**Electronic Supplementary Materials**

**For**

**Strong partitioning of soil bacterial community composition and co-occurrence networks along a small-scale elevational gradient on Zijin mountain**

**Table S1.** Environmental factors of soil samples among three elevations. Values are means (SD). Values at the same columns followed by different letters differed significantly at $P < 0.05$ (Duncan' s test). Abbreviations for edaphic factors as SM: soil moisture, TN: total N, TC: total C, DOC: dissolved organic carbon, DON: dissolved organic nitrogen.

| Variables | | Hillfoot | Hillside | Hilltop |
|---|---|---|---|---|
| Moisture | $g\ kg^{-1}$ | 369.9 (14.60)$^{a}$ | 370.9 (54.46)$^{a}$ | 543.9 (126.26)$^{b}$ |
| pH | / | 4.572 (0.27)$^{a}$ | 4.396 (0.26)$^{a}$ | 4.310 (0.20)$^{a}$ |
| TC | $g\ kg^{-1}$ | 33.44 (5.15)$^{a}$ | 40.50 (10.25)$^{a}$ | 79.40 (18.35)$^{b}$ |
| TN | $g\ kg^{-1}$ | 2.40 (0.37)$^{a}$ | 3.40 (0.77)$^{ab}$ | 4.94 (0.97)$^{b}$ |
| DOC | $mg\ kg^{-1}$ | 63.04 (9.18)$^{a}$ | 48.85 (11.67)$^{a}$ | 87.76 (13.15)$^{b}$ |
| DON | $mg\ kg^{-1}$ | 22.86 (3.57)$^{a}$ | 31.87 (3.28)$^{b}$ | 43.97 (6.74)$^{c}$ |
| $NH_4^+$-N | $mg\ kg^{-1}$ | 6.70 (0.99)$^{a}$ | 6.348 (1.11)$^{a}$ | 11.79 (4.21)$^{b}$ |
| $NO_3^-$-N | $mg\ kg^{-1}$ | 7.12 (1.35)$^{a}$ | 10.74 (2.28)$^{b}$ | 10.06 (1.41)$^{b}$ |
| Forest | *type* | mixed pine and broadleaved forest | mixed pine and broadleaved | mixed pine and broadleaved |

**Table S2.** Relative abundance of bacterial phyla/subphyla among elevations. Values are means (SD). Values at the same columns followed by different letters differed significantly at $P < 0.05$ (Duncan' s test). Non-parametric difference test among elevations adopted Kruskal-Wallis method.

| **Taxonomy** (%) | **Elevations** | | | **Kruskal-Wallis** | |
|---|---|---|---|---|---|
| | Hillfoot | Hillside | Hilltop | H(K) | *P* |
| Acidobacteria | 0.349 (0.064)$^{a}$ | 0.345(0.033)$^{a}$ | 0.258(0.106)$^{a}$ | 2.160 | 0.340 |
| Alphaproteobacteria | 0.133 (0.012)$^{b}$ | 0.110(0.017)$^{b}$ | 0.191(0.029)$^{a}$ | 10.820 | 0.004 |
| Actinobacteria | 0.067 (0.012)$^{b}$ | 0.056 (0.014)$^{b}$ | 0.149 (0.097)$^{a}$ | 9.782 | 0.008 |
| Bacteroidetes | 0.093 (0.033)$^{a}$ | 0.079 (0.011)$^{a}$ | 0.078 (0.034)$^{a}$ | 0.847 | 0.655 |
| Verrucomicrobia | 0.082 (0.021)$^{a}$ | 0.076 (0.024)$^{a}$ | 0.063 (0.013)$^{a}$ | 1.825 | 0.402 |
| Gammaproteobacteria | 0.052 (0.030)$^{a}$ | 0.059 (0.018)$^{a}$ | 0.070 (0.026)$^{a}$ | 2.000 | 0.368 |
| Crenarchaeota | 0.047 (0.022)$^{b}$ | 0.092 (0.029)$^{a}$ | 0.027 (0.012)$^{b}$ | 8.896 | 0.012 |
| Planctomycetes | 0.034 (0.005)$^{a}$ | 0.039 (0.007)$^{a}$ | 0.034 (0.006)$^{a}$ | 1.101 | 0.577 |
| Betaproteobacteria | 0.027 (0.010)$^{a}$ | 0.036 (0.009)$^{a}$ | 0.035 (0.01)$^{a}$ | 2.480 | 0.289 |
| Chloroflexi | 0.030 (0.012)$^{a}$ | 0.015 (0.005)$^{a}$ | 0.018 (0.013)$^{a}$ | 2.745 | 0.253 |
| Deltaproteobacteria | 0.016 (0.002)$^{a}$ | 0.014 (0.003)$^{a}$ | 0.014 (0.002)$^{a}$ | 1.860 | 0.395 |
| Gemmatimonadetes | 0.007 (0.003)$^{a}$ | 0.008 (0.002)$^{a}$ | 0.007 (0.004)$^{a}$ | 0.564 | 0.754 |
| Chlamydiae | 0.005 (0.003)$^{a}$ | 0.006 (0.003)$^{a}$ | 0.003 (0.001)$^{a}$ | 4.912 | 0.086 |
| Cyanobacteria | 0.002 (0.001)$^{a}$ | 0.006 (0.003)$^{a}$ | 0.004 (0.003)$^{a}$ | 4.390 | 0.111 |
| OD1 | 0.004 (0.002)$^{a}$ | 0.004 (0.002)$^{a}$ | 0.003 (0.002)$^{a}$ | 1.256 | 0.534 |
| WPS2 | 0.003 (0.002)$^{a}$ | 0.003 (0.002)$^{a}$ | 0.004 (0.002)$^{a}$ | 0.128 | 0.938 |
| FCPU426 | 0.002 (0.001)$^{a}$ | 0.004 (0.001)$^{a}$ | 0.002 (0.001)$^{a}$ | 4.488 | 0.106 |
| OP3 | 0.003 (0.002)$^{a}$ | 0.002 (0.001)$^{a}$ | 0.002 (0.002)$^{a}$ | 2.420 | 0.298 |
| Elusimicrobia | 0.002 (0.001)$^{a}$ | 0.003 (0.001)$^{a}$ | 0.001 (0.001)$^{b}$ | 7.444 | 0.024 |
| AD3 | 0.003 (0.002)$^{a}$ | 0.002 (0.001)$^{a}$ | 0.002 (0.001)$^{a}$ | 1.157 | 0.561 |
| Others | 0.038 (0.005)$^{a}$ | 0.041 (0.004)$^{a}$ | 0.036 (0.001)$^{a}$ | 1.644 | 0.440 |

