

Multiples nucleotide sequence alignment of wtMth212 and Mth212/D151N (clone 4)

	1	10	20	30	40	50	60	70	80	90
Mth212_WT	ATGACCGTGCTAAAATAATATCTCTGGACGCTCAACGGCCTCAGGGCGGTCCACAGGAAGGGGTTCCTTAATGGTTTCATGGAAGAG									
Mth212D151N_clone4_F	ACCATTGGCCGTGCTAAAATAATATCTCTGGACGCTCAACGGCCTCAGGGCGGTCCACAGGAAGGGGTTCCTTAATGGTTTCATGGAAGAG									
Mth212D151N_clone4_R	ACCATTGGCCGTGCTAAAATAATATCTCTGGACGCTCAACGGCCTCAGGGCGGTCCACAGGAAGGGGTTCCTTAATGGTTTCATGGAAGAG									
Consensus	accATGcCGGTGCTAAAATAATATCTCTGGACGCTCAACGGCCTCAGGGCGGTCCACAGGAAGGGGTTCCTTAATGGTTTCATGGAAGAG									
	91	100	110	120	130	140	150	160	170	180
Mth212_WT	AAGCCAGACATCCTGTGCTTCAGGAGATAAAGCAGCGCTGACAGCTCCCCAGGAAGCTCAGGCACGTTGAGGGTTACAGAGCTTC									
Mth212D151N_clone4_F	AAGCCAGACATCCTGTGCTTCAGGAGATAAAGCAGCGCTGACAGCTCCCCAGGAAGCTCAGGCACGTTGAGGGTTACAGAGCTTC									
Mth212D151N_clone4_R	AAGCCAGACATCCTGTGCTTCAGGAGATAAAGCAGCGCTGACAGCTCCCCAGGAAGCTCAGGCACGTTGAGGGTTACAGAGCTTC									
Consensus	AAGCCAGACATCCTGTGCTTCAGGAGATAAAGCAGCGCTGACAGCTCCCCAGGAAGCTCAGGCACGTTGAGGGTTACAGAGCTTC									
	181	190	200	210	220	230	240	250	260	270
Mth212_WT	TTCACCCCTGCGGAGAGAAAGGGGTACAGCGGGGTTGCCATGTACACAAGGTAACCCCTCTTCTACTGAGGGAGGGTTTCGGTGTGGAG									
Mth212D151N_clone4_F	TTCACCCCTGCGGAGAGAAAGGGGTACAGCGGGGTTGCCATGTACACAAGGTAACCCCTCTTCTACTGAGGGAGGGTTTCGGTGTGGAG									
Mth212D151N_clone4_R	TTCACCCCTGCGGAGAGAAAGGGGTACAGCGGGGTTGCCATGTACACAAGGTAACCCCTCTTCTACTGAGGGAGGGTTTCGGTGTGGAG									
Consensus	TTCACCCCTGCGGAGAGAAAGGGGTACAGCGGGGTTGCCATGTACACAAGGTAACCCCTCTTCTACTGAGGGAGGGTTTCGGTGTGGAG									
	271	280	290	300	310	320	330	340	350	360
Mth212_WT	AGATTTCGACACCGAGGGGTGGGATACAGATCGCAGACTTTGACGACTTCCTCCTCTACACATATATCTTCCCCAACGGTAGAGTGTACAGAG									
Mth212D151N_clone4_F	AGATTTCGACACCGAGGGGTGGGATACAGATCGCAGACTTTGACGACTTCCTCCTCTACACATATATCTTCCCCAACGGTAGAGTGTACAGAG									
Mth212D151N_clone4_R	AGATTTCGACACCGAGGGGTGGGATACAGATCGCAGACTTTGACGACTTCCTCCTCTACACATATATCTTCCCCAACGGTAGAGTGTACAGAG									
Consensus	AGATTTCGACACCGAGGGGTGGGATACAGATCGCAGACTTTGACGACTTCCTCCTCTACACATATATCTTCCCCAACGGTAGAGTGTACAGAG									
	361	370	380	390	400	410	420	430	440	450
Mth212_WT	GAGAGGGTGAAGTATAAAGTGAATTCCTATGACGCATTCTTGGAGGACGTCACCCGGGAGAGGGATTTCGGGGAGGAGACGTGATTATATGT									
