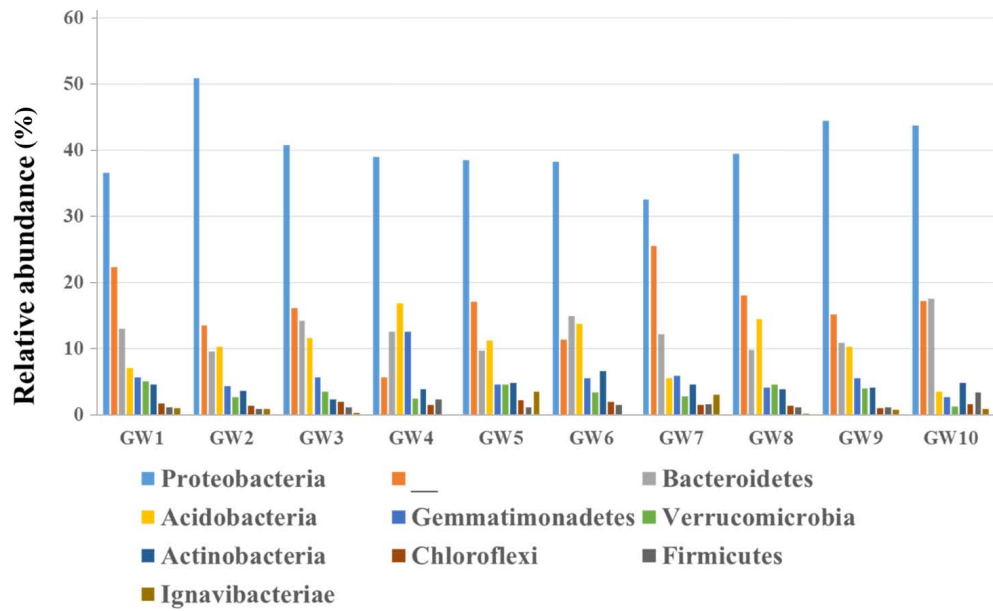
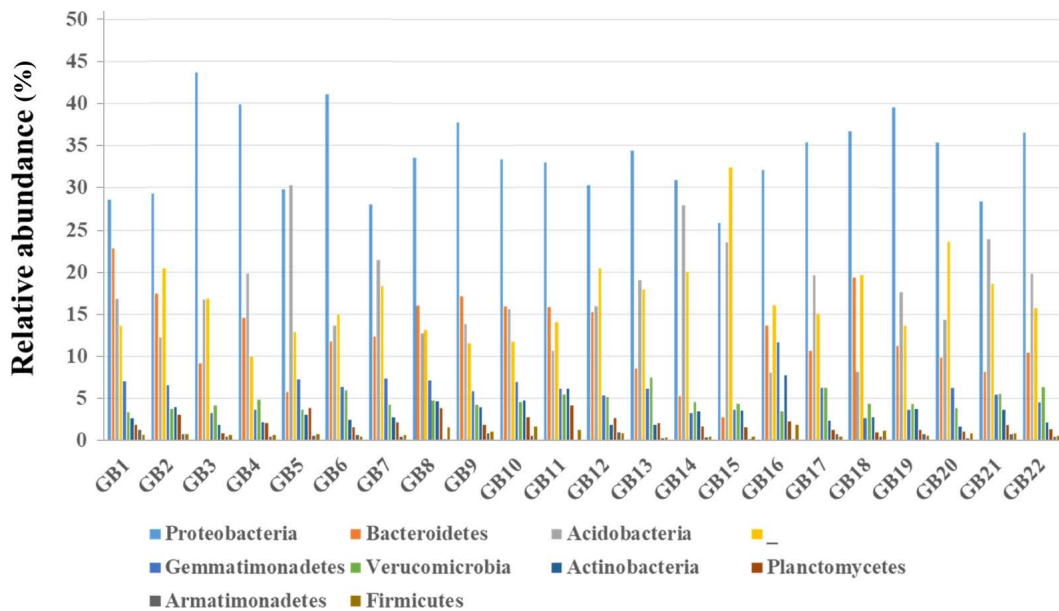


