

Supplementary

Supplementary Data

Supp. data 1. Synthetic DNA used as qPCR quantification reference sample

Sequence of fungal 18S rRNA gene DNA used as a standard:

CGATAACGAACGAGACCTTACTCTGCTAAATAGCCAGGCTAGCTTTGGCTGGTCGCCGGCTTCTTAGA
GAGACTATCAACTCAAGTTGATGGAAGTTTGAGGCAATAACAGGTCTGTGATGCCCTTAGATGTTCTG
GGCCGCACGCGCGCTACACTGACAGAGCCAACGAGTTCTTCACCTTGGCCGAAAGTCTTGGGTAATC
TTGTTAAACTCTGTCGTGCTGGGGATAAAGCATTGCAATTATTGCTTTTCAACGAGGAATGCCTAGTAA
GCGCGTGTATCAGCATGCGTTGATTACGTCCCTGACCTTTGTACACACCGCCCGTCGCTAHTACCGATT
GAATGGHT

Sequence of bacterial 16S rRNA gene DNA used as a standard:

CCTACGGGAGGCAGCAGTGGGGAATATTGGACAATGGGCGAAAGCCTGATCCAGCCATGCCGCGTGT
GTGAAGAAGGTCTTCGGATTGTAAAGCACTTTAAGTTGGGAGGAAGGGCAGTAAATTAATACTTTGCT
GTTTTGACGTTACCGACAGAATAAGCACCGGCTAACTCTGTGCCAGCAGCCGCGGTAATACAGAGGGT
GCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCGCTAGGTGGTTTGTAAAGTTGGATGTGAAATC
CCCGGGCTCAACCTGGGAACTGCATTCAAACTGACAAGCTAGAGTATGGTAGAGGGTGGTGGGAATT
TCCTGTGTAGCGGTGAAATGCGTAGATATAGGAAGGAACACCAGTGGCGAAGGCGACCACCTGGACT
GATACTGACACTGAGGTGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCG
TAAACGATGTCAACTAGCCGTTGGGAGCCTTGAGCTCTTAGTGCGCAGCTAACGCATTAAGTTGACC
GCCTGGGGAGTACGGCCGCAAGGTTAAAACTCAAATGAATTGACGGGGGCCCGCACAAAGCGGTGGA
GCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGCCTTGACATCCAATGAACTTTCCAGA
GATGGATTGGTGCCTTCGGGAACATTGAGACAGGTGCTGCATGGCTGTCGTCAGCTCGTGTCTGAGA
TGTTGGGTAAAGTCCCGTAACGAGCGCAACCCTTGTCTTAGTTACCAGCACGTAATGGTGGGCACTCT
AAGGAGACTGCCGTGACAAACCGGAGGAAGGTGGGGATGACGT

