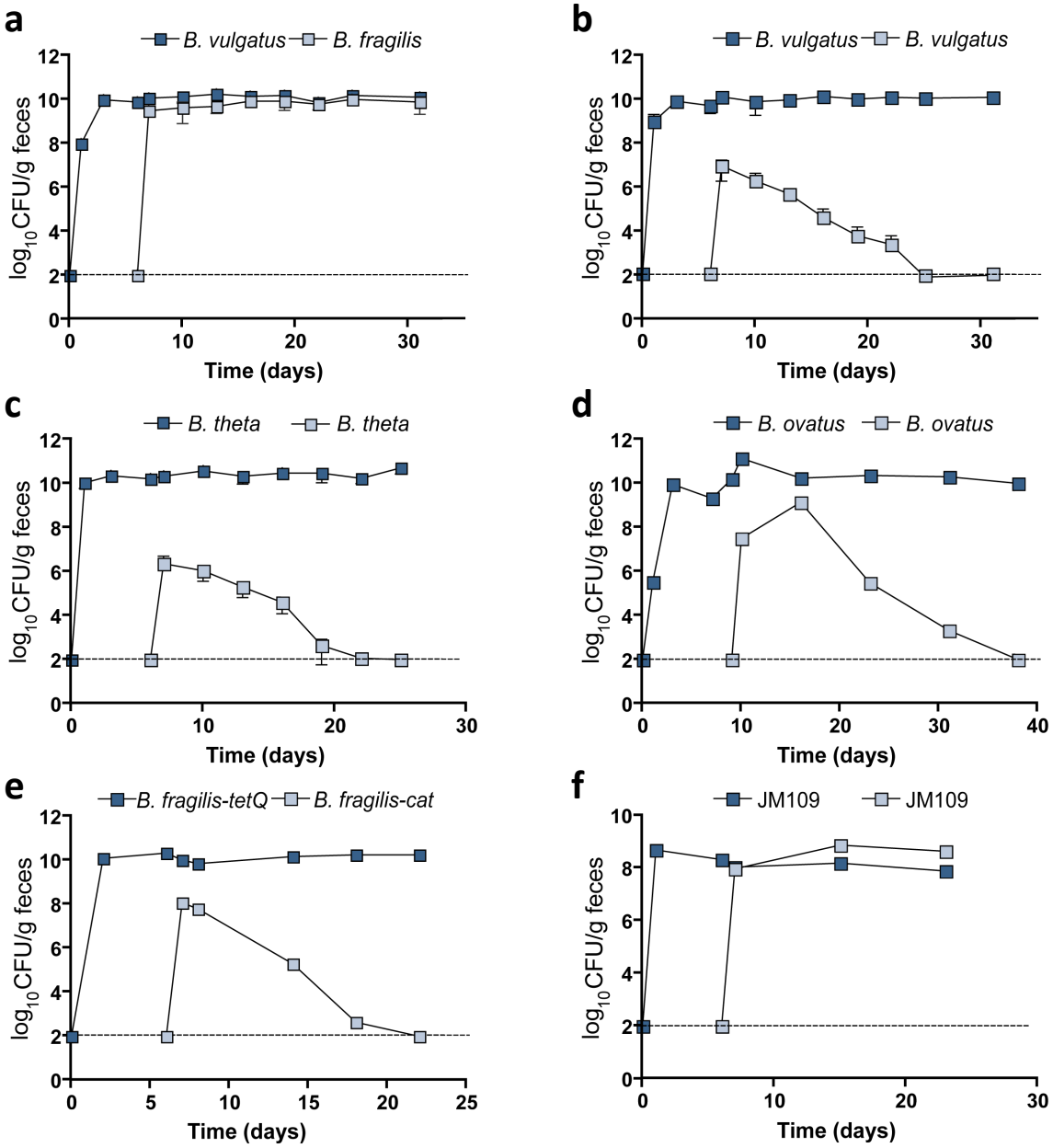
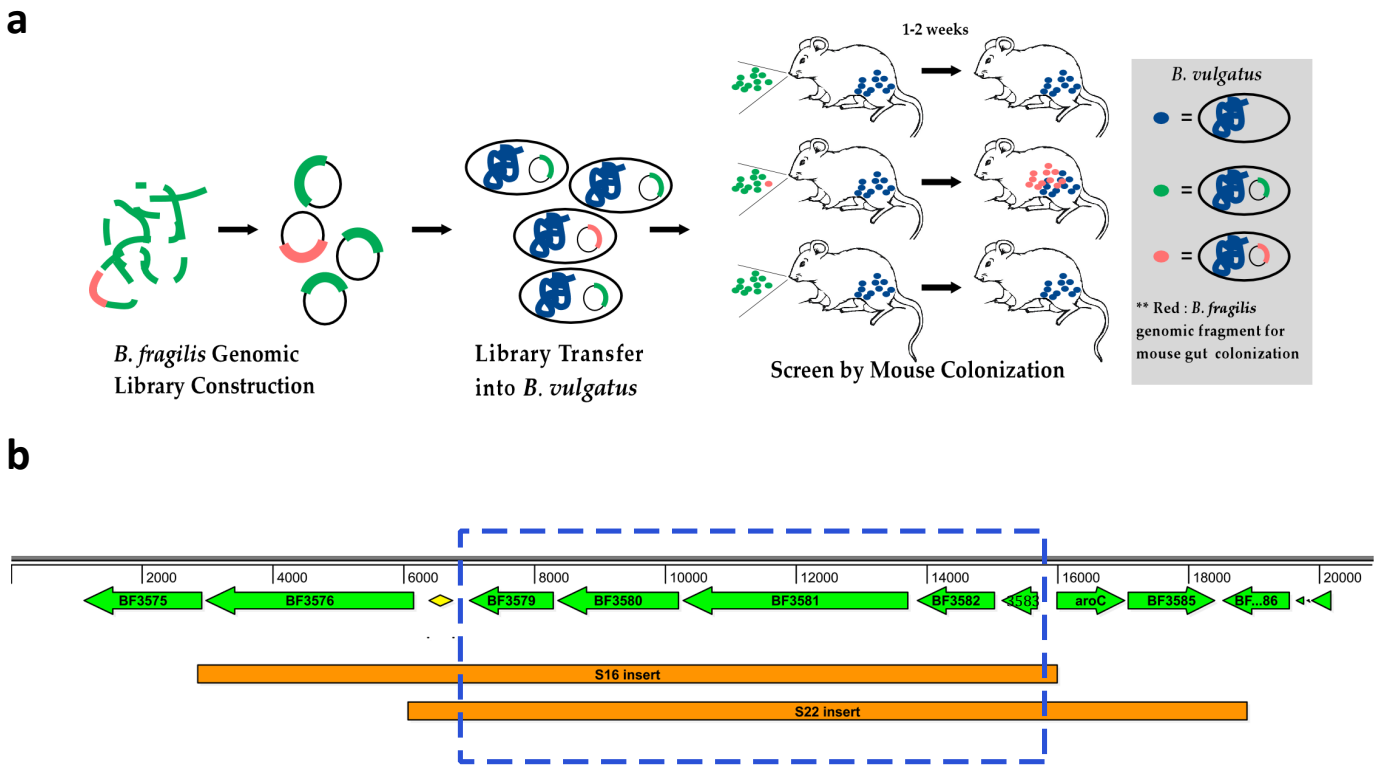
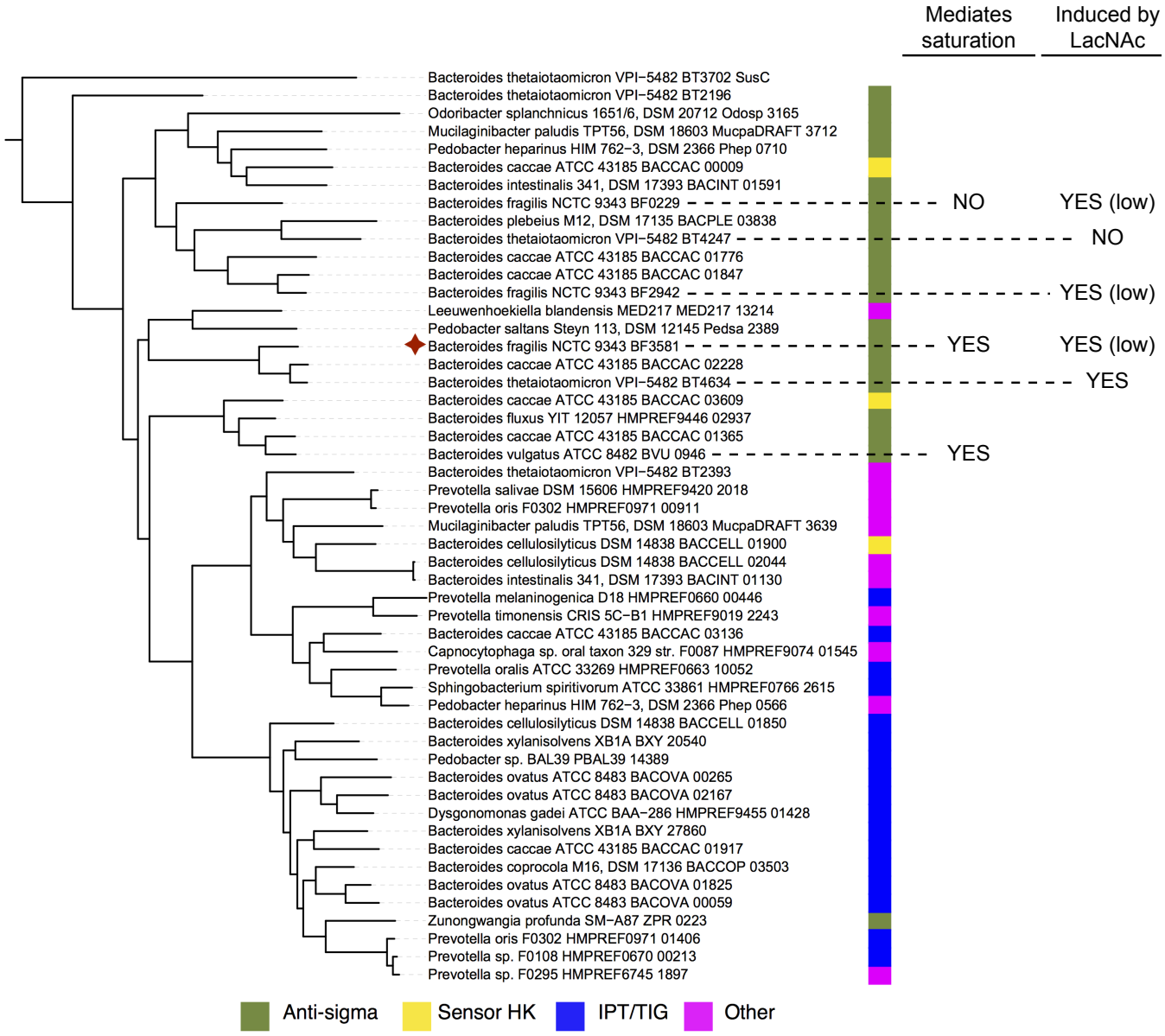
doi:10.1038/nature12447