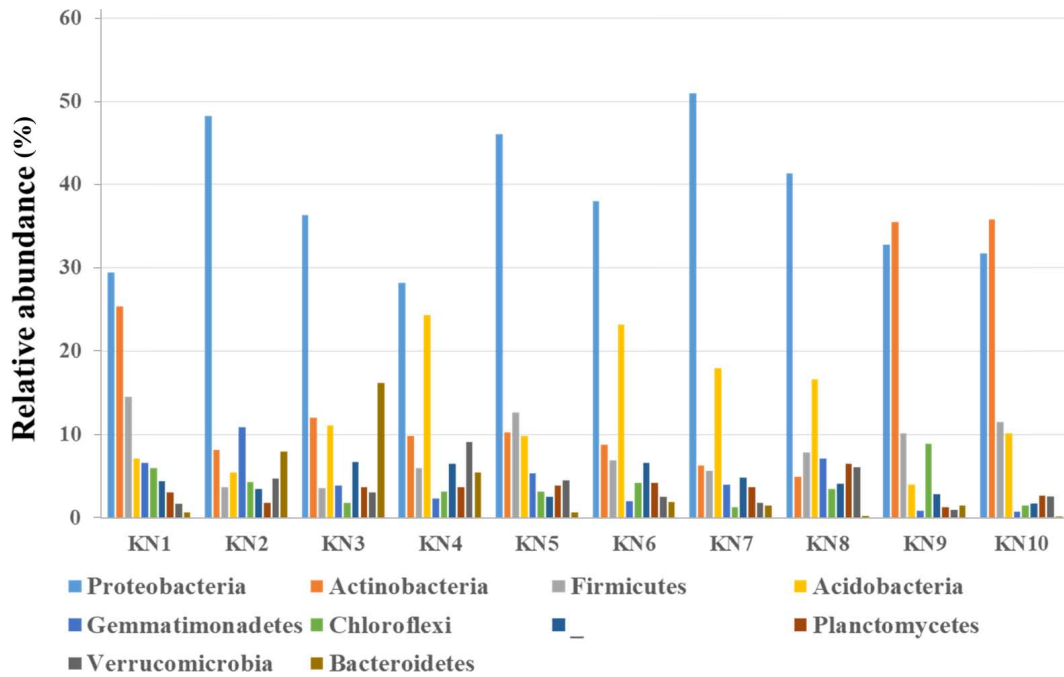
**Supplementary Fig. 1.** Location of soil samples collection using global positioning system (GPS).



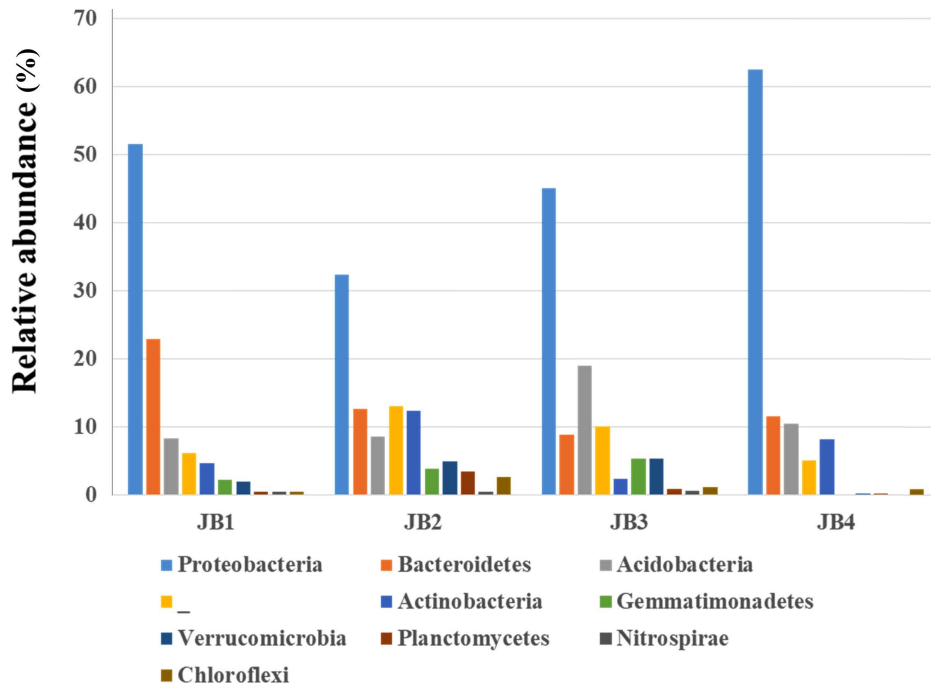
**Supplementary Fig. 2.** Top 10 most abundant phylum from the watermelon cultivated soils from Gangwon-do. \_\_ denotes the unidentified phylum detected in the soil samples. The different color bars shown in the bar diagram indicated the dominant bacterial phylum detected in the soil samples from Gangwon-do (GW1-GW10). x-axis indicates soil samples collected from Gangwon-do (GW1-GW10) and y-axis indicates abundancy ratio of dominant bacterial phylum.



