Supplementary Table 1. Analysis of similarity (ANOSIM) and permutational multivariate analysis of variance (PERMANOVA) of microbial communities among different groups

	ANOSIM		PERMANOVA	
	R	*P*-value	R^2	*P*-value
EC levels	0.6278	0.001	0.3073	0.001
Rhizocompartments	0.4294	0.001	0.1523	0.001

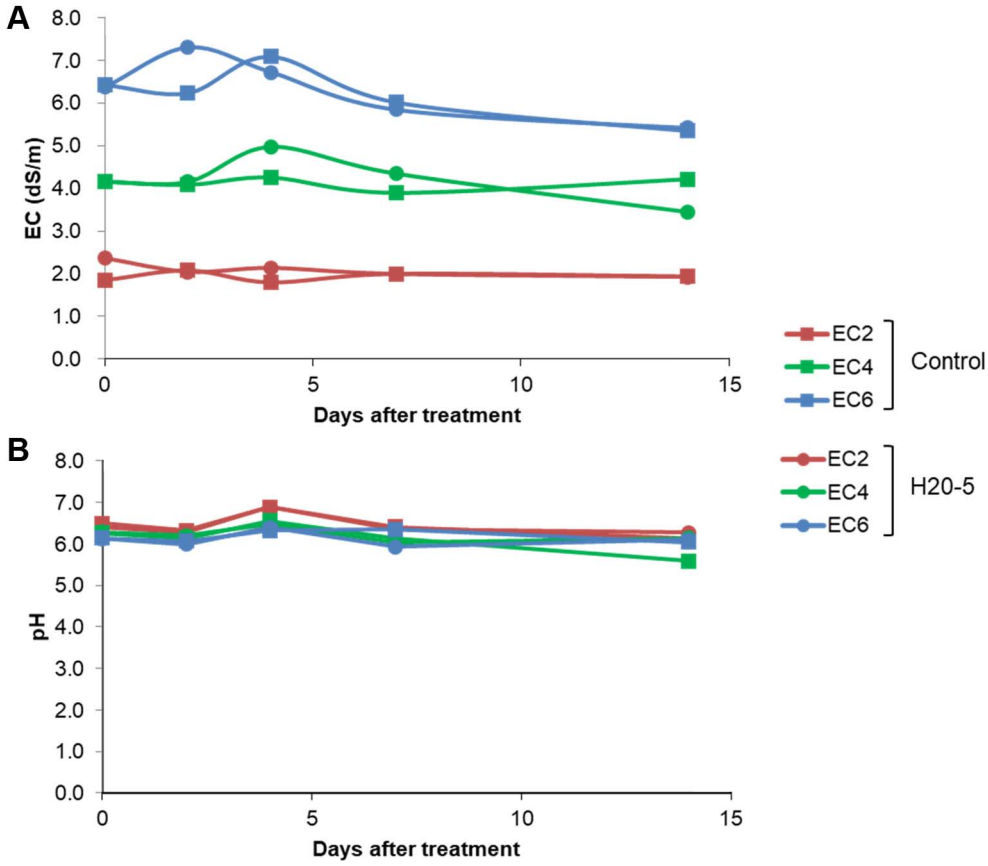
Supplementary Table 2. Topological descriptors of microbial network in the rhizosphere soils of control and H20-5 treatment groups

Topological descriptor	Control	H20-5
Descriptors based on distances		
Harary index	10,511.7	23,777.8
Descriptors based on other graph-invariants		
Index of total adjacency	1,346	1,839
Zagreb index	2,692	3,678
Randić complexity index	138.7	216.2
Classical Entropy-based descriptors		
Topological information content	7.588	8.189
Bertz complexity index	4,866	8,429

