

The soil microbiome of the laurel forest in Garajonay National Park (La Gomera, Canary Islands), comparing unburned and burned habitats after a wildfire.

Pablo J. Villadas¹, Sara Díaz-Díaz², Antonio Rodríguez-Rodríguez³, Marcelino del Arco-Aguilar⁴, Antonio J. Fernández-González¹, Juan Pérez-Yépez², Carmen Arbelo³, Juana M. Mancebo⁴, Manuel Fernández-López¹ and Milagros León-Barrios^{2*}

***Corresponding author:** Milagros León-Barrios. E-mail: mileonba@ull.edu.es

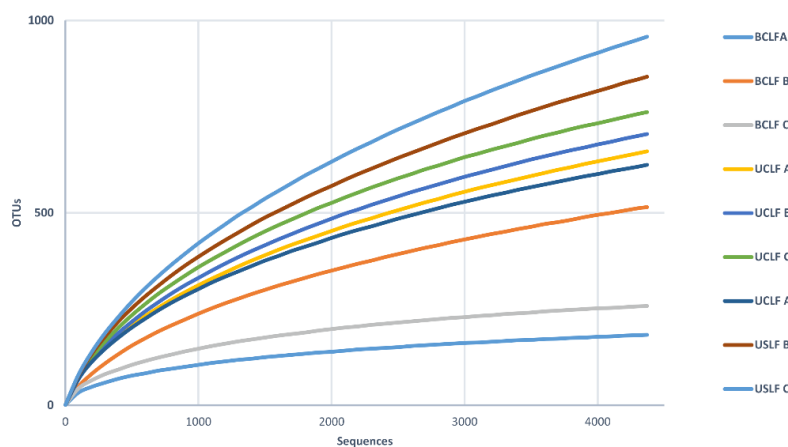


Figure S1. Rarefaction normalized curve calculated at OTU level (97% sequence similarity). Sampling sites correspond to USLF (unburned slope laurel forest), UCLF (unburned crest laurel forest) and BCLF (burned crest laurel forest). A, B and C refer to replicates for each sampled soil. Samples were normalized to 4370 sequences.

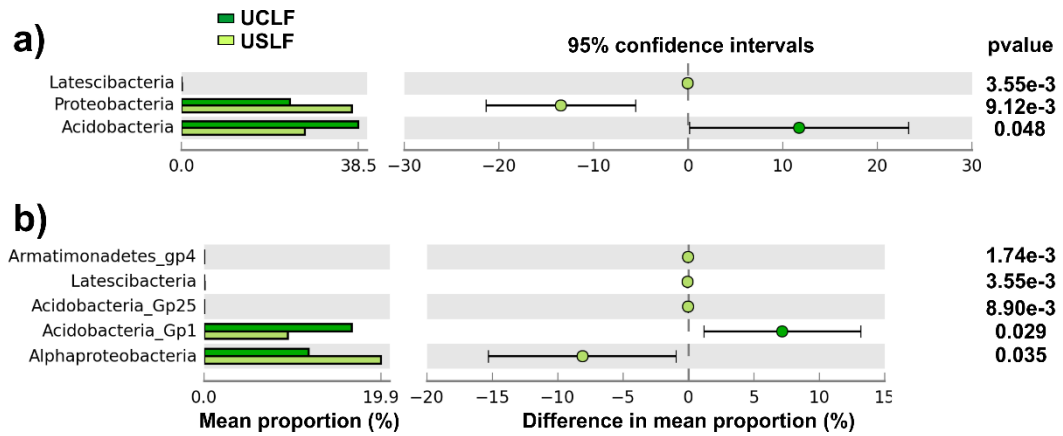


Figure S2. Significant differences at phylum level (a) and class level (b) between the soil microbiomes of the unburned laurel forests on the crest and slope (UCLF and USLF), at 95% confidence interval.

