**Table S2.** Six hundred and nineteen SSR primer pairs were designed in the contigs including tri-nucleotide motif.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Code | Motifs |  | Forward primer (5'-3') | Reverse primer (5'-3') |
| mdNGS145 | (AAT) | 7 | TGGTGTCAATAGTGGTGATGG | GGATATAATGGTTATTTCAGCAAAA |
| mdNGS146 | (TAA) | 18 | TGTTTCAAACGCATAGCTGC | CCCAAGTCAACCTTTCTCCA |
| mdNGS147 | (CAA) | 5 | ACGATGCCTGAGGGTTACTG | CAGCATAGGCTCCCACAAAT |
| mdNGS148 | (TTA) | 5 | ACTCTTGGATGCCCCATTTT | CTAAAGGGTGTGGCCCTATC |
| mdNGS149 | (TTC) | 5 | CCGAGCATTAAACCATTTCG | CAACAACCGATTTGTGCATC |
| mdNGS150 | (AAT) | 5 | AGTCCTGGCCCCAAGATTAT | ATGCAGTAATTCTGGCCTGC |
| mdNGS151 | (AAT) | 5 | AGTCCTGGGCAGCCTTTTAT | AGAATAGTGCCACCACGACC |
| mdNGS152 | (ATG) | 5 | AGAAAAAGATGTCGATGCCC | GAGATGAGGGGAGTACCGTG |
| mdNGS153 | (ATA) | 5 | TGCATTGATTATGCATATTTGG | TCATATTCCTGTCTGTGGCAA |
| mdNGS154 | (CTT) | 6 | TACCTGACTCTTGTCGGCCT | AACTTGCTGCCCAAGTCCTA |
| mdNGS155 | (ATA) | 5 | CTTGGGTGTCTGTCAGGGAT | AACAGAGGCACCTGAGCAAT |
| mdNGS156 | (ATA) | 5 | GCAGCTCCGATATTGATGGT | AACTTCTCACAAAAACATGTAGCA |
| mdNGS157 | (TAT) | 5 | TGTCATCATGAGTTTTTCGCTT | TCTTCGGATGCATCTTCTCC |
| mdNGS158 | (TTA) | 7 | AATAGGGCTTGGGGAAGAAC | TGCTGGTGAAATCAGATGCT |
| mdNGS159 | (ATC) | 5 | TGGCTTCTCTCGGATCATTT | GCATAAAATTGCATCCCCAC |
| mdNGS160 | (CTT) | 6 | TACGTTGTTGTCGTCCCTCC | GAAAAATTCAGCCCGCAATA |
| mdNGS161 | (ATA) | 5 | CAAAAGAGAGGAGGGAGAGGA | ATGGTAGTCCAGAGCCAAGC |
| mdNGS162 | (CTT) | 5 | CAGATCCATGAGGAGGGAGA | TGGAAGAGGAAATAGTAGAGGAGG |
| mdNGS163 | (TAT) | 6 | CACGAGGACAATTCGAGGAT | TCCTTCCTTCTCAATTAATTTTAGTCA |
| mdNGS164 | (AAT) | 9 | TTGTGAATAGCGTATGGGAGC | TATGCAAGCGGATGAAGATG |
| mdNGS165 | (ATG) | 5 | TTTTGTGCTGCTTTGTCACC | TGTGAATGTGGGATGAAGGA |
| mdNGS166 | (TTC) | 7 | TGGCTCACATAATTTGGGGT | TCGCATTATTTTCTTTTCCCC |
| mdNGS167 | (TCT) | 5 | CAAAACTCAATGGCATCCAA | CGAACATTGTCTGCTCAGGA |
| mdNGS168 | (TTA) | 5 | TCCTGGAGATGCTCTGTCCT | CCCTCACTCGACTATTTGGC |
| mdNGS169 | (GAA) | 5 | CATGTTGGATGTGTCAAAGGA | GCTTGCGGCTTATCAGAATC |
| mdNGS170 | (TAA) | 5 | GGGATCATCAACTCTTTCTCG | TGAAAGGGATAGGACCATGC |
| mdNGS171 | (ATG) | 5 | TGCCTTAATTTCTCAACCAAAAA | GCAGGGTAAAGAAGTGAGCAA |
| mdNGS172 | (TCT) | 5 | CCCCCAACTTCAGTTCAGAC | GATCACCTGATGGATGCCTT |
| mdNGS173 | (ATC) | 7 | TTGGATTTTTCATCTTGCCC | CTTTCTTACACCCAACCCCA |
| mdNGS174 | (TTC) | 7 | AAGACAAAATGCCGTTCGAT | GGGGTTGTAACTTGTCACCG |
| mdNGS175 | (GAA) | 5 | GTCAATGACCCCTTTGTGCT | TTGAAGACCAATGGAACCCT |
| mdNGS176 | (TTA) | 7 | CTGTGATGCAATCAGAGAGAGAG | GAAAAAGGAAAAAGAAAAAGAAAAAGA |
| mdNGS177 | (AAT) | 5 | CCGAGTTGGTGGTTTCTCAT | CCATTTCTCGAGCTTTGTCA |
| mdNGS178 | (GAA) | 5 | CGCGGGAAGAAAAGAAAAG | GAGAGAAAGGAGGGAGAGGAA |
| mdNGS179 | (ATC) | 5 | GCATAATTGATGGGAGGCAG | TTCTTTGTTCGAGGCGGTAT |
| mdNGS180 | (TTC) | 5 | GAGGAACTATCCGGCCTACC | CCTTCCCTCAGCCTCCTAAC |
| mdNGS181 | (GCA) | 5 | CTTGGGGGATGATGATATGG | GAACTCTGTGGAGCCTGACG |
| mdNGS182 | (ATA) | 17 | GCAAATGACAACCATTATTTGCT | TTTCATTTGCATCATTTTGAAC |
| mdNGS183 | (AAT) | 18 | TTCTCTTGATGGTACTCTTACGTG | TGGATCGATTTCATGCTCAA |
| mdNGS184 | (TTC) | 5 | TCATGTCTTTCAGCTCAGCG | CGTGCAGGCCTACCTAAGAG |
| mdNGS185 | (ATA) | 23 | TTGTGGTTAGGGATGGGGTA | TTCTTGTCAAACGAAGCACG |
| mdNGS186 | (ATC) | 6 | TAGGCTGCTCCTCTCCAAAA | GCTGCCACTTCAAAGCCTAC |
| mdNGS187 | (AAT) | 9 | TTTGCTCTTTTGTTGTGCTCTC | AACAGTCAACAAGGCTGGCT |
| mdNGS188 | (TGC) | 5 | TGGATAGGGCTACGGTCTCA | CCAACACACATTGCCATGAA |
| mdNGS189 | (TGA) | 6 | CGAGTTGCTTAACAAGCTGAGA | TCTGAGAGCTGCAACAGCAT |
| mdNGS190 | (AGA) | 5 | GGGAAGAAGGGAGAGTGGTC | ATCAGGGGTCAACATCAAGC |
| mdNGS191 | (TTA) | 5 | TCTTGATGAGTTGAAGAGTGACG | ATCGTCGTCTGTCTCCTGGT |
| mdNGS192 | (ATA) | 5 | AGAGCTGTGGCTTTTTGCAT | TGCAAACTATGATCTCCCCTG |
| mdNGS193 | (AAT) | 5 | TCCGTGACTGCTGCAATAGA | TTCCACATGCATCATTCCAT |
| mdNGS194 | (TTC) | 5 | CATCTGACAAAGTAGCCCCAA | CCCTCCTTATGTGAGACCCA |
| Code | Motifs |  | Forward primer (5'-3') | Reverse primer (5'-3') |
| mdNGS195 | (TCT) | 9 | CTTTTTCTGCACTGCTGCTG | CCCTCCTTATGTGAGACCCA |
| mdNGS196 | (CAT) | 6 | CAGCAAGGACCCATGCTAAT | TCTATACTGATCCCTCTCTCAAGGA |
| mdNGS197 | (TAA) | 5 | CTCCTCACAAAAACATGTAGCAG | TGGTCAAAATTGACTGAGCCT |
| mdNGS198 | (CTT) | 7 | TCTAGCTGTGGCAAGTGCAT | CAAGGTTGTCAGTGGGAGGT |
| mdNGS199 | (TTC) | 5 | TCTTCTTCAAGTGCCCATCC | GCTCAAAACAGCAGAGAGCC |
| mdNGS200 | (TCT) | 5 | GACTGCAGGATCAACTCCTTG | CTCTTCCTTTCCACACCCAA |
| mdNGS201 | (ATA) | 7 | ATGGGCCAGGTAGTCTCCTT | TTTTTGTCTCCTTCCCATTACC |
| mdNGS202 | (AAT) | 6 | AAAATTTTATTTTGTTTAGTGGCAA | CATGCTCAAATCAAAACCGA |
| mdNGS203 | (AGA) | 5 | TGTGGATCAATTGGAAGCAA | TGCTCCTGCTTAGTTAATGCT |
| mdNGS204 | (ATA) | 7 | TCAGGGCGTTGAGTAGGTCT | GCCTTCACCTCATCCAATGT |
| mdNGS205 | (TAT) | 5 | TCTCTCACAATATCACGTGTCAAG | TAATTAGCGCTCAACCCCAT |
| mdNGS206 | (TTA) | 13 | GCCGCCTCTTCTCTACTCCT | GTCCACGAGATCTGAAAGGG |
| mdNGS207 | (AAT) | 5 | CCTTTATAAGCCAGCACCCA | CCCAACTTATTTATTGCTAGTCCC |
| mdNGS208 | (GAA) | 5 | TGATCCTGCAATCCCTTCTT | TCGTTGGTCTTCTTTGGAGC |
| mdNGS209 | (TCA) | 5 | GCCAATTACTGCACCAACCT | TGTACCTCAGTGGAGTGGCA |
| mdNGS210 | (CAT) | 5 | TGGTCTTCATCTCCGCTTTC | GGCGGTGGAATAAATTCTGA |
| mdNGS211 | (AAT) | 5 | TCCTGAATGATGGTGTTTGTTT | AAACGGTCTGGTTTGGTTTG |
| mdNGS212 | (TTA) | 8 | CTGCATTCACAACTCCTCACA | TTGACTAAGCCTAACCAAGTTCG |
| mdNGS213 | (TTC) | 6 | TCTTCACCTCTTCCTCTTCTTCC | ATAGATGCCGAGTTGGATGC |
| mdNGS214 | (TTA) | 5 | CTGTTCGGCATCAGTTAGCA | GCCACCTGGTTGACATTTCT |
| mdNGS215 | (TTC) | 5 | TGGAACAATGTTTGGGAACAC | GGACTTCTGGTGTCATCTGGA |
| mdNGS216 | (TCT) | 5 | ACATATGTCCGGCCTCTACG | TCATACACCTAGAAAAAGTTCTGATGA |
| mdNGS217 | (TTC) | 7 | GAAATCCTCTTGTCTGCGGT | AACACTGATCGTCTCTGGGC |
| mdNGS218 | (AGA) | 5 | CAAGGTGGTTGCATCAAATG | TGACCTGGTCCCTATGGAAT |
| mdNGS219 | (GAG) | 6 | CTTCGACGCATGGGATTTAT | ATCCCATCTCATCCTCTCCC |
