

Supplementary materials Raitzz et al.

File S1. Sweep Analyses

In this study, not all results were performed on specific scripts. In some cases, the results were obtained step by step in the MATLAB® command window and in other data of interchange between the various applied software. Below, is included excerpts from scripts with details and the links to the tools used that can assist in understanding the methods.

- 1) Function to calculate the distance of SWeeP Vectors:

```
pdist()
```

pdist() is a standard function in MATLAB® that calculate the pairwise distance (by default Euclidean distances) between observations (vectors);

- 2) Excerpt of script to obtain neighbour joining:

```
treeout = seqneighjoin(xdist,'equivar',xnames);
```

Were *xdist* is a *pdist* vector (MATLAB standart result from a *pdist()* function call) and *xname* is a cell var with the nodes names.

- 3) Normalization by the mean of ANI matrices:

Here, the normalization was performed for the upper and lower ANI matrices separately (see the script below). First, ANI was converted into dissimilarity matrices and then the lower and upper matrices were divided by their corresponding mean values. It was decided to normalize the mean to guarantee a better correspondence between the matrices in the visualization. This technique allowed us to compare different distance / dissimilarity matrices in the same heat map.

```
% ANI matrix  
MANI  
  
% Transforms lower and upper ANI matrices in dissimilarity  
matrices
```

```

D1 = 100 - tril(MANI)+tril(MANI)';
D2 = 100 - triu(MANI)+triu(MANI) '
% iani1 - Order for Lower triangular part of the ANI matrix
[~ iani1] = HFclus(distmat2pdist(D1),'Method','Nj');
% iani2 - Order for upper triangular part of the ANI matrix
[~ iani2] = HFclus(distmat2pdist(D2),'Method','Nj');
% HFclus is an 'in house' function used for several purposes;
here it receives a MATLAB pdist vector and returns de order
of the leaves in the corresponding neighbour joining
phylogenetic tree (exploiting the MATLAB bioinformatics
toolbox functions)

% Normalization and matrix reordering for Heat map
Mx = tril(D1)/mean(D1(:))+triu(D2)/mean(D2(:));
Mx = Mx(iani1,iani2);
% Transforms matrix into image
xHeat = mat2im3(Mx);

```

4) Links to all the programs used in this study:

FastQC

<https://www.bioinformatics.babraham.ac.uk/projects/fastqc/>

Trimmomatic

<http://www.usadellab.org/cms/?page=trimmomatic>

BBMap

<https://sourceforge.net/projects/bbmap/>

SPAdes

<https://cab.spbu.ru/software/spades/>

Prokka

<https://github.com/tseemann/prokka>

QUAST

<http://quast.sourceforge.net/>

FastANI

<https://github.com/ParBLISS/FastANI>

RAFTS3G

<https://sourceforge.net/projects/rafts-g/>

SWeeP

<https://sourceforge.net/projects/spacedwordsprojection/>

Dendroscope

<https://software-ab.informatik.uni-tuebingen.de/download/dendroscope3/welcome.html>

Clustal Omega

<https://www.ebi.ac.uk/Tools/msa/clustalo/>

IQ-Tree

<http://www.iqtree.org/>

File S2. Growth conditions for assessment of nitrogenase activity using the acetylene reduction assay

Azoarcus olearius DQS-4^T, *Az. communis* Swub3^T, *Az. communis* LMG 5514 (LMG), *Az. indigenus* VB32^T, and *Azoarcus* sp. TTM-91 were grown on SM or CVM media, prepared following the composition described in [1]. The SM medium was supplemented with a vitamin solution (1 mg L⁻¹ thiamine hydrochloride, 2 mg L⁻¹ D-pantothenic acid, 1 mg L⁻¹ nicotinic acid, and 0.1 mg L⁻¹ biotin) modified from UMS medium [2]. Semi solid medium (SM or ½CVM) was prepared at the moment of use by mixing pre-warmed solid (1.5% agar) and liquid media to reach a final concentration of 0.18% agar. ½CVM is CVM [1] but with half of the amount of bactopeptone and yeast extract *i.e.* 1.5 and 0.5 g L⁻¹, respectively. *Aromatoleum* sp. CIB and *Ar. toluovorans* Td21^T were grown on MNF medium [3] supplemented with 3 mM sodium benzoate as carbon source.

