

Table S1. End sequencing of SMG clones

Clone	Best hit microorganism	Top blastx hit	e-value	% coverage	% identity	Phylum
SMG 1	<i>Bacteroides thetaiotamicron</i> VPI-5482	Hypothetical protein BT_1366	0.00E+00	100%	100%	Bacteroidetes
SMG 2	<i>Collinsella aerofaciens</i> ATCC 25986	Hypothetical protein COLAER_01951	1.00E-133	99%	96%	Actinobacteria
SMG 3	<i>Collinsella aerofaciens</i> ATCC 25986	Hypothetical protein COLAER_01951	2.00E-146	99%	88%	Actinobacteria
SMG 4	<i>Collinsella aerofaciens</i> ATCC 25986	Hypothetical protein COLAER_01951	2.00E-41	99%	95%	Actinobacteria
SMG 5	<i>Eggerthella</i> sp. YY7918	Aldehyde ferredoxin oxidoreductase	6.00E-120	99%	42%	Actinobacteria
SMG 6	<i>Bacteroides thetaiotamicron</i> VPI-5482	Hypothetical protein BT_1366	0.00E+00	100%	100%	Bacteroidetes
SMG 7	<i>Bacteroides</i> sp. 4_3_47FAA	Two-component system; response regulator sensor kinase	1.00E-135	83%	98%	Bacteroidetes
SMG 8	<i>Bacteroides</i> sp. 3_1_40A	Hypothetical protein HMPREF9011_03915	3.00E-160	99%	99%	Bacteroidetes
SMG 9	<i>Alistipes putredinis</i> DSM 17216	Hypothetical protein ALIPUT_02368	0.00E+00	47%	72%	Bacteroidetes
SMG 10	<i>Paraprevotella xylaniphila</i> YIT 11841	Helicase protein	8.00E-143	99%	99%	Bacteroidetes
SMG 11	<i>Bacteroides</i> sp. 3_1_40A	Dipeptidyl aminopeptidase	0.00E+00	99%	99%	Bacteroidetes
SMG 12	<i>Collinsella aerofaciens</i> ATCC 25986	Hypothetical protein COLAER_01951	6.00E-48	92%	98%	Actinobacteria
SMG 13	<i>Bacteroides stercoris</i> ATCC 43183	Hypothetical protein BACSTE_02336	5.00E-80	91%	64%	Bacteroidetes
SMG 14	<i>Bacteroides</i> sp. D2	TonB-dependent receptor	1.00E-65	99%	55%	Bacteroidetes
SMG 15	n/a	No sequence data	n/a	n/a	n/a	n/a
SMG 16	<i>Pseudomonas syringae</i> pv. <i>aceris</i> str. M302273PT	Phage integrase, putative	7.00E-31	69%	47%	Proteobacteria (γ)
SMG 17	<i>Pseudomonas syringae</i> pv. <i>aceris</i> str. M302273PT	Phage integrase, putative	1.00E-32	50%	51%	Proteobacteria (γ)
SMG 18	n/a	No sequence data	n/a	n/a	n/a	n/a
SMG 19	<i>Prevotella copri</i> DSM 18205	Putative Tat pathway signal sequence	2.00E-26	59%	52%	Bacteroidetes
SMG 20	<i>Slackia heliotrinireducens</i> DSM 20476	Fe-S oxidoreductase, coproporphyrinogen III oxidase	2.00E-18	22%	70%	Actinobacteria

