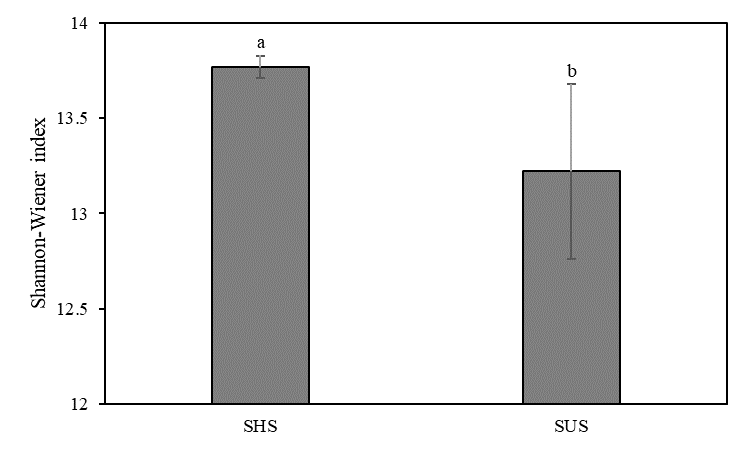
**Supplementary materials**

**Table S1**. The characterization of the plant communities feature on the different slopes.

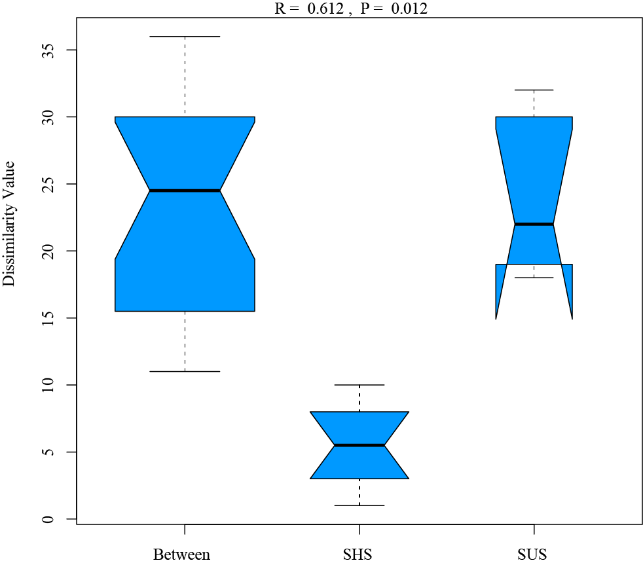
|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | Species richness | Coverage (%) | Shannon-Wiener index | Dominant species |
| SHS | 42.8±3.70a | 76.2±4.32a | 2.06±0.17a | *Myrsine africana* Linn.  *Debregeasia orientalis* C. J. Chen  *Ternstroemia gymnanthera* (Wight et Arn.) Beddome |
| SUS | 29.8±5.06b | 60.0±5.94b | 1.77±0.12a | *Quercus guyavifolia*  *Quercus variabilis* Bl. |

