

Table S2. Primers used in this study

Regions or genes	Primers	Sequences 5'-3'	Length
<i>ngrA</i> mutant construction	L-PCR1- <i>ngrA</i> -XbaI	GCGCTCTAGAGGCCAGTACTTCACGATTGG	579 bp
	R-PCR1- <i>ngrA</i> -BamHI	GCGCGGATCCGGAACGGTCTTTGGCATTG	
<i>ngrA</i> mutant verification	L- <i>ngrA</i> 2bis-BamHI	GCGGATCCCAATCGCACTGTGAACATCA	522 bp
	R- <i>ngrA</i> 2bis-ApaI	GCGGGCCCCAGTCATTGGTGGTTTGACG	
<i>ngrA</i> gene	L- <i>ngrA</i> -mut	CAGCAGCACAACAGACCAAT	6 kb
	L-PCR1- <i>ngrA</i> -XbaI	GCGCTCTAGAGGCCAGTACTTCACGATTGG	
<i>oatA</i> mutant construction	L-SacI-b	GCGAGCTCATGTCATCGCACACTTGCTC	595 bp
	R-SpeI- <i>oatA</i>	GCACTAGGGCATGAGCAACATATCACC	
<i>oatA</i> mutant verification	L-SalI- <i>oatA</i>	GCGTCGACGGATCACCGTCTGCTATGAG	611 bp
	R-ApaI- <i>odl1</i>	GCGGGCCCAGATTCCGCCTCATCTCAC	
<i>oatA</i> mutant verification	R-Km-PvuI	GCCGATCG TCATTTGCAACCCAGAGTC	1791- bp
	L-b-KpnI	GGCGGTACCCCGAAAGTCAAACCCAGAGA	
	M13-F	GTAAAACGACGGCCAG	3 kb
	R- <i>odl1</i> -F1q	TTCTACAGAAATATCGAAGCTGACC	
p15A- <i>odl</i> -BGC Red/ET cloning (LLHR)	<i>odl</i> -bis1	TTGTTCTGGTTTGGAAACGATGATACTAACATCAACC CCCCGCATTGCGGCTGTACAAATGGTTACGCCCG CCCTGCCACTC	44.5 kb
	<i>odl</i> -bis2	CGGAAATGTTTCGACAATATGAACGAGCTTTTACT CATAATTATTGAATATCTCTTCCACGGTAACGAATC AGACAATTGACG	
p15A- <i>P_{ter}</i> - <i>odl</i> -BGC Red/ET cloning (LCHR1)	p15A- <i>odilo</i> -5	TCTGCAAACCCTATGCTACTCCGTCAAGCCGTCAAT TGCTGATTCTGTTACCTAATGCGGTAGTTTATCACA	2093 bp
	p15A- <i>odilo</i> -3	AAATGTTTCGACAATATGAACGAGCTTTTACTCAT AATTATTGAATATCTCTTCCACATGAATTCCTCTG CTAGAT	
p15A- <i>P_{ter}</i> - <i>odl</i> -BGC-mob Red/ET cloning (LCHR2)	L-Gm-Km	ATAAATAAAATGGCGCCACAGGTGCGGTTGCTGGC GCCTCGACCAAGTACCGCCAAGAGAGCGGTTTGC GTATT	2786 bp
	R-oriV-Ptet	CCGTTTCGTATAGCATAACATTATACGAAGTTATTCGG CTTGAACGAATTGTTAGGGGGGCTTGTGATCGAC TG	
<i>defghij</i> region	L-d-KpnI	GGCGGTACCTTTATGGGCGGTTGGTGTAT	7205 bp
	R-j-SacI	GGCGAGCTCATTGGTTTAGCGGCATCGGA	
<i>abc</i> region	L- <i>ectB</i> -KpnI	GGCGGTACCAAAAAGAGGTTAAAGTGAAGAGA	2764 bp
	R-c-SacI	GGCGAGCTCTCAAGTTACGGCTTCGTTG	
<i>ectB</i> gene	L- <i>ectB</i> -KpnI	GGCGGTACCAAAAAGAGGTTAAAGTGAAGAGA	1395 bp
	R- <i>ectB</i> -SacI	GGCGAGCTCTGCGATGACATTCATTCTGA	
<i>b</i> gene	L-b-KpnI	GGCGGTACCCCGAAAGTCAAACCCAGAGA	999 bp
	R-b-SacI	GGCGAGCTCGACACATCACATCTTCATAGTTGTC	
<i>oatA</i> gene	L-c-KpnI	GGCGGTACCCCGTCCGTACCTTAATTATATTCT	591 bp
	R-c-SacI	GGCGAGCTCTCAAGTTACGGCTTCGTTG	
pET- <i>oatA</i>	F-Nterm- <i>oatA</i> -NdeI	GGCCATATGAAAGTAACTTTGACTGATGTG	478 bp
	R-Stop- <i>oatA</i> -SalI	GGCGTCGACTTGGGTATAGGATCATTA	
<i>oatA</i> <i>Photorhabdus</i>	L- <i>oatA</i> -photo-KpnI	GGCGGTACCGTATCTTAATTATATTCTTAAA	592 bp
	R- <i>oatA</i> -photo-SacI	GGCGAGCTCGGAATAACAAGCGGTTCAACTT	
<i>oatA</i> -like <i>X. hominickii</i>	L- <i>oatA</i> -xh-KpnI	GGCGGTACCTCAAAGTATCTTCCGCACCTT	589 bp
	R- <i>oatA</i> -xh-SacI	GGCGAGCTCATAAGCGGGAGAGGCAGTTT	
<i>oatA</i> -like <i>X. innexi</i>	L- <i>oatA</i> -xi-KpnI	GGCGGTACCTCAATAAACTGATGGCAATTACA	473 bp
	R- <i>oatA</i> -xi-SacI	GGCGAGCTCCATTTCTTCATGCTCATCAAA	
<i>oatA</i> -like <i>X. cabanillassii</i>	L- <i>oatA</i> -xc-KpnI	GGCGGTACCTGTGATTCAAAGGGAGAGCA	430 bp
	R- <i>oatA</i> -xc-SacI	GGCGAGCTCATTCTTTTCGCAAGCTCCAG	
<i>oatA</i> -like <i>X. stockiae</i>	L- <i>oatA</i> -xs-KpnI	GGCGGTACCTGGCTATTACATTGTGATTATGGA	527 bp
	R- <i>oatA</i> -xs-SacI	GGCGAGCTCTGTTTCATTTTAAAGAGAAGTTCACA	

In red : Forward homology arm

In blue : Reverse homology arm

Regions or genes	Primers	Sequences 5'-3'	used for
<i>gyrB</i>	F- <i>gyrB</i> -Ecq	ACCCGAATATCTTCTACTTCTCCAC	qPCR
	R- <i>gyrB</i> -Ecq	CTGTAGCCTTCTTTGTCCATGTAG	
<i>ectB</i>	F- <i>ectB</i> -F1q	TCTGGGCTATATTCTCAAATCACAC	qPCR
	R- <i>ectB</i> -F1q	CGCCTTGTACAGTCTCAAGAATAAC	
<i>odl1</i>	F- <i>odl1</i> -F1q	ATCAGAACATCTGGCTTATGTGATT	qPCR
	R- <i>odl1</i> -F1q	TTCTACAGAAATATCGAAGCTGACC	