Table S1. DNA sequences of the oligonucleotides used in this study

Primer	Sequence 5'-3'	Purpose
s089WF	GGGTGACTCCTTCAAAACCAACATAAGGAGTCACCAGTGTAGGCTGGAGCTGCTTCG	Deletion of *s089* from SXT
s089WR	GAGTGTTACTTGGTTTTTCATGATGTTCTCCTCGTCATTCCGGGGATCCGTCGACC	Deletion of *s089* from SXT and R391
ssb1WF	GTGTGCACTGAGTTCAACTAAGACGAGGAGAACATCGTGTAGGCTGGAGCTGCTTCG	Deletion of *ssb* from SXT
ssb1WR	AAGTACTCCCGGCTGGGTTAAAGCGTTTTTGCTCGGATTCCGGGGATCCGTCGACC	Deletion of *ssb* from SXT
R66WF	GGGTGACTCCTTCAAAACCAAATTATGGAGTCACCAGTGTAGGCTGGAGCTGCTTCG	Deletion of *s089* from R391
ssb2WF	GTGTGCACAGAGTTCAACTAAGACGAGGAGAACATCGTGTAGGCTGGAGCTGCTTCG	Deletion of *ssb* from R391
ssb2WR	AAGTACTCCCGGCTGGGTTAAAGCGTTTTCGCTCGGATTCCGGGGATCCGTCGACC	Deletion of *ssb* from R391
setD2wF	CTATCGCAATATTTTACATGAACTGGAGGTCCGTCAATTCCGGGGATCCGTCGACC	Deletion of *setDC* from SXT
setC2wR	CACGGGCGGTGCACAATCAAATCATGTATCAGCATGGTGTAGGCTGGAGCTGCTTCG	Deletion of *setDC* from SXT
65lacZ42BF	ATTGTCGGAGTCCACAATGGAAAAACCAAAGCTAATCCAAGCCGTCGTTTTACAACGTCGT	LacZ fusion of *bet* in SXT
65lacZ42BR	AGAATAATCCCGTCAGGGTTAGTAAAATGAATGCGTGGCGGTGTAGGCTGGAGCTGCTTCG	LacZ fusion of *bet* in SXT
66lacZ42BF	CCTCAAAGGAGACAATATGAAGGTTATCGACCTATCACAAGCCGTCGTTTTACAACGTCGT	LacZ fusion of *exo* in SXT
66lacZ42BR	AGCGCATGAGAAAGGAGCCGAAATCGGCTCCAAGTGAACGGTGTAGGCTGGAGCTGCTTCG	LacZ fusion of *exo* in SXT
setDF	CTGGAATTCGCAAAGAGTGCTTTCTATCTA	Construction of pGG2B
setC2R	TTGCTTAAGTAGTACTCTCAAAGTGCACG	Construction of pGG2B
orfZTOPOF	TAATTTGGAGATCTTCCATGACTAA	Construction of pGG7
corfZR	TTACTTTGCAGCTTGTGCTAAC	Construction of pGG7
6389F	CGATTCCGTAAAGCGCACTGACC	Construction of pGG32
6389R	CGAGCAAGCAATCGCAAAAGCG	Construction of pGG32
s089-C	TGCAAAACTGAGCTGGTCG	RT-qPCR *s089*
s089-D	GTCGTACTGATGTGGCTCTTTG	RT-qPCR *s089*
ssb-A	TTCGAGATCGTGGTGGATTAA	RT-qPCR *ssb*
ssb-B	CAGATGCTTTGTTCACATTATCAAG	RT-qPCR *ssb*
bet-A	AAACAAAGTCTCCCTGGATGG	RT-qPCR *bet*
bet-B	ATGGACCATCTACACGGTAAGG	RT-qPCR *bet*
exo-A	ACTTTCTTCTGCCGTTATGTGC	RT-qPCR *exo*
exo-B	GATGCTGTACTTGCACCCAATA	RT-qPCR *exo*
orfZ-A	GACTAAATCAGCCTCACTTTTTCG	RT-qPCR *orfZ*
orfZ-B	CTTTGCAGCTTGTGCTAACGC	RT-qPCR *orfZ*
RTlacZF	GTGACGTCTCGTTGCTGCAT	RT-qPCR *lacZ*
RTlacZR	CACCCTGCCATAAAGAAACTG	RT-qPCR *lacZ*
s073RT	GCATGACGAGTCACCACGACAG	Reverse transcription *s073*
TSS89up4	GTTTAAGGAGGCTAGCTACCTC	Primer extension analysis
betTAlacZF1	TAAGGAGTCCACAATGGAAAAACC	Construction of pDPL373
betTAlacZF2	TAACCACTTTGATTGTCGGAGTCC	Construction of pDPL374
betTAlacZF3	TAAGGGAGTACTTTCCCGTCAGG	Construction of pDPL375
exoTAlacZF1	TAAAGGAGACAATATGAAGGTTATCG	Construction of pDPL376
exoTAlacZF2	TAATTCTCTCCTTCGGGGGAGTCT	Construction of pDPL377
exoTAlacZF3	TAAAGGGGAGTTCTCTCCTTCGG	Construction of pDPL378
lacZTAcommonR	TTATTTTTGACACCAGACCAACTGG	Construction of pDPL plasmids

Table S2. RecT and YqaJ family proteins

RecT				YqaJ									
ACCESSION #	**GI**	**PROTEIN ID**	**SIZE**	**ACCESSION #**	**GI**	**PROTEIN ID**	**SIZE**	**STRAIN/MICROORGANISM**	**TAXON (ORDER)**	**LOCALIZATION**	**ICE or Plasmid**	**FAMILY**	**NOTES**
AAL59710.1	GI:21885304	SXT bet	272 aa	AAL59709.1	GI:21885303	SXT exo	338 aa	Vibrio cholerae MO10	vibrionales	ICE	SXT	SXT/R391	ssb-bet-orfZ-exo
AAM08027.1	GI:20095161	R391 bet	272 aa	AAM08015.1	GI:20095149	R391 exo	338 aa	Providencia rettgeri	enterobacteriales	ICE	R391	SXT/R391	ssb-bet-orfZ-exo
YP_962550.1	GI:120597976	phage recombination protein Bet	272 aa	YP_962551.1	GI:120597977	endonuclease-like phage-like protein	338 aa	Shewanella sp. W3-18-1	alteromonadales	ICE	ICESpuPO1	SXT/R319	ssb-bet-orfZ-exo
YP_002152166.1	GI:197286294	phage recombination protein	272 aa	YP_002152164.1	GI:197286292	plasmid-like protein	338 aa	Proteus mirabilis HI4320	enterobacteriales	ICE	ICEPmiUSA1	SXT/R319	ssb-bet-orfZ-exo
YP_002879411.1	GI:229608763	hypothetical protein VCD_003685	272 aa	YP_002879409.1	GI:229608761	DNA recombination protein	338 aa	Vibrio cholerae MJ-1236	vibrionales	ICE	ICEVchBan9	SXT/R391	ssb-bet-orfZ-exo
YP_004936301.1	GI:360034538	phage recombination protein	272 aa	YP_004936303.1	GI:360034540	endonuclease-like phage-related protein	338 aa	Vibrio cholerae O1 str. 2010EL-1786	vibrionales	ICE	UD	SXT/R391	ssb-bet-orfZ-exo
YP_908670.1	GI:118601970	DNA recombination protein	343 aa	YP_908671.1	GI:118601971	hypothetical protein P91278ORF_073	336 aa	Photobacterium damselae subsp. piscicida	vibrionales	Plasmid	pP91278	IncA/C	ssb-bet-exo
YP_908491.1	GI:118614708	DNA recombination protein	343 aa	YP_908492.1	GI:118614709	hypothetical protein P99018ORF_081	336 aa	Photobacterium damselae subsp. piscicida	vibrionales	Plasmid	pP99-018	IncA/C	ssb-bet-exo