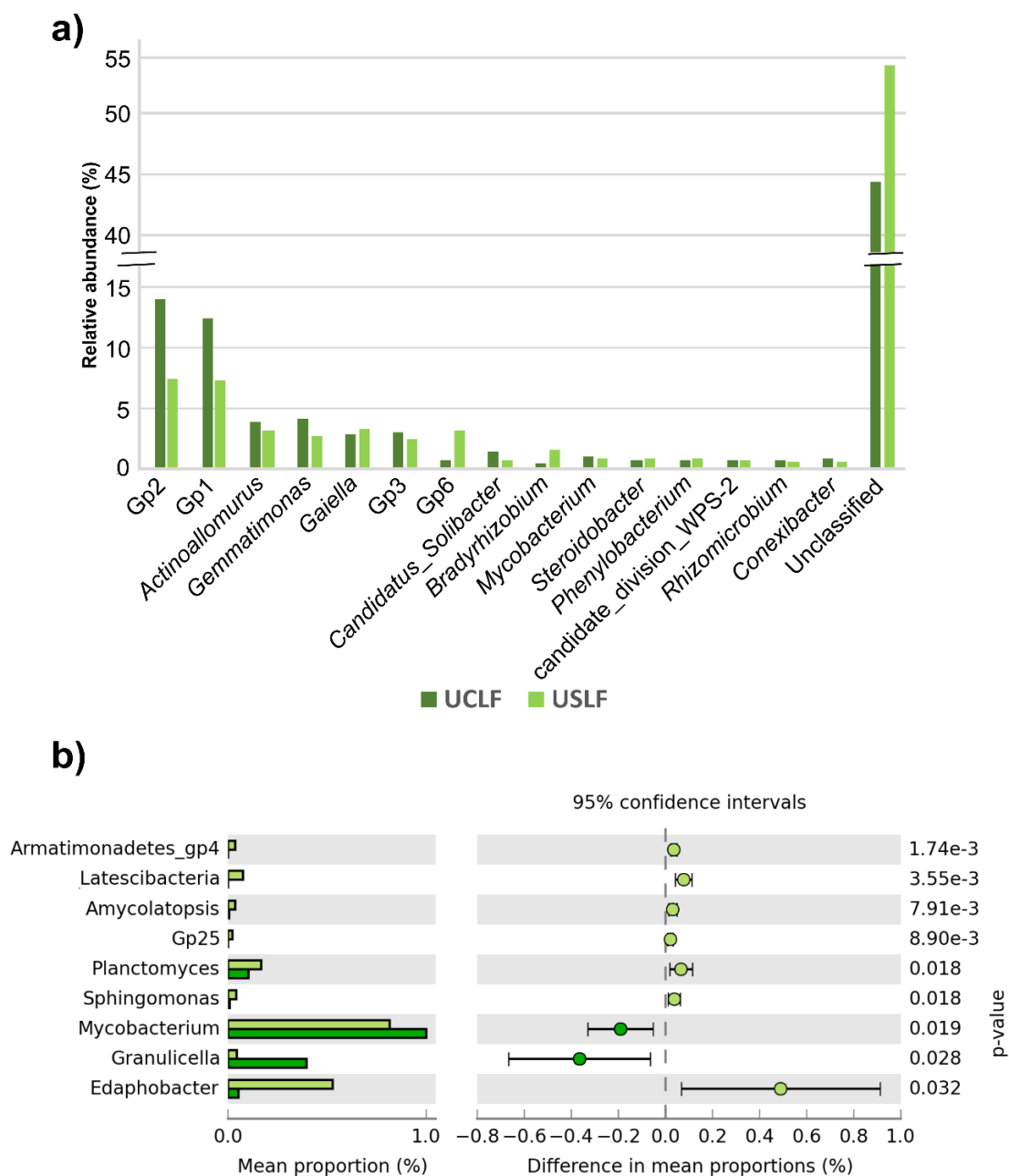


Figure S3. The soil microbiome in the unburned laurel forest soils. **(a)** Relative abundance at the genus level in the soil microbiome from undisturbed laurel forest on the crest and slope (UCLF and USLF) of the mountain. Only the genera above 0.7% relative abundance in some of the three locations are shown. ‘Others’ represent less abundant genera (below 0.7%). Unclassified: sequences showing no homology with currently described genera. Asterisk (*) indicates significant differences (STAMP at 95% confidence interval). **(b)** Genera with statistically significant differences in soils from unburned crest and slope laurel forests (UCLF and USLF) obtained by a t-test (at 95% confidence).

