Supplementary Material:

**S1 Table 1. Differential abundance comparison of alfalfa when grown alone (1 plant) and alfalfa plant densities.** Enriched column shows which treatment the bacterial taxa is enriched (A1: single alfalfa plant, A24: 24 alfalfa plants, A48: 48 alfalfa plants). Bacterial taxa which were enriched in only one treatment of increasing plant density is highlighted in orange. Bacterial taxa which were enriched all density treatment is highlighted in sky blue.

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| **A24** |  |  |  | **A48** |  |  |  |
| Bacterial Taxa | Enriched | Log Fold | P-adjust | Bacterial Taxa | Enriched | Log Fold | P-adjust |
| *Larkinella insperata* | A1 | -20.12 | 1.28E-03 | *Ammoniphilus oxalaticus* | A1 | -29.96 | 2.79E-24 |
| *Leptolyngbya* sp. O-77 | A1 | -18.44 | 2.44E-03 | *Oscillatoria nigro-viridis* | A1 | -23.81 | 2.36E-12 |
| *Halomicronema hongdechloris* | A1 | -19.20 | 2.52E-03 | *Larkinella harenae* | A1 | -25.78 | 2.18E-11 |
| *Anabaena cylindrica* | A1 | -18.15 | 2.52E-03 | *Paenibacillus* sp. 37 | A1 | -20.93 | 2.19E-10 |
| *Telluribacter humicola* | A1 | -18.03 | 2.52E-03 | *Azospirillum brasilense* | A1 | -23.21 | 2.19E-10 |
| *Adhaeribacter aerophilus* | A24 | 12.61 | 2.52E-03 | *Paenibacillus xylanexedens* | A1 | -21.14 | 2.00E-09 |
| *Arthrobacter* sp. KBS0702 | A24 | 9.46 | 5.63E-06 | *Larkinella rosea* | A1 | -24.28 | 6.07E-09 |
| *Arthrobacter* sp. UKPF54-2 | A24 | 9.16 | 3.68E-03 | *Adhaeribacter swui* | A48 | 16.43 | 3.61E-15 |
| *Arthrobacter* sp. QXT-31 | A24 | 5.15 | 7.57E-03 | *Pseudarthrobacter* sp. NIBRBAC000502771 | A48 | 19.10 | 3.61E-15 |
| *Adhaeribacter swui* | A24 | 17.11 | 7.43E-18 | *Pseudarthrobacter phenanthrenivorans* | A48 | 19.80 | 4.04E-20 |
| *Pseudarthrobacter* sp. NIBRBAC000502771 | A24 | 18.79 | 4.51E-16 |  |  |  |  |
| *Pseudarthrobacter phenanthrenivorans* | A24 | 19.83 | 6.73E-22 |  |  |  |  |

**S2 Table. Differential abundance comparison of alfalfa when grown alone (1 plant) and alfalfa-brassica mixtures.** Enriched column shows which treatment the bacterial taxa is enriched (A1: single alfalfa plant, Ab2: single alfalfa and brassica plant, Ab24: 12 alfalfa and brassica plants, Ab48: 24 alfalfa and brassica plants). Bacterial taxa which were enriched when alfalfa was grown alone as compared to multiple density treatments. Bacterial taxa which were enriched in only one treatment of increasing plant density is highlighted in orange. Bacterial taxa which were enriched in more than one diversity treatment is highlighted in light sky blue. Bacterial taxa which were enriched all density treatment is highlighted in sky blue.

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| **Ab2** |  |  |  | **Ab24** |  |  |  | **Ab48** |  |  |  |
| Bacterial Taxa | Enriched | Log Fold | P-adjust | Bacterial Taxa | Enriched | Log Fold | P-adjust | Bacterial Taxa | Enriched | Log Fold | P-adjust |
| *Dyadobacter sediminis* | A1 | -19.86 | 4.05E-09 | *Bacillus carboniphilus* | A1 | -26.49 | 2.35E-44 | *Achromobacter insolitus* | A1 | -29.96 | 1.32E-31 |
| *Ensifer adhaerens* | A1 | -20.52 | 1.40E-04 | *Bacillus mannanilyticus* | A1 | -6.39 | 6.33E-03 | *Luteolibacter pohnpeiensis* | A1 | -21.51 | 3.72E-07 |
| *Exiguobacterium aurantiacum* | A1 | -17.87 | 8.40E-08 | *Devosia geojensis* | A1 | -22.10 | 5.95E-16 | *Planomicrobium chinense* | A1 | -22.23 | 2.30E-09 |
| *Exiguobacterium mexicanum* | A1 | -29.94 | 4.45E-43 | *Azohydromonas australica* | A1 | -25.49 | 1.60E-03 | *Stenotrophomonas* sp. MYb57 | A1 | -9.74 | 7.78E-03 |
| *Larkinella harenae* | A1 | -28.32 | 1.43E-15 | *Trichocoleus desertorum* | A1 | -21.31 | 1.61E-05 | *Larkinella insperata* | A1 | -21.46 | 1.20E-04 |
| *Larkinella rosea* | A1 | -24.96 | 1.82E-10 | *Gemmata* sp. SH-PL17 | Ab24 | 17.99 | 6.27E-03 | *Leptolyngbya* sp. O-77 | A1 | -19.67 | 2.77E-04 |
| *Lysobacter helvus* | A1 | -21.48 | 1.77E-03 | *Metabacillus indicus* | Ab24 | 2.91 | 1.74E-03 | *Anabaena cylindrica* | A1 | -19.67 | 3.32E-04 |
| *Noviherbaspirillum suwonense* | A1 | -7.31 | 3.49E-04 | *Arthrobacter* sp. KBS0702 | Ab24 | 8.23 | 1.36E-04 | *Azohydromonas australica* | A1 | -26.41 | 4.47E-04 |
| *Peribacillus simplex* | A1 | -16.77 | 8.34E-03 | *Gemmata massiliana* | Ab24 | 19.13 | 5.65E-04 | *Trichocoleus desertorum* | A1 | -21.58 | 7.63E-06 |
| *Pontibacter chitinilyticus* | A1 | -30.00 | 7.74E-30 | *Pseudarthrobacter* sp. NIBRBAC000502771 | Ab24 | 18.39 | 1.29E-15 | *Adhaeribacter aerophilus* | Ab48 | 15.14 | 3.92E-05 |
| *Pontibacter rhizosphera* | A1 | -16.65 | 8.81E-05 | *Pseudarthrobacter phenanthrenivorans* | Ab24 | 20.86 | 1.02E-24 | *Arthrobacter* sp. KBS0702 | Ab48 | 8.09 | 1.20E-04 |
| *Pseudomonas stutzeri* | A1 | -17.05 | 3.27E-03 | *Adhaeribacter swui* | Ab24 | 17.54 | 4.30E-19 | *Pseudarthrobacter* sp. NIBRBAC000502771 | Ab48 | 18.04 | 5.26E-15 |
| *Sinorhizobium fredii* | A1 | -18.50 | 1.95E-06 |  |  |  |  | *Pseudarthrobacter phenanthrenivorans* | Ab48 | 19.21 | 6.43E-21 |
| *Paucimonas lemoignei* | Ab2 | 17.31 | 8.34E-03 |  |  |  |  | *Adhaeribacter swui* | Ab48 | 17.16 | 2.44E-18 |
| *Gemmata massiliana* | Ab2 | 15.96 | 8.01E-03 |  |  |  |  |  |  |  |  |
| *Adhaeribacter swui* | Ab2 | 18.52 | 2.16E-21 |  |  |  |  |  |  |  |  |

**S3 Table. Differential abundance comparison of alfalfa when grown alone (1 plant) and alfalfa-fescue mixtures.** Enriched column shows which treatment the bacterial taxa is enriched (A1: single alfalfa plant, Af2: single alfalfa and fescue plant, Af24: 12 alfalfa and fescue plants, Af48: 24 alfalfa and fescue plants). Bacterial taxa which were enriched when alfalfa was grown alone as compared to multiple density treatments. Bacterial taxa which were enriched in only one treatment of increasing plant density is highlighted in orange. Bacterial taxa which were enriched in more than one diversity treatment is highlighted in light sky blue. Bacterial taxa which were enriched all density treatment is highlighted in sky blue.

