

**Table S1. Annotation of all sequences in all samples at various taxonomic levels and ASVs.**

Sample	Kingdom	Phylum	Class	Order	Family	Genus	Species	OTU
bacteria	1	37	98	160	261	551	376	10152
fungi	1	4	12	26	42	43	29	4123

**Table S2. Low abundance taxa at the bacterial phylum level in each sampling point (ranked 20th and beyond in terms of abundance among all taxa).**

Phylum	diseased_6h	diseased_24h	diseased_3d	diseased_5d	diseased_11d	diseased_14d	diseased_20d	diseased_70d	diseased_90d
Chloroflexi	0.001847328	7.92E-05	0	8.86E-05	0.000956111	0.022474754	0.010706722	0.00030698	0.000903586
Bdellovibrionota	0.001423408	8.97E-05	0.00021824	0.000408523	0.000198707	0.00150949	0.002047527	0.00122637	0.004152385
Myxococcota	0.000875509	0.000176453	0.00050126	0.000183456	0.000187155	0.0046654	0.003299577	0.002065139	0.000722768
Desulfobacterota	0.000816367	0	0.00014298	0.000294641	0.000125154	0.007999244	0.004134508	0.000659916	0
Deinococcota	0.000941672	5.48E-05	3.01E-05	0.000412012	0.000120768	0.000206709	0.000569523	0.002712669	0.005517733
Armatimonadota	0.000132639	2.96E-05	0	0.000262727	9.02E-05	0.00026734	0.000119772	0.00016769	0.004441327
Verrucomicrobiota	0.000647924	1.76E-05	0.00013544	0.000172337	0.000233673	0.004668615	0.003854182	0.000302018	0
Gemmatimonadota	0.000162227	0	0.00011461	1.36E-05	0.000179544	0.006437728	0.002247704	0.000144357	4.56E-05
Abditibacteriota	0	0	0	0.000265008	0	0.000206214	0.000248099	0.000761593	0.007706625
Nitrospirota	0.000185283	0.000121142	0	0	0.000167395	0.003398942	0.003336911	0.000461437	0.000106341
Planctomycetota	0.000173491	0.000149694	0	0	0.000184721	0.002640515	0.001149031	0.000598049	0
Dependentiae	7.30E-05	0	0.00027841	0	0	0.001311843	0	0	4.19E-05
Fusobacteriota	0.000212044	0	4.31E-05	0	0	0.000672988	0.000136882	0.000134259	0
Elusimicrobiota	7.42E-05	0	6.16E-05	0.000216811	0	0.000412429	0.001121604	0.00052613	7.52E-05
NB1_j	2.10E-05	1.48E-05	0.00014981	0	0	0.000472356	0.000767226	9.17E-05	5.24E-05
Other	0.002059552	0.000670499	0.00028391	0.000177301	0.000345381	0.007332592	0.006029252	0.000424055	4.66E-05

Phylum	healthy_6h	healthy_24h	healthy_3d	healthy_5d	healthy_11d	healthy_14d	healthy_20d	healthy_70d	healthy_90d
Chloroflexi	0	0.001227172	0.00232728	0.001191956	0.000104552	0.00053184	0.00156522	0.012518753	0.000344525
Bdellovibrionota	0.002797073	0.00279135	0.00125571	0.001189554	0.002305952	0.001126752	0.000545918	0.002363565	0.005419279
Myxococcota	0.000974259	0.000864432	0.00294246	0.000745036	0.002203031	0.000886609	0.00103496	0.003291598	0.003931118
Desulfobacterota	0.000317788	0.000452309	0.00055393	0.00012848	0.000510263	0.000785498	0.00040599	0.004112245	7.97E-05
Deinococcota	0.001664372	0.000269592	0.00023312	0.000415346	0.000133156	5.53E-05	0.002441331	0.000353581	0.002527446

Armatimonadota	0.00218155	0.000142794	6.17E-05	0.007105436	0	0.000210821	0	0.000680093	0.001367487
Verrucomicrobiota	0.000806395	0.000178992	0	0	0.000628558	0.000809187	0.001455958	0.001463867	0.000185908
Gemmatimonadota	0.000101128	0.000383618	0.00068134	0.000143317	1.12E-05	0.000816387	0	0.002358205	6.89E-05
Abditibacteriota	0	0.000119947	0	0.001673012	0	0.001122742	0	0	0.001186271
Nitrospirota	0.001647446	0.000271839	0	0	0.00034662	0	0.001026915	0.000120034	0
Planctomycetota	0.000144469	0.000271985	0.0013948	0	0	0	0.000150908	0.000271214	0.00050238
Dependentiae	0.000330994	0.000295464	0.00070998	0	0.001335072	0	0.000669292	0	0
Fusobacteriota	0.00046291	7.89E-05	0.00014903	0.000407285	0.000147635	0.001043643	0.000283162	0	0
Elusimicrobiota	6.02E-05	0.000176965	0.00060542	0	0	0	0.000193065	0.000474978	0
NB1_j	0	0.000256463	0	0	0.000464969	0	0.000271635	0.000948945	0
Other	0.001149294	0.001301437	0.00024068	0.000634199	0.000636018	0	0.00053894	0.002725284	8.86E-05

**Table S3. Low abundance taxa at the bacterial class level in each sampling point (ranked 20th and beyond in terms of abundance among all taxa).**

