Supplementary material for

Changes in bacterial community composition across natural grassland and pine forests in the Bunya Mountains in subtropical Australia

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Table S1. The basic information for Bunya sites and bacterial sequence analysis

Treatment	Land use	Zone	Raw sequences	Quality sequences	OTU
BF1	Forest	Bunya pine segment	2482	1140	630
			2902	1459	646
			2134	1359	560
BG1	Grass bald	Bunya pine segment	4677	3484	546
			7852	6099	557
			6392	5077	546
BG2	Grass bald	Hoop pine segment	22083	12451	649
			11425	7084	536
			13714	7783	621
BF2	Forest	Hoop pine segment	16741	8336	688
			15839	7832	634
			18339	8930	615

Table S2. Soil chemical properties across different sites

All the values are means ± SD. The unit for TC, TN, TP, TS is g kg^{-1}, for EC is µs cm^{-1}, for Moisture is %. Abbreviations: TC, total carbon; TN, total nitrogen; TP, total phosphorus; C:N, the ratio of TC to TN; EC, electrical conductivity. Different lowercase letters in the same row indicate significant difference between sites ($P < 0.05$)

	BF1	BG1	BG2	BF2
TC	104±16c	55±2a	75±3b	99±10c
TN	8.17±0.7c	4.63±0.24a	5.86±0.37b	7.42±0.59c
$\delta^{13}C$	-26.2±0.3d	-15.2±0.7a	-16.1±0.2b	-23.7±0.2c
$\delta^{13}N$	12.6±0.4b	10.1±0.5a	12.7±0.5b	10.6±0.2a
TP	2.09±0.08d	1.49±0.07c	1.09±0.06a	1.20±0.07b
TS	0.79±0.07b	0.40±0.01a	0.66±0.08b	0.71±0.02b
pH	6.15±0.06c	5.36±0.16b	4.95±0.30a	5.57±0.04b
EC	202±49b	55±3a	68±30a	162±57b
C:N	12.7±0.8a	11.9±0.2a	12.8±0.3a	13.4±0.7a
Moisture	26.3±1.6b	18.8±0.3a	25.2±1.4b	21.9±4.5ab

Table S3. Significance tests of bacterial community structure in grassland and pine forest across upper and lower slopes with three different statistical approaches

Abbreviations: ANOSIM, analysis of similarity; MRPP, multiresponse permutation procedure

Data sets	Partial predictor	PERMANOVA[A]		ANOSIM		MRPP	
		F	P	R	P	δ	P
Forest vs grass	-	2.207	**0.006[B]**	0.587	**0.002**	0.746	**0.005**
	Slope	2.201	**0.004**	0.587	**0.008**	0.746	**0.004**
Upper vs lower slope	-	1.524	0.072	0.2241	0.073	0.728	0.051

[A]All three tests are non-parametric multivariate analyses based on dissimilarities among samples

[B]*P*-value of corresponding significance test. The values in bold indicate the significant difference between the groups (at the levels of P<0.01, or P<0.05) by the tests.