| mdNGS220 | (AAT) | 5 | TGTTGTTTGCCGCTTTGATA | CTCTCAACCGTTTGTCCCAT |
| mdNGS221 | (TAT) | 11 | TCGCAGCCATTTCTACAAGA | TGAATAAGACCCCAGGTTGG |
| mdNGS222 | (TGA) | 5 | GCATCCAGCTGCATTAGAGA | GCTCCCACAGACATGTTAGGA |
| mdNGS223 | (TTA) | 5 | TCCAAACACGGATCATTTTACA | TGGTGGATAGGATGCATAGG |
| mdNGS224 | (TAA) | 5 | CGTAAAAATTTCGGCAGCAT | TGAGCCGTAGATCCCTGTTC |
| mdNGS225 | (GAA) | 5 | CCCCATCTCCATCTGGGTA | TTTCAGCGGGAGAGATAGGA |
| mdNGS226 | (TCA) | 5 | CATTTTCAATGCCATCATCG | GGATGGCGGAGTATTTTCAA |
| mdNGS227 | (TTA) | 6 | TCGATGATCCGACGATGTAA | AAGCAAAAGTGGAGGGATGTT |
| mdNGS228 | (CAT) | 5 | GTGAAGAGAGGGCGGTGTAG | TGTTTCCCAATGTGTTGAGG |
| mdNGS229 | (TTA) | 10 | GAAGAAAGGAAACCAGGGGA | CAATCGATAACGGATTGAATTTT |
| mdNGS230 | (AAT) | 5 | GGATATCTCCTCGTAATCTCTAACAAA | TCATCATGGATGGTGAAAAAGA |
| mdNGS231 | (AAT) | 5 | TCTCCCCATAATCTCTAACAGG | AAGATTTTCTGAATCATTTAACACCA |
| mdNGS232 | (TAT) | 6 | TATTGCCCTTCGTCCATTTC | GTCGGTCGAGAGAGAGGAGA |
| mdNGS233 | (GAT) | 5 | TTTTGGAAGGCATAAGGTCAA | CATCCAAATGTACGATCCCC |
| mdNGS234 | (TCT) | 7 | TTCCCCGGTCTCTCCTAAAT | TCCGAAACAAAACTGATCAAGA |
| mdNGS235 | (AAT) | 5 | ATCGTCGTCTGTCTCCTGGT | AGAGGGCGACGATCAGTTTA |
| mdNGS236 | (AAT) | 5 | TCTCCAGATTTAAGTGCTTGCTT | CCCCCTTCAATTACAACAAAA |
| mdNGS237 | (AGA) | 5 | CCTTCCCTCAGCCTCCTAAC | GAGGAACTATCCGGCCTACC |
| mdNGS238 | (TAT) | 19 | CGTCTAGTGGAGAGATGGGG | ACGAACACCTTCAAAGGCTC |
| mdNGS239 | (AAT) | 6 | CCCTATCTCTTTCCTTTCTCCC | TTCCAGCCATTTGATTTTCA |
| mdNGS240 | (CTT) | 5 | ATCCCGTGGCTCTTTGAGT | ATTGGATCACAACCACAGCA |
| mdNGS241 | (AAT) | 5 | ACTTAGAATAGAGACGTTGATTTTGA | CAAAATTTTCTTACTCAAACCCTCA |
| mdNGS242 | (TTA) | 6 | CACCCTCGTTTCTTGGTCTT | CATCCATGTTGGGTCATTCA |
| mdNGS243 | (TAA) | 5 | TCTTGGAGAACCATTGGGAG | CCTTCCACCAATTTAATGAAGC |
| mdNGS244 | (TTA) | 5 | AAGATCGCTCTTGGCTTATGTT | TGTCTTGCATGTATAGCTCGAAA |
| mdNGS245 | (AAT) | 5 | GATGCACTAGGGTTAGCCGA | CGAACGGAGGGATAGTGTGT |
| mdNGS246 | (TTC) | 5 | CCAGTATCTTGCTTTGCCGT | GCTCCACTTCTTCTTGTGGG |
| mdNGS247 | (AAT) | 8 | TCAAAAGCAGCCTAAGGTGAA | TGATTGGTCATCCCACACAC |
| Code | Motifs |  | Forward primer (5'-3') | Reverse primer (5'-3') |
| mdNGS248 | (CAT) | 5 | ACAATTTGGTGCATGTTTGG | GTGGTGTCAATACGGCACTG |
| mdNGS249 | (GAG) | 6 | GGGGTGAAGAAGGGCAAG | TGCTTCCATAATACCGCACA |
| mdNGS250 | (TCT) | 5 | CAGTCTCCTCGGGAGTGCTA | ACCCTAAATCCTAGCGCCAT |
| mdNGS251 | (TCT) | 8 | CGTCTGGTGCATCTCTGTTC | ACTTGACTGGTTGGGTGAGG |
| mdNGS252 | (TCT) | 5 | AGCTCAAAACACCCACCTTT | CAGTCCGACCTTCACCAAAT |
| mdNGS253 | (CAT) | 5 | TGCAAACACCATGTTTTCGT | TGCCAGAAAAACAATGCAAA |
| mdNGS254 | (AAT) | 5 | GCAATTTGGTTTGTTTTATCG | TCAACCAAAAGAAAAAGCTTGA |
| mdNGS255 | (GTC) | 5 | GGTCCCACATCTGAGAGGAA | CTGACCAAATTGAATGGCAA |
| mdNGS256 | (CTT) | 6 | AAAAGGCTGAATGCAGGAGA | GGTTGCTCGAAACCCTGATA |
| mdNGS257 | (TTA) | 5 | CCCAACTCGAATTTCAGATCA | GGAGAACCATGAGGAGATGC |
| mdNGS258 | (TTA) | 6 | TTGGCAAGGTTCTCTCAAAA | CCTCCTGCAAAACCAGAAAA |
| mdNGS259 | (AAG) | 7 | TAGCAATTTGCCACAATCCC | GGTTGTAATGGGGCTATGGT |
| mdNGS260 | (TAA) | 5 | TCAACCATGGCGTATGATCT | CCTGGACTGAAGAGGAGCAC |
| mdNGS261 | (GAA) | 5 | GAAGAGGAGCCAAGAAAGATGA | TTCTTTTGGGGTGCTTTTTG |
| mdNGS262 | (AAT) | 5 | CCTTGTCAATTTTCAATGCATATAGT | ATGCAGGTGGTTCTCTCCAA |
| mdNGS263 | (AAG) | 7 | ATTTGATTTGCCCTTCAAGC | GCTTGGGAGCCTGATAGTTG |
| mdNGS264 | (CTT) | 5 | CTGCTTTCTGTGCCATTCAA | ATTTCTGCAGCTTGTCCCAC |
| mdNGS265 | (TTC) | 5 | TTGTTGCTCTTTTTCTCCCC | ACAGTTTGGAGTTGCACACG |
| mdNGS266 | (TTA) | 6 | AAGCACGTGTGAGAGATAGCC | TCGATTATTCGTTGACAATATTTTAG |
| mdNGS267 | (TCT) | 5 | TTGGTACTCCAAAATTCAGCC | GCCCTCTCTTCATCTCCCTT |
| mdNGS268 | (TTA) | 5 | CAATCCAATGGGTCCAACTC | TTGGTTTAAGGTGTTCTGATCG |
| mdNGS269 | (TTA) | 5 | GGCGCAACATAGAAGTCACTC | CATCTAGTGTTGCTAGTGGCAGA |
| mdNGS270 | (AAT) | 25 | GGCAATTCATTTCATTGTTGA | GCCACATTGTAGGTGAAGGG |
| mdNGS271 | (GAT) | 5 | AGATACGTGACCATGCTGCT | TGAACCTTCTGTGCATTAACAA |
| mdNGS272 | (AAT) | 5 | TCATTCGCCTGCATGATTTA | TCCTGTGTTAGCCATATGCAAG |
| mdNGS273 | (GAT) | 5 | GCAGCGGTCGATACAACTTT | GCCCAAATTCAGGAACAAGA |
| mdNGS274 | (GAA) | 5 | CCCTTTGTGCAAACTCAACA | TTTTGGAGCATCCAACTTTGT |
| mdNGS275 | (GAA) | 5 | GCACGGTGATCTTATTTTGGA | CATCAACAATTGATATCCTGAAAA |
| mdNGS276 | (TCT) | 7 | AGAGAAGGTGGTTCGCTACG | TGAAAACTGTGTCCCTTCCC |
| mdNGS277 | (AGA) | 5 | TTGTAGCCACCAAATCAAAAG | CTGAAGATTGGTCGGTGGAT |
| mdNGS278 | (TCT) | 5 | CACTCGGATATCAGGGCAGT | ATCCTGTCGAACCATTGACC |
| mdNGS279 | (AAT) | 13 | CAAACATAACGAATGAGCAGAA | GACCCCAATGAATGACAAGC |
| mdNGS280 | (TTA) | 13 | TGCCAAACCCTATTTTTGGA | GGAGAAAAAGAAAGCAAGAAAAA |
| mdNGS281 | (TCT) | 5 | CATCGCCTGATGTTTACCCT | GATTTGAGGCAGGTGGAGAG |
| mdNGS282 | (ATA) | 5 | TTGGTGTTGATGGATCATGC | TCTTCATTCACAACTCCTCACAA |
| mdNGS283 | (TCA) | 5 | AAATTCGGCATTGTGGTAGG | GAGCCAATTCTGTCTCAGCC |
| mdNGS284 | (TAA) | 5 | TGGTGGATAGTGTGCGTAGG | AAGTGTGGCCCTATCCCTTT |
| mdNGS285 | (TTC) | 5 | TCTGGTAGCTGTCTGGTCACA | TGCATGGCCTGTTCAAATAA |
| mdNGS286 | (TTA) | 6 | AACCTCTCAAGACCCTGCAA | TTTTGAAATCCAGCAAGGTT |
| mdNGS287 | (AAT) | 5 | TTCTTGGATCCTTGGATTGC | CAAGCAGGAGAGATTGGAGC |
| mdNGS288 | (TTC) | 5 | ATCATGCTTTGCCGTCCTAT | ACCAGTTTGCTGACCCCTTT |
| mdNGS289 | (TAA) | 11 | CATCAACGTCCATTGCTGTC | GCATTGGGCCAACTGTTAAT |
| mdNGS290 | (TTA) | 6 | GCGTGCGCCTCTATTTATTC | CTAGCAAAAGACGCATGCAA |
| mdNGS291 | (TCT) | 5 | CATCTTGATCTGGACTGCGA | CTTTCCACATGCCAAGAGGT |
| mdNGS292 | (TCT) | 5 | CTGCAATCAAAGCCAAGTCA | AATCACCGCAATCCAAGAAG |
| mdNGS293 | (TTA) | 10 | GCCTTCTTCTTCTGCTGGTG | CTGCGGGAGATTCCAACTTA |
| mdNGS294 | (CAT) | 7 | TTCCTTGTCACAGGGCAAAC | TCTCCAGCATGCATCTTGTC |
| mdNGS295 | (ACA) | 6 | CCGACCCATAAAATACTGCC | GGCTCAATTCTTCTTCCCCT |
| mdNGS296 | (AGA) | 5 | CCCACTTTTTGGCTAGTTGC | TCAGCCTGAAACAACCCTCT |
| mdNGS297 | (TCT) | 5 | GAATTTTTGGAGCATCCAACTC | TCGAGCCATTCATTATGAGC |
