

**Supplementary tables and figures:****Supplementary Table S1****Supplementary Table S1** Statistics of 16S rDNA amplicon sequences in grapevine samples of variety Cabernet sauvignon

ample	Raw_Tags	Raw_Bases	Valid_Tags	Valid_Bases	Valid%	Q20%	Q30%	GC%
C1	85982	42.99M	83455	20.84M	97.06	98.52	95.17	54.79
C2	83579	41.79M	80653	20.24M	96.49	99.24	97.03	53.85
C3uS	83906	41.95M	78692	19.67M	93.72	96.33	90.15	55.01
C3uL	84046	42.02M	81829	20.53M	97.37	98.93	96.30	54.64
C3uS	84220	42.11M	81633	20.41M	96.92	99.11	96.64	54.73
C3lL	81040	40.52M	79013	19.82M	97.50	99.27	97.08	54.65
C3R	85681	42.84M	79813	20.03M	93.14	98.93	96.06	53.77
C4uS	85178	42.59M	82764	20.64M	97.17	99.08	96.59	54.68
C4uL	83941	41.97M	81320	20.33M	96.87	97.75	93.41	54.81
C4mS	85429	42.71M	82883	20.69M	97.02	98.74	95.59	54.10
C4mL	82863	41.43M	80493	20.13M	97.14	98.95	96.17	54.72
C4lS	80663	40.33M	77418	19.35M	95.98	97.32	92.39	54.22
C4lL	85159	42.58M	83217	20.87M	97.72	99.58	98.17	54.67
C4R	85013	42.51M	79074	19.78M	93.03	97.53	92.84	53.99

**Supplementary Table S2****Supplementary Table S2.** Statistics of 16S rDNA amplicon sequences in grapevine samples of variety Rose honey

Sample	Raw_Tags	Raw_Bases	Valid_Tags	Valid_Bases	Valid%	Q20%	Q30%	GC%
R1	84506	42.25M	82055	20.51M	97.11	98.89	95.97	53.83
R2	83514	41.76M	80717	20.21M	96.64	98.69	95.44	54.18
R3uS	82698	41.35M	80343	20.07M	97.15	99.10	96.66	54.75
R3uL	84642	42.32M	80051	20.09M	94.59	96.05	89.16	54.85
R3uS	86034	43.02M	83535	20.87M	97.10	99.19	96.81	54.75
R3lL	83342	41.67M	80687	20.24M	96.82	98.19	94.17	54.56
R3R	84861	42.43M	80417	20.18M	94.77	98.87	96.00	53.15
R4uS	83702	41.85M	81304	20.30M	97.12	98.81	95.81	54.78
R4uL	84058	42.03M	81661	20.42M	97.15	99.01	96.36	54.66
R4mS	83636	41.82M	80474	20.10M	96.27	96.80	91.13	55.04
R4mL	85474	42.74M	82893	20.74M	96.98	98.69	95.50	54.74
R4lS	83146	41.57M	80733	20.17M	97.10	99.12	96.79	54.85
R4lL	81802	40.90M	78825	19.72M	96.35	97.14	91.81	54.89
R4R	84367	42.18M	74283	18.58M	88.01	98.80	95.71	53.55

**Supplementary Table S3****Supplementary Table S3.** Statistics of ITS amplicon sequences in grapevine samples of variety Cabernet sauvignon

Sample	Raw_Tags	Raw_Bases	Valid_Tags	Valid_Bases	Valid%	Q20%	Q30%	GC%
C1	81273	40.64M	80704	24.88M	99.30	99.63	98.54	71.38
C2	84008	42.00M	83024	22.21M	98.84	99.79	99.18	62.53
C3uS	84666	42.34M	82424	21.52M	97.37	99.84	99.36	59.20
C3uL	84543	42.27M	83132	25.04M	98.34	99.10	96.80	69.99
C3uS	82973	41.48M	81999	20.59M	98.83	99.88	99.50	56.45
C3lL	46984	23.49M	46348	11.64M	97.30	98.44	96.06	61.54
C3R	81593	40.80M	79087	24.12M	96.93	99.60	98.34	39.07
C4uS	83270	41.63M	82595	22.57M	99.19	99.80	99.21	61.90
C4uL	84283	42.14M	83530	21.86M	99.10	99.80	99.21	57.43
C4mS	86588	43.30M	86055	21.03M	99.39	99.93	99.70	57.92
C4mL	83770	41.88M	82859	22.81M	98.92	99.61	98.51	58.19
C4lS	86675	43.34M	86001	22.89M	99.23	99.72	98.85	62.78
C4lL	82122	41.06M	81717	25.44M	99.51	99.62	98.44	72.35
C4R	84433	42.21M	83362	24.44M	98.74	99.72	98.80	44.87

