

Multiples nucleotide sequence alignment of wtMth212 and Mth212/D151N (clone 2)

| | | | | | | | | | | | | |
|--|----------------------|---|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| | | 1 | 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 | 90 | |
| | Mth212_WT | ----- ----- ----- ----- ----- ----- ----- | | | | | | | | | | |
| | Mth212D151N_clone2_F | ATGACCGTGCTAAAATATATCTCTGGAACGTCACCGGCTCAGGGCGGTCCACAGGAAGGGGTTCCCTTAARTGGTTCATGGAAGAG | | | | | | | | | | |
| | Mth212D151N_clone2_R | ACCATGGCCGTGCTAAAATATATCTCTGGAACGTCACCGGCTCAGGGCGGTCCACAGGAAGGGGTTCCCTTAARTGGTTCATGGAAGAG | | | | | | | | | | |
| | Consensus | accATGgCCGTGCTAAAATATATCTCTGGAACGTCACCGGCTCAGGGCGGTCCACAGGAAGGGGTTCCCTTAARTGGTTCATGGAAGAG | | | | | | | | | | |
| | | 91 | 100 | 110 | 120 | 130 | 140 | 150 | 160 | 170 | 180 | |
| | Mth212_WT | ----- ----- ----- ----- ----- ----- ----- | | | | | | | | | | |
| | Mth212D151N_clone2_F | AAGCCAGACATCTGTGCCTTCAGGAGATAAAGCAGCGCCTGACACGCTCCCCAGGAAGCTCAGGCACGTTGAGGGTTACAGAAGCTTC | | | | | | | | | | |
| | Mth212D151N_clone2_R | AAGCCAGACATCTGTGCCTTCAGGAGATAAAGCAGCGCCTGACACGCTCCCCAGGAAGCTCAGGCACGTTGAGGGTTACAGAAGCTTC | | | | | | | | | | |
| | Consensus | AAGCCAGACATCTGTGCCTTCAGGAGATAAAGCAGCGCCTGACACGCTCCCCAGGAAGCTCAGGCACGTTGAGGGTTACAGAAGCTTC | | | | | | | | | | |
| | | 181 | 190 | 200 | 210 | 220 | 230 | 240 | 250 | 260 | 270 | |
| | Mth212_WT | ----- ----- ----- ----- ----- ----- ----- | | | | | | | | | | |
| | Mth212D151N_clone2_F | TTCACCCCTGCGGAGAGAAAGGGGTACAGCGGGGTTGCCATGTACACAAAGGTACCCCTCTTCACTAGGGGAGGGTTTCGGTGTGGAG | | | | | | | | | | |
| | Mth212D151N_clone2_R | TTCACCCCTGCGGAGAGAAAGGGGTACAGCGGGGTTGCCATGTACACAAAGGTACCCCTCTTCACTAGGGGAGGGTTTCGGTGTGGAG | | | | | | | | | | |
| | Consensus | TTCACCCCTGCGGAGAGAAAGGGGTACAGCGGGGTTGCCATGTACACAAAGGTACCCCTCTTCACTAGGGGAGGGTTTCGGTGTGGAG | | | | | | | | | | |
| | | 271 | 280 | 290 | 300 | 310 | 320 | 330 | 340 | 350 | 360 | |
| | Mth212_WT | ----- ----- ----- ----- ----- ----- ----- | | | | | | | | | | |
| | Mth212D151N_clone2_F | AGATTTCGACACCGAGGGTCGGATACAGATCGCAGACTTTGACGACTTCTCCTCTACACATATACTTCCCAACGGTAGATGTCAGAG | | | | | | | | | | |
| | Mth212D151N_clone2_R | AGATTTCGACACCGAGGGTCGGATACAGATCGCAGACTTTGACGACTTCTCCTCTACACATATACTTCCCAACGGTAGATGTCAGAG | | | | | | | | | | |
| | Consensus | AGATTTCGACACCGAGGGTCGGATACAGATCGCAGACTTTGACGACTTCTCCTCTACACATATACTTCCCAACGGTAGATGTCAGAG | | | | | | | | | | |
| | | 361 | 370 | 380 | 390 | 400 | 410 | 420 | 430 | 440 | 450 | |
| | Mth212_WT | ----- ----- ----- ----- ----- ----- ----- | | | | | | | | | | |
