

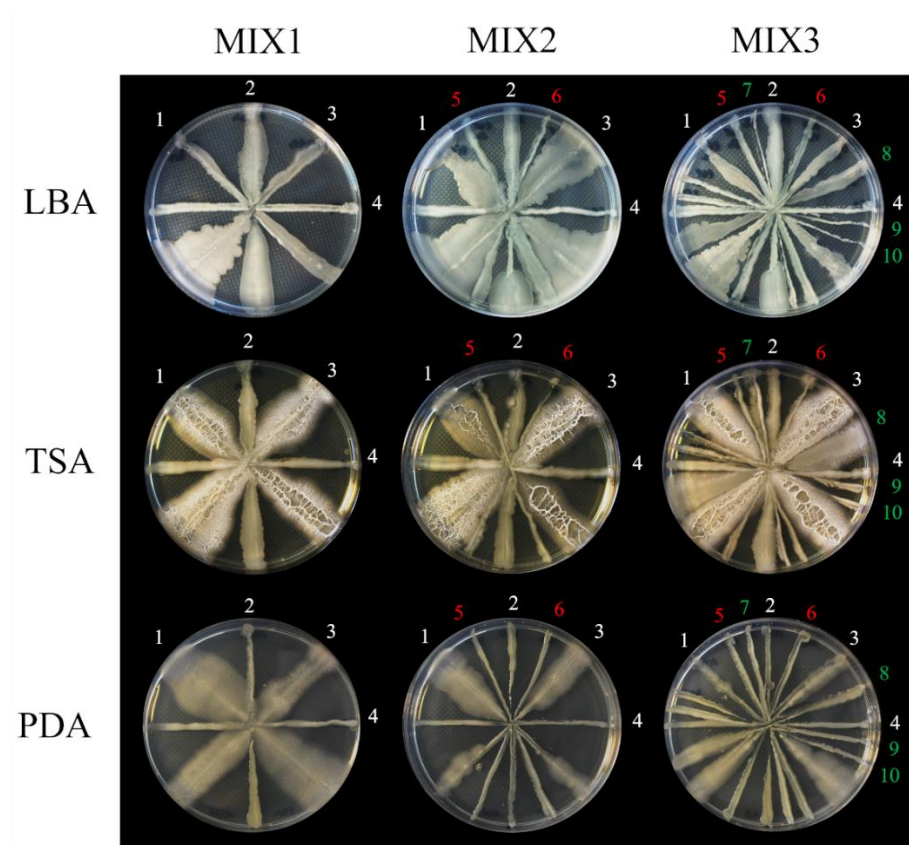


Figure S1: Co-growth of SynCom strains cultured together in one plate. 1, *B. velezensis* PFE42; 2, *G. halophytocola* PFE44; 3, *B. velezensis* PSE31B; 4, *Leclercia* sp. S52; 5, *P. salmasensis* POE54; 6, *P. simiae* POE78A; 7, *Paenarthrobacter* sp. S56; 8, *B. velezensis* PFE11; 9, *P. ureafaciens* S54; 10, *Chryseobacterium* sp. POE47. Red and green colours indicate the strains progressively added to MIX1 to obtain MIX2 and MIX3, respectively. LBA, Luria Broth Agar; TSA, Tryptic Soy Agar; PDA, Potato Dextrose Agar.

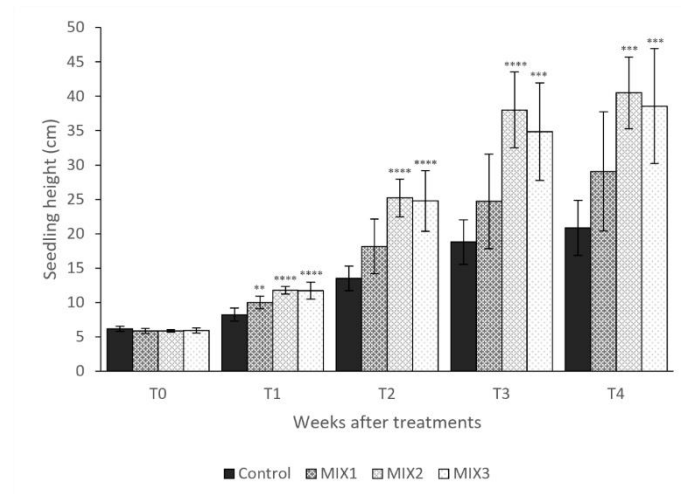


Figure S2: Time-course evaluation of tomato seedling height: T0 (a few hours after SynCom treatment), T1-4 (1-4 weeks after the treatment). Asterisks denote statistical significance compared to the untreated plants (Control) based on post-hoc Tukey HSD test [******, $0.001 \leq p \leq 0.01$; *******, $0.0001 \leq p \leq 0.001$; ********, $p < 0.0001$]. [Control = water-drenched plants; MIX1 = plants treated with the four-strains SynCom MIX1; MIX2 = plants treated with the six-strains SynCom MIX2; MIX3 plants treated with the ten-strains SynCom MIX3].

