

**Table S1.** Primers and plasmids used in this work

Primer	Sequence (5'-3')	PCR product and purpose	Plasmid (related strain)
ermE*p insertion			
EcoRI-EP1	TATAGAATTCGCTGACTTCGAGGAAGTGGT	2769-bp fragment for ermE*p insertion upstream (-104 bp from start codon) of jomP1 in chromosome	pEjomP1 (G-pErm*)
PstI-EP1	TATACTGCAGCCCGCAATTCAGGTTCTTTA		
Gene mutation			
EcoRI-P1	TATAGAATTCGAGAGTTCTGCTTCGGGATG	2938-bp fragment for jomP1 interruption	pIjomP1 (jomP1 <sup>-</sup> )
HindIII-P1	TATAAAGCTTGCGTCGCAGTACTTCGGTAT		
EcoRI-N	TATAGAATTCGCTGGTCGGTGTCCTCTC	2246-bp fragment for jomN interruption	pIjomN (jomN <sup>-</sup> )
HindIII-N	TATAAAGCTTGTCTCTCTACGACGCCTTG		
NsiI-orf8	TATAATGCATCTTCCGCATCAGAGGACAGT	2590-bp upstream flanking region for orf8deletion	pDorf8 (Δorf8-araC)
SpeI-orf98	TATAACTAGT GATGTTCCATTCGCCTGTCT		
EcoRV- orf8	TATAGATATCGGTCGGTACAACGTCGTCTT	2433-bp downstream flanking region for orf8 deletion	
BamHI- orf8	TATAGGATCCCTTCATCGACGCCTTCAACT		
NsiI-orf9	TATAATGCATTGACGACAGTTGCCTTCTTG	2501-bp upstream flanking region for orf9 deletion	pDorf9 (Δorf9)
SpeI-orf9	TATAACTAGTCAGTTCCACCAACTCCACCT		
EcoRV-orf9	TATAGATATCACATGTGTCGATCCCGAAGAGT	2495-bp downstream flanking region for orf9 deletion	
BglII-orf9	TATAAGATCTCCTCCTACGAAGGGGAGTTC		
SpeI-orf16	TATAACTAGTCCCTTCTTGAAAGGACCACA	2659-bp upstream flanking region for orf16 deletion	pDorf16 (Δorf16-luxR)
NsiI-orf16	TATAATGCATGAGTCATGATCACGCTCCAG		
BamHI-orf16	TATAGGATCCGTCCTCGCGAAGCTACAGTT	2592-bp downstream flanking region for orf16 deletion	
EcoRV-orf16	TATAGATATCATCTCCGTGAGAGTGGCATC		
SpeI-orf20	TATAACTAGTTCGCGTACAACATCATCGAG	2510-bp upstream flanking region for orf20 deletion	pDorf20 (Δorf20-marR)
NsiI-orf20	TATAATGCAT GTGCTGGGTGACGTCCTT		
BamHI-orf20	TATAGGATCCCGTCTACGCCGTGCGAACAG	2353-bp downstream flanking region for orf20 deletion	
EcoRV-orf20	TATAGATATCAAGTGGTTGCCGATGAAGAG		

