Supplementary Table 1. Longitudinal alpha diversity measures of fecal samples from 32 women with breast cancer participating in a presurgical weight loss trial[a] having low versus high *Akkermansia muciniphila* abundance.

	Low *A. muciniphila* (n=16)					High *A. muciniphila* (n=16)					
	Baseline		Follow-up			Baseline		Follow-up			
	Mean	SD	Mean	SD	p[b]	Mean	SD	Mean	SD	p[b]	p[c]
Observed species[d]	282.4	69.6	303.6	73.0	0.342	360.8	84.8	330.8	70.9	0.054	0.058
Chao1[e]	341.6	71.2	361.5	75.4	0.335	418.4	90.2	379.9	75.3	0.044	0.036
Whole tree phylogeny[f]	20.7	4.3	21.7	5.0	0.416	25.8	5.8	24.6	4.7	0.168	0.144
Shannon Index[g]	4.735	0.729	5.113	0.858	0.201	5.395	0.559	4.970	0.736	0.012	0.017

[a] Mean time from baseline to follow-up was 30±9 days.

[b] Within group differences from baseline to follow-up

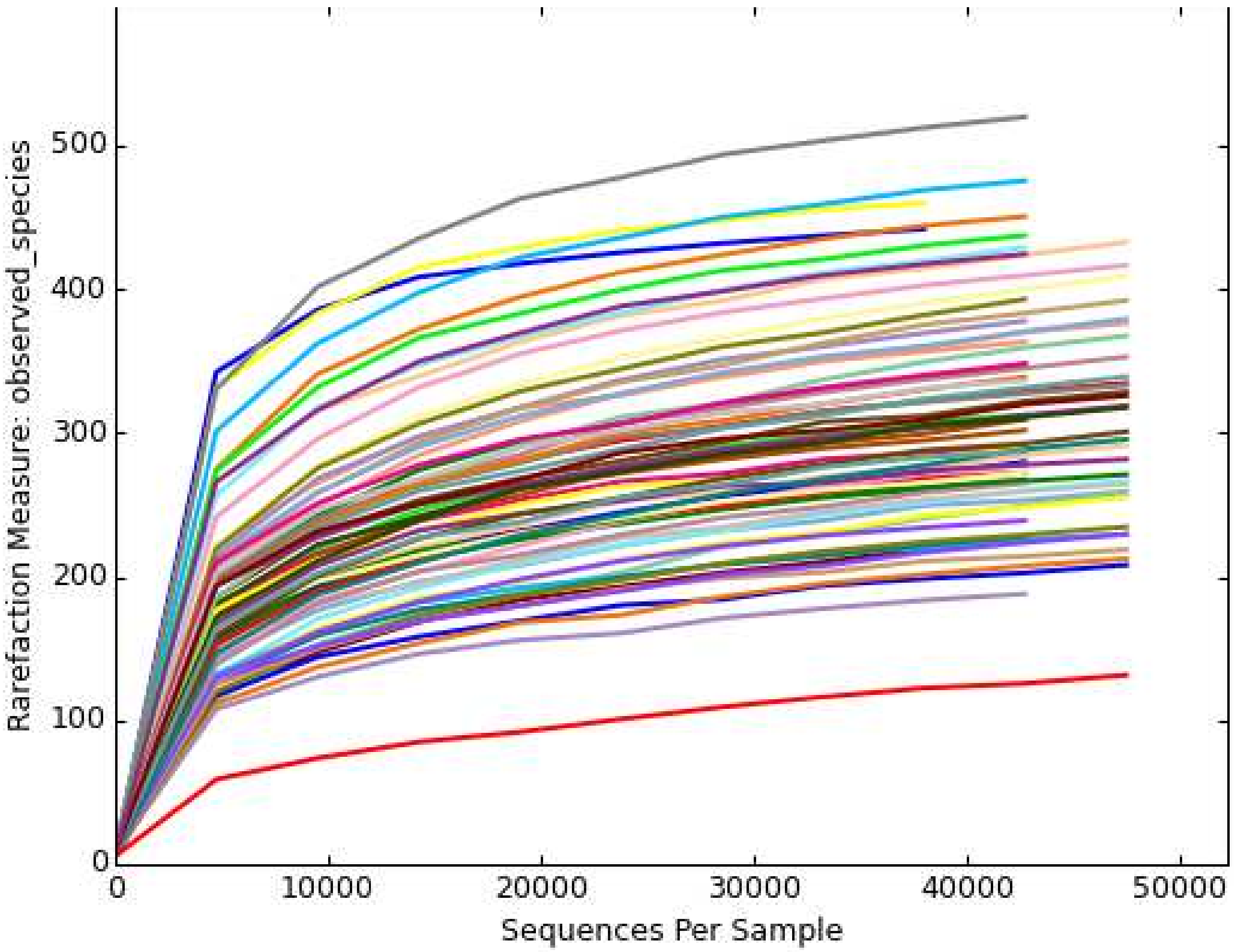
[c] Differences between groups from baseline to follow-up

