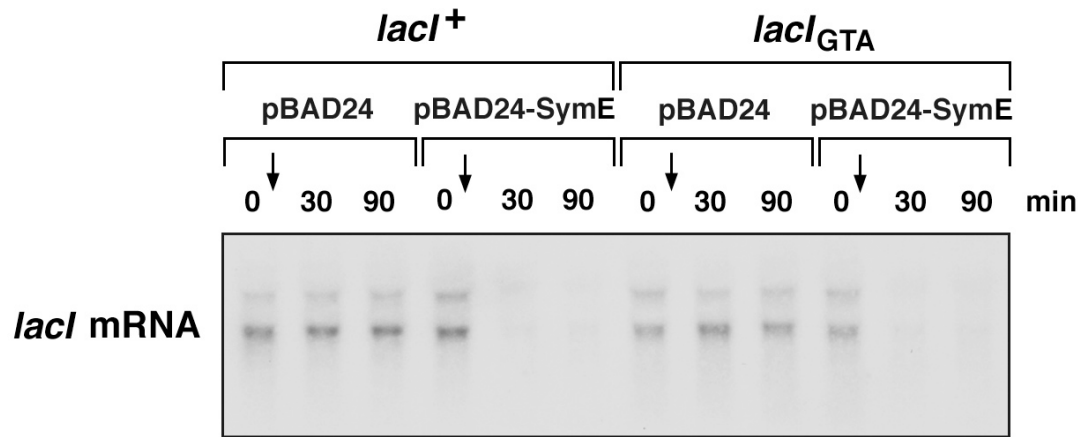


**Fig. S1.** SymE overexpression leads to reduced levels of *lacI* mRNA with and without a start codon.

MG1655 P<sub>cp18</sub>-*araE* and MG1655 P<sub>cp18</sub>-*araE lacI*<sub>GTA</sub> (GSO129) carrying either pBAD24 or pBAD-SymE were grown to OD<sub>600</sub> ~0.5 at 37°C in M9 minimal medium supplemented with glycerol and casamino acids. Total RNA isolated at 0, 30, and 90 min after treatment with 0.02% arabinose (indicated by the arrow). Samples (5 µg) were analyzed by Northern hybridization using an oligonucleotide probe specific to *lacI*. The start codon mutation in *lacI* was generated in GSO120 using the mini-λ Red recombination method (Court et al., 2003) and a single-stranded oligonucleotide with a single mutation (ATG to GTA).



**Fig. S2.** Multiple alignment of the SymE family and other members of the AbrB superfamily

Proteins are denoted by gene name, species abbreviation, and gi number; separated by underscores. The gi number can be used as a unique identifier to recover the protein from the Genbank database. Amino acid residues are colored according to side chain properties and the percentage of conservation as indicated in the consensus below the alignment. Consensus similarity designations and coloring scheme are as follows: ‘h’, hydrophobic residues (ACFILMVWY) and their aromatic subset, ‘a’ are shaded yellow; ‘s’ small residues (AGSVCDN) shaded aqua and their tiny subset (GAS) are shaded green; polar residues ‘p’ are colored orange. Secondary structure assignments obtained from the JPRED prediction for the SymE family and from the crystal structures like 1mvf and 1ub4 for the rest of the AbrB superfamily are shown above the alignment where E represents a strand and H represents a helix. The boundaries of the alignment are shown to the right. Species abbreviations are as follows: *Amac* : *Alteromonas macleodii*; *Amet* : *Alkaliphilus metalliredigenes*; *Ana* : *Nostoc sp.*; *Atum* : *Agrobacterium tumefaciens*; *Bcla* : *Bacillus clausii*; *Bsp.* : *Burkholderia sp.*; *Bvie* : *Burkholderia vietnamiensis*; *Bxen* : *Burkholderia xenovorans*; *Cchl* : *Chlorobium chlorochromatii*; *Drad* : *Deinococcus radiodurans*; *Ecar* : *Erwinia carotovora subsp.