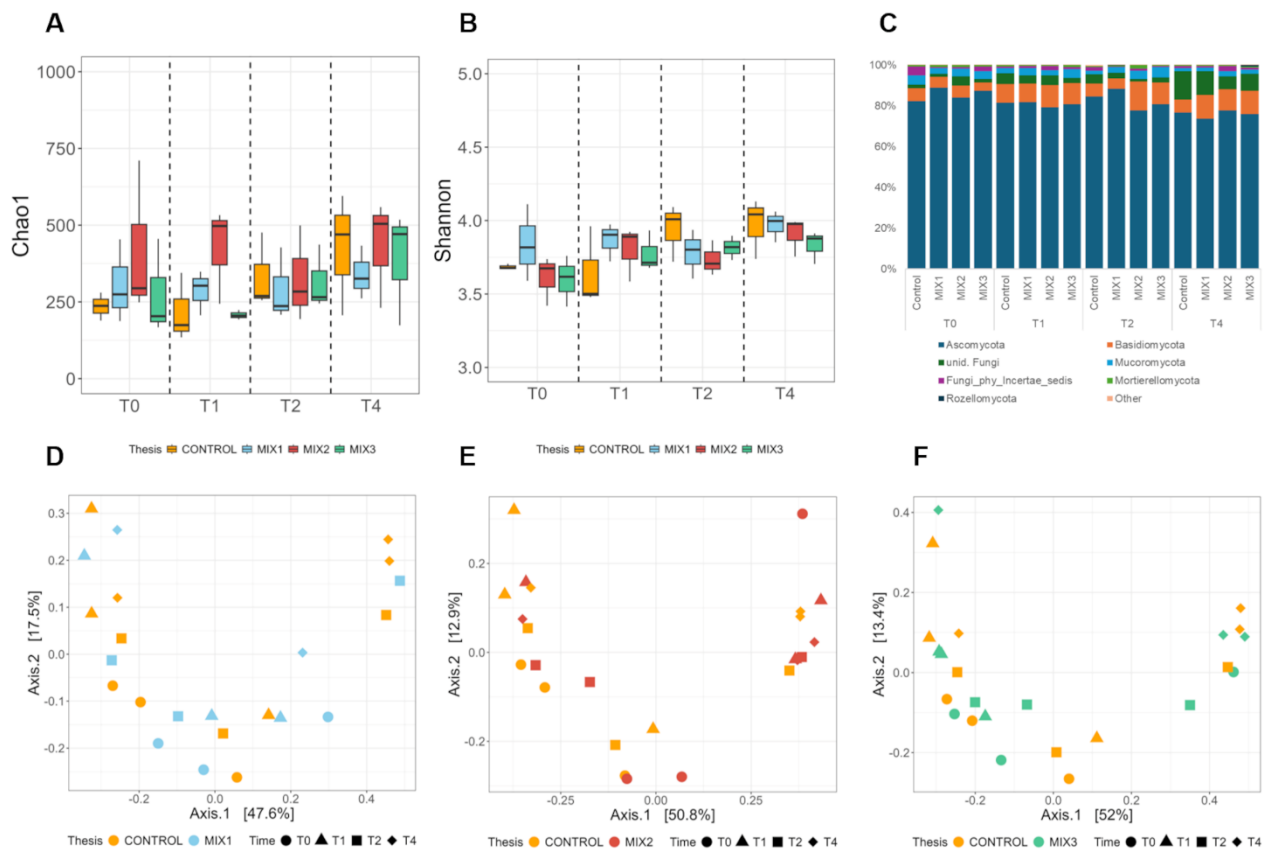


Figure S3: Estimation of the alpha diversity of the microbiome fungal (A-B) communities in the rhizosphere of control and SynCom-treated tomato plants based on amplicon sequencing data. The observed Chao1 and Shannon indices were used in the alpha diversity analysis. (C) Relative abundances of fungal communities at the phylum taxonomic level in the rhizosphere of control and SynCom plants. Taxa less abundant than 1% are reported as “Other taxa”. (D-F) PCoA of rhizosphere fungal communities in the control and SynCom-treated tomato plants based on amplicon sequencing data. Sample clustering was based on the Bray–Curtis dissimilarity matrix. Each point on the graph corresponds to a single sample (biological replication). No statistically significant effects due to time, except for MIX3 (p -value > 0.05 : MIX1, $R^2 = 0.2$; MIX2, $R^2 = 0.15$; p -value < 0.05 : MIX3, $R^2 = 0.27$; PERMANOVA, 999 permutations), treatment (p -value > 0.05 : MIX1, $R^2 = 0.02$; MIX2, $R^2 = 0.06$; MIX3, $R^2 = 0.01$; PERMANOVA, 999 permutations) or their interactions (p -value > 0.05 : MIX1, $R^2 = 0.9$; MIX2, $R^2 = 0.1$; MIX3, $R^2 = 0.06$; PERMANOVA, 999 permutations) were found. [Control = water-drenched plants; MIX1 = plants treated with the four-strains SynCom MIX1; MIX2 = plants treated with the six-strains SynCom MIX2; MIX3 plants treated with the ten-strains SynCom MIX3].

