

Table S1. Range and median of relative abundance of each bacterial taxa

Phylum	Median occupancy (%)			
	Week 0	Week 4	Week 8	Week 12
Firmicutes	67.25	78.06	66.61	70.50
	(56.80 - 79.51)	(52.43 - 87.44)	(44.03 - 90.02)	(61.38 - 94.03)
Actinobacteria	4.03	6.39#	9.70 #	6.58
	(1.75 - 5.91)	(1.99 - 10.87)	(3.29 - 13.38)	(3.00 - 9.55)
Fusobacteria	6.92	1.48#	1.38#	2.28
	(1.54 - 11.29)	(0.55 - 8.22)	(0.75 - 5.27)	(0.02 - 4.59)
Bacteroidetes	4.10	2.26	2.66	0.79*
	(1.14 - 5.07)	(0.84 - 6.38)	(0.68 - 3.54)	(0.00 - 0.81)
Proteobacteria	2.16	1.27	0.88	0.40
	(0.62 - 3.72)	(0.25 - 5.54)	(0.25 - 2.40)	(0.02 - 2.28)
Tenericutes	0.00	0.00	0.00	0.00
	(0.00 - 0.00)	(0.00 - 0.00)	(0.00 - 0.00)	(0.00 - 0.00)
Rejected hit †	15.54	10.54	18.77	19.45
	(9.28 - 22.14)	(6.81 - 28.18)	(4.11 - 34.10)	(2.93 - 30.41)
Genus §	Week 0	Week 4	Week 8	Week 12
Lactobacillus	39.14	49.04	45.65	46.49
	(10.79 - 47.51)	(19.22 - 68.46)	(9.51 - 60.79)	(34.58 - 75.80)
Blautia	11.84	12.29	8.65	9.55
	(10.61 - 21.55)	(5.58 - 13.34)	(7.62 - 10.69)	(7.17 - 14.89)
Peptoclostridium	4.49	5.42	4.11	5.26
	(3.55 - 8.61)	(1.98 - 8.33)	(3.91 - 5.34)	(2.60 - 7.39)
Bifidobacterium	0.63	4.19#	7.64#	5.83
	(0.01 - 4.82)	(0.25 - 9.73)	(1.85 - 11.75)	(2.21 - 8.42)
Romboutsia	3.11	4.03	1.43	2.88
	(0.25 - 14.41)	(0.38 - 6.87)	(0.34 - 10.66)	(1.69 - 10.09)
Fusobacterium	7.42	1.53#	1.44#	2.41
	(1.54 - 11.29)	(0.55 - 8.22)	(0.75 - 5.27)	(0.02 - 4.59)
Streptococcus	1.54	1.70	1.29	0.07
	(0.05 - 3.31)	(0.00 - 7.06)	(0.00 - 18.13)	(0.00 - 1.03)
Prevotella	2.24	1.46	1.78	0.59*
	(0.57 - 4.20)	(0.22 - 5.60)	(0.31 - 2.73)	(0.00 - 0.64)
Enterococcus	1.19	1.00	0.73	0.39
	(0.04 - 4.56)	(0.01 - 5.17)	(0.11 - 3.51)	(0.00 - 3.67)
Clostridium	0.89	0.81	0.42	1.25
	(0.62 - 7.44)	(0.01 - 1.73)	(0.12 - 4.30)	(0.01 - 1.61)
Collinsella	1.83	1.49	1.37	0.96
	(0.74 - 3.03)	(0.81 - 1.96)	(0.72 - 2.21)	(0.59 - 0.98)
Faecalibacterium	2.01	1.14	1.16	0.85
	(1.18 - 3.00)	(0.73 - 1.18)	(0.43 - 1.75)	(0.01 - 1.71)
Achnoclostridium	0.97	1.05	1.00	0.73
	(0.68 - 1.87)	(0.70 - 1.49)	(0.41 - 1.81)	(0.41 - 1.10)