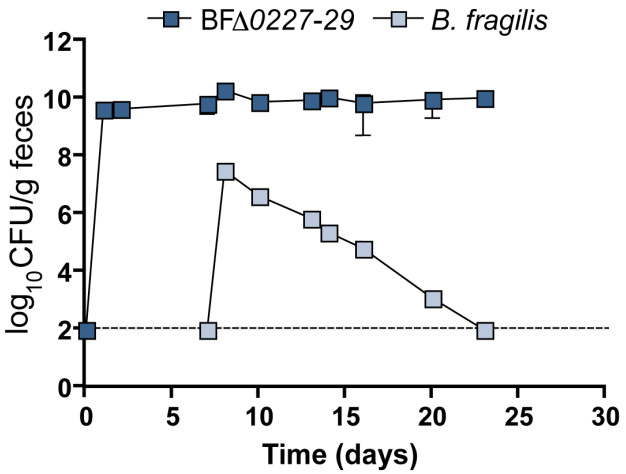
Supplementary Figure 1. a-d, Sequential colonization profiles reveal that *Bacteroides* species exhibit saturable niche colonization. Germ-free Swiss Webster (SW) mice were mono-associated with a chloramphenicol resistant (Cm^r) bacterial strain containing pFD340-*cat* for 6-9 days and subsequently challenged orally with ~10^8 CFU of tetracycline resistant (Tet^r) bacterial strain containing pFD340-*tetQ* (see legend for species). CFU was determined by plating serial dilutions of homogenized feces on BHIS agar plate with either Cm or Tet selection to distinguish strains. In each panel, initial (dark blue) and challenge (light blue) strains are shown. **e**, Germ-free SW mice were mono-associated with *B. fragilis* pFD340-*tetQ* for 6 days and subsequently challenged with ~10^8 CFU of *B. fragilis* pFD340-*cat*. This is the reverse order of colonization compared to Fig. 1c. **f,** Germ-free SW mice were mono-associated with *E. coli* JM109 containing pNJR6 (kanamycin resistant) for 6 days and subsequently challenged with ~10^8 CFU of *E. coli* JM109 containing pFD340 (ampicillin resistant). In all panels, dashed line indicates the limit of detection at 100 CFU/g feces. Results are representative of at least 2 independent trials per experiment (n=1-3 animals/group). Error bars indicate SD.



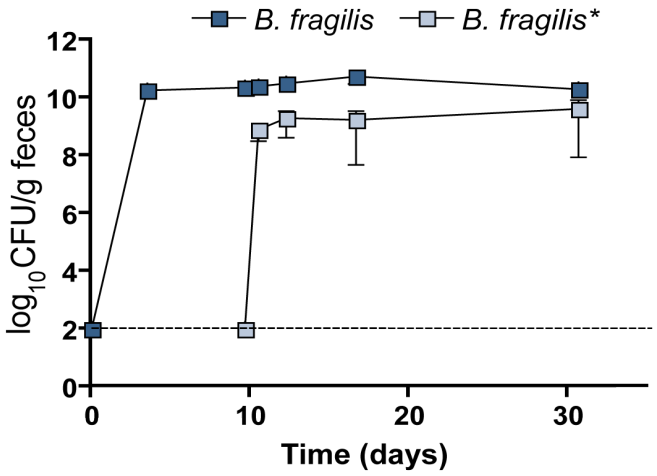
Supplementary Figure 2. a, Schematic of functional *in vivo* screen of the *B. fragilis* genome for mouse gut colonization. 9-10 kb fragments of *B. fragilis* genomic DNA generated by partial digestion with *Sau3*AI were ligated into the *E. coli-Bacteroides* shuttle plasmid pFD340-*catBII* (Cm^r). Each individual clone was conjugally transferred into *B. vulgatus*, generating a library of *B. vulgatus* strains carrying a unique *B. fragilis* genomic DNA fragment. The library was screened for *B. fragilis*-specific niche colonization phenotype in animals mono-associated with *B. vulgatus*. **b,** Of 2,100 clones screened, only 2 persisted in mice after 30 days. The minimal genetic element common to the two clones (named S16 and S22) that displayed a colonization phenotype from the *in vivo* screen contains 5 hypothetical open reading frames: BF3583, BF3582, BF3581, BF3580 and BF3579.



