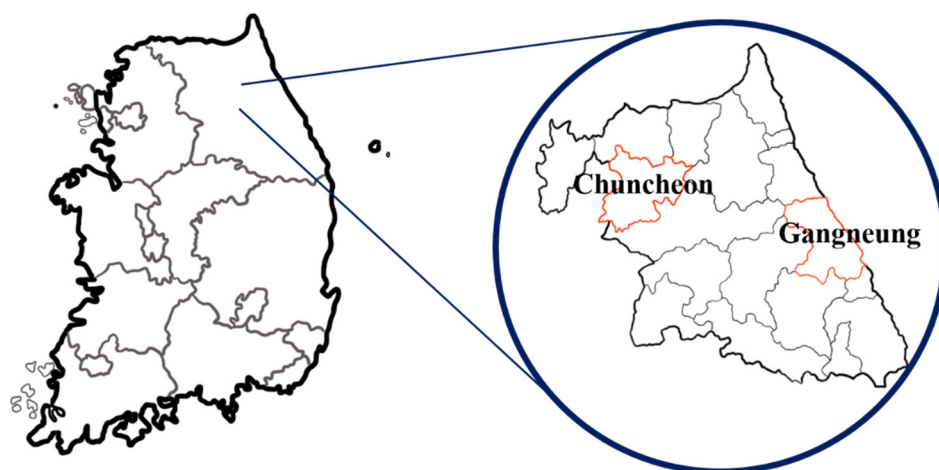


Supplementary figures and tables



Experiment Information			
Province	Location	Latitude	Longitude
Gangneung	Gangneung Potato Research Center (Experimental field facility)	37°48'47.2"N	128°49'58.1"E
Chuncheon	Gangwon-do Agricultural Research and Extension Services (Chuncheon experimental field)	37°57'05.5"N	127°46'29.5"E

Figure S1. Details of soil sampling sites and its exact GPS (Global Positioning System) locations.

Table S1. Average environmental conditions for a week to each locations (Gangneung and Chuncheon) during pre and post harvesting of potato.

Gangneung Location		
Parameters	April 27 to May 3	July 20–26
One week mean temperature (°C)	19.3	22.1
One week maximum temperature (°C)	24.4	24.6
One week minimum temperature (°C)	12.9	19.7
One week mean precipitation (mm)	0.36	28.13
Chuncheon Location		
	May 4–10	August 10 to 16
One week mean temperature (°C)	18.0	26.8
One week maximum temperature (°C)	23.8	29.6
One week minimum temperature (°C)	12.5	24.3
One week mean precipitation (mm)	6.04	15.39

Note: April 27 to May 3 -> environmental parameters before planting of potato in Gangneung field location.

July 20 – 26 - environmental parameters after harvesting of potato in Gangneung field location.

May 4 -10 -> environmental parameters before planting of potato in Chuncheon field location.

August 10 to 16 -> environmental parameters after harvesting of potato in Chuncheon.

field location.