| mdNGS298 | (CTT) | 10 | TGGGAAAAACATTACCCCAT | ATAATCAAGCCAGCATTGCC |
| mdNGS299 | (TTA) | 12 | TGAGATTTCCAGCTCAATTCAA | CGCCTCAAAGTCTACTGCAC |
| mdNGS300 | (GAA) | 5 | TAGTGTCCACCAAGCATCCA | CGATGGCTTTGATGAGATGA |
| Code | Motifs |  | Forward primer (5'-3') | Reverse primer (5'-3') |
| mdNGS301 | (TCT) | 5 | TTGGCTAGGTTCGTACTTGGA | GGGGTCTAGATTAGAACAATCTCC |
| mdNGS302 | (TTA) | 5 | TTGTCTGCACACGACTTGTT | TGCTTGTTTAGCACGCAGTT |
| mdNGS303 | (GAT) | 6 | AGACAAAGCCTCCGTTTGAA | CACACCACGTGTCTGCTCTT |
| mdNGS304 | (TTA) | 5 | CGGAGAAGGATCTACACATCG | TGCAGGATCCTCTGACAATG |
| mdNGS305 | (AGA) | 5 | CTATTCTCTTCCACGCCCAA | CACCTTGATCTGGACTGCAA |
| mdNGS306 | (GAT) | 5 | GAGGTGGTGATGAAGACGGT | CCATCTCCACCGCTATTGTT |
| mdNGS307 | (TAA) | 5 | GCCTTTCAATTCCAGATCCA | CTCGCGATTTCCAGAAGGTA |
| mdNGS308 | (AGA) | 8 | CACAATCCTTGCAATTCTGC | ACCCTGCCCTACAAACACAC |
| mdNGS309 | (GAA) | 6 | GTCAATGACCCCTTTGTGCT | TGGAGCATTCAACTCTGCAT |
| mdNGS310 | (TTA) | 5 | CGATTACTATGATTCGGATGAGG | AGGTAATTGTGAACGCGACC |
| mdNGS311 | (GAA) | 5 | CCCCCTACTCATGCTGTCAA | CACAGCAATGCTAAGGGGTAG |
| mdNGS312 | (CAT) | 6 | TGTTAACCTTGGCTTCGGTC | AAGCTGGAAAAGCACATGGT |
| mdNGS313 | (AAT) | 7 | AATGGCGGTTATGAAGCAAG | CACTGGGATAGGTTACCGGA |
| mdNGS314 | (TTA) | 6 | TGGAGAAGAGAGTGGTTCGG | TGCAATATAAGATGCCATCCA |
| mdNGS315 | (TTC) | 5 | TCCACTTCTTCCTCTTCTTCCA | CTCGTTCATGATCGCCAATA |
| mdNGS316 | (ATA) | 5 | TCCATGGGAGATCATGGAAT | GCCACTTTGAGATTTCTTTCG |
| mdNGS317 | (GAA) | 6 | CACAACACCAGAACCACCAG | CCACTGATTTATTATTGTATGCCC |
| mdNGS318 | (AAT) | 5 | GCACCAAAGCAAACAATAACAA | TTCTTATATGGGATTACCTCCAAA |
| mdNGS319 | (TGA) | 5 | TGAGGTACCGTGCAATTCAA | TGGAGGTTGTGAGTGGTCAA |
| mdNGS320 | (ATA) | 6 | GACGCATCCTTGTGTGTCTG | CGTGAAGAACATCGACATGG |
| mdNGS321 | (ATG) | 5 | TGCATAAAGCTTGCTTGTGG | GAAAGGCACTTGATGGAACC |
| mdNGS322 | (TCT) | 5 | GTGCTAGCTCGCAAGGATCT | TTAACCCAAAACCCTAGCCC |
| mdNGS323 | (ATA) | 6 | CCTCATATGGAAAGGATGATACA | CTTTGCCGGATAAATTGGAA |
| mdNGS324 | (TAT) | 7 | GTGTAGGGCGAGCAGACTTC | TCTCATAGTATCCAAAACCATCACA |
| mdNGS325 | (TTC) | 5 | GATTTGACCCCCAACACTTG | TCATTATCGAATGACGAAGCC |
| mdNGS326 | (AAT) | 5 | CATTGAAACCTTCGTCACCA | GCATTGAATATGCCAGCAAAC |
| mdNGS327 | (TCT) | 5 | TTGTTGCAATTGTAGCATGTGA | TGGCTCAAAGAGAGGAAGAGA |
| mdNGS328 | (AAT) | 9 | CAAAGATGGCCCTAAAACCA | GCAAATGTTCGGCATTCTTT |
| mdNGS329 | (GAG) | 5 | ATGGGAATCTAAACAGGGGG | GTTGAGGCCATTGTTGTGTG |
| mdNGS330 | (AAT) | 7 | AAAATCATCGGTTGAATCGG | TACACCCTGGATGTCCCTGT |
| mdNGS331 | (GAA) | 6 | GGAGTCAAAATATCCCCCGT | GGAGAGAGGGAAGAGAGGGA |
| mdNGS332 | (TCT) | 5 | TCTCCTCGAGAGCTCTGTCC | ATCCTCCCCAAGAAAGGAAA |
| mdNGS333 | (AGA) | 5 | TCCTTCTTGTCAAATCCTTGG | TGGACATGTCTCCCTCTTCC |
| mdNGS334 | (AAT) | 6 | TGAAGGAGGTGCAGTATCTTGA | GCCACTGTGTTTTAGTGCAAG |
| mdNGS335 | (CAT) | 5 | TGCAAGCTTTCCCAAAGAGT | TAATGGCTGTTCCTGGTTCC |
| mdNGS336 | (AGA) | 5 | GTATCTTCTTCAGACGGGCG | TCGGATCAAGGGAAGAAATG |
| mdNGS337 | (TAT) | 5 | TCAGTGTACACCCTAAATGGCTT | TAATATGCGAGGCCTCTTGG |
| mdNGS338 | (ATA) | 5 | TGGTGTTGCGAAAGATTATCC | CTGATTTGGGAGGCCAACTA |
| mdNGS339 | (TCT) | 5 | GGAGTGCTTGATGGTGTACTTG | TTCTGATATGCAATCAAGGGTC |
| mdNGS340 | (GAG) | 5 | ATTAATGAGGATGCTCGGGA | TCTAGCCTTCTCCTCCCCTC |
| mdNGS341 | (AAT) | 5 | TCCCAAACTCCCAATCTTTG | TCACCAGCTAGACATGAGCAA |
| mdNGS342 | (GAA) | 6 | CCTGACCTGAGTTTTTCCCA | AGGAAGAGGATGGCCACTTT |
| mdNGS343 | (AGA) | 5 | AGAGAGAAAATTATAAGGATCCAAAG | CGGAAAGATGGTTGATGACC |
| mdNGS344 | (TAT) | 16 | GAACCGAGGCATATCTGAGC | GTAGTGTCTTGGTGGGCCTC |
| mdNGS345 | (TCT) | 6 | TTGGAGCATCCAACTTGACA | CCACGATATGGGCTTATTGAA |
| mdNGS346 | (TTC) | 5 | TTTGGGGGCGTGAGATATAG | ATAATGACGGCTCTGGATGG |
| mdNGS347 | (TAT) | 6 | CATTGGTTTTTGATGGGACC | CGCATGCATATGCTTTTCAA |
| mdNGS348 | (TAT) | 5 | GTTGTCCTCCTGGTTTTTGG | GAGTTGAAGTGCGGTGTGTG |
| mdNGS349 | (ATG) | 5 | TTCCATAGGGAGACGGTGAC | AGTCATGGTTGTTGTTGCCA |
| mdNGS350 | (AAT) | 5 | TAGGGGAGGCAGAAGAGACA | AGAACCCCATACAATGCACG |
| mdNGS351 | (AGA) | 5 | TCAAATCCGGTCAAACCCTA | GCCAAACATGACTCCTGGAT |
| mdNGS352 | (CAT) | 5 | GGCATTCTAAAAATTTCAAAAAGAA | CTGTGAGCCGGATGGTTAAG |
| mdNGS353 | (TAA) | 5 | AGGCACCGTATTCACGTCAT | GGCCCTATCCCTTTCAAAAA |
| Code | Motifs |  | Forward primer (5'-3') | Reverse primer (5'-3') |
| mdNGS354 | (CTT) | 5 | CTCAAACTGCACACACGTCC | TTCCTTTCCACACCCAAGAG |
| mdNGS355 | (AGT) | 5 | TGCCTAGGGTAAGAACTGGC | ATGTTTGGGGTTGGAATTGA |
| mdNGS356 | (TCT) | 5 | TCGCTTCTGATGATCTTGGA | TCCAAAAGTTGGGTGCTTTC |
| mdNGS357 | (TCA) | 5 | CCACAGTGCACAATGTTTCC | GCGCTTGGTGAAGAAAGAAC |
| mdNGS358 | (AAT) | 7 | ATCCCCTGGTACCGATCTTT | TCATATGTTATTTTTGGTTCGCA |
| mdNGS359 | (ATA) | 8 | GCCTGAGGTGCAAAAGATGT | TCAAGGTTCCAGATTGCATTA |
| mdNGS360 | (GAT) | 5 | CTTGGTGCTGTGCTCCATAA | TCAAATTGGCATCCATTACG |
| mdNGS361 | (AAT) | 5 | CGAATGTCGTCGTCTGTCTC | AGGGCGACGATCAGTTCATA |
| mdNGS362 | (AAT) | 6 | ATCATCCCAAGTGCATCTCC | TGCCGCACTATCAACTGTTC |
| mdNGS363 | (AAT) | 9 | GAATGTAGTTATTGCGCATCG | TGCATCCATGAAAAGTTGGA |
| mdNGS364 | (AAT) | 9 | GAATGTAGTTATTGCGCATCG | TGCATCCATGAAAAGTTGGA |
| mdNGS365 | (TCT) | 5 | ATGGCTGAGCGAGCACTATT | TCTGAAGGGCATGACCAAGT |
| mdNGS366 | (ATA) | 6 | GCATGGATGCAAAACTAGCA | GGACTACAAAGTGGGGGAGA |
| mdNGS367 | (TGA) | 5 | TAAGTTAAGCGTGGATGCCC | CTCCCTTCAGTTCTCACGCT |
| mdNGS368 | (ATC) | 5 | TGGGATGTTTTGGATATGGTG | AGATAAGCCATGGGCATGAA |
| mdNGS369 | (AGA) | 5 | GGACGCACGTTCCAAGTTAT | GAATCTGAACGAAGCCTGGA |
| mdNGS370 | (TAA) | 5 | GGTGGATAGGATGTGTAGGCA | CCTTCCACCAATTTAATGAAGC |
| mdNGS371 | (AGA) | 5 | GGCAGATTCTCAGCTCCAAC | GGAGTGATTGGGTGGACATT |
| mdNGS372 | (CAT) | 5 | TTTGAGCAAGAGTTTTCTAAAATTGA | GCAACAATATGAAAAGATGCTGA |
| mdNGS373 | (AGA) | 5 | TGGGTGGCTCTAATAATGTGTG | GGTCTAGGACTCTCTTAGGATTTTCA |
| mdNGS374 | (TTA) | 6 | GAAATGAGCATCATGGGGTT | CACAGAGGCACTGCACAAAT |
