Supplemental Table 5

	RYGB (TG)	RYGB (M12)	AGB (TG)	AGB (M12)	p	q	status	size	NA_pc	BMC_pc	BMS	Bit_id1	Bit_id	Taxo_level	species	genus	family	order	class	phylum	name	bc_bmi	bc_dxa_fm_pc	dxa_fm	dxa_fm_tbc	dxa_gynoid_tg	vo_adipo_kepin	metab_bmr	adipok_adiponectin	neutrophil	mucr_g_richness	dxa_bc_bmi	rho_bc_dxa_fm_g	rho_bc_dxa_fm_tr	rho_bc_dxa_gynoid	rho_lipid_tg	rho_inone_hbatc	rho_bc_weight	rho_bc_dxa_fm_g	rho_adipok_kepin	rho_metab_bmr	rho_adipok_adiponectin	rho_infl_neutrophil	rho_micr_g_richness
GU:87	1.1e-07 +/- 1.7e-07	5.8e-07 +/- 4.4e-07	6.1e-07 +/- 7.4e-07	5.2e-07 +/- 1.7e-07	1.40e-08	3.72E-05	M12	1877	14.2		44 Oscillibacter sp. 1-3	78.1	79.7	genus	NA	Oscillibacter	Oscillospiraceae	Clostridiales	Clostridia	Firmicutes	GU:87 Oscillibacter	2.15E-01	1.24E-01	1.11E-03	1.24E-01	6.21E-01	4.86E-01	9.20E-01	1.04E-01	2.62E-01	6.75E-01	6.72E-01	1.97E-01	8.10E-01	2.64E-01	2.67E-01	-0.37	-0.32	-0.33	0.16	-0.11	0.36	0.34	-0.31	-0.10	0.00	0.12	0.28	0.27
GU:58	1.1e-07 +/- 1.1e-07	1.1e-07 +/- 1.1e-07	8.9e-08 +/- 1.4e-07	2.8e-07 +/- 1.4e-07	1.14e-05	3.72E-05	M12	2699	12.4	99.6	Clostridium sp. CAG:58	99.2	99.4	species	Clostridium sp. CAG:58	Clostridium	Unclassified Clostridiales	Unclassified Clostridiales	Clostridiales	Clostridia	Firmicutes	GU:58 Clostridium sp. CAG:58	2.15E-01	1.24E-01	1.11E-03	1.24E-01	6.21E-01	4.86E-01	9.20E-01	1.04E-01	2.62E-01	6.75E-01	6.72E-01	1.97E-01	8.10E-01	2.64E-01	2.67E-01	-0.37	-0.32	-0.33	0.16	-0.11	0.36	0.34	-0.31	-0.10	0.00	0.12	0.28	0.27
GU:126	3.1e-07 +/- 1.7e-07	1.4e-06 +/- 1.4e-06	3e-07 +/- 1.4e-07	3e-07 +/- 7e-07	3.19e-06	3.72E-05	M12	1429	9.6	98.3	Butyricimonas virosa DSM 23226	99.2	96	species	Butyricimonas virosa	Butyricimonas	Porphyromonadaceae	Bacteroidales	Bacteroidia	Bacteroidetes	GU:215 Butyricimonas virosa	8.86E-01	9.42E-01	7.99E-01	4.26E-01	2.15E-01	9.62E-01	4.20E-01	3.27E-01	9.58E-01	4.65E-01	8.64E-01	6.78E-01	6.31E-01	5.60E-01	1.16E-01	-0.33	-0.32	0.01	-0.17	0.26	-0.01	-0.05	0.16	0.01	0.23	-0.23	0.13	0.23
