Table S1 Primer sequences

Primer name	Sequence
127-41	5'-GCTCGCGGGCTTGCTAT-3'
127-42	5'-TCGGTTTAAAAGCTGGTCATCA-3'
141-25	5'-TTcAAccAccgcAcgATAgAg-3'
141-77-2	5'-gcgTAcccTgTTcAccggTAgcAAAgAAcg-3'
141-62	5'-CATTTTCCGTGACGTCTCGTT-3'
141-63	5'-GCAACATGGAAATCGCTGATT-3'
170-23	5'-AAGGTGCGCCGTACAGCTA-3'
170-24	5'-CGGCACCAGATGGTTTTTGT-3'
178-21	5'-ATCCTCACCGATCTGCAAAAAG-3'
178-22	5'-GCGCAGCAGGGCAATG-3'
178-23	5'-AACGCTACTGCTGCCCAAA-3'
178-24	5'-GGGCGTCGGTCAAATCG-3'
178-25	5'-GGCAGCCGATTATGAAAATCA-3'
178-26	5'-GACAATGGGCGCATCGA-3'
198-12	5'-ATGGGTCGGGCCATTGT-3'
198-13	5'-GGGCTGGTCCCAGTACCAT-3'
224-7	5'-CCCGCCACAAGGTCATAAGA-3'
224-8	5'-AAGGAAGAACGAGAAGCCATGT-3'
225-10	5'-ggAgATcTTcTTTcAAcAgcgTTTcgcg-3'
225-24	5'-ccAAgcTT TTATTTTTTTccTTcAAcccATTTgccATc-3'
225-34	5'-GTGCCCTTAAACGCCTGGTGCTACGCCTGAATAAGTGAAATAACCTTTAATTCTGTCAGG-3'
225-35	5'-AGATATCGTGAGCATCAACACGCAC-3'
225-40	5'-CGAAGAGTTGAACGAAACGCATCAG-3'
225-41	5'-TTGGCCCAGGGCTTCCCGGTATCAACAGGGACACCAG AGCTTTACCCATATTCACCTTAC-3'
273-14	5'- AAGCAACTGGTCTGTTCCTGACT-3'
273-15	5' - TTCGCACCAGCGGTGAT-3'
343-15	5'- GGTCAGCGGCCTGAGTGA-3'
343-16	5' - AGCCTTACGACGGCTTGAAC-3'
377-10	5'-AgATgggcgATcTgTATcTgATcAATggTg-3'
377-24	5'-ccgAATTcTAcAAccTgAcAcTcTcTcg-3'
377-27	5'-gAAggATcTcgTTgAgAcTc-3'
377-29	5'-TTggTgcccTTAAAcgccTggTgcTAcgccTgAATAAgTgggcgATTTAAAcgccTggcg-3'
377-30	5'-TccTcTTcTgAgATgAgTTTTTgTTcgccgccgccATATcccTgcTcgAAATAgcTTTcg-3'
377-37-2	5'-ccgTcgAcTAcAAccTgAcAcTcTcTcg-3'
377-38	5'-ttggtctggatatcatcggc-3'
378-11	5'-AgcTggATTTTgccgTgTcg-3'
378-8	5'-TTgcggccgcgTcAcAAAAgcTggAAgTgg-3'
387-16	5'-GCGGGCTACCAGCAGGTA-3'
387-17	5'-CGTTTGCGGATGCAGAAAC-3'
397-42	5'-ccggATcc AcAgAgATgATTAcTgcgccAgTTg-3'
397-43	5'-ccggATcc gcTAcAgTTTATTAcgcTTcgTcAccg-3'
447-50	5'-ccgAgcTccTggTAAccATTATTcAgcAg-3'
447-96	5'-acttaactcgctgcaaggcg-3'
448-13	5'-TTgggcccggcAAcAgTTTAccggcATc-3'
448-17	5'-gAgccAATTTcTAccgcAcg-3'
448-23	5'-CACCCGCGAAACCTACAAA-3'
448-24	5'-GCATCTTTCTTGGCGGACAT-3'
454-30	5'-ccAgATcT gTcAgTTgAAAgAgTTccTcgAcgc-3'
454-31	5'-ccAgATcT ggAATTTTccTAAcATcgccAgcg-3'
454-32	5'-GCGGCAGCCTGACCATT-3'
454-33	5'-GTCCATTTTAGAACCGGTATCGA-3'
454-31	5'-ccAgATcT ggAATTTTccTAAcATcgccAgcg-3'
454-37	5'-cgccAccATATccATTAgcggAATg-3'
454-56	5'-ATGGGTCGGGATCTGTACGACGATGACGATAAG ATGAATCTTACCGAATTAAAGAATACG-3'
466-22	5'- TCAGTACGGCGGCTCTGTAA -3'
466-23	5' - CCGGCTGAGCAAACAGTTCT -3'
466-46	5'- GTTCGCGTCACGGAAGGT -3'