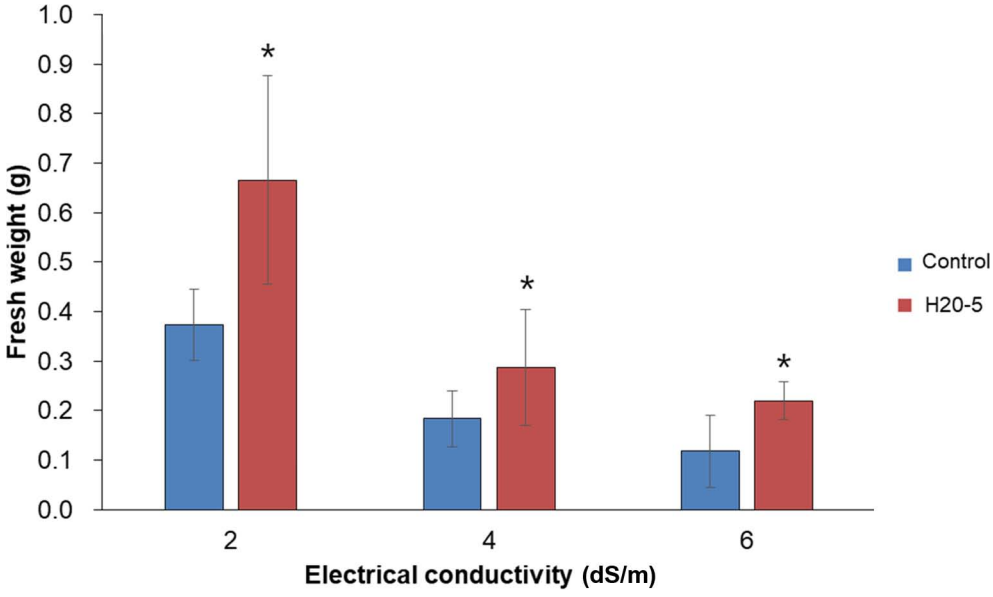
Supplementary Table 3. The OTUs showing significantly different relative abundances between the *Bacillus mesonae* H20-5 treatment and control groups

OTU	Phylum	Class	Order	Family	Genus	Value	Relative abundance (%)	
							Control	H20-5
OTU117	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingobium	0.70**	2.06	0.96
OTU89	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Erythrobacteraceae	Altererythrobacter	0.50*	0.59	0.37
OTU122	Proteobacteria	Alphaproteobacteria	Rhizobiales	Hyphomicrobiaceae	Devosia	0.50*	0.30	0.17
OTU62	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Sinobacteraceae	Steroidobacter	0.82***	0.10	0.19
OTU164	Actinobacteria	Actinobacteria	Actinomycetales	Kineosporiaceae	Kineosporia	0.70***	0.06	0.13
OTU72	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	0.69***	0.50	0.70
OTU131	Actinobacteria	Actinobacteria	Actinomycetales	Micromonosporaceae	Virgisporangium	0.69***	0.20	0.31
OTU81	Nitrospirae	Nitrospira	Nitrospirales	Nitrospiraceae	Nitrospira	0.68**	0.08	0.13
OTU70	Proteobacteria	Alphaproteobacteria	Rhizobiales	Xanthobacteraceae	Pseudolabrys	0.66**	0.07	0.11
OTU99	Actinobacteria	Actinobacteria	Actinomycetales	Micromonosporaceae	Actinoplanes	0.65**	0.17	0.28
OTU90	Proteobacteria	Alphaproteobacteria	Rhizobiales	Unclassified	Unclassified	0.63**	0.12	0.17
OTU12	Proteobacteria	Alphaproteobacteria	Rhizobiales	Bradyrhizobiaceae	Bradyrhizobium	0.61**	0.26	0.38
OTU79	Actinobacteria	Actinobacteria	Gaiellales	Gaiellaceae	Gaiella	0.60**	0.23	0.34
OTU119	Acidobacteria	Acidobacteria_Gp1	Gp1	Unclassified	Unclassified	0.57*	0.08	0.12
OTU112	Actinobacteria	Actinobacteria	Actinomycetales	Geodermatophilaceae	Blastococcus	0.56*	0.24	0.33
OTU66	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	0.55*	0.21	0.33
OTU127	Proteobacteria	Betaproteobacteria	Sulfuricellales	Sulfuricellaceae	Sulfuriferula	0.54*	0.13	0.18
OTU38	Unclassified	Unclassified	Unclassified	Unclassified	Unclassified	0.53*	0.18	0.26
OTU436	Actinobacteria	Actinobacteria	Gaiellales	Gaiellaceae	Gaiella	0.53*	0.15	0.22
OTU98	Proteobacteria	Alphaproteobacteria	Rhizobiales	Hyphomicrobiaceae	Hyphomicrobium	0.53*	0.08	0.12
OTU78	Actinobacteria	Actinobacteria	Solirubrobacterales	Solirubrobacteraceae	Solirubrobacter	0.52*	0.21	0.31
OTU174	Actinobacteria	Actinobacteria	Actinomycetales	Micromonosporaceae	Unclassified	0.52*	0.07	0.12