**Table S3.** Relative abundance of bacterial dominant order among elevations. Values are means (SD). Values at the same columns followed by different letters differed significantly at $P < 0.05$ (Duncan' s test). Non-parametric difference test among elevations adopted Kruskal-Wallis method.

| **Taxonomy** (%) | **Elevations** | | | **Kruskal-Wallis** | |
|---|---|---|---|---|---|
| p_Phyla;o_Order | Hillfoot | Hillside | Hilltop | H(K) | *P* |
| p_Acidobacteria;o_Ellin6513 | 0.136 (0.044)$^{ab}$ | 0.16 (0.032)$^{a}$ | 0.08 (0.034)$^{b}$ | 6.320 | 0.042 |
| p_Acidobacteria;o_Acidobacteriales | 0.094 (0.019)$^{a}$ | 0.071 (0.011)$^{a}$ | 0.088 (0.045)$^{a}$ | 2.240 | 0.326 |
| p_Actinobacteria;o_Actinomycetales | 0.042 (0.009)$^{b}$ | 0.035 (0.01)$^{b}$ | 0.106 (0.065)$^{a}$ | 9.620 | 0.008 |
| p_Acidobacteria;o_Solibacterales | 0.05 (0.006)$^{ab}$ | 0.056 (0.007)$^{a}$ | 0.042 (0.013)$^{b}$ | 3.260 | 0.196 |
| p_Proteobacteria;o_Ellin329 | 0.045 (0.004)$^{a}$ | 0.041 (0.008)$^{a}$ | 0.058 (0.019)$^{a}$ | 3.620 | 0.164 |
| p_Proteobacteria;o_Rhizobiales | 0.044 (0.009)$^{ab}$ | 0.033 (0.005)$^{b}$ | 0.065 (0.022)$^{a}$ | 8.420 | 0.015 |
| p_Verrucomicrobia;o_Pedosphaerales | 0.043 (0.009)$^{a}$ | 0.043 (0.007)$^{a}$ | 0.044 (0.012)$^{a}$ | 0.180 | 0.914 |
| p_Proteobacteria;o_Xanthomonadales | 0.031 (0.007)$^{b}$ | 0.041 (0.013)$^{ab}$ | 0.051 (0.016)$^{a}$ | 3.660 | 0.160 |
| p_Bacteroidetes;o_Saprospirales | 0.041 (0.016)$^{a}$ | 0.039 (0.003)$^{a}$ | 0.035 (0.013)$^{a}$ | 0.260 | 0.878 |
| p_Proteobacteria;o_Rhodospirillales | 0.028 (0.004)$^{b}$ | 0.025 (0.002)$^{b}$ | 0.046 (0.008)$^{a}$ | 10.220 | 0.006 |
| p_Crenarchaeota;o_Cenarchaeales | 0.02 (0.016)$^{b}$ | 0.06 (0.023)$^{a}$ | 0.016 (0.007)$^{b}$ | 8.060 | 0.018 |
| p_Bacteroidetes;o_Sphingobacteriales | 0.026 (0.01)$^{a}$ | 0.024 (0.004)$^{a}$ | 0.028 (0.01)$^{a}$ | 0.140 | 0.932 |
| p_Verrucomicrobia;o_Chthoniobacterales | 0.022 (0.01)$^{a}$ | 0.017 (0.012)$^{a}$ | 0.008 (0.005)$^{a}$ | 4.560 | 0.102 |
| p_Actinobacteria;o_Gaiellales | 0.016 (0.008)$^{a}$ | 0.011 (0.002)$^{a}$ | 0.016 (0.009)$^{a}$ | 1.940 | 0.379 |
| p_Planctomycetes;o_WD2101 | 0.014 (0.002)$^{a}$ | 0.016 (0.002)$^{a}$ | 0.012 (0.004)$^{a}$ | 2.340 | 0.310 |
| p_Proteobacteria;o_Burkholderiales | 0.013 (0.005)$^{a}$ | 0.013 (0.003)$^{a}$ | 0.015 (0.005)$^{a}$ | 0.140 | 0.932 |
| p_Chloroflexi;o_Thermogemmatisporales | 0.019 (0.007)$^{a}$ | 0.007 (0.004)$^{b}$ | 0.007 (0.005)$^{b}$ | 7.340 | 0.025 |
| p_Planctomycetes;o_Pirellulales | 0.008 (0.003)$^{a}$ | 0.011 (0.003)$^{a}$ | 0.011 (0.004)$^{a}$ | 2.960 | 0.228 |
| p_Crenarchaeota;o_Nitrososphaerales | 0.009 (0.006)$^{b}$ | 0.017 (0.004)$^{a}$ | 0.004 (0.003)$^{b}$ | 9.260 | 0.010 |
| p_Proteobacteria;o_Unassigned | 0.004 (0.001)$^{b}$ | 0.011 (0.004)$^{ab}$ | 0.012 (0.007)$^{a}$ | 6.660 | 0.036 |
| p_Actinobacteria;o_Solirubrobacterales | 0.005 (0.001)$^{b}$ | 0.006 (0.002)$^{ab}$ | 0.014 (0.009)$^{a}$ | 7.580 | 0.023 |
| p_Planctomycetes;o_Gemmatales | 0.008 (0.001)$^{a}$ | 0.008 (0.001)$^{a}$ | 0.008 (0.002)$^{a}$ | 0.020 | 0.990 |
| p_Proteobacteria;o_Myxococcales | 0.009 (0.004)$^{a}$ | 0.008 (0.002)$^{a}$ | 0.008 (0.003)$^{a}$ | 0.260 | 0.878 |
| Other | 0.273 (0.028)$^{a}$ | 0.247 (0.03)$^{ab}$ | 0.225 (0.017)$^{b}$ | 1.820 | 0.403 |

