TABLE S1 Summary of longitude, latitude, mean annual temperature (MAT), and mean annual precipitation (MAP) at sampling plots.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Plot Name | longitude (°) | latitude (°) | MAT (℃) | MAP (mm) |
| MP1 | 123 | 44.5 | 5.10 | 373 |
| MP2 | 121 | 44.5 | 5.80 | 320 |
| MP3 | 120 | 45.1 | 3.72 | 320 |
| MP4 | 118 | 44.7 | 0.56 | 336 |
| MP5 | 116 | 44.2 | 1.17 | 262 |
| MP6 | 116 | 43.5 | 0.16 | 321 |
| MP7 | 117 | 44.5 | 1.96 | 287 |
| MP8 | 114 | 44.0 | 0.10 | 234 |
| MP9 | 113 | 43.8 | 2.47 | 177 |
| MP10 | 112 | 43.6 | 3.69 | 140 |
| LP1 | 113 | 36.2 | 11.8 | 469 |
| LP2 | 112 | 35.9 | 9.96 | 492 |
| LP3 | 111 | 35.9 | 10.6 | 471 |
| LP4 | 110 | 36.0 | 10.7 | 444 |
| LP5 | 109 | 36.7 | 9.50 | 415 |
| LP6 | 107 | 36.9 | 7.46 | 365 |
| LP7 | 107 | 37.5 | 5.23 | 329 |
| LP8 | 105 | 37.4 | 5.87 | 266 |
| LP9 | 104 | 37.4 | 7.56 | 194 |
| LP10 | 104 | 37.4 | 7.71 | 179 |
| TP1 | 95.4 | 31.4 | 0.41 | 516 |
| TP2 | 93.5 | 31.8 | -1.50 | 447 |
| TP3 | 92.0 | 31.6 | -4.37 | 417 |
| TP4 | 90.7 | 31.3 | -6.76 | 439 |
| TP5 | 89.7 | 31.5 | -3.06 | 369 |
| TP6 | 87.8 | 31.8 | -2.57 | 324 |
| TP7 | 85.8 | 31.9 | -3.77 | 313 |
| TP8 | 83.3 | 32.4 | -3.90 | 264 |
| TP9 | 81.2 | 32.3 | -3.49 | 242 |
| TP10 | 80.1 | 32.4 | -1.27 | 159 |

TABLE S2 Summary of environmental factors (soil environment, plant properties, climate) in three transects.

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | MP | | | LP | | | TP | | |
|  | MG | TG | DS | MG | TG | DS | MG | TG | DS |
| soil environment | | | | | | | | | |
| pH | 8.18±0.14 | 7.59±0.05 | 7.95±0.02 | 8.05±0.02 | 8.09±0.02 | 8.23±0.12 | 6.92±0.07 | 8.16±0.03 | 8.23±0.04 |
| SOC (%) | 1.30±0.18 | 1.81±0.05 | 0.61±0.07 | 1.21±0.05 | 0.75±0.04 | 0.48±0.03 | 5.10±0.30 | 0.81±0.04 | 0.41±0.04 |
| TN (%) | 0.13±0.02 | 0.19±0.01 | 0.06±0.01 | 0.14±0.01 | 0.09±0.01 | 0.06±0.01 | 0.42±0.02 | 0.09±0.02 | 0.05±0.01 |
| NH4+ (mg/kg) | 1.16±0.08 | 2.18±0.24 | 0.58±0.04 | 2.03±0.13 | 2.16±0.28 | 1.32±0.11 | 4.00±0.22 | 1.11±0.07 | 1.40±0.21 |
| NO3-(mg/kg) | 23.4±1.37 | 35.3±3.33 | 14.3±1.97 | 9.14±2.13 | 14.6±2.89 | 6.34±0.88 | 39.6±4.57 | 19.6±2.08 | 4.31±1.37 |
| AP (mg/kg) | 2.85±0.20 | 4.99±0.20 | 3.28±0.27 | 2.61±0.21 | 1.98±0.12 | 4.25±0.41 | 3.24±0.39 | 2.10±0.22 | 3.99±0.18 |
| WC % | 0.16±0.01 | 0.12±0.01 | 0.07±0.01 | 0.13±0.01 | 0.09±0.01 | 0.04±0.02 | 0.33±0.03 | 0.13±0.01 | 0.06±0.01 |
| EC (us/cm) | 771±35.2 | 204±13.1 | 246±21.4 | 215±6.36 | 313±67.4 | 277±48.4 | 238±34.0 | 560±141 | 410±99.1 |
| plant properties | | | | | | | | | |
| PS | 1.55±0.12 | 1.42±0.05 | 1.34±0.07 | 1.48±0.09 | 1.58±0.06 | 1.36±0.08 | 1.65±0.13 | 1.42±0.04 | 0.91±0.09 |
| PB(g/m2) | 125±7.40 | 56.6±5.04 | 22.3±2.31 | 155.4±20.0 | 101±8.23 | 74.2±9.87 | 95.0±9.45 | 53.0±7.87 | 25.4±2.04 |
| RWD (kg/m2) | 0.30±0.01 | 0.54±0.05 | 0.12±0.01 | 0.46±0.01 | 0.27±0.02 | 0.21±0.01 | 1.49±0.10 | 0.27±0.01 | 0.33±0.03 |
| RD (mm) | 0.54±0.01 | 0.52±0.01 | 0.56±0.01 | 0.52±0.01 | 0.49±0.01 | 0.51±0.02 | 0.60±0.02 | 0.47±0.01 | 0.60±0.01 |
| climate | | | | | | | | | |
| MAT (℃) | 4.87±0.18 | 0.96±0.12 | 2.09±0.30 | 10.82±0.16 | 8.23±0.37 | 7.04±0.17 | -1.82±0.40 | -4.04±0.29 | -2.89±0.24 |
| MAP (mm) | 338±5.14 | 301±5.08 | 184±7.89 | 478±2.11 | 388±7.87 | 213±7.78 | 460±8.45 | 361±8.74 | 222±9.20 |
| AI | 27.3±0.46 | 33.3±0.85 | 19.1±1.33 | 27.6±0.32 | 25.5±0.06 | 15.2±0.72 | 70.5±2.68 | 84.8±7.97 | 39.5±2.61 |

