Supporting Information

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Table S1. Bacterial strains and plasmids used in this study

Strain	Relevant characteristics	Source
Bacteroides fragilis		
ADB77	TM4000Δ*thyA*, Tp^R, 638R derivative	1
ADB267	ADB77Δ*oxe*	Present study
ADB266	ADB77Δ*cydAB*	2
IB260	638RΔ*kat*::Tet^R	3
IB263	638R*oxyR*^{c}	4
MBD616	TM4000 $thyA_2$Δ*sodA*	Laboratory strain
ADB267/616	ADB77Δ*oxe*Δ*sod*	Present study
YT135	TM4000 *batD*::Tn*4400*′	5
BM28	ADB77Δ*ahpC*	6
BM37	ADB77Δ*kat*	6
BM50	BM28Δ*kat*	6
BM95	ADB77Δ*tpx*	6
BM105	BM50 Δ*tpx*	6
BM104	ADB267Δ*ahpC*Δ*kat*Δ*tpx*	Present study
BM131	BM28 Δ*tpx*	Present study
BM2	ADB77Δ*rub*	Present study
BM118	ADB77Δ*oxyR*	Present study
BM134	Δ*rubrerythrins*	Present study
Escherichia coli		
DH5∝	λ nonlysogen	7
HB101	*rpsL20*, host strain for pRK231	8
Plasmids		
RK231	RP4 derivative, Tet^R, tra^+	9
pADB242	pYT102 derivative, 0·35 kb BamHI–HindIII fragment replaced by 18 bp BamHI–HindIII fragment from pCR2.1-TOPO (Invitrogen) Cm^R	10
pADB267	pADB242::Δ*oxe*	Present study
pADB293	pJST61*oxe*$^+$	Present study
pJST61	*B. fragilis–E. coli* shuttle vector, Erm^R, Amp^R	8

oxyR^c, constitutively-active oxyR. R, resistant.

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5. Tang YP, Dallas MM, Malamy MH (1999) Characterization of the Batl (*Bacteroides* aerotolerance) operon in *Bacteroides fragilis*: Isolation of a *B. fragilis* mutant with reduced aerotolerance and impaired growth in *in vivo* model systems. *Mol Microbiol* 32:139–149.
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7. Woodcock DM, et al. (1989) Quantitative evaluation of *Escherichia coli* host strains for tolerance to cytosine methylation in plasmid and phage recombinants. *Nucleic Acids Res* 17: 3469–3478.
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9. Godoy VG, Dallas MM, Russo TA, Malamy MH (1993) A role for *Bacteroides fragilis* neuraminidase in bacterial growth in two model systems. *Infect Immun* 61:4415–4426.
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Table S2. Primers used in this study

Primer no.	Region of homology	Sequence
61RAB	pADB242	GGCGCGCCGTAAGGAAAGTGGCTCTCAG
646J	Tn*4400′*	GACTTGGATACCTCACGC
Bacteroides fragilis		
oxe1	Upstream of *oxe*	GAAGAAGCTTTGAGTGTGGACGG
oxe2	*oxe*	GGGCCATGGGCCACATTCCCTCAAAGAGG
oxe3	*oxe*	AGACCATGGCACGTGCTATGGCC
oxe4	*nagB*	TGCGGATCCAGGTGATCTGCTTCG
oxe5	upstream of *oxe*	GCAATGACTGCGGATCGAGGTG
oxe6	upstream of *oxe*	CCTGGGATCCGATCTGATACTTGAGCG
oxe7	*nagB*	CGCCGGATCCGAAACGGACTGATAGTCCG
BAM21	*rubredoxin*	CGATGGATCCGGACTTGGAACGATCTGC
BAM22	*rubredoxin*	TGACCCATGGCTTCCGGATCACCTATCTC
BAM23	*rubredoxin*	GGCACCATGGGGTATGCCCTCTGTGTGGAG
BAM24	*rubredoxin*	AGGTGCGGCCGCGGAGGTATGCTTTCTAC
BAM25	*rubredoxin*	GACGATGGCATTCAGTGG
BAM251	*oxyR*	ACATGGATCCGGAGATTATTGAATTTACCAAACG
BAM252	*oxyR*	ACATCCATGGCGGAACTGGTCCACAG
BAM253	*oxyR*	ACATCCATGGGAAAGAGGAGATTCAGGCGG
BAM254	*oxyR*	ATATGCGGCCGCACAATGAAGATTCCC
BAM255	*oxyR*	CGGCAAGCAGTTGCTGTAATGACAGTACG
BAM263	*rubrerythrinA*	GCAGATGTTGCAGAACAGGA
BAM264	*rubrerythrinA*	AGACATGCCGGACATACCTC
BAM265	*rubrerythrinA*	TCATGGGCGAATGTACTGAA
BAM266	*rubrerythrinA*	CATACGCAATCACCCAACAG
BAM267	*rubrerythrinA*	ACATGGATCCCGAATATGTCAGCAATCTGGG
BAM268	*rubrerythrinB*	ACATTCTAGAAGCAAATGATGTCAGCAAATTC
BAM269	*rubrerythrinB*	ATTATCTAGATGTCTGCATCCACAAGCATAC
BAM270	*rubrerythrinB*	ACATGCGGCCGCGGAAGAGACTAAAAAAC
BAM271	*rubrerythrinB*	CACCAGTTGACTGTGTCGAAATGCCG
BAM272	*rubrerythrinB*	ACATGGATCCGTATTAAAGGCACTCAGACAG
BAM273	*rubrerythrinB*	ATTAGCGGCCGCCCTTTTTCTGCAATAGAG
Bacteroides thetaiotaomicron		
BAM110	Upstream of *oxe*	AAGAATGAAAGAAAGGGGAGC
BAM111	*oxe*	GAATCCTTCAATCATGCCGAA
BAM112	*oxe*	GGAGGACTGCCTATCACTACC
BAM113	*nagB*	AATGTGCAGCCCACTGAGATA