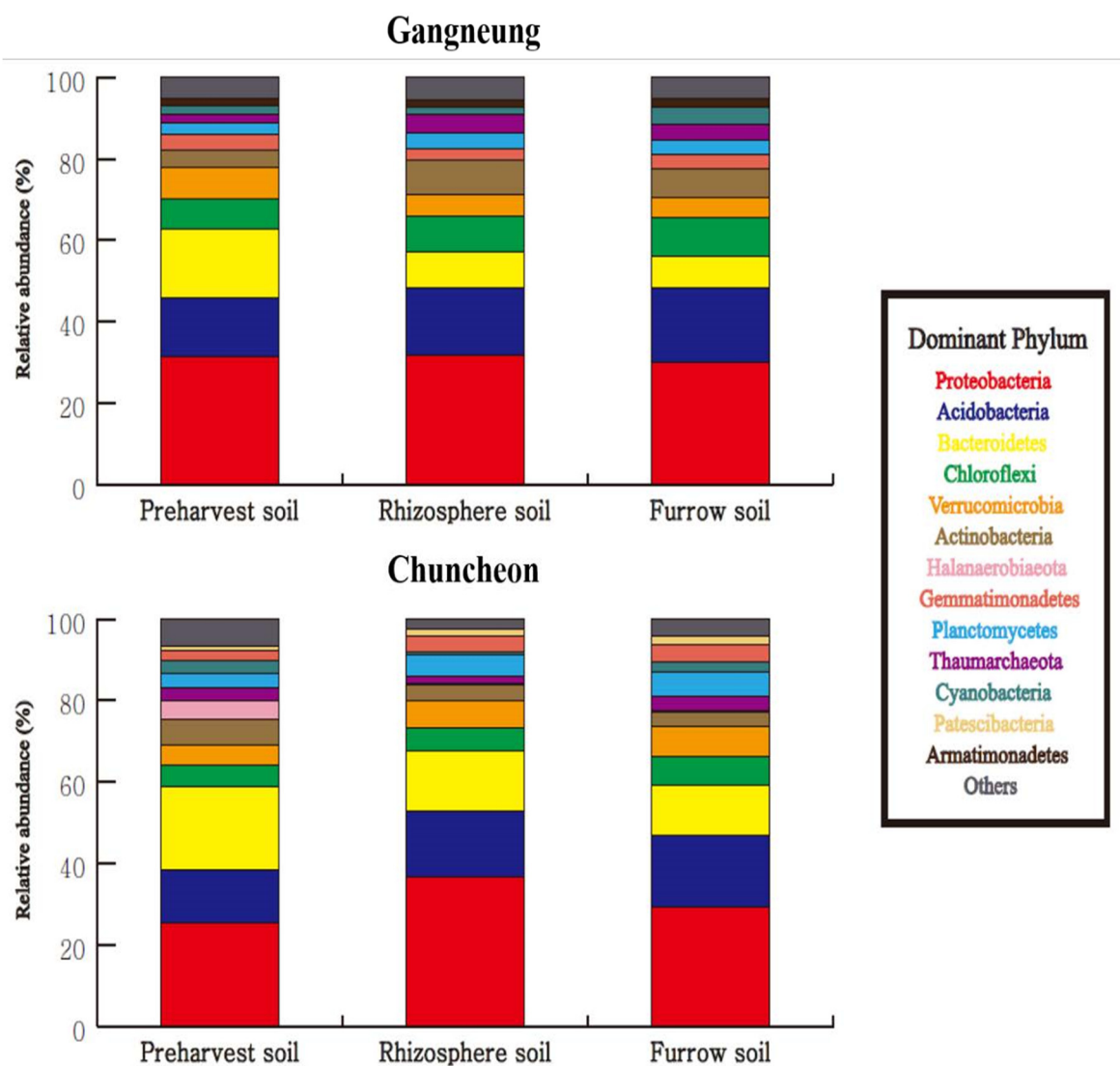


Figure S2. Dominant bacterial phylum according to sites, spatial locations and harvest time.

Note: Others -> unidentified bacterial groups. Preharvest; time of potato harvesting. Rhizosphere and furrow; spatial locations