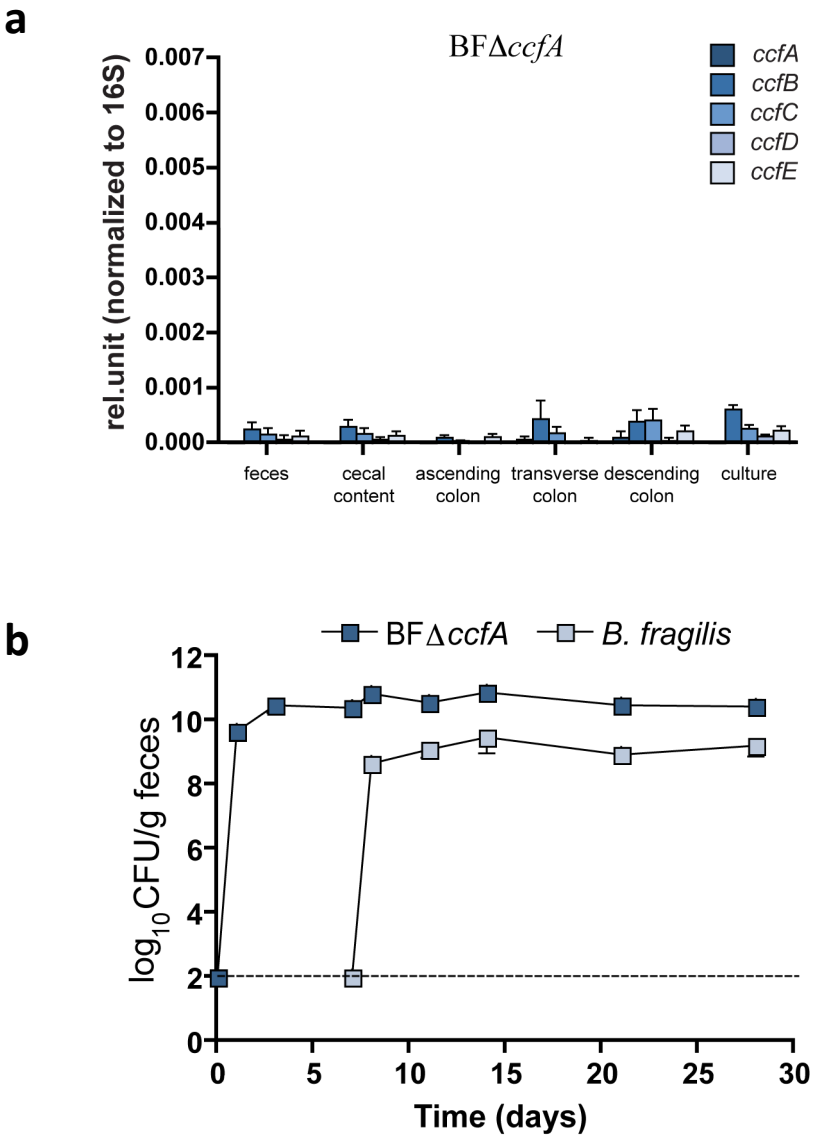
Supplementary Figure 3. Phylogenetic tree of CCF homologs based on similarity to BF3581 and BF3580 in the phylum *Bacteroidetes*. Labels indicate the locus ID of the BF3581 homologs. Amino acid sequences of BF3581 and BF3580 were used to query sequenced genomes using JGI's Integrated Microbial Genomes site[1]. Hits with expected values less than 10^{-10} were examined for operon organization resemblance to BF3579-BF3583. For inclusion in the tree, candidate operons were required to have a downstream BF3579 homolog with at least one of either the F5/F8 Type C domain (pfam00754) or DUF1735 (pfam08522), which are present in BF3579. Also, candidate operons were required to have one of the following transmembrane regulatory domains: anti-sigma factors, IPT/TIG domain-containing transmembrane proteins (pfam01833), sensor histidine kinases, and transmembrane 6-bladed NHL-repeat beta-propellers (pfam01436). The canonical *sus* operon (BT3702) from *B. thetaiotaomicron* is included as an outgroup for comparison to distantly related genes. Operons from redundant strains of single species and the 22 draft genomes of unnamed *Bacteroides* sp. isolates were not included. Amino acid sequences of BF3581 and BF3580 homologs were concatenated and locally aligned using MUSCLE[2]. The tree was constructed using PhyML[3] and displayed using iTOL[4]. Functional results from the animal colonization experiments and the gene expression during growth on N-acetyllactosamine (LacNAc) are summarized to the right of the tree for those operons tested (see main text for more details).



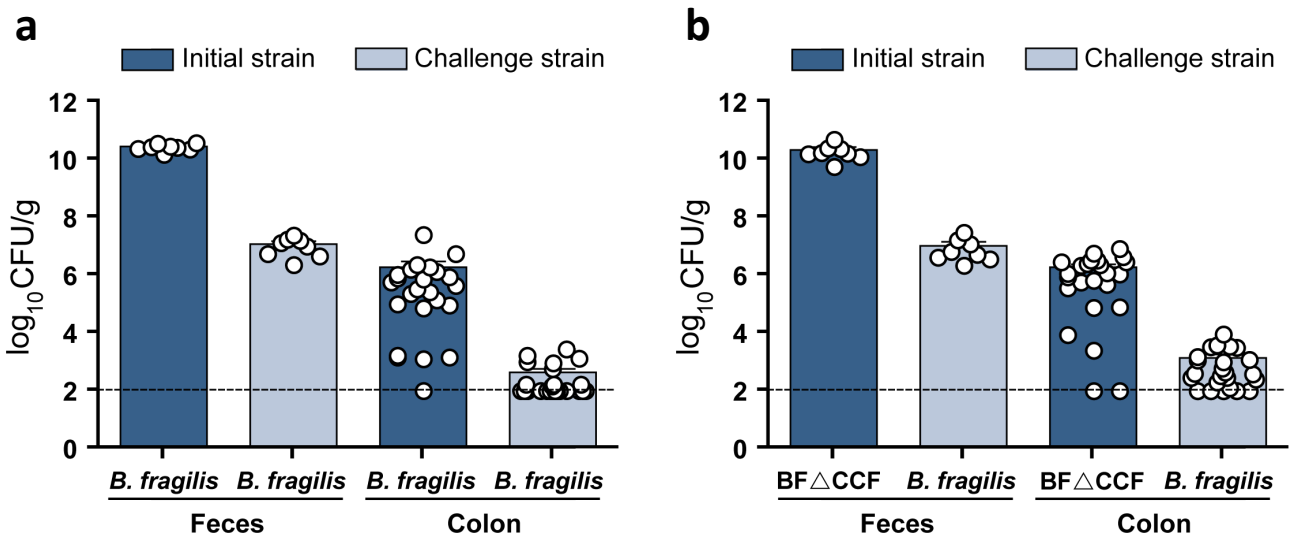
Supplementary Figure 4. Saturable niche colonization is specific to the identified operon and not the nearest *B. fragilis* homolog. Germ-free mice were mono-associated with a BF0227-BF0229 deletion mutant *B. fragilis* strain containing pFD340-*cat* (Cm^r) for 7 days and subsequently challenged orally with ~10^8 CFU of wild-type *B. fragilis* containing pFD340-*tetQ* (Tet^r). CFU was determined by serial dilution plating of fecal homogenate on BHIS plate with either Cm or Tet. Dashed line indicates the limit of detection at 100 CFU/g feces (n=2 animals/group). Results are representative of 2 independent trials (n=2 animals/group). Error bars indicate SD.



