



Figure S1. Phylogenetic tree of the 163 MACPF-containing proteins encoded by Bacteroidetes/Chlorobi species. BSAP-1, the subject of this study, is highlighted in green font. Those in blue font are from non-Bacteroidia classes including Sphingobacteria, Flavobacteria, and Chlorobia. Those in red font were subsequently analyzed for growth inhibitory activity as shown in Table S4. Yellow font represents those present on a mobile genetic element transferred between Bacteroides strains co-resident in the human gut. Only one protein is listed for each orthologous protein clustering at 99% similarity with the number and letter in the preceding box listing the number of strains and cluster where each strain/gene can be found in Table S3. Evolutionary distance represents the number of amino acid substitutions per site.

Table S1 – Ability of *B. fragilis* strains to inhibit growth of strain NCTC 9343 in the agar spot overlay assay

		Growth inhibition of strain NCTC 9343
1	638R	+
2	23745	+
3	B20	+
4	13141	-
5	CM13	-
6	379	+
7	B35	+
8	B127	-
9	26877	-
10	VPI-13784	-
11	LM2	+
12	1284-2	-
13	17905	-
14	US365	-
15	12905	-
16	2429	-
17	US2244	+
18	B124	+
19	419	+
20	LM8	+
21	B16	+
22	LM16	-
23	LM2	+
24	1277476	-
25	1279-2	+
26	TAL2480	-
27	1279155-I	-
28	CM11	-
29	US1206	-
30	B117	+
31	LM46	+
32	B272	+
33	38310	+
34	1286265-I	-
35	IL89375-II	+
36	1285531-I	-
37	B110	+
38	US326	-
39	CM3	+
40	CL03T12C07	-
41	CL05T12C13	-
42	CL07T12C05	+

+ sensitive (growth inhibition)
 - no growth inhibition

Table S2. Distribution of the 324 proteins with a MACPF domain among the 15,948 sequenced bacterial genomes collected

phylum (# genomes with a MACPF protein/total # genomes in phylum)	genome	genome bioproject accession	MACPF-encoding gene
Acidobacteria (1/9)	Terriglobus roseus DSM 18391	PRJNA63509	Terro_2974
Actinobacteria (2/1970)	Clavibacter michiganensis NCPPB 382	PRJNA19643	CMM_2382
	Nocardia seriolae N 2927	PRJDB1598	NS07_contig00091-0002
Bacteroidetes (106/466)	Alistipes finegoldii DSM 17242	PRJNA40775	Alfi_1691
	Bacteroides 1 1 14	PRJNA38765	HMPREF9007_04731
	Bacteroides 1 1 30	PRJNA41955	HMPREF0127_02494
	Bacteroides 1 1 6	PRJNA32435	BSIG_1300
	Bacteroides 2 1 16	PRJNA38347	HMPREF0101_01895
	Bacteroides 2 1 22	PRJNA38349	HMPREF0102_00396
	Bacteroides 2 1 56FAA	PRJNA40013	HMPREF1018_01740
			HMPREF1018_02853
	Bacteroides 2 2 4	PRJNA32439	BSCG_02855
	Bacteroides 20 3	PRJNA38767	HMPREF9008_02040
	Bacteroides 3 1 23	PRJNA38771	HMPREF9010_04345
			HMPREF9010_04348
			HMPREF9010_04403
	Bacteroides 3 1 33FAA	PRJNA38353	HMPREF0105_2069
	Bacteroides 3 1 40A	PRJNA38773	HMPREF9011_00463
	Bacteroides 3 2 5	PRJNA32441	BSHG_0134
	Bacteroides 4 1 36	PRJNA39357	HMPREF1007_00197
	Bacteroides 9 1 42FAA	PRJNA32445	BSBG_00812
			BSBG_00813
	Bacteroides caccae CAG 21	PRJEB759	BN535_00964
	Bacteroides CAG 754	PRJEB996	BN772_00356
	Bacteroides cellulosilyticus CL02T12C19	PRJNA64803	HMPREF1062_02094
			HMPREF1062_02095
			HMPREF1062_02120
			HMPREF1062_02121
			HMPREF1062_02122
			HMPREF1062_02123
			HMPREF1062_02124
			HMPREF1062_02883
			HMPREF1062_05373
	Bacteroides cellulosilyticus DSM 14838	PRJNA30027	BACCELL_01585

