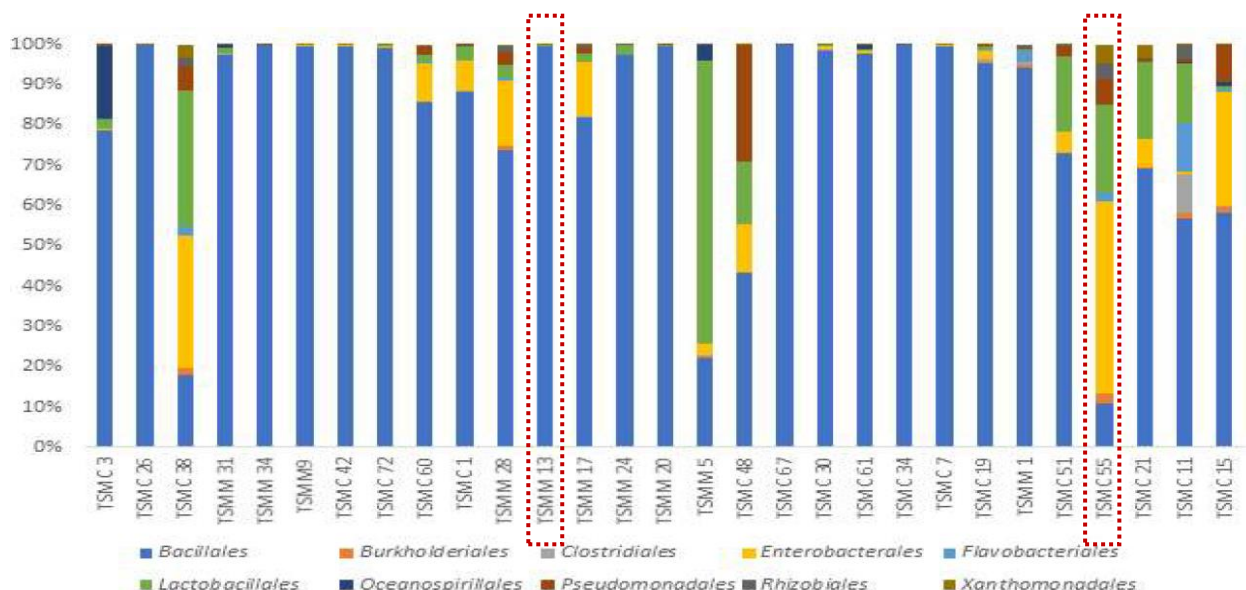
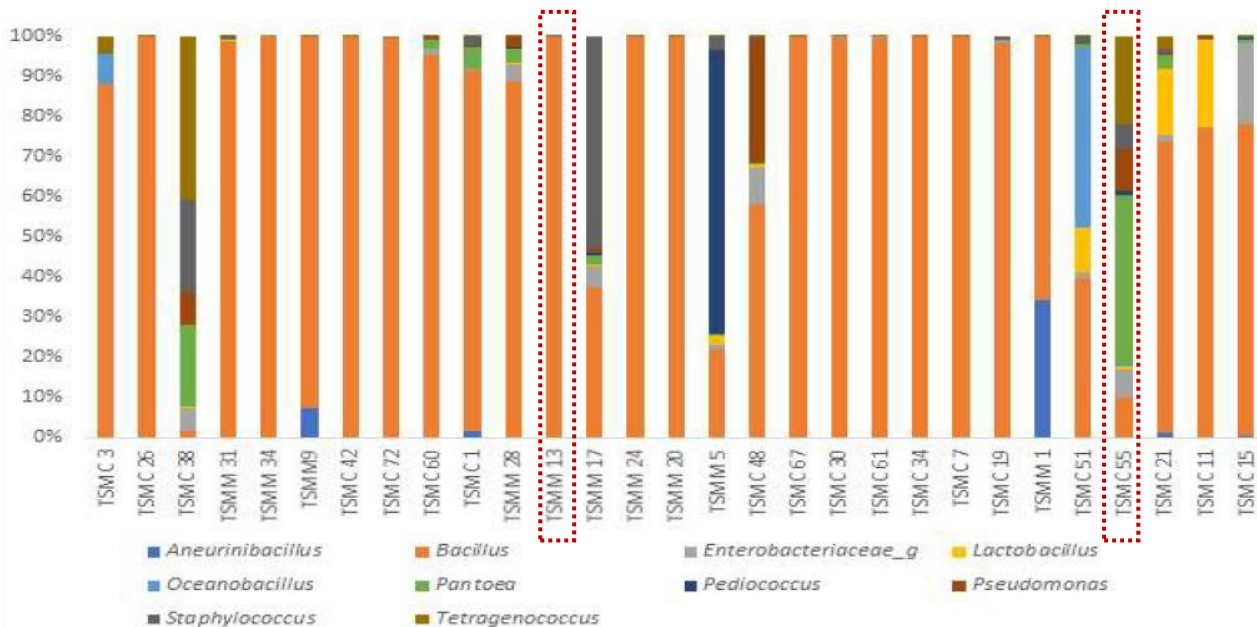


Supplemental Figure S1 .