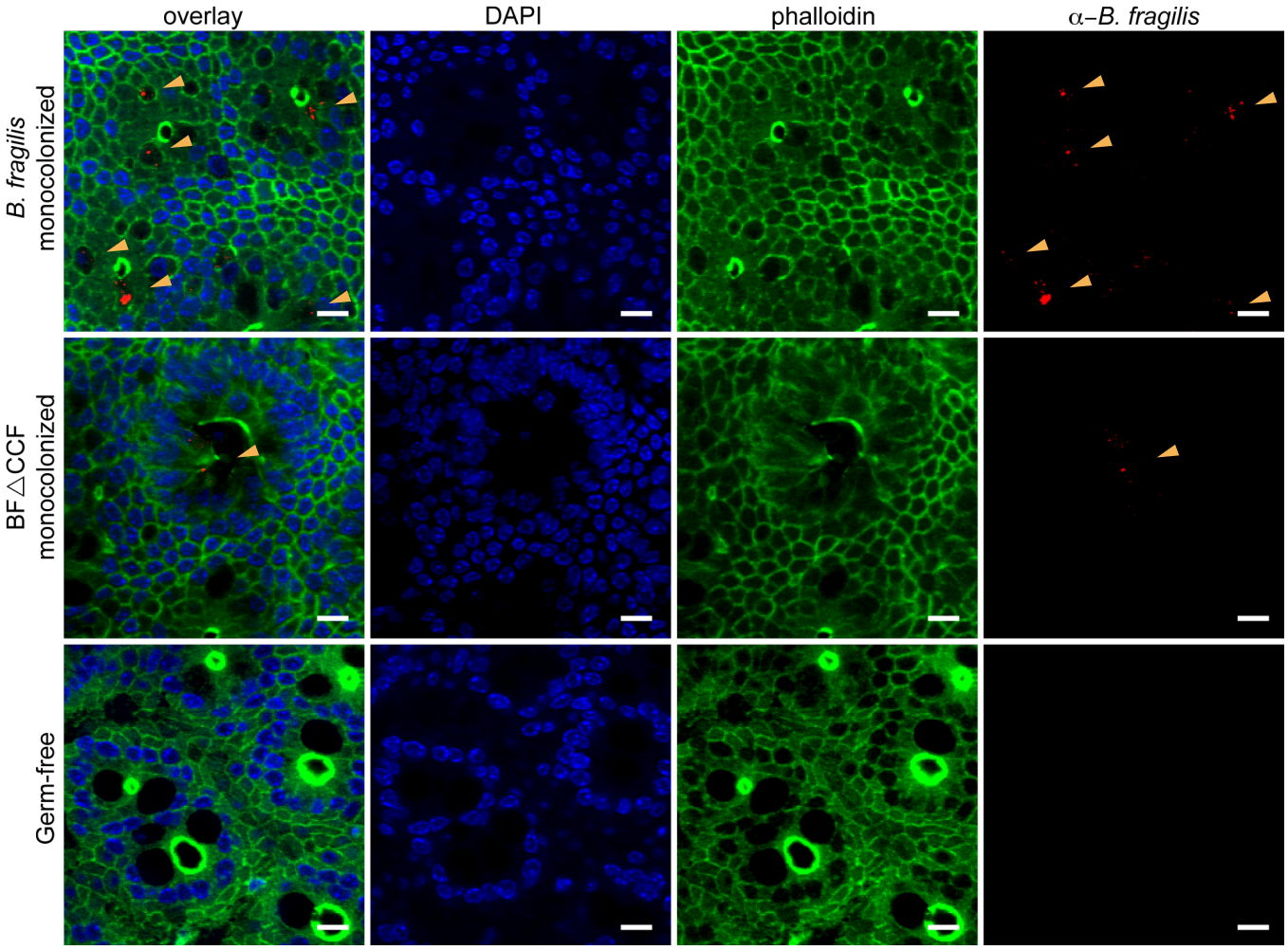
Supplementary Figure 5. Germ-free mice were mono-associated with WT *B. fragilis* pFD340-*cat* for 10 days and subsequently challenged orally with 1x10^8 CFU of *B. fragilis* pFD340-*tetQ* harvested from cecal content (*) of a donor mouse (n=3 animals/group, 1 donor). CFU was determined by serial dilution plating of fecal homogenate on BHIS plate with either Cm or Tet. Dashed line indicates the limit of detection at 100 CFU/g feces. Results are from 3 independent experiments. All error bars indicate SD.



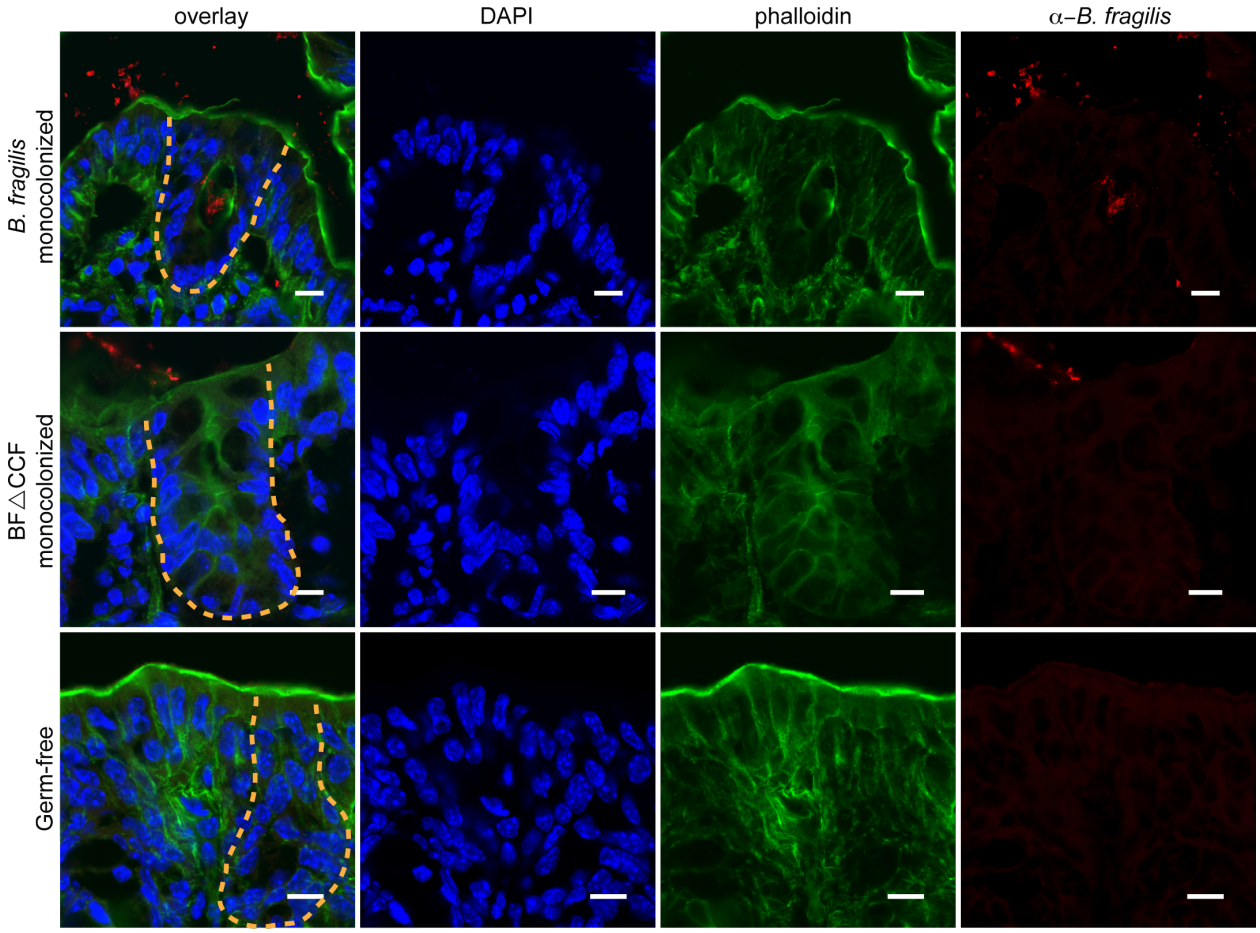
Supplementary Figure 6. a, *ccfA* regulates gene expression and colonization resistance. qRT-PCR of *ccf* gene expression levels from *B. fragilis*Δ*ccfA* (in-frame *ccfA* deletion) mono-associated animal feces, cecal content and colon tissues (n=3 animals/group) and culture. The y-axis range was fixed according to Figure 2a. Error bars indicate SEM. **b**, Fecal bacterial colonization levels measured from germ-free mice mono-associated with *B. fragilis*Δ*ccfA* and subsequently challenged with 10^8 CFU of WT *B. fragilis.* Error bars indicate SD.



