Supplementary Table 1: Members of the mouse gut microbiota unique to SPF or CONV housing conditions. Only microorganisms that were exclusively found either in SPF or CONV TNF^{deltaARE} mice are displayed. Analysis was performed using high-throughput 16S rRNA gene sequencing, FELASA-guided analysis or cultivation (yeast-specific Sabourand-agar). Sequencing was done as described in the supplementary methods (taxa with a sequence abundance >0.5% are shown). For FELASA analysis, results of three different analysis time points were considered (previous, during and after performing the experiments). Samples from sentinel mice were taken from intestinal content, fur swaps, organs and rectum swaps. Analysis was performed by an independent, certified lab according to FELASA recommendations from 2014. *microorganisms generally regarded as pathogenic to rodents.[69]

Housing	**Taxon**	**relative abundance (% ± SD)**	**Lineage**	**Method of analysis**
SPF	*unknown_Clostridiales*	2.4 ± 1.2	Bacteria	sequencing
	unknown_Desulfovibrionales	0.5 ± 0.3	Bacteria	sequencing
CONV	*Helicobacteraceae**	9.6 ± 3.4	Bacteria	sequencing
	Bacteroidaceae	5.5 ± 2.9	Bacteria	sequencing
	Desulfovibrionaceae	5.1 ± 1.6	Bacteria	sequencing
	Verrucomicrobiaceae	2.8 ± 1.6	Bacteria	sequencing
	Prevotellaceae	2.0 ± 1.0	Bacteria	sequencing
	Deferribacteraceae	1.5 ± 0.9	Bacteria	sequencing
	Defluviitaleaceae	1.0 ± 0.7	Bacteria	sequencing
	Sutterellaceae	0.9 ± 0.4	Bacteria	sequencing
	Bifidobacteriaceae	0.8 ± 0.9	Bacteria	sequencing
	Erysipelotrichaceae	0.8 ± 0.7	Bacteria	sequencing
	Clostridiaceae	0.7 ± 1.1	Bacteria	sequencing
	Peptostreptococcaceae	0.6 ± 0.9	Bacteria	sequencing
	*Chlamydiaceae**	0.6 ± 0.6	Bacteria	sequencing
	*Murine norovirus**	positive	Virus	FELASA
	*Helicobacter spp.**	positive	Bacteria	FELASA
	*Pasteurella spp.**	positive	Bacteria	FELASA
	*Syphacia spp.**	positive	Animalia	FELASA
	*Trichomonas spp.**	positive	Animalia	FELASA
	Candida tropicalis	positive	Fungi	cultivation
	Kazachstania heterogenica	positive	Fungi	cultivation