

# Acquired interbacterial defense systems protect against interspecies antagonism in the human gut microbiome

Benjamin D. Ross<sup>1,\*</sup>, Adrian J. Verster<sup>2,\*</sup>, Matthew C. Radey<sup>1</sup>, Danica T. Schmidtke<sup>1</sup>, Christopher E. Pope<sup>3</sup>, Lucas R. Hoffman<sup>1,3,4</sup>, Adeline Hajjar<sup>5</sup>, S. Brook Peterson<sup>1</sup>, Elhanan Borenstein<sup>2,6,7,8,9,†</sup> and Joseph D. Mougous<sup>1,10,11,†</sup>

## **Supplemental Data Table 1:**

List of *B. fragilis*-specific type VI secretion system cognate immunity genes. Related to Fig. 1

## **Supplemental Data Table 2:**

List of orphan i6 and i7 immunity genes associated with AID-1 and -2 systems. Related to Fig 2.

## **Supplemental Data Table 3:**

Comprehensive list of genes within AID-1 and -2 systems; those with homology to cognate immunity are indicated along with the percent amino acid identity. Related to Fig. 2.

## **Supplemental Data Table 4:**

Comprehensive list of genes found within *r*AID-1 systems from six Bacteroidales strains. Related to Fig. 4.

## **Supplemental Data Table 5:**

List of all *r*AID-1 recombinase genes in Bacteroidales. Homology (tblastn e-value) with the *B. fragilis* NCTC 9343 *r*AID-1 recombinase is indicated, as well as the number of genes in the cluster. Related to Fig. 4 and Supplemental Fig. 4.

## **Supplemental Data Table 6:**

List of all strains, plasmids, and primers used in this study.

## Supplemental Data Table 1

List of *B. fragilis*- specific T6SS cognate immunity (GA3 subtype)

<b>Immunity #</b>	<b>Immunity locus tag</b>	<b>Immunity accession</b>
GA3_i1	M117_RS0122600	WP_008659772.1
GA3_i2	M117_RS11245	WP_008659758.1
GA3_i3	M117_RS11255	WP_008659747.1
GA3_i4	M074_RS10750	WP_025814152.1
GA3_i5	M074_RS10805	WP_011202655.1
GA3_i6	BF9343_1936	WP_005787090.1
GA3_i7	BF9343_1927	WP_010992797.1
GA3_i8	M068_2000	WP_005787075.1
GA3_i9	M065_2764	WP_005794673.1
GA3_i10	M065_2759	WP_005794684.1
GA3_i11	M069_2106	WP_009292150.1
GA3_i12	M069_2103	WP_032571500.1
GA3_i13	M073_1832	WP_032562840.1
GA3_i14	HMPREF1205_03575	WP_005819890.1
GA3_i15	HMPREF1205_RS15320	WP_005819898.1
GA3_i16	M068_RS11155	WP_005787063.1

## Supplemental Data Table 2

Related to Fig 2. panels A and B. List of strain names and accessions

Clade	Abbreviation	Strain	Genome accession	Immunity locus tag
i6-cI	<i>B. fr</i> 32	<i>B. fragilis</i> 321_BFRA	GCF_001056335.1	ADB44_RS08460
	<i>B. fr</i> I1	<i>B. fragilis</i> I1345	GCF_000598785.2	M066_2029
	<i>B. fr</i> A7	<i>B. fragilis</i> A7 (UDC12-2)	GCF_000598985.1	M070_RS11175
	<i>B. fr</i> BO	<i>B. fragilis</i> BOB25	GCF_000965785.1	VU15_RS08380
	<i>B. fr</i> J1	<i>B. fragilis</i> J-143-4	GCF_000598525.1	M067_RS12915
	<i>B. fr</i> 9343	<i>B. fragilis</i> NCTC 9343	GCF_000025985.1	BF9343_RS09445
	<i>B. fr</i> S2	<i>B. fragilis</i> S24L34	GCF_000599325.1	M134_RS11155
	<i>B. fr</i> J3	<i>B. fragilis</i> J38-1	GCF_000598645.1	M068_RS11090
i6-cII	<i>B. xy</i> H4	<i>B. xylanisolvens</i> H204	this study	n.a.
	<i>B. xy</i> H207	<i>B. xylanisolvens</i> H207	this study	n.a.
i6-cIII	<i>B. ov</i> 3725	<i>B. ovatus</i> 3725 D1 iv	GCF_000699725.1	M088_RS11470
	<i>B. fr</i> 638R	<i>B. fragilis</i> 638R	GCF_000210835.1	BF638R_RS09610
	<i>B. fr</i> DC	<i>B. fragilis</i> DCMOUH0042B	GCF_000724795.1	HR50_RS01170
	<i>B. fr</i> 35	<i>B. fragilis</i> 3_2_5	GCF_000159855.2	BSHG_RS08305
	<i>B. fr</i> 3986	<i>B. fragilis</i> 3986 T(B)9	GCF_000598465.1	M083_RS12250
i7-cl	<i>B. fr</i> JC	<i>B. fragilis</i> JCM 11017	GCF_000613425.1	n.a.
	<i>B. fr</i> 9343	<i>B. fragilis</i> NCTC 9343	GCF_000025985.1	BF9343_RS09400
	<i>B. fr</i> BE	<i>B. fragilis</i> BE1	GCF_001286525.1	BN2301_RS09100
i7-cIII	<i>B. fr</i> 638R	<i>B. fragilis</i> 638R	GCF_000210835.1	BF638R_RS09665
	<i>B. ov</i> 3725	<i>B. ovatus</i> 3725 D1 iv	GCF_000699725.1	M088_RS11485
i7-cIV	<i>B. fr</i> 3986	<i>B. fragilis</i> 3986 T(B)9	GCF_000598465.1	M083_RS12280
	<i>B. fr</i> N3	<i>B. fragilis</i> 3986 N3	GCF_000601115.1	M113_RS10845
	<i>B. fr</i> 10	<i>B. fragilis</i> 1007-1-F #4	GCF_000598545.2	M147_RS11600
	<i>B. fr</i> DC	<i>B. fragilis</i> DCMOUH0042B	GCF_000724795.1	HR50_RS06680

Supplemental Data Table 3

*B. fragilis* orphan immunity in GREEN

**AID-1 gene clusters**

<b>Actinobacteria fragilis 43SR (cluster 1)</b>															
Position in cluster	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
Locus Tag	BF43SR_RS09610	BF43SR_RS09615	BF43SR_RS09620	BF43SR_RS09625	BF43SR_RS09630	BF43SR_RS09635	BF43SR_RS09640	BF43SR_RS09645	BF43SR_RS09650	BF43SR_RS09655	BF43SR_RS09660	BF43SR_RS09665	BF43SR_RS09670	BF43SR_RS09675	BF43SR_RS09680
Identity (%) with cognate immunity	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.
Homology	GAT 4	ToRb transcriptional regulator	YvaK anti-toxin	hypothetical pseudogene	hypothetical pseudogene	GAT 15	hypothetical	hypothetical	hypothetical	hypothetical	GAT 17a	GAT 17b	GAT 17c	GAT 17d	GAT 17e

  

<b>Actinobacteria fragilis 396 N3</b>															
Position in cluster	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
Locus Tag	M113_RS10873	M113_RS102040	M113_RS10870	M113_RS012045	M113_RS012050	M113_RS10885	M113_RS10890	M113_RS10885	M113_RS10890	M113_RS10895	M113_RS10845	M113_RS10840	M113_RS012060	M113_RS10835	M113_RS10830
Identity (%) with cognate immunity	87	56	n.a.	n.a.	70	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	100	78	41	87
Homology	GAT 4	GAT 4	ToRb transcriptional regulator	YvaK anti-toxin	GAT 11	hypothetical pseudogene	GAT 15	hypothetical	hypothetical	hypothetical	hypothetical	GAT 17b	GAT 17c	GAT 17d	GAT 17e

  