A

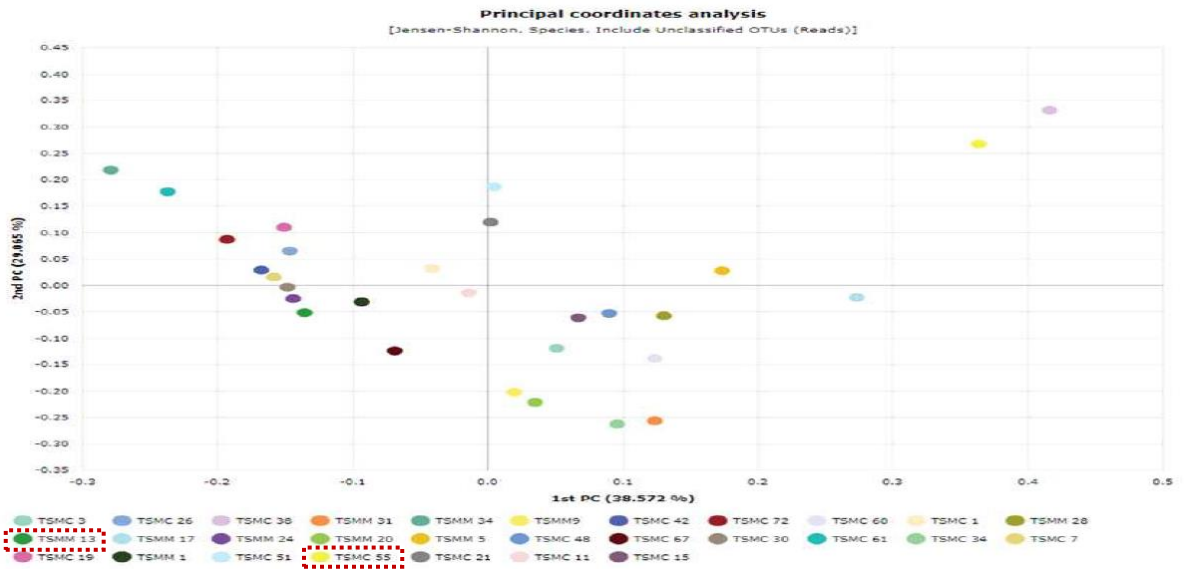


B



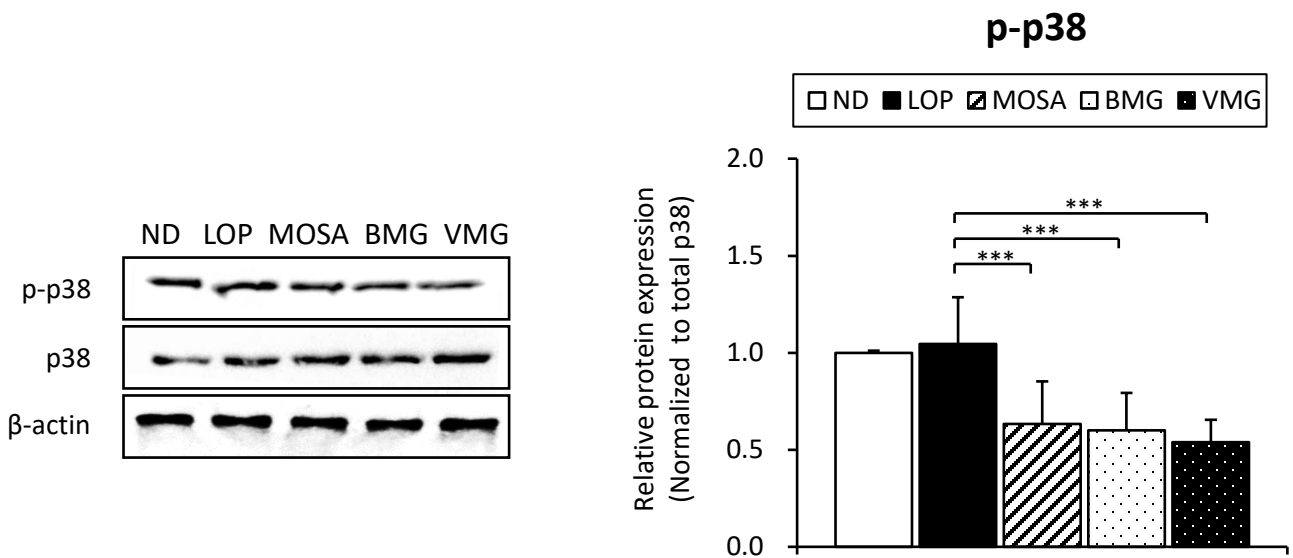
Taxonomic Composition Analysis of 29 Candidate *Gochujang* for Screening ($n = 1$ *Gochujang*). (A) 29 kinds of *Gochujang* taxonomic composition at order level and (B) at genus level. TSMC13(BMG) was selected as the representative of *Gochujang* with a high proportion of beneficial microorganisms. TSMC55(VMG) was chosen as the representative of *Gochujang* having a greater variety of species.

