Supplemental Table S1. Differential abundance of genus level bacteria identified in participan

hash ID	Base Mean	log2 Fold Change	lfcSE	Statistic
098c3bbd8234f4ac198;	2644.797543	0.636678934	2.919656061	126.4650425
803eb52cfe3d77bdf9fe	3.71967458	-1.595559731	1.252152435	43.60717769
cbb17c39cfea0aa84321	19.58395687	2.053827386	2.93652842	21.01484623
a3f9e91d15a189d0cf1e	61.07314628	-0.936009287	1.534221748	9.663043489
a0798db0c868e9ad608	142.8544936	0.63230722	2.935199284	25.48475532
6960eba3db7d4d863d(	47.066038	0.762509259	2.914439392	63.01935241

ts whose median AUC-TMAO was less than versus greater than 29.25 uM/hr. Differential abur

P-value	Adj P-value	Kingdom	Phylum	Class
2.43E-29	1.26E-27	k__Bacteria	p__Bacteroidetes	c__Bacteroidia
4.01E-11	6.96E-10	k__Bacteria	p__Actinobacteria	c__Coriobacteriia
4.56E-06	4.74E-05	k__Bacteria	p__Firmicutes	c__Bacilli
0.001880119	0.016294363	k__Bacteria	p__Firmicutes	c__Erysipelotrichi
4.46E-07	5.80E-06	k__Bacteria	p__Firmicutes	c__Erysipelotrichi
2.05E-15	5.32E-14	k__Bacteria	p__Firmicutes	c__Clostridia

...dance was performed with the log ratio test in DESeq2.

Order	Family	Genus
o__Bacteroidales	f__Prevotellaceae	g__Prevotella
o__Coriobacteriales	f__Coriobacteriaceae	g__Eggerthella
o__Lactobacillales	f__Lactobacillaceae	g__Lactobacillus
o__Erysipelotrichales	f__Erysipelotrichaceae	g__Clostridium
o__Erysipelotrichales	f__Erysipelotrichaceae	g__Catenibacterium
o__Clostridiales	f__Veillonellaceae	g__Dialister