Prior to the nitrogenase activity assay, *Az. olearius*, DQS-4^T, *Az. communis* Swub3^T, *Az. communis* LMG 5514 (LMG), *Az. indigenus* VB32^T, and *Azoarcus* sp. TTM-91 were streaked from glycerol stocks into CVM amended with 20 mM NH₄Cl (CVM+N) and incubated at 30°C for 3–5 days. Isolated colonies were then inoculated into 3 mL of liquid CVM+N (in 30 mL plastic universal tubes) and incubated at 30°C and 120 rpm. Once the culture reached saturation, a further inoculation (1/100) in liquid medium was performed before the inoculation into semi-solid medium (SM amended with 0.5 mM sodium glutamate for *Az. olearius*, DQS-4^T, *Az. communis* Swub3^T, and *Az. communis* LMG 5514, or ½CVM for *Az. indigenus* VB32^T, and *Azoarcus* sp. TTM-91). The semi-solid medium (3 mL) was set in a 7 mL glass vial (Fisherbrand™ #14873562). Liquid cultures (15–60 µL), pre-grown as above, were used for inoculation into the center-bottom of vials of semi-solid media which was aimed at achieving approximately the same number of cells (OD_{600nm} = 0.01 approximately) across the different inocula. Cells were incubated for 18–24 hours, or until the bacterial pellicle reached the meniscus. Once the pellicle was formed, the plastic cap from the vial was replaced by a suba-seal rubber stopper (n° 21) and the substrate, acetylene (10% of the gas phase), for the nitrogenase activity assay was injected. A similar pre-inoculation procedure was used to assay the nitrogenase activity in *Aromatoleum* sp. CIB and *Ar. toluovorans* Td21^T except that MNF medium was supplemented with 3 mM sodium benzoate as carbon source and 5 mM KNO₃ as nitrogen source. The second re-inoculation into liquid medium was performed on a higher volume, 20 mL of medium in a 100 mL Erlenmeyer flask at 30°C and 120 rpm. Cells were then washed in MNF + 3 mM sodium benzoate to remove excess nitrate and then re-inoculated into fresh medium without nitrate to an OD_{600nm} of approximately 0.01. Ten mL cells (OD_{600nm} of 0.01), were transferred to 20 mL glass universal tubes, sealed with suba-seal rubber stopper n°41 and incubated for 24 hours at 30°C and 120 rpm before injection of the acetylene (10% of the gas phase). *Ar. diolicum* 22Lin^T was grown on UMS medium supplemented with 30 mM malate as carbon source and 20 mM NH₄Cl. Prior to the acetylene reduction assay, 50 mL cells were collected by centrifugation (4000 rpm, 8 min) and re-suspended to an initial O.D₆₀₀ of 0.4 (20 mL in an 100 mL Pyrex Erlenmeyer flask) in UMS plus 30 mM malate without added ammonium. The flask was stoppered with a suba-seal (n° 37) and the internal flask atmosphere was adjusted to approximately 1% O₂. After 6 hours incubation, the acetylene reduction assay was performed as above.

References

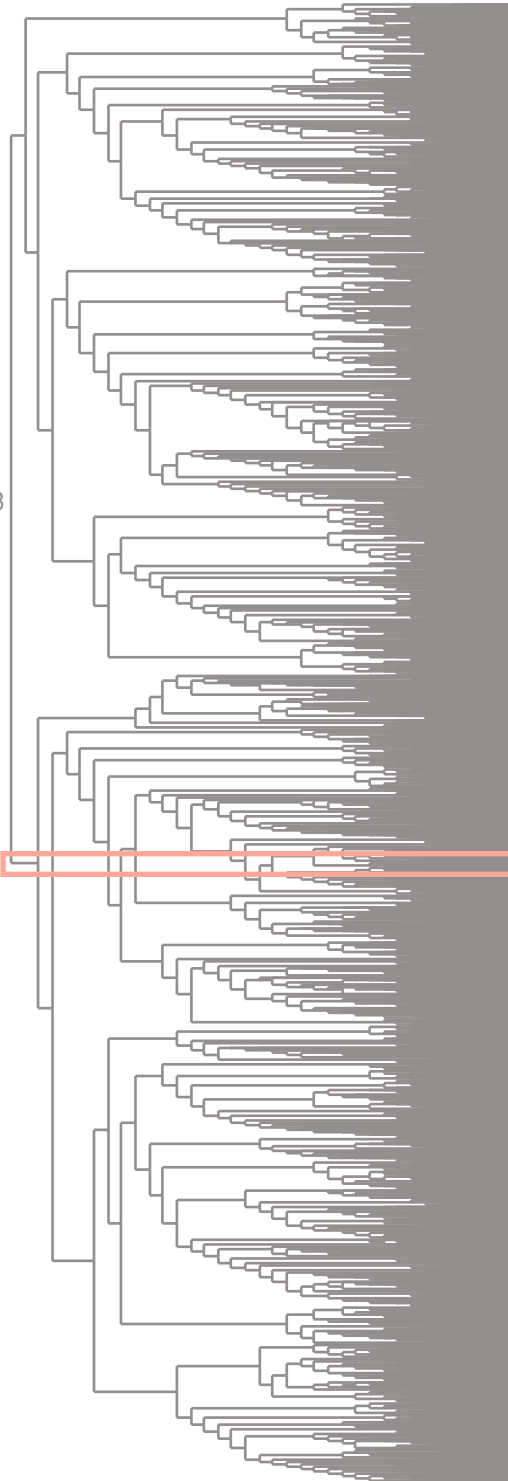
1. Krause, A.; Julich, H.; Mankar, M.; Reinhold-Hurek, B. The regulatory network controlling ethanol-induced expression of alcohol dehydrogenase in the endophyte *Azoarcus* sp. strain BH72. *Mol. Plant-Microbe Interact.* **2017**, 30, 778-785, doi:MPMI-01-17-0013-R.
2. Pini, F.; East, A.K.; Appia-Ayme, C.; Tomek, J.; Karunakaran, R.; Mendoza-Suarez, M.; Edwards, A.; Terpolilli, J.; Rowoth, J.; Downie, J.A.; et al. Bacterial biosensors for in vivo