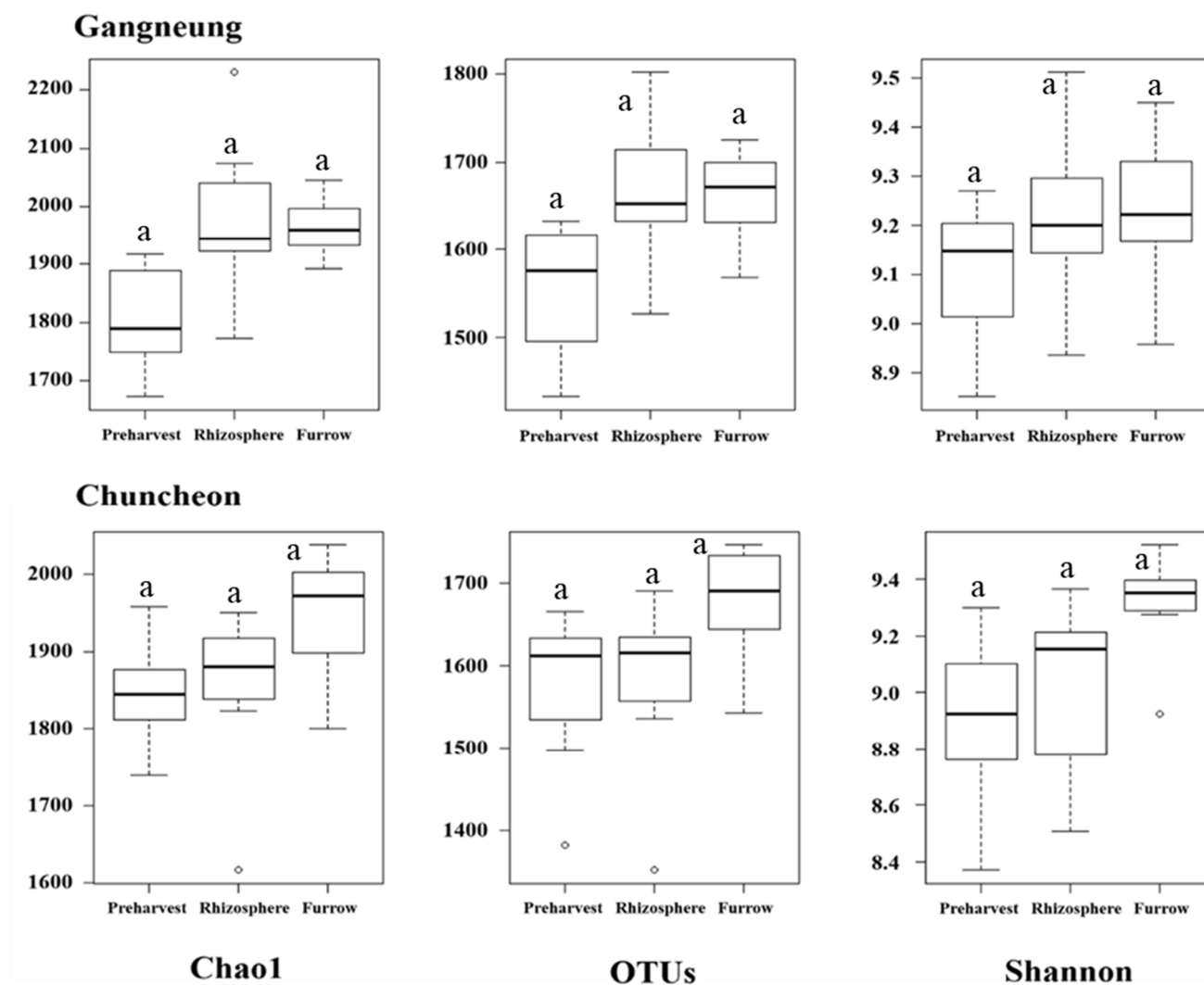


Figure S3. Bacterial diversity indices in Gangneung and Chuncheon.

Note: Postharvest - > time of potato harvesting

Rhizosphere and furrow - > spatial locations

Chao1 -> bacterial community richness

OTUs -> operational taxonomic units

Shannon -> bacterial diversity index

Note: Each box plots is represented with 3 average values. The values with same alphabetic letters are not significantly different at $P < 0.05$.