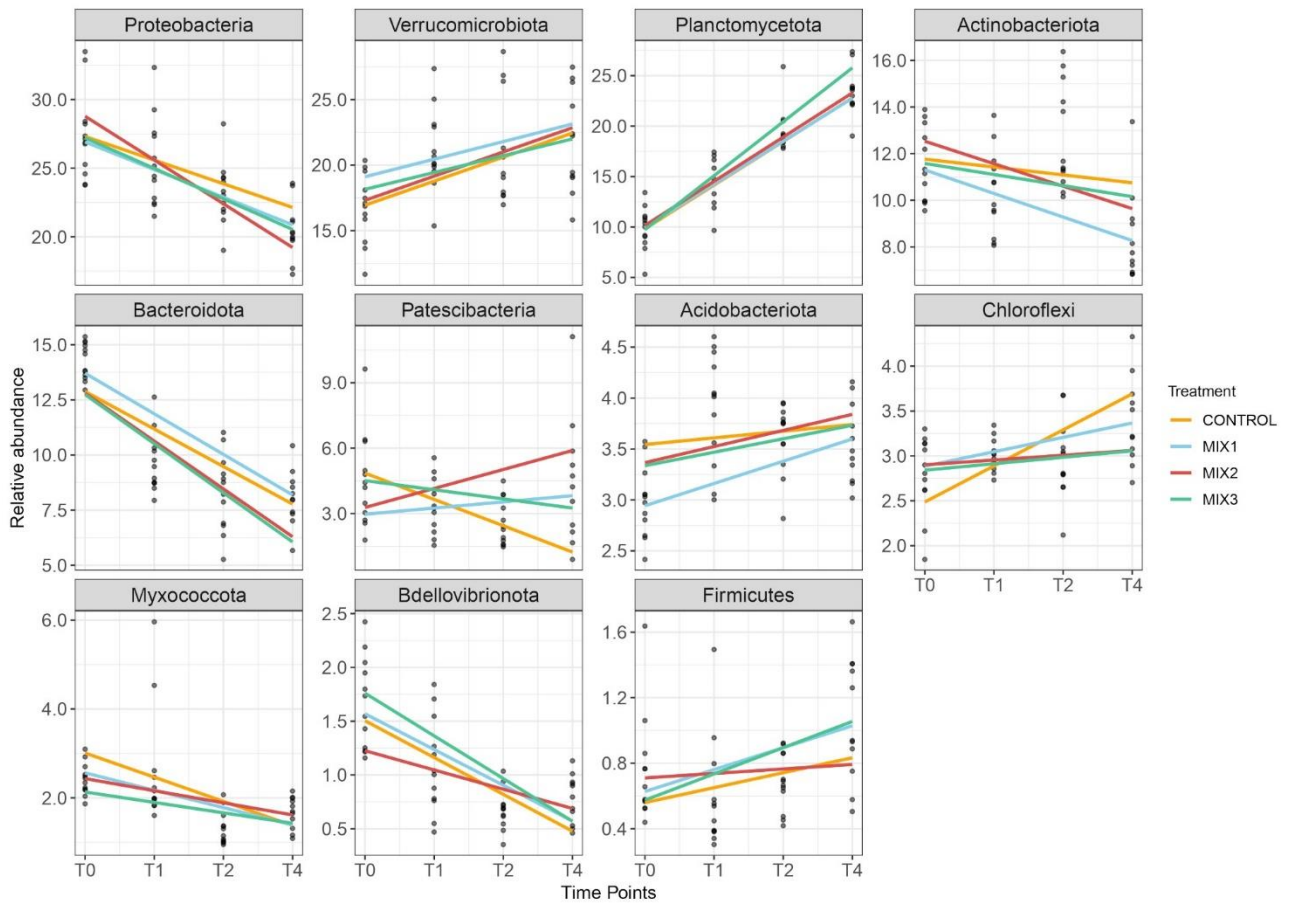


Figure S4: Linear regression analysis between the relative abundance of the most abundant bacterial phyla and time points. Dots represent individual samples collected at different time points for each treatment, while lines depict treatment-specific linear models fitted within each phylum to describe temporal trends.