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| **Af2** |  |  |  | **Af24** |  |  |  | **Af48** |  |  |  |
| Bacterial Taxa | Enriched | Log Fold | P-adjust | Bacterial Taxa | Enriched | Log Fold | P-adjust | Bacterial Taxa | Enriched | Log Fold | P-adjust |
| *Achromobacter insolitus* | A1 | -25.05 | 3.76E-21 | *Leptolyngbya* sp. O-77 | A1 | -19.09 | 2.64E-03 | *Massilia plicata* | A1 | -21.49 | 1.45E-10 |
| *Arthrobacter* sp. Rue61a | A1 | -17.25 | 7.55E-11 | *Lysobacter helvus* | A1 | -21.19 | 6.71E-03 | *Metabacillus indicus* | A1 | -3.36 | 2.17E-04 |
| *Azospirillum brasilense* | A1 | -22.15 | 3.85E-10 | *Methylophilus* sp. TWE2 | A1 | -20.97 | 1.04E-03 | *Peribacillus simplex* | A1 | -17.36 | 5.00E-03 |
| *Azospirillum* sp. TSH58 | A1 | -19.02 | 2.10E-04 | *Pseudomonas stutzeri* | A1 | -18.31 | 3.87E-03 | *Solibacillus silvestris* | A1 | -18.34 | 1.06E-06 |
| *Dyadobacter sediminis* | A1 | -19.09 | 4.62E-08 | *Roseimicrobium gellanilyticum* | A1 | -20.03 | 3.31E-06 | *Stenotrophomonas* sp. G4 | A1 | -27.73 | 7.93E-36 |
| *Larkinella rosea* | A1 | -23.79 | 4.13E-09 | *Telluribacter humicola* | A1 | -18.03 | 5.48E-03 | *Azospirillum* sp. TSA2s | A1 | -16.36 | 4.13E-03 |
| *Luteolibacter pohnpeiensis* | A1 | -19.70 | 1.39E-05 | *Azospirillum* sp. TSA2s | A1 | -16.89 | 8.24E-03 | *Exiguobacterium acetylicum* | A1 | -23.24 | 6.13E-14 |
| *Pontibacter rhizosphera* | A1 | -16.04 | 4.74E-04 | *Exiguobacterium acetylicum* | A1 | -21.95 | 1.10E-10 | *Exiguobacterium* sp. U13-1 | A1 | -23.57 | 2.85E-14 |
| *Sphingoaurantiacus polygranulatus* | A1 | -21.37 | 3.34E-12 | *Exiguobacterium* sp. U13-1 | A1 | -21.99 | 1.10E-10 | *Paenibacillus* sp. 37 | A1 | -21.25 | 3.34E-12 |
| *Paenibacillus* sp. 37 | A1 | -19.93 | 3.85E-10 | *Adhaeribacter aerophilus* | Af24 | 15.77 | 9.40E-05 | *Paenibacillus xylanexedens* | A1 | -21.19 | 9.35E-11 |
| *Paenibacillus xylanexedens* | A1 | -19.51 | 1.48E-08 | *Arthrobacter* sp. KBS0702 | Af24 | 7.65 | 1.57E-03 | *Planomicrobium chinense* | A1 | -21.48 | 6.42E-09 |
| *Planomicrobium chinense* | A1 | -20.21 | 2.40E-07 | *Pseudarthrobacter phenanthrenivorans* | Af24 | 17.83 | 5.07E-16 | *Flavisolibacter tropicus* | Af48 | 3.44 | 5.00E-03 |
| *Adhaeribacter swui* | Af2 | 15.50 | 9.61E-14 | *Adhaeribacter swui* | Af24 | 17.16 | 5.07E-16 | *Paucimonas lemoignei* | Af48 | 18.26 | 4.06E-03 |
| *Pseudarthrobacter* sp. NIBRBAC000502771 | Af2 | 17.93 | 8.12E-14 | *Pseudarthrobacter* sp. NIBRBAC000502771 | Af24 | 17.52 | 2.02E-12 | *Arthrobacter* sp. KBS0702 | Af48 | 7.72 | 3.21E-04 |
|  |  |  |  |  |  |  |  | *Pseudarthrobacter phenanthrenivorans* | Af48 | 18.26 | 7.54E-19 |
|  |  |  |  |  |  |  |  | *Adhaeribacter swui* | Af48 | 17.59 | 5.30E-19 |
|  |  |  |  |  |  |  |  | *Pseudarthrobacter* sp. NIBRBAC000502771 | Af48 | 18.09 | 5.80E-15 |

**S4 Table. Differential abundance comparison of alfalfa when grown alone (1 plant) and alfalfa-brassica-fescue mixtures.** Enriched column shows which treatment the bacterial taxa is enriched (A1: single alfalfa plant, Abf2: single alfalfa, brassica, and fescue plant, Abf24: 8 alfalfa, brassica, and fescue plants, Af48: 16 alfalfa, brassica, and fescue plants). Bacterial taxa which were enriched when alfalfa was grown alone as compared to multiple density treatments. Bacterial taxa which were enriched in only one treatment of increasing plant density is highlighted in orange. Bacterial taxa which were enriched in more than one diversity treatment is highlighted in light sky blue. Bacterial taxa which were enriched all density treatment is highlighted in sky blue.

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| **Abf3** |  |  |  | **Abf24** |  |  |  | **Abf48** |  |  |  |
| Bacterial Taxa | Enriched | Log Fold | P-adjust | Bacterial Taxa | Enriched | Log Fold | P-adjust | Bacterial Taxa | Enriched | Log Fold | P-adjust |
| *Exiguobacterium aurantiacum* | A1 | -19.23 | 7.32E-09 | *Paenibacillus xylanexedens* | A1 | -19.80 | 4.56E-09 | *Azospirillum brasilense* | A1 | -24.73 | 3.48E-13 |
| *Larkinella insperata* | A1 | -21.27 | 3.07E-04 | *Planctomyces* sp. SH-PL14 | A1 | -19.66 | 1.30E-05 | *Azospirillum* sp. TSH58 | A1 | -20.80 | 9.12E-06 |
| *Halomicronema hongdechloris* | A1 | -20.27 | 1.23E-03 | *Arthrobacter* sp. KBS0702 | Abf24 | 7.59 | 9.20E-04 | *Exiguobacterium sibiricum* | A1 | -5.99 | 9.10E-03 |
| *Adhaeribacter aerophilus* | Abf3 | 16.67 | 5.19E-06 | *Adhaeribacter aerophilus* | Abf24 | 13.02 | 1.77E-03 | *Exiguobacterium undae* | A1 | -6.34 | 3.74E-04 |
| *Adhaeribacter swui* | Abf3 | 20.30 | 2.07E-25 | *Adhaeribacter swui* | Abf24 | 17.74 | 2.78E-19 | *Leptolyngbya* sp. O-77 | A1 | -19.31 | 4.38E-04 |
| *Pseudarthrobacter* sp. NIBRBAC000502771 | Abf3 | 14.59 | 3.29E-09 | *Pseudarthrobacter* sp. NIBRBAC000502771 | Abf24 | 19.22 | 6.70E-17 | *Methylophilus* sp. TWE2 | A1 | -21.39 | 1.19E-04 |
| *Pseudarthrobacter phenanthrenivorans* | Abf3 | 14.37 | 6.88E-11 | *Pseudarthrobacter phenanthrenivorans* | Abf24 | 18.53 | 2.78E-19 | *Oscillatoria nigro-viridis* | A1 | -23.79 | 6.89E-14 |
|  |  |  |  |  |  |  |  | *Paenibacillus* sp. 37 | A1 | -21.67 | 1.56E-12 |
|  |  |  |  |  |  |  |  | *Peribacillus simplex* | A1 | -17.70 | 4.17E-03 |
|  |  |  |  |  |  |  |  | *Planomicrobium chinense* | A1 | -21.86 | 5.45E-09 |
|  |  |  |  |  |  |  |  | *Roseimicrobium gellanilyticum* | A1 | -20.28 | 2.01E-07 |
|  |  |  |  |  |  |  |  | *Trichocoleus desertorum* | A1 | -20.95 | 1.77E-05 |
|  |  |  |  |  |  |  |  | *Halomicronema hongdechloris* | A1 | -20.09 | 7.63E-04 |
|  |  |  |  |  |  |  |  | *Planctomyces* sp. SH-PL14 | A1 | -21.54 | 5.45E-07 |
|  |  |  |  |  |  |  |  | *Arthrobacter* sp. KBS0702 | Abf48 | 8.57 | 3.70E-05 |
|  |  |  |  |  |  |  |  | *Adhaeribacter aerophilus* | Abf48 | 13.97 | 2.51E-04 |
|  |  |  |  |  |  |  |  | *Adhaeribacter swui* | Abf48 | 16.98 | 1.66E-17 |
|  |  |  |  |  |  |  |  | *Pseudarthrobacter* sp. NIBRBAC000502771 | Abf48 | 17.66 | 5.31E-14 |
|  |  |  |  |  |  |  |  | *Pseudarthrobacter phenanthrenivorans* | Abf48 | 18.40 | 1.33E-18 |