**Table S4.** Permutational Multivariate Analysis of Variance (Adonis) test of bacterial community composition, based on Bray-Curtis distance. The number of permutations is 999.

| **Groups** | **F** | $R^2$ | ***P*** |
|---|---|---|---|
| Hillfoot&Hillside | 1.753 | 0.180 | 0.022 |
| Hillfoot&Hilltop | 1.833 | 0.186 | 0.011 |
| Hillside&Hilltop | 1.843 | 0.187 | 0.014 |

**Table S5.** The normal distribution test for edaphic factors, using Shapiro-Wilk test. The hypothesis of $H_0$ is not to follow a normal distribution. Abbreviations of edaphic factors as Table S1.

| **Variables** | **Shapiro-Wilk W** | ***P*** |
|---|---|---|
| SM | 0.823 | **0.007** |
| pH | 0.949 | 0.502 |
| TC | 0.874 | **0.039** |
| TN | 0.926 | 0.242 |
| DOC | 0.978 | 0.950 |
| DON | 0.899 | 0.091 |
| $NH_4^+$-N | 0.761 | **0.001** |
| $NO_3^-$-N | 0.944 | 0.428 |
| **Log transformation** | | |
| SM_transformed | 0.895 | 0.081 |
| TC_transformed | 0.936 | 0.340 |
| $NH_4^+$-N_transformed | 0.887 | 0.053 |

**Table S6.** Generalized variance inflation factors to determine the multicollinearity of a linear model. Abbreviations of edaphic factors as Table S1.

| Variables | VIF | VIF without TC |
|---|---|---|
| SM | 48.1 | 15.7 |
| pH | 2.45 | 2.17 |
| TC | 450.25 | *Deleted* |
| TN | 213.96 | 13.56 |
| DOC | 132.93 | 10.39 |
| DON | 1.6 | 1.53 |
| $NH_4^+$-N | 5.32 | 5.3 |
| $NO_3^-$-N | 4.94 | 4.19 |
| Elevation | 18.96 | 5.82 |

**Table S7.** Permutational Multivariate Analysis of Variance (Adonis) test to evaluate the influence of environmental factors on bacterial community composition, based on Bray-Curtis distance. The number of permutations is 999. Abbreviations of edaphic factors as Table S1.

| Adonis | | |
|---|---|---|
| **Variables** | **$R^2$** | ***P*** |
| SM | 0.114 | **0.004** |
| pH | 0.132 | **0.001** |
| TC | 0.130 | **0.002** |
| TN | 0.125 | **0.002** |
| DOC | 0.125 | **0.001** |
| DON | 0.070 | 0.496 |
| $NH_4^+$-N | 0.094 | 0.063 |
| $NO_3^-$-N | 0.096 | **0.048** |
| Elevation | 0.117 | **0.003** |

**Table S8.** Analysis of correlations between alpha diversity and environmental factors, based on the Pearson method. Bold and italic values indicate a significant correlation. Abbreviations of edaphic factors as Table S1.

| Variables | OTU Richness | | Phylogenetic Diversity | |
|---|---|---|---|---|
| | **r** | ***P*** | **r** | ***P*** |
| SM | 0.061 | 0.830 | -0.142 | 0.613 |
| pH | 0.505 | 0.055 | ***0.549*** | ***0.034*** |
| TC | 0.098 | 0.728 | -0.109 | 0.699 |
| TN | 0.102 | 0.717 | -0.066 | 0.816 |
| DOC | 0.070 | 0.803 | -0.166 | 0.554 |
| DON | -0.346 | 0.207 | -0.279 | 0.315 |
| $NH_4^+$-N | 0.273 | 0.325 | 0.111 | 0.693 |
| $NO_3^-$-N | -0.035 | 0.902 | -0.050 | 0.858 |
| Elevation | -0.006 | 0.984 | -0.174 | 0.535 |