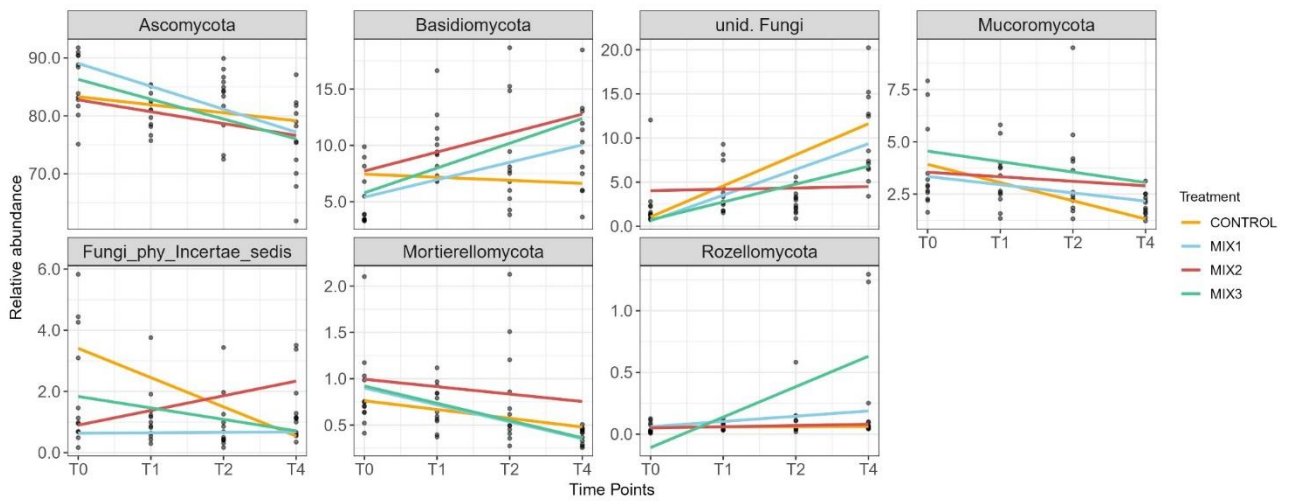


Figure S5: Linear regression analysis between the relative abundance of the most abundant fungal phyla and time points. Dots represent individual samples collected at different time points for each treatment, while lines depict treatment-specific linear models fitted within each phylum to describe temporal trends.

Figure S6: Significant differentially abundant bacterial genera (p-value < 0.05) in the rhizosphere of ‘Proxy’ plants treated with SynComs at T1 (A) and T2 (B). The log₂FoldChange of each bacterial taxon (on the left) is coloured according to depleted (red), not differentiated (white), and enriched (green) conditions of the samples compared to control ones. The relative abundance (%) of each bacterial taxon (on the right) is coloured according to low (light brown) to high (dark brown) abundance. Taxa that are not present or not significant in a specific treatment are indicated by gray colour. [MIX1_MIX2_MIX3 = taxa in common between MIX1, MIX2 and MIX3; MIX1_MIX2 = taxa in common between MIX1 and MIX2; MIX1_MIX3 = taxa in common between MIX1 and MIX3; MIX2_MIX3 = taxa in common between MIX2 and MIX3; Control = water-drenched plants; MIX1 = plants treated with the four-strains SynCom MIX1; MIX2 = plants treated with the six-strains SynCom MIX2; MIX3 plants treated with the ten-strains SynCom MIX3]