YP_001101797.1	GI:134044549	phage recombination protein Bet	329 aa	YP_001101798.1	GI:134044499	hypothetical protein YR71pYR1_0104	336 aa	Yersinia ruckeri	enterobacteriales	Plasmid	pYR1	IncA/C	ssb-bet-exo
YP_001102187.1	GI:134044924	phage recombination protein Bet	329 aa	YP_001102188.1	GI:134044856	putative phage-type endonuclease	336 aa	Yersinia pestis biovar Orientalis str. IP275	enterobacteriales	Plasmid	pIP1202	IncA/C	ssb-bet-exo
YP_001101983.1	GI:134047188	phage recombination protein Bet	329 aa	YP_001101984.1	GI:134047100	phage-type endonuclease	336 aa	Salmonella enterica subsp. enterica serovar Newport str. SL254	enterobacteriales	Plasmid	pSN254	IncA/C	ssb-bet-exo
YP_002894450.1	GI:237810011	Bet	329 aa	YP_002894451.1	GI:237810012	hypothetical protein pAR060302_0105	336 aa	Escherichia coli	enterobacteriales	Plasmid	pAR060302	IncA/C	ssb-bet-exo
YP_002894646.1	GI:237810207	Bet	329 aa	YP_002894647.1	GI:237810208	hypothetical protein pAM04528_0111	336 aa	Salmonella enterica	enterobacteriales	Plasmid	pAM04528	IncA/C	ssb-bet-exo
YP_002995586.1	GI:242348025	phage recombination protein Bet	331 aa	YP_002995587.1	GI:242348026	putative phage-type endonuclease	336 aa	Aeromonas hydrophila	aeromonadales	Plasmid	pRA1	IncA/C	ssb-bet-exo
YP_002474064.1	GI:219857032	DNA recombination protein	373 aa	YP_002474069.1	GI:219857037	putative DNA recombination protein	352 aa	Pseudomonas sp. CA10	pseudomonadales	Plasmid	pCAR1.2	IncP-7	ssb-bet-exo
YP_003617122.1	GI:296100205	DNA single-strand annealing protein	363 aa	YP_003617126.1	GI:296100209	putative DNA-processing protein	347 aa	Pseudomonas putida	pseudomonadales	Plasmid	pDK1	IncP-7	ssb-bet-exo
NP_758659.1	GI:27228609	DNA recombination protein	373 aa	NP_758663.1	GI:27228613	putative DNA recombination protein	352 aa	Pseudomonas resinovorans	pseudomonadales	Plasmid	pCAR.1	IncP-7	ssb-bet-exo
NP_640183.1	GI:21233885	DNA recombination protein	510 aa	NP_640184.1	GI:21233886	DNA recombination protein	375 aa	Proteus vulgaris	enterobacteriales	Plasmid	Rts1	IncT	ssb-bet-exo
YP_957258.1	GI:120537201	RecT protein	319 aa	YP_957256.1	GI:120537199	Phage-related protein endonuclease-like	334 aa	Marinobacter aquaeolei VT8	alteromonadales	Plasmid	pMAQU02	UD	ssb-bet-exo
YP_003456916.1	GI:288986953	phage recombination protein Bet	299 aa	YP_003456917.1	GI:288986954	phage-type endonuclease	334 aa	Allochromatium vinosum DSM 180	chromatiales	Plasmid	pALVIN02	UD	bet-exo
NP_040617.1	GI:9626281	bet	261 aa	NP_040616.1	GI:9626280	exonuclease	226 aa	Enterobacteria phage lambda	enterobacteriales	Bacteriophage	Lambda	Siphoviridae	gam-bet-exo
NP_049474.1	GI:9632480	Bet protein	261 aa	NP_049473.1	GI:9632479	exonuclease	225 aa	Enterobacteria phage 933W	enterobacteriales	Bacteriophage			
NP_050513.1	GI:9633410	bet	261 aa	NP_050512.1	GI:9633409	exonuclease	226 aa	Enterobacteria phage VT2-Sakai	enterobacteriales	Bacteriophage			
NP_286500.1	GI:15800488	Bet recombination protein of prophage CP-933K	215 aa	NP_286499.1	GI:15800487	exonuclease	226 aa	Escherichia coli O157:H7 str. EDL933	enterobacteriales	Prophage-like			
NP_286953.1	GI:15800937	betW gene product	261 aa	NP_286952.1	GI:15800936	exoW gene product	225 aa	Escherichia coli O157:H7 str. EDL933	enterobacteriales	Prophage-like			
NP_288694.1	GI:15802667	recombination protein Bet of prophage CP-933V	261 aa	NP_288695.1	GI:15802668	exonuclease of prophage CP-933V	225 aa	Escherichia coli O157:H7 str. EDL933	enterobacteriales	Prophage-like			
NP_309202.1	GI:15830429	recombination protein Bet	261 aa	NP_309201.1	GI:15830428	exonuclease	226 aa	Escherichia coli O157:H7 str. Sakai	enterobacteriales	Prophage-like			
NP_311028.1	GI:15832255	hypothetical protein ECs3001	261 aa	NP_311029.1	GI:15832256	exonuclease	225 aa	Escherichia coli O157:H7 str. Sakai	enterobacteriales	Prophage-like			
NP_298937.1	GI:15838249	hypothetical protein XF1648	308 aa	NP_298936.1	GI:15838248	hypothetical protein XF1647	547 aa	Xylella fastidiosa 9a5c	xanthomonadales	Prophage-like			
NP_390505.1	GI:16079681	DNA recombination protein; skin element	284 aa	NP_390506.1	GI:16079682	nuclease; skin element	319 aa	Bacillus subtilis subsp. subtilis str. 168	bacillales	Prophage-like			
NP_463513.1	GI:16798835	putative recombinase	271 aa	NP_463512.1	GI:16798834	gp47	319 aa	Listeria phage A118	bacillales	Bacteriophage			
NP_612983.1	GI:20065900	Bet protein	261 aa	NP_612980.1	GI:20065897	hypothetical protein Stx2Ip102	225 aa	Stx2 converting phage I	enterobacteriales	Bacteriophage			
NP_690727.1	GI:22855121	hypothetical protein SPP1p076	287 aa	NP_690722.1	GI:22855116	hypothetical protein SPP1p071	311 aa	Bacillus phage SPP1	bacillales	Bacteriophage			
