

Supplementary Material to:

**Identification of iron-regulated genes of *Bifidobacterium breve* UCC2003 as a basis for controlled gene expression**

Michelle Cronin, Aldert Zomer, Gerald Fitzgerald and Douwe van Sinderen  
Bioengineered Bugs 2012 ; 3(3): In Press. DOI: 10.4161/bbug.3.3.18985

**Table S1.** Gram-positive bacterial pathogens iron uptake systems

Organism	Transporter	Function	Reference
<i>S. aureus</i>	Staphyloferrin a	Siderophore, (transferrin)	62 63
	Staphyloferrin b	Siderophore (unknown)	64
	Aurochelin	Siderophore (unknown)	65
	FhuABC	ABC transporter (ferrichrome uptake)	66 67 68
	SirABC	ABC transporter (unknown)	69
	SstABCD	ABC transporter (unknown)	70
	SitABC	ABC transporter (unknown)	71
	Glyceraldehyde 3 phosphate dehydrogenase	Transferrin receptor	72
	IsdE	Heme	73
<i>S. pyogenes</i>	FeoB	Transmembrane transporter	74
	SiuADG	ABC transporter	75
	MtsABC	ABC transporter (multi-metal transporter)	76
<i>S. pneumoniae</i>	SiaABC	ABC transporter (Heme)	77
	PiaABCD	ABC transporter	78
	PiuBCDA	ABC transporter	78
<i>B. anthracis</i>	PitADBC	ABC transporter	79
	IsdX1 & IsdX2,	Heme transport	80
<i>C. diphtheriae</i>	ciuABCD	ABC transporter (siderophore)	81
	HmuTUV	ABC transporter (Haemin & haemoglobin)	82
	HmuO	Haem oxygenase	83
<i>L. monocytogenes</i>	FhuCBDG	Heterologous siderophore (ferric hydroxymate transporter)	84
	FeoAB	Uptake of ferrous iron	84
	hupDGC	ABC transporter (Haemin/haemoglobin)	84
<i>M. tuberculosis</i>	irtAB	Transporter of Fe-carboxymycobactin	85

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Figure S1. Cluster consensus alignment of FTR1 homologs from *B. breve*, *B. longum*, *T. denticola*, *E. coli*, *Campylobacter jejuni*, *Bacillus subtilis*, *Listeria monocytogenes*, *Streptococcus thermophilus*, *Mycobacterium smegmatis* and *Saccharomyces cerevisiae*.

See next page.

# Supplementary Figure 1

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      10      20      30      40      50      60      70      80
B. breve      -----MVRRA CQSAELNTI REHDTIVADS FARAMOVDAE HQQSSEFISAR
B. longum     -----MVRRA QALRSV-----
T. denticola  -----
E. coli       MHVRNFRNSL LVTFLGLFIS MSVWASTN-Y APLIEDIEQR LDKTAELYQQ QHAEARRTV QMAYFEVFN LEGPFRINIS
C. jejuni     --MKIFK--L LPLITSLFIS SSAPARVDDY INEAKLTKDM LKQSIETYYK GDNIGAKKLS EDAYFQHFEN MEGPFRGNIG
B. subtilis   -----
L. monocytogenes -----
S. thermophilus -----M LVLLAWRKEA TLVKHSLKKD LVLGLLALF WTYPVAESY SDLYKITA TTAVQNKDQA
M. smegmatis  -----
S. cerevisiae -----
Clustal Consensu -----

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      90      100     110     120     130     140     150     160
B. breve      AMAAVVFLFA LIAATFLPAA VIPQSAPADP PCATVVTAAD KTDTSQVEYT TWADVSKAIE AQLQAGAKRY KSCNT-----
B. longum     VLAIVFLFA KVIATVADAV TAP-MAFADS STS----SSS SSSSSVSDYA TWAEVSKAMD KQLNSGLKTY KCGNT-----
T. denticola  -----
E. coli       ARKSYEMESA FGEIRRMIGE KKLADYQAR LDKLKAALRE VEPVLGGHR LVAEELQNAL SRDDIAVHWQ ES-----
C. jejuni     -RKAITMRK FVNLRMYKD KAPLITQNAL LDSIYYIDLR VAPLQNGYR LKAGASITNY DKAKARKSSI KANAKRQADA
B. subtilis   --GLALITFS LKLVFG-- SAHAARDFP TAALITQNKQ MTKSVKDCDM DSAQQTDTTF -----
L. monocytogenes LIGRFMLLS VLAVVLCVNF SETFAAEKPK LDKPKALEQ TETAVALDY FKAKEAFQED -----
S. thermophilus KAKELVALIK TDFETKENHD SKAGKVSKA LDKGDTSEE DLTSISSALL KFEKQNPVD LDAEKEKLET HFN-----
M. smegmatis  -----
S. cerevisiae -----
Clustal Consensu -----