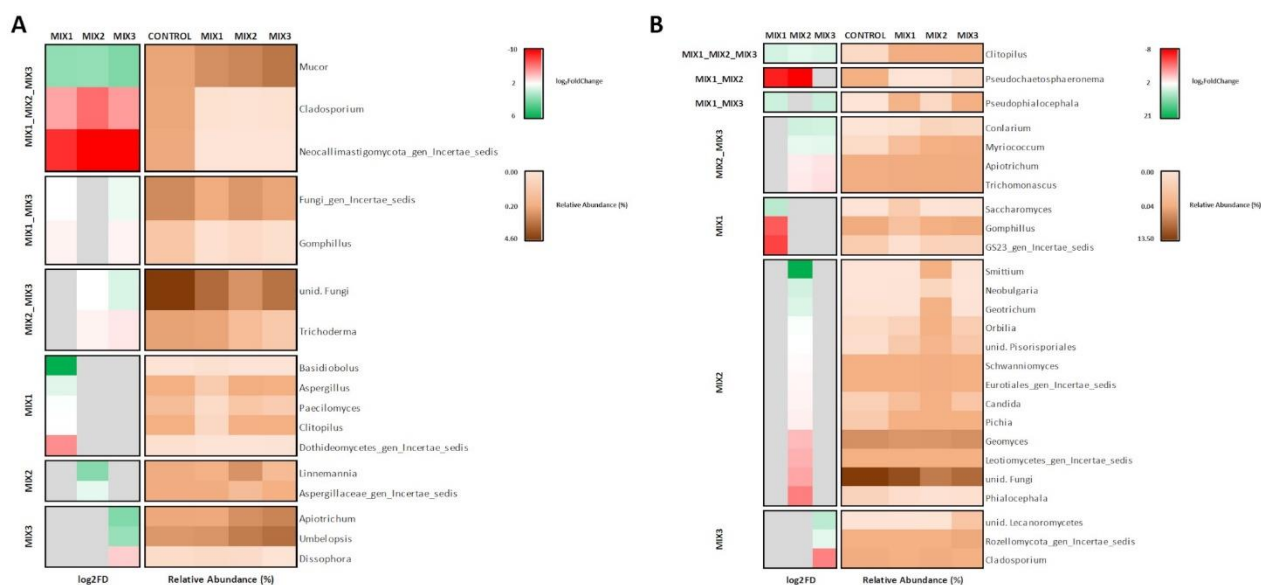


Figure S7: Significant differentially abundant fungal genera (p -value < 0.05) in the rhizosphere of ‘Proxy’ plants treated with SynComs at T2 (A) and T4 (B). The $\log_2$ FoldChange of each fungal taxon (on the left) is coloured according to depleted (red), not differentiated (white), and enriched (green) conditions of the samples compared to control ones. The relative abundance (%) of each fungal taxon (on the right) is coloured according to low (light brown) to high (dark brown) abundance. Taxa that are not present or not significant in a specific treatment are indicated by gray colour. [MIX1_MIX2_MIX3 = taxa in common between MIX1, MIX2 and MIX3; MIX1_MIX2 = taxa in common between MIX1 and MIX2; MIX1_MIX3 = taxa in common between MIX1 and MIX3; MIX2_MIX3 = taxa in common between MIX2 and MIX3; Control = water-drenched plants; MIX1 = plants treated with the four-strains SynCom MIX1; MIX2 = plants treated with the six-strains SynCom MIX2; MIX3 plants treated with the ten-strains SynCom MIX3]

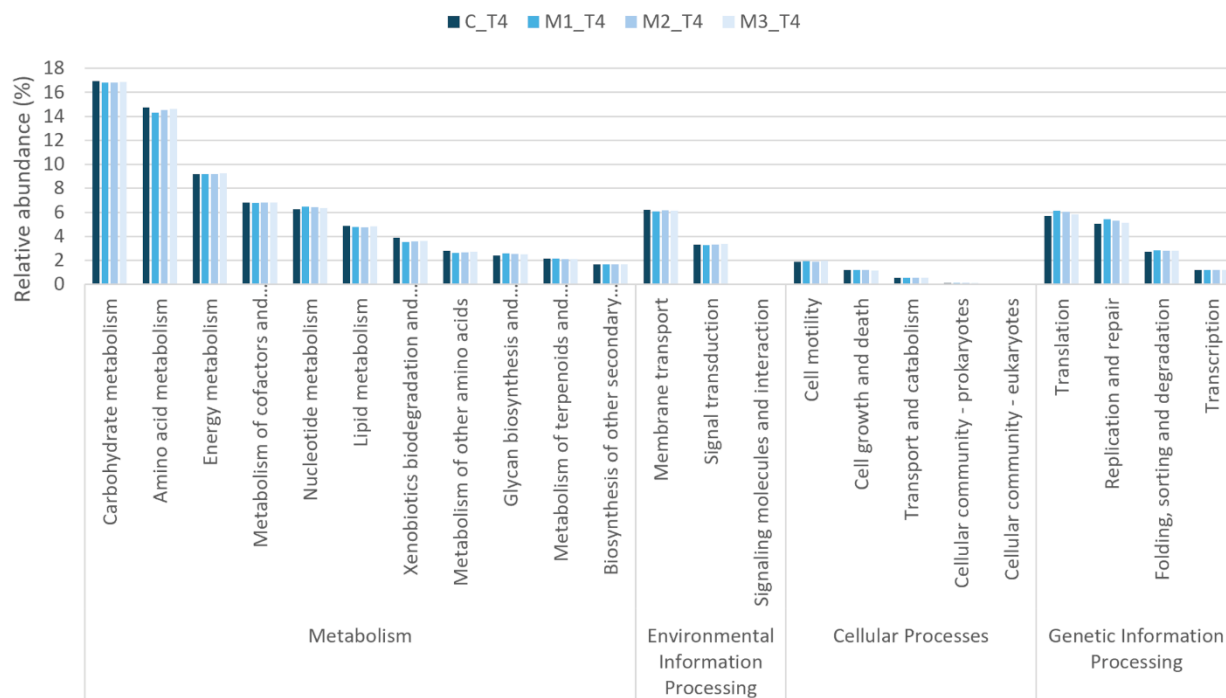


Figure S8: Relative abundance of the predicted functions grouped according KEGG level 1 and 2 categories of the rhizosphere bacterial communities of the control and SynCom-treated plants. [C = water-drenched plants; M1 = plants treated with the four-strains SynCom MIX1; M2 = plants treated with the six-strains SynCom MIX2; M3 = plants treated with the ten-strains SynCom MIX3].

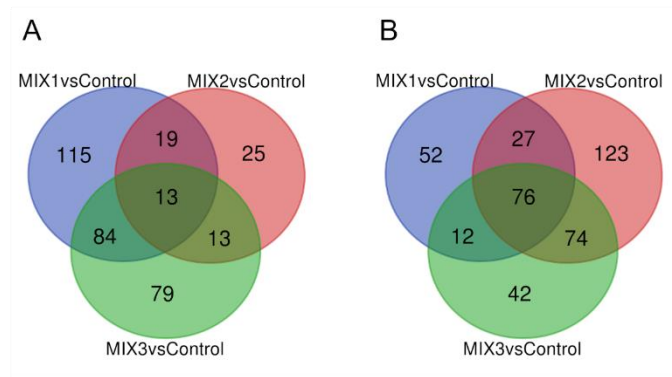


Figure S9: Number of exclusive or shared predicted genes significantly (p -value < 0.05, FDR) up- (A) or down-regulated (B) in the rhizosphere bacterial communities of SynCom-treated plants compared to control plants. [Control = water-drenched plants; MIX1 = plants treated with the four-strains SynCom MIX1; MIX2 = plants treated with the six-strains SynCom MIX2; MIX3 = plants treated with the ten-strains SynCom MIX3].