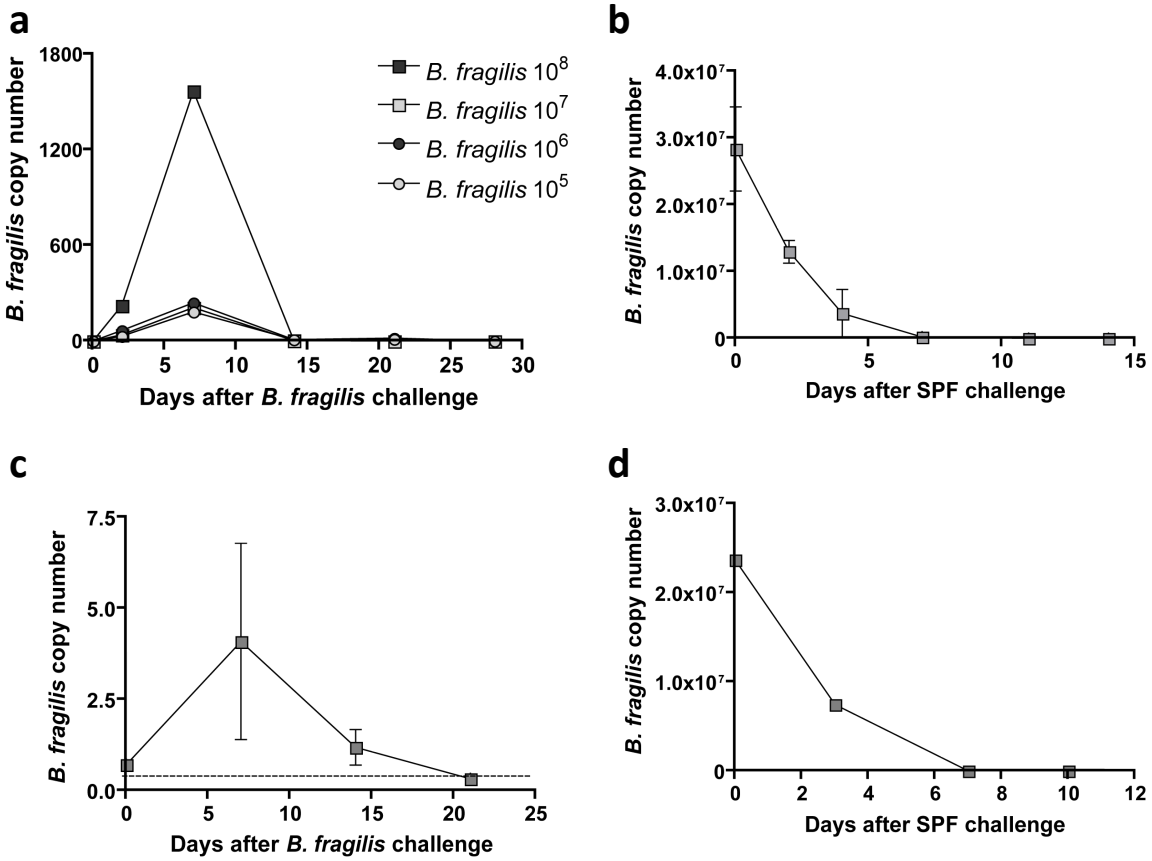
Supplementary Figure 7. a-b, CFU data for Fig. 2b showing that WT *B. fragilis* inhibits mucosal association of challenge bacteria better than *B. fragilis*ΔCCF. Germ-free Swiss Webster mice were mono-associated with (**a**) WT *B. fragilis* or (**b**) *B. fragilis*ΔCCF strain for 1 week and subsequently challenged with ~10^8 CFU of WT *B. fragilis* by oral gavage. Feces and colon tissues were harvested 24 hrs after the challenge and homogenized in PBS for CFU determination. Mucus layer was scraped off from the tissue before homogenization (n = 8 animals/group). Dashed line indicates the limit of detection at 100 CFU/g feces. Each symbol represents one stool or colon tissue sample.



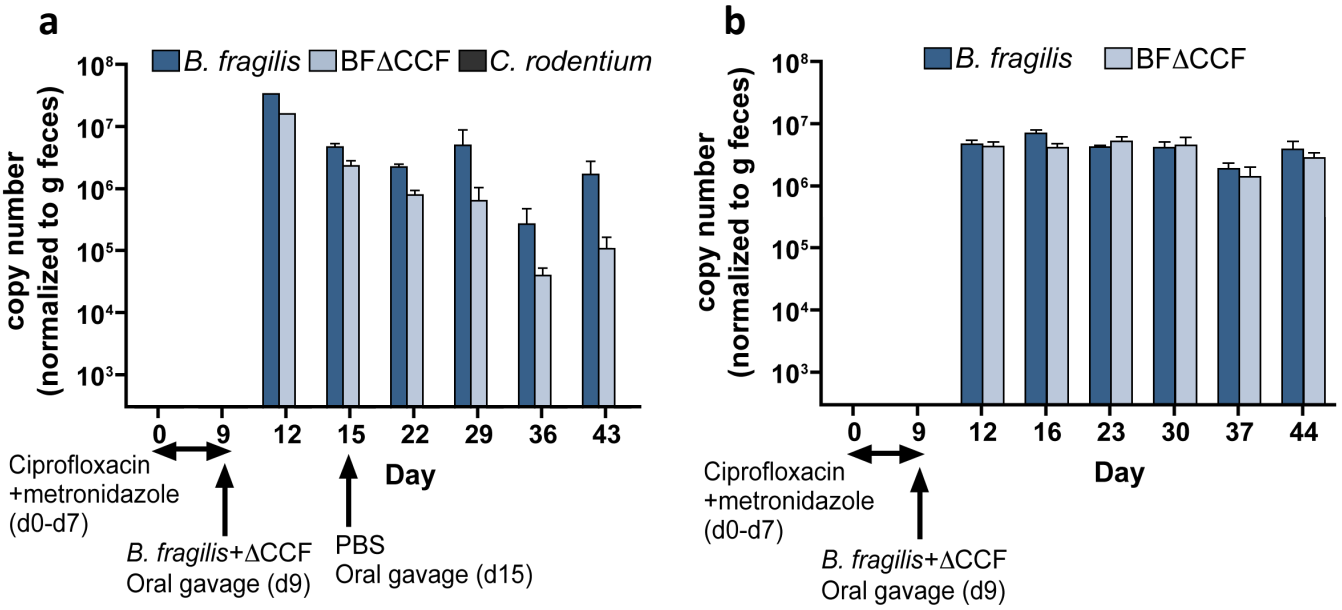
Supplementary Figure 8. WT *B. fragilis* is physically associated with colonic crypts. Confocal micrographs of fixed whole-mount colon tissue from germ-free, WT *B. fragilis* or *B. fragilis*ΔCCF mono-associated mice. Colonic crypts are visualized by DAPI (nuclei, blue) and phalloidin (F-actin, green). Bacteria (red, arrowheads) are visualized by IgY polyclonal antibody raised against *B. fragilis*. Images are representative of seven different sites analyzed from at least two different colons. Scale bar: 10 μm.



