Electronic Supplementary Material (ESI) for Food & Function.

[Supplement]

Alleviation of cognitive impairment by anti-inflammatory *Lactobacillus plantarum* and *Bifidobacterium longum* in mice

Table S1. The whole genomes of NK151 and NK173

	NK151	NK173
Platform	RS2	Sequel
No. of contigs	5	1
Sequencing depth of coverage	169.0x	943.0x
Genome size (bp)	3,288,981	2,507,434
N50 (bp)	2,365,629	2,507,434
GC content	44.5%	59.9%
No. of CDS	3,930	2,077
No. of rRNA genes	16	12
No. of tRNA genes	70	59

Table S2. Effects of NK151 and NK172 on the gut microbiota composition at the phylum level in mice with *Escherichia coli* K1-induced cognitive impairment

Taxon Name	Composition (%)				
	NC	EC	EC-NK151	EC-NK173	EC-NKm
Firmicutes	56.92±11.02	38.56±17.23$^{\#}$	39.53±12.58	44.34±18.20	53.78±24.16
Bacteroidetes	38.81±9.97	54.23±19.63	54.42±13.92	51.75±18.34	41.25±25.15
Proteobacteria	3.07±2.05	6.06±5.24	4.88±2.61	2.85±2.27	2.70±1.78
Actinobacteria	0.46±0.11	0.56±0.54	0.35±0.17	0.43±0.22	0.72±0.42
Verrucomicrobia	0.39±0.24	0.03±0.03$^{\#}$	0.28±0.38	0.32±0.26*	0.51±0.73
Tenericutes	0.21±0.14	0.17±0.14	0.17±0.07	0.16±0.11	0.18±0.10
Deferribacteres	0.08±0.07	0.27±0.46	0.12±0.15	0.12±0.15	0.41±0.81
Cyanobacteria	0.04±0.03	0.12±0.08$^{\#}$	0.24±0.37	0.01±0.01*	0.44±1.09
Saccharibacteria_TM7	0.01±0.01	0.00±0.00$^{\#}$	0.01±0.01*	0.01±0.01*	0.01±0.01*

Values indicate means±SD. $^{\#}p<0.05$ vs. NC. *$p<0.05$ vs. EC.

Table S3. Effects of NK151 and NK172 on the gut microbiota composition at the family level in mice with *Escherichia coli* K1-induced cognitive impairment

Taxon Name	Composition (%)				
	NC	EC	EC-NK151	EC-NK173	EC-NKm
Lachnospiraceae	39.57±13.50	24.93±14.13	27.16±14.16	32.89±16.54	28.88±21.06

Muribaculaceae	27.09±6.14	36.67±18.19	38.16±13.69	41.67±13.67	30.96±18.74
Lactobacillaceae	8.43±5.40	4.39±4.93	4.39±4.87	6.14±4.07	17.88±13.00*
Ruminococcaceae	7.65±0.98	8.08±2.65	6.99±1.77	4.37±2.00*	5.75±2.06
Prevotellaceae	5.77±4.10	5.85±6.76	10.99±5.69	4.05±2.59	6.19±6.75
Bacteroidaceae	2.74±2.21	3.23±1.91	2.54±1.10	3.33±3.27	2.24±1.57
Rikenellaceae	2.19±1.52	5.67±3.75#	1.89±0.54*	1.75±1.22*	1.38±0.70*
Helicobacteraceae	2.12±1.78	4.72±4.66	3.82±2.61	1.88±1.78	1.56±1.08
Desulfovibrionaceae	0.73±0.22	1.15±0.86	0.75±0.41	0.83±0.55	0.95±0.95
Odoribacteraceae	0.59±0.53	2.04±2.19	0.31±0.35	0.28±0.18	0.10±0.08*
Akkermansiaceae	0.39±0.24	0.03±0.03#	0.28±0.38	0.32±0.26*	0.51±0.73
Coriobacteriaceae	0.35±0.15	0.56±0.54	0.29±0.15	0.36±0.22	0.72±0.42
Dehalobacterium_f	0.32±0.05	0.17±0.15#	0.20±0.11	0.20±0.12	0.09±0.06
Porphyromonadaceae	0.29±0.25	0.23±0.09	0.38±0.17	0.33±0.21	0.28±0.19
Clostridiaceae	0.24±0.10	0.25±0.28	0.17±0.21	0.18±0.12	0.28±0.19
Christensenellaceae	0.21±0.13	0.46±0.30	0.14±0.06*	0.09±0.03*	0.22±0.16
Enterococcaceae	0.17±0.06	0.10±0.13	0.12±0.13	0.13±0.06	0.28±0.32
AC160630_f	0.15±0.16	0.53±0.26#	0.14±0.06*	0.34±0.34	0.10±0.11*
Erysipelotrichaceae	0.13±0.05	0.09±0.04	0.16±0.08	0.15±0.13	0.26±0.33
Bifidobacteriaceae	0.11±0.04	0.00±0.00#	0.06±0.03*	0.07±0.03*	0.00±0.00
PAC000197_f	0.10±0.05	0.07±0.08	0.10±0.08	0.10±0.05	0.09±0.05
Sutterellaceae	0.10±0.09	0.09±0.06	0.14±0.11	0.09±0.10	0.11±0.08
Mogibacterium_f	0.09±0.03	0.07±0.05	0.12±0.03	0.06±0.04	0.06±0.06
Deferribacteraceae	0.08±0.07	0.27±0.46	0.12±0.15	0.12±0.15	0.41±0.81
Pseudomonadaceae	0.08±0.06	0.00±0.00#	0.02±0.05	0.02±0.04	0.00±0.00

Values indicate means±SD. #$p<0.05$ vs. NC. *$p<0.05$ vs. EC.