Table S1: *In vitro* reciprocal growth inhibition of bacterial strains evaluated on PDA. 0, no inhibition; 1, inhibition; 2, partial inhibition.

	<i>Bacillus velezensis</i> PFE11	<i>Bacillus velezensis</i> PFE42	<i>Bacillus velezensis</i> PSE31B	<i>Pseudomonas salmasensis</i> POE54	<i>Pseudomonas simiae</i> POE78A	<i>Leclercia</i> sp. S52	<i>Chryseobacterium</i> sp. POE47	<i>Glutamicibacter halophytocola</i> PFE44	<i>Paenarthrobacter ureafaciens</i> S54	<i>Paenarthrobacter</i> sp. S56
<i>Bacillus velezensis</i> PFE11	0	1	1	1	1	0	0	0	0	0
<i>Bacillus velezensis</i> PFE42	1	0	0	1	1	2	0	0	0	0
<i>Bacillus velezensis</i> PSE31B	1	0	0	1	1	0	0	0	0	0
<i>Pseudomonas salmasensis</i> POE54	1	1	1	0	2	1	1	1	1	1
<i>Pseudomonas simiae</i> POE78A	1	1	1	2	0	0	1	1	1	1
<i>Leclercia</i> sp. S52	0	2	0	1	0	0	1	0	1	1
<i>Chryseobacterium</i> sp. POE47	0	0	0	1	1	1	0	0	0	0
<i>Glutamicibacter halophytocola</i> PFE44	0	0	0	1	1	0	0	0	0	0
<i>Paenarthrobacter ureafaciens</i> S54	0	0	0	1	1	1	0	0	0	0
<i>Paenarthrobacter</i> sp. S56	0	0	0	1	1	1	0	0	0	0

Table S2: Linear regression analysis between the relative abundance of the most abundant bacterial phyla and time points [Control = water-drenched plants; MIX1 = plants treated with the four-strains SynCom MIX1; MIX2 = plants treated with the six-strains SynCom MIX2; MIX3 = plants treated with the ten-strains SynCom MIX3].

Treatment	Phylum	Slope	StdError	tValue	pValue	r2
MIX1	Acidobacteriota	0.218612327	0.129564596	1.687284445	0.125822166	0.630017731
MIX3	Acidobacteriota	0.132113224	0.09523679	1.387207867	0.195515914	0.365950012
MIX2	Acidobacteriota	0.157950706	0.157047237	1.005752847	0.338250279	0.758927945
CONTROL	Acidobacteriota	0.065356045	0.147578497	0.44285615	0.667295766	0.676075813
MIX1	Actinobacteriota	-1.01080048	0.486160691	-2.079148928	0.067358032	0.824715234
MIX2	Actinobacteriota	-0.964061788	0.671851662	-1.434932503	0.181833631	0.694031971
CONTROL	Actinobacteriota	-0.338359828	0.53760339	-0.629385591	0.543207009	0.182174579
MIX3	Actinobacteriota	-0.47475743	0.768270922	-0.617955744	0.550417953	0.681865308
MIX2	Bacteroidota	-2.168759227	0.376226254	-5.76450793	0.000181532	0.950395245
MIX1	Bacteroidota	-1.838906375	0.315411701	-5.83017805	0.000249862	0.866568601
MIX3	Bacteroidota	-2.227690861	0.529749084	-4.205181146	0.001813728	0.930047952
CONTROL	Bacteroidota	-1.701475124	0.526385636	-3.232373776	0.008984742	0.834282598
MIX3	Bdellovibrionota	-0.397058451	0.075321832	-5.271492241	0.000362035	0.796257803
CONTROL	Bdellovibrionota	-0.342357766	0.099378656	-3.444982841	0.006278749	0.677205783
MIX1	Bdellovibrionota	-0.332429442	0.13955404	-2.382083965	0.041087104	0.683305407
MIX2	Bdellovibrionota	-0.179038071	0.088128811	-2.031549834	0.069624045	0.755823225
CONTROL	Chloroflexi	0.401489931	0.119626924	3.356183692	0.007289016	0.691592106
MIX1	Chloroflexi	0.160134661	0.124034318	1.29105124	0.228859956	0.330426435
MIX3	Chloroflexi	0.071743967	0.056762699	1.263928044	0.234923291	0.279477904
MIX2	Chloroflexi	0.053110278	0.102380409	0.518754306	0.615216765	0.412406158
MIX1	Firmicutes	0.133873079	0.047294945	2.830600148	0.019703098	0.527953886
MIX3	Firmicutes	0.160190361	0.123718941	1.294792535	0.2244882	0.537870272
CONTROL	Firmicutes	0.091241342	0.080987979	1.12660352	0.286218794	0.632684759
MIX2	Firmicutes	0.027415408	0.09198306	0.298048442	0.771766776	0.087251264
MIX2	Myxococcota	-0.272665859	0.102480505	-2.660660757	0.023872196	0.557774821
MIX3	Myxococcota	-0.2342872	0.099216921	-2.36136334	0.039860424	0.732493981
CONTROL	Myxococcota	-0.543934791	0.322346731	-1.687421458	0.122414482	0.562050427
MIX1	Myxococcota	-0.390760905	0.268287636	-1.456499862	0.179237986	0.554006918
CONTROL	Patescibacteria	-1.206941026	0.335708617	-3.595204194	0.00488667	0.664939633
MIX3	Patescibacteria	-0.420156192	0.287351223	-1.462169492	0.174398458	0.25065934
MIX2	Patescibacteria	0.870973896	0.811420693	1.073393745	0.308313185	0.500751618
MIX1	Patescibacteria	0.283409743	0.348796535	0.812536005	0.437448322	0.592154427
MIX1	Planctomycetota	4.263727883	0.378086597	11.27711988	1.3048E-06	0.93788109
MIX3	Planctomycetota	5.345546889	0.555781327	9.618075716	2.26868E-06	0.913847849
CONTROL	Planctomycetota	4.326111656	0.457963047	9.446420797	2.67217E-06	0.926345395
MIX2	Planctomycetota	4.381169734	0.79564947	5.506406901	0.000259447	0.850143738
MIX2	Proteobacteria	-3.186565175	0.825113058	-3.861973998	0.003150098	0.889340443
MIX3	Proteobacteria	-2.224491483	0.690131889	-3.223284589	0.009124204	0.512258305
MIX1	Proteobacteria	-2.014288486	0.738261456	-2.728421578	0.023284615	0.791094864
CONTROL	Proteobacteria	-1.723439244	0.650309278	-2.650184001	0.024305378	0.620569404
MIX2	Verrucomicrobiota	1.848810236	0.743047362	2.488145885	0.032091961	0.416614681
MIX3	Verrucomicrobiota	1.283170289	0.848860022	1.511639442	0.161563726	0.275976665
CONTROL	Verrucomicrobiota	1.8359977	1.268675194	1.447177109	0.178458077	0.3268987
MIX1	Verrucomicrobiota	1.343863635	1.037124729	1.295758935	0.22730216	0.601921722