Class	diseased_6h	diseased_24h	diseased_3d	diseased_5d	diseased_11d	diseased_14d	diseased_20d	diseased_70d	diseased_90d
Bacteroidia	0.01864567	0.01025847	0.00608732	0.00795762	0.0208291	0.06405695	0.06573949	0.01690357	0.02040729
Thermoleophilia	0.00224116	0.00033422	0.00307307	0.00178269	0.00145125	0.03367159	0.01469781	0.0033328	0.00244854
Acidobacteriae	0.00090534	0.00054567	0.00110664	0.00046698	0.00049876	0.01115474	0.00467069	0.0038426	0.00051146
Acidimicrobiia	0.00012819	6.23E-05	0.00083163	0.00013715	0.00010024	0.01028707	0.00454476	0.00045809	0.00017053
Bdellovibrionia	0.00096366	6.23E-05	8.28E-05	0.00021347	7.02E-05	0.0008661	0.00111362	0.00119478	0.00353312
Polyangia	0.00076327	0.00015884	0.00026902	0.00015566	0.00013704	0.0033411	0.00259252	0.00095718	0.00027462
AD3	0	0	0	0	5.01E-05	0.00900325	0.00545299	0	0
Deinococci	0.00094167	5.48E-05	3.01E-05	0.00041201	0.00012077	0.00020671	0.00056952	0.00271267	0.00551773
Fimbriimonadia	0.00013264	2.96E-05	0	0.00026273	9.02E-05	0.00026734	0.00011977	0.00016769	0.00410711
MB_A2_108	0	2.96E-05	0.00016214	0	0.00027279	0.00351208	0.00561934	0	0
Limnochordia	0	0	0	0	0.00037088	0.00563505	0.00759239	0	0
TK10	0	0	0	0	8.02E-05	0.00415309	0.00216775	0	0.00010485
Gemmatimonadetes	0.00013669	0	6.38E-05	1.36E-05	0.00014947	0.00619244	0.00200108	0.00014436	0
Abditibacteria	0	0	0	0.00026501	0	0.00020621	0.0002481	0.00076159	0.00770663
unclassified	0.00075957	0.00018453	0	0	0	0.0008865	0.00202546	0.00043994	0.00353765
Other	0.00963474	0.00184514	0.00231822	0.00170905	0.00277583	0.05118783	0.03235216	0.00628924	0.00291553

Class	healthy_6h	healthy_24h	healthy_3d	healthy_5d	healthy_11d	healthy_14d	healthy_20d	healthy_70d	healthy_90d
Bacteroidia	0.03533521	0.03826801	0.03673052	0.01390706	0.02181452	0.03562631	0.0588622	0.04827124	0.05024898
Thermoleophilia	0.00467204	0.00449386	0.00374468	0.00808934	0.00118318	0.00401224	0.00371092	0.01681338	0.00042995
Acidobacteriae	0.00346688	0.00118795	0.00532147	0.00074287	0.00141542	0.00232793	0.00324489	0.00909536	0.00122928
Acidimicrobiia	0.00090992	0.00124456	0.00019806	0.00059541	0.00102683	0.00152927	0.00039485	0.00682691	0.00059933
Bdellovibrionia	0.00237751	0.00251063	0.00085226	0.00100513	0.00131523	0.00086235	0.00054592	0.00192752	0.00435445
Polyangia	0.00046272	0.00065101	0.00241622	0.0005975	0.00220303	0.00073967	0.00077226	0.00277049	0.00153165
AD3	0	0	0	0	0	0	0	0.0053182	0
Deinococci	0.00166437	0.00026959	0.00023312	0.00041535	0.00013316	5.53E-05	0.00244133	0.00035358	0.00252745

Fimbriimonadia	0.00218155	0.00014279	6.17E-05	0.00710544	0	0.00021082	0	0.00068009	0.00136749
MB_A2_108	0.0003395	0.00146335	0	0.00035049	0	0.0016743	0	0.00200892	0
Limnochordia	0	0	0	0	0	0	0	0.00070079	0
TK10	0	0.00070291	0.00218111	0.0005188	0	0.00029207	0	0.00244491	6.89E-05
Gemmatimonadetes	4.33E-05	0.00026871	0.00068134	0.00014332	0	0.0005721	0	0.00218892	6.89E-05
Abditibacteria	0	0.00011995	0	0.00167301	0	0.00112274	0	0	0.00118627
unclassified	0.00081625	0.00010023	2.09E-05	0	0.000348	0.0002677	0.00040599	0.00098206	0
Other	0.00694707	0.00582844	0.00516027	0.00272639	0.00539086	0.00458926	0.00694975	0.02034713	0.00703531

**Table S4.** Low abundance taxa at the fungal    phylum level in each sampling point  
(ranked 20th and beyond in terms of abundance among all taxa).

name	diseased_6h	diseased_24h	diseased_3d	diseased_5d	diseased_11d	diseased_14d	diseased_20d	diseased_70d	diseased_90d
Ascomycota	0.764599339	0.484791526	0.619890296	0.514730729	0.763981195	0.825546438	0.636687252	0.56601028	0.681654128
Basidiomycota	0.006511188	0.014042673	0.009844644	0.011366461	0.013905674	0.00480353	0.011969271	0.002200219	0.003130325
Mortierellomycota	0	0	0	0	0	0	0	0.000392619	0
Rozellomycota	0.000327577	0	0	0.000938764	0	0	0	0.001359802	0
unclassified	0.307562765	0.501165801	0.37026506	0.472964046	0.222113131	0.169650032	0.351343477	0.43003708	0.532720909

name	healthy_6h	healthy_24h	healthy_3d	healthy_5d	healthy_11d	healthy_14d	healthy_20d	healthy_70d	healthy_90d
Ascomycota	0.889392732	0.796216466	0.78272912	0.742425317	0.861845954	0.686115383	0.489002504	0.417531354	0.512898576
Basidiomycota	0.00528348	0.026763774	0.017504094	0.008165167	0.004040991	0.007038348	0.022849032	0.01352015	0.007508982
Mortierellomycota	0	0.000270022	0	0	0	0	0	0	0
Rozellomycota	0	0	0	0	0	0.000967697	0	0	0
unclassified	0.105323788	0.176749738	0.199766786	0.334933347	0.134113055	0.305878573	0.488148464	0.680375735	0.683134952