Supplementary Figures

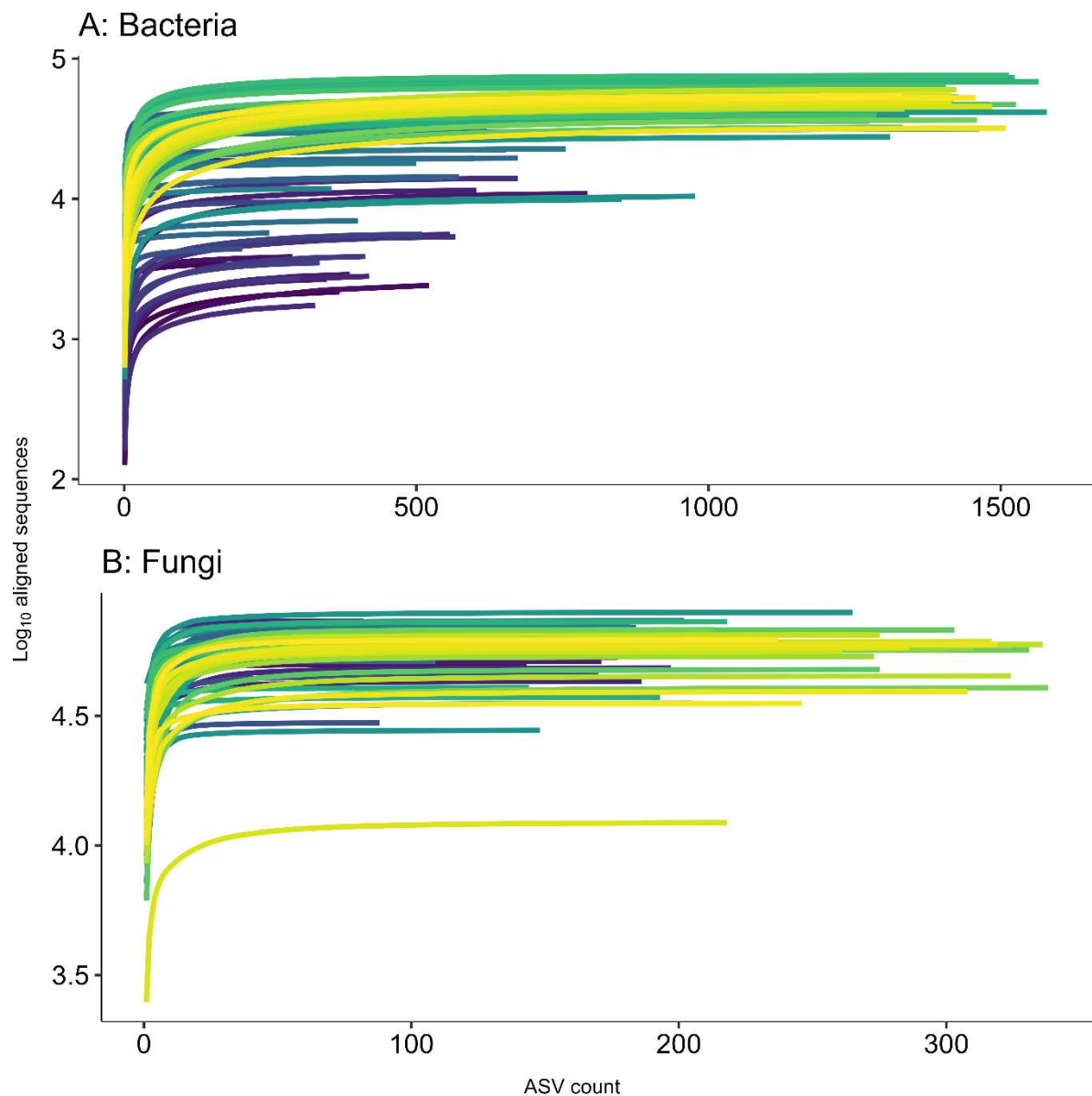


Figure S1. Rarefaction curves. Accumulated number of 16S (A) and ITS (B) sequence reads plotted against the number of ASVs indicating sufficient sequencing depth for 16S (90 samples) and ITS (95 samples).

Supplementary Tables

Table S1. ASV summary. The number of ASVs found in each sample type (before and after rare ASVs were filtered out), and ASVs shared between four sample types (top and base leaf scars, rhizosphere and roots). Samples were collected from M9 apple rootstock plants six months after their roots were treated with *Sphingomonas* consortia or water.

	Bacteria				Fungi			
	Leaf scar		Rhizosphere	Root	Leaf scar		Rhizosphere	Root
	Top	Base			Top	Base		
Number of ASVs								
Before filtering	2186	2652	2238	2818	492	882	683	855
After filtering	2023	2340	2152	2691	361	629	626	762
Normalised reads per Sample								
Minimum	1118		31833	19523	37621		38841	22803
Maximum	86533		65779	69192	91437		75979	106555
Median	8449		45088	31432	69291		49431	53625
Normalised reads per ASV								
Minimum	0.4		6	0.1	81		16	6
Maximum	43619		23679	74397	1062590		230854	394795
Median	21		218	63	159		105	63
Shared ASVs (after filtering out rare ASVs)								
	Base scar		Rhizosphere	Roots	Base scar		Rhizosphere	Roots
Top scar	1739		1262	1742	350		87	234
Base scar			1471	1947			192	360
Rhizosphere				2053				542

*: ASV data from top and base leaf scar samples were pooled together for statistical analysis.