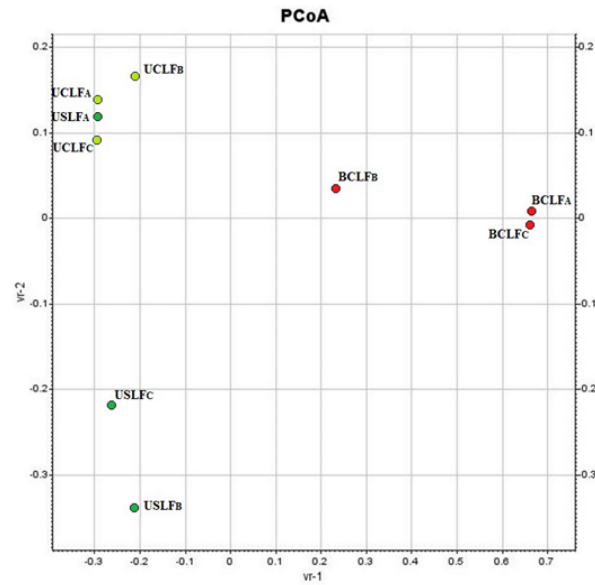


Figure S4. Principal Coordinate Analysis (PCoA) based on 16S rRNA gene sequences classified at genus level from unburned and burned laurel forest soils. USLF, Unburned Slope Laurel forest; UCLF, Unburned Crest Laurel Forest and BCLF, Burned Crest Laurel Forest.

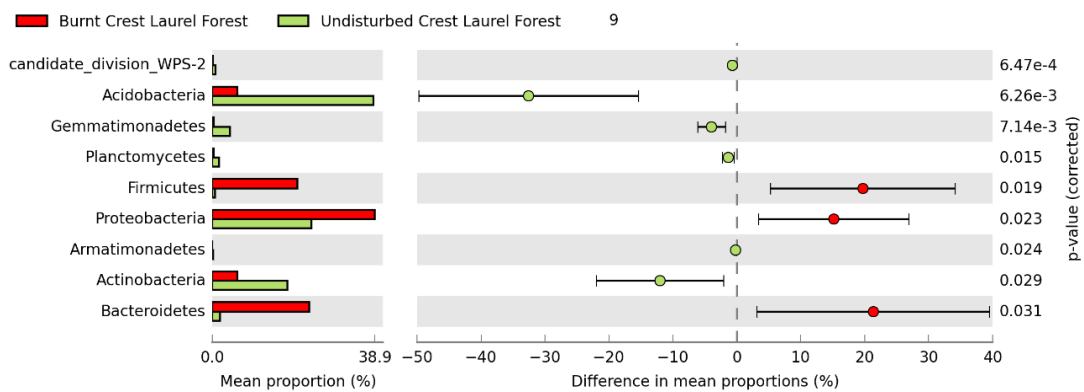


Figure S5. Phyla with statistically significant differences in soils from unburned crest forest (UCLF) and burned crest forest (BCLF), at 95% confidence interval.

