

SUPPORTING INFORMATION for

A clostripain-like protease plays a major role in generating the secretome of enterotoxigenic *Bacteroides fragilis*

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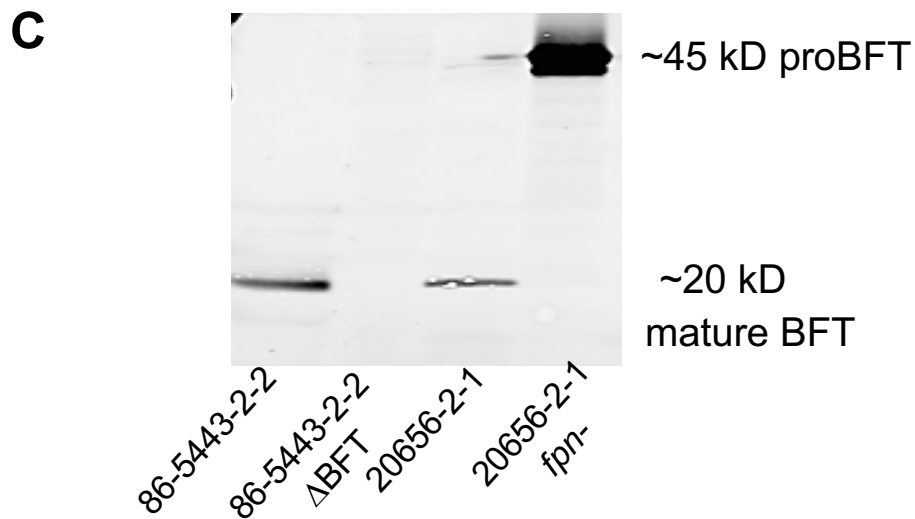
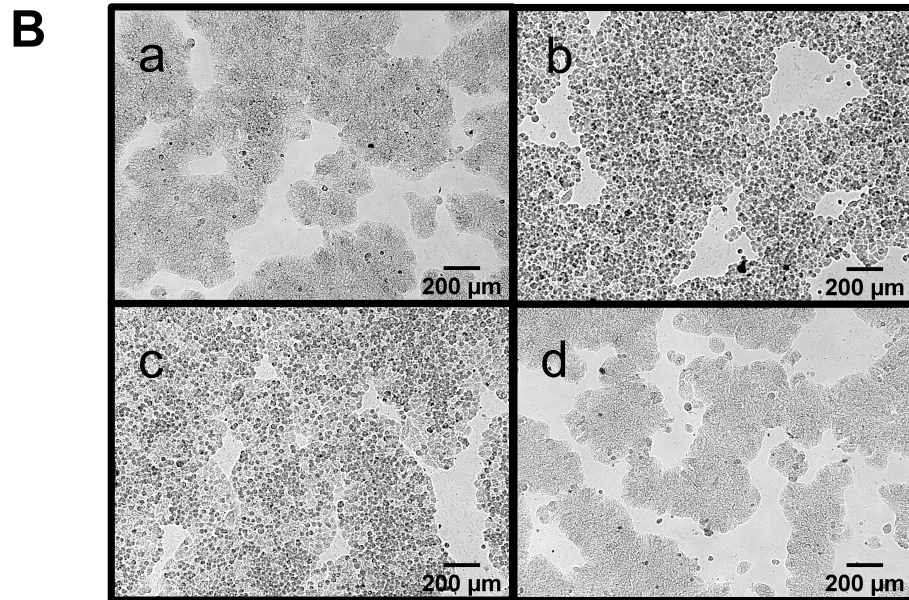
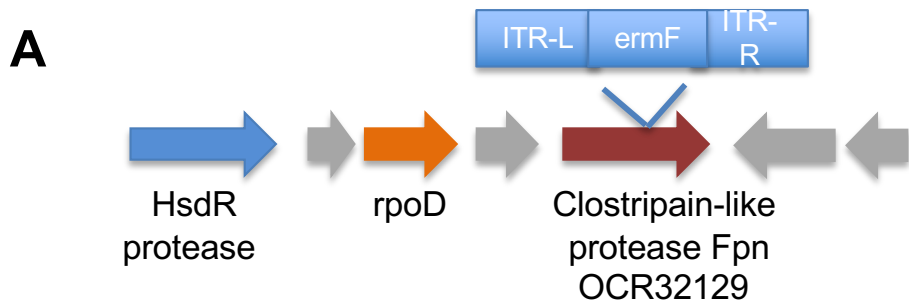


Figure S1. Identification of a transposon insertion that blocks BFT maturation. *A*, Diagram of the transposon insertion site in ETBF strain 20656-2-1. The putative function of neighboring genes is indicated. Genes of unknown function are shown in gray. *B*, HT29 cells were incubated with culture medium from *B. fragilis* strain NCTC 9343 (a), NCTC 9343 pFD340:BFT (b), ETBF 20656-2-1 (c) or ETBF 20656-2-1 *fpn*⁻ (d) and observed after 6 h. Fixed cells were examined at 10X magnification. The rounding up of cells in (b) and (c) shows intoxication with BFT. *C*, The culture medium of the indicated strains was analyzed by Western blot using an anti-BFT antiserum.

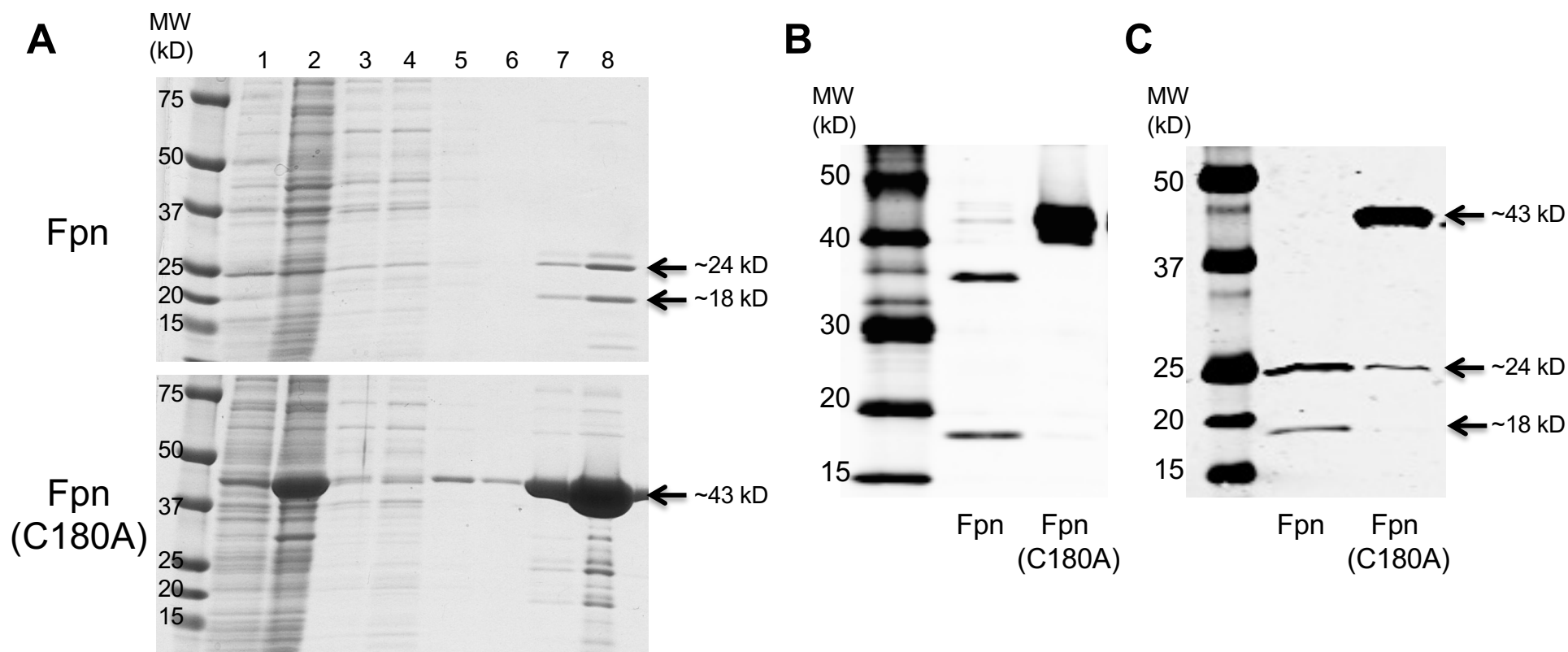


Figure S2. Purification of the *B. fragilis* Fpn protease. A, Fpn protease and the Fpn (C180A) mutant containing an N-terminal 6xHis tag in place of the signal peptide were expressed in *E. coli* and purified on a Ni-NTA column. Lanes: 1, uninduced; 2, induced; 3, Ni-NTA input (diluted ~5 fold); 4, flow through; 5-6, washes; 7-8, elution fractions. Following SDS-PAGE proteins were detected by Coomassie Blue staining. The purified proteins were analyzed by Western blot using anti-6xHis (B) and anti-Fpn (C) antisera.

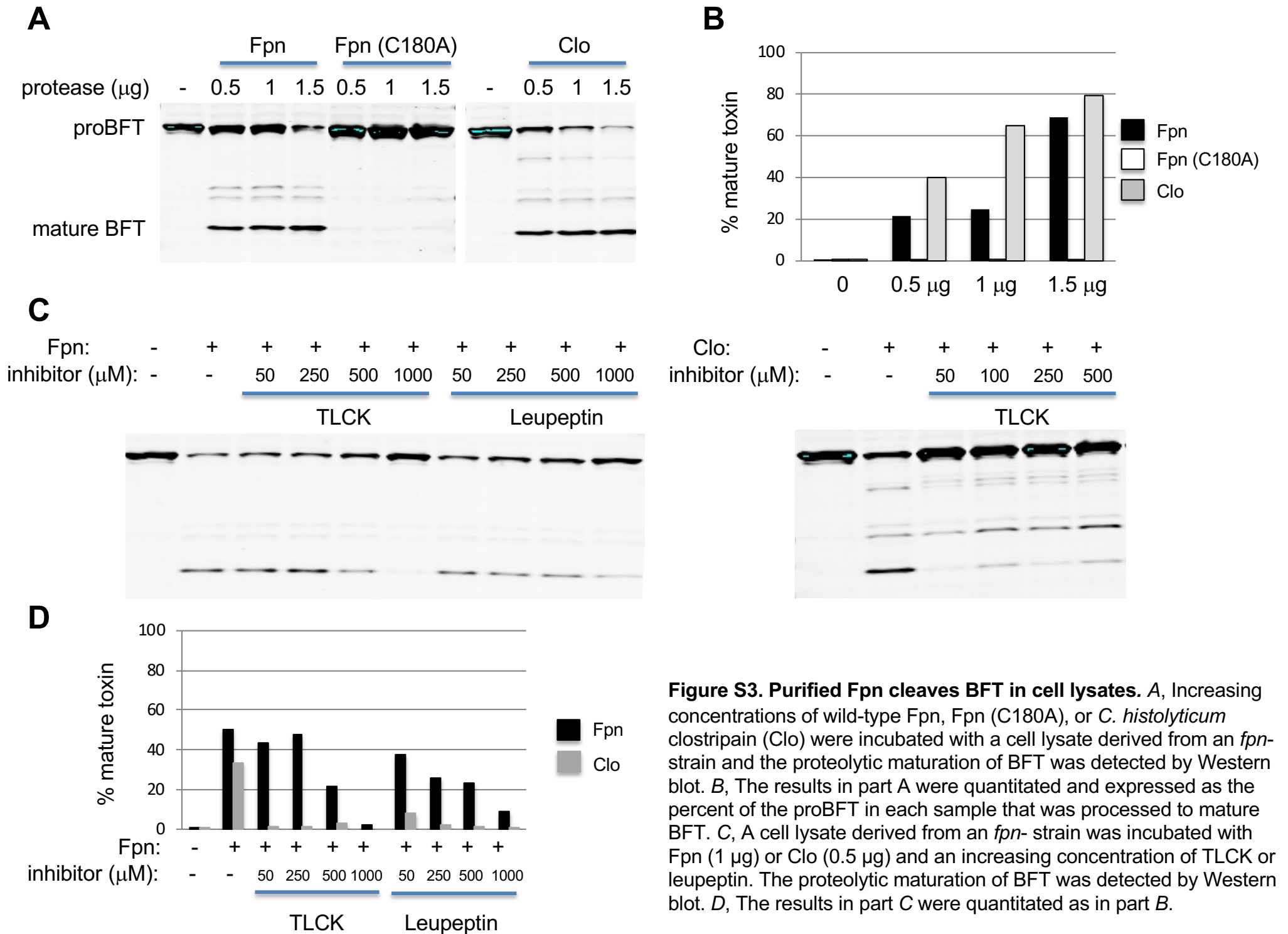


Figure S3. Purified Fpn cleaves BFT in cell lysates. *A*, Increasing concentrations of wild-type Fpn, Fpn (C180A), or *C. histolyticum* clostripain (Clo) were incubated with a cell lysate derived from an *fpn*-strain and the proteolytic maturation of BFT was detected by Western blot. *B*, The results in part *A* were quantitated and expressed as the percent of the proBFT in each sample that was processed to mature BFT. *C*, A cell lysate derived from an *fpn*- strain was incubated with Fpn (1 μg) or Clo (0.5 μg) and an increasing concentration of TLCK or leupeptin. The proteolytic maturation of BFT was detected by Western blot. *D*, The results in part *C* were quantitated as in part *B*.

