Supplementary data

Supplementary Table s1. Relative abundance (%) of major prokaryotic phyla, families, and genera at 3H *in vitro* incubation (which represented at least 0.1% of the average relative abundance across all samples) discussed in this study

Microbiota	Overall average (%)	Inoculum		Diet			SEM
		HWG	JBG	Growing	Early fattening	Late fattening	
Phylum level							
Firmicutes	84.54	84.21	84.87	85.25	84.33	84.03	0.49
Patescibacteria	5.13	3.86	6.39	4.53	5.15	5.70	0.37
Actinobacteriota	3.17	3.71	2.63	3.10	3.21	3.21	0.20
Proteobacteria	2.66	3.40	1.92	2.85	2.84	2.28	0.37
Bacteroidota	2.21	3.03	1.39	2.19	1.85	2.60	0.35
Euryarchaeota	1.37	0.82	1.91	1.25	1.38	1.46	0.21
Family level							
Lachnospiraceae	16.05	16.16	15.95	16.97	16.94	14.35	0.51
Planococcaceae	14.08	9.59	18.57	13.34	11.86	12.55	0.99
Ruminococcaceae	13.59	16.96	10.22	16.45	14.47	13.21	0.96
Oscillospiraceae	7.97	8.22	7.72	7.98	7.63	8.56	0.46
Succinivibrionaceae	5.87	10.01	1.72	6.10	7.81	7.83	1.39
Peptostreptococcaceae	5.08	2.79	7.37	3.81	4.58	4.57	0.53
Saccharimonadaceae	4.28	2.55	6.02	3.40	3.60	4.12	0.39
Christensenellaceae	4.25	5.73	2.76	4.34	4.84	5.04	0.40
[Eubacterium]_coprostanoligenes_group	4.10	2.99	5.22	3.21	3.71	4.28	0.40
Clostridia UCG-014	3.58	3.24	3.93	3.36	3.26	3.78	0.22
Atopobiaceae	2.02	2.07	1.96	2.03	2.06	2.02	0.19
Prevotellaceae	1.82	2.41	1.23	2.07	1.71	2.28	0.20
Anaerovoracaceae	1.64	1.63	1.66	1.53	1.82	1.56	0.09
Clostridiaceae	1.44	0.67	2.22	1.04	1.10	1.42	0.18
Methanobacteriaceae	1.26	0.61	1.91	0.99	0.99	1.16	0.17
Oscillospirales UCG-010	0.77	0.74	0.80	0.76	0.69	0.82	0.07
Eubacteriaceae	0.51	0.76	0.25	0.60	0.60	0.58	0.07
Monoglobaceae	0.48	0.49	0.47	0.38	0.52	0.55	0.09
Eggerthellaceae	0.33	0.38	0.28	0.42	0.34	0.29	0.05
Absconditabacteriales_(SR1)	0.31	0.27	0.36	0.30	0.31	0.28	0.04
Rikenellaceae	0.26	0.39	0.12	0.27	0.24	0.39	0.06
Hungateiclostridiaceae	0.20	0.22	0.19	0.17	0.20	0.26	0.04
Bacillaceae	0.20	0.24	0.16	0.24	0.18	0.21	0.06
Bifidobacteriaceae	0.17	0.04	0.30	0.12	0.16	0.11	0.03
Clostridia_vadinBB60_group	0.16	0.13	0.20	0.09	0.16	0.21	0.04
Oscillospirales UCG-011	0.14	0.03	0.25	0.05	0.20	0.05	0.07
Anaerolineaceae	0.11	0.10	0.12	0.08	0.09	0.14	0.03
Acholeplasmataceae	0.09	0.13	0.04	0.12	0.09	0.10	0.03
Genus level							
Solibacillus	13.30	8.77	17.84	13.86	12.26	13.79	1.32
Ruminococcaceae CAG-352	6.02	8.82	3.21	7.00	5.70	5.35	0.73
[*Eubacterium*] coprostanoligenes group	5.06	4.90	5.22	4.25	5.10	5.83	0.22
Oscillospiraceae NK4A214 group	5.03	4.02	6.05	5.07	4.33	5.70	0.40
Candidatus *Saccharimonas*	4.82	3.63	6.02	4.25	4.77	5.45	0.36
Clostridia UCG-014	4.02	4.12	3.93	3.77	3.84	4.46	0.22
Ruminococcus	3.72	5.00	2.43	3.85	4.19	3.10	0.41
Christensenellaceae R-7 group	3.57	4.38	2.76	3.29	3.30	4.13	0.32
Paeniclostridium	3.28	2.33	4.22	2.80	3.56	3.47	0.29
Succinivibrio	2.51	3.31	1.72	2.65	2.76	2.12	0.35

Romboutsia	2.48	1.95	3.01	2.28	2.50	2.66	0.20
Pseudobutyrivibrio	2.25	1.64	2.87	2.43	2.31	2.02	0.27
Prevotella	1.78	2.36	1.20	1.83	1.45	2.06	0.29
Clostridium sensu stricto 1	1.66	1.11	2.22	1.43	1.49	2.06	0.18
Ruminococcaceae UCG-001	1.64	1.49	1.78	1.93	1.51	1.47	0.11
Oscillospiraceae UCG-002	1.52	1.55	1.49	1.02	1.45	2.09	0.15
[*Eubacterium*] ruminantium group	1.52	1.90	1.14	1.50	1.58	1.47	0.19
Howardella	1.47	1.34	1.59	1.29	1.49	1.63	0.09
Methanobrevibacter	1.37	0.82	1.91	1.25	1.38	1.46	0.21
[*Ruminococcus*] gauvreauii group	1.13	0.73	1.54	1.02	1.08	1.29	0.15
Acetitomaculum	0.99	0.79	1.18	0.87	1.00	1.09	0.08
Lachnospiraceae UCG-008	0.82	0.86	0.79	0.60	1.08	0.78	0.10