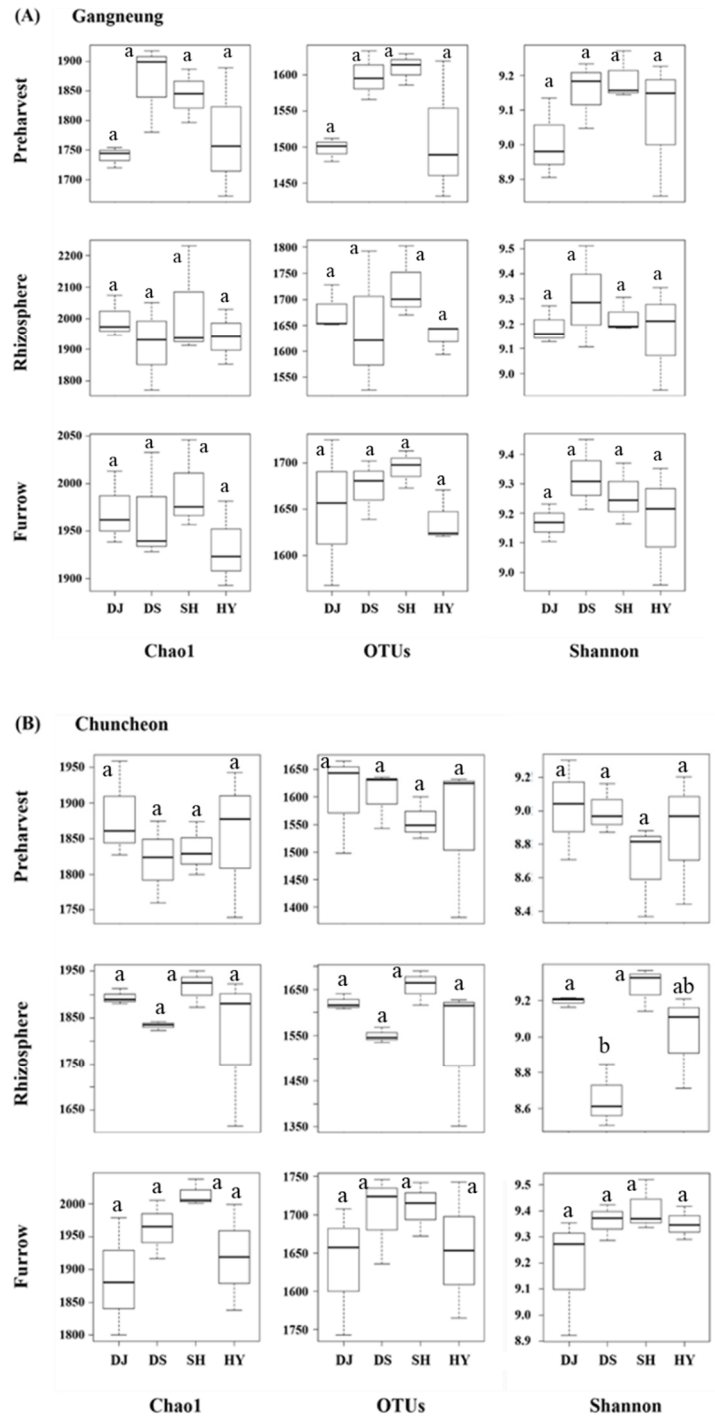
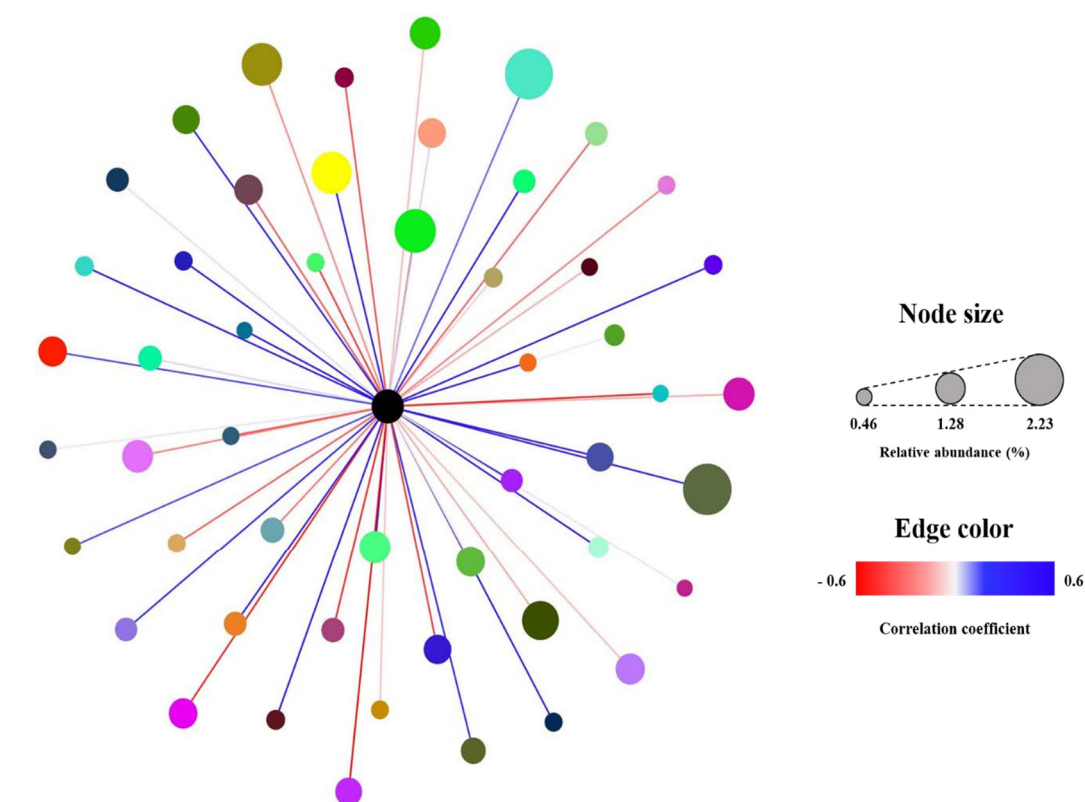


Figure S4. Bacterial diversity indices obtained after metagenomics sequencing from different varieties of potato cultivated soils in two different sites (Gangneung and Chuncheon) and spatial locations (rhizosphere and furrow). (A) Gangneung (B) Chuncheon. Each box plots is represented with 3 average values. The values with same alphabetic letters are not significantly different at $P < 0.05$.