**Supplementary Table S4****Supplementary Table S4.** Statistics of ITS amplicon sequences in grapevine samples of variety  
Rose honey

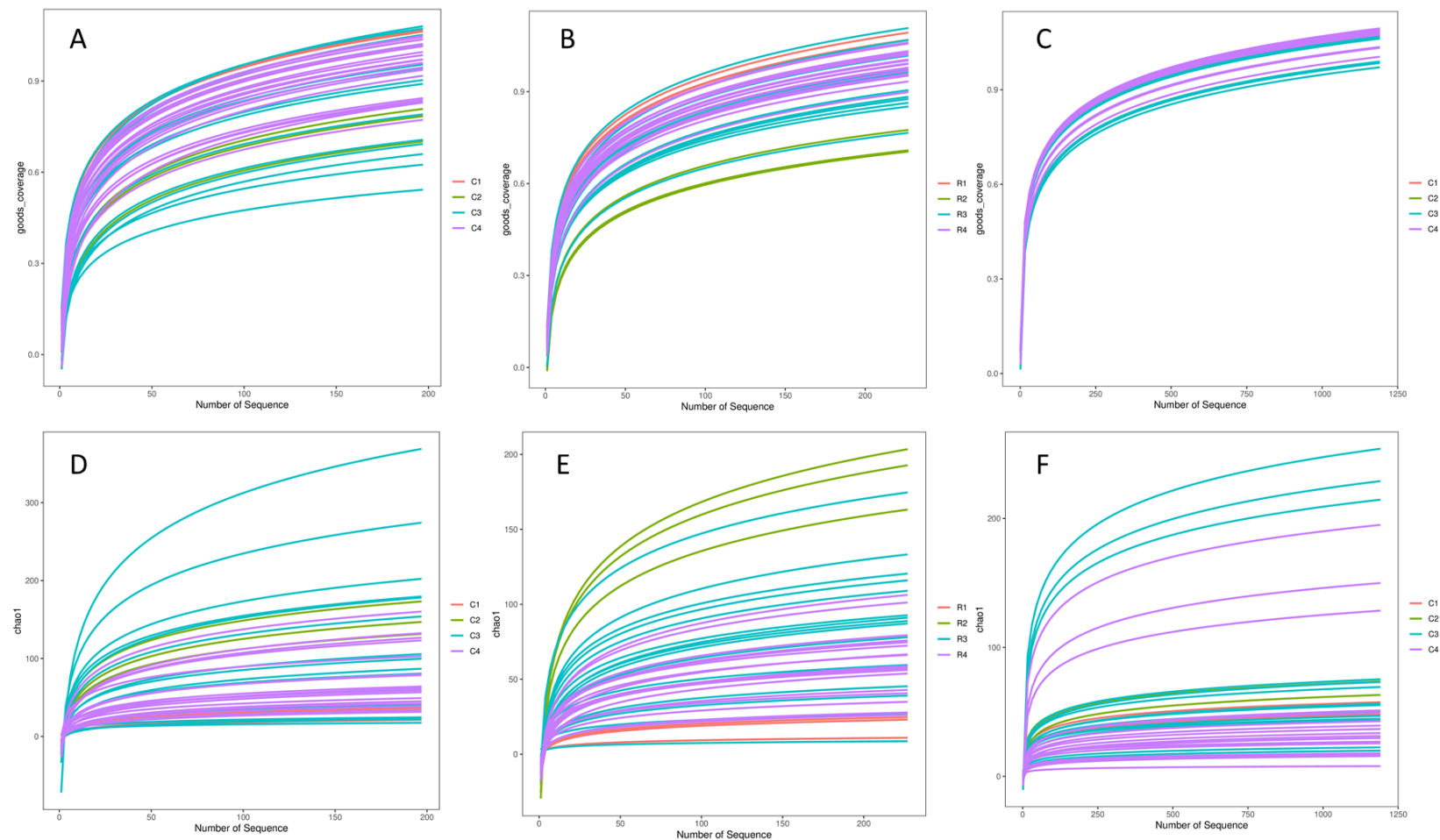
Sample	Raw_Tags	Raw_Bases	Valid_Tags	Valid_Bases	Valid%	Q20%	Q30%	GC%
R1	84726	42.36M	84012	25.94M	99.16	99.35	97.43	68.77
R2	83699	41.85M	78826	20.96M	94.23	99.76	99.18	59.89
R3uS	84029	42.01M	83014	21.03M	98.78	99.88	99.50	58.35
R3uL	83468	41.73M	82690	25.96M	99.07	98.96	96.57	72.52
R3uS	84389	42.20M	83166	20.65M	98.55	99.87	99.41	56.98
R3lL	83388	41.69M	82312	22.39M	98.71	99.71	98.79	61.31
R3R	86388	43.19M	84956	25.18M	98.34	99.33	97.49	42.81
R4uS	82128	41.06M	81434	22.57M	99.15	99.73	98.93	59.51
R4uL	84801	42.40M	84191	23.20M	99.28	99.79	99.18	57.94
R4mS	82977	41.49M	82120	22.79M	98.98	99.75	99.04	58.46
R4mL	85019	42.51M	84525	23.43M	99.42	99.81	99.28	57.94
R4lS	83966	41.98M	83422	22.29M	99.35	99.70	98.78	62.61
R4lL	81195	40.60M	80695	22.30M	99.38	99.78	99.15	58.00
R4R	81504	40.75M	79939	23.81M	98.07	99.59	98.45	41.17

