

Additional File 10. Relative abundance of outset bacterial genera (mean of 3 pre-diet days) between the three weight-loss groups (n = 5/group).

	Low	Mid	High	SED	Benjamini-Hochberg P-value
<i>Unclassified</i>	0.691	0.616	0.581	0.032	0.434
<i>Fibrobacter</i>	0.083	0.181	0.221	0.070	0.328
<i>Treponema</i>	0.034	0.034	0.016	0.020	0.205
<i>Phascolarctobacterium</i>	0.026	0.018	0.013	0.019	0.424
<i>Alkalitalea</i>	0.023	0.016	0.021	0.069	0.880
<i>Prevotella</i>	0.015	0.013	0.020	0.029	0.872
<i>Paraprevotella</i>	0.013	0.015	0.012	0.020	0.880
<i>Barnesiella</i>	0.011	0.004	0.026	0.043	0.690
<i>Ruminococcus</i>	0.011	0.012	0.009	0.018	0.872
<i>Paludibacter</i>	0.010	0.015	0.022	0.041	0.872
<i>Alloprevotella</i>	0.009	0.004	0.002	0.023	0.706
<i>Clostridium XIVa</i>	0.008	0.005	0.005	0.010	0.476
<i>Oscillibacter</i>	0.008	0.007	0.006	0.010	0.872
<i>Phocaeicola</i>	0.006	0.011	0.009	0.026	0.872
<i>Anaeroplasma</i>	0.006	0.003	0.003	0.012	0.559
<i>Rikenella</i>	0.006	0.009	0.006	0.010	0.434
<i>Lachnospiracea</i>	0.006	0.005	0.004	0.007	0.770
<i>Faecalitalea</i>	0.003	0.002	0.001	0.010	0.434
<i>Asteroleplasma</i>	0.003	0.001	0.001	0.016	0.872
<i>Anaerovorax</i>	0.002	0.002	0.001	0.005	0.144
<i>Coprobacter</i>	0.002	0.002	0.001	0.012	0.750
<i>Sporobacter</i>	0.002	0.002	0.001	0.004	0.328
<i>Sphaerochaeta</i>	0.002	0.001	0.000	0.007	0.150
<i>Macellibacteroides</i>	0.002	0.001	0.000	0.019	0.872
<i>Pseudoflavonifractor</i>	0.002	0.009	0.004	0.030	0.872
<i>Lachnobacterium</i>	0.002	0.001	0.001	0.008	0.872
<i>Intestinimonas</i>	0.002	0.002	0.003	0.007	0.640
<i>Clostridium IV</i>	0.002	0.002	0.002	0.005	0.706
<i>Faecalicoccus</i>	0.001	0.001	0.000	0.006	0.328
<i>Mobilitalea</i>	0.001	0.001	0.000	0.004	0.041
<i>Anaerorhabdus</i>	0.001	0.000	0.001	0.009	0.746
<i>Roseburia</i>	0.001	0.001	0.001	0.004	0.872
<i>Saccharofermentans</i>	0.001	0.000	0.001	0.005	0.690
<i>Vampirovibrio</i>	0.001	0.001	0.001	0.005	0.872
<i>Saccharibacteria</i>	0.001	0.001	0.001	0.005	0.872
<i>Ethanoligenens</i>	0.001	0.001	0.001	0.008	0.872
<i>Anaerocella</i>	0.001	0.001	0.000	0.006	0.872
<i>Mogibacterium</i>	0.001	0.001	0.001	0.005	0.872
<i>Candidatusendomicrobium</i>	0.000	0.000	0.001	0.007	0.915
<i>Catabacter</i>	0.000	0.000	0.000	0.004	0.872
<i>Streptococcus</i>	0.000	0.000	0.001	0.007	0.287

ANOVA analysis was employed to evaluate group differences in the relative abundance of bacterial phyla, and the resulting P-values were adjusted for multiple testing using the Benjamini-Hochberg correction.