[d] Observed species: number of unique species observed per sample

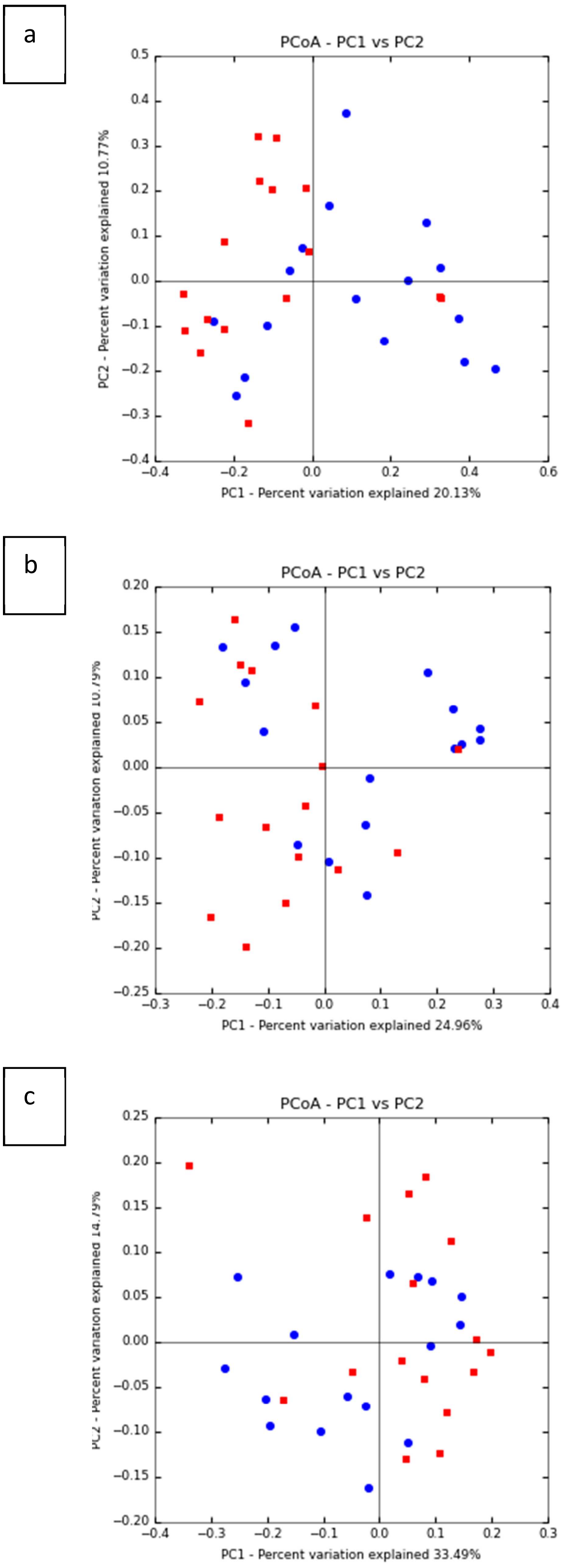
[e] Chao1: estimate of species richness including rare species