**Table S5.** Low abundance taxa at the fungal class level in each sampling point  
(ranked 20th and beyond in terms of abundance among all taxa).

name	diseased_6h	diseased_24h	diseased_3d	diseased_5d	diseased_11d	diseased_14d	diseased_20d	diseased_70d	diseased_90d
Dothideomycetes	0.002848321	0.01943549	0.11593811	0.04400194	0.026355838	0.006158407	0.019237643	0.496687072	0.449142732
Eurotiomycetes	0.058787657	0.04168089	0.12389434	0.02709832	0.162208072	0.040749906	0.151423254	0.031613569	0.000705419
Leotiomycetes	0	0.00359988	0.00011819	0.00131204	0.000199866	0	0.000347737	0	0
Pezizomycetes	0	1.7576E-05	0.00239046	0	0.001977341	0	0.001421916	0.001175965	0
Saccharomycetes	0.001169919	0	0	0	0.001579403	2.88157E-05	0.004597685	0	4.59464E-05
Sordariomycetes	0.003608576	0.00134785	0.02656974	0.03311592	0.003883664	0.004763893	0.02039573	0.009777447	0.010401599
Agaricomycetes	0.00647375	0.00857248	0.00441813	0.00436835	0.01361513	0.001598531	0.010620004	0.002200219	0.00173186
Cystobasidiomycetes	0	0.0022497	0.00336951	0.00024873	0	0	0	0	9.30238E-05
Malasseziomycetes	3.74374E-05	0.00016231	0.00052899	5.7045E-05	0.000290544	0.001620133	0.000321509	0	0
Tremellomycetes	0	0.00305818	0.0006838	0	0	0	0.001027757	0	2.32559E-05
Mortierellomycetes	0	0	0	0	0	0	0	0.000392619	0
Rozellomycotina	0.000327577	0	0	0.00093876	0	0	0	0.001359802	0
unclassified	0.926746762	0.91987565	0.72208873	0.8888589	0.789890143	0.945080314	0.790606765	0.456793308	0.537856163

name	healthy_6h	healthy_24h	healthy_3d	healthy_5d	healthy_11d	healthy_14d	healthy_20d	healthy_70d	healthy_90d
Dothideomycetes	0.003472178	0.02595918	0.04087869	0.04438286	0.029151206	0.008331235	0.003964312	0.194570851	0.483528556
Eurotiomycetes	0.255794104	0.241981	0.49383528	0.26833957	0.032098955	0.062967283	0.092859585	0.056968022	0.002199817
Leotiomycetes	0.000195972	0.00040234	0.00098594	0	0	0.005303312	0.004970021	0	0
Pezizomycetes	0.000923559	0	0.00035067	0	0.003561019	0.000528413	0.002100875	0.002881958	7.04442E-05
Saccharomycetes	0.000576587	0	0.00031091	9.2539E-05	0	0.000779643	0.00013733	0.002000263	8.80553E-05
Sordariomycetes	0.004413693	0.00783718	0.00222537	0.008729	0	0.022805715	0.018874151	0.004362056	0.00453967
Agaricomycetes	0.005217147	0.02611444	0.01509592	0.00210531	0.002553168	0.005908241	0.019486455	0.012322624	0.006823802
Cystobasidiomycetes	0	0	0	0.00591164	0	0	0	0	0
Malasseziomycetes	6.6333E-05	0.00019423	8.0544E-05	3.365E-05	9.75622E-05	7.07204E-05	0.001522205	0	0
Tremellomycetes	0	0	0.00186515	0	0	0.001059387	0.000908191	0	3.21897E-05
Mortierellomycetes	0	0.00027002	0	0	0	0	0	0	0
Rozellomycotina	0	0	0	0	0	0.000967697	0	0	0
unclassified	0.729340428	0.69724161	0.44437153	0.67040543	0.93253809	0.891278354	0.855176875	0.726894225	0.502717466

**Table S6.** Unweighted-permanova data analysis was conducted for fungal  
bacterial communities in four periods. Specific evaluation parameters were shown  
in the table.

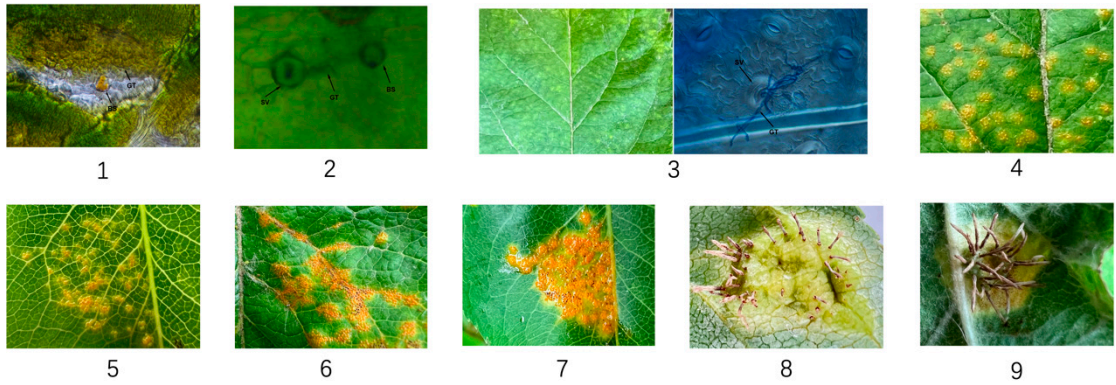
Healthy group-bacteria						
Group 1	Group 2	Sample size	Permutations	pseudo-F	p-value	q-value
A	B	12	999	1.19379719	0.146	0.146
A	C	12	999	1.90947393	0.002	0.006
A	D	12	999	2.26252768	0.001	0.006
B	C	12	999	1.39293589	0.086	0.1032
B	D	12	999	1.77209408	0.004	0.0075
C	D	12	999	1.61386405	0.005	0.0075