**Table S2.** The gene number of CAZy class on the different slopes.

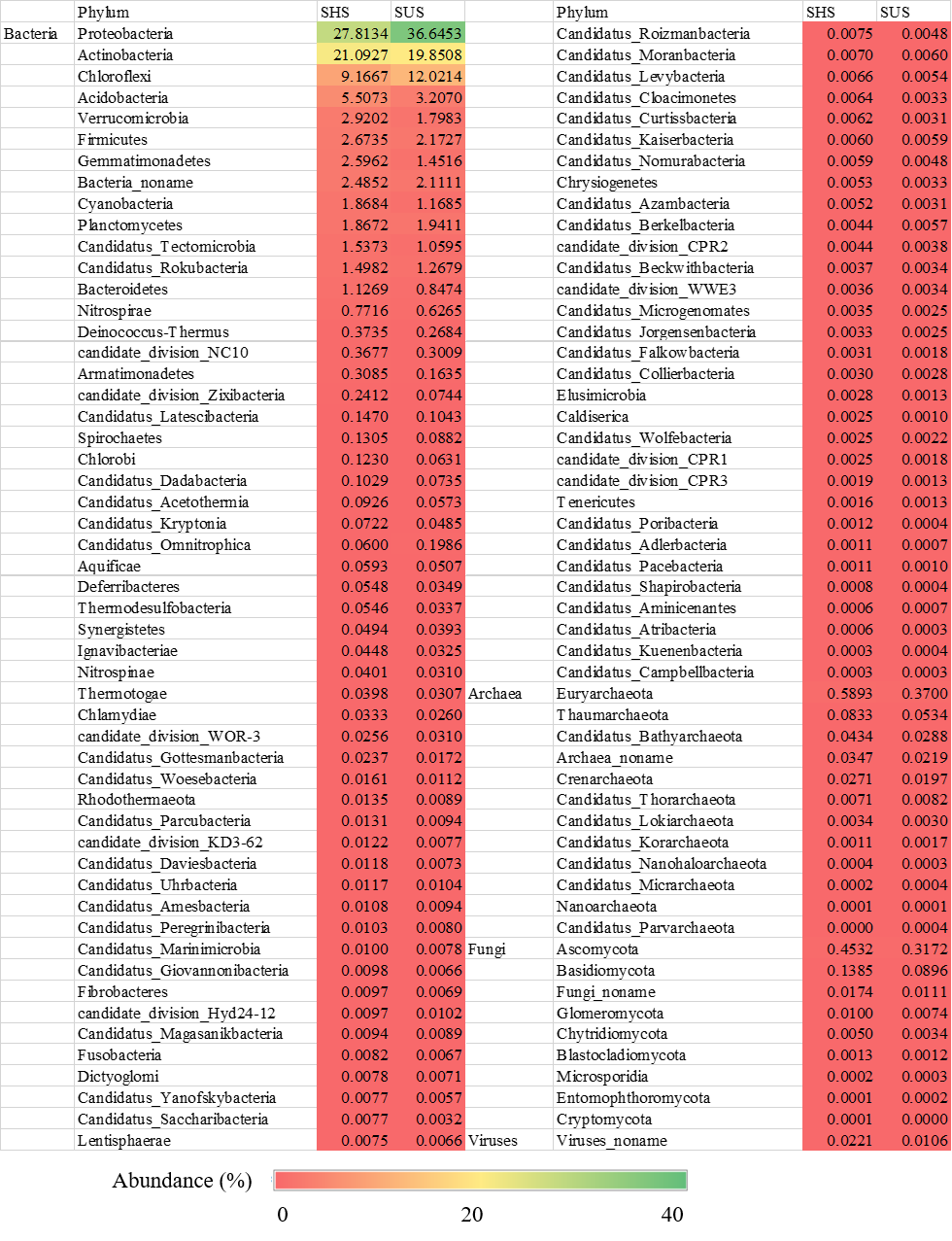
|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **CAZy Class** | **CAZy Abbr** | **SHS** | **SUS** | **P value** |
| Auxiliary Activities | AA5 | 0.1396 | 0.1849 | 0.018 |
| Carbohydrate-Binding Modules | CBM12 | 0.0745 | 0.0980 | 0 |
|  | CBM38 | 0.0265 | 0.0186 | 0.028 |
|  | CBM40 | 0.0223 | 0.0279 | 0.011 |
|  | CBM41 | 0.0240 | 0.0337 | 0.05 |
|  | CBM51 | 0.0182 | 0.0137 | 0.02 |
|  | CBM61 | 0.0195 | 0.0145 | 0.015 |
| Carbohydrate Esterases | CE1 | 0.0147 | 0.0074 | 0.001 |
|  | CE15 | 0.0111 | 0.0139 | 0.005 |
|  | CE16 | 0.0108 | 0.0195 | 0.006 |
|  | CE2 | 0.0157 | 0.0104 | 0.016 |
|  | CE3 | 0.0117 | 0.0077 | 0 |
| Glycoside Hydrolases | GH100 | 0.0109 | 0.0074 | 0.027 |
|  | GH104 | 0.0063 | 0.0036 | 0.017 |
|  | GH119 | 0.0083 | 0.0040 | 0.011 |
|  | GH12 | 0.0071 | 0.0047 | 0.042 |
|  | GH13 | 0.0041 | 0.0024 | 0.012 |
|  | GH17 | 0.0030 | 0.0013 | 0.005 |
|  | GH19 | 0.0025 | 0.0052 | 0.014 |
|  | GH2 | 0.0031 | 0.0020 | 0.04 |
|  | GH25 | 0.0054 | 0.0017 | 0.002 |
|  | GH29 | 0.0021 | 0.0013 | 0.046 |
|  | GH30 | 0.0048 | 0.0020 | 0.018 |
|  | GH4 | 0.0025 | 0.0010 | 0.012 |
|  | GH46 | 0.0030 | 0.0017 | 0.043 |
|  | GH49 | 0.0023 | 0.0008 | 0.02 |
|  | GH50 | 0.0023 | 0.0005 | 0.001 |
|  | GH53 | 0.0016 | 0.0006 | 0.005 |
|  | GH54 | 0.0016 | 0.0011 | 0.038 |
|  | GH55 | 0.0016 | 0.0006 | 0 |
|  | GH57 | 0.0016 | 0.0010 | 0.021 |
|  | GH68 | 0.0014 | 0.0008 | 0.039 |
|  | GH7 | 0.0019 | 0.0004 | 0.009 |
|  | GH70 | 0.0011 | 0.0003 | 0.001 |
|  | GH75 | 0.0008 | 0.0004 | 0.028 |
|  | GH76 | 0.0008 | 0.0004 | 0.039 |
|  | GH78 | 0.0010 | 0.0006 | 0.022 |
|  | GH94 | 0.0010 | 0.0002 | 0.006 |
| Glycosyl Transferases | GT12 | 0.0007 | 0.0002 | 0.029 |
|  | GT14 | 0.0003 | 0.0000 | 0.002 |
|  | GT2 | 0.0005 | 0.0002 | 0.015 |
|  | GT21 | 0.0003 | 0.0001 | 0.01 |
|  | GT26 | 0.0010 | 0.0002 | 0.043 |
|  | GT30 | 0.0002 | 0.0007 | 0.014 |
|  | GT39 | 0.0003 | 0.0001 | 0.008 |
|  | GT40 | 0.0001 | 0.0000 | 0.003 |
|  | GT47 | 0.0005 | 0.0001 | 0.044 |
|  | GT58 | 0.0002 | 0.0000 | 0.018 |