Anaerovoracaceae Family XIII AD3011 group	0.74	0.51	0.97	0.69	0.88	0.64	0.09
Oscillospirales UCG-010	0.71	0.61	0.80	0.73	0.60	0.78	0.10
Monoglobus	0.65	0.83	0.47	0.47	0.66	0.82	0.12
Pseudoramibacter	0.63	1.00	0.25	0.63	0.59	0.66	0.10
Mogibacterium	0.60	0.73	0.46	0.48	0.70	0.61	0.07
[*Eubacterium*] ventriosum group	0.57	0.42	0.72	0.54	0.52	0.65	0.06
Roseburia	0.55	0.72	0.38	0.76	0.53	0.34	0.14
Absconditabacteriales (SR1)	0.30	0.23	0.36	0.27	0.37	0.25	0.05
Rikenellaceae RC9 gut group	0.28	0.44	0.12	0.33	0.16	0.35	0.08
Saccharofermentans	0.24	0.29	0.19	0.18	0.23	0.31	0.06
Oribacterium	0.24	0.10	0.37	0.55	0.08	0.08	0.10
Bacillus	0.22	0.32	0.11	0.25	0.10	0.29	0.09
Ruminococcaceae uncultured	0.21	0.01	0.42	0.21	0.32	0.11	0.07
Lachnospiraceae XPB1014 group	0.20	0.03	0.37	0.00	0.30	0.31	0.09
[*Eubacterium*] hallii group	0.16	0.02	0.30	0.34	0.08	0.07	0.06
Blautia	0.13	0.00	0.27	0.21	0.13	0.07	0.05
Oscillospirales UCG-011	0.13	0.00	0.25	0.00	0.29	0.08	0.10
Paenibacillus	0.11	0.15	0.08	0.13	0.00	0.22	0.04
Clostridia vadinBB60 group	0.11	0.01	0.20	0.05	0.11	0.16	0.05

HWG, Hanwoo inoculum-treated group; JBG, Jeju Black inoculum-treated group; SEM, standard error of the mean.

Supplementary Table s2. Relative abundance (%) of major prokaryotic phyla, families, and genera at 24H *in vitro* incubation (which represented at least 0.1% of the average relative abundance across all samples) discussed in this study

Microbiota	Overall average (%)	Inoculum		Diet			SEM
		HWG	JBG	Growing	Early fattening	Late fattening	
Phylum level							
Firmicutes	74.91	74.46	75.37	77.28	73.45	74.01	1.08
Proteobacteria	15.91	16.98	14.85	13.24	17.92	16.58	1.02
Bacteroidota	2.96	2.75	3.16	2.92	2.69	3.25	0.24
Patescibacteria	2.20	1.77	2.62	2.33	2.12	2.13	0.15
Actinobacteriota	1.46	1.34	1.57	1.93	1.20	1.23	0.14
Euryarchaeota	0.58	0.40	0.75	0.64	0.50	0.59	0.09
Chloroflexi	0.27	0.15	0.38	0.26	0.21	0.33	0.04
Synergistota	0.21	0.07	0.35	0.21	0.25	0.16	0.05
Cyanobacteria	0.15	0.19	0.10	0.25	0.11	0.07	0.05
Verrucomicrobiota	0.12	0.14	0.11	0.12	0.09	0.16	0.03
Family level							
Lachnospiraceae	19.44	18.17	20.70	20.19	20.56	17.55	0.95
Succinivibrionaceae	15.68	16.72	14.63	13.07	17.79	16.18	1.01
Oscillospiraceae	11.65	10.63	12.67	11.55	11.86	11.54	0.41
Ruminococcaceae	10.69	13.27	8.10	11.41	10.07	10.57	0.71
Planococcaceae	10.40	9.27	11.54	12.56	9.28	9.37	0.85
Christensenellaceae	6.26	7.08	5.45	5.65	6.42	6.71	0.35
Prevotellaceae	2.43	2.35	2.52	2.51	2.12	2.67	0.22
Clostridia_UCG-014	2.19	2.35	2.02	2.16	1.99	2.41	0.13
Saccharimonadaceae	1.88	1.47	2.28	1.93	1.85	1.85	0.14
Anaerovoracaceae	1.75	1.60	1.90	1.56	1.54	2.15	0.11
Peptostreptococcaceae	1.62	1.20	2.04	1.76	1.46	1.64	0.16
[Eubacterium]_coprostanoligenes_group	1.26	1.08	1.43	1.14	1.11	1.52	0.10
Atopobiaceae	1.10	1.04	1.16	1.48	0.88	0.94	0.10
Oscillospirales UCG-010	0.93	0.86	1.01	0.75	1.02	1.04	0.08
Methanobacteriaceae	0.58	0.40	0.75	0.64	0.50	0.59	0.09
Rikenellaceae	0.45	0.34	0.56	0.39	0.52	0.44	0.06
Eubacteriaceae	0.40	0.53	0.26	0.40	0.38	0.40	0.05
Clostridiaceae	0.33	0.23	0.44	0.28	0.41	0.31	0.05
Absconditabacteriales_(SR1)	0.32	0.30	0.33	0.40	0.26	0.29	0.03
Acidaminococcaceae	0.31	0.27	0.35	0.27	0.32	0.36	0.06
Clostridia_vadinBB60_group	0.30	0.25	0.36	0.19	0.31	0.41	0.06
Acholeplasmataceae	0.28	0.27	0.29	0.36	0.21	0.26	0.03
Oscillospirales UCG-011	0.27	0.05	0.48	0.39	0.31	0.11	0.09
Anaerolineaceae	0.27	0.15	0.38	0.26	0.21	0.33	0.04
Eggerthellaceae	0.25	0.27	0.23	0.33	0.22	0.21	0.04