spatiotemporal mapping of root secretion. *Plant Physiol.* **2017**, 174, 1289-1306, doi:10.1104/pp.16.01302

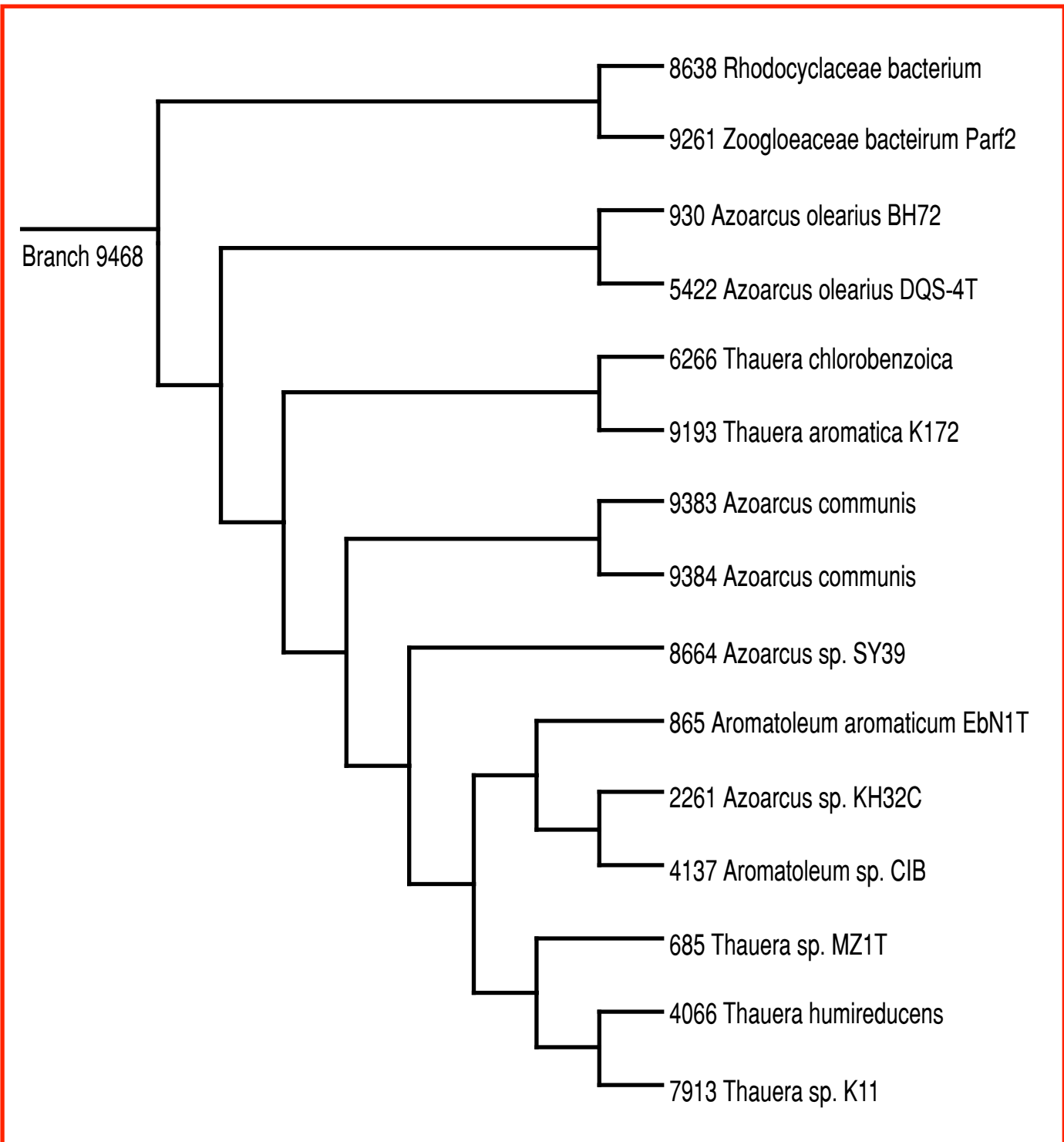
3. Fernández, H.; Prandoni, N.; Fernández-Pascual, M.; Fajardo, S.; Morcillo, C.; Díaz, E.; Carmona, M. *Azoarcus* sp. CIB, an anaerobic biodegrader of aromatic compounds shows an endophytic lifestyle. *PLoS One* **2014**, 9, e110771, doi:10.1371/journal.pone.0110771