		BACCELL_02330
		BACCELL_05502
Bacteroides D1	PRJNA32447	BSAG_00140
Bacteroides D20	PRJNA38355	HMPREF0969_01421
Bacteroides D22	PRJNA41953	HMPREF0106_01001
		HMPREF0106_02882
Bacteroides dorei CL03T12C01	PRJNA64809	HMPREF1065_02384
		HMPREF1065_02385
		HMPREF1065_04347
Bacteroides eggerthii 1 2 48FAA	PRJNA61869	HMPREF1016_03647
Bacteroides faecis MAJ27	PRJNA72171	BfaeM_010100023705
Bacteroides fragilis 1007 1 F 10	PRJNA206138	M104_2757
		M104_4085
Bacteroides fragilis 1007 1 F 5	PRJNA206182	M148_1670
		M148_2852
Bacteroides fragilis 1007 1 F 6	PRJNA206183	M149_1805
		M149_2962
Bacteroides fragilis 1007 1 F 7	PRJNA206135	M100_1591
		M100_2810
Bacteroides fragilis 1007 1 F 8	PRJNA206136	M101_2609
Bacteroides fragilis 1009 4 F 10	PRJNA206140	M106_1597
		M106_1841
Bacteroides fragilis 1009 4 F 7	PRJNA206139	M105_2100
		M105_3134
Bacteroides fragilis 2 F 2 4	PRJNA206111	M076_1635
Bacteroides fragilis 2 F 2 5	PRJNA206112	M077_1747
Bacteroides fragilis 2 F 2 7	PRJNA206113	M078_1667
Bacteroides fragilis 3 1 12	PRJNA32433	BFAG_00915
		BFAG_00974
		BFAG_03570
Bacteroides fragilis 3 F 2 6	PRJNA206178	M144_1629
		M144_2717
Bacteroides fragilis 3397 N2	PRJNA206143	M109_2574
Bacteroides fragilis 3397 T10	PRJNA206115	M080_2450
Bacteroides fragilis 3397 T14	PRJNA206142	M108_2648
Bacteroides fragilis 34 F 2 13	PRJNA206179	M145_1554
Bacteroides fragilis 3719 A10	PRJNA206150	M116_1647
Bacteroides fragilis 3719 T6	PRJNA206149	M115_1539
Bacteroides fragilis 3725 D9 v	PRJNA206141	M107_2338
		M107_2399
		M107_2891

Bacteroides fragilis 3783N1 8	PRJNA206154	M120_1906
Bacteroides fragilis 3976T8	PRJNA206157	M123_1651
		M123_1767
Bacteroides fragilis 3986 N B 22	PRJNA206148	M114_1392
Bacteroides fragilis 3986 T B 13	PRJNA206146	M112_1592
Bacteroides fragilis 3986 T B 9	PRJNA206118	M083_1493
Bacteroides fragilis 3986T B 10	PRJNA206145	M111_4148
Bacteroides fragilis 3996 N B 6	PRJNA206114	M079_1648
		M079_2797
Bacteroides fragilis 3998T B 3	PRJNA206159	M125_2032
Bacteroides fragilis 638R	PRJNA50405	BF638R_1646
		BF638R_2714
Bacteroides fragilis B1 UDC16 1	PRJNA206104	M069_1710
		M069_1772
		M069_5973
Bacteroides fragilis CL07T00C01	PRJNA64819	HMPREF1055_00045
		HMPREF1055_01288
Bacteroides fragilis CL07T12C05	PRJNA64821	HMPREF1056_01634
		HMPREF1056_02880
Bacteroides fragilis DS 71	PRJNA206108	M073_1472
Bacteroides fragilis HMW 610	PRJNA71525	HMPREF1203_00874
		HMPREF1203_04347
Bacteroides fragilis HMW 615	PRJNA71527	HMPREF1204_03336
Bacteroides fragilis HMW 616	PRJNA71529	HMPREF1205_04263
Bacteroides fragilis I 1345	PRJNA206101	M066_1626
Bacteroides fragilis J 143 4	PRJNA206102	M067_1727
Bacteroides fragilis J 38 1	PRJNA206103	M068_0191
		M068_1622
Bacteroides fragilis S24L15	PRJNA206166	M132_1451
		M132_2481
Bacteroides fragilis S24L26	PRJNA206167	M133_1503
		M133_2565
Bacteroides fragilis YCH46	PRJNA13067	BF1566
		BF1634
		BF2685
Bacteroides helcogenes P 36 108	PRJNA41913	Bache_1009
		Bache_1010
		Bache_1011
		Bache_2425
		Bache_2426
Bacteroides intestinalis CAG 315	PRJEB828	BN604_01094