Synergistaceae	0.21	0.07	0.35	0.21	0.25	0.16	0.05
Gastranaerophilales	0.15	0.19	0.10	0.25	0.11	0.07	0.05
Rhodospirillales uncultured	0.14	0.14	0.13	0.11	0.08	0.22	0.03
Victivallales vadinBE97	0.12	0.13	0.10	0.11	0.09	0.15	0.03
Monoglobaceae	0.11	0.15	0.07	0.15	0.14	0.04	0.03
Hungateiclostridiaceae	0.11	0.15	0.06	0.08	0.12	0.11	0.03
Genus level							
Succinivibrio	13.56	14.28	12.84	11.36	15.44	13.89	0.85
Solibacillus	9.48	8.32	10.64	11.53	8.56	8.35	0.79
Christensenellaceae R-7 group	6.22	7.06	5.38	5.65	6.41	6.60	0.34
Oscillospiraceae NK4A214 group	6.01	5.05	6.96	5.65	5.86	6.51	0.37
Oscillospiraceae UCG-002	5.27	5.34	5.20	5.54	5.56	4.71	0.16
Ruminococcus	5.06	6.65	3.46	4.92	5.42	4.83	0.48
Ruminococcaceae CAG-352	2.72	3.73	1.71	2.66	2.45	3.04	0.28

Pseudobutyrivibrio	2.37	1.57	3.17	2.76	2.53	1.81	0.35
Prevotella	2.34	2.20	2.48	2.32	2.07	2.64	0.21
Clostridia UCG-014	2.19	2.35	2.02	2.16	1.99	2.41	0.13
Roseburia	1.95	2.37	1.54	1.69	1.97	2.20	0.16
Candidatus Saccharimonas	1.88	1.47	2.28	1.93	1.85	1.85	0.14
Succinivibrionaceae UCG-002	1.51	1.98	1.04	1.02	1.72	1.78	0.20
[*Eubacterium*] ruminantium group	1.33	1.67	0.99	1.24	1.58	1.18	0.12
[*Eubacterium*] coprostanoligenes group	1.26	1.08	1.43	1.14	1.11	1.52	0.10
Acetitomaculum	1.22	1.01	1.42	1.28	1.12	1.25	0.08
[*Ruminococcus*] gauvreauii group	1.20	0.72	1.69	1.21	1.17	1.22	0.15
Paeniclostridium	0.96	0.71	1.20	1.01	0.88	0.98	0.09
Oscillospirales UCG-010	0.93	0.86	1.01	0.75	1.02	1.04	0.08
Coprococcus	0.91	1.20	0.62	0.73	1.17	0.82	0.10
Ruminococcaceae uncultured	0.87	0.72	1.02	1.46	0.63	0.53	0.14
Lachnospiraceae XPB1014 group	0.82	0.41	1.22	0.93	0.99	0.54	0.12
Romboutsia	0.65	0.48	0.83	0.74	0.58	0.63	0.08
Anaerobiospirillum	0.60	0.44	0.75	0.68	0.63	0.48	0.07
Anaerovoracaceae Family XIII AD3011 group	0.59	0.51	0.67	0.62	0.53	0.63	0.06
Methanobrevibacter	0.57	0.40	0.75	0.63	0.50	0.59	0.09
Lachnospiraceae NK4A136 group	0.51	0.55	0.48	0.59	0.54	0.41	0.09
Ruminococcaceae UCG-001	0.51	0.30	0.71	0.64	0.44	0.44	0.08
Anaerovorax	0.49	0.45	0.54	0.45	0.45	0.58	0.03
Mogibacterium	0.48	0.44	0.53	0.42	0.46	0.57	0.03
Lachnospiraceae UCG-008	0.47	0.47	0.47	0.42	0.48	0.52	0.03
Rikenellaceae RC9 gut group	0.45	0.34	0.56	0.39	0.52	0.44	0.06
Pseudoramibacter	0.40	0.53	0.26	0.40	0.38	0.40	0.05
Clostridium sensu stricto 1	0.33	0.23	0.44	0.28	0.41	0.31	0.05
Absconditabacteriales (SR1)	0.32	0.30	0.33	0.40	0.26	0.29	0.03
Clostridia vadinBB60 group	0.30	0.25	0.36	0.19	0.31	0.41	0.06
[*Eubacterium*] xylanophilum group	0.29	0.28	0.30	0.36	0.31	0.20	0.04
Howardella	0.28	0.19	0.37	0.25	0.29	0.30	0.05
Anaeroplasma	0.28	0.27	0.29	0.36	0.21	0.26	0.03
Oscillospirales UCG-011	0.27	0.05	0.48	0.39	0.31	0.11	0.09
Flexilinea	0.27	0.15	0.38	0.26	0.21	0.33	0.04
Oscillospiraceae uncultured	0.23	0.13	0.32	0.29	0.24	0.15	0.05
Blautia	0.22	0.00	0.45	0.18	0.22	0.27	0.07
Oribacterium	0.20	0.11	0.28	0.41	0.10	0.08	0.10
Coriobacteriaceae UCG-002	0.19	0.27	0.12	0.34	0.09	0.15	0.05
Ruminococcaceae	0.19	0.27	0.11	0.18	0.18	0.21	0.04
Synergistaceae uncultured	0.15	0.04	0.27	0.20	0.16	0.11	0.04
Gastranaerophilales	0.15	0.19	0.10	0.25	0.11	0.07	0.05
Rhodospirillales uncultured	0.14	0.14	0.13	0.11	0.08	0.22	0.03
Victivallales vadinBE97	0.12	0.13	0.10	0.11	0.09	0.15	0.03
[*Eubacterium*] hallii group	0.12	0.05	0.18	0.15	0.09	0.11	0.03
Monoglobus	0.11	0.15	0.07	0.15	0.14	0.04	0.03
Saccharofermentans	0.11	0.15	0.06	0.08	0.12	0.11	0.03

HWG, Hanwoo inoculum-treated group; JBG, Jeju Black inoculum-treated group; SEM, standard error of the mean.