<b>Actinobacteria fragilis 4C MDR100420</b>														
Position in cluster	1	2	3	4	5	6	7	8	9	10	11	12	13	14
Locus Tag	HR30_RS01170	HR30_RS012045	HR30_RS012050	HR30_RS012055	HR30_RS012060	HR30_RS01165	HR30_RS01160	HR30_RS01155	HR30_RS01150	HR30_RS06675	HR30_RS06680	HR30_RS06685	HR30_RS06690	HR30_RS06695
Identity (%) with cognate immunity	87	56	n.a.	n.a.	98	n.a.	n.a.	n.a.	n.a.	100	100	78	41	87
Homology	GAT 4	GAT 4	ToRb transcriptional regulator	epithelial pseudogene	pseudogene	hypothetical	GAT 15	hypothetical	hypothetical	hypothetical	GAT 17a	GAT 17b	GAT 17c	GAT 17d

  

<b>Actinobacteria fragilis 396c TDR9</b>															
Position in cluster	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
Locus Tag	M083_RS12250	M083_RS0121510	M083_RS12255	M083_RS0121505	M083_RS0121500	M083_RS12260	M083_RS12265	M083_RS12270	M083_RS0121495	M083_RS12275	M083_RS0121490	M083_RS12280	M083_RS12285	M083_RS12290	M083_RS12295
Identity (%) with cognate immunity	87	56	n.a.	n.a.	70	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.
Homology	GAT 4	GAT 4	ToRb transcriptional regulator	YvaK anti-toxin	GAT 11	hypothetical pseudogene	GAT 15	hypothetical	hypothetical	hypothetical	hypothetical	GAT 17a	GAT 17b	GAT 17c	GAT 17d

  

<b>Actinobacteria fragilis 3725 D14</b>														
Position in cluster	1	2	3	4	5	6	7	8						
Locus Tag	M083_RS11470	M083_RS11475	M083_RS11480	M083_RS0120425	M083_RS11485	M083_RS11490	M083_RS11495							
Identity (%) with cognate immunity	90	n.a.	n.a.	n.a.	90	43	pseudogene	pseudogene						
Homology	GAT 4	hypothetical	hypothetical	GAT 17a	GAT 17b	GAT 15	GAT 15							

**AID-2 gene clusters**

<b>Actinobacteria vulnificans H207</b>			
Position in cluster	1	2	3
Locus Tag	E01DMPPF_04287	E01DMPPF_04288	E01DMPPF_04289
Identity (%) with cognate immunity	n.a.	n.a.	n.a.
Homology	hypothetical	GAT 15	GAT 16

Note: Cluster is flanked by inverted repeats and associated with a DDE transposase consistent with an Insertion Sequence mobile element

**Other AID gene clusters**

<b>Actinobacteria fragilis 43SR (cluster 2)</b>															
Position in cluster	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
Locus Tag	BF43SR_RS08270	BF43SR_RS08275	BF43SR_RS08280	BF43SR_RS08285	BF43SR_RS08290	BF43SR_RS08295	BF43SR_RS08300	BF43SR_RS08305	BF43SR_RS08310	BF43SR_RS08315	BF43SR_RS08320	BF43SR_RS08325	BF43SR_RS08330	BF43SR_RS08335	BF43SR_RS08340
Identity (%) with cognate immunity	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.
Homology	ToRb transcriptional regulator	YvaK anti-toxin	GAT 15	GAT 13	hypothetical	GAT 4	hypothetical	GAT 11	hypothetical	hypothetical	GAT 11	GAT 13	GAT 4	n.a.	GAT 17a

  

<b>Actinobacteria fragilis 397G18</b>															
Position in cluster	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
Locus Tag	M123_RS06740	M123_RS0122125	M123_RS06735	M123_RS06730	M123_RS06725	M123_RS06720	M123_RS06715	M123_RS06710	M123_RS06705						
Identity (%) with cognate immunity	n.a.	n.a.	n.a.	85	93	n.a.	80	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.
Homology	ToRb transcriptional regulator	YvaK anti-toxin	hypothetical	GAT 18	GAT 16a	hypothetical	GAT 4	hypothetical	GAT 17a						

  

<b>Actinobacteria fragilis 3725 D14a</b>															
Position in cluster	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
Locus Tag	M107_RS11435	M107_RS11440	M107_RS11425	M107_RS11420	M107_RS11415	M107_RS11410	M107_RS11405	M107_RS11400	M107_RS11395	M107_RS11390	M107_RS11385	M107_RS11380	M107_RS11375		
Identity (%) with cognate immunity	n.a.	n.a.	61	100	n.a.	n.a.	n.a.	n.a.	90	79	n.a.	65	65	n.a.	n.a.
Homology	ToRb transcriptional regulator	YvaK anti-toxin	GAT 15	GAT 13	hypothetical	hypothetical	GAT 4	GAT 11	GAT 13	hypothetical	GAT 4	hypothetical	GAT 17a		

  

<b>Actinobacteria vulnificans P36-108</b>														
Position in cluster	1	2	3	4	5	6	7	8	9					
Locus Tag	BACHE_RS13600	BACHE_RS13595	BACHE_RS13590	BACHE_RS13585	BACHE_RS13580	BACHE_RS13575	BACHE_RS13570	BACHE_RS13565	BACHE_RS13560					
Identity (%) with cognate immunity	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.					
Homology	ToRb transcriptional regulator	YvaK anti-toxin	GAT 18	GAT 10	hypothetical	hypothetical	GAT 11	hypothetical	hypothetical					

  

<b>Actinobacteria coprococcus DSM 17136</b>														
Position in cluster	1	2	3	4	5	6	7	8	9					
Locus Tag	BACCCOP_RS14550	BACCCOP_RS14545	BACCCOP_RS14540	BACCCOP_RS14535	BACCCOP_RS14530	BACCCOP_RS14525	BACCCOP_RS14520	BACCCOP_RS14515	BACCCOP_RS14510					
Identity (%) with cognate immunity	n.a.	n.a.	n.a.	n.a.	n.a.	65	n.a.	n.a.	69					
Homology	AraC transcriptional regulator	hypothetical	hypothetical	hypothetical	hypothetical	GAT 13	hypothetical	hypothetical	GAT 15					

  

<b>Actinobacteria coprococcus DSM 17136</b>														
Position in cluster	1	2	3	4	5	6	7	8	9	10	11			
Locus Tag	BACCCOP_RS03400	BACCCOP_RS03405	BACCCOP_RS03410	BACCCOP_RS03415	BACCCOP_RS03420	BACCCOP_RS03425	BACCCOP_RS03430	BACCCOP_RS03435	BACCCOP_RS03440	BACCCOP_RS03445	BACCCOP_RS03450			
Identity (%) with cognate immunity	n.a.	n.a.	69	n.a.	n.a.	64	n.a.	n.a.	n.a.	n.a.	n.a.			
Homology	DDE transposase	GAT 15	GAT 15	hypothetical	hypothetical	GAT 13	hypothetical	hypothetical	hypothetical	hypothetical	hypothetical			

  

<b>Actinobacteria vulnificans 27983FDY 0834007</b>																		
Position in cluster	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18
Locus Tag	ARB20_RS07450	ARB20_RS07455	ARB20_RS07460	ARB20_RS07465	ARB20_RS07470	ARB20_RS07475	ARB20_RS07480	ARB20_RS07485	ARB20_RS07490	ARB20_RS07495	ARB20_RS07500	ARB20_RS07505	ARB20_RS07510	ARB20_RS07515	ARB20_RS07520	ARB20_RS07525	ARB20_RS07530	ARB20_RS07535
Identity (%) with cognate immunity	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	57	n.a.	76	79	n.a.	89	n.a.	n.a.	n.a.
Homology	ToRb	ToRb	hypothetical	hypothetical	ToRb	AraC transcriptional regulator	hypothetical	hypothetical	hypothetical	GAT 13	hypothetical	GAT 15	GAT 15	hypothetical	GAT 18	hypothetical	hypothetical	hypothetical



