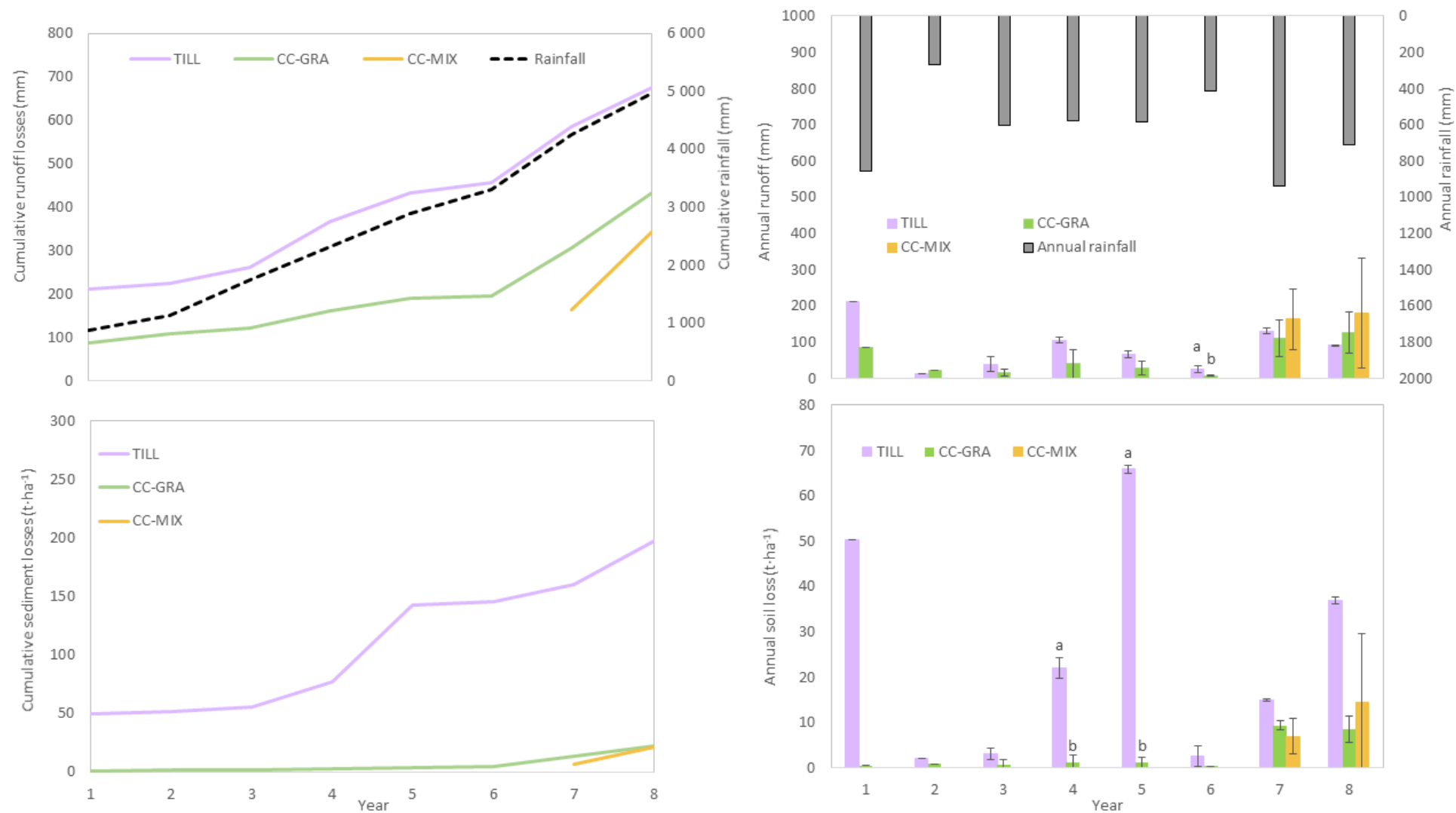
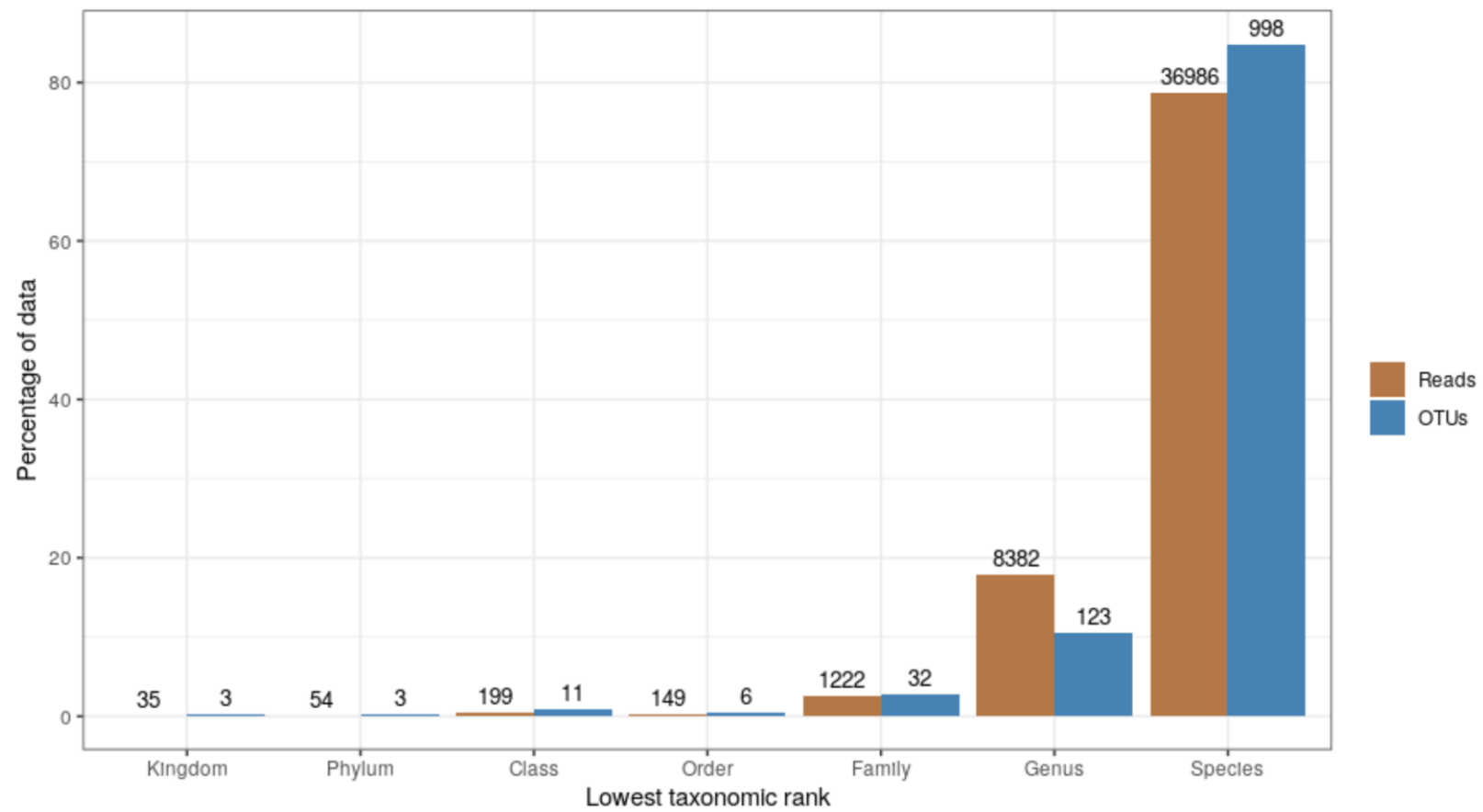