# Supplementary Table S5

**Supplementary Table S5.** List the most 5 dominant (top 5) distribution endophytic ASVs in different staged grapevines.

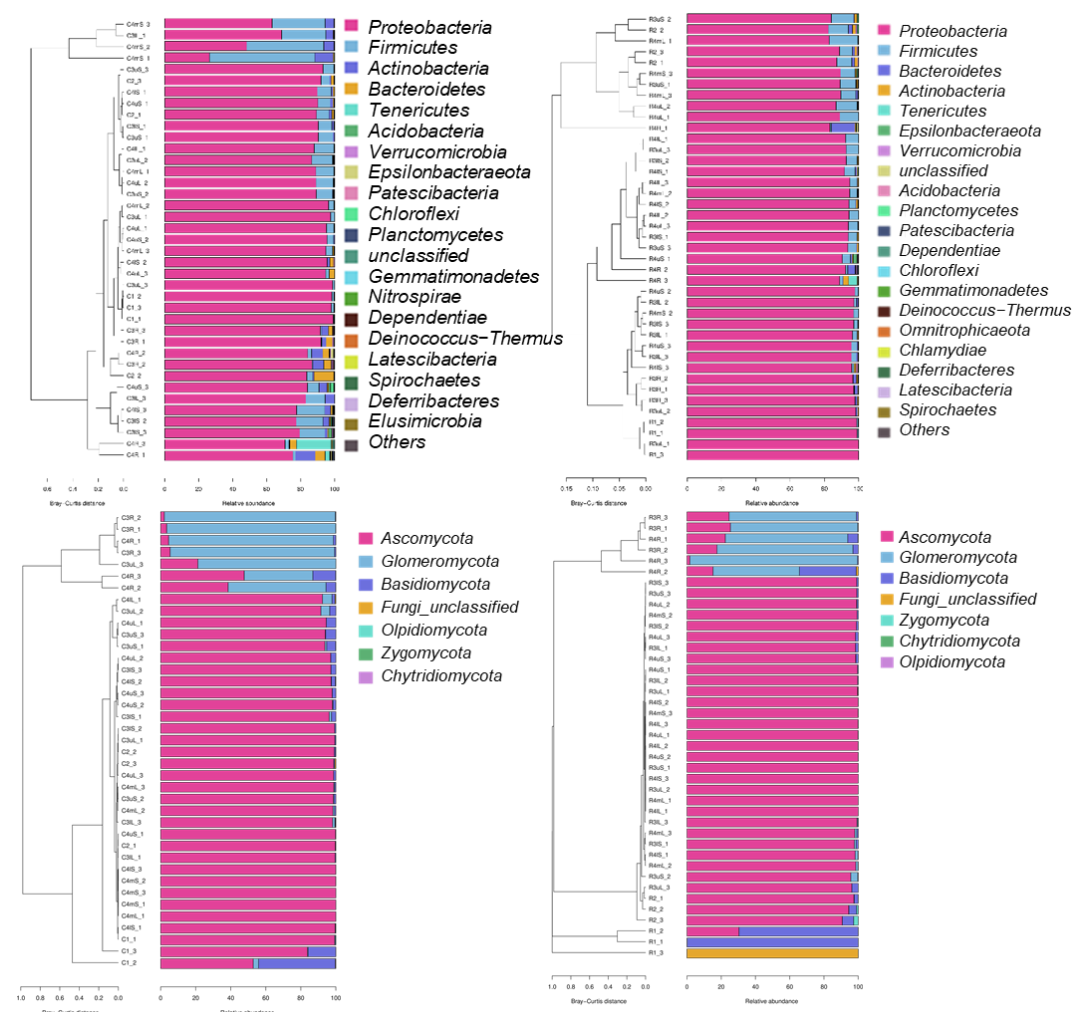
Taxonomy	ASV ID	Genus
<b>Bacterial</b>	Bc01/Br02	<i>Cupriavidus</i>
	Bc02/Br03	<i>Ralstonia</i>
	Bc03/Br04	<i>Sphingomonas</i>
	Bc04/Br11	<i>Ralstonia</i>
	Bc05/Br10	<i>Sphingomonas</i>
	Bc08/Br08	<i>Bradyrhizobium</i>
	Bc32/Br48	<i>Novosphingobium</i>
	Bc59	<i>Burkholderia</i>
	Bc57/Br26	<i>Aquabacterium</i>
	Bc74/Br68	<i>Cellvibrio</i>
	Bc2-5	<i>Ohtaekwangia</i>
	Bc3-4,	Burkholderiales_unclassified
	Bc2-23	<i>Rhizobium</i>
	Bc2-123	<i>Rhizobium</i>
	Bc98	<i>Lactococcus</i>
	Bc12/Br01,	<i>Acinetobacter</i>
	Br05	<i>Acinetobacter</i>
	Br52	<i>Pseudomonas</i>