*; *Ecol* : *Escherichia coli*; *Efae* : *Enterococcus faecalis*; *Gkau* : *Geobacillus kaustophilus*; *Gmet* : *Geobacter metallireducens*; *Goxy* : *Gluconobacter oxydans*; *Gura* : *Geobacter uraniumreducens*; *Gvio* : *Gloeobacter violaceus*; *Hche* : *Hahella chejuensis*; *Ipla* : *IncL/M plasmid*; *Lint* : *Leptospira interrogans*; *Maqu* : *Marinobacter aquaeolei*; *Mcel* : *Mycobacterium celatum*; *Moth* : *Moorella thermoacetica*; *Neur* : *Nitrosomonas europaea*; *Ngon* : *Neisseria gonorrhoeae*; *Nmen* : *Neisseria meningitidis*; *Nmob* : *Nitrococcus mobilis*; *Paci* : *Pediococcus acidilactici*; *Plum* : *Photorhabdus luminescens*; *Pnap* : *Polaromonas naphthalenivorans*; *Ppha* : *Pelodictyon phaeoclathratiforme*; *Ppro* : *Photobacterium profundum*; *Pput* : *Pseudomonas putida*; *Psyr* : *Pseudomonas syringae*; *Reut* : *Ralstonia eutropha*; *Rfer* : *Rhodoferrax ferrireducens*; *Rnub* : *Roseovarius nubinhibens*; *Rpal* : *Rhodopseudomonas palustris*; *Sent* : *Salmonella enterica*; *Sfle* : *Shigella flexneri*; *Sfri* : *Shewanella frigidimarina*; *Smut* : *Streptococcus mutans*; *Srub* : *Salinibacter ruber*; *Styp* : *Salmonella typhimurium*; *Susi* : *Solibacter usitatus*; *Swol* : *Syntrophomonas wolfei*; *Syn* : *Synechococcus sp.*; *Vcho* : *Vibrio cholerae*; *Xaxo* : *Xanthomonas axonopodis*; *Xcam* : *Xanthomonas campestris*; *Xory* : *Xanthomonas oryzae*; *Ypes* : *Yersinia pestis*; *Ypse* : *Yersinia pseudotuberculosis*.

Secondary Struc.

SymE\_Ecol\_49176495

SF4363\_Sfle\_24054893
yjiW\_Sent\_62182949
yjiW\_Styp\_16767767
plu3716\_Plum\_36787014
YintA\_01002156\_Yint\_77978014
ECA2121\_Ecar\_49611575
YP3938\_Ypes\_45438536
ECA4295\_Ecar\_49613741
ECA3402\_Ecar\_49612852
ECA4289\_Ecar\_49613735
ECA3392\_Ecar\_49612842
ECA3418\_Ecar\_49612868
orf8\_Plum\_27497170
plu3380\_Plum\_36786688
XCC3569\_Xcam\_21114842
XCC3103\_Xcam\_21114326
XOO2821\_Xory\_58582444
XOO1835\_Xory\_84367432
XOO1938\_Xory\_58426155
XOO0917\_Xory\_58580540
XOO0162\_Xory\_58579785
XOO0141\_Xory\_84365738
XAC1914\_Xaxo\_21108128
XAC2863\_Xaxo\_21109161
STM0296\_Styp\_16418797
STM0294.1N\_Styp\_39546291
STY0328\_Sent\_16501578
SF0591\_Sfle\_24050834
plu3699\_Plum\_36786998