**S5 Table. Differential Abundance Comparison of brassica when grown alone (1 plant) and brassica plant densities.** Enriched column shows which treatment the bacterial taxa is enriched (B1: single brassica plant, Ba2: single brassica and alfalfa plants, B24: 24 brassica plants, B48: 48 brassica plants). Bacterial taxa which were enriched when brassica was grown alone as compared to multiple density treatments. Bacterial taxa which were enriched in only one treatment of increasing plant density is highlighted in orange. Bacterial taxa which were enriched in more than one diversity treatment is highlighted in light sky blue. Bacterial taxa which were enriched all density treatment is highlighted in sky blue.

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| **B24** |  |  |  | **B48** |  |  |  |
| Bacterial Taxa | Enriched | Log Fold | P-adjust | Bacterial Taxa | Enriched | Log Fold | P-adjust |
| *Anabaena cylindrica* | B1 | -25.48 | 7.77E-03 | *Pontibacter populi* | B1 | -7.88 | 1.65E-04 |
| *Aneurinibacillus soli* | B1 | -22.03 | 2.20E-03 | *Tumebacillus flagellatus* | B48 | 7.75 | 1.24E-07 |
| *Halomicronema hongdechloris* | B1 | -24.41 | 1.36E-03 | *Nocardioides alpinus* | B48 | 18.21 | 7.89E-04 |
| *Leptolyngbya boryana* | B1 | -21.67 | 7.32E-03 | *Nocardioides cavernae* | B48 | 18.51 | 1.67E-07 |
| *Paenibacillus odorifer* | B1 | -20.30 | 3.97E-04 | *Solibacillus silvestris* | B48 | 19.40 | 9.28E-05 |
| *Paenibacillus* sp. FSL H7-0357 | B1 | -19.47 | 9.55E-03 |  |  |  |  |
| *Nocardioides alpinus* | B24 | 18.50 | 6.35E-04 |  |  |  |  |
| *Nocardioides cavernae* | B24 | 19.14 | 7.50E-08 |  |  |  |  |
| *Solibacillus silvestris* | B24 | 19.32 | 1.42E-04 |  |  |  |  |

**S6 Table. Differential abundance comparison of brassica when grown alone (1 plant) and brassica-alfalfa mixtures.** Enriched column shows which treatment the bacterial taxa is enriched (B1: single brassica plant, Ba24: 12 brassica and alfalfa plants, Ba48: 24 brassica and alfalfa plants). Bacterial taxa which were enriched when brassica was grown alone as compared to multiple density treatments. Bacterial taxa which were enriched in only one treatment of increasing plant density is highlighted in orange. Bacterial taxa which were enriched in more than one diversity treatment is highlighted in light sky blue. Bacterial taxa which were enriched all density treatment is highlighted in sky blue.

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| **Ba2** |  |  |  | **Ba24** |  |  |  | **Ba48** |  |  |  |
| Bacterial Taxa | Enriched | Log Fold | P-adjust | Bacterial Taxa | Enriched | Log Fold | P-adjust | Bacterial Taxa | Enriched | Log Fold | P-adjust |
| *Aneurinibacillus soli* | B1 | -21.67 | 2.93E-05 | *Adhaeribacter aerophilus* | B1 | -17.55 | 9.95E-13 | *Exiguobacterium sibiricum* | B1 | -4.68 | 4.13E-03 |
| *Azospirillum* sp. TSH58 | B1 | -.23.08 | 1.11E-10 | *Daejeonella composti* | B1 | -25.64 | 1.62E-08 | *Exiguobacterium* sp. MH3 | B1 | -8.38 | 3.20E-03 |
| *Domibacillus robiginosus* | B1 | -18.17 | 1.35E-13 | *Ensifer adhaerens* | B1 | -16.90 | 3.33E-04 | *Exiguobacterium undae* | B1 | -4.97 | 9.69E-04 |
| *Exiguobacterium aurantiacum* | B1 | -24.54 | 9.03E-20 | *Massilia plicata* | B1 | -20.09 | 3.13E-12 | *Prosthecobacter fluviatilis* | B1 | -22.62 | 2.80E-07 |
| *Pseudarthrobacter* sp. NIBRBAC000502771 | B1 | -7.96 | 1.66E-04 | *Methylotenera mobilis* | B1 | -7.26 | 3.07E-06 | *Stenotrophomonas* sp. G4 | B1 | -9.69 | 1.37E-03 |
| *Anabaena cylindrica* | B1 | -25.21 | 1.20E-04 | *Paenibacillus xylanexedens* | B1 | -21.99 | 1.65E-16 | *Stenotrophomonas* sp. MYb57 | B1 | -23.06 | 1.08E-13 |
| *Paenibacillus* sp. FSL H7-0357 | B1 | -19.22 | 1.71E-04 | *Pirellula* sp. SH-Sr6A | B1 | -9.45 | 9.17E-05 | *Anabaena cylindrica* | B1 | -25.68 | 3.66E-03 |
| *Spirosoma linguale* | Ba2 | 18.90 | 1.53E-04 | *Pontibacter populi* | B1 | -7.56 | 2.69E-06 | *Halomicronema hongdechloris* | B1 | -24.47 | 9.25E-04 |
| *Nocardioides alpinus* | Ba2 | 17.23 | 1.89E-05 | *Pontibacter rhizosphera* | B1 | -24.29 | 4.72E-10 | *Larkinella arboricola* | B1 | -21.22 | 9.75E-03 |
| *Nocardioides cavernae* | Ba2 | 17.69 | 3.04E-09 | *Rhizobacter gummiphilus* | B1 | -22.21 | 1.86E-04 | *Larkinella insperata* | B1 | -20.92 | 9.25E-04 |
| *Solibacillus silvestris* | Ba2 | 19.39 | 4.24E-07 | *Roseomonas ludipueritiae* | B1 | -20.58 | 2.64E-04 | *Leptolyngbya boryana* | B1 | -21.94 | 3.20E-03 |
|  |  |  |  | *Sinorhizobium fredii* | B1 | -18.59 | 6.57E-07 | *Lysobacter soli* | B1 | -25.10 | 9.75E-03 |
|  |  |  |  | *Telluribacter humicola* | B1 | -20.17 | 5.52E-06 | *Bacillus* sp. Y1 | Ba48 | 3.65 | 4.25E-04 |
|  |  |  |  | *Trichocoleus desertorum* | B1 | -25.81 | 2.57E-13 | *Metabacillus litoralis* | Ba48 | 2.44 | 9.75E-03 |
|  |  |  |  | *Halomicronema hongdechloris* | B1 | -24.22 | 1.31E-05 | *Spirosoma linguale* | Ba48 | 19.90 | 3.20E-03 |
|  |  |  |  | *Larkinella arboricola* | B1 | -20.75 | 3.76E-04 | *Nocardioides alpinus* | Ba48 | 17.36 | 1.00E-03 |
|  |  |  |  | *Larkinella insperata* | B1 | -21.14 | 9.13E-06 | *Nocardioides cavernae* | Ba48 | 17.33 | 1.15E-06 |
|  |  |  |  | *Leptolyngbya boryana* | B1 | -20.96 | 1.42E-04 | *Solibacillus silvestris* | Ba48 | 20.24 | 1.83E-05 |
|  |  |  |  | *Lysobacter soli* | B1 | -24.72 | 3.74E-04 |  |  |  |  |
|  |  |  |  | *Paenibacillus* sp. FSL H7-0357 | B1 | -18.94 | 2.12E-04 |  |  |  |  |
|  |  |  |  | *Metabacillus indicus* | Ba24 | 4.38 | 1.07E-10 |  |  |  |  |
|  |  |  |  | *Pseudomonas stutzeri* | Ba24 | 18.65 | 4.42E-04 |  |  |  |  |
|  |  |  |  | *Nocardioides alpinus* | Ba24 | 15.74 | 1.04E-04 |  |  |  |  |
|  |  |  |  | *Nocardioides cavernae* | Ba24 | 19.99 | 1.80E-11 |  |  |  |  |
|  |  |  |  | *Solibacillus silvestris* | Ba24 | 20.04 | 1.71E-07 |  |  |  |  |