Table S3: Linear regression analysis between the relative abundance of the most abundant fungal phyla and time points [Control = water-drenched plants; MIX1 = plants treated with the four-strains SynCom MIX1; MIX2 = plants treated with the six-strains SynCom MIX2; MIX3 = plants treated with the ten-strains SynCom MIX3].

Treatment	Phylum	Slope	StdError	tValue	pValue	r2
MIX1	Ascomycota	-3.9505	1.417	-2.78794	0.019187616	0.85092737
MIX3	Ascomycota	-3.41923	1.82534	-1.8732	0.090530283	0.2912478
MIX2	Ascomycota	-2.04502	1.16088	-1.76161	0.108620409	0.307888093
CONTROL	Ascomycota	-1.38304	1.42895	-0.96788	0.35593194	0.289654827
MIX3	Basidiomycota	2.19782	1.04491	2.10337	0.061726612	0.435005273
MIX1	Basidiomycota	1.54495	0.74471	2.07456	0.064786321	0.780959888
MIX2	Basidiomycota	1.68241	1.23269	1.36483	0.202226544	0.388810013
CONTROL	Basidiomycota	-0.27259	0.59049	-0.46164	0.654219334	0.326855728
CONTROL	Fungi_phy_Incertae_sedis	-0.95563	0.38591	-2.47629	0.032750377	0.717398108
MIX2	Fungi_phy_Incertae_sedis	0.47953	0.29801	1.60911	0.138670491	0.34630341
MIX3	Fungi_phy_Incertae_sedis	-0.37506	0.25809	-1.45321	0.17681567	0.380341269
MIX1	Fungi_phy_Incertae_sedis	0.01258	0.10472	0.12011	0.906778331	0.41847205
MIX3	Mortierellomycota	-0.18637	0.04762	-3.91363	0.00289617	0.883752122
CONTROL	Mortierellomycota	-0.09447	0.04194	-2.25234	0.047988404	0.472798232
MIX1	Mortierellomycota	-0.18241	0.11794	-1.54667	0.152981233	0.242428974
MIX2	Mortierellomycota	-0.08005	0.14974	-0.53458	0.60462008	0.791849469
CONTROL	Mucoromycota	-0.86985	0.41974	-2.07238	0.06502345	0.353624966
MIX1	Mucoromycota	-0.39205	0.27225	-1.44	0.180429189	0.334063598
MIX3	Mucoromycota	-0.50087	0.65546	-0.76415	0.462429675	0.243187189
MIX2	Mucoromycota	-0.21679	0.33912	-0.63925	0.537026037	0.304524983
MIX3	Rozellomycota	0.24663	0.10059	2.45192	0.034145341	0.585310046
MIX2	Rozellomycota	0.00991	0.00929	1.06568	0.311620865	0.194827818
MIX1	Rozellomycota	0.04254	0.04047	1.05093	0.318023973	0.209711027
CONTROL	Rozellomycota	0.00189	0.01126	0.16803	0.869909947	0.065229204
MIX1	unid. Fungi	2.91621	0.84217	3.46273	0.006094784	0.783444024
CONTROL	unid. Fungi	3.51851	1.02288	3.43981	0.006333409	0.696075354
MIX3	unid. Fungi	2.02397	0.82489	2.45363	0.034045542	0.524741337
MIX2	unid. Fungi	0.15175	0.96975	0.15649	0.878762246	0.2751529

