

**Table S1.** Sequence of primer used in this study. Specific endonuclease restriction sites are indicated in bold.

<b>gene</b>	<b>Sequence (restriction endonuclease)</b>	<b>Application</b>
<i>eccB<sub>5</sub></i> ( <i>rv1782</i> )	AGATGAACAAGGTGGTGTCTGT ATTGGGAGCGTGTCTGTGCTC	Expression studies, RT-PCR
<i>eccC<sub>5</sub></i> (5' terminus) ( <i>rv1783</i> )	ATCAAGCCCGAGAATATTGTCC ATGTCCAGCATCAACATGAACT	Expression studies, RT-PCR
<i>eccC<sub>5</sub></i> (3' terminus) ( <i>rv1784</i> )	CTGCTGTTCTTGGATATGAAAT TTCGAGGTCGGTGATGATCC	Expression studies, RT-PCR
<i>eccB<sub>5</sub></i>	TCCACTCAAATCTGCCGGT GACTCTTTGGCGAGAACGAT ATCTGGCTTGACCGAACCAG	Retrotranscription in 5'RACE reactions 1 <sup>st</sup> nested amplification in 5'RACE reactions 2 <sup>nd</sup> nested amplification in 5'RACE reactions
<i>eccC<sub>5</sub></i>	CCAACCACAATCAGCCACCA GTGTCGATAGGACAATATTCTC ATGTTGAGGTAGGTGCCGAC	Retrotranscription in 5'RACE reactions 1 <sup>st</sup> nested amplification in 5'RACE reactions 2 <sup>nd</sup> nested amplification in 5'RACE reactions
<i>eccB<sub>5</sub></i> upstream region	<b>GGACTAGT</b> ACCGAAAGCTACCAACAG ( <i>SpeI</i> ) G <b>CTCTAG</b> ATAGATCACCTTCCGGTCTGC ( <i>XbaI</i> )	Amplification of <i>eccB<sub>5</sub></i> upstream region for knockout construction
<i>eccC<sub>5</sub></i> downstream region	G <b>CTCTAG</b> ATTCGGCCAAACCGATCAGCT ( <i>XbaI</i> ) ATAAGAAT <b>GCGGCCG</b> CACAAGAACGGAGACACGAAAG ( <i>NotI</i> )	Amplification of <i>eccC<sub>5</sub></i> downstream region for knockout construction
<i>aph</i>	G <b>CTCTAG</b> AGCTGCAAGGCGATTAAGT ( <i>XbaI</i> ) G <b>CTCTAG</b> AATTAGGCACCCAGGCTTTA ( <i>XbaI</i> )	Amplification of <i>aph</i> cassette
<i>rv1780</i> <i>aph</i> <i>rv1786</i> <i>aph</i>	TCATCAATGTGGCCGAACAATT GCAATGTAACATCAGAGATTTTGTGAG ATAGCACTGCGCATGACCCA CACGAGGCAGACCT	Screening of Kana <sup>r</sup> /Sac <sup>r</sup> transformants
<i>eccB<sub>5</sub></i> <i>eccC<sub>5</sub></i>	<b>GGACTAGT</b> GTGGCTGAAGAGAGCCGCGG ( <i>SpeI</i> ) A <b>ATCGTTAAC</b> CTACCGACGCACCTCGGTG ( <i>HpaI</i> )	Construction of Mtb488 merodiploid strain
<i>eccB<sub>5</sub></i>	TGCAT <b>GCAT</b> GCTGAAGAGAGCCGCGGG ( <i>NsiI</i> ) TGCAT <b>GCATA</b> CTACCAGCGTTCTGCAG ( <i>NsiI</i> )	Construction of Mtb <sub><i>p<sub>ptr</sub></i></sub> <i>eccB<sub>5</sub>-eccC<sub>5</sub></i> conditional mutant
<i>eccC<sub>5</sub></i>	TGCAT <b>GCATA</b> AAGCGTGGTTTTGCCCGCC ( <i>NsiI</i> ) TGCAT <b>GCAT</b> CAAACTCACGAACCGAGGTG ( <i>NsiI</i> )	Construction of Mtb <sub><i>p<sub>ptr</sub></i></sub> <i>eccC<sub>5</sub></i> conditional mutant
<i>ptr</i> promoter <i>eccB<sub>5</sub></i> <i>eccC<sub>5</sub></i>	CAGCGTATGGGAATCTCTTG AGAGAGATCCAACCGATTACAC CGTGTCGAGGCGTGAAGAA	Screening of Mtb <sub><i>p<sub>ptr</sub></i></sub> <i>eccB<sub>5</sub>-eccC<sub>5</sub></i> and Mtb <sub><i>p<sub>ptr</sub></i></sub> <i>eccC<sub>5</sub></i> strains