Table S1. Principal component loadings (correlation between original loading variable and principal component) as a measure of influence of a loading variable on treatment differences.

Loading Variable	**PC1 (70.20%)** †	**PC2 (10.16%)**
Amines	0.898 ‡	−0.267
Amino acids	0.869 ‡	−0.284
Carbohydrates	0.888 ‡	−0.195
Carboxylic acids	0.857 ‡	−0.028
Phenolic compounds	0.722 ‡	0.480
Polymers	0.779 ‡	0.434

† Percent of total variance in data set, including treatments attributed to principal component 1 (PC1) and 2 (PC2). ‡ Factor loadings statistically significant ($P < 0.05$). A high positive or negative correlation indicates higher degree of influence of loading variable on differences among treatments determined for a principal component.

Table S2. Population diversity of bacterial communities in bare control and cover cropping samples collected during three months.

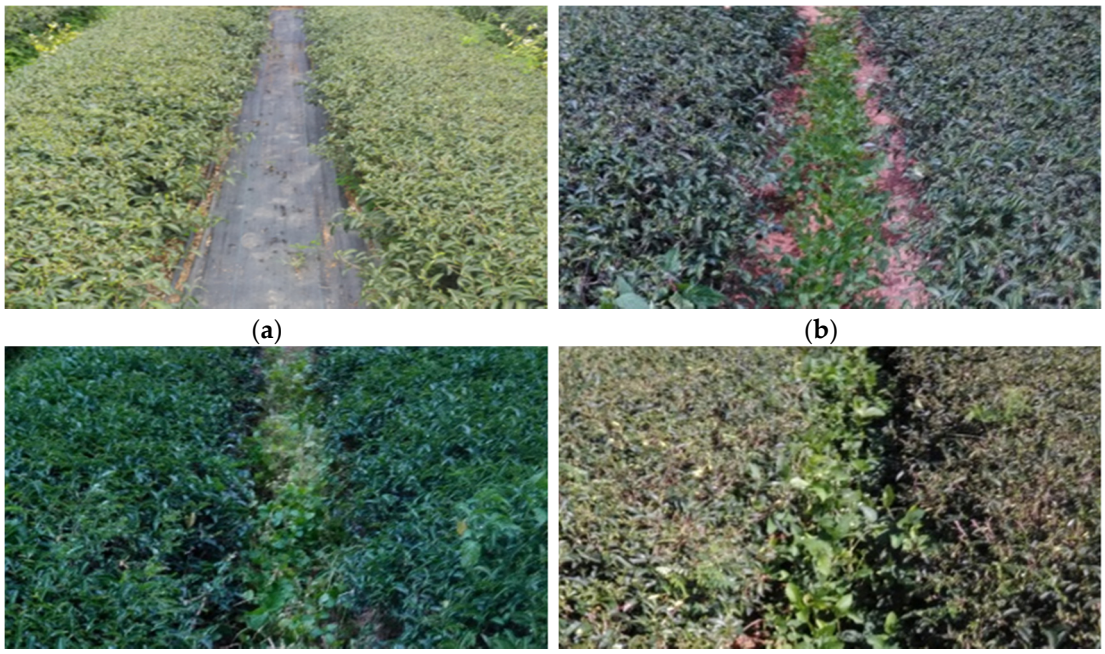
Treatment	1 month				2 months				3 months			
	OTUs	**Chao1**	**Shannon**	**InvSimpson**	**OTUs**	**Chao1**	**Shannon**	**InvSimpson**	**OTUs**	**Chao1**	**Shannon**	**InvSimpson**
Bare control	22496 a †	272 a	6.216 a	40.634 a	20427 a	268 a	6.004 a	33.884 a	20928 a	269 a	6.310 a	49.662 a
Cover cropping	19639 a	312 a	6.317 a	43.921 a	23847 a	271 a	6.011 a	31.610 a	23219 a	281 a	6.099 a	37.340 b

† In columns, means followed by the same letters were not significantly different ($P < 0.05$) in one-way ANOVA.

Table S3. Principal component loadings (correlation between original loading variable and principal component) as a measure of influence of a loading variable on treatment differences.

Loading variable	PC1 (47.21%) †	PC2 (24.89%)
Bacterial phylum		
Acidobacteria	−0.896 ‡	−0.137
Actinobacteria	0.956 ‡	−0.153
Bacteroidetes	−0.105	0.857 ‡
Chloroflexi	0.840 ‡	−0.333
Gemmatimonadetes	−0.393	−0.290
Planctomycetes	−0.646 ‡	−0.391
Proteobacteria	−0.549 ‡	0.801 ‡
Verrucomicrobia	−0.516 ‡	−0.671 ‡
WPS–2	−0.821 ‡	−0.147
Loading variable	PC1 (49.57%) †	PC2 (20.64%)
Bacterial family		
Acetobacteraceae	0.360	−0.372
Acidobacteriaceae	−0.839 ‡	0.032
Acidothermaceae	0.975 ‡	0.102
Burkholderiaceae	−0.234	0.766 ‡
Chthoniobacteraceae	−0.225	−0.561 ‡
Enterobacteriaceae	−0.419	0.462
Gemmataceae	0.901 ‡	−0.206
Gemmatimonadaceae	−0.486	−0.271
Ktedonobacteraceae	0.911 ‡	0.151
Pseudonocardiaceae	0.976 ‡	−0.049
Rhodanobacteraceae	−0.371	0.895 ‡
Solibacteraceae	−0.737 ‡	−0.357
Solirubrobacteraceae	0.983 ‡	−0.044
Sphingomonadaceae	−0.807 ‡	−0.364
Xanthobacteraceae	0.845 ‡	0.267
Xanthomonadaceae	−0.152	0.873 ‡

