Supplementary material for

Vineyard soil microbial community under conventional, sustainable and organic management practices in a Mediterranean climate

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Table S1. Correlation among soil parameters (r and *P* values; *P* < 0.05 bold)

	EC	*Hygr*	WFC	SOM	CaCO$_3$	DOC	TDC	DIC	TDN	C:N ratio
clay (%)	0.16, (0.21)	**-0.27, (0.035)**	**0.29, (0.019)**	-0.03, (0.79)	**-0.27, (0.029)**	0.03, (0.81)	-0.35, (0.005)	**-0.34, (0.006)**	-0.14, (0.26)	-0.19, (0.13)
silt (%)	**0.26, (0.036)**	-0.21, (0.10)	0.08, (0.53)	0.01, (0.91)	**-0.26, (0.036)**	0.21, (0.10)	-0.27, (0.033)	**-0.27, (0.035)**	-0.12, (0.34)	-0.03, (0.83)
sand (%)	**-0.25, (0.047)**	**0.26, (0.039)**	-0.19, (0.14)	0.01, (0.97)	**0.30, (0.016)**	-0.16, (0.22)	0.34, (0.007)	**0.33, (0.008)**	0.15, (0.25)	0.10, (0.42)
pH	**-0.66 (<0.001)**	0.03 (0.82)	0.05 (0.67)	**-0.32, (<0.001)**	**0.34 (0.006)**	**-0.47, (<0.001)**	**-0.44, (<0.001)**	-0.02 (0.87)	**-0.31 (0.015)**	0.2 (0.12)
EC		-0.23 (0.07)	0.07 (0.58)	**0.26 (0.03)**	0.14 (0.27)	**0.53 (<0.001)**	**0.51 (<0.001)**	0.1 (0.42)	**0.38 (0.002)**	-0.24 (0.055)
Hygr			**0.4 (0.001)**	**-0.63 (<0.001)**	**-0.37 (0.003)**	**-0.47 (<0.001)**	**-0.43 (<0.001)**	0.03 (0.81)	**-0.3 (0.018)**	0.2 (0.11)
WFC				**0.73 (<0.003)**	-0.04 (0.76)	-0.16 (0.2)	-0.15 (0.24)	0.01 (0.92)	-0.09 (0.5)	0.01 (0.96)
SOM					0.21 (0.11)	**0.87 (<0.001)**	**0.86 (<0.001)**	0.03 (0.8)	**0.68 (<0.001)**	-0.06 (0.61)
CaCO$_3$						0.18 (0.15)	0.19 (0.15)	0.12 (0.36)	0.16 (0.21)	0.08 (0.56)
DOC							**0.99 (<0.001)**	**0.47 (<0.001)**	**0.64 (<0.001)**	-0.04 (0.75)
TDC								**0.57 (<0.001)**	**0.62 (<0.001)**	0.03 (0.84)
DIC									0.17 (0.19)	**0.49 (<0.001)**
TDN										**-0.55 (<0.001)**

Table S2. Alpha diversity indices for bacterial and fungal communities (additional to Table 1)

	Good's coverage	Berger Parker	Shannon's Entropy	Inverse Simpson	Exponential Shannon	Chao1
Bacteria						
Nat.	0.95 ab	0.04 ab	5.80 a	154 a	329 a	1871 a
Conv2	0.95 b	0.03 a	5.79 a	153 a	326 a	1765 ab
Conv1	0.96 a	0.03 a	5.76 a	151 a	318 a	1565 c
Org3	0.95 b	0.05 b	5.79 a	155 a	328 a	1814 ab
Org2	0.95 b	0.03 a	5.79 a	153 a	326 a	1790 ab
Org1	0.95 ab	0.03 a	5.67 b	143 b	291 b	1185 d
Sust2	0.95 b	0.03 a	5.78 a	153 a	324 a	1693 bc
Sust1	0.95 b	0.04 ab	5.79 a	154 a	328 a	1847 a
Fungi						
Nat.	0.98 ab	0.34 a	4.21 ab	20.2 a	60.1 bc	916 e
Conv2	0.98 ab	0.23 abc	3.88 c	17.5 b	50.5 d	491 g
Conv1	0.99 a	0.16 c	4.16 b	19.9 a	64.8 c	802 f
Org3	0.98 ab	0.30 ab	4.30 ab	20.7 a	73.6 ab	1129 bc
Org2	0.98 ab	0.21 abc	4.25 ab	20.4 a	70.2 ab	992 cd
Org1	0.98 ab	0.18 bc	4.27 ab	20.5 a	71.9 abc	1066 de
Sust2	0.97 b	0.21 abc	4.31 a	20.7 a	74.7 a	1178 ab
Sust1	0.98 ab	0.22 abc	4.33 a	20.8 a	75.6 a	1223 a