Bacteroides intestinalis DSM 17393	PRJNA20523	BN604_02420 BACINT_00423 BACINT_00829 BACINT_03190
Bacteroides massiliensis B84634 DSM 17679	PRJNA170352	HMPREF1534_02177
Bacteroides oleiciplenus YIT 12058	PRJNA46377	HMPREF9447_05370
Bacteroides ovatus SD CC 2a	PRJNA47359	CW1_1049
Bacteroides ovatus SD CMC 3f	PRJNA42769	CUY_2106
Bacteroides plebeius DSM 17135	PRJNA27829	BACPLE_01336
Bacteroides pyogenes JCM 6292	PRJDB556	JCM6292_3817
Bacteroides salyersiae CL02T12C01	PRJNA64829	HMPREF1071_01444 HMPREF1071_03696
Bacteroides thetaiotaomicron dnLKV9	PRJNA175974	C799_03772
Bacteroides thetaiotaomicron VPI 5482	PRJNA399	BT_3437
Bacteroides uniformis ATCC 8492	PRJNA18195	BACUNI_00959
Bacteroides uniformis CAG 3	PRJEB818	BN594_02326
Bacteroides uniformis CL03T00C23	PRJNA64833	HMPREF1072_01167 HMPREF1072_03071 HMPREF1072_04153
Bacteroides uniformis CL03T12C37	PRJNA64835	HMPREF1073_02064 HMPREF1073_03392 HMPREF1073_04081
Bacteroides uniformis dnLKV2	PRJNA175976	C801_00210
Bacteroides vulgatus CL09T03C04	PRJNA64837	HMPREF1058_01764 HMPREF1058_01765
Bacteroides vulgatus dnLKV7	PRJNA175975	C800_03444
Bacteroides xylanisolvens SD CC 1b	PRJNA47865	CW3_1454
Bacteroides xylanisolvens XB1A	PRJNA39177	BXY_26810 BXY_27570
Barnesiella intestinihominis YIT 11860	PRJNA46375	HMPREF9448_02774
Chryseobacterium gleum ATCC 35910	PRJNA30953	HMPREF0204_11601
Dokdonia donghaensis MED134	PRJNA13544	MED134_03544
Elizabethkingia anophelis Ag1	PRJNA77829	EAAG1_10627
Elizabethkingia anophelis R26	PRJNA178189	D505_04224
Krokinobacter 4H 3 7 5	PRJNA62895	Krodi_0142
Leeuwenhoekiella blandensis MED217	PRJNA13573	MED217_10914
Mucilaginibacter paludis DSM 18603	PRJNA43733	Mucpa_5412
Parabacteroides D13	PRJNA38359	HMPREF0619_03645
Parabacteroides distasonis CL09T03C24	PRJNA64885	HMPREF1059_02732
Parabacteroides merdae CL03T12C32	PRJNA64891	HMPREF1060_03364
Paraprevotella xylaniphila YIT 11841	PRJNA48503	HMPREF9442_03422

Chlamydiae (120/137)

Pedobacter V48	PRJNA214790	HMPREF9442_03423
Porphyromonas endodontalis ATCC 35406	PRJNA31385	N824_23675
Porphyromonas oral taxon 279 F0450	PRJNA78907	POREN0001_1212
Prevotella ruminicola 23	PRJNA10619	HMPREF1323_1106
Solitalea canadensis DSM 3403	PRJNA60421	PRU_2520
		Solca_1704
		Solca_3841
Sphingobacterium spiritivorum ATCC 33300	PRJNA31529	HMPREF0765_1250
Zunongwangia profunda SM A87	PRJNA38641	ZPR_2061
Chlamydia trachomatis A 363	PRJEA71065	A363_00159
Chlamydia trachomatis A 5291	PRJEA71067	A5291_00158
Chlamydophila psittaci Mat116	PRJNA28637	AO9_02945
Chlamydia psittaci 84 55	PRJNA171856	B595_0657
Chlamydia psittaci MN	PRJNA171914	B599_0612
Chlamydia psittaci VS225	PRJNA171915	B600_0655
Chlamydia psittaci M56	PRJNA171917	B602_0619
Chlamydia psittaci WC	PRJNA171918	B603_0619
Chlamydophila psittaci CP3	PRJNA172450	B711_0655
Chlamydophila psittaci NJ1	PRJNA172451	B712_0614
Chlamydia trachomatis IU824	PRJEB223	BN197_1541
Chlamydia trachomatis IU888	PRJEB627	BN442_1541
Chlamydia trachomatis E Bour	PRJEA71077	BOUR_00160
Chlamydophila felis Fe C 56	PRJNA370	CF0443
Chlamydia muridarum MopnTet14	PRJNA39295	CmurM_010100002220
Chlamydia muridarum Weiss	PRJNA38161	CmurW_010100002228
Chlamydia psittaci 02DC14	PRJNA77079	CP02DC14_1040
Chlamydia psittaci 02DC16	PRJNA77083	CP02DC16_1026
Chlamydia psittaci 02DC21	PRJNA77087	CP02DC21_1006
Chlamydia psittaci 02DC24	PRJNA77093	CP02DC24_0299
Chlamydia psittaci 03DC29	PRJNA77097	CP03DC29_0722
Chlamydia psittaci 03DC35	PRJNA77101	CP03DC35_1019
Chlamydia psittaci 04DC42	PRJNA77103	CP04DC42_1020
Chlamydophila pneumoniae AR39	PRJNA247	CP0593
Chlamydia psittaci 09DC77	PRJNA77109	CP09DC77_1034
Chlamydia psittaci 09DC79	PRJNA77113	CP09DC79_0747
Chlamydia psittaci 84 8471 1	PRJNA77033	CP8484711_1340A
Chlamydia psittaci 99DC5	PRJNA77075	CP99DC5_1023
Chlamydophila pneumoniae TW 183	PRJNA420	CpB0179
Chlamydia psittaci C6 98	PRJNA77071	CPC698_0917
Chlamydia pecorum PV3056 3	PRJNA175545	CPE1_0549

