

Table S1. Difference in bacterial community relative abundances at phylum level (%).

| | Tif.TS | Tif.NT | Com.TS | Com.NT |
|------------------|-------------|-------------|-------------|-------------|
| Acidobacteria | 29.45±0.53b | 35.89±0.41a | 30.69±0.47b | 34.79±0.60a |
| Proteobacteria | 19.22±0.24b | 23.97±0.21a | 22.55±0.31a | 23.38±0.25a |
| Chloroflexi | 19.10±0.18a | 11.78±0.10c | 15.18±0.21b | 15.10±0.11b |
| Actinobacteria | 9.62±0.12a | 4.15±0.06d | 7.17±0.08b | 5.00±0.13c |
| Nitrospirae | 5.64±0.11a | 3.82±0.08c | 4.69±0.08b | 3.50±0.06c |
| Verrucomicrobia | 4.80±0.23a | 4.19±0.18b | 5.04±0.20a | 3.35±0.15c |
| Planctomycetes | 4.46±0.25a | 3.44±0.21c | 3.85±0.24b | 3.91±0.12b |
| Bacteroidetes | 2.96±0.12b | 2.14±0.10d | 4.87±0.18a | 2.46±0.13c |
| Patescibacteria | 0.70±0.06c | 3.51±0.12a | 1.48±0.08c | 2.74±0.11b |
| Chlamydiae | 0.34±0.05d | 3.54±0.13a | 1.30±0.07c | 2.18±0.10b |
| Gemmatimonadetes | 1.35±0.09a | 0.76±0.05c | 0.99±0.06b | 0.79±0.07c |
| Firmicutes | 0.80±0.08a | 0.52±0.04c | 0.87±0.07a | 0.74±0.07b |
| (Unassigned) | 0.59±0.05c | 0.72±0.07b | 0.56±0.06c | 0.83±0.07a |
| Spirochaetes | 0.64±0.06b | 0.75±0.07a | 0.41±0.05c | 0.59±0.06b |
| Elusimicrobia | 0.32±0.04c | 0.80±0.11a | 0.34±0.05c | 0.63±0.06b |
| others | 0.00 | 0.00 | 0.00 | 0.00 |

Table S2. Difference in bacterial community relative abundances at order level (%).

| Order | Tif.TS | Tif.NT | Com.TS | Com.NT |
|----------------------|--------------|-------------|-------------|-------------|
| Acidobacteriales | 14.05±0.41c | 20.52±0.57a | 16.53±0.43b | 19.95±0.39a |
| Ktedonobacterales | 11.85±0.20ab | 8.23±0.11c | 11.42±0.17b | 12.12±0.18a |
| (Unassigned) | 10.08±0.18a | 9.36±0.14b | 8.92±0.12c | 9.17±0.17bc |
| Subgroup_2 | 8.99±0.21ab | 9.23±0.17a | 8.19±0.20c | 8.81±0.15b |
| Solibacterales | 6.61±0.18a | 6.33±0.16b | 6.04±0.13c | 5.86±0.17d |
| Betaproteobacterales | 4.93±0.13b | 6.03±0.19a | 4.22±0.11c | 5.04±0.13b |
| Pedosphaerales | 4.22±0.09a | 3.59±0.12b | 4.28±0.14a | 2.78±0.09c |
| Rhizobiales | 4.52±0.20a | 2.99±0.10d | 3.90±0.16b | 3.45±0.14c |
| uncultured | 2.20±0.11c | 3.23±0.13a | 2.20±0.08c | 2.64±0.10b |
| Anaerolineales | 3.98±0.20a | 1.57±0.10b | 1.74±0.12b | 1.00±0.08c |
| Xanthomonadales | 1.05±0.07d | 1.28±0.09c | 3.80±0.24a | 1.86±0.12b |
| Chlamydiales | 0.38±0.05d | 3.85±0.32a | 1.41±0.10c | 2.35±0.18b |
| Gemmatales | 2.15±0.09a | 1.69±0.04c | 1.70±0.09c | 1.80±0.07b |
| Elsterales | 1.15±0.08c | 1.92±0.17a | 1.36±0.10b | 2.08±0.15a |
| Frankiales | 2.07±0.16a | 1.14±0.08c | 1.85±0.12b | 1.26±0.09c |
| others | 21.75±0.35a | 19.04±0.43b | 22.42±0.41a | 19.81±0.33b |

Table S3. Alpha diversity (ACE, Chao1, shannon and simpson indexes) index of soil bacterial community structure under traffic stress.

| | Tif.TS | Tif.NT | Com.TS | Com.NT |
|---------|----------------|----------------|----------------|----------------|
| ACE | 2618.63±22.65b | 2688.09±23.96a | 2471.56±30.12d | 2566.87±25.63c |
| Chao1 | 2610.47±21.58b | 2689.75±28.21a | 2472.21±27.12d | 2569.87±24.36c |
| shannon | 9.08±0.03b | 9.17±0.02a | 9.10±0.02b | 9.20±0.03a |
| simpson | 0.0065±0.0002a | 0.0053±0.0003c | 0.0059±0.0003b | 0.0051±0.0002c |