Supplementary Table s3. Major predicted enzymes (which represented at least 0.1% of the average relative abundance across all samples) differentially abundant by inoculum effect ($q \leq 0.05$) at 3 h of incubation

Enzymes	EC number	Relative abundance (%)		SEM	Coefficient	*p*-value	*q*-value
		HWG	JBG				
Alcohol dehydrogenase	EC:1.1.1.1	0.208	0.224	0.0043	0.0250	<0.0001	0.0019
dTDP-4-dehydrorhamnose reductase	EC:1.1.1.133	0.110	0.099	0.0022	-0.0152	<0.0001	0.0025
3-hydroxybutyryl-CoA dehydrogenase	EC:1.1.1.157	0.125	0.141	0.0032	0.0210	0.0020	0.0258
5-amino-6-(5-phosphoribosylamino)uracil reductase	EC:1.1.1.193	0.107	0.111	0.0013	0.0073	0.0002	0.0040
Histidinol dehydrogenase	EC:1.1.1.23	0.147	0.142	0.0014	-0.0074	<0.0001	0.0006
Shikimate dehydrogenase	EC:1.1.1.25	0.194	0.184	0.0024	-0.0151	<0.0001	0.0010
Isocitrate dehydrogenase (NADP(+))	EC:1.1.1.42	0.125	0.120	0.0009	-0.0043	0.0038	0.0399
Ketol-acid reductoisomerase (NADP(+))	EC:1.1.1.86	0.144	0.140	0.0014	-0.0050	0.0007	0.0119
Glycerol-3-phosphate dehydrogenase (NAD(P)(+))	EC:1.1.1.94	0.154	0.150	0.0009	-0.0052	0.0033	0.0368
Phosphoglycerate dehydrogenase	EC:1.1.1.95	0.203	0.198	0.0028	-0.0107	0.0006	0.0103
Glycerol-3-phosphate dehydrogenase	EC:1.1.5.3	0.110	0.120	0.0015	0.0121	<0.0001	0.0005
Peroxiredoxin	EC:1.11.1.15	0.209	0.213	0.0029	0.0119	0.0013	0.0183
Glutathione peroxidase	EC:1.11.1.9	0.123	0.110	0.0025	-0.0131	0.0015	0.0214
Hydrogen dehydrogenase (NADP(+))	EC:1.12.1.3	0.258	0.227	0.0103	-0.0479	0.0002	0.0038
Ribonucleoside-diphosphate reductase	EC:1.17.4.1	0.151	0.168	0.0049	0.0276	<0.0001	0.0007
Aldehyde dehydrogenase (NAD(+))	EC:1.2.1.3	0.125	0.152	0.0075	0.0421	0.0006	0.0103
N-acetyl-gamma-glutamyl-phosphate reductase	EC:1.2.1.38	0.147	0.142	0.0014	-0.0075	<0.0001	0.0006
Glutamate-5-semialdehyde dehydrogenase	EC:1.2.1.41	0.145	0.138	0.0016	-0.0098	<0.0001	0.0018
Pyruvate synthase	EC:1.2.7.1	0.308	0.281	0.0099	-0.0422	0.0003	0.0053
Indolepyruvate ferredoxin oxidoreductase	EC:1.2.7.8	0.130	0.110	0.0044	-0.0294	0.0004	0.0082
Arsenate reductase (glutaredoxin)	EC:1.20.4.1	0.138	0.151	0.0021	0.0179	<0.0001	0.0001
Coproporphyrinogen dehydrogenase	EC:1.3.99.22	0.297	0.290	0.0021	-0.0100	0.0006	0.0108
Glutamate dehydrogenase (NADP(+))	EC:1.4.1.4	0.145	0.136	0.0016	-0.0140	<0.0001	<0.0001
L-aspartate oxidase	EC:1.4.3.16	0.133	0.126	0.0018	-0.0107	0.0039	0.0402
Glycine dehydrogenase (aminomethyl-transferring)	EC:1.4.4.2	0.108	0.120	0.0026	0.0165	<0.0001	0.0005
Methylenetetrahydrofolate reductase (NAD(P)H)	EC:1.5.1.20	0.112	0.099	0.0026	-0.0178	<0.0001	0.0011
Dihydrofolate reductase	EC:1.5.1.3	0.103	0.112	0.0021	0.0109	<0.0001	0.0002
NADH:ubiquinone reductase (H(+)-translocating)	EC:1.6.5.3	0.489	0.450	0.0079	-0.0443	0.0011	0.0164
Dihydrolipoyl dehydrogenase	EC:1.8.1.4	0.147	0.156	0.0039	0.0173	0.0049	0.0480
Uroporphyrinogen-III C-methyltransferase	EC:2.1.1.107	0.141	0.149	0.0031	0.0149	0.0002	0.0040
Methionine synthase	EC:2.1.1.13	0.182	0.164	0.0046	-0.0255	<0.0001	0.0011
16S rRNA (cytosine(967)-C(5))-methyltransferase	EC:2.1.1.176	0.159	0.153	0.0023	-0.0077	0.0004	0.0077
23S rRNA (pseudouridine(1915)-N(3))-methyltransferase	EC:2.1.1.177	0.145	0.141	0.0012	-0.0060	0.0001	0.0036
23S rRNA (uracil(1939)-C(5))-methyltransferase	EC:2.1.1.190	0.223	0.204	0.0027	-0.0249	<0.0001	<0.0001