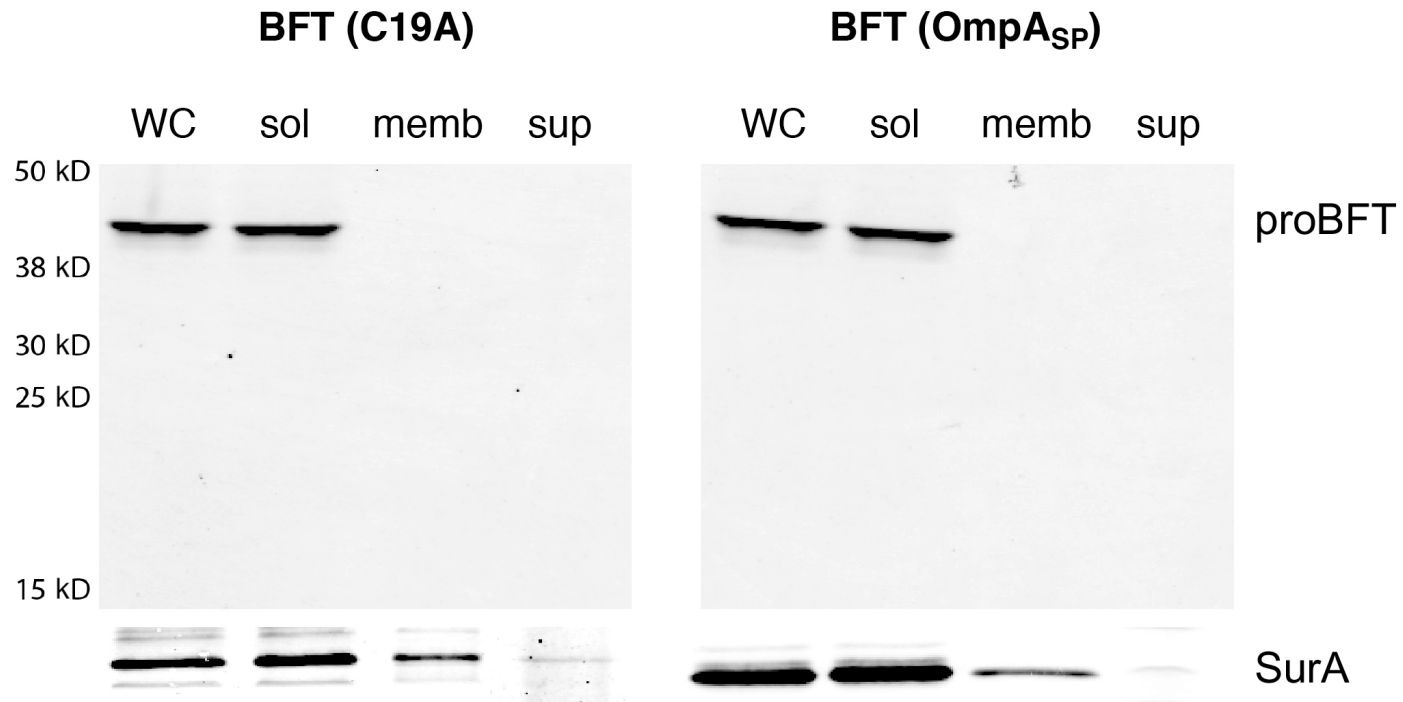


Figure S4. Mutations in the BFT lipobox or signal peptide abolish proteolytic processing. A wild-type ETBF strain transformed with pFD340 containing the gene that encodes BFT C19A or BFT (OmpA_{SP}) was grown to mid-log phase, and cells were separated from the culture medium (sup) by centrifugation. Whole cell lysates (WC) were then separated into membrane (memb) and soluble (sol) fractions. Samples were analyzed by Western blot using antisera against BFT and SurA.

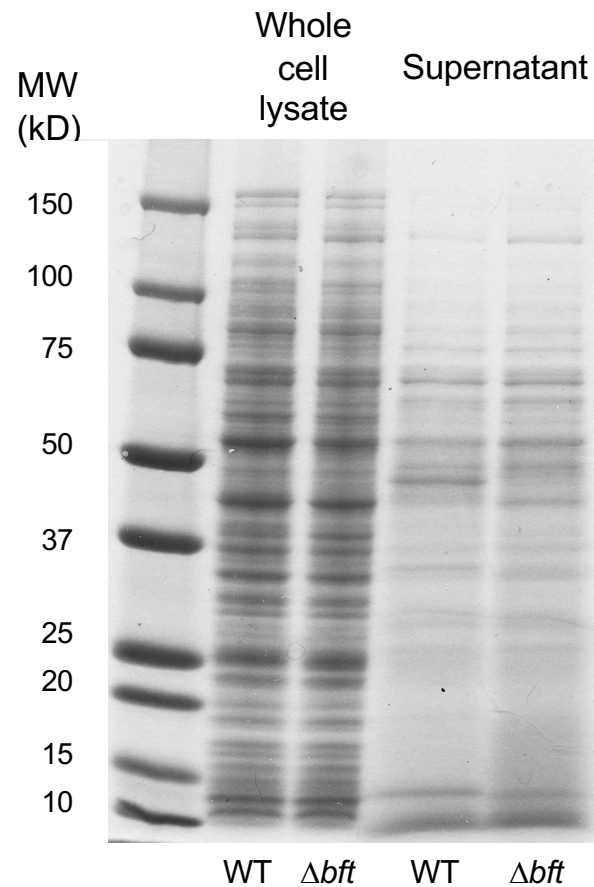
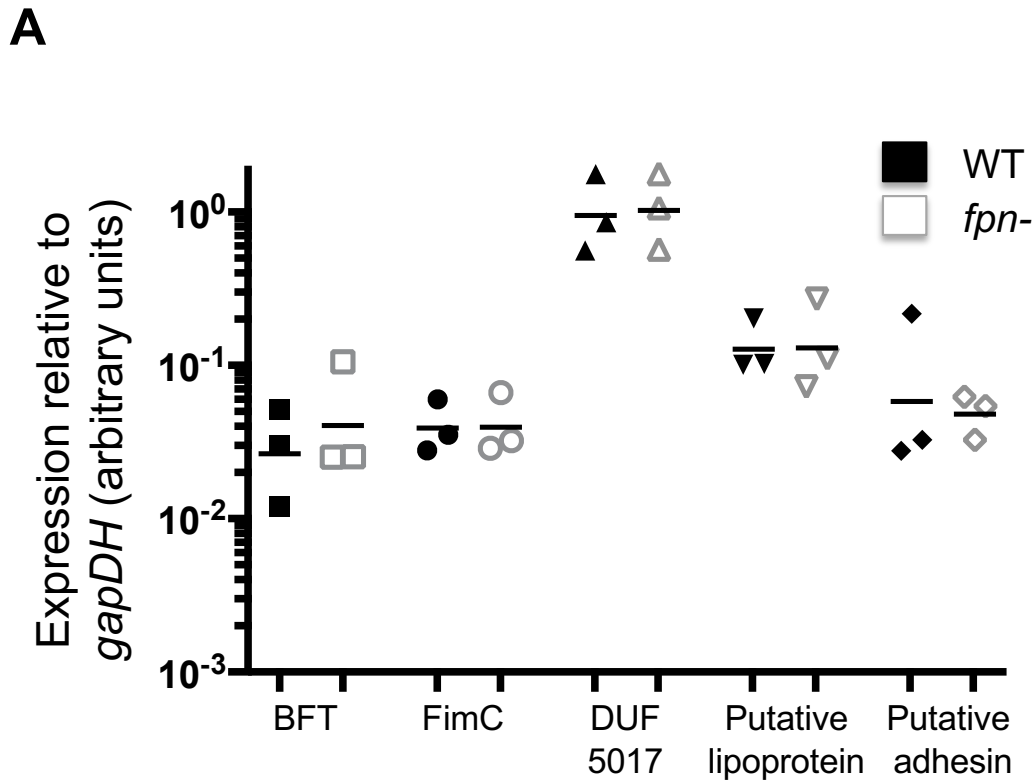


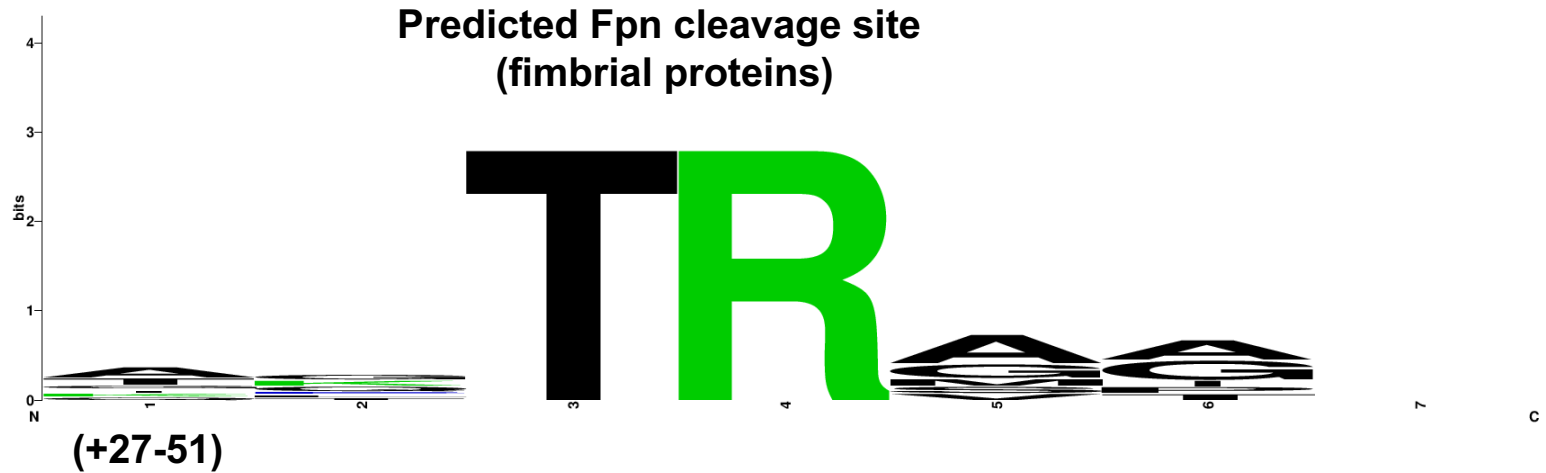
Figure S5. BFT plays only a minor role in the generation of the ETBF secretome. Cultures of wild-type strain 86-5543-2-2 (WT) and an isogenic Δbft strain were grown to log phase. Cells were then isolated by centrifugation, and the protein content of the whole cell lysate and culture medium (supernatant) was analyzed by SDS-PAGE and Colloidal Blue staining. Culture medium samples were 20x more concentrated than the cell lysate samples.