**S7 Table. Differential abundance comparison of brassica when grown alone (1 plant) and brassica-fescue mixtures.** Enriched column shows which treatment the bacterial taxa is enriched (B1: single brassica plant, Bf1: single brassica and fescue plants, Bf24: 12 brassica and fescue plants, Bf48: 24 brassica and fescue plants). Bacterial taxa which were enriched when brassica was grown alone as compared to multiple density treatments. Bacterial taxa which were enriched in only one treatment of increasing plant density is highlighted in orange. Bacterial taxa which were enriched in more than one diversity treatment is highlighted in light sky blue. Bacterial taxa which were enriched all density treatment is highlighted in sky blue.

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| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Bf2** |  | |  |  | **Bf24** |  | |  | |  | **Bf48** |  |  |  |
| Bacterial Taxa | Enriched | Log Fold | | P-adjust | Bacterial Taxa | Enriched | Log Fold | | P-adjust | | Bacterial Taxa | Enriched | Log Fold | P-adjust |
| *Aneurinibacillus soli* | B1 | -21.27 | | 3.02E-03 | *Daejeonella composti* | B1 | -23.22891 | | 1.48E-06 | | *Anabaena cylindrica* | B1 | -25.74 | 5.50E-03 |
| *Exiguobacterium aurantiacum* | B1 | -23.78 | | 6.01E-16 | *Paenarthrobacter nicotinovorans* | B1 | -19.0309 | | 2.22E-09 | | *Halomicronema hongdechloris* | B1 | -24.49 | 8.58E-04 |
| *Larkinella insperata* | B1 | -21.17 | | 7.62E-04 | *Paenibacillus* sp. 37 | B1 | -22.05469 | | 1.92E-15 | | *Oscillatoria nigro-viridis* | B1 | -26.77 | 4.80E-14 |
| *Pontibacter populi* | B1 | -7.48 | | 3.62E-04 | *Paenibacillus xylanexedens* | B1 | -22.52285 | | 2.56E-15 | | *Rhizobacter gummiphilus* | B1 | -23.10 | 5.80E-03 |
| *Pontibacter rhizosphera* | B1 | -24.22 | | 1.37E-07 | *Nocardioides alpinus* | Bf24 | 17.17779 | | 5.64E-05 | | *Sphingoaurantiacus capsulatus* | B1 | -22.04 | 1.25E-17 |
| *Prosthecobacter fluviatilis* | B1 | -21.33 | | 1.05E-06 | *Nocardioides cavernae* | Bf24 | 18.14108 | | 8.26E-09 | | *Sphingoaurantiacus polygranulatus* | B1 | -22.36 | 1.95E-16 |
| *Spirosoma linguale* | Bf2 | 19.25 | | 6.60E-03 |  |  | |  | |  | *Prosthecobacter fluviatilis* | B1 | -22.69 | 9.91E-08 |
| *Solibacillus silvestris* | Bf2 | 15.39 | | 4.98E-03 |  |  | |  | |  | *Nocardioides alpinus* | Bf48 | 18.71 | 3.05E-04 |
| *Nocardioides cavernae* | Bf2 | 17.57 | | 6.95E-07 |  |  | |  | |  | *Solibacillus silvestris* | Bf48 | 16.33 | 1.56E-03 |
|  |  | |  |  |  |  | |  | |  | *Nocardioides cavernae* | Bf48 | 18.50 | 7.24E-08 |

**S8 Table. Differential abundance comparison of brassica when grown alone (1 plant) and brassica-alfalfa-fescue mixtures.** Enriched column shows which treatment the bacterial taxa is enriched (B1: single brassica plant, Baf1: single brassica, alfalfa, and fescue plants, Baf24: 8 brassica, alfalfa, and fescue plants, Baf48: 16 brassica, alfalfa, and fescue plants). Bacterial taxa which were enriched when brassica was grown alone as compared to multiple density treatments. Bacterial taxa which were enriched in only one treatment of increasing plant density is highlighted in orange. Bacterial taxa which were enriched in more than one diversity treatment is highlighted in light sky blue. Bacterial taxa which were enriched all density treatment is highlighted in sky blue.

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| **Baf3** |  |  |  | **Baf24** |  |  |  | **Baf48** |  |  |  |
| Bacterial Taxa | Enriched | Log Fold | P-adjust | Bacterial Taxa | Enriched | Log Fold | P-adjust | Bacterial Taxa | Enriched | Log Fold | P-adjust |
| *Daejeonella oryzae* | B1 | -23.20 | 1.23E-13 | *Aneurinibacillus soli* | B1 | -20.95 | 4.56E-03 | *Azospirillum* sp. TSH58 | B1 | -23.14 | 7.89E-09 |
| *Exiguobacterium aurantiacum* | B1 | -20.41 | 1.03E-10 | *Daejeonella composti* | B1 | -25.20 | 7.92E-06 | *Exiguobacterium acetylicum* | B1 | -22.59 | 5.47E-20 |
| *Gemmata massiliana* | B1 | -21.30 | 7.67E-09 | *Pontibacter rhizosphera* | B1 | -24.00 | 4.18E-07 | *Exiguobacterium antarcticum* | B1 | -4.71 | 3.69E-03 |
| *Gemmata* sp. SH-PL17 | B1 | -21.26 | 1.61E-05 | *Tumebacillus flagellatus* | Baf24 | 4.89 | 4.56E-03 | *Exiguobacterium sibiricum* | B1 | -4.44 | 7.68E-03 |
| *Larkinella insperata* | B1 | -23.77 | 1.71E-05 | *Nocardioides cavernae* | Baf24 | 16.46 | 8.50E-06 | *Exiguobacterium* sp. MH3 | B1 | -7.89 | 6.12E-03 |
| *Prosthecobacter fluviatilis* | B1 | -19.85 | 4.00E-06 | *Solibacillus silvestris* | Baf24 | 19.05 | 9.46E-05 | *Exiguobacterium* sp. U13-1 | B1 | -22.94 | 2.51E-19 |
| *Sphingoaurantiacus polygranulatus* | B1 | -20.69 | 2.49E-12 | *Nocardioides alpinus* | Baf24 | 18.27 | 6.21E-04 | *Exiguobacterium undae* | B1 | -5.19 | 2.71E-04 |
| *Daejeonella composti* | B1 | -20.21 | 1.25E-04 |  |  |  |  | *Leptolyngbya boryana* | B1 | -21.33 | 4.00E-03 |
| *Pontibacter rhizosphera* | B1 | -19.68 | 1.42E-05 |  |  |  |  | *Paenibacillus odorifer* | B1 | -20.06 | 1.43E-04 |
| Nocardioides alpinus | Baf3 | 18.59 | 5.58E-05 |  |  |  |  | *Paenibacillus* sp. 37 | B1 | -22.36 | 1.43E-15 |
|  |  |  |  |  |  |  |  | *Paenibacillus* sp. FSL H7-0357 | B1 | -19.24 | 5.81E-03 |
|  |  |  |  |  |  |  |  | *Paenibacillus xylanexedens* | B1 | -22.42 | 5.93E-15 |
|  |  |  |  |  |  |  |  | *Pseudomonas koreensis* | B1 | -20.06 | 8.10E-03 |
|  |  |  |  |  |  |  |  | *Stenotrophomonas* sp. MYb57 | B1 | -22.33 | 1.77E-13 |
|  |  |  |  |  |  |  |  | *Trichocoleus desertorum* | B1 | -26.03 | 1.49E-11 |
|  |  |  |  |  |  |  |  | *Spirosoma linguale* | Baf48 | 19.37 | 4.00E-03 |
|  |  |  |  |  |  |  |  | *Nocardioides cavernae* | Baf48 | 18.64 | 2.64E-08 |
|  |  |  |  |  |  |  |  | *Solibacillus silvestris* | Baf48 | 18.12 | 1.43E-04 |
|  |  |  |  |  |  |  |  | *Nocardioides alpinus* | Baf48 | 18.24 | 2.71E-04 |

