Supplementary Table S1. Comparison of gut microbiota abundance at the phylum level between rIMb and rHMb mice (%).

phylum	rIMb	rHMb	*p*
Bacteroidetes	47.78 (37.00~57.08)	53.70 (42.17~65.47)	0.293[b]
Firmicutes	45.60 ± 11.97	34.61 ± 12.59	0.085[a]
Proteobacteria	4.61 ± 3.97	5.78 ± 4.41	0.569[a]
Actinobacteria	0.51 (0.39~1.24)	4.26 (1.43~6.34)	0.004[b]
TM7	0.42 (0.17~1.00)	0.32 (0.01~0.77)	0.483[b]
Verrucomicrobia	0.00 (0.00~0.02)	0.00 (0.00~0.02)	0.625[b]
Deferribacteres	0.01 (0.00~0.08)	0.02 (0.00~0.13)	0.860[b]
Cyanobacteria	0.03 ± 0.03	0.04 ± 0.02	0.693[a]
Tenericutes	0.03 ± 0.03	0.02 ± 0.03	0.563[a]
Spirochaetes	0.00 (0.00~0.00)	0.00 (0.00~0.00)	0.945[b]

a indicates that the statistical method used is the independent-samples t test; b indicates that the statistical method used is the Mann-Whitney U test. Significance was accepted at $p<0.05$.

IMb: IgAV microbiota; HMb: healthy microbiota; rIMb: recipient of IgAV microbiota; rHMb: recipient of healthy microbiota.

Supplementary Table S2. Comparison of gut microbiota abundance at the family level between rIMb and rHMb mice (%).

family	rIMb	rHMb	*p*
S24-7	40.77 ± 7.54	46.04 ± 11.27	0.242[a]
Lactobacillaceae	36.99 ± 15.88	22.53 ± 12.47	0.067[a]
Helicobacteraceae	2.25 (0.37~6.27)	2.95 (1.13~5.22)	0.599[b]
Lachnospiraceae	1.05 (0.49~2.56)	1.69 (1.01~6.17)	0.430[b]
Rikenellaceae	1.88 ± 1.52	2.71 ± 1.90	0.322[a]
Coriobacteriaceae	0.41 (0.30~0.56)	2.71 (1.33~4.95)	0.001[b]
Prevotellaceae	0.79 (0.61~2.21)	0.94 (0.47~1.94)	0.661[b]
Erysipelotrichaceae	0.18 (0.08~0.31v	0.74 (0.30~7.28)	0.054[b]
[Paraprevotellaceae]	0.61 (0.14~0.86)	1.68 (0.41~3.39)	0.079[b]
Ruminococcaceae	0.81 (0.43~1.88)	1.38 (0.80~2.10)	0.335[b]

a indicates that the statistical method used is the independent-samples t test; b indicates that the statistical method used is the Mann-Whitney U test. Significance was accepted at $p<0.05$.

IMb: IgAV microbiota; HMb: healthy microbiota; rIMb: recipient of IgAV microbiota; rHMb: recipient of healthy microbiota.

Supplementary Table S3. Comparison of gut microbiota abundance at the genus level between rIMb and rHMb mice (%).

genus	rIMb	rHMb	*p*
Lactobacillus	36.45 ± 15.71	22.43 ± 12.43	0.072[a]
Flexispira	0.75 (0.08~5.12)	1.87 (0.05~2.79)	0.599[b]
[Prevotella]	0.59 (0.10~0.85)	1.66 (0.37~3.36)	0.096[b]
Allobaculum	0.02 (0.00~0.12)	0.03 (0.02~7.21)	0.188[b]
Desulfovibrio	0.39 (0.25~0.74)	0.83 (0.21~3.78)	0.726[b]
Adlercreutzia	0.38 (0.25~0.53)	1.37 (1.00~3.92)	0.001[b]
Prevotella	0.53 (0.24~1.73)	0.61 (0.34~1.31)	0.861[b]
Helicobacter	0.32 (0.12~0.54)	0.33 (0.14~4.02)	0.483[b]
Bacteroides	0.76 ± 0.61	0.71 ± 0.41	0.856[a]
Odoribacter	0.54 (0.24~0.70)	0.61 (0.23~1.18)	0.661[b]

a indicates that the statistical method used is the independent-samples t test; b indicates that the statistical method used is the Mann-Whitney U test. Significance was accepted at $p<0.05$.

IMb: IgAV microbiota; HMb: healthy microbiota; rIMb: recipient of IgAV microbiota; rHMb: recipient of healthy microbiota.