NP_753445.1	GI:26247405	recombination protein Bet of prophage	261 aa	NP_753443.1	GI:26247403	exonuclease encoded by prophage	226 aa	Escherichia coli CFT073	enterobacteriales	Prophage-like			
NP_779225.1	GI:28198911	hypothetical protein	308 aa	NP_779226.1	GI:28198912	hypothetical protein	550 aa	Xylella fastidiosa Temecula1	xanthomonadales	Prophage-like			
NP_781721.1	GI:28210777	hypothetical protein CTC01075	268 aa	NP_781720.1	GI:28210776	hypothetical protein CTC01074	447 aa	Clostridium tetani E88	clostridiales	Prophage-like			
NP_782702.1	GI:28211758	recT protein	268 aa	NP_782703.1	GI:28211759	hypothetical protein CTC02146	306 aa	Clostridium tetani E88	clostridiales	Prophage-like			
NP_805690.1	GI:29142348	bacteriophage recombination protein	261 aa	NP_805691.1	GI:29142349	exonuclease	226 aa	Salmonella enterica subsp. enterica serovar Typhi str. Ty2	enterobacteriales	Prophage-like			
NP_848242.1	GI:30387413	RecT	340 aa	NP_848243.1	GI:30387414	hypothetical protein epsilon15p35	299 aa	Enterobacteria phage epsilon15	enterobacteriales	Bacteriophage			
NP_888735.1	GI:33601175	phage-related DNA recombination protein	328 aa	NP_888734.1	GI:33601174	phage-related exonuclease	215 aa	Bordetella bronchiseptica RB50	burkholderiales	Prophage-like			
NP_944238.1	GI:38640317	Bcep22gp10	337 aa	NP_944240.1	GI:38640319	Bcep22gp12	303 aa	Burkholderia phage Bcep22	burkholderiales	Bacteriophage			
YP_063133.1	GI:50955845	phage recombination protein	261 aa	YP_063132.1	GI:50955844	phage recombination protein	331 aa	Leifsonia xyli subsp. xyli str. CTCB07	actinomycetales	Prophage-like			
YP_070310.1	GI:51596119	hypothetical protein YPTB1784	280 aa	YP_070309.1	GI:51596118	hypothetical protein YPTB1783	534 aa	Yersinia pseudotuberculosis IP 32953	enterobacteriales	Prophage-like			
YP_078630.1	GI:52079839	recombination and repair protein RecT	273 aa	YP_078629.2	GI:163119372	phage-like protein	312 aa	Bacillus licheniformis DSM 13 = ATCC 14580	bacillales	Prophage-like			
YP_235897.1	GI:66046056	RecT protein	295 aa	YP_235898.1	GI:66046057	hypothetical protein	553 aa	Pseudomonas syringae pv. syringae B728a	pseudomonadales	Prophage-like			
YP_248965.1	GI:68249853	recombinational DNA repair protein, RecE pathway	306 aa	YP_248964.1	GI:68249852	hypothetical protein NTHI1491	214 aa	Haemophilus influenzae 86-028NP	pasteurellales	Prophage-like			
YP_403019.1	GI:82776670	bet gene product	261 aa	YP_403018.1	GI:82776669	exonuclease	226 aa	Shigella dysenteriae Sd197	enterobacteriales	Prophage-like			
YP_454855.1	GI:85059153	recombination and repair protein RecT	337 aa	YP_454856.1	GI:85059154	hypothetical protein SG1176	298 aa	Sodalis glossinidius str. 'morsitans'	enterobacteriales	Prophage-like			
YP_497969.1	GI:87200712	rect protein	294 aa	YP_497970.1	GI:87200713	Phage-like protein endonuclease-like	303 aa	Novosphingobium aromaticivorans DSM 12444	sphingomonadales	Prophage-like			
YP_540289.1	GI:91210303	recombination protein Bet of prophage	261 aa	YP_540288.1	GI:91210302	prophage CP-933K exonuclease	226 aa	Escherichia coli UTI89	enterobacteriales	Prophage-like			
YP_669053.1	GI:110641323	bacteriophage recombination protein	261 aa	YP_669052.1	GI:110641322	exonuclease	226 aa	Escherichia coli 536	enterobacteriales	Prophage-like			
YP_695388.1	GI:110800960	RecT family protein	289 aa	YP_695387.1	GI:110800330	hypothetical protein CPF_0938	303 aa	Clostridium perfringens ATCC 13124	clostridiales	Prophage-like			
YP_719631.1	GI:113461562	phage recombinase	311 aa	YP_719632.1	GI:113461563	hypothetical protein HS_1420	222 aa	Haemophilus somnus 129PT	pasteurellales	Prophage-like			
YP_764458.1	GI:115334612	DNA-binding phage-related protein	289 aa	YP_764457.1	GI:115334611	YqaJ	321 aa	Geobacillus phage GBSV1	bacillales	Bacteriophage			
YP_794099.1	GI:116222044	recombination protein Bet	261 aa	YP_794098.1	GI:116222043	exonuclease	226 aa	Stx2-converting phage 86	enterobacteriales	Bacteriophage			
YP_852238.1	GI:117623325	recombination protein Bet of prophage	261 aa	YP_852237.1	GI:117623324	exonuclease encoded by prophage CP-933K	226 aa	Escherichia coli APEC O1	enterobacteriales	Prophage-like			
YP_853641.1	GI:117624728	recT gene product	340 aa	YP_853640.1	GI:117624727	hypothetical protein	299 aa	Escherichia coli APEC O1	enterobacteriales	Prophage-like			
YP_917501.1	GI:119386446	Fis family transcriptional regulator	323 aa	YP_917502.1	GI:119386447	hypothetical protein	322 aa	Paracoccus denitrificans PD1222	rhodobacterales	Prophage-like			
YP_001375846.1	GI:152976329	recombination and repair protein RecT	268 aa	YP_001375848.1	GI:152976331	YqaJ protein	311 aa	Bacillus cytotoxicus NVH 391-98	bacillales	Prophage-like			