S1.

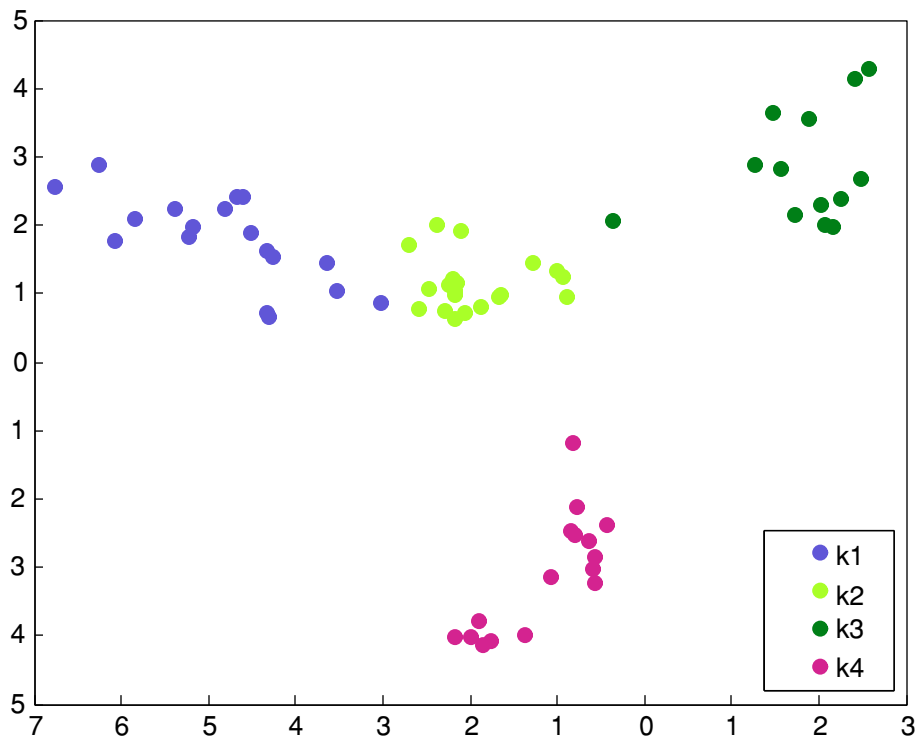
Branch 10323