Table S4. Effects of NK151 and NK172 on the gut microbiota composition at the genus level in mice with *Escherichia coli* K1-induced cognitive impairment

Taxon Name	Composition (%)				
	NC	EC	EC-NK151	EC-NK173	EC-NKm
Lactobacillus	8.36±5.36	4.35±4.91	4.35±4.79	6.10±4.05	17.81±12.96*
PAC001068_g	6.82±1.30	9.54±4.84	9.18±2.73	11.39±3.98	9.85±6.16
PAC000186_g	6.51±3.02	9.77±4.85	10.99±4.66	10.20±4.64	7.93±4.83
KE159538_g	5.32±4.12	2.95±3.28	2.82±3.31	1.82±3.46	1.70±2.78
LLKB_g	3.94±6.08	1.09±0.80	1.87±1.29	0.16±0.07*	1.30±2.16
Bacteroides	2.74±2.21	3.23±1.91	2.53±1.11	3.33±3.27	2.24±1.57
PAC001512_g	2.71±1.93	2.26±1.67	2.26±1.04	1.90±0.72	0.44±0.55
Eubacterium_g6	2.59±3.34	4.04±5.97	1.70±1.65	9.54±14.76	11.64±18.13
PAC000198_g	2.41±1.01	3.63±1.86	4.76±2.57	4.42±1.14	2.53±1.74
PAC000664_g	2.28±1.84	1.43±1.09	2.17±1.34	3.61±3.69	1.01±0.86
Helicobacter	2.12±1.78	4.71±4.66	3.82±2.61	1.88±1.78	1.56±1.08
PAC001092_g	2.07±1.63	0.60±0.33#	2.48±2.64	1.75±1.73	1.84±1.78
PAC001124_g	1.91±2.20	1.24±1.59	0.43±0.63	3.72±3.66	1.54±2.69
Paraprevotella	1.88±1.58	1.51±3.32	2.11±1.98	1.36±1.23	1.01±1.56
Pseudoflavonifractor	1.85±0.67	1.95±1.05	1.44±0.85	1.15±0.68	0.97±0.39*
PAC001074_g	1.77±0.94	2.16±1.55	2.17±1.13	3.10±1.15	2.14±1.61
Oscillibacter	1.75±0.81	3.25±2.03	1.06±0.77*	0.71±0.51*	0.64±0.41*
Prevotellaceae_uc	1.74±1.62	2.09±2.52	5.67±4.45*	0.91±0.73	2.37±4.43
PAC002367_g	1.74±3.66	1.18±2.29	1.04±1.37	0.65±0.83	0.19±0.24
PAC001066_g	1.47±1.12	1.01±0.39	1.04±0.56	1.10±0.31	0.52±0.42*
KE159571_g	1.38±1.51	1.16±1.06	1.02±0.88	0.41±0.40	0.53±0.36

Alistipes	1.34±1.18	4.17±2.57$^{\#}$	1.17±0.49*	1.06±0.87*	0.79±0.55*
Alloprevotella	1.33±2.15	0.54±0.49	0.26±0.49	0.87±0.90	1.02±1.91
PAC001091_g	1.11±1.03	0.65±1.01	1.09±1.13	0.46±0.49	0.49±0.64
PAC001112_g	1.07±0.43	1.15±0.82	1.55±0.84	1.85±0.55	1.44±0.92

Values indicate means±SD. $^{\#}p<0.05$ vs. NC. *$p<0.05$ vs. EC.

Table S5. Effects of NK151 and NK172 on the gut microbiota composition at the species level in mice with *Escherichia coli* K1-induced cognitive impairment

Taxon Name	Composition (%)				
	NC	EC	EC-NK151	EC-NK173	EC-NKm
PAC001065_s group	4.54±1.75	6.26±4.07	6.71±2.57	5.65±3.32	5.99±4.28
PAC001093_s	4.27±3.84	0.32±0.78$^{\#}$	0.58±1.13	0.22±0.50	0.39±0.68
Lactobacillus reuteri group	3.15±1.87	0.67±0.77$^{\#}$	1.48±2.06	1.27±1.23	4.50±4.73
AB626939_s	3.06±5.65	0.37±0.65	0.67±0.85	0.03±0.03	0.92±1.75
Lactobacillus murinus group	2.86±1.73	2.98±4.83	1.81±2.26	2.65±3.14	10.75±13.70
EU791023_s	2.68±1.92	2.15±1.58	2.17±1.01	1.86±0.71	0.37±0.50*
EF097112_s	2.68±0.74	4.35±1.51$^{\#}$	4.56±1.65	4.52±1.65	2.66±1.65
FJ880724_s	1.88±1.58	1.51±3.32	2.11±1.97	1.36±1.23	1.00±1.55
PAC001124_g_uc	1.74±2.11	0.71±1.22	0.28±0.43	0.81±1.11	1.16±1.90
PAC002367_s	1.74±3.65	1.17±2.28	1.04±1.37	0.65±0.83	0.19±0.24
PAC001064_s	1.69±1.60	2.80±1.17	3.97±2.45	4.11±1.28	1.59±1.71
PAC001071_s	1.60±0.85	2.16±1.02	1.05±0.62*	1.21±0.56	1.04±0.49*
Helicobacter japonicus	1.54±1.78	1.94±2.36	1.21±1.43	0.90±0.63	0.91±0.94
Eubacterium_g6_uc	1.54±3.56	0.15±0.15	0.10±0.14	8.02±15.01	10.84±17.81
PAC001074_s	1.52±0.89	1.74±1.32	1.84±0.84	2.08±0.97	1.77±1.31
Bacteroides acidifaciens group	1.50±1.25	1.41±0.80	0.93±0.55	1.74±1.76	1.10±1.01
PAC001066_s	1.47±1.12	1.01±0.39	1.04±0.55	1.09±0.30	0.52±0.42*
PAC002479_s	1.32±2.15	0.54±0.49	0.26±0.49	0.87±0.90	1.01±1.89
PAC001139_s	1.10±0.80	2.13±1.21	1.85±0.77	2.35±0.78	0.86±0.48*
Lactobacillus gasseri group	1.09±1.14	0.36±0.32	0.70±0.62	1.73±2.08	1.26±1.24
PAC001092_s	1.09±1.30	0.30±0.23	1.94±2.55	1.10±1.66	0.91±1.65
Lactobacillus intestinalis	1.08±1.34	0.24±0.22	0.23±0.13	0.32±0.42	1.07±1.51
PAC001070_s group	0.85±0.71	1.04±1.65	1.16±0.96	1.80±1.13	2.98±3.02
KE159628_s	0.85±1.14	0.53±0.46	0.38±0.37	0.22±0.36	0.09±0.15
PAC001072_s	0.82±0.58	1.31±1.27	1.18±0.56	2.31±1.21	1.94±

Values indicate means±SD. $^{\#}p<0.05$ vs. NC. *$p<0.05$ vs. EC.

