Inventory of Supplemental Information

Table S1.
Species-level bacterial phylotypes identified from 16S rRNA-based analyses as significantly different in their proportional representation in the fecal microbiota of TRUC versus *Rag*2-/- mice.
Supplemental material for Fig. 1

Table S2.
Table S2. All bacterial species identified in the culture-dependent time course screen of *Rag*2$^{-/-}$ and TRUC fecal microbiota
Supplemental material for Fig. 2

Supplemental Fig. 1
Dextran sulfate sodium does not alter fecal levels of culturable *Klebsiella pneumoniae* and *Proteus mirabilis* in *Rag2*$^{-/-}$ and WT mice.
These data support the results in the paper (e.g. Fig. 2 and Fig. 3) that WT and *Rag2-/-* mice do not have live recoverable *K. pneumoniae* or *P. mirabilis* in their fecal material (at our detection limit) even in response to the colitogenic, mucosal disruptant, dextran sulfate sodium. Thus the presence of these Enterobacteriaceae in TRUC mice is not solely attributable to the presence of colonic inflammation (an observation also supported by Fig. 4).

Supplemental Fig. 2
Colitis scores for Rag2$^{-/-}$ and WT cross-fostered TRUC mice.
These data are the colitis scores for a sub-set of mice in Fig. 3B.

Supplemental Fig. 3
Histologic colitis scores for anti-TNF-α and T-regulatory cell infused TRUC mice off-therapy.
These data are the colitis scores for the mice in the experiments in Fig. 4.

Supplemental Fig. 4.
TNF-α does not affect the growth kinetics of *Klebsiella pneumoniae* or *Proteus mirabilis* cultured *in vitro*
These data supplement the data in Fig. 4 and demonstrate that the observed effects in Fig. 4 are not simply attributable to a direct effect of TNF-α on bacterial growth kinetics.

Fig. S5.
Increased pro-inflammatory cytokines in TRUC vs *Rag2*$^{-/-}$ milk.
These data seek to address the contribution of non-microbial maternal/foster-related environmental factors that may impact microbial colonization of the gut post-natally. These data supplement interpretation of data in Fig. 1 and Fig. 3.

Supplemental Text and Figures

Table S1. Species-level bacterial phylotypes identified from 16S rRNA-based analyses as significantly different in their proportional representation in the fecal microbiota of TRUC versus *Rag2*-/- animals.