Table S3. Confusion matrices obtained with a neural network prediction algorithm (Multi-layer Perceptron algorithm(Pedregosa, Varoquaux et al. 2011) as implemented in Orange3 (Demsar, Curk et al. 2013)). Bacterial and fungal OTUs abundances were standardized using the Hellinger method (Legendre and Gallagher 2001); soil parameters were standardized as z-scores, i.e. units of standard deviation around the mean)

Predictions based on soil abiotic parameters (83% accuracy)
(Correct assignment to management: Nat, 83%; Org, 77%; Sust, 89%; Conv, 83%)

|		Nat.	Org3	Org2	Org1	Sust2	Sust1	Conv2	Conv1	$\sum$
						Predicted				
Actual	Nat.	**5**	1	0	0	0	0	0	0	**6**
	Org3	0	**8**	0	0	0	1	0	0	**9**
	Org2	0	0	**3**	3	0	0	3	0	**9**
	Org1	0	0	3	**4**	0	2	0	0	**9**
	Sust2	0	0	1	0	**8**	0	0	0	**9**
	Sust1	0	0	0	0	0	**8**	0	1	**9**
	Conv2	0	0	0	0	1	0	**7**	1	**9**
	Conv1	0	0	0	0	2	0	1	**6**	**9**
	$\sum$	**5**	**9**	**7**	**7**	**11**	**11**	**11**	**8**	**69**

Predictions based on bacterial OTU structure (75% accuracy)
(Correct assignment to management: Nat, 67%; Org, 62%; Sust, 79%; Conv, 94%)

		Nat.	Org3	Org2	Org1	Sust2	Sust1	Conv2	Conv1	$\sum$
						Predicted				
Actual	Nat.	**4**	0	0	0	2	0	0	0	**6**
	Org3	0	**5**	1	0	0	0	2	1	**9**
	Org2	0	2	**5**	0	0	0	1	0	**8**
	Org1	0	1	0	**2**	2	2	0	2	**9**
	Sust2	3	0	0	0	**6**	0	0	0	**9**
	Sust1	0	0	0	0	1	**8**	0	1	**10**
	Conv2	0	0	0	0	1	0	**8**	0	**9**
	Conv1	0	0	0	0	0	0	0	**9**	**9**
	$\sum$	**7**	**8**	**6**	**2**	**12**	**10**	**11**	**13**	**69**

Predictions based on fungal OTU structure (78% accuracy
(Correct assignment to management: Nat, 17%; Org, 81%; Sust, 79%; Conv, 100%)

		Nat.	Org3	Org2	Org1	Sust2	Sust1	Conv2	Conv1	$\sum$
						Predicted				
Actual	Nat.	**1**	0	1	0	0	3	0	1	**6**
	Org3	1	**6**	0	0	0	2	0	0	**9**
	Org2	0	0	**4**	2	1	1	0	0	**8**
	Org1	0	0	1	**8**	0	0	0	0	**9**
	Sust2	0	0	0	0	**9**	0	0	0	**9**
	Sust1	3	0	0	0	0	**6**	0	0	**9**
	Conv2	0	0	0	0	0	0	**8**	1	**9**
	Conv1	0	0	0	0	0	0	0	**9**	**9**
	$\sum$	**5**	**6**	**6**	**10**	**10**	**12**	**8**	**11**	**68**

Table S4. Redundancy analysis for bacterial and fungal OTU datasets. Analysis carried out with the ordiR2 step function (stepwise selection of explanatory variables) in the "vegan" package (Oksanen, Guillaume Blanchet et al. 2017) in R (R Core Team 2018). Microbial data was transformed using the Hellinger algorithm to minimise the excessive effect of rare taxa (Legendre and Gallagher 2001).