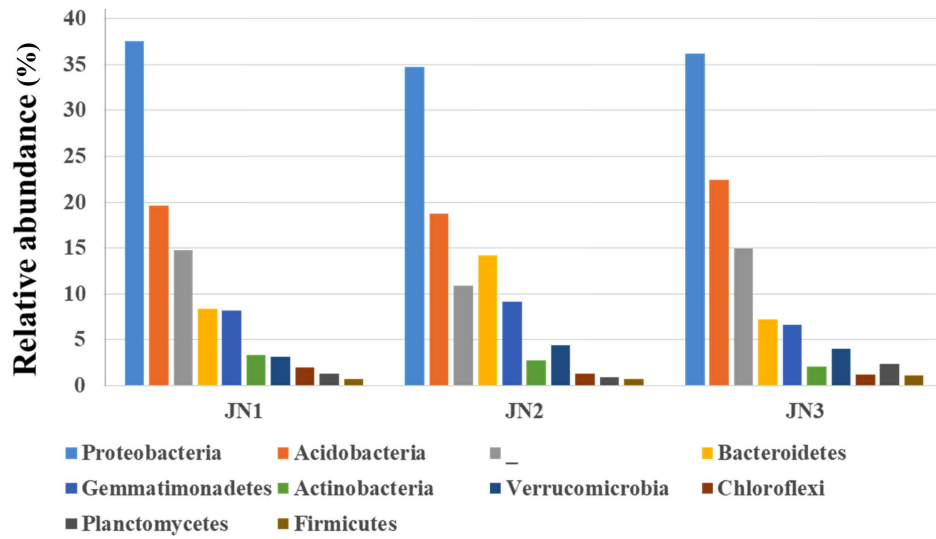
**Supplementary Fig. 3.** Top 10 most abundant phylum from the watermelon cultivated soils in Gyeongsangbuk-do. \_\_ denotes the unidentified phylum detected in the soil samples. The different color bars shown in the diagram indicated the dominant bacterial phylum detected in the soil samples from Gyeongsangbuk-do (GB1-GB22). x-axis indicates soil samples collected from Gangwon-do (GW1-GW22) and y-axis indicates abundancy ratio of dominant bacterial phylum.



