Supporting Information

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SI Materials and Methods

Recipes for the Rich Medium and the Minimal Medium. ***Rich medium (per liter).*** Twenty grams proteose peptone, 5 g yeast extract, 5 g NaCl, 5 g glucose, 5 g K_2HPO_4, 0.5 g L-cysteine, 5 mg hemi, and 2.5 μL vitamin K_1.

Minimal medium (per liter). One gram $(NH_4)_2SO_4$, 1 g Na_2CO_3, 5 g glucose, 0.5 g L-cysteine, 5 mg hemin, 2.5 μL vitamin K_1, 2 mg $FeSO_4{\cdot}7H_2O$, 5 μg vitamin B_{12}, and 20 mL mineral solution (per liter: 18 g KH_2PO_4, 18 g NaCl, 530 mg $CaCl_2{\cdot}2H_2O$, 400 mg $MgCl_2{\cdot}6H_2O$, 200 mg $MnCl_2{\cdot}4H_2O$, and 20 mg $CoCl_2{\cdot}6H_2O$).

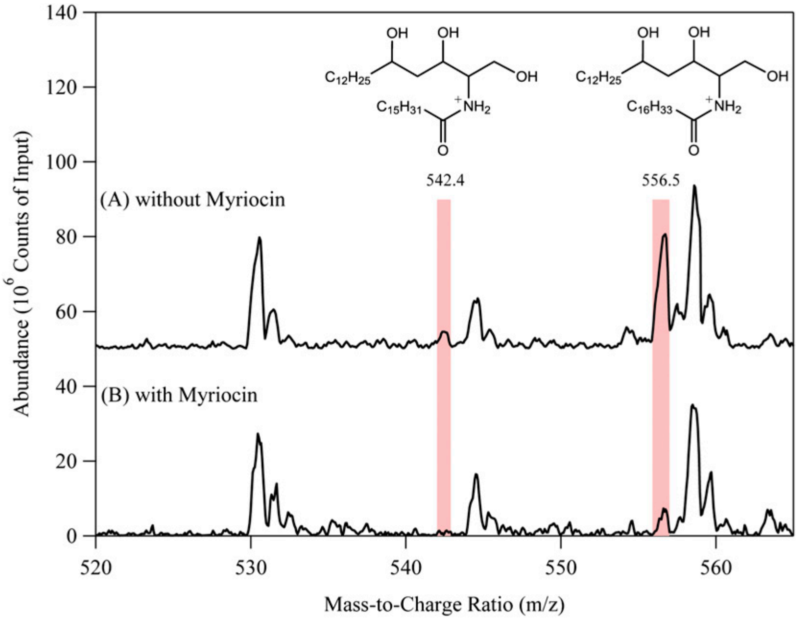

Fig. S1. Myriocin-treated *B. fragilis* cells have diminished sphingolipid production. Electrospray ionization mass spectra (ESI/MS) of lipids extracted from wild-type *B. fragilis* cells that were grown (*A*) without or (*B*) with added myriocin. In presence of myriocin, the relative abundances of the molecules represented by the two peaks at *m/z* 542.4 and 556.5 in ESI/MS are greatly reduced. The reduction of the peak area is calculated to be 77% and 68%, respectively. Further analyses of these two peaks by tandem mass spectra (Figs. S2 and S3) show that they stand for ceramide-like structures (phytoceramide). ESI/MS was performed with three separate 5-μL injections of samples into the ionization chamber of a mass spectrometer (Thermo Finnigan TSQ 7000). The ESI/MS is a triple quadrupole mass spectrometer, operating under positive ionization mode.