Table S6. Effects of NK151 and NK172 on the gut microbiota composition at the phylum level in mice with LPS-induced cognitive impairment

Taxon Name	Composition (%)				
	NC	LPS	EC-NK151	EC-NK173	EC-NKm
Bacteroidetes	55.0±19.2	49.5±16.9	54.9±22.0	64.2±9.9	69.2±12.6*
Firmicutes	37.4±17.3	44.7±14.6	40.5±19.9	30.3±8.6*	26.9±11.7*
Proteobacteria	6.9±4.4	5.1±2.5	4.1±2.0	4.3±4.1	2.9±1.4
Tenericutes	0.4±0.6	0.1±0.1	0.1±0.1	0.5±0.7	0.4±0.4
Actinobacteria	0.2±0.2	0.2±0.1	0.2±0.1	0.2±0.2	0.2±0.1
Cyanobacteria	0.2±0.2	0.1±0.1	0.0±0.0	0.1±0.2	0.1±0.1
Deferribacteres	0.0±0.1	0.4±0.5	0.1±0.1	0.0±0.0	0.1±0.1

Verrucomicrobia	0.0±0.0	0.0±0.0	0.0±0.0	0.4±0.7	0.2±0.3
Saccharibacteria_TM7	0.0±0.0	0.0±0.0	0.0±0.0$^{\#}$	0.0±0.0	0.0±0.0

Values indicate means±SD. $^{\#}p<0.05$ vs. NC. *$p<0.05$ vs. EC.

Table S7. Effects of NK151 and NK172 on the gut microbiota composition at the family level in mice with LPS-induced cognitive impairment

Taxon Name	Composition (%)				
	NC	LPS	EC-NK151	EC-NK173	EC-NKm
Muribaculaceae	31.6±9.4	35.0±11.0	42.5±17.8	49.5±9.8$^{\#*}$	46.3±6.7$^{\#*}$
Lachnospiraceae	26.4±16.7	34.5±12.4	31.1±19.6	21.3±6.7*	18.3±9.4*
Prevotellaceae	13.5±11.5	9.3±7.4	4.5±4.8	5.1±3.8	8.2±4.2
Ruminococcaceae	7.3±2.3	7.6±2.4	6.1±3.1	5.6±2.3	4.7±3.6
Helicobacteraceae	5.6±4.0	3.8±2.4	3.3±1.7	3.2±4.0	1.6±1.2$^{\#}$
Rikenellaceae	4.9±2.4	2.8±1.1	4.1±1.8	5.3±1.5*	5.9±3.0*
Bacteroidaceae	3.3±1.8	1.3±0.3$^{\#}$	1.7±1.2	2.2±1.4	5.8±3.7*
Lactobacillaceae	2.9±2.2	1.7±0.7	2.6±3.0	2.5±1.2	2.7±1.5
Desulfovibrionaceae	1.0±0.6	1.1±0.7	0.7±0.5	1.0±0.8	0.6±0.6
AC160630_f	0.8±0.6	0.4±0.1	0.9±0.5*	0.6±0.5	0.4±0.1
Odoribacteraceae	0.6±0.6	0.4±0.4	0.8±0.9	1.2±1.0	2.1±1.5*
Christensenellaceae	0.4±0.3	0.5±0.3	0.4±0.5	0.6±0.5	0.8±0.6
Porphyromonadaceae	0.4±0.2	0.3±0.1	0.4±0.4	0.4±0.3	0.5±0.1*
Mycoplasmataceae	0.3±0.5	0.0±0.0	0.0±0.1	0.0±0.0	0.0±0.0
Dehalobacterium_f	0.2±0.1	0.2±0.1	0.2±0.2	0.1±0.1	0.1±0.0$^{\#*}$
Coriobacteriaceae	0.2±0.1	0.2±0.1	0.2±0.1	0.2±0.2	0.2±0.1
FR888536_f	0.2±0.2	0.1±0.1	0.0±0.0	0.1±0.2	0.1±0.1
Rhodospirillaceae	0.1±0.2	0.0±0.0	0.0±0.0	0.0±0.0	0.1±0.1
Sutterellaceae	0.1±0.1	0.1±0.1	0.0±0.0	0.1±0.1	0.6±0.7
Erysipelotrichaceae	0.1±0.1	0.0±0.0	0.0±0.0	0.1±0.1	0.2±0.1
Mogibacterium_f	0.1±0.0	0.0±0.0	0.0±0.0	0.0±0.0	0.0±0.0*
PAC000197_f	0.0±0.1	0.0±0.0	0.0±0.0	0.0±0.0	0.0±0.0
Clostridiaceae	0.0±0.0	0.0±0.0	0.1±0.1	0.1±0.1$^{\#*}$	0.1±0.1
Deferribacteraceae	0.0±0.1	0.4±0.5	0.1±0.1	0.0±0.0	0.1±0.1
Enterococcaceae	0.0±0.1	0.0±0.0	0.0±0.0	0.0±0.0	0.0±0.0

Values indicate means±SD. $^{\#}p<0.05$ vs. NC. *$p<0.05$ vs. EC.

Table S8. Effects of NK151 and NK172 on the gut microbiota composition at the genus level in mice with LPS-induced cognitive impairment

Taxon Name	Composition (%)				
	NC	LPS	EC-NK151	EC-NK173	EC-NKm
PAC000186_g	8.4±3.3	9.0±2.7	11.4±4.7	10.0±2.1	11.7±2.6
Prevotellaceae_uc	7.7±8.5	7.3±6.5	0.6±0.7$^{\#}$*	0.7±1.2*	1.5±1.3
PAC001068_g	7.6±2.5	7.7±3.1	8.6±4.7$^{\#}$*	12.2±3.5	10.0±2.5
Helicobacter	5.6±4.0	3.8±2.4	3.3±1.7$^{\#}$	3.2±4.0	1.6±1.2
KE159538_g	4.5±3.0	5.8±5.5	3.3±4.1	3.6±3.4	2.9±2.0
Alistipes	3.9±2.2	2.1±1.1	3.3±1.9	4.6±1.4*	5.3±3.1
PAC000198_g	3.5±0.6	4.7±1.5	6.1±3.5	8.9±3.9$^{\#}$*	5.9±1.0$^{\#}$
Bacteroides	3.3±1.8	1.3±0.3$^{\#}$	1.7±1.2	2.2±1.4	5.8±3.7*
Paraprevotella	3.1±3.4	0.2±0.3$^{\#}$	0.2±0.2$^{\#}$	1.3±2.3	2.1±2.9
Lactobacillus	2.8±2.1	1.7±0.7	2.6±3.0	2.5±1.2	2.6±1.5
Oscillibacter	2.5±1.5	2.9±1.4	2.3±1.4	2.4±1.4	1.8±1.7