SMG 21	<i>Bacteroides caccae</i> ATCC 43185	Hypothetical protein BACCAC_01367	1.00E-126	58%	98%	Bacteroidetes
SMG 22	<i>Prevotella oulorum</i> F0390	Hypothetical protein HMPREF9431_01698	7.00E-61	58%	65%	Bacteroidetes
SMG 23	<i>Clostridium methylpentosum</i> DSM 5476	Hypothetical protein CLOSTMETH_00476	8.00E-19	97%	23%	Firmicutes
SMG 24	<i>Bacteroides eggerthii</i> 1_2_48FAA	TonB-dependent receptor	3.00E-123	100%	54%	Bacteroidetes
SMG 25	<i>Akkermansia muciniphila</i> ATCC BAA-835	DNA polymerase III, alpha subunit Amuc_0374	0.00E+00	99%	95%	Verrucomicrobia
SMG 26	<i>Bacteroides fragilis</i> 3_1_12	Excinuclease ABC subunit B	1.00E-34	73%	82%	Bacteroidetes
SMG 27	<i>Alistipes</i> sp. HGB 7	Glycosyl hydrolase, family 57	0.00E+00	97%	95%	Bacteroidetes
SMG 28	<i>Pseudomonas fluorescens</i> Pf-5	Efflux; ABC transporter ATP-binding protein	1.00E-72	79%	53%	Proteobacteria (γ)
SMG 29	Uncultured rumen bacterium	Beta-D-xylosidase/alpha-L-arabinosidase	1.00E-90	82%	66%	Bacteroidetes
SMG 30	<i>Bacteroides caccae</i> ATCC 43185	Hypothetical protein BACCAC_01367	2.00E-90	59%	98%	Bacteroidetes
SMG 31	n/a	No sequence data	n/a	n/a	n/a	n/a
SMG 32	<i>Lacinutrix</i> sp. 5H-3-7-4	Primosomal protein N'	9.00E-74	92%	44%	Bacteroidetes
SMG 33	<i>Capnocytophaga</i> sp. oral taxon 329 str. F0087	RND transporter, HAE1/HME family, permease protein	6.00E-84	98%	47%	Bacteroidetes
SMG 34	<i>Bacterium Ellin514</i>	Antibiotic biosynthesis monooxygenase	8.00E-41	54%	40%	Verrucomicrobia
SMG 35	<i>Alistipes</i> sp. HGB5	Transporter; major facilitator family protein (sugar phosphate permease)	9.00E-67	73%	56%	Bacteroidetes
SMG 36	<i>Bacteroides coprosuis</i> DSM 18011	Hypothetical protein Bcop_0579	5.00E-69	99%	48%	Bacteroidetes
SMG 37	<i>Pseudomonas fluorescens</i> SBW25	Putative integrase	1.00E-60	66%	61%	Proteobacteria (γ)
SMG 38	<i>Prevotella buccae</i> D17	Glycine dehydrogenase (decarboxylating), subunit 2	1.00E-57	35%	75%	Bacteroidetes
SMG 39	<i>Bacteroides</i> sp. 4_3_47FAA	Dipeptidyl peptidase IV	0.00E+00	99%	98%	Bacteroidetes
SMG 40	<i>Oxalobacter formigenes</i> OXCC13	Conserved hypothetical protein	3.00E-130	81%	79%	Proteobacteria (β)
SMG 41	<i>Alistipes</i> sp. HGB5	3-dehydroquinate dehydratase, type II	2.00E-16	45%	78%	Bacteroidetes
SMG 42	<i>Bacteroides</i> sp. 9_1_42FAA	V-type ATP synthase subunit E	2.00E-128	53%	100%	Bacteroidetes
SMG 43	<i>Eubacterium rectale</i> DSM 17629	RecA-family ATPase	3.00E-131	88%	99%	Firmicutes
SMG 44	n/a	No sequence data	n/a	n/a	n/a	n/a

SMG 45	<i>Blastocystis hominis</i>	Unnamed protein product	4.00E-17	91%	47%	Heterokontophyta
SMG 46	<i>Akkermansia muciniphila</i> ATCC BAA-835	Hypothetical protein Amuc_0150	7.00E-25	66%	36%	Verrucomicrobia
SMG 47	<i>Pseudomonas fluorescens</i> Pf0-1	GCN5-like N-acetyltransferase	2.00E-82	48%	81%	Proteobacteria (γ)
SMG 48	Unidentified	No significant similarity	n/a	n/a	n/a	n/a
SMG 49	<i>Bacteroides ovatus</i> SD CMC 3f	Conserved hypothetical protein	7.00E-94	98%	48%	Bacteroidetes
SMG 50	<i>Alistipes</i> sp. HGB5	Putative membrane protein	7.00E-45	52%	90%	Bacteroidetes
SMG 51	<i>Akkermansia muciniphila</i> ATCC BAA-835	Small multidrug resistance protein Amuc_0621	3.00E-39	32%	88%	Verrucomicrobia
SMG 52	<i>Bacteroides thetaiotamicron</i> VPI-5482	Hypothetical protein (BT_1366)	0.00E+00	100%	100%	Bacteroidetes
SMG 53	<i>Bifidobacterium bifidum</i> PRL2010	TrpS Tryptophanyl-tRNA synthetase	1.00E-118	100%	99%	Actinobacteria

