Supporting information for

A synthetic bacterial community derived from a desert rhizosphere confers salt stress resilience to tomato in the presence of a soil microbiome

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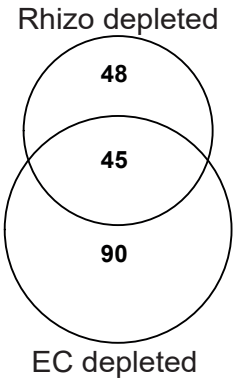
Figures

Fig. S1: Former agricultural areas in the Jizan desert, which suffer from high salinity, are scarcely populated with indigofera.

Fig. S2: Venn diagram showing number of depleted OTUs in the Rhizo and EC of *I. argentea* in comparison to the Soil. See Dataset S2.



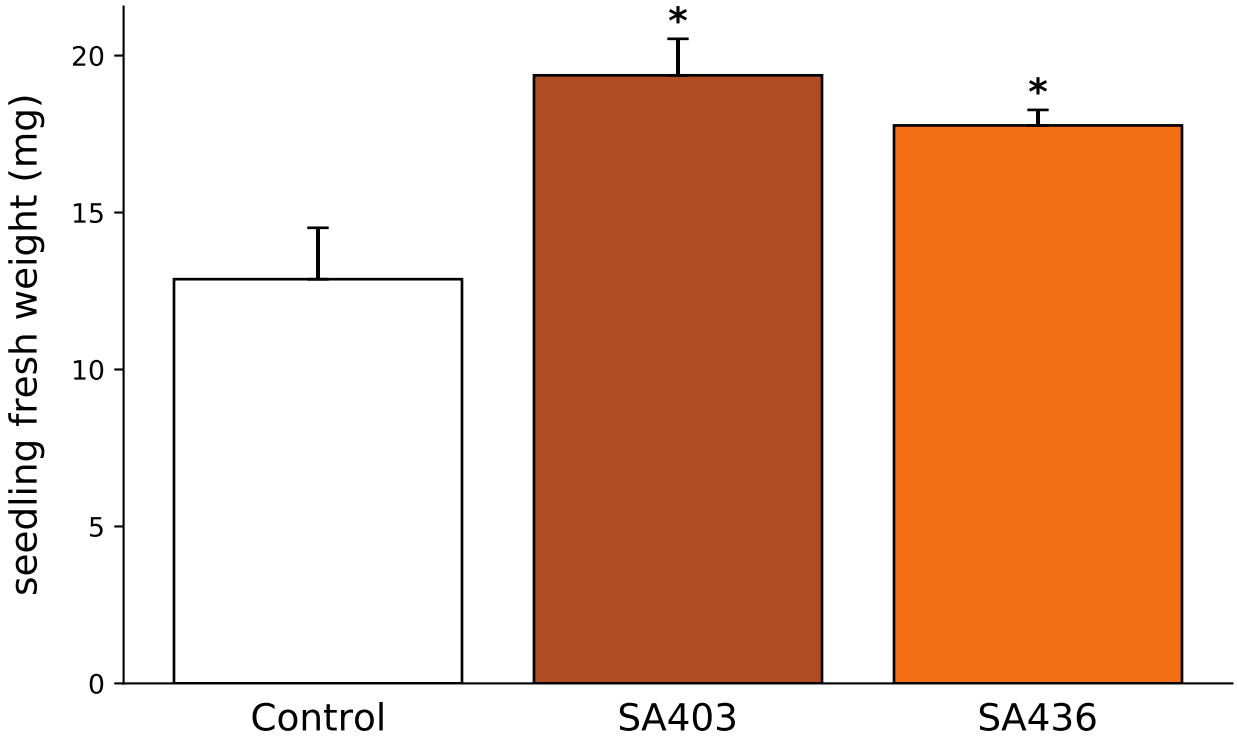
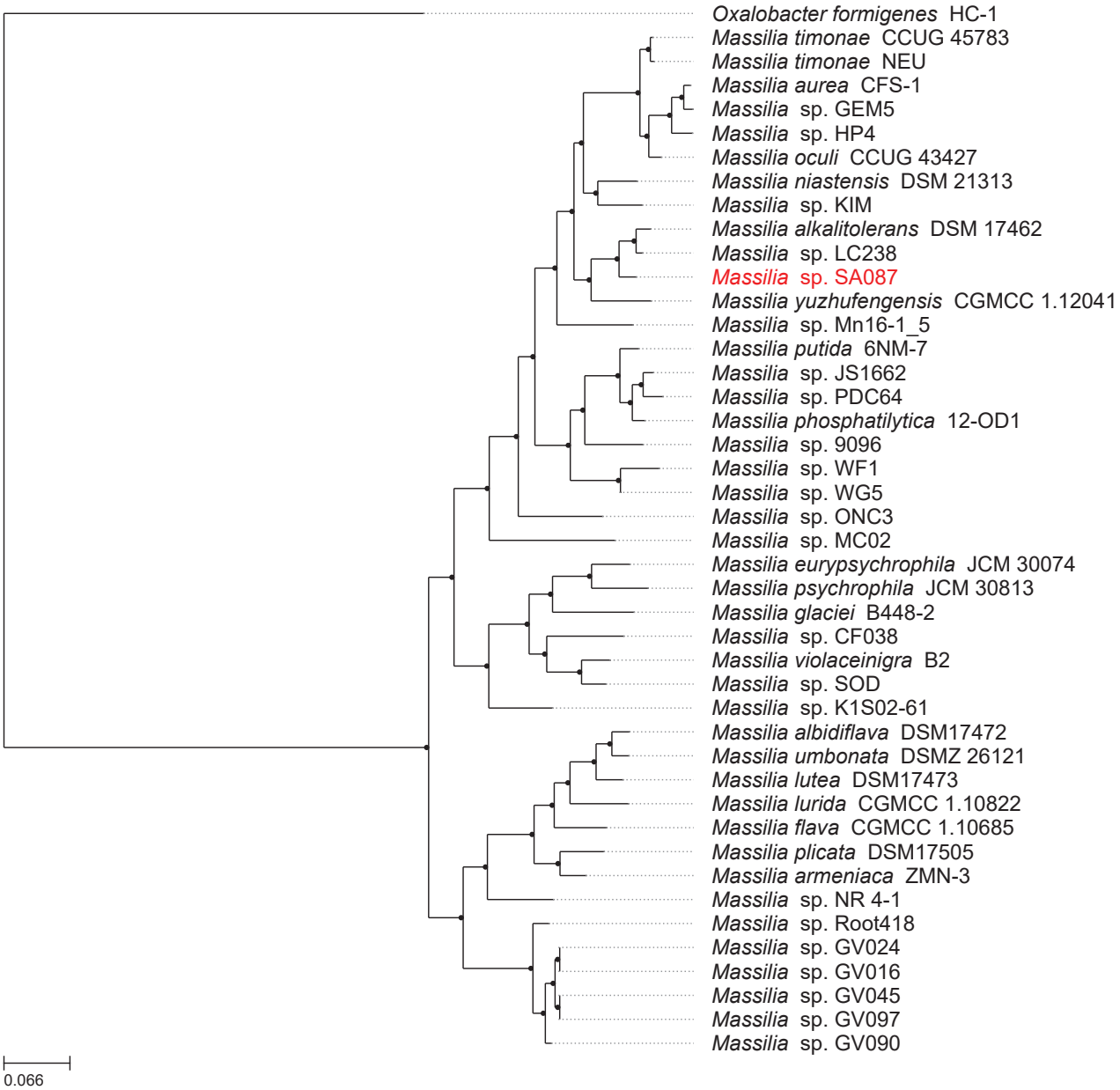


Fig. S3 : Growth promotion of arabidopsis by the Jizan strains *Ensifer* sp. SA403 and *Bacillus* sp. SA436. Ten arabidopsis seeds were grown on a plate which was the experimental unit. There were four experimental units per inoculation which also included a sterile control. Seedling fresh weight was defined as the average weight per experimental unit and determined eleven days post bacterial inoculation. The y-axis shows the average seedling fresh weights with the standard deviation as error bars. An asterisk is a significant difference ($p < 0.05$) from the control per Dunnett's test. Strains SA436 and SA403 were grown in 5 mL $1/10^{th}$ TSB or 5 mL YEM liquid medium, respectively, for 48 hours at 28°C. Bacterial cells were washed and resuspended in 10 mM $MgSO_4$ and the final suspension had an OD_{600} of 1.0 (~109 cfu/mL). Seeds of *Arabidopsis thaliana* Columbia-0 were surface steriled by washing with ethanol and soaking in 1/4 strength commercial bleach for 10 minutes. Seeds were transferred to wet filter paper in Petri dishes. After incubating at 4°C for 3 days, 10 seeds were sown on plates containing 50 mL $1/2^{th}$ Murashige Skoog medium. Two µL of the bacterial suspension was applied to the root tips of one-week-old seedlings. Control plants were inoculated with 2 µL of 10 mM $MgSO_4$.