Table S4: Absolute abundance (number of reads) and relative abundance (in brackets) of the ASVs matching the inoculated strains in the rhizosphere of the tomato plants treated with the Syncoms. T0, a few hours after SynCom treatment; T1-4 one to four weeks after SynCom treatment. [Control = water-drenched plants; MIX1 = plants treated with the four-strains SynCom MIX1; MIX2 = plants treated with the six-strains SynCom MIX2; MIX3 = plants treated with the ten-strains SynCom MIX3].

STRAIN	ASV	CONTROL				MIX1				MIX2				MIX3			
		T0	T1	T2	T4	T0	T1	T2	T4	T0	T1	T2	T4	T0	T1	T2	T4
<i>Bacillus velezensis</i> PFE11, PFE42, PSE31B	407	11.67 (0.026)	31.33 (0.0064)	50.00 (0.0104)	8.00 (0.0035)	581.67 (0.2071)	137.67 (0.0349)	226.00 (0.0604)	24.00 (0.0141)	344.67 (0.1213)	107.67 (0.0546)	52.00 (0.0210)	30.67 (0.0144)	383.00 (0.1446)	150.00 (0.0358)	33.00 (0.0172)	19.00 (0.0084)
<i>Glutamicibacter halophytocola</i> PFE44	541	0.00 (0.000)	0.00 (0.000)	44.00 (0.0141)	0.00 (0.000)	579.00 (0.1998)	163.67 (0.0415)	161.33 (0.0436)	28.00 (0.0141)	318.00 (0.1113)	47.33 (0.0239)	23.00 (0.0102)	24.67 (0.0114)	172.00 (0.0654)	71.33 (0.0169)	12.33 (0.0074)	7.00 (0.0027)
<i>Paenarthrobacter ureafaciens</i> S54	1004	80.67 (0.0307)	25.67 (0.0049)	71.67 (0.0217)	10.33 (0.0036)	1.67 (0.0004)	220.00 (0.0557)	42.00 (0.0119)	120.00 (0.0472)	72.00 (0.0258)	51.67 (0.0246)	27.67 (0.0104)	16.00 (0.0086)	125.33 (0.0478)	3.67 (0.0009)	0.67 (0.0003)	15.00 (0.0057)
<i>Pseudomonas salmasensis</i> POE54	2503	0.33 (0.0001)	0.00 (0.000)	0.33 (0.0001)	0.00 (0.000)	0.00 (0.000)	0.00 (0.000)	0.00 (0.000)	0.00 (0.000)	105.67 (0.0374)	1.33 (0.0006)	0.00 (0.000)	37.67 (0.0152)	76.33 (0.0283)	12.00 (0.0033)	3.33 (0.0016)	0.00 (0.000)
<i>Chryseobacterium</i> sp. POE47	2685	0.00 (0.000)	0.00 (0.000)	0.00 (0.000)	0.00 (0.000)	0.00 (0.000)	0.00 (0.000)	0.00 (0.000)	0.00 (0.000)	0.00 (0.000)	18.00 (0.0089)	5.67 (0.0022)	0.00 (0.000)	185.67 (0.0691)	0.00 (0.000)	0.00 (0.000)	3.00 (0.0014)
<i>Paenarthrobacter</i> sp. S56	3124	1.67 (0.0003)	0.00 (0.000)	0.00 (0.000)	0.00 (0.000)	4.67 (0.0017)	1.00 (0.0003)	0.00 (0.000)	1.50 (0.0006)	30.67 (0.0111)	14.67 (0.0069)	9.00 (0.0048)	0.00 (0.000)	94.00 (0.0355)	10.33 (0.0018)	0.00 (0.000)	1.33 (0.0005)
<i>Leclercia</i> sp. S52	2430	4.00 (0.0009)	1.00 (0.0002)	0.33 (0.0001)	0.00 (0.000)	126.67 (0.0479)	3.00 (0.0008)	7.67 (0.0022)	0.00 (0.000)	54.33 (0.0193)	12.33 (0.0075)	0.67 (0.0004)	1.00 (0.0004)	24.67 (0.0090)	5.33 (0.0013)	5.33 (0.0023)	1.00 (0.0003)
<i>Pseudomonas simiae</i> POE78A	6620	3.00 (0.0007)	0.33 (0.0001)	0.00 (0.000)	0.00 (0.000)	0.67 (0.0004)	1.00 (0.0003)	0.00 (0.000)	0.00 (0.000)	13.33 (0.0047)	1.00 (0.0005)	0.67 (0.0004)	0.00 (0.000)	15.67 (0.0059)	3.33 (0.0008)	0.00 (0.000)	0.67 (0.0002)