YP_001425586.1	GI:155042919	DNA binding phage related protein RecT	289 aa	YP_001425585.1	GI:155042966	Putative endonuclease	322 aa	Bacillus virus 1	bacillales	Bacteriophage			
YP_001461932.1	GI:157155950	phage recombination protein Bet	261 aa	YP_001461931.1	GI:157156284	exonuclease	226 aa	Escherichia coli E24377A	enterobacteriales	Prophage-like			
YP_001468882.1	GI:157325459	gp42	271 aa	YP_001468881.1	GI:157325458	gp41	319 aa	Listeria phage A006	bacillales	Bacteriophage			
YP_001562941.1	GI:160897359	RecT protein	307 aa	YP_001562940.1	GI:160897358	exonuclease	209 aa	Delftia acidovorans SPH-1	burkholderiales	Prophage-like			
YP_001587229.1	GI:161613264	hypothetical protein SPAB_00974	261 aa	YP_001587228.1	GI:161613263	hypothetical protein SPAB_00973	226 aa	Salmonella enterica subsp. enterica serovar Paratyphi B str. SPB7	enterobacteriales	Prophage-like			
YP_001730203.1	GI:170080883	RecT protein	305 aa	YP_001730202.1	GI:170080882	exonuclease	226 aa	Escherichia coli str. K-12 substr. DH10B	enterobacteriales	Prophage-like			
YP_001648906.1	GI:170783624	Bet protein	261 aa	YP_001648905.1	GI:170783623	exonuclease	225 aa	Enterobacteria phage Min27	enterobacteriales	Bacteriophage			
YP_001829779.1	GI:182681619	phage recombination protein Bet	308 aa	YP_001829780.1	GI:182681620	hypothetical protein XfasM23_1078	550 aa	Xylella fastidiosa M23	xanthomonadales	Prophage-like			
YP_001852190.1	GI:183983899	RecT-family phage protein	375 aa	YP_001852192.1	GI:183983901	hypothetical protein MMAR_3929	359 aa	Mycobacterium marinum M	actinomycetales	Prophage-like			
YP_001968261.1	GI:190149736	phage recombinase	318 aa	YP_001968260.1	GI:190149735	hypothetical protein APP7_0466	229 aa	Actinobacillus pleuropneumoniae serovar 7 str. AP76	pasteurellales	Prophage-like			
YP_001986912.1	GI:191637746	RecT protein	295 aa	YP_001986910.1	GI:191637744	hypothetical protein LCABL_09660	291 aa	Lactobacillus casei BL23	lactobacillales	Prophage-like			
YP_002045006.1	GI:194449120	recombination protein bet	261 aa	YP_002045005.1	GI:194450183	exonuclease	226 aa	Salmonella enterica subsp. enterica serovar Heidelberg str. SL476	enterobacteriales	Prophage-like			
YP_002242032.1	GI:206599593	gp49	355 aa	YP_002242031.1	GI:206599592	gp48	335 aa	Mycobacterium phage Brujita	actinomycetales	Bacteriophage			
YP_002269409.1	GI:209397607	recombination protein bet	215 aa	YP_002269408.1	GI:209396861	exo gene product	226 aa	Escherichia coli O157:H7 str. EC4115	enterobacteriales	Prophage-like			
YP_002271823.1	GI:209399367	bet gene product	261 aa	YP_002271824.1	GI:209397437	exo gene product	226 aa	Escherichia coli O157:H7 str. EC4115	enterobacteriales	Prophage-like			
YP_002271521.1	GI:209399455	bet gene product	261 aa	YP_002271522.1	GI:209399863	exo gene product	225 aa	Escherichia coli O157:H7 str. EC4115	enterobacteriales	Prophage-like			
YP_002274151.1	GI:209427740	Bet protein	261 aa	YP_002274150.1	GI:209427739	putative exonuclease	226 aa	Enterobacteria phage YYZ-2008	enterobacteriales	Bacteriophage			
YP_002274222.1	GI:209447137	Bet recombination protein	261 aa	YP_002274221.1	GI:209447136	exonuclease	226 aa	Stx2-converting phage 1717	enterobacteriales	Bacteriophage			
YP_002288537.1	GI:209884680	rect protein	461 aa	YP_002288539.1	GI:209884682	hypothetical protein OCAR_5543	311 aa	Oligotropha carboxidovorans OM5	rhizobiales	Prophage-like			
YP_002291843.1	GI:209917759	phage recombination protein	261 aa	YP_002291842.1	GI:209917758	phage exonuclease	226 aa	Escherichia coli SE11	enterobacteriales	Prophage-like			
YP_002351899.1	GI:217966221	recombinase, phage RecT family protein	271 aa	YP_002351898.1	GI:217966220	gp47	319 aa	Listeria monocytogenes HCC23	bacillales	Prophage-like			
YP_002383833.1	GI:218550042	Recombination protein bet from phage origin	261 aa	YP_002383834.1	GI:218550043	exonuclease from phage origin	226 aa	Escherichia fergusonii ATCC 35469	enterobacteriales	Prophage-like			
YP_002386220.1	GI:218553307	Recombination protein bet from phage origin	261 aa	YP_002386219.1	GI:218553306	exonuclease from phage origin	226 aa	Escherichia coli IAI1	enterobacteriales	Prophage-like			
YP_002390941.1	GI:218558028	Recombination protein bet from phage origin	261 aa	YP_002390940.1	GI:218558027	exonuclease from phage origin	226 aa	Escherichia coli S88	enterobacteriales	Prophage-like			
YP_002397109.1	GI:218688897	Recombination protein bet from phage origin	261 aa	YP_002397108.1	GI:218688896	exonuclease from phage origin	226 aa	Escherichia coli ED1a	enterobacteriales	Prophage-like			