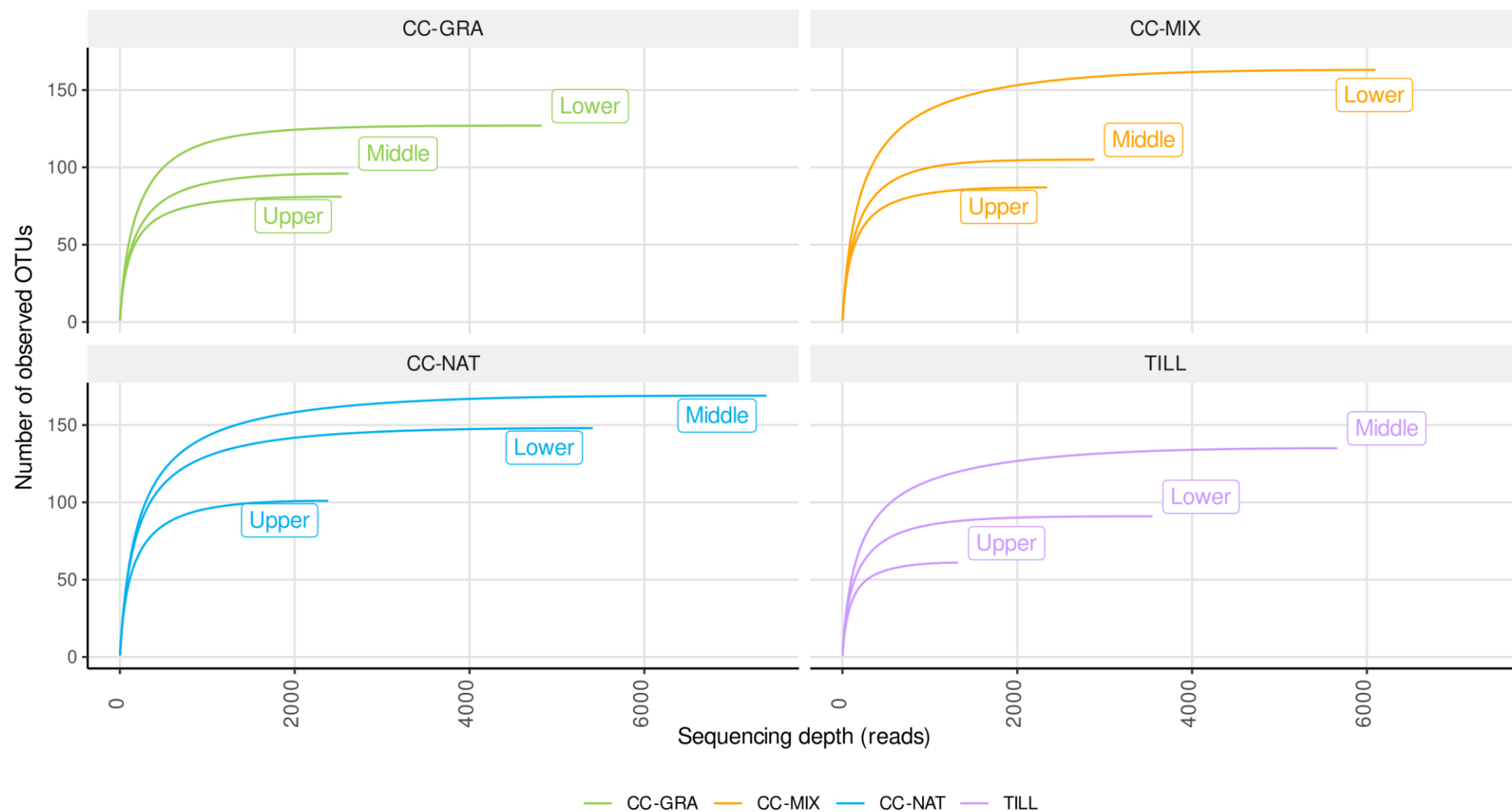
**Figure S1.** Location of the trial and aerial view of the sampled managements (from Google Earth): TILL: tillage, CC-GRA: sown cover crop with gramineous, CC-MIX: sown cover crop with a mixture of species, and CC-NAT: cover crop with spontaneous vegetation.