23S rRNA (adenine(2503)-C(2))-methyltransferase	EC:2.1.1.192	0.156	0.154	0.0009	-0.0040	0.0045	0.0446
DNA (cytosine-5-)-methyltransferase	EC:2.1.1.37	0.222	0.202	0.0048	-0.0278	0.0001	0.0030
Methylated-DNA--[protein]-cysteine S-methyltransferase	EC:2.1.1.63	0.121	0.136	0.0020	0.0232	<0.0001	0.0001
Site-specific DNA-methyltransferase (adenine-specific)	EC:2.1.1.72	0.576	0.496	0.0138	-0.0790	<0.0001	<0.0001
Protein-glutamate O-methyltransferase	EC:2.1.1.80	0.105	0.115	0.0022	0.0150	0.0005	0.0093
Phosphoribosylglycinamide formyltransferase	EC:2.1.2.2	0.159	0.155	0.0009	-0.0067	<0.0001	0.0023
Phosphoribosylaminoimidazolecarboxamide formyltransferase	EC:2.1.2.3	0.159	0.155	0.0010	-0.0072	0.0003	0.0057
Methionyl-tRNA formyltransferase	EC:2.1.2.9	0.155	0.152	0.0009	-0.0055	0.0021	0.0266
Transaldolase	EC:2.2.1.2	0.105	0.113	0.0016	0.0112	0.0005	0.0092
Acetolactate synthase	EC:2.2.1.6	0.433	0.417	0.0060	-0.0177	0.0011	0.0167
Amino-acid N-acetyltransferase	EC:2.3.1.1	0.150	0.144	0.0021	-0.0059	0.0016	0.0222
Beta-ketoacyl-[acyl-carrier-protein] synthase II	EC:2.3.1.179	0.222	0.192	0.0035	-0.0343	<0.0001	<0.0001
Beta-ketoacyl-[acyl-carrier-protein] synthase III	EC:2.3.1.180	0.154	0.167	0.0023	0.0177	<0.0001	0.0007
N(6)-L-threonylcarbamoyladenine synthase	EC:2.3.1.234	0.218	0.208	0.0033	-0.0147	0.0013	0.0192
Serine O-acetyltransferase	EC:2.3.1.30	0.154	0.151	0.0010	-0.0061	0.0008	0.0122
Homoserine O-succinyltransferase	EC:2.3.1.46	0.140	0.132	0.0015	-0.0129	<0.0001	<0.0001
1-acylglycerol-3-phosphate O-acyltransferase	EC:2.3.1.51	0.203	0.197	0.0022	-0.0100	0.0015	0.0204
Maltose O-acetyltransferase	EC:2.3.1.79	0.135	0.119	0.0033	-0.0224	<0.0001	0.0014

Phosphate acetyltransferase	EC:2.3.1.8	0.157	0.150	0.0021	-0.0108	0.0005	0.0093
Acetyl-CoA C-acetyltransferase	EC:2.3.1.9	0.164	0.192	0.0052	0.0363	0.0004	0.0082
Citrate (Si)-synthase	EC:2.3.3.1	0.153	0.148	0.0015	-0.0091	<0.0001	0.0018
Peptidoglycan glycosyltransferase	EC:2.4.1.129	0.117	0.106	0.0020	-0.0185	<0.0001	0.0018
1,4-alpha-glucan branching enzyme	EC:2.4.1.18	0.167	0.148	0.0042	-0.0280	<0.0001	0.0005
Starch synthase	EC:2.4.1.21	0.142	0.135	0.0021	-0.0136	0.0002	0.0037
4-alpha-glucanotransferase	EC:2.4.1.25	0.112	0.103	0.0028	-0.0174	<0.0001	0.0025
Orotate phosphoribosyltransferase	EC:2.4.2.10	0.200	0.186	0.0027	-0.0176	<0.0001	0.0001
Amidophosphoribosyltransferase	EC:2.4.2.14	0.211	0.200	0.0032	-0.0162	0.0001	0.0034
ATP phosphoribosyltransferase	EC:2.4.2.17	0.143	0.137	0.0015	-0.0060	<0.0001	0.0020
Adenine phosphoribosyltransferase	EC:2.4.2.7	0.151	0.146	0.0008	-0.0061	0.0002	0.0042
S-adenosylmethionine:tRNA ribosyltransferase-isomerase	EC:2.4.99.17	0.160	0.156	0.0009	-0.0073	0.0002	0.0040
Cob(I)yrinic acid a,c-diamide adenosyltransferase	EC:2.5.1.17	0.145	0.152	0.0016	0.0087	0.0007	0.0119
Thiamine-phosphate diphosphorylase	EC:2.5.1.3	0.169	0.162	0.0012	-0.0094	0.0003	0.0057
Heptaprenyl diphosphate synthase	EC:2.5.1.30	0.151	0.156	0.0024	0.0074	0.0039	0.0402
Cysteine synthase	EC:2.5.1.47	0.249	0.232	0.0025	-0.0192	<0.0001	0.0011
O-acetylhomoserine aminocarboxypropyltransferase	EC:2.5.1.49	0.258	0.241	0.0035	-0.0254	<0.0001	0.0001
UDP-N-acetylglucosamine 1-carboxyvinyltransferase	EC:2.5.1.7	0.249	0.242	0.0026	-0.0087	0.0049	0.0474
tRNA dimethylallyltransferase	EC:2.5.1.75	0.159	0.155	0.0010	-0.0067	0.0006	0.0102