466-47	5'- TCGTCAATTTCGCCCATACC -3'
466-48	5'- GACGAAAACGAACTGGGTGAA -3'
466-49	5'- CGCGGCTACGAACAACGT -3'
466-50	5'- GACGAAAACGAACTGGGTGAA -3'
466-51	5'- CGCGGCTACGAACAACGT -3'
Cm N	5'-cTggTgTcccTgTTgATAcc-3'
Cm C	5'-cAcTTATTcAggcgTAgcAc-3'
CmC-BNH	5'-ccggATccgcggccgcAAgcTTcAcTTATTcAggcgTAgcAc-3'
L39-2B-CmC	5'-cTgATgcgAcgcTAAcgcgTcTTATcAgAccTATAgccgcAcTTATTcAggcgTAgcAc-3'
L39-8A-CmN	5'-ATATTcTcAccATgccTggTgTggcAggAcAcgccTgATgcTggTgTcccTgTTgATAcc-3'
Myc-N	5'-ggcggcggcgAAcAAAAAcT-3'
pBAD-ApU2Not	5'-TTTgcggccgcccgggAgcggATTTgAAcgTTgcg-3'
pBAD-ApURNot	5'-TTTgcggccgccggATTTgTccTAcTcAggAgAgcg-3'
pBAD-C2	5'-CCCGATTGTCCTCCTTAATTGGTAC-3'
pBAD-EK	5'-cTTATcgTcATcgTcgTAcAg-3'
pBAD-N4	5'-gATcgATggggATccgAgc-3'
pBAD-N5	5'-cccTcgAgATcTgcAgcTggTAccATATggg-3'
Sa-ApL-R	5'-TgAAAgAAggTgTTgAAATggc-3'
Sa-ApR	5'-ATAAATcTcgAAAATAATAgAggg-3'
tnaC(mut)-A	5'-caaaattgtcgatcacagaccttgatttgcccttctgtagccatcaccagagccaaaccg-3'
tnaC(mut)-AR	5'-cggtttggctctggtgatggctacagaagggcaaatcaaggtctgtgatcgacaattttg-3'
tnaC(mut)-D	5'-caaaattgtcgatcacagatagtgatttgcccttctgtagccatcaccagagccaaaccg-3'
tnaC(mut)-DR	5'-cggtttggctctggtgatggctacagaagggcaaatcactatctgtgatcgacaattttg-3'
tnaC(mut)-E	5'-caaaattgtcgatcactgatttgcccttctgtagccatcaccagagccaaaccg-3'
tnaC(mut)-ER	5'-cggtttggctctggtgatggctacagaagggcaaatcagtgatcgacaattttg-3'
tnaC(mut)-F	5'-caaaattgtcgatcacctggcttgatttgcccttctgtagccatcaccagagccaaaccg-3'
tnaC(mut)-FR	5'-cggtttggctctggtgatggctacagaagggcaaatcaagccaggtgatcgacaattttg-3'
tnaC(mut)-G	5'-taaccatgaatatcttacatatatgtgtgacctcaaaatccgtcaatattgacaacaaaa-3'
tnaC(mut)-GR	5'-ttttgttgtcaatattgacggattttgaggtcacacatatatgtaagatattcatggtta-3'
tnaC(mut)-H	5'-caaaattgtcgatcaccgcccttgatgagccaaaccgattagattcaatgtgatc-3'
tnaC(mut)-HR	5'-gatcacattgaatctaatcggtttggctcatcaagggcggtgatcgacaattttg-3'
yqgF-A103I-F	5'-ctccatgacgagcgtcttagcactgtggaaatccgttccggtctgtttgaacagggcggc-3'
yqgF-A103I-R	5'-gccgccctgttcaaacagaccggaacggatttccacagtgctaagacgctcgtcatggag-3'