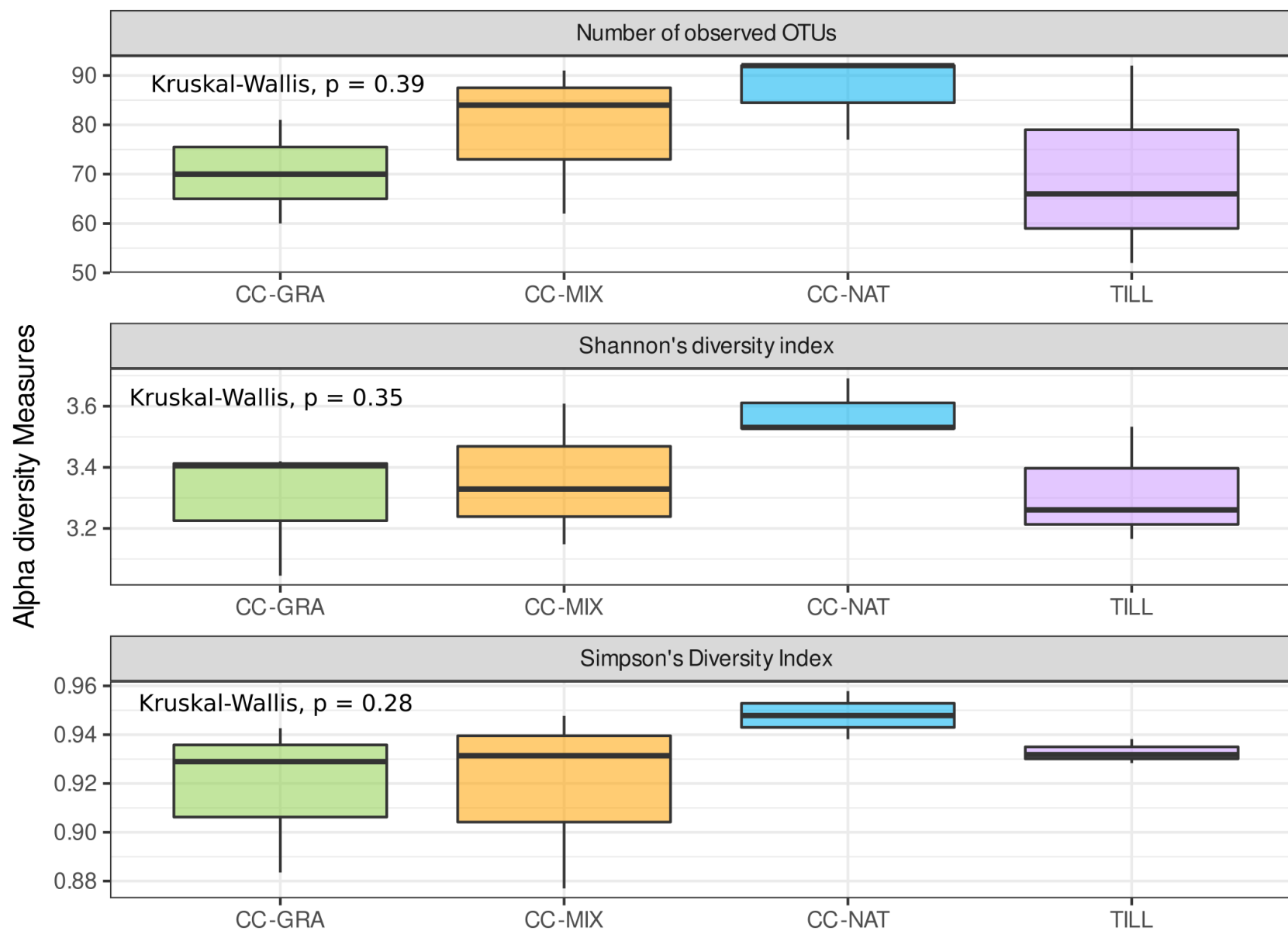
**Figure S2.** Erosion measurements during the 8-year period: precipitation and runoff (both in mm) and soil losses ( $\text{t}\cdot\text{ha}^{-1}$ ) measured in the erosion plots. (a) Cumulative values and (b) Mean annual measurements with standard deviation. Different letters on the bars indicate statistically significant differences based in the ANOVA test ( $p < 0.05$ ). Soil managements are: TILL: tillage, CC-GRA: sown cover crop with gramineous, CC-MIX: sown cover crop with a mixture of species.



