

Multiples nucleotide sequence alignment of wtMth212 and Mth212/D151S (clone 2)

| | 1 | 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 | 90 |
|----------------------|---|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Mth212_WT | ATGACCGTGC TAAAAATAATATCTCGAACGCTCAACGGCCTCAGGGCGGTCACAGGAGGGGTTCCCTTAATGGTTCATGGAGAG | | | | | | | | | |
| Mth212D151S_clone2_F | ACCATGGCCGTGC TAAAAATAATATCTCGAACGCTCAACGGCCTCAGGGCGGTCACAGGAGGGGTTCCCTTAATGGTTCATGGAGAG | | | | | | | | | |
| Mth212D151S_clone2_R | ACCATGGCCGTGC TAAAAATAATATCTCGAACGCTCAACGGCCTCAGGGCGGTCACAGGAGGGGTTCCCTTAATGGTTCATGGAGAG | | | | | | | | | |
| Consensus | accATGgCCGTGC TAAAAATAATATCTCGAACGCTCAACGGCCTCAGGGCGGTCACAGGAGGGGTTCCCTTAATGGTTCATGGAGAG | | | | | | | | | |
| | 91 | 100 | 110 | 120 | 130 | 140 | 150 | 160 | 170 | 180 |
| Mth212_WT | AAGCCAGACATCCTGTGCTTCAGGAGATAAAGCAGCGCCTGACACGCTCCCGAGGAGCTCAGGCACGTTGAGGGTTACAGAGCTTC | | | | | | | | | |
| Mth212D151S_clone2_F | AAGCCAGACATCCTGTGCTTCAGGAGATAAAGCAGCGCCTGACACGCTCCCGAGGAGCTCAGGCACGTTGAGGGTTACAGAGCTTC | | | | | | | | | |
| Mth212D151S_clone2_R | AAGCCAGACATCCTGTGCTTCAGGAGATAAAGCAGCGCCTGACACGCTCCCGAGGAGCTCAGGCACGTTGAGGGTTACAGAGCTTC | | | | | | | | | |
| Consensus | AAGCCAGACATCCTGTGCTTCAGGAGATAAAGCAGCGCCTGACACGCTCCCGAGGAGCTCAGGCACGTTGAGGGTTACAGAGCTTC | | | | | | | | | |
| | 181 | 190 | 200 | 210 | 220 | 230 | 240 | 250 | 260 | 270 |
| Mth212_WT | TTCACCCCTCGGGAGAGAAAGGGGTACAGCGGGGTTGCCATGTACACAAAGGTACCCCCCTTCTACTGAGGGAGGGTTTCGGTGTGGAG | | | | | | | | | |
| Mth212D151S_clone2_F | TTCACCCCTCGGGAGAGAAAGGGGTACAGCGGGGTTGCCATGTACACAAAGGTACCCCCCTTCTACTGAGGGAGGGTTTCGGTGTGGAG | | | | | | | | | |
| Mth212D151S_clone2_R | TTCACCCCTCGGGAGAGAAAGGGGTACAGCGGGGTTGCCATGTACACAAAGGTACCCCCCTTCTACTGAGGGAGGGTTTCGGTGTGGAG | | | | | | | | | |
| Consensus | TTCACCCCTCGGGAGAGAAAGGGGTACAGCGGGGTTGCCATGTACACAAAGGTACCCCCCTTCTACTGAGGGAGGGTTTCGGTGTGGAG | | | | | | | | | |
| | 271 | 280 | 290 | 300 | 310 | 320 | 330 | 340 | 350 | 360 |
| Mth212_WT | AGATTTCGACACCGAGGGTCGGATACAGATCGCAGACTTTGACGACTTCCTCCTCTACACATATACTTCCCAACGGTAGATGTCAGAG | | | | | | | | | |
| Mth212D151S_clone2_F | AGATTTCGACACCGAGGGTCGGATACAGATCGCAGACTTTGACGACTTCCTCCTCTACACATATACTTCCCAACGGTAGATGTCAGAG | | | | | | | | | |
| Mth212D151S_clone2_R | AGATTTCGACACCGAGGGTCGGATACAGATCGCAGACTTTGACGACTTCCTCCTCTACACATATACTTCCCAACGGTAGATGTCAGAG | | | | | | | | | |
| Consensus | AGATTTCGACACCGAGGGTCGGATACAGATCGCAGACTTTGACGACTTCCTCCTCTACACATATACTTCCCAACGGTAGATGTCAGAG | | | | | | | | | |
| | 361 | 370 | 380 | 390 | 400 | 410 | 420 | 430 | 440 | 450 |
| Mth212_WT | GAGAGGCTGAGGTATARAAC TGGAAATTCATGACGCATTCTTGAGGACGCTCAACCGGAGAGGGATTCTGGGGAGGACGTCGATTATATGT | | | | | | | | | |