Supplemental Data Table 5

Strain	Genome accession	Recombinase protein ID	e-value	Number of genes in <i>rAID-1</i> cluster
<i>Alistipes onderdonkii</i> WAL 8169 = DSM 19147	GCF_000374505.1	WP_004319196.1		0
<i>Alistipes putredinis</i> DSM 17216	GCF_000154465.1	WP_004329685.1	1.00E-102	5
<i>Alistipes shahii</i> WAL 8301	GCF_000210575.1	WP_004319196.1		0
<i>Bacteroides barnesiae</i> DSM 18169 = JCM 13652	GCF_000374585.1	WP_018709302.1	3.00E-99	9
<i>Bacteroides caccae</i> CL03T12C61	GCF_000273725.1	WP_004319196.1		0
<i>Bacteroides cellulosilyticus</i> WH2	GCF_001318345.1	WP_004319196.1		0
<i>Bacteroides cellulosilyticus</i> WH2	GCF_001318345.1	WP_029427642.1	3.00E-104	15
<i>Bacteroides cellulosilyticus</i> KLE1257	GCF_001580105.1	WP_032575359.1	5.00E-61	6
<i>Bacteroides cellulosilyticus</i> KLE1257	GCF_001580105.1	WP_041579541.1		0
<i>Bacteroides cellulosilyticus</i> WH2	GCF_000463315.1	WP_004319196.1		0
<i>Bacteroides cellulosilyticus</i> WH2	GCF_000463315.1	WP_029427371.1		0
<i>Bacteroides coprocola</i> DSM 17136	GCF_000154845.1	WP_007565622.1		0
<i>Bacteroides coprocola</i> DSM 17136	GCF_000154845.1	WP_007566045.1	4.00E-27	2
<i>Bacteroides dorei</i> CL02T00C15	GCF_000273035.1	WP_007845703.1	1.00E-103	7
<i>Bacteroides dorei</i> CL02T12C06	GCF_000273055.1	WP_007845703.1	1.00E-103	7
<i>Bacteroides dorei</i> CL03T12C01	GCF_000273075.1	WP_004319196.1		0
<i>Bacteroides eggerthii</i> 1_2_48FAA	GCF_000185605.1	WP_034717210.1		0
<i>Bacteroides eggerthii</i> 1_2_48FAA	GCF_000273465.1	WP_004319196.1		0
<i>Bacteroides faecichinchillae</i> JCM 17102	GCF_000614145.1	WP_025073740.1	1.00E-28	2
<i>Bacteroides finegoldii</i> CL09T03C10	GCF_000269545.1	WP_007762162.1	6.00E-28	2
<i>Bacteroides finegoldii</i> DSM 17565	GCF_000156195.1	WP_007757814.1	7.00E-107	2
<i>Bacteroides finegoldii</i> DSM 17565	GCF_000156195.1	WP_032532373.1	2.00E-102	9
<i>Bacteroides fragilis</i>	GCF_000965785.1	WP_032573111.1	2.00E-53	5
<i>Bacteroides fragilis</i>	GCF_000965785.1	WP_045899093.1	8.00E-102	7
<i>Bacteroides fragilis</i>	GCF_001286525.1	WP_053873782.1	4.00E-61	5
<i>Bacteroides fragilis</i>	GCF_000710365.1	WP_007480249.1	7.00E-103	3
<i>Bacteroides fragilis</i>	GCF_000710365.1	WP_032530216.1	1.00E-177	12
<i>Bacteroides fragilis</i>	GCF_000710375.1	WP_032541534.1	1.00E-180	14
<i>Bacteroides fragilis</i>	GCF_000724665.1	WP_044300451.1	8.00E-101	5
<i>Bacteroides fragilis</i>	GCF_000724795.1	WP_005817965.1	1.00E-56	5
<i>Bacteroides fragilis</i>	GCF_000724805.1	WP_032530216.1	1.00E-177	2
<i>Bacteroides fragilis</i>	GCF_000724815.1	WP_032539385.1	6.00E-178	14
<i>Bacteroides fragilis</i>	GCF_001058755.1	WP_009292164.1	7.00E-61	5
<i>Bacteroides fragilis</i>	GCF_001580095.1	WP_032575359.1	5.00E-61	6
<i>Bacteroides fragilis</i>	GCF_001580095.1	WP_041579541.1		0
<i>Bacteroides fragilis</i>	GCF_001693695.1	WP_032541534.1	1.00E-180	31
<i>Bacteroides fragilis</i>	GCF_001699855.1	WP_005800292.1	7.00E-52	6
<i>Bacteroides fragilis</i>	GCF_001699865.1	WP_009292164.1	7.00E-61	7
<i>Bacteroides fragilis</i>	GCF_001816225.1	WP_042986887.1	2.00E-60	5
<i>Bacteroides fragilis</i>	GCF_001997325.1	WP_041579541.1		0
<i>Bacteroides fragilis</i> 3_1_12	GCF_000157015.1	WP_032541534.1	1.00E-180	19
<i>Bacteroides fragilis</i> 638R	GCF_000210835.1	WP_014298729.1	1.00E-60	7
<i>Bacteroides fragilis</i> 638R	GCF_000210835.1	WP_041161350.1	3.00E-103	8
<i>Bacteroides fragilis</i> CL03T00C08	GCF_000273095.1	WP_005787123.1	1.00E-60	7
<i>Bacteroides fragilis</i> CL03T12C07	GCF_000273115.1	WP_005787123.1	1.00E-60	7
<i>Bacteroides fragilis</i> CL03T12C07	GCF_000273115.1	WP_029427371.1		0
<i>Bacteroides fragilis</i> CL03T12C07	GCF_000273115.1	WP_032532373.1	2.00E-102	11
<i>Bacteroides fragilis</i> CL05T00C42	GCF_000269525.1	WP_005800292.1	7.00E-52	5
<i>Bacteroides fragilis</i> CL05T00C42	GCF_000273765.1	WP_005800292.1	7.00E-52	5
<i>Bacteroides fragilis</i> CL05T12C13	GCF_000273135.1	WP_005800292.1	7.00E-52	5
<i>Bacteroides fragilis</i> CL07T00C01	GCF_000263115.1	WP_005794646.1	1.00E-60	5
<i>Bacteroides fragilis</i> CL07T12C05	GCF_000273155.1	WP_005794646.1	1.00E-60	5
<i>Bacteroides fragilis</i> HMW 610	GCF_000297695.1	WP_032538046.1	5.00E-179	15
<i>Bacteroides fragilis</i> HMW 615	GCF_000297735.1	WP_005817965.1	1.00E-56	5
<i>Bacteroides fragilis</i> NCTC 9343	GCF_000025985.1	WP_032575359.1	5.00E-61	5
<i>Bacteroides fragilis</i> NCTC 9343	GCF_000025985.1	WP_041579541.1		0
<i>Bacteroides fragilis</i> str. 1007-1-F #10	GCF_000598685.2	WP_032533094.1	2.00E-52	5
<i>Bacteroides fragilis</i> str. 1007-1-F #3	GCF_000599265.1	WP_032533094.1	2.00E-52	6
<i>Bacteroides fragilis</i> str. 1007-1-F #4	GCF_000598545.2	WP_032533094.1	2.00E-52	5
<i>Bacteroides fragilis</i> str. 1007-1-F #5	GCF_000601035.1	WP_032533094.1	2.00E-52	6
<i>Bacteroides fragilis</i> str. 1007-1-F #6	GCF_000601095.1	WP_032533094.1	2.00E-52	6
<i>Bacteroides fragilis</i> str. 1007-1-F #7	GCF_000599145.2	WP_032533094.1	2.00E-52	5
<i>Bacteroides fragilis</i> str. 1007-1-F #8	GCF_000598265.1	WP_032533094.1	2.00E-52	6
<i>Bacteroides fragilis</i> str. 1007-1-F #9	GCF_000598885.1	WP_032533094.1	2.00E-52	6
<i>Bacteroides fragilis</i> str. 1009-4-F #10	GCF_000598705.1	WP_032573111.1	2.00E-53	5
<i>Bacteroides fragilis</i> str. 1009-4-F #7	GCF_000599285.2	WP_032573111.1	2.00E-53	4
<i>Bacteroides fragilis</i> str. 2-F-2 #4	GCF_000598825.1	WP_032570367.1	3.00E-53	6
<i>Bacteroides fragilis</i> str. 2-F-2 #5	GCF_000598285.1	WP_032570367.1	3.00E-53	5
<i>Bacteroides fragilis</i> str. 2-F-2 #7	GCF_000598145.1	WP_032570367.1	3.00E-53	6
<i>Bacteroides fragilis</i> str. 20793-3	GCF_000598905.1	WP_005800292.1	7.00E-52	6
<i>Bacteroides fragilis</i> str. 3-F-2 #6	GCF_000598865.1	WP_032581328.1	4.00E-103	13
<i>Bacteroides fragilis</i> str. 3-F-2 #6	GCF_000598865.1	WP_032581437.1		0
<i>Bacteroides fragilis</i> str. 34-F-2 #13	GCF_000598425.1	WP_032570367.1	3.00E-53	7
<i>Bacteroides fragilis</i> str. 3719 A10	GCF_000598845.1	WP_005817965.1	1.00E-56	5