Notes. SOC: soil organic carbon; TN: total nitrogen; NH4+: ammonium-nitrogen; NO3-: nitrate-nitrogen; AP: available phosphorus; WC: water content; EC: electrical conductivity; PS: plant Shannon index; PB: plant biomass; RDW: root dry weight; RD: root diameter; MAT: mean annul temperature; MAP: mean annul precipitation; and AI: arid index.

TABLE S3 Results of PERMANOVA test for bacterial communities among transects and habitat types.

|  |  |  |  |
| --- | --- | --- | --- |
| Community | | Bray-curtis | |
|  | | F | R2 |
| MP - LP | | 19.1 | 0.107\*\* |
| MP - TP | | 13.0 | 0.076\*\* |
| LP - TP | | 11.8 | 0.069\*\* |
| MP | MG - TG | 6.55 | 0.110\*\* |
|  | MG - DS | 9.58 | 0.172\*\* |
|  | TG - DS | 19.6 | 0.266\*\* |
| LP | MG - TG | 6.15 | 0.102\*\* |
|  | MG - DS | 17.5 | 0.275\*\* |
|  | TG - DS | 14.3 | 0.208\*\* |
| TP | MG - TG | 21.2 | 0.281\*\* |
|  | MG - DS | 26.0 | 0.361\*\* |
|  | TG - DS | 11.5 | 0.175\*\* |

Notes. \*P < 0.05; \*\*P < 0.01. MP: Inner Mongolia Plateau; LP: Loess Plateau; TP: Tibet Plateau; MG: Meadow grassland; TG: Typical grassland; DS Desert steppe.

TABLE S4 The proportion of different ecological processes based on β-nearest taxon index (βNTI).

|  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | MP | LP | TP | MP | | | LP | | | TP | | |
|  | MG | TG | DS | MG | TG | DS | MG | TG | DS |
| Heterogeneous selection | 4.65 | 8.67 | 4.24 | 7.97 | 1.09 | 0.00 | 0.20 | 11.7 | 7.66 | 0.00 | 3.26 | 0.00 |
| Homogeneous selection | 53.9 | 27.5 | 41.5 | 36.2 | 47.8 | 75.7 | 67.3 | 23.2 | 41.1 | 38.0 | 47.1 | 38.4 |
| Dispersal limitation | 34.4 | 50.6 | 48.9 | 50.7 | 17.8 | 16.7 | 11.9 | 33.9 | 31.7 | 35.5 | 40.2 | 49.6 |
| Homogeneous dispersal | 0.98 | 0.35 | 0.51 | 0.72 | 3.26 | 0.72 | 2.42 | 0.20 | 2.42 | 6.16 | 0.36 | 0.72 |
| Drift | 6.08 | 12.9 | 4.94 | 4.35 | 30.1 | 6.88 | 18.2 | 31.1 | 17.1 | 20.3 | 9.06 | 11.2 |

Notes. MP: Inner Mongolia Plateau; LP: Loess Plateau; TP: Tibet Plateau; MG: Meadow grassland; TG: Typical grassland; DS Desert steppe.

TABLE S5 Mantel tests of environmental variables against the relative importance of homogeneous selection and dispersal limitation in shaping soil bacterial communities.