| Mth212D151S_clone2_F | GAGAGGCTGAGGTATARAAC TGGAAATTCATGACGCATTCTTGAGGACGCTCAACCGGAGAGGGATTCTGGGGAGGACGTCGATTATATGT | | | | | | | | | |
| Mth212D151S_clone2_R | GAGAGGCTGAGGTATARAAC TGGAAATTCATGACGCATTCTTGAGGACGCTCAACCGGAGAGGGATTCTGGGGAGGACGTCGATTATATGT | | | | | | | | | |
| Consensus | GAGAGGCTGAGGTATARAAC TGGAAATTCATGACGCATTCTTGAGGACGCTCAACCGGAGAGGGATTCTGGGGAGGACGTCGATTATATGT | | | | | | | | | |
| | 451 | 460 | 470 | 480 | 490 | 500 | 510 | 520 | 530 | 540 |
| Mth212_WT | GGGAGCTTCACACACAGCCACAGGGAGATAGACCTTGCAGGCCAAGGAAACAGCAGACGTATCAGGTTTCTTCCCGTTGAGAGGGCC | | | | | | | | | |
| Mth212D151S_clone2_F | GGGTCATTACACACAGCCACAGGGAGATAGACCTTGCAGGCCAAGGAAACAGCAGACGTATCAGGTTTCTTCCCGTTGAGAGGGCC | | | | | | | | | |
| Mth212D151S_clone2_R | GGGTCATTACACACAGCCACAGGGAGATAGACCTTGCAGGCCAAGGAAACAGCAGACGTATCAGGTTTCTTCCCGTTGAGAGGGCC | | | | | | | | | |
| Consensus | GGG Lca TTACACACAGCCACAGGGAGATAGACCTTGCAGGCCAAGGAAACAGCAGACGTATCAGGTTTCTTCCCGTTGAGAGGGCC | | | | | | | | | |
| | 541 | 550 | 560 | 570 | 580 | 590 | 600 | 610 | 620 | 630 |
| Mth212_WT | TGGATCGATAAATTTATTGAAATGGGTACGTGGACACCTTCAGGATGTTCAACAGTGACCCGGACAGTACACATGGTGGAGCTACAGG | | | | | | | | | |
| Mth212D151S_clone2_F | TGGATCGATAAATTTATTGAAATGGGTACGTGGACACCTTCAGGATGTTCAACAGTGACCCGGACAGTACACATGGTGGAGCTACAGG | | | | | | | | | |
| Mth212D151S_clone2_R | TGGATCGATAAATTTATTGAAATGGGTACGTGGACACCTTCAGGATGTTCAACAGTGACCCGGACAGTACACATGGTGGAGCTACAGG | | | | | | | | | |
| Consensus | TGGATCGATAAATTTATTGAAATGGGTACGTGGACACCTTCAGGATGTTCAACAGTGACCCGGACAGTACACATGGTGGAGCTACAGG | | | | | | | | | |
| | 631 | 640 | 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 |
| Mth212_WT | ACAGGGGCCGTGAGAGGAGACGTCGGCTGGAGACTCGACTACTTCTTTGTAACAGGAGGTTCAAGGGGAGGTTAAAGGCTCTGGATA | | | | | | | | | |
| Mth212D151S_clone2_F | ACAGGGGCCGTGAGAGGAGACGTCGGCTGGAGACTCGACTACTTCTTTGTAACAGGAGGTTCAAGGGGAGGTTAAAGGCTCTGGATA | | | | | | | | | |
| Mth212D151S_clone2_R | ACAGGGGCCGTGAGAGGAGACGTCGGCTGGAGACTCGACTACTTCTTTGTAACAGGAGGTTCAAGGGGAGGTTAAAGGCTCTGGATA | | | | | | | | | |
| Consensus | ACAGGGGCCGTGAGAGGAGACGTCGGCTGGAGACTCGACTACTTCTTTGTAACAGGAGGTTCAAGGGGAGGTTAAAGGCTCTGGATA | | | | | | | | | |
| | 721 | 730 | 740 | 750 | 760 | 770 | 780 | 790 | 798 | |
| Mth212_WT | CTCTCAGATGTCATGGGCTCAGACCACTGTCCCATAGGACTGGAATAGACATATAA | | | | | | | | | |
| Mth212D151S_clone2_F | CTCTCAGATGTCATGGGCTCAGACCACTGTCCCATAGGACTGGAATAGACATCTCAGACCAACCACCACCACCAC | | | | | | | | | |
| Mth212D151S_clone2_R | CTCTCAGATGTCATGGGCTCAGACCACTGTCCCATAGGACTGGAATAGACATCTCAGACCAACCACCACCACCAC | | | | | | | | | |
| Consensus | CTCTCAGATGTCATGGGCTCAGACCACTGTCCCATAGGACTGGAATAGACAT ctc gagaccaccaccaccaccacc | | | | | | | | | |