LLKB_g	2.3±3.5	3.0±1.8	2.9±2.9	1.5±1.3	1.0±0.6*
PAC000664_g	2.3±1.7	2.6±2.8	1.1±1.0	2.9±2.8	1.1±0.7
PAC001074_g	2.1±1.1	2.1±0.9	2.6±1.4	3.1±2.2	5.0±2.2*
Pseudoflavonifractor	2.1±0.9	2.0±0.4	1.8±1.0	1.6±0.9	1.5±1.2
Prevotella	2.0±1.4	1.3±0.9	1.6±1.5	0.9±0.6	2.1±1.3
Muribaculum	1.9±0.6	1.7±0.7	1.6±1.8	2.0±1.1	1.5±0.5
PAC001512_g	1.5±1.2	2.8±1.8	3.6±2.1$^{\#}$	4.5±2.3$^{\#}$	1.8±1.1
PAC001124_g	1.2±1.7	1.1±1.0	1.7±2.4	0.5±0.9	0.2±0.4
PAC001127_g	1.2±0.9	1.8±0.6	1.3±1.1$^{\#}$	2.2±0.6	2.1±1.4
PAC001092_g	1.1±1.1	1.7±0.7	2.3±3.5	0.8±0.6*	0.3±0.3*
Lachnospiraceae_uc	1.1±1.4	0.7±0.6	0.5±0.7	0.2±0.3	0.3±0.4
KE159600_g	1.0±2.0	0.7±0.7	2.2±3.0	0.3±0.3	0.5±0.3
Eubacterium_g6	0.9±0.8	1.2±0.8	1.4±1.0	1.8±2.2	1.2±2.3
PAC002400_g	0.9±0.6	0.7±0.3	1.6±0.4$^{\#}$*	1.8±0.6$^{\#}$*	1.7±0.8*

Values indicate means±SD. $^{\#}p<0.05$ vs. NC. *$p<0.05$ vs. EC.

Table S9. Effects of NK151 and NK172 on the gut microbiota composition at the species level in mice with LPS-induced cognitive impairment

Taxon Name	Composition (%)				
	NC	LPS	EC-NK151	EC-NK173	EC-NKm
PAC001065_s group	5.9±3.5	6.5±2.3	6.1±3.5	6.8±1.0	6.5±1.5
Helicobacter rodentium group	3.3±2.2	3.0±2.5	2.4±1.5	2.7±4.2	0.8±1.1$^{\#}$
FJ880724_s	3.1±3.4	0.2±0.3$^{\#}$	0.2±0.2$^{\#}$	1.3±2.3	2.1±2.9
PAC001072_s	2.3±1.1	1.0±0.7$^{\#}$	0.5±0.2$^{\#}$*	0.6±0.3$^{\#}$	0.8±0.2$^{\#}$
Lactobacillus murinus group	2.2±1.9	0.6±0.3$^{\#}$	0.7±0.8	1.1±0.9	1.9±1.2
Helicobacter japonicus	2.1±1.6	0.7±0.7	0.9±0.9	0.4±0.4$^{\#}$	0.8±0.5
PAC001074_s	2.0±1.1	1.9±0.6	2.3±1.3	2.4±1.2	4.1±1.8$^{\#}$*
EF097112_s	1.9±0.9	4.3±1.5$^{\#}$	4.3±2.1$^{\#}$	5.5±2.2$^{\#}$	4.8±1.4$^{\#}$
PAC001064_s	1.8±1.2	2.1±0.6	4.5±1.9$^{\#}$*	2.4±1.4	4.1±1.0$^{\#}$*
AB626939_s	1.4±2.4	1.3±1.4	0.1±0.1*	0.5±0.5	0.2±0.3
KE159538_g_uc	1.4±3.3	0.0±0.1	1.9±4.5	0.0±0.0	0.8±1.9
AB599946_s	1.3±1.3	0.7±0.3	0.4±0.3*	1.0±0.9	1.9±1.7
PAC001139_s	1.2±0.8	2.7±0.9$^{\#}$	3.5±2.1$^{\#}$	2.6±1.1$^{\#}$	3.9±0.7$^{\#}$*
PAC001696_s	1.2±1.6	0.3±0.6	0.0±0.0	0.0±0.0	0.4±0.8
PAC001071_s	1.2±0.6	1.2±0.5	2.8±1.9$^{\#}$	3.0±1.5$^{\#}$*	2.0±0.8
PAC002399_s	1.2±0.9	1.8±0.5	1.3±1.1$^{\#}$	2.2±0.6	2.1±1.4
PAC001070_s group	1.1±0.7	0.4±0.4$^{\#}$	0.7±0.6	2.3±1.6*	1.6±1.2
Bacteroides acidifaciens group	1.1±0.7	0.4±0.1$^{\#}$	1.1±0.9*	0.7±0.4*	2.5±1.5*
PAC002445_s	1.0±0.9	0.5±0.4	0.3±0.2	1.1±0.5*	1.5±1.3
EU622763_s group	1.0±1.5	0.3±0.3	0.0±0.0	0.0±0.0	0.1±0.2
KE159538_s	1.0±0.7	0.7±0.6	0.5±0.5	0.7±1.1	1.3±0.6
PAC001075_s	0.9±0.3	0.9±0.3	0.8±0.4	1.2±0.6	0.9±0.4
PAC002444_s	0.9±0.8	0.4±0.7	1.4±1.1	1.4±1.2	1.0±1.1
PAC002400_s	0.9±0.6	0.7±0.3	1.6±0.4*	1.8±0.5*	1.7±0.8*
PAC001077_s	0.8±0.3	0.7±0.2	0.9±1.5	1.0±0.8	0.4±0.2$^{\#}$*

Values indicate means±SD. $^{\#}p<0.05$ vs. NC. *$p<0.05$ vs. EC.