B

Ratio (<i>fpn-</i> WT)	Protein
0.24	BFT
0.16	FimC
0.008	DUF5017*
0.022	Putative lipoprotein*
0.006	Putative adhesin

Figure S6. The loss of Fpn does not affect the expression of genes encoding secreted proteins. *A*, The relative expression of genes encoding five proteins in wild-type ETBF and isogenic *fpn-* mutant strains was determined by quantitative RT-PCR using the oligonucleotides listed in Table S3. Expression was normalized to the level of *gapDH* in each strain and is shown in arbitrary units. *B*, The ratio of proteins analyzed in part *A* in the culture medium of the two strains as determined by quantitative mass spectrometry is indicated. Asterisks denote proteins that were identified as highly abundant secretome components (see Fig. 3).

A**B**

Band 6 (Fig. 3)	+ ³⁴ QI TR SS	
Band 3 (Fig. 3)	+ ⁸¹ AT TR SA	
BF9343_2214	+ ²⁷ AN TR ST	
BF638R_4428	+ ²⁶ PG TR AA	N-terminal arginine
BF9343_0726	+ ¹¹ AV TR VS	
BF4433	+ ²⁷ AS SR AI	
BF1567	+ ¹⁹⁵ TA SR GA	Unique arginine
BFT	+ ¹⁹⁰ SQ TR AV	Mapped Fpn cleavage site

Figure S7. Identification of a potential Fpn cleavage motif. *A*, An arginine residue located near the N terminus of all nine fimbrial proteins whose levels were strongly reduced in the secretome of an *fpn*- strain (Fig. 4D) is embedded in a conserved sequence motif identified using Logo plot software (<https://weblogo.berkeley.edu/logo.cgi?>). The arginine is the first arginine in the mature region of seven of the proteins and is the predicted site of Fpn cleavage. *B*, The most N-terminal arginine residue of some of the proteins that were strongly reduced in the secretome of an *fpn*- strain (see Fig. 3, Table S2) as well as the sole arginine in BF1567 is embedded in a sequence motif that is similar to the motif identified in *A*. For comparison, the mapped Fpn cleavage site in BFT is shown.

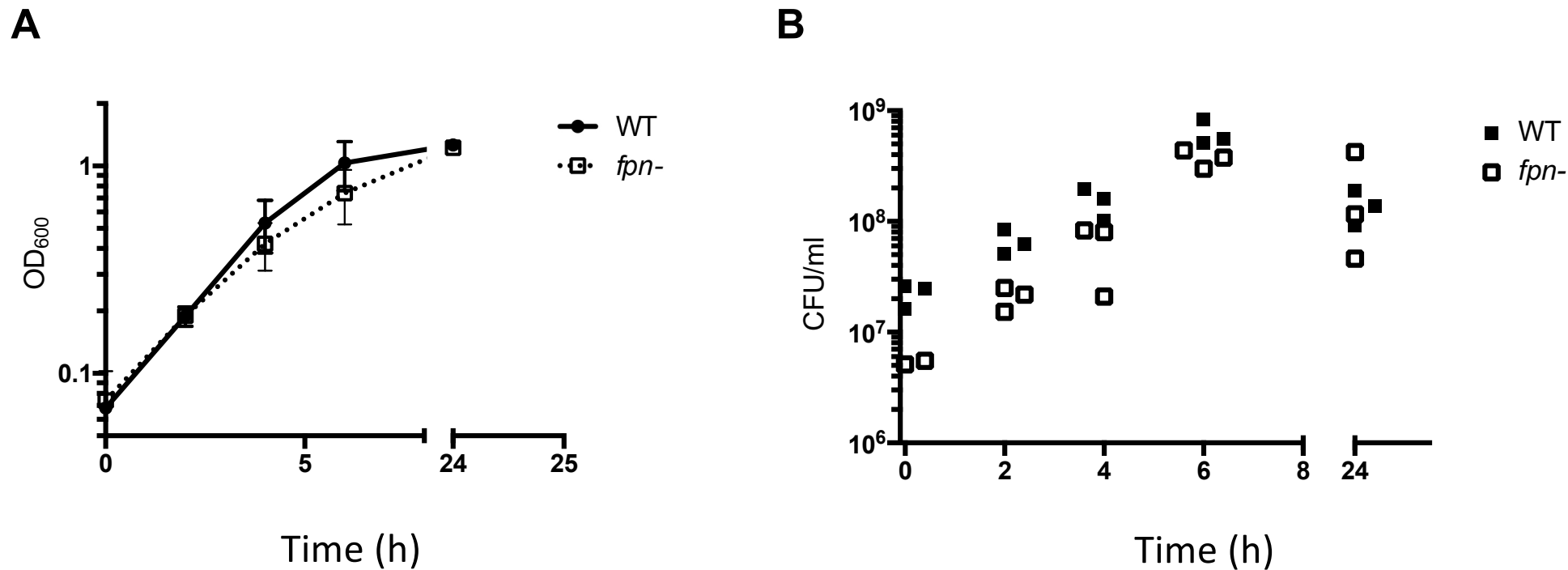


Figure S8. The loss of Fpn does not affect cell viability during stationary phase. *A*, The growth of wild-type (WT) ETBF and isogenic *fpn*⁻ strains in rich medium was monitored at OD₆₀₀. The standard deviation of three cultures is shown. *B*, Samples were removed from the cultures in *A* at various time points and the number of colony forming units (CFU) per ml was determined to assess cell viability.

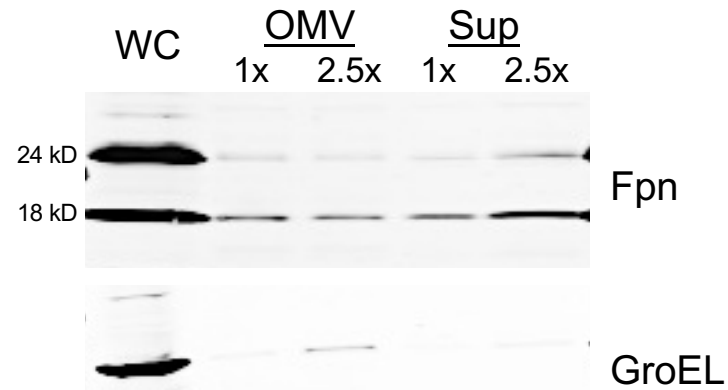


Figure S9. Fpn is retained on the cell surface. A wild-type ETBF strain was grown to mid-log phase and cells were separated from outer membrane vesicles (OMV) and the culture medium by centrifugation. A total cell lysate and the two extracellular fractions were then analyzed by Western blot using antisera against Fpn and GroEL. Protein derived from two and a half times as many cell equivalents was loaded in lanes marked “2.5x”.

Table S1. Peptides identified in gel slices by mass spectrometry

Band	Predicted size (no SP)	Apparent size	KEGG ID	pSORT		Fold change (<i>fjn</i> - <i>WT</i>)*	Annotation
				Predicted Localization	SP II+ (Lipoprotein)		
1	108	100	BF3307	OM	No	0.52	TonB-dependent receptor / SusC-like
2	83	78	BF638R_4406	Periplasmic	Yes	0.04	Putative lipoprotein
3	65	65	BF9343_3471	Unknown	Yes	0.04	PCDM domain, Lipocalin-like
4	68	63	BF1992	Unknown	Yes	0.008	DUF 5017, Bacteroidetes-specific protein
5	54	51	BF0669	Unknown	Yes	0.061	SusD-like
6	54	49	BF2685	Unknown	Yes	0.014	MACPF domain, pore forming toxin
7	43	40	BF1929	Unknown	Yes	0.052	DUF4856, Bacteroides-specific protein
8	40	37	BF1298	OM	No	0.406	OmpA-like
9	27	28	BF9343_2956	Unknown	Yes	0.022	Putative lipoprotein

* Data from quantitative comparison

Peptide coverage (identified peptides shown in red)

Band	KEGG ID	Peptide 1	Peptide 2	Peptide 3	Peptide 4	Peptide 5
Band 9:	BF9343_2956	1 MKQLKMLVLT	LTLMLGTMFT	SCMDSGESGP	QQWAGVVKVN.	DRMGVYTFD
		51 AAGTELIPTN	TIPVTLNARM	AYIYQVDEG	QDLSTNPKSI	KITLLADPTG
		101 IDATAITTPK	VGESGDVTTN	APVGSLSFVS	GYSTVAPFKY	SENTIVLPVL
		151 YRVKVVITTE	DIKNELAKHT	FTLVCYTDDI	KSQDITLKLQ	LRKYVEDEPA
		201 AIAERATRIS	SFKAYEISQI	LREYTLKSGQ	TKPAKITIVA	QQNEYNNKLE
		251 DTSTIEKVEE	IEYKTAE			
Band 8:	BF1298	1 MKKSIFMFAL	ATLMSASVFA	QDNDAKRLPG	YKTFEGNGF	WNNWFMSANF
		51 GAQSLFAENS	KDAKFRNTIT	FMPTLVSGKW	FNPYNGVRLQ	GTGGSLHGF
		101 SGANSMHYQ	YGAVHADFMF	GLINFFAPYK	ENRRFDIVPF	AGIGGAFIRK
		151 GDQSFITNAG	IQARYRISKR	FDINVEYQGA	ILDDDMVVRG	GFPNDGISGL
		201 TAQVTRFRGK	TGFKKGYSSR	QYNAIKSNYS	DLEANATLK	KENAAQQAIEI
		251 AELKARKPEI	VKEETVIDNS	EIKALPSTIT	FPFNSSKIEL	SQEVSIFFNIA
		301 EFLKANPEIR	VRLTYGADKR	GSEQANRIVS	ERRANAVTEV	FVNYKGIADK
		351 RITTEFKGTS	TKFENDMNR	AVVVELIK		
Band 7:	BF1929	1 MNYLLKCLFL	SCLLISVVAC	TDGINETVIS	AYQLPVLPEP	SYKFSRNGES
		51 SVNVLCEGFL	KSPIDRIFSE	YMNARMSTK	RDYDEALRIY	HEGNFGLKPK
		101 KEVSASSKHL	KDRDKILKDI	DANFETSARI	AGLGANIPSY	EHRNREAVKG
		151 LTGYVNGIG	KDKICVYDER	GIAVAEVYKY	AIMGAIYLDK	ILNIHLEQI
		201 LENNEVLVRN	DLTQLLPGHN	YTELEHHWDL	AYGYDFWKT	LAQSDGLPAL
		251 KDCHLRISRS	FVKGRAIMTT	SQYDEMRLQA	DTIRQELSRV	VAVRAMHLLV
		301 GPNTLANLKE	NPRRAFRLLS	QAYGLYAAQ	FARNMQGKSF	LTNEETGILL
		351 HELEKGDGLW	DKERLLGREQ	TEGALYNLAV	RIGEKFDVSP	EDIKK
Band 6:	BF2685	1 MKREEISYKN	YSKLLIKLSL	LGISFIIIVSC	NKTDLITDNP	NNELGQLPQE
		51 NGITTKITITY	SPQITRSGGD	GANDLIGYGY	NCLYATGDNP	NGAANKVIDL
		101 KRFESGVGID	PMTGKIKIFP	KGIIEESIMH	GDVTATEIFE	KSKKEFKKSI
		151 SAKGKLLKGF	LPWGGIQFSA	EYDSNFETKD	EYSFYKMDII	RNVRRLLYSS
		201 SSIERLKYFL	TDEFRYALKH	ASGTEIINDY	GTHVLVDFVL	GGKLSVWTS
		251 IDHSNKKDEL	KFKSTIKFKI	ISASASSSIS	KSNYLKNTSL	TILQAGGSEI
		301 QAVKRYIEED	GITNSDIFNY	KEWIKSINKE	TSVLVASDTK	KMIGIWEITD
		351 DPKIKTKILA	ELEKRGNNLG	IIGSKSGEIV	TGKSTPMYKL	QNEKTGELAK
		401 APNDRGYKFP	LYCQGEYGKE	MTGIGFMNYL	LSYRDFQPYQ	SAPASNDEKS
		451 WSIKFTPDGY	ITVLNKHNLK	FLCTDYKFRT	ISEDDTNSRL	WIPRYTLNMM
501 DDDTIQ						
Band 5:	BF0669	1 MKKIYKSITL	VAAILSLSSC	GNDWLDKPA	DGIPSEDAIT	NYNDALTART
		51 GMYDGIQNS	NATSYGARM	FYDGDVRAAD	MQARTQGMRS	SSCYEMLYTV
		101 DDAPNMWNI	YNVIRANRNL	IEATINEKVT	DATEAQIGKI	YSEALVVRAL
		151 VHFDLVRIY	MPYTADNGAS	LGVPVIVKPL	ERNDLPSRNT	VAEYTVQVIT
		201 DLTDAINSGY	LAKDQTPGYI	NEWAAKALLT	RVYLTGQDNE	NALKVAEDII
		251 TNSPYKLWITN	EEYVNAVYKS	NGAHTNEMIF	EVVNASNDW	TDNRGAIYLL
		301 NENGYADAIV	TKSFMNLSQ	DPKDVRIGMV	LPAQYDKDLQ	EEYGDAKIFI
		351 NKFPADKDDV	GEMRLNPLPL	LRLSEVYLSA	AEEAAKLGGH	QDKAAKYLNE
401 IVQRANPEAK	ATSEADATVE	RILERRKEM	IGEGQRYFDA	LRNNETIVRY		
451 KDEGDGKYHY	SLIKESQSFD	RTYFRALPI	PVDETNVNP	LRAQQNPGY		
Band 4:	BF1992	1 MNRNLLMPVA	VSLILLSGCK	YNDNFEGLD	DMTQPTNLMK	IEYTLTDADY
		51 ATISSNSTNK	KIATDAGVSK	DLENVKTNMY	LTEKITGADY	IPAFLLDKYY
		101 TADKSSSAKI	TYKYEAMSS	LLSEYASVKY	LKPTDAEYKL	VYGENAFAPY
		151 LNEKTEGQMS	KILNEKFKDA	EKGTAVFDY	KLGGEGLENP	LMNQNFALP
		201 TGDLEKLGW	FISSTGDTQM	KVTSYDDNQY	VQYSANGTKG	ACVGMVTPA
		251 ISVTAGDYLA	FDVTVGYNA	SCLSVLISEN	FDGENVGTAN	WVDVTSDFSI
		301 PTKPTSGYGT	FASAGKPLS	AYAGKKVYVA	FKYEGDGANK	KTTTYIDNII
		351 MVGTSIPANS	LSTPTYAVKV	YDGNKWNKS	NSVYVLYAD	YDGMGQSKRY
401 FTSVPAVNY	LPALYSKQVA	YPVDGARVV	VYRYNGTDL	KIYSDEYTS		

