

Table S1. Summary of analyzed metagenome shotgun sequence information.

Sample	Season	No. of reads	Avg. length	No. of reads after trim	% Trimmed	Avg. length after trim	No. of features
0h-4-2_S1	Summer	10,829,594	246.3	10,811,704	99.83	234.9	210
6-CJ-R1-2_S2	Summer	9,182,086	260.7	9,175,594	99.93	242.1	315
6-CJ-R2-2_S3	Summer	8,971,656	255.1	8,963,927	99.91	241.1	262
A-0h-2-1_S4	Summer	7,964,866	245.7	7,954,126	99.87	232.6	295
CJ01-R2_S1	Winter	7,981,914	260.3	7,978,013	99.95	245	325
CJ01-R6_S2	Winter	9,582,472	254.7	9,576,491	99.94	243.8	328
CJ02-M13_S3	Winter	10,680,326	258.2	10,675,424	99.95	244.8	162
CJ02-M14_S4	Winter	9,517,026	257.7	9,511,638	99.94	247.3	188

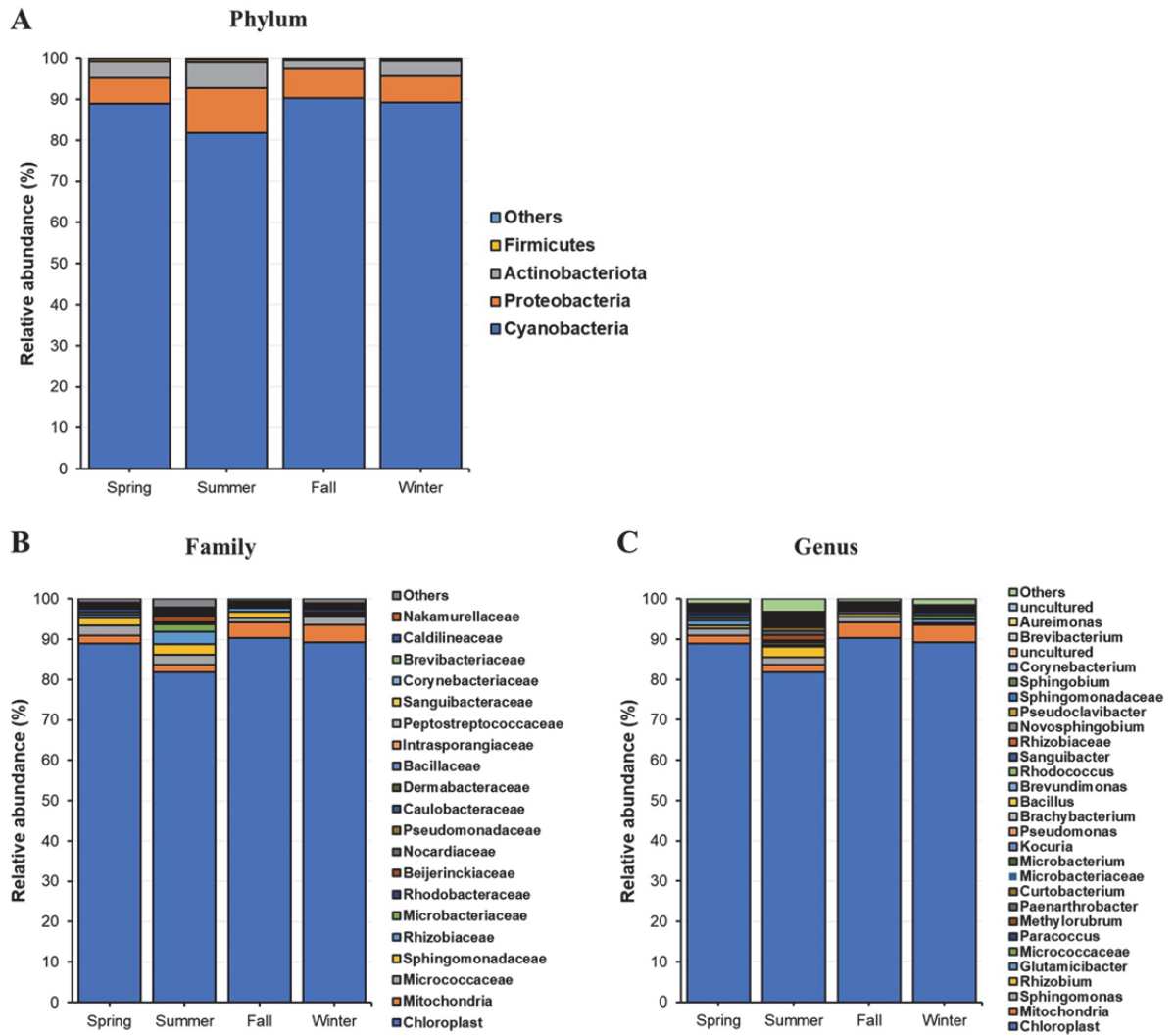
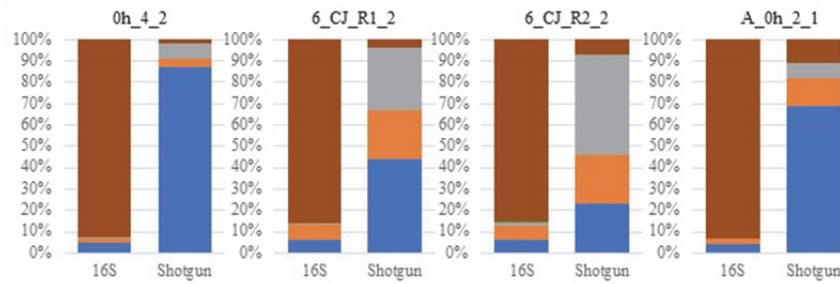