**Table S9.** Analysis of correlations between relative abundance of dominant phyla and environmental factors, based on the Spearman method. Bold values indicate a significant correlation. Abbreviations of edaphic factors as Table S1.

| Phyla | Statics | SM | pH | TC | TN | DOC | DON | $NH_4^+$-N | $NO_3^-$-N | Elevation |
|---|---|---|---|---|---|---|---|---|---|---|
| Acidobacteria | r | -0.255 | 0.107 | -0.504 | -0.465 | -0.345 | 0.501 | -0.332 | -0.310 | -0.451 |
| | *P* | 0.360 | 0.705 | 0.055 | 0.080 | 0.208 | 0.057 | 0.227 | 0.261 | 0.092 |
| Actinobacteria | r | 0.322 | -0.227 | 0.474 | 0.375 | 0.456 | -0.365 | 0.205 | 0.217 | 0.481 |
| | *P* | 0.243 | 0.415 | 0.075 | 0.168 | 0.088 | 0.181 | 0.463 | 0.437 | 0.070 |
| Bacteroidetes | r | -0.082 | 0.218 | -0.003 | -0.005 | 0.023 | -0.159 | 0.103 | -0.061 | -0.279 |
| | *P* | 0.771 | 0.435 | 0.990 | 0.987 | 0.936 | 0.571 | 0.715 | 0.829 | 0.313 |
| Verrucomicrobia | r | -0.289 | **0.645**$^{**}$ | -0.293 | -0.249 | -0.292 | -0.114 | -0.044 | -0.133 | -0.369 |
| | *P* | 0.297 | 0.009 | 0.289 | 0.370 | 0.291 | 0.687 | 0.878 | 0.636 | 0.176 |
| Planctomycetes | r | 0.052 | -0.096 | 0.229 | 0.329 | 0.025 | -0.028 | -0.058 | 0.384 | 0.035 |
| | *P* | 0.855 | 0.734 | 0.411 | 0.231 | 0.930 | 0.920 | 0.837 | 0.158 | 0.903 |
| Chloroflexi | r | **-0.541**$^{*}$ | 0.318 | **-0.532**$^{*}$ | **-0.618**$^{*}$ | -0.334 | -0.198 | -0.246 | **-0.605**$^{*}$ | -0.400 |
| | *P* | 0.037 | 0.249 | 0.041 | 0.014 | 0.223 | 0.480 | 0.376 | 0.017 | 0.139 |
| Gemmatimonadetes | r | 0.009 | 0.375 | 0.054 | 0.130 | -0.148 | -0.281 | -0.131 | 0.422 | 0.063 |
| | *P* | 0.974 | 0.169 | 0.847 | 0.645 | 0.598 | 0.311 | 0.641 | 0.117 | 0.824 |
| Alphaproteobacteria | r | **0.624**$^{*}$ | -0.248 | **0.769**$^{**}$ | **0.671**$^{**}$ | **0.726**$^{**}$ | -0.308 | **0.684**$^{**}$ | 0.162 | **0.640**$^{*}$ |
| | *P* | 0.013 | 0.373 | 0.001 | 0.006 | 0.002 | 0.265 | 0.005 | 0.565 | 0.010 |
| Gammaproteobacteria | r | 0.500 | **-0.550**$^{*}$ | **0.542**$^{*}$ | **0.567**$^{*}$ | 0.449 | 0.088 | 0.214 | 0.339 | 0.323 |
| | *P* | 0.058 | 0.034 | 0.037 | 0.027 | 0.093 | 0.754 | 0.443 | 0.216 | 0.241 |
| Betaproteobacteria | r | 0.233 | 0.238 | 0.303 | 0.395 | 0.072 | -0.033 | 0.231 | **0.554**$^{*}$ | 0.264 |
| | *P* | 0.403 | 0.394 | 0.272 | 0.145 | 0.799 | 0.908 | 0.407 | 0.032 | 0.342 |
| Deltaproteobacteria | r | -0.170 | **0.700**$^{**}$ | -0.174 | -0.168 | -0.136 | -0.269 | 0.104 | -0.113 | -0.268 |
| | *P* | 0.544 | 0.004 | 0.535 | 0.550 | 0.629 | 0.333 | 0.713 | 0.689 | 0.334 |

* represents $P < 0.05$; ** represents $P < 0.01$.

**Table S10.** Key topological properties of co-occurrence networks among three elevations.

| Key traits of networks | Hillfoot Network | Hillside Network | Hilltop Network | Clarifications |
|---|---|---|---|---|
| Node | 453 | 421 | 452 | A taxa, e.g., the bacterial OTUs in this study |
| Edge | 2201 | 1925 | 2283 | The lines connecting nodes, representing the correlations between OTUs |
| Average number of neighbors | 9.739 | 9.145 | 10.079 | The average number of correlations within OTUs in the network, representing the extent to the members closely related to each other in the network |
| Clustering coefficient | 0.084 | 0.088 | 0.083 | Transitivity. The connectedness among members of a network |
| Network density | 0.022 | 0.022 | 0.022 | The portion of the potential connections in a network that are actual connections |
| Positive correlations | 52.5% | 60.2% | 64.1% | The relations of cooperation between the bacterial OTUs in this study |
| Negative correlations | 47.5% | 39.8% | 35.9% | The relations of competition between the bacterial OTUs in this study |