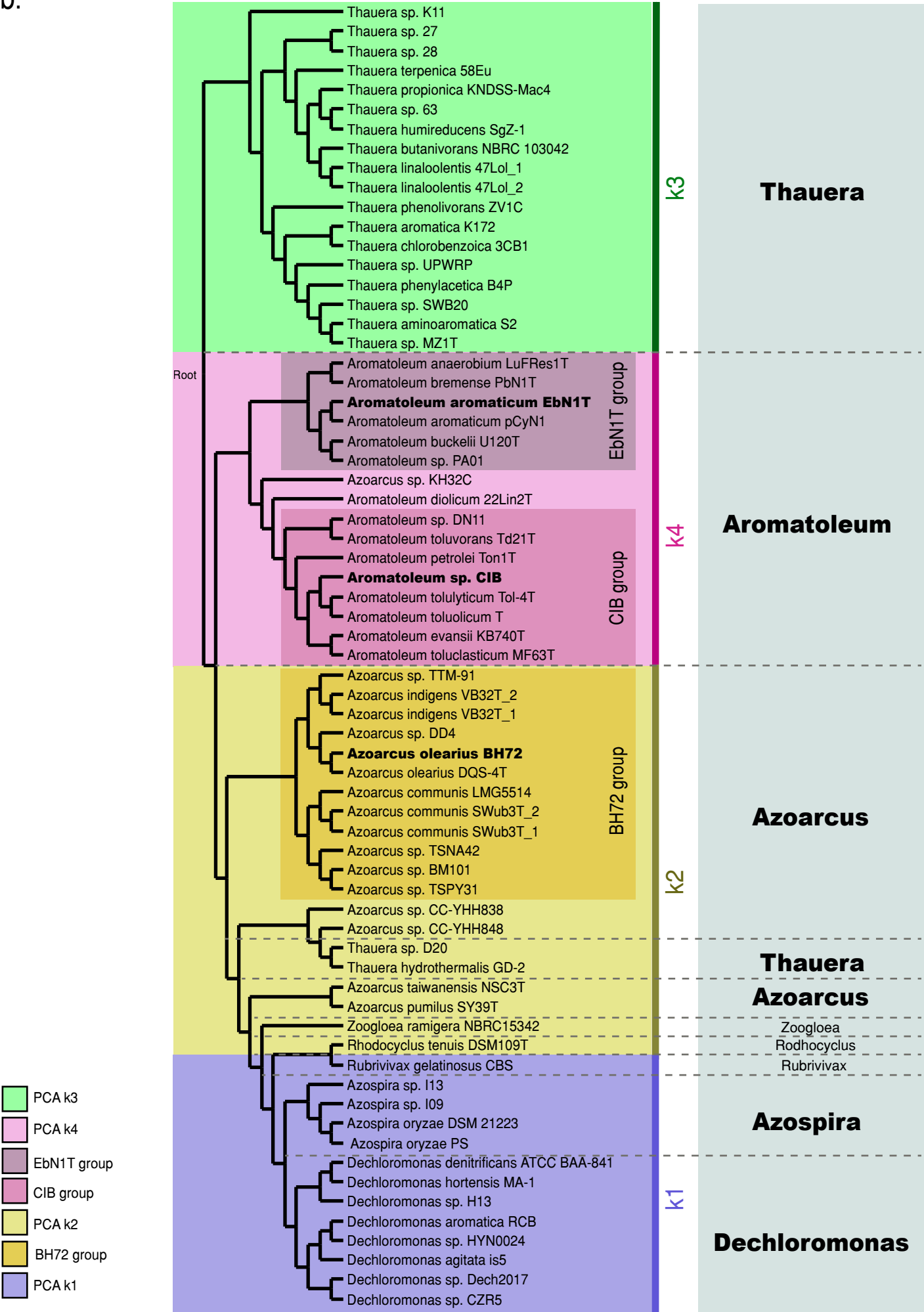
Branch 9468

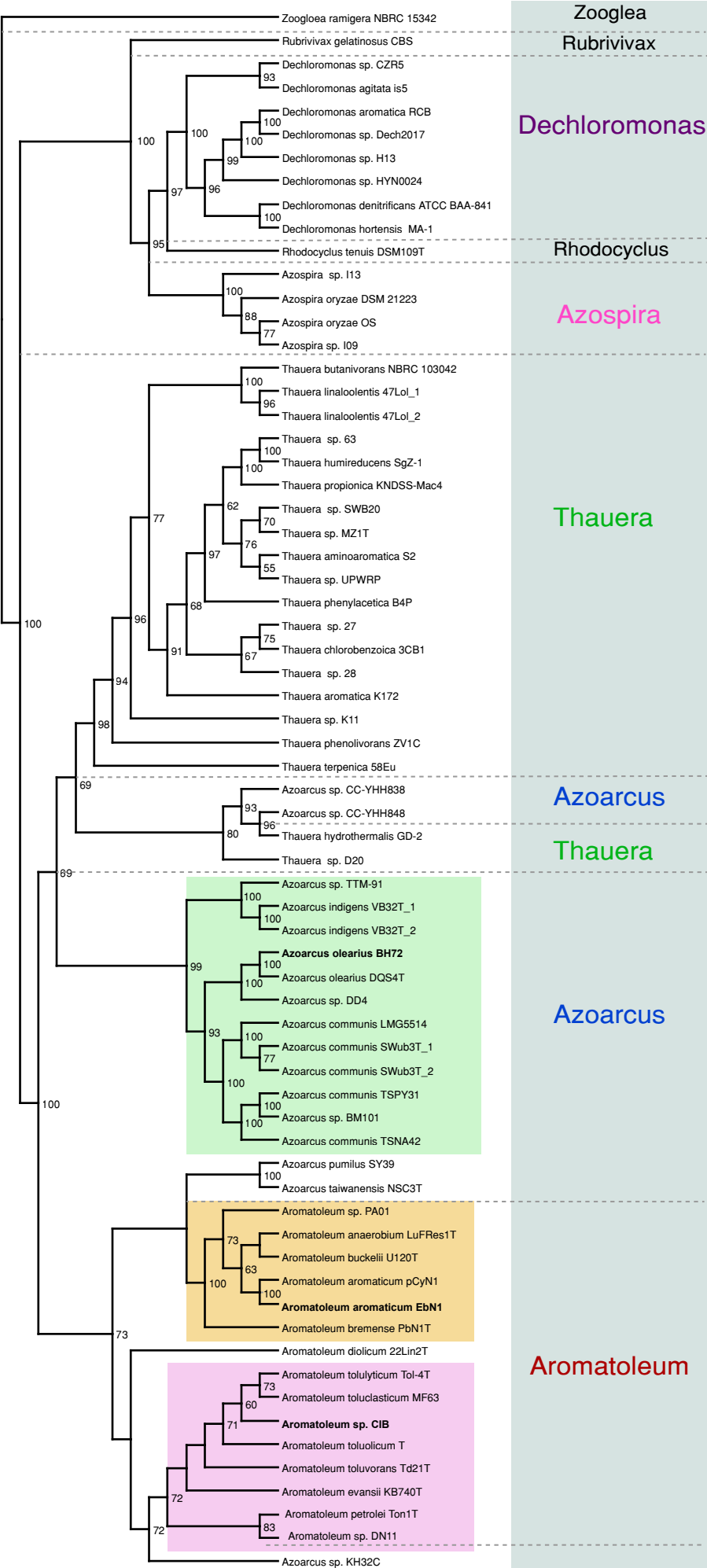


S2a.