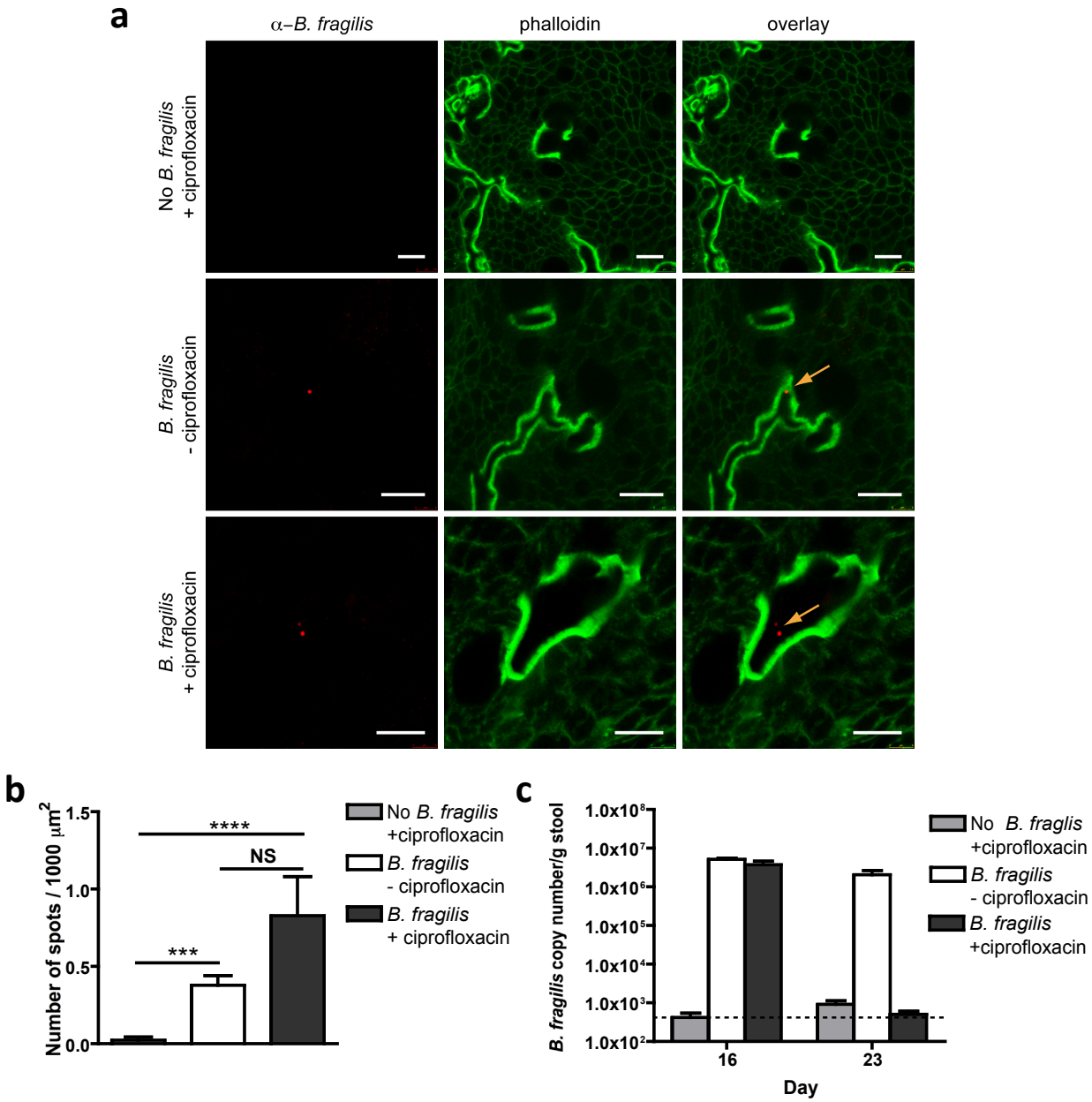
Supplementary Figure 9. WT *B. fragilis* is physically associated with colonic crypts. Cross-section view of confocal micrographs of frozen colon tissue sections from germ-free, WT *B. fragilis* or *B. fragilis*ΔCCF mono-associated mice. The colon crypts are outlined (dashed line) and stained with DAPI (nuclei, blue) and phalloidin (F-actin, green). Bacteria (red) are visualized by IgY polyclonal antibody raised against *B. fragilis*. Scale bar: 10 μm.



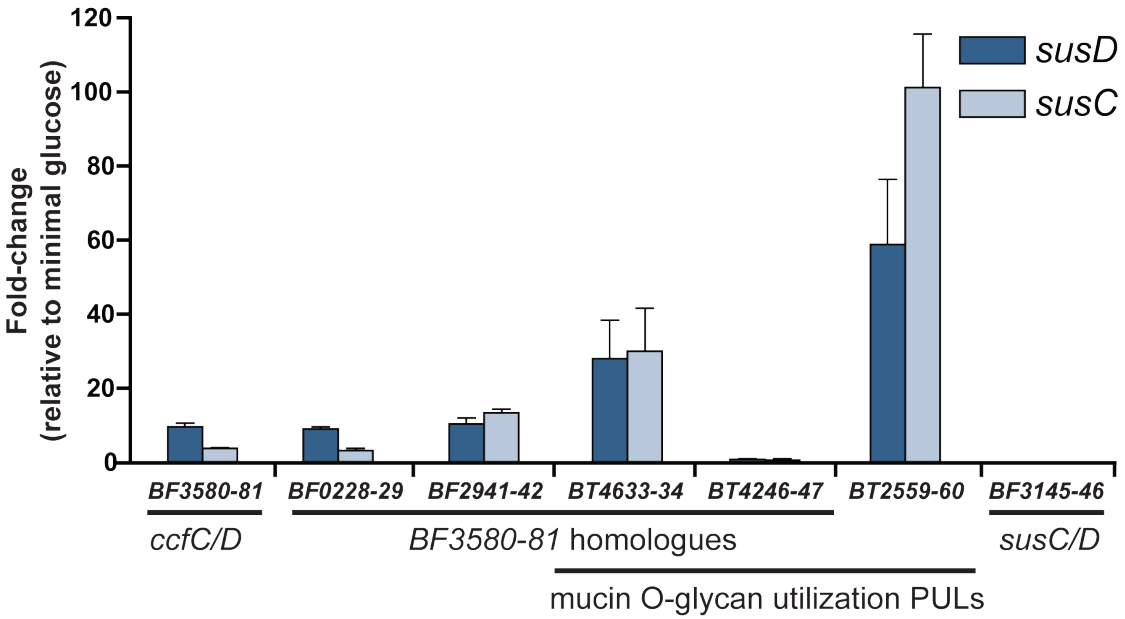
Supplementary Figure 10. *B. fragilis* does not colonize SPF mice. Bacterial colonization levels as relative copy number was determined by fecal DNA qPCR for the following animal experiments: **a,** SPF SW mice were challenged with 10^8, 10^7, 10^6, or 10^5 CFU of *B. fragilis* by oral gavage. **b,** Germ-free SW mice were mono-associated with *B. fragilis* for 2 weeks and orally challenged with cecal content from SPF SW mice. **c,** SPF C57BL/6 mice were challenged with 10^8 CFU of *B. fragilis* by oral gavage. **d,** C57BL/6 mice mono-associated with *B. fragilis* from birth were orally challenged with cecal content from SPF C57BL/6 mice. Dashed line indicates the limit of detection set by the no-template control. Results are representative of 2 independent trials (n=2 animals/group). Error bars indicate SEM.



Supplementary Figure 11. a, Real-time qPCR analysis of bacterial colonization levels in feces from SPF mice that were antibiotic treated to allow co-association with WT *B. fragilis* and *B. fragilis*ΔCCF. After 6 days, mice were orally gavaged with PBS (n=4 animals/group). Compare results to Fig. 3e, where *Citrobacter rodentium* was given, showing CCF phenotype is dependent on perturbation. **b**, Real-time qPCR analysis of bacterial colonization levels in feces from SPF mice that were antibiotic treated and co-associated with WT *B. fragilis* and *B. fragilis*ΔCCF (n=4 animals/group). Compare results to Fig. 3f, where a second round of antibiotic was given, showing CCF phenotype is dependent on perturbation. Results are representative of at least 2 independent trials per experiment. Error bars indicate SEM.



Supplementary Figure 12. WT *B. fragilis* occupies crypts even during antibiotic treatment that clears bacteria from feces. **a,** Confocal micrographs of fixed whole-mount colon tissues from *B. fragilis* colonized SPF mice that were treated with ciprofloxacin in drinking water (1 mg/ml) for 7 days. Crypts were visualized by phalloidin (F-actin, green) and bacteria (red) were stained with IgY polyclonal antibody raised against *B. fragilis*. Arrows show *B. fragilis* in crypts. Scale bar: 10 µm. **b**, Quantification of the proportion of crypts associated with bacteria identified by *B. fragilis* signal level above threshold from z-stacks. Error bars indicate SEM. ND: not detected. ***p<0.001. ****p<0.0001. **c**, qPCR analysis of the *B. fragilis* copy numbers from stool DNA at the beginning (day 16) and at the end of the ciprofloxacin treatment (day 23). Animals were sacrificed and colon tissues were fixed for immunofluorescence staining on day 23. Dashed line indicates the limit of detection set by the no template control. Error bars indicate SEM.