Phylotype Identification Number	Taxonomic assignment	T-bet-/-.Rag2-/- (TRUC) mice Relative abundance of phylotype, % average ± SEM *	Rag2-/- mice Relative abundance of phylotype, % average ± SEM	Mann Whitney U	P value	P value with Bonferroni correction **	P value with FDR correction
otu_107	Actinobacteria;Actinobacteria;Coriobacteridae;Coriobacteriales;Coriobacterineae;Coriobacteriaceae;Denitrobacterium	0.01 ± 0.01	0.17 ± 0.06	37	2.17E-04	7.00E-01	3.33E-02
otu_464	Bacteroidetes	1.89 ± 0.48	0.01 ± 0.01	1	8.01E-07	2.59E-03	2.59E-03
otu_807	Bacteroidetes	0.38 ± 0.14	0.00 ± 0.00	16	3.59E-06	1.16E-02	2.90E-03
otu_126	Bacteroidetes	0.24 ± 0.05	0.02 ± 0.01	13.5	7.20E-06	2.32E-02	3.32E-03
otu_1090	Bacteroidetes	0.71 ± 0.20	0.00 ± 0.00	18	1.03E-05	3.32E-02	3.69E-03
otu_1947	Bacteroidetes	0.17 ± 0.03	0.00 ± 0.00	25.5	2.24E-05	7.25E-02	3.45E-03
otu_842	Bacteroidetes	0.11 ± 0.03	0.00 ± 0.00	32	3.49E-05	1.13E-01	5.36E-03
otu_2027	Bacteroidetes	0.01 ± 0.01	0.53 ± 0.14	31	8.02E-05	2.59E-01	1.23E-02
otu_572	Bacteroidetes	0.23 ± 0.05	0.02 ± 0.02	30	8.58E-05	2.77E-01	1.32E-02
otu_1544	Bacteroidetes	0.31 ± 0.14	0.00 ± 0.00	40	9.92E-05	3.20E-01	1.53E-02
otu_3215	Bacteroidetes	0.76 ± 0.30	0.00 ± 0.00	40	9.92E-05	3.20E-01	1.53E-02
otu_823	Bacteroidetes	0.12 ± 0.03	0.00 ± 0.00	40	9.92E-05	3.20E-01	1.53E-02
otu_870	Bacteroidetes	0.13 ± 0.04	0.00 ± 0.00	40	9.92E-05	3.20E-01	1.53E-02
otu_893	Bacteroidetes	0.09 ± 0.02	0.00 ± 0.00	40	9.92E-05	3.20E-01	1.53E-02
otu_1598	Bacteroidetes	0.45 ± 0.17	0.00 ± 0.00	42.5	2.30E-04	7.42E-01	3.53E-02
otu_1100	Bacteroidetes	0.46 ± 0.18	0.00 ± 0.00	48	2.67E-04	8.61E-01	4.10E-02
otu_814	Bacteroidetes	0.18 ± 0.10	0.00 ± 0.00	48	2.67E-04	8.61E-01	4.10E-02
otu_110	Bacteroidetes;Bacteroidetes;Bacteroidales	0.66 ± 0.12	0.03 ± 0.01	10.5	5.90E-06	1.91E-02	3.18E-03
otu_846	Bacteroidetes;Bacteroidetes;Bacteroidales	0.33 ± 0.08	0.00 ± 0.00	32	3.49E-05	1.13E-01	5.36E-03
otu_1459	Bacteroidetes;Bacteroidetes;Bacteroidales;Bacteroidaceae;Bacteroides	0.21 ± 0.05	0.00 ± 0.00	9.5	2.00E-06	6.46E-03	2.15E-03
otu_386	Bacteroidetes;Bacteroidetes;Bacteroidales;Bacteroidaceae;Bacteroides	3.44 ± 0.53	0.25 ± 0.23	8	4.80E-06	1.55E-02	3.10E-03
otu_1476	Bacteroidetes;Bacteroidetes;Bacteroidales;Bacteroidaceae;Bacteroides	0.14 ± 0.03	0.00 ± 0.00	24	1.16E-05	3.73E-02	3.11E-03
otu_225	Bacteroidetes;Bacteroidetes;Bacteroidales;Bacteroidaceae;Bacteroides	0.27 ± 0.06	0.01 ± 0.01	19	1.24E-05	4.00E-02	2.50E-03
otu_1115	Bacteroidetes;Bacteroidetes;Bacteroidales;Bacteroidaceae;Bacteroides	0.16 ± 0.04	0.00 ± 0.00	32	3.49E-05	1.13E-01	5.36E-03
otu_1552	Bacteroidetes;Bacteroidetes;Bacteroidales;Bacteroidaceae;Bacteroides	0.10 ± 0.03	0.00 ± 0.00	32	3.49E-05	1.13E-01	5.36E-03
otu_1042	Bacteroidetes;Bacteroidetes;Bacteroidales;Bacteroidaceae;Bacteroides	0.11 ± 0.03	0.00 ± 0.00	40	9.92E-05	3.20E-01	1.53E-02
otu_1130	Bacteroidetes;Bacteroidetes;Bacteroidales;Bacteroidaceae;Bacteroides	0.07 ± 0.03	0.00 ± 0.00	40	9.92E-05	3.20E-01	1.53E-02
otu_675	Bacteroidetes;Bacteroidetes;Bacteroidales;Bacteroidaceae;Bacteroides	0.20 ± 0.04	0.20 ± 0.20	33	1.41E-04	4.55E-01	2.16E-02
otu_812	Bacteroidetes;Bacteroidetes;Bacteroidales;Porphyromonadaceae;Parabacteroides	0.36 ± 0.07	0.00 ± 0.00	8	1.04E-06	3.36E-03	1.68E-03
otu_1998	Bacteroidetes;Bacteroidetes;Bacteroidales;Porphyromonadaceae;Parabacteroides	0.17 ± 0.05	0.00 ± 0.00	24	1.16E-05	3.73E-02	2.87E-03
otu_1496	Bacteroidetes;Bacteroidetes;Bacteroidales;Porphyromonadaceae;Parabacteroides	0.14 ± 0.04	0.00 ± 0.00	40	9.92E-05	3.20E-01	1.53E-02
otu_1288	Bacteroidetes;Bacteroidetes;Bacteroidales;Rikenellaceae;Alistipes	0.02 ± 0.01	0.29 ± 0.06	16	1.79E-05	5.78E-02	3.04E-03
otu_1283	Bacteroidetes;Bacteroidetes;Bacteroidales;Rikenellaceae;Alistipes	0.06 ± 0.03	0.45 ± 0.09	32	2.39E-04	7.71E-01	3.67E-02