451 AEKARWELNT	RIVDKTEQFV	LSDGKWNFD	STVVTLKAEK	GDAETAIFYQ
501 TITDVIANK	GQEYAPIFSG	KSNNEYYS	SAYQNFDFR	PAKWRQNA
551 AYGNMSADL	TKLMFERLPE	AFLPGLKAIY	GSADVVEGVD	VFYTIINFAIY
601 DGSSTTQYTI	KYKVTGKQF	EYVADSLKKV	E	

Band 3: BF9343_3471

1 MKNLLYLSC	ALMCLGFLS	SKDDEKEIP	PVVEDVAQY	TGDKVKVTLG
51 GEAVSGDAQI	DLVQDDKSL	TIKLLNIIPD	VKEFSIPNAE	FEATTRSAYI
101 SKLSGKVSNA	VVGVDVTFEG	VVDEGLTAS	ITATEIKGDS	INAKKAGLTG
151 KTFKGMKTIN	VSNIPTPIEM	EQRVYTSVVS	KDTSAILKIKI	NDFAFQGLKL
201 GDISLDTAV	RHRGEQDGKP	IYGFKTSQE	MTLEAVGKVL	IDANGTIIGE
251 KMELSLNVNA	VTAGLTVGVD	FSGNIVEEST	DTKATITVTG	DAVAEGVTVS
301 GNTYTFKWE	STPDDQLVFI	PKIEIPATAV	LDSIIIDNR	NKKSVAEPPN
351 TAIDFSQLKE	NYVGYHVTP	EDIRYPSKMM	LKMVRIAEIN	PVYDMATWVA
401 DGFDEKPNGL	TTSNLAFAFF	PMFGIDVPTP	VVKASDAAE	ITTSRTVSAT
451 LPSTLVPQVT	AGTMFLGEFK	VDITNTLKST	HFGVPYRVKP	VNFKITYKYT
501 PGTTYFKTVV	KNNANDTEVV	PNEKDECSIN	AYLYEVDSYA	ETLDGTNINT
551 SNKVIMKAVL	EDGSAKADYV	TLTIIPFKETG	NGSFDPTKKK	YKLAIVCSSS
601 KKGDDQFMGAD	GSKLWVKYLE	VTR		

Band 2: BF638R_4406

1 MNLFKSSVLC	GMVIVSFMST	CTDVIDTMPK	GPKGDTGLSA	YEFWKEKQVAD
51 GTVNMFKDQT	EVADFFKFLK	GKDGKDGKDG	QSAFEQWKDM	IASGSVDDPH
101 NPGEKWPSEN	NTVQDFWRFL	TGASGEDGQT	PHIGDNGNWF	IGKEDTGIGA
151 RGRDGDQDKD	GKDGINGRDA	IPPTVTIGDN	GNWYINGTDT	GKPAFGKDGK
201 DGKDGKDAVP	PTVTIIGDNG	WVFDGTDGK	KAVGQDGKSP	EVAIGDNGNW
251 YINGDITGKP	AFGKDGKDGK	DGKDGANGAN	GKSAYELWKE	YISSGDVDPN
301 HNPDKQIPAD	RNKQDFWDF	LTGKSSVIEI	EVGKYNVIPE	YWNSSLKEYV
351 VPSDQSVLFT	VYDKTGKVT	AGVKVSDLPG	VSSTDAFITN	EEGQFKVTDY
401 KLPDNKGLSE	RNGSVTVTVYD	KTQETSAGNT	LVPNRINVRNA	IITSAVLSNW
451 SNTSIDIYRT	LNVYYSFERQ	VDGEMDKYPT	SITTPYNSMK	SARVKDINRP
501 VNEGVDKQDQ	LVRYSNNGSY	LYIIRPLVLT	ETEKANVAKN	DTVGLKAKYE
551 WDQNTNYAAL	YFGDGTGSYN	DYQQTIYLDQ	KIHVPEVYPA	PSFKENSVFI
601 EIKQGITMWM	GEIDTDLQD	FYKTYAYPTG	QKFTKEEGT	NVMKHEPKLL
651 PASELEENRA	VFIEMRTFIN	GTGGTVHTGS	KPLSTGGKRF	KLSTYPNW
701 IGLDIRRRTTE	STDKITYNIS	NEYRGRYAYY	LLKEEDKYLL	VDFADWSKRM
751 PLPIKDCPVD	WMN			

Band 1: BF3307

1 MKQVNLRVCR	MILPLFLGFL	LSLSAYAQQV	SVKGHVKDST	GEPIGANVV
51 VKDNSSIGTI	TDLNGNFVLS	VPQNSTLVIS	FIGYKPVEMK	AAPSVTVTLH
101 EDAVMLQEAV	VIGYGVTKKN	DVTGSVMAID	ADKMKVGMAT	SASDLLVGKA
151 AGVSVITDGG	APGAGATIRV	RGSSSMSASN	DPLIVIDGVP	VDNTEIKGMG
201 NPLSTVHPND	IETFTILKDA	SATAIYGSRA	SNGVJIIITTK	KGQSGRVKVD
251 YSGTFSISTK	SNTVDVMKAE	DFRNFVIEKF	GENSLQANAL	GKSTDMQDE
301 IFRTAFTSDH	NVSVSGAVPH	MPYRVSVAYT	NENGLKTSN	MQRLTGAINL
351 NPNFFDKKLN	IQLNVKGVYN	KNRFADRAAI	GLATQYDPTQ	PVYMEGNPYG
401 NGYFMYMKQE	GDKASPIDIG	LANPVMALLE	KDDKSTVYRS	IGNAQIDYKF
451 HFLPELRANL	NLGYDVSXSK	GDVLIADNSP	LYCTGNFKN	GFGENSHYQ
501 LKRNTLLDFY	LNYANTFGVN	YIDVMAGYSW	QHFYNSTTNS	YPYSAAYA EK
551 TGEFFYKKG	DYASESYLVS	FFGRLLNYTLL	NRYLVTFTLR	NDGSSRFSPD
601 NRWGLFPSVA	LAWKLNEESF	LKNVNAISDL	KLRLGYGVGTG	QQNLGNGDYP
651 YMARYMYSKA	GANYFYGDE	YSLIAPQPYD	QNLKWEETTT	WNVGIDYGFL
701 NGRITGTIDY	YFRKTKDLLN	TVTAPAGTNF	SNQLLTVNGT	LENKGFESI
751 NAHAVSTQDW	NNWIGNYISY	NKNKITKMTF	NDDPNYAGVI	HGGIDGGTGY
801 NALIHVRGEA	FNSFYVFEQI	YGPDKPIEG	AYVDQGNQ	INDADLICFK
851 KAAPDVFMGL	TSQLSYKND	FSFALRGSFG	NYVYNNVQSN	REAYEGANNY
901 DQTGFLKNRL	TSARSTDFKN	AQYRSSYYVQ	NASFVRMDNI	SLGYTFNKL F
951 NDKQ SARVYA	TVQNPVITK	YKGLDPEISG	EGIDNNIYPR	PRVFMIGLNL

1001

Table S2. Comparison of the secretome of wild-type ETBF and isogenic *fpn-* strains by quantitative mass spectrometry