Chlamydia pecorum W73	PRJNA175546	CPE2_0549
Chlamydia pecorum P787	PRJNA175547	CPE3_0549
Chlamydia pecorum IPTaLE	PRJNA229197	CpecA_0811
Chlamydia pecorum DBDeUG	PRJNA229199	CpecF_0809
Chlamydia pecorum MC MarsBar	PRJNA229198	CpecG_0809
Chlamydia pecorum VR629	PRJNA229200	CpecS_0807
Chlamydomphila pneumoniae J138	PRJNA257	CPj0176
Chlamydomphila pneumoniae LPCoLN	PRJNA17947	CPK_ORF00685
Chlamydomphila pneumoniae CWL029	PRJNA248	CPn0176
Chlamydomphila psittaci 01DC11	PRJNA159527	CPS0A_0617
Chlamydomphila psittaci 02DC15	PRJNA159521	CPS0B_0614
Chlamydomphila psittaci C19 98	PRJNA159523	CPS0C_0621
Chlamydomphila psittaci 08DC60	PRJNA159525	CPS0D_0616
Chlamydomphila psittaci RD1	PRJEA60445	Cpsi_5581
Chlamydomphila psittaci 6BC	PRJNA63621	CPSIT_0608
Chlamydia trachomatis D UW 3 CX	PRJNA45	CT_153
Chlamydia trachomatis A HAR 13	PRJNA13885	CTA_0162
Chlamydia trachomatis B TZ1A828 OT	PRJEA32653	CTB_1521
Chlamydia trachomatis D EC	PRJNA48087	CTDEC_0153
Chlamydia trachomatis D LC	PRJNA48089	CTDLC_0153
Chlamydia trachomatis G 9301	PRJNA45851	CTG9301_00790
Chlamydia trachomatis J 6276tet1	PRJNA53863	CTJTET1_00800
Chlamydia trachomatis 434 Bu	PRJNA28583	CTL0408
Chlamydia trachomatis L2c	PRJNA47581	CTL2C_436
Chlamydia trachomatis L2 434 Bu f	PRJNA182165	CTLFINAL_02150
Chlamydia trachomatis L2 434 Bu i	PRJNA182150	CTLINITIAL_02150
Chlamydia trachomatis L2b UCH 1 proctitis	PRJNA28585	CTLon_0404
Chlamydia trachomatis A2497	PRJNA159993	CTO_0162
Chlamydia trachomatis 6276s	PRJNA32185	Ctra6_010100000785
Chlamydia trachomatis 6276	PRJNA32183	Ctra62_010100000790
Chlamydia trachomatis 70s	PRJNA32189	Ctra7_010100000820
Chlamydia trachomatis 70	PRJNA32187	Ctra70_010100000805
Chlamydia trachomatis D s 2923	PRJNA32539	CtraD_010100000810
Chlamydia trachomatis L2tet1	PRJNA39293	CtraL_010100002315
Chlamydia trachomatis RC J s 122	PRJNA53859	CTRC122_00815
Chlamydia trachomatis RC L2 s 3	PRJNA53855	CTRC3_00815
Chlamydia trachomatis RC F s 342	PRJNA53857	CTRC342_00820
Chlamydia trachomatis RC L2 s 46	PRJNA53847	CTRC46_00805
Chlamydia trachomatis RC L2 55	PRJNA66013	CTRC55_00805
Chlamydia trachomatis RC F 69	PRJNA53845	CTRC69_00805
Chlamydia trachomatis RC F s 852	PRJNA53849	CTRC852_00825