**Table S11.** Analysis of variance (ANOVA) of degree scores and betweenness centralities.

| | Degree scores | | | Betweenness centralities | | |
|---|---|---|---|---|---|---|
| | Hillfoot Hillside | Hillfoot Hilltop | Hillside Hilltop | Hillfoot Hillside | Hillfoot Hilltop | Hillside Hilltop |
| F | 12.600 | 3.747 | 29.109 | 7.378 | 0.293 | 10.229 |
| *P* | 0.001 | 0.053 | 0.001 | 0.007 | 0.588 | 0.001 |

**Table S12.** Summary of topological network properties and taxonomic information of network and module hubs.

| OUT ID | Roles | Radiality | Degree scores | Betweenness centrality | Taxonomy | Relative Abundance |
|---|---|---|---|---|---|---|
| denovo124438 | Network hubs | 0.58 | 18 | 0.0035 | Phylum Proteobacteria; Order Ellin329 | 0.20% |
| 291945 | Network hubs | 0.58 | 20 | 0.0045 | Phylum Acidobacteria; Family Koribacteraceae | 0.10% |
| denovo5335 | Module hubs | 0.54 | 16 | 0.0032 | Phylum Acidobacteria; Order Ellin6513 | 0.41% |
| denovo173697 | Module hubs | 0.54 | 14 | 0.0019 | Phylum Acidobacteria; Family Koribacteraceae | 0.37% |
| denovo153364 | Module hubs | 0.58 | 19 | 0.0043 | Phylum Proteobacteria; Order Rhizobiales | 0.29% |
| denovo172651 | Module hubs | 0.55 | 16 | 0.0033 | Phylum Crenarchaeota; Order NRP-J | 0.17% |
| denovo65042 | Module hubs | 0.55 | 15 | 0.0026 | Phylum Proteobacteria; Family Sinobacteraceae | 0.16% |
| denovo139762 | Module hubs | 0.57 | 17 | 0.0039 | Phylum Gemmatimonadetes; Class Gemm-1 | 0.12% |
| denovo114756 | Module hubs | 0.55 | 14 | 0.0023 | Phylum Acidobacteria; Family Koribacteraceae | 0.11% |
| 248716 | Module hubs | 0.56 | 17 | 0.0035 | Phylum Acidobacteria; Family Koribacteraceae | 0.08% |
| denovo95684 | Module hubs | 0.57 | 17 | 0.0033 | Phylum Actinobacteria; Order Actinomycetales | 0.09% |
| denovo250717 | Module hubs | 0.54 | 16 | 0.0026 | Phylum Proteobacteria; Family Burkholderiaceae | 0.07% |
| denovo58422 | Module hubs | 0.52 | 14 | 0.0022 | Phylum Proteobacteria; Order Rhizobiales | 0.07% |
| denovo248978 | Module hubs | 0.57 | 19 | 0.0043 | Phylum Verrucomicrobia; Family Chthoniobacteraceae | 0.07% |
| denovo111533 | Module hubs | 0.57 | 15 | 0.0024 | Phylum Proteobacteria; Order Ellin329 | 0.06% |
| denovo120408 | Module hubs | 0.58 | 20 | 0.0043 | Phylum Proteobacteria; Family Xanthomonadaceae | 0.06% |

**Table S13.** Correlations between relative abundance of network and module hubs and environmental factors using the Spearman method. Bold values indicate a significant correlation. Abbreviations of edaphic factors as Table S1.