<i>Bacteroides fragilis</i> str. 3719 T6	GCF_000598725.1	WP_032591763.1	4.00E-61	5
<i>Bacteroides fragilis</i> str. 3725 D9(v)	GCF_000598585.1	WP_011202667.1	5.00E-61	7
<i>Bacteroides fragilis</i> str. 3725 D9(v)	GCF_000598585.1	WP_032588375.1	2.00E-103	7
<i>Bacteroides fragilis</i> str. 3783N1-2	GCF_000598325.1	WP_032576242.1	3.00E-53	3
<i>Bacteroides fragilis</i> str. 3783N1-6	GCF_000599065.2	WP_032576242.1	3.00E-53	5
<i>Bacteroides fragilis</i> str. 3783N1-8	GCF_000598605.1	WP_032576242.1	3.00E-53	5
<i>Bacteroides fragilis</i> str. 3986 N(B)19	GCF_000598445.1	WP_032583251.1	1.00E-62	5
<i>Bacteroides fragilis</i> str. 3988 T1	GCF_000598205.1	WP_022347519.1	4.00E-51	7
<i>Bacteroides fragilis</i> str. 3988T(B)14	GCF_000598365.1	WP_022347519.1	4.00E-51	2
<i>Bacteroides fragilis</i> str. 3998T(B)3	GCF_000598485.1	WP_042971802.1	0	3
<i>Bacteroides fragilis</i> str. A7 (UDC12-2)	GCF_000598985.1	WP_032573111.1	2.00E-53	5
<i>Bacteroides fragilis</i> str. DS-166	GCF_000598245.1	WP_009292164.1	7.00E-61	7
<i>Bacteroides fragilis</i> str. DS-208	GCF_000598505.1	WP_032569346.1	4.00E-53	5
<i>Bacteroides fragilis</i> str. Ds-233	GCF_000598805.1	WP_009292164.1	7.00E-61	5
<i>Bacteroides fragilis</i> str. DS-71	GCF_000599085.1	WP_032589960.1	2.00E-61	3
<i>Bacteroides fragilis</i> str. I1345	GCF_000598785.2	WP_032573111.1	2.00E-53	4
<i>Bacteroides fragilis</i> str. J-143-4	GCF_000598525.1	WP_032564756.1	6.00E-60	5
<i>Bacteroides fragilis</i> str. J38-1	GCF_000598645.1	WP_009292164.1	7.00E-61	5
<i>Bacteroides fragilis</i> str. S23 R14	GCF_000598665.1	WP_032562849.1	2.00E-59	6
<i>Bacteroides fragilis</i> str. S23L17	GCF_000601055.1	WP_032562849.1	2.00E-59	5
<i>Bacteroides fragilis</i> str. S23L24	GCF_000599305.1	WP_032562849.1	2.00E-59	6
<i>Bacteroides fragilis</i> str. S24L15	GCF_000599005.1	WP_009292164.1	7.00E-61	7
<i>Bacteroides fragilis</i> str. S24L15	GCF_000599005.1	WP_032568676.1	0	14
<i>Bacteroides fragilis</i> str. S24L15	GCF_000599005.1	WP_032568998.1	5.00E-114	7
<i>Bacteroides fragilis</i> str. S24L26	GCF_000598745.1	WP_009292164.1	7.00E-61	7
<i>Bacteroides fragilis</i> str. S24L26	GCF_000598745.1	WP_032568676.1	0	14
<i>Bacteroides fragilis</i> str. S24L26	GCF_000598745.1	WP_032568998.1	5.00E-114	7
<i>Bacteroides fragilis</i> str. S24L34	GCF_000599325.1	WP_009292164.1	7.00E-61	7
<i>Bacteroides fragilis</i> str. S24L34	GCF_000599325.1	WP_032568676.1	0	14
<i>Bacteroides fragilis</i> str. S24L34	GCF_000599325.1	WP_032568998.1	5.00E-114	7
<i>Bacteroides fragilis</i> str. S36L11	GCF_000599125.1	WP_009292164.1	7.00E-61	4
<i>Bacteroides fragilis</i> str. S36L12	GCF_000599345.1	WP_009292164.1	7.00E-61	5
<i>Bacteroides fragilis</i> str. S36L5	GCF_000599025.1	WP_009292164.1	7.00E-61	5
<i>Bacteroides fragilis</i> str. S38L3	GCF_000598765.2	WP_032575359.1	5.00E-61	5
<i>Bacteroides fragilis</i> str. S38L5	GCF_000599365.1	WP_032575359.1	5.00E-61	6
<i>Bacteroides fragilis</i> str. S6L3	GCF_000599225.1	WP_009292164.1	7.00E-61	7
<i>Bacteroides fragilis</i> str. S6L8	GCF_000599385.1	WP_009292164.1	7.00E-61	7
<i>Bacteroides fragilis</i> str. S6R5	GCF_000599045.1	WP_009292164.1	7.00E-61	7
<i>Bacteroides fragilis</i> str. S6R6	GCF_000599245.1	WP_009292164.1	7.00E-61	7
<i>Bacteroides fragilis</i> str. S6R8	GCF_000601075.2	WP_009292164.1	7.00E-61	6
<i>Bacteroides fragilis</i> YCH46	GCF_000009925.1	YP_098675.1	2.00E-103	9
<i>Bacteroides fragilis</i> YCH46	GCF_000009925.1	YP_099248.1	5.00E-61	7
<i>Bacteroides gallinarum</i> DSM 18171 = JCM 13651	GCF_000374365.1	WP_018668258.1	2.00E-100	9
<i>Bacteroides gallinarum</i> DSM 18171 = JCM 13651	GCF_000613665.1	WP_018668258.1	2.00E-100	9
<i>Bacteroides ihuae</i>	GCF_900104585.1	WP_071147699.1	7.00E-28	2
<i>Bacteroides intestinalis</i>	GCF_001578635.1	WP_007565622.1	0	6
<i>Bacteroides luti</i>	GCF_900128905.1	WP_073402179.1	8.00E-24	2
<i>Bacteroides nordii</i> CL02T12C05	GCF_000273175.1	WP_004319196.1	0	16
<i>Bacteroides nordii</i> CL02T12C05	GCF_000273175.1	WP_007482838.1	2.00E-28	16
<i>Bacteroides nordii</i> CL02T12C05	GCF_000273175.1	WP_044166385.1	3.00E-104	7
<i>Bacteroides nordii</i> WAL 11050 = JCM 12987	GCF_000613465.1	WP_002558314.1	4.00E-25	20
<i>Bacteroides oleiciplenus</i> YIT 12058	GCF_000315485.1	WP_009132147.1	0	15
<i>Bacteroides ovatus</i>	GCF_001314995.1	WP_004296526.1	1.00E-24	2
<i>Bacteroides ovatus</i>	GCF_001535615.1	WP_004317151.1	2.00E-25	2
<i>Bacteroides ovatus</i>	GCF_001578575.1	WP_022199412.1	3.00E-24	2
<i>Bacteroides ovatus</i>	GCF_900100465.1	WP_008646540.1	1.00E-24	2
<i>Bacteroides ovatus</i>	GCF_900107475.1	WP_004296526.1	1.00E-24	2
<i>Bacteroides ovatus</i> 3_8_47FAA	GCF_000218325.1	WP_004303812.1	0	5
<i>Bacteroides ovatus</i> ATCC 8483	GCF_000154125.1	WP_004296526.1	1.00E-24	2
<i>Bacteroides ovatus</i> CL02T12C04	GCF_000273195.1	WP_004317151.1	2.00E-25	2
<i>Bacteroides ovatus</i> CL02T12C04	GCF_000273195.1	WP_004319196.1	0	14
<i>Bacteroides ovatus</i> CL03T12C18	GCF_000273215.1	WP_029427371.1	0	16
<i>Bacteroides ovatus</i> CL03T12C18	GCF_000273215.1	WP_032532373.1	2.00E-102	11
<i>Bacteroides ovatus</i> SD CMC 3f	GCF_000178275.1	WP_004309994.1	1.00E-102	5
<i>Bacteroides ovatus</i> str. 3725 D1 iv	GCF_000699725.1	WP_004319196.1	0	9
<i>Bacteroides ovatus</i> str. 3725 D1 iv	GCF_000699725.1	WP_004319196.1	0	8
<i>Bacteroides ovatus</i> str. 3725 D1 iv	GCF_000699725.1	WP_032588375.1	2.00E-103	10
<i>Bacteroides ovatus</i> str. 3725 D9 iii	GCF_000699665.1	WP_004319196.1	0	10
<i>Bacteroides ovatus</i> str. 3725 D9 iii	GCF_000699665.1	WP_029427371.1	0	5
<i>Bacteroides ovatus</i> str. 3725 D9 iii	GCF_000699665.1	WP_032588375.1	2.00E-103	6
<i>Bacteroides ovatus</i> V975	GCF_900095495.1	WP_004296526.1	1.00E-24	2
<i>Bacteroides paurosaccharolyticus</i> JCM 15092	GCF_000613805.1	WP_024993116.1	2.00E-28	4
<i>Bacteroides plebeius</i> DSM 17135	GCF_000187895.1	WP_007558964.1	0	20
<i>Bacteroides salanitronis</i> DSM 18170	GCF_000190575.1	WP_013619075.1	5.00E-101	14
<i>Bacteroides sahyersiae</i>	GCF_001405695.1	WP_004319196.1	0	9
<i>Bacteroides sahyersiae</i> CL02T12C01	GCF_000273235.1	WP_007480249.1	7.00E-103	5
<i>Bacteroides sahyersiae</i> WAL 10018 = DSM 18765	GCF_000381365.1	WP_005926302.1	3.00E-102	9