yqgF-D122A-F	5'-ctatcgggcgctcaacaaaggcaaagttgcctctgcctctgcggttattattctcgaaag-3'
yqgF-D122A-R	5'-ctttcgagaataataaccgcagaggcagaggcaactttgcctttgttgagcgcccgatag-3'
yqgF-D125A-F2	5'-ctatcgggcgctcaacaaaggcaaagttgactctgccgctgcggttattattctcgaaag-3'
yqgF-D9A-F	5'-atgagtggaaccttactcgccttcgccttcggcaccaaaagcattggcgtagcggtcggc-3'
yqgf-D9A-R	5'-tggccgaccgctacgccaatgcttttggtgccgaaggcgaaggcgagtaaggttccactg-3'
yqgF-E96A-F	5'-cgtttcggtgttgaagtaaagctccatgacgcgcgtcttagcactgtggaagcccgttcc-3'
yqgF-E96A-R	5'-ggaacgggcttccacagtgctaagacgcgcgtcatggagctttacttcaacaccgaaacg-3'
yqgF-S105I-F	5'-gacgagcgtcttagcactgtggaagcccgtatcggtctgtttgaacagggcggctatcgg-3'
yqgF-S105I-R	5'-ccgatagccgccctgttcaaacagaccgatacgggcttccacagtgctaagacgctcgtc-3'
yqgF-S125A-R2	5'-ctttcgagaataataaccgcagcggcagagtcaactttgcctttgttgagcgcccgatag-3'
yqgF-T100I-F	5'-gtaaagctccatgacgagcgtcttagcattgtggaagcccgttccggtctgtttgaacag-3'
yqgF-T100I-R	5'-ctgttcaaacagaccggaacgggcttccacaatgctaagacgctcgtcatggagctttac-3'
yqgF-L6H-F	5'-ATGAGTGGAACCTTACACGCCTTCGACTTCGGCACCAAAAGCATTGGCGTAGCGGTCGGC-3'
yqgF-L6H-R	5'-GCCGACCGCTACGCCAATGCTTTTGGTGCCGAAGTCGAAGGCGTGTAAGGTTCCACTCAT-3'
yqgF-E46G-F	5'-GACGGTACGCCGGACTGGAACATTATCGGGCGTTTACTGAAAGAGTGGCAGCCGGACGAA-3'
yqgF-E46G-R	5'-TTCGTCCGGCTGCCACTCTTTCAGTAAACGCCCGATAATGTTCCAGTCCGGCGTACCGTC-3'
yqgF-E109G-F	5'-CGTCTTAGCACTGTGGAAGCCCGTTCCGGTCTGTTTGGACAGGGCGGCTATCGGGCGCTC-3'
yqgF-E109G-R	5'-GAGCGCCCGATAGCCGCCCTGTCCAAACAGACCGGAACGGGCTTCCACAGTGCTAAGACG-3'
yqgF-N117D-F	5'-CAGGGCGGCTATCGGGCGCTCGACAAAGGCAAAGTTGACTCTGCCTCTGCGGTTATTATT-3'
yqgF-N117D-R	5'-AATAATAACCGCAGAGGCAGAGTCAACTTTGCCTTTGTCGAGCGCCCGATAGCCGCCCTG-3'
HJ-1	5'-GACGCTGCCGAATTCTGGCGTTAGGAGATACCGATAAGCTTCGGCTTAA-3'
HJ-2	5'-CTTAAGCCGAAGCTTATCGGTATCTTGCTTACGACGCTAGCAAGTGATC-3'
HJ-3	5'-TGATCACTTGCTAGCGTCGTAAGCAGCTCGTGCTGTCTAGAGACATCGA-3'
HJ-4	5'-ATCGATGTCTCTAGACAGCACGAGCCCTAACGCCAGAATTCGGCAGCGT-3'
HJ-5	5'-CTTAAGCCGAAGCTTATCGGTATCTCCTAACGCCAGAATTCGGCAGCGT-3'
HJ-7	5'-CTTAAGCCGAAGCTTATCGGTATCT-3'
HJ-8	5'-GCTCGTGCTGTCTAGAGACATCGAG-3'