6,7-dimethyl-8-ribityllumazine synthase	EC:2.5.1.78	0.108	0.113	0.0013	0.0088	<0.0001	0.0008
Riboflavin synthase	EC:2.5.1.9	0.108	0.113	0.0013	0.0088	<0.0001	0.0007
Aspartate transaminase	EC:2.6.1.1	0.167	0.184	0.0020	0.0163	0.0003	0.0068
Acetylornithine transaminase	EC:2.6.1.11	0.148	0.143	0.0013	-0.0071	<0.0001	0.0021
Phosphoserine transaminase	EC:2.6.1.52	0.131	0.121	0.0013	-0.0146	<0.0001	<0.0001
Histidinol-phosphate transaminase	EC:2.6.1.9	0.175	0.166	0.0024	-0.0103	<0.0001	0.0010
Ribokinase	EC:2.7.1.15	0.116	0.129	0.0018	0.0165	<0.0001	<0.0001
Adenosylcobinamide kinase	EC:2.7.1.156	0.099	0.110	0.0012	0.0099	<0.0001	0.0006
Glucokinase	EC:2.7.1.2	0.178	0.173	0.0024	-0.0148	0.0001	0.0030
NAD(+) kinase	EC:2.7.1.23	0.163	0.159	0.0006	-0.0061	<0.0001	0.0007
Dephospho-CoA kinase	EC:2.7.1.24	0.153	0.150	0.0010	-0.0051	0.0032	0.0356
Homoserine kinase	EC:2.7.1.39	0.137	0.132	0.0010	-0.0071	0.0017	0.0229
Uridine kinase	EC:2.7.1.48	0.164	0.182	0.0033	0.0200	<0.0001	0.0009
Hydroxymethylpyrimidine kinase	EC:2.7.1.49	0.139	0.131	0.0010	-0.0097	<0.0001	0.0003
1-phosphofructokinase	EC:2.7.1.56	0.110	0.102	0.0023	-0.0142	0.0031	0.0346
Galactokinase	EC:2.7.1.6	0.111	0.102	0.0015	-0.0150	<0.0001	0.0010
Shikimate kinase	EC:2.7.1.71	0.210	0.205	0.0027	-0.0114	0.0002	0.0048
Non-specific serine/threonine protein kinase	EC:2.7.11.1	0.480	0.456	0.0092	-0.0268	<0.0001	<0.0001
Histidine kinase	EC:2.7.13.3	0.897	0.955	0.0080	0.0508	<0.0001	0.0001
Acetate kinase	EC:2.7.2.1	0.142	0.137	0.0020	-0.0099	0.0051	0.0490
Glutamate 5-kinase	EC:2.7.2.11	0.145	0.138	0.0016	-0.0099	<0.0001	0.0017
Aspartate kinase	EC:2.7.2.4	0.232	0.226	0.0012	-0.0065	<0.0001	0.0014
Acetylglutamate kinase	EC:2.7.2.8	0.147	0.141	0.0013	-0.0075	<0.0001	0.0006
Phosphoenolpyruvate--protein phosphotransferase	EC:2.7.3.9	0.167	0.147	0.0024	-0.0213	<0.0001	0.0001
Phosphomethylpyrimidine kinase	EC:2.7.4.7	0.139	0.131	0.0010	-0.0097	<0.0001	0.0003
2-amino-4-hydroxy-6-hydroxymethyldihydropteridine diphosphokinase	EC:2.7.6.3	0.108	0.113	0.0029	0.0094	0.0003	0.0064
Nicotinate-nucleotide adenylyltransferase	EC:2.7.7.18	0.156	0.155	0.0009	-0.0040	0.0035	0.0379
Glucose-1-phosphate thymidylyltransferase	EC:2.7.7.24	0.129	0.122	0.0025	-0.0135	0.0007	0.0111
Glucose-1-phosphate adenylyltransferase	EC:2.7.7.27	0.257	0.251	0.0043	-0.0175	0.0010	0.0156
2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase	EC:2.7.7.60	0.215	0.191	0.0042	-0.0285	<0.0001	0.0001
Adenosylcobinamide-phosphate guanylyltransferase	EC:2.7.7.62	0.100	0.112	0.0013	0.0115	<0.0001	<0.0001
[Ribosomal protein S12] (aspartate(89)-C(3))-methylthiotransferase	EC:2.8.4.4	0.126	0.119	0.0030	-0.0138	0.0008	0.0119
tRNA (N(6)-L-threonylcarbamoyladenosine(37)-C(2))-methylthiotransferase	EC:2.8.4.5	0.132	0.131	0.0017	-0.0055	0.0036	0.0386
Phosphoglycolate phosphatase	EC:3.1.3.18	0.314	0.290	0.0050	-0.0335	<0.0001	0.0002
Protein-tyrosine-phosphatase	EC:3.1.3.48	0.273	0.278	0.0013	0.0081	0.0018	0.0245

dGTPase	EC:3.1.5.1	0.132	0.124	0.0030	-0.0150	0.0009	0.0137
Alpha-amylase	EC:3.2.1.1	0.149	0.087	0.0082	-0.0840	<0.0001	<0.0001
Beta-glucosidase	EC:3.2.1.21	0.226	0.221	0.0046	-0.0271	0.0036	0.0387
Cellulase	EC:3.2.1.4	0.188	0.164	0.0046	-0.0348	<0.0001	0.0007
Beta-N-acetylhexosaminidase	EC:3.2.1.52	0.121	0.102	0.0027	-0.0312	<0.0001	<0.0001
Uracil-DNA glycosylase	EC:3.2.2.27	0.100	0.104	0.0018	0.0070	0.0011	0.0159