otu_1466	Bacteroidetes;Bacteroidetes;Bacteroidales;Rikenellaceae;Alistipes	0.21 ± 0.09	0.00 ± 0.00	48	2.67E-04	8.61E-01	4.10E-02
otu_1418	Firmicutes	0.58 ± 0.17	0.07 ± 0.07	22	2.70E-05	8.72E-02	4.15E-03
otu_1769	Firmicutes	0.00 ± 0.00	0.06 ± 0.02	48	2.67E-04	8.61E-01	4.10E-02
otu_2410	Firmicutes;Bacilli;Lactobacillales;Lactobacillaceae;Lactobacillus	10.01 ± 2.67	0.98 ± 0.39	14	1.89E-05	6.09E-02	3.04E-03
otu_1921	Firmicutes;Bacilli;Lactobacillales;Lactobacillaceae;Lactobacillus	3.04 ± 1.48	0.32 ± 0.32	29	7.25E-05	2.34E-01	1.12E-02
otu_829	Firmicutes;Clostridia;Clostridiales	0.29 ± 0.09	0.00 ± 0.00	24	1.16E-05	3.73E-02	3.39E-03
otu_105	Firmicutes;Clostridia;Clostridiales	0.00 ± 0.00	0.17 ± 0.04	27	4.00E-05	1.29E-01	6.16E-03
otu_470	Firmicutes;Clostridia;Clostridiales	0.01 ± 0.01	0.18 ± 0.06	27	4.00E-05	1.29E-01	6.16E-03
otu_276	Firmicutes;Clostridia;Clostridiales	0.04 ± 0.02	0.33 ± 0.06	25	8.03E-05	2.59E-01	1.24E-02
otu_178	Firmicutes;Clostridia;Clostridiales	0.01 ± 0.01	0.53 ± 0.24	35	8.87E-05	2.86E-01	1.36E-02
otu_2	Firmicutes;Clostridia;Clostridiales	0.07 ± 0.03	0.73 ± 0.23	24.5	9.13E-05	2.95E-01	1.40E-02
otu_7	Firmicutes;Clostridia;Clostridiales	0.00 ± 0.00	0.49 ± 0.34	40	9.92E-05	3.20E-01	1.53E-02
otu_369	Firmicutes;Clostridia;Clostridiales	0.05 ± 0.02	0.25 ± 0.05	30.5	2.29E-04	7.40E-01	3.53E-02
otu_1304	Firmicutes;Clostridia;Clostridiales	0.00 ± 0.00	0.06 ± 0.02	48	2.67E-04	8.61E-01	4.10E-02
otu_14	Firmicutes;Clostridia;Clostridiales;Lachnospiraceae	0.04 ± 0.02	0.40 ± 0.08	13	1.18E-05	3.79E-02	2.71E-03
otu_33	Firmicutes;Clostridia;Clostridiales;Lachnospiraceae	0.01 ± 0.01	0.52 ± 0.14	19	1.24E-05	4.00E-02	2.67E-03
otu_52	Firmicutes;Clostridia;Clostridiales;Lachnospiraceae	0.13 ± 0.05	1.02 ± 0.14	13	1.37E-05	4.42E-02	2.45E-03
otu_205	Firmicutes;Clostridia;Clostridiales;Lachnospiraceae	0.01 ± 0.00	0.15 ± 0.02	21	2.26E-05	7.31E-02	3.48E-03
otu_59	Firmicutes;Clostridia;Clostridiales;Lachnospiraceae	0.00 ± 0.00	0.12 ± 0.06	32	3.49E-05	1.13E-01	5.36E-03
otu_1777	Firmicutes;Clostridia;Clostridiales;Lachnospiraceae	0.05 ± 0.03	0.26 ± 0.04	21	4.18E-05	1.35E-01	6.43E-03
otu_2407	Firmicutes;Clostridia;Clostridiales;Lachnospiraceae	0.01 ± 0.00	0.11 ± 0.02	32.5	1.30E-04	4.19E-01	2.00E-02
otu_375	Firmicutes;Clostridia;Clostridiales;Lachnospiraceae	0.01 ± 0.01	0.14 ± 0.04	41	2.47E-04	7.97E-01	3.80E-02
otu_1298	Firmicutes;Clostridia;Clostridiales;Lachnospiraceae	0.00 ± 0.00	0.07 ± 0.02	43.5	2.72E-04	8.79E-01	4.18E-02
otu_3	Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Lachnospiraceae Incertae Sedis	0.27 ± 0.09	1.46 ± 0.16	15	2.22E-05	7.17E-02	3.41E-03
otu_1934	Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Lachnospiraceae Incertae Sedis	0.38 ± 0.10	0.02 ± 0.02	33	1.12E-04	3.63E-01	1.73E-02
otu_79	Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Lachnospiraceae Incertae Sedis	0.06 ± 0.03	0.28 ± 0.04	27	1.28E-04	4.14E-01	1.97E-02
otu_173	Firmicutes;Clostridia;Clostridiales;Lachnospiraceae;Roseburia	0.00 ± 0.00	0.11 ± 0.02	25.5	2.24E-05	7.25E-02	3.45E-03
otu_10	Firmicutes;Clostridia;Clostridiales;Ruminococcaceae	0.19 ± 0.10	2.09 ± 0.34	11	9.00E-06	2.91E-02	3.63E-03
otu_12	Firmicutes;Clostridia;Clostridiales;Ruminococcaceae	0.03 ± 0.03	0.63 ± 0.14	18	1.32E-05	4.27E-02	2.51E-03
otu_2017	Unclassified Bacteria	0.20 ± 0.05	0.00 ± 0.00	20	1.12E-05	3.60E-02	3.60E-03
otu_1190	Unclassified Bacteria	0.24 ± 0.07	0.00 ± 0.00	32	3.49E-05	1.13E-01	5.36E-03
otu_1930	Unclassified Bacteria	0.36 ± 0.10	0.00 ± 0.00	32	3.49E-05	1.13E-01	5.36E-03
otu_1149	Unclassified Bacteria	0.10 ± 0.03	0.00 ± 0.00	40	9.92E-05	3.20E-01	1.53E-02
otu_658	Unclassified Bacteria	0.24 ± 0.07	0.02 ± 0.02	40	2.09E-04	6.75E-01	3.22E-02
otu_1475	Unclassified Bacteria	0.80 ± 0.31	0.00 ± 0.00	48	2.67E-04	8.61E-01	4.10E-02
otu_2816	Unclassified Bacteria	0.27 ± 0.06	0.04 ± 0.03	39	2.98E-04	9.63E-01	4.59E-02