Supplementary Figure 13. *In vitro* induction of *ccf* genes and other polysaccharide utilization loci (PULs). qRT-PCR analsis of *susC/D* gene expression in response to N-acetyllactosamine (LacNAc) in minimal medium compared to glucose during growth of *B. thetaiotaomicron* and *B. fragilis*. *BF3580-81* homologs from *B. fragilis* and *B. thetaiotaomicron* were selected based on the phylogenetic tree in Supplementary Figure 3. Of these homologs, *BT4633-34* and *BT4246-47* are part of PULs that respond to mucin O-glycans as substrates. *BT4633-34* and *BT2559-60* are specifically induced by LacNAc diasaccharide whereas *BT4246-47* respond to core 1 disaccharide[5]. The canonical *sus* genes from *B. fragilis* (*BF3145-46*) are included as a negative control. Results are representative of 2 independent experiments. Error bars indicate SEM from triplicate cultures.

$$N = \frac{\ln(1-P)}{\ln(1-\frac{i}{G})} = \frac{\ln(1-P)}{\ln(1-\frac{9.5\times10^{3}}{5.2\times10^{6}})} = 2100$$

$$P = 0.979$$

Supplementary Equation 1. Optimal number of clones in the genomic library[6]. P denotes the probability of isolating a particular DNA sequence. The total number of clones screened (N) is 2100; average insert size (i) is 9.5 kb and the *B. fragilis* genome size (G) is $5.2\text{x}10^6$ bp.

Supplementary References

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Supplementary Table 1. Strains and plasmids used in this study.

Strain or plasmid	Description	Reference or source
E. cloni® 10G	F- *mcrA Δ(mrr-hsdRMS-mcrBC) endA1 recA1 Φ80dlacZΔM15 ΔlacX74 araD139 Δ(ara,leu)7697 galU galK rpsL nupG λ- tonA*; Standard cloning strain	Lucigen
E. coli JM109	F`[*traD36 proA+B+ laclq* Δ*(lacZ)M15*] Δ*(lac-proAB) glnV44 (supE44) e14- (McrA-) thi gyrA96 (NalR) endA1 hsdR17(rk-mk+) relA1 recA1*; standard cloning strain	Zymo Research
Bacteroides fragilis NCTC 9343	Type strain	[1]
B. fragilis 9343ΔPSA Δ*mpi*.off (CPM1)	*B. fragilis* 9343ΔPSA mutant with chromosomal deletion of 534-of 591-bp in the *mpi* gene; invertible promoters for PSA, PSB, and PSD-H all in "off" orientation	[2]
B. fragilis 9343Δ*ccfA*	*B. fragilis* 9343 mutant with chromosomal deletion in *ccfA* gene (BF3583); 312 bp of the 579-bp *ccfA* gene removed	This study
B. fragilis 9343Δ*ccfC*	*B. fragilis* 9343 mutant with chromosomal deletion in *ccfC* gene (BF3581); 2148 bp of the 3477-bp *ccfC* gene removed	This study
B. fragilis 9343Δ*ccfD*	*B. fragilis* 9343 mutant with chromosomal deletion in *ccfD* gene (BF3580); 1086 bp of the 1887-bp *ccfD* gene removed	This study
B. fragilis 9343Δ*ccfE*	*B. fragilis* 9343 mutant with chromosomal deletion in *ccfE* gene (BF3579); 1006 bp of the 1323-bp *ccfE* gene removed	This study
B. fragilis 9343Δ*ccfC-E* (*B. fragilis*ΔCCF)	*B. fragilis* 9343 mutant with chromosomal deletion of CCF operon in biosynthesis genes *ccfC-E* (BF3581-79); 6059 bp removed	This study
B. fragilis 9343Δ*BF0227-29*	*B. fragilis* 9343 mutant with chromosomal deletion of BF0227-29); 6664 bp removed	This study
B. vulgatus ATCC 8482	Type strain	[3]
*B. vulgatus*Δ*ccfC-E* (*B. vulgatus*ΔCCF)	*B. vulgatus* mutant with chromosomal deletion of CCF operon in biosynthesis genes *ccfC-E* (BVU946-8); 6304 bp removed	This study
B. vulgatus::BFCCF	*B. vulgatus* complemented with *B fragilis* CCF operon. Clone S16 isolated from the *in vivo* chromosomal library screen.	This study
*B. fragilis*ΔCCF::BFCCF	*B. fragilis*ΔCCF complemented with *B fragilis* CCF operon. BFCCF plasmid isolated from clone S16 and transformed into *B. fragilis*ΔCCF.	This study
B. thetaiotaomicron ATCC 29148	Type strain; VPI-5482	[4]
B. ovatus ATCC 8483	Type strain	[3]
Citrobacter rodentium DBS100	Type strain; ATCC 51459	[5]
pNJR6	*Bacteroides* suicide vector; mob^+ Tra^- Km^r (*E. coli*) Em^r (*Bacteroides*)	[6]
R751	Mobilizable mating plasmid to move constructs from *E. coli* to *Bacteroides*; Tra^+ Tp^r	[7]
RK231	Mobilizable mating plasmid to move constructs from *E. coli* to *Bacteroides*, RK2 derivative; Tra^+ Tet^r Km^r	[8]
pFD340	*E. coli-Bacteroides* shuttle vector, IS4351 promoter; Amp^r (*E. coli*) Em^r (*Bacteroides*)	[9]
pFD340-*cat*	Modified pFD340 plasmid containing *cat* gene PCR amplified from *E. Coli* K12/pACYC184 (accession #: X06403) cloned into a *Sma*I site; Amp^r (*E. coli*) Cm^rEm^r (*Bacteroides*)	[2]
pFD340-*cat*BII	*E.coli-Bacteroides* shuttle vector containing IS4351-*cat* cassette PCR amplified from pFD340-*cat*, *Bgl*II restriction site encoded at the 5'-end by PCR primer, and cloned into *Bam*HI/*Pst*I digested	This study

	and blunted pFD340 backbone; Amp^r (*E. coli*) Cm^{r}Em^r (*Bacteroides*)	
pFD340-*tetQ*	Modified pFD340 plasmid containing *tetQ* gene PCR amplified from *Parabacteroides merdae* ATCC 43184 cloned into *Bam*HI/*Kpn*I site; Amp^r (*E. coli*) Tet^{r}Em^r (*Bacteroides*)	This study

Supplementary Table 2. Sequences of primers used in this study.

Primers used for cloning recombinant genes and generating deletion constructs (bold: 5' addition)