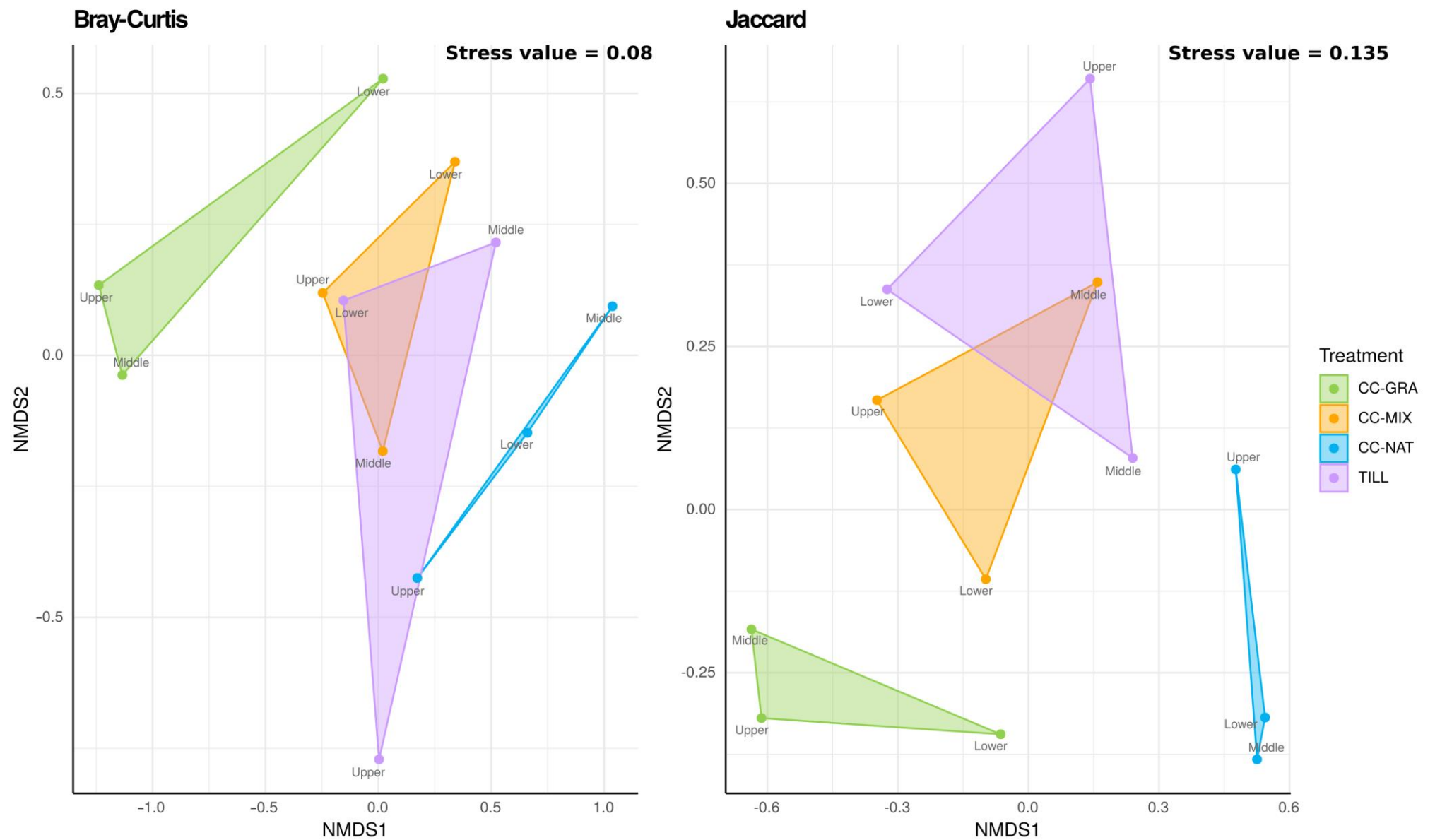
**Figure S3.** Taxonomic resolution of OTUs classified with the SILVA 138 databases for bacteria. For each taxonomic classification, the lowest level was determined by plotting the total number of Reads and OTUs associated with the lowest level of classification.



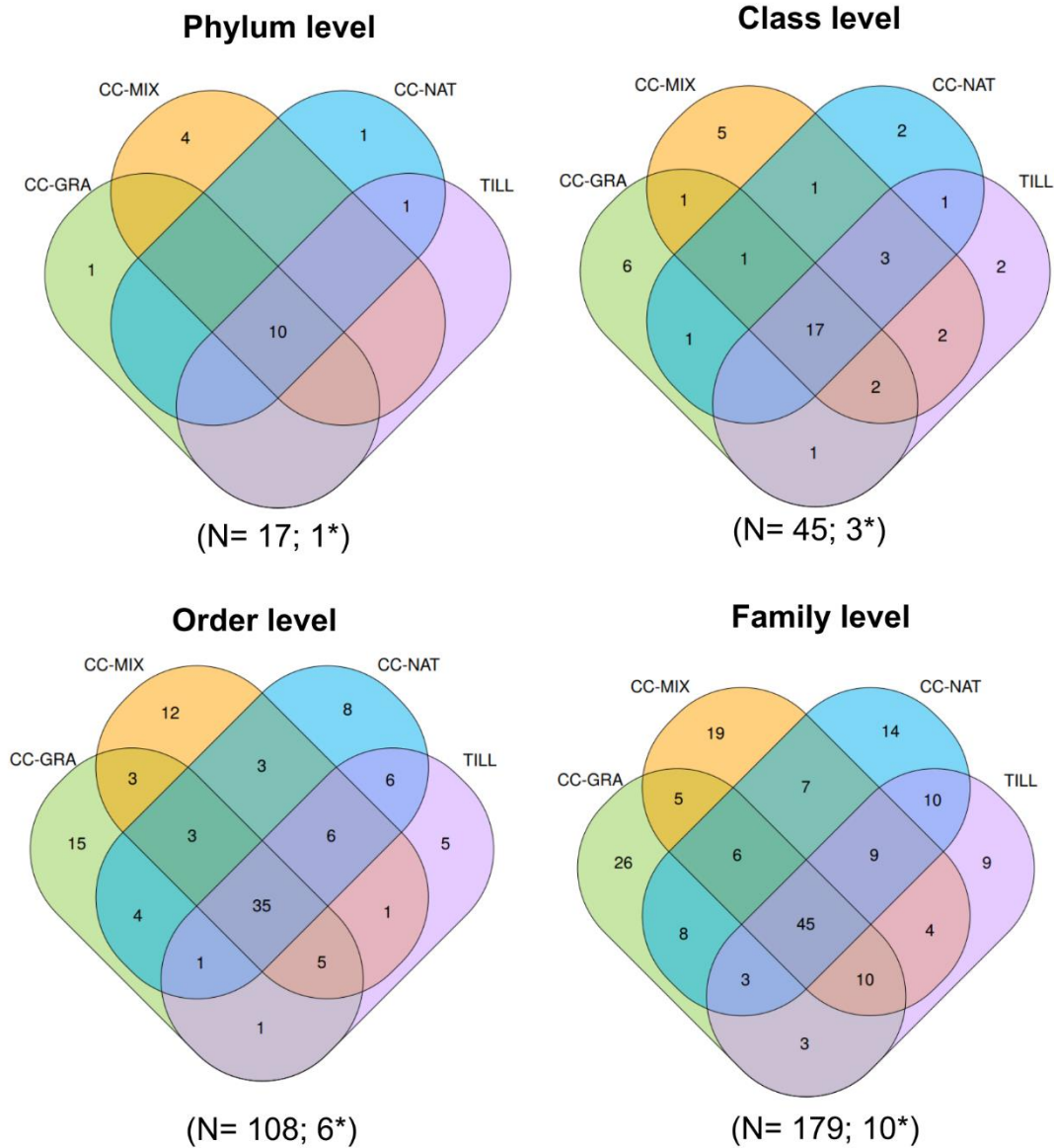
**Figure S4.** Comparison of rarefaction curves of observed OTUs obtained from an olive orchard soil under different cover crop managements (TILL: tillage, CC-GRA: sown cover crop with gramineous, CC-MIX: sown cover crop with a mixture of species) and CC-NAT (cover crop with spontaneous vegetation) and for each sampling point on the slope. The sampling points on the slope of the field for each treatment. Data shown are before rarefaction.