Chlamydia trachomatis RC J 943	PRJNA53851	CTRC943_00795
Chlamydia trachomatis RC J 953	PRJNA53853	CTRC953_00800
Chlamydia trachomatis RC J 966	PRJNA53861	CTRC966_00810
Chlamydia trachomatis RC J 971	PRJNA66011	CTRC971_00805
Chlamydia trachomatis C TW 3	PRJNA230246	CTW3_00820
Chlamydia trachomatis E 11023	PRJNA43141	E11023_00800
Chlamydia trachomatis E 150	PRJNA43143	E150_00810
Chlamydia trachomatis E C599	PRJEA74569	EC599_1581
Chlamydia trachomatis E SW3	PRJEA71079	ESW3_1541
Chlamydia trachomatis F SW4	PRJEA71085	FSW4_1541
Chlamydia trachomatis F SW5	PRJEA71087	FSW5_1541
Chlamydia trachomatis G 11074	PRJNA43149	G11074_00790
Chlamydia trachomatis G 11222	PRJNA43147	G11222_00790
Chlamydophila psittaci Cal10	PRJNA62891	G5Q_0588
Chlamydophila pecorum E58	PRJNA62893	G5S_0929
Chlamydia trachomatis G 9768	PRJNA43145	G9768_00790
Chlamydia trachomatis B Jali20 OT	PRJEA32655	JALI_1521
Chlamydia trachomatis L1 115	PRJEA71101	L1115_00157
Chlamydia trachomatis L1 224	PRJEA71103	L1224_00157
Chlamydia trachomatis L1 440 LN	PRJEA71099	L1440_00157
Chlamydia trachomatis L2 25667R	PRJEA71105	L225667R_00157
Chlamydia trachomatis L2b 795	PRJEA71115	L2B795_00157
Chlamydia trachomatis L2b 8200 07	PRJEA71107	L2B8200_00157
Chlamydia trachomatis L2b Ams1	PRJEA71117	L2BAMS1_00157
		B602_0620
Chlamydia trachomatis L2b Ams2	PRJEA71119	L2BAMS2_00157
Chlamydia trachomatis L2b Ams3	PRJEA71121	L2BAMS3_00157
Chlamydia trachomatis L2b Ams4	PRJEA71123	L2BAMS4_00157
Chlamydia trachomatis L2b Ams5	PRJEA71125	L2BAMS5_00157
Chlamydia trachomatis L2b Canada1	PRJEA71457	L2BCAN1_00158
Chlamydia trachomatis L2b Canada2	PRJEA71459	L2BCAN2_00157
Chlamydia trachomatis L2b CV204	PRJEA71113	L2BCV204_00157
Chlamydia trachomatis	PRJEA71111	L2BLST_00157
Chlamydia trachomatis L2b UCH 2	PRJEA71109	L2BUCH2_00157
Chlamydia trachomatis L3 404 LN	PRJEA71127	L3404_00157
Chlamydia suis MD56	PRJNA221336	Q499_0165
Chlamydia trachomatis D SotonD1	PRJEA71071	SOTOND1_00157
Chlamydia trachomatis D SotonD5	PRJEA71073	SOTOND5_00157
Chlamydia trachomatis D SotonD6	PRJEA71075	SOTOND6_00157
Chlamydia trachomatis	PRJEA71081	SOTONE4_00157
Chlamydia trachomatis E SotonE8	PRJEA71083	SOTONE8_00157

	Chlamydia trachomatis	PRJEA71089	SOTONF3_00157
	Chlamydia trachomatis G SotonG1	PRJEA71091	SOTONG1_00156
	Chlamydia trachomatis Ia SotonIa1	PRJEA71093	SOTONIA1_00157
	Chlamydia trachomatis	PRJEA71095	SOTONIA3_00157
	Chlamydia trachomatis K SotonK1	PRJEA71097	SOTONK1_00157
	Chlamydia trachomatis Sweden2	PRJEA43167	SW2_1541
	Chlamydia trachomatis F SWFPminus	PRJEA74571	SWFP_1631
	Chlamydia muridarum Nigg	PRJNA57785	TC_0431
Chlorobi (2/12)			
	Chlorobium limicola DSM 245	PRJNA12606	Clim_0052
	Chlorobium phaeobacteroides DSM 266	PRJNA12609	Cpha266_0063
Cyanobacteria (4/129)			
	Cyanothece PCC 7822	PRJNA28535	Cyan7822_6553
	Leptolyngbya PCC 7375	PRJNA43137	Lepto7375DRAFT_7535
	Lyngbya majuscula 3L	PRJNA60895	LYNGBM3L_24480
	Trichodesmium erythraeum IMS101	PRJNA318	Tery_0815
Euryarchaeota (1/195)			
	Halorubrum kocurii JCM 14978	PRJNA174917	C468_01225
Firmicutes (6/6259)			
	Clostridium CAG 307	PRJEB822	BN598_00407
			BN598_01207
	Filifactor alocis ATCC 35896	PRJNA30485	HMPREF0389_01644
	Lachnospiraceae bacterium 3 1	PRJNA175981	C806_02722
	Lachnospiraceae bacterium 3 1 57FAA CT1	PRJNA39383	HMPREF0994_05290
	Paenibacillus mucilaginosus 3016	PRJNA77661	PM3016_3694
	Paenibacillus mucilaginosus KNP414	PRJNA67335	KNP414_04256
Proteobacteria (21/6039)			
	Beggiatoa PS	PRJNA18683	BGP_1327
	Bradyrhizobium YR681	PRJNA83113	PMI42_07046
	Candidatus Entotheonella TSY2	PRJNA230051	ETSY2_16640
	Chondromyces apiculatus DSM 436	PRJNA167109	A176_05694
	Chondromyces apiculatus DSM 436	PRJNA192263	A176_3469
	Marinomonas MED121	PRJNA13587	MED121_03928
	Myxococcus fulvus HW 1	PRJNA27837	LILAB_21670
	Photorhabdus asymbiotica ATCC 43949	PRJNA59243	PAU_02991
	Photorhabdus luminescens laumondii TTO1	PRJNA9605	plu1415
	Plesiocystis pacifica SIR 1	PRJNA19341	PPSIR1_00475
	Pseudogulbenkiania ferrooxidans EGD HP2	PRJNA215707	O166_11535
	Pseudomonas brassicacearum NFM421	PRJEA63495	PSEBR_a5064
	Pseudomonas fluorescens F113	PRJNA76715	PSF113_1304
	Pseudomonas fluorescens Q2 87	PRJNA67535	PflQ2_4938