Diseased group-bacteria						
Group 1	Group 2	Sample size	Permutations	pseudo-F	p-value	q-value
A	B	12	999	1.53413578	0.035	0.035
A	C	12	999	2.23165862	0.018	0.0288
A	D	12	999	1.68385656	0.011	0.0288
B	C	12	999	2.2735224	0.023	0.0288
B	D	12	999	1.40173125	0.024	0.0288
C	D	12	999	2.39046314	0.008	0.0288

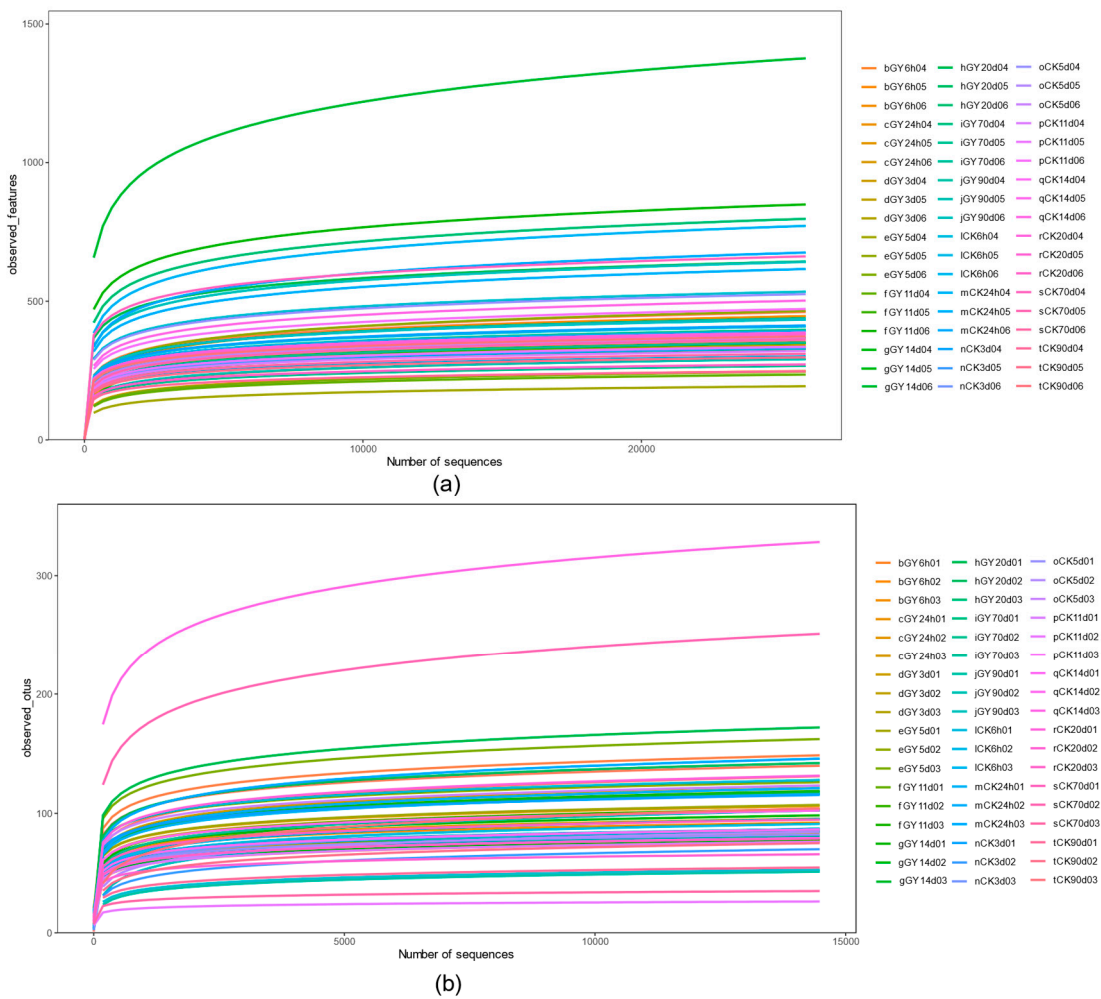
Healthy group-fungi						
Group 1	Group 2	Sample size	Permutations	pseudo-F	p-value	q-value
A	B	12	999	1.05545888	0.326	0.489
A	C	12	999	0.77693211	0.906	0.906
A	D	12	999	2.37783951	0.005	0.012
B	C	12	999	1.00237994	0.421	0.5052
B	D	12	999	2.14025578	0.004	0.012
C	D	12	999	2.05297857	0.006	0.012

Diseased group-fungi						
Group 1	Group 2	Sample size	Permutations	pseudo-F	p-value	q-value
A	B	12	999	0.87567365	0.75	0.75
A	C	12	999	1.56824199	0.002	0.006
A	D	12	999	2.06524003	0.009	0.0135
B	C	12	999	1.51759079	0.004	0.008
B	D	12	999	1.70784349	0.015	0.018
C	D	12	999	2.80369598	0.002	0.006

**Figure S1** After being infected by *Gymnosporangium Yamadae*, apple leaves undergo a series of pathological changes both at the micro and macro level ( Real shot pictures).



