

Multiples nucleotide sequence alignment of wtMth212 and Mth212/D151A (clone 1)

	1	10	20	30	40	50	60	70	80	90
Mth212_WT	ATGACCGTGCTAAAAATATATATCTTGGACGCTCAACGGCCTCAGGGCGGTCCACAGGAGGGGTTCTTAAATGGTTCATGGAAGAC									
Mth212D151A_clone1_F	ACCATG6CCGTGCTAAAAATATATATCTTGGACGCTCAACGGCCTCAGGGCGGTCCACAGGAGGGGTTCTTAAATGGTTCATGGAAGAC									
Mth212D151A_clone1_R	ACCATG6CCGTGCTAAAAATATATATCTTGGACGCTCAACGGCCTCAGGGCGGTCCACAGGAGGGGTTCTTAAATGGTTCATGGAAGAC									
Consensus	accATG6cCGTGCTAAAAATATATATCTTGGACGCTCAACGGCCTCAGGGCGGTCCACAGGAGGGGTTCTTAAATGGTTCATGGAAGAC									
	91	100	110	120	130	140	150	160	170	180
Mth212_WT	AAGCCAGACATCCTGTGCCCTTCAGGAGATAAAGCAGCGCCTGAACAGCTCCCGAGGAGCTCAGGCACGTTGAGGGTTACAGAGCTTC									
Mth212D151A_clone1_F	AAGCCAGACATCCTGTGCCCTTCAGGAGATAAAGCAGCGCCTGAACAGCTCCCGAGGAGCTCAGGCACGTTGAGGGTTACAGAGCTTC									
Mth212D151A_clone1_R	AAGCCAGACATCCTGTGCCCTTCAGGAGATAAAGCAGCGCCTGAACAGCTCCCGAGGAGCTCAGGCACGTTGAGGGTTACAGAGCTTC									
Consensus	AAGCCAGACATCCTGTGCCCTTCAGGAGATAAAGCAGCGCCTGAACAGCTCCCGAGGAGCTCAGGCACGTTGAGGGTTACAGAGCTTC									
	181	190	200	210	220	230	240	250	260	270
Mth212_WT	TTCACCCCTGCGGAGAGAAAGGGGTACAGCGGGGTTGCCATGTACACAAAGGTACCCCCCTTCTACTGAGGGAGGGGTTTCGGTGTGGAG									
Mth212D151A_clone1_F	TTCACCCCTGCGGAGAGAAAGGGGTACAGCGGGGTTGCCATGTACACAAAGGTACCCCCCTTCTACTGAGGGAGGGGTTTCGGTGTGGAG									
Mth212D151A_clone1_R	TTCACCCCTGCGGAGAGAAAGGGGTACAGCGGGGTTGCCATGTACACAAAGGTACCCCCCTTCTACTGAGGGAGGGGTTTCGGTGTGGAG									
Consensus	TTCACCCCTGCGGAGAGAAAGGGGTACAGCGGGGTTGCCATGTACACAAAGGTACCCCCCTTCTACTGAGGGAGGGGTTTCGGTGTGGAG									
	271	280	290	300	310	320	330	340	350	360
Mth212_WT	AGATTTCGACACCGAGGGTCGGATACAGATCGCAGACTTTGACGACTTCCTCCTTACACATATACTTCCCACGGTAGAGTGTACAGAG									
Mth212D151A_clone1_F	AGATTTCGACACCGAGGGTCGGATACAGATCGCAGACTTTGACGACTTCCTCCTTACACATATACTTCCCACGGTAGAGTGTACAGAG									
Mth212D151A_clone1_R	AGATTTCGACACCGAGGGTCGGATACAGATCGCAGACTTTGACGACTTCCTCCTTACACATATACTTCCCACGGTAGAGTGTACAGAG									
Consensus	AGATTTCGACACCGAGGGTCGGATACAGATCGCAGACTTTGACGACTTCCTCCTTACACATATACTTCCCACGGTAGAGTGTACAGAG									