YP_002398474.1	GI:218690262	Recombination protein bet from phage origin	261 aa	YP_002398475.1	GI:218690263	exonuclease from phage origin	226 aa	Escherichia coli ED1a	enterobacteriales	Prophage-like			
YP_002401864.1	GI:218694197	Recombination protein bet from phage origin	261 aa	YP_002401863.1	GI:218694196	exonuclease from phage origin	226 aa	Escherichia coli 55989	enterobacteriales	Prophage-like			
YP_002407960.1	GI:218700331	Recombination protein bet from phage origin	261 aa	YP_002407961.1	GI:218700332	exonuclease from phage origin	226 aa	Escherichia coli IAI39	enterobacteriales	Prophage-like			
YP_002411346.1	GI:218703827	recombination protein bet from phage origin	261 aa	YP_002411345.1	GI:218703826	exonuclease from phage origin	226 aa	Escherichia coli UMN026	enterobacteriales	Prophage-like			
YP_002412137.1	GI:218704618	recombination protein bet from phage origin	261 aa	YP_002412136.1	GI:218704617	exonuclease from phage origin	226 aa	Escherichia coli UMN026	enterobacteriales	Prophage-like			
YP_002475179.1	GI:219870804	phage recombinase, recombinational DNA repair protein, RecE pathway	312 aa	YP_002475180.1	GI:219870805	hypothetical protein HAPS_0579	222 aa	Haemophilus parasuis SH0165	pasteurellales	Prophage-like			
YP_002475717.1	GI:219871342	phage recombination protein Bet	288 aa	YP_002475716.1	GI:219871341	putative bacteriophage exonuclease	204 aa	Haemophilus parasuis SH0165	pasteurellales	Prophage-like			
YP_002497906.1	GI:220922604	hypothetical protein Mnod_2640	334 aa	YP_002497905.1	GI:220922603	phage-like protein endonuclease-like protein	316 aa	Methylobacterium nodulans ORS 2060	rhizobiales	Prophage-like			
YP_002498798.1	GI:220923496	hypothetical protein Mnod_3586	303 aa	YP_002498797.1	GI:220923495	hypothetical protein Mnod_3585	316 aa	Methylobacterium nodulans ORS 2060	rhizobiales	Prophage-like			
YP_002501391.1	GI:220926089	hypothetical protein Mnod_6283	345 aa	YP_002501390.1	GI:220926088	phage-like protein endonuclease-like protein	316 aa	Methylobacterium nodulans ORS 2060	rhizobiales	Prophage-like			
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YP_002773048.1	GI:226313154	hypothetical protein BBR47_35670	314 aa	YP_002773049.1	GI:226313155	hypothetical protein BBR47_35680	289 aa	Brevibacillus brevis NBRC 100599	bacillales	Prophage-like			
YP_002872416.1	GI:229590297	hypothetical protein PFLU2837	272 aa	YP_002872415.1	GI:229590296	putative phage-like protein	542 aa	Pseudomonas fluorescens SBW25	pseudomonadales	Prophage-like			
YP_002863331.1	GI:237795779	RecT	294 aa	YP_002863332.1	GI:237795780	putative YqaJ	349 aa	Clostridium botulinum Ba4 str. 657	clostridiales	Prophage-like			
YP_002922678.1	GI:238801622	RecT-like protein	342 aa	YP_002922679.1	GI:238801623	RecB-like nuclease	343 aa	Burkholderia phage BcepIL02	burkholderiales	Bacteriophage			
YP_002928889.1	GI:238903093	Recombination protein bet	261 aa	YP_002928888.1	GI:238903092	Exonuclease	226 aa	Escherichia coli BW2952	enterobacteriales	Prophage-like			
YP_002971742.1	GI:240850349	bacteriophage recombination protein	275 aa	YP_002971741.1	GI:240850348	phage-related exonuclease	207 aa	Bartonella grahamii as4aup	rhizobiales	Prophage-like			
YP_003006972.1	GI:251792250	Bet	260 aa	YP_003006971.1	GI:251792249	hypothetical protein NT05HA_0469	203 aa	Aggregatibacter aphrophilus NJ8700	pasteurellales	Prophage-like			
YP_003037099.1	GI:253774268	phage recombination protein Bet	261 aa	YP_003037100.1	GI:253774269	exodeoxyribonuclease (lambda-induced)	226 aa	Escherichia coli 'BL21-Gold(DE3)pLysS AG'	enterobacteriales	Prophage-like			
YP_003076768.1	GI:254791931	Bet recombination protein of prophage CP-933K	215 aa	YP_003076767.1	GI:254791930	exonuclease encoded by prophage CP-933K	226 aa	Escherichia coli O157:H7 str. TW14359	enterobacteriales	Prophage-like			
YP_003078845.1	GI:254794008	protein bet	261 aa	YP_003078846.1	GI:254794009	exonuclease of prophage CP-933V	225 aa	Escherichia coli O157:H7 str. TW14359	enterobacteriales	Prophage-like			
YP_003079134.1	GI:254794297	Bet recombination protein	261 aa	YP_003079135.1	GI:254794298	exonuclease	226 aa	Escherichia coli O157:H7 str. TW14359	enterobacteriales	Prophage-like			
YP_003222764.1	GI:260844986	DNA recombination protein Bet	316 aa	YP_003222765.1	GI:260844987	exonuclease	229 aa	Escherichia coli O103:H2 str. 12009	enterobacteriales	Prophage-like			
YP_003224981.1	GI:260847203	recombinase	261 aa	YP_003224980.1	GI:260847202	exonuclease	226 aa	Escherichia coli O103:H2 str. 12009	enterobacteriales	Prophage-like			
YP_003227650.1	GI:260853759	recombination protein	261 aa	YP_003227649.1	GI:260853758	exonuclease	226 aa	Escherichia coli O26:H11 str. 11368	enterobacteriales	Prophage-like			