Note: Preharvest; before harvesting of potato. Rhizosphere and furrow; spatial locations. Chao1; bacterial community richness. OTUs; operational taxonomic units. Shannon; bacterial diversity index



Phylum	Class	Order	Family	Genus (Mark)
Thaumarchaeota	Nitrososphaeria	Nitrososphaerales	Nitrososphaeraceae	uncultured bacterium
Acidobacteria	Acidobacteria	Acidobacteriales	uncultured	Other
		Soilbacteriales	Soilbacteriaceae Subgroup 3	Bryobacter
	Blautiaellia Subgroup 4	Blautiaelliales	Blautiaellaceae	Blautiaellia
			JGI 1001 1001	OLB17
		metagenome	metagenome	metagenome
			uncultured Acidobacteria bacterium	uncultured Acidobacteria bacterium
	Subgroup 6	uncultured proteobacterium	uncultured proteobacterium	uncultured proteobacterium
			Other	Other
		Other	Other	Other
		Other	Other	Other
Actinobacteria	Actinobacteria	Micrococcales	Micrococcaceae	Pseudarthrobacter
Bacteroidetes	Bacteroidia	Chitinophagales	Chitinophagaceae	Flavobacter
			Chitinophagaceae	Terrimonas
		Cytophagales	Micrococcaceae	uncultured
			Flavobacteriaceae	Flavobacterium
		Sphingobacteriales	ens OPS 17	uncultured bacterium
Chloroflexi	Chloroflexia	Anaerolineae	SR1101	AB
		Chloroflexiales	Roseiflexaceae	uncultured
		KD4 96	metagenome	metagenome
Gemmatimonadetes	Gemmatimonadetes	Gemmatimonadales	Gemmatimonadaceae	Gemmatimonas
Nitrospirae	Nitrospira	Nitrospirales	Nitrospiraceae	uncultured
Patescibacteria	Saccharinimadia	Saccharinimadales	uncultured bacterium	uncultured bacterium
Planctomycetes	Planctomycetes	Planctomycetales	WD2101 soil group	uncultured bacterium
	Planctomycetes	Planctomycetales	Other	Other

Proteobacteria	Alphaproteobacteria	Micropepsales	Micropepsaceae	uncultured
		Rhizobiales	Xanthobacteraceae	Pseudolabrys
		Sphingomonadales	Sphingomonadaceae	uncultured
	Deltaproteobacteria	Myxococcales	Haliangiaceae	Sphingomonas
				Haliangium
	Gammaproteobacteria	Betaproteobacteriales	A21b	uncultured Rhodocyclaceae bacterium
			Burkholderiaceae	Massilia
				Other
			Nitrosomonadaceae	Ellin6067
		Cellvibrionales	Cellvibrionaceae	MSD1
				uncultured beta proteobacterium
			Cellvibrionaceae	Cellvibrio
	Verrucomicrobia	Gammaproteobacteria Incertae Sedis	Unknown	Acidibacter
		Pseudomonadales	Pseudomonadaceae	Pseudomonas
		Steroidobacteriales	Steroidobacteraceae	Steroidobacter
		Xanthomonadales	Rhodanobacteraceae	Rhodanobacter
		Xanthomonadales	Xanthomonadaceae	Luteimonas
		Chthoniobacteriales	Chthoniobacteraceae	Chthoniobacter
Other	Other	Other	Other	Lacunisphaera
				Opitutia
				Other

Figure S5. Correlation network analysis between *Streptomyces* spp. and other bacterial communities. The network was undirected and binary network as only microbial communities (color node) related with *Streptomyces* spp. (black node). The network analysis was performed on the basis of Spearman correlation analysis of microbial communities at the Genus level at a relative ratio (cut off $> 0.1\%$).

Note: Colored column in the tables represents the different bacterial genus names used in the correlation network analysis with *Streptomyces* spp.