	361	370	380	390	400	410	420	430	440	450
Mth212_WT	GAGAGGCTGAAGTATAAATCGGAATTCATGACGATTCTCTGAGGACGTCACCGGAGAGGGGATTCGGGGAGGAGACGTGATTATATGT									
Mth212D151A_clone1_F	GAGAGGCTGAAGTATAAATCGGAATTCATGACGATTCTCTGAGGACGTCACCGGAGAGGGGATTCGGGGAGGAGACGTGATTATATGT									
Mth212D151A_clone1_R	GAGAGGCTGAAGTATAAATCGGAATTCATGACGATTCTCTGAGGACGTCACCGGAGAGGGGATTCGGGGAGGAGACGTGATTATATGT									
Consensus	GAGAGGCTGAAGTATAAATCGGAATTCATGACGATTCTCTGAGGACGTCACCGGAGAGGGGATTCGGGGAGGAGACGTGATTATATGT									
	451	460	470	480	490	500	510	520	530	540
Mth212_WT	GGGGACTTCACACAGCCCCACAGGGAGATAGACTTTCARAGGCCAAGAGGAACAGCAGCATACAGGTTTCCTCCCGTTGAGAGGGCC									
Mth212D151A_clone1_F	GGGGCAATTCACACAGCCCCACAGGGAGATAGACTTTCARAGGCCAAGAGGAACAGCAGCATACAGGTTTCCTCCCGTTGAGAGGGCC									
Mth212D151A_clone1_R	GGGGCAATTCACACAGCCCCACAGGGAGATAGACTTTCARAGGCCAAGAGGAACAGCAGCATACAGGTTTCCTCCCGTTGAGAGGGCC									
Consensus	GGGGcaATTCACACAGCCCCACAGGGAGATAGACTTTCARAGGCCAAGAGGAACAGCAGCATACAGGTTTCCTCCCGTTGAGAGGGCC									
	541	550	560	570	580	590	600	610	620	630
Mth212_WT	TGGATCGATAAATTTATTGAATGGGTACGTGGACACCTTCAGGATGTTCAACAGTGACCCGGACAGTACACATGGTGGAGCTACAGG									
Mth212D151A_clone1_F	TGGATCGATAAATTTATTGAATGGGTACGTGGACACCTTCAGGATGTTCAACAGTGACCCGGACAGTACACATGGTGGAGCTACAGG									
Mth212D151A_clone1_R	TGGATCGATAAATTTATTGAATGGGTACGTGGACACCTTCAGGATGTTCAACAGTGACCCGGACAGTACACATGGTGGAGCTACAGG									
Consensus	TGGATCGATAAATTTATTGAATGGGTACGTGGACACCTTCAGGATGTTCAACAGTGACCCGGACAGTACACATGGTGGAGCTACAGG									
	631	640	650	660	670	680	690	700	710	720
Mth212_WT	ACAGGGGCCCGTGAGAGGACGTCGGCTGGAGACTCGACTACTTCTTTGTAACAGGAGGTTCAAGGGGAGGTTAAAGGTCCTGGATA									
Mth212D151A_clone1_F	ACAGGGGCCCGTGAGAGGACGTCGGCTGGAGACTCGACTACTTCTTTGTAACAGGAGGTTCAAGGGGAGGTTAAAGGTCCTGGATA									
Mth212D151A_clone1_R	ACAGGGGCCCGTGAGAGGACGTCGGCTGGAGACTCGACTACTTCTTTGTAACAGGAGGTTCAAGGGGAGGTTAAAGGTCCTGGATA									
Consensus	ACAGGGGCCCGTGAGAGGACGTCGGCTGGAGACTCGACTACTTCTTTGTAACAGGAGGTTCAAGGGGAGGTTAAAGGTCCTGGATA									
	721	730	740	750	760	770	780	790	798	
Mth212_WT	CTCTCAGATGTCATGGGCTCAGACCACCTGTCCATAGGACTGGAATAGAACTATAA									
Mth212D151A