Table S1. Determination of soil parameters and nutrients and supplements performed according to DIN-standards inhouse and by Eurofins Agricultural Analytics Germany (Jena)

Determination of	According to
Soil class*	DIN 19682-2 (2014-07)
Total OS*	DIN ISO 10694: 1996-08
Clay content*	DIN ISO 11277: 2002-08
Magnesium	VDLUFA method book volume I, chapter 6.2.4.1
Potassium	VDLUFA method book volume I, chapter 6.2.1.2
Phosphorum	VDLUFA method book volume I, chapter 6.2.1.2
pH value	VDLUFA method book volume I, chapter 5.1.1

OS = organic substance; * determination by Eurofins Agricultural Analytics Germany (Jena); accrediting: DIN EN ISO/IEC 17025:2018 DAkkS D-PL-20226-01-00

Table S2. (A) Analysis of pathogenic organisms of the soil samples of sites A, B and C before the experiment (2017); **(B)** number of nematodes per cm2 soil in samples of soils of sites A, B and C.

(A)

Detected Microorganisms	DNA-Multiscan hybridisation signal		
	Site A	Site B	Site C
Alternaria sp.	2	2	0
Fusarium sp.	6	6	4
Fusarium oxysporum	2	2	2
Fusarium solani	2	2	2
Pythium sp.	4	4	4
Pythium sylvaticum	2	4	4
Pythium ultimum	4	4	0
Verticillium sp.	0	2	2
Verticilium dahliae	0	2	2

The intensity of the hybridisation signals is proportional to the amount of DNA (i.e., to the amount of biomass); 0 = not detected; 1–2 = weak; 3–4 = moderate signal; 5–6 = strong signal. Analyses by Scientia Terrae Research Institute, Antwerp, Belgium.

(B)

Nematodes per cm² soil	Site A	Site B	Site C
Pratylenchus thornei	25	3	49
Tylenchorhynchus	5	3	4
Paratylenchus spp.	247	53	18
Meloidogyne hapla	9	-	12
Rotylenchus	-	1	-
Heterodera	-	1	-
Trychodorus/Paratrychodorus	-	-	8

Table S3. Analysis of pathogenic organisms (DNA-multiscan) in non-sterilised and sterilised (at 100 °C) soils of sites A, B, and C 12 weeks after plant growth (pot trial 1), median over three singly analysed pots.

Detected	Soil A		Soil B		Soil C	
Microorganisms	Non-ster	Ster	Non-ster	Ster	Non-ster	Ster
Alternaria sp.	0	0	0	0	0	0
Fusarium sp.	2	0	2	0	2	0
Fusarium oxysporum	2	0	1	0	2	0
Fusarium solani	1	0	1	0	0	0
Pythium sp.	5	0	2	0	2	0
Pythium irregulare	3	0	0	0	0	0
Pythium sylvaticum	5	0	2	0	0	0
Pythium ultimum	0	0	2	0	2	0
Stemphylium sp.	1	2	0	0	0	0

Non-ster = non-sterilised soil; ster = sterilised soil. Analysis of pathogenic organisms (DNA-multiscan) in soils of sites A, B and C in non-sterilised and sterilised (at 100 °C). Median over three pots.

Table S4. Growth increase (GI) of average trunk cross-sectional areas (CSA) per tree (cm^2) from 2018-2022 in control and treated soils in sites A, B and C.

	Site A	Site B	Site C
Control	5.6 ± 0.2	5.3 ± 0.3	8.6 ± 1.7
Mc-compost	5.6 ± 0.3	5.2 ± 0.3	
Champost	5.5 ± 0.2	5.6 ± 0.3	5.3 ± 0.6
M-dam	6.8 ± 0.3	7.3 ± 0.5	
Leonardite			6.7 ± 1.0
M9/Gala	5.6 ± 0.2	6.6 ± 0.3	
M9/GalaRed	6.4 ± 0.3		
G11/Gala	5.5 ± 0.2	5.1 ± 0.2	
G11/GalaRed	6.1 ± 0.3		

± Standard error

Table S5. Yield (kg) of apples harvested per tree from 2019 to 2022 in terms of treatments and rootstock/variety combination at sites A and B and from 2020 to 2022 at site C.