| Hubs ID | Statics | SM | pH | TC | TN | DOC | DON | $NH_4^+$-N | $NO_3^-$-N | Elevation |
|---|---|---|---|---|---|---|---|---|---|---|
| denovo111533 | r | -0.234 | -0.075 | -0.189 | -0.307 | 0.071 | -0.048 | 0.157 | -0.356 | -0.059 |
| | *P* | 0.401 | 0.791 | 0.500 | 0.266 | 0.801 | 0.866 | 0.576 | 0.193 | 0.833 |
| denovo120408 | r | 0.048 | 0.191 | -0.042 | -0.065 | 0.197 | -0.176 | 0.206 | -0.136 | -0.273 |
| | *P* | 0.866 | 0.496 | 0.882 | 0.818 | 0.482 | 0.530 | 0.461 | 0.630 | 0.325 |
| denovo139762 | r | 0.241 | -0.177 | 0.262 | 0.109 | 0.409 | -0.056 | 0.427 | -0.112 | 0.244 |
| | *P* | 0.386 | 0.528 | 0.346 | 0.700 | 0.130 | 0.844 | 0.112 | 0.690 | 0.381 |
| 248716 | r | -0.485 | 0.068 | **-.537*** | **-.695*** | -0.186 | 0.168 | -0.271 | **-.712*** | **-.751*** |
| | *P* | 0.067 | 0.809 | 0.039 | 0.004 | 0.506 | 0.549 | 0.328 | 0.003 | 0.001 |
| denovo172651 | r | **-.574*** | 0.045 | **-.750*** | **-.728*** | **-.701*** | 0.121 | **-.717**** | -0.326 | **-.757*** |
| | *P* | 0.025 | 0.873 | 0.001 | 0.002 | 0.004 | 0.668 | 0.003 | 0.236 | 0.001 |
| denovo173697 | r | -0.212 | -0.169 | -0.285 | -0.325 | -0.345 | **.538*** | -0.276 | -0.176 | -0.105 |
| | *P* | 0.448 | 0.548 | 0.302 | 0.237 | 0.208 | 0.039 | 0.318 | 0.531 | 0.711 |
| denovo114756 | r | 0.064 | 0.241 | 0.091 | -0.096 | 0.432 | -0.102 | 0.483 | -0.238 | -0.096 |
| | *P* | 0.822 | 0.386 | 0.748 | 0.733 | 0.108 | 0.717 | 0.068 | 0.393 | 0.733 |
| 291945 | r | -0.396 | 0.142 | -0.393 | -0.504 | -0.040 | -0.118 | 0.340 | -0.449 | -0.260 |
| | *P* | 0.143 | 0.614 | 0.148 | 0.056 | 0.887 | 0.674 | 0.215 | 0.093 | 0.350 |
| denovo95684 | r | 0.502 | -0.164 | 0.485 | **.588*** | 0.105 | 0.222 | -0.059 | **.569*** | 0.342 |
| | *P* | 0.056 | 0.560 | 0.067 | 0.021 | 0.710 | 0.426 | 0.835 | 0.027 | 0.212 |
| denovo124438 | r | 0.375 | -0.243 | 0.418 | 0.447 | 0.367 | 0.265 | **.563*** | 0.241 | 0.488 |
| | *P* | 0.169 | 0.384 | 0.121 | 0.095 | 0.178 | 0.340 | 0.029 | 0.387 | 0.065 |
| denovo248978 | r | -0.247 | -0.067 | -0.258 | -0.156 | -0.380 | 0.129 | -0.286 | 0.182 | -0.147 |
| | *P* | 0.375 | 0.813 | 0.354 | 0.579 | 0.162 | 0.648 | 0.302 | 0.517 | 0.601 |
| denovo65042 | r | **.858*** | -0.384 | **.781*** | **.704*** | **.629*** | 0.226 | 0.492 | 0.490 | **.774*** |
| | *P* | 0.000 | 0.158 | 0.001 | 0.003 | 0.012 | 0.419 | 0.063 | 0.064 | 0.001 |
| denovo250717 | r | **.646*** | -0.183 | **.749*** | **.745*** | **.666*** | -0.177 | 0.499 | 0.303 | **.727*** |
| | *P* | 0.009 | 0.515 | 0.001 | 0.001 | 0.007 | 0.527 | 0.058 | 0.272 | 0.002 |
| denovo5335 | r | -0.036 | -0.485 | -0.056 | -0.054 | -0.231 | 0.464 | -0.406 | 0.027 | -0.095 |

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| denovo153364 | *P* | 0.899 | 0.067 | 0.844 | 0.849 | 0.408 | 0.082 | 0.133 | 0.924 | 0.737 |
| | r | -0.158 | 0.276 | -0.151 | -0.287 | 0.156 | -0.276 | 0.039 | -0.433 | -0.304 |
| | *P* | 0.574 | 0.318 | 0.592 | 0.299 | 0.578 | 0.320 | 0.889 | 0.107 | 0.271 |
| denovo58422 | r | **.551*** | -0.495 | **.580*** | 0.392 | **.805*** | -0.172 | **.515*** | -0.048 | 0.394 |
| | *P* | 0.033 | 0.061 | 0.024 | 0.148 | 0.000 | 0.540 | 0.049 | 0.864 | 0.146 |

* represents $P < 0.05$

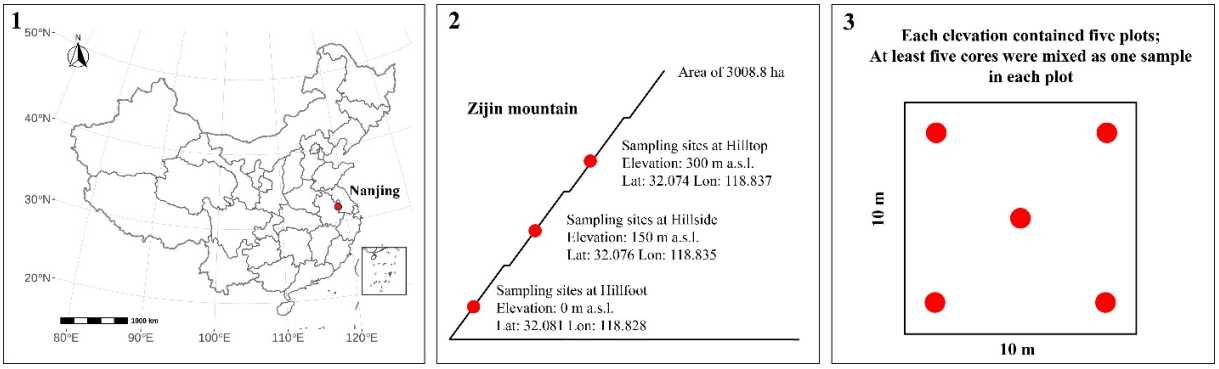


**Fig. S1.** The sampling concept map. 1) The location of sampling site Zijin mountain in China; 2) The information of sampling elevations and coordinates; 3) The sampling strategy at each elevation.