plu3591\_Plum\_36786895
plu1147\_Plum\_36784541
ECA2120\_Ecar\_49611574
ECA3393\_Ecar\_49612843
ECA3410\_Ecar\_49612860
ECA3419\_Ecar\_49612869
YPTB3619\_Ypse\_51591192
YP3939\_Ypes\_45438537
EF\_2302\_Efae\_29344269
HCH\_03808\_Hche\_83646529
ECA0399\_Ecar\_49609882
Bcep18194\_B2924\_Bsp\_77971656
Bxe\_A4510\_Bxen\_91782963
consensus/90%

-----EEEEEE-----eEEEE.HHHHHH-----EEEEEE-----EEEEEE-----

ANNRHVTVGYASRYP-----DYSRI PAITLKGQWLEAAGFATGTAVDVKVMEGCIVLTAQPPAA [ 18- 76]
ANNRQLTVSYASRYP-----DYSRI PAITLKGQWLEAAGFATGTAVDVKVMEGCIVLTAQPPAA [ 18- 76]
ANNRHLLTVSYASSYP-----EYTRI PAITLKGQWLEADAGFTTGTQVDVVMNGCIVLTAQQPQP [ 18- 76]
TNNRHLLTVSYASRYP-----DYTRI PALTMKGWLEAAGFATGTEVDVVMNGCIVLTAQQPQP [ 18- 76]
VKPRHYTVGYRPNRG-----KPNPY PQLTIKGRWLAALGFTTGKPIITITSEAGQLIIQLAEND- [ 18- 75]
PQARKSIVGYRPNNG-----RPNPL PQLTIRGRWLEPLGFTTGQKIEVITEFGQLIIRLAVEG- [ 13- 70]
APASPVSSGYRTNGG-----KPNPL PQLTIKGRWLEALGFTKGQPVSIITAEHGQLIIRRTAPATK [ 7- 65]
KTERYYTVGYVPQRG-----KRNPP PAINLKGRWLEALGFSSGQPVLIITVEHGRLLVIQPEIKI- [ 17- 74]
KIARYYTVGYALKNG-----KPNPP PAIDLKCRWLESSGFMTGIPITITVVERRRLVIEETEINL- [ 13- 70]
KTERYYTVGYASHNG-----KPNPP SAINLKGRWLEECGFITGMPVTVTVERGRIIIETQINL- [ 17- 74]
KTERYYTVGYAPHNG-----RPNPP SAINLKGRWLEESGFMTGMPITVTVVERGRIVIEETEINL- [ 17- 74]
QAERFTRVGYRPIK-----GNHDT PAINIAGQWLKDAAGFTTGQSLKLRIMPGCIVITTTQDIHE [ 17- 74]
QAERFTRVGYRPIK-----GNHAT PAINIAGQWLKDAAGFTTGQPLRLRIMPGCIVITTTQDIHE [ 17- 74]
KTERYYTVGYVPNGNR-----VNDAT PAIBLKGQWLROAGFNTGGQITVVMMDGCLVLIIPDSEAT [ 17- 76]
KRDNKTIRRIISQAERFGK-----VAKNG ISLKGKWLQEAAGFTFGMPLKIRVMPDCIVITTAQNTQE [ 3- 62]
RRPRQCTVSYTYLPGAHDHA---GDQHV PHVRLSGLWLQQLGFAIGTKLRITASVGRLLMEVLPVVG [ 38-101]
RTPTSCYTVGYAFYEAEPGRP---HSQRI PSVRLRGLWLEQLGFAVGCCKLQITARKGELVVTVVERAPS [ 80-143]
RRPRQCTVSYTHYPGAHDHA---GDQHV PHVRLSGLWLQQLGFAIGTKLRITANAGQLLMEVLPVVE [ 65-128]
RTPTRCTVGYAFYDAEPGRP---DSQRI PNVRLRGLWLEQLGFAVGCCKLQITARNGELVVTVVAED-- [ 70-131]
RTPTRCTVGYAFYDAEPGRP---DSQRI PNVRLRGLWLEQLGFAVGCCKLQITARNGELVVTVVAED-- [ 36- 97]
RPTKQCTVGYGYYPN-----SQQRV PTLRLRGGWLEQLGFAIGSKLRVTVHDCALVIAVIDEEC [194-252]
RATQQCTMGYGYYPD-----SHQRV PALRLRGRWLEQLGFAIGCKLRITVRDSELVITTVVGGEE- [112-169]
RATQQCTMGYGYYPD-----SHQRV PALRLRGRWLEQLGFAIGCKLRITVRDSELVITTVVGGEE- [ 63-120]