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | Homogeneous selection | | | | Dispersal limitation | | | |
|  | Total | MP | LP | TP | Total | MP | LP | TP |
| AP | 0.001\*\* | 0.015\*\* | 0.000 | 0.012\*\* | 0.007\*\* | 0.021\*\* | 0.044\*\* | 0.010\*\* |
| AI | 0.013\*\* | 0.109\*\* | 0.018\*\* | 0.001 | 0.029\*\* | 0.222\*\* | 0.189\*\* | 0.027\*\* |
| EC | 0.074\*\* | 0.001 | 0.002\* | 0.154\*\* | 0.033\*\* | 0.013\*\* | 0.001 | 0.089\*\* |
| MAP | 0.042\*\* | **0.149**\*\* | **0.042**\*\* | 0.154\*\* | **0.096**\*\* | **0.312**\*\* | **0.314**\*\* | **0.277**\*\* |
| MAT | 0.042\*\* | 0.011\*\* | 0.017\*\* | 0.001 | 0.089\*\* | 0.078\*\* | 0.153\*\* | 0.040\*\* |
| NH4+ | 0.015\*\* | 0.023\*\* | 0.000 | 0.082\*\* | 0.019\*\* | 0.055\*\* | 0.013\*\* | 0.117\*\* |
| NO3- | 0.014\*\* | 0.001 | 0.001 | 0.102\*\* | 0.024\*\* | 0.012\*\* | 0.010\*\* | 0.094\*\* |
| pH | **0.125**\*\* | 0.002\* | 0.011\*\* | **0.263**\*\* | 0.060\*\* | 0.037\*\* | 0.002\* | 0.229\*\* |
| PB | 0.005\*\* | 0.000 | 0.002\* | 0.022\*\* | 0.012\*\* | 0.041\*\* | 0.005\* | 0.025\*\* |
| PS | 0.002\*\* | 0.001 | 0.001 | 0.011\*\* | 0.005\*\* | 0.009\*\* | 0.003\* | 0.038\*\* |
| RDW | 0.041\*\* | 0.001 | 0.022\*\* | 0.185\*\* | 0.021\*\* | 0.048\*\* | 0.143\*\* | 0.166\*\* |
| RD | 0.000\*\* | 0.055\*\* | 0.000 | 0.000 | 0.008\*\* | 0.141\*\* | 0.024\*\* | 0.060\*\* |
| SOC | 0.064\*\* | 0.122\*\* | 0.014\*\* | 0.196\*\* | 0.045\*\* | 0.291\*\* | 0.121\*\* | 0.194\*\* |
| TN | 0.065\*\* | 0.119\*\* | 0.009\*\* | 0.213\*\* | 0.058\*\* | 0.291\*\* | 0.123\*\* | 0.221\*\* |
| WC | 0.058\*\* | 0.002\* | 0.032\*\* | 0.140\*\* | 0.027\*\* | 0.018\*\* | 0.043\*\* | 0.103\*\* |

Notes. \*P < 0.05; \*\*P < 0.01. AP: available phosphorus; AI: arid index; EC: electroconductibility; MAT: mean annul temperature; MAP: mean annul precipitation; NH4+: ammonium-nitrogen; NO3-: nitrate-nitrogen; PB: plant biomass; PS: plant Shannon index; RDW: root dry weight; RD: root diameter; SOC: soil organic carbon; TN: total nitrogen; and WC: water content. The optimal predictor was bolded.