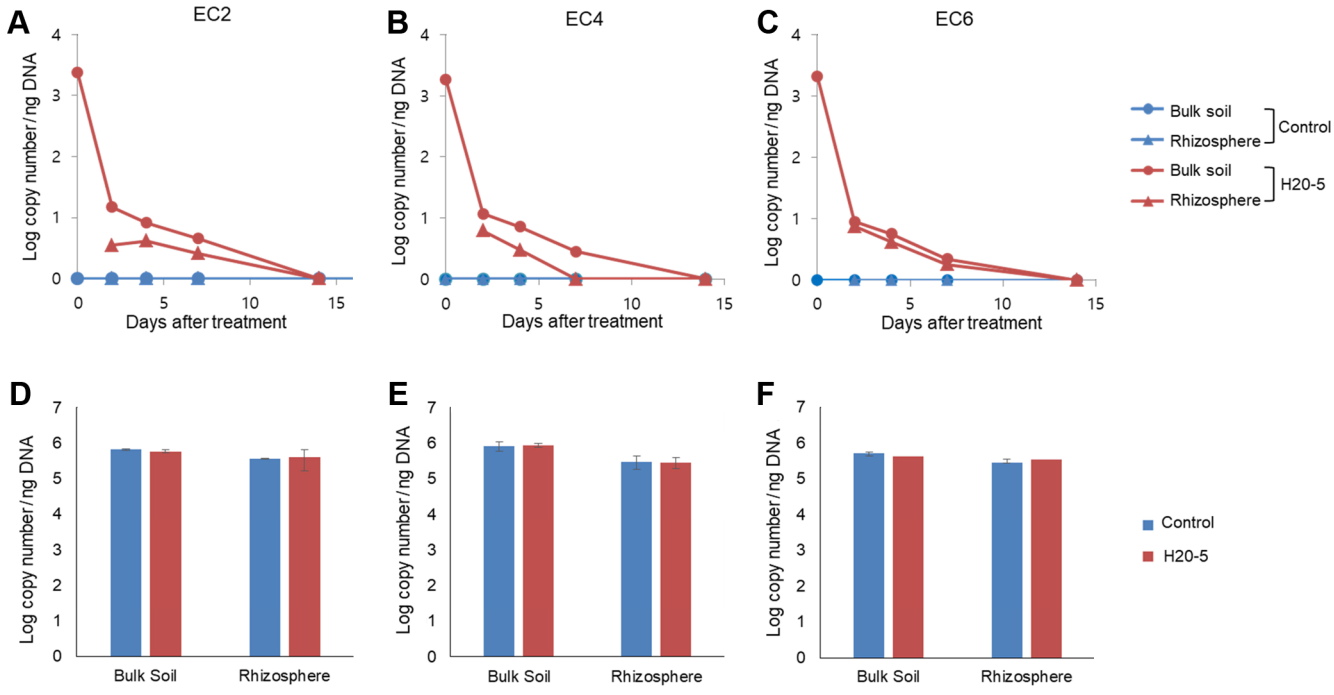
The indicator species analysis was performed using point biserial correlation. The operational taxonomic units (OTUs) with high indicator values (>0.5) and high abundances (>0.1% relative abundance) are listed. The significance level was set at $P < 0.001$.