Methionyl aminopeptidase	EC:3.4.11.18	0.222	0.208	0.0027	-0.0181	<0.0001	0.0002
Tripeptide aminopeptidase	EC:3.4.11.4	0.119	0.134	0.0034	0.0168	<0.0001	0.0014
C-terminal processing peptidase	EC:3.4.21.102	0.170	0.182	0.0030	0.0167	0.0018	0.0242
Peptidase Do	EC:3.4.21.107	0.211	0.201	0.0031	-0.0157	<0.0001	0.0011
Signal peptidase I	EC:3.4.21.89	0.285	0.297	0.0018	0.0148	<0.0001	0.0012
Sortase A	EC:3.4.22.70	0.360	0.302	0.0126	-0.0689	<0.0001	<0.0001
Prepilin peptidase	EC:3.4.23.43	0.133	0.142	0.0014	0.0125	<0.0001	0.0009
Asparaginase	EC:3.5.1.1	0.129	0.124	0.0007	-0.0071	<0.0001	0.0009
N-acetylglucosamine-6-phosphate deacetylase	EC:3.5.1.25	0.120	0.124	0.0023	0.0082	0.0003	0.0061
N-acetylmuramoyl-L-alanine amidase	EC:3.5.1.28	0.553	0.573	0.0064	0.0218	0.0036	0.0387
Nicotinamide-nucleotide amidase	EC:3.5.1.42	0.152	0.150	0.0009	-0.0048	0.0037	0.0391
Peptide deformylase	EC:3.5.1.88	0.248	0.241	0.0020	-0.0082	0.0002	0.0049
IMP cyclohydrolase	EC:3.5.4.10	0.160	0.157	0.0010	-0.0055	0.0017	0.0231
dCMP deaminase	EC:3.5.4.12	0.131	0.130	0.0017	-0.0057	0.0022	0.0273
GTP cyclohydrolase I	EC:3.5.4.16	0.104	0.112	0.0016	0.0095	<0.0001	0.0010
Phosphoribosyl-AMP cyclohydrolase	EC:3.5.4.19	0.148	0.143	0.0014	-0.0073	<0.0001	0.0011
GTP cyclohydrolase II	EC:3.5.4.25	0.125	0.131	0.0019	0.0108	0.0025	0.0303
Diaminohydroxyphosphoribosylaminopyrimidine deaminase	EC:3.5.4.26	0.107	0.111	0.0013	0.0073	0.0002	0.0040
tRNA(adenine(34)) deaminase	EC:3.5.4.33	0.154	0.151	0.0009	-0.0047	0.0047	0.0465
Cytidine deaminase	EC:3.5.4.5	0.110	0.122	0.0012	0.0134	<0.0001	<0.0001
Inorganic diphosphatase	EC:3.6.1.1	0.237	0.247	0.0012	0.0097	0.0001	0.0030
Undecaprenyl-diphosphate phosphatase	EC:3.6.1.27	0.395	0.368	0.0060	-0.0300	<0.0001	0.0003
Phosphoribosyl-ATP diphosphatase	EC:3.6.1.31	0.174	0.157	0.0026	-0.0214	<0.0001	<0.0001
Monosaccharide-transporting ATPase	EC:3.6.3.17	0.331	0.366	0.0054	0.0319	<0.0001	0.0002
Iron-chelate-transporting ATPase	EC:3.6.3.34	0.348	0.392	0.0109	0.0618	<0.0001	0.0016
Cu(+) exporting ATPase	EC:3.6.3.54	0.109	0.117	0.0014	0.0141	<0.0001	<0.0001
DNA helicase	EC:3.6.4.12	1.480	1.453	0.0078	-0.0199	0.0034	0.0375
Diaminopimelate decarboxylase	EC:4.1.1.20	0.190	0.180	0.0024	-0.0131	<0.0001	0.0011
Indole-3-glycerol-phosphate synthase	EC:4.1.1.48	0.142	0.137	0.0014	-0.0068	<0.0001	0.0007
Fructose-bisphosphate aldolase	EC:4.1.2.13	0.197	0.189	0.0017	-0.0110	0.0028	0.0322
3,4-dihydroxy-2-butanone-4-phosphate synthase	EC:4.1.99.12	0.108	0.114	0.0013	0.0089	<0.0001	0.0008
Cyclic pyranopterin phosphate synthase	EC:4.1.99.18	0.132	0.145	0.0024	0.0154	0.0036	0.0386
Imidazoleglycerol-phosphate dehydratase	EC:4.2.1.19	0.147	0.142	0.0014	-0.0074	<0.0001	0.0006
Tryptophan synthase	EC:4.2.1.20	0.346	0.318	0.0043	-0.0279	<0.0001	<0.0001
Aconitate hydratase	EC:4.2.1.3	0.145	0.141	0.0014	-0.0063	0.0008	0.0132
Prephenate dehydratase	EC:4.2.1.51	0.156	0.151	0.0013	-0.0076	<0.0001	0.0007
3-hydroxyacyl-[acyl-carrier-protein] dehydratase	EC:4.2.1.59	0.187	0.169	0.0026	-0.0197	<0.0001	<0.0001
Uroporphyrinogen-III synthase	EC:4.2.1.75	0.118	0.125	0.0013	0.0110	0.0004	0.0074
Threonine synthase	EC:4.2.3.1	0.156	0.154	0.0014	-0.0050	0.0023	0.0278
L-serine ammonia-lyase	EC:4.3.1.17	0.188	0.209	0.0030	0.0255	<0.0001	0.0001
Lactoylglutathione lyase	EC:4.4.1.5	0.122	0.130	0.0017	0.0106	<0.0001	0.0007