	Bc43/Br22	<i>Methylophilus</i>
	Br2-20	<i>Rhizobium</i>
<b>Fungal</b>	Fc01	<i>Trichomeriaceae_un</i>
	Fc02/Fr2-15	<i>Davidiella</i>
	Fc03	<i>Malassezia</i>
	Fc04	<i>Didymella</i>
	Fc05	Hypocreales_Incertae_sedis_unclassified
	Fc07/Fr2-1	<i>Sarocladium</i>
	Fc22	<i>Eurotium</i>
	Fc12	<i>Gibberella</i>
	Fc15	<i>Acremonium</i>
	Fc09/Fr2-2	<i>Aspergillus</i>
	Fc10/Fr15	<i>Davidiella</i>
	Fc34	<i>Davidiella</i>
	Fc16/Fr05	<i>Cladosporium</i>
	Fc49	<i>Pilidiella</i>
	Fc20/Fr2-82	<i>Erysiphe</i>
	Fc2-126	<i>Stachybotrys</i>
	Fc3-256	<i>Fusarium</i>
	Fr01/Fc98	<i>Malassezia</i>
	Fr02	<i>Schizophyllum</i>
	Fr03	<i>Coprinellus</i>
	Fr04	<i>Exidia</i>
	Fr2-3/Fc18	<i>Penicillium</i>
	Fr2-4/Fc17	<i>Penicillium</i>
	Fr2-28/Fc34	<i>Davidiella</i>
	Fr2-148/Fc61	<i>Clitopilus</i>

