

PCR Primers for *Brucella* MLSA-9 and MLSA-21 schemes

9 locus – Whatmore *et al.* BMC Microbiol 7:34

21 locus – Whatmore *et al.* 2016. Submitted.

<u>Locus</u>	<u>Putative function</u>	<u>Primer sequences</u>	<u>Core sequence length</u>	<u>Location in <i>B. abortus</i> 9-941 sequence</u>	
MLSA-9					
<i>gap</i>	glyceraldehyde 3-phosphate dehydrogenase	5' YGCCAAGCGCGTCATCGT 3' 5' GCGGYTGGAGAAGCCCCA 3'	589 bp	AE017223	1685083-1685671
<i>aroA</i>	3-phosphoshikimate1-carboxyvinyltransferase	5' GACCATCGACGTGCCGGG 3' 5' YCATCAKGCCCATGAATTC 3'	565 bp	AE017223	29974-30538
<i>glk</i>	glucokinase	5' TATGGAAMAGATCGGCGG 3' 5' GGGCCTTGTCTCGAAGG 3'	475 bp [#]	AE017224	988660-989134
<i>dnaK</i>	chaperone protein	5' CGTCTGGTCTGAATATCTGG 3' 5' GCGTTTCAATGCCGAGCGA 3'	470 bp	AE017223	2066742-2067211
<i>gyrB</i>	DNA gyrase B subunit	5' ATGATTTTCATCCGATCAGGT 3' 5' CTGTGCCGTTGCATTGTC 3'	469 bp	AE017223	142378-141910
<i>trpE</i>	anthranilate synthase	5' GCGCGCMTGGTATGGCG 3' 5' CKCSCCGCCATAGGCTTC 3'	486 bp	AE017223	1538194-1537709
<i>omp25</i>	25 kDa outer-membrane protein	5' ATGCGCACTCTTAAGTCTC 3' 5' GCCSAGGATGTTGTCCGT 3'	490 bp [#]	AE017223	710041-710530
<i>cobQ</i>	cobyrinic acid synthase	5' GCGGGTTTTCAAATGCTTGGA 3' 5' GCGTCAATCATGCCAGC 3'	422 bp [#]	AE017223	1289341-1288920
<i>int-hyp</i>	upstream and extreme 5' of hypothetical protein	5' CAACTACTCTGTTGACCCGA 3' 5' GCAGCATCATAGCGACGGA 3'	430 bp [#]	AE017223	1372708-1372279
Additional loci for MLSA-21					
<i>prpE</i>	propionate-CoA ligase	5' GGTGCTGTTACGCTGGAA 3' 5' AGGTTTTTCGCAGGCGGCGAA 3'	468 bp	AE017223	1687838-1688305
<i>caiA</i>	acyl-CoA dehydrogenase	5' TGTGTTCGCAAGCCTTTG 3' 5' GGTCAAAAGACGTGCCACA 3'	449 bp	AE017224	633492-633940

<i>csdB</i>	cysteine desulfhydrase	5' CGTCACTTCCTGGATCATTTTC 3' 5' GCCACCGACGCTTATGAGAA 3'	487 bp	AE017223	930109-929623
<i>soxA</i>	sarcosine oxidase alpha subunit	5' CCTCGTAAAGCGCCTTCC 3' 5' TGTTGATGCCTCCACATTGG 3'	486 bp	AE017223	245488-245003
<i>leuA</i>	2-isopropylmalate synthase	5' TCAACCGGATGAAGGAAGTC 3' 5' CCCTCGATAGTCTTGGTGACA 3'	482 bp	AE017223	1534688-1534207
<i>mviM</i>	glucose-fructose oxidoreductase precursor	5' ATCGCCCGTTCGGTGAC 3' 5' TGTTGCGCCGTCCTTGTCC 3'	447 bp [#]	AE017223	1990600-1990154
<i>fumC</i>	fumarate hydratase C	5' CGACCATGTCAATATGAGCC 3' 5' GATATCGTTGGCGATCTTGAA 3'	452 bp	AE017224	180504-180055
<i>fbaA</i>	fructose-bisphosphate aldolase	5' CGTGAAATAACCTGATCTCAC 3' 5' CATGCCGGTTTCAAGCGAAC 3'	458 bp	AE017224	360206-360663
<i>ddlA</i>	D-alanine-D-alanine ligase A	5' TTTTCAGTGCCTCGAACAG 3' 5' GTTCTTCAATGATGAGATTAAA 3'	553 bp	AE017223	1251848-1251296
<i>putA</i>	proline dehydrogenase	5' GTGGGCGTGACGCTTTTCG 3' 5' CCTGTGTGAGTACGAGCGG 3'	527 bp	AE017224	512957-513483
<i>mutL</i>	DNA mismatch repair protein	5' ACATCCAAGCTGACCGAC 3' 5' TCCCGTGCGATCACATCCGA 3'	549 bp	AE017224	208009-207461
<i>acnA</i>	aconitate hydratase	5' GAAGGCCGCATCCCCTG 3' 5' GCGGCGAGGCAAGGTAAT 3'	490 bp	AE017223	99997-99508

[#]Size variants identified in these loci.