Fig. S4: Maximum likelihood trees based on the AMPHORA gene alignments of nine different genera. (a) *Massilia*, (b) *Streptomyces*, (c) *Ensifer*, (d) *Bacillus*, (e) *Enterobacter*, (f) *Acinetobacter*, (g) *Ochrobactrum*, (h) *Pseudomonas*, (i) *Ralstonia*. Each tree contains at least one of the strains found in the Jizan SynCom, representative genomes and plant-associated strains for that genus. All trees are rooted on a suitable outgroup and the Jizan strains are colored in red. The distance scale indicates the number of differences between sequences.

a



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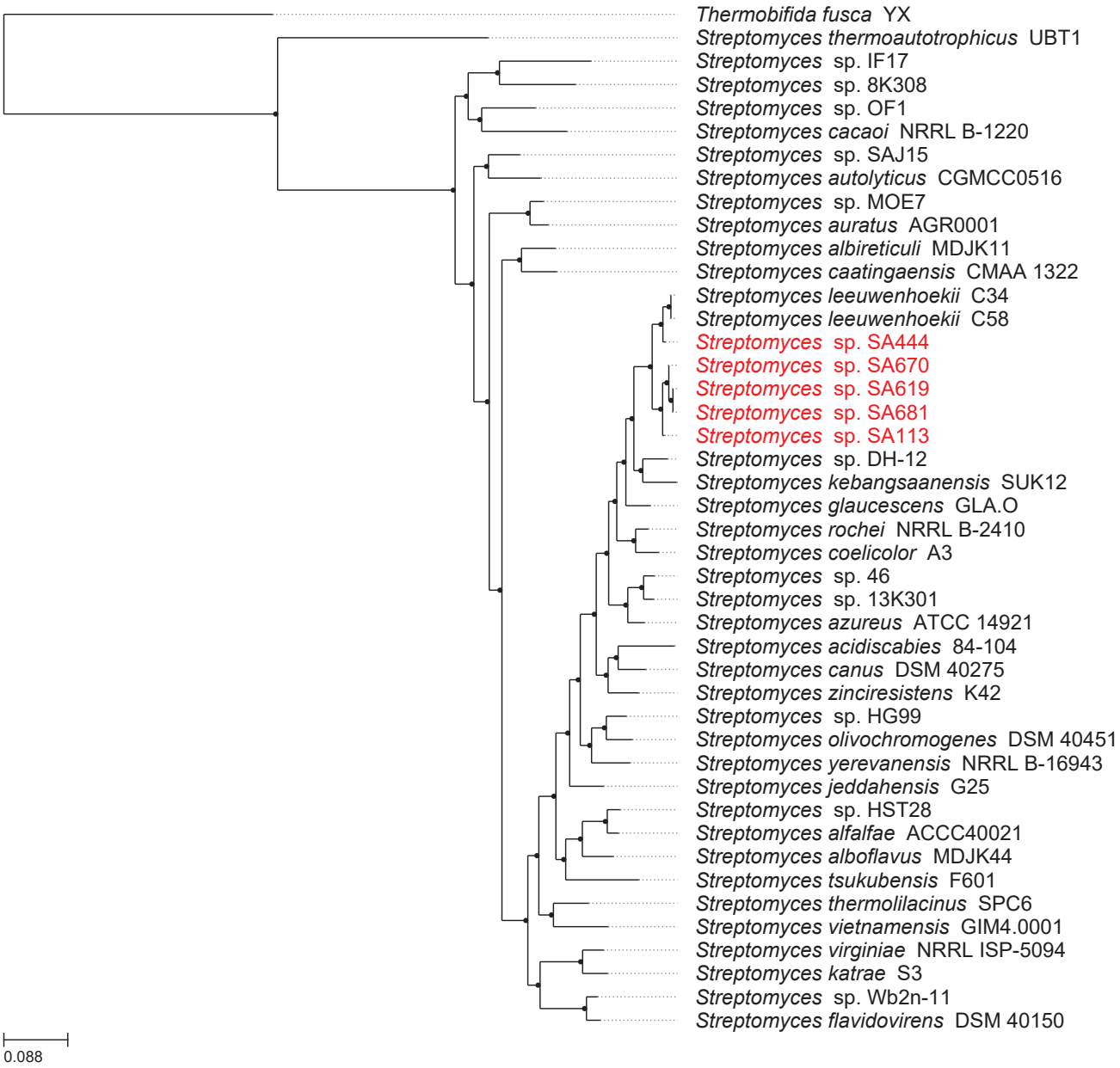
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Streptomyces sp. SAJ15
Streptomyces autolyticus CGMCC0516
Streptomyces sp. MOE7
Streptomyces auratus AGR0001
Streptomyces albireticuli MDJK11
Streptomyces caatingaensis CMAA 1322
Streptomyces leeuwenhoekii C34
Streptomyces leeuwenhoekii C58
Streptomyces sp. SA444
Streptomyces sp. SA670
Streptomyces sp. SA619
Streptomyces sp. SA681
Streptomyces sp. SA113
Streptomyces sp. DH-12
Streptomyces kebangsaanensis SUK12