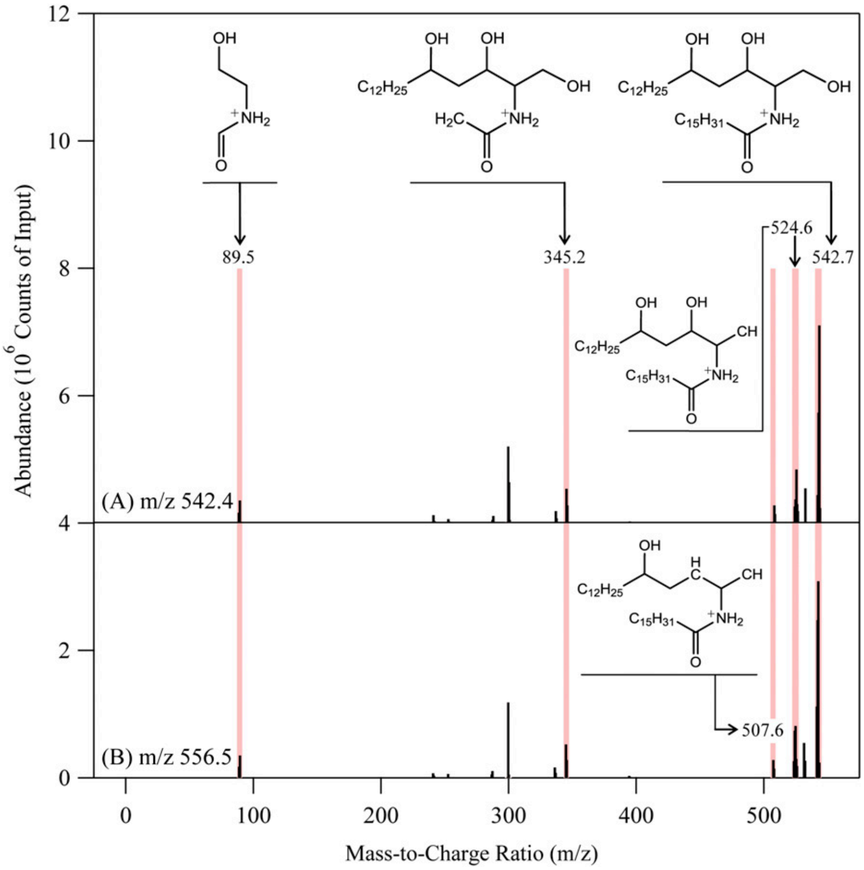

Fig. S2. Tandem mass spectra of the peaks at (*A*) *m/z* = 542.4 and (*B*) *m/z* = 556.5 acquired at 15 eV. Only one structure is proposed for each ion fragment. Isomeric structures are not shown.

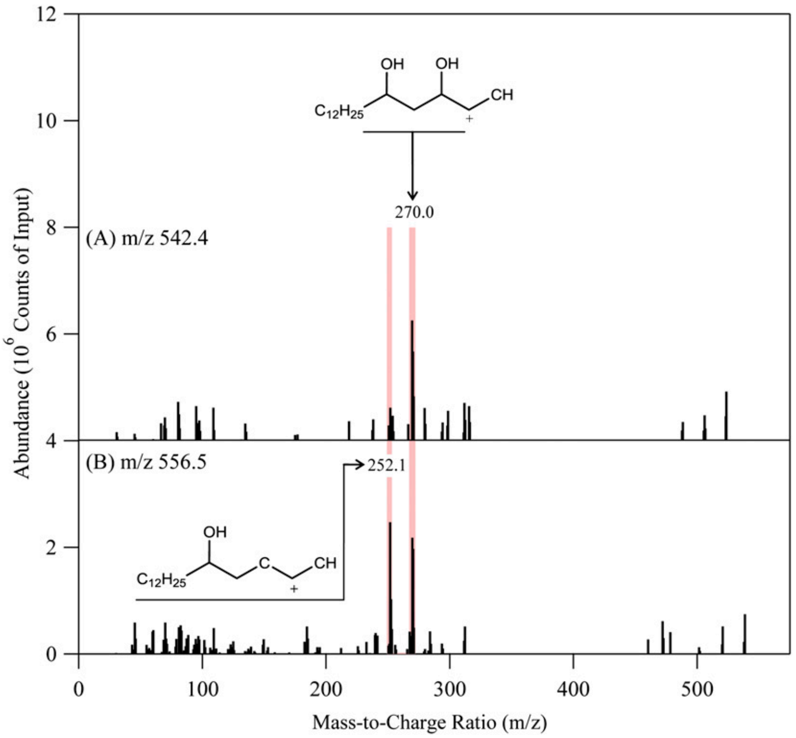

Fig. S3. Tandem mass spectra of the peaks at (*A*) *m/z* = 542.4 and (*B*) *m/z* = 556.5 acquired at 35 eV and 40 eV, respectively. Only one structure is proposed for each ion fragment. Isomeric structures are not shown.