† Percent of total variance in data set, including treatments attributed to principal component 1 (PC1) and 2 (PC2). ‡ Factor loadings statistically significant ($P < 0.05$). A high positive or negative correlation indicates higher degree of influence of loading variable on differences among treatments determined for a principal component.

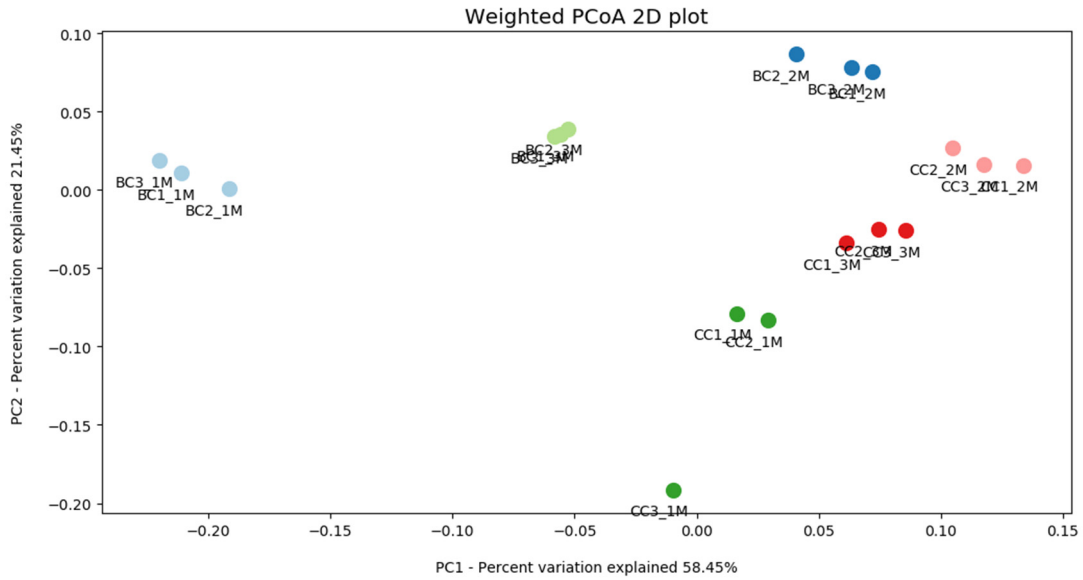


(**a**) (**b**)

(**c**) (**d**)

Figure S1. Photograph of experimental plots representing (**a**) bare control (**b**) one-month cover cropping (**c**) two-month cover cropping (**d**) three-month cover cropping in the tea plantation.

(a)



(b)