Streptomyces glaucescens GLA.O
Streptomyces rochei NRRL B-2410
Streptomyces coelicolor A3
Streptomyces sp. 46
Streptomyces sp. 13K301
Streptomyces azureus ATCC 14921
Streptomyces acidiscabies 84-104
Streptomyces canus DSM 40275
Streptomyces zinciresistens K42
Streptomyces sp. HG99
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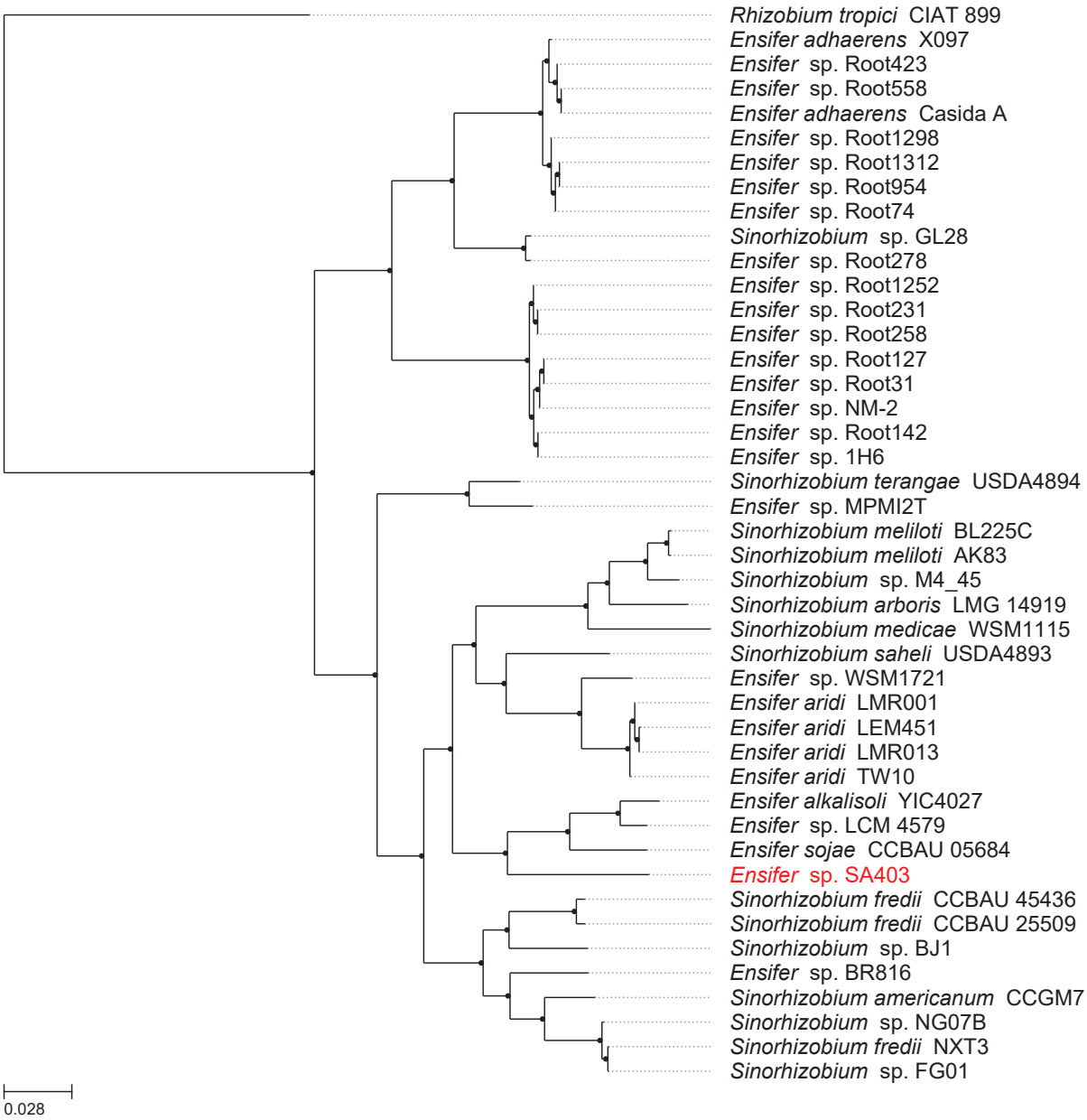
c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Ensifer sp. Root278
Ensifer sp. Root1252
Ensifer sp. Root231
Ensifer sp. Root258
Ensifer sp. Root127
Ensifer sp. Root31
Ensifer sp. NM-2
Ensifer sp. Root142
Ensifer sp. 1H6
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Sinorhizobium medicae WSM1115
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Ensifer aridi LMR001
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Ensifer alkalisoli YIC4027
Ensifer sp. LCM 4579
Ensifer sojae CCBAU 05684
Ensifer sp. SA403
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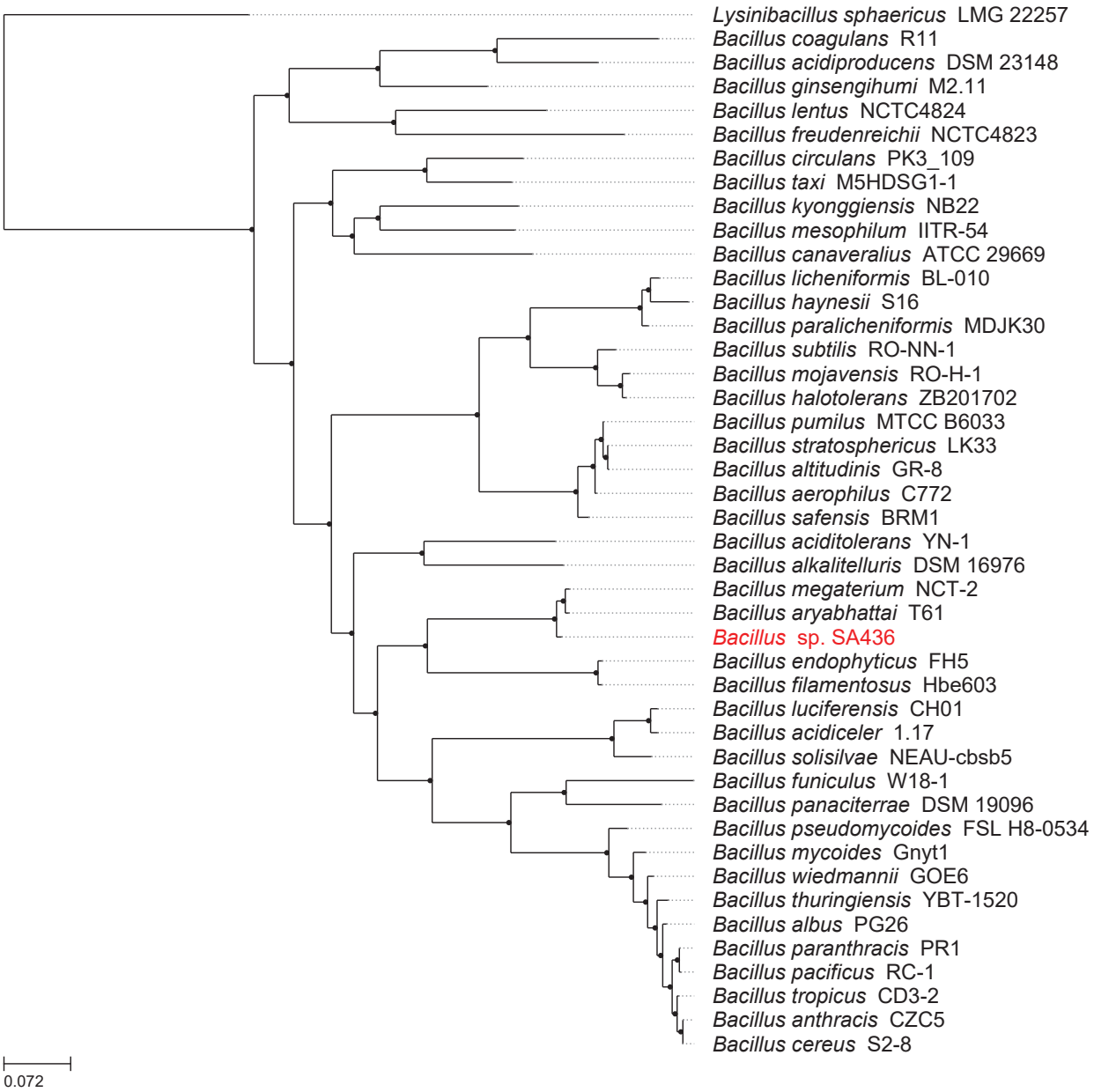
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Bacillus circulans PK3_109
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Bacillus canaveralius ATCC 29669