**Figure S2** Rarefaction curves based on OTUs.

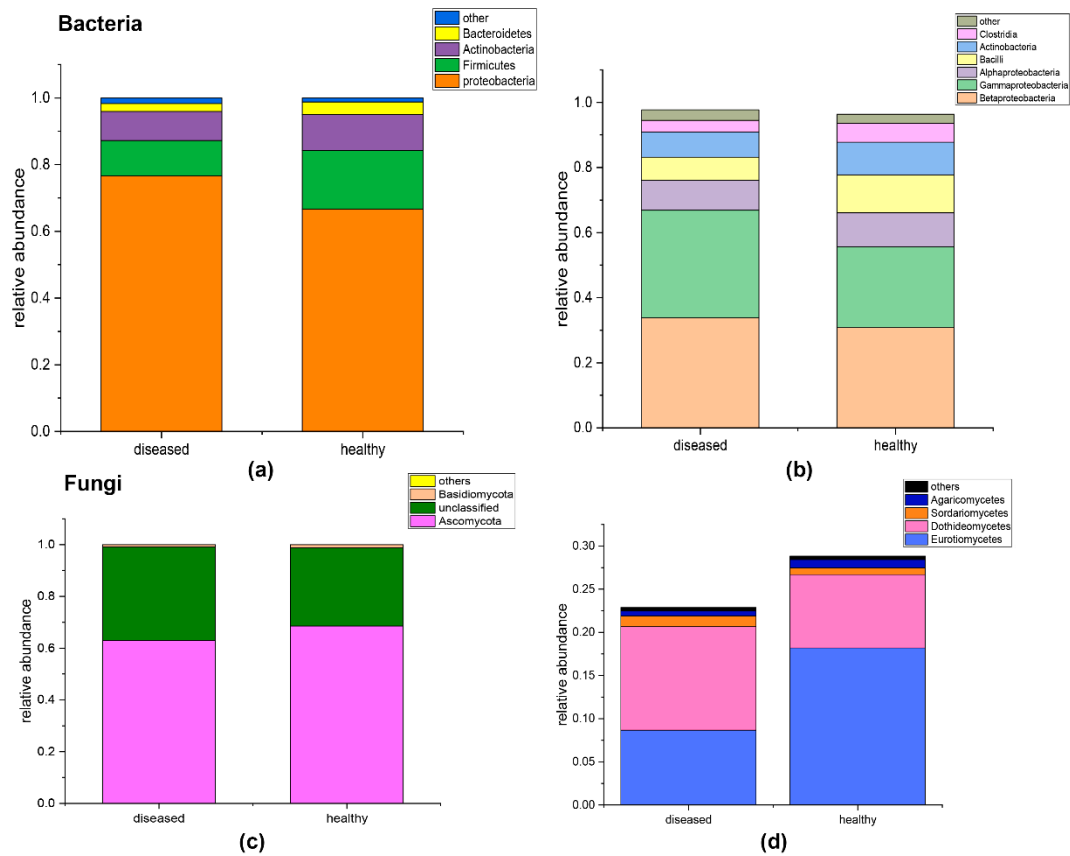


**Figure S3** Histogram of sequence annotation degree of each sample at each

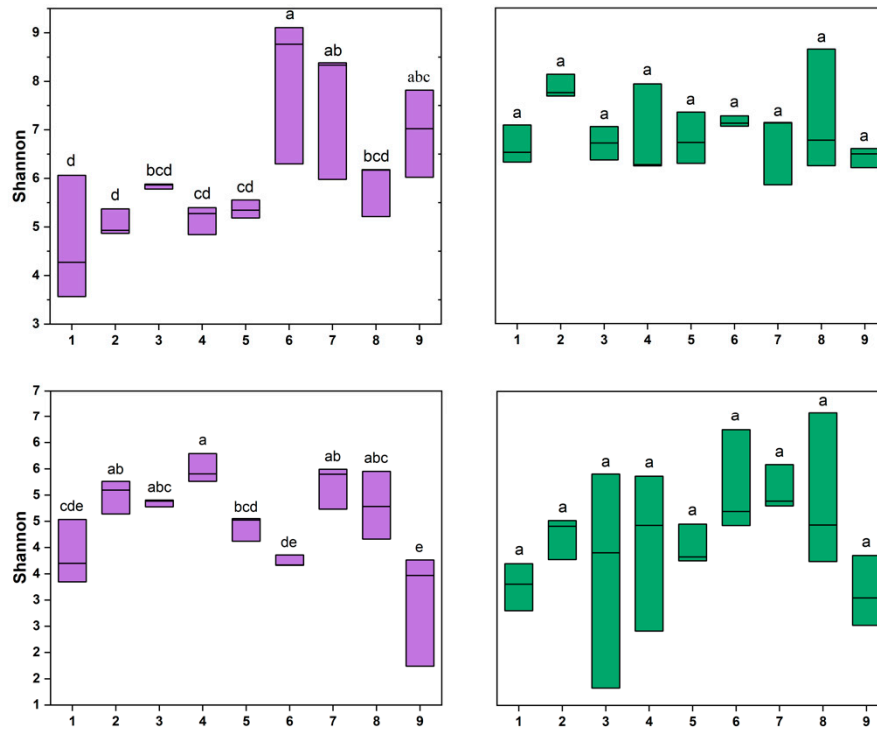
classification level. The X-axis (Sample Name) represents the sample name during sequencing, and the Y-axis (Sequence Number Percent) indicates the proportion of annotated sequences at each level compared to the total annotated data. The color order of the bars from top to bottom corresponds to the color order in the legend on the right. The maximum value at each taxonomic level is 1, representing 100% of the sequences that have been annotated at least at that level.