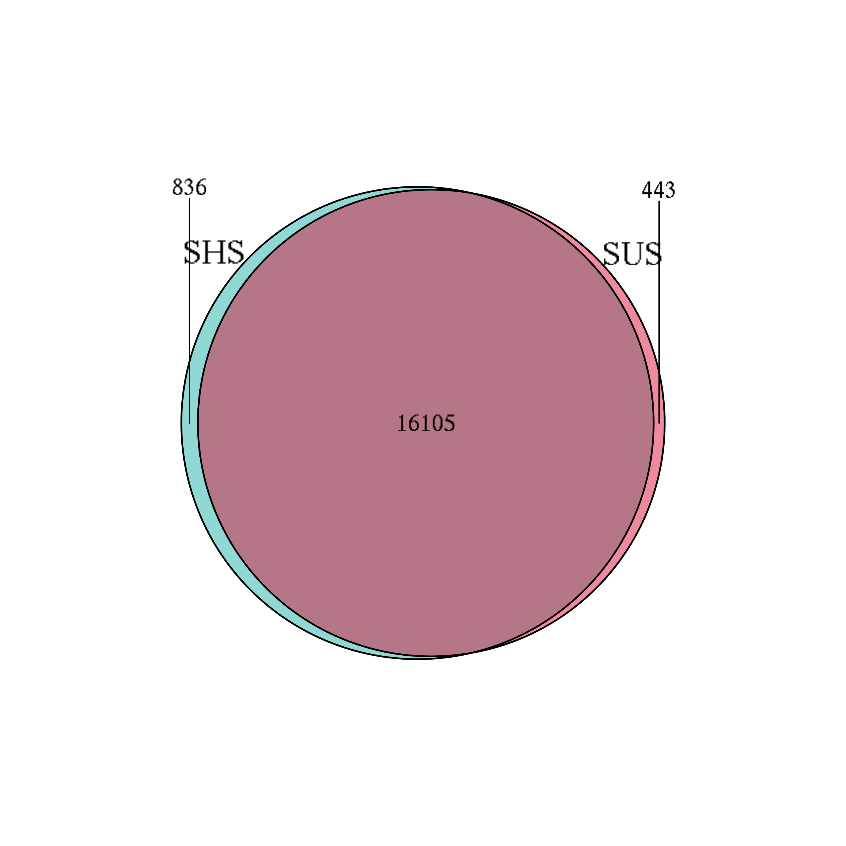
**Figure S1.** The Shannon-Wiener index of microbial community on the different slopes.



