

Table S1: Genus contributing to the top 70% of significant dissimilarity of bacteria between day 7 and 18 age groups as determined by SIMPER. Overall average dissimilarity between ages is 51%.

Phyla	Class	Order	Family	Genus	Day 7 Average Abundance	Day 18 Average Abundance	%
Actinobacteria	Actinobacteria	Actinomycetales	<i>Actinomycetaceae</i>	<i>Actinomyces</i>	0.57	0.24	0.74
	Coriobacteriia	Coriobacteriales	<i>Coriobacteriaceae</i>	<i>Collinsella</i>	0.51	0.61	0.57
Bacteroidetes	Bacteroidia	Bacteroidales	<i>Bacteroidaceae</i>	<i>Bacteroides</i>	2.1	1.63	1.03
			<i>Marinifilaceae</i>	<i>Butyricimonas</i>	0.82	0.81	0.9
				<i>Sanguibacteroides</i>	0.08	0.42	0.59
				CAG-873	0.01	1.1	1.68
			<i>Marinifilaceae</i>		0.38	0.78	0.91
			<i>Marinifilaceae</i>		0.78	1.04	0.97
			<i>p-2534-18B5 gut group</i>		0.06	0.7	1.04
			<i>Prevotellaceae</i>	<i>Alloprevotella</i>	0.46	0.83	0.89
				<i>Prevotella 2</i>	0.95	1.11	1.3
				<i>Prevotella 7</i>	0.22	0.42	0.56
				<i>Prevotellaceae NK3B31 group</i>	0.62	0.68	0.77
				<i>Prevotellaceae UCG-003</i>	0.26	0.64	0.89
				<i>Prevotellaceae UCG-004</i>	0.11	0.48	0.68
			<i>Prevotellaceae</i>		0.64	0.52	0.89
			<i>Prevotellaceae</i>		0.27	0.42	0.55
			<i>Rikenellaceae</i>	<i>Alistipes</i>	0.39	0.62	0.77
Epsilonbacteraeota	Campylobacteria	Campylobacterales		<i>dgA-11 gut group</i>	0.04	0.38	0.56
				<i>RC9 gut group</i>	0.79	1.17	0.95
			<i>Campylobacteraceae</i>	<i>Campylobacter</i>	0.58	0.83	0.97
			<i>Helicobacteraceae</i>	<i>Helicobacter</i>	0.12	0.41	0.6
Firmicutes	Bacilli	Lactobacillales	<i>Enterococcaceae</i>	<i>Enterococcus</i>	0.36	0.31	0.64
			<i>Lactobacillaceae</i>	<i>Lactobacillus</i>	1.4	1.24	1
			<i>Streptococcaceae</i>	<i>Streptococcus</i>	0.82	0.58	0.53
Firmicutes	Clostridia	Clostridiales	<i>Christensenellaceae</i>	<i>Christensenellaceae R-7 group</i>	0.38	1.36	1.56
			<i>Clostridiaceae</i>	<i>Clostridium sensu stricto 1</i>	1.16	0.58	1

	<i>Clostridium sensu stricto 2</i>	0.92	0.14	1.31
<i>Clostridiales vadinBB60 group</i>		0.05	0.67	0.97
<i>Clostridiales vadinBB60 group</i>		0.18	1.15	1.56
<i>Family XIII</i>	<i>[Eubacterium] nodatum group</i>	0.29	0.46	0.51
	<i>Family XIII AD3011 group</i>	0.15	0.59	0.72
<i>Lachnospiraceae</i>	<i>[Eubacterium] fissicatena group</i>	0.92	0.61	0.67
	<i>[Ruminococcus] gausvreauii group</i>	0.32	0.53	0.68
	<i>Blautia</i>	0.44	0.49	0.51
	<i>Dorea</i>	0.51	0.72	0.72
	<i>Eisenbergiella</i>	0.73	0.45	0.65
	<i>Hungatella</i>	0.56	0.43	0.48
	<i>Lachnoclostridium</i>	1.44	1.43	0.75
	<i>Lachnospiraceae FCS020 group</i>	0.15	0.39	0.53
	<i>Lachnospiraceae UCG-002</i>	0.07	0.31	0.47
	<i>Lachnospiraceae UCG-010</i>	0.11	0.4	0.56
<i>Lachnospiraceae</i>		0.2	0.74	0.98
	<i>Roseburia</i>	0.47	0.51	0.78
	<i>Tyzzerella</i>	0.59	0.31	0.72
<i>Peptostreptococcaceae</i>	<i>Clostridioides</i>	0.3	0.13	0.47
	<i>Peptostreptococcus</i>	0.66	0.21	0.81
	<i>Romboutsia</i>	0.48	0.55	0.47
<i>Ruminococcaceae</i>	<i>[Eubacterium] coprostanoligenes group</i>	1.14	1.14	0.62
	<i>Butyricicoccus</i>	0.59	0.48	0.51
	<i>Faecalibacterium</i>	0.08	0.33	0.5
	<i>GCA-900066225</i>	0.23	0.35	0.45
	<i>Hydrogenoanaerobacterium</i>	0.38	0.64	0.56
	<i>Intestinimonas</i>	0.62	0.97	0.66
	<i>Oscillibacter</i>	0.12	0.52	0.7
	<i>Oscillospira</i>	0.22	0.65	0.83
	<i>Ruminiclostridium 9</i>	0.57	0.83	0.71
	<i>Ruminococcaceae NK4A214 group</i>	0.51	1.01	0.9
	<i>Ruminococcaceae UCG-002</i>	0.75	1.24	1.04
	<i>Ruminococcaceae UCG-003</i>	0.26	0.54	0.72
	<i>Ruminococcaceae UCG-005</i>	0.22	0.83	0.98