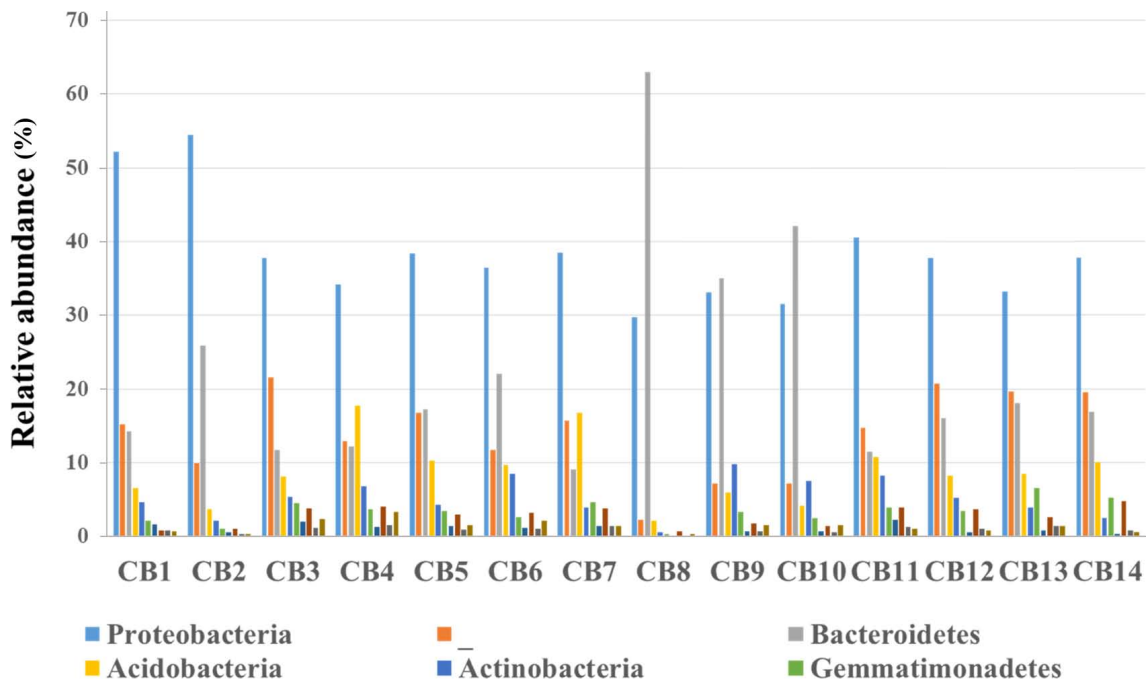
**Supplementary Fig. 4.** Top 10 most abundant phylum from the watermelon cultivated soils in Gyeongsangnam-do. \_\_\_ denotes the unidentified phylum detected in the soil samples. The different color bars shown in the diagram indicated the dominant bacterial phylum detected in the soil samples from Gyeongsangnam-do (KN1-KN10). x-axis indicates soil samples collected from Gangwon-do (KN1-KN10) and y-axis indicates abundancy ratio of dominant bacterial phylum.



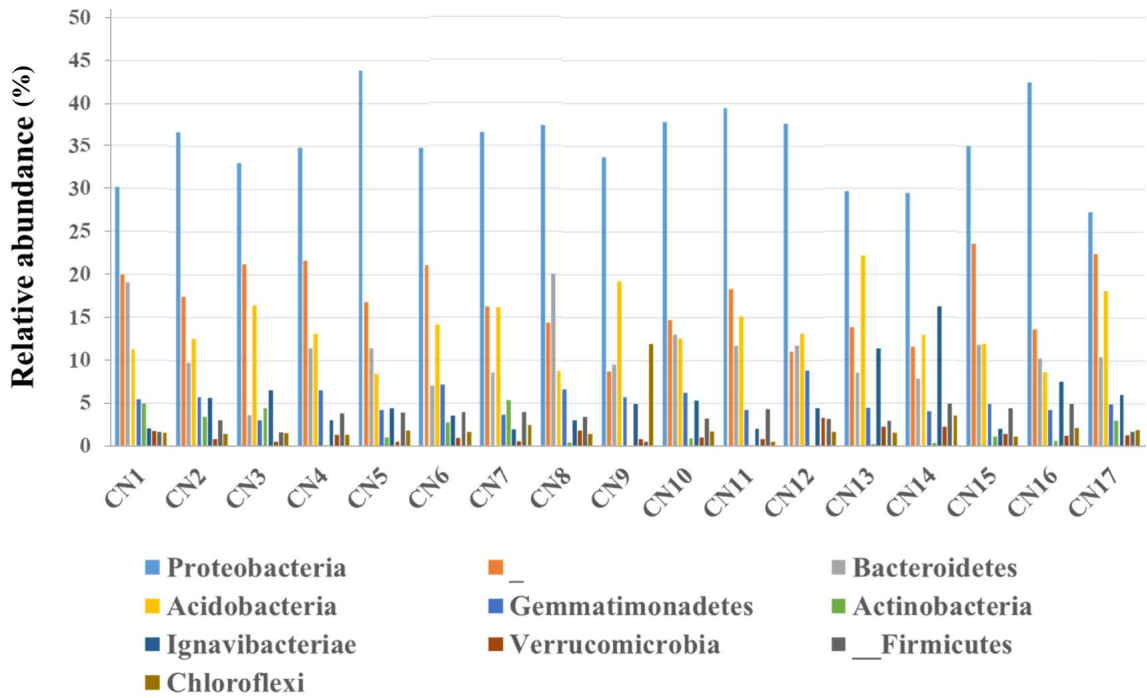
**Supplementary Fig. 5.** Top 10 most abundant phylum from the watermelon cultivated soils in Jeollabuk-do. \_\_\_ denotes the unidentified phylum detected in the soil samples. X-axis indicates dominant bacterial phylum detected in soil samples collected from Jeollabuk-do (JB1-JB4) and y-axis indicates abundancy ratio of dominant bacterial phylum.