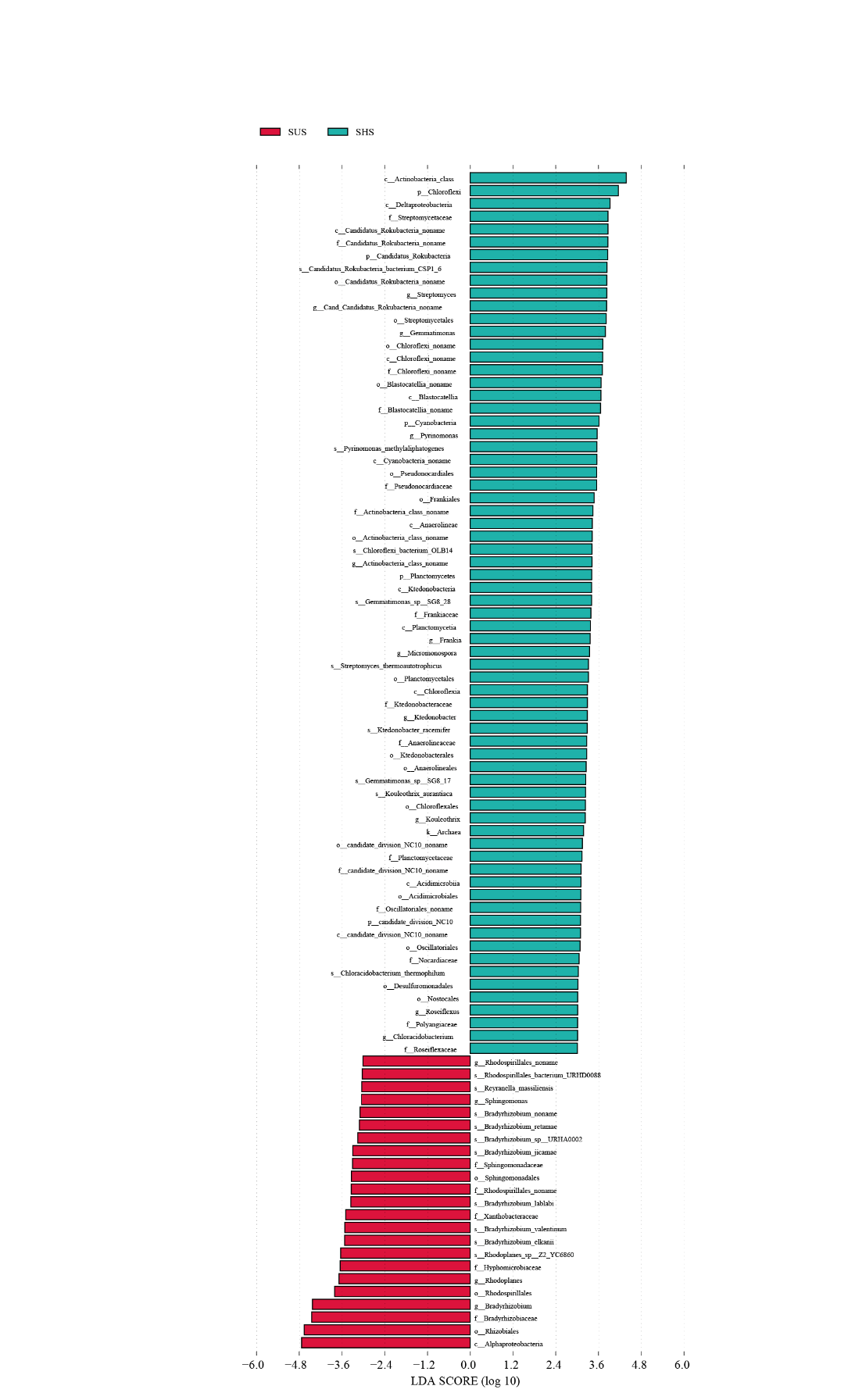
**Figure S2.** The analysis of similarities (AMOSIM) of microbial community on the different slopes.