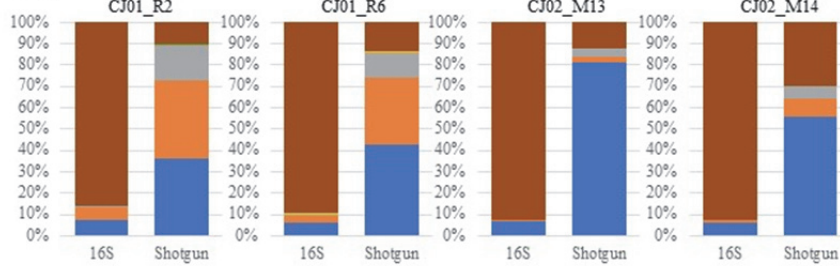
Fig. S1. Relative abundance of various bacterial taxa at the **A** phylum, **B** family, and **C** genus levels in the lettuce samples collected during all four seasons.

A. 16S (all) vs. Shotgun

Summer

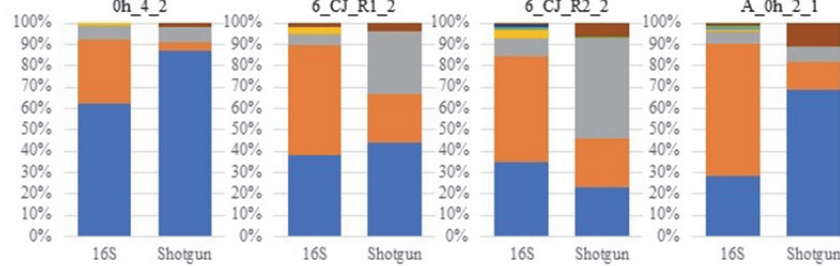


Winter



B. 16S (without Chloroplast, Mitochondria) vs. Shotgun

Summer



Winter

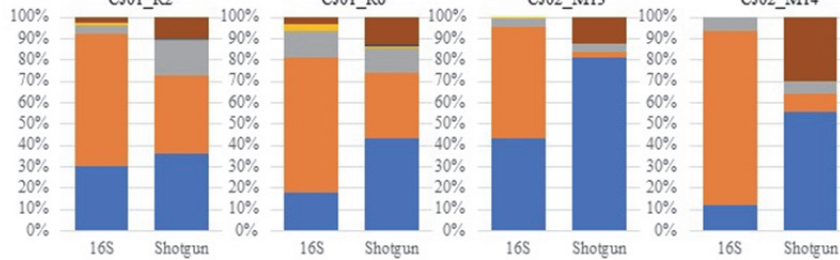


Fig. S2. Comparison of bacterial taxa plots for the same sample. (A) 16S rRNA gene-based sequencing (non-filtered) vs. metagenome shotgun sequencing (B) 16S rRNA gene-based sequencing (without chloroplast-related reads) vs. metagenome shotgun sequencing

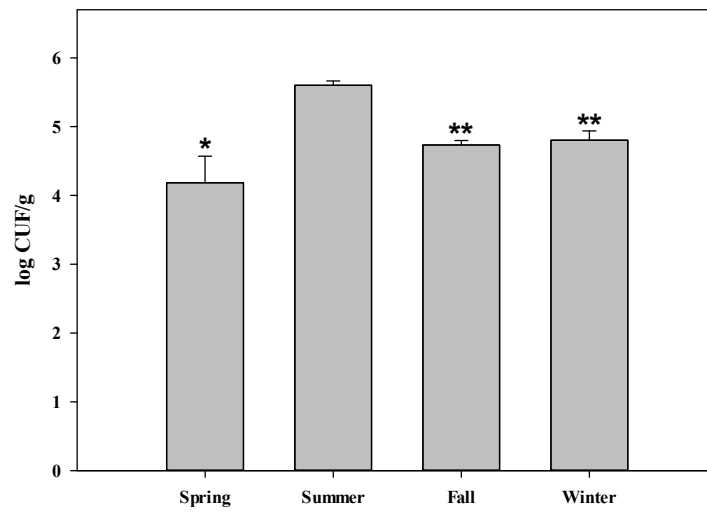


Fig. S3. Cell counts of total aerobic bacteria in lettuce at four seasons. The lettuce samples are as follows: Error bars represent the standard error among the three replicates. *, $p < 0.05$; **, $p < 0.01$ compared with the lettuce of summer group using the Mann-Whitney U test.