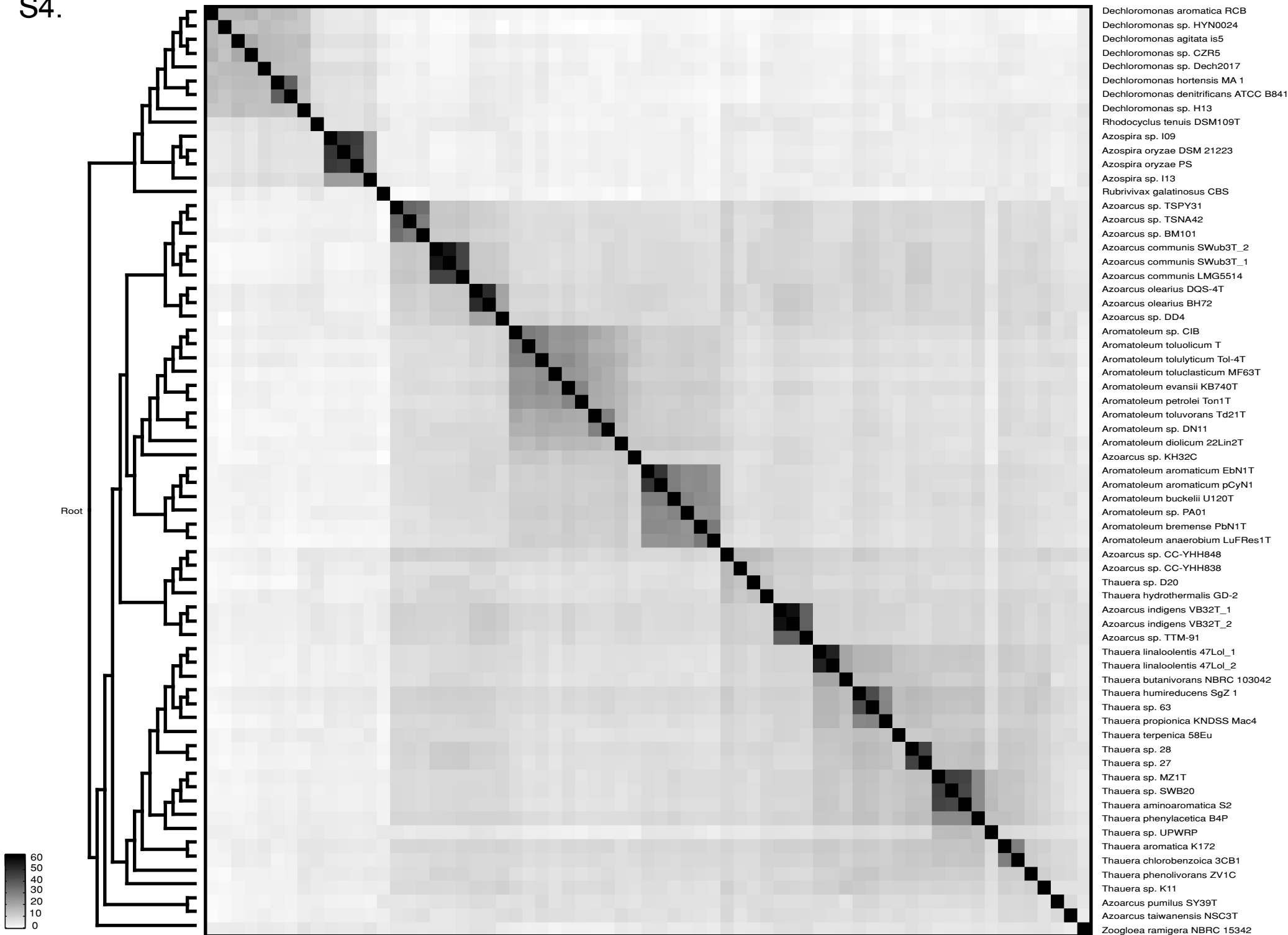


S2b.