Ratio (<i>fpn-</i> / <i>WT</i>) Protein Abundance		KEGG ID	Predicted Function	Category	Size (kD)	Signal peptide	PFAM Domains	InterPro Domains	pSORT localization (score)	SP /SP II cleavage site
						+				
0.006	BF1567	DUF 5074	Bacteroidetes specific, PKD domain	Bacteroidetes specific	50.6	Yes	PF16819:PFam:entry name:DUF5074:match status:1:	IPR031815:InterPro:entry name:DUF5074:	Unknown	Spl
0.006	BF3230	DUF 2807	Trimeric autotransporter like adhesin	Adhesin	34.0	Yes	PF10988:PFam:entry name:DUF2807:match status:1:	IPR021255:InterPro:entry name:DUF2807:	Extracellular 9.65	Spl
0.008	BF0506		Uncharacterized protein	Unknown	49.8	Yes			Extracellular 9.65	Spl
0.008	BF1992	DUF 5017	Unknown	Unknown	70.3		PF16409:PFam:entry name:DUF5017:match status:1:	IPR032185:InterPro:entry name:DUF5017:	Unknown	Spl
0.009	BF0090	DUF 3836	Bacteroidales specific	Bacteroidetes specific	15.3	Yes	PF12930:PFam:entry name:DUF3836:match status:1:	IPR024339:InterPro:entry name:DUF3836:	Unknown	Spl
0.011	BF4025		Uncharacterized protein	Unknown	95.8				Unknown	x
0.011	BF2542		Uncharacterized protein	Unknown	16.8				Unknown	Spl
0.011	BF1424		Putative quinoprotein amine dehydrogenase	Enzyme, Other	37.6	Yes		IPR011044:InterPro:entry name:Quino_amine_DH_bsu:	Unknown	Spl
0.012	BF1637		Uncharacterized protein	Unknown	16.8	Yes			Unknown	Spl
0.014	BF2685		MACPF domain, bacteriocin-like, pore forming	MACPF domain	57.1		PF01823:PFam:entry name:MACPF:match status:1:	IPR020864:InterPro:entry name:MACPF:	Unknown	Spl
0.014	BF2541		Uncharacterized protein	Unknown	15.5				Unknown	Spl
0.014	BF9343_1295		Uncharacterized protein	Unknown	43.3				Unknown	Spl
0.016	BF1524		Uncharacterized protein	Unknown	13.9	Yes			Unknown	Spl
0.016	BF9343_2214		Putative lipoprotein	Lipoprotein	21.9	Yes			Unknown	Spl
0.016	BF4024		Mfa2 Fimbrillin_C	Fimbriae	59.0		PF08842:PFam:entry name:Mfa2:match status:1:match status 1	IPR014941:InterPro:entry name:FimA_assoc_Mfa1/Mfa2:	Unknown	Spl
0.017	BF2686		Lipocalin-like, extracellular, pro-inflammatory	Lipocalin	30.2	Yes	PF13944:PFam:entry name:Calycin_like:match status:1:	IPR024311:InterPro:entry name:Lipocalin-like:	OuterMembrane 9.52	Spl
0.020	BF4311		Uncharacterized protein	Unknown	45.7				Unknown	Spl
0.021	BF638R_1207		Putative lipoprotein	Lipoprotein	54.1	Yes			Unknown	Spl
0.021	pBFP35 orf2*		Putative integral membrane protein	Membrane, Other	22.3				Unknown	x
0.022	BF9343_2956		Putative lipoprotein	Lipoprotein	29.5	Yes			Unknown	Spl
0.023	BF1209	DUF 4252	Unknown	Unknown	26.0	Yes	PF14060:PFam:entry name:DUF4252:match status:1:	IPR025348:InterPro:entry name:DUF4252:	Unknown (may have multiple localization sites.)	Spl
0.024	BF4030		Uncharacterized protein	Unknown	34.3				Unknown	x
0.024	HMPREF1080_03218*		SusD, TPR domain	SusD-like	77.9		PF07980:PFam:entry name:SusD:match status:1:	IPR011990:InterPro:entry name:TPR-like_helical_dom:	Unknown	x
0.025	BF4433	DUF 5305	Unknown	Unknown	37.2	Yes	PF17231:pfam:entry name:DUF5305:match status:1:	IPR035185:InterPro:entry name:DUF5305	Extracellular 9.65	Spl
0.025	BF638R_4428		Putative lipoprotein	Lipoprotein	28.6	Yes			Unknown	Spl
0.026	BF1680	DUF 3869	3XOG-like, putative adhesin	Adhesin	37.6	Yes	PF12985:PFam:entry name:DUF3869:match status:1:	IPR008969:InterPro:entry name:CarboxyPept-like_regulatory	Unknown	Spl
0.026	pBFP35 orf1*		Hypothetical lipoprotein	Lipoprotein	28.6				Extracellular 9.65	Spl
0.027	BF9343_3469		Putative exported protein, PCMD domain, carbol	Carbohydrate utilization	40.1	Yes	PF13201:PFam:entry name:PCMD:match status:1:	IPR025112:InterPro:entry name:PCMD:	Unknown	Spl
0.031	BF0970		SusD, TPR domain	SusD-like	77.2	Yes	PF07980:PFam:entry name:SusD:match status:1:	IPR011990:InterPro:entry name:TPR-like_helical_dom:	Unknown (may have multiple localization sites.)	Spl
0.032	BF1909		Peptidase_S41 domain, PDZ domain	Protease	47.7		PF03572:PFam:entry name:Peptidase_S41:match status:1:	IPR001478:InterPro:entry name:PDZ:	Unknown	Spl
0.033	BF1257		Endo/exonuclease/phosphatase domains	Enzyme, Other	38.1		PF03372:PFam:entry name:Exo_endo_phos:match status:1:	IPR005135:InterPro:entry name:Endo/exonuclease/phospha:	Unknown	x
0.033	BF1926		Peptidase_Mx1, metalloprotease	Protease	38.9	Yes	PF15890:PFam:entry name:Peptidase_Mx1:match status:1:	IPR030890:InterPro:entry name:LP_HEXxH_w_tonB:	Unknown (may have multiple localization sites.)	Spl
0.034	BF1330		Exo-alpha sialidase	Carbohydrate utilization	37.3	Yes	PF08522:PFam:entry name:DUF1735:match status:1:	IPR011048:InterPro:entry name:Haem_d1:	OuterMembrane 9.49	Spl
0.037	BF1568		Uncharacterized protein	Unknown	75.2				Unknown	Spl
0.038	BF1329	DUF 1735	acylhydrolase	Enzyme, Other	42.1		PF08522:PFam:entry name:DUF1735:match status:1:	IPR013728:InterPro:entry name:DUF1735:	Unknown	Spl
0.038	BF3877		Uncharacterized protein	Unknown	13.0	Yes			Unknown	Spl
0.038	BF1034		LolA_2 Bacteroides outer membrane lipoprotein	Lipoprotein	24.2	Yes	PF16584:PFam:entry name:LolA_2:match status:1:	IPR029046:InterPro:entry name:LolA/LolB/LppX:	Unknown	Spl
0.038	BF3899	DUF 4827	Bacteroides specific	Bacteroidetes specific	24.5	Yes	PF16109:PFam:entry name:DUF4827:match status:1:	IPR023252:InterPro:entry name:DUF4827:	Unknown	Spl
0.040	BF9343_3471		PCMD domain, carbohydrate binding	Carbohydrate utilization	67.7	Yes	PF13201:PFam:entry name:PCMD:match status:1:	IPR025112:InterPro:entry name:PCMD:	Unknown	Spl
0.041	BF1675		CarboxypepD_reg CarbopepD_reg_2	Carbohydrate utilization	79.0	Yes	PF13620:PFam:entry name:CarboxypepD:match status:1:	IPR013784:InterPro:entry name:Carb-bd-like_fold:	Unknown	Spl
0.043	BF4449		Putative outer membrane protein probably invol	SusD-like	75.6	Yes	PF07980:PFam:entry name:SusD:match status:1:	IPR011990:InterPro:entry name:TPR-like_helical_dom:	Unknown	Spl
0.043	BF4299	DUF 1349	Unknown	Unknown	25.3	Yes	PF07081:PFam:entry name:DUF1349:match status:1:	IPR015987:InterPro:entry name:UCP022704:	Unknown	Spl
0.043	BF1955		TssC	Other	52.2				Unknown (may have multiple localization sites.)	x
0.044	BF0772		NigD-like, Bacteroides specific, lipoprotein, puts	NigD like	27.9	Yes	PF12667:PFam:entry name:NigD:match status:1:	IPR024299:InterPro:entry name:NigD-like:	Unknown (may have multiple localization sites.)	Spl
0.044	BF0965		Lipocalin-like, Bacteroides specific	Lipocalin	19.2	Yes	PF16139:PFam:entry name:DUF4847:match status:1:	IPR023216:InterPro:entry name:DUF4847:	Unknown	Spl
0.045	BF4461		Putative outer membrane protein probably invol	SusD-like	77.1	Yes	PF07980:PFam:entry name:SusD:match status:1:	IPR011990:InterPro:entry name:TPR-like_helical_dom:	Unknown	Spl
0.045	BF0947		Possible outer membrane protein, SusD like, Ra	SusD-like	66.6		PF07980:PFam:entry name:SusD:match status:1:	IPR012944:InterPro:entry name:SusD_RagB_dom:	Unknown	Spl
0.047	BF3740		TolR, iron uptake TBDR	TBDR	22.4		PF02472:PFam:entry name:ExbD:match status:1:	IPR003400:InterPro:entry name:ExbD:	Unknown	x
0.048	BF0702		Peptidase M43, metalloprotease, Bacteroides	Protease	40.6		PF05572:PFam:entry name:Peptidase_M43:match status:1:	IPR023852:InterPro:entry name:Metalloprotease_lipop_Bf	Unknown	x
0.048	BF1925		SusD like, TPR domain	SusD-like	58.3		PF07980:PFam:entry name:SusD:match status:1:	IPR011990:InterPro:entry name:TPR-like_helical_dom:	OuterMembrane 9.52	Spl
0.048	BF0393		SusD-like, TPR domain	SusD-like	56.8	Yes	PF07980:PFam:entry name:SusD:match status:1:	IPR011990:InterPro:entry name:TPR-like_helical_dom:	Unknown	Spl
0.050	BF3274	DUF3836	Bacteroidales specific	Bacteroidetes specific	19.6	Yes	PF12930:PFam:entry name:DUF3836:match status:1:	IPR024339:InterPro:entry name:DUF3836:	Unknown	Spl
0.050	BF4129		Putative TPR-repeat family protein	TPR	53.5	Yes	PF13414:PFam:entry name:TPR_11:match status:1:	IPR019734:InterPro:entry name:TPR_repeat:	Unknown	Spl
0.050	BF1724		SusD like, Rag B like	SusD-like	58.6		PF07980:PFam:entry name:SusD:match status:1:	IPR012944:InterPro:entry name:SusD_RagB_dom:	Unknown	x
0.051	BF1723		Putative outer membrane protein probably invol	SusD-like	59.2	Yes	PF07980:PFam:entry name:SusD:match status:1:	IPR011990:InterPro:entry name:TPR-like_helical_dom:	Unknown	Spl
0.051	BF1748		LRR domain, common cell surface domain	LRR domain	38.9	Yes	PF13306:PFam:entry name:LRR_S:match status:2:	IPR022675:InterPro:entry name:LRR_dom-like:	Unknown (may have multiple localization sites.)	Spl
0.052	BF3757		IgG-like fold, collagen like protein	Adhesin	71.6	Yes	PF16130:PFam:entry name:DUF4842:match status:1:	IPR032295:InterPro:entry name:DUF4842:	Unknown	Spl
0.052	BF1634		MACPF domain, bacteriocin like, pore forming	MACPF domain	41.0	Yes	PF01823:PFam:entry name:MACPF:match status:1:	IPR020864:InterPro:entry name:MACPF:	Unknown	Spl
0.052	BF1929		DUF4856 Bacteroides specific	Bacteroidetes specific	44.9	Yes	PF16148:PFam:entry name:DUF4856:match status:1:	IPR023231:InterPro:entry name:DUF4856:	Unknown (may have multiple localization sites.)	Spl
0.052	BF1074		TPR domain	TPR	48.1			IPR013026:InterPro:entry name:TPR_contain_dom:	Unknown	Spl
0.052	BF0590		NigD-like, Bacteroides specific, lipoprotein, puts	NigD like	27.6	Yes	PF12667:PFam:entry name:NigD:match status:1:	IPR024299:InterPro:entry name:NigD-like:	Unknown	Spl
0.056	BF0408		Putative outer membrane protein probably invol	SusD-like	54.6	Yes	PF07980:PFam:entry name:SusD:match status:1:	IPR011990:InterPro:entry name:TPR-like_helical_dom:	Unknown	Spl
0.057	BF638R_0923		Putative outer membrane protein, SusD like, Ra	SusD-like	61.7		PF07980:PFam:entry name:SusD:match status:1:	IPR012944:InterPro:entry name:SusD_RagB_dom:	Unknown	Spl
0.057	BF9343_1425		Fimbrillin-like, adhesion, gut microbiome enhar	Fimbriae	69.2		PF13149:PFam:entry name:Mfa_like_1:match status:1:	IPR025049:InterPro:entry name:Mfa_like_1:	Unknown	Spl
0.059	BF9343_2885		Putative lipoprotein, Ig-like, putative adhesin	Lipoprotein, Adhesin	43.0				Unknown (may have multiple localization sites.)	Spl
0.060	BF1261		DUF 4890 Bacteroides specific	Bacteroidetes specific	18.0	Yes	PF16231:PFam:entry name:DUF4890:match status:1:	IPR032612:InterPro:entry name:DUF4890:	Unknown	Spl
0.061	BF0669		SusD like, TPR domain	SusD-like	56.2	Yes	PF07980:PFam:entry name:SusD:match status:1:	IPR011990:InterPro:entry name:TPR-like_helical_dom:	Unknown (may have multiple localization sites.)	Spl
0.061	BF1714		Putative outer membrane protein probably invol	SusD-like	60.7	Yes	PF07980:PFam:entry name:SusD:match status:1:	IPR011990:InterPro:entry name:TPR-like_helical_dom:	Unknown	Spl
0.062	BF1335		NigD-like, Bacteroides specific, lipoprotein, puts	NigD like	28.1	Yes	PF12667:PFam:entry name:NigD:match status:1:	IPR024299:InterPro:entry name:NigD-like:	Unknown	Spl
0.062	BF9343_1939		TssD	Other	16.1		PF17642:PFam:entry name:TssD:match status:1:	Unknown	Unknown	x
0.063	BF3194		Stress responsive A/B barrel	Other	11.3		PF07876:PFam:entry name:Dabb:match status:1:	IPR013097:InterPro:entry name:Dabb:	Unknown	x
0.064	BF2738		Putative periplasmic protein	Inhibitor, Other	16.7	Yes	PF11396:PFam:entry name:PepsY_like:match status:1:	IPR021533:InterPro:entry name:PepsY_like:	Unknown	Spl
0.064	BF4082		Putative RNA-binding protein RbpA	Other	8.9		PF00076:PFam:entry name:RRM_1:match status:1:	IPR000504:InterPro:entry name:RRM_dom:	Unknown	x
0.064	BF1451		DUF4468	Unknown	39.8	Yes	PF14730:PFam:entry name:DUF4468:match status:1:	IPR027823:InterPro:entry name:DUF4468:	Unknown	Spl
0.065	BF1711		Putative outer membrane protein probably invol	SusD-like	59.2	Yes	PF07980:PFam:entry name:SusD:match status:1:	IPR011990:InterPro:entry name:TPR-like_helical_dom:	Unknown	Spl