				<i>Ruminococcaceae</i> UCG-010	0.46	0.83	0.74
				<i>Ruminococcus</i> 2	0.92	0.81	0.68
				<i>Subdoligranulum</i>	0.08	0.45	0.66
				UBA1819	0.6	0.48	0.45
			<i>Ruminococcaceae</i>		0.77	0.97	0.68
	Erysipelotrichia	Erysipelotrichales	<i>Erysipelotrichaceae</i>	<i>Catenibacterium</i>	0.17	0.33	0.48
				<i>Erysipelotrichaceae</i> UCG-004	0.19	0.47	0.65
				<i>Holdemanella</i>	0.52	0.56	0.49
			<i>Erysipelotrichaceae</i>		0.12	0.71	0.97
	Negativicutes	Selenomonadales	<i>Acidaminococcaceae</i>	<i>Phascolarctobacterium</i>	0.85	1.1	0.54
			<i>Veillonellaceae</i>	<i>Allisonella</i>	0.31	0.12	0.49
				<i>Megasphaera</i>	0.18	0.43	0.68
				<i>Veillonella</i>	0.77	0.42	0.69
Fusobacteria	Fusobacteriia	Fusobacteriales	<i>Fusobacteriaceae</i>	<i>Fusobacterium</i>	1.71	0.88	1.54
Lentisphaerae	Lentisphaeria	Victivallales	<i>Victivallaceae</i>	<i>Victivallis</i>	0.12	0.38	0.54
	Oligosphaeria	Oligosphaerales	<i>Oligosphaeraceae</i>	Z20	0.04	0.38	0.57
Planctomycetes	Planctomycetacia	Pirellulales	<i>Pirellulaceae</i>	<i>p-1088-a5 gut group</i>	0.09	0.38	0.55
Proteobacteria	Deltaproteobacteria	Bradymonadales			0.12	0.33	0.52
		Desulfovibrionales	<i>Desulfovibrionaceae</i>	<i>Bilophila</i>	0.32	0.59	0.57
				<i>Mailhella</i>	0.17	0.36	0.5
			<i>Desulfovibrionaceae</i>		0.06	0.31	0.47
	Gammaproteobacteria	Betaproteobacteriales	<i>Burkholderiaceae</i>	<i>Sutterella</i>	0.8	0.73	0.49
		Enterobacteriales	<i>Enterobacteriaceae</i>	<i>Escherichia-Shigella</i>	1.37	1.09	0.94
		Pasteurellales	<i>Pasteurellaceae</i>	<i>Actinobacillus</i>	0.58	0.5	0.48
Spirochaetes	Spirochaetia	Spirochaetales	<i>Spirochaetaceae</i>	<i>Sphaerochaeta</i>	0.13	0.36	0.53
				<i>Treponema</i> 2	0.08	0.45	0.64
Synergistetes	Synergistia	Synergistales	<i>Synergistaceae</i>	<i>Pyramidobacter</i>	0.02	0.6	0.91
				<i>Synergistes</i>	0	0.37	0.57
Tenericutes	Mollicutes	Mollicutes RF39			0	0.36	0.55