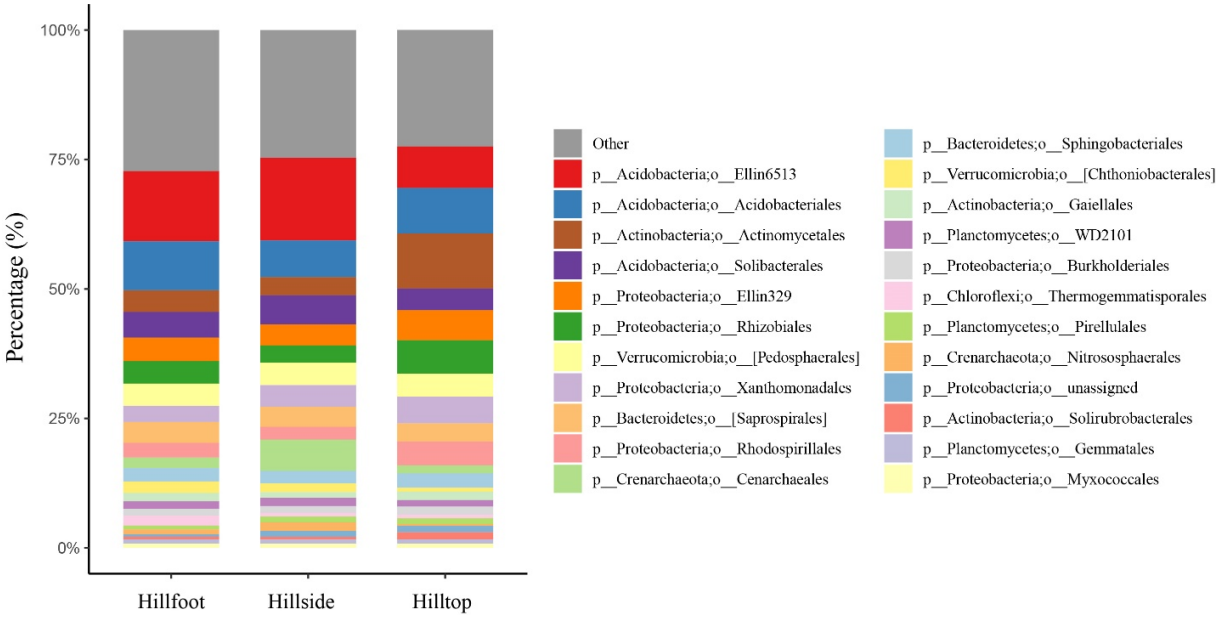


**Fig. S2.** Relative abundance of bacterial dominant order in soils separated according to elevations. Relative abundance is based on the proportional frequencies of those DNA sequences that could be classified at the order level.

