

Primer name	Sequence (5'-3')	Target gene	Gene annotation
Bacteroid			
mlr9289F	TCTCAATTGCCGCGAAAAG	mlr9289	Unknown
mlr9289R	ATTCTGCCGCCCGA		
mlr5943F	TCGTTGCGAAATACCCCAA	mlr5943	L-2,4-Diaminobutyric acid transaminase
mlr5943R	GCCGGCCATCAGACCAC		
mlr6282F	TGCCTGTTGATCCATCGGA	mlr6282	Phosphinothricin tripeptide synthetase B
mlr6282R	TGGCGTTCTGTGTTGCG		
mlr5972F	AAATGGGTGCGCGATCTG	mlr5972	Transposase
mlr5972R	ATCTGCCCGTGGCCG		
mll6075F	GCTGATGACGATGATCGCCT	mll6075	Transposase
mll6075R	CCCCTCCCGCTTGTGTTG		
mll9123F	TTCTGCGCCCGGC	mll9123	NTA monooxygenase component A
mll9123R	ATCGGAATGCGCGTTCATA		
mlr5876F	TTGAGCTCGATCCACCGG	mlr5876	Cytochrome P450
mlr5876R	GCGAAAGCAGCGACTGA		
mlr5906F	CCGCGGCGTTTCACA	mlr5906	<i>nifD</i>
mlr5906R	AATCGCGGATCGCATCATT		
mlr5932F	GTTTTTTTCCAGCGGGCTC	mlr5932	1-Aminocyclopropane-1-carboxylate deaminase
mlr5932R	TTGATGGCCGGCGC		
mlr7226F	TTCCAAGATCGAATGGTTTTCC	mlr7226	Sugar ABC transporter, permease protein
mlr7226R	TGGCGAAGGTGACGGC		
mll3068F	CCAGAATGATGCGGGTGAG	mll3068	Sulfate ABC transporter, permease protein
mll3068R	TCGACGGCTGCGCC		
mll3069F	ACAAGGACCTGGTAAGGTTTC	mll3069	ABC transporter, periplasmic binding protein
mll3069R	TTGGCGAATCCGGCTT		
mll2921F	CGGTCCGAAACGCTTGAA	mll2921	<i>flgH</i>
mll2921R	CGTTCGGCAAGACGTCG		
mlr9251F	TCGTCAAGCGCAATGACGT	mlr9251	Conjugal transfer protein
mlr9251R	ATTGACAAGCTGCACCAGGAA		
mlr6617F	TCCTGGACACACGCCAGAT	mlr6617	Two-component system, regulatory protein
mlr6617R	CGAAAGCGCAACGGGA		
mll0870F	CCGCGATCTGGCCGA	mll0870	DNA polymerase III alpha subunit
mll0870R	CCAATTCGACATAGAGCCGG		
mlr0325F	CATCAAGGAGATCGCCATCC	mlr0325	DNA-directed RNA polymerase alpha subunit
mlr0325R	TTGCGCACGACCATGC		
mll6624F	TCGTGCTGCTTGTTCATTG	mll6624	<i>fixI</i>
mll6624R	CCGGTGAATTTGGCATCG		
mlr6417F	CGTGATGGTCAAGGACGGA	mlr6417	<i>fixI</i>
mlr6417R	TCGAATACCGCCACGTCTATC		
mlr6210F	ATCCGGTCGACACGCGT	mlr6210	Glutamine synthetase III
mlr6210R	CCAGTCGCGCTCAGCAA		
mll7254F	ATGTGGCGGAGATTTTCCC	mll7254	Glutamine synthetase
mll7254R	CCTGGCGTTTGCAGGC		
Microaerobic			
mlr5857F	TCATATGCGCCACCAACAA	mlr5857	<i>nifA</i>
mlr5857R	GCACCACATTGATGCGGTAATA		
mll6593F	GCCTCTCGATTGCATCGAA	mll6593	Hypothetical protein
mll6593R	AGAAGGCAAGGTCGTACAGAACA		
mll6600F	TGGTCTTACCTCTGGCTTTGT	mll6600	5-Aminolevulinic acid synthase
mll6600R	ATCATCGAGGCGTGGTTCA		
mll6607F	TTACAGCACTCGCGAAATG	mll6607	<i>fixL</i>
mll6607R	TGCCTTTGAGGTAGTTTCGTGATC		
mll6630F	GAGCCTTTCCGACAGCATATGT	mll6630	<i>fixN</i>
mll6630R	ACTTGTTGTCGCGAAGAACA		
mll6639F	ATGCAATATGCCAGCCAGAAC	mll6639	Aldehyde dehydrogenase
mll6639R	CAGCGGAACATGACGAA		
mlr5905F	CGTCATCACCTCGATCAACTTC	mlr5905	<i>nifH</i>
mlr5905R	CCAGCACGTCGTAGGAGACATA		
mlr6411F	CGTCGTTCTAAGCCTGTTGCT	mlr6411	<i>fixN</i>
mlr6411R	CTGTGTTGCGCAGCAGGAT		
mlr6580F	TGTATGGAAGTGGACAGGTCTCA	mlr6580	Serine/threonine kinase
mlr6580R	TGCGAAACAGGCTGGTGAT		
mlr6618F	GATACTGGTTCCGGCAACCTT	mlr6618	Two-component sensor protein
mlr6618R	GCCCCTTGAATTCCTTGATCTC		
mlr6622F	CAGGAACTTGGCGACATCTATG	mlr6622	Nodulin 21
mlr6622R	GCCGTTGTCATCTCCGAAAT		
mlr6633F	CGGCGTTCAGGATTCGAT	mlr6633	Anaerobic coproporphyrinogen III oxidase
mlr6633R	CTCTTGGTCAGCAGGAAGCTTT		