0.065	BF1655	Aldose-1-epimerase, carbohydrate binding	Carbohydrate utilization	40.2		PF01263:Pfam:entry name:Aldose_epim:match status:1:	IPR014718:InterPro:entry name:Glyco_hydro-type_carb-bd_	Unknown (may have multiple localization sites.)	x
0.069	BF0492	NigD-like, Bacteroides specific, lipoprotein, putative	NigD-like	26.1		PF12667:Pfam:entry name:NigD:match status:1:	IPR024299:InterPro:entry name:NigD-like:	Unknown (may have multiple localization sites.)	Spl
0.069	BF9343_4231	Fimbrillin-like, adhesion, gut microbiome enhancer	Fimbrae	35.5		PF13149:Pfam:entry name:Mfa_1k_1:match status:1:	IPR025049:InterPro:entry name:Mfa_1k_1:	Extracellular 9.64	Spl
0.070	BF3295	Alpha-amylase	Carbohydrate utilization	70.9	Yes	PF10438:Pfam:entry name:Cyc_maltodex_C:match status:1:	IPR015902:InterPro:entry name:Glyco_hydro_13:	Unknown (may have multiple localization sites.)	Spl
0.073	BF0953	Putative outer membrane protein probably involved	SusD-like	67.8		PF07980:Pfam:entry name:SusD:match status:1:	IPR011990:InterPro:entry name:TPR-like_helical_dom:	Unknown (may have multiple localization sites.)	Spl
0.074	BF4430	Uncharacterized protein	Unknown	160.7	Yes			Unknown (may have multiple localization sites.)	Spl
0.074	BF3787	Putative chitinase	Carbohydrate utilization	48.2		PF08522:Pfam:entry name:DUF1735:match status:2:	IPR008979:InterPro:entry name:Galactose-bd-like:	Unknown (may have multiple localization sites.)	Spl
0.075	BF6388_4424	FimA, P. gingivalis, adhesion, virulence	Fimbrae	122.2	Yes	PF06321:Pfam:entry name:P_gingi_FimA:match status:1:	IPR029141:InterPro:entry name:FimA_N:	Unknown	Spl
0.076	BF2036	Putative xylanase	Carbohydrate utilization	28.7	Yes	PF07313:Pfam:entry name:DUF1460:match status:1:	IPR023360:InterPro:entry name:Put_xylanase-like_C	Unknown (may have multiple localization sites.)	Spl
0.076	BF2976	Tetrapeptide repeat family protein	TPR	62.8	Yes	PF07179:Pfam:entry name:TPR_2:match status:1:	IPR011990:InterPro:entry name:TPR-like_helical_dom:	Unknown	Spl
0.079	BF2725	Uncharacterized protein	Unknown	24.8	Yes			Unknown (may have multiple localization sites.)	Spl
0.079	BF1254	SusD-like_2 SusD-like SusD-like_3	SusD-like	57.9	Yes	PF12771:Pfam:entry name:SusD-like:match status:1:	IPR011990:InterPro:entry name:TPR-like_helical_dom:	Unknown	Spl
0.079	BF2640	Putative glycerophosphodiester phosphodiester:Enzyme, Other	Enzyme, Other	28.5	Yes	PF03009:Pfam:entry name:GDP:match status:1:	IPR017946:InterPro:entry name:PLC-like_Pdiesterase_TIM-b	Unknown (may have multiple localization sites.)	Spl
0.082	BF3228	Putative lipoprotein DUF 4876	Lipoprotein	44.6	Yes	PF16215:Pfam:entry name:DUF4876:match status:1:	IPR032627:InterPro:entry name:DUF4876:	Unknown	Spl
0.083	BF2267	RNA binding protein	Other	9.1		PF0076:Pfam:entry name:RRM_1:match status:1:	IPR000504:InterPro:entry name:RRM_dom:	Unknown	x
0.085	BF0886	Putative glycosylhydrolase	Carbohydrate utilization	51.4	Yes	PF01120:Pfam:entry name:Alpha_L_fucos:match status:1:	IPR000933:InterPro:entry name:Glyco_hydro_29:	Unknown	Spl
0.085	BF3905	Sua5/Yco/YrdC/YwIC family protein	Other	19.4		PF01300:Pfam:entry name:Sua5_yco_yrdC:match status:1:	IPR006070:InterPro:entry name:YrdC-like_dom:	Unknown	x
0.086	BF3075	Protease/ glutamine aminotransferase	Protease	21.8		PF01965:Pfam:entry name:Di_1_Ppl:match status:1:	IPR029062:InterPro:entry name:Class_I_gatase-like:	Unknown	x
0.087	BF1328	Putative secreted endoglycosidase	Carbohydrate utilization	39.5	Yes	PF16141:Pfam:entry name:DUF4849:match status:1:	IPR013781:InterPro:entry name:Glyco_hydro_catalytic_dom	Extracellular 9.71	Spl
0.087	BF4473	Putative outer membrane protein probably involved	SusD-like	73.7	Yes	PF07980:Pfam:entry name:SusD:match status:1:	IPR012944:InterPro:entry name:SusD_RagB_dom:	Unknown	Spl
0.090	BF0192	Glycoside hydrolase family 2, beta galactosidase	Carbohydrate utilization	118.2	Yes	PF00703:Pfam:entry name:Glyco_hydro_2:match status:1:	IPR023312:InterPro:entry name:LaC2_4:	Unknown	Spl
0.092	BF0751	SusD-like SusD-like_2	SusD-like	66.2	Yes	PF12741:Pfam:entry name:SusD-like:match status:1:	IPR011990:InterPro:entry name:TPR-like_helical_dom:	Unknown	Spl
0.092	BF0727	Aminopeptidase	Protease	37.6	Yes	PF04389:Pfam:entry name:Peptidase_M28:match status:1:	IPR007484:InterPro:entry name:Peptidase_M28:	Extracellular 9.71	Spl
0.093	BF3375	Beta-galactosidase	Carbohydrate utilization	150.6	Yes	PF02929:Pfam:entry name:Bgal_small_N:match status:1:	IPR006102:InterPro:entry name:Glyco_hydro_2_lg-like:	OuterMembrane 9.49	Spl
0.093	BF0439	SusD like, RagB like	SusD-like	63.7		PF07980:Pfam:entry name:SusD:match status:1:	IPR012944:InterPro:entry name:SusD_RagB_dom:	Unknown	Spl
0.094	BF0287	Alpha-galactosidase	Carbohydrate utilization	82.2	Yes	PF16875:Pfam:entry name:Glyco_hydro_36N:match status:1:	IPR013705:InterPro:entry name:Glyco_hydro_36_C:	Unknown (may have multiple localization sites.)	Spl
0.096	BF1332	Glycosyl hydrolase, mannin catalysis	Carbohydrate utilization	37.5		PF04041:Pfam:entry name:DUF377:match status:1:	IPR023296:InterPro:entry name:Glyco_hydro_beta-prop:	Unknown	x
0.096	BF9343_2925	DPP-7 like, cell surface serine protease, P. gingivalis	Protease	81.5	Yes	PF10459:Pfam:entry name:Peptidase_S46:match status:1:	IPR019500:InterPro:entry name:Pep_S46:	Unknown (may have multiple localization sites.)	Spl
0.098	BF2230	Putative phosphatidylinositol-4-phosphate 5-kinase	Enzyme, Other	44.0	Yes	PF02493:Pfam:entry name:MDRN:match status:14:	IPR003409:InterPro:entry name:MORN:	Unknown	Spl
0.100	BF0503	Cationic outer membrane protein OmpH	OMP	19.2	Yes	PF03938:Pfam:entry name:OmpH:match status:1:	IPR005632:InterPro:entry name:Chaperone_Skp:	Unknown	Spl
0.100	BF1087	Uncharacterized protein Bacteroides specific	Bacteroidetes specific	39.0	Yes	PF16115:Pfam:entry name:DUF4831:match status:1:	IPR032265:InterPro:entry name:DUF4831:	Unknown	Spl
0.101	BF3420	Alpha-L-fucosidase	Carbohydrate utilization	49.5	Yes	PF01120:Pfam:entry name:Alpha_L_fucos:match status:1:	IPR017853:InterPro:entry name:Glycoside_hydrolase_SF:	Unknown	Spl
0.106	BF3304	Alpha-amylase	Carbohydrate utilization	106.7		PF00128:Pfam:entry name:Alpha-amylase:match status:2:	IPR013781:InterPro:entry name:Glyco_hydro_catalytic_dom	Unknown (may have multiple localization sites.)	Spl
0.106	BF9343_1339	Putative dipeptidase	Protease	61.5	Yes	PF03577:Pfam:entry name:Peptidase_C69:match status:2:	IPR005322:InterPro:entry name:Peptidase_C69:	Unknown	Spl
0.106	BF9343_1408	Fimbrillin-like, adhesion, gut microbiome enhancer	Fimbrae	34.6	Yes	PF13149:Pfam:entry name:Mfa_1k_1:match status:1:	IPR025049:InterPro:entry name:Mfa_1k_1:	Unknown	Spl
0.107	BF3122	Uncharacterized protein	Unknown	12.2				Unknown	x
0.114	BF2010	Putative aminopeptidase C	Protease	53.1	Yes	PF03051:Pfam:entry name:Peptidase_C1_2:match status:1:	IPR004134:InterPro:entry name:Peptidase_C1B:	Unknown (may have multiple localization sites.)	Spl
0.114	BF1616	Uncharacterized protein	Unknown	60.5	Yes			Unknown	Spl
0.116	BF1785	Uncharacterized protein Bacteroides specific	Bacteroidetes specific	59.3	Yes	PF16432:Pfam:entry name:DUF5029:match status:1:	IPR032210:InterPro:entry name:DUF5029:	Unknown	Spl