**Table S1.** Primers and plasmids used in this work (continued)

Primer	Sequence (5'-3')	PCR product and purpose	Plasmid (related strain)
Gene mutation			
SpeI-orf29	TATA <u>ACTAGT</u> CCTGGAGATATCCCTCACCA	2392-bp upstream flanking region for <i>orf29</i> deletion	pDorf29 (Δorf29-gntR)
NsiI-orf29	TATA <u>ATGCAT</u> GCTGGGACAGCTGGAAATAC		
BglII-orf29	TATA <u>AGATCT</u> GTTACGCCTTCGAGTTCCAG	2609-bp downstream flanking region for <i>orf29</i> deletion	
EcoRV-orf29	TATA <u>GATATC</u> CCTGCGATCGAGAAGAAAAGG		
SpeI-orf31	TATA <u>ACTAGT</u> GTCTCCAGCGTGAGACCACT	2345-bp upstream flanking region for <i>orf31</i> deletion	pDorf31 (Δorf31)
NsiI-orf31	TATA <u>ATGCAT</u> GTGAAGGGGCGGTAGTCG		
BglII-orf31	TATA <u>AGATCT</u> ACGACGAGTTCAAGGCGTAT	2316-bp downstream flanking region for <i>orf31</i> deletion	
EcoRV-orf31	TATA <u>GATATC</u> ATGACGCAGAGCACCTTCTT		
SpeI-M	TATA <u>ACTAGT</u> CCTCGCGTACGTCATCTACA	2506-bp upstream flanking region for <i>jomM</i> deletion	pDjomM (ΔjomM)
NsiI-M	TATA <u>ATGCAT</u> CGTGGTTGTACACCTCGGATA		
BglII-M	TATA <u>AGATCT</u> GACTACCTCCCCACACTGGA	2751-bp downstream flanking region for <i>jomM</i> deletion	
EcoRV-M	TATA <u>GATATC</u> CGGGAGCTGAACTGTAGCTT		
Gene expression			
EcoRV-araC	TATA <u>GATATC</u> GTGGTGGCGAGCCCTAAG	917-bp fragment containing <i>orf8</i> (-31 bp from start codon) for gene overexpression	pSAraC (G- pSAraC)
BamHI-araC	TATA <u>GGATCC</u> CTCTGTGGGTCTTCCGTCC		
EcoRV-luxR	TATA <u>GATATC</u> CCTACCGCGCCGGCCGCT	2376-bp fragment containing <i>orf16</i> (-100 bp from start codon) for gene overexpression	pSLuxR (G- pSLuxR)
XbaI-luxR	TATA <u>TCTAGA</u> GTGTCCCTTCCGGAGCAAAG		
EcoRV-marR	TATA <u>GATATC</u> GTCAATTCCTCCAGGGCCG	547-bp fragment containing <i>orf20</i> (-84 bp from start codon) for gene overexpression	pSMarR (G- pSMarR)
BamHI-marR	TATA <u>GGATCC</u> TGGGGTCTTCCTCACTCCTT		
EcoRV-gntR	TATA <u>GATATC</u> CAGGCGGACGGAATGACC	888-bp fragment containing <i>orf29</i> (-60 bp from start codon) for gene over-expression	pSGntR (G- pSGntR)
BamHI-gntR	TATA <u>GGATCC</u> TGTCCGGACAATGTGACCTC		
SmaI-jomM	ATAT <u>CCCGGG</u> CTGTGGGTCTAGCTGGCGG	1035-bp fragment containing <i>jomM</i> (-38 bp from start codon) for mutant complementation	pSEJomM (ΔM- pSEJomM)
BamHI-jomM	ATAT <u>GGATCCCC</u> GAAGAGCTTGGTCAACGA		
EcoRI-KanR	TATA <u>GAATTC</u> GAAATCTCGTGATGGCAGGT	930-bp fragment containing gene <i>aph(3) II</i> (-86 bp from start codon) for pSETk construction	pSETk (G- pSETk)
EcoRV-KanR	TATA <u>GATATC</u> TTTCTTGCCGCCAAGGATCT		