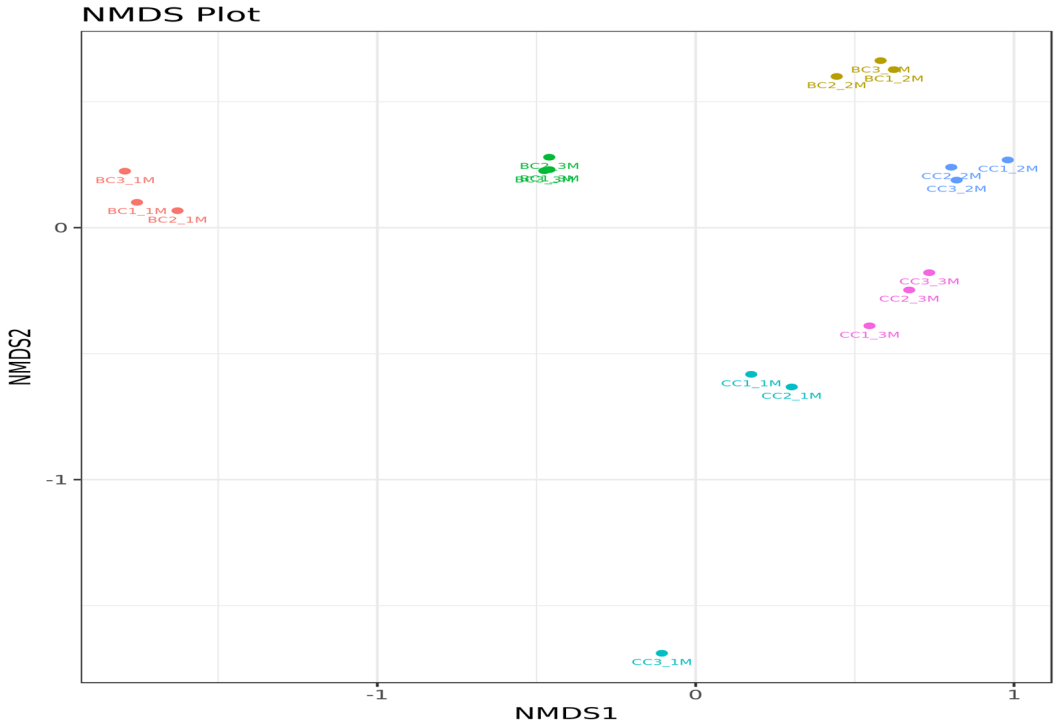


Figure S2. Ordination diagrams of (**a**) principal coordinates analysis (PCoA) and (**b**) non-metric multidimensional scaling (NMDS) of the relative abundance data from next generation sequencing. Bare control (BC) and cover cropping (CC) samples collected during three months were compared. PCoA and NMDS were performed based on weighted UniFrac distance metric. Loading variables (whole bacterial community) explaining variation in different treatments.

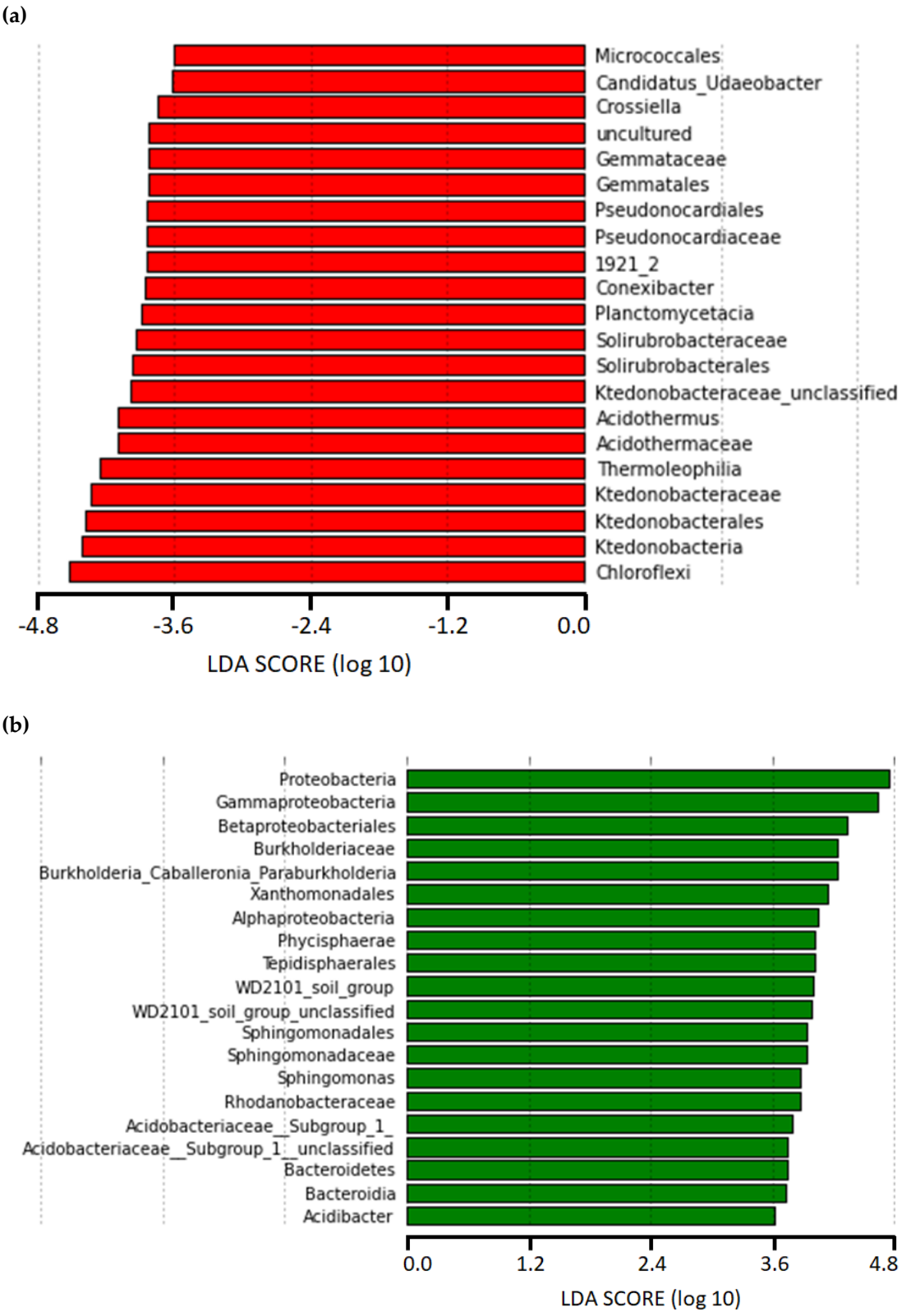


Figure S3. LEfSe analysis showing the bacterial taxa enriched in (**a**) bare control and (**b**) cover crop treatment. The bars which represent the effect size (LDA) for particular taxa were given.