	Pseudomonas fluorescens Q8r1 96	PRJNA67537	PflQ8_5199
	Pseudomonas fuscovaginae UPB0736	PRJNA84441	PfusU_010100000662
	Serratia proteamaculans 568	PRJNA17459	Spro_2388
	Skermanella stibioresistens SB22	PRJNA214805	N825_02095
	Sulfurospirillum barnesii SES 3	PRJNA63451	Sulba_1023
	Sulfurospirillum deleyianum DSM 6946	PRJNA29529	Sdel_1215
Spirochaetes (1/315)	uncultured Thiohalocapsa PB PSB1	PRJNA215075	N838_01415
	Spirochaeta smaragdinae DSM 11293	PRJNA32637	Spirs_3309
Tenericutes (1/128)	Acholeplasma palmae J233	PRJEB1742	BN85402230

Table S3 - Clusters of MACPF domain containing proteins from Bacteroidetes strains with at least 99% identity among each cluster

cluster	genome	MACPF domain gene	size (aa)	gi
cluster A (29 genomes)				
	<i>Bacteroides fragilis</i> 638R	BF638R_1646	372	375357946
	<i>Bacteroides fragilis</i> YCH46	BF1634	372	53712924
	<i>Bacteroides fragilis</i> 3 1 12	BFAG_00974	372	313146153
	<i>Bacteroides fragilis</i> 2 1 56FAA	HMPREF1018_01740	372	336409237
	<i>Bacteroides fragilis</i> CL07T00C01	HMPREF1055_01288	372	423258088
	<i>Bacteroides fragilis</i> CL07T12C05	HMPREF1056_01634	372	423264944
	<i>Bacteroides fragilis</i> I 1345	M066_1626	372	596282837
	<i>Bacteroides fragilis</i> B1 UDC16 1	M069_1772	372	596123585
	<i>Bacteroides fragilis</i> 2 F 2 5	M077_1747	372	595897619
	<i>Bacteroides fragilis</i> 1009 4 F 7	M105_2100	372	596184650
	<i>Bacteroides fragilis</i> 1009 4 F 10	M106_1597	372	596179785
	<i>Bacteroides fragilis</i> 3725 D9 v	M107_2399	372	596099258
	<i>Bacteroides fragilis</i> 3783N1 8	M120_1906	372	596105509
	<i>Bacteroides fragilis</i> S24L15	M132_1451	372	596227992
	<i>Bacteroides fragilis</i> S24L26	M133_1503	372	596233194
	<i>Bacteroides fragilis</i> 3 F 2 6	M144_1629	372	596117941
	<i>Bacteroides fragilis</i> 1007 1 F 5	M148_1670	372	598884198
	<i>Bacteroides fragilis</i> 1007 1 F 6	M149_1805	372	598892530
	<i>Bacteroides fragilis</i> J 143 4	M067_1727	364	596045352
	<i>Bacteroides fragilis</i> J 38 1	M068_1622	364	596131568
	<i>Bacteroides fragilis</i> 2 F 2 4	M076_1635	364	596078823
	<i>Bacteroides fragilis</i> 2 F 2 7	M078_1667	364	595902282
	<i>Bacteroides fragilis</i> 3996 N B 6	M079_1648	364	595997100
	<i>Bacteroides fragilis</i> 1007 1 F 7	M100_1591	364	596072905
	<i>Bacteroides fragilis</i> 1007 1 F 10	M104_4085	364	596160913
	<i>Bacteroides fragilis</i> 3719 T6	M115_1539	364	596201381
	<i>Bacteroides fragilis</i> 3976T8	M123_1767	364	596111621
	<i>Bacteroides fragilis</i> 3998T B 3	M125_2032	364	596006232
	<i>Bacteroides fragilis</i> 34 F 2 13	M145_1554	359	595927946
cluster B (21 genomes)				
	<i>Bacteroides fragilis</i> 638R	BF638R_2714	506	375358975
	<i>Bacteroides fragilis</i> YCH46	BF2685	506	53713977
	<i>Bacteroides fragilis</i> 2 1 16	HMPREF0101_01895	506	265764327
	<i>Bacteroides fragilis</i> 2 1 56FAA	HMPREF1018_02853	506	336410356
	<i>Bacteroides fragilis</i> CL07T00C01	HMPREF1055_00045	506	423256845
	<i>Bacteroides fragilis</i> CL07T12C05	HMPREF1056_02880	506	423266190
	<i>Bacteroides fragilis</i> 3996 N B 6	M079_2797	506	595995905
	<i>Bacteroides fragilis</i> 3397 T10	M080_2450	506	595908723
	<i>Bacteroides fragilis</i> 1007 1 F 7	M100_2810	506	596071634
	<i>Bacteroides fragilis</i> 1007 1 F 10	M104_2757	506	596161846
	<i>Bacteroides fragilis</i> 1009 4 F 7	M105_3134	506	596183673
	<i>Bacteroides fragilis</i> 1009 4 F 10	M106_1841	506	596179494
	<i>Bacteroides fragilis</i> 3725 D9 v	M107_2891	506	596098974
	<i>Bacteroides fragilis</i> 3397 T14	M108_2648	506	596088191
	<i>Bacteroides fragilis</i> 3397 N2	M109_2574	506	596082827
	<i>Bacteroides fragilis</i> S24L15	M132_2481	506	596226905
	<i>Bacteroides fragilis</i> S24L26	M133_2565	506	596232110