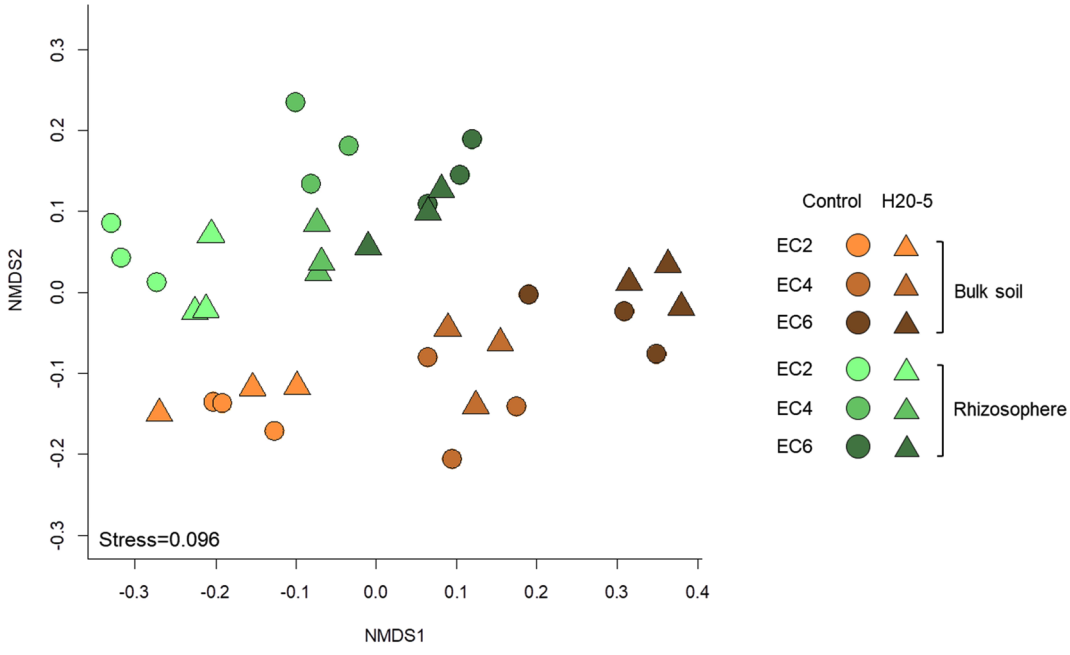
Supplementary Fig. 1. The electrical conductivity (EC) and pH values of the soil treated with different concentration of salt solutions to establish soils with EC 2, 4, 6 dS/m gradient. Soil EC and pH were measured at 0, 2, 4, 7, and 14 days after salt solution treatments.



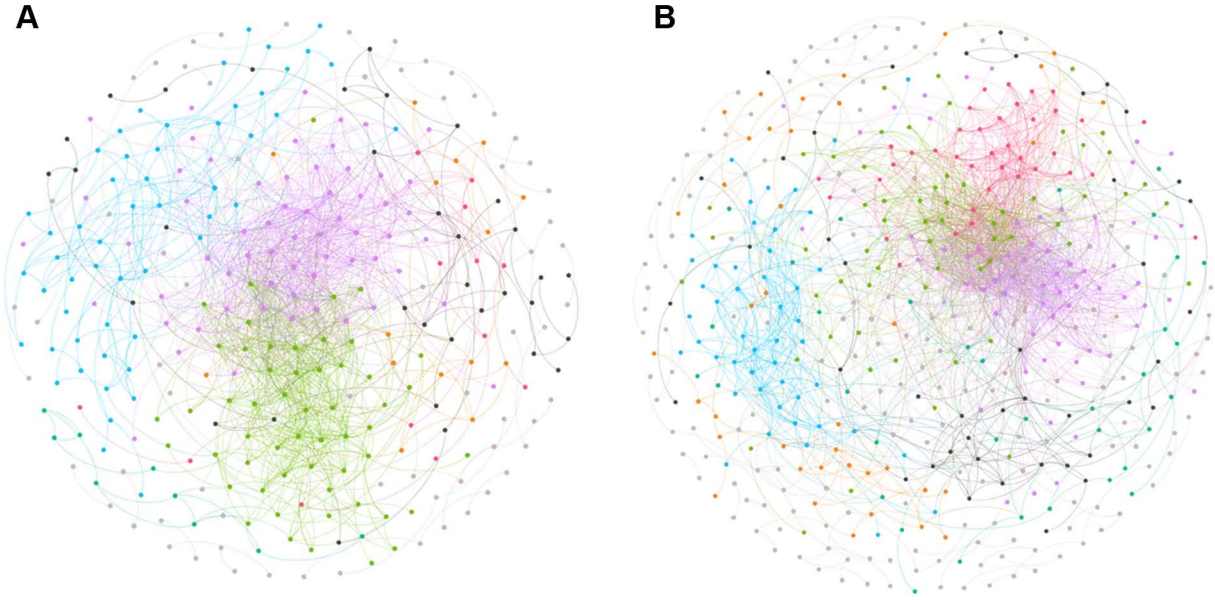
Supplementary Fig. 2. The effects of *Bacillus mesonae* H20-5 on tomato growth under different soil salinity levels. Fresh weight of tomato plant was measured after 14 days of treatment. An asterisk indicates significants differences between the treatment and control determined by Student's t-test ($P < 0.05$). Error bars indicate standard error.