**Figure S5.** Alpha diversity comparison of an olive orchard soil under different cover crop managements (TILL: tillage, CC-GRA: sown cover crop with gramineous, CC-MIX: sown cover crop with a mixture of species) and CC-NAT (cover crop with spontaneous vegetation). The Kruskal-Wallis H test was performed to determine the existence of significant differences among the treatments. Data were rarified to 1,324 sequences before analysis.

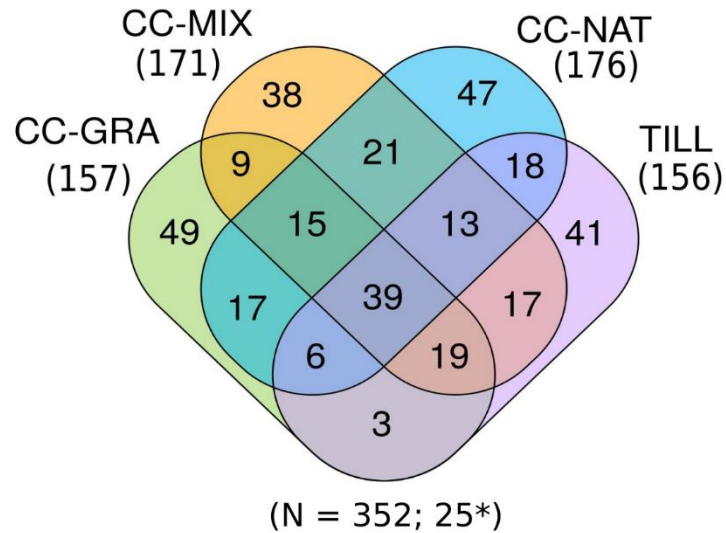


**Figure S6.** Non-metric multidimensional scaling (NMDS) plot based on Bray-Curtis (left) and Jaccard (right) dissimilarity distances from an olive orchard soil under different cover crop managements (TILL: tillage, CC-GRA: sown cover crop with gramineous, CC-MIX: sown cover crop with a mixture of species) and CC-NAT (cover crop with spontaneous vegetation) for each sampling point on the slope. Stress values of the ordination analysis are shown at the top right of each plot.



**Figure S7.** Prevalence Venn diagram showing the unique and shared bacterial taxa at different taxonomic levels obtained from an olive orchard soil under different cover crop managements (TILL: tillage, CC-GRA: sown cover crop with gramineous, CC-MIX: sown cover crop with a mixture of species) and CC-NAT (cover crop with spontaneous vegetation). The total number of taxa is indicated between brackets. \*Number of taxa that stopped at a higher taxonomic level.





**Acidobacteriota:** Subgroup 10  
**Actinobacteriota:** 67-14, *Blastococcus*, *Microbacterium*, *Arthrobacter*, *Actinoplanes*, *Nocardioides*, *Pseudonocardia*, *Solirubrobacter*, *Streptomyces*, *Unc. Microtrichales*, *f\_\_Kineosporiaceae*  
**Bacteroidota:** *Bacteroides*, *unc. Chitinophagaceae*, *Ohtaekwangia*, *unc. Microscillaceae*, *Alistipes*  
**Chloroflexi:** A4b  
**Firmicutes:** *Bacillus*, *Faecalibacterium*, *f\_\_Lachnospiraceae*  
**Gemmatimonadota:** *unc. Gemmatimonadaceae*  
**Myxococcota:** *Haliangium*, *unc. Sandaracinaceae*  
**Proteobacteria:** *Craurococcus-Caldovatus*, *Roseomonas*, *Skermanella*, *Microvirga*, *Psychroglaciecola*, *Phenylobacterium*, *Rhizobacter*, *Variovorax*, *Devosia*, *MND1*, *Massilia*, *Novosphingobium*, *Steroidobacter*, *Acidibacter*, *Bradyrhizobium*

**CC-GRA**  
(49)

**CC-MIX**  
(38)

**CC-NAT**  
(47)

**TILL**  
(41)

**Acidobacteriota:** *Stenotrophobacter*, *Candidatus Solibacter*, Subgroup 2, Subgroup 5, *f\_\_Acidobacteriaceae*(Subgroup 1), *Unc. Acidobacteriales*  
**Actinobacteriota:** *Actinomyces*, *Slackia*, *Jatrophilhabitans*, *Glycomyces*, *Angustibacter*, *Crossiella*  
**Bacteroidota:** *Parafilimonas*, *Terrimonas*, *Kapabacteriales*, *Muribaculaceae*  
**Chloroflexi:** AD3, SBR1031  
**Cyanobacteria:** *Sericytochromati*  
**Fibrobacterota:** possible genus 04  
**Firmicutes:** *Clostridia vadinBB60* group, *Erysipelotrichaceae* UCG-003, *Ruminococcus*, *o\_\_Oscillospirales*  
**Gemmatimonadota:** BD2-11 terrestrial group  
**Myxococcota:** P3OB-42, *Vitiosangium*, *Pajaroellobacter*  
**Proteobacteria:** A0839, A21b, *Acidiphilium*, *Burkholderia*, *Caulobacter*, *Pelomonas*, *Elsteraceae*, *unc. Elsteraceae*, *unc. Magnetospiraceae*, *unc. Micropepsaceae*, IS-44, *mle1-7*, *Phyllobacterium*, *unc. Rhizobiaceae*, SC-I-84, JTB255 marine benthic group, *Rhodopseudomonas*, *unc. Xanthobacteraceae*, *o\_\_Burkholderiales*, *f\_\_Acetobacteraceae*, *Unc. Alphaproteobacteria*