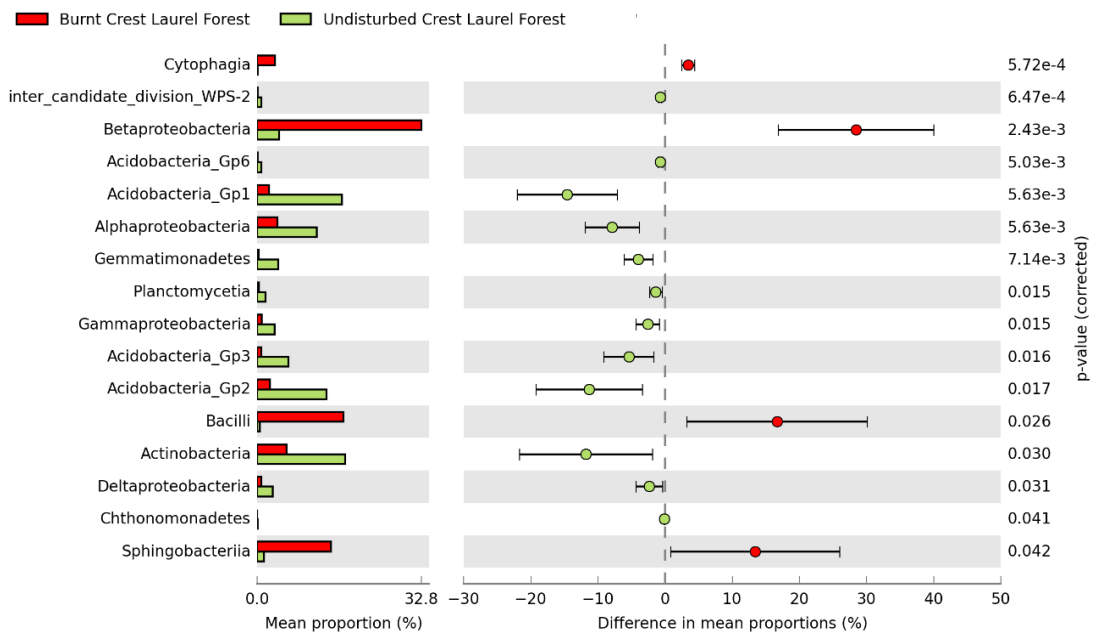


Figure S6. Classes showing statistically significant differences in soils from burned crest forest (BCLF) and unburned crest forest (UCLF) (with t test, 95% confidence interval).