| mdNGS375 | (AAT) | 10 | GCCAAAACCAATTTTTGGAA | ACAAATAGCTTTCTAAGGGAAGG |
| mdNGS376 | (TCT) | 5 | TGCATTAAACGGTTGCTGAC | GGCCAACCAATTTGATGTTT |
| mdNGS377 | (TAT) | 7 | GCTTGAGGAAGGACATGGAG | CCCCATGGGTAAATGGGTAT |
| mdNGS378 | (GAT) | 6 | TATTTCATGACGAATGGGCA | CATCTGTAGAAGCCCCCAAG |
| mdNGS379 | (TAT) | 5 | CCCAAATGCATGCAATGATA | TGCACCCAAGCACATTAACT |
| mdNGS380 | (TGA) | 5 | ATTGGGCAAAACGATATCCA | GCGAGGCTGCTTGATAAAAT |
| mdNGS381 | (AAT) | 7 | TGGACAAACAACAATAAATCAAA | CAATGTGTCTGCTATGGTCATATTT |
| mdNGS382 | (GAA) | 5 | TCGAGCCGTTTATTACGTGC | GCATCCAACTCGGCATCTAT |
| mdNGS383 | (AGA) | 5 | TGATGGCCAACATGAGAAGA | ATGGATGGCAATGCAAGATT |
| mdNGS384 | (AAT) | 5 | TCAGATCTAAATTAAAACATGCATCA | GGGTTTACCCCCAATATTAAAAA |
| mdNGS385 | (TAA) | 6 | CGTCTCACTCAAACCCGTCT | TTTTGCATGCTCAACTGCTT |
| mdNGS386 | (ATA) | 7 | ACAGGCCTCCCATTCTCTCT | TTGTCCAAGCAAGTCTTCCC |
| mdNGS387 | (TAA) | 5 | TAGGCACCATTTTCACATCG | CGATCTGGATCCAAACATGA |
| mdNGS388 | (AAT) | 5 | TCGTCTGTCTCTTGATGCCA | GTCGGAGGACGACAATCAGT |
| mdNGS389 | (TTA) | 5 | CAGGTGTGGTCCTATCCCTT | TCTGTCCACTGTTCTCCGAGT |
| mdNGS390 | (GAA) | 5 | TGGTGTCTTTGAATAGATCCGA | TCAATGGAAATAAGTGCCTCA |
| mdNGS391 | (CAT) | 7 | TTGTGCATCGCATACTCCAT | TGCATGGGCTTAAATTGTGA |
| mdNGS392 | (TTA) | 6 | TGAAATCCCCCTATACACAAAAA | GCAAAACATATATTGAGGATATTGGA |
| mdNGS393 | (TTA) | 5 | CAAACTAGATCCCGATCCGA | CACGTCATATACTTGGAGAACCA |
| mdNGS394 | (TCT) | 5 | GTCGGTGGTCGTGAAAGAAT | TACAAAGCAGCAACGTACCG |
| mdNGS395 | (ATG) | 6 | TTGGTTATTGGCTTGTAGAAGGA | GGCAAATAGTAGGCTCTGCAA |
| mdNGS396 | (ATA) | 12 | GGGATGAGAGTGCTAATATGGTG | GGCTTATTGGCCTTCAGGAT |
| mdNGS397 | (CAA) | 5 | AGAGAGGAAGAGAGGCGAGG | TTTTAATCTGTTGAGGGCCG |
| mdNGS398 | (AAT) | 6 | CGATTGGGATGATTGGATCT | AGGGAGAGAGTGGGTGGAGT |
| mdNGS399 | (TTC) | 5 | TCGGAAGGTCATTTCCTCAC | CCACATGTTCACCTTGCATC |
| mdNGS400 | (TAA) | 5 | CTCACTGGCGTGATCTCATC | CCCTACAAGCCAATCACATACA |
| mdNGS401 | (TTA) | 5 | GCATTCCGAATTCCAGCTAA | ATGGTGGATAGGGTGCGTAG |
| mdNGS402 | (TTA) | 22 | ACTTGGAGTGGGTCCTGATG | TCCGAAATTGTTCCCCTACA |
| mdNGS403 | (AAT) | 14 | CGCAAGTGAAGCAACAACAT | ATGGGGAAGGATTTATTGGC |
| mdNGS404 | (ATA) | 6 | CTGACCAACAAGAGGCCAAT | CCTCTCACCTGCCCAACTTA |
| mdNGS405 | (GAA) | 5 | TAGGAAAAACTGGCCCATTG | CCCGTGGACGTAGGAGTATC |
| mdNGS406 | (AGA) | 5 | TGTATCTGGCAATCATTATTTTATCC | AGGGCTCGAAGGTAACCTCA |
| Code | Motifs |  | Forward primer (5'-3') | Reverse primer (5'-3') |
| mdNGS407 | (AAT) | 5 | ATCGTGCTTGGCACTCTTCT | TAAGCCCATCCTCCTCAATG |
| mdNGS408 | (TAT) | 5 | GCAATTCAAAGTGGCCAGAA | AAAGGACGTAAGAATCATAAAAGAAAA |
| mdNGS409 | (TGC) | 5 | GGGGACTGACTCAGGCACTA | GTTGGCGACCGAAAACTTTA |
| mdNGS410 | (ATA) | 5 | TGGTTTTGAATGCAACTGACA | GCAAGTGGCATTTTAAGGTTG |
| mdNGS411 | (ACA) | 6 | AGCTTTCTTCACATGCCCAC | CCAAAGTCATGCTGCTACGA |
| mdNGS412 | (AAT) | 8 | CATGCTCCAAGACATGATCC | TTAGGCATCACTGCCTTCCT |
| mdNGS413 | (AAT) | 12 | TGCTAGAACTAGGCCAGACCA | TTTCTGAAAGCATGAAAGAAATTG |
| mdNGS414 | (CAA) | 6 | CGACACGCTGAGATTTATGC | GGAGCTCCCCTGAGATTGAT |
| mdNGS415 | (TAT) | 5 | CCCCTATATTGAAAAGGTTGTCC | TTCATTGCATGCATTAGTGACTT |
| mdNGS416 | (GAT) | 6 | ATCAAATGGTCCTGAGGTGC | GATCTGAGAACATGGCAAAGC |
| mdNGS417 | (TCT) | 5 | TGGATTCAAACTCAAGATAGGGA | TTCTGACTGCAGGCATTGTC |
| mdNGS418 | (GAA) | 6 | CAATGCAATCAGCAATTTGG | ACCAGTTTTCGGAGCAAGAA |
| mdNGS419 | (AAT) | 5 | GAGATAAAAGCCCGAAAGCA | TGACCGTAAGTGACCAACCA |
| mdNGS420 | (AAT) | 23 | TGGAGGAGATTTTTGGGATG | TGTGCTCGTCATGCACATATT |
| mdNGS421 | (AAT) | 7 | CACTAACGATCAACCCCACA | GGATCATTGATTGGATGGCT |
| mdNGS422 | (GAA) | 6 | AATTGCATTGAGATCGCGT | TGACATCATTTACGGTCCCA |
| mdNGS423 | (TTC) | 5 | TTGATTGGAGGATGAATTTGC | TTGCATGCAGTTCAACAAATC |
| mdNGS424 | (TTA) | 5 | GTTTTCGAAGTGCTTCAGCC | TTGTCCCTCCTTTTTGGTGT |
| mdNGS425 | (TAT) | 5 | CTTCTAAGCTTTATGCTGTGAATTT | ACTCAACCCCCATGCTACTG |
| mdNGS426 | (GAA) | 5 | AAAGGAAAGATTGGTGGGCT | CACATATGCGATTGGCTTGT |
| mdNGS427 | (TTC) | 5 | CCCTAGCCAATCACCAAAAA | ATGACAGCAGAGCTCGACAA |
| mdNGS428 | (TCT) | 5 | GGAGGAACTTGCTCTCCCTT | GGTGCAAATTTTCCAGAACAG |
| mdNGS429 | (TTC) | 5 | GGTGAGGGCAATACAAAGGA | CCTCCATTTTGGTTTGTTCG |
| mdNGS430 | (AGA) | 5 | GAGTGCTAGCTCCCTTGCAG | TCCCTTTTGTCGATGTTTGG |
| mdNGS431 | (ATC) | 5 | TCTCCACCAGCCAGCTATTT | TTTGATGGTGGTCCTGTTGA |
| mdNGS432 | (AGA) | 5 | CGGATGGAGAAGAAGGACAT | CCTCTTCTTCAACTTCAACTTCTTG |
| mdNGS433 | (AAT) | 7 | AATTAGTTGCGGGACACACTG | CATTTTGCTCCCATGTCTCA |
| mdNGS434 | (TAT) | 5 | CCAGAATTATGAGAAACAGGCAA | TCTTGATTGACATATTTTGGTATGA |
| mdNGS435 | (ATG) | 5 | GGTACATGGATTGGTGGTAATC | ATGGACTGGACCCAATTCTG |
| mdNGS436 | (TTC) | 5 | CATTGTTGCCAGGTATGCAG | TGAAAAGTTCAAGGGAAACGA |
| mdNGS437 | (TCT) | 7 | AAAGGGCCTCTCTTTTCAGC | GATTGCCTAGGGGCATTACA |
| mdNGS438 | (TCT) | 5 | TAGATGGAAGGGGAGCAAGA | TCTCATTCCGGTAGCCAATC |
| mdNGS439 | (TTC) | 5 | GGGGATGCAAACTCAGAAAA | TTTTATTTTCTTCACCGCCG |
| mdNGS440 | (GAA) | 6 | TCACTTTTACCACATGCCACA | GGTCCATTCAACATCAACCC |
| mdNGS441 | (AAT) | 5 | ACATCGTCGTCTGTGTCCTG | AGGGCGACGATCAGTTCATA |
| mdNGS442 | (TTA) | 5 | TCACTTAACATTGGTCCCCC | TGCTGGTCGTCTGAGTCATC |
| mdNGS443 | (TGA) | 5 | GGGACGATGACTGGGTAGAA | GATCTTCGACCAGCGCTAAC |
| mdNGS444 | (TCT) | 5 | CAGCTTGGAACGGTCCTCTA | TGATAGCAGCACATAGCAAGAAA |
| mdNGS445 | (TTA) | 5 | CATGGCAACAAATGAACAGC | CGGCCTAGTCTGGTGGAATA |
| mdNGS446 | (TTC) | 7 | AGCCCATGAAGAAAGCTGAA | AGCTTACCCATTGTGATGCC |
| mdNGS447 | (TAT) | 5 | CCAGCGGAGAGAGAGAAGAA | ACGGTGGGTGGTGTACAAAT |
| mdNGS448 | (AAT) | 7 | AAACCCATCTGGCTTTCCTT | TTGCAGTTTCCTATAACAGCCA |
| mdNGS449 | (AAT) | 5 | CCACTGTAGGGCCCTGTTTA | TTGCTTTTGAATTTTCTTGTATCC |
| mdNGS450 | (AAT) | 5 | GGAAAAAGAAAAGAAAAGGAAGAAA | GAACGACTTTAGAGAGGGATGAGA |
| mdNGS451 | (CAT) | 6 | AAGGCCTCAGTAACTGCCAA | GCAAGGGCAGTTCTACCAAA |
| mdNGS452 | (TTA) | 6 | TCAAAGCCAAGCATATGAGA | TTGCTTTGATACCATGTTTTGC |
