

Table S5. Dominant taxa in RF-FACs by TEA treatment.

Phylum	Class	Order	Subgroup	SG	SG + NO3	SG + Fe	SG + SO4	P
Archaea								
Methanobacteria	Methanobrevibacter	Methanobacterium	subterraneum	0.8 +/- 0.6	0	0.3 +/- 0.3	0	.
Methanomicrobia	Methanosarcinales	Methanosarcinaceae	Methanosarcina	0.2 +/- 0.1	0	0.4 +/- 0.5	0.1 +/- 0	
Bacteria								
Acidobacteria	Acidobacteriales	UA1		0.3 +/- 0	0	0.5 +/- 0.5	0.1 +/- 0.1	
Actinobacteria	Actinobacteridae	Actinomycetales	Propionibacterineae; Nocardioideaceae	0	2.1 +/- 2.2	2.8 +/- 2.5	0	
Bacteroidetes	Bacteroidales	BCf7-02		13.2 +/- 4	0	16.4 +/- 14.3	13.3 +/- 1.5	
Bacteroidetes	Bacteroidales	Bacteroidetes	bacterium_PPf50E2; E1-K9; BA017	0.6 +/- 0.9	0	2.8 +/- 2.8	0	
Bacteroidetes	Bacteroidales	Dysgonomonaceae		0	0	1.6 +/- 1.4	0	.
Bacteroidetes	Bacteroidales	Proteophilaceae		0	16.7 +/- 28.9	0	0	
Firmicutes	Bacillales	Bacillaceae	Bacillus	0	4.2 +/- 5	0	0	
Firmicutes	Bacillales	Paenibacillaceae	Paenibacillus	0	0.2 +/- 0.2	0.9 +/- 1	0	
Firmicutes	Clostridia	Clostridiales		1.5 +/- 0.9	0	0	0 +/- 0	*
Firmicutes	Clostridia	Clostridiales	Clostr; Clostridium	0	0	0	11.8 +/- 14.6	
Firmicutes	Clostridia	Clostridiales	Clostr; Clostridium	6 +/- 2.7	37.2 +/- 32.9	1.6 +/- 1.5	19.7 +/- 7.8	
Firmicutes	Clostridia	Clostridiales	Clostr; Clostridium	7.3 +/- 4	0	0	9.7 +/- 4.9	**
Firmicutes	Clostridia	Clostridiales	Clostr; Clostridium	1.6 +/- 0.4	27.2 +/- 20	0.3 +/- 0.3	0.8 +/- 0.8	*
Firmicutes	Clostridia	Clostridiales	Clostr; Clostridium	3.5 +/- 0.2	0	0.1 +/- 0.1	5.2 +/- 0.6	***
Firmicutes	Clostridia	Clostridiales	Clostr; Clostridium	0.9 +/- 0.3	0	0.5 +/- 0.5	0.6 +/- 0.1	*
Firmicutes	Clostridia	Clostridiales	Clostr; Clostridium	6.6 +/- 3.3	0	0	3.6 +/- 4	*
Firmicutes	Clostridia	Clostridiales	Clostr; Clostridium	0	0	2.1 +/- 1.8	0.3 +/- 0.1	.
Firmicutes	Clostridia	Clostridiales	Clostr; Clostridium	1.6 +/- 1.3	0.6 +/- 0.8	0	1.4 +/- 0.2	
Firmicutes	Clostridia	Clostridiales	Clostr; Clostridium	7.4 +/- 2.7	0	0	0.9 +/- 1.1	***
Firmicutes	Clostridia	Clostridiales	Clostridiaceae	5.5 +/- 2.4	0	0	0.7 +/- 0.2	**
Firmicutes	Clostridia	Clostridiales	Clostridiaceae	0	0	41.7 +/- 50.7	0	
Firmicutes	Clostridia	Clostridiales	Clostridiaceae	1.4 +/- 0.7	4.9 +/- 5.7	0	2.4 +/- 0.8	
Firmicutes	Clostridia	Clostridiales	Clostridium aminovalericum	0	0.1 +/- 0.1	9.6 +/- 8.3	0	.
Firmicutes	Clostridia	Clostridiales	Faecalibacterium	0.1 +/- 0	0	0.1 +/- 0	0.1 +/- 0	**
Firmicutes	Clostridia	Clostridiales	Ruminococcus	0	0	0	1.6 +/- 2.3	
Firmicutes	Clostridia	Clostridiales	Ruminococcus; Ruminococcus_bromii	2.7 +/- 1.3	0.3 +/- 0.5	0	0.5 +/- 0.2	*
Firmicutes	Clostridia	Clostridiales	UC7-69	0	0	0	1.8 +/- 0.8	**
Proteobacteria	Alphaproteobacteria	Ellin329		28.6 +/- 3.7	1.2 +/- 1	5.9 +/- 5.2	15.1 +/- 3.1	***
Proteobacteria	Alphaproteobacteria	Rhizobiales		0.6 +/- 0.6	0	3.2 +/- 2.7	0	
Proteobacteria	Deltaproteobacteria	Desulfovibrionales	Desulfovibrionaceae; Desulfovibrio	0.2 +/- 0.2	0	0.9 +/- 0.8	3 +/- 0.1	***
Proteobacteria	Gammaproteobacteria	Enterobacteriales	Enterobacteriaceae; Enterobacter	0	1.4 +/- 2.5	1.5 +/- 1.9	0	
Eukaryota								
stramenopiles	Oomycetes	Peronosporales	Phytophthora	0	0	0	0	

P. <0.1; * <0.05; ** <0.01; *** <0.001