**S9 Table. Differential abundance comparison of fescue when grown alone (1 plant) and fescue plant densities**. Enriched column shows which treatment the bacterial taxa is enriched (F1: single fescue plant, F24: 24 fescue plants, F48: 48 fescue plants). Bacterial taxa which were enriched when fescue was grown alone as compared to multiple density treatments. Bacterial taxa which were enriched in only one treatment of increasing plant density is highlighted in orange. Bacterial taxa which were enriched in more than one diversity treatment is highlighted in light sky blue. Bacterial taxa which were enriched all density treatment is highlighted in sky blue.

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| **F24** |  |  |  | **F48** |  |  | |  |
| Bacterial Taxa | Enriched | Log Fold | P-adjust | Bacterial Taxa | Enriched | | Log Fold | P-adjust |
| *Telluribacter humicola* | F1 | -19.97 | 5.94E-06 | *Kaistia defluvii* | F1 | | -24.00 | 2.26E-08 |
| *Lysobacter helvus* | F1 | -22.62 | 7.67E-04 | *Pseudomonas stutzeri* | F1 | | -22.96 | 2.03E-08 |
| *Lysobacter* sp. TY2-98 | F1 | -21.69 | 2.12E-03 | *Adhaeribacter terreus* | F48 | | 8.53 | 7.45E-04 |
| *Metabacillus indicus* | F24 | 2.64 | 7.35E-03 | *Adhaeribacter swui* | F48 | | 5.51 | 6.84E-03 |
| *Sinorhizobium meliloti* | F24 | 7.52 | 7.08E-03 | *Dyadobacter sediminis* | F48 | | 18.80 | 1.23E-07 |
| *Trichormus azollae* | F24 | 20.06 | 8.95E-03 | *Ensifer adhaerens* | F48 | | 16.76 | 7.45E-04 |
| *Adhaeribacter aerophilus* | F24 | 14.77 | 5.94E-06 | *Adhaeribacter aerophilus* | F48 | | 15.30 | 1.25E-06 |
| *[Brevibacterium] frigoritolerans* | F24 | 18.96 | 7.67E-04 | *[Brevibacterium] frigoritolerans* | F48 | | 20.12 | 1.60E-04 |
| *Larkinella arboricola* | F24 | 19.42 | 3.03E-05 | *Larkinella arboricola* | F48 | | 18.29 | 8.47E-05 |
| *Larkinella insperata* | F24 | 19.98 | 7.80E-07 | *Larkinella insperata* | F48 | | 18.63 | 2.32E-06 |
| *Paenibacillus* sp. 37 | F24 | 17.39 | 5.86E-10 | *Paenibacillus* sp. 37 | F48 | | 17.15 | 9.81E-10 |

**S10 Table. Differential abundance comparison of fescue when grown alone (1 plant) and fescue-alfalfa mixtures.** Enriched column shows which treatment the bacterial taxa is enriched (F1: single fescue plant, Fa1: single fescue and alfalfa plants, Fa24: 12 fescue and alfalfa plants, Fa48: 24 fescue and alfalfa plants). Bacterial taxa which were enriched when fescue was grown alone as compared to multiple density treatments. Bacterial taxa which were enriched in only one treatment of increasing plant density is highlighted in orange. Bacterial taxa which were enriched in more than one diversity treatment is highlighted in light sky blue. Bacterial taxa which were enriched all density treatment is highlighted in sky blue.

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| **Fa2** |  |  |  | **Fa24** |  |  |  | **Fa48** |  |  |  |
| Bacterial Taxa | Enriched | Log Fold | P-adjust | Bacterial Taxa | Enriched | Log Fold | P-adjust | Bacterial Taxa | Enriched | Log Fold | P-adjust |
| *Anabaena cylindrica* | F1 | -23.61 | 1.94E-09 | *Lysobacter helvus* | F1 | -21.88 | 7.45E-04 | *Azospirillum* sp. TSA2s | F1 | -21.84 | 2.32E-05 |
| *Azospirillum brasilense* | F1 | -20.75 | 3.79E-08 | *Lysobacter* sp. TY2-98 | F1 | -20.78 | 2.58E-03 | *Nostoc flagelliforme* | F1 | -21.72 | 6.09E-03 |
| *Azospirillum* sp. TSH58 | F1 | -20.48 | 3.72E-05 | *Noviherbaspirillum malthae* | F1 | -7.31 | 7.37E-03 | *Stenotrophomonas* sp. G4 | F1 | -22.37 | 6.45E-29 |
| *Calothrix* sp. PCC 7507 | F1 | -17.47 | 2.44E-03 | *Pararcticibacter amylolyticus* | F1 | -18.75 | 1.40E-05 | *Sinorhizobium meliloti* | Fa48 | 8.19 | 1.54E-03 |
| *Halomicronema hongdechloris* | F1 | -18.51 | 5.70E-06 | *Phenylobacterium haematophilum* | F1 | -8.10 | 9.63E-05 | *Adhaeribacter aerophilus* | Fa48 | 15.73 | 5.86E-07 |
| *Peribacillus muralis* | F1 | -7.54 | 2.72E-03 | *Pseudomonas stutzeri* | F1 | -21.91 | 7.67E-08 | *Dyadobacter sediminis* | Fa48 | 17.57 | 1.12E-06 |
| *Peribacillus simplex* | F1 | -17.07 | 9.67E-04 | *Pseudoxanthomonas mexicana* | F1 | -22.30 | 1.44E-05 | *Paenibacillus* sp. 37 | Fa48 | 16.81 | 1.47E-09 |
| *Sinorhizobium meliloti* | Fa2 | 7.81 | 3.72E-03 | *Telluribacter humicola* | F1 | -18.64 | 2.04E-05 | *Ensifer adhaerens* | Fa48 | 14.87 | 6.09E-03 |
| *Ensifer adhaerens* | Fa2 | 16.80 | 1.24E-03 | *Trichormus azollae* | Fa24 | 20.99 | 3.35E-03 | *Larkinella arboricola* | Fa48 | 19.06 | 2.85E-05 |
| *Larkinella arboricola* | Fa2 | 17.97 | 2.08E-04 | *[Brevibacterium] frigoritolerans* | Fa24 | 15.99 | 6.63E-03 | *Larkinella insperata* | Fa48 | 19.82 | 5.58E-07 |
| *Larkinella insperata* | Fa2 | 17.38 | 3.72E-05 | *Paenibacillus* sp. 37 | Fa24 | 20.29 | 4.50E-14 |  |  |  |  |
|  |  |  |  | *Dyadobacter sediminis* | Fa24 | 19.97 | 2.48E-08 |  |  |  |  |
|  |  |  |  | *Adhaeribacter aerophilus* | Fa24 | 16.71 | 7.67E-08 |  |  |  |  |
|  |  |  |  | *Ensifer adhaerens* | Fa24 | 19.30 | 4.07E-05 |  |  |  |  |
|  |  |  |  | *Larkinella arboricola* | Fa24 | 18.57 | 4.60E-05 |  |  |  |  |
|  |  |  |  | *Larkinella insperata* | Fa24 | 18.80 | 2.39E-06 |  |  |  |  |

