

Table S2. Analysis of variance for each response (lactic acid bacteria and yeasts cell counts, pH, total titratable acidity [TTA], total phenolics content [TPC], DPPH radical scavenging activity, and overall acceptability [OA]).

Source	Sum of squares	DF	Mean squares	F-value	Signif.%
Lactic acid bacteria cells count log (CFU/ml)					
Model	3.1541	5	0.6308	95.6258	***
Residual	0.0462	7	0.0066		
Lack of fit	0.0218	3	0.0073	1.1900	42.0%
Pure error	0.0244	4	0.0061		
total	3.2002	12			

$R^2=0.986$; Adj- $R^2=0.975$

(* $p < 0.05$, ** $p < 0.01$, and *** $p < 0.001$).

Source	Sum of squares	DF	Mean squares	F-value	Signif.%
Yeasts cells count (log CFU/ml)					
Model	5.18015E-0001	5	1.03603E-0001	6598.9158	***
Residual	4.17591E-0002	7	5.96559E-0003		
Lack of fit	4.16963E-0002	3	1.38987E-0002	885.2720	***
Pure error	6.28000E-0005	4	1.57000E-0005		
total	5.59774E-0001	12			

$R^2=0.925$; Adj- $R^2=0.872$

(* $p < 0.05$, ** $p < 0.01$, and *** $p < 0.001$).

Source	Sum of squares	DF	Mean squares	F-value	Signif.%
pH					
Model	0.0349	5	0.0070	58.0935	**
Residual	0.0056	7	0.0008		
Lack of fit	0.0051	3	0.0017	14.2800	*
Pure error	0.0005	4	0.0001		
total	0.0405	12			

$R^2=0.861$; Adj- $R^2=0.762$

(* $p < 0.05$, ** $p < 0.01$, and *** $p < 0.001$).

Source	Sum of squares	DF	Mean squares	F-value	Signif.%
TTA					
Model	0.0878	5	0.0176	219.3988	***
Residual	0.0077	7	0.0011		
Lack of fit	0.0073	3	0.0024	30.6142	**
Pure error	0.0003	4	0.0001		
total	0.0954	12			

$R^2=0.920$; Adj- $R^2=0.862$

(* $p < 0.05$, ** $p < 0.01$, and *** $p < 0.001$).

Source	Sum of squares	DF	Mean squares	F-value	Signif.%
TPC (mg GAE/mL)					
Model	230.2032	5	46.0406	580.3687	***
Residual	45.4356	7	6.4908		
Lack of fit	45.1183	3	15.0394	189.5807	***
Pure error	0.3173	4	0.0793		
total	275.6389	12			

$R^2=0.835$; Adj- $R^2=0.717$

(* $p < 0.05$, ** $p < 0.01$, and *** $p < 0.001$).

Source	Sum of squares	DF	Mean squares	F-value	Signif.%
DPPH radical scavenging activity (%)					
Model	210.5275	5	42.1055	57.6211	**
Residual	47.5512	7	6.7930		
Lack of fit	44.6283	3	14.8761	20.3579	**
Pure error	2.9229	4	0.7307		
total	258.0787	12			
R ² = 0.816 ; Adj-R ² =0.684					
(* <i>p</i> < 0.05, ** <i>p</i> < 0.01, and *** <i>p</i> < 0.001).					

Source	Sum of squares	DF	Mean squares	F-value	Signif.%
OA (5 point hedonic scale)					
Model	0.6039	5	0.1208	38.8140	***
Residual	0.0218	7	0.0031		
Lack of fit	0.0069	3	0.0023	0.6132	64.3%
Pure error	0.0149	4	0.0037		
total	0.6257	12			
R ² = 0.965; Adj-R ² =0.940					
(* <i>p</i> < 0.05, ** <i>p</i> < 0.01, and *** <i>p</i> < 0.001).					