For each phylotype, a taxonomic assignment based on the RDP classifier implemented in QIIME software (http://sourceforge.net/projects/qiime/) is shown, followed by the average proportional representation of that phylotype in the fecal microbiota of TRUC (T-bet-/- x Rag2-/-) and Rag2-/- mice (n=16 fecal samples from 4 mice per genotype). *Relative abundance as % of assigned bacterial 16S rRNA gene sequences for each sample. **A total of 3,229 species-level OTUs were identified among all fecal microbiota surveyed, but only the 69 shown here passed the threshold FDR-corrected value of p<0.05.

Supplemental Text and Figures

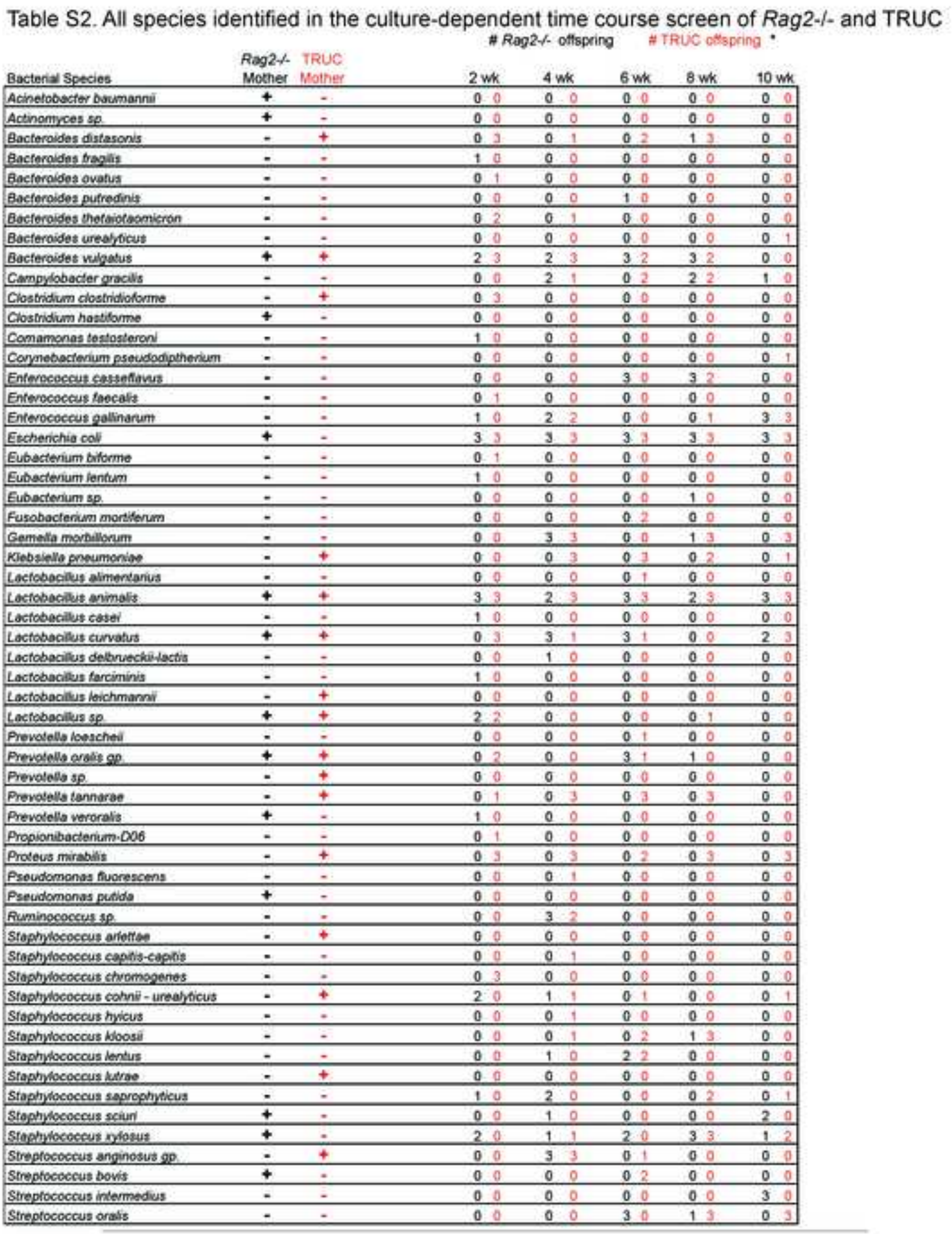


Table S2. All species identified in the culture-dependent time course screen of *Rag2-/-* and TRUC