**S11 Table. Differential abundance comparison of fescue when grown alone (1 plant) and fescue-brassica mixtures.** Enriched column shows which treatment the bacterial taxa is enriched (F1: single fescue plant, Fb1: single fescue and brassica plants, Fb24: 12 fescue and brassica plants, Fb48: 24 fescue and brassica plants). Bacterial taxa which were enriched when fescue was grown alone as compared to multiple density treatments. Bacterial taxa which were enriched in only one treatment of increasing plant density is highlighted in orange. Bacterial taxa which were enriched in more than one diversity treatment is highlighted in light sky blue. Bacterial taxa which were enriched all density treatment is highlighted in sky blue.

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| **Fb2** |  |  |  | **Fb24** |  | |  |  | **Fb48** |  |  |  |
| Bacterial Taxa | Enriched | Log Fold | P-adjust | Bacterial Taxa | Enriched | Log Fold | | P-adjust | Bacterial Taxa | Enriched | Log Fold | P-adjust |
| *Lysobacter helvus* | F1 | -21.99 | 1.23E-03 | *Anabaena cylindrica* | F1 | -24.97 | | 2.26E-09 | *Anabaena cylindrica* | F1 | -24.75 | 3.70E-11 |
| *Lysobacter* sp. TY2-98 | F1 | -20.69 | 4.37E-03 | *Azospirillum* sp. TSA2s | F1 | -22.24 | | 1.01E-04 | *Leptolyngbya* sp. O-77 | F1 | -23.95 | 2.27E-11 |
| *Azohydromonas australica* | F1 | -22.04 | 1.97E-03 | *Azospirillum* sp. TSH58 | F1 | -21.42 | | 5.94E-05 | *Nostoc flagelliforme* | F1 | -22.85 | 1.96E-03 |
| *Calothrix* sp. PCC 7507 | F1 | -18.91 | 6.96E-04 | *Calothrix* sp. PCC 7507 | F1 | -18.38 | | 2.42E-03 | *Oscillatoria nigro-viridis* | F1 | -26.59 | 7.75E-23 |
| *Ensifer adhaerens* | Fb2 | 20.85 | 1.35E-05 | *[Brevibacterium] frigoritolerans* | Fb24 | 20.90 | | 3.08E-04 | *Calothrix* sp. PCC 7507 | F1 | -20.36 | 6.17E-05 |
| *Adhaeribacter aerophilus* | Fb2 | 15.95 | 8.42E-07 | *Adhaeribacter aerophilus* | Fb24 | 15.25 | | 1.38E-05 | *Azohydromonas australica* | F1 | -22.99 | 4.75E-04 |
| *Dyadobacter sediminis* | Fb2 | 18.17 | 8.42E-07 | *Dyadobacter sediminis* | Fb24 | 14.96 | | 4.12E-04 | *[Brevibacterium] frigoritolerans* | Fb48 | 15.83 | 6.88E-03 |
| *Larkinella arboricola* | Fb2 | 17.29 | 5.05E-04 | *Larkinella arboricola* | Fb24 | 15.13 | | 8.77E-03 | *Ensifer adhaerens* | Fb48 | 19.07 | 4.32E-05 |
| *Larkinella insperata* | Fb2 | 17.78 | 1.63E-05 | *Larkinella insperata* | Fb24 | 16.49 | | 3.08E-04 | *Adhaeribacter aerophilus* | Fb48 | 15.45 | 5.67E-07 |
| *Paenibacillus* sp. 37 | Fb2 | 20.05 | 1.26E-13 | *Paenibacillus* sp. 37 | Fb24 | 16.27 | | 8.37E-08 | *Dyadobacter sediminis* | Fb48 | 18.89 | 7.28E-08 |
|  |  |  |  |  |  | |  |  | *Larkinella arboricola* | Fb48 | 20.09 | 5.48E-06 |
|  |  |  |  |  |  | |  |  | *Larkinella insperata* | Fb48 | 20.81 | 6.40E-08 |
|  |  |  |  |  |  | |  |  | *Paenibacillus* sp. 37 | Fb48 | 14.65 | 2.32E-07 |

**S12 Table. Differential abundance comparison of fescue when grown alone (1 plant) and fescue-alfalfa-brassica mixtures.** Enriched column shows which treatment the bacterial taxa is enriched (F1: single fescue plant, Fab1: single fescue, alfalfa, and brassica plants, Fab24: 8 fescue, alfalfa, and brassica plants, Fab48: 16 fescue, alfalfa, and brassica plants). Bacterial taxa which were enriched when fescue was grown alone as compared to multiple density treatments. Bacterial taxa which were enriched in only one treatment of increasing plant density is highlighted in orange. Bacterial taxa which were enriched in more than one diversity treatment is highlighted in light sky blue. Bacterial taxa which were enriched all density treatment is highlighted in sky blue.

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| **Fba3** |  |  |  | **Fab24** |  |  |  | **Fab48** |  |  |  |
| Bacterial Taxa | Enriched | Log Fold | P-adjust | Bacterial Taxa | Enriched | Log Fold | P-adjust | Bacterial Taxa | Enriched | Log Fold | P-adjust |
| Planctomyces sp. SH-PL14 | F1 | -24.16 | 2.55E-10 | Daejeonella oryzae | F1 | -19.11 | 5.81E-06 | Azospirillum brasilense | F1 | -22.10 | 1.13E-09 |
| Planomicrobium chinense | F1 | -20.01 | 8.77E-09 | Leptolyngbya sp. O-77 | F1 | -23.64 | 1.29E-10 | Limisphaera ngatamarikiensis | F1 | -3.43 | 3.00E-04 |
| Calothrix sp. PCC 7507 | F1 | -19.38 | 7.11E-04 | [Brevibacterium] frigoritolerans | Fab24 | 17.49 | 2.80E-03 | Oscillatoria nigro-viridis | F1 | -25.25 | 2.55E-20 |
| Nostoc flagelliforme | F1 | -22.24 | 9.13E-03 | Trichormus azollae | Fab24 | 20.50 | 7.39E-03 | Calothrix sp. PCC 7507 | F1 | -19.37 | 2.68E-04 |
| Adhaeribacter terreus | Fab3 | 8.42 | 2.50E-03 | Paenibacillus sp. 37 | Fab24 | 17.33 | 3.63E-10 | Nostoc flagelliforme | F1 | -22.17 | 4.23E-03 |
| Adhaeribacter swui | Fab3 | 5.80 | 8.52E-03 | Ensifer adhaerens | Fab24 | 19.02 | 7.16E-05 | Leptolyngbya sp. O-77 | F1 | -23.55 | 8.80E-11 |
| Paenibacillus sp. 37 | Fab3 | 19.72 | 5.57E-13 | Larkinella arboricola | Fab24 | 18.96 | 4.23E-05 | Planomicrobium chinense | F1 | -19.94 | 5.62E-09 |
| Adhaeribacter aerophilus | Fab3 | 18.42 | 2.54E-09 | Larkinella insperata | Fab24 | 20.29 | 2.31E-07 | Planctomyces sp. SH-PL14 | F1 | -24.22 | 1.02E-10 |
| Dyadobacter sediminis | Fab3 | 17.29 | 3.99E-06 | Adhaeribacter aerophilus | Fab24 | 14.58 | 5.97E-06 | Sinorhizobium meliloti | Fab48 | 8.81 | 3.23E-04 |
|  |  |  |  | Dyadobacter sediminis | Fab24 | 19.49 | 4.89E-08 | Ensifer adhaerens | Fab48 | 19.73 | 2.81E-05 |
|  |  |  |  |  |  |  |  | Larkinella arboricola | Fab48 | 17.71 | 1.74E-04 |
|  |  |  |  |  |  |  |  | Larkinella insperata | Fab48 | 18.35 | 3.84E-06 |
|  |  |  |  |  |  |  |  | Adhaeribacter aerophilus | Fab48 | 15.84 | 4.34E-07 |
|  |  |  |  |  |  |  |  | Dyadobacter sediminis | Fab48 | 17.20 | 2.27E-06 |