RRPRQCTVSYTHYPGAHDHA---GDQHV PHVRLSGLWLQQLGFAIGTKLRITASEGQLLMEVLPVVE [ 65-128]
RPPQCTIGYGYAA-----TQQYV PTVRLRGRWLEQLGFAVVGSKLDIRMREGELVMSLAHKD- [ 60-117]
MARLCGILTYSRV-----ERLSVRLYGEWMPQAGFINGMPVKVRVMDRCIVITTPQHHTG [ 1- 54]
NSETCMTACYSQI-----PSQHLKGDWLEEAGFETGHHGVTVKISEGCLILIIAETDEV [ 12- 63]
MARLCGILTYSRV-----ERLSVRLYGEWMPQAGFINGMPVKVRVMDRCIVITTPQHTRG [ 1- 54]
DRKTGIARYYSQH-----PSLHLKGDWLKEAGFDTGRGVTVKISEGGLTIIADSDEV [ 30- 81]
DRHTGMTRYYSQH-----PSLHLKGNWLEEAGFVTVGQPVQVSVEHGQLIIRLVENS- [ 30- 80]
DRSTGMTRYYSQH-----PSLHLKGNWLEEAGFATGQPVQVSVEHGQLIIRLVENG- [ 30- 80]
DRSTGMTRYYSQH-----PSLHLKGNWLEEAGFATGQPVQVSVEHGQLIIRLVEYN- [ 30- 80]
QQRQDLGADWVRE-----NGGVIIISGDWLTESDIARAEQLEVTAAASGVIRLQRREEV [ 59-111]
DGSETEGADWVGD-----NGELTLAGDWLTQSGL-LGQSLSIEVLLGKITIQAERGNM [ 61-112]
DGNEAEGADWVSD-----NGELTLAGDWLTQSGL-PDQPLIIEVLPGRITIRAVQGNM [ 61-112]
DGNEAEGADWVSD-----NGELTLAGDWLTQSGL-LDQPLIIEVLPGRITIRAVQGNM [ 61-112]
ENDNHIGMDWIQD-----NGELSLSGEWLTQTGL-TGQPLAISVMAGKVIIRGQQGNM [ 64-115]
LKYNNIVMAWIQD-----NGELSLSGEWLTQTGL-TGQPLAISVMAGKVIIRGQQGNM [ 10- 61]
LTVCYGHGNYKQA-----PTQIVLQGWLEQAGFSVGDKITVVKCQQGQLTITKNETGN [ 16- 68]
QRRLKVRKGYDYHLSSSRYDYGFKFPVWMLIKGYWLEQAGFGVDTEVEVSVEGGRIVFTAGAG-- [ 22- 86]
SQALLHLISVSRRHADRSDMTRYYSRSPSLHLQDHWLEAAGFEIDIPVVIITVEQQLVIRPAPE-- [ 9- 73]
PRTSFQTRRIVPHLKLADMA---PPVLHLWMLKSSHWIEAAGFDPEQPLKIEVMHKRLVITPIEDRR [ 19- 82]
PRKPKPGRDWRTPR-----FFSWLRLIAGMWLEQAGFSPQRVRIEVOHGRLVITTPD---- [ 23- 73]
.....a.....s.lpl.G.Wlp..Gh..s..l.lph..spl.hp.....

**Secondary Struc.**

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MazE_Ecol_31616033 (1mvf)  -MIHSSVKKRWGNS-----PAVRIIPATLMQALNINIDDEVKIDLVLDGKLIIEPVRKEP [ 1-52]
chpR_Ecar_49611137        -MIDVPPVKKWGNS-----PAIRLSSSSVMQAFDMTFNDSFDMREIRETEIALIIPKPKKPK [ 1-51]
SMU_172_Smut_24378686     --MQLVINKRWGNS-----SAIRLPKQLVQELQQLQTNLDVLDYKVSNGKIILEKVNINIP [ 1-50]
RPC_3251_Rpal_90424742    --MKVKVAKRWGNS-----LGIIRLPSAAADS VGATVSGELDLTIENGELRLRSIRKTS [ 1-50]
MaquDRAFT_1702_Maqu_77953495
MazE_Ppro_11344928        -AMRTQIRKIGNS-----LGSIIIPATFIRQLELAEGAEIDVKTVDGKIVIEPIRKMK [ 1-51]
VchoR_01000034_Vcho_75824896
MADE_08556_Amac_88793356 --MRTQIRKIGNS-----LGNIIIPATFIRQLGLVEGADIEVKTEGKRIIIIEPVERQK [ 1-50]
MazE_Paci_31442758        --METVIRKYGNS-----KGVIIIPAAALLKELDLVDVNEKIDVKTENGRIIIIEPMRQLE [ 1-50]