Rag2-/- offspring # TRUC offspring *

Bacterial Species	*Rag2-/-* Mother	TRUC Mother	2 wk		4 wk		6 wk		8 wk		10 wk	
Acinetobacter baumannii	+	-	0	0	0	0	0	0	0	0	0	0
Actinomyces sp.	+	-	0	0	0	0	0	0	0	0	0	0
Bacteroides distasonis	-	+	0	3	0	1	0	2	1	3	0	0
Bacteroides fragilis	-	-	1	0	0	0	0	0	0	0	0	0
Bacteroides ovatus	-	-	0	1	0	0	0	0	0	0	0	0
Bacteroides putredinis	-	-	0	0	0	0	1	0	0	0	0	0
Bacteroides thetaiotaomicron	-	-	0	2	0	1	0	0	0	0	0	0
Bacteroides urealyticus	-	-	0	0	0	0	0	0	0	0	0	1
Bacteroides vulgatus	+	+	2	3	2	3	3	2	3	2	0	0
Campylobacter gracilis	-	-	0	0	2	1	0	2	2	2	1	0
Clostridium clostridioforme	-	+	0	3	0	0	0	0	0	0	0	0
Clostridium hastiforme	+	-	0	0	0	0	0	0	0	0	0	0
Comamonas testosteroni	-	-	1	0	0	0	0	0	0	0	0	0
Corynebacterium pseudodiptherium	-	-	0	0	0	0	0	0	0	0	0	1
Enterococcus casseflavus	-	-	0	0	0	0	3	0	3	2	0	0
Enterococcus faecalis	-	-	0	1	0	0	0	0	0	0	0	0
Enterococcus gallinarum	-	-	1	0	2	2	0	0	0	1	3	3
Escherichia coli	+	-	3	3	3	3	3	3	3	3	3	3
Eubacterium biforme	-	-	0	1	0	0	0	0	0	0	0	0
Eubacterium lentum	-	-	1	0	0	0	0	0	0	0	0	0
Eubacterium sp.	-	-	0	0	0	0	0	0	1	0	0	0
Fusobacterium mortiferum	-	-	0	0	0	0	0	2	0	0	0	0
Gemella morbillorum	-	-	0	0	3	3	0	0	1	3	0	3
Klebsiella pneumoniae	-	+	0	0	0	3	0	3	0	2	0	1
Lactobacillus alimentarius	-	-	0	0	0	0	0	1	0	0	0	0
Lactobacillus animalis	+	+	3	3	2	3	3	3	2	3	3	3
Lactobacillus casei	-	-	1	0	0	0	0	0	0	0	0	0
Lactobacillus curvatus	+	+	0	3	3	1	3	1	0	0	2	3
Lactobacillus delbrueckii-lactis	-	-	0	0	1	0	0	0	0	0	0	0
Lactobacillus farciminis	-	-	1	0	0	0	0	0	0	0	0	0
Lactobacillus leichmannii	-	+	0	0	0	0	0	0	0	0	0	0
Lactobacillus sp.	+	+	2	2	0	0	0	0	0	1	0	0
Prevotella loescheii	-	-	0	0	0	0	0	1	0	0	0	0
Prevotella oralis gp.	+	+	0	2	0	0	3	1	1	0	0	0
Prevotella sp.	-	+	0	0	0	0	0	0	0	0	0	0
Prevotella tannarae	-	+	0	1	0	3	0	3	0	3	0	0
Prevotella veroralis	+	-	1	0	0	0	0	0	0	0	0	0
Propionibacterium-D06	-	-	0	1	0	0	0	0	0	0	0	0
Proteus mirabilis	-	+	0	3	0	3	0	2	0	3	0	3
Pseudomonas fluorescens	-	-	0	0	0	1	0	0	0	0	0	0
Pseudomonas putida	+	-	0	0	0	0	0	0	0	0	0	0
Ruminococcus sp.	-	-	0	0	3	2	0	0	0	0	0	0
Staphylococcus arlettae	-	+	0	0	0	0	0	0	0	0	0	0
Staphylococcus capitis-capitis	-	-	0	0	0	1	0	0	0	0	0	0
Staphylococcus chromogenes	-	-	0	3	0	0	0	0	0	0	0	0
Staphylococcus cohnii - urealyticus	-	+	2	0	1	1	0	1	0	0	0	1
Staphylococcus hyicus	-	-	0	0	0	1	0	0	0	0	0	0
Staphylococcus kloosii	-	-	0	0	0	1	0	2	1	3	0	0
Staphylococcus lentus	-	-	0	0	1	0	2	2	0	0	0	0
Staphylococcus lutrae	-	+	0	0	0	0	0	0	0	0	0	0
Staphylococcus saprophyticus	-	-	1	0	2	0	0	0	0	2	0	1
Staphylococcus sciuri	+	-	0	0	1	0	0	0	0	0	2	0
Staphylococcus xylosus	+	-	2	0	1	1	2	0	3	3	1	2
Streptococcus anginosus gp.	-	+	0	0	3	3	0	1	0	0	0	0
Streptococcus bovis	+	-	0	0	0	0	0	2	0	0	0	0
Streptococcus intermedius	-	-	0	0	0	0	0	0	0	0	3	0
Streptococcus oralis	-	-	0	0	0	0	3	0	1	3	0	3