| mdNGS453 | (TTA) | 5 | CGGAGTATGACGGAAGACAGA | TCCTAGCATCTACTTGCAATAAAAA |
| mdNGS454 | (TTC) | 7 | TTTTTGTCTTAATTTATCAGGCATTG | CCCCTTGGAGTCCTACATCA |
| mdNGS455 | (CAT) | 7 | TCTTGCATTTCAGATGCTGC | CCATGAGAGCAACACAACCA |
| mdNGS456 | (GCA) | 6 | TGAACGCAATCAACATCTCTG | GGATGTTGGGGCTTGAAGTA |
| mdNGS457 | (CTT) | 6 | ATGCACCATCCAATCTCCTC | TCCCGAAATTCTTCTGGTTG |
| mdNGS458 | (TTA) | 6 | TTGTCCTGGAGATAATGCCA | AGCATCCTCCAATGATGAGG |
| mdNGS459 | (TCA) | 6 | GTCCTCCTTAGCCCTATGCC | AGCCATCACACCCCTTTATG |
| Code | Motifs |  | Forward primer (5'-3') | Reverse primer (5'-3') |
| mdNGS460 | (ATG) | 6 | CTTCGCTGCAAGCCATATTC | GAACAGGTTTGTGTAGGCCC |
| mdNGS461 | (TAT) | 5 | CCCATACATTAGAAAAATGGAGC | CTAGGAAGGTTGGGGGAAAA |
| mdNGS462 | (TTC) | 10 | GGGTGTTTCACTAGGGGTGA | ATGAGGAGCCAATCCCTCTT |
| mdNGS463 | (ATG) | 5 | TCTGGGCTGTGAGTCAAATG | TATCATGGAGGTTCGTGCAA |
| mdNGS464 | (AGA) | 5 | TTGGCTATGCTGAATGAATGA | TAAGGAGCCCATGGAGAATG |
| mdNGS465 | (AAT) | 21 | TTCATTGAAAAGTCCAGGGAA | CCAAAGCTGTCACGGATCAT |
| mdNGS466 | (TTC) | 6 | CCTTTCTGCCTTCTCTCCTTT | CTGCTCTGGTATGATATTGGGA |
| mdNGS467 | (TTA) | 5 | TGCACAATCCTATCCATTTCA | CTTGGAGAACCATGGGAAGA |
| mdNGS468 | (TTC) | 8 | TGTTCCTCAAATGCCTCCTC | GGACGTGGACCTTTCATCAC |
| mdNGS469 | (TCT) | 5 | TCAATGTGCCCTTCCTTTTC | TTTTGGGTTTTCTTTGGAACA |
| mdNGS470 | (TTA) | 5 | CAAACTGGTTGCATCTGTGG | TTGTTGACAGGGGAGTTCCT |
| mdNGS471 | (AGA) | 5 | AGAAACAGGTGCATCAATGTG | TCCAGCAACTATCCAAAGCA |
| mdNGS472 | (AAG) | 7 | GTCCAACCATATGGGACTCG | TCAGTGCATCATTGGGTGTT |
| mdNGS473 | (TAA) | 10 | GGACATCCCATTACCTTCCA | CAAAGGCAAGGAAACTCCAC |
| mdNGS474 | (TTA) | 5 | CGTTATGGAGGGTTTGCATT | GGCCGTTAGCTTTTTAGGGA |
| mdNGS475 | (AAG) | 6 | CTGGAATGAATCTTATACCACGA | TCCATGGTGAGTGAAATTGG |
| mdNGS476 | (TAA) | 5 | CATGGAGAGATGCTGCTGAA | TCGAACCAAATCCCGATCTA |
| mdNGS477 | (GAA) | 5 | ACCATGCAGTTTGAGGTGGT | TCTTTTGGCAACCAAGCTCT |
| mdNGS478 | (AAT) | 5 | TGAGAACTTTGGGGACATGC | TTACTAGCAGGTGTGGCCCT |
| mdNGS479 | (TGA) | 7 | TTTTGCCATTAATGCTGTGC | CCAAGTTGATTGGCACCTTT |
| mdNGS480 | (AAT) | 7 | TGCAACAAGGAGATCGTGAG | CCAAACCAAGGCAAGTTTCT |
| mdNGS481 | (AAG) | 8 | TAGCGGCACAGAAGTTGATG | AGAGGCTGTTTCAGAGGTTCC |
| mdNGS482 | (TCT) | 5 | TCAGCCTGAAACAACCCTCT | CCCACTTTTTGGCTAGTTGC |
| mdNGS483 | (AGA) | 5 | TGAAGCCACACAAGTATCCG | TGGTACATGGGTTTTAGGAAGAA |
| mdNGS484 | (AAT) | 5 | CACCAAGCAAAATTGGAAGC | ATCAATTTTTGGTGCCGTTG |
| mdNGS485 | (GAA) | 5 | GGCATGGTGAATTCATGCTA | CAATTTCAGTTGAGCCGACC |
| mdNGS486 | (AAT) | 5 | CAGCATTGGAAATTGGTGAA | CGATTGTAGTGATTCGAAGGAG |
| mdNGS487 | (TTC) | 5 | TCCTTTACTTCAGCCTTCTTCG | GGAGCAGACTTCTTCATCCAA |
| mdNGS488 | (TTA) | 5 | CGAATCCAGATACGGATCACT | AAAATCATGGGGAGATGCTG |
| mdNGS489 | (GAA) | 5 | GAAGGAAAGATTGGTGGGCT | CATGTTGGCCATCTTCACAT |
| mdNGS490 | (TAT) | 11 | CGCGTAAGATACCAACGGTAA | AGAGGAGCCATAATGATTTAGATG |
| mdNGS491 | (TTC) | 5 | GAAGACAGATCTTCTCCTTCAGTACA | CAAAGAGTTGGAGCATGGTG |
| mdNGS492 | (TAA) | 5 | CATCGTATACTTGGAGAATCATGG | TCTTTTCGACATTCAGGCAA |
| mdNGS493 | (TTA) | 5 | AAATACATGTTTGCTACGTATGTTTTA | AAAATTCAATCACTCGACCG |
| mdNGS494 | (TTC) | 5 | TGAAGCATCCAACTCTGCAT | TGTCAATGACCCTTTTGTGC |
| mdNGS495 | (AAG) | 5 | TTGGGTGCCTCTTTCTTGTT | TTTAGCTGCACAAGTGTCCG |
| mdNGS496 | (TTA) | 5 | TCTTGATGAGTTGGAGGACG | CGTCATCATCTATCTCCTCCGT |
| mdNGS497 | (AAG) | 6 | AGGTCTGGCGACAAAGAAAA | CCCAACAGTTGTCTCCCACT |
| mdNGS498 | (GAA) | 5 | CACCCAACCCTTTCTCTTGA | AGGTTTCATTGAAGATGGCA |
| mdNGS499 | (TAA) | 5 | GGATGCGTAGGCACCATATT | TGGTCCTATCCCTTTCAAAAA |
| mdNGS500 | (AAT) | 6 | GAAACTTTCTCTCTCTGCTCTCTCTC | AACAGCATCCAGGATTTTCG |
| mdNGS501 | (TTC) | 8 | AGTGCCCCTGCTTCTTACAA | GGGAGGGTCTTCTTCTGGTC |
| mdNGS502 | (TTA) | 6 | TTCGATCCGAATCCAAAAAT | CCATAGGGAGATGTTGTCGAA |
| mdNGS503 | (TTA) | 5 | TCTTCACGAAAGAGGGAGGA | GAAAAAGGAAAAGGAAAAGGAAA |
| mdNGS504 | (TAA) | 5 | CCTTGGAGAACCATGAGGAG | TGTGGCCCTATCTCTTTCAGA |
| mdNGS505 | (TAA) | 5 | CCTTGGAGAACCATGAGGAG | GGATCCAAACACGGATCATT |
| mdNGS506 | (TAA) | 5 | CTACGCACCCTATCCACCAT | GCGTTGAGCCATAGATTTCC |
| mdNGS507 | (TTA) | 5 | CAGGTGTGGCCCTATCTCTT | TCTGTCCATTGTTCTCCGAGT |
| mdNGS508 | (TTC) | 5 | TCATGATTTATGGAGAAGGGTTC | GAAAAAGAGGGATGGTGTGG |
| mdNGS509 | (AAT) | 8 | GATGAAATTTGTTTTCGTCGC | ACGAAAAAGTTCGCAGCATT |
| mdNGS510 | (AAT) | 6 | ACACTGGAGCCCGAATACAG | CTGATGAGCTTGTCGCTGTC |
| mdNGS511 | (AAT) | 5 | CATGGGGTGAATTGAAATTGT | CCTTTCCATCTCTATAAAATCAGGA |
| mdNGS512 | (AGA) | 5 | GGTCAAGCAGGGTTCTAGGTT | CGGTCTAGGACCCCTTAGGA |
| Code | Motifs |  | Forward primer (5'-3') | Reverse primer (5'-3') |
| mdNGS513 | (AGA) | 6 | GGCTTCCTTGTCAAACCAAA | TGGAAAGAGCTTTGGCATCT |
| mdNGS514 | (GGA) | 5 | CCCTAGTGGCCATTCTTTCA | TAGTTCGTTGCACAATGGGA |
| mdNGS515 | (AGA) | 5 | AGTTTTCCATCATGCCCAAG | CTGAACGAAGCCTAGATCGC |
| mdNGS516 | (TAA) | 5 | TCTGTCCACTGTTCTCCGAGT | ATGGATCGACATGAATACCG |
| mdNGS517 | (AAG) | 5 | CAGTTTTGACTGTGAAGCGG | GTCGCCAGATAGGTCGGATA |
| mdNGS518 | (AAT) | 23 | TAGCCACAAAGGTGCTTCCT | ATTGCCCAATGATTGAGGTT |
| mdNGS519 | (AAT) | 6 | TCATCGTTTGTCTCATAATGCC | TGATGAGTCAGAGGACGACG |
| mdNGS520 | (TAT) | 5 | CAGTGCATCTAATGTATGTCCCA | TGCTCAAGAAACCAGAGCCT |
| mdNGS521 | (TTC) | 5 | TTTGCAATGGTAGGAGTAGCC | TGCCACAGTAGAAGCAGATGA |
| mdNGS522 | (TGA) | 5 | ACCGTGCAATTCAATCCTTC | TGGAGGTTGTGAGTGGTCAA |
| mdNGS523 | (AAG) | 8 | TAAGAGAAGCAGGGGCCATT | TAAACCCGATTGACATGCCT |
| mdNGS524 | (ATA) | 6 | ATTGTGAAAGCACGAGGAGC | CCAATGCAACCCTACTGTGT |
| mdNGS525 | (TCT) | 5 | TGACTAAGGCGACAATACCAGA | AAGGCTAATGGGAAATTGATG |
| mdNGS526 | (TTC) | 5 | ATTGATGATGAGCAGAGGCA | GCCAACCAAGAAAATCCAGA |
| mdNGS527 | (TTA) | 5 | GGAGGAGGACCTACACATCG | GTAGACTGCGAACGCAAACA |
| mdNGS528 | (AGA) | 6 | GGCCAATAAAGTGCACGAAT | AAACGGATTTTTGCACCAAC |
| mdNGS529 | (TTA) | 5 | CAGAGGAGGACCTCTACATCG | AATGGAGATCGGTGAAGGTG |
| mdNGS530 | (AAT) | 5 | CCCCTCCACTATCACCAGAA | TAGTACGAGGGCACTGCTGA |
