

Figure S1. Cluster analysis in the RTE chicken meat samples based on (A, C) storage time and (B, D) temperature at the (A, B) phylum and (C, D) species level.

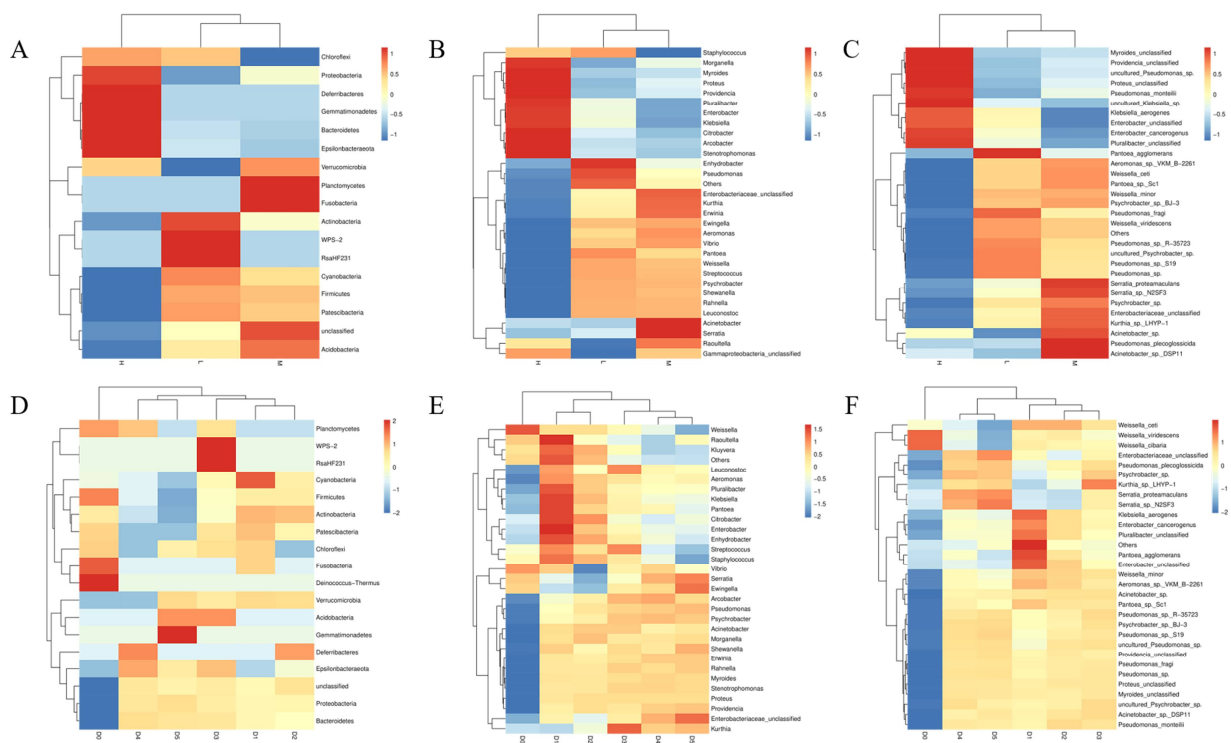


Figure S2. Heatmap analysis in the RTE chicken meat samples based on (A - C) storage temperature and (D - F) time at the (A, D) phylum, (B, E) genus and (C, F) species level.

Table S1. Species-level microbial interactions detected by SparCC in the bacterial communities of chicken meat samples stored at 4, 8 and 22 °C.