YP_003230160.1	GI:260856269	recombinase	261 aa	YP_003230161.1	GI:260856270	exonuclease	225 aa	Escherichia coli O26:H11 str. 11368	enterobacteriales	Prophage-like			
YP_003251764.1	GI:261418082	recombination and repair protein RecT	281 aa	YP_003251762.1	GI:261418080	phage-type endonuclease	311 aa	Geobacillus sp. Y412MC61	bacillales	Prophage-like			
YP_003347581.1	GI:281416232	RecT family protein	267 aa	YP_003347580.1	GI:281416231	endonuclease YqaJ superfamily	293 aa	Enterococcus phage phiFL3A	lactobacillales	Bacteriophage			
YP_003347474.1	GI:281416340	RecT family protein	296 aa	YP_003347473.1	GI:281416339	endonuclease YqaJ superfamily	313 aa	Enterococcus phage phiFL1A	lactobacillales	Bacteriophage			
YP_003347309.1	GI:281416508	RecT family protein	296 aa	YP_003347307.1	GI:281416506	endonuclease YqaJ superfamily	231 aa	Enterococcus phage phiFL2A	lactobacillales	Bacteriophage			
YP_003477226.1	GI:289578599	RecT protein	283 aa	YP_003477227.1	GI:289578600	phage-type endonuclease	312 aa	Thermoanaerobacter italicus Ab9	thermoanaerobacterales	Prophage-like			
YP_003497915.1	GI:291281097	Bet protein	261 aa	YP_003497914.1	GI:291281096	Exonuclease	226 aa	Escherichia coli O55:H7 str. CB9615	enterobacteriales	Prophage-like			
YP_003498272.1	GI:291281454	Bet protein	261 aa	YP_003498271.1	GI:291281453	exonuclease encoded by prophage CP-933K	226 aa	Escherichia coli O55:H7 str. CB9615	enterobacteriales	Prophage-like			
YP_003498535.1	GI:291281717	bacteriophage recombination protein	247 aa	YP_003498534.1	GI:291281716	Exonuclease	226 aa	Escherichia coli O55:H7 str. CB9615	enterobacteriales	Prophage-like			
YP_003500772.1	GI:291283954	Recombination protein Bet	261 aa	YP_003500773.1	GI:291283955	exonuclease encoded by prophage CP-933K	226 aa	Escherichia coli O55:H7 str. CB9615	enterobacteriales	Prophage-like			
YP_003609870.1	GI:295681296	DNA single-strand annealing protein RecT-like protein	389 aa	YP_003609871.1	GI:295681297	phage-type endonuclease	307 aa	Burkholderia sp. CCGE1002	burkholderiales	Prophage-like			
YP_003828959.1	GI:302393129	recombination protein Bet	261 aa	YP_003828958.1	GI:302393128	exonuclease	226 aa	Stx2 converting phage II	enterobacteriales	Bacteriophage			
YP_003848869.1	GI:302861168	recombination protein Bet	261 aa	YP_003848868.1	GI:302861167	exonuclease	226 aa	Stx1 converting phage	enterobacteriales	Bacteriophage			
YP_003919148.1	GI:308172443	DNA recombination protein	279 aa	YP_003919146.1	GI:308172441	nuclease; skin element	167 aa	Bacillus amyloliquefaciens DSM 7	bacillales	Prophage-like			
YP_003947700.1	GI:310642942	rect protein	298 aa	YP_003947701.1	GI:310642943	endonuclease yqaj superfamily	315 aa	Paenibacillus polymyxa SC2	bacillales	Prophage-like			
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YP_004100874.1	GI:317120871	RecT protein	308 aa	YP_004100873.1	GI:317120870	phage-type endonuclease	318 aa	Thermaerobacter marianensis DSM 12885	clostridiales	Prophage-like			
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YP_004138192.1	GI:319775704	recombinational DNA repair protein, RecE pathway	316 aa	YP_004138191.1	GI:319775703	hypothetical protein HICON_10450	216 aa	Haemophilus influenzae F3047	pasteurellales	Prophage-like			
YP_004138677.1	GI:319776189	recombinational DNA repair protein	306 aa	YP_004138676.1	GI:319776188	hypothetical protein HICON_15410	231 aa	Haemophilus influenzae F3047	pasteurellales	Prophage-like			
YP_004134950.1	GI:319896756	recombinational DNA repair protein, rece pathway	316 aa	YP_004134951.1	GI:319896757	hypothetical protein HIBPF04260	216 aa	Haemophilus influenzae F3031	pasteurellales	Prophage-like			
YP_004204415.1	GI:321312128	putative DNA recombination protein	284 aa	YP_004204416.1	GI:321312129	putative nuclease	318 aa	Bacillus subtilis BSn5	bacillales	Prophage-like			
YP_004355228.1	GI:330810766	gifsy-1 prophage protein	322 aa	YP_004355229.1	GI:330810767	phage exonuclease	222 aa	Pseudomonas brassicacearum subsp. brassicacearum NFM421	pseudomonadales	Prophage-like			
YP_004413770.1	GI:330839190	RecT protein	303 aa	YP_004413771.1	GI:330839191	phage-type endonuclease	311 aa	Selenomonas sputigena ATCC 35185	selenomonadales	Prophage-like			
YP_004488026.1	GI:333914294	RecT protein	353 aa	YP_004488027.1	GI:333914295	YqaJ recombinase family protein	269 aa	Delftia sp. Cs1-4	burkholderiales	Prophage-like			
YP_004594671.1	GI:336250961	hypothetical protein	281 aa	YP_004594672.1	GI:336250962	exonuclease	226 aa	Enterobacter aerogenes KCTC 2190	enterobacteriales	Prophage-like			
YP_004633391.1	GI:337741663	RecT family protein	461 aa	YP_004633389.1	GI:337741661	endonuclease	311 aa	Oligotropha carboxidovorans OM5	rhizobiales	Prophage-like			
