Table S1. Primer sequences for qPCR

Target gene or bacteria	Direction	Sequence (5′ to 3′)
Rpl13a	Forward	CCATTGTGGCCAAGCAGGTA
	Reverse	CTCGGGAGGGGTTGGTATTC
TNF-a	Forward	TAGCCCACGTCGTAGCAAAC
	Reverse	GCAGCCTTGTCCCTTGAAGA
Adiponectin	Forward	GTCTGGCTCCAGGTGTATGG
	Reverse	AGCTGAAAGTGTGTCGACTGT
F4/80	Forward	CTGGGATCCTACAGCTGCTC
	Reverse	AGGAGCCTGGTACATTGGTG
CD11c	Forward	CTGGATAGCCTTTCTTCTGCTG
	Reverse	GCACACTGTGTCCGAACTCA
Tjp1	Forward	GCCAGAGAAAAGTTGGCAAG
	Reverse	TTGGATACCACTGCGCATAA
Muc2	Forward	GCTGACGAGTGGTTGGTGAATG
	Reverse	GATGAGGTGGCAGACAGGAGAC
Eubacterium	Forward	ACTCCTACGGGAGGCAGCAGT
	Reverse	ATTACCGCGGCTGCTGGC
Akkermansia muciniphila	Forward	CAGCACGTGAAGGTGGGGAC
	Reverse	CCTTGCGGTTGGCTTCAGAT
Parabacteroides goldsteinii	Forward	GCAGCACGATGTAGCAATACA
	Reverse	TTAACAAATATTTCCATGTGGAAC

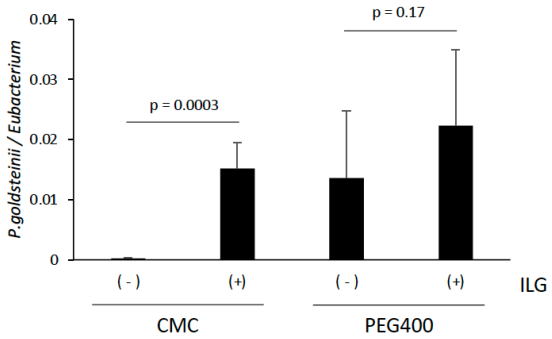

Figure S1. Relative abundance of *P. goldsteinii* in mice administered with ILG dispersed in CMC or PEG400. RT-PCR analysis of eubacterium and *P. goldsteinii* in fecal DNA isolated from ND-fed mice administered with CMC or PEG400 (40%) in the presence or absence of ILG (*n* = 6). ILG dispersed in CMC or PEG400 was administered for two weeks post-acclimation.