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Bacillus haynesii S16
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Bacillus megaterium NCT-2
Bacillus aryabhattai T61
Bacillus sp. SA436
Bacillus endophyticus FH5
Bacillus filamentosus Hbe603
Bacillus luciferensis CH01
Bacillus acidiceler 1.17
Bacillus solisilvae NEAU-cbsb5
Bacillus funiculus W18-1
Bacillus panaciterrae DSM 19096
Bacillus pseudomycoides FSL H8-0534
Bacillus mycoides Gnyt1
Bacillus wiedmannii GOE6
Bacillus thuringiensis YBT-1520
Bacillus albus PG26
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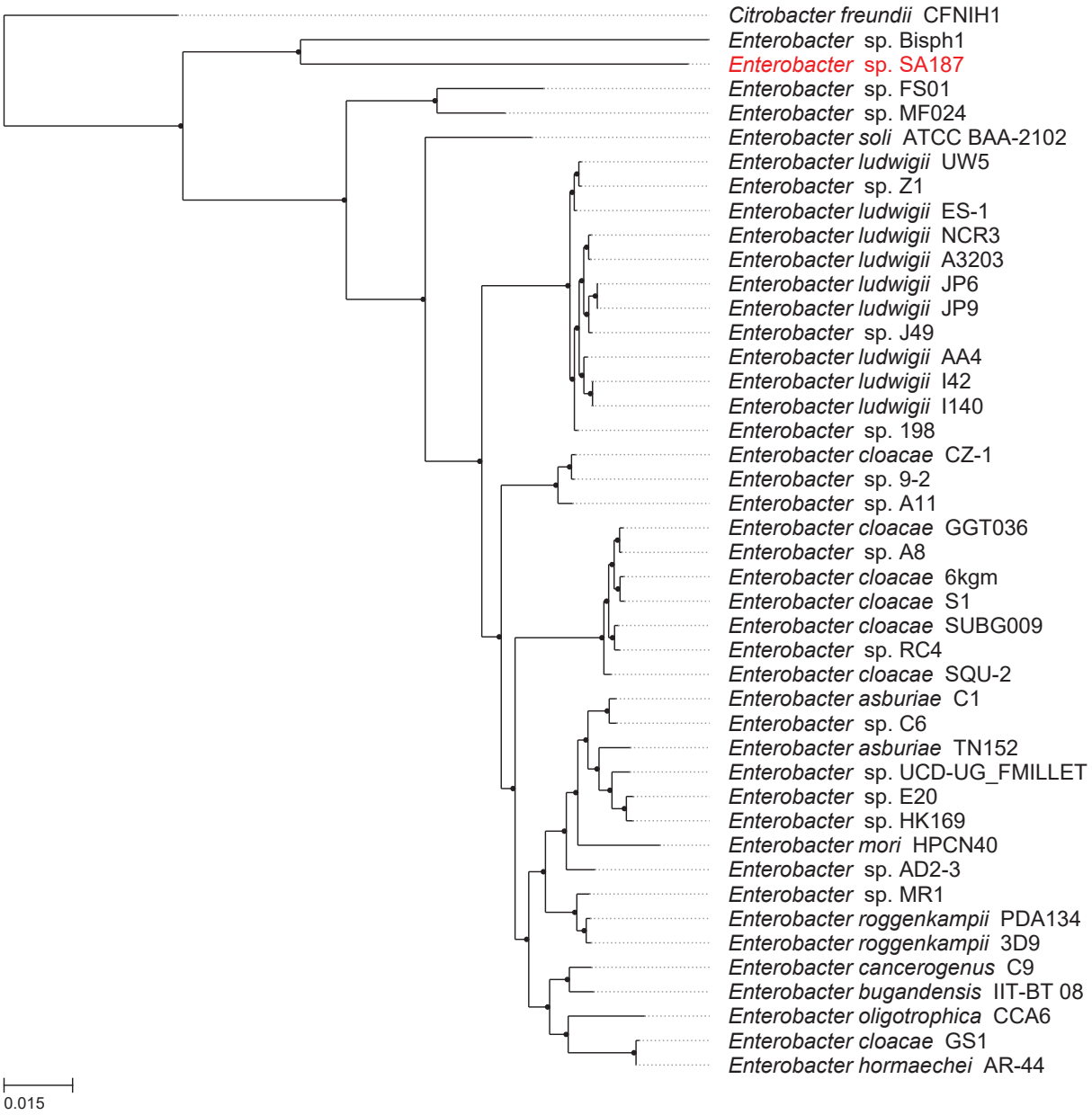
e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Enterobacter ludwigii ES-1
Enterobacter ludwigii NCR3
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Enterobacter ludwigii JP6
Enterobacter ludwigii JP9
Enterobacter sp. J49
Enterobacter ludwigii AA4
Enterobacter ludwigii I42
Enterobacter ludwigii I140
Enterobacter sp. 198
Enterobacter cloacae CZ-1
Enterobacter sp. 9-2
Enterobacter sp. A11
Enterobacter cloacae GGT036
Enterobacter sp. A8
Enterobacter cloacae 6kgm
Enterobacter cloacae S1