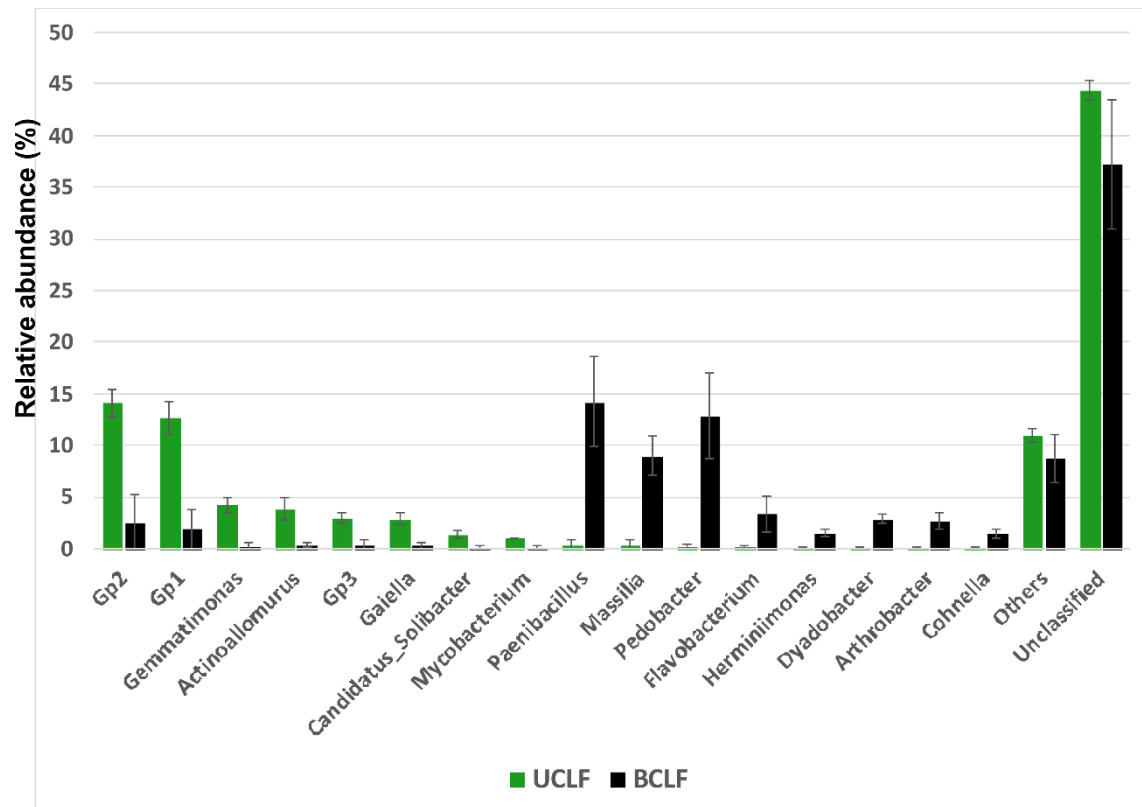


Figure S7. Relative abundance of genera in the bacterial communities from soils in unburned crest laurel forest (UCLF) and in a crest forest burned after a wildfire (BCLF). Only genera with relative abundance above 1% in at least one location are shown, while less abundant genera are under ‘Others’. Unclassified: sequences with no homology with currently described genera.

PCA (Correlation Biplot)

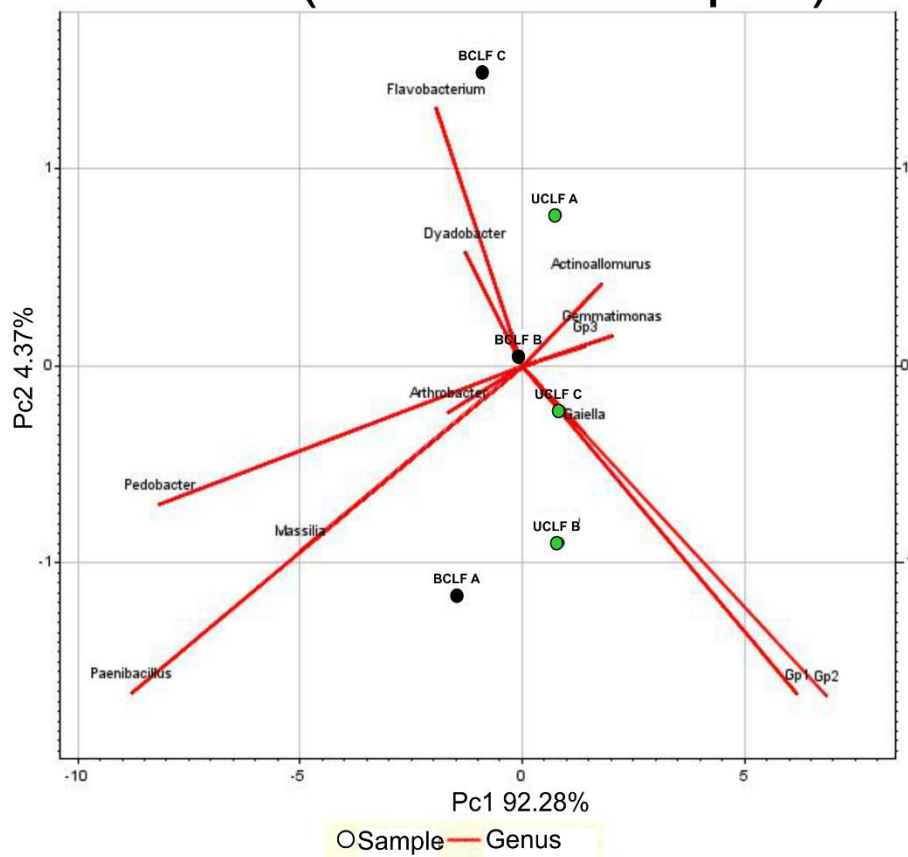


Figure S8. Principal component analysis (PCA) plot of the genera distribution (only genera above 1% are shown) in unburned (UCLF) and burned (BCLF) crest laurel forest soils.