	Site A					
	2019	2020	2021	2022	2019-2022	
Control	4.2 ± 0.2	9.7 ± 0.4	10.3 ± 0.6	9.1 ± 0.4	33.3 ± 1.0	b
Mc-compost	4.0 ± 0.2	9.7 ± 0.5	10.2 ± 0.6	9.9 ± 0.4	33.8 ± 0.9	b
Champost	4.4 ± 0.1	9.1 ± 0.4	10.7 ± 0.6	10.1 ± 0.3	34.3 ± 0.9	ab
M-dam	4.5 ± 0.2	10.1 ± 0.2	11.5 ± 0.5	11.1 ± 0.4	37.2 ± 0.9	a
M9/Gala	4.5 ± 0.1	8.9 ± 0.4	11.3 ± 0.5	10.3 ± 0.5	34.9 ± 1.2	A
M9/GalaRed	4.2 ± 0.2	10.1 ± 0.4	9.9 ± 0.6	10.7 ± 0.3	34.9 ± 0.7	A
G11/Gala	4.3 ± 0.2	9.8 ± 0.3	11.6 ± 0.6	10.1 ± 0.3	35.8 ± 0.9	A
G11/GalaRed	4.1 ± 0.3	9.8 ± 0.3	9.9 ± 0.5	9.1 ± 0.4	33.0 ± 0.8	A

± Standard error; different letters depict significance over summed years; Tukey test $p \leq 0.05$.

	Site B					
	2019	**2020**	**2021**	**2022**	**2019-2022**	
Control	2.3 ± 0.2	8.9 ± 0.5	13.8 ± 0.8	12.5 ± 0.7	37.6 ± 1.4	a
Mc-compost	2.6 ± 0.3	8.8 ± 0.5	14.3 ± 0.7	12.9 ± 0.9	38.5 ± 1.9	a
Champost	2.9 ± 0.3	9.8 ± 0.5	14.7 ± 0.8	13.9 ± 0.7	43.5 ± 2.7	a
M-dam	2.2 ± 0.3	10.8 ± 0.3	16.2 ± 0.6	14.3 ± 0.6	43.5 ± 1.3	a
M9/Gala	2.3 ± 0.2	9.4 ± 0.4	14.5 ± 0.6	13.6 ± 0.6	39.9 ± 1.3	A
M9/GalaRed						
G11/Gala	2.6 ± 0.2	9.7 ± 0.3	15.0 ± 0.5	14.3 ± 1.2	42.6 ± 1.6	A
G11/GalaRed						

± Standard error; different letters depict significance over summed years; Tukey test p≤0.05.

	Site C				
	2020	**2021**	**2022**	**2020-2022**	
Control	0.3 ± 0.2	5.7 ± 1.4	6.7 ± 0.7	12.9 ± 2.0	a
Champost	0.6 ± 0.1	4.1 ± 1.0	6.9 ± 0.6	11.6 ± 1.7	a
Leonardite	0.3 ± 0.1	4.3 ± 0.3	5.7 ± 1.3	10.3 ± 1.6	a

± Standard error; different letters depict significance over summed years; Tukey test p≤0.05.