Megamonas	1.15	0.43	0.58	0.02*
	(0.17 - 4.05)	(0.22 - 1.26)	(0.20 - 1.70)	(0.00 - 0.49)
Bacteroides	0.71	0.69	0.60	0.17*
	(0.33 - 2.07)	(0.42 - 0.74)	(0.37 - 1.80)	(0.00 - 0.28)
Parasutterella	0.16	0.68	0.56	0.17
	(0.00 - 1.96)	(0.00 - 2.61)	(0.01 - 2.06)	(0.00 - 0.43)
Anaerobiospirillum	0.36	0.01	0.00	0.01
	(0.00 - 1.41)	(0.00 - 3.77)	(0.00 - 0.28)	(0.00 - 1.40)
Ruminococcus	0.44	0.41	0.39	0.48
	(0.19 - 0.82)	(0.21 - 0.57)	(0.20 - 0.77)	(0.10 - 0.72)
Ascolactobacterium	0.42	0.33	0.52	0.11
	(0.10 - 0.97)	(0.27 - 1.04)	(0.08 - 1.01)	(0.01 - 0.26)
Asipilatoclostridium	0.33	0.22	0.30	0.38
	(0.15 - 0.76)	(0.17 - 0.54)	(0.13 - 0.39)	(0.17 - 0.43)
Allobaculum	0.55	0.25	0.11	0.33
	(0.00 - 1.08)	(0.03 - 0.37)	(0.09 - 0.22)	(0.04 - 0.52)
Terrisporobacter	0.12	0.09	0.04	0.02
	(0.00 - 2.91)	(0.00 - 0.27)	(0.00 - 0.24)	(0.01 - 0.44)
Escherichia	0.40	0.05	0.00	0.00
	(0.00 - 1.83)	(0.00 - 0.20)	(0.00 - 0.54)	(0.00 - 0.09)
Slackia	0.29	0.20	0.15	0.15
	(0.17 - 0.64)	(0.05 - 0.36)	(0.05 - 0.17)	(0.10 - 0.36)
Sutterella	0.25	0.10	0.09	0.02
	(0.07 - 0.94)	(0.03 - 0.20)	(0.01 - 0.15)	(0.00 - 0.07)
Turicibacter	0.27	0.02	0.04	0.02
	(0.00 - 0.51)	(0.00 - 0.21)	(0.00 - 0.53)	(0.00 - 0.31)
Helicobacter	0.06	0.05	0.03	0.01
	(0.00 - 0.20)	(0.01 - 0.40)	(0.00 - 0.20)	(0.00 - 0.45)
Butyricoccus	0.11	0.12	0.10	0.05*
	(0.07 - 0.12)	(0.09 - 0.18)	(0.08 - 0.17)	(0.01 - 0.12)
Lactonifactor	0.09	0.05	0.04	0.04
	(0.05 - 0.24)	(0.02 - 0.13)	(0.02 - 0.11)	(0.01 - 0.22)
Campylobacter	0.11	0.04	0.01	0.00
	(0.00 - 0.17)	(0.00 - 0.57)	(0.00 - 0.06)	(0.00 - 0.13)
Catenibacterium	0.04	0.02	0.03	0.01
	(0.02 - 0.42)	(0.00 - 0.18)	(0.01 - 0.08)	(0.00 - 0.15)
Adlercreutzia	0.06	0.06	0.07	0.07
	(0.00 - 0.08)	(0.01 - 0.10)	(0.02 - 0.09)	(0.04 - 0.10)

$p < 0.1$ vs. 0 weeks* $p < 0.05$ vs. 8 weeks

† Rejected hit include those whose sequences shared less than 97% homology to any species listed in TechnoSuruga Lab Microbial Identification database DB-BA 10 (TechnoSuruga Laboratory, Shizuoka, Japan).

§ Genus whose median occupancy exceeded 0.1% are listed.