GU:53	7.8e-08 +/- 1.3e-07	5.5e-07 +/- 5.8e-07	3.2e-07 +/- 6.1e-07	1.7e-07 +/- 1.8e-07	4.04e-07	3.72E-05	M12	1748	0	99.8	Alistipes sp. CAG:53	97.8	99.1	species	Alistipes shahii	Alistipes	Rikenellaceae	Bacteroidales	Bacteroidia	Bacteroidetes	GU:53 Alistipes shahii	1.28E-01	2.09E-01	2.37E-01	8.02E-01	1.20E-01	9.61E-01	9.19E-01	6.18E-02	1.24E-01	1.94E-01	2.66E-01	1.29E-01	8.95E-02	2.75E-01	6.57E-02	-0.33	-0.39	-0.33	0.05	-0.30	0.06	-0.33	-0.27	-0.23	-0.17	0.22	0.24	0.38
GU:159	9.3e-08 +/- 2.6e-07	1.2e-06 +/- 2.2e-06	1.6e-07 +/- 1.6e-07	4e-07 +/- 6.8e-07	1.36e-05	3.72E-05	M12	3271	17.2	98.5	Butyricimonas virosa DSM 23226	92.1	96.9	genus	NA	Butyricimonas	Porphyromonadaceae	Bacteroidales	Bacteroidia	Bacteroidetes	GU:159 Butyricimonas	1.75E-01	1.85E-01	1.87E-01	2.37E-01	1.65E-01	4.90E-01	9.68E-01	3.17E-01	2.57E-01	5.16E-01	1.61E-01	2.38E-01	6.18E-01	3.18E-01	6.50E-01	-0.39	-0.38	-0.18	-0.25	0.21	0.10	-0.35	-0.14	-0.18	-0.16	-0.15	0.21	0.24
GU:228	6.7e-09 +/- 9.7e-09	8.1e-08 +/- 1.2e-07	2.1e-09 +/- 6.3e-09	1.2e-08 +/- 3e-08	1.12e-06	3.72E-05	M12	3327	0	99.9	Clostridium hathewayi CAG:224	99.8	100	species	Hungatella hathewayi 1	Hungatella	Clostridiaceae	Clostridiales	Clostridia	Firmicutes	GU:224 Hungatella hathewayi 1	1.04E-02	1.35E-02	1.04E-02	4.05E-01	5.71E-01	1.28E-02	9.35E-01	6.65E-01	2.98E-02	1.08E-01	1.61E-01	3.82E-01	8.64E-01	3.22E-01	7.09E-01	-0.68	-0.52	-0.58	0.18	-0.12	0.42	-0.66	-0.34	-0.39	0.00	0.01	0.21	-0.08
GU:149	0 +/- 0	5.8e-08 +/- 7.6e-08	2.6e-09 +/- 7.4e-09	0 +/- 0	5.64E-06	3.72E-05	M12	1607	0	97.7	Fusobacterium sp. CAG:149	99.6	98.5	species	Fusobacterium nucleatum	Fusobacterium	Fusobacteriaceae	Fusobacteriales	Fusobacteriia	Fusobacteria	GU:149 Fusobacterium nucleatum	2.62E-02	2.62E-02	2.76E-02	9.11E-02	5.19E-01	1.21E-01	7.80E-02	7.68E-01	1.51E-02	1.68E-01	6.19E-02	2.45E-02	1.75E-01	1.69E-01	7.18E-01	-0.45	-0.41	-0.43	0.35	-0.14	-0.15	-0.46	-0.29	-0.45	-0.21	0.16	0.29	0.28
GU:99	7.3e-08 +/- 2e-07	9.2e-07 +/- 1.2e-06	1.6e-07 +/- 2.1e-07	4.6e-07 +/- 1.9e-07	8.59E-07	4.18E-05	M12	1794	20.2	99.3	Roseburia sp. CAG:85	68.6	77.6	genus	NA	Roseburia	Lachnospiraceae	Clostridiales	Clostridia	Firmicutes	GU:99 Roseburia	1.42E-01	1.77E-01	8.96E-02	1.31E-01	1.60E-01	7.78E-01	2.78E-01	8.18E-02	1.72E-01	6.19E-01	2.09E-01	8.75E-01	2.66E-01	2.10E-01	2.75E-02	-0.30	-0.36	-0.67	0.31	-0.28	0.12	-0.32	-0.14	-0.34	-0.25	0.32	0.27	0.45