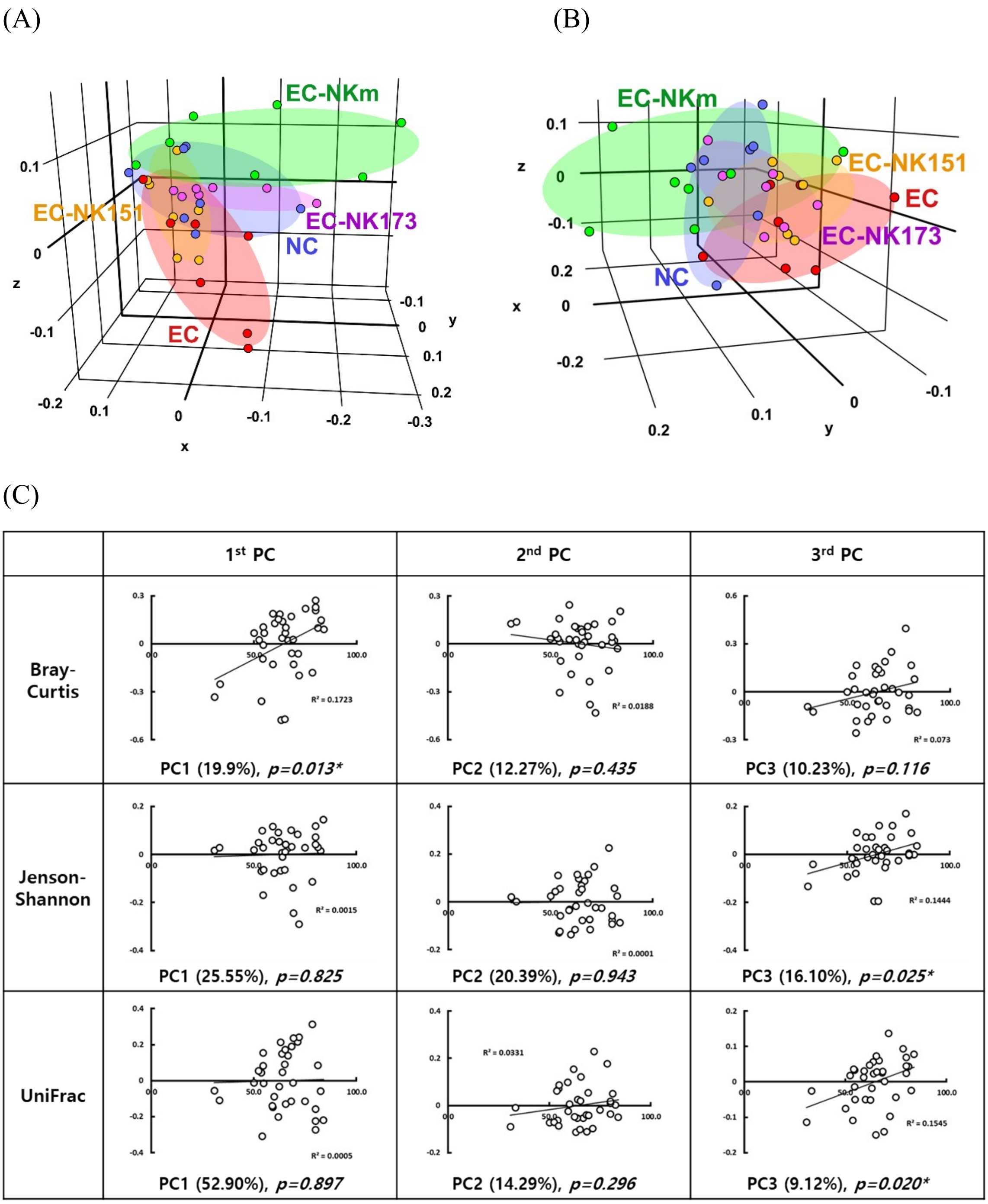
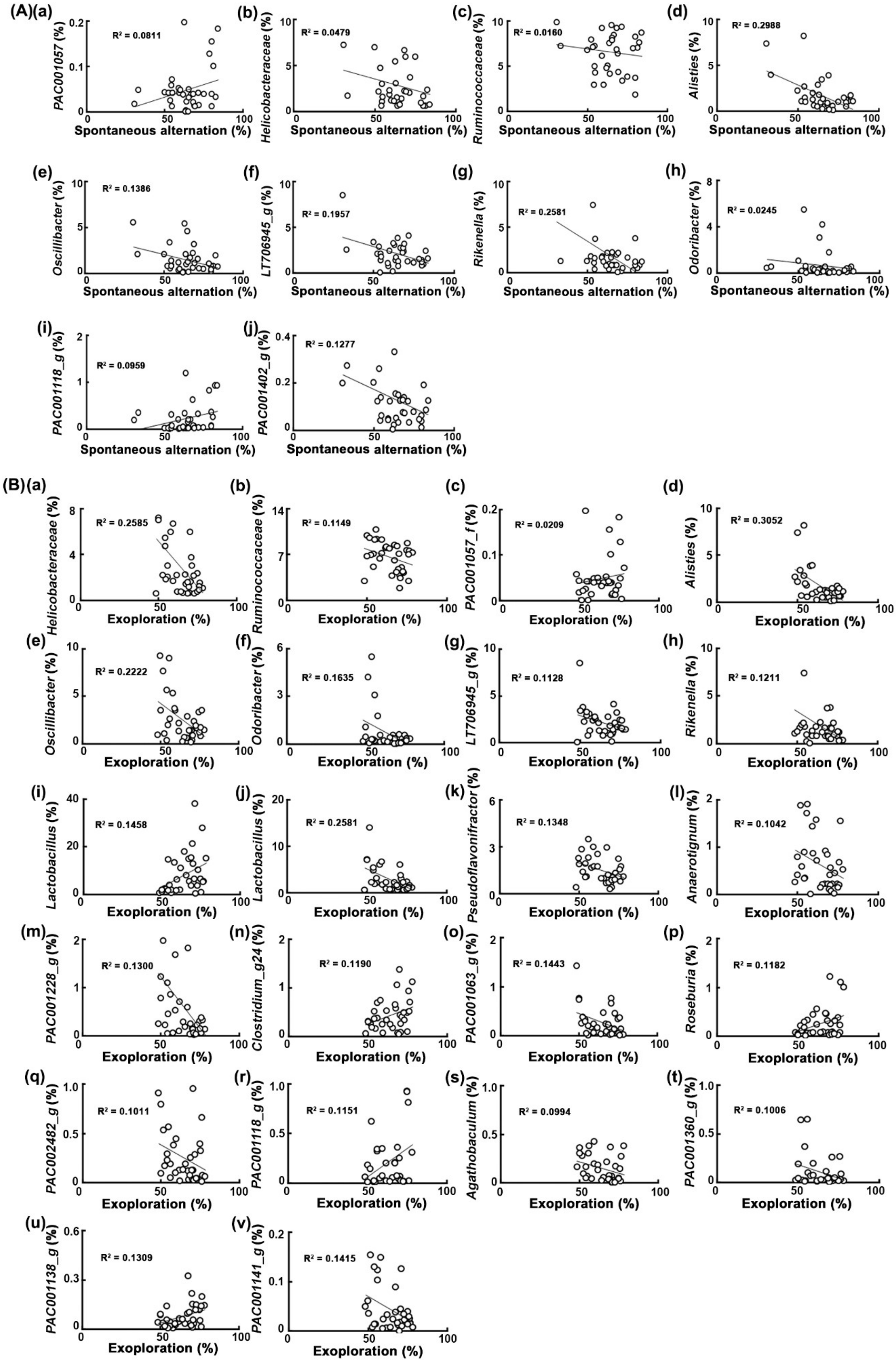