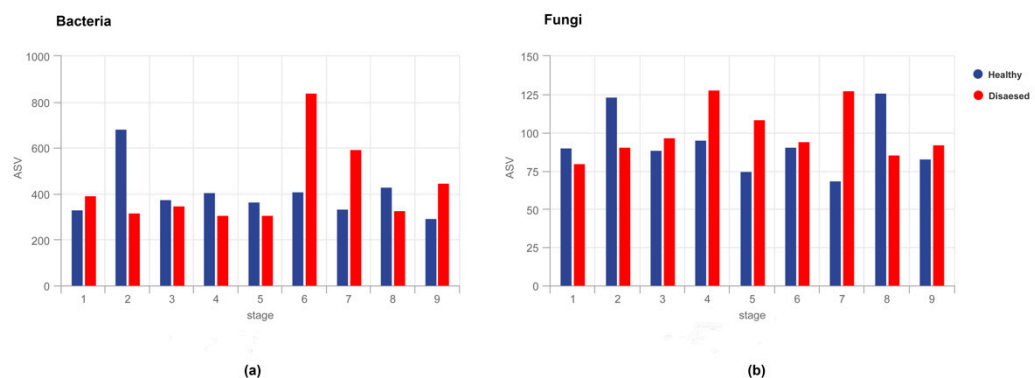
**Figure S4 Histogram of the relative distribution of diseased and healthy samples at phyla and class levels.**



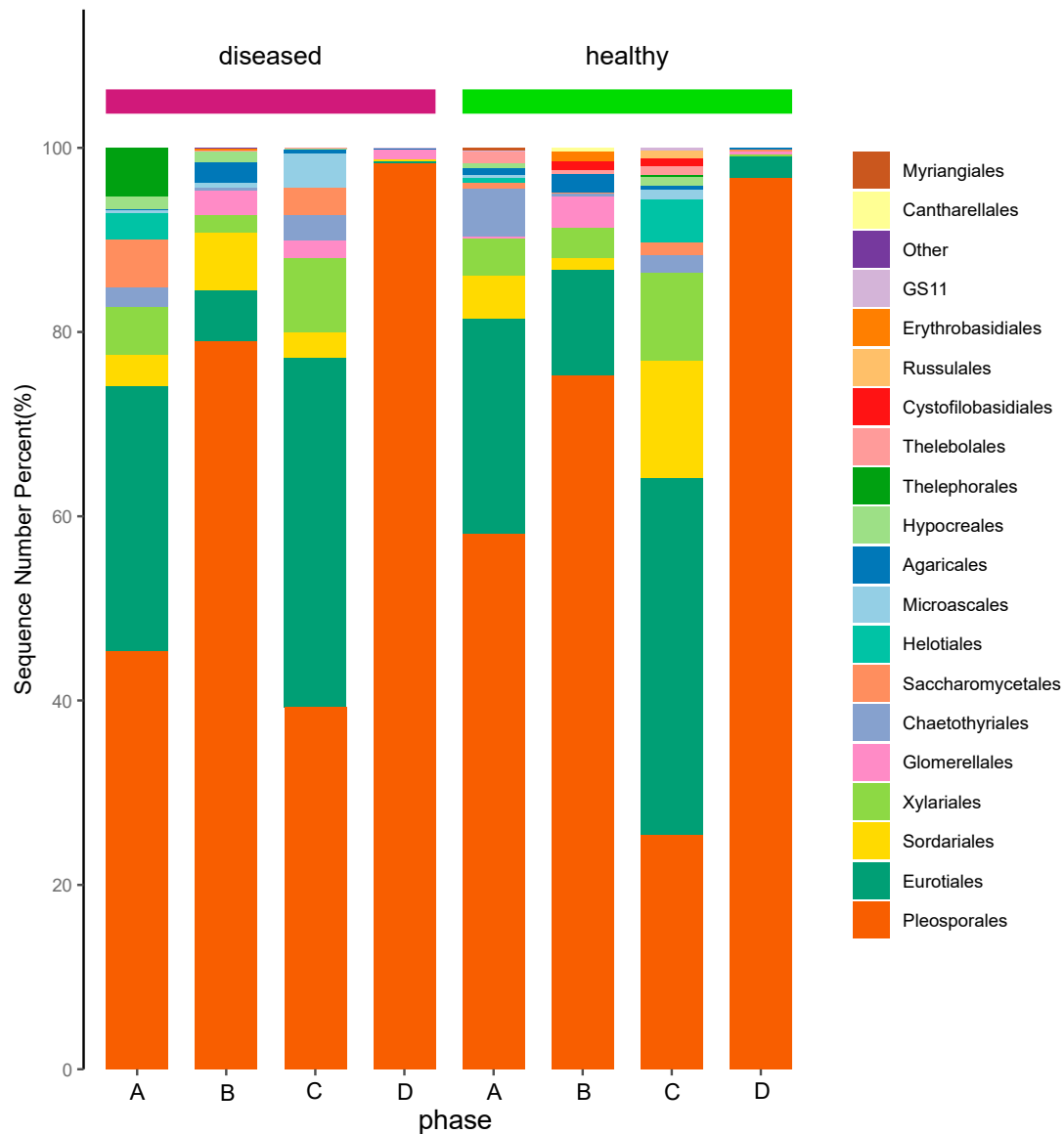
**Figure S5** Changes in alpha diversity (indicated by Shannon index) of endophytic bacteria and fungi communities in healthy apple leaves and diseased leaves at 9 stages of infection were compared. Different letters represent statistically significant differences between stages, as determined by one-way Anova with *post hoc* Tukey's HSD test ( $P < 0.05$ ). The boxplots show the estimated range between the 25th and 75th percentiles, as well as the median, minimum, and maximum values of the observed data in each dataset.