Primer name	Sequence	Purpose
IS4351-F2	**AAAGATCT**GAAAGAGAGACAATGTCCCC	clone IS4351-*cat*
cat2-X	**AACTCGAG**CGAATTTCTGCCATTCATCCG	clone IS4351-*cat*
tetQ-F2	**AAGGATCC**GTAATCGTTATGCGGCAGTAATAATA TACA	clone *tetQ*
tetQ-R	**AAGGTACC**GAGCTCGTCTATTTTTTTATTGCCAAG	clone *tetQ*
delBF3583L_F	**CTGTCGAC**CGAGGGAAGCATCACTTCAT	delete *ccfA* – left flank
delBF3583L_R	**TTCCCGGTAT**TCTCCCAGACAGCGAGAGAT	delete *ccfA* – left flank
delBF3583R_F	**GTCTGGGAGA**ATACCGGGAATATAGCCATGC	delete *ccfA* – right flank
delBF3583R_R	**ATGTCGAC**TTGTGATACGTCCGTCGGTA	delete *ccfA* – right flank
delBF3581L_F	**GTGGATCC**TAGTTAAACTGACCGAACGATTGA	delete *ccfC* – left flank
delBF3581L_R	**TGCCATTAC**TTTTACCCGGAATAAAATTCTTGA	delete *ccfC* – left flank
delBF3581R_F	**CGGGTAAAA**GTAATGGCACCTATGGTAGGATTC	delete *ccfC* – right flank
delBF3581R_R	**TTGGATCC**TGTGAATGTTTATAGGCAGAAGGA	delete *ccfC* – right flank
delBF3580L_F	**GTGGATCC**GGCTGATTTTATCAGAGTTCCTGT	delete *ccfD* – left flank
delBF3580L_R	**TCGTCAGGC**TATTATTTTCCGTTTGGCAGATTT	delete *ccfD* – left flank
delBF3580R_F	**AAAATAATA**GCCTGACGAATGTATTTGTAACAG	delete *ccfD* – right flank
delBF3580R_R	**TTGGATCC**ACTGTAGGGGTAGATCTCGCTATG	delete *ccfD* – right flank
delBF3579L_F	**AAGGATCC**TTGGCATATCCGGAATTCAT	delete *ccfE* – left flank
delBF3579L_R	**TAGGCGAAAAG**CGATCGGTCAGTTTGGTTTT	delete *ccfE* – left flank
delBF3579R_F	**TGACCGATCG**CTTTTCGCCTACATTATAAGATTGC	delete *ccfE* – right flank
delBF3579R_R	**ATGGATCC**GCGTCGACCAGTCCAATTAT	delete *ccfE* – right flank
delBF3579L_F	**AAGGATCC**TTGGCATATCCGGAATTCAT	delete *ccfC-E* – left flank
delBF3579L_Rb	**TGCCATTAC**CGATCGGTCAGTTTGGTTTT	delete *ccfC-E* – left flank
delBF3581R_Fb	**TGACCGATCG**GTAATGGCACCTATGGTAGGATTC	delete *ccfC-E* – right flank
delBF3581R_R	**TTGGATCC**TGTGAATGTTTATAGGCAGAAGGA	delete *ccfC-E* – right flank
delBF0227L_F	**AAGGATCC**GAACCGTTAATGCGTCGTTT	delete *BF0227-29* – left flank
delBF0227L_R	**CTTCACGCAA**ATTCCGGTACATGGGATCAA	delete *BF0227-29* – left flank
delBF0229R_F	**GTACCGGAAT**TTGCGTGAAGCGTAAAAACA	delete *BF0227-29* – right flank
delBF0229R_R	**AAGGATCC**ATCGTCTATTCGGCAACAGG	delete *BF0227-29* – right flank
delBVU946L_F	**CTGTCGAC**GGATTTCGTCTTGCACAGGT	delete *ccfC-E* – left flank (*B. vulgatus*)
delBVU946L_R	**TGGGGAATCC**ACGTTGCTGCCCTCAAATAC	delete *ccfC-E* – left flank (*B. vulgatus*)
delBVU948R_F	**GCAGCAACGT**GGATTCCCCACTGCTACAAA	delete *ccfC-E* – right flank (*B. vulgatus*)
delBVU948R_R	**ATGTCGAC**TCGACTCCGTAGATCCCATC	delete *ccfC-E* – right flank (*B. vulgatus*)

Primers used for quantitative PCR

Primer name	Sequence	Target	Reference or source
BF3583 QF	GGAATTTGCATGACACTTAT	*B. fragilis ccfA*	This study
BF3583 QR	CTGAGAGGTTTCATCTTCTG	*B. fragilis ccfA*	This study
BF3582 QF	AGTGTCCCCACTTCATCGTC	*B. fragilis ccfB*	This study
BF3582 QR	TGAAACTTTTGCCGGAGAAT	*B. fragilis ccfB*	This study
BF3581 QF	GATGAACTGATAGCCCATTA	*B. fragilis ccfC*	This study
BF3581 QR	TAGCGATGACTAAAGGTGTT	*B. fragilis ccfC*	This study
BF3580 QF	CGGTTATATGCTTTTCAAAC	*B. fragilis ccfD*	This study
BF3580 QR	CAAATAGAAATCTGCCAAAC	*B. fragilis ccfD*	This study
BF3579 QF	TGCTATTTGCACGGGTAACA	*B. fragilis ccfE*	This study
BF3579 QR	CCGAAACTCCGATTCTTCAT	*B. fragilis ccfE*	This study
BF0229 QF	CCGGACGTGTTACCTATGCT	*B. fragilis ccfC homologue*	This study
BF0229 QR	ACAGCGAGTGAAGGGAAGAA	*B. fragilis ccfC homologue*	This study
BF0228 QF	GAAAACTGCCATGGACGAAT	*B. fragilis ccfD homologue*	This study
BF0228 QR	GGTTGAATTCCGGCAGATTA	*B. fragilis ccfD homologue*	This study
BF2942 QF	GATCGATTCAGTCGGTTCGT	*B. fragilis ccfC homologue*	This study
BF2942 QR	CGGTTCTCCACTACGTTGGT	*B. fragilis ccfC homologue*	This study
BF2941 QF	AAATGCTTCGCAAGCAGAAT	*B. fragilis ccfD homologue*	This study
BF2941 QR	TACGTATGGCAGGCAATGAA	*B. fragilis ccfD homologue*	This study
BF3146 QF	ACCTCTACCGACTGGCAAGA	*B. fragilis susC homologue*	This study
BF3146 QR	CGGACACACGATAAGGCATA	*B. fragilis susC homologue*	This study
BF3145 QF	ACCTCGATACGGTTCCACTG	*B. fragilis susD homologue*	This study
BF3145 QR	GCCATGCCTGCATAAATCTT	*B. fragilis susD homologue*	This study
Bfragilis16S F	TGATTCCGCATGGTTTCATT	*B. fragilis* 16S rRNA	[10]
Bfragilis16S R	CGACCCATAGAGCCTTCATC	*B. fragilis* 16S rRNA	[10]
BT4634 QF	AACGGTAGTGGCATCGAAAC	*B. thetaiotaomicron susC homologue*	This study
BT4634 QR	CGATAATGCCGTCTCCATTT	*B. thetaiotaomicron susC homologue*	This study
BT4633 QF	ATGCAGCAAACATGGGTTTT	*B. thetaiotaomicron susD homologue*	This study
BT4633 QR	CCATTGGCAGCTATTGGTTT	*B. thetaiotaomicron susD homologue*	This study
BT4247 QF	ATTCACGCATTACCGGCTAC	*B. thetaiotaomicron susC homologue*	This study
BT4247 QR	TCCGACCTTGGGTGTAGAAC	*B. thetaiotaomicron susC homologue*	This study
BT4246 QF	GAACGGAAGTTTCCCCTACC	*B. thetaiotaomicron susD homologue*	This study
BT4246 QR	TGCTCTTTCCCATTTGCTCT	*B. thetaiotaomicron susD homologue*	This study
BT2560 QF	CCAGCCGTTGTATGTGATTG	*B. thetaiotaomicron susC homologue*	This study
BT2560 QR	GGAGATACCGTCACCTGCAT	*B. thetaiotaomicron susC homologue*	This study
BT2559 QF	AATGAAGGCTGGGGAGAAGT	*B. thetaiotaomicron susD homologue*	This study
BT2559 QR	TATCACCACCTTCCGCTTTC	*B. thetaiotaomicron susD homologue*	This study
Btheta16S F	GGTAGTCCACACAGTAAACGATGAA	*B. thetaiotaomicron* 16S rRNA	[11]
Btheta16S R	CCCGTCAATTCCTTTGAGTTTC	*B. thetaiotaomicron* 16S rRNA	[11]
BF3581 QF3	CACCGATACCCTGCGTAAAT	WT *B. fragilis* specific	This study
BF3581 QR3	GGCGGACTGGTAACGATAAA	WT *B. fragilis* specific	This study
delCCF QF	CGGTGCTAACGTTGTCGTAA	*B. fragilis*ΔCCF specific	This study
delCCF QR	ATTTTAGTGCGGCATCCTGA	*B. fragilis*ΔCCF specific	This study
CfcH QF	GGTAAATCCACCACCCTGAA	*C. rodentium* specific	This study
CfcH QR	GTATTCCACGGGGTCTTCAA	*C. rodentium* specific	This study
UniF334	ACTCCTACGGGAGGCAGCAGT	Universal 16S	[12]
UniR514	ATTACCGCGGCTGCTGGC	Universal 16S	[12]

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