

Supplementary Table 1. Meta-analysis of all seven included studies for gut taxa with differential relative abundances between baseline and end-point of RS intake.

Bacterial taxa (genus)	Pooled <i>p</i> - <i>value</i>	BS median	RS median	Log2fc
<i>g__Blautia</i>	0.0200	0.0506	0.0411	-0.3007
<i>g__Roseburia</i>	0.0194	0.0094	0.0067	-0.5031
<i>g__Ruminococcaceae.UCG.013</i>	0.0000	0.0025	0.0011	-1.1430
<i>g__Agathobacter</i>	0.0417	0.0102	0.0155	0.6014
<i>g__Faecalibacterium</i>	0.0006	0.0505	0.0683	0.4362
<i>g__Ruminococcus.2</i>	0.0001	0.0060	0.0141	1.2355
<i>g__Fusicatenibacter</i>	0.0127	0.0115	0.0076	-0.5964
<i>g__Ruminococcus.torques.group</i>	0.0000	0.0073	0.0038	-0.9659
<i>g__Eubacterium.ventriosum.group</i>	0.0038	0.0008	0.0003	-1.4905
<i>g__Ruminococcaceae.NK4A214.group</i>	0.0074	0.0014	0.0005	-1.4775
<i>g__Erysipelotrichaceae.UCG.003</i>	0.0011	0.0019	0.0008	-1.1983
<i>g__Bifidobacterium</i>	0.0031	0.0070	0.0156	1.1606
<i>g__Eubacterium.eligens.group</i>	0.0008	0.0023	0.0008	-1.4527
<i>g__UBA1819</i>	0.0022	0.0004	0.0002	-1.2213
<i>g__Coprococcus.3</i>	0.0255	0.0033	0.0021	-0.6141

Only those with pooled *p*-values < 0.05 are shown.