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      170     180     190     200     210     220     230     240
B. breve      -----AGS TSAFMSAYNT IYASNPFAV
B. longum     -----AGA TSDFMGAYNK IYVASNPFAV
T. denticola  -----
E. coli       -----
C. jejuni     KALTAQMGCV DKKDLAQSSI TTTQASTPANN DTPSKLTDINA GTDIQAAAAM DARIQPTLGN ISTKFSQAAK APKKKNYQAS
B. subtilis   -----
L. monocytogenes -----
S. thermophilus -----
M. smegmatis  -----
S. cerevisiae -----
Clustal Consensu -----

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      250     260     270     280     290     300     310     320
B. breve      VRDTISSDKQ TAQQQAFQDI QNLSYTAGND DQLCQKIDAL SADL-DATAQ QLDANTQLAK PKQYKENLQK QIAKE----
B. longum     VHDITGADKQ LAQQQAFQSV QNLSYTPSND DQLAQKIDAL TADL-DATAQ QLDNTADLAK PKAYEALQA QIAKE----
T. denticola  -----
E. coli       SQHVQARVYQ GEKNSMEMMS LRQNRSAKDA ASINQQFSSL LALTAQPDHL N-DVSYQVIT LQDIEELIF GLPTTRDUQQ
C. jejuni     KDFLNDALFS DYRNTKVRTI VKKPTKAGND QKTQQATRTI TRQNDAKTD FKGLRDGLGN TRFQFDFVFI QTPNS----
B. subtilis   -----K AKWKEEFSI KKENLSSHSE MDANIAMISL SFINQDARKL KIQLEELASH LETYQAVVL KKTSS----
L. monocytogenes -----K LKWSENKQVV KEKSYDLAQQ IDRQIABISL GILNNDKQQA MDGITSLSHLN LKTYQEGTYT DKE-----
S. thermophilus RRTYGELKNA WTRNEAVVRD HSTAYYKIE TAISLSSSI ETEPTDFTSI QSSYDDLKGG IDDFIKGVPL DSTSS----
M. smegmatis  -----
S. cerevisiae -----MPNKV FNVAVFVVF RECLEAVIVI SVILSPKQA IGHDRALYR KIRIQ----
Clustal Consensu -----

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      330     340     350     360     370     380     390     400
B. breve      ---RKELDAK KRRTKN-TAK QNKDVADAML PILDNAYKAY EGGDAAKGAT LVNDAYYQHY EKLGFERTVL SAISGNRVSQ
B. longum     ---RKELDAK KKNPKGNR SWKDVANEMT PILDNAYKAY EKGDGAKGAT LVNNAYYQY EKLGFERNVM NAISGNRVSQ
T. denticola  ---KEDLST----- -WTKIVEKME IELNAYELY TQGTREAYD EVNAAVFRYY ESKGMKCTM SYLSGARKTA
E. coli       VAAAQSAUN: PAADRGNRRY DWAEVITGIN QSIQCAIARY QGGDAKNAII DIDDYDFRF EASGMEN-KI GSRDSAPKTT
C. jejuni     ---ELSSLQI SGFNDETRKR DYARVSNDR LALDGLKNY DGFAS-IVD DLGGIYLDIF EASGMEN-KI GAVDSGLKLL
B. subtilis   -----G QSRASLTAYI QSLKDTKQFI EKKQLDEASS AIDNLTSWL AVESGVVSQS KEAYTCHQN
L. monocytogenes -----G NTNITLSSYI AKLTATKKLI DEKEWAKAST QIQDLKTEWL AVESGVVSQS QAAVNTDRD
S. thermophilus -----S LTKLYGI KLEKALSQF QAGDEKATA SMKKFITWP TIEDDVSTIN PSLYAS----
M. smegmatis  -----
S. cerevisiae -----VWGVVILGPI ICAACAGPI GAYYSQKD IEGSARDIWE GIPCMIAITM ISMMGIPMR
Clustal Consensu -----

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