| mdNGS531 | (TTA) | 5 | TCCTTAAGATGTGTTATGAAGATGC | CCATTGCTGGAGATCTAGGC |
| mdNGS532 | (TCT) | 6 | GCCTTTTTCATCACCTTGTTTT | GCAATCACACCAGTACCATCC |
| mdNGS533 | (TCT) | 6 | TTTCTTTGGTCTTGCTTTGTTG | GCATAAAAGGCATCTCATTGG |
| mdNGS534 | (CTT) | 6 | TTGGTCATGAGGCAAAGATG | TTGGGGCTACTCGCTAAAAA |
| mdNGS535 | (TTA) | 5 | GAAGCAAAAATGCATGATCC | GGTGGATAGGGTGTGTAGGC |
| mdNGS536 | (TAT) | 5 | CAGCCCTAATTTGGCATCAT | TGAGCTCTATCAGTCCCTTTCA |
| mdNGS537 | (TAT) | 6 | GGTTCATGCACGCTATCCTC | AGATTTGAGTCGTTAGGCACAA |
| mdNGS538 | (GAG) | 5 | AGGAGGCAAAGAAGGGAAAG | TTTTCCTCCTCAGTGTTGGC |
| mdNGS539 | (AGA) | 5 | AGAGTTGGGCATCCCTTTTT | ATGGCTATCCACCAGGATCA |
| mdNGS540 | (CTA) | 6 | TTGGATCAAGTCAGATACTAAGCC | GTCAGAATGGATCCAGGGAA |
| mdNGS541 | (CTA) | 7 | CTTGAATTTTGGGGCGAGTA | GTCAGAATGGATCCAGGGAA |
| mdNGS542 | (TCT) | 5 | GCTGAATTTGAACGAAGCCT | AGCAGCACATAGCAAGAAAAA |
| mdNGS543 | (TCT) | 6 | TCTGTCATAGTGGCCTGCAT | TGGGGAAAGTGAGGTTGAAG |
| mdNGS544 | (TTC) | 5 | TCTCATGATTTATGGAGAAGAAAGG | GAGAAAGAGGGATGGCATTG |
| mdNGS545 | (AAT) | 5 | ATTCCTTTGGGGCTCAATTC | GGTTGCCACATCGAATTTTT |
| mdNGS546 | (TAT) | 5 | TGGTACCAAACTTTGTGGCAT | GCTTTATGGTCCGGTAAGGA |
| mdNGS547 | (TAT) | 5 | TCCTTACCGGACCATAAAGC | TCATCCTGCAACTTAGACAACAA |
| mdNGS548 | (CAG) | 7 | AAGACAATTGCATCCCCAAA | CAGAACCACGAGGAGTGGAT |
| mdNGS549 | (TTA) | 5 | ATGCATGTACCAATGCAACC | CGCATCTAGGCTGATTCACA |
| mdNGS550 | (ATG) | 5 | TGATGTGTCCTTGAATCATCC | CCCACACTTATGGTCCTGTG |
| mdNGS551 | (ATG) | 6 | CAATGGGAGCAAACATTCTG | AAAAAGACTGTTGGATTTATGAAGAA |
| mdNGS552 | (ATG) | 5 | TTTCTTCATAAATCCAACAGTCTTTTT | GCACGAGAATATGGATACATTGA |
| mdNGS553 | (ATC) | 5 | GCCTCATATGGTGGGACATC | CACGTGCCAGACTAGAAGGA |
| mdNGS554 | (TCT) | 5 | GGGAAGAGGTGAACTCAGCA | GAGTATAGGGGCAGCATGGA |
| mdNGS555 | (AGA) | 5 | AGGATTTTAGGTTGTCAAATGG | TCCCTAGGACTCTCATCTCTCG |
| mdNGS556 | (TTA) | 6 | TGATGCTGGTAGGAGGAATTG | GGATAATGTCGATTAAGTTGGAGAA |
| mdNGS557 | (ATA) | 5 | GGATGGCTCTGATACTACTATTAAAAA | TTTAAAAGTATGAGGGGTCTAGATTT |
| mdNGS558 | (ATA) | 5 | GGATGGCTCTGATACTACTATTAAAAA | TTTAAAAGTATGAGGGGTCTAGATTT |
| mdNGS559 | (AAT) | 5 | GGCATAGAGCAGACAAAGCA | TGTTAATGCATGGCCTTGTT |
| mdNGS560 | (AAT) | 8 | GTTGCATGCATTCTACATTCATA | CCTACTTCATGCAAGTTACCTATTTT |
| mdNGS561 | (AAT) | 6 | GAAACAACTCTTCATGAATCACAA | TCCTTCCCCAAGGAACTTCT |
| mdNGS562 | (AAT) | 5 | TCGGATATTATGCTTTGTGGA | GCACCATACGTAGCTGTTCG |
| mdNGS563 | (TCT) | 6 | TAGATGCTCGAGCCACACAC | TCTCTTCCATGCCCAAGAGT |
| mdNGS564 | (TTC) | 5 | CGGATCAAGGAAAGCAATGT | CATCTTCTTCAGGTGGGCAT |
| mdNGS565 | (ATC) | 5 | ACCCACCAAAACAGAGCAAC | GACTGCCCATTTTTCCAAGA |
| Code | Motifs |  | Forward primer (5'-3') | Reverse primer (5'-3') |
| mdNGS566 | (GAT) | 5 | ATATTTCATGGCGAACGGAC | AAGGCATCGGTACAAAAACG |
| mdNGS567 | (AGA) | 5 | CGCCCTCTTTTCTTCTCCTT | TGAATGAAACCTGGATCGTG |
| mdNGS568 | (TCT) | 5 | AGCCACACAAGTATCCGGTC | CGCATCCCAAGTAGTTCCAT |
| mdNGS569 | (TAT) | 5 | TGGCACTTGATGCATACGAT | GCTCTCTGAGGGACAGCAAC |
| mdNGS570 | (TTC) | 6 | CCATACAAATCAAAGCTCAAACC | CAATCATTTGATGGCTGCAC |
| mdNGS571 | (TCT) | 5 | AAGCCTAGATTGCGATCAACA | CCTAGAGCATCCAAACCAGC |
| mdNGS572 | (CTT) | 5 | TGACCTGAAGTCTCTGCAATG | GGGGGTCAGACCGTAAAGTT |
| mdNGS573 | (GAA) | 5 | GGCATGGTGAATTCATGCTA | TGCTAGGATATGACAAGACCTTC |
| mdNGS574 | (AAT) | 5 | GGTGCCATACCTGCAATTCT | ATGTCTCGTATTCGGGCTTG |
| mdNGS575 | (TTA) | 5 | CATTCTGAATTCCAGCCAAAA | CTTGGAGAATCATGGGAAGA |
| mdNGS576 | (TAA) | 6 | TCTGTTCACTATTCTCCGGG | TGTGGCCCTATCCTTTTCAG |
| mdNGS577 | (TCA) | 5 | CCACTTTGAGATATGTGTGGGA | CAACATCCCAGAAAAGCCAT |
| mdNGS578 | (ATA) | 15 | TGATAATATTGGCCAAGTGGG | TCGATTCTTAAGTATAATCAGGTGC |
| mdNGS579 | (AAT) | 7 | ATCTTCGTTTACACAGCGGC | CGGAGCTTTCCTGTAATGGT |
| mdNGS580 | (TAT) | 24 | GGCCATAACATTCATGATATAAGACA | TCCAAACATAGCAATAGCCTCA |
| mdNGS581 | (AAT) | 5 | GATGAAGGTGCCTCAACCTC | TGTGATTCGGAGGAGGATCT |
| mdNGS582 | (GAA) | 5 | TGGTGAATTCATGCTCCAAA | CATCAACAATTGATATCCTGAAAA |
| mdNGS583 | (TTA) | 6 | GGGGAGCATGCTAGATCACT | CTTACACGCATGCAAGGCTA |
| mdNGS584 | (AAG) | 6 | GGAAAAGAAAGAAAAGAAAAAGAAAA | TCGGAGCAATCTCAGATCAT |
| mdNGS585 | (TCT) | 5 | AAATCTGAACGAAGCCTGGA | ATACACCCCTTCCTTGGGAC |
| mdNGS586 | (TCA) | 5 | TATGAGTGGCCAAGCTCTCA | CCGACTTTGCTCAATGGTTT |
| mdNGS587 | (AGA) | 5 | TAGTCCCTCACACCCAAAGG | TTCTCCAAAATTCAGCCTGC |
| mdNGS588 | (TAT) | 6 | AGCATAAAGATAAGGTTGCATTTT | TTGACATGTTTGGTATGGCA |
| mdNGS589 | (AGA) | 5 | CATAGCAAAGAAAAATTCTAGAAAAGA | GAGGCTCTCTATTAGCCGCA |
| mdNGS590 | (AAG) | 5 | AGGAGCTCGGCAGATAACAA | CATGAGGCTTGCAATGATGT |
| mdNGS591 | (TAT) | 5 | TATGCATTGGAATGTGGCTC | TCCCACTCATATATCGGTGAAAT |
| mdNGS592 | (ATG) | 5 | CAAGGTCCCATTCCATGAAC | GCACGCACAACAACGTAAAT |
| mdNGS593 | (TCT) | 6 | CTGCAGGATCAACTCCATGA | GGGAGGTCTCTAGGGTTTCTTG |
| mdNGS594 | (AGA) | 5 | ATTCAACCAGCCATTGATCC | ATTGCTGAAGAGGCATTTGG |
| mdNGS595 | (TAA) | 5 | TTTCATGCAAATCATTGACCA | TGTCATGAGGGGTTCAACAA |
| mdNGS596 | (TTA) | 8 | TAGATGAGTCGGAGGGCAAC | TCTTAGTGCCATATCTACAAGAATTGA |
| mdNGS597 | (AAT) | 5 | CCCATGGATGCACTAAGGTT | GTCGCTATCCAACAGCGAAT |
| mdNGS598 | (ATC) | 5 | TCATAGCCTCAACTAAATCCCA | AGCATGCCACTAGCATCAAA |
| mdNGS599 | (AAT) | 5 | CAGCCTTCGGATAAGACTGC | CAAAGGAGGACCTACACATCG |
| mdNGS600 | (TCA) | 5 | TCATGCAAACGAAGTTGAGG | GTACGGGATACGGCACTCAT |
| mdNGS601 | (ATC) | 5 | CGATGCAGCACTCCTATCAA | ATGATGCTTACGATGTGCCA |
| mdNGS602 | (AAT) | 5 | ATAAAGGCCACGTTGAACCA | TTTAAGCGCAATTAGGTGCC |
| mdNGS603 | (TTA) | 5 | GGAAAAAGAAAATGGCCAAG | TTGACTCAAGCAATCACAACG |
| mdNGS604 | (TTC) | 10 | ACGCCAGAAACGAAAGAAAA | CATGGCTTTGCATCAATCCT |
| mdNGS605 | (TTA) | 5 | GGAGGCATGTACAAAATGGG | AAAGTGCACCACCCAAGAGT |
| mdNGS606 | (GAT) | 9 | AGCAGACCATGACATTATTGGA | TCCTTTGCCTCTTGAAGTATTTG |
| mdNGS607 | (CTT) | 5 | AAATGCAAGCTTGATGATTCC | ATCGCTTTCTTTGATCCGAA |