Figure S1. Effects of NK151 and NK173 on the fecal microbiota composition in mice with EC-induced cognitive impairment. (A) Effects on fecal microbiota composition: the principal coordinate analysis (PCoA) plot based on Jensen-Shannon (A) and UniFrac analyses (B). (C) The relationship between the spontaneous alternation in the Y-maze task and the PC1, PC2, or PC3 of the gut bacteria PCoA plot based on Bray-Curtis, Jenson-Shannon, and UniFrac anlyses. NK151, NK173, and their mixture (NKm) (1×10^9 CFU/mice/day) were orally gavaged 24 h after the final peritoneal injection of EC. The control group (NC) was treated with vehicle instead of test agents.


(A)(a)
PAC001057 (%)
R² = 0.0811
Spontaneous alternation (%)
(b)
Helicobacteraceae (%)
R² = 0.0479
Spontaneous alternation (%)
(c)
Ruminococcaceae (%)
R² = 0.0160
Spontaneous alternation (%)
(d)
Alisties (%)
R² = 0.2988
Spontaneous alternation (%)
(e)
Oscillibacter (%)
R² = 0.1386
Spontaneous alternation (%)
(f)
LT706945_g (%)
R² = 0.1957
Spontaneous alternation (%)
(g)
Rikenella (%)
R² = 0.2581
Spontaneous alternation (%)
(h)
Odoribacter (%)
R² = 0.0245
Spontaneous alternation (%)
(i)
PAC001118_g (%)
R² = 0.0959
Spontaneous alternation (%)
(j)
PAC001402_g (%)
R² = 0.1277
Spontaneous alternation (%)
(B)(a)
Helicobacteraceae (%)
R² = 0.2585
Exoploration (%)
(b)
Ruminococcaceae (%)
R² = 0.1149
Exoploration (%)
(c)
PAC001057_f (%)
R² = 0.0209
Exoploration (%)
(d)
Alisties (%)
R² = 0.3052
Exoploration (%)
(e)
Oscillibacter (%)
R² = 0.2222
Exoploration (%)
(f)
Odoribacter (%)
R² = 0.1635
Exoploration (%)
(g)
LT706945_g (%)
R² = 0.1128
Exoploration (%)
(h)
Rikenella (%)
R² = 0.1211
Exoploration (%)
(i)
Lactobacillus (%)
R² = 0.1458
Exoploration (%)
(j)
Lactobacillus (%)
R² = 0.2581
Exoploration (%)
(k)
Pseudoflavonifractor (%)
R² = 0.1348
Exoploration (%)
(l)
Anaerotignum (%)
R² = 0.1042
Exoploration (%)
(m)
PAC001228_g (%)
R² = 0.1300
Exoploration (%)
(n)
Clostridium_g24 (%)
R² = 0.1190
Exoploration (%)
(o)
PAC001063_g (%)
R² = 0.1443
Exoploration (%)
(p)
Roseburia (%)
R² = 0.1182
Exoploration (%)
(q)
PAC002482_g (%)
R² = 0.1011
Exoploration (%)
(r)
PAC001118_g (%)
R² = 0.1151
Exoploration (%)
(s)
Agathobaculum (%)
R² = 0.0994
Exoploration (%)
(t)
PAC001360_g (%)
R² = 0.1006
Exoploration (%)
(u)
PAC001138_g (%)
R² = 0.1309
Exoploration (%)
(v)
PAC001141_g (%)
R² = 0.1415
Exoploration (%)
0
50
100