Sirohydrochlorin ferrochelatase	EC:4.99.1.4	0.108	0.120	0.0021	0.0178	<0.0001	0.0017
Alanine racemase	EC:5.1.1.1	0.203	0.193	0.0028	-0.0145	0.0005	0.0093
Glutamate racemase	EC:5.1.1.3	0.150	0.146	0.0010	-0.0058	0.0046	0.0455
Diaminopimelate epimerase	EC:5.1.1.7	0.126	0.137	0.0017	0.0137	<0.0001	<0.0001
Ribulose-phosphate 3-epimerase	EC:5.1.3.1	0.183	0.168	0.0023	-0.0212	<0.0001	<0.0001
dTDP-4-dehydrorhamnose 3,5-epimerase	EC:5.1.3.13	0.112	0.106	0.0018	-0.0110	0.0021	0.0266
UDP-N-acetylglucosamine 2-epimerase (non-hydrolyzing)	EC:5.1.3.14	0.115	0.123	0.0016	0.0085	0.0022	0.0273
Aldose 1-epimerase	EC:5.1.3.3	0.116	0.103	0.0020	-0.0204	<0.0001	<0.0001
NAD(P)H-hydrate epimerase	EC:5.1.99.6	0.157	0.143	0.0037	-0.0207	0.0002	0.0042
Triose-phosphate isomerase	EC:5.3.1.1	0.170	0.165	0.0011	-0.0086	0.0011	0.0159

isomerase	EC:5.3.1.16	0.148	0.144	0.0014	-0.0055	0.0004	0.0069
Phosphoribosylanthranilate isomerase	EC:5.3.1.24	0.137	0.128	0.0013	-0.0109	<0.0001	<0.0001
Mannose-6-phosphate isomerase	EC:5.3.1.8	0.110	0.095	0.0022	-0.0224	<0.0001	0.0003
Glutamate-1-semialdehyde 2,1-aminomutase	EC:5.4.3.8	0.112	0.119	0.0017	0.0132	0.0002	0.0047
23S rRNA pseudouridine(2605) synthase	EC:5.4.99.22	0.128	0.122	0.0010	-0.0071	0.0034	0.0373
23S rRNA pseudouridine(955/2504/2580) synthase	EC:5.4.99.24	0.110	0.103	0.0031	-0.0127	0.0002	0.0047
DNA topoisomerase (ATP-hydrolyzing)	EC:5.99.1.3	0.477	0.464	0.0062	-0.0212	0.0005	0.0093
Aspartate--tRNA ligase	EC:6.1.1.12	0.184	0.172	0.0025	-0.0147	<0.0001	0.0011
Glutamine--tRNA ligase	EC:6.1.1.18	0.123	0.116	0.0023	-0.0139	<0.0001	0.0014
Asparagine--tRNA ligase	EC:6.1.1.22	0.112	0.118	0.0019	0.0077	0.0003	0.0058
Lysine--tRNA ligase	EC:6.1.1.6	0.166	0.163	0.0007	-0.0049	0.0041	0.0421
Alanine--tRNA ligase	EC:6.1.1.7	0.212	0.221	0.0010	0.0101	<0.0001	<0.0001
Long-chain-fatty-acid--CoA ligase	EC:6.2.1.3	0.168	0.186	0.0056	0.0274	0.0044	0.0436
Adenosylcobinamide-phosphate synthase	EC:6.3.1.10	0.102	0.113	0.0012	0.0101	<0.0001	0.0001
Glutamate--ammonia ligase	EC:6.3.1.2	0.313	0.298	0.0044	-0.0209	<0.0001	0.0003
Dihydrofolate synthase	EC:6.3.2.12	0.186	0.190	0.0009	0.0052	0.0022	0.0268
Tetrahydrofolate synthase	EC:6.3.2.17	0.186	0.190	0.0009	0.0052	0.0022	0.0268
Phosphoribosylaminoimidazole succinocarboxamide synthase	EC:6.3.2.6	0.173	0.177	0.0009	0.0070	0.0015	0.0209
5-formyltetrahydrofolate cyclo-ligase	EC:6.3.3.2	0.153	0.149	0.0010	-0.0086	<0.0001	0.0009
tRNA(Ile)-lysidine synthetase	EC:6.3.4.19	0.154	0.152	0.0009	-0.0047	0.0047	0.0465
CTP synthase (glutamine hydrolyzing)	EC:6.3.4.2	0.149	0.146	0.0013	-0.0057	0.0002	0.0050
Nicotinate phosphoribosyltransferase	EC:6.3.4.21	0.156	0.151	0.0008	-0.0067	0.0002	0.0042
Argininosuccinate synthase	EC:6.3.4.5	0.151	0.148	0.0010	-0.0048	0.0010	0.0152
NAD(+) synthase (glutamine-hydrolyzing)	EC:6.3.5.1	0.128	0.122	0.0026	-0.0122	0.0017	0.0226
Adenosylcobyric acid synthase (glutamine-hydrolyzing)	EC:6.3.5.10	0.097	0.107	0.0011	0.0100	<0.0001	<0.0001
Phosphoribosylformylglycinamidine synthase	EC:6.3.5.3	0.213	0.218	0.0026	0.0105	0.0010	0.0155
Carbamoyl-phosphate synthase (glutamine-hydrolyzing)	EC:6.3.5.5	0.375	0.370	0.0013	-0.0068	0.0010	0.0158

EC, enzyme commission; HWG, Hanwoo inoculum-treated group; JBG, Jeju Black inoculum-treated group; SEM, standard error of the mean.