| mdNGS608 | (TCT) | 5 | TTCTCCAAAATTCAGCCTGC | TGTTGGGCATCCATTGATTA |
| mdNGS609 | (ATA) | 7 | TAAATGGGGTTGGGTCACAT | TTTGGGACTTTTTCCTTTGC |
| mdNGS610 | (TGA) | 6 | TCATGTCAAGCCCAAATACCT | GGGATGTTCTGAATTTGGTGA |
| mdNGS611 | (ACT) | 12 | TTTTGCAGTTCTGGCTCAAA | GGCTTACCACGGTTGTCTTG |
| mdNGS612 | (AAG) | 6 | AAACCCTAAGGCAGGCATTT | GCAAAAGTGTGAGCCACAGA |
| mdNGS613 | (TCT) | 5 | ATTCTCCCCTACCACAAGCC | TGAAGAGCCTGTTGGTTTGA |
| mdNGS614 | (AAG) | 5 | GCTTTGGGTTGTGAAGAAGG | TGTCACGTGCTGTGAACAAA |
| mdNGS615 | (AAG) | 5 | CCAGATAACCTTGTCCACGAA | CCTTAGGCCCCCATCTTTAG |
| mdNGS616 | (AGA) | 5 | GCTTTTCCACATGCCAAGAG | CGGACAGATATTCACCGCTT |
| mdNGS617 | (GAA) | 5 | GGCACATGCATAGACCAGTG | CATTGCACACGTTGGCTTAT |
| mdNGS618 | (GAG) | 5 | GGCTCGGAGATGCTAGTCTG | ATTCATGGCACCCTTTCTTG |
| Code | Motifs |  | Forward primer (5'-3') | Reverse primer (5'-3') |
| mdNGS619 | (AAG) | 5 | TTTTGAATTGCGAAGAAAGC | GCCGTTAGATGGAGCTTGAA |
| mdNGS620 | (AAG) | 11 | TGAATGGGATTGGGCTTTAG | TCATGTCTTCATGGGGTCAA |
| mdNGS621 | (AAG) | 9 | TGAATGGGATTGGGCTTTAG | TCATGTCTTCATGGGGTCAA |
| mdNGS622 | (TAT) | 5 | AGGGGCATCTTGATAATTTACTAAT | TCTGTAGTACCCCCTAAAAGCA |
| mdNGS623 | (AGA) | 5 | ATCTGAGCGGTCCATTGAAG | CCTTCTTCCATCGTACTCCG |
| mdNGS624 | (CTG) | 5 | TGACTCCAAAGATGGTGCAG | GGAGGATGAAATATCGGCAA |
| mdNGS625 | (AAT) | 6 | TCACTGGGACTAACGACATCC | TCTCAAAAATGGCATGTGGA |
| mdNGS626 | (AAT) | 8 | ATCGTCTGTCTCCTGATGCC | GAGGGTGACGATCCATTCAT |
| mdNGS627 | (AGA) | 5 | TCCAAAGGGATCCCAACATA | TTGATTGACCTACTTGATTGTTAACTG |
| mdNGS628 | (TCT) | 5 | GAATTTGAACGAAGCCTGGA | AGTTTGGGTGCCTCTTCCTT |
| mdNGS629 | (TTA) | 5 | TCCAACCAAAATCTCGATCC | ATGGTGGATAGGGTGCGTAG |
| mdNGS630 | (ATA) | 6 | AAGACTCGATCATCCAACCG | TTTTATAGATCATGATATCTTTTGGCA |
| mdNGS631 | (CAG) | 5 | CCTGCAGCAACAATGACAGT | CAAGGCAAATATGGAGATGGA |
| mdNGS632 | (TCA) | 11 | CTGGAATTCCCAGCTTTTCA | CCACATTCTTGAGATTGGCA |
| mdNGS633 | (TCA) | 9 | CAGGAATTCCCAGCTTTTCA | CCACATTCTTGAGATTGGCA |
| mdNGS634 | (AAT) | 5 | AGACCTAACGCATCCCAATG | AATTCGATCCCACTGCACTC |
| mdNGS635 | (TCA) | 5 | TTCCCCATCTTTTGCATCTC | AAATTAAGGGGGCAATTTCG |
| mdNGS636 | (TTC) | 5 | GCACTACTCATCGGCCTCTT | ATGATGGCGAACATGAGGA |
| mdNGS637 | (TTC) | 5 | GGGACTTTAGCCCTTCTATTTACC | ATTTGGGCCTAAACATTGGG |
| mdNGS638 | (CAT) | 5 | GCAGTGTCCTCATCTCCTCC | CGTGAATTGGCATCATGTTC |
| mdNGS639 | (AGA) | 5 | TGGAAAACTGGAGATGAGGC | ATTGGCGCTAGAGGAAAGGT |
| mdNGS640 | (TTC) | 5 | TCCTCTTCAGTCTTGTTTTCTTCA | GATGCATTGGATGGTGTTGA |
| mdNGS641 | (AAT) | 7 | CCCACTTCCCATGTCTTTGT | GTCAGTTGCTTGTTGCTGGA |
| mdNGS642 | (AGA) | 5 | AGTTGGGTGCCTCTCTTTCA | CACGTATCCAATCTCTACGGG |
| mdNGS643 | (AGA) | 5 | AACCTTCCAACAACCACCAG | GAAGGAGAAAGTGGTTTGGC |
| mdNGS644 | (TAT) | 8 | TCCTAAACGGTTTGGCATTT | TGATCCTTAATGATGGTGTTCG |
| mdNGS645 | (AAT) | 5 | TTATGCTTTGTGGACATGGA | AGGCGGAGAGAGAGATGTGA |
| mdNGS646 | (GAA) | 5 | AGTGAGTCAGGATCGTTTCCA | TCCGTACCCCTTAGAGATAAGC |
| mdNGS647 | (AAT) | 6 | CGAATGCAGTCCGTGTAGATT | TCGAAATTGGGTCCGATAAG |
| mdNGS648 | (TTA) | 6 | GTGTGGCCCTATTCCTTTCA | ATGGTGGATAGGGTGCGTAG |
| mdNGS649 | (AGA) | 7 | CCTGCAATCTCTCCCAATGT | GCATTATGTTCATGTTTTCTTGC |
| mdNGS650 | (TTC) | 6 | CCCGATGGCTGTCTCATTA | TGAAGAAGGGGAAAAGTTGAAA |
| mdNGS651 | (CTT) | 5 | ATGTGTCCGACCTCTATGGG | TCTTCTCTCCCTCTCCATGC |
| mdNGS652 | (AAG) | 6 | CACTGCCAGAATGCCCTACT | TACCGAGCTGCCATAAATCC |
| mdNGS653 | (CTT) | 6 | TCTTGTTAGGCCTGTTTGGG | GTCCTCTGCTAGGCGTCATC |
| mdNGS654 | (GCT) | 5 | ATCCACCCATCATTCCTCAA | AGAAGTGGCTGAGCTTCGAG |
| mdNGS655 | (TTA) | 6 | CCCAAATGGACATATCTGGA | TGCGACCTAGCATTTCAACA |
| mdNGS656 | (CAT) | 5 | GATCCGATCGTCCTCCAGTA | AGCGATCTCCGATTTAGGGT |
| mdNGS657 | (TGA) | 5 | AGAGCATCATCTTTGTGGGG | TGCAACCTTGGAACCCTACT |
| mdNGS658 | (TTA) | 7 | TGATTGCTTGAGACTTGGGA | TGCATGCAAGGCTACAAATC |
| mdNGS659 | (ATC) | 5 | CCTGATCTGCCACCAAGAAT | GTTGGAGCTTGAAGAGTGGC |
| mdNGS660 | (TAA) | 5 | CTACGCACCCTATCCACCAT | TTGATCGAGATTGACTCTTGGA |
| mdNGS661 | (TTA) | 5 | GAAGCAGAGAATCAGTGCCC | ACAATCCTTGCGAAACATGA |
| mdNGS662 | (AAT) | 5 | CTATGGGCATTGCATACCTG | CAATGGCGAGGATATACCGA |
| mdNGS663 | (ATA) | 5 | CTAGCACTCAACCCCCATGT | TCCGGATAAAATTCAAGAAAGC |
| mdNGS664 | (AAG) | 5 | TCCAGATTTGAAGAAAAGGATTG | TCGCAATCAACATTTGGTCT |
| mdNGS665 | (GAA) | 5 | GATGGCCAACATGAGGAAGT | ACATCGGTTGGTGGTCTAGC |
| mdNGS666 | (TCT) | 5 | CTGAATCTGAATGAAGCCTGG | GAGTTTCATGCCCAAGGTGT |
| mdNGS667 | (CAT) | 5 | CATCAATAAATCATGAAGGGCA | TGGATCAATCATACACCCGA |
| mdNGS668 | (TCA) | 5 | CGGTGTACCTTGGCACATAGT | AAAGAGGGGACGGAAATCAG |
| mdNGS669 | (TAT) | 6 | ACCAATCCCAATCTTCTCCC | ATGGGCCAGGTAGTCTCCTT |
| mdNGS670 | (AGA) | 6 | GTCCAAAGTCAGTTGCACCA | CCACCTGACGTCCTTGATTT |
| mdNGS671 | (AAG) | 5 | CCCATCTAAAAGGAGGTCCA | CCTTCAGGTTGCTTGTAGCC |
| Code | Motifs |  | Forward primer (5'-3') | Reverse primer (5'-3') |
| mdNGS672 | (AAT) | 5 | TTGTGATGGGTTATTCAAAATGA | TGCCAAACATCACATAACTCAA |
| mdNGS673 | (TCT) | 5 | GAATCTGAACGAAGCCTGGA | CCAAGGAGTCCCACACCTAA |
| mdNGS674 | (CAT) | 5 | AGGACACCCATCATCATCGT | TATACCACCACATGCCTCCC |
| mdNGS675 | (AGA) | 5 | CCATCTCCATGCCTTCTCTC | CACATGTGTTCGGCCTCTAC |
| mdNGS676 | (TTC) | 5 | CGTCGGCCTCTACAGATGTT | CAGAAGAAGAATCCGAAGGG |
| mdNGS677 | (AAT) | 8 | CCGAATGCAGTCTGTGTGAA | GTTGGGATCGTTGAGCTTGT |
| mdNGS678 | (GGC) | 5 | GGGAAAGAAAAGATTATTGAGGAA | TCATCTCCAAGGCTAATGTCG |
| mdNGS679 | (ATA) | 5 | TGGATTGAATGCACATGATGA | TGCTCTGAGATTTGCCTTGA |
| mdNGS680 | (AAT) | 5 | AATGGGTGAAGGCATCTCAG | TGCACATCGAGGAAGATACG |
| mdNGS681 | (CTT) | 6 | AGACTGCGGCATCAACTCTT | AATTGGGTGTCCCCTTTTTC |
| mdNGS682 | (TAT) | 5 | GCGTCTCATCATGAACCCTT | ACTTGGGACGGCTTAGACCT |
| mdNGS683 | (AAT) | 5 | TCATCATCTGTCTCCTGGTGTC | TTGATGAGTTAGAGGGTGACGA |
| mdNGS684 | (AAT) | 5 | AAAAGAAGAAAAACAACCAATCA | ACACACATAGCAGCACCGAC |