Fig. S1. Venn diagram showing shared and unique numbers of OTU among sites. OTUs were defined at 97% nucleotide similarity and the taxonomic assignment of representative sequences utilized the Ribosomal Database Project (RDP) Classifier
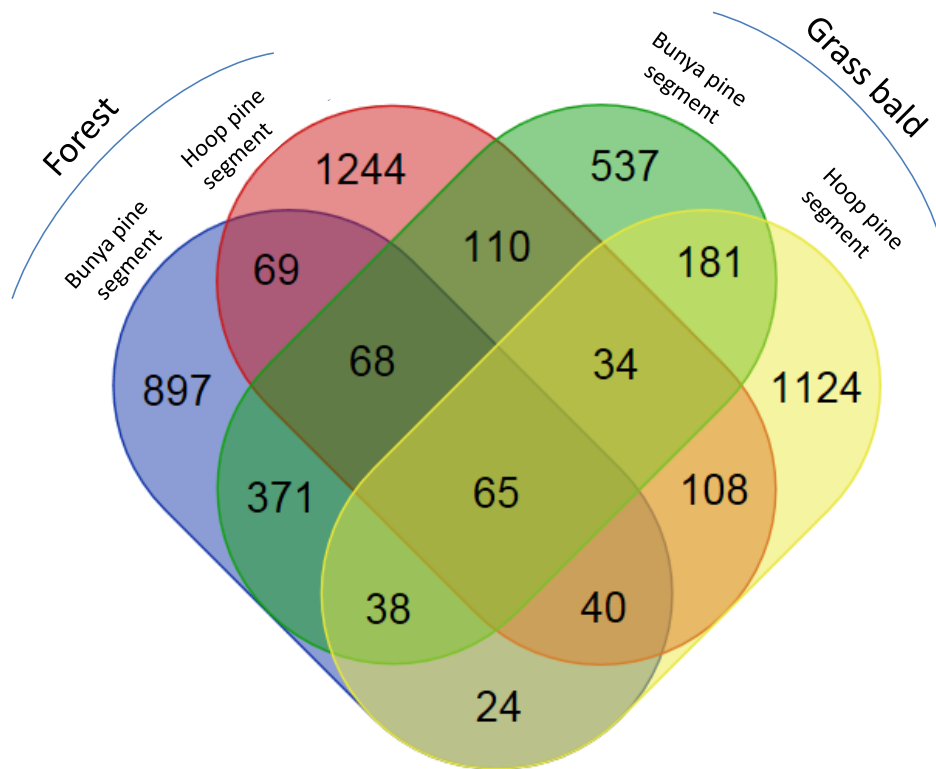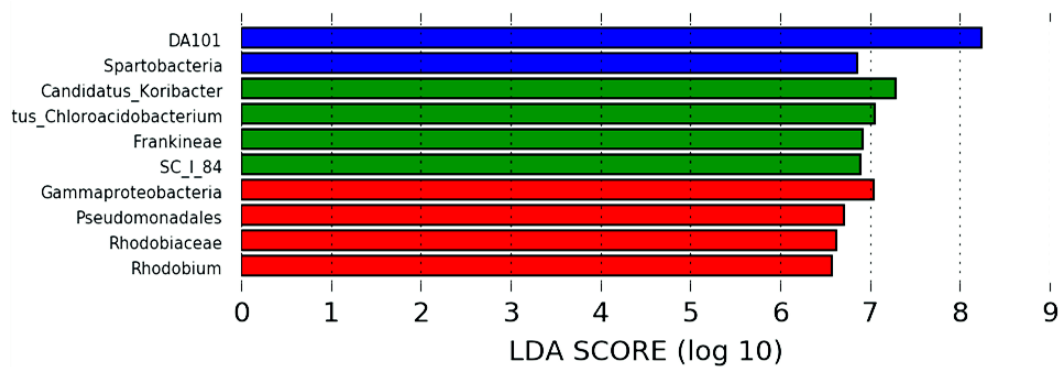

Fig. S2. Linear discriminant analysis effect size of bacterial OTUs among vegetation types

Red, green and blue bars represent forest site at upper slope (BF1), grass site at the upper (BG1) and lower slope (BG2), respectively.