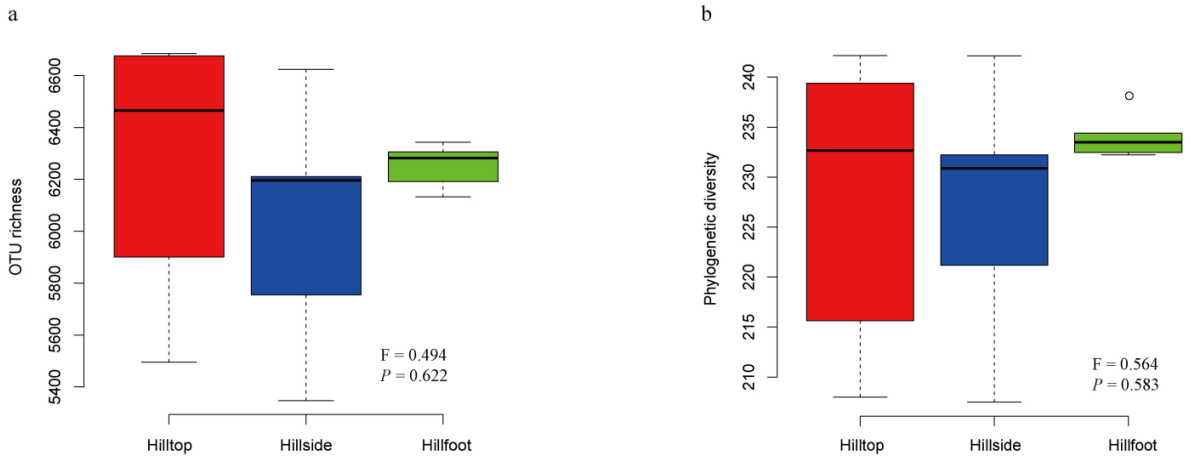


**Fig. S3.** Alpha diversity indices, including OTU richness (a) and phylogenetic diversity (b), sorted by elevations.

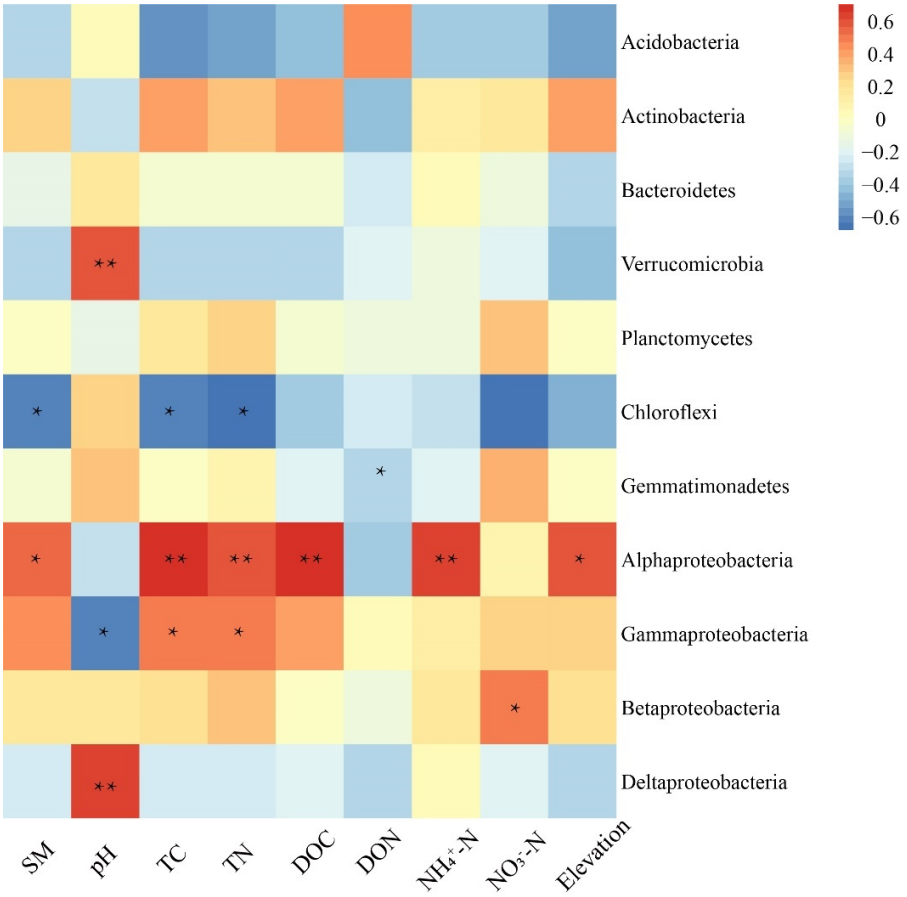


**Fig. S4.** Heat map for correlations between relative abundance of dominant phyla and environmental factors, based on *Spearman* method. * represents $P < 0.05$; ** represents $P < 0.01$. Abbreviations of edaphic factors as Table 1.

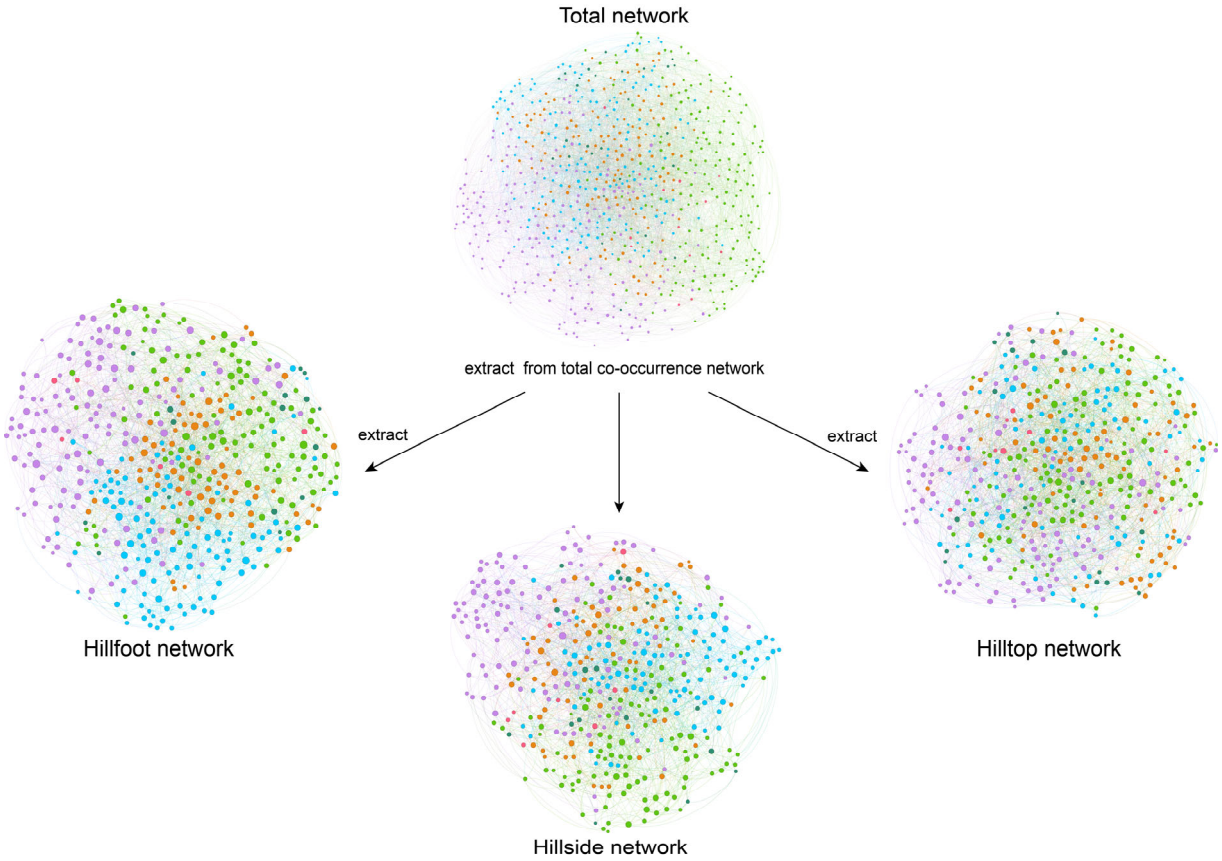


**Fig. S5.** Species co-occurrence networks of dominant bacterial communities across each elevation at OTU levels. Different network modules of OTUs were indicated by different colors. The network layout was arranged according to degree scores at the OTU level, following the ForceAtlas2 settings in Gephi software.