Supplemental Figure S2 .



Beta-diversity analysis of 29 kinds of *Gochujang* ($n = 29$). TSMC13(BMG) and TSMC(VMG) have different the structure of bacterial community.

Supplemental Figure S3 .



Effect of BMG and VMG on proteins involved in MAPK signaling in the colon tissue of ICR mice with Lop-induced constipation. Western blot bands of p-p38 and p38, and relative protein expression of p-p38. ND, nonconstipation group, LOP, loperamide (5 mg/kg BW) + vehicle-treated group, MOSA, loperamide (5 mg/kg BW) + mosapride citrate (3 mg/kg BW), BMG, loperamide (5 mg/kg BW) + BMG *Gochujang* (2 g/kg BW), VMG, loperamide (5 mg/kg BW) + VMG *Gochujang* (2 g/kg BW). Data were expressed as the mean \pm SD ($n = 7$ mice per group). *, $p < 0.001$, **, $p < 0.01$ and ***, $p < 0.01$ were showed significant between different groups. Abbreviations: ICR, Institute of Cancer Research; Lop, loperamide; MAPK, mitogen-activated protein kinase; p-p38, phospho-p38 kinase.

Supplemental Table S1. Alpha-diversity analysis of 29 kinds of *Gochujang*

No.	Sample name	Target reads	OTUs	CHAO	Shannon	Phylogenetic diversity	Good's coverage of libraries (%)
1	TSMC 1	91,231	74	80.43	2.27	185	99.99
2	TSMC 5	60,166	266	288.86	1.91	358	99.91
3	TSMC 9	73,279	141	168.75	1.02	207	99.95
4	TSMC 13	98,480	158	193.05	1.36	301	99.96
5	TSMC 17	54,885	470	545.96	2.05	686	99.78
6	TSMC 20	99,492	73	84	0.62	128	99.99
7	TSMC 24	94,360	126	136	1.69	204	99.98
8	TSMC 28	19,877	242	259.18	2.61	426	99.86
9	TSMC 31	98,076	61	74.2	0.78	128	99.99
10	TSMC 34	96,738	115	136.12	1.39	151	99.97
11	TSMC 1	84,179	238	257.38	2.65	366	99.96
12	TSMC 3	93,917	152	173	2.54	291	99.98
13	TSMC 7	96,767	88	97.56	0.95	167	99.98
14	TSMC 11	61,895	2729	2866.38	4.86	3564	99.29
15	TSMC 15	78,118	446	477.13	2.79	580	99.9
16	TSMC 19	70,853	432	486.01	1.89	536	99.84
17	TSMC 21	72,455	260	282.5	2.82	452	99.95
18	TSMC 26	85,901	151	190.42	1.05	203	99.95
19	TSMC 30	86,358	132	142.56	1.71	229	99.98
20	TSMC 34	99,366	50	61.25	0.33	101	99.99
21	TSMC 38	34,456	645	778.91	3.31	961	99.49
22	TSMC 42	92,549	150	165	1.48	243	99.97
23	TSMC 48	60,014	226	255.17	2.6	312	99.92
24	TSMC 51	36,990	459	501.36	3.27	557	99.75
25	TSMC 55	32,254	710	801.08	3.92	1041	99.53
26	TSMC 60	28,832	196	255.11	1.58	334	99.8
27	TSMC 61	75,904	173	194.5	1.26	292	99.94
28	TSMC 67	98,675	54	67	0.83	118	99.99
29	TSMC 72	84,905	207	241.45	1.54	297	99.94