Fig. S3. Predicted functions of the bacterial communities found in forest sites and grass sites. All the sequence reads were used to predict functions against the KEGG database (http://www. genome.jp/ kegg/), which is incorporated in PICRUSt (http://picrust.github.io/picrust/) bioinformatics package. Green bars represent grassy balds while red bars represent the forest sites.
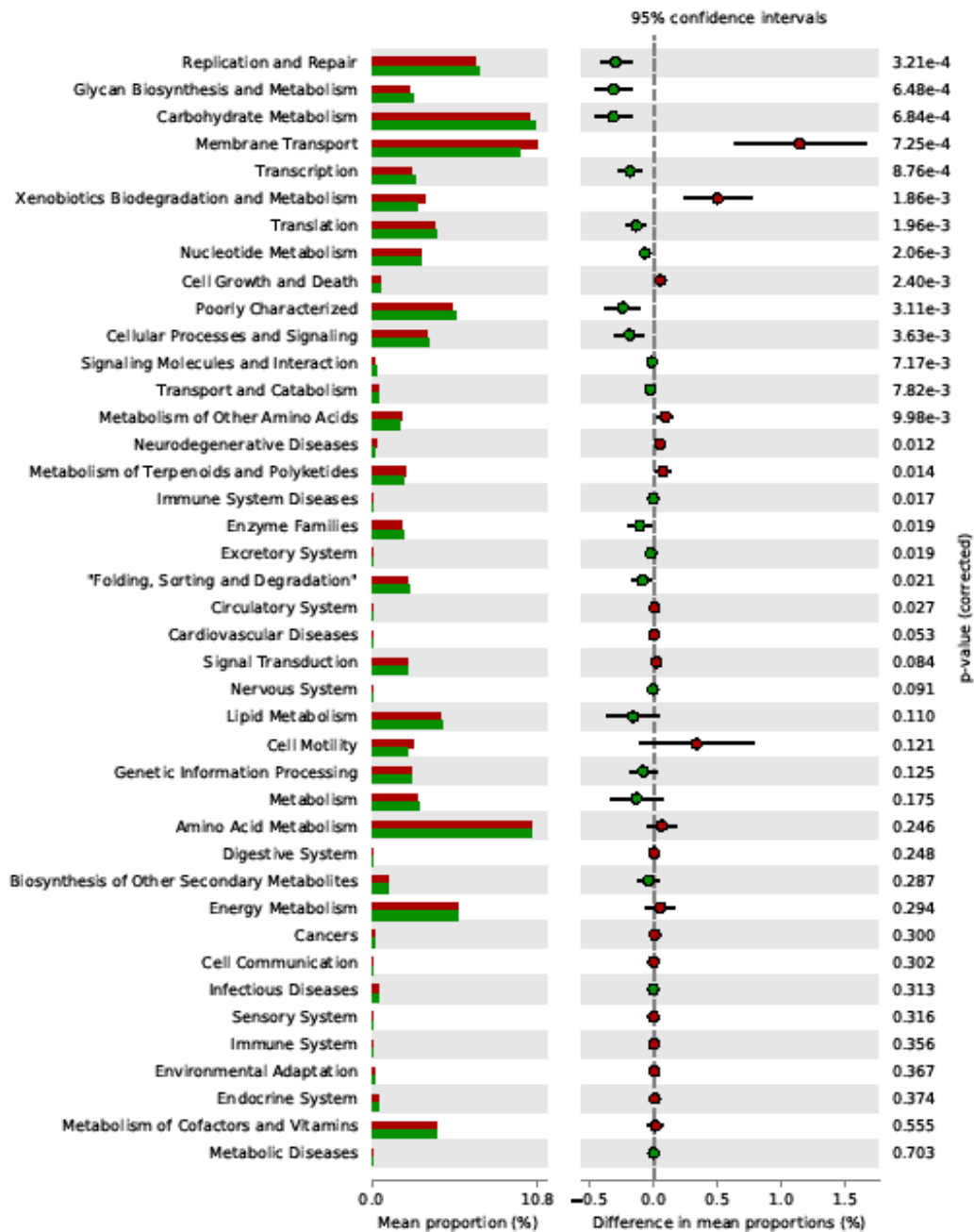
Fig. S4. Multivariate regression tree of soil bacteria diversity based on main relative abundance of OTUs. The label in the figure indicates the categorical factors grouping samples. C13, $\delta^{13}C$; TC (total carbon); TP (total phosphorous)