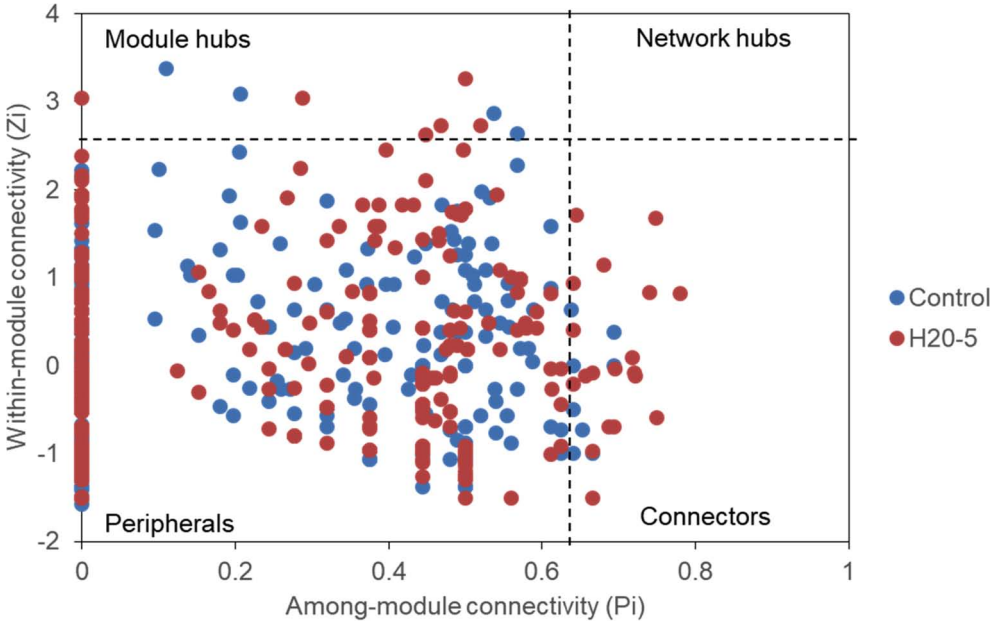
Supplementary Fig. 3. The abundance of strain H20-5 (A-C) and bacteria (D-F) in the bulk and rhizosphere soils with salinity gradients (EC2, 4, and 6 dS/m) after treatment.



Supplementary Fig. 4. The non-metric multidimensional scaling (NMDS) biplot of samples from the bulk and rhizosphere samples.



Supplementary Fig. 5. The submodule structure of microbial network in the rhizosphere soils of control (A) and H20-5 treatment (B) groups based on the fast greedy modularity optimization method. Nodes represent microbial operational taxonomic units and the colors denote different modules.



Supplementary Fig. 6. ZP-plot classifying nodes to module-based topological roles. Each dot represents an operational taxonomic unit (OUT) in the rhizosphere with and without H20-5 treatment. The threshold values of Zi and Pi for categorizing OTUs as module hubs and connecters were 2.5 and 0.62, respectively.