TABLE S6 The relative abundance of each bin and interpretation for homogeneous selection process among transects and habitat types.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  |  |  |  |  |  | MP |  |  | LP |  |  | TP |  |
|  | RA | MP | LP | TP | MG | TG | DS | MG | TG | DS | MG | TG | DS |
| bin1 | 0.006 | 0.006 | 0.006 | 0.002 | 0.007 | 0.004 | 0.007 | 0.006 | 0.007 | 0.005 | 0.000 | 0.004 | 0.004 |
| bin2 | 0.016 | 0.004 | 0.003 | 0.002 | 0.003 | 0.002 | 0.009 | 0.005 | 0.003 | 0.002 | 0.000 | 0.003 | 0.001 |
| bin3 | 0.004 | 0.058 | 0.040 | 0.044 | 0.055 | 0.071 | 0.044 | 0.039 | 0.049 | 0.028 | 0.075 | 0.037 | 0.023 |
| bin4 | 0.02 | 0.016 | 0.016 | 0.014 | 0.016 | 0.015 | 0.020 | 0.015 | 0.017 | 0.019 | 0.009 | 0.018 | 0.015 |
| bin5 | 0.01 | 0.000 | 0.000 | 0.001 | 0.000 | 0.000 | 0.001 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.009 |
| bin6 | 0.012 | 0.001 | 0.003 | 0.000 | 0.003 | 0.000 | 0.000 | 0.005 | 0.002 | 0.008 | 0.000 | 0.001 | 0.000 |
| bin7 | 0.01 | 0.020 | 0.015 | 0.009 | 0.020 | 0.019 | 0.020 | 0.011 | 0.017 | 0.017 | 0.001 | 0.012 | 0.016 |
| bin8 | 0.026 | 0.007 | 0.004 | 0.006 | 0.007 | 0.026 | 0.000 | 0.011 | 0.003 | 0.000 | 0.032 | 0.000 | 0.005 |
| bin9 | 0.005 | 0.015 | 0.013 | 0.016 | 0.013 | 0.018 | 0.011 | 0.013 | 0.018 | 0.008 | 0.008 | 0.029 | 0.006 |
| bin10 | 0.006 | 0.003 | 0.000 | 0.003 | 0.003 | 0.002 | 0.003 | 0.000 | 0.000 | 0.000 | 0.004 | 0.005 | 0.000 |
| bin11 | 0.005 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.000 | 0.000 | 0.001 | 0.001 | 0.002 | 0.000 | 0.000 |
| bin12 | 0.01 | 0.001 | 0.000 | 0.004 | 0.002 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.005 | 0.008 |
| bin13 | 0.033 | 0.002 | 0.000 | 0.003 | 0.000 | 0.003 | 0.001 | 0.000 | 0.000 | 0.000 | 0.004 | 0.005 | 0.000 |
| bin14 | 0.015 | 0.006 | 0.018 | 0.008 | 0.006 | 0.006 | 0.004 | 0.020 | 0.014 | 0.021 | 0.005 | 0.007 | 0.015 |
| bin15 | 0.016 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.001 |
| bin16 | 0.074 | 0.000 | 0.007 | 0.002 | 0.003 | 0.000 | 0.000 | 0.001 | 0.007 | 0.013 | 0.000 | 0.005 | 0.002 |
| bin17 | 0.114 | 0.002 | 0.003 | 0.001 | 0.001 | 0.001 | 0.004 | 0.003 | 0.002 | 0.002 | 0.000 | 0.001 | 0.002 |
| bin18 | 0.012 | 0.000 | 0.002 | 0.001 | 0.002 | 0.000 | 0.000 | 0.001 | 0.002 | 0.003 | 0.000 | 0.001 | 0.002 |
| bin19 | 0.004 | 0.002 | 0.001 | 0.000 | 0.002 | 0.003 | 0.001 | 0.000 | 0.000 | 0.002 | 0.001 | 0.000 | 0.000 |
| bin20 | 0.009 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.004 | 0.000 | 0.000 | 0.000 |
| bin21 | 0.01 | 0.018 | 0.010 | 0.014 | 0.011 | 0.030 | 0.010 | 0.007 | 0.009 | 0.010 | 0.032 | 0.009 | 0.005 |
| bin22 | 0.021 | 0.001 | 0.024 | 0.002 | 0.001 | 0.004 | 0.000 | 0.005 | 0.021 | 0.047 | 0.003 | 0.003 | 0.000 |
| bin23 | 0.05 | 0.070 | 0.090 | 0.061 | 0.065 | 0.073 | 0.071 | 0.109 | 0.107 | 0.050 | 0.062 | 0.070 | 0.049 |
| bin24 | 0.016 | 0.122 | 0.105 | 0.115 | 0.118 | 0.143 | 0.096 | 0.124 | 0.121 | 0.064 | 0.154 | 0.124 | 0.062 |
| bin25 | 0.021 | 0.011 | 0.012 | 0.009 | 0.013 | 0.008 | 0.011 | 0.016 | 0.017 | 0.002 | 0.013 | 0.012 | 0.002 |
| bin26 | 0.018 | 0.000 | 0.002 | 0.000 | 0.000 | 0.000 | 0.000 | 0.002 | 0.001 | 0.005 | 0.000 | 0.000 | 0.001 |
| bin27 | 0.02 | 0.000 | 0.001 | 0.001 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.007 | 0.001 | 0.000 | 0.004 |
| bin28 | 0.013 | 0.006 | 0.001 | 0.007 | 0.003 | 0.008 | 0.007 | 0.000 | 0.005 | 0.000 | 0.010 | 0.006 | 0.005 |
| bin29 | 0.017 | 0.006 | 0.001 | 0.000 | 0.004 | 0.007 | 0.006 | 0.001 | 0.000 | 0.001 | 0.000 | 0.000 | 0.000 |
| bin30 | 0.068 | 0.014 | 0.015 | 0.016 | 0.011 | 0.014 | 0.018 | 0.013 | 0.018 | 0.015 | 0.022 | 0.012 | 0.015 |
| bin31 | 0.039 | 0.016 | 0.018 | 0.020 | 0.014 | 0.015 | 0.021 | 0.011 | 0.014 | 0.033 | 0.004 | 0.020 | 0.041 |
| bin32 | 0.061 | 0.001 | 0.006 | 0.004 | 0.000 | 0.002 | 0.000 | 0.002 | 0.002 | 0.014 | 0.005 | 0.000 | 0.019 |
| bin33 | 0.021 | 0.013 | 0.005 | 0.000 | 0.008 | 0.019 | 0.008 | 0.001 | 0.000 | 0.026 | 0.001 | 0.000 | 0.003 |
| bin34 | 0.112 | 0.005 | 0.003 | 0.006 | 0.004 | 0.007 | 0.002 | 0.006 | 0.008 | 0.000 | 0.010 | 0.011 | 0.006 |
| bin35 | 0.017 | 0.019 | 0.004 | 0.012 | 0.013 | 0.026 | 0.013 | 0.005 | 0.006 | 0.002 | 0.019 | 0.011 | 0.007 |
| bin36 | 0.016 | 0.050 | 0.045 | 0.030 | 0.060 | 0.075 | 0.017 | 0.049 | 0.052 | 0.029 | 0.063 | 0.040 | 0.016 |
| bin37 | 0.052 | 0.014 | 0.021 | 0.030 | 0.001 | 0.009 | 0.032 | 0.004 | 0.005 | 0.044 | 0.002 | 0.029 | 0.051 |
| bin38 | 0.022 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 |

Notes. MP: Inner Mongolia Plateau; LP: Loess Plateau; TP: Tibet Plateau; MG: Meadow grassland; TG: Typical grassland; DS: Desert steppe.

