SUPPLEMENTARY FIGURE 1: **BF and HF fecal bacteria communities profile before and after dietary fiber supplementation with cellulose.** Fecal bacteria communities were profiled using high depth sequencing of amplicons of 16S rRNA. Prior to dietary modification all animals contained similar gut bacterial communities. After 2 weeks on different diets we observed a shift in the composition of the intestinal microbiota in HF-fed mice characterized by a decline in the relative abundance of a family of Bacteroidales, *Lactobacillus* and Clostridiales and by a significant increase in *Akkermansia* and Lachnospiraceae members. LEfSe was used to identify biomarkers ($P \leq 0.05$) for either the initial, BF and HF sample groups. Taxa displayed here are those with high relative abundance across sample groups (> 0.01).

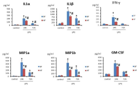
IL1α
IL1β
IFN-γ
MIP1a
MIP1b
GM-CSF
pg/ml
control
24h
72h
LPS
BF
HF
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Fig. 1