| mdNGS685 | (TCT) | 5 | CTGCTGAATCTGAACGAAGC | CAATTTGCTGGTTGCTGATG |
| mdNGS686 | (ATA) | 8 | CGCTTGCCAGCAAATTAAAC | AAGGAGCCAGAGTTGCAATG |
| mdNGS687 | (TCT) | 5 | TTTTGTGCATGTACGCTGGT | AAAGGCTGCAGCTCAGTGAT |
| mdNGS688 | (GAA) | 6 | TTCAAAGAAAGCATTGAACCC | GCCCCTGCAATGACTTACAT |
| mdNGS689 | (AAG) | 8 | CCAGCCCCATAGAGTAACCA | GGATGTGTGCATTTTGCTTG |
| mdNGS690 | (ATG) | 5 | TGAATGCTTTTCATTCCTACCA | GGTCATGTCTTACATTCACATGG |
| mdNGS691 | (TCT) | 5 | TCAGCCTGCTGAATGTGAAC | CTTTGGGCATCTTCTCCTTG |
| mdNGS692 | (AAT) | 28 | TTGGACAATCACAAATTGGC | TTGGGCCCATTATCAGAAAC |
| mdNGS693 | (TTC) | 5 | GAAAAGGGTCCTAAGAGAAGACA | GCATGGCGATCTTATTTTGG |
| mdNGS694 | (TAA) | 5 | CCGGAGAACAATGGACAGAT | CGAATGCACGTTCAAAGATG |
| mdNGS695 | (TAT) | 5 | TGGATACGAGGAAGCAAAGC | ATACTCAACCCCCACATTGC |
| mdNGS696 | (AAG) | 6 | TGCACCTTTACTCCCTGTTG | CTTGATGCTTCCTCCACCAT |
| mdNGS697 | (CTT) | 5 | GGCTTTCAGTATCCAATACCCA | CTTTTGCAAGAAGCAGGGTC |
| mdNGS698 | (ATC) | 5 | CACCCTACCTCCATGGACAC | TTACATGGTCCTCATTGCCA |
| mdNGS699 | (TAA) | 5 | GACTAAACCAGCGATCCTTCA | TTGGAAATGCACCAGTTAAGA |
| mdNGS700 | (AGA) | 5 | CTTTCTTTCCATGCCCAAAG | CTCTACGAGTATCCACCGGG |
| mdNGS701 | (TAT) | 5 | TGGTCAGGCAAGTCATCAAG | GACCAAATCTGGCCAAAAGA |
| mdNGS702 | (AGA) | 6 | TCATAAGTTGAACATGCACCAA | TGAATTTCATAATGAGGCACCA |
| mdNGS703 | (TTC) | 5 | TTCACCTTTCCTCAGCCTTC | AAGAAGGCCACAAACAAGGA |
| mdNGS704 | (CTT) | 6 | TGTTTCAGGGAATGGGCTTA | CCTACTTATCGGACAGAAGCAAA |
| mdNGS705 | (AAT) | 6 | CCTTCGGGGTAGACTGTGAA | GCCATCCTCGGGATTATGTT |
| mdNGS706 | (AAG) | 5 | CAAAAATCGAAGGAAAGTCAGC | TCAGTGAACTCTGATAGCAGCAC |
| mdNGS707 | (ATA) | 5 | GACCGTCGTCGTCTATCTCC | AGGGCGACGATCAGTTCATA |
| mdNGS708 | (AAG) | 7 | TTGAACTCAAGCCCTGTTCC | TGCACTTTCCACTGCACATT |
| mdNGS709 | (AGA) | 5 | TGGTGACTTAGAGATTGAAGATCG | CTCATTACCCTGGTGTGGGT |
| mdNGS710 | (TCT) | 5 | TGGTTCTCCAAAATTCAGCC | GATGCACGTTCCAAGGAGTT |
| mdNGS711 | (CTT) | 5 | CGGGTATCTATCGGGATCAA | TCCCTCTCTTCCTTTCCACA |
| mdNGS712 | (ATA) | 6 | GGCATGGCATTGCTTAAAAT | AGGCCCTGTAATCGGTTTTT |
| mdNGS713 | (AAG) | 8 | GCTGCCATTAGTAGGAGGACC | TTGGAGGGAGAAAGTGGAGA |
| mdNGS714 | (AAT) | 31 | TCCAAGCCAAACGAGTTTCT | ATCCGGATAGAAGGGCAACT |
| mdNGS715 | (AAT) | 12 | TGATGCGTATCATAGAGTACCGA | ACCATTGGACGCAGCTAGAA |
| mdNGS716 | (AGA) | 5 | GCACCATCTTTTGGGATGTC | TGAACGAAGTCTGGATCGTG |
| mdNGS717 | (CTT) | 5 | ATCATCAGCTTCGCCTTGTT | CCTCCACCCAACTGTTCTTG |
| mdNGS718 | (AGA) | 5 | TTCCTCTCTCCATCTCCACG | AACCTTGGCCTTGAGGATCT |
| mdNGS719 | (AGA) | 5 | TTTCTTTTCATGCCCAAAGG | CACGTATTCGGCCTCTATGG |
| mdNGS720 | (AAT) | 7 | AACTATTCAATAATAAACCCCGAA | GGTCCCCACTCCACTCCTAT |
| mdNGS721 | (AAG) | 5 | GTGGCACGATCTCGAACATA | AAAAGCAACAGTTGGGGATG |
| mdNGS722 | (AGA) | 6 | AAACTTATTGATCTCACCAGAGTGC | GCGTAGAGAACATCATCCTCC |
| mdNGS723 | (TTA) | 5 | TTGATAAGTCGAAGGGCGAC | ATCATCTGTCTCCAGGTGCC |
| mdNGS724 | (AGA) | 5 | TCCCAAGTTATCTCATGCCC | TGAACGAAGTCTGGATCACG |
| Code | Motifs |  | Forward primer (5'-3') | Reverse primer (5'-3') |
| mdNGS725 | (TAT) | 8 | TCAATATGGCTCCAAATACATCA | CCACCCATCAGGACACAATA |
| mdNGS726 | (TTA) | 5 | TTCTCTTGTAATAATGGTATGCGA | GTGCAAGACCCTCTGGTGAT |
| mdNGS727 | (GAA) | 5 | AGGCAACAAACAAGCTTTGG | TGGATTGGTGCAGTCTCATC |
| mdNGS728 | (TTC) | 5 | CCTTTTCTTTTTCCTTTCTTTTCC | AAGAGGTCACCACTCATCGG |
| mdNGS729 | (AAT) | 7 | GCCTCTTTGAGTAGCGATGC | AATTGGAGTTTGACCCCCTC |
| mdNGS730 | (GAA) | 5 | CAAAGAGTTGGAGCATGGTG | AGGGGTCCTAAGAGAAGACAGA |
| mdNGS731 | (CTT) | 5 | TCTCCCTGAGATTTTGTGGG | AAAGGAGGAGAAGAGTGGGG |
| mdNGS732 | (AAG) | 5 | TAGAGCGAGCTTCCTAAGCG | TCATCAAGCAGGTTGGACAG |
| mdNGS733 | (AAT) | 5 | AGCCACTTCCAATTCGTGAG | TTTTCAAACATCTTTTTCCACTT |
| mdNGS734 | (CCG) | 5 | TCATCCTCAAGGCTAATGTCG | GGAAAGAAAAGGTTGTTGAGGA |
| mdNGS735 | (ATC) | 5 | TTGGTAAATGCTGGTGATGG | GCCAGCAATTCCTCATTCAT |
| mdNGS736 | (CAT) | 8 | GAAGTGGTGCCACTCCCTAT | GGCGGTTGAAAGTGGTCTTA |
| mdNGS737 | (AGA) | 5 | AGACCTTTGGGTCATGGAGA | TAGGGCTCCTCCAAAGATGA |
| mdNGS738 | (TTA) | 5 | AATAGGTGTGGCCCTATCCC | TAGGCACCATATTCACGTCG |
| mdNGS739 | (AAG) | 5 | GGGGGAAAAGAGAAAGAAAAA | TCGAATAGAATCGGACTGGG |
| mdNGS740 | (TCT) | 5 | ACTTGGAGTGCTCGAAGGTG | TCGGATTGTTTTGATTGATTTC |
| mdNGS741 | (AGA) | 5 | GGGCGTCCCATATTTTCATA | GCCACACATATGTTCGGTCTC |
| mdNGS742 | (ATG) | 5 | CGAAACAATGACTGTTGGGA | ATGCCAACTAACTGCCCTTG |
| mdNGS743 | (TCT) | 6 | CACATCACTGAAGACCACCG | GAAGAGGGGGAGAGAGAGGA |
| mdNGS744 | (TCA) | 5 | TTTGCATCCTTCTCCATGCT | ACAGGCCATCCAATTAGCAA |
| mdNGS745 | (GAA) | 5 | ACCCTGCCTAAGCTGTTGAA | TCTTGTTCTTCACGCTCCCT |
| mdNGS746 | (CAT) | 5 | TCTCTCTCTGCTCATGCTGTTC | TCATTGGCTGCGTAGAGATG |
| mdNGS747 | (TAA) | 5 | ATTGACTCTTGGATGTCCCG | GGTGTGACCCTATCTCTTTCACA |
| mdNGS748 | (TAA) | 5 | TTGGTGGAAGGAGATTTTCTG | CAGGTGTGGTCCTATCCCTT |
| mdNGS749 | (TTA) | 8 | CTGTGATTCGGATGAGGATCT | CGTCTATCTCCTGGTGCCAT |
| mdNGS750 | (AAT) | 6 | TGCAGTCCGTGTGGATTCTA | GTTGGGTTCGATGAGCTTGT |
| mdNGS751 | (TAT) | 11 | TTATGCACGCTATCCTCGAA | AGAGTTGGAAGATCAGGCCA |
| mdNGS752 | (AAG) | 5 | CCCTCCTCCCTCTCATCTCT | CGCATACGTGTCTGGTCTCT |
| mdNGS753 | (TAT) | 12 | TTGAGCATGGTTTGGTTTGA | TCTTGATGGTACTCGTATGTGAAAA |
| mdNGS754 | (TAT) | 5 | TGCACATGGATTTGAATGTC | TCCTTCAATTAGGTGGCTTCA |
| mdNGS755 | (ATA) | 6 | CACGTGAGGGGCTTAGAAAA | TTTGACATGTGGTATTGCGA |
| mdNGS756 | (CTT) | 5 | GTCGTCAGATAGGCCGGATA | TGGTAATAGCTGAGGGCACC |
| mdNGS757 | (TTA) | 5 | TGCATGATCCTATCCATTTCA | CAGGCACCATATTCACATCG |
| mdNGS758 | (TTA) | 5 | TAACAGGTGTGGCCCTATCC | TCTTGGATGTCCTGTATTCGG |
| mdNGS759 | (CTT) | 5 | ATCCATCGGGATCAATCTCA | GGCATCCCATATTTCCACAC |
| mdNGS760 | (TCT) | 5 | TCAGCCTAAAACAGCCCTCT | GCATCGAATCCTTGTTGGTT |
| mdNGS761 | (TCA) | 5 | CCACCTTCATCGCTACCATT | GTGGCTGAGTGTGAGCATGT |
| mdNGS762 | (GAA) | 5 | CCTTCCTTGGTTCTTCTCCC | CGCTGCATGATCTTGAAAAA |
| mdNGS763 | (GAA) | 5 | TTGAAGAATTCAAGGGGCAC | CAGCATCATGGTGGAAACAC |