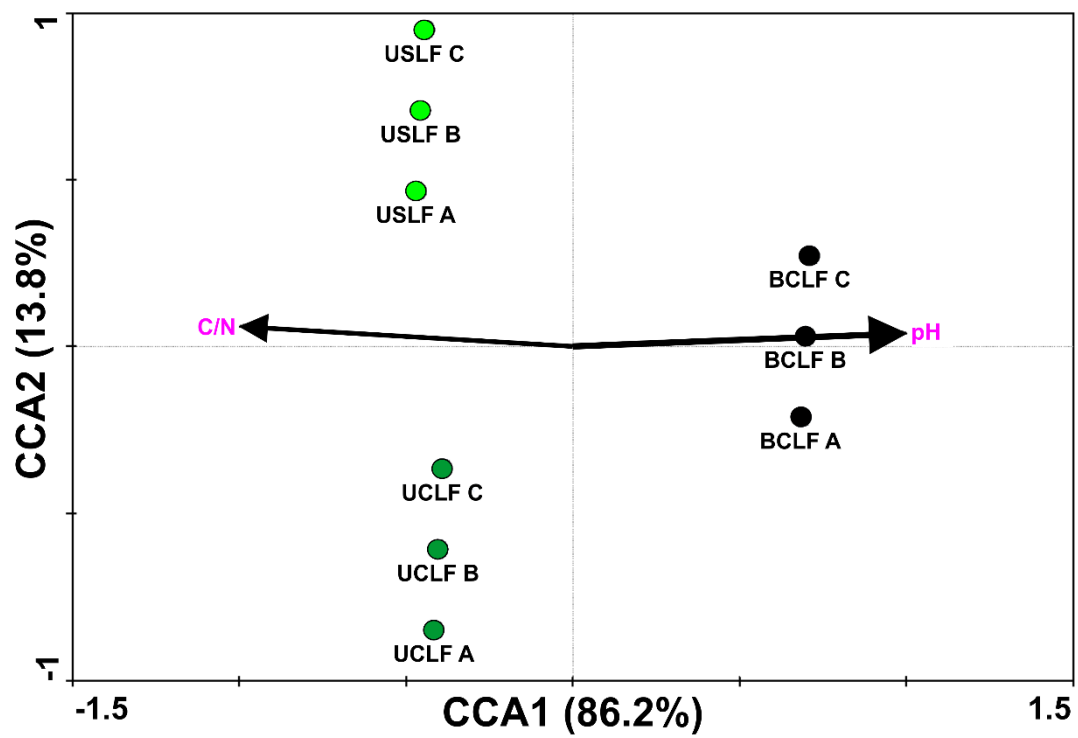


Figure S9. Canonical correspondence analysis (CCA) of 16S rRNA gene sequences (at genus level) in the three types of soil samples. Pink colour indicates vectors of environmental variables significantly influencing genera distribution. USLF, Unburned Slope Laurel Forest; UCLF, Unburned Crest Laurel Forest and BCLF, Burnt Crest Laurel Forest.

Table S1. Genera with percentage of exclusive sequences above 0.1% and detected OTUs in soils from an undisturbed laurel forest growing on the mountain slope (USLF).

Genera	Sequences %	OTUs				
<i>Gaiella</i>	0.2212052	Otu00047	Otu00143	Otu00302	Otu00346	Otu00479
		Otu00559	Otu00600	Otu00625	Otu00695	Otu00713
		Otu00810	Otu00891	Otu00960	Otu03592	Otu04076
		Otu04094	Otu04236	Otu04249	Otu04515	Otu04767
		Otu05446				
<i>Gp6</i>	0.1779812	Otu00214	Otu00292	Otu00339	Otu00485	Otu00709
		Otu00737	Otu00796	Otu00826	Otu00898	Otu00916
		Otu00921	Otu00988	Otu00994	Otu01132	Otu01316
		Otu01360	Otu01395	Otu01483	Otu01583	Otu01670
		Otu01761	Otu02193	Otu03162	Otu03232	Otu04163
		Otu04265	Otu04294	Otu04624	Otu04711	Otu04875
		Otu05460				
<i>Anaeromyxobacter</i>	0.1678108	Otu00093	Otu01041	Otu01094		

Table S2. Genera with percentage of exclusive sequence above 0.1% and detected OTUs in soil samples from the undisturbed crest laurel forest (UCLF).