Starvation

mll6527f1	TGCTCGCCCTCGTTCAACTG	mll6527	Isocitrate lyase
mll6527r1	GAGCGTGATGAACTGGAACCTGTAG		
mll3076f	AGCGACAGCAGACGGATACC	mll3076	Hypothetical protein
mll3076r	CCAGCCTCTCCTCGACGATG		
mlr4771f	GAACTCTACAAGAAGGGCAACC	mlr4771	Secreted sugar-binding protein
mlr4771r	AGATGAAGCCGTGGATGACC		
mlr2341f	CGTACCGATGCTCTCCGATGC	mlr2341	Hypothetical protein
mlr2341r	AGGACGGCAGCCATAATTGAC		
mlr2339f	GACAAGTCGTCGCCATATCTGAAG	mlr2339	Hypothetical protein
mlr2339r	CGCTGGTCTCGCCGTCATG		
mll1629f	GCTGCCTGCGACTATTCTTCC	mll1629	Dihydropyrimidinase
mll1629r	TCTCGTCGTCGCCACCATCAG		
mll1631f	CCAGTACAAGGTCGAGCAGGTC	mll1631	N-Carbamoyl-beta-alanine amidohydrolase
mll1631r	CGATGTTGCCGTGCGTATAGC		
mll3075f	GCCTGTTGCTGCCGATCTATACG	mll3075	Amino acid/metabolite permease
mll3075r	CCGACCAGACGACCGACATGAC		
mll1644f2	TGCCACGCCCGACGACTATC	mll1644	Sterol methyltransferase
mll1644r2	GCTTCTTGCCCTCCGCTTGC		
mll0710f2	CGTTTCGTGCTGCCCTATGC	mll0710	Glycerol-3-phosphate dehydrogenase
mll0710r2	GCTTGCCATGTGCGAGTGCCTG		
mlr2338f	CGCTCCGAGCGACGACCATC	mlr2338	Hypothetical protein
mlr2338r	CGCCAGGTGCCCTCCATCTCC		
mlr1634f	CCGCCGAAGGAAGACATTCAC	mlr1634	Transcriptional regulator
mlr1634r	CGCAGCTCAGTCATCGGATCG		
mll3795f	ACGACATCGCCAAGGCTAGG	mll3795	Transcriptional regulator
mll3795r	GATCGGAACAACCGACATC		
mll4697f	AGATAGTGATTGCTGACGACCATCC	mll4697	Two-component system response regulator
mll4697r	ACCCTGTCTCGCCATTGTC		
mll4698f	CAGTCTCAGCCGAAGCGTCAAAGC	mll4698	Two-component system histidine protein kinase
mll4698r	GTGCCGCCGCCAACCCAAAG		
mll6710f	CAGCCGCAGGACCGTGATAG	mll6710	Transcriptional regulator
mll6710r	CGAGCGTTGAAAAGGACAGAGG		
mlr0480f	CGCTTCCGAGCCTCTACCACTAC	mlr0480	Unknown protein
mlr0480r	CACTGTTGCCGCTCACCGTTAG		
mlr0479f2	GCTTCGCCTCGTGTGGTGAC	mlr0479	<i>exol</i>
mlr0479r2	GGAAATGGCTACTGGCTTTGGCTTG		
mlr2852f	CCTTGGCGTGCTGATCTATG	mlr2852	Cardiolipin synthase
mlr2852r	GCTCATTCTTGCCGATACC		

Standard

MLsigAf1	GCCCTCTGCTCGACCTTTCC	mll2466	<i>sigA</i>
MLsigAr1	AGCATCGCCATCGTGCTCTC		

Other

MLsym1	GGAGGTTATGCTGGGAAAATGAGTTGCAGC	mlr8755	<i>nodA</i>
MLsym2	TGGTCCTGGCTCAAACTCTTACCTGC	mlr6164	<i>nodI</i>
MLsym3	CTCGATGACAGATGGAAGGTGCAGAG	mlr6175	<i>nodB</i>
MLsym4	GTCACGGTATGCGAATTGCCGCTGCCA	mlr8755	<i>nodA</i>
MLsym5	TGGGAGGCAGATCGAGGTACACGTC	ml6179,mlr6182	<i>nodD1, nodD2</i>
MLnodD1	GCAGCATCAACCTTAGTCAGCCG		
MLnodD2	ACGAGCTGTGCCTGAGACCATC		
MLsigA1	AAGAAAGAGCCGACTGACCGACCGA		
MLsigA2	GACCGAGAAGTGTGGCCGACTTCTT	mll2466	<i>sigA</i>
MLsigA3	GGGGTACCCAGCTTTACGACATCAACAAGCGCCTGG		
MLsigA4	CGGGATCCTGACCGAGAAGTGTGGCCGACTTCT		