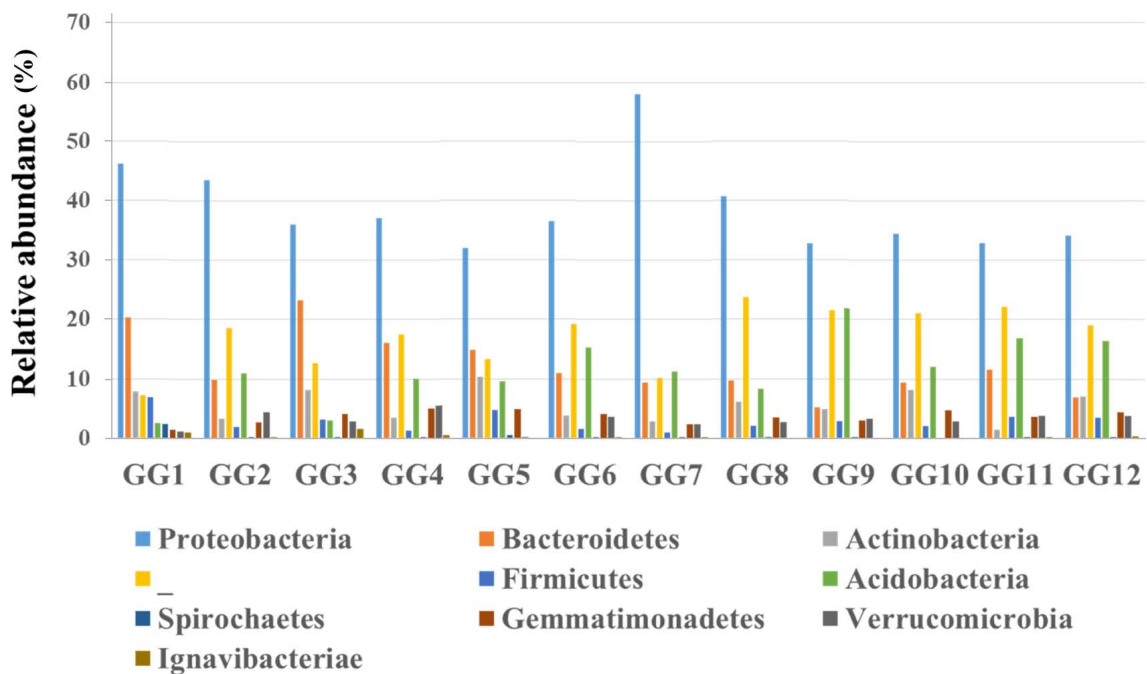
**Supplementary Fig. 6.** Top 10 most abundant phylum from the watermelon cultivated soils in Jeollanam-do. \_ denotes the unidentified phylum detected in the soil samples. X-axis indicates dominant bacterial phylum detected in soil samples collected from Jeollabuk-do (JN1-JN3) and y-axis indicates abundancy ratio of dominant bacterial phylum.