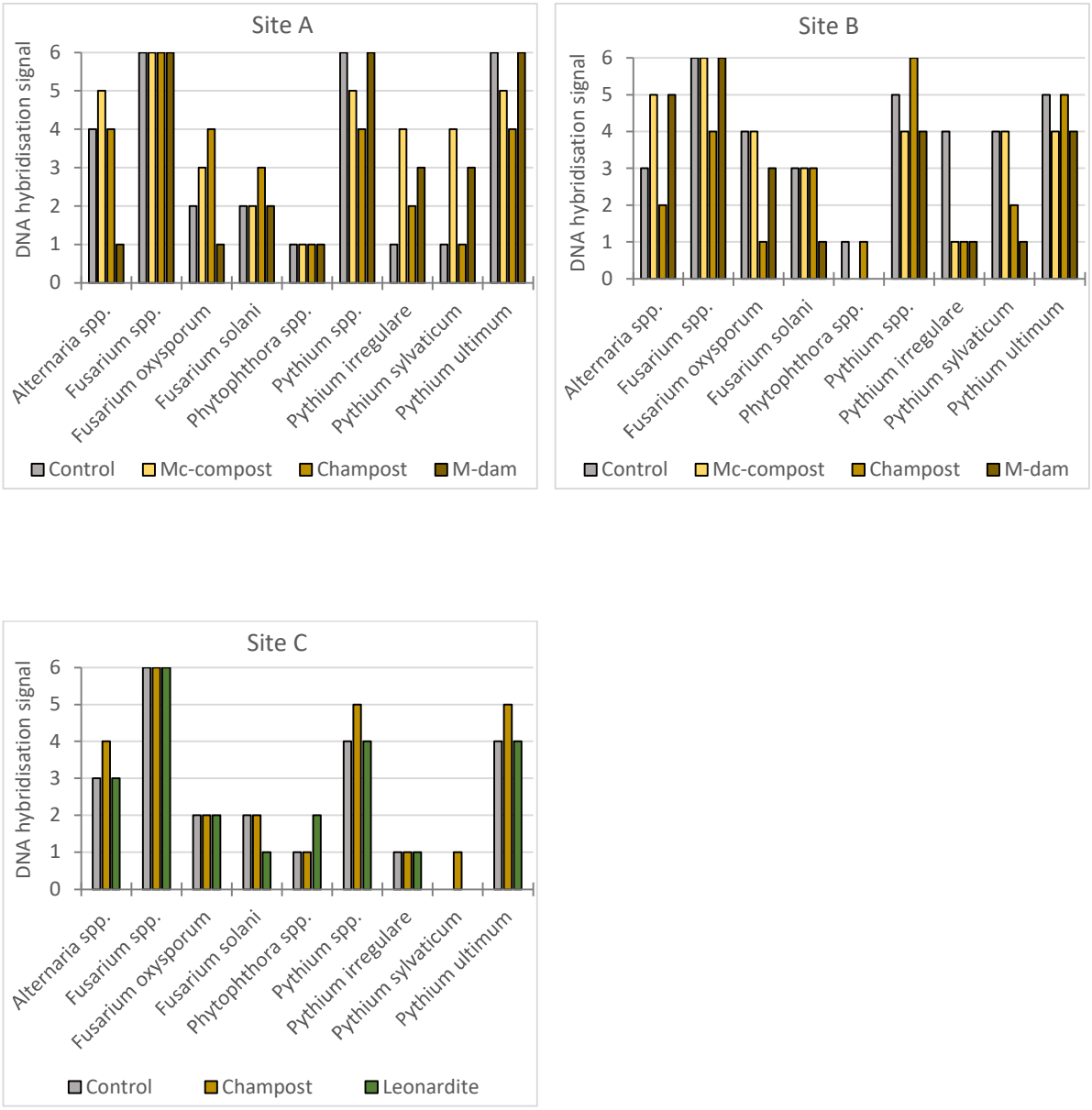

Figure S1. DNA Multiscan hybridisation signal intensities for predominantly fungal pathogenic microorganisms, detected in soil samples from sites A, B and C in 2022, 5 years after the soil treatments. The intensity of the DNA hybridisation signals (displayed in the respective bars) is proportional to the amount of DNA in the soil samples: 0 (not detected) to 6 (strongest).