Fig. S1

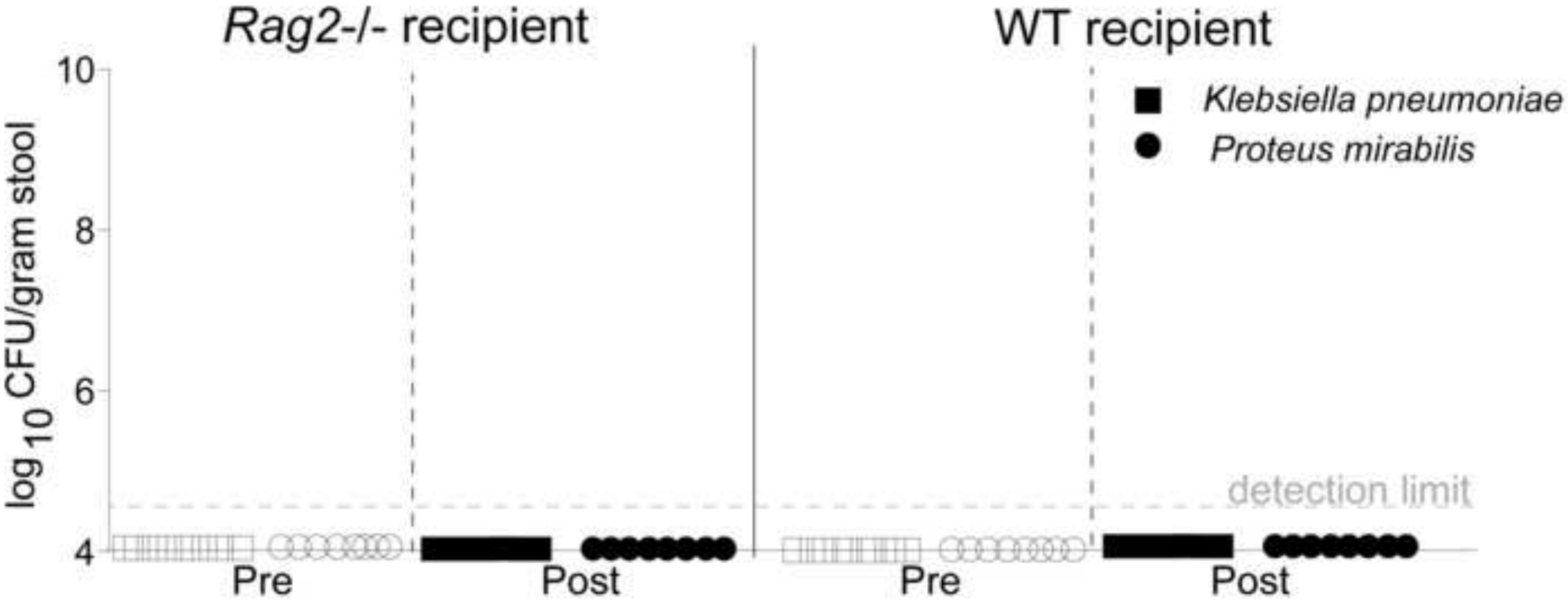

Rag2-/- recipient
WT recipient
log10 CFU/gram stool
10
8
6
4
■ *Klebsiella pneumoniae*
● *Proteus mirabilis*
detection limit
Pre
Post
Pre
Post