**S13 Table. 1st, 2nd, and 3rd largest module by plant network.**

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| --- | --- | --- | --- |
| Network | Module 1: 17.31% | Module 2: 17.31% | Module 3: 13.46% |
| A | *Alkalihalobacillus halodurans*  *Bacillus infantis*  *Bacillus methanolicus*  *Bacillus* sp. S3  *Bacillus* sp. X1(2014)  *Bacillus* sp. 1NLA3E  *Mesobacillus subterraneus*  *Mesobacillus foraminis*  *Paenibacillus beijingensis* | *Bacillus circulans*  *Cohnella abietis*  *Cohnella phaseoli*  *Cohnella massiliensis*  *Cytobacillus oceanisediminis*  *Limisphaera ngatamarikiensis*  *Paenibacillus swuensis*  *Paenibacillus chitinolvticus*  *Paenibacillus tyrfis* | *Arthrobacter* sp. KBS0702  *Arthrobacter* sp. PGP41  *Arthrobacter* sp. QXT-31  *Arthrobacter* sp. UKPF54-2  *Pseudarthrobacter* sp. NIBRBAC000502771  *Pseudarthrobacter phenanthrenivorans* |
| Network | Module 1: 13.43% | Module 2: 8.96% | Module 3: 8.96% |
| Ab | *Flavisolibacter galbus*  *Flavisolibacter ginsengisoli*  *Flavisolibacter ginsenosidimutans*  *Microvirga aerilata*  *Microvirga ossetica*  *Microvirga soli*  *Microvirga subterranean*  *Microvirga zambiensis*  *Microvirga* sp. 17 mud 1-3 | *Bacillus* sp. X1(2014)  *Bacillus* sp. 1NLA3E  *Bacillus* sp. S3  *Bacillus infantis*  *Bacillus* sp. Y1.  *Neobacillus niacin* | *Anabaena cylindrica*  *Exiguobacterium antarcticum*  *Exiguobacterium sibiricum*  *Exiguobacterium undae*  *Stenotrophomonas* sp. G4  *Stenotrophomonas* sp. MYb57 |
| Network | Module 1: 16.22% | Module 2: 13.51% | Module 3: 8.11% |
| Af | *Bacillus infantis*  *Bacillus mediterraneensis*  *Bacillus methanolicus*  *Bacillus* sp. 1NLA3E  *Mesobacillus foraminis*  *Mesobacillus subterraneus* | *Achromobacter xylosoxidans*  *Ensifer adhaerens*  *Exiguobacterium mexicanum*  *Stenotrophomonas* sp. G4  *Stenotrophomonas* sp. MYb57 | *Massilia agri*  *Massilia oculi*  *Massilia* sp. WG5 |
| Network | Module 1: 14.55% | Module 2: 12.73% | Module 3: 10.91% |
| Abf | *Massilia agri*  *Massilia albidiflava*  *Massilia oculi*  *Massilia putida*  *Massilia timonae*  *Massilia umbonata*  *Massilia violaceinigra*  *Massilia* sp. WG5 | *Bacillus acidicola*  *Bacillus carboniphilus*  *Bacillus mediterraneensis*  *Bacillus licheniformis*  *Bacillus paralicheniformis*  *Mesobacillus foraminis*  *Mesobacillus subterraneus* | *Alkalihalobacillus halodurans*  *Bacillus circulans*  *Bacillus dafuensis*  *Bacillus infantis*  *Bacillus methanolicus*  *Cytobacillus gottheili* |
| Network | Module 1: 22.41% | Module 2: 13.79% | Module 3: 4.9% |
| B | *Ammoniphilus resinae*  *Alkalihalobacillus halodurans*  *Bacillus mediterraneensis*  *Bacillus methanolicus*  *Bacillus infantis*  *Bacillus* sp. 1NLA3E  *Cytobacillus gottheilii*  *Mesobacillus foraminis*  *Mesobacillus subterraneus*  *Oxalophagus oxalicus*  *Paenibacillus beijingensis*  *Paenibacillus chitinolyticus*  *Paenibacillus vunnanensis* | *Cohnella abietis*  *Cohnella candidum*  *Cohnella massiliensis*  *Cohnella phaseoli*  *Cytobacillus oceanisediminis*  *Tumebacillus algifaecis*  *Tumebacillus ginsengisoli*  *Tumebacillus soli* | 4 way tie  *Exiguobactrium* sp.  *Flavisolibacter*, *Bacillus* sp.  *Microvirga* sp. |
| Network | Module 1: 14.89% | Module 2: 12.77% | Module 3: 8.51% |
| Ba | Alkalihalobacillus halodurans  Bacillus dafuensis  Bacillus mediterraneensis  Bacillus methanolicus  Cytobacillus gottheilli  Paenibacillus beijingensis  Paenibacillus chitinolyticus | *Bacillus infantis*  *Bacillus* sp. 1NLA3E  *Bacillus* sp. Y1.  *Cytobacillus Oceanisediminis*  *Mesobacillus foraminis*  *Mesobacillus litoralis* | *Bacillus* sp. S3  *Bacillus* sp. X1(2014)  *Neobacillus mesonae*  *Neobacillus niacin* |
| Network | Module 1: 23.33% | Module 2: 18.33% | Module 3: 11.67% |
| Bf | *Bacillus infantis*  *Bacillus mediterraneensis*  *Bacillus* *methanolicus*  *Bacillus* sp. S3  *Bacillus* sp. X1(2014)  *Bacillus* sp. Y1.  *Bacillus* sp. 1NLA3E  *Cytobacillus gottheilii*  *Cytobacillus Oceanisediminis*  *Mesobacillus foraminis*  *Metabacillus litoralis*  *Mesobacillus subterraneus*  *Neobacillus niacin*  *Neobacillus mesonae* | *Massilia armeniaca*  *Massilia namucuonensis*  *Massilia putida*  *Massilia oculi*  *Massilia umbonate*  *Massilia violaceinigra*  *Microvirga ossetica*  *Microvirga subterranean*  *Microvirga* sp. 17 mud 1-3  *Paracoccus* sp. Arc7-R13 | *Exiguobacterium acetylicum*  *Exiguobacterium antarcticum*  *Exiguobacterium sibiricum*  *Exiguobacterium undae*  *Exiguobacterium* sp. U13-1  *Exiguobacterium* sp. ZWU0009  *Flavisolibacter* sp. 17J28-1 |
| Network | Module 1: 18.87% | Module 2: 13.21% | Module 3: 7.55% |
| Baf | *Alkalihalobacillus halodurans*  *Bacillus mediterraneensis*  *Bacillus* *methanolicus*  *Devosia* sp. A16  *Flaviaesturaribacter luteus*  *Mesobacillus foraminis*  *Mesobacillus stamsii*  *Mesobacillus subterraneus*  *Paenibacillus chitinolyticus*  *Pontibacter populi* | *Massilia agri*  *Massilia alkalitolerans*  *Massilia oculi*  *Massilia putida*  *Massilia Umbonata*  *Massilia violaceinigra*  *Massilia* sp. WG5 | *Bacillus* sp. S3  *Bacillus* sp. X1(2014)  *Bacillus* sp. 1NLA3E  *Neobacillus mesonae* |
| Network | Module 1: 12.5% | Module 2: 9.38% | Module 3: 9.38% |
| F | *Microvirga ossetica*  *Microvirga soli*  *Microvirga subterranean*  *Microvirga* sp. 17 mud 1-3 | *Exiguobacterium antarcticum*  *Exiguobacterium sibiricum*  *Exiguobacterium undae* | *Noviherbaspirillum aurantiacum*  *Noviherbaspirillum massiliense*  *Noviherbaspirillum soli* |
| Network | Module 1: 19.15% | Module 2: 10.64% | Module 3: 8.51% |
| Fa | *Alkalihalobacillus halodurans*  *Bacillus ciccensis*  *Bacillus infantis*  *Bacillus mediterraneensis*  *Bacillus methanolicus*  *Cytobacillus gottheili*  *Mesobacillus foraminis*  *Mesobacillus subterraneus*  *Paenibacillus chitinolvticus* | *Massilia agri*  *Massilia oculi*  *Massilia putida*  *Massilia umbonate*  *Massilia* sp. WG5 | *Herbaspirillum* sp. meg3  *Herbaspirillum seropedica*  *Noviherbaspirillum aurantiacum*  *Noviherbaspirillum soli* |
| Network | Module 1: 20.73% | Module 2: 14.63% | Module 3: 14.63% |
| Fb | *Ammoniphilus resinae*  *Bacillus infantis*  *Bacillus mediterraneensis*  *Bacillus methanolicus*  *Bacillus* sp. S3  *Bacillus* sp. X1(2014)  *Bacillus* sp. 1NLA3E  *Cytobacillus gottheili*  *Cytobacillus oceanisediminis*  *Mesobacillus foraminis*  *Mesobacillus stamsii*  *Mesobacillus subterraneus*  *Oxalophagus oxalicus*  *Paenibacillus mucilaginosus*  *Pedobacter mongoliensis*  *Roseisolibacter agri*  *Rufibacter* sp. DG31D | *Massilia albidiflava*  *Massilia armeniaca*  *Massilia namucuonensis*  *Massilia oculi*  *Massilia putida*  *Massilia umbonate*  *Massilia*  *Microvirga ossetica*  *Microvirga subterrânea*  *Microvirga zambiensis*  *Microvirga* sp. 17 mud 1-3  *Ramlibacter tataouinensis* | *Achromobacter insolitus*  *Achromobacter spanius*  *Achromobacter xylosoxidans*  *Chthoniobacter flavus*  *Flavisolibacter ginsenosidimutans*  *Flavisolibacter tropicus*  *Metabacillus litoralis*  *Methylotenera versatilis*  *Pontibacter chitinilvticus*  *Pontibacter korlensis*  *Pontibacter Populi*  *Rubellimicrobium roseum*  Fescue-alfalfa-brassica plant mixture |
| Network | Module 1: 20% | Module 2: 16.67% | Module 3: 10% |
| Fab | *Bacillus methanolicus*  *Bacillus* sp. S3  *Bacillus* sp. X1(2014)  *Bacillus* sp. 1NLA3E  *Neobacillus mesonae*  *Paenibacillus yunnanensis* | *Microvirga ossetica*  *Microvirga soli*  *Microvirga subterranean*  *Microvirga zambiensis*  *Rubellimicrobium roseum* | 5 way tie |