| | Mth212D151N_clone2_F | GAGAGGCTGAAGTATAAATCGGAATCTATGACGATTCCCTTGAGGACGTCACCGGGAGAGGGATTCTGGGGAGGACGCTGATTATATGT | | | | | | | | | | |
| | Mth212D151N_clone2_R | GAGAGGCTGAAGTATAAATCGGAATCTATGACGATTCCCTTGAGGACGTCACCGGGAGAGGGATTCTGGGGAGGACGCTGATTATATGT | | | | | | | | | | |
| | Consensus | GAGAGGCTGAAGTATAAATCGGAATCTATGACGATTCCCTTGAGGACGTCACCGGGAGAGGGATTCTGGGGAGGACGCTGATTATATGT | | | | | | | | | | |
| | | 451 | 460 | 470 | 480 | 490 | 500 | 510 | 520 | 530 | 540 | |
| | Mth212_WT | ----- ----- ----- ----- ----- ----- ----- | | | | | | | | | | |
| | Mth212D151N_clone2_F | GGGGAACCTCAACACAGCCCCAGGGAGATAGACCTTGCAGGGCCAAAGGAAACAGCAGCGTATCAGGTTTCCTTCCCGTTGAGAGGGCC | | | | | | | | | | |
| | Mth212D151N_clone2_R | GGGGAACCTCAACACAGCCCCAGGGAGATAGACCTTGCAGGGCCAAAGGAAACAGCAGCGTATCAGGTTTCCTTCCCGTTGAGAGGGCC | | | | | | | | | | |
| | Consensus | GGGGAACCTCAACACAGCCCCAGGGAGATAGACCTTGCAGGGCCAAAGGAAACAGCAGCGTATCAGGTTTCCTTCCCGTTGAGAGGGCC | | | | | | | | | | |
| | | 541 | 550 | 560 | 570 | 580 | 590 | 600 | 610 | 620 | 630 | |
| | Mth212_WT | ----- ----- ----- ----- ----- ----- ----- | | | | | | | | | | |
| | Mth212D151N_clone2_F | TGGATCGATAAATTTATTGAAATGGGTACGTGGACACCTTCAGGATGTTCAACAGTGACCCCGGACAGTACACATGGTGGAGCTACAGG | | | | | | | | | | |
| | Mth212D151N_clone2_R | TGGATCGATAAATTTATTGAAATGGGTACGTGGACACCTTCAGGATGTTCAACAGTGACCCCGGACAGTACACATGGTGGAGCTACAGG | | | | | | | | | | |
| | Consensus | TGGATCGATAAATTTATTGAAATGGGTACGTGGACACCTTCAGGATGTTCAACAGTGACCCCGGACAGTACACATGGTGGAGCTACAGG | | | | | | | | | | |
| | | 631 | 640 | 650 | 660 | 670 | 680 | 690 | 700 | 710 | 720 | |
| | Mth212_WT | ----- ----- ----- ----- ----- ----- ----- | | | | | | | | | | |
| | Mth212D151N_clone2_F | ACAGGGGCCCGTGAGAGGACGTCGGCTGGAGACTCGACTACTTCTTTGTAAACGAGGAGTTCAAGGGGAGGTTAAAGGCTCTGGATA | | | | | | | | | | |
| | Mth212D151N_clone2_R | ACAGGGGCCCGTGAGAGGACGTCGGCTGGAGACTCGACTACTTCTTTGTAAACGAGGAGTTCAAGGGGAGGTTAAAGGCTCTGGATA | | | | | | | | | | |
| | Consensus | ACAGGGGCCCGTGAGAGGACGTCGGCTGGAGACTCGACTACTTCTTTGTAAACGAGGAGTTCAAGGGGAGGTTAAAGGCTCTGGATA | | | | | | | | | | |
| | | 721 | 730 | 740 | 750 | 760 | 770 | 780 | 790 | 798 | | |
| | Mth212_WT | ----- ----- ----- ----- ----- ----- ----- | | | | | | | | | | |
| | Mth212D151N_clone2_F | CTCTCAGATGTCATGGGCTCAGACCCTGTCCATAGGACTGGAATAGAACTATTA | | | | | | | | | | |
| | Mth212D151N_clone2_R | CTCTCAGATGTCATGGGCTCAGACCCTGTCCATAGGACTGGAATAGAACTATTCGAGCACCCACCCACCCACCCAC | | | | | | | | | | |
| | Consensus | CTCTCAGATGTCATGGGCTCAGACCCTGTCCATAGGACTGGAATAGAACTATTCGAGCACCCACCCACCCACCCAC | | | | | | | | | | |