Mth212D151N_clone4_F	GAGAGGGTGAAGTATAAAGTGAATTCCTATGACGCATTCTTGGAGGACGTCACCCGGGAGAGGGATTTCGGGGAGGAGACGTGATTATATGT									
Mth212D151N_clone4_R	GAGAGGGTGAAGTATAAAGTGAATTCCTATGACGCATTCTTGGAGGACGTCACCCGGGAGAGGGATTTCGGGGAGGAGACGTGATTATATGT									
Consensus	GAGAGGGTGAAGTATAAAGTGAATTCCTATGACGCATTCTTGGAGGACGTCACCCGGGAGAGGGATTTCGGGGAGGAGACGTGATTATATGT									
	451	460	470	480	490	500	510	520	530	540
Mth212_WT	GGGGACTTCACACAGGCCACAGGGAGATAGACCTTGACAGGCCAAGGGAACACAGCAGATATCAGGTTTCCTCCCGTTGAGAGGGCC									
Mth212D151N_clone4_F	GGGGACTTCACACAGGCCACAGGGAGATAGACCTTGACAGGCCAAGGGAACACAGCAGATATCAGGTTTCCTCCCGTTGAGAGGGCC									
Mth212D151N_clone4_R	GGGGACTTCACACAGGCCACAGGGAGATAGACCTTGACAGGCCAAGGGAACACAGCAGATATCAGGTTTCCTCCCGTTGAGAGGGCC									
Consensus	GGGgACTTCACACAGGCCACAGGGAGATAGACCTTGACAGGCCAAGGGAACACAGCAGATATCAGGTTTCCTCCCGTTGAGAGGGCC									
	541	550	560	570	580	590	600	610	620	630
Mth212_WT	TGGATCGATAAATTTATTGAAGTGGGTACGTGGACACCTTCAGGATGTTTCACAGTGACCCCGGACAGTACACATGGTGGAGCTACAGG									
Mth212D151N_clone4_F	TGGATCGATAAATTTATTGAAGTGGGTACGTGGACACCTTCAGGATGTTTCACAGTGACCCCGGACAGTACACATGGTGGAGCTACAGG									
Mth212D151N_clone4_R	TGGATCGATAAATTTATTGAAGTGGGTACGTGGACACCTTCAGGATGTTTCACAGTGACCCCGGACAGTACACATGGTGGAGCTACAGG									
Consensus	TGGATCGATAAATTTATTGAAGTGGGTACGTGGACACCTTCAGGATGTTTCACAGTGACCCCGGACAGTACACATGGTGGAGCTACAGG									
	631	640	650	660	670	680	690	700	710	720
Mth212_WT	ACAAGGGCCCGTGAGAGGAACGCTCGGCTGGAGACTCGACTACTTCTTTGTAACAGGAGGTTCAAGGGAGAGGTTAAAGGTCCTGGATA									
Mth212D151N_clone4_F	ACAAGGGCCCGTGAGAGGAACGCTCGGCTGGAGACTCGACTACTTCTTTGTAACAGGAGGTTCAAGGGAGAGGTTAAAGGTCCTGGATA									
Mth212D151N_clone4_R	ACAAGGGCCCGTGAGAGGAACGCTCGGCTGGAGACTCGACTACTTCTTTGTAACAGGAGGTTCAAGGGAGAGGTTAAAGGTCCTGGATA									
Consensus	ACAAGGGCCCGTGAGAGGAACGCTCGGCTGGAGACTCGACTACTTCTTTGTAACAGGAGGTTCAAGGGAGAGGTTAAAGGTCCTGGATA									
	721	730	740	750	760	770	780	790	798	
Mth212_WT	CTCTCAGATGTCTATGGGCTCAGACCCTGTCCCATAGGACTGGAAATAGAACTATAA									
Mth212D151N_clone4_F	CTCTCAGATGTCTATGGGCTCAGACCCTGTCCCATAGGACTGGAAATAGAACTACTCGAGCACCACCACCACCACCAC									
Mth212D151N_clone4_R	CTCTCAGATGTCTATGGGCTCAGACCCTGTCCCATAGGACTGGAAATAGAACTACTCGAGCACCACCACCACCACCAC									
Consensus	CTCTCAGATGTCTATGGGCTCAGACCCTGTCCCATAGGACTGTCCCATAGGACTGGAAATAGAACTactcgagcaccaccaccaccaccac									