RDA analysis, Bacterial data				
Parameter	AIC	F	p	Cumulative R^2 adjusted
Hygr	-71.47	3.6393	0.002 **	0.037
CN	-72.382	2.8454	0.002 **	0.063
WFC	-73.665	3.167	0.002 **	0.093
pH	-74.849	3.0225	0.002 **	0.120
DIC	-75.644	2.6046	0.002 **	0.142
SOM	-75.873	-2.035	0.002 **	0.156
DOC	-75.706	1.6034	0.002 **	0.164
RDA Model: formula = speB.hel ~ Hygr + CN + WFC + pH + DIC + SOM, Constrained proportion: 23%				

RDA analysis, Fungal data				
Parameter	AIC	F	p	Cumulative R^2 adjusted
TDC	-58.984	3.4553	0.002 **	0.035
pH	-60.835	3.7865	0.002 **	0.076
CN	-62.797	3.8374	0.002 **	0.115
Hygr	-64.309	3.3373	0.002 **	0.146
SOM	-67.999	5.4063	0.002 **	0.203
WFC	-69.851	3.5503	0.002 **	0.235
RDA model: formula = speF.hel ~ TDC + pH + CN + Hygr + SOM + WFC, Constrained proportion: 31%				
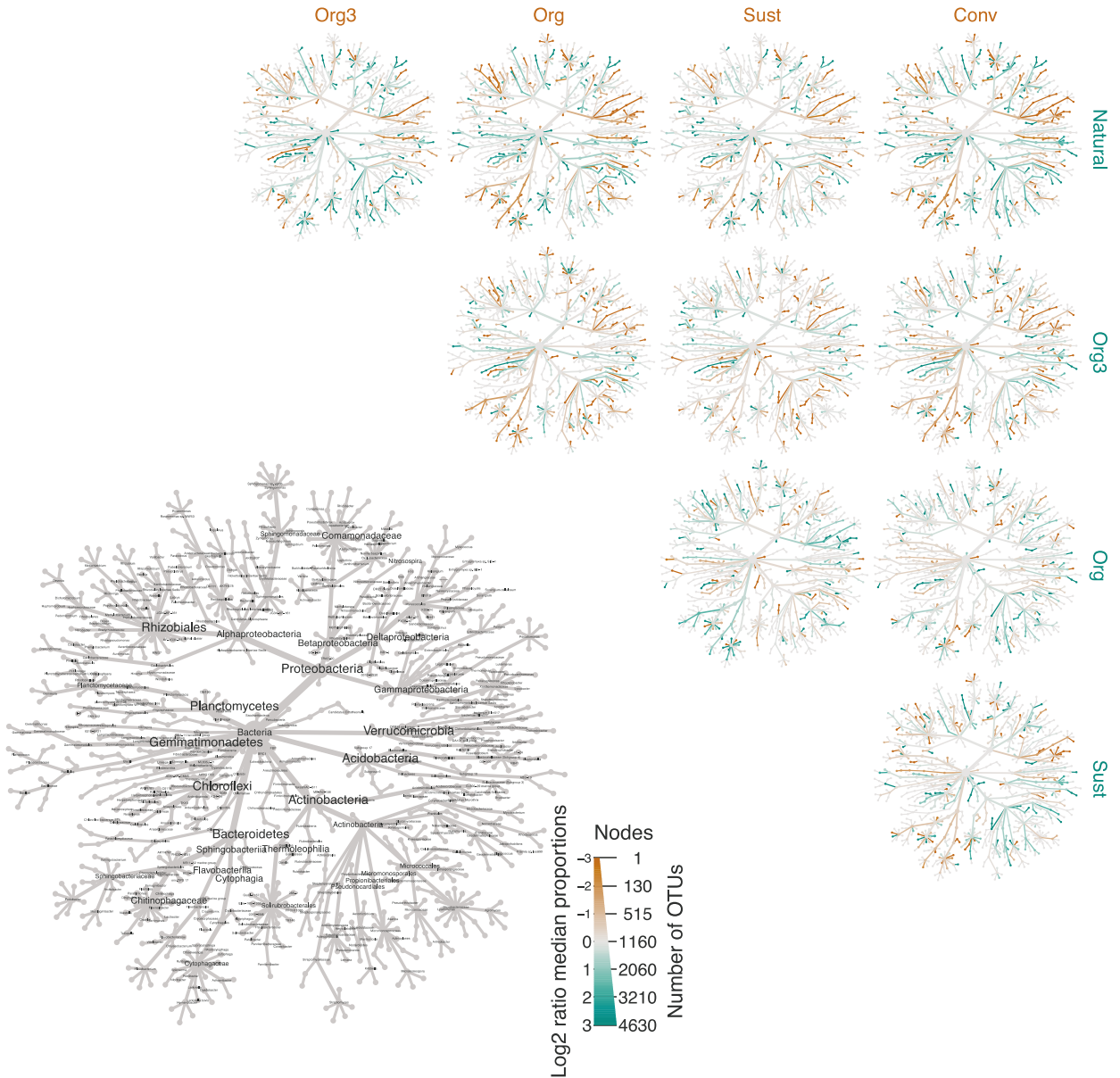
Fig. S1. Comparison of bacterial similarities across treatments(Foster, Sharpton et al. 2017). The color intensity describes the differences in taxonomic proportional abundance between two compared treatments, on a scale from log2 of 0 to 3. Analysis carried out in Metacoder R-package (Foster, Sharpton et al. 2017).