**S14 Table. Bacteriome Network Statistics.** First capitalized letter denotes plant species rhizosphere; lower case letter denotes neighboring plant species.

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Network | Node | Edge | Avg. Weight Degree | Graph Density | Connected Components | Modularity | Avg. Clustering Coefficient | Avg. Path Length |
| A | 52 | 58 | 2.037 | 0.044 | 12 | 0.858 | 0.627 | 2.065 |
| Ab | 71 | 56 | 1.577 | 0.023 | 27 | 0.898 | 0.576 | 1.71 |
| Af | 42 | 26 | 1.141 | 0.03 | 19 | 0.876 | 0.515 | 1.537 |
| Abf | 55 | 49 | 1.597 | 0.033 | 18 | 0.873 | 0.636 | 1.54 |
| B | 58 | 80 | 2.454 | 0.048 | 13 | 0.714 | 0.678 | 2.88 |
| Ba | 47 | 38 | 1.454 | 0.035 | 15 | 0.861 | 0.525 | 2.184 |
| Bf | 60 | 99 | 2.993 | 0.056 | 10 | 0.761 | 0.688 | 2.942 |
| Baf | 53 | 54 | 1.822 | 0.039 | 15 | 0.819 | 0.676 | 2.139 |
| F | 32 | 21 | 1.206 | 0.042 | 14 | 0.898 | 0.926 | 1.087 |
| Fa | 47 | 35 | 1.34 | 0.032 | 16 | 0.874 | 0.473 | 1.775 |
| Fb | 82 | 136 | 2.948 | 0.041 | 10 | 0.682 | 0.478 | 5.331 |
| Fab | 30 | 26 | 1.556 | 0.06 | 9 | 0.835 | 0.562 | 1.452 |

**S15 Table. Bacterial taxa characterization for alfalfa and brassica related microbes.**

|  |  |  |
| --- | --- | --- |
| Bacterial Taxa | Characterization | Citation |
| *Adhaeribacter swui* | Tested positive for oxidase and catalase | Kim et al. [60] |
| *Neorhizobium* sp. SOG26 | Metal ion binding properties | NCBI 2060726  uniprot.org |
| *Pseudarthrobacter* sp. NIBRBAC000502771 | Capable of producing auxin (Indol-3-glycerol phosphate synthase) and has heavy metal (copper and arsenic) resistance | Park et al. [61] |
| *Pseudarthrobacter phenanthrenivornans* | Produces several phytohormones (abscisic acid, auxin, cytokinin, ethylene, gibberellins, jasmonic acid, and salicylic acid) | Tshishonga et al. [62] |
| *Pseudarthrobacter oxydans* | Synthesizes indole-3-acetic acid, fix nitrogen (ammonia production), solubilize phosphorus, and is resistant to heavy metals (cadmium, copper, and nickel) | Bushra et al. [63] |
| *Paucimonas lemoignei* | Flagellated and a potential nitrogen fixer | Jendrossek et al. [64] |
| *Arthrobacter sp.* UKPF54-2 | Promotes growth for *Brassica* sp., fix nitrogen, produce acetolactate synthase (dihydroxy acid dehydratase and ketol acid reductoisomerase), and produce five genes attributed to antimicrobial properties | Shen et al. [65] |
| *Adhaeribacter aerophilus* | Oxidase positive and may hydrolyze starch | Weon et al. [71] |
| *Larkinella arboricola* | Indole producer | Kulichevskaya et al. [72] |
| *Larkinella insperata* | Bared no remarkable plant related characteristics | Anandham et al. [73]  Vancanneyt et al. [74] |
| *Dyadobacter sediminis* | Produces catalase, oxidase, alkaline phosphatase, and acid phosphatase | Tian et al. [75] |
| *Paenibacillus* sp. 37 | Possible plant growth promotor due to its ability for siderophore biosynthesis, antimicrobial production (paeninodin, bacitracin, paenilipoheptin, xenocoumacin, pellasoren, and octapeptin), and its phytohormone-associated genes | Garcia-Lemos et al. [76] |
| *Brevibacterium frigrotolerans* | Shown to solubilize phosphate, produce indole-3-acetic acid, and produce siderophores | Tara et al. [77] |
| *Trichormus azollae* | Nitrogen fixer for ferns | Gunawardana et al. [78] |
| *Ensifer adhaerens* | Nitrogen fixer and may produce indole-3-acetic acid, exopolysaccharides, ammonia, siderophores, salicylic acid (for abiotic stress), and even promote seed germination for soybean | Zhou et al. [79] |
| *Sinorhizobium meliloti* | Nitrogen fixing symbiont of alfalfa | Galibert et al. [80] |