<i>Bacteroides salyersiae</i> WAL 10018 = DSM 18765	GCF_000381365.1	WP_044097441.1	1.00E-103	7
<i>Bacteroides salyersiae</i> WAL 10018 = DSM 18765	GCF_000613685.1	WP_005926302.1	3.00E-102	9
<i>Bacteroides</i> sp. 1_1_30	GCF_000218365.1	WP_008642435.1	4.00E-25	2
<i>Bacteroides</i> sp. 2_1_22	GCF_000162155.1	WP_004317151.1	2.00E-25	2
<i>Bacteroides</i> sp. 2_1_56FAA	GCF_000218345.1	WP_009292164.1	7.00E-61	8
<i>Bacteroides</i> sp. 2_1_56FAA	GCF_000218345.1	WP_032496509.1	4.00E-103	13
<i>Bacteroides</i> sp. 2_2_4	GCF_000157055.1	WP_008646540.1	1.00E-24	2
<i>Bacteroides</i> sp. 3_1_13	GCF_001185845.1	WP_004317151.1	2.00E-25	2
<i>Bacteroides</i> sp. 3_1_23	GCF_000162555.1	WP_008646540.1	1.00E-24	2
<i>Bacteroides</i> sp. 3_1_23	GCF_000162555.1	WP_032532373.1	2.00E-102	5
<i>Bacteroides</i> sp. 3_2_5	GCF_000159855.2	WP_005817965.1	1.00E-56	5
<i>Bacteroides</i> sp. D1	GCF_000157095.2	WP_004317151.1	2.00E-25	2
<i>Bacteroides</i> sp. D2	GCF_000159075.2	WP_009001080.1	2.00E-25	2
<i>Bacteroides</i> sp. D22	GCF_000163675.1	WP_004317151.1	2.00E-25	2
<i>Bacteroides</i> sp. HMSC067B03	GCF_001811315.1	WP_055295521.1	1.00E-103	9
<i>Bacteroides</i> sp. HMSC073E02	GCF_001815255.1	WP_007480249.1	7.00E-103	5
<i>Bacteroides</i> sp. HMSC073E02	GCF_001815255.1	WP_070782541.1	0	7
<i>Bacteroides</i> sp. HPS0048	GCF_000382465.1	WP_002558314.1	4.00E-25	2
<i>Bacteroides</i> sp. Marseille-P2653	GCF_900155865.1	WP_007480249.1	7.00E-103	16
<i>Bacteroides</i> sp. Marseille-P2653	GCF_900155865.1	WP_077152863.1	5.00E-25	2
<i>Bacteroides</i> sp. Marseille-P3108	GCF_900108345.1	WP_071148900.1	0	6
<i>Bacteroides</i> sp. Marseille-P3108	GCF_900108345.1	WP_071150249.1	3.00E-26	7
<i>Bacteroides</i> sp. Marseille-P3132	GCF_900130125.1	WP_073343607.1	3.00E-36	6
<i>Bacteroides</i> sp. Marseille-P3132	GCF_900130125.1	WP_073348178.1	7.00E-101	8
<i>Bacteroides</i> sp. Marseille-P3208T	GCF_900128495.1	WP_071150249.1	3.00E-26	7
<i>Bacteroides</i> sp. UW	GCF_000785025.1	WP_032530216.1	1.00E-177	12
<i>Bacteroides stercoris</i> CC31F	GCF_000413395.1	WP_016662012.1	9.00E-104	9
<i>Bacteroides thetaiotaomicron</i>	GCF_001405095.1	WP_032851361.1	0	6
<i>Bacteroides thetaiotaomicron</i>	GCF_900109385.1	WP_065540254.1	6.00E-103	8
<i>Bacteroides thetaiotaomicron</i> dnLKV9	GCF_000403155.2	WP_016268162.1	3.00E-180	6
<i>Bacteroides uniformis</i>	GCF_001406135.1	WP_007565622.1	0	15
<i>Bacteroides uniformis</i>	GCF_001406135.1	WP_041579541.1	0	12
<i>Bacteroides uniformis</i>	GCF_001406635.1	WP_007565622.1	0	14
<i>Bacteroides uniformis</i>	GCF_900107315.1	WP_005647591.1	0	5
<i>Bacteroides uniformis</i> ATCC 8492	GCF_000154205.1	WP_005647591.1	0	5
<i>Bacteroides uniformis</i> CL03T00C23	GCF_000273785.1	WP_032532373.1	2.00E-102	11
<i>Bacteroides uniformis</i> CL03T12C37	GCF_000273275.1	WP_032532373.1	2.00E-102	11
<i>Bacteroides uniformis</i> dnLKV2	GCF_000403175.1	WP_035458146.1	7.00E-103	8
<i>Bacteroides vulgatus</i> PC510	GCF_000178195.1	WP_032938614.1	0	5
<i>Bacteroides vulgatus</i> str. 3975 RP4	GCF_000699865.1	WP_004319196.1	0	6
<i>Bacteroides vulgatus</i> str. 3975 RP4	GCF_000699865.1	WP_032953256.1	0	3
<i>Bacteroides xylanisolvens</i>	GCF_001405055.1	WP_004317151.1	2.00E-25	2
<i>Bacteroides xylanisolvens</i>	GCF_900107825.1	WP_004317151.1	2.00E-25	2
<i>Bacteroides xylanisolvens</i>	GCF_900114865.1	WP_004317151.1	2.00E-25	2
<i>Bacteroides xylanisolvens</i> CL03T12C04	GCF_000273315.1	WP_004317151.1	2.00E-25	2
<i>Bacteroides xylanisolvens</i> CL03T12C04	GCF_000273315.1	WP_029427371.1	0	16
<i>Bacteroides xylanisolvens</i> CL03T12C04	GCF_000273315.1	WP_032532373.1	2.00E-102	11
<i>Bacteroides xylanisolvens</i> SD CC 1b	GCF_000178215.1	WP_004316061.1	4.00E-110	2
<i>Bacteroides xylanisolvens</i> SD CC 1b	GCF_000178215.1	WP_004317151.1	2.00E-25	2
<i>Bacteroides xylanisolvens</i> SD CC 1b	GCF_000577295.1	WP_004316061.1	4.00E-110	6
<i>Bacteroides xylanisolvens</i> SD CC 1b	GCF_000577295.1	WP_004317151.1	2.00E-25	2
<i>Bacteroides xylanisolvens</i> SD CC 2a	GCF_000178295.1	WP_004316061.1	4.00E-110	3
<i>Bacteroides xylanisolvens</i> SD CC 2a	GCF_000178295.1	WP_004317151.1	2.00E-25	2
<i>Bacteroides xylanisolvens</i> SD CC 2a	GCF_000577955.1	WP_004316061.1	4.00E-110	7
<i>Bacteroides xylanisolvens</i> SD CC 2a	GCF_000577955.1	WP_004317151.1	2.00E-25	2
<i>Parabacteroides distasonis</i> CL03T12C09	GCF_000307455.1	WP_029427371.1	0	16
<i>Parabacteroides distasonis</i> str. 3999B T(B) 4	GCF_000699905.1	WP_034503414.1	9.00E-104	10
<i>Parabacteroides goldsteinii</i>	GCF_001039445.1	WP_007565622.1	0	20
<i>Parabacteroides goldsteinii</i>	GCF_001039445.1	WP_046147928.1	8.00E-28	2
<i>Parabacteroides goldsteinii</i> CL02T12C30	GCF_000307395.1	WP_007654016.1	7.00E-109	13
<i>Parabacteroides goldsteinii</i> dnLKV18	GCF_000403825.2	WP_007565622.1	0	9
<i>Parabacteroides goldsteinii</i> dnLKV18	GCF_000403825.2	WP_032581328.1	4.00E-103	4
<i>Parabacteroides gordonii</i> DSM 23371	GCF_000428565.1	WP_007480249.1	7.00E-103	9
<i>Parabacteroides gordonii</i> DSM 23371	GCF_000428565.1	WP_028728892.1	0	16
<i>Parabacteroides gordonii</i> DSM 23371	GCF_000428565.1	WP_028729533.1	6.00E-103	5
<i>Parabacteroides gordonii</i> MS-1	GCF_000969825.1	WP_007480249.1	7.00E-103	9
<i>Parabacteroides gordonii</i> MS-1	GCF_000969825.1	WP_028728892.1	0	16
<i>Parabacteroides gordonii</i> MS-1	GCF_000969825.1	WP_028729533.1	6.00E-103	5
<i>Parabacteroides merdae</i> CL03T12C32	GCF_000307345.1	WP_005647591.1	0	25
<i>Parabacteroides merdae</i> CL03T12C32	GCF_000307345.1	WP_034503414.1	9.00E-104	14
<i>Parabacteroides</i> sp. ASF519	GCF_000364265.1	WP_032581328.1	4.00E-103	4
<i>Parabacteroides</i> sp. D13	GCF_000162275.1	WP_009017658.1	0	8
<i>Paraprevotella xylaniphila</i> YIT 11841	GCF_000205165.1	WP_040602870.1	0	11
<i>Porphyromonas endodontalis</i> ATCC 35406	GCF_000174815.1	WP_040581485.1	4.00E-25	3