0.117	BF2283	DUF3332	Unknown	19.9		PF11810:Pfam:entry name:DUF3332:match status:1:	IPR021768:InterPro:entry name:DUF3332:	Unknown	x
0.117	BF4420	Ig-like fold, putative adhesion	Adhesion	36.5		PF16130:Pfam:entry name:DUF4842:match status:1:	IPR032295:InterPro:entry name:DUF4842:	Unknown	Spl
0.121	BF3780	Putative outer membrane protein probably involved	SusD-like	68.2	Yes	PF07980:Pfam:entry name:SusD:match status:1:	IPR012944:InterPro:entry name:SusD_RagB_dom:	Unknown (may have multiple localization sites.)	Spl
0.122	BF4322	Putative mannose-1-phosphate guanylyltransferase	Carbohydrate utilization	40.5		PF00483:Pfam:entry name:ntp_transferase:match status:1:	IPR029044:InterPro:entry name:Nucleotide-diphosphate_tra	Unknown	x
0.122	BF2948	Uncharacterized protein DUF 4494	Unknown	17.6		PF14902:Pfam:entry name:DUF4494:match status:1:	IPR027848:InterPro:entry name:DUF4494:	Unknown	x
0.123	BF1858	Putative xylanase	Carbohydrate utilization	80.3		PF06452:Pfam:entry name:CBM9_1:match status:1:	IPR010502:InterPro:entry name:Carb-bd_dom_fam9:	Unknown (may have multiple localization sites.)	Spl
0.125	BF3871	Uncharacterized protein	Unknown	16.3	Yes			Unknown	Spl
0.127	BF3892	Putative hydrogenase	Enzyme, Other	54.4		PF02906:Pfam:entry name:Fe_hyd_lg_C:match status:1:	IPR004108:InterPro:entry name:Fe_hydrogenase_lsu_C:	Unknown (may have multiple localization sites.)	x
0.129	BF1895	SusD like	SusD-like	71.3	Yes	PF12741:Pfam:entry name:SusD-like:match status:1:	IPR024302:InterPro:entry name:SusD-like:	OuterMembrane 9.52	Spl
0.133	BF4026	Putative outer membrane protein, TolB like	OMP	88.2		PF03160:Pfam:entry name:Calx-beta:match status:3:	IPR011042:InterPro:entry name:6-blade_b-propeller_TolB-III	Unknown	Spl
0.133	BF2440	Uncharacterized protein	Unknown	46.3				Unknown (may have multiple localization sites.)	Spl
0.137	BF4000	Subtilisin-like serine proteases	Protease	49.1	Yes	PF00082:Pfam:entry name:Peptidase_S8:match status:1:	IPR000209:InterPro:entry name:Peptidase_S8/S53_dom:	Unknown	Spl
0.138	BF1733	Beta-mannosidase	Carbohydrate utilization	99.0		PF02837:Pfam:entry name:Glyco_hydro_2_N:match status:1:	IPR008979:InterPro:entry name:Galactose-bd-like:	Unknown	Spl
0.138	BF0085	DPP-4 like, serine protease, T cell activation	Protease	80.7	Yes	PF00930:Pfam:entry name:DPPV_N:match status:1:	IPR002469:InterPro:entry name:Peptidase_S98_N:	Unknown (may have multiple localization sites.)	Spl
0.140	BF9343_1548	Putative ATP/GTP-binding protein	Other	60.6				Unknown	x
0.140	BF3305	SusE like	SusD-like	58.2	Yes	PF14292:Pfam:entry name:SusE:match status:1:	IPR025970:InterPro:entry name:SusE:	Extracellular 9.65	Spl
0.148	BF9343_1938	TsxD	Other	15.4		PF17642:Pfam:entry name:TsxD:match status:1:		Unknown	x
0.148	BF4937	putative protease	Extracellular, Other	120.2		PF07676:Pfam:entry name:PDZ:match status:3:	IPR001478:InterPro:entry name:PDZ:	Unknown	Spl
0.150	BF4526	Putative outer membrane protein probably involved	SusD-like	66.7	Yes	PF07980:Pfam:entry name:SusD:match status:1:	IPR012944:InterPro:entry name:SusD_RagB_dom:	Unknown	Spl
0.151	BF0977	Dipeptidyl peptidase IV, DPP-4 like, serine protease	Protease	84.1	Yes	PF00930:Pfam:entry name:DPPV_N:match status:1:	IPR001375:InterPro:entry name:Peptidase_S9:	Unknown	Spl
0.155	VU15_18680*	MplI	Virulence	44.4	Yes	PF16376:Pfam:entry name:fragilysinNterm:match status:1:	IPR001843:InterPro:entry name:Fragilysin:	Extracellular 9.72	Spl
0.156	BF4459	Glycoside hydrolase family 65, alpha fucosidase	Carbohydrate utilization	93.1	Yes	PF14498:Pfam:entry name:Glyco_hyd_65N_2:match status:1:	IPR016518:InterPro:entry name:Alpha-L-fucosidase:	Unknown	Spl
0.159	BF0662	Uncharacterized protein	Unknown	31.7	Yes			Unknown (may have multiple localization sites.)	Spl
0.159	BF2126	Fimbrillin C, major fimbrial subunit related to P. jimbriae	Fimbrae	58.2	Yes	PF15495:Pfam:entry name:Fimbrillin_C:match status:1:	IPR029141:InterPro:entry name:FimA_N:	Unknown (may have multiple localization sites.)	Spl
0.160	BF9343_2554	LysM, bacterial cell wall degradation, peptidoglycan	Enzyme, Other	67.1	Yes	PF01476:Pfam:entry name:LysM:match status:3:	IPR018392:InterPro:entry name:LysM_dom:	Unknown	Spl
0.165	BF4565	DUF2059	Unknown	17.0	Yes	PF09832:Pfam:entry name:DUF2059:match status:1:	IPR018637:InterPro:entry name:DUF2059:	Unknown	Spl
0.167	BF1144	Alpha-xyloridase	Carbohydrate utilization	144.3	Yes	PF16338:Pfam:entry name:DUF4968:match status:1:	IPR016134:InterPro:entry name:Cellulose_entz_dockerin_1:	OuterMembrane 9.52	Spl
0.173	BF1566	MACPF domain, bacteriocin like, pore forming	MACPF domain	54.7		PF01823:Pfam:entry name:MACPF:match status:1:	IPR020864:InterPro:entry name:MACPF:	Unknown	Spl
0.175	BF1327	SusD-like SusD-like_2 SusD-like_3	SusD-like	57.3	Yes			Unknown	Spl
0.176	BF1185	Uncharacterized protein	Unknown	20.0	Yes			Unknown	Spl
0.177	BF3907	DUF4114	Unknown	76.7	Yes	PF13448:Pfam:entry name:DUF4114:match status:1:	IPR031025:InterPro:entry name:LruC_dom:	Unknown	Spl
0.180	BF2219	Putative outer membrane protein involved in nuTDR	Unknown	121.2	Yes	PF07715:Pfam:entry name:Plug:match status:1:	IPR014766:InterPro:entry name:CarboxyPept_regulatory_do	Unknown	Spl
0.181	BF6388_3874	Putative exported protein, BACON domain	BACON	90.8	Yes	PF13004:Pfam:entry name:BACON:match status:1:	IPR024361:InterPro:entry name:BACON:	OuterMembrane 9.52	Spl
0.186	BF9343_2008	DUF 1573	Unknown	14.4	Yes	PF07101:Pfam:entry name:DUF1573:match status:1:	IPR011467:InterPro:entry name:DUF1573:	Unknown	Spl
0.189	BFAG_01064*	SusD family protein, RagB like	SusD-like	76.1		PF07980:Pfam:entry name:SusD:match status:1:	IPR012944:InterPro:entry name:SusD_RagB_dom:	Unknown	Spl
0.190	BF2101	Uncharacterized protein Bacteroidetes specific	Bacteroidetes specific	24.4	Yes	PF16246:Pfam:entry name:DUF4903:match status:1:	IPR025970:InterPro:entry name:DUF4903:	Unknown (may have multiple localization sites.)	Spl
0.190	BF3306	Putative outer membrane protein probably involved	SusD-like	60.3	Yes	PF07980:Pfam:entry name:SusD:match status:1:	IPR012944:InterPro:entry name:SusD_RagB_dom:	Unknown	Spl
0.192	BF1680	3KOG like, putative pore forming toxin, putative	Adhesion	38.0	Yes	PF12985:Pfam:entry name:DUF3869:match status:1:	IPR024620:InterPro:entry name:DUF3869:	Unknown	Spl
0.193	BF0927	Uncharacterized protein Bacteroidetes specific	Bacteroidetes specific	24.4	Yes	PF11644:Pfam:entry name:DUF3256:match status:1:	IPR021670:InterPro:entry name:DUF3256:	Unknown	Spl
0.196	BF9343_3703	Mfa2, Fimbrillin associated anchor proteins	Mfa2, Fimbrae	44.6	Yes	PF08842:Pfam:entry name:Mfa2:match status:1:	IPR014941:InterPro:entry name:FimA-assoc_Mfa1/Mfa2:	Unknown	Spl
0.201	BF4485	TPR domain	TPR	60.3		PF13181:Pfam:entry name:TPR_8:match status:1:	IPR011990:InterPro:entry name:TPR-like_helical_dom:	Unknown	x
0.203	BF1563	Mfa2, lipoprotein, Mfa1/2 major fimbrial subunit	Fimbrae	37.4		PF08842:Pfam:entry name:Mfa2:match status:2:	IPR014941:InterPro:entry name:FimA-assoc_Mfa1/Mfa2:	Extracellular 9.64	Spl