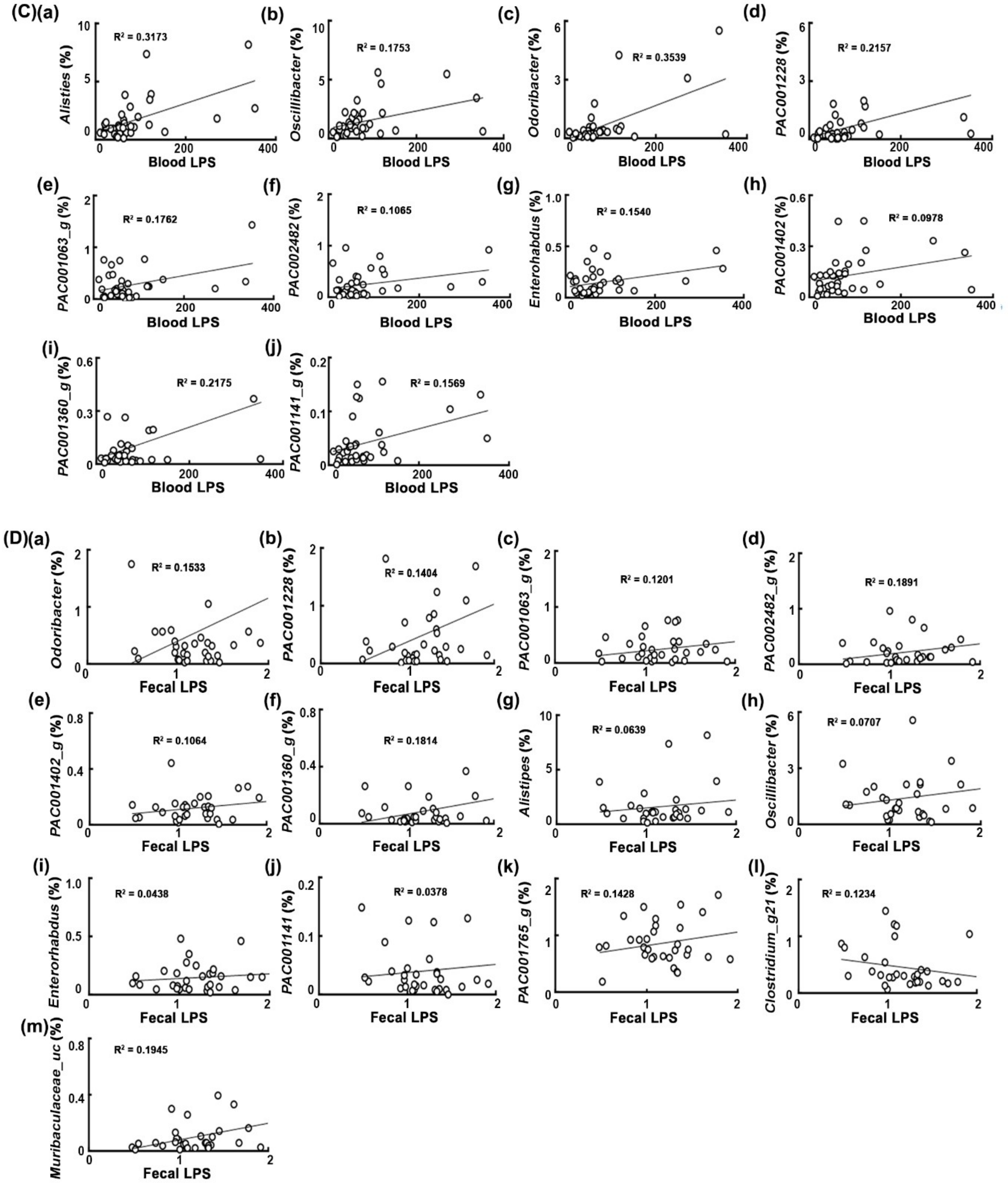
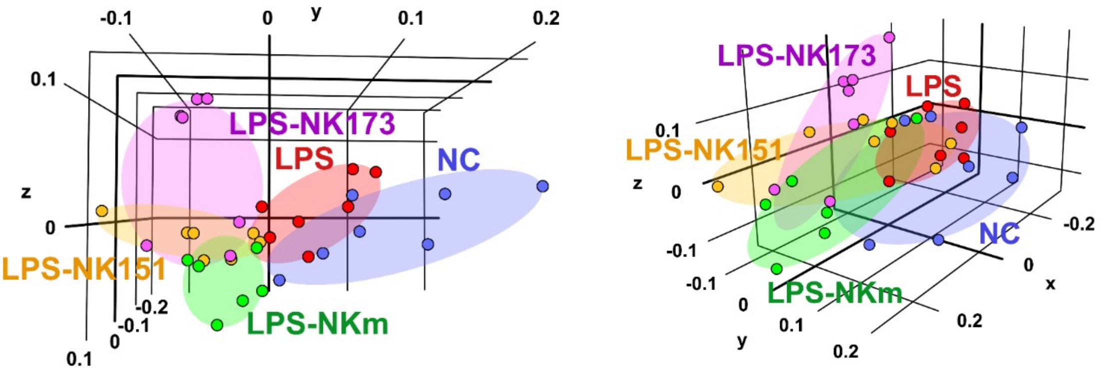


Figure S2. Effects of NK151 and NK173 on the fecal microbiota composition in mice with *Escherichia coli* K1-induced cognitive impairment. (A) The relationship between the spontaneous alternation in the Y-maze task and gut bacteria. (B) The relationship between the preference index in the novel object recognition task and gut bacteria. (C) The relationship between the blood LPS level and gut bacteria. NK151, NK173, and their mixture (NKm), *Escherichia coli* K1 (EC, $1x10^9$ CFU/mice/day) was orally gavaged. Control group (NC) was treated with vehicle instead of test agents.

(A) (B)



(C)

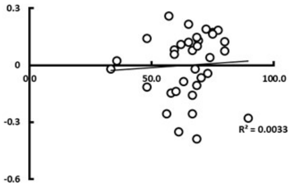
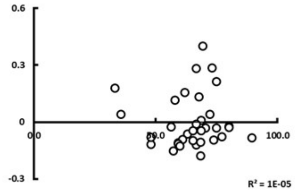
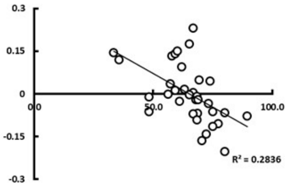
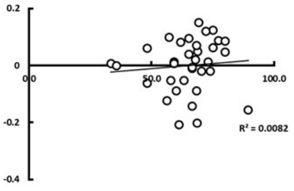
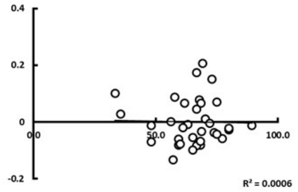
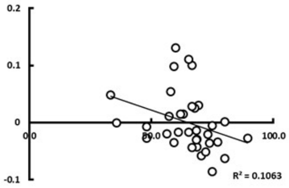
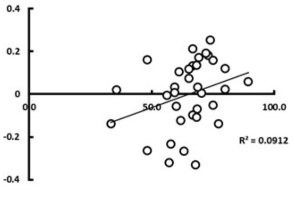
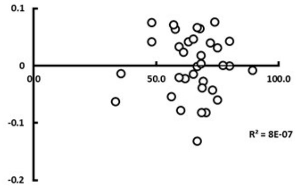
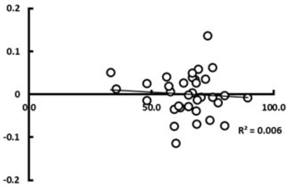
	1st PC	2nd PC	3rd PC
Bray-Curtis	 PC1 (19.41%), *p=0.751*	 PC2 (13.12%), *p=0.986*	 PC3 (6.98%), *p=0.001**
Jenson-Shannon	 PC1 (26.77%), *p=0.613*	 PC2 (20.49%), *p=0.889*	 PC3 (8.26%), *p=0.060*
UniFrac	 PC1 (61.29%), *p=0.083*	 PC2 (6.88%), *p=0.999*	 PC3 (5.69%), *p=0.664*