[f] Whole tree phylogeny: metric of phylogenetic diversity among species

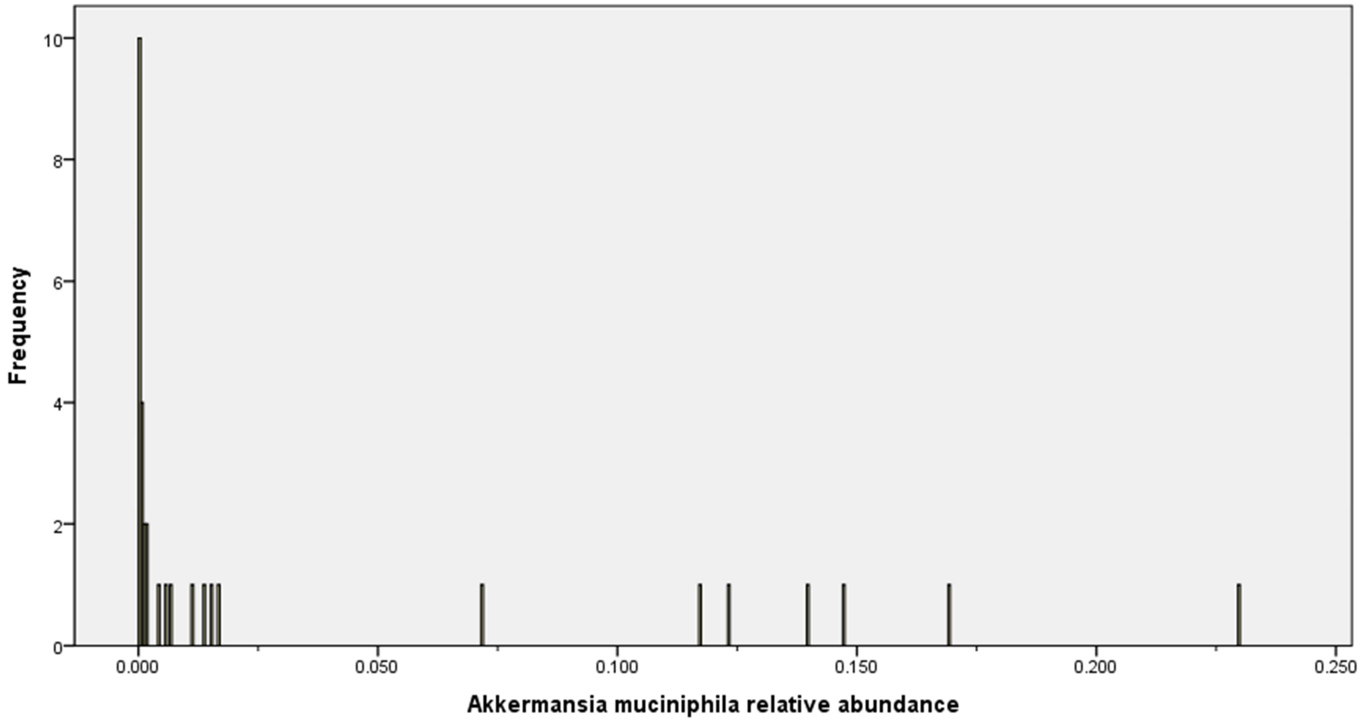
[g] Shannon Index: estimate of species richness



Supplementary Figure 1. Rarefaction curves with number of species observed in each sample as a function of sequences sampled per sample in all fecal samples provided by 32 women with breast cancer participating in a presurgical weight loss trial.



Supplementary Figure 2. Principal coordinate analysis (PCoA) plots of all fecal samples from 32 women with breast cancer participating in a presurgical weight loss trial at baseline. Red squares = LAM; Blue circles = HAM a) Bray-Curtis, p = 0.002, b) Unweighted Unifrac, p = 0.014, c) Weighted Unifrac, p = 0.028.



Supplementary Figure 3. Distribution of 32 women with breast cancer participating in a presurgical weight loss trial by relative abundance of *Akkermansia Muciniphila.*