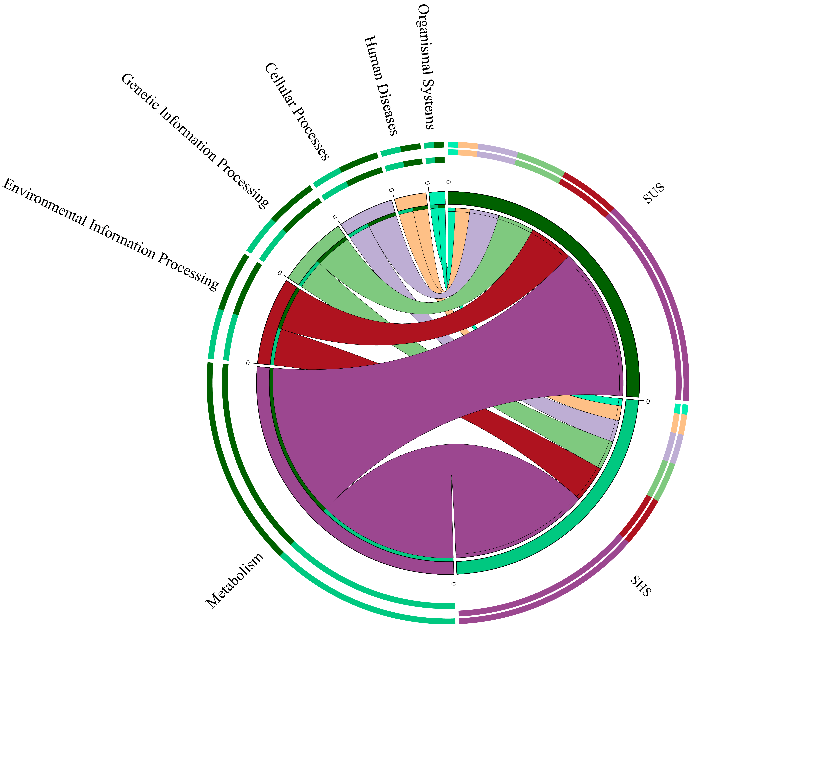
**Figure S3.** The abundance of microbial community composition on the different slopes.