Figure S3. Effects of NK151 and NK173 on the fecal microbiota composition in mice with LPS-induced cognitive impairment. (A) Effects on fecal microbiota composition: the principal coordinate analysis (PCoA) plot based on Jensen-Shannon (A) and UniFrac analyses (B). (C) The relationship between the spontaneous alternation in the Y-maze task and the PC1, PC2, or PC3 of the gut bacteria PCoA plot based on Bray-Curtis, Jenson-Shannon, and UniFrac anlyses. NK151, NK173, and their mixture (NKm) (1×10^9 CFU/mice/day) were orally gavaged 24 h after the final peritoneal injection of EC.

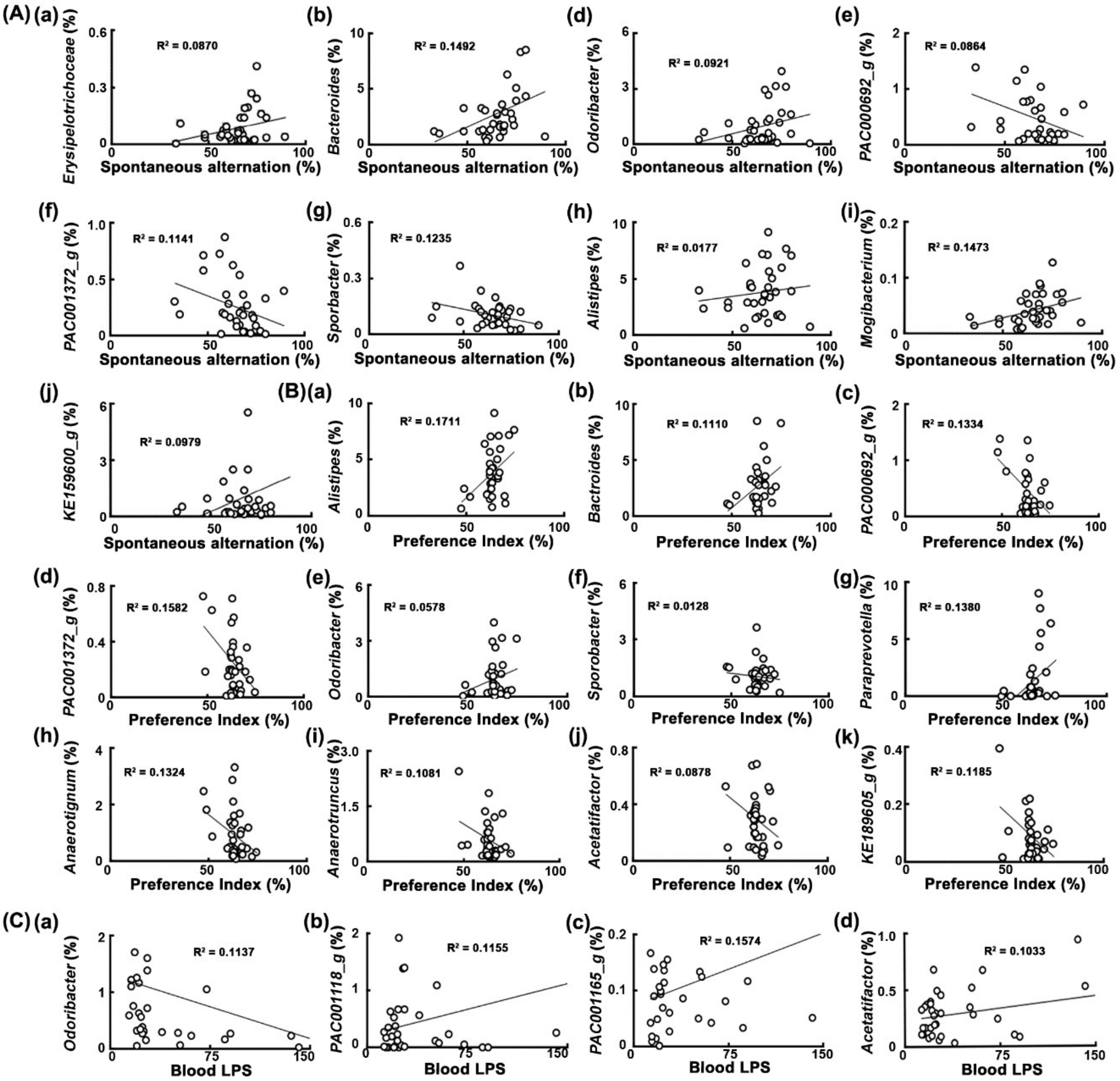


Figure S4. Effects of NK151 and NK173 on the fecal microbiota composition in mice with LPS-induced cognitive impairment. (A) The relationship between the spontaneous alternation in the Y-maze task and gut bacteria. (B) The relationship between the preference index in the novel object recognition task and gut bacteria. (C) The relationship between the blood LPS level and gut bacteria. NK151, NK173, and their mixture (NKm) (1×10^9 CFU/mice/day) was orally gavaged 24 h after the final peritoneal injection of LPS. Control group (NC) was treated with vehicle instead of test agents.