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YP_005129299.1	GI:375361260	putative protein yqaK	280 aa	YP_005129298.1	GI:375361259	putative protein yqaJ	316 aa	Bacillus amyloliquefaciens subsp. plantarum CAU B946	bacillales	Prophage-like			
YP_005217573.1	GI:378960087	hypothetical protein	261 aa	YP_005217574.1	GI:378960088	exonuclease	174 aa	Salmonella enterica subsp. enterica serovar Typhi str. P-stx-12	enterobacteriales	Prophage-like			
NP_244410.1	GI:15616105	hypothetical protein BH3543	292 aa	NP_244411.1	GI:15616106	hypothetical protein BH3544	320 aa	Bacillus halodurans C-125	bacillales	Genomic Island			
NP_455496.1	GI:16759879	bacteriophage recombination protein	261 aa	NP_455495.1	GI:16759878	exonuclease	226 aa	Salmonella enterica subsp. enterica serovar Typhi str. CT18	enterobacteriales	Genomic Island			
NP_469431.1	GI:16799163	putative recombinase	271 aa	NP_469430.1	GI:16799162	hypothetical protein lin0084	319 aa	Listeria innocua Clip11262	bacillales	Genomic Island			
NP_471743.1	GI:16801475	hypothetical protein lin2413	271 aa	NP_471744.1	GI:16801476	hypothetical protein lin2414	319 aa	Listeria innocua Clip11262	bacillales	Genomic Island			
NP_879361.1	GI:33591717	phage-related DNA recombination protein	328 aa	NP_879360.1	GI:33591716	phage-related exonuclease	215 aa	Bordetella pertussis Tohama I	burkholderiales	Genomic Island			
NP_930169.1	GI:37526825	hypothetical protein plu2935	306 aa	NP_930170.1	GI:37526826	hypothetical protein plu2936	227 aa	Photorhabdus luminescens subsp. laumondii TTO1	enterobacteriales	Genomic Island			
YP_091037.1	GI:52785208	recombination and repair protein RecT	273 aa	YP_091036.1	GI:52785207	hypothetical protein BLi01440	312 aa	Bacillus licheniformis DSM 13 = ATCC 14580	bacillales	Genomic Island			
YP_120257.1	GI:54026015	recombination and repair protein RecT	295 aa	YP_120258.1	GI:54026016	hypothetical protein nfa40460	329 aa	Nocardia farcinica IFM 10152	actinomycetales	Genomic Island			
YP_264268.1	GI:71065541	hypothetical protein	348 aa	YP_264269.1	GI:71065542	hypothetical protein	338 aa	Psychrobacter arcticus 273-4	pseudomonadales	Genomic Island			
YP_001292323.1	GI:148827570	hypothetical protein CGSHiGG_04985	306 aa	YP_001292324.1	GI:148827571	hypothetical protein CGSHiGG_04990	216 aa	Haemophilus influenzae PittGG	pasteurellales	Genomic Island			
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YP_002560350.1	GI:222151196	recombination and repair protein RecT	276 aa	YP_002560349.1	GI:222151195	hypothetical protein MCCL_0946	313 aa	Macrococcus caseolyticus JCSC5402	bacillales	Genomic Island			
YP_002795496.1	GI:226940422	Recombination protein bet	262 aa	YP_002795495.1	GI:226940421	Exonuclease	203 aa	Laribacter hongkongensis HLHK9	neisseriales	Genomic Island			
YP_002835493.1	GI:227833786	phage recombinase	272 aa	YP_002835494.1	GI:227833787	hypothetical protein cauri_1963	332 aa	Corynebacterium aurimucosum ATCC 700975	actinomycetales	Genomic Island			
YP_003113797.1	GI:256392233	RecT protein	313 aa	YP_003113798.1	GI:256392234	endonuclease-like protein	312 aa	Catenulispora acidiphila DSM 44928	actinomycetales	Genomic Island			
YP_003325187.1	GI:269955398	phage recombination protein Bet	327 aa	YP_003325188.1	GI:269955399	hypothetical protein Xcel_0591	310 aa	Xylanimonas cellulosilytica DSM 15894	actinomycetales	Genomic Island			
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YP_004748640.1	GI:340782033	hypothetical protein Atc_1291	294 aa	YP_004748641.1	GI:340782034	heme peroxidase	505 aa	Acidithiobacillus caldus SM-1	acidithiobacillales	Genomic Island			
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YP_004896617.1	GI:352684632	recombination and repair protein recT	262 aa	YP_004896618.1	GI:352684633	hypothetical protein	329 aa	Acidaminococcus intestini RyC-MR95	selenomonadales	Genomic Island			
YP_005162586.1	GI:376290339	hypothetical protein	309 aa	YP_005162588.1	GI:376290341	hypothetical protein	341 aa	Corynebacterium diphtheriae C7 (beta)	actinomycetales	Genomic Island			
YP_005179769.1	GI:378697811	recombinational DNA repair protein, RecE pathway	306 aa	YP_005179770.1	GI:378697812	hypothetical protein	216 aa	Haemophilus influenzae 10810	pasteurellales	Genomic Island			

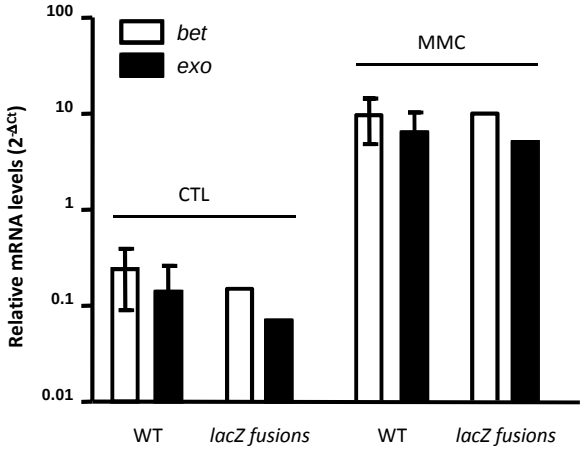

Figure S1. Comparison of mRNA levels of *bet* and *exo* in a WT context and of *lacZ* in the *bet*'-'*lacZ* and *exo*'-'*lacZ* fusions, in control (CTL) and MMC-induced conditions (MMC). Results are expressed as the relative transcription of each gene compared to *rpoZ* ($2^{-\Delta Ct}$).

