Supplementary Table S2. Primers used in this work.

|  |  |  |
| --- | --- | --- |
| Primer name | Sequence (5’-3’) a. b | Experiment |
| leuAF | TGCTCCCTACCAACTCTATTC | Selective marker amplification, PCR validation |
| leuAR | GTCGAGTTGACCAGAATGTAC | Selective marker amplification |
| dmt2-F5’ | GCCTGCACGGTATACTGACG | *dmt2* deletion construct |
| dmt2-R5’+ leuA | GAATAGAGTTGGTAGGGAGCATCAAGAAGGTGGAGGAGAAACA | *dmt2* deletion construct |
| dmt2-F3’+ leuA | GTACATTCTGGTCAACTCGACAGCATAGTAAAAGATAGATGGAGCGT | *dmt2* deletion construct |
| dmt2-R3’ | CACGCGGAATCTGAATGACG | *dmt2* deletion construct |
| dmt3-F5 | CGGTTGCCCTTTTCTTTCTCG | *dmt3* deletion construct |
| dmt3-R5+leuA | GAATAGAGTTGGTAGGGAGCATCTCTTTGTGATGAAGGTTGGA | *dmt3* deletion construct |
| dmt3-F3+leuA | GTACATTCTGGTCAACTCGACAGCCCATTTTGTGATTTGAGGT | *dmt3* deletion construct |
| dmt3-R3 | GTCCCGGTAAGTACAACTGCA | *dmt3* deletion construct |
| pkaR4-TR-F | AGTCTGGCCTTGCCGTGTTT | RT-qPCR |
| pkaR4-TR-R | GCAACGACCGTAGCTGCTCT | RT-qPCR |
| dmt1-F+ XhoI | TCCCTCGAGAGGTCCCCCTTGACACGTGGTTC | *dmt1* ORF |
| dmt1-R+SacII | TCACCGCGGAGTGCACCATTGGATTCCTTGTCC | *dmt1* ORF |
| P1 | GAAAGCCTGCATTGGATTGGC | *dmt2* replacement confirmation |
| P2 | CGAAAAGTGGCCCCTATCGG | *dmt2* replacement confirmation |
| P3 | GTACACTGTTGCTCTCCATGTG | *dmt3* replacement confirmation |
| P4 | AGCAAATCGTCGTGGATGGT | *dmt3* replacement confirmation |
| pyrGF | TGCCTCAGCATTGGTACTTG | Selective marker amplification |
| pyrGR | GTACACTGGCCATGCTATCG | Selective marker amplification |
| 85076 F | ACAATCTCGGCCTCGGAACAAGTGC | *dmt1* deletion construct |
| 85076 RpyrG | CAAGTACCAATGCTGAGGCATGCACCTTGCTGTCATGGCAACAAGC | *dmt1* deletion construct |
| 85076 FpyrG | CGATAGCATGGCCAGTGTACGCTTGGACCAATGGATACCTACTGAC | *dmt1* deletion construct |
| 85076 R | ATCCCCCTTGACACGTGGTTCGTAGC | *dmt1* deletion construct |
| 115786 F | CTCCATGCTGATATCTGTACGCTGT | *dmt3* deletion construct |
| 115786 RpyrG | CAAGTACCAATGCTGAGGCATGAGGTTCAGCTGTGATTTGGCTCCA | *dmt3* deletion construct |
| 115786 FpyrG | CGATAGCATGGCCAGTGTACTGCTGCTGGTGATTGACAGTTGCTG | *dmt3* deletion construct |
| 115786 R | GATGGCTACTGACAAGATCGTTGCTG | *dmt3* deletion construct |
| 106998 F | AGAGCACGCGGAATCTGAATGACG | *dmt2* deletion construct |
| 106998 RpyrG | CAAGTACCAATGCTGAGGCAGTCTATCCACGACATCAGAGCGAGGA | *dmt2* deletion construct |
| 106998 FpyrG | CGATAGCATGGCCAGTGTACCGAAAATAGTGTGCGCCAGCAGGATG | *dmt2* deletion construct |
| 106998 R | CTTGTGGACATGGAAGATGCTGCT | *dmt2* deletion construct |
| CarRP11 | CATACAAAGCACGAGTTTCC | PCR validation |
| dmt1-TR-F | TGCCTCGTAAACCCAACCACT | PCR validation |
| qPCR-EF1-F | GTCCGTGATATGCGTCAAACC | RT-qPCR |
| qPCR-EF1-R | AGCGGCCTTGGTGACCTTAC | RT-qPCR |
| Udmt1F | ACAATCTCGGCCTCGGAACAAGTGC | Southern blot validadtion |
| Ddmt1-pyrGR | CAAGTACCAATGCTGAGGCATGCACCTTGCTGTCATGGCAACAAGC | Southern blot validadtion |
| Udmt2F | AGAGCACGCGGAATCTGAATGACG | Southern blot validadtion |
| Udmt2-pyrGR | CAAGTACCAATGCTGAGGCAGTCTATCCACGACATCAGAGCGAGGA | Southern blot validadtion |
| Udmt3F | CTCCATGCTGATATCTGTACGCTGT | Southern blot validadtion |
| Ddmt3-pyrGR | CAAGTACCAATGCTGAGGCATGAGGTTCAGCTGTGATTTGGCTCCA | Southern blot validadtion |
| a Underlined sequences are complementary to selection marker *pyrG* or *leuA* | | |
| b Bold bases corresponding to the cutting sites to restriction enzymes | | |