Gmet_2502_Gmet_78194957  IKEQTRLAKWGNS-----KAARIPSQIIKQLKLLDDNQDMTITIENGSIIVLTPPIKKNP [ 31-82]
gsr0095_Gvio_35210655    --MRTNIIIRIGNS-----QGIRIPKVLLEQSHL--GAEVELEVEDEKIIIRSASRPR [ 1-48]
mazE_Ana_17132307         --MKSQVARKWGNS-----LAFRIIPRQIVIQGLKPHHTLLCSVEAGALVVRPVREVK [ 1-50]
PP0770_Pput_26987506      --MTTVVAKWGNS-----LAVRIPRSIAEQAHVTEGTDINFVSEGNISIVITPKRRKK [ 1-50]
Psysr_0889_Psysr_63254851
RPEDRAFT_3008_Rpal_77740482
NGO0517_Ngon_59800955    --MQIKIQQWGNS-----AAIRLPAAVLQKQMRGLVGGSTLSLDTTGETMVLKPVRSKP [ 1-50]
GK1647_Gkau_56380024     --MEVKIQQWGNS-----AAIRLPAANVLKQMSLSSGDVLTLDASAIEVITLKPAAKAKL [ 1-50]
Cag_0428_Cchl_78170605   --MKGQVAQWGNS-----AALRLPKSVLEDLKVAPGSEVEMVVEAGELVRRAAPRIV [ 1-50]
RS9917_04555_Syn_87123100
DR_0416_Drad_6458096     ---MLRLQKWGNS-----AAVRLPARLLTALNAKIGDALETEIRNGELLIRPVKR-- [ 1-47]
PphaDRAFT_1569_Ppha_68550788
Moth_1020_Moth_83589868  SIMTITVQKWGNS-----LAVRIPSVIAERLALHQGSEVEMIVENQAIKLIPKPKK-- [ 10-60]
LA1780_Lint_24214480     --MLTQVKKWGNS-----FALKIPKAIIVSDAKIERDSFIDINIVKGQITIEENVTTQR [ 1-50]
WH5701_04345_Syn_87300647
pemI_Reut_38638041       --MKVKVQAWGNS-----LGLRIPKVFANALGVGSGSEMEVKVEDGALLARPAAA-- [ 1-48]
PnapDRAFT_2207_Pnap_84713095
Rfer_3405_Rfer_89902174  --MTSQIQKWGNS-----LALRIPKALAQQVGLTQSSEVELLLQDQGQIVIRPVPARQ [ 1-50]
SRU_2815_Srub_83815344   --MLTKVQKWGNS-----LALRIPKTWALEARLENNSEVEISLVEGKLVITPVVTIK [ 1-50]
ABC1016_Bcla_56909028    IVMQPHVQKWGNS-----LGIIRIPLSLAQKIGLREGTPVDLQVDEDAIIIRRKQ--- [ 3-51]
XAC2188_Xaxo_21108422    --MESIIQKWGNS-----LGIIRIPKAMATELELNDGSHVELQYEGDKIVIYPMKK-- [ 1-48]
NE0975_Neur_30138595     TPSRQALRRWGNS-----LGIIRLPAAIAREARLQEDQAVELSVVEGRVLRIPVQPR- [ 6-56]
pemI_Xaxo_59938898       KSATLTIQKWGNS-----LAVRIP TAVARS AHFAEQEVEVSVDEIGVTVRVPVGRRA [ 3-54]
SF3433_Sfle_24053885     -MHILKLTQIGNS-----VGVVLPKEALARLKLKGETVFLTETPDGYTLTPYD--- [ 1-48]
GuraDRAFT_3227_Gura_88935131
MazE_Mcel_13810878       -MTTLKLSQIGNS-----VGVILPKELLARLHLEKGDVVFMTDTVNGFTTISPYD--- [ 1-48]
AGR_C1711_Atum_15155939  MPEETTIRRIGNS-----SGLTIPKDLLDRQHLEEGDQVHLVETEDGLLITPYD--- [ 1-49]
AbrB_Bsub_113009 (1yfb)  -MKTTRLRKVGNS-----YGF TIPKELMDKYNLNEGVELNIIIEQNDGFALTPYD--- [ 1-48]
consensus/90%            --MSFKVHPWGNS-----SAVPVPSHVVRKVLGIENGSEVEIEVKDGMIVKPVKGD- [ 1-49]