Supplemental Data Table 6

Bacterial species and strains	Genotype	Notes
<i>Escherichia coli</i> EC1000	F <sup>-</sup> <i>metA</i> (Δ <i>mir-bcdRMS-mecB</i> C) o80[ <i>hlsZAM15</i> <i>AlacX74</i> <i>recA1</i> <i>endA1</i> <i>araD139</i> <i>Δ(ara, leu)</i> 7697	
<i>Escherichia coli</i> S17-1 <i>pir</i>	<i>galI</i> <i>galK</i> $\lambda$ - <i>rpsL</i> . <i>nupG</i> <i>pir-116</i> (DHFR)	
<i>B. fragilis</i> NCTC 9343 <i>tdk</i>	BF9343_0556, F <sub>UdR</sub> <sup>R</sup>	Parental deletion background
<i>B. fragilis</i> NCTC 9343 <i>tdk tssC</i>	BF9343_1941, F <sub>UdR</sub> <sup>R</sup>	Type VI secretion system inactive
<i>B. fragilis</i> NCTC 9343 <i>tdk e-16</i>	BF9343_1936-7, F <sub>UdR</sub> <sup>R</sup>	E-16 mutant ( <i>bte-11</i> )
<i>B. fragilis</i> NCTC 9343 <i>tdk e-17ab</i>	BF9343_1926-8, F <sub>UdR</sub> <sup>R</sup>	E-17ab mutant ( <i>bte-12ab</i> )
<i>B. fragilis</i> NCTC 9343 <i>tdk rAID-1 orf1</i>	BF9343_1926-8, F <sub>UdR</sub> <sup>R</sup>	rAID-1 orf1 mutant
<i>B. fragilis</i> 638R	Wildtype, F <sub>UdR</sub> <sup>R</sup>	Gift from Sears lab, Johns Hopkins University
<i>B. fragilis</i> 638R <i>tdk</i>	BF638R_0630, F <sub>UdR</sub> <sup>R</sup>	Parental deletion background, retains <i>tdk</i> resistance
<i>B. fragilis</i> 638R <i>tdk o16</i>	BF638R_2042, F <sub>UdR</sub> <sup>R</sup>	Orphan 16 mutant
<i>B. fragilis</i> 638R <i>tdk o17ab</i>	BF638R_2053-4, F <sub>UdR</sub> <sup>R</sup>	Orphan 17ab mutant
<i>B. fragilis</i> 638R <i>tdk o16 o17ab</i>	BF638R_2042, BF638R_2053-4, F <sub>UdR</sub> <sup>R</sup>	Orphan 16/17ab double mutant
<i>Bacteroides ovatus</i> 8483 <i>tdk</i>	F <sub>UdR</sub> <sup>R</sup>	Parental
<i>Bacteroides ovatus</i> 3725 D1 <i>iv</i>	F <sub>UdR</sub> <sup>R</sup>	Wildtype strain, naturally tet resistant.
<i>Bacteroides ovatus</i> 3725 D1 <i>iv tdk</i>	M088_RS16410, F <sub>UdR</sub> <sup>R</sup>	Parental deletion background
<i>Bacteroides ovatus</i> 3725 D1 <i>iv tdk o16</i>	M088_RS11470, F <sub>UdR</sub> <sup>R</sup>	Orphan 16 mutant
<i>Bacteroides ovatus</i> 3725 D1 <i>iv tdk o17ab</i>	M088_RS11485-90, F <sub>UdR</sub> <sup>R</sup>	Orphan 17ab mutant
<i>Bacteroides ovatus</i> 3725 D1 <i>iv tdk o16 o17ab</i>	M088_RS11470, M088_RS11485-90, F <sub>UdR</sub> <sup>R</sup>	Orphan 16/17ab double mutant
<i>Bacteroides xylanisolvens</i> H204	F <sub>UdR</sub> <sup>R</sup>	Wildtype strain, naturally tet resistant
<i>Bacteroides xylanisolvens</i> H207	F <sub>UdR</sub> <sup>R</sup>	Wildtype strain, naturally tet resistant
<i>Bacteroides xylanisolvens</i> H207 <i>tdk</i>	E0JDMPIF_00853, F <sub>UdR</sub> <sup>R</sup>	Parental deletion background, naturally tet resistant
<i>Bacteroides xylanisolvens</i> H207 <i>tdk o16</i>	E0JDMPIF_04289, F <sub>UdR</sub> <sup>R</sup>	Orphan 16 mutant, naturally tet resistant
<i>Bacteroides fragilis</i> YCH46	F <sub>UdR</sub> <sup>R</sup>	Wildtype strain
<i>Bacteroides fragilis</i> YCH46 <i>tdk</i>	BF0659, F <sub>UdR</sub> <sup>R</sup>	Parental deletion background
<i>Bacteroides fragilis</i> YCH46 <i>tdk GA1 tssR</i>	BF2842, F <sub>UdR</sub> <sup>R</sup>	BF2842 ( <i>tssR</i> ) mutant, GA1 T6SS inactivating
Plasmids	Purpose	Reference/Source
pKNOCK-erm	Suicide vector, allelic exchange	Gift from Goodman lab, Yale. PMID: 18611383
pKNOCK- <i>tdk</i> -BF9343_0556	Deletion of thymidine kinase gene from <i>B. fragilis</i> 638R	Gift from Goodman lab, Yale. PMID: 26957597
pKNOCK-Bov- <i>tdk</i>	Deletion of thymidine kinase gene M088_RS16410 from <i>B. ovatus</i> 3725 D1 <i>iv</i>	This study
pKNOCK-Bxy- <i>tdk</i>	Deletion of thymidine kinase gene E0JDMPIF_00853 from <i>B. xylanisolvens</i> H207	This study
pExchange <i>tdk</i>	Suicide vector, allelic exchange	Gift from Goodman lab, Yale. PMID: 18611383
pExchange <i>tdk</i> _BF638R_o16	Deletion of BF638R_2042 from <i>B. fragilis</i> 638R	This study
pExchange <i>tdk</i> _BF638R_o17ab	Deletion of BF638R_2053-4 from <i>B. fragilis</i> 638R	Gift from Goodman lab, Yale. PMID: 18611383
pExchange <i>tdk</i> _Bov3725_o16	Deletion of M088_RS11470 from <i>B. ovatus</i> 3725 D1 <i>iv</i>	Gift from Goodman lab, Yale. PMID: 18611383
pExchange <i>tdk</i> _Bov3725_o17ab	Deletion of M088_RS11485-90 from <i>B. ovatus</i> 3725 D1 <i>iv</i>	Gift from Goodman lab, Yale. PMID: 18611383
pExchange <i>tdk</i> _BxyH207_o16	Deletion of E0JDMPIF_04289 from <i>B. xylanisolvens</i> H207	Gift from Goodman lab, Yale. PMID: 18611383