Table S2 Specific Primers used for construction of mutant *yqgF*

Plasmids with mutant *yqgF*	1st PCR (1)		1st PCR (2)		2nd PCR	
mF-Ap3-KmNot-*yqgF*(D9A)	377-10	yqgF-D9A-R	Sa-Ap-R	yqgF-D9A-F	377-38	Sa-ApL-R
mF-Ap3-KmNot-*yqgF*(E96A)	377-10	yqgF-E96A-R	Sa-Ap-R	yqgF-E96A-F	377-38	Sa-ApL-R
mF-Ap3-KmNot-*yqgF*(D122A)	377-10	yqgF-D122A-R	Sa-Ap-R	yqgF-D122A-F	377-38	Sa-ApL-R
mF-Ap3-KmNot-*yqgF*(S125A)	377-10	yqgF-S125A-R2	Sa-Ap-R	yqgF-D125A-F2	377-38	Sa-ApL-R
mF-Ap3-KmNot-*yqgF*(T100I)	377-10	yqgF-T100I-R	Sa-Ap-R	yqgF-T100I-F	377-38	Sa-ApL-R
mF-Ap3-KmNot-*yqgF*(A103I)	377-10	yqgF-A103I-R	Sa-Ap-R	yqgF-A103I-F	377-38	Sa-ApL-R
mF-Ap3-KmNot-*yqgF*(S105I)	377-10	yqgF-S105I-R	Sa-Ap-R	yqgF-S105I-F	377-38	Sa-ApL-R
mF-Ap3-KmNot-*yqgF*(deletionE96-G119)	377-10	yqgF-deletion-R2	Sa-Ap-R	yqgF-deletion-F2	377-38	Sa-ApL-R
mF-Ap3-KmNot-*yqgF*(deletionF108-A115)	377-10	R-yqgF-del(F108-A115)	Sa-Ap-R	F-yqgF-del(F108-A115)	377-38	Sa-ApL-R

Table S3 Specific Primers used for construction of mutant *tnaC*

Plasmids with mutant *tnaC*	1st PCR (1)		1st PCR (2)		2nd PCR	
pHSG415-*tnaC* (A)	tnaC(mut)-A	448-17	tnaC(mut)-AR	447-96	447-50	448-13
pHSG415-*tnaC* (D)	tnaC(mut)-D	448-17	tnaC(mut)-DR	447-96	447-50	448-13
pHSG415-*tnaC* (E)	tnaC(mut)-E	448-17	tnaC(mut)-ER	447-96	447-50	448-13
pHSG415-*tnaC* (F)	tnaC(mut)-F	448-17	tnaC(mut)-FR	447-96	447-50	448-13
pHSG415-*tnaC* (G)	tnaC(mut)-G	448-17	tnaC(mut)-GR	447-96	447-50	448-13
pHSG415-*tnaC* (H)	tnaC(mut)-H	448-17	tnaC(mut)-HR	447-96	447-50	448-13

Table S4 Specific Primers used for qRT-PCR

Gene	Primer (1)	Primer (2)
cca	387-16	387-17
dnaE	127-41	127-42
galE	178-21	178-22
galK	178-25	178-26
galT	178-23	178-24
gapA	273-14	273-15
lacZ	141-62	141-63
lnt	170-23	170-24
nusA	466-50	466-51
ompA	198-12	198-13
pnp	466-48	466-49
rho	454-32	454-33
rnc	343-15	343-16
tnaA	448-23	448-24
tpiA	466-22	466-23
trpE	224-7	224-8
truB	466-46	466-47