

Table S1: Relative abundance of the top 20 genera following ST colonization.

Genus	D8		D14			D21		
	Control	SA	Control	SA	SN	Control	SA	SN
Clostridiales_unclassified	15.70	13.80	15.61	11.52	8.76	19.73	20.80	18.31
Oscillospira	21.65	11.76	13.40	8.37	13.08	14.22	11.74	12.19
Ruminococcaceae_unclassified	11.09	10.23	15.70	15.39	14.18	15.54	10.53	9.75
Butyricicoccus	3.40	5.47	4.03	9.86	11.96	6.03	10.95	7.61
Lachnospiraceae_unclassified	7.92	8.56	2.93	7.45	1.55	5.60	13.00	10.88
Subdoligranulum	14.63	8.52	0.27	14.01	0.11	0.43	7.55	1.88
Bacteroides	0.00	2.43	0.00	10.39	11.67	0.01	7.39	13.79
Lactobacillus	4.51	22.04	11.67	0.53	0.24	1.92	1.84	0.68
Coprobacillus	3.79	5.25	6.12	2.53	5.59	3.40	3.78	5.83
Enterococcus	3.04	1.45	4.52	2.98	9.08	6.56	2.01	0.90
Escherichia	2.05	0.95	3.32	1.74	2.43	8.44	2.58	4.47
Bacillaceae_unclassified	0.77	3.16	9.93	6.83	0.95	1.47	1.28	0.88
Erysipelatoclostridium	3.73	5.80	1.78	1.57	3.95	3.64	1.46	1.62
cc_115	2.26	1.78	3.60	4.26	4.13	1.51	1.95	0.62
Ruminococcus	1.44	0.60	2.58	0.81	2.82	2.60	2.50	3.12
Dorea	0.12	0.39	0.79	0.53	7.31	2.77	1.20	2.58
Erysipelotrichaceae_unclassified	1.91	1.69	2.74	1.70	2.87	1.57	1.45	1.74
Turicibacter	0.04	0.00	2.86	0.01	0.09	2.72	0.02	0.07
RF39_unclassified	0.74	0.10	0.38	0.49	2.00	0.35	0.34	0.84
Enterobacteriaceae_unclassified	0.51	0.01	0.11	0.75	0.07	0.00	0.68	0.91
Anaeroplasma	0.00	0.00	0.68	0.00	0.37	0.35	0.34	0.91
Christensenellaceae_unclassified	0.50	0.09	0.30	0.07	0.17	0.48	0.10	0.26
Coprococcus	0.24	0.15	0.20	0.04	0.36	0.13	0.48	0.33
Clostridium	0.02	0.12	0.07	0.05	0.40	0.12	0.21	0.12
Mogibacteriaceae_unclassified	0.08	0.00	0.21	0.09	0.13	0.19	0.14	0.21
Lachnospira	0.09	0.06	0.17	0.13	0.24	0.13	0.03	0.12
ML615J-28_unclassified	0.00	0.00	0.83	0.00	0.00	0.00	0.00	0.00
Dehalobacteriaceae_unclassified	0.00	0.00	0.07	0.00	0.03	0.12	0.35	0.05
Blautia	0.16	0.00	0.01	0.06	0.12	0.04	0.05	0.11
Proteus	0.00	0.16	0.02	0.10	0.03	0.03	0.06	0.09
rc4-4	0.00	0.00	0.00	0.00	0.00	0.48	0.00	0.00
Enterobacter	0.00	0.00	0.00	0.00	0.11	0.00	0.22	0.06
Faecalibacterium	0.00	0.02	0.07	0.07	0.04	0.07	0.04	0.05
Holdemania	0.05	0.00	0.04	0.00	0.08	0.02	0.09	0.06
Pediococcus	0.05	0.02	0.11	0.00	0.10	0.00	0.00	0.00
[Eubacterium]	0.02	0.00	0.19	0.00	0.04	0.00	0.00	0.00
Klebsiella	0.00	0.02	0.03	0.04	0.03	0.01	0.00	0.04
Salmonella	0.00	0.11	0.00	0.04	0.00	0.00	0.00	0.00
[Ruminococcus]	0.00	0.02	0.00	0.01	0.00	0.04	0.05	0.00
SHA-98_unclassified	0.00	0.00	0.06	0.00	0.00	0.06	0.00	0.00
Bacteria_unclassified	0.00	0.00	0.00	0.06	0.03	0.00	0.01	0.00
Peptostreptococcaceae_unclassified	0.00	0.00	0.06	0.00	0.00	0.01	0.02	0.00
Shigella	0.03	0.00	0.04	0.00	0.00	0.00	0.00	0.00
EtOH8_unclassified	0.00	0.00	0.00	0.00	0.00	0.07	0.00	0.00

Weissella	0.01	0.02	0.03	0.01	0.00	0.00	0.00	0.00
Clostridiaceae_unclassified	0.00	0.00	0.02	0.00	0.04	0.00	0.00	0.00
Firmicutes_unclassified	0.00	0.00	0.04	0.00	0.00	0.00	0.00	0.01
Staphylococcus	0.00	0.00	0.01	0.01	0.00	0.01	0.00	0.00
Enterococcaceae_unclassified	0.00	0.00	0.00	0.00	0.00	0.02	0.00	0.00

\*Data is shown as percent relative abundance of normalized data.