TABLE S7 The interpretation of each bin for dispersal limitation process among transects and habitat types.

|  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  |  |  |  |  | MP |  |  | LP |  |  | TP |  |
|  | MP | LP | TP | MG | TG | DS | MG | TG | DS | MG | TG | DS |
| bin1 | 0.001 | 0.000 | 0.003 | 0.001 | 0.002 | 0.000 | 0.000 | 0.000 | 0.000 | 0.007 | 0.001 | 0.000 |
| bin2 | 0.004 | 0.008 | 0.007 | 0.005 | 0.002 | 0.002 | 0.002 | 0.007 | 0.010 | 0.000 | 0.010 | 0.007 |
| bin3 | 0.000 | 0.000 | 0.005 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.013 | 0.000 |
| bin4 | 0.004 | 0.005 | 0.007 | 0.010 | 0.001 | 0.001 | 0.007 | 0.004 | 0.001 | 0.013 | 0.006 | 0.000 |
| bin5 | 0.098 | 0.112 | 0.075 | 0.090 | 0.055 | 0.159 | 0.146 | 0.088 | 0.106 | 0.015 | 0.092 | 0.130 |
| bin6 | 0.017 | 0.015 | 0.010 | 0.023 | 0.018 | 0.005 | 0.017 | 0.016 | 0.006 | 0.015 | 0.007 | 0.005 |
| bin7 | 0.000 | 0.000 | 0.003 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.006 | 0.000 | 0.000 |
| bin8 | 0.047 | 0.034 | 0.050 | 0.053 | 0.040 | 0.022 | 0.030 | 0.047 | 0.003 | 0.056 | 0.052 | 0.015 |
| bin9 | 0.009 | 0.004 | 0.004 | 0.027 | 0.000 | 0.004 | 0.000 | 0.001 | 0.010 | 0.006 | 0.000 | 0.007 |
| bin10 | 0.014 | 0.016 | 0.010 | 0.016 | 0.012 | 0.014 | 0.019 | 0.017 | 0.010 | 0.010 | 0.009 | 0.009 |
| bin11 | 0.003 | 0.005 | 0.002 | 0.004 | 0.003 | 0.003 | 0.007 | 0.006 | 0.003 | 0.002 | 0.001 | 0.001 |
| bin12 | 0.021 | 0.016 | 0.017 | 0.018 | 0.022 | 0.022 | 0.020 | 0.013 | 0.016 | 0.004 | 0.017 | 0.021 |
| bin13 | 0.005 | 0.010 | 0.005 | 0.003 | 0.003 | 0.009 | 0.013 | 0.011 | 0.007 | 0.000 | 0.006 | 0.008 |
| bin14 | 0.001 | 0.000 | 0.002 | 0.000 | 0.000 | 0.001 | 0.001 | 0.000 | 0.000 | 0.001 | 0.003 | 0.001 |
| bin15 | 0.006 | 0.012 | 0.010 | 0.002 | 0.007 | 0.008 | 0.015 | 0.012 | 0.008 | 0.006 | 0.009 | 0.014 |
| bin16 | 0.019 | 0.021 | 0.025 | 0.019 | 0.012 | 0.020 | 0.028 | 0.020 | 0.010 | 0.031 | 0.023 | 0.016 |
| bin17 | 0.003 | 0.001 | 0.004 | 0.011 | 0.000 | 0.000 | 0.000 | 0.001 | 0.004 | 0.000 | 0.004 | 0.008 |
| bin18 | 0.005 | 0.004 | 0.003 | 0.013 | 0.000 | 0.001 | 0.001 | 0.002 | 0.008 | 0.000 | 0.004 | 0.004 |
| bin19 | 0.004 | 0.004 | 0.005 | 0.005 | 0.002 | 0.005 | 0.001 | 0.005 | 0.004 | 0.003 | 0.002 | 0.011 |
| bin20 | 0.021 | 0.035 | 0.042 | 0.019 | 0.019 | 0.020 | 0.034 | 0.037 | 0.031 | 0.034 | 0.048 | 0.041 |
| bin21 | 0.000 | 0.002 | 0.000 | 0.001 | 0.000 | 0.000 | 0.006 | 0.001 | 0.000 | 0.000 | 0.000 | 0.000 |
| bin22 | 0.002 | 0.008 | 0.005 | 0.000 | 0.001 | 0.003 | 0.001 | 0.004 | 0.021 | 0.000 | 0.013 | 0.000 |
| bin23 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 |
| bin24 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 |
| bin25 | 0.000 | 0.001 | 0.002 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 0.002 | 0.000 | 0.001 | 0.003 |
| bin26 | 0.001 | 0.004 | 0.003 | 0.001 | 0.001 | 0.000 | 0.003 | 0.004 | 0.005 | 0.000 | 0.001 | 0.007 |
| bin27 | 0.002 | 0.005 | 0.005 | 0.001 | 0.000 | 0.005 | 0.005 | 0.007 | 0.011 | 0.000 | 0.004 | 0.017 |
| bin28 | 0.004 | 0.006 | 0.003 | 0.005 | 0.002 | 0.004 | 0.007 | 0.007 | 0.001 | 0.000 | 0.004 | 0.004 |
| bin29 | 0.017 | 0.013 | 0.021 | 0.013 | 0.013 | 0.023 | 0.004 | 0.008 | 0.018 | 0.008 | 0.013 | 0.040 |
| bin30 | 0.001 | 0.002 | 0.000 | 0.002 | 0.000 | 0.000 | 0.001 | 0.000 | 0.005 | 0.000 | 0.001 | 0.000 |
| bin31 | 0.000 | 0.004 | 0.005 | 0.000 | 0.000 | 0.000 | 0.002 | 0.007 | 0.000 | 0.004 | 0.004 | 0.001 |
| bin32 | 0.005 | 0.011 | 0.011 | 0.006 | 0.005 | 0.002 | 0.011 | 0.008 | 0.012 | 0.011 | 0.006 | 0.004 |
| bin33 | 0.009 | 0.011 | 0.017 | 0.008 | 0.001 | 0.022 | 0.007 | 0.004 | 0.012 | 0.004 | 0.015 | 0.028 |
| bin34 | 0.005 | 0.010 | 0.008 | 0.005 | 0.001 | 0.011 | 0.008 | 0.001 | 0.020 | 0.000 | 0.001 | 0.015 |
| bin35 | 0.003 | 0.009 | 0.003 | 0.005 | 0.000 | 0.008 | 0.005 | 0.009 | 0.012 | 0.003 | 0.001 | 0.005 |
| bin36 | 0.026 | 0.013 | 0.038 | 0.026 | 0.011 | 0.030 | 0.008 | 0.010 | 0.021 | 0.002 | 0.030 | 0.048 |
| bin37 | 0.026 | 0.010 | 0.013 | 0.034 | 0.040 | 0.002 | 0.023 | 0.014 | 0.000 | 0.051 | 0.001 | 0.001 |
| bin38 | 0.068 | 0.041 | 0.052 | 0.056 | 0.062 | 0.085 | 0.040 | 0.033 | 0.071 | 0.017 | 0.058 | 0.088 |