Enterobacter cloacae SUBG009
Enterobacter sp. RC4
Enterobacter cloacae SQU-2
Enterobacter asburiae C1
Enterobacter sp. C6
Enterobacter asburiae TN152
Enterobacter sp. UCD-UG_FMILLET
Enterobacter sp. E20
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Enterobacter mori HPCN40
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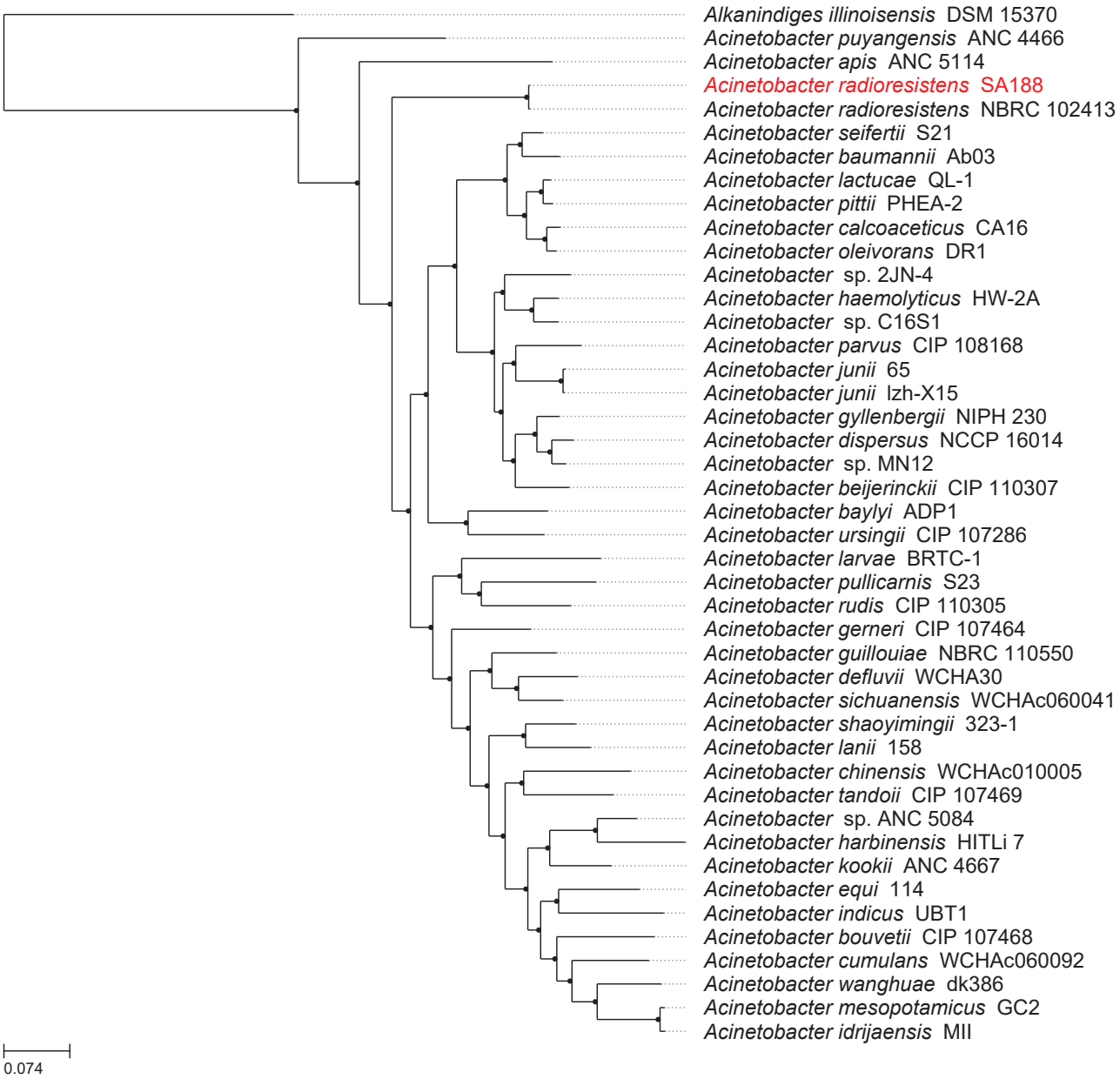
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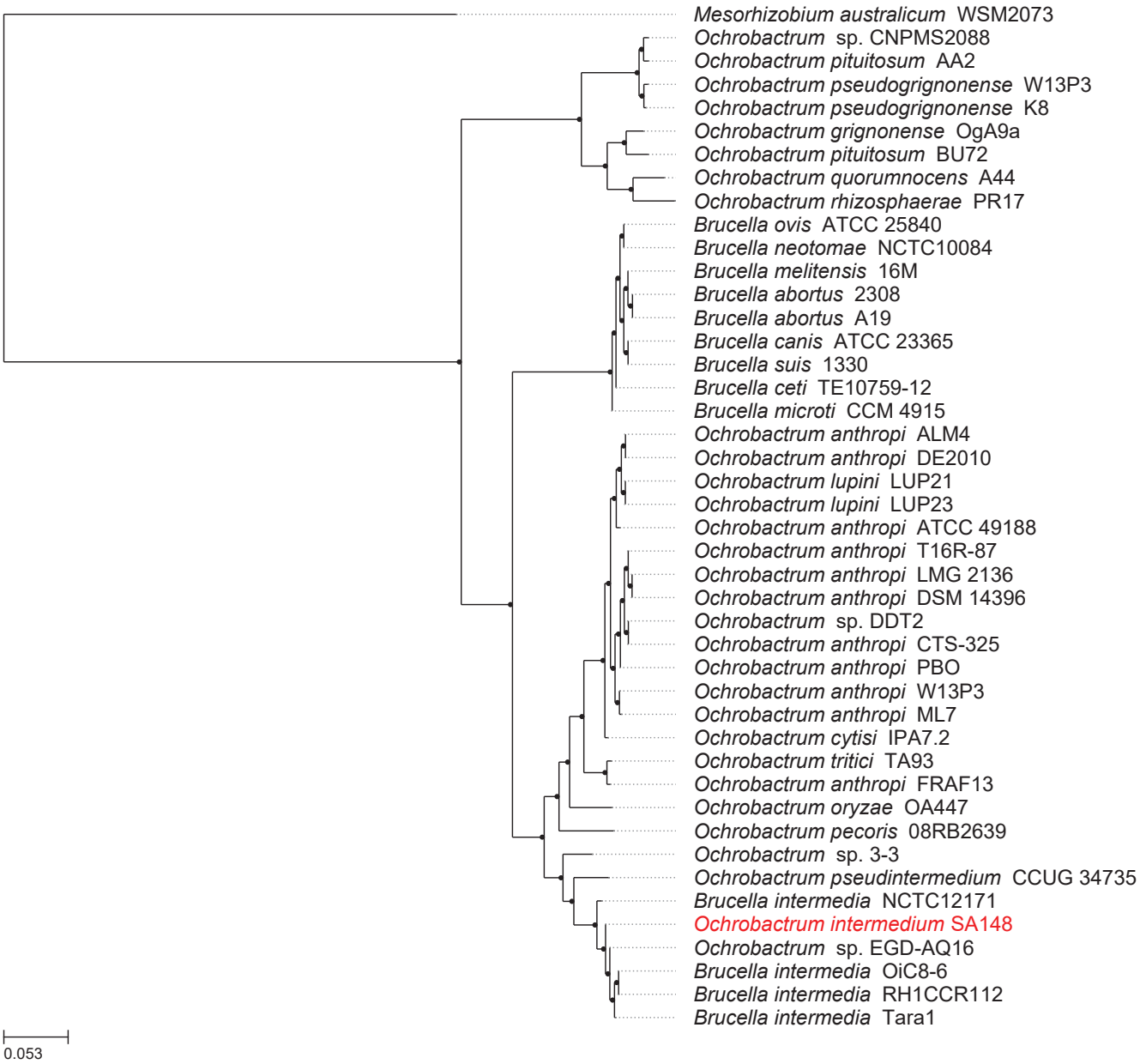
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Brucella neotomae NCTC10084
Brucella melitensis 16M
Brucella abortus 2308
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Brucella canis ATCC 23365
Brucella suis 1330
Brucella ceti TE10759-12
Brucella microti CCM 4915
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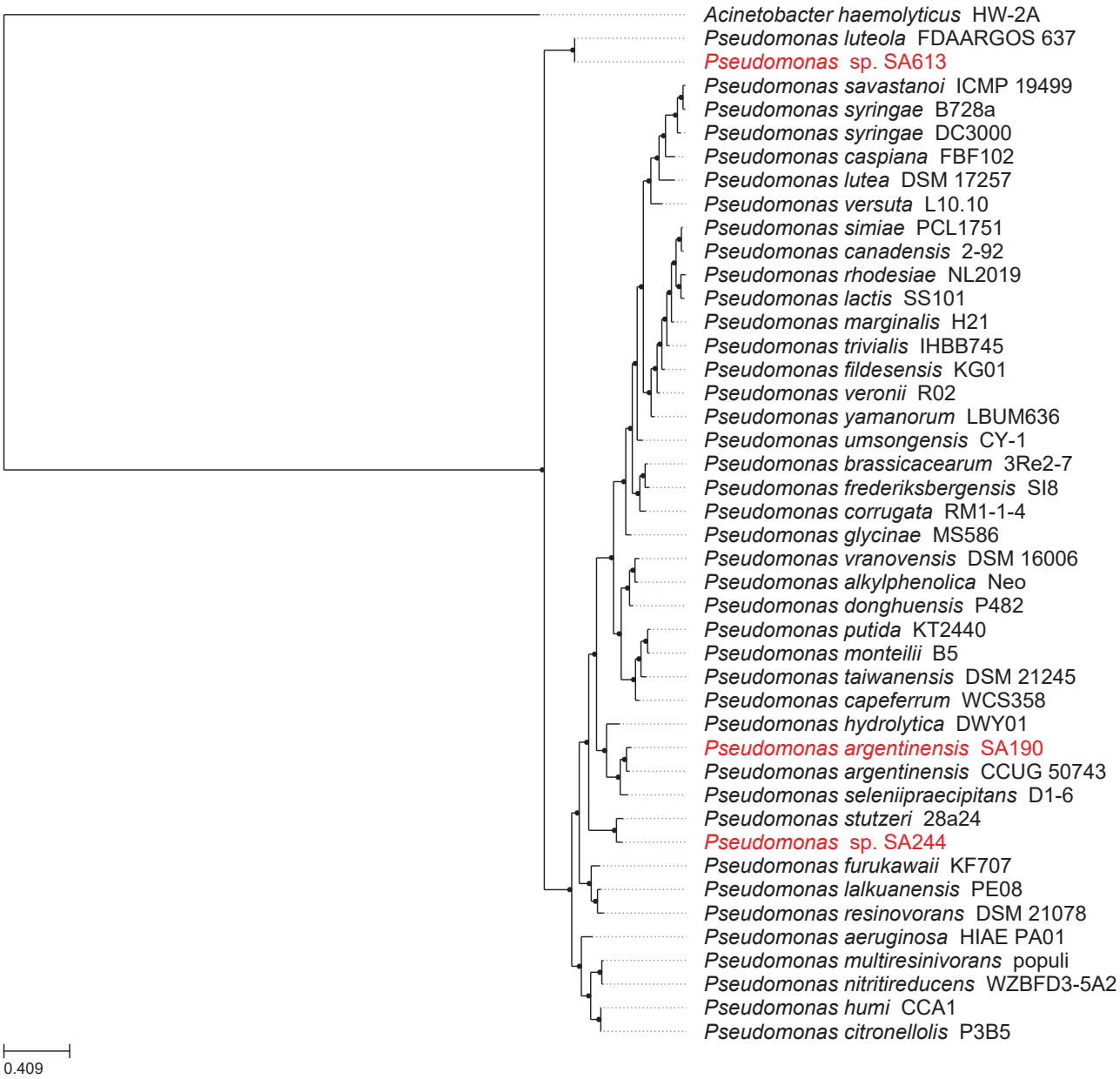
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Pseudomonas veronii R02
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Pseudomonas glycinae MS586
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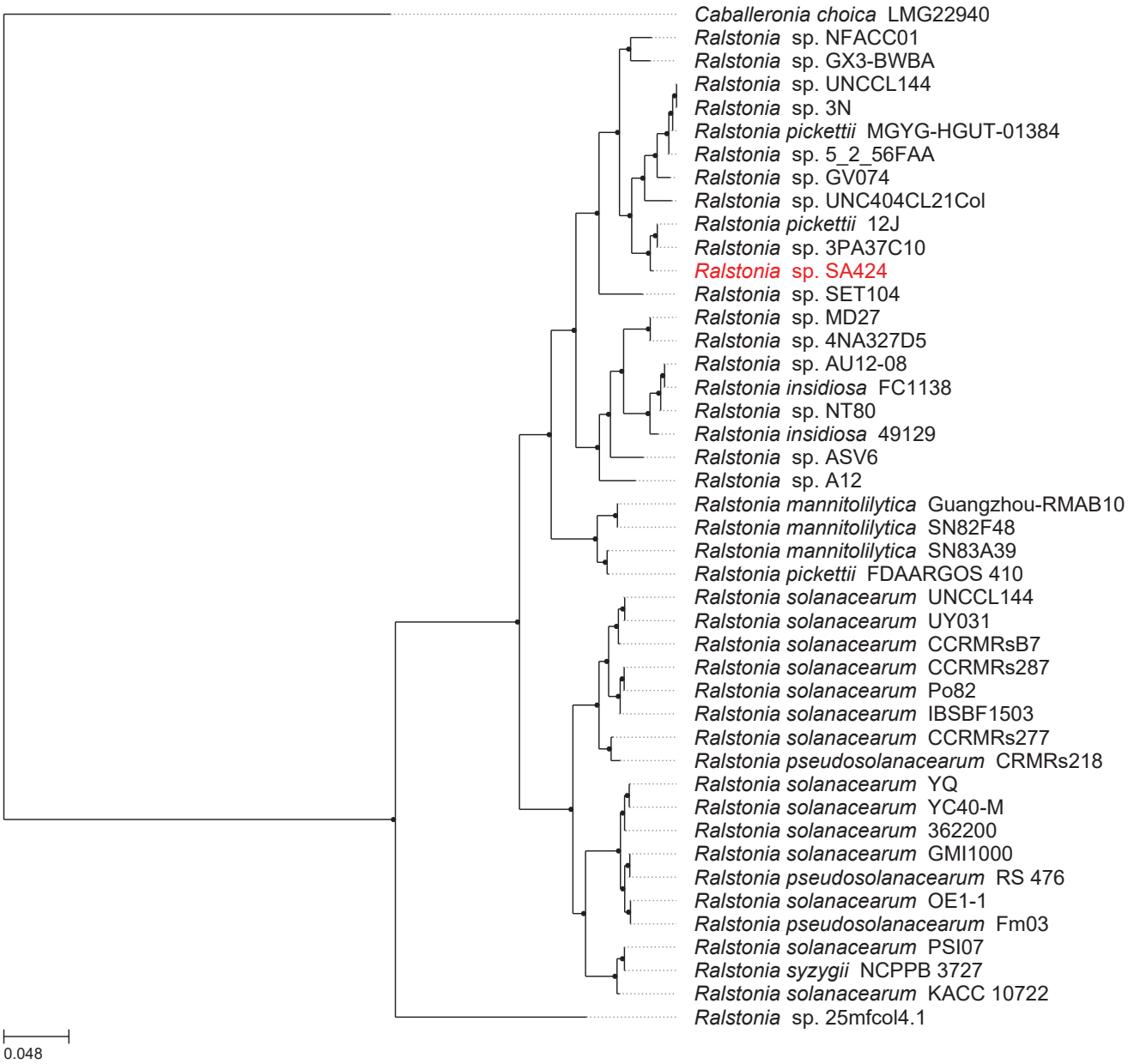
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0.048