Fig. S2

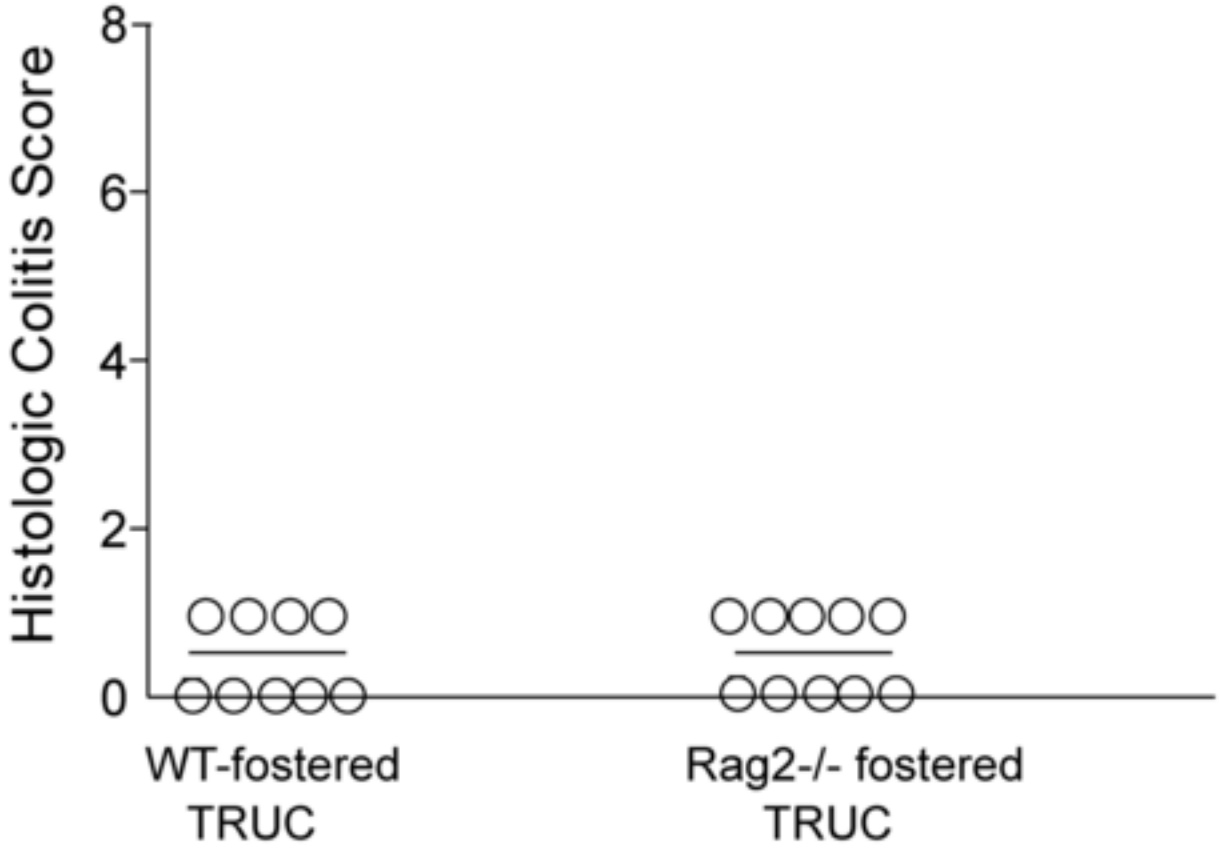

Histologic Colitis Score
8
6
4
2
0
WT-fostered TRUC
Rag2-/- fostered TRUC

Fig. S3

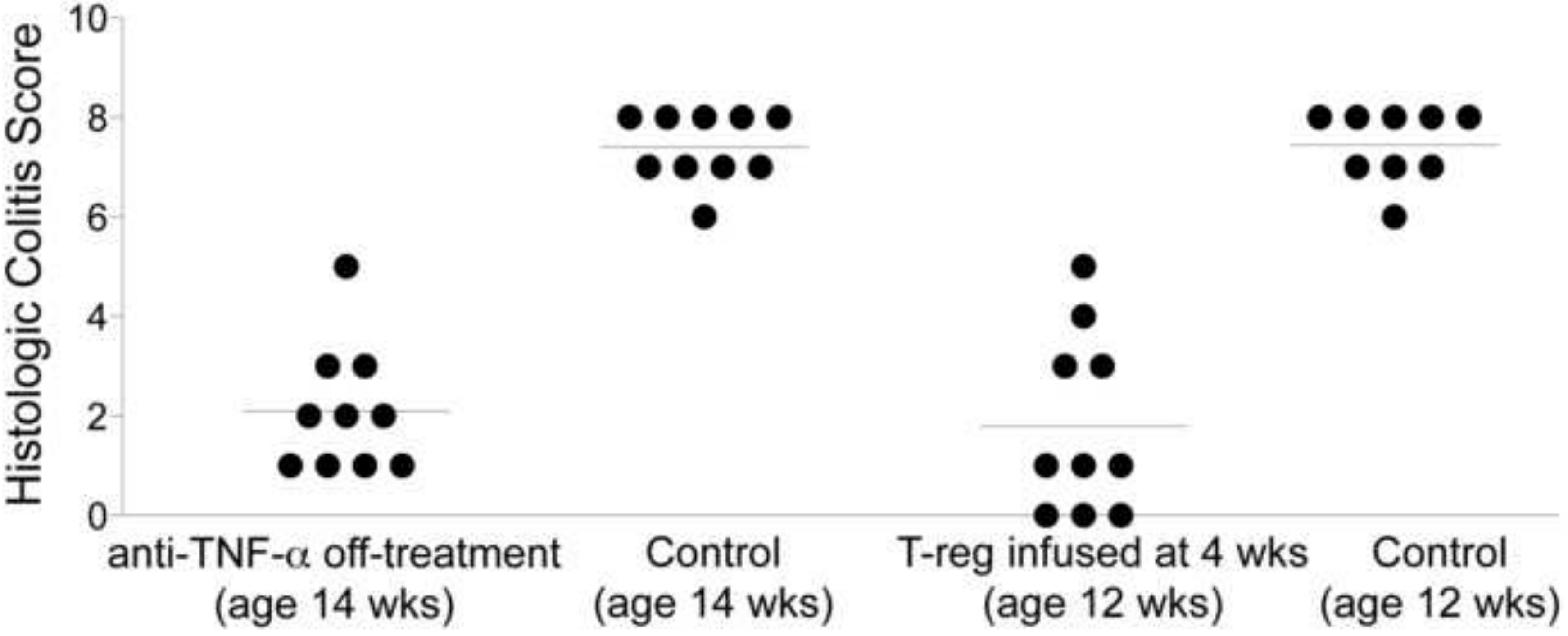
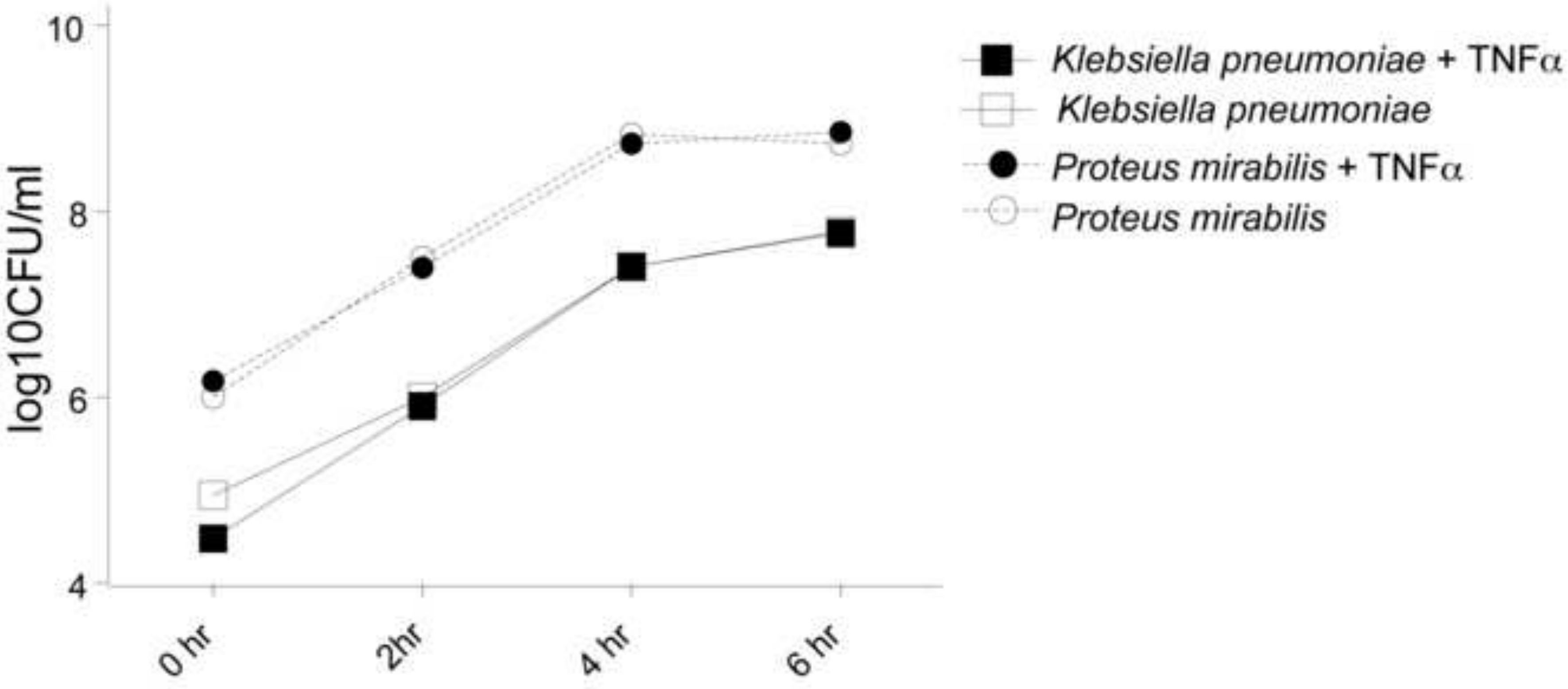

Histologic Colitis Score
10
8
6
4
2
0
anti-TNF-α off-treatment
(age 14 wks)
Control
(age 14 wks)
T-reg infused at 4 wks
(age 12 wks)
Control
(age 12 wks)

Fig. S4


10
8
6
4
log10CFU/ml
0 hr
2hr
4 hr
6 hr
■ *Klebsiella pneumoniae* + TNFα
□ *Klebsiella pneumoniae*
● *Proteus mirabilis* + TNFα
○ *Proteus mirabilis*

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