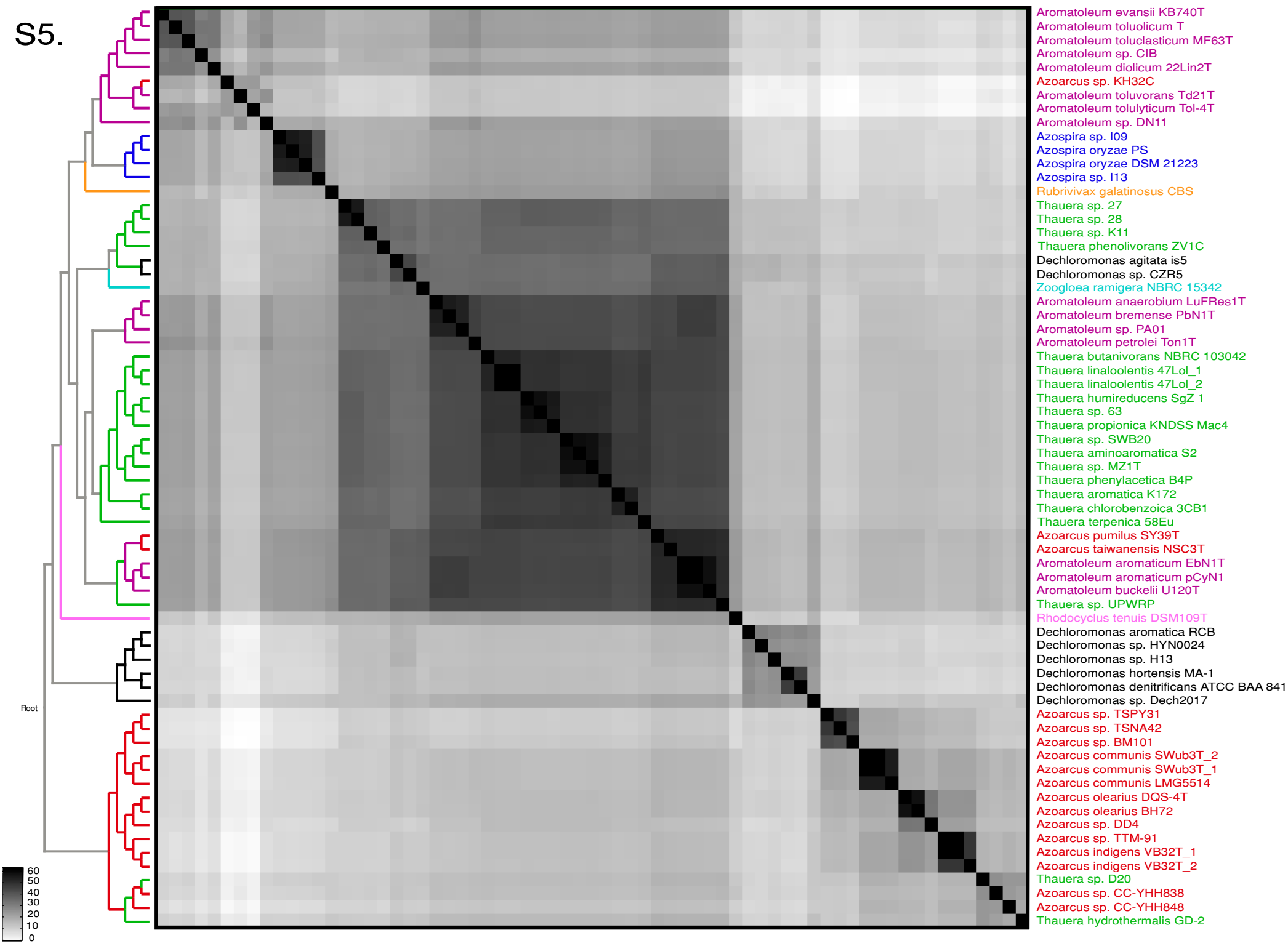