Fig. S5: Tomato salt stress assay. The salt stress assay was adapted from a protocol by Awlia et al., 2016. Pots with plants are soaked in a saline solution for about 30 minutes. As the WHC is always maintained at 60%, there is a certain volume of water already present in the substrate. When the saline solution enters through the bottom of the cups during the soaking, the salt concentration lowers as the solution is diluted by the water present in the substrate. The volume of saline solution that enters the pot is equal to the remaining 40% WHC plus extra air. This extra air volume is a result of the supersaturation by the soaking method which exceeds the amount predicted by 100% WHC. As the WHC returns to 60% due to evaporation and transpiration, the diluted saline solution will concentrate to a target concentration in the substrate.

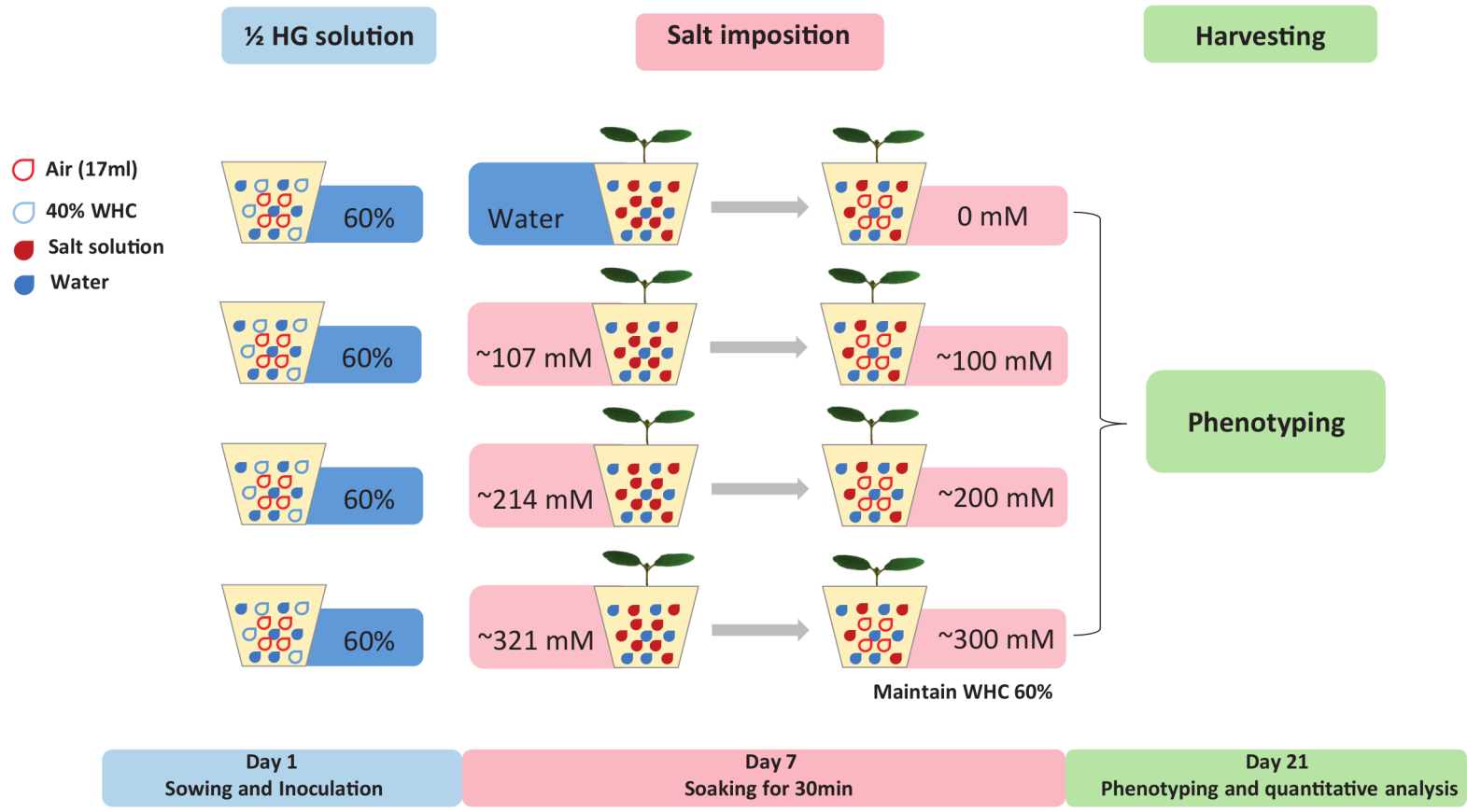
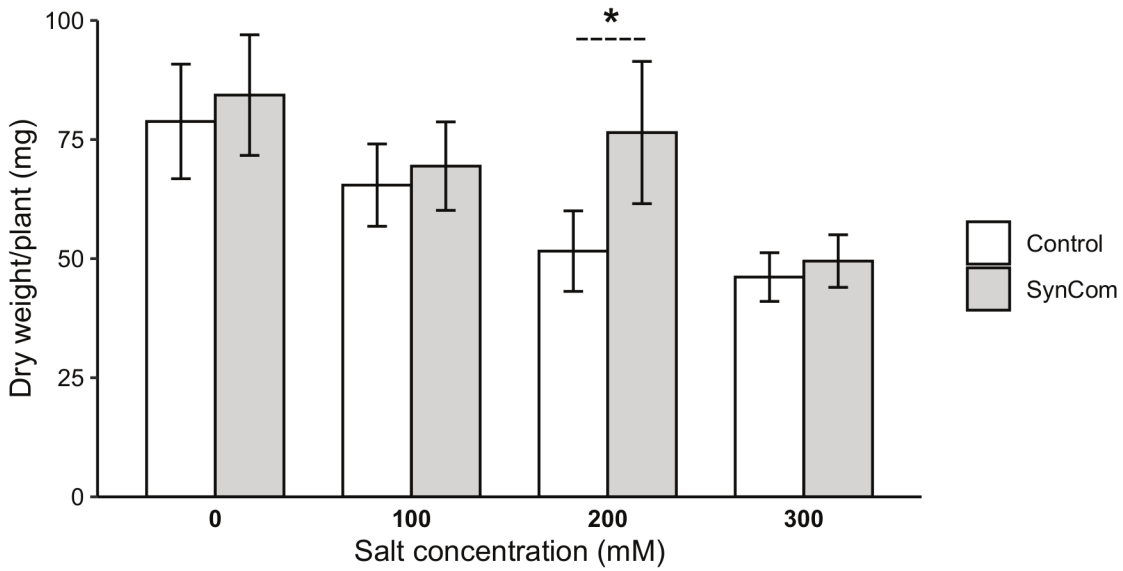