0.206 BF0475	DUF4699	Unknown	24.6	Yes			Unknown		Spl
0.207 BF638R_3592	putative exported lipoprotein	Lipoprotein	55.6	Yes	PF16272: Pfam:entry name:DUF4925:match status:1:	IPR032573: InterPro:entry name:DUF4925:	Unknown		Spl
0.210 BF4022	Hyaluronoglucosaminidase	Carbohydrate utilization	84.3	Yes	PF02838: Pfam:entry name:Glyco_hydro_20b:match status:1:	IPR017853: InterPro:entry name:Glycoside_hydrolyase_SF:	Unknown		Spl
0.211 BF1698	Putative cell surface antigen LRR domain	LRR domain	57.2	Yes	PF13306: Pfam:entry name:LRR_5:match status:2:	IPR032675: InterPro:entry name:l_dom_like:	Unknown		Spl
0.212 BF0887	Glycanase, copper binding	Carbohydrate utilization	46.5	Yes	PF09112: Pfam:entry name:N-glycanase_N:match status:1:	IPR014784: InterPro:entry name:Cu2_ascorb_mOase-like_C:	Unknown		Spl
0.224 BF1404	Secreted protein, putative porin, CFG group bac	Extracellular	30.7	Yes	PF15283: Pfam:entry name:DUF4595:match status:1:	IPR027931: InterPro:entry name:DUF4595:	Unknown (may have multiple localization sites.)		Spl
0.230 BF9343_1843	Uncharacterized protein	Unknown	47.9	Yes			Unknown		Spl
0.235 BF9343_0726	Putative lipoprotein	Lipoprotein	40.9	Yes			Unknown		Spl
0.235 BF3627	Lipoprotein DUF4493	Lipoprotein	78.7	Yes	PF14900: Pfam:entry name:DUF4493:match status:1:	IPR027840: InterPro:entry name:DUF4493:	Unknown		Spl
0.236 BF1662	SPOR domain, cell division	Other	17.8	Yes	PF05036: Pfam:entry name:SPOR:match status:1:	IPR007730: InterPro:entry name:SPOR_dom:	Unknown		Spl
0.238 VU15_18690*	Fragilysin	Virulence	44.4	Yes	PF16376: Pfam:entry name:fragilysinNterm:match status:1:	IPR024079: InterPro:entry name:MetalloPept_cat_dom:	Extracellular	10.00	Spl
0.252 BF0572	Lipoprotein, PDZ domain	Lipoprotein	24.3	Yes	PF13590: Pfam:entry name:DUF4136:match status:1:	IPR025411: InterPro:entry name:DUF4136:	Unknown		Spl
0.256 BF3813	Uncharacterized protein Bacteroides specific	Bacteroidetes specific	18.9	Yes	PF16438: Pfam:entry name:DUF5035:match status:1:	IPR022216: InterPro:entry name:DUF5035:	Unknown (may have multiple localization sites.)		Spl
0.257 BF0931	Glycosyl hydrolase family 109 protein 1	Carbohydrate utilization	52.1	Yes	PF01408: Pfam:entry name:GFO_IDH_MockA:match status:1:	IPR016040: InterPro:entry name:NAD(P)-bd_dom:	Unknown (may have multiple localization sites.)		Spl
0.264 BF9343_1449	Uncharacterized protein	Unknown	9.2	Yes			Unknown		x
0.269 BF3626	Lipoprotein DUF4493	Lipoprotein	24.3	Yes	PF14900: Pfam:entry name:DUF4493:match status:1:	IPR027840: InterPro:entry name:DUF4493:	Unknown		Spl
0.275 BF1217	Putative secreted protein, META domain	Extracellular	28.1	Yes	PF03724: Pfam:entry name:META:match status:2:	IPR005184: InterPro:entry name:DUF306_Meta_HsII:	Unknown		Spl
0.281 BF2929	TBDR	TBDR	45.8	Yes		IPR008969: InterPro:entry name:CarboxyPept-like_regulatory	Unknown		Spl
0.293 BF1460	Putative outer membrane protein	Membrane, Other	54.6	Yes			OuterMembrane	9.49	Spl
0.294 BF1682	Major outer membrane protein OmpA	OMP	40.0	Yes	PF00691: Pfam:entry name:OmpA:match status:1:	IPR006665: InterPro:entry name:OmpA/MotB_C:	OuterMembrane	9.93	Spl
0.295 BF4019	B-galactosidase	Carbohydrate utilization	71.1	Yes	PF01301: Pfam:entry name:Glyco_hydro_35:match status:1:	IPR026283: InterPro:entry name:B-gal_1-like:	Unknown		Spl
0.301 BF3631	Lipoprotein DUF4493	Lipoprotein	47.7	Yes	PF14900: Pfam:entry name:DUF4493:match status:1:	IPR027840: InterPro:entry name:DUF4493:	Unknown		Spl
0.302 BF0875	Alpha/beta hydrolase	Enzyme, Other	49.7	Yes	PF12695: Pfam:entry name:Abhydrolase_5:match status:1:	IPR024981: InterPro:entry name:DUF3887:	Unknown (may have multiple localization sites.)		Spl
0.303 BF2739	Putative beta lactamase inhibitor, PepSY like	Inhibitor, Other	31.9	Yes	PF11396: Pfam:entry name:PepSY_like:match status:2:	IPR021533: InterPro:entry name:PepSY_like:	Unknown (may have multiple localization sites.)		Spl
0.303 BF2659	Putative outer membrane protein DUF 4842, Ig- Adhesin		89.5	Yes	PF16130: Pfam:entry name:DUF4842:match status:1:	IPR032295: InterPro:entry name:DUF4842:	Unknown		Spl
0.305 BF1991	Putative TonB-dependent outer membrane prot	TBDR	102.0	Yes	PF07715: Pfam:entry name:Plug:match status:1:	IPR012910: InterPro:entry name:Plug_dom:	OuterMembrane	9.52	Spl
0.309 BF3275	Beta-glucanase	Carbohydrate utilization	31.1	Yes	PF00722: Pfam:entry name:Glyco_hydro_16:match status:1:	IPR013320: InterPro:entry name:ConA-like_dom:	Unknown		Spl
0.313 BF1897	OmpA family outer membrane protein	OMP	23.1	Yes	PF00691: Pfam:entry name:OmpA:match status:1:	IPR006664: InterPro:entry name:OMP_bac:	OuterMembrane	9.45	Spl
0.314 BF4555	Uncharacterized protein	Unknown	44.4	Yes	PF14298: Pfam:entry name:DUF4374:match status:1:	IPR025401: InterPro:entry name:DUF4374:	Unknown		Spl
0.326 BF9343_3342	Putative exported protein Lipoprotein DUF4493	Lipoprotein	65.5	Yes	PF14900: Pfam:entry name:DUF4493:match status:1:	IPR025112: InterPro:entry name:DUF4493:	OuterMembrane	9.52	Spl
0.327 BF3667	Flavodoxin	Redox, Other	18.5	Yes	PF02568: Pfam:entry name:Flavodoxin_1:match status:1:	IPR010086: InterPro:entry name:Flavodoxin_1c:	Unknown		x
0.349 BF638R_3589	PCDM domain, carbohydrate metabolism	Carbohydrate utilization	40.2	Yes	PF13201: Pfam:entry name:PCMD:match status:1:	IPR025112: InterPro:entry name:PCMD:	Unknown		Spl
0.361 BF1198	Collagen like, extracellular	Extracellular	85.3	Yes	PF01391: Pfam:entry name:Collagen:match status:1:	IPR008160: InterPro:entry name:Collagen:	Unknown		x
0.363 BF3101	Discoidin domain, BACON domain	BACON	103.6	Yes	PF00754: Pfam:entry name:F5_F8_type_C:match status:1:	IPR024361: InterPro:entry name:BACON:	Unknown		Spl
0.371 BF3632	Putative exported protein Lipoprotein DUF4493	Lipoprotein	29.1	Yes	PF14900: Pfam:entry name:DUF4493:match status:1:	IPR027840: InterPro:entry name:DUF4493:	Unknown		Spl
0.375 BF4037	Major outer membrane protein OmpA	OMP	43.3	Yes	PF00691: Pfam:entry name:OmpA:match status:1:	IPR006665: InterPro:entry name:OmpA/MotB_C:	OuterMembrane	9.93	Spl
0.393 BF3370	Putative outer membrane protein probably invol	SusD-like	64.6	Yes	PF07980: Pfam:entry name:SusD:match status:1:	IPR011990: InterPro:entry name:TPR-like_helical_dom:	Unknown (may have multiple localization sites.)		Spl
0.406 BF1298	Putative outer membrane protein OmpA	OMP	42.4	Yes	PF00691: Pfam:entry name:OmpA:match status:1:	IPR011250: InterPro:entry name:OMP/PagP_b-ri:	OuterMembrane	9.93	Spl
0.408 BF9343_0883	Uncharacterized protein DUF 4272	Unknown	56.2	Yes	PF14092: Pfam:entry name:DUF4270:match status:1:	IPR025366: InterPro:entry name:DUF4270:	Unknown		Spl
0.481 BF2138	Putative outer membrane protein probably invol	TBDR	123.5	Yes	PF07715: Pfam:entry name:Plug:match status:1:	IPR008969: InterPro:entry name:CarboxyPept-like_regulatory	OuterMembrane	9.52	Spl
0.486 BF2203	Uncharacterized protein	Unknown	26.6	Yes			Unknown		Spl
0.495 BF2536	OMP beta barrel domain	OMP	18.9	Yes	PF13505: Pfam:entry name:OMP_b-ri:match status:1:	IPR027385: InterPro:entry name:OMP_b-ri:	Unknown		Spl
0.516 BF2675	TonB-dependent outer membrane receptor	TPR	85.6	Yes	PF00593: Pfam:entry name:TonB_dep_Rec:match status:1:	IPR008969: InterPro:entry name:CarboxyPept-like_regulatory	OuterMembrane	9.93	Spl
0.520 BF3307	Outer membrane protein probably involved in n	TBDR	111.0	Yes	PF07715: Pfam:entry name:Plug:match status:1:	IPR012910: InterPro:entry name:Plug_dom:	OuterMembrane	9.52	Spl
0.539 BF3102	Putative chitinase	Carbohydrate utilization	33.0	Yes	PF00754: Pfam:entry name:F5_F8_type_C:match status:1:	IPR032527: InterPro:entry name:DUF4959:	Unknown		Spl
0.549 BF9343_1433	Putative cholesteryltransferase	Enzyme, Other	37.2	Yes	PF02275: Pfam:entry name:CBAH:match status:1:	IPR029055: InterPro:entry name:Ntn_hydrolases_N:	Unknown		x
0.549 BF3103	SusD like, RagB like	SusD-like	71.7	Yes	PF07980: Pfam:entry name:SusD:match status:1:	IPR012944: InterPro:entry name:SusD_RagB_dom:	Unknown		Spl
0.570 BF3628	PCDM domain, carbohydrate metabolism	Carbohydrate utilization	59.4	Yes	PF13201: Pfam:entry name:PCMD:match status:1:	IPR013783: InterPro:entry name:lg-like_fold:	OuterMembrane	9.49	Spl
0.590 BF9343_0567	Putative membrane protein, TBDR plug domain	TBDR	111.7	Yes	PF07715: Pfam:entry name:Plug:match status:1:	IPR012910: InterPro:entry name:Plug_dom:	Unknown (may have multiple localization sites.)		Spl
0.607 BF3397	Mfa2, Fimbriin associated anchor proteins Mf	Fimbrae	43.7	Yes	PF08842: Pfam:entry name:Mfa2:match status:1:	IPR014941: InterPro:entry name:FimA-assoc_Mfa1/Mfa2:	Unknown		Spl
0.625 BF1894	Outer membrane protein OmpI21	OMP	124.7	Yes	PF07715: Pfam:entry name:Plug:match status:1:	IPR012910: InterPro:entry name:Plug_dom:	Unknown		Spl
0.634 BF2687	HmuV, heme binding, extracellular	Hmu family	25.0	Yes	PF14064: Pfam:entry name:HmuV:match status:1:	IPR025921: InterPro:entry name:HmuV:	Extracellular	9.64	Spl
0.653 BF0571	OMP beta barrel domain	OMP	23.3	Yes	PF13505: Pfam:entry name:OMP_b-ri:match status:1:	IPR027385: InterPro:entry name:OMP_b-ri:	Unknown		Spl
0.735 BF0671	SusD like, RagB like	SusD-like	51.9	Yes	PF07980: Pfam:entry name:SusD:match status:1:	IPR012944: InterPro:entry name:SusD_RagB_dom:	Unknown		Spl
0.757 BF2844	TsxD Sfil_C	Unknown	14.7	Yes			Unknown		x
0.779 BF4460	Putative outer membrane protein probably invol	TBDR	120.8	Yes	PF07715: Pfam:entry name:Plug:match status:1:	IPR023996: InterPro:entry name:TonB-dep_OMP_SusC/RagA	OuterMembrane	9.52	Spl
0.827 BF1193	Uncharacterized protein	Unknown	57.7	Yes			OuterMembrane	9.52	Spl
1.050 BF9343_3355	SusD like, TPR domain	SusD-like	55.7	Yes	PF07980: Pfam:entry name:SusD:match status:1:	IPR011990: InterPro:entry name:TPR-like_helical_dom:	Unknown		Spl
1.663 BF1116	HmuV, heme binding, extracellular	Hmu family	23.1	Yes	PF14064: Pfam:entry name:HmuV:match status:1:	IPR025921: InterPro:entry name:HmuV:	Unknown (may have multiple localization sites.)		Spl
1.669 BF9343_3356	Putative lipoprotein DUF 4929 Bacteroides spec	Lipoprotein	45.2	Yes	PF16283: Pfam:entry name:DUF4929:match status:1:	IPR032562: InterPro:entry name:DUF4929:	Unknown		Spl
1.961 BF2099	LRR domain, common cell surface domain	LRR domain	52.9	Yes		IPR032675: InterPro:entry name:l_dom_like:	Unknown		Spl
3.527 BF0019	HmuR, Ferrichrome-iron receptor	Hmu family	89.6	Yes	PF00593: Pfam:entry name:TonB_dep_Rec:match status:1:	IPR014766: InterPro:entry name:CarboxyPept_regulatory_dor	OuterMembrane	10.00	Spl
4.069 HMPREF1080_02980*	Lipocalin-like	Lipocalin	13.9	Yes	PF13944: Pfam:entry name:Calycin_like:match status:1:	IPR024311: InterPro:entry name:Lipocalin-like:	Unknown		Spl
6.382 BF2334	Uncharacterized protein	Unknown	82.4	Yes	PF08614: Pfam:entry name:ATG16		Unknown		x
9.702 BF4004	Putative Antimicrobial protein, inhibitor, gamm	Extracellular, Other	31.8	Yes		IPR011024: InterPro:entry name:G_crystallin-rel:	Unknown		Spl

* Gene IDs are from Genbank

Table S3. Primers used for qRT-PCR

Primer	Sequence
BFT	see reference 5
FimC	F 5'-TGATTCATCTGCAGCTGCTAT-3' R 5'-TTCTCTGCGCCTGTCGGAAGAGTT-3'
DUF5017	F 5'-GCCGAAAAGCGAGATGGGAGTT-3' R 5'-TGCGGCAGCCTCTACATTACC C-3'
Putative lipoprotein	F 5'-GGATATTCAACTGTGGCCCCATTT-3' R 5'-TCAGCAATAGCAGCAGGTTTCATCC-3'
Putative Adhesin	F 5'-CCGGACAGTTGGATGGCTCAG-3' R 5'-GCCGTTACATTTTCAGCATCCAGT-3'
GapDH	F 5'-CACTTCATACGCAGGACAGGACATCA-3' R 5'-ACGCGGAATGCCATACCAGTCA-3'