Notes. MP: Inner Mongolia Plateau; LP: Loess Plateau; TP: Tibet Plateau; MG: Meadow grassland; TG: Typical grassland; DS: Desert steppe.

TABLE S8 Number and relative abundance of the dominant microbial groups among phylum.

|  |  |  |  |
| --- | --- | --- | --- |
| The dominant microbial groups | Abundant taxa | Moderate taxa | Rare taxa |
| Group1 |  |  |  |
| Acidobacteria | 42(0.065) | 202(0.061) | 516(0.045) |
| Actinobacteria | 21(0.012) | 176(0.046) | 394(0.038) |
| Bacteroidetes | 7(0.011) | 99(0.024) | 428(0.010) |
| Total | 70(0.088) | 477(0.131) | 1338(0.093) |
|  |  |  |  |
| Group2 |  |  |  |
| Proteobacteria | 17(0.092) | 176(0.044) | 423(0.013) |
| Actinobacteria | 7(0.017) | 106(0.031) | 202(0.006) |
| Gemmatimonadetes | 8(0.015) | 40(0.010) | 225(0.005) |
| Acidobacteria | 2(0.002) | 33(0.009) | 96(0.003) |
| Nitrospirae |  | 36(0.008) | 63(0.002) |
| Total | 34(0.126) | 391(0.103) | 1009(0.029) |

**Captions for Supplementary Figures:**

Fig. S1 The relative abundances of Acidobacteria, Actinobacteria, and Proteobacteria in three transects and grassland types. Low-case letters indicate significant differences based on LSD test between the transects and habitat types at P < 0.05. Error bars represent standard errors of the means.

Fig. S2 The relative abundance of bacterial in order level in three transects and grassland types

Fig. S3 Proportions of community pairs assembled by heterogeneous selection, drift, selection and SD (selection/dispersal limitation) in three transects and grassland types. Low-case letters indicate significant difference based on bootstrapping test between transects and habitat types at P < 0.05.

Fig. S4 Pie charts show the contribution of dominant bacterial taxa driven by ecological process in three transects and grassland types.

