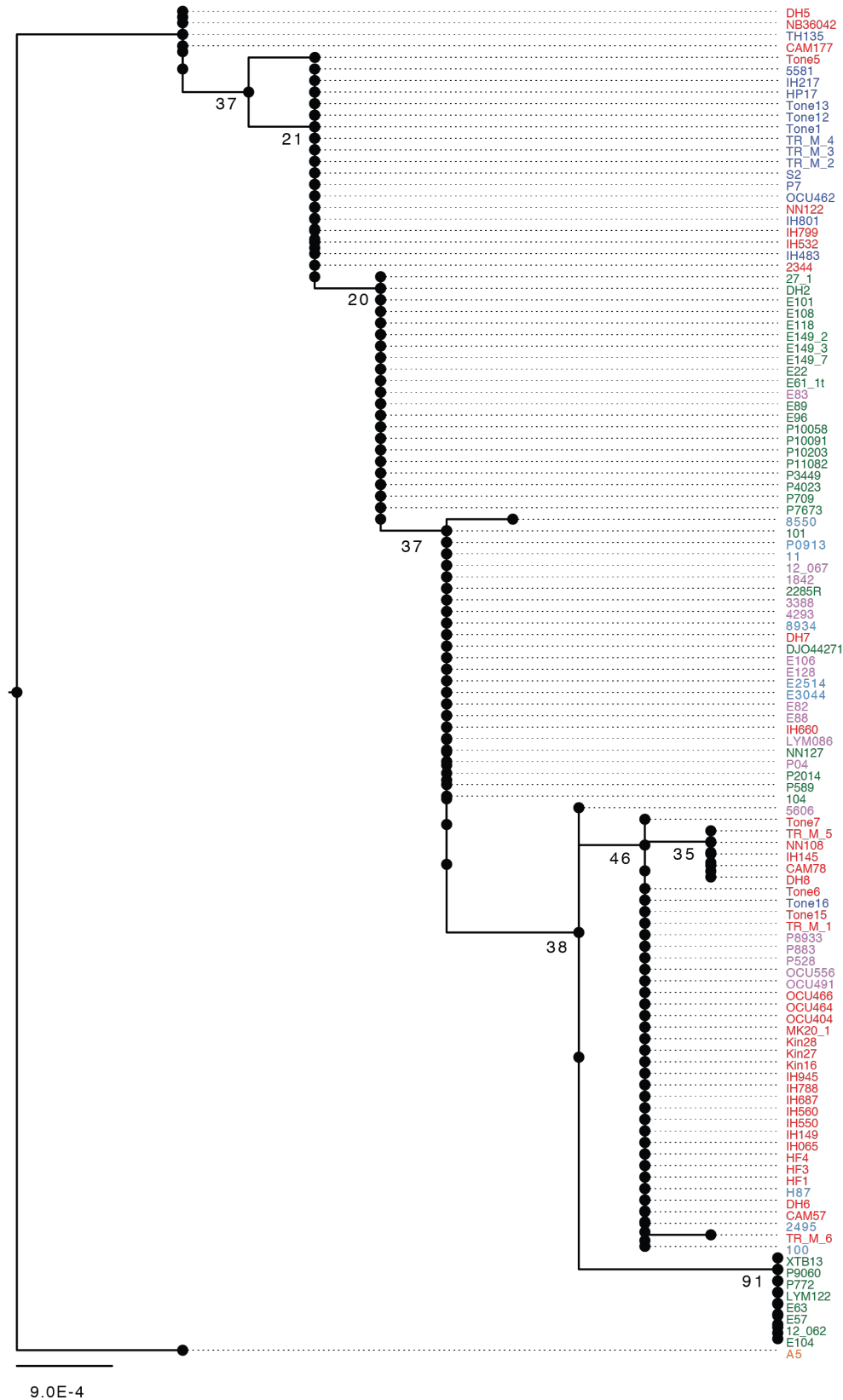
nuc.diversity: 2.7827

hap.diversity: 0.8262

n.allele: 12

TH135 coordinate: 4,400,278

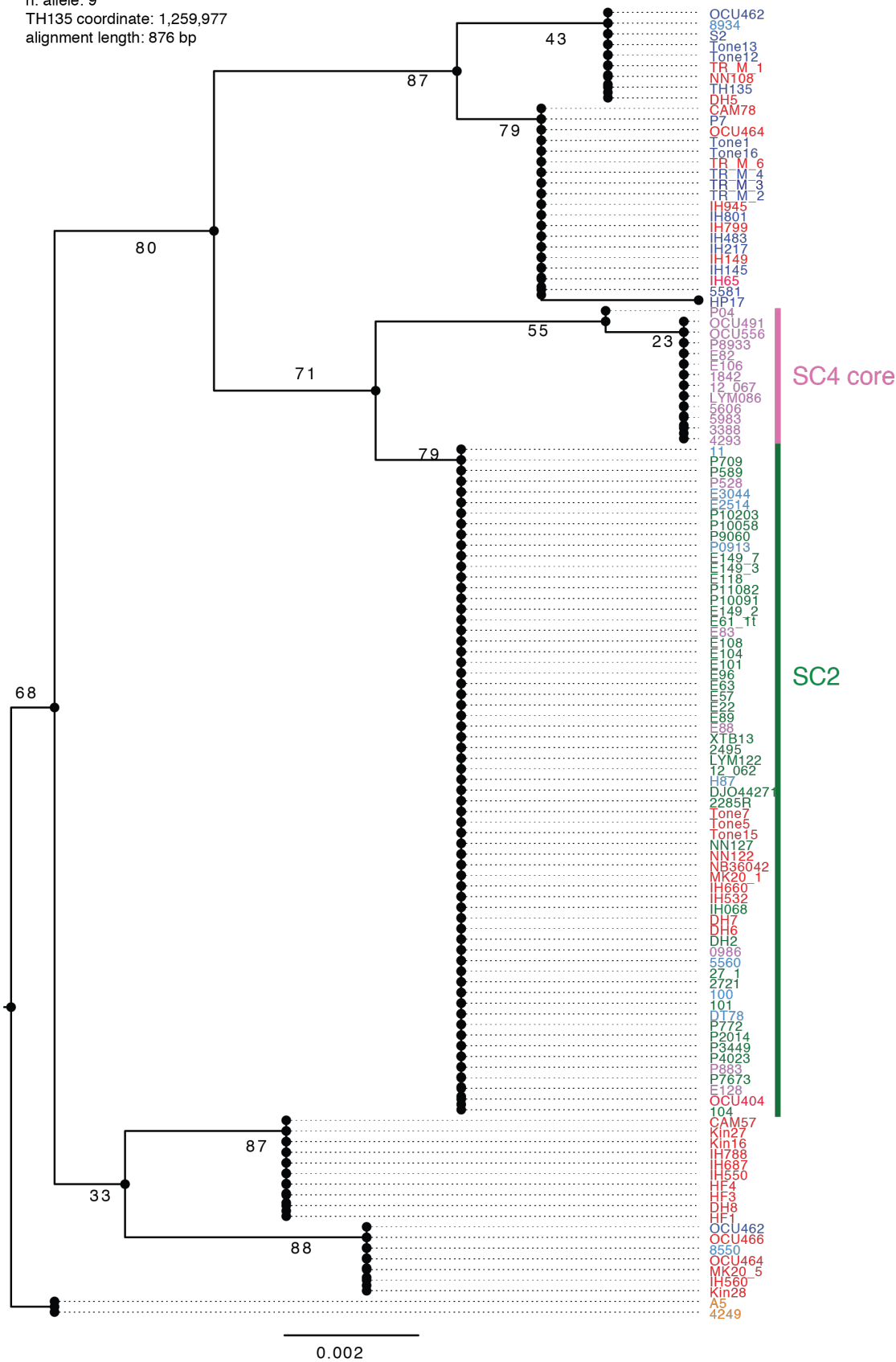
alignment length: 1,623 bp



Additional file 3

(vii) MAV\_1375

locus tag: MAH\_1236 in strain TH135; MAV\_1375 in strain 104  
gene name: *sugA*  
product name: trehalose ABC transporter permease  
nuc.diversity: 4.909769  
hap.diversity: 0.6967880  
n. allele: 9  
TH135 coordinate: 1,259,977  
alignment length: 876 bp



(viii) MAV\_2820

A phylogenetic tree illustrating the evolutionary relationships among 100 bacterial strains. The tree is rooted on the left and branches out to the right. Bootstrap values are indicated at the nodes, representing the confidence in the branching order. The strains are listed on the right side of the tree, color-coded by group: blue for the first large cluster, red for the second large cluster, and black for the third large cluster. The tree shows a high degree of genetic differentiation between the three main clusters, with bootstrap values of 98 at the base of each major branch. Within each cluster, there are several sub-clusters with varying degrees of support.