Table S1. Conservation of serine palmitoyl transferase orthologs in *Bacteroides* and related genera

Organisms	Score	E value
Porphyromonas gingivalis W83 [CFB group bacteria] taxid 242619	192	5E-47
Porphyromonas gingivalis ATCC 33277 [CFB group bacteria] taxid 431947	191	7E-47
Porphyromonas endodontalis ATCC 35406 [CFB group bacteria] taxid 553175	189	2E-46
Parabacteroides merdae ATCC 43184 [CFB group bacteria] taxid 411477	187	1E-45
Bacteroides caccae ATCC 43185 [CFB group bacteria] taxid 411901	187	1E-45
Bacteroides finegoldii DSM 17565 [CFB group bacteria] taxid 483215	187	1E-45
Parabacteroides johnsonii DSM 18315 [CFB group bacteria] taxid 537006	187	2E-45
Bacteroides ovatus ATCC 8483 [CFB group bacteria] taxid 411476	187	2E-45
Bacteroides sp. D2 [CFB group bacteria] taxid 556259	186	2E-45
Prevotella veroralis F0319 [CFB group bacteria] taxid 649761	186	3E-45
Bacteroides sp. D1 [CFB group bacteria] taxid 556258	186	4E-45
Bacteroides sp. 2_1_22 [CFB group bacteria] taxid 469588	186	4E-45
Bacteroides sp. 2_2_4 [CFB group bacteria] taxid 469590	186	4E-45
Bacteroides sp. 2_1_7 [CFB group bacteria] taxid 457388	181	6E-44
Parabacteroides distasonis ATCC 8503 [CFB group bacteria] taxid 435591	181	6E-44
Parabacteroides sp. D13 [CFB group bacteria] taxid 563193	181	6E-44
Bacteroides sp. 2_1_33B [CFB group bacteria] taxid 469589	181	6E-44
Bacteroides fragilis NCTC 9343 [CFB group bacteria] taxid 272559	179	4E-43
Bacteroides sp. 3_2_5 [CFB group bacteria] taxid 457392	179	4E-43
Bacteroides sp. 2_1_16 [CFB group bacteria] taxid 469587	179	4E-43
Bacteroides fragilis YCH46 [CFB group bacteria] taxid 295405	179	4E-43
Prevotella bivia JCVIHMP010 [CFB group bacteria] taxid 553171	177	1E-42
Prevotella bergensis DSM 17361 [CFB group bacteria] taxid 585502	177	1E-42
Bacteroides fragilis 3_1_12 [CFB group bacteria] taxid 457424	176	3E-42
Bacteroides eggerthii DSM 20697 [CFB group bacteria] taxid 483216	175	4E-42
Bacteroides stercoris ATCC 43183 [CFB group bacteria] taxid 449673	175	6E-42
Sphingobacterium spiritivorum ATCC 33300 [CFB group bacteria] taxid 525372	173	2E-41
Sphingobacterium spiritivorum ATCC 33861 [CFB group bacteria] taxid 525373	173	2E-41
Sphingobacterium spiritivorum [CFB group bacteria] taxid 258	173	2E-41
Bacteroides uniformis ATCC 8492 [CFB group bacteria] taxid 411479	172	3E-41
Prevotella tannerae ATCC 51259 [CFB group bacteria] taxid 626522	172	4E-41
Prevotella melaninogenica ATCC 25845 [CFB group bacteria] taxid 553174	172	5E-41
Pedobacter heparinus DSM 2366 [CFB group bacteria] taxid 485917	172	6E-41
Pedobacter sp. BAL39 [CFB group bacteria] taxid 391596	171	1E-40
Bacteroides sp. D20 [CFB group bacteria] taxid 585543	171	1E-40
Chitinophaga pinensis DSM 2588 [CFB group bacteria] taxid 485918	169	2E-40
Bacteroides thetaiotaomicron VPI-5482 [CFB group bacteria] taxid 226186	168	6E-40
Bacteroides sp. 1_1_6 [CFB group bacteria] taxid 469586	168	6E-40
Bacteroides coprocola DSM 17136 [CFB group bacteria] taxid 470145	168	8E-40
Bacteroides intestinalis DSM 17393 [CFB group bacteria] taxid 471870	167	8E-40
Bacteroides cellulosilyticus DSM 14838 [CFB group bacteria] taxid 537012	167	8E-40
Prevotella copri DSM 18205 [CFB group bacteria] taxid 537011	167	9E-40
Bacteroides dorei DSM 17855 [CFB group bacteria] taxid 483217	167	1E-39
Bacteroides sp. 9_1_42FAA [CFB group bacteria] taxid 457395	167	1E-39
Bacteroides dorei 5_1_36/D4 [CFB group bacteria] taxid 556260	167	1E-39
Bacteroides sp. 3_1_33FAA [CFB group bacteria] taxid 457391	167	1E-39
Bacteroides vulgatus ATCC 8482 [CFB group bacteria] taxid 435590	167	1E-39
Bacteroides sp. 4_3_47FAA [CFB group bacteria] taxid 457394	167	1E-39

Homology is compared with human serine palmitoyl transferase enzyme subunit SPTLC1 by BLASTP (2.2.22+) standard search. CFB, *Cytophaga-Flavobacteria-Bacteroides*.