Fig S1

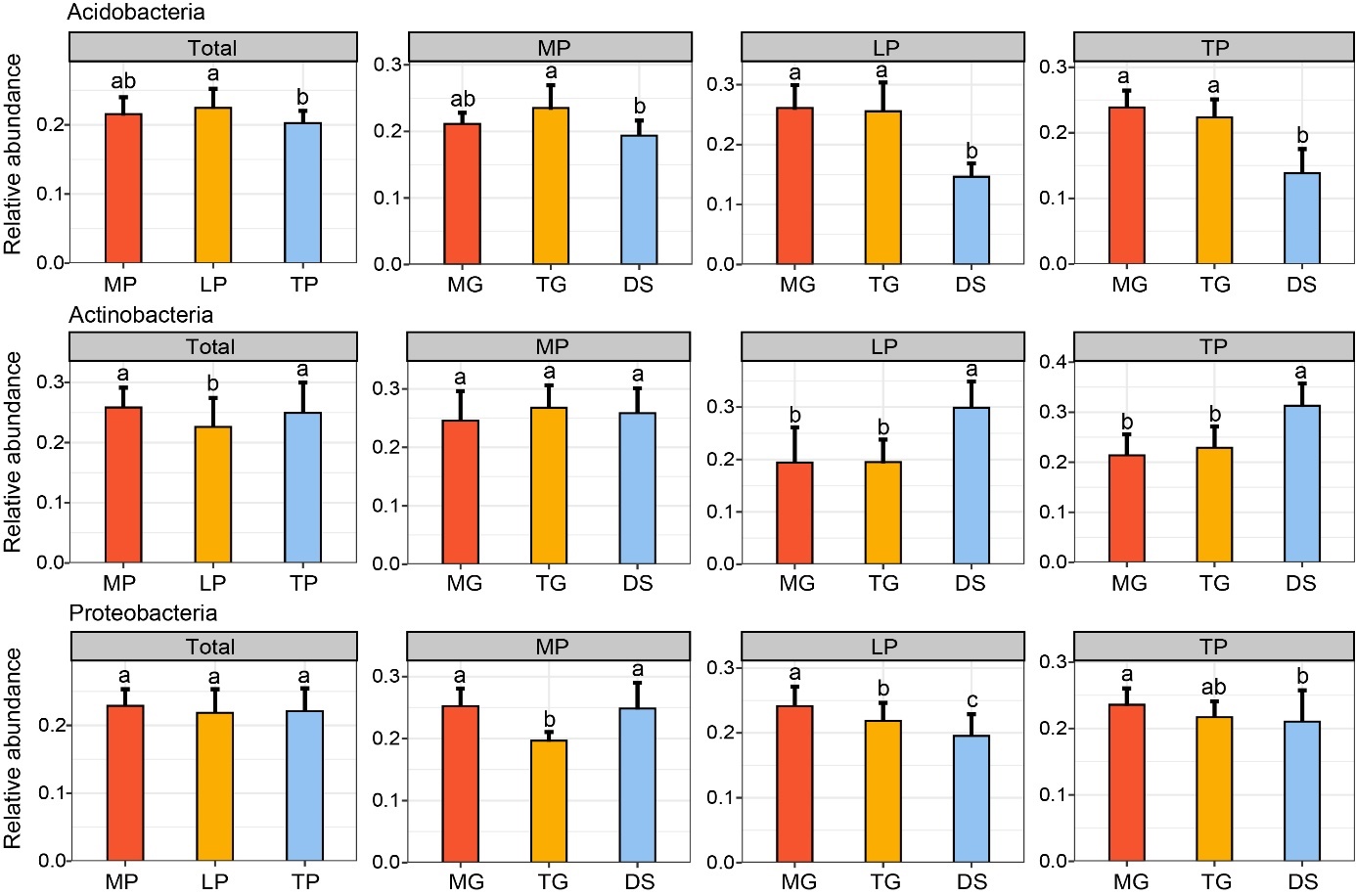


Fig S2

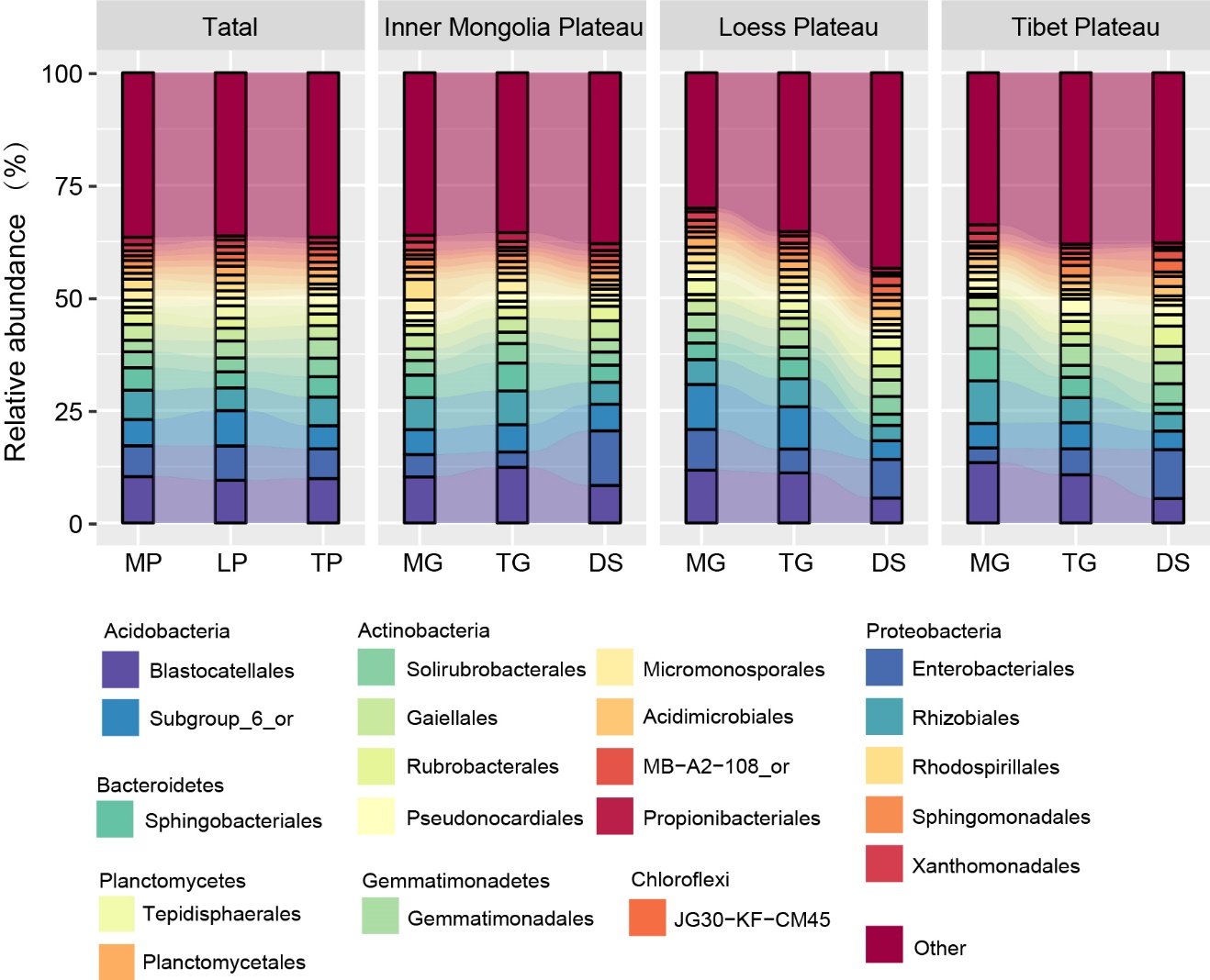