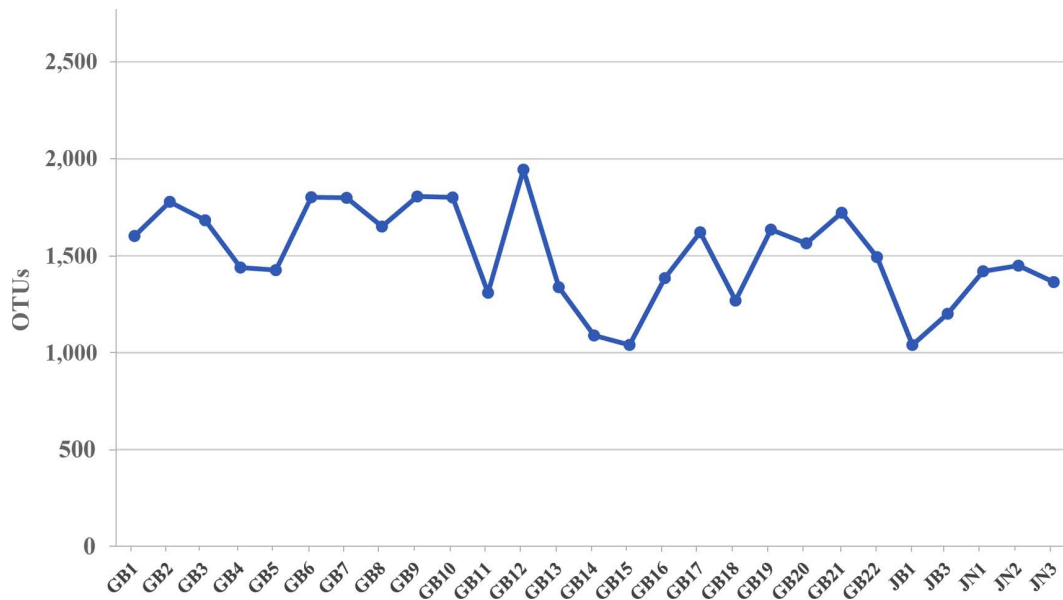
**Supplementary Fig. 7.** Top 10 most abundant phylum from the watermelon cultivated soils in Chungcheongbuk-do. \_ denotes the unidentified phylum detected in the soil samples. The different color bars shown in the diagram indicated the dominant bacterial phylum detected in the soil samples from Chungcheongbuk-do (CB1-CB14). x-axis indicates soil samples collected from Chungcheongbuk-do (CB1-CB14) and y-axis indicates abundancy ratio of dominant bacterial phylum.



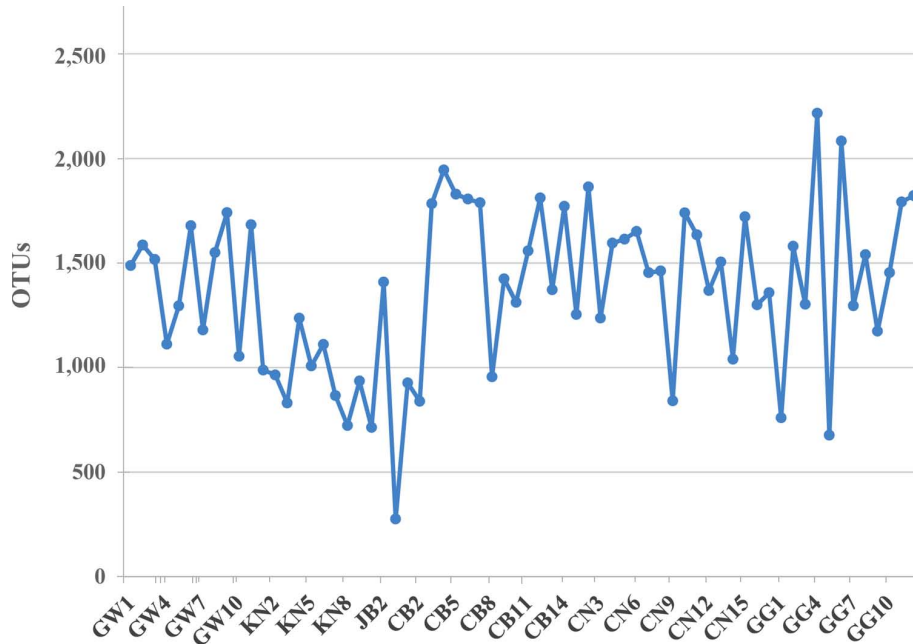
**Supplementary Fig. 8.** Top 10 most abundant phylum from the watermelon cultivated soils in Chungcheongnam-do. \_\_ denotes the unidentified phylum detected in the soil samples. The different color bars shown in the diagram indicated the dominant bacterial phylum detected in the soil samples from Chungcheongnam-do (CN1-CN17). x-axis indicates soil samples collected from Chungcheongbuk-do (CN1-CN17) and y-axis indicates abundancy ratio of dominant bacterial phylum.



