

Table S2. Bacterial community composition across intestinal compartments (feces, cecum, and ileum) at the family level.

feces			relative abundance (%)				
phylum	class	family	WT	v-IL-15tg	logFC	PValue	FDR
Actinobacteria	Actinobacteria	<i>Bifidobacteriaceae</i>	0.73	0.33	0.7921911	0.2858	0.3036
Bacteroidetes	Bacteroidia	<i>Bacteroidaceae</i>	2.00	6.85	-1.7379271	0.0049	0.0141
		<i>Prevotellaceae</i>	0.58	1.21	-1.3098976	0.0517	0.0732
		<i>Rikenellaceae</i>	3.37	2.08	1.6591556	0.0050	0.0141
		S24-7	62.11	46.17	0.8518989	0.1133	0.1482
		[<i>Odoribacteraceae</i>]	0.97	0.47	2.4851926	0.0045	0.0141
		[<i>Paraprevotellaceae</i>]	6.79	7.74	0.6487954	0.2160	0.2448
		fam. not assigned	0.64	3.07	-2.8777891	7.527E-07	6.398E-06
Firmicutes	Bacilli	<i>Lactobacillaceae</i>	4.94	7.33	-0.9008724	0.1455	0.1766
		<i>Turicibacteraceae</i>	0.48	0.00	3.1163517	0.0045	0.0141
	Clostridia	<i>Clostridiaceae</i>	0.96	0.20	1.7926073	0.0376	0.0581
		<i>Lachnospiraceae</i>	1.64	2.66	-1.4578893	0.0229	0.0534
Proteobacteria	Erysipelotrichi	<i>Ruminococcaceae</i>	2.44	1.56	1.4318648	0.0260	0.0534
	Deltaproteobacteria	fam. not assigned	8.64	6.48	1.2569871	0.0282	0.0534
	Erysipelotrichaceae	1.07	2.63	-1.6506351	0.0355	0.0581	
	Desulfovibrionaceae	0.29	0.62	-0.925956	0.4557	0.4557	
Verrucomicrobia	Verrucomicrobiae	<i>Verrucomicrobiaceae</i>	0.24	7.91	-4.7844848	2.444E-10	4.156E-09
cecum			relative abundance (%)				
phylum	class	family	WT	v-IL-15tg	logFC	PValue	FDR
Bacteroidetes	Bacteroidia	<i>Bacteroidaceae</i>	1.36	3.99	-1.6809302	0.0029	0.0093
		<i>Prevotellaceae</i>	0.37	0.59	-1.7630516	0.0356	0.0713
		<i>Rikenellaceae</i>	4.54	3.48	1.2812665	0.0059	0.0156
		S24-7	40.22	36.58	0.2994091	0.5620	0.5620
		[<i>Odoribacteraceae</i>]	2.36	0.35	3.2840747	0.0005	0.0026
		[<i>Paraprevotellaceae</i>]	4.72	4.44	0.6222448	0.2784	0.3897
		fam. not assigned	0.45	2.27	-2.4275481	0.0017	0.0069
Deferribacteres	Deferribacteres	<i>Deferribacteraceae</i>	1.07	0.66	0.7436959	0.4766	0.5600
		<i>Lactobacillaceae</i>	1.22	4.32	-1.6012775	0.0068	0.0156
		<i>Clostridiaceae</i>	0.26	0.37	-0.4145128	0.5356	0.5620
		<i>Lachnospiraceae</i>	3.84	7.88	-0.6772985	0.2165	0.3463
Firmicutes	Bacilli	<i>Ruminococcaceae</i>	9.16	4.81	1.6047906	0.0004	0.0026
		fam. not assigned	25.63	21.62	0.7383458	0.0408	0.0725
		<i>Desulfovibrionaceae</i>	2.26	1.95	0.4520553	0.4900	0.5600
Proteobacteria	Deltaproteobacteria	<i>Anaeroplasmataceae</i>	0.52	1.12	-0.8408389	0.2922	0.3897
Tenericutes		<i>Verrucomicrobiaceae</i>	0.10	2.95	-3.0706332	0.0001	0.0024
ileum			relative abundance (%)				
phylum	class	family	WT	v-IL-15tg	logFC	PValue	FDR
Actinobacteria	Actinobacteria	<i>Bifidobacteriaceae</i>	1.55	0.22	2.1434885	0.0535	0.1300
		<i>Coriobacteriaceae</i>	0.09	0.40	-0.8523897	0.3187	0.4341
	Bacteroidetes	<i>Bacteroidaceae</i>	0.01	0.29	-0.9015356	0.3905	0.4426
		S24-7	2.48	13.61	-2.8896138	0.0104	0.0353
		[<i>Odoribacteraceae</i>]	0.07	0.16	0.207351	0.8683	0.9175
		[<i>Paraprevotellaceae</i>]	0.04	1.11	-1.3981053	0.1143	0.2429
		fam. not assigned	0.00	0.45	-1.2057727	0.1713	0.3175
Firmicutes	Bacilli	<i>Lactobacillaceae</i>	20.84	43.40	-1.3101401	0.1867	0.3175
		<i>Streptococcaceae</i>	1.55	0.04	3.3815733	0.0002	0.0014
		<i>Clostridiaceae</i>	65.27	23.02	1.0872175	0.3575	0.4341
	Clostridia	<i>Lachnospiraceae</i>	0.24	0.97	-0.8238579	0.3486	0.4341
		<i>Ruminococcaceae</i>	0.86	0.59	2.7586418	0.0140	0.0396
		fam. not assigned	0.86	6.44	-3.222775	0.0086	0.0353
Proteobacteria	Deltaproteobacteria	<i>Erysipelotrichaceae</i>	4.55	3.72	0.141341	0.9175	0.9175
		<i>Desulfovibrionaceae</i>	0.40	0.98	-0.9947364	0.3327	0.4341
		<i>Mycoplasmataceae</i>	0.00	0.68	-2.8517619	0.0099	0.0353
Tenericutes	Mollicutes	<i>Verrucomicrobiaceae</i>	0.00	2.09	-4.0655816	0.0002	0.0014