	<i>Bacteroides fragilis</i> 3 F 2 6	M144_2717	506	596116817
	<i>Bacteroides fragilis</i> 1007 1 F 5	M148_2852	506	598880300
	<i>Bacteroides fragilis</i> 1007 1 F 6	M149_2962	506	598891202
	<i>Bacteroides fragilis</i> 1007 1 F 8	M101_2609	247	595889845
cluster C (12 genomes)				
	<i>Bacteroides fragilis</i> YCH46	BF1566	486	53712858
	<i>Bacteroides fragilis</i> 3 2 5	BSHG_0134	486	383117721
	<i>Bacteroides fragilis</i> HMW 615	HMPREF1204_03336	486	423284915
	<i>Bacteroides fragilis</i> B1 UDC16 1	M069_1710	486	596123523
	<i>Bacteroides fragilis</i> 3725 D9 v	M107_2338	486	596099197
	<i>Bacteroides fragilis</i> 3986 T B 13	M112_1592	486	596210719
	<i>Bacteroides fragilis</i> 3986 N B 22	M114_1392	486	596206604
	<i>Bacteroides fragilis</i> 3719 A10	M116_1647	486	596094037
	<i>Bacteroides fragilis</i> 3976T8	M123_1651	486	596111718
	<i>Bacteroides fragilis</i> 3986 T B 9	M083_1493	479	595979045
	<i>Bacteroides fragilis</i> DS 71	M073_1472	352	596031736
	<i>Bacteroides fragilis</i> 3986T B 10	M111_4148	187	595960642
cluster D (11 genomes)				
	<i>Bacteroides dorei</i> CL03T12C01	HMPREF1065_04347	559	423242619
	<i>Bacteroides intestinalis</i> DSM 17393	BACINT_00423	559	189464088
	<i>Bacteroides plebeius</i> DSM 17135	BACPLE_01336	559	198275178
	<i>Bacteroides fragilis</i> 3 1 12	BFAG_03570	559	313148745
	<i>Bacteroides faecis</i> MAJ27	BfaeM_010100023705	559	380696948
	<i>Bacteroides xylanisolvens</i> D22	HMPREF0106_02882	559	298482417
	<i>Bacteroides eggerthii</i> 1 2 48FAA	HMPREF1016_03647	559	317477434
	<i>Parabacteroides merdae</i> CL03T12C32	HMPREF1060_03364	559	423348007
	<i>Bacteroides uniformis</i> CL03T00C23	HMPREF1072_04153	559	423307215
	<i>Bacteroides uniformis</i> CL03T12C37	HMPREF1073_04081	559	423311363
	<i>Bacteroides fragilis</i> B1 UDC16 1	M069_5973	559	596126173
cluster E (8 genomes)				
	<i>Bacteroides xylanisolvens</i> 2 2 4	BSCG_02855	549	237720387
	<i>Bacteroides ovatus</i> SD CMC 3f	CUY_2106	549	293370465
	<i>Bacteroides ovatus</i> SD CC 2a	CW1_1049	549	294646213
	<i>Bacteroides xylanisolvens</i> SD CC 1b	CW3_1454	549	294809120
	<i>Bacteroides xylanisolvens</i> 2 1 22	HMPREF0102_00396	549	262405432
	<i>Bacteroides xylanisolvens</i> D22	HMPREF0106_01001	549	298480572
	<i>Bacteroides xylanisolvens</i> 1 1 30	HMPREF0127_02494	549	336404486
	<i>Bacteroides xylanisolvens</i> D1	BSAG_00140	360	345510621
cluster F (4 genomes)				
	<i>Bacteroides uniformis</i> ATCC 8492	BACUNI_00959	656	160888542
	<i>Bacteroides uniformis</i> CAG 3	BN594_02326	658	524694523
	<i>Bacteroides uniformis</i> 4 1 36	HMPREF1007_00197	658	317477897
	<i>Bacteroides uniformis</i> D20	HMPREF0969_01421	651	270294900
cluster G (3 genomes)				
	<i>Bacteroides uniformis</i> dnLKV2	C801_00210	508	507752131
	<i>Bacteroides uniformis</i> CL03T00C23	HMPREF1072_01167	508	423304228
	<i>Bacteroides uniformis</i> CL03T12C37	HMPREF1073_03392	508	423310658
cluster H (3 genomes)				
	<i>Bacteroides dorei</i> 9 1 42FAA	BSBG_00813	491	237711430

Table S4 – Agar overlay assay results of ability of strains listed in red font to secrete molecules that inhibits the growth of strains listed in blue font.