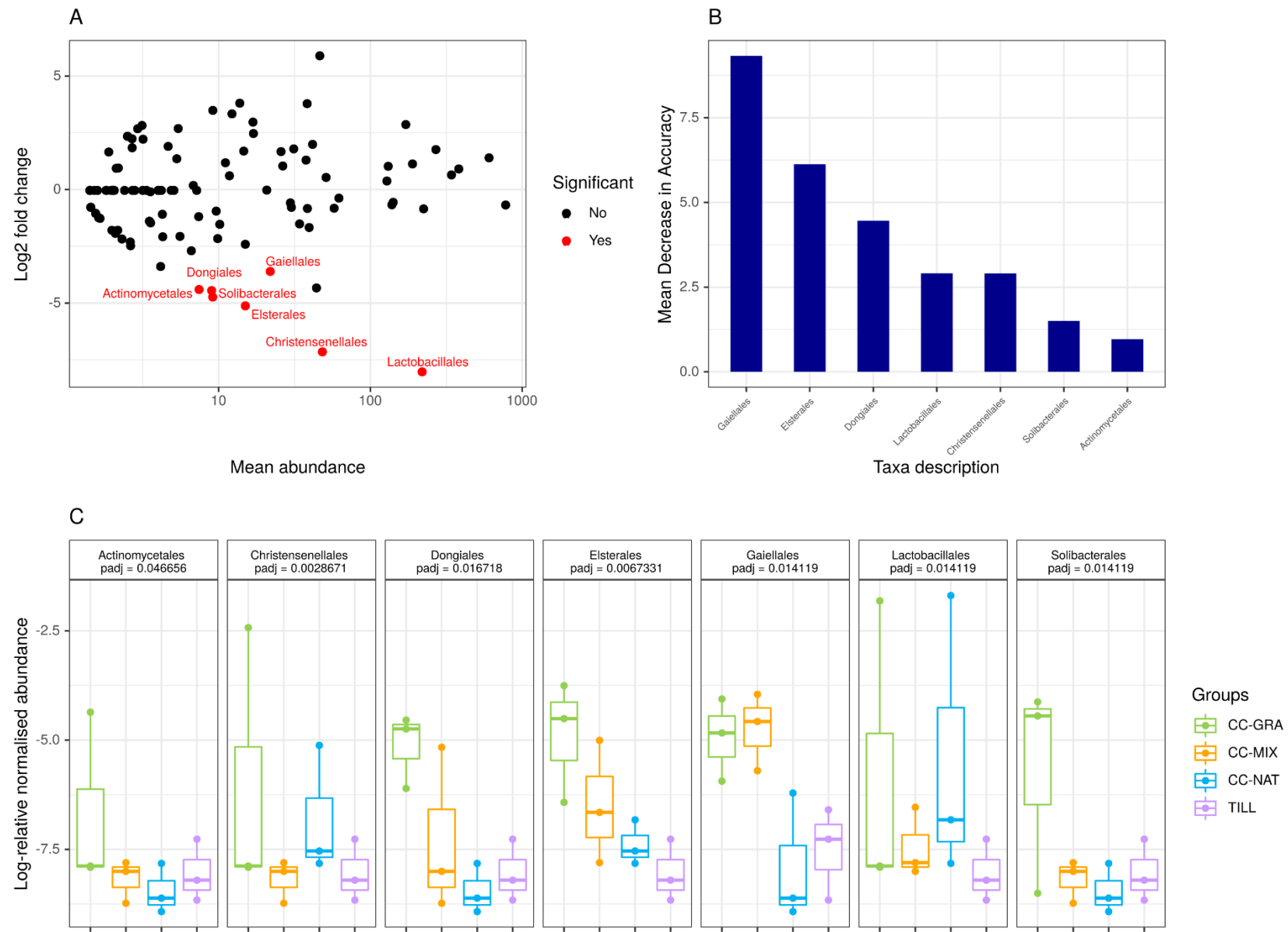
**Acidobacteriota:** *Vicinamibacter*, *c\_\_Vicinamibacteria*  
**Actinobacteriota:** 0319-7L14, *Curtobacterium*, *Pseudarthrobacter*, *Catenuloplanes*, *Longispora*, IMCC26207, *Nakamurella*, *Unc. Frankiales*  
**Bacteroidota:** *Coprobacter*, *Chitinophaga*, UTBCD1, *Unc. Cytophagales*  
**Bdellovibrionota:** 0319-6G20  
**Chloroflexi:** *unc. Chloroflexi*  
**Firmicutes:** DTU014, *Fusicatenibacter*, *Lachnospiraceae* ND3007 group, *Colidextribacter*, *Paenibacillus*, *Melghirimyces*, *f\_\_Bacillaceae*, *f\_\_Peptostreptococcaceae*  
**Gemmatimonadota:** *f\_\_Gemmatimonadaceae*  
**Myxococcota:** *Angiococcus*, *unc. Myxococcaceae*  
**Patescibacteria:** TM7a  
**Planctomycetota:** *unc. Isosphaeraceae*  
**Proteobacteria:** *Roseococcus*, *Achromobacter*, *Ferrovibrio*, *Pseudorhizobium*, *Luteimonas*, *f\_\_Rhodobacteraceae*, *Unc. Azospirillales*  
**RCP2:** RCP2-54  
**SAR324:** SAR324 clade(Marine group B)