**Table S1.** Primers and plasmids used in this work (continued)

Primer	Sequence (5'-3')	PCR product and purpose	Plasmid (related strain)
JAs BGC heterologous expression			
XhoI-2TAR	TATA <u>CTCGAG</u> CTTAGGGCTCGCCACCAC	1081-bp arm flanking JAs BGC (left) for capture by TAR cloning	<b>pCL2-CAP</b> (Sc-pJATAR and Sa-pJATAR)
NsiI-U2TAR	TATA <u>ATGCAT</u> AGCTCATGGGACTGAACACC		
NsiI-L2TAR	TATA <u>ATGCAT</u> GAGCGTGATCATGACGAGGT	945-bp arm flanking JAs BGC (right) for capture by TAR cloning	
SpeI-2TAR	TATA <u>ACTAGT</u> TGGTGTTGATCACCCACAAT		
dApra-pErm	caggttcttagggcagggcgaccgtcctctcggtcgattTTTTCTACGGGGTCTGACGC	Amplification of a <i>aac(3)IV-ermE*p</i> assembled fragment to be inserted upstream of <i>jomP1</i> at pJATAR	<b>pNTARe</b> (Sc-pJATARe and Sa-pJATARe)
dApra	TTTTCTACGGGGTCTGACGC		
NsiI-rvApra	TATA <u>ATGCAT</u> TCGTTAGTCGGAGGCCAAAC		
dNsiI-pErm	TATA <u>ATGCAT</u> GTAAAACGACGGCCAGTGC		
rvApra-pErm	tcaccggcggtcttcattcaacatccccaatttcatgaagtTACGAATTCGATATCGCGCG		
rvpErm	TACGAATTCGATATCGCGCG		
Mutant confirmation			
apraI	TGAGAAGCTGACCGATGAGCTC	reverse primer annealing <i>aac(3)IV</i>	
apraII	GAGCTCATCGGTCAGCTTCTCA	forward primer annealing <i>aac(3)IV</i>	
dcfErm	CGGTTGGTAGGATCCAGACCTG	Confirmation of <i>ermE*p</i> insertion upstream of <i>jomP1</i>	
rvcfErm	GAACCTGTGAGGCCAGCGA		
cfP1up	GGACTGATGAAGGTGGTGCTGT	used with apraI for confirmation of <i>jomP1</i> interruption with pJomP1	
cfP1dw	CAGGTGGAAGTAGTCGTCCTCG	used with apraII for confirmation of <i>jomP1</i> interruption with pJomP1	
cfNup	TCCTCGTACCACTGGAAGAGA	used with apraI for upstream confirmation of <i>jomN</i> interruption with pJomN	
cfNdw	GAGAACTCCACCTGCCATTCT	used with apraII for downstream confirmation of <i>jomN</i> interruption with pJomN	
cf8up	CGGTTGTTGGGCGACTTGATC	used with apraI for upstream confirmation of <i>orf8</i> deletion	
cf8dw	CTTCAGGTACGGGGTGTGATC	used with apraII for downstream confirmation of <i>orf8</i> deletion	
cf9up	CTTCGATCCTGGTGATCCGCC	used with apraI for upstream confirmation of <i>orf9</i> deletion	
cf9dw	TCCCTTGATGCCAGCTGTAGAC	used with apraII for downstream confirmation of <i>orf9</i> deletion	

**Table S1.** Primers and plasmids used in this work (continued)

Primer	Sequence (5'-3')	PCR product and purpose
<b>Mutant confirmation</b>		
cf16up	AGGAATGGCAGGTGGAGTTCTC	used with apraI for upstream confirmation of <i>orf16</i> deletion
cf16dw	AGCACAAAAACGGAGCAGGTTG	used with apraII for downstream confirmation of <i>orf16</i> deletion
cf20up	CCATGAACTCGATGGGCAGGTA	used with apraI for upstream confirmation of <i>orf20</i> deletion
cf20dw	TCTCGTCGGTGATGTGCTTGAT	used with apraII for downstream confirmation of <i>orf20</i> deletion
cf29up	GAAAATGCCGTATCCGCCGTAG	used with apraI for upstream confirmation of <i>orf29</i> deletion
cf29dw	CCTCCATATCGGCGATGGTCTT	used with apraII for downstream confirmation of <i>orf29</i> deletion
cf31up	CGGATACCGTGGTGCCATAGG	used with apraI for upstream confirmation of <i>orf31</i> deletion
cf31dw	CTCGATCGAGGACTGCGAGTTC	used with apraII for downstream confirmation of <i>orf31</i> deletion
cfMup	ATCCTGCTGGACGAACAGACC	used with apraI for upstream confirmation of <i>jomM</i> deletion
cfMdw	CTCTTCATCGGCAACCACTT	used with apraII for downstream confirmation of <i>jomM</i> deletion

**Figure S27. Confirmation by PCR amplification of *S. caniferus* GUA-06-05-006A derivative strains generated in this work.** Recombinant strain (RS) G-pErm\* and mutant strains (M) were subjected to colony PCR with the indicated primer pairs (see table S1). In all cases a negative PCR control (WT) consisting in wild type *S. caniferus* GUA-06-05-006A DNA was processed. Band sizes were compared with 0.1 µg of lambda/PstI DNA marker.





