

Table S1. Bacterial community composition across intestinal compartments (feces, cecum, and ileum) at the phylum level.

feces					
	relative abundance (%)				
phylum	WT	v-IL-15tg	logFC	PValue	FDR
Actinobacteria	0.82	0.56	1.263	0.0814	0.1645
Bacteroidetes	77.03	68.09	0.658	0.0987	0.1645
Firmicutes	20.35	21.05	0.071	0.8531	0.8531
Proteobacteria	0.63	1.17	-1.004	0.3469	0.4336
Verrucomicrobia	0.24	7.91	-4.363	1.072E-07	5.362E-07

cecum					
	relative abundance (%)				
phylum	WT	v-IL-15tg	logFC	PValue	FDR
Bacteroidetes	54.36	52.01	1.061	0.0219	0.0402
Deferribacteres	1.07	0.66	1.145	0.2224	0.2669
Firmicutes	40.89	40.03	1.102	0.0029	0.0087
Proteobacteria	2.47	2.31	1.367	0.0268	0.0402
Tenericutes	0.60	1.23	-0.434	0.5557	0.5557
Verrucomicrobia	0.10	2.95	-2.411	0.0021	0.0087

ileum					
	relative abundance (%)				
phylum	WT	v-IL-15tg	logFC	PValue	FDR
Actinobacteria	1.63	0.62	2.561	0.0024	0.0073
Bacteroidetes	2.64	16.21	-2.184	0.0120	0.0241
Firmicutes	94.24	78.31	-0.133	0.8689	0.8689
Proteobacteria	0.94	1.21	0.675	0.2073	0.2487
Tenericutes	0.01	0.74	-3.219	0.0358	0.0538
Verrucomicrobia	0.00	2.09	-2.771	0.0004	0.0023