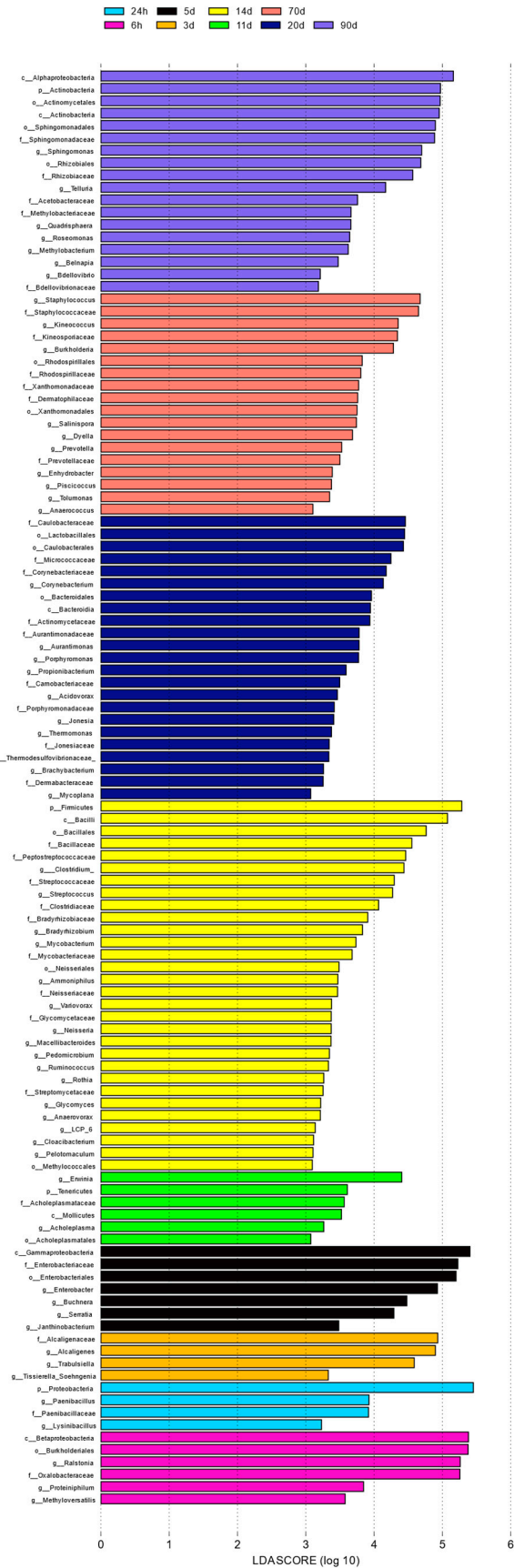
**Figure S6** Bar chart of the number of OTUs at each stage for healthy samples and disease samples.



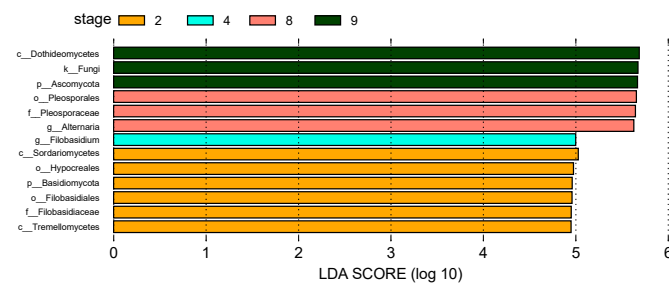
**Figure S7** Taxonomic compositions of the leaves endophytic fungal community at the order level of the diseased and healthy groups.



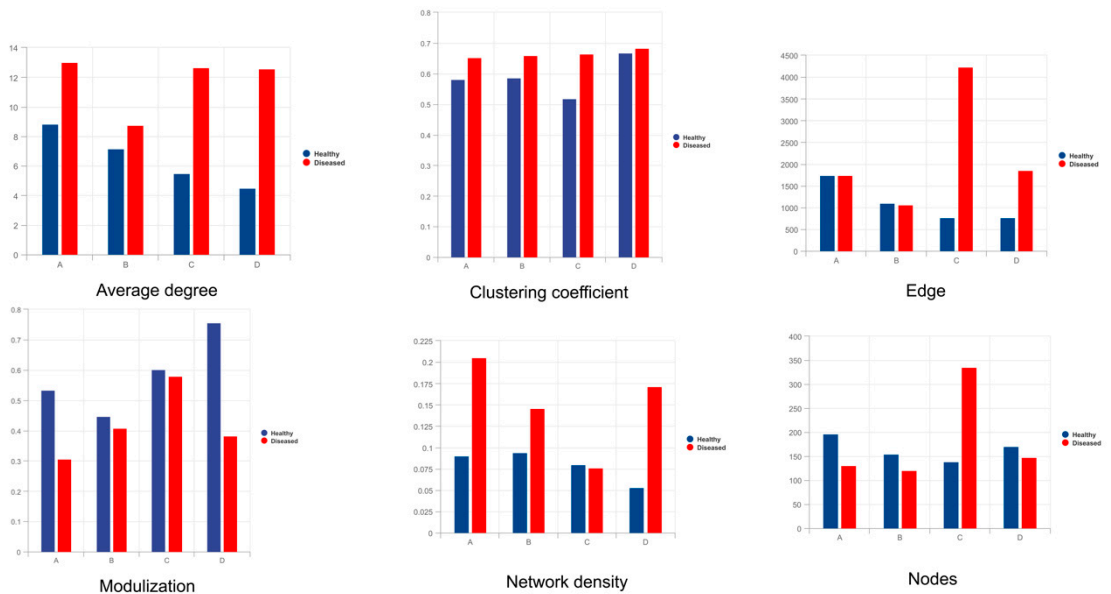
**Figure S8** LEfSe Analysis LDA Barplot for endophytic bacteria. Each horizontal bar represents a species, and the length of the bar corresponds to the LDA value. A higher LDA value indicates a larger difference. The color of the bar corresponds to which group the species is a biomarker for, indicating higher abundance of the biomarker in the corresponding group.