pNBU2_erm	To confer antibiotic resistance to strains following chromosomal insertion at <i>Bacteroides</i> NBU2 att sites	Gift from Goodman lab, Yale. PMID: 26957597
pNBU2_tet	To confer antibiotic resistance to strains following chromosomal insertion at <i>Bacteroides</i> NBU2 att sites	Gift from Goodman lab, Yale. PMID: 26957597
pNBU2_erm_us1311	For constitutive gene expression following chromosomal insertion at <i>Bacteroides</i> NBU2 att sites, used in	Gift from Goodman lab, Yale. PMID: 24439897
pSchaB2-V	For inducible expression of proteins in <i>Escherichia coli</i>	PMID: 15925406
pSchaB2-V-BF2850-toxCT	For inducible expression of the C-terminal toxin domain (residue 1353 to 1481) of BF2850 in <i>E. coli</i>	PMID: 15925406
pPSV39-CV	For inducible expression of proteins in <i>Escherichia coli</i>	PMID: 23954347
pPSV39-BF2851-CV	For inducible expression of BF2851 cognate immunity in <i>E. coli</i>	PMID: 23954347
pPSV39-CV-BF9343_1657=CV	For inducible expression of BF9343_1657 orphan immunity in <i>E. coli</i>	PMID: 23954347
Primers	Sequence	Purpose
E0JDMPIF_03980 F	GAGAGAAACITTTGTCATCCCC	qPCR, <i>B. xylanisolvens</i> H207
E0JDMPIF_03980 R	GAGACGCTCTTTGAAGAATTC	qPCR, <i>B. xylanisolvens</i> H207
BACOVA_04916 F	GTTTGGCGGAGGAATGATGTC	qPCR, <i>B. ovatus</i>
BACOVA_04916 R	CATCGTCTTCCAAAGAAAGTCACATGA	qPCR, <i>B. ovatus</i>
BF638R_1320 F	AGGAGGCATCGGGATTITTTGAC	qPCR, <i>B. fragilis</i>
BF638R_1320 R	CAATACGCTATCTCCTGTGGAAGTC	qPCR, <i>B. fragilis</i>
BF638R_o16_left_fwd	gaagagagaataaacttgaggagcctaattgttagagagcaac	For deletion of BF638R_2042 by Gibson Assembly into BamHI and Sall linearized pExchange <i>tdk</i>
BF638R_o16_left_rev	tcacagggtctatccctactctcaaaaacaaatctcc	For deletion of BF638R_2042 by Gibson Assembly into BamHI and Sall linearized pExchange <i>tdk</i>
BF638R_o16_right_fwd	atggtagagacccttgaaatgcaaacatttattatc	For deletion of BF638R_2042 by Gibson Assembly into BamHI and Sall linearized pExchange <i>tdk</i>
BF638R_o16_right_rev	eggcgcctgttagctgacattttataaaatccggctggc	For deletion of BF638R_2042 by Gibson Assembly into BamHI and Sall linearized pExchange <i>tdk</i>
BF638R_o17ab_left_fwd	gaagagagaataaacttgaggagcctaattgttagagagcaac	For deletion of BF638R_2053-4 by Gibson Assembly into BamHI and Sall linearized pExchange <i>tdk</i>
BF638R_o17ab_left_rev	gtcatctctcctttatctgtttttgttttc	For deletion of BF638R_2053-4 by Gibson Assembly into BamHI and Sall linearized pExchange <i>tdk</i>
BF638R_o17ab_right_fwd	caatgaagaagcagactatgacagaaaaaacaggtg	For deletion of BF638R_2053-4 by Gibson Assembly into BamHI and Sall linearized pExchange <i>tdk</i>
BF638R_o17ab_right_rev	eggcgcctgttagctgacattttataaaatccggctggc	For deletion of BF638R_2053-4 by Gibson Assembly into BamHI and Sall linearized pExchange <i>tdk</i>
Bxy_H207_o16_#1	TCAGTAACGGATCCCGACCGCACTGTGTGAGGACCCATTAC	For deletion of E0JDMPIF_04289 by Gibson Assembly into BamHI and Sall linearized pKNOCK
Bxy_H207_o16_#2	CGTCCAGGAGGCGCTCTCTCTAGCTCTCTGTATGTTGG	For deletion of E0JDMPIF_00853 by Gibson Assembly into BamHI and Sall linearized pKNOCK
Bxy_H207_o16_#3	CTAGAAGAAGGCGCTCGTCCAGGAGGGAAGATGAGC	For deletion of E0JDMPIF_00853 by Gibson Assembly into BamHI and Sall linearized pKNOCK
Bxy_H207_o16_#4	TCAGAAATGTGCACTAGCCATGGGAAATCGATAATCAGGAAGC	For deletion of E0JDMPIF_00853 by Gibson Assembly into BamHI and Sall linearized pExchange <i>tdk</i>
Bxy_H207_o16_#1	TCAGTAACGGATCCCGACCGCACTGTGTGAGGACCCATTAC	For deletion of E0JDMPIF_04289 by Gibson Assembly into BamHI and Sall linearized pExchange <i>tdk</i>
Bxy_H207_o16_#2	GACCCCACTCGGAGCGCGCAAAAACAATGCCTCTTCAAAAAATAAATGATTC	For deletion of E0JDMPIF_04289 by Gibson Assembly into BamHI and Sall linearized pExchange <i>tdk</i>
Bxy_H207_o16_#3	CATTTGTTTTGCTGGCTCGGATGGGTCAGATAATAAATACTAGTTG	For deletion of E0JDMPIF_04289 by Gibson Assembly into BamHI and Sall linearized pExchange <i>tdk</i>
Bxy_H207_o16_#4	TCAGAAATGTGCACTAGCCATGGGAAATCGATAATCAGGAAGC	For deletion of E0JDMPIF_04289 by Gibson Assembly into BamHI and Sall linearized pExchange <i>tdk</i>
BOV_tdk_Sall_F1	CTGAAGATCGAC GTGATCTCCGCCAAATCAGATC	For deletion of M088_RS16410 from <i>B. ovatus</i> 3725 D1 <i>iv</i> by SOE and restriction-ligation cloning into BamHI and Sall linearized pKNOCK
BOV_tdk_SOE_R1	GAGATTTTTGGTTTTCTGATATAAATAATGCCTTCCATCAATCTGTTTCTTTATAGAGT	For deletion of M088_RS16410 from <i>B. ovatus</i> 3725 D1 <i>iv</i> by SOE and restriction-ligation cloning into BamHI and Sall linearized pKNOCK