Supplemental Table S2. The relative abundances of microorganisms in BMG at the species level

Order	Species	Percentage	Order	Species	Percentage
<i>Bacillales</i>	<i>Bacillus subtilis</i>	92.77%	<i>Burkholderiales</i>	<i>Aquabacterium parvum</i>	0.01%
	<i>Bacillus hisashii</i>	5.94%	<i>Corynebacteriales</i>	<i>Corynebacterium casei</i>	0.01%
	<i>Bacillus wiedmannii</i>	0.33%	<i>Enterobacterales</i>	<i>Proteus mirabilis</i>	0.01%
	<i>Brevibacillus borstelensis</i>	0.22%		<i>Enterobacter cloacae</i>	0.01%
	<i>Bacillus rhizosphaerae</i>	0.12%	<i>Lactobacillales</i>	<i>Lactobacillus rennini</i>	0.09%
	<i>Bacillus subterraneus</i>	0.07%		<i>Enterococcus hirae</i>	0.04%
	<i>Bacillus zhangzhouensis</i>	0.04%		<i>Lactococcus raffinolactis</i>	0.03%
	<i>Staphylococcus sciuri</i>	0.03%		<i>Leuconostoc mesenteroides</i>	0.01%
	<i>Bacillus chungangensis</i>	0.03%	<i>Micrococcales</i>	<i>Brevibacterium ravenpurgense</i>	0.03%
	<i>Bacillus smithii</i>	0.01%		<i>Brevibacterium sediminis</i>	0.01%
	<i>Bacillus oleronius</i>	0.01%		<i>Oscillatoriales</i>	<i>Aerosakkonema funiforme</i>
	<i>Bacillus zanthoxyli</i>	0.01%	<i>Pseudomonadales</i>		<i>Acinetobacter baumannii</i>
	<i>Kroppenstedtia eburnea</i>	0.01%		<i>Moraxella osloensis</i>	0.02%
	<i>Aneurinibacillus thermoaerophilus</i>	0.01%		<i>Pseudomonas thermotolerans</i>	0.01%
	<i>Bacillus thermoamylovorans</i>	0.01%		<i>Pseudomonas deceptionensis</i>	0.01%
	<i>Sporosarcina saromensis</i>	0.01%	<i>Sphingobacteriales</i>	<i>Sphingobacterium thermophilum</i>	0.01%
	<i>Staphylococcus gallinarum</i>	0.01%		Other	0.01%
	<i>Bacillus coagulans</i>	0.01%			
	<i>Bacillus plakortidis</i>	0.01%			
	<i>Exiguobacterium indicum</i>	0.01%			

Supplemental Table S3. The relative abundances of microorganisms in VMG at the species level