**Actinobacteriota:** *Acidothermus*, *Actinotalea*, *Enterorhabdus*, *Kineococcus*, *Cryobacterium*, *Lysinimonas*, *Naasia*, *Rathayibacter*, *Dactylosporangium*, *Actinocorallia*, *f\_\_Nocardioidaceae*  
**Bacteroidota:** *Edaphobaculum*, *Flavobacterium*, *Hymenobacter*, *Pedobacter*  
**Cyanobacteria:** *Gastranaerophilales*, *Phormidium* SAG 37.90.  
**Firmicutes:** *Acidaminococcus*, *Granulicatella*, *Clostridia* UCG-014, *Clostridium sensu stricto* 13, *Asteroleplasma*, *[Eubacterium] xylanophilum* group, *Agathobacter*, *Butyrivibrio*, *Coprococcus*, UCG-005, UCG-010, *Planomicrobium*, *[Eubacterium] siraeum* group, CAG-352, *Veillonella*  
**Myxococcota:** MSB-4B10, *Phaselicystis*, *o\_\_Polyangiales*  
**Proteobacteria:** *Pusillimonas*, *Methylocella*, *Lautropia*, *Ideonella*, *Paucibacter*, *Rhodoferax*, *unc. Comamonadaceae*, *Filomicrobium*, *Chiayiivirga*, *Erythrobacter*, *Sphingosinicella*  
**Verrucomicrobiota:** *Candidatus Udaeobacter*

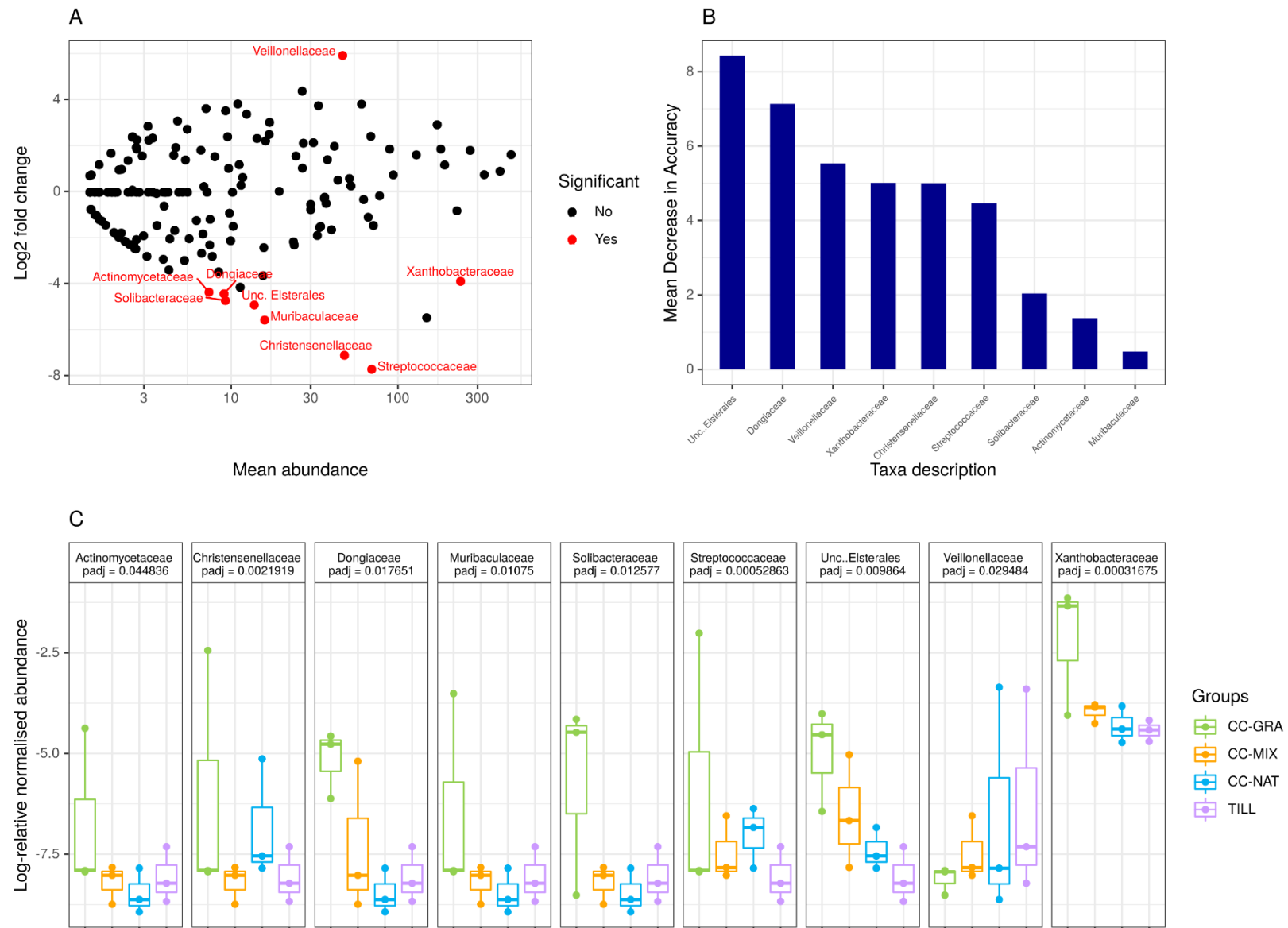
**Acidobacteriota:** *f\_\_Blastocatellaceae*  
**Actinobacteriota:** *Brevibacterium*, *unc. Ilumatobacteraceae*, *Kineosporiaceae*, *Pseudokineococcus*, *Marisediminicola*, *Salinibacterium*, *Asanoa*, *Catellatospora*, *Rubrobacter*, *Solirubrobacteraceae*, *Actinomadura*, *p\_\_Actinobacteriota*  
**Bacteroidota:** *Aurantisolimonas*, *Flaviaeusturariibacter*, *Flavitalea*, *Puia*, *Chryseolinea*, *Larkinella*, *Unc. Chitinophagales*  
**Chloroflexi:** AKYG1722, JG30-KF-CM45  
**Cyanobacteria:** *Geitlerinema*  
**Firmicutes:** *Phascolarctobacterium*, *Anaerostipes*, *unc. Lachnospiraceae*, *Flavonifractor*, *Oscillibacter*, *Oscillospira*, UBA1819, *Megasphaera*  
**Gemmatimonadota:** *Longimicrobiaceae*  
**Myxococcota:** *Stigmatella*, *Aetherobacter*  
**Patescibacteria:** LWQ8  
**Proteobacteria:** *unc. Azospirillaceae*, CCD24, *Pseudofulvimonas*, *Lysobacter*, *Pseudoxanthomonas*, *f\_\_Hyphomicrobiaceae*

**Figure S8.** Prevalence Venn diagram showing the unique and shared bacterial genera obtained from an olive orchard soil under different cover crop managements (TILL: tillage, CC-GRA: sown cover crop with gramineous, CC-MIX: sown cover crop with a mixture of species) and CC-NAT (cover crop with spontaneous vegetation). The total number of genera is indicated between brackets and the core and unique genera names for each treatment. \*Number of OTUs that stopped at a higher taxonomic level.