                    --MAMQVAKWGNS-----LAVRLPSSLVEALELREGDDIETVVDPRFLFAVRKKPGP [ 1-50]
                    --MLQTLRKAGGS-----LVMTVPKSFIEQNGLSEGSQVELHHLHGKMMIVEAPARPR [ 1-50]
                    -MHTTNLRKVGGS-----VMLAVFPALLDVLHIGAGAKVGLAVDNGRLVVEPHARPR [ 1-51]
                    VEAVLGIKQWGNN-----LGVRLP VNVARAAHLHVDQKVRIAVEEGRVIIITPVDDAA [ 4-55]
                    -MFTTKLRKVGGS-----VMLATIPALLEMLDLNAGAPVGLSVDAGQLVVDQPVRPH [ 1-51]
                    -MQTVKLRQGGGA-----MIVTIPRDLAIDLWSPGTELTVEKKGDSVNLRAATEHKP [ 1-51]
                    MTVTTKIRRQGGGA-----AVMTIPALLKMLGLEIQEQLTLEVDNGALVASPVRLK [ 16-67]
                    --MDQAIIRKSSK-----RQITIPAAIYKKLGTQPGQKLFLEVHGDKLIIWPKTKSY [ 1-50]
                    MKSTGIVRKVDEL-----GRVVIPIELRRTLGIAEKDALEIYVDDEKIIILKKYKPN- [ 3-53]
                    .....1.phGsS                ..h.lP..hh..h.h..s..l.h.....h.lps.....

```

**Table S1.** Strains used in study

<u>Strain</u>	<u>Relevant genotype</u>	<u>Source or reference</u>
MG1655	<i>E. coli</i> F $\lambda$ <i>ilvG</i> <i>rfb-50 rph-1</i>	lab stock
DY330	W3110 $\Delta$ <i>lacU169 gal490</i> $\lambda$ <i>cI85</i> $\Delta$ ( <i>cro-bioA</i> )	D. Court
NM1100	MG1655 mini- $\lambda$ - <i>tet</i>	N. Majdalani
GSO114	MG1655 <i>symE</i> -SPA	this study
GSO115	MG1655 <i>symR-10 mutant</i>	this study
GSO116	MG1655 <i>symE</i> -SPA <i>symR-10 mutant</i>	this study
GSO117	MG1655 $\Delta$ <i>symER::kan</i>	this study
GSO118	MG1655 $\Delta$ <i>symER</i>	this study
GSO119	MG1655 <i>kan</i> -P <sub>CP18</sub> - <i>araE</i>	this study
GSO120	MG1655 P <sub>CP18</sub> - <i>araE</i>	this study
GSO122	MG1655 <i>symE</i> -SPA <i>hfq-1::</i> $\Omega$	this study
GSO123	MG1655 <i>symE</i> -SPA <i>rnc-14::</i> $\Delta$ Tn10	this study
GSO124	MG1655 <i>symE</i> -SPA <i>lon146::</i> Tn10	this study
GSO125	MG1655 <i>symE</i> -SPA <i>clpP::cat</i>	this study
GSO126	MG1655 <i>symE</i> -SPA <i>symR-10 mutant lon146::</i> Tn10	this study
GSO127	MG1655 $\Delta$ <i>symER lon146::</i> Tn10	this study
GSO128	MG1655 <i>symR-10 mutant lon146::</i> Tn10	this study

**Table S2.** Plasmids used in study

<u>Plasmid</u>	<u>Resistance markers</u>	<u>Source or reference</u>
pACYC184	(Tc <sup>R</sup> )	Chang and Cohen, 1978
pACYC-SymR	(Tc <sup>R</sup> )	this study