Fig S3

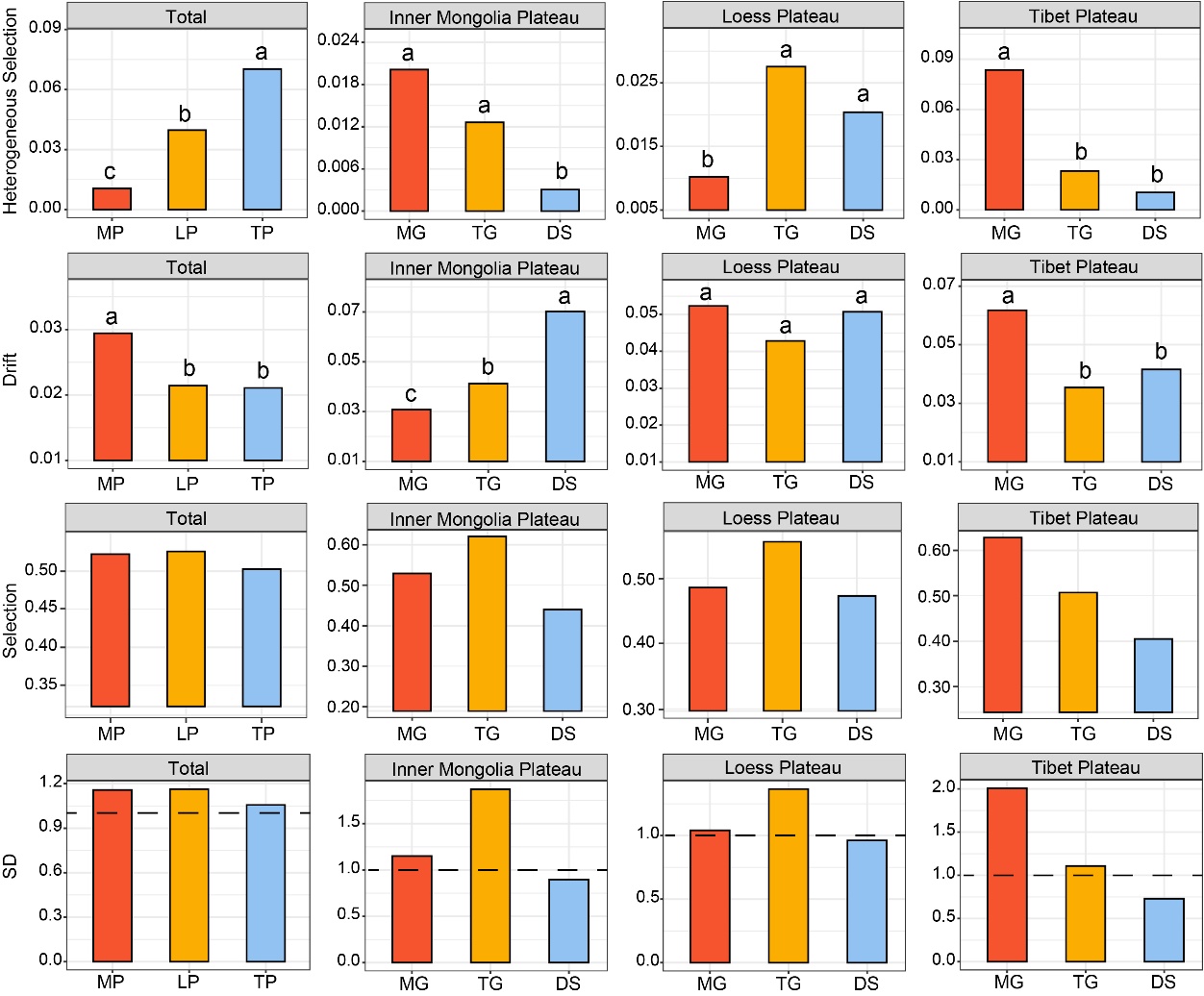


Fig S4