Fig. S6: Salt tolerance test of tomato plants grown with or without SynCom inoculation. Shoot dry weight of 21-day-old tomato plantlets exposed to 0, 100, 200, 300 mM NaCl (for 14 days) and inoculated with or without SynCom C. Plants were grown in the non-sterile substrate. An asterisk represents a statistically significant ($p < 0.05$) difference between the two inoculations per Student's t-test.



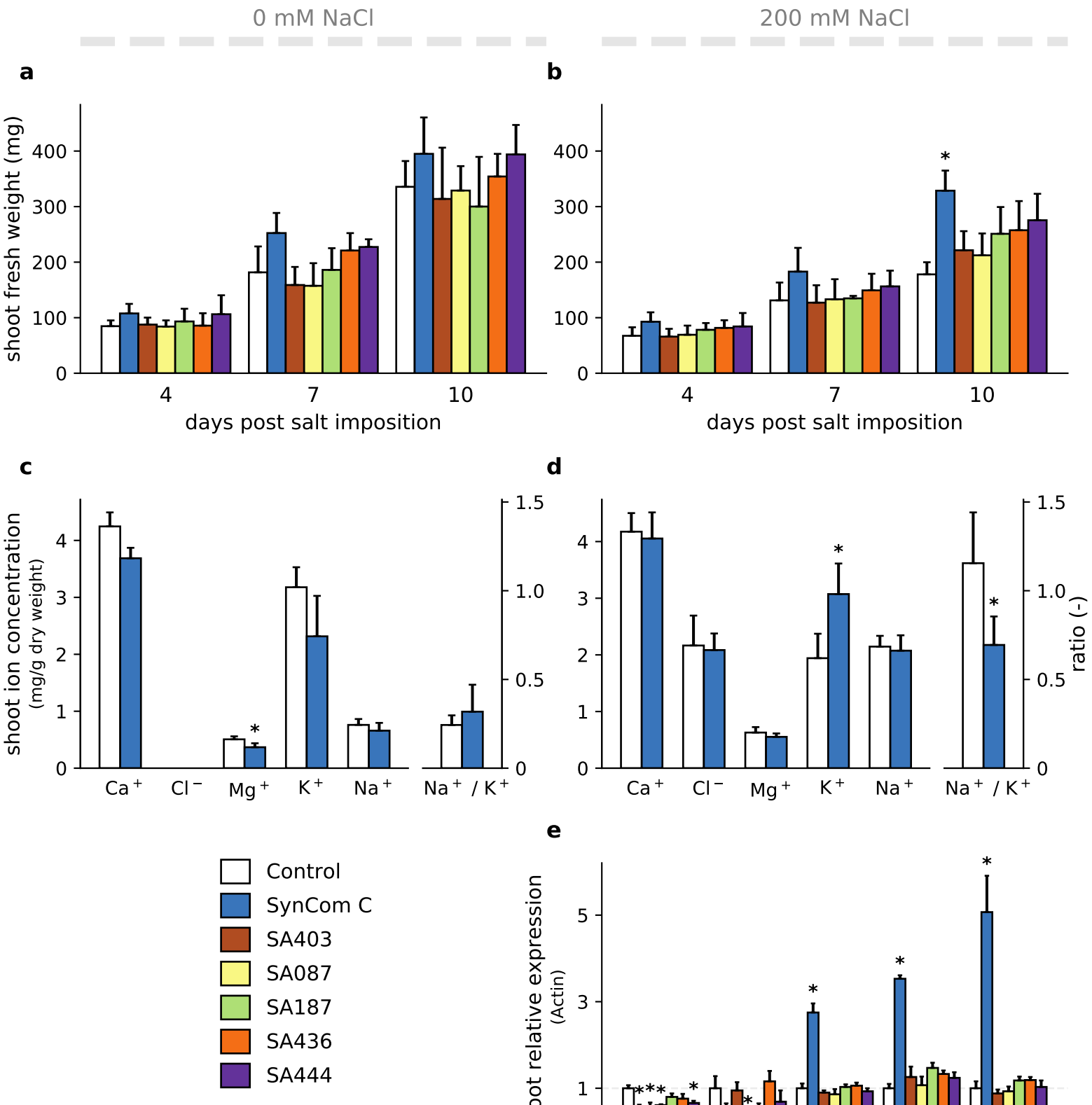


Fig. S7 : Tomato plants were grown in the sterile substrate and inoculated with SynCom C or individually with the five SynCom C strains. A control condition without inoculum was also included. Plants were exposed to 0 or 200 mM NaCl at 7 days post sowing. Shoot and root tissue was harvested at 4, 7 and 10 days post salt imposition. Unless otherwise indicated, error bars represent the standard deviation and an asterisk is a significant difference ($p < 0.05$) from the control per Dunnett's test. **(a & b)** Average shoot fresh weights (n=5) for each of the three time points and the 0 and 200 mM NaCl, respectively. **(c & d)** Average shoot ion content (n=5) as determined by ion chromatography ten days after the salt imposition for 0 and 200 mM NaCl, respectively. The left axis shows the average concentration in mg / g of dry weight for each ion. The right axis shows the dimensionless ratio between the concentrations of the Sodium and Potassium ions. Significance was determined by Student's t-test. **(e & f)** Relative expression against Actin in the root and shoot, respectively, of salt stress related genes in plants four days after being treated with 200 mM NaCl (n=5). The error bars represent the standard error of the mean of the fold changes per sample.