**Supplementary Fig. 9.** Top 10 most abundant phylum from the watermelon cultivated soils in Gyeonggi-do. \_\_ denotes the unidentified phylum detected in the soil samples. The different color bars shown in the diagram indicated the dominant bacterial phylum detected in the soil samples from Gyeonggi-do (GG1-GG12). x-axis indicates soil samples collected from Gyeonggi-do (GG1-GG12) and y-axis indicates abundancy ratio of dominant bacterial phylum.

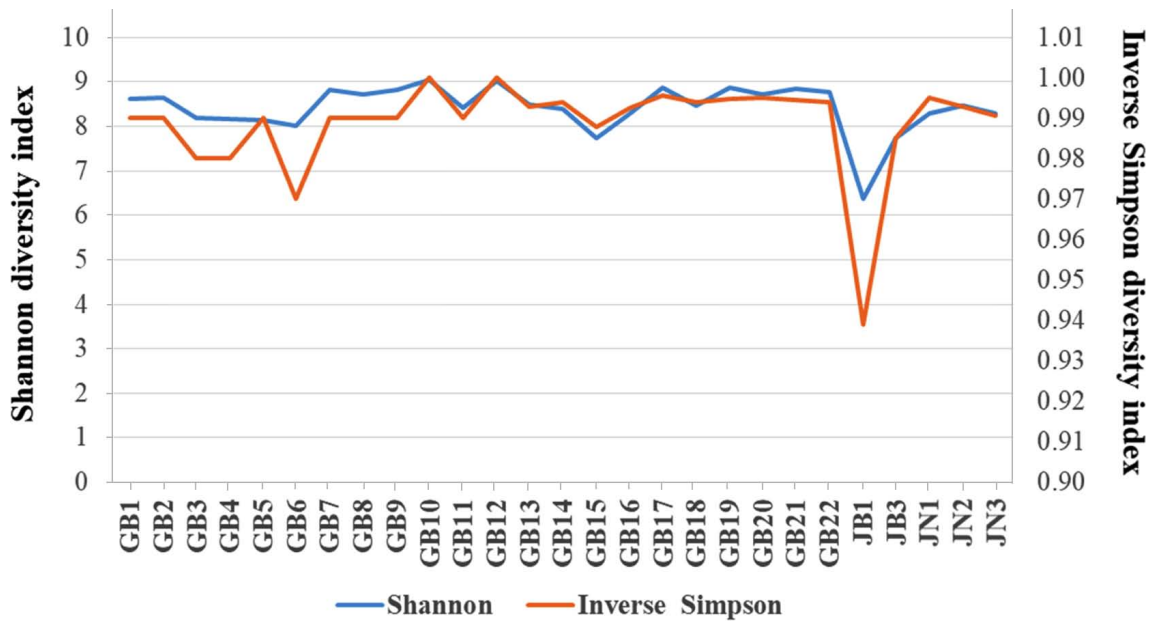


**Supplementary Fig. 10.** Operational taxonomic units (OTUs) of the bacterial community obtained from watermelon cultivated on open field soils. x-axis indicates soil samples from open field soils collected from Gyeongsangbuk-do (GB1-GB22), Jeollabuk-do (JB1-JB4), and Jeollanam-do (JN1-JN4) and y-axis indicates OTUs count. GB, Gyeongsangbuk-do; JB, Jeollabuk-do; JN, Jeollanam-do.