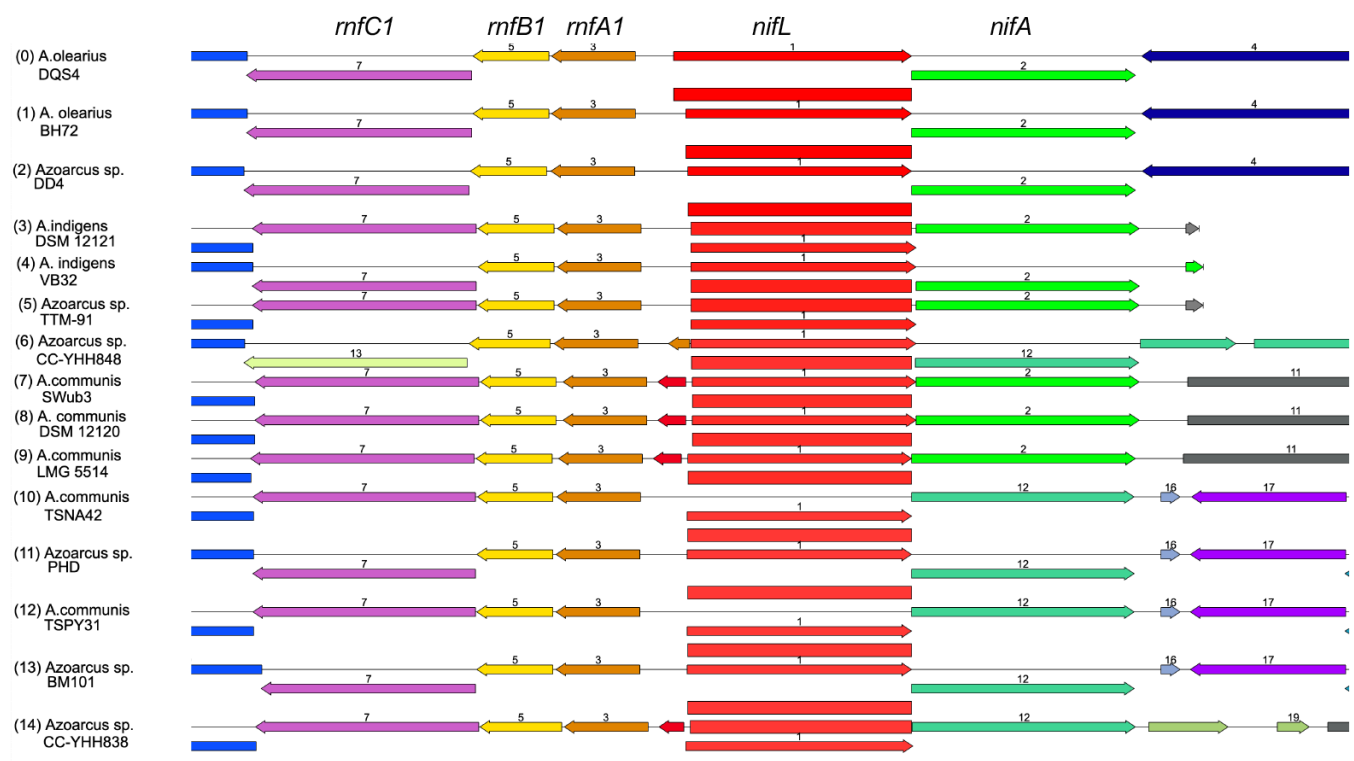
S4.



S5.



S6.
A.



B.