pAZ3	(Cm <sup>R</sup> )	this study
pAZ3-anti-SymR	(Cm <sup>R</sup> )	this study
pBAD24	(Ap <sup>R</sup> )	Guzman et al., 1995
pBAD24-SymE	(Ap <sup>R</sup> )	this study
pBAD24-SymE-SPA	(Ap <sup>R</sup> )	this study
pJL148	(Ap <sup>R</sup> )	Zeghouf et al., 2004
pKD4	(Km <sup>R</sup> )	Datsenko and Wanner, 2000
pCP20	(Ap <sup>R</sup> , Cm <sup>R</sup> )	Cherepanov and Wackernagel, 1995

**Table S3.** Oligonucleotides used in study

<u>Name</u>	<u>Sequence (5' to 3', with relevant restriction sites underlined)</u>	<u>Use</u>
yjiW-AR20	CGCATAACCGACGGTGACATGACCGG	<i>symE</i> mRNA Northern
RyjC-R	AGCGCGGTGCGGATGTGCG	SymR RNA Northern , SymR RNA synthesis
Stm-F	CAATCACTATTTTAGGGAATAGCCATCATGACT	SymR RNA (S.tm) Northern
recA-R	TCGTTCGATAGCCATTTTACTCC	<i>recA</i> mRNA Northern
ompA-R	GCCACTGCAATCGCGATAGCTGTCTTTTCAT	<i>ompA</i> mRNA Northern
RdID-R	GCTAAGCTTAGAAAACCCCGCACGTTGCAGGTATG	RdID RNA Northern
6S-R	CCAACCGCGGAGCGCCACATTCTTGTGGTATG	6S RNA Northern
lacI-R	CAGCTCCGCCATCGCCGCTTCC	<i>lacI</i> mRNA Northern
TF-yjiW	GCAGGTGCAGGCGTTTATTGGAGTGATTGCCGGTAAACAGAAAAGTCGCGTCCATGGAAAAGAGAAG	GSO114 PCR
TR-yjiW	CTATTGAGTCAGTGGAAGGCTCCCGGTGGTTAACCGGAGTAAACGCTGCATATGAATATCCTCCTTAG	GSO114 PCR
yjiW-P1KO	CCCGCATCGCTAATCACAATCACTATTCTGGAGAATAGCAGTTTAGCCATGGTCCATATGAATATCC	GSO117 PCR
yjiW-P2KO	TGGAAGGCTCCCGGTGGTTAACCGGAGTAAACGCTGTTAGTGTAGGCTGGAGCTGCTTC	GSO117 PCR
P-10F-PAGE	CACAATCACTATTCTGGAGAATAGCAGTTATGACTGACACGCACTCCATTGCACAACCGTTCGAAGCAGAAGTCTCCCGGCAAATAACCGTC	GSO115 recombineering
lacI-GTA	GATAGCGCCCGGAAGAGAGTCAATTCAGGGTGGTGAATGTAAAACAGTAACGTTATACGATGTCGCAGAGTATGCCGGTG	lacI <sub>GTA</sub> mutant
yjiW-Eco2	TGAGAATTCAGGGTGATGCGGGGAATACG	pACYC-SymR PCR
yjiW-F2	TATGAATTCGTATTTAGCGCGGTGCGGATGTGC	pACYC-SymR PCR
AryjC-Eco	CAGGAATTCAGCGCGGTGCGGATGTGCGCCAAC	pAZ3-anti-SymR PCR
AryjC-Hin	CAAAAGCTTAAAAAAAAGTCCTAACTGCTATTCTCCAGG	pAZ3-anti-SymR PCR
YjiW-NS	ACTGACACGCATTCTATTGCACAACC	pBAD-SymE & pBAD-SymE-SPA PCR
YjiW-C	TTACGCGACTTTCTGTTTACCG	pBAD-SymE PCR
SPA-C	CTACTTGTCATCGTCATCCTTGTAGTCG	pBAD-SymE-SPA PCR
yjiW-5-T7	TAATACGACTCACTATAGGGTATTTAGCGCGGTGCGGATGTGC	<i>symE</i> mRNA synthesis
YjiW-3	GAAGGCTCCCGGTGGTTAACC	<i>symE</i> mRNA synthesis
AyjiW-F-T7	TAATACGACTCACTATAGGGAGTCATAACTGCTATTCTCCAGG	SymR RNA synthesis