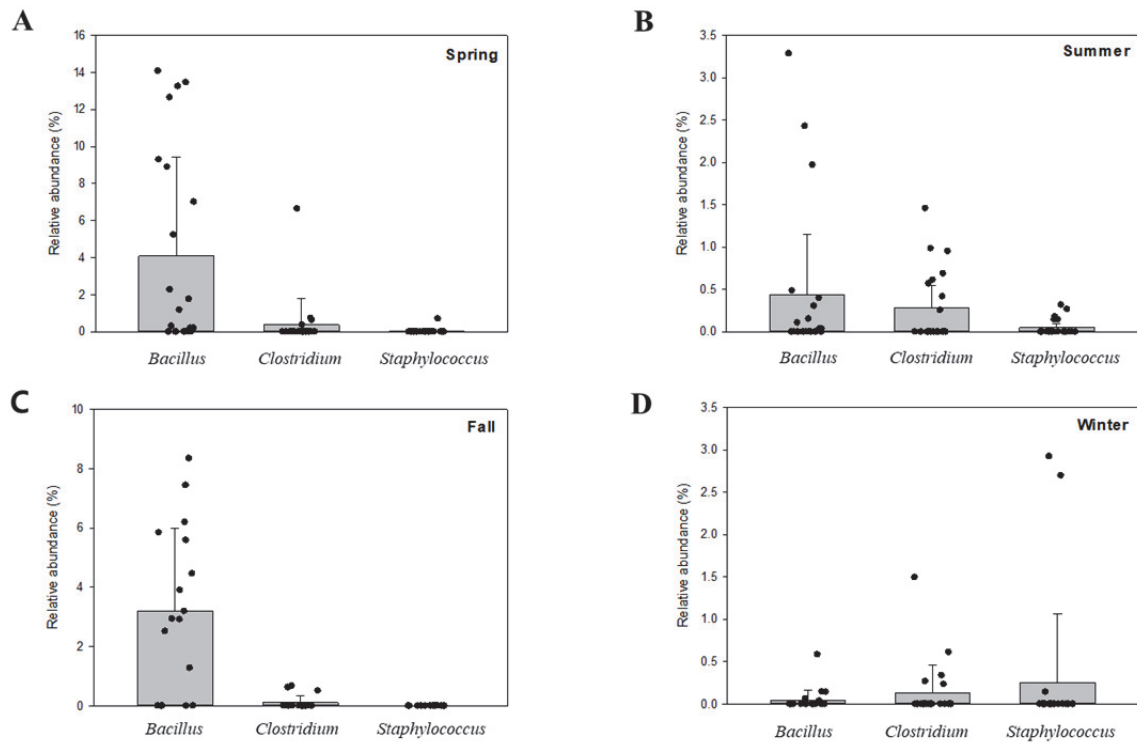


Fig. S4. Bacterial monitoring for potential pathogens in the lettuce samples harvested during different seasons. Three genera of potential foodborne pathogens (*Bacillus*, *Clostridium*, and *Staphylococcus*) were monitored in lettuce samples in **A** spring, **B** summer, **C** fall, and **D** winter.

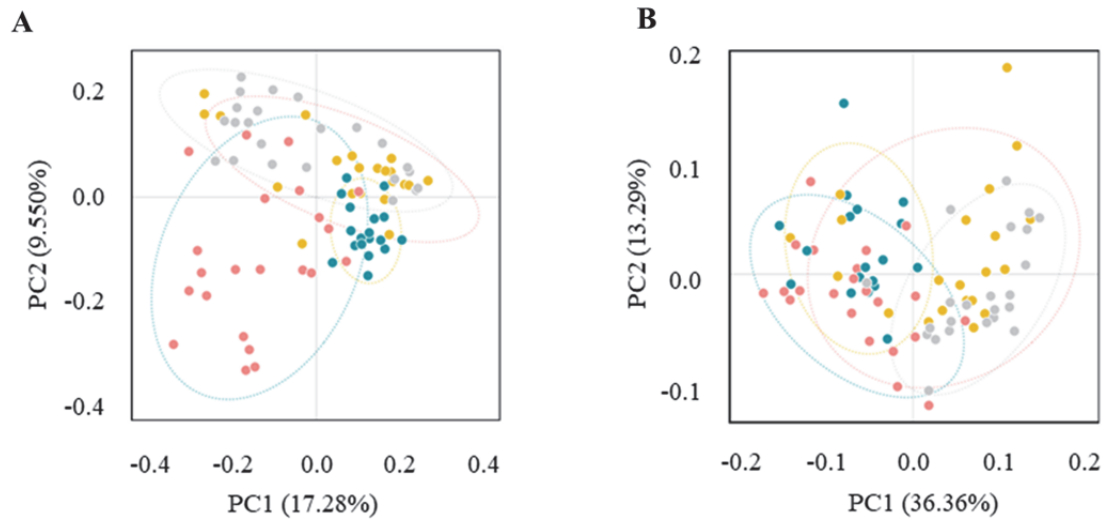


Fig. S5. Comparison of microbial beta diversity in the lettuce samples collected from different seasons. Lettuce microbiota composition across four seasons was compared using a PCoA plot based on the unweighted **A** and weighted **B** UniFrac distance.