	Bf 638R	Bf 638R pMCL140	638R pMCL177 (BF638R_2714)	Bf CM13 pMCL140	Bf CM13 pMCL177			
Bf 12905	+	+	+					
Bf CM13	+	+	+					
Bf 9343	+	+	+					
Bf CL03T12C07	+	+	+					
Bf CL05T12C13	+	+	+					
Bf US326	+	+	+					
	Bu ATCC 8492	Bu pMCL178 (BACUNI_00905)	CM13 pMCL140	CM13 pMCL178				
Bf 12905	slight	slight						
Bf CM13								
Bf 9343								
Bf CL03T12C07								
Bf CL05T12C13								
Bf US326								
Bu CL03T12C16	slight	slight						
Bu CL06T06C18	slight	slight						
Bu CL07T00C16	slight	slight						
Bu CL09T06C01								
Bu CL10T00C10								
Bu CL12T00C13								
Bu CL12T12C47								
Bu CL14T09C07	slight	slight						
	Bt VPI-5482	Bt pMCL176 (BT_3120)	Bt pMCL175 (BT_3437)	Bt pMCL174 (BT_3439)	CM13 pMCL140	CM13 pMCL176	CM13 pMCL175	CM13 pMCL174
Bf 12905	+	+	+	+				
Bf CM13								
Bf 9343								
Bf CL03T12C07								
Bf CL05T12C13								
Bf US326								
Bt CL04T06C10								
Bt CL04T12C04								
Bt CL05T03C12	slight	slight	slight	slight				
Bt CL06T03C18								
Bt CL06T12C08								
Bt CL07T03C06								
Bt CL07T12C01								
Bt CL08T00C07								
Bt CL08T06C15								
Bt CL09T03C10								
Bt CL10T00C23								
Bt CL10T12C19								
Bt CL11T00C19								
Bt CL11T12C02								
Bt CL12T00C04								
Bt CL12T12C02								
Bt CL13T03C02								
Bt CL13T12C04								
Bt CL15T03C05								
Bt CL15T12C11								

Results are only shown for those strains that are growth inhibited (+/slight). Blank cells are equivalent to no inhibitory activity.

Table S5. Primers used in this study

Purpose	Primer	Primer sequence ^a
Sequencing out of tn junction		GACTTGGATACCTCACGCC
Cloning of BF1646	forward	GTTTGGATCCGGTTTTGCTTGGTATTTTCATTTG
	reverse	ACGAGGATCCAGAAAAGCCCTGTATAAAAAGCA
Cloning of His-BF1646	forward	AGAACATATGACTAATGATGATTTTTCTGTATTACAGGAAAATGAAGA
	reverse	GATTCATATGTTATGGTCTCCTATAAGTACTTCTATTTCCATTAG
Cloning of BT_3120	forward	CGATGGATCCTTCTCATTCCCTTTTATCTACCTTTAGC
	reverse	TTCCGGATCCGGTATGGCCTTATGCTTATACCTT
Cloning of BT_3437	forward	AGTAGGATCCACCAAAGTATCAACCATAAGAAACATGA
	reverse	GTAAGGATCCGTGTTTTAGCGATTATCCTCAATG
Cloning of BT_3439	forward	GAAGGGATCCCTTTTTAAATTATACGCAAATGAAGAAG
	reverse	ACATGGATCCGGAACATTAATTCTGTTTATTGTTACTACA
Cloning of BACUNI_00959	forward	TTAGGATCCTTATAACAATCATAACAACAACATACATTA
	reverse	TTCCGGATCCAAGTTATCTCTAACACATTGGTACACCTT
Cloning of BF638R_2714	forward	TATGGATCCCCACCTACCTTTGCAAACAGTTAT
	reverse	CTGCGGATCCGCCCTTCTTATTGTATTGTATCGTC
Creation of Δ BF1646	left flank forward	TACTGGATCCGAGTACGCTGAACGCATCAT
	left flank reverse	CGATACGCGTAAGCGGCAAATGTGAATAGC
	right flank forward	GGTAACGCGTCGAGTTATTGGGGCTAATGG
	right flank reverse	ATGAGGATCCCGCGTTTCGTGATGTGAGTA
Creation of site-directed mutants	VL>AA forward	CTTTTATTATTCAACATTATGGGACACATGCAGCAACTGATATTACTTTGGGAGGAAGAATAAC
	VL>AA reverse	GTTATTCTTCCTCCCAAAGTAATATCAGTTGCTGCATGTGTCCATAATGTTGAATAATAAAAAG
	W>A forward	TCTAAAAATCCATCCGTAATTGATATATCATCAGCGCAACAGAGTTGTGATG
	W>A reverse	CATCACAACCTCTGTTGCGCTGATGATATATCAATTACGGATGGATTTT TAGA

^a Restriction sites are underlined.