**Supplementary Figure S1**



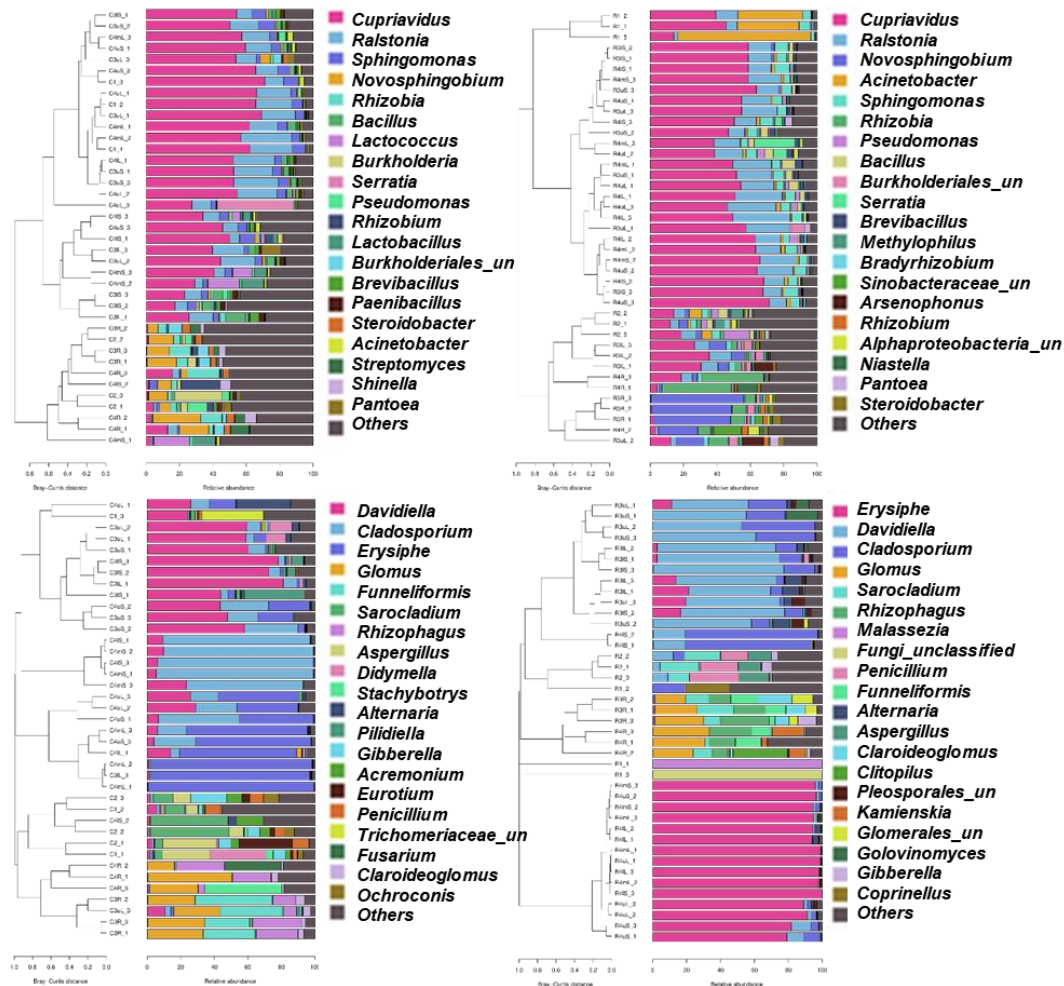
**Supplementary Figure S1 The Goods coverage (A-C) and Chao 1 (D-E) rarefaction curves for 16r rRNA (A, B, D and E) and ITS DNA sequencing in grapevine samples of the cultivar CS (A, C, D, E) and RH (B and E).**

**Supplementary Figure S2**



**Supplementary Figure S2. The cluster and composition of the top 20 dominant endophytic phyla in different-staged and compartmentalized grapevines.** C1-C2 and R1-R2 separately represent the stage 1 to stage 2 grapevine samples of the two cultivars. Grapevines of stages 3 and 4 of the both grapevine cultivars were further divided sectionally into stems (C3S, C4S, R3S and R4S), leaves (C3L, C4L, R3L and R4L) and roots (C3R, C4R, R3R and R4R) as summarized in Table S1. Replicates of all samples are shown in the plots.