BOV_tdk_SOE_F2	ACTCTATAAAGAAACAGATATAGGAAAGC CATATTTATTTAATCAAGAAACACAAAF	For deletion of M088_RS16410 from <i>B. ovatus</i> 3725 D1 <i>iv</i> by SOE and restriction-ligation cloning into BamHI and Sall linearized pKNOCK
BOV_tdk_BamHI_R2	CAACAAGATCC GAAGGTATCCTGTATGATTTGTACGAT	For deletion of M088_RS16410 from <i>B. ovatus</i> 3725 D1 <i>iv</i> by SOE and restriction-ligation cloning into BamHI and Sall linearized pKNOCK
Bov_3725_o16_#1	TCAGTAACGGATCCAAATCGGGAACGACCCACCGCT	For deletion of M088_RS11470 by Gibson Assembly into BamHI and Sall linearized pExchange <i>tdk</i>
Bov_3725_o16_#2	CCCATCGGAGCGAGCGATAAAGATAACACTCACT	For deletion of M088_RS11470 by Gibson Assembly into BamHI and Sall linearized pExchange <i>tdk</i>
Bov_3725_o16_#3	CTTTCATCCGGCTCCTCCGATGGGAGTCAGATAATGAAGTTC	For deletion of M088_RS11470 by Gibson Assembly into BamHI and Sall linearized pExchange <i>tdk</i>
Bov_3725_o16_#4	TCAGAAATGTGCACTAGCCATGGGAAATCGATAATCAGGAAGC	For deletion of M088_RS11470 by Gibson Assembly into BamHI and Sall linearized pExchange <i>tdk</i>
Bov_3725_o17ab_#1	TCAGTAACGGATCCCAATGATGACTACTTATAAGGAATG	For deletion of M088_RS11485-90 by Gibson Assembly into BamHI and Sall linearized pExchange <i>tdk</i>
Bov_3725_o17ab_#2	CTCTCTGTATTGCTGCCAATGATGACTACTTATAAGGAATG	For deletion of M088_RS11485-90 by Gibson Assembly into BamHI and Sall linearized pExchange <i>tdk</i>
Bov_3725_o17ab_#3	GTATCTGAAATGGGCTAGGCAAAATACAGGAAGAATAACAATAAACAAG	For deletion of M088_RS11485-90 by Gibson Assembly into BamHI and Sall linearized pExchange <i>tdk</i>
Bov_3725_o17ab_#4	TCAGAAATGGGCGCGCAATCGATCTGACTAGACTGAATATAAG	For deletion of M088_RS11485-90 by Gibson Assembly into BamHI and Sall linearized pExchange <i>tdk</i>
YCH46_BF2842_LEFT_fwd	gaagagagaataaacttgaggagcctaattgttagagagcaac	For deletion of BF2842 (GA1 TssR) by Gibson Assembly into BamHI and Sall linearized pExchange <i>tdk</i>
YCH46_BF2842_LEFT_rev	ttacagattgttttcaatttataaaatctgtgtgac	For deletion of BF2842 (GA1 TssR) by Gibson Assembly into BamHI and Sall linearized pExchange <i>tdk</i>
YCH46_BF2842_RIGHT_fwd	atgaagaacatfactgtaaaataaaatggaaccacac	For deletion of BF2842 (GA1 TssR) by Gibson Assembly into BamHI and Sall linearized pExchange <i>tdk</i>
YCH46_BF2842_RIGHT_rev	eggcgcctgttagctgacattttataaaatccggctggc	For deletion of BF2842 (GA1 TssR) by Gibson Assembly into BamHI and Sall linearized pExchange <i>tdk</i>
BF9343_1657_LEFT_fwd	TCAGTAACGGATCCCGACCGCACTGTGTGAGGACCCATTAC	For deletion of <i>B. fragilis</i> 9343 rAID-1 orf1 (BF9343_1657) by SOE and restriction-ligation cloning into BamHI and Sall linearized pExchange <i>tdk</i>
BF9343_1657_LEFT_rev	CCGTTGTAACGTTCAGCTCCGGAAATCGAAATGACCCGAC	For deletion of <i>B. fragilis</i> 9343 rAID-1 orf1 (BF9343_1657) by SOE and restriction-ligation cloning into BamHI and Sall linearized pExchange <i>tdk</i>
BF9343_1657_RIGHT_fwd	CCGAACTGACGACGCTTACAAAGGATCTCAATTTGGAACTATATG	For deletion of <i>B. fragilis</i> 9343 rAID-1 orf1 (BF9343_1657) by SOE and restriction-ligation cloning into BamHI and Sall linearized pExchange <i>tdk</i>
BF9343_1657_RIGHT_rev	TCAGAAATGTGCACTAGCCATGGGAAATCGATAATCAGGAAGC	For deletion of <i>B. fragilis</i> 9343 rAID-1 orf1 (BF9343_1657) by SOE and restriction-ligation cloning into BamHI and Sall linearized pExchange <i>tdk</i>
BF9343_1657_F_Sael_hcpRBS	TCAAGTACTAGACCTACCGGAGGAAAGATGAGTAAAGTAAATGGGTTGGC	For inducible expression of orphan immunity from <i>B. fragilis</i> NCTC 9343 from pPSV39-CV (untagged), RBS from <i>P. aeruginosa</i> hcp1
BF9343_1657_R_Xba_1_NS	TCATCAGTACTAGATCTGCAATATAAGTTTCCAAATAATGAATACC	For inducible expression of orphan immunity from <i>B. fragilis</i> NCTC 9343 from pPSV39-CV (untagged), RBS from <i>P. aeruginosa</i> hcp1
YCH46_BF2851_F_Sael_hcpRBS	CTGAA GAGCTC <i>ACGGGAGGAAAG</i> ATGAATAAAATAATGATTTGGGTTGGTC	For inducible expression of cognate immunity from <i>B. fragilis</i> YCH46 into pPSV39-CV (VsvG-tagged), RBS from <i>P. aeruginosa</i> hcp1
YCH46_BF2851_R_Xba1-ns	CAACA tetaq CTATCCCGCTATATATGTTCTTAAATAATG	For inducible expression of cognate immunity from <i>B. fragilis</i> YCH46 into pPSV39-CV (VsvG-tagged), RBS from <i>P. aeruginosa</i> hcp1
YCH46_BF2850F_Nde I	TAGTACACTACATATGGCGTCTCCATGGGACG	For inducible expression of the C-terminal toxin domain of <i>B. fragilis</i> YCH46 BF2850 (untagged)
YCH46_BF2850_Xba_1_STOP	TCAATCAGTACTAGATTTTATTAAGAATACTACTACATGC	For inducible expression of the C-terminal toxin domain of <i>B. fragilis</i> YCH46 BF2850 (untagged)