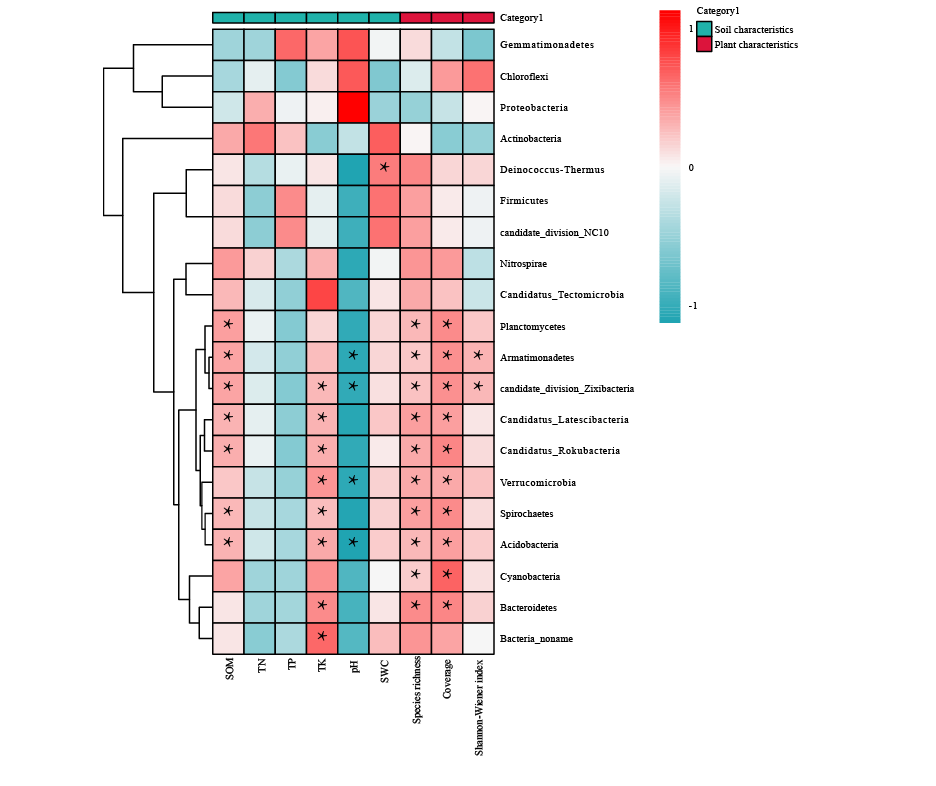
**Figure S4.** The veen diagrams of microbial composition on the different slopes.



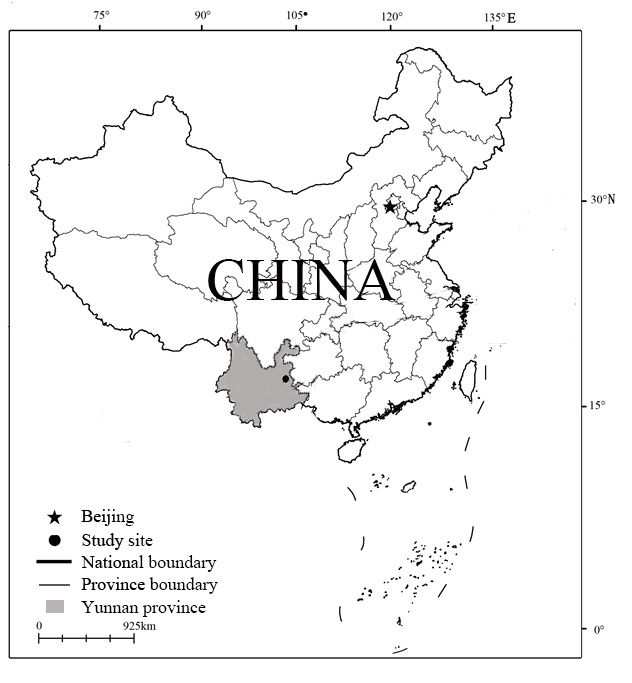
**Figure S5.** The LEfSe analysis of microbial community composition on the different slopes (LDA > 3).



**Figure S6.** The microbial community function pathways on the different slopes.



**Figure S7.** The correlation between the microbial community (at phylum level) and environmental variables. \* correlation significant at the 0.05 level. SWC, soil water content; SOM, soil organic matter; TN, total nitrogen; TP, total phosphorus; TK, total potassium.



**Figure S8.** Location of the study site in Yunnan Province, China.