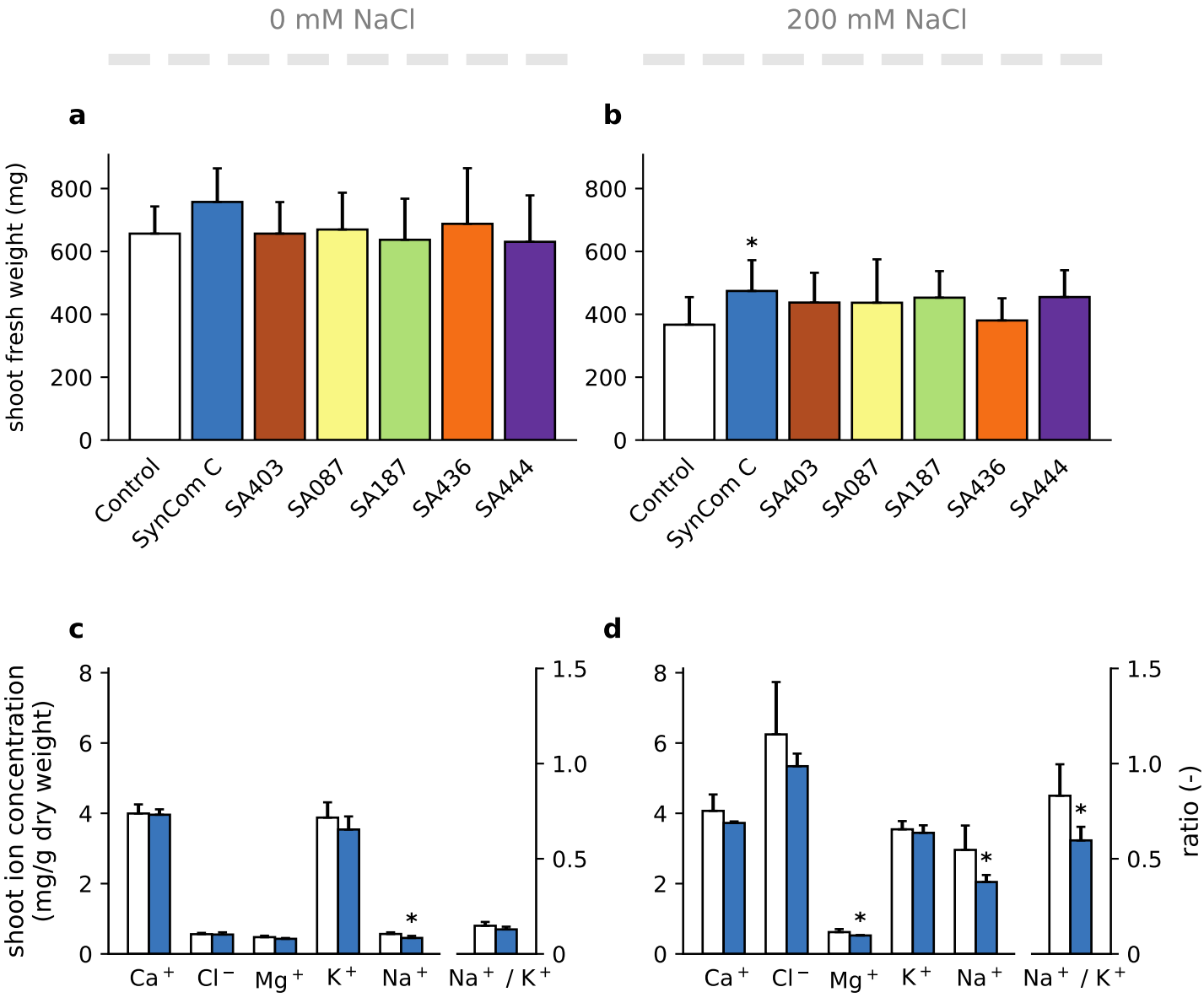


Fig. S8 : Tomato plants were grown in the non-sterile substrate and inoculated with SynCom C or individually with the five SynCom C strains. A control condition without inoculum was also included. Plants were exposed to 0 or 200 mM NaCl one week after sowing. Shoot tissue was harvested at ten days post salt imposition for fresh weight and ion content analysis. The standard deviation is shown by the error bars. **(a & b)** Average shoot fresh weights (n=15) for the 0 & 200 mM NaCl treated plants, respectively. An asterisk indicates a significant difference ($p < 0.05$) from the control per Dunnett's test. **(c & d)** Average shoot ion content as determined by ion chromatography for the 0 & 200 mM NaCl salt levels, respectively. Five random plants were selected from the control and SynCom C inoculated plants. The left axis shows the concentration in mg / g of dry weight for each ion. The right axis shows the dimensionless ratio between the concentrations of the Sodium and Potassium ions. An asterisk is a significant difference ($p < 0.05$) per Student's t-test.

Fig. S9: ASVs of Jizan strains which did not pass the detection criteria for the root colonization of tomato.

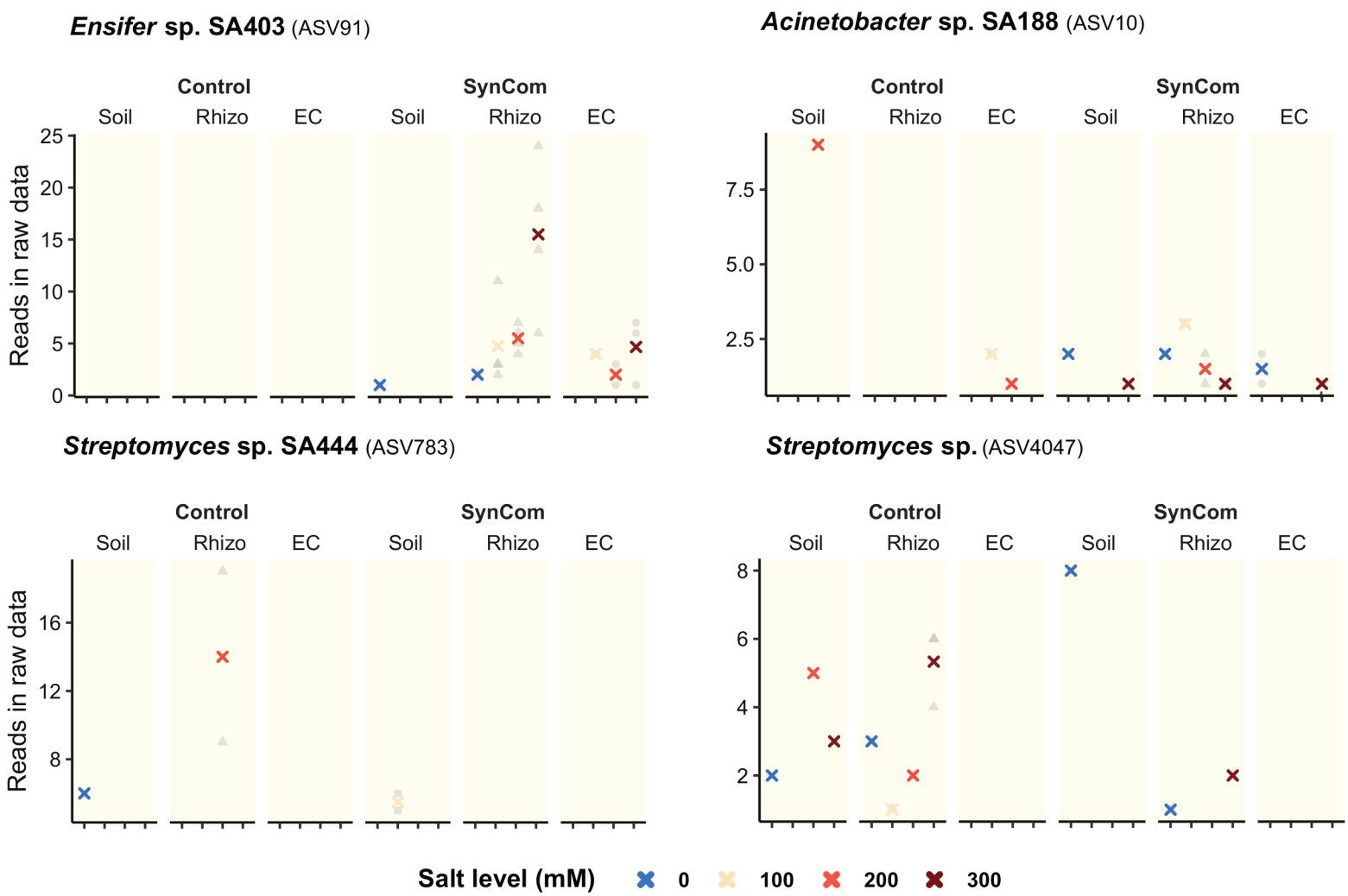


Fig. S10: Positive correlation between bacterial ASVs and salt concentration. Log2-transformed normalized read counts of ASVs found in the Rhizo (a) and EC (b) of tomato growing in the non-sterile substrate and inoculated with the Jizan SynCom. The ASVs that were enriched in any of the salt levels and with a positive correlation to the salt gradient are shown here. Crosses indicate mean log2-transformed normalized read counts of each ASV under each salt level. Blue crosses indicate ASVs matching a SynCom strain detected in this analysis.