Table S6. Bacterial diversity, Jaccard similarity index (mean and n); all SE <0.01

	Nat	Conv2	Conv1	Sust2	Sust1	Org3	Org2	Org1
Nat	0.53 n=10	0.48 n=45	0.47, n=45	0.51, n=45	0.47, n=45	0.46, n=45	0.47, n=40	0.52, n=45
Conv2		0.52 n=36	0.44, n=81	0.54, n=81	0.47, n=81	0.49, n=81	0.44, n=72	0.44, n=81
Conv1			0.51, n=36	0.47, n=81	0.48,n=81	0.52, n=81	0.49, n=72	0.48, n=81
Sust2				0.49, n=36	0.48, n=81	0.45, n=81	0.51, n=72	0.46, n=81
Sust1					0.50, n=36	0.46 , n=81	0.53, n=72	0.46, n=81
Org3						0.46, n=36	0.47, n=72	0.51, n=81
Org2							0.50, n=28	0.52, n=72
Org1								0.46, n=36
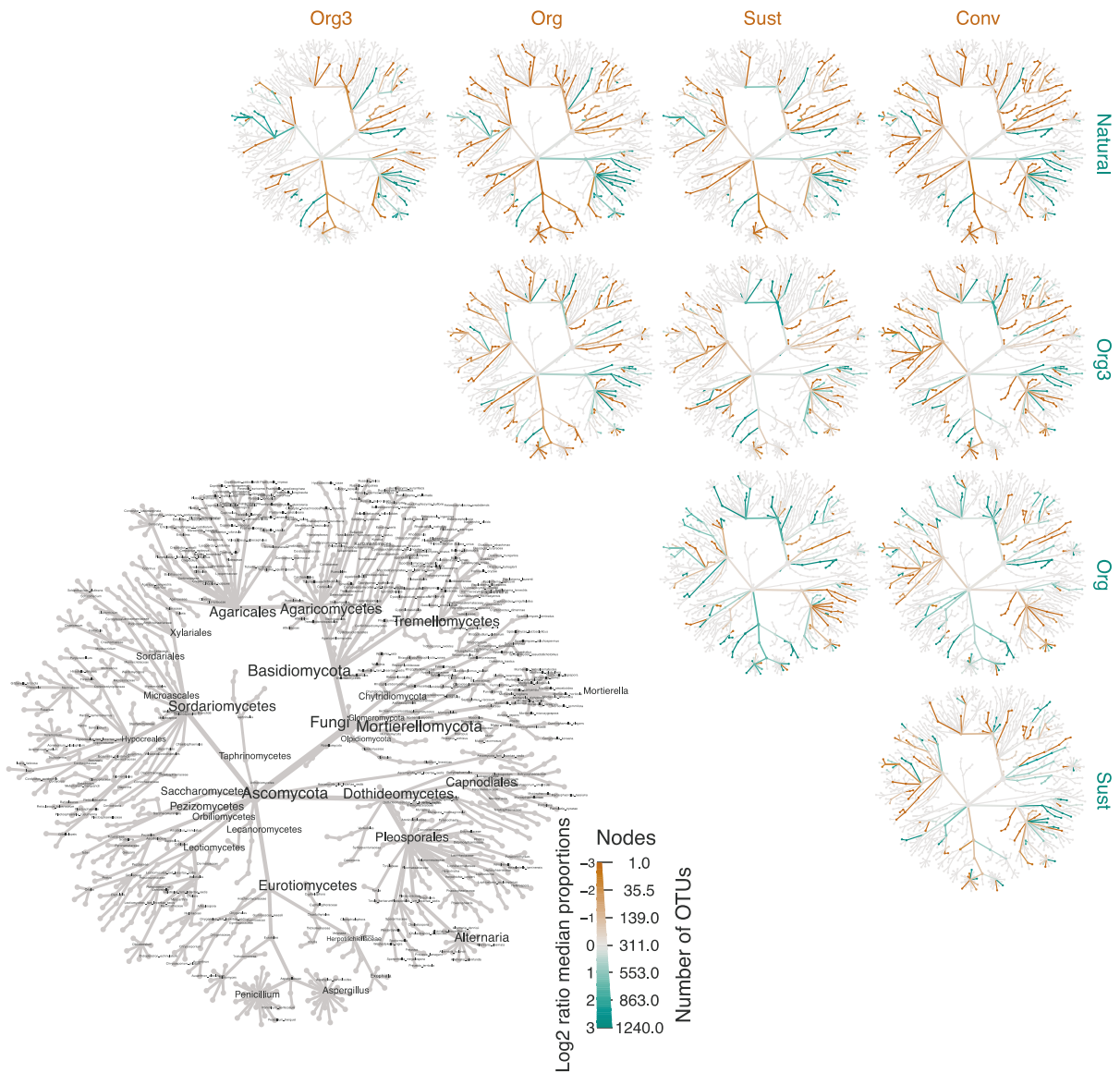
Fig. S2.Comparison of fungal similarities across treatments(Foster, Sharpton et al. 2017). The color intensity describes the differences in taxonomic proportional abundance between two compared treatments, on a scale from log2 of 0 to 3. Analysis carried out in Metacoder R-package (Foster, Sharpton et al. 2017).

Table S7. Fungal diversity, Jaccard similarity index (mean and n); SE <0.01, unless otherwise mentioned

	Nat	Conv2	Conv1	Sust2	Sust1	Org3	Org2	Org1
Nat	0.36[*], n=10	0.26, n=45	0.24, n=45	0.31, n=45	0.27, n=45	0.27, n=45	0.25, n=40	0.22, n=45
Conv2		0.33, n=36	0.27, n=81	0.24, n=81	0.26, n=81	0.28, n=81	0.25, n=72	0.19, n=81
Conv1			0.41, n=36	0.24, n=81	0.33, n=81	0.30, n=81	0.24, n=72	0.18, n=81
Sust2				0.33, n=36	0.25, n=81	0.24, n=81	0.22, n=72	0.24, n=81
Sust1					0.39, n=36	0.31, n=81	0.27, n=72	0.20, n=81
Org3						0.37, n=36	0.29, n=72	0.19, n=81
Org2							0.32, n=28	0.18, n=72
Org1								0.21[#], n=36