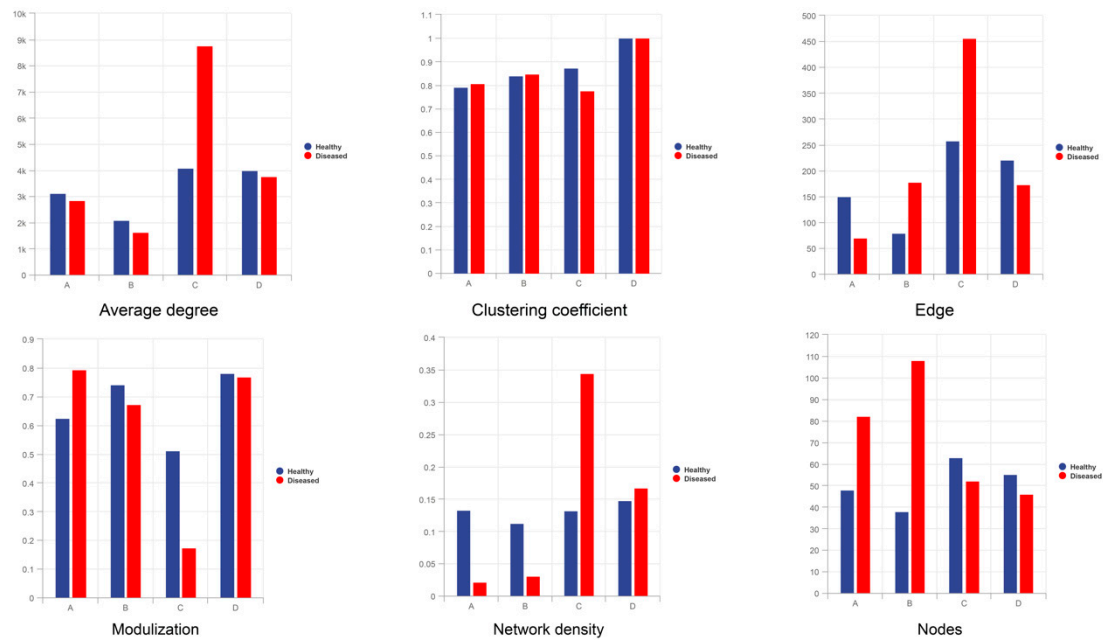
**Figure S9** LEfSe Analysis LDA Barplot for endophytic fungi. Each horizontal bar represents a species, and the length of the bar corresponds to the LDA value. A higher LDA value indicates a larger difference. The color of the bar corresponds to which group the species is a biomarker for, indicating higher abundance of the biomarker in the corresponding group.



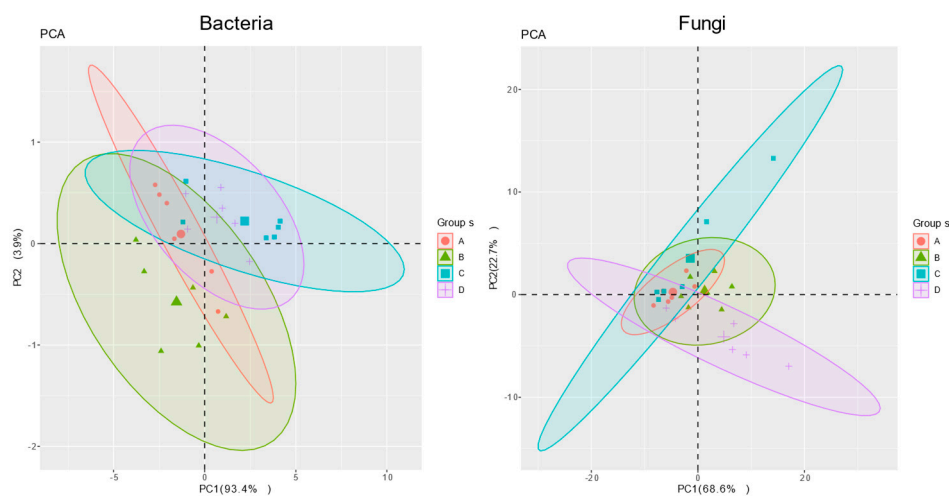
**Figure S10** Relevant parameters of endophytic bacteria community co-occurrence network at different stages.



**Figure S11** Relevant parameters of endophytic fungi community co-occurrence network at different stages.



**Figure S12** The functional enrichment of endophytic bacterial and fungal sequences on MetaCyc pathway in healthy and diseased apple leaves was demonstrated by PCA analysis.



**Figure S13** Functional categories in which fungal community sequences are significantly enriched at various phases. Different letters indicate statistically significant differences among stages.