Genera	Sequences %	OTUs				
<i>Gp1</i>	0.2364607	Otu00495	Otu00584	Otu00741	Otu00966	Otu01035
		Otu01061	Otu01078	Otu01102	Otu01155	Otu01199
		Otu01406	Otu01498	Otu01801	Otu01859	Otu01934
		Otu02003	Otu02165	Otu02397	Otu02433	Otu02553
		Otu02765	Otu03130	Otu03185	Otu03517	Otu03700
		Otu04042	Otu04316	Otu04755	Otu04852	Otu04985
		Otu06062	Otu06133	Otu06376	Otu06551	Otu06562
<i>Gp2</i>	0.2339181	Otu00814	Otu00824	Otu01364	Otu01536	Otu01634
		Otu01805	Otu01809	Otu01961	Otu02004	Otu02039
		Otu02129	Otu02156	Otu02442	Otu03204	Otu03209
		Otu03332	Otu03691	Otu03794	Otu03849	Otu03984
		Otu03995	Otu04017	Otu04019	Otu04160	Otu04332
		Otu04335	Otu04369	Otu04381	Otu04779	Otu04786
		Otu04904	Otu04918	Otu04928	Otu04996	Otu05093
		Otu05145	Otu05204	Otu05521	Otu05903	Otu06056
		Otu06096	Otu06223	Otu06238	Otu06327	Otu06452
		Otu06486	Otu06556	Otu06561	Otu06565	
<i>Gemmatimonas</i>	0.1678108	Otu00444	Otu00706	Otu00944	Otu01021	Otu02593
		Otu03524	Otu04540	Otu04871	Otu06018	Otu06061
		Otu06461				

Table S3. Genera with percentage of exclusive sequences above 0.1% and detected OTUs in soil samples from the burned crest laurel forest (BCLF).

Genera	% Sequences	OTUs				
<i>Flavobacterium</i>	0.5466565	Otu00085 Otu01170 Otu05635	Otu00447 Otu01338	Otu00723 Otu01414	Otu00799 Otu04253	Otu00914 Otu05575
<i>Pedobacter</i>	0.4373252	Otu00165	Otu00481	Otu01619	Otu04752	Otu06192
<i>Paenibacillus</i>	0.41698449	Otu00246 Otu01839 Otu04244	Otu00873 Otu02070 Otu04487	Otu01122 Otu02086 Otu04817	Otu01541 Otu04102	Otu04114 Otu04243
<i>Amycolatopsis</i>	0.24408848	Otu00231				
<i>Dyadobacter</i>	0.22374778	Otu01245	Otu01712	Otu02541		
<i>Delftia</i>	0.15764048	Otu00299				

Table S4. Genera with percentage of exclusive sequences above 0.6% and detected OTUs in the core microbiome.

Genera	% Sequences	OTUs				
<i>Gp1</i>	6.130180524	Otu00001	Otu00035	Otu00061	Otu00071	Otu00075
		Otu00091	Otu00124	Otu00132	Otu00211	Otu00308
		Otu00342	Otu00379	Otu00545	Otu00694	Otu01236
<i>Gp2</i>	6.076786168	Otu00004	Otu00027	Otu00028	Otu00029	Otu00045
		Otu00076	Otu00078	Otu00141	Otu00149	Otu00184
		Otu00220	Otu00235	Otu00334	Otu01272	
<i>Massilia</i>	3.206203916	Otu00009				
<i>Pedobacter</i>	3.185863209	Otu00012				
<i>Actinoallomurus</i>	2.405288584	Otu00003	Otu00050	Otu00116		
<i>Gp3</i>	1.688278668	Otu00016	Otu00057	Otu00089	Otu00100	Otu00107
		Otu00167	Otu00187	Otu00197	Otu00406	Otu00439
		Otu00661				
<i>Gaiella</i>	1.685736079	Otu00017	Otu00039	Otu00068	Otu00082	Otu00158
		Otu00319	Otu00409			
<i>Gemmatimonas</i>	1.34502924	Otu00042	Otu00144	Otu00153	Otu00189	Otu00191
		Otu00270	Otu00293			
<i>Arthrobacter</i>	0.894991101	Otu00064				
<i>Gp6</i>	0.884820748	Otu00008	Otu00044			
<i>Candidatus_Solibacter</i>	0.732265446	Otu00034	Otu00113	Otu00254		
<i>Bradyrhizobium</i>	0.671243326	Otu00007				
<i>Flavobacterium</i>	0.666158149	Otu00051	Otu00058			
<i>Mycobacterium</i>	0.666158149	Otu00014				