Supplementary Materials:

Table S1. Description of the most abundant phyla, families, and Amplicon Sequence Variants (ASVs) (% mean ± SD) found in the fecal microbiota of cats fed with either a control or an inulin-supplemented diet at the start of the experiment (T0) and six weeks after.

		T0		6 weeks	
		Control	Inulin	Control	Inulin
Main Phylums	Firmicutes	70.73 ± 7.81	70.66 ± 8.52	62.83 ± 13.09	71.7 ± 6.68
	Bacteroidetes	9.67 ± 8.87	7.26 ± 7.05	18.00 ± 14.66	7.87 ± 4.74
	Actinobacteria	17.21 ± 7.75	20.39 ± 11.28	14.81 ± 10.18	18.59 ± 6.92
	Proteobacteria	2.02 ± 2.11	1.48 ± 2.43	2.93 ± 3.12	1.53 ± 0.73
	Fusobacteria	0.15 ± 0.23	0.11 ± 0.25	1.31 ± 3.57	0.15 ± 0.28
Main Families	*Veillonellaceae*	17.82 ± 8.48	20.06 ± 8.96	16.31 ± 10.50	19.23 ± 8.39
	Lachnospiraceae	17.94 ± 7.88	14.99 ± 6.01	13.33 ± 6.07	13.81 ± 4.85
	Prevotellaceae	8.38 ± 7.71	6.29 ± 5.92	13.77 ± 10.14	6.74 ± 4.14
	Erysipelotrichaceae	11.98 ± 3.87	12.84 ± 5.66	11.17 ± 5.50	13.62 ± 5.70
	Peptostreptococcaceae	8.26 ± 2.09	8.37 ± 5.04	8.02 ± 3.87	10.01 ± 3.51
	Coriobacteriaceae	9.97 ± 3.67	8.47 ± 3.86	7.58 ± 3.14	10.81 ± 1.68
	Ruminococcaceae	6.54 ± 4.33	5.79 ± 3.08	6.07 ± 2.57	8.04 ± 4.84
	Lactobacillaceae	4.38 ± 5.62	4.82 ± 3.80	4.25 ± 4.53	2.33 ± 2.10
	Bifidobacteriaceae	4.61 ± 5.04	5.69 ± 6.10	6.28 ± 8.53	5.3 ± 4.86
	Bacteroidaceae	0.92 ± 0.99	0.51 ± 0.82	3.56 ± 5.82	0.74 ± 0.59
	Atopobiaceae	2.31 ± 3.33	5.93 ± 8.41	0.66 ± 0.77	2.03 ± 2.54
	Acidaminococcaceae	1.71 ± 1.16	1.96 ± 0.94	2.04 ± 0.85	2.14 ± 1.27
	Fusobacteriaceae	0.15 ± 0.23	0.11 ± 0.25	1.31 ± 3.57	0.15 ± 0.28
	Enterobacteriaceae	0.02 ± 0.05	0 ± 0	0.01 ± 0.01	0.01 ± 0.03
	Succinivibrionaceae	1.37 ± 1.80	1.2 ± 2.08	1.81 ± 2.04	1.01 ± 0.67
	Burkholderiaceae	0.41 ± 0.52	0.23 ± 0.30	1.06 ± 1.25	0.39 ± 0.31
Main Genus	*Megasphaera*	10.57 ± 6.79	16.74 ± 9.22	11.03 ± 8.72	13.72 ± 7.65
	Prevotella 9	7.33 ± 7.18	5.66 ± 5.44	11.39 ± 8.36	6.12 ± 3.84
	Blautia	12.06 ± 5.66	10.07 ± 4.47	8.27 ± 4.35	8.53 ± 3.30
	Peptoclostridium	6.43 ± 2.43	6.04 ± 4.07	7.05 ± 3.59	7.84 ± 2.67
	Collinsella	9.91 ± 3.65	8.41 ± 3.82	7.52 ± 3.11	10.68 ± 1.61
	Lactobacillus	4.39 ± 5.63	4.82 ± 3.80	4.23 ± 4.52	2.33 ±2.08
	Bifidobacterium	4.63 ± 5.03	5.68 ± 6.08	6.28 ± 8.52	5.30 ± 4.85
	Solobacterium	4.98 ± 3.44	5.85 ± 4.26	4.78 ± 4.14	7.15 ± 4.64
	Megamonas	5.22 ± 3.19	1.14 ± 0.82	3.49 ± 2.27	2.96 ± 2.83
	Bacteroides	0.92 ± 0.97	0.52 ± 0.84	3.57 ± 5.81	0.75 ± 0.58
	Catenibacterium	3.83 ± 2.67	3.66 ± 3.36	3.41 ± 2.22	2.20 ± 1.62
	Lachnospiraceae	2.44 ± 0.83	2.34 ± 1.37	2.33 ± 1.31	2.56 ± 1.75
	Fusobacterium	0.14 ± 0.23	0.11 ± 0.26	1.31 ± 3.58	0.15 ± 0.3
	Holdemanella	2.04 ± 1.49	1.82 ± 1.08	2.05 ± 1.20	2.03 ± 1.38
	Olsenella	1.93 ± 3.22	5.29 ±8.52	0.11 ± 0.19	1.35 ± 2.33
	Dialister	1.72 ±1.72	1.76 ± 1.63	1.44 ± 1.42	2.03 ± 2.03
	Succinivibrio	1.12 ± 1.79	1.16 ± 2.08	1.49 ±1.92	0.87 ± 0.74
	Alloprevotella	0.80 ± 0.91	0.39 ± 0.78	1.72 ± 2.30	0.25±0.23
	Acidaminococcus	1.03 ± 1.04	1.67 ± 1.02	1.03 ± 0.95	1.72 ±1.31
	Negativibacillus	1.43 ± 0.81	1.27 ± 0.63	1.46 ± 0.79	1.99 ±0.89
	Faecalibacterium	1.24 ±1.10	0.85 ± 0.81	1.33 ± 1.03	1.14 ±0.92
	Subdoligranulum	1.56 ±1.68	1.65 ± 1.20	0.90 ± 0.85	2.05 ± 2.30
	Faecalitalea	0.97 ±0.98	1.38 ± 1.13	0.52 ± 0.79	1.59 ±1.53
	Peptostreptococcaceae	1.33 ± 1.42	1.90 ± 1.51	0.92 ± 1.00	1.47 ±2.20