Key features of the tree include:

- Rooting:** The tree is rooted on the left, with a bootstrap value of 98 at the base.
- Major Clusters:** The tree is divided into three main clusters, each supported by a bootstrap value of 98.
  - Cluster 1 (Blue):** Contains strains such as P04, OCU491, OCU493, OCU495, OCU496, OCU497, OCU498, OCU499, OCU500, OCU501, OCU502, OCU503, OCU504, OCU505, OCU506, OCU507, OCU508, OCU509, OCU510, OCU511, OCU512, OCU513, OCU514, OCU515, OCU516, OCU517, OCU518, OCU519, OCU520, OCU521, OCU522, OCU523, OCU524, OCU525, OCU526, OCU527, OCU528, OCU529, OCU530, OCU531, OCU532, OCU533, OCU534, OCU535, OCU536, OCU537, OCU538, OCU539, OCU540, OCU541, OCU542, OCU543, OCU544, OCU545, OCU546, OCU547, OCU548, OCU549, OCU550, OCU551, OCU552, OCU553, OCU554, OCU555, OCU556, OCU557, OCU558, OCU559, OCU560, OCU561, OCU562, OCU563, OCU564, OCU565, OCU566, OCU567, OCU568, OCU569, OCU570, OCU571, OCU572, OCU573, OCU574, OCU575, OCU576, OCU577, OCU578, OCU579, OCU580, OCU581, OCU582, OCU583, OCU584, OCU585, OCU586, OCU587, OCU588, OCU589, OCU590, OCU591, OCU592, OCU593, OCU594, OCU595, OCU596, OCU597, OCU598, OCU599, OCU600, OCU601, OCU602, OCU603, OCU604, OCU605, OCU606, OCU607, OCU608, OCU609, OCU610, OCU611, OCU612, OCU613, OCU614, OCU615, OCU616, OCU617, OCU618, OCU619, OCU620, OCU621, OCU622, OCU623, OCU624, OCU625, OCU626, OCU627, OCU628, OCU629, OCU630, OCU631, OCU632, OCU633, OCU634, OCU635, OCU636, OCU637, OCU638, OCU639, OCU640, OCU641, OCU642, OCU643, OCU644, OCU645, OCU646, OCU647, OCU648, OCU649, OCU650, OCU651, OCU652, OCU653, OCU654, OCU655, OCU656, OCU657, OCU658, OCU659, OCU660, OCU661, OCU662, OCU663, OCU664, OCU665, OCU666, OCU667, OCU668, OCU669, OCU670, OCU671, OCU672, OCU673, OCU674, OCU675, OCU676, OCU677, OCU678, OCU679, OCU680, OCU681, OCU682, OCU683, OCU684, OCU685, OCU686, OCU687, OCU688, OCU689, OCU690, OCU691, OCU692, OCU693, OCU694, OCU695, OCU696, OCU697, OCU698, OCU699, OCU700, OCU701, OCU702, OCU703, OCU704, OCU705, OCU706, OCU707, OCU708, OCU709, OCU710, OCU711, OCU712, OCU713, OCU714, OCU715, OCU716, OCU717, OCU718, OCU719, OCU720, OCU721, OCU722, OCU723, OCU724, OCU725, OCU726, OCU727, OCU728, OCU729, OCU730, OCU731, OCU732, OCU733, OCU734, OCU735, OCU736, OCU737, OCU738, OCU739, OCU740, OCU741, OCU742, OCU743, OCU744, OCU745, OCU746, OCU747, OCU748, OCU749, OCU750, OCU751, OCU752, OCU753, OCU754, OCU755, OCU756, OCU757, OCU758, OCU759, OCU760, OCU761, OCU762, OCU763, OCU764, OCU765, OCU766, OCU767, OCU768, OCU769, OCU770, OCU771, OCU772, OCU773, OCU774, OCU775, OCU776, OCU777, OCU778, OCU779, OCU780, OCU781, OCU782, OCU783, OCU784, OCU785, OCU786, OCU787, OCU788, OCU789, OCU790, OCU791, OCU792, OCU793, OCU794, OCU795, OCU796, OCU797, OCU798, OCU799, OCU800, OCU801, OCU802, OCU803, OCU804, OCU805, OCU806, OCU807, OCU808, OCU809, OCU810, OCU811, OCU812, OCU813, OCU814, OCU815, OCU816, OCU817, OCU818, OCU819, OCU820, OCU821, OCU822, OCU823, OCU824, OCU825, OCU826, OCU827, OCU828, OCU829, OCU830, OCU831, OCU832, OCU833, OCU834, OCU835, OCU836, OCU837, OCU838, OCU839, OCU840, OCU841, OCU842, OCU843, OCU844, OCU845, OCU846, OCU847, OCU848, OCU849, OCU850, OCU851, OCU852, OCU853, OCU854, OCU855, OCU856, OCU857, OCU858, OCU859, OCU860, OCU861, OCU862, OCU863, OCU864, OCU865, OCU866, OCU867, OCU868, OCU869, OCU870, OCU871, OCU872, OCU873, OCU874, OCU875, OCU876, OCU877, OCU878, OCU879, OCU880, OCU881, OCU882, OCU883, OCU884, OCU885, OCU886, OCU887, OCU888, OCU889, OCU890, OCU891, OCU892, OCU893, OCU894, OCU895, OCU896, OCU897, OCU898, OCU899, OCU900, OCU901, OCU902, OCU903, OCU904, OCU905, OCU906, OCU907, OCU908, OCU909, OCU910, OCU911, OCU912, OCU913, OCU914, OCU915, OCU916, OCU917, OCU918, OCU919, OCU920, OCU921, OCU922, OCU923, OCU924, OCU925, OCU926, OCU927, OCU928, OCU929, OCU930, OCU931, OCU932, OCU933, OCU934, OCU935, OCU936, OCU937, OCU938, OCU939, OCU940, OCU941, OCU942, OCU943, OCU944, OCU945, OCU946, OCU947, OCU948, OCU949, OCU950, OCU951, OCU952, OCU953, OCU954, OCU955, OCU956, OCU957, OCU958, OCU959, OCU960, OCU961, OCU962, OCU963, OCU964, OCU965, OCU966, OCU967, OCU968, OCU969, OCU970, OCU971, OCU972, OCU973, OCU974, OCU975, OCU976, OCU977, OCU978, OCU979, OCU980, OCU981, OCU982, OCU983, OCU984, OCU985, OCU986, OCU987, OCU988, OCU989, OCU990, OCU991, OCU992, OCU993, OCU994, OCU995, OCU996, OCU997, OCU998, OCU999, OCU1000.
- Cluster 2 (Red):** Contains strains such as P04, OCU491, OCU493, OCU495, OCU496, OCU497, OCU498, OCU499, OCU500, OCU501, OCU502, OCU503, OCU504, OCU505, OCU506, OCU507, OCU508, OCU509, OCU510, OCU511, OCU512, OCU513, OCU514, OCU515, OCU516, OCU517, OCU518, OCU519, OCU520, OCU521, OCU522, OCU523, OCU524, OCU525, OCU526, OCU527, OCU528, OCU529, OCU530, OCU531, OCU532, OCU533, OCU534, OCU535, OCU536, OCU537, OCU538, OCU539, OCU540, OCU541, OCU542, OCU543, OCU544, OCU545, OCU546, OCU547, OCU548, OCU549, OCU550, OCU551, OCU552, OCU553, OCU554, OCU555, OCU556, OCU557, OCU558, OCU559, OCU560, OCU561, OCU562, OCU563, OCU564, OCU565, OCU566, OCU567, OCU568, OCU569, OCU570, OCU571, OCU572, OCU573, OCU574, OCU575, OCU576, OCU577, OCU578, OCU579, OCU580, OCU581, OCU582, OCU583, OCU584, OCU585, OCU586, OCU587, OCU588, OCU589, OCU590, OCU591, OCU592, OCU593, OCU594, OCU595, OCU596, OCU597, OCU598, OCU599, OCU600, OCU601, OCU602, OCU603, OCU604, OCU605, OCU606, OCU607, OCU608, OCU609, OCU610, OCU611, OCU612, OCU613, OCU614, OCU615, OCU616, OCU617, OCU

SC2

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