GU:188	0 +/- 0	1.1e-07 +/- 2e-07	0 +/- 0	0 +/- 0	5.51E-01	4.18E-05	M12	1281	0.2	99.8	Dialister sp. CAG:188	98.1	99.9	species	Dialister sp. CAG:188	Dialister	Veillonellaceae	Selenomonadales	Negativicutes	Firmicutes	GU:188 Dialister sp. CAG:188	2.84E-01	3.74E-01	5.31E-02	3.70E-02	1.39E-01	7.18E-01	2.09E-01	1.37E-01	2.46E-02	6.71E-02	2.62E-01	1.21E-01	7.71E-02	1.54E-01	6.23E-01	-0.45	-0.48	-0.42	0.43	-0.33	0.05	-0.45	-0.38	-0.33	-0.24	0.22	0.30	0.18
GU:235	9.1e-07 +/- 1.3e-06	2.6e-07 +/- 3.6e-07	5.6e-07 +/- 7.1e-07	6.7e-07 +/- 6.3e-07	1.36e-07	3.72E-05	T0	1641	0	99	bacterium LF-3	99.5	98.8	species	Coprobacillus sp. CAG:235	Coprobacillus	Erysipelotrichaceae	Erysipelotrichales	Erysipelotrichia	Firmicutes	GU:235 Coprobacillus sp. CAG:235	4.37E-02	1.39E-02	9.71E-03	1.86E-01	2.91E-01	8.42E-01	4.04E-02	9.45E-01	6.27E-02	2.33E-01	1.15E-01	1.90E-01	9.90E-01	1.12E-01	1.38E-01	0.62	0.64	0.35	-0.28	0.22	-0.06	0.62	0.27	0.35	0.20	0.09	-0.33	0.31
GU:25	1.1e-06 +/- 1.8e-06	5.8e-07 +/- 9.2e-07	3.1e-07 +/- 2.9e-07	6.9e-07 +/- 5.4e-07	6.14E-07	4.18E-05	T0	1686	0	99.8	Lachnospiraceae bacterium 5_1_63FAA	99.3	99	species	Acetatifactor fissihirs	Acetatifactor	Lachnospiraceae	Clostridiales	Clostridia	Firmicutes	GU:25 Acetatifactor fissihirs	1.97E-02	1.34E-02	2.24E-02	1.47E-01	2.98E-01	6.18E-01	1.47E-01	1.51E-01	3.20E-02	1.47E-01	7.82E-02	2.83E-01	7.80E-01	2.65E-01	7.12E-02	0.62	0.64	0.49	-0.20	0.22	-0.17	0.65	0.31	0.32	0.21	-0.05	-0.24	0.27
GU:203	7.5e-07 +/- 2.5e-06	9.5e-08 +/- 1.9e-06	9.5e-08 +/- 2.8e-07	2.8e-07 +/- 6.3e-07	4.51E-01	1.00E+00	M12	1660	0	99.7	Bacteroides finegoldii CAG:203	98.3	99.7	species	Bacteroides finegoldii	Bacteroides	Bacteroidaceae	Bacteroidales	Bacteroidia	Bacteroidetes	GU:203 Bacteroides finegoldii	3.23E-02	1.68E-02	1.70E-02	7.10E-01	9.69E-01	4.27E-01	2.25E-01	1.69E-01	2.76E-02	2.17E-01	1.77E-01	2.26E-02	2.23E-01	2.84E-01	1.68E-02	0.45	0.50	0.45	-0.11	0.05	-0.25	0.47	0.24	0.45	0.42	0.24	-0.23	0.32