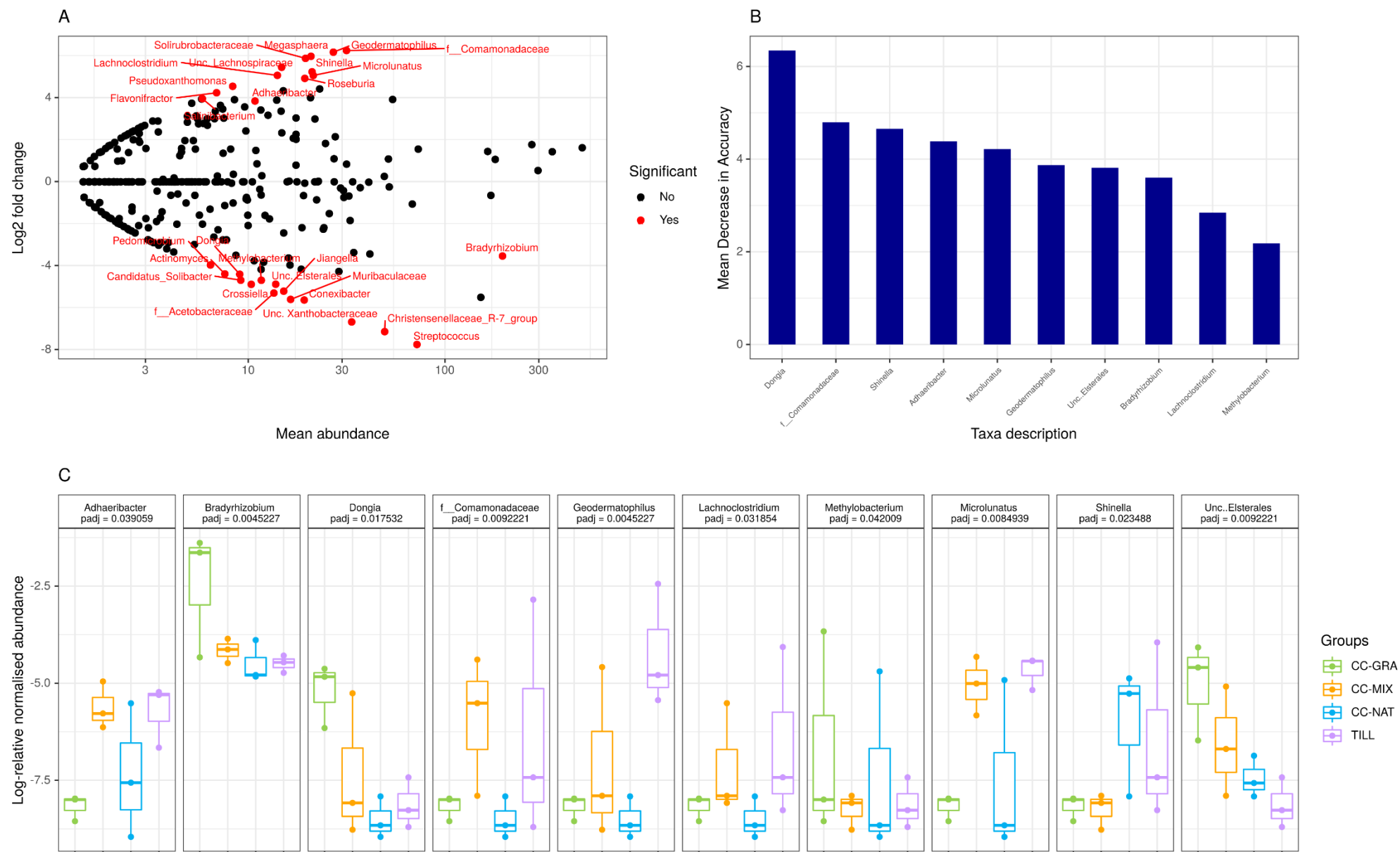




**Figure S9.** Differential OTU abundance analysis with DESeq2 R package at the order level. **(A)** Volcano plot representation of bacterial orders that are either up or down regulated; **(B)** Mean Decrease Accuracy plot of most important differentially expressed bacterial orders for microbial community obtained by random forest classifier; **(C)** Box-plot representation of the seven most abundant orders with a different significant abundance, for each taxon is represented the Log-relative normalised abundance among soil treatments and  $p$ -values from Wald test.



**Figure S10.** Differential OTU abundance analysis with DESeq2 R package at the family level. (A) Volcano plot representation of bacterial families that are either up or down regulated; (B) Mean Decrease Accuracy plot of most important differentially expressed bacterial families for microbial community obtained by random forest classifier; (C) Box-plot representation of the seven most abundant families with a different significant abundance, for each taxon is represented the Log-relative normalised abundance among soil treatments and *p*-values from Wald test.



**Figure S11.** Differential OTU abundance analysis with DESeq2 R package at the genus level. (A) Volcano plot representation of bacterial genera that are either up or down regulated; (B) Mean Decrease Accuracy plot of most important differentially expressed bacterial genera for microbial community obtained by random forest classifier; (C) Box-plot representation of the seven most abundant genera with a different significant abundance, for each taxon is represented the Log-relative normalised abundance among soil treatments and  $p$ -values from Wald test.