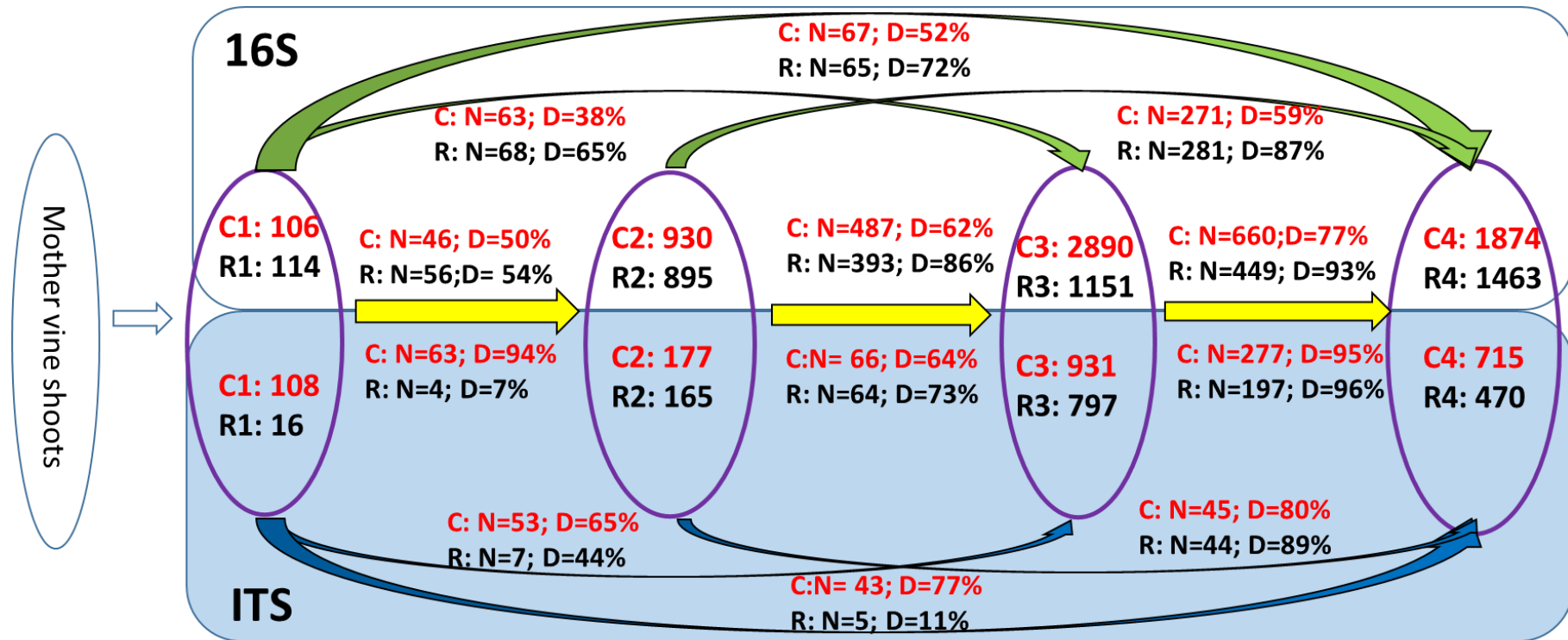
**Supplementary Figure S3**



**Supplementary Figure S3. The cluster and composition of the top 20 dominant endophytic genera in different-staged and compartmentalized grapevines.** C1-C2 and R1-R2 separately represent the stage 1 to stage 2 grapevines of the two cultivars. Grapevines of stages 3 and 4 of the both grapevine cultivars were further divided sectionally into stems (C3S, C4S, R3S and R4S), leaves (C3L, C4L, R3L and R4L) and roots (C3R, C4R, R3R and R4R) as summarized in Supplementary Table S1. Replicates of all samples are shown in the plots.



Supplementary Figure S4



**Supplementary Figure S4. Dynamic changes in endophytic ASV numbers and relative abundances along staged grapevines.** The succeeded numbers (N) of endophytic ASVs (16S: bacterial; ITS: fungal) and the relative abundances (D) in different staged grapevines are listed in the figure. The total detected numbers of endophytic ASVs in different staged vines and variants are listed accordingly inside the ellipses. C1-C4 and R1-R4 separately represent the stage 1 to stage 4 grapevines of the two cultivars Cabernet sauvignon (CS) and rose honey (RH).