Temperature (°C)	Interaction	Pearson correlation†	Relation
4	<i>Weissella_minor</i> ↔ <i>Weissella_viridescens</i>	0.653	Copresence
	<i>Pseudomonas_fragi</i> ↔ <i>Pseudomonas_sp._S19</i>	0.6491	Copresence
	<i>Pseudomonas_fragi</i> ↔ <i>Pseudomonas_sp._R-35723</i>	0.5624	Copresence
	<i>Pseudomonas_sp._R-35723</i> ↔ <i>Pseudomonas_sp._S19</i>	0.5401	Copresence
	<i>Pseudomonas_fragi</i> ↔ <i>Pseudomonas_sp._R-35723</i>	0.5241	Copresence
	<i>Pseudomonas_sp._R-35723</i> ↔ <i>Pseudomonas_sp._S19</i>	0.4964	Copresence
	<i>Pseudomonas_sp._R-35723</i> ↔ <i>Pseudomonas_sp._55D</i>	0.4567	Copresence
	<i>Weissella_ceti</i> ↔ <i>Weissella_minor</i>	0.4556	Copresence
	<i>Pseudomonas_sp._55D</i> ↔ <i>Pseudomonas_sp._S19</i>	0.4311	Copresence
	<i>Psychrobacter_sp._BJ-3</i> ↔ <i>Psychrobacter_sp._BJ-3</i>	0.4305	Copresence
	<i>Pseudomonas_sp._55D</i> ↔ <i>Weissella_viridescens</i>	0.4186	Copresence
	<i>Pseudomonas_sp._R-35723</i> ↔ <i>Weissella_minor</i>	-0.4597	Mutual exclusion
	<i>Pseudomonas_sp._R-35723</i> ↔ <i>Weissella_viridescens</i>	-0.4649	Mutual exclusion
	<i>Pseudomonas_sp._R-35723</i> ↔ <i>Weissella_viridescens</i>	-0.4682	Mutual exclusion
	<i>Pseudomonas_sp._R-35723</i> ↔ <i>Weissella_viridescens</i>	-0.482	Mutual exclusion
	<i>Pseudomonas_sp._S19</i> ↔ <i>Weissella_minor</i>	-0.5245	Mutual exclusion
	<i>Pseudomonas_sp._S19</i> ↔ <i>Weissella_viridescens</i>	-0.5452	Mutual exclusion
	<i>Pseudomonas_fragi</i> ↔ <i>Weissella_viridescens</i>	-0.5982	Mutual exclusion
	<i>Pseudomonas_fragi</i> ↔ <i>Weissella_minor</i>	-0.6072	Mutual exclusion
	<i>Weissella_minor</i> ↔ <i>Weissella_viridescens</i>	-0.6223	Mutual exclusion
	<i>Serratia_proteamaculans</i> ↔ <i>Serratia_sp._N2SF3</i>	0.7217	Copresence
	<i>Weissella_ceti</i> ↔ <i>Weissella_viridescens</i>	0.6608	Copresence
	<i>Enterobacteriaceae_unclassified</i> ↔ <i>Serratia_proteamaculans</i>	0.6434	Copresence
	<i>Pseudomonas_plecoglossicida</i> ↔ <i>Serratia_proteamaculans</i>	0.6273	Copresence
	<i>Psychrobacter_sp._BJ-3</i> ↔ <i>Psychrobacter_sp._BJ-3</i>	0.6183	Copresence
8	<i>Weissella_ceti</i> ↔ <i>Weissella_viridescens</i>	0.6125	Copresence
	<i>Acinetobacter_sp._DSP11</i> ↔ <i>Acinetobacter_sp._DSP11</i>	0.586	Copresence
	<i>Enterobacteriaceae_unclassified</i> ↔ <i>Serratia_sp._N2SF3</i>	0.5672	Copresence
	<i>Pseudomonas_fragi</i> ↔ <i>Pseudomonas_sp._S19</i>	0.567	Copresence
	<i>Pseudomonas_plecoglossicida</i> ↔ <i>Serratia_sp._N2SF3</i>	0.5039	Copresence
	<i>Enterobacteriaceae_unclassified</i> ↔ <i>Pseudomonas_plecoglossicida</i>	0.4947	Copresence
	<i>Pseudomonas_fragi</i> ↔ <i>Pseudomonas_sp._R-35723</i>	0.4714	Copresence
	<i>Pseudomonas_fragi</i> ↔ <i>Pseudomonas_sp._R-35723</i>	0.454	Copresence
	<i>Pseudomonas_fragi</i> ↔ <i>Psychrobacter_sp._BJ-3</i>	0.4321	Copresence
	<i>Acinetobacter_sp._R-35723</i> ↔ <i>Pseudomonas_plecoglossicida</i>	0.42	Copresence
	<i>Pseudomonas_sp._R-35723</i> ↔ <i>Pseudomonas_sp._S19</i>	0.4048	Copresence
	<i>Serratia_sp._N2SF3</i> ↔ <i>Weissella_ceti</i>	0.4035	Copresence
	<i>Pseudomonas_fragi</i> ↔ <i>Weissella_viridescens</i>	-0.4009	Mutual exclusion
	<i>Enterobacteriaceae_unclassified</i> ↔ <i>Weissella_minor</i>	-0.4098	Mutual exclusion
	<i>Serratia_proteamaculans</i> ↔ <i>Weissella_ceti</i>	-0.4246	Mutual exclusion
	<i>Serratia_sp._N2SF3</i> ↔ <i>Weissella_minor</i>	-0.425	Mutual exclusion
	<i>Enterobacteriaceae_unclassified</i> ↔ <i>Weissella_viridescens</i>	-0.438	Mutual exclusion
	<i>Serratia_proteamaculans</i> ↔ <i>Weissella_viridescens</i>	-0.4794	Mutual exclusion
	<i>Serratia_sp._N2SF3</i> ↔ <i>Weissella_viridescens</i>	-0.4807	Mutual exclusion
	<i>Serratia_sp._N2SF3</i> ↔ <i>Weissella_viridescens</i>	-0.5003	Mutual exclusion
	<i>Serratia_proteamaculans</i> ↔ <i>Weissella_viridescens</i>	-0.5295	Mutual exclusion
	<i>Proteus_unclassified</i> ↔ <i>Providencia_unclassified</i>	0.4832	Copresence
	<i>Klebsiella_aerogenes</i> ↔ <i>Pluralibacter_unclassified</i>	0.4312	Copresence
	<i>Enterobacter_unclassified</i> ↔ <i>Klebsiella_aerogenes</i>	0.4211	Copresence
	<i>Klebsiella_aerogenes</i> ↔ <i>Pantoea_agglomerans</i>	0.4129	Copresence
22	<i>Proteus_unclassified</i> ↔ <i>Pseudomonas_plecoglossicida</i>	0.4059	Copresence
	<i>Klebsiella_aerogenes</i> ↔ <i>Providencia_unclassified</i>	-0.4377	Mutual exclusion
	<i>Enterobacter_unclassified</i> ↔ <i>Proteus_unclassified</i>	-0.4402	Mutual exclusion
	<i>Acinetobacter_sp._R-35723</i> ↔ <i>Providencia_unclassified</i>	-0.4439	Mutual exclusion
	<i>Pantoea_agglomerans</i> ↔ <i>Proteus_unclassified</i>	-0.4812	Mutual exclusion
	<i>Pluralibacter_unclassified</i> ↔ <i>Proteus_unclassified</i>	-0.4866	Mutual exclusion
	<i>Klebsiella_aerogenes</i> ↔ <i>Proteus_unclassified</i>	-0.5782	Mutual exclusion

†The threshold values of Pearson correlation in the three constructed networks were >0.4 or <-0.4.