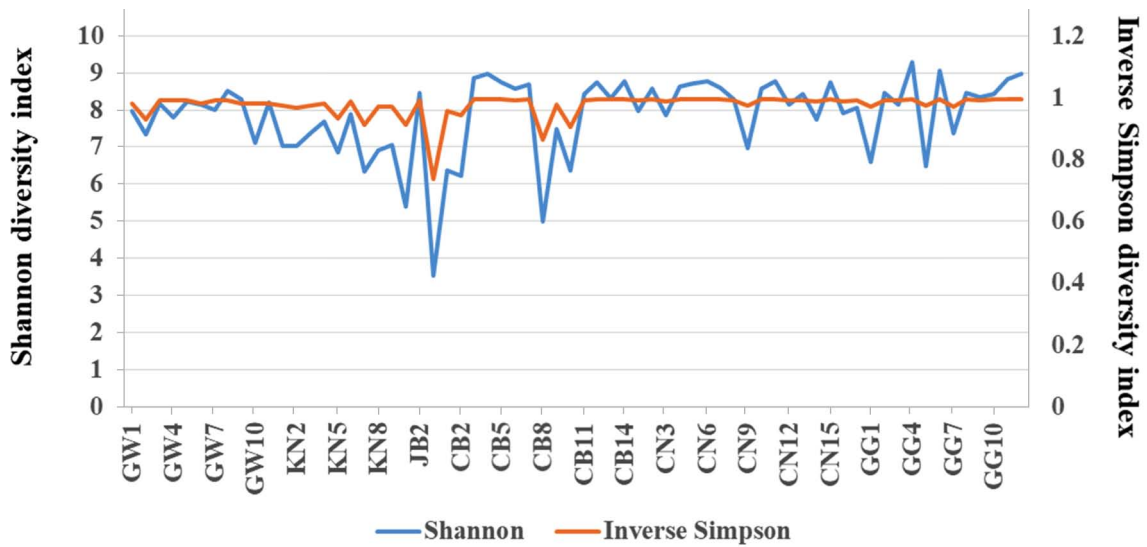


**Supplementary Fig. 11.** Operational taxonomic units (OTUs) of the bacterial community obtained from watermelon cultivated in greenhouse soils. x-axis indicates soil samples from greenhouse soils collected from Gangwon-do (GW1-GW10), Gyeongsangnam-do (KN1-KN10), Chungcheongbuk-do (CB1-CB14), Chungcheongnam-do (CN1-CN17), and Gyeonggi-do (GG1- GG12) and y-axis indicates OTUs count. CB, Chungcheongbuk-do; CN, Chungcheongnam-do; GG, Gyeonggi-do; GW, Gangwon-do; KN, Gyeongsangnam-do.





**Supplementary Fig. 12.** Bacterial community richness and diversity obtained from watermelon cultivated on open-field soil. X-axis indicates soil samples from open field soils collected from Gyeongsangbuk-do (GB1-GB22), Jeollabuk-do (JB1-JB4), and Jeollanam-do (JN1-JN4). GB, Gyeongsangbuk-do; JB, Jeollabuk-do; JN, Jeollanam-do.



**Supplementary Fig. 13.** Bacterial community richness and diversity obtained from watermelon cultivated in greenhouse soil. X-axis indicates soil samples from greenhouse soils collected from, Gangwon-do (GW1-GW10), Gyeongsangnam-do (KN1-KN10), Chungcheongbuk-do (CB1-CB14), Chungcheongnam-do (CN1-CN17), and Gyeonggi-do (GG1-GG12). CB, Chungcheongbuk-do; CN, Chungcheongnam-do; GG, Gyeonggi-do; GW, Gangwon-do; JB, Jeollabuk-do; KN, Gyeongsangnam-do.