Order	Species	Percentage	Order	Species	Percentage	
<i>Oscillatoriales</i>	<i>Aerosakkonema funiforme</i>	66.93%		<i>Pseudomonas deceptionensis</i>	0.10%	
<i>Enterobacterales</i>	<i>Enterobacter cloacae</i>	12.38%	<i>Pseudomonadales</i>	<i>Pseudomonas composti</i>	0.03%	
	<i>Serratia nematodiphila</i>	0.51%		<i>Pseudomonas xiamenensis</i>	0.03%	
	<i>Providencia thailandensis</i>	0.29%		<i>Pseudomonas trivialis</i>	0.02%	
	<i>Rosenbergiella epipactidis</i>	0.11%		<i>Acinetobacter baumannii</i>	0.02%	
	<i>Cronobacter sakazakii</i>	0.11%		<i>Acinetobacter rudis</i>	0.01%	
	<i>Serratia quinivorans</i>	0.06%	<i>Xanthomonadales</i>	<i>Xanthomonas nasturtii</i>	0.72%	
	<i>Pectobacterium carotovorum</i>	0.02%		<i>Pseudomonas geniculata</i>	0.48%	
	<i>Pantoea vagans</i>	0.02%	<i>Rhizobiales</i>	<i>Ochrobactrum pseudogrignonense</i>	0.63%	
	<i>Escherichia fergusonii</i>	0.01%		<i>Agrobacterium larrymoorei</i>	0.40%	
	<i>Proteus mirabilis</i>	0.01%		<i>Paenochrobactrum gallinarii</i>	0.05%	
<i>Rouxiiella chamberiensis</i>	0.01%	<i>Methylorubrum populi</i>		0.02%		
		<i>Ochrobactrum intermedium</i>		0.02%		
<i>Lactobacillales</i>	<i>Tetragenococcus halophilus</i>	5.18%		<i>Aureimonas ureilytica</i>	0.01%	
	<i>Vagococcus penaei</i>	1.62%	<i>Burkholderiales</i>	<i>Corticimicrobacter populi</i>	0.20%	
	<i>Leuconostoc mesenteroides</i>	0.41%		<i>Alcaligenes aquatilis</i>	0.13%	
	<i>Enterococcus hirae</i>	0.32%		<i>Bordetella bronchiseptica</i>	0.04%	
	<i>Weissella confusa</i>	0.21%		<i>Lampropedia puyangensis</i>	0.03%	
	<i>Pediococcus stilesii</i>	0.20%		<i>Kerstesia similis</i>	0.01%	
	<i>Weissella fabalis</i>	0.10%		<i>Acidovorax soli</i>	0.01%	
	<i>Lactococcus lactis</i>	0.07%		<i>Aquabacterium parvum</i>	0.01%	
	<i>Lactobacillus sakei</i>	0.07%		<i>Verticella sediminum</i>	0.01%	
	<i>Facklamia tabacinasalis</i>	0.06%		<i>Flavobacteriales</i>	<i>Myroides odoratus</i>	0.13%
	<i>Lactobacillus plantarum</i>	0.01%			<i>Myroides injenensis</i>	0.12%
	<i>Lactobacillus brevis</i>	0.01%	<i>Myroides odoratimimus</i>		0.04%	
	<i>Lactobacillus homohiochii</i>	0.01%	<i>Flavobacterium ceti</i>		0.01%	
				<i>Myroides xuanwuensis</i>	0.01%	
			<i>Wautersiella enshiensis</i>	0.01%		
<i>Bacillales</i>	<i>Bacillus subtilis</i>	1.63%	<i>Micrococcales</i>	<i>Leucobacter tardus</i>	0.11%	
	<i>Staphylococcus gallinarum</i>	0.93%		<i>Microbacterium fluvii</i>	0.04%	
	<i>Staphylococcus sciuri</i>	0.35%		<i>Brevibacterium sediminis</i>	0.02%	
	<i>Bacillus zhangzhouensis</i>	0.21%		<i>Populibacterium corticicola</i>	0.02%	
	<i>Bacillus zanthoxyli</i>	0.17%		<i>Arthrobacter echini</i>	0.01%	
	<i>Bacillus wiedmannii</i>	0.12%	<i>Leucobacter musarum</i>	0.01%		
	<i>Bacillus rhizosphaerae</i>	0.09%	<i>Corynebacteriales</i>	<i>Corynebacterium terpenotabidum</i>	0.05%	
	<i>Bacillus hisashii</i>	0.05%		<i>Corynebacterium casei</i>	0.01%	
	<i>Bacillus plakortidis</i>	0.04%	<i>Erysipelotrichales</i>	<i>Erysipelothrix inopinata</i>	0.05%	
	<i>Rummeliibacillus stabekisii</i>	0.02%	<i>Caulobacterales</i>	<i>Brevundimonas olei</i>	0.01%	
	<i>Bacillus velezensis</i>	0.01%		<i>Brevundimonas albigilva</i>	0.01%	
	<i>Lysinibacillus boronitolerans</i>	0.01%	<i>Cellvibrionales</i>	<i>Cellvibrio diazotrophicus</i>	0.02%	
	<i>Oceanobacillus timonensis</i>	0.01%	<i>Rhodospirillales</i>	<i>Acetobacter orientalis</i>	0.02%	
	<i>Saccharibacillus endophyticus</i>	0.01%	<i>Nostocales</i>	<i>Loriellopsis cavernicola</i>	0.01%	
<i>Macrocooccus canis</i>	0.01%	<i>Rhodobacterales</i>		<i>Falsirhodobacter halotolerans</i>	0.01%	
<i>Pseudomonadales</i>	<i>Pseudomonas oryzihabitans</i>	0.88%	Other		2.10%	
	<i>Pseudomonas lactis</i>	0.55%				
	<i>Pseudomonas japonica</i>	0.16%				

Supplemental Table S4. Nutritional ingredients of BMG and VMG

	BMG	VMG
Calories (kcal/100g)	187.63	254.45
Total Carbohydrate (g/100g)	34.34	57.02
Sugars (g/100g)	9.54	31.14
Protein (g/100g)	6.11	3.96
Total Fat (g/100g)	2.87	1.17
Saturated Fat (g/100g)	0.09	0.04
Trans Fat (g/100g)	0.00	0.00
Cholesterol (mg/100g)	Not Detect	Not Detect
Sodium (mg/100g)	2,665.64	3,185.48