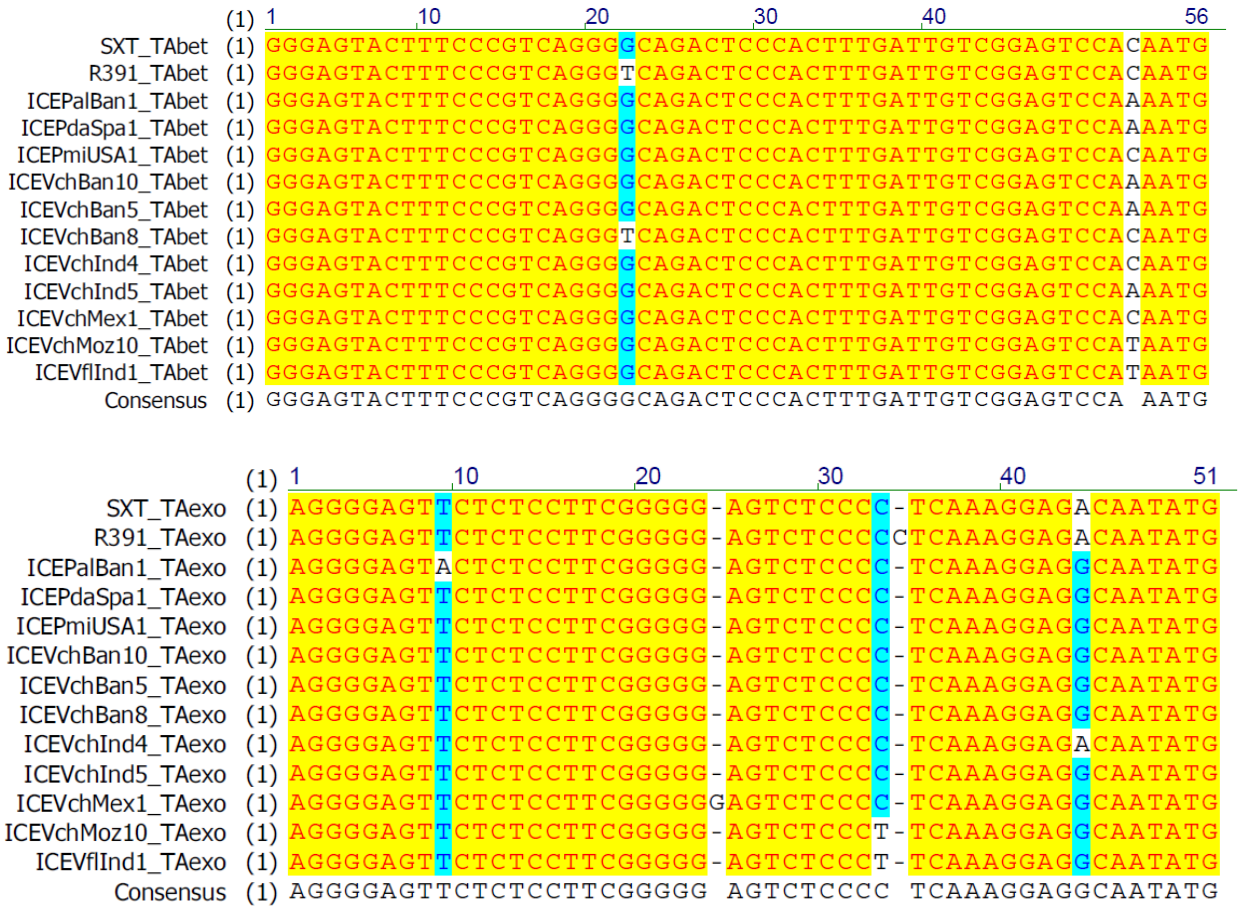

Figure S2. Alignment of the predicted translational attenuators found upstream *bet* (TA*bet*) and upstream *exo* (TA*exo*) in sequenced SXT/R391 ICEs.

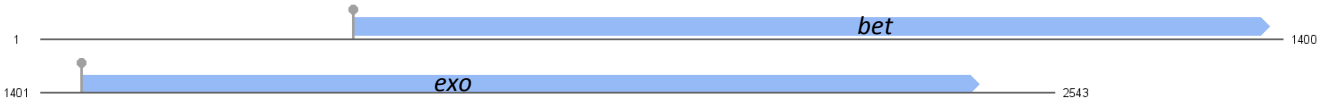

Figure S3. Translational attenuators predicted by RibEx upstream *bet* and *exo* in IncA/C plasmid pIP1202.

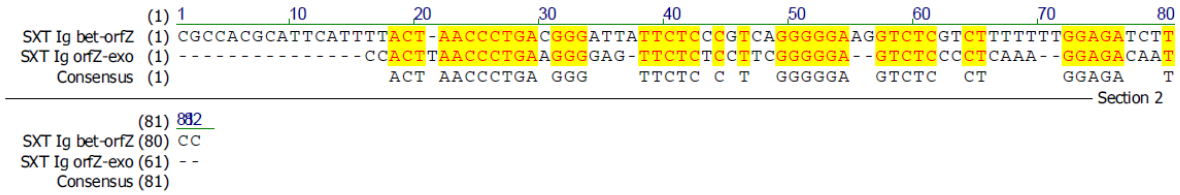

Figure S4. Alignment of the intergenic regions located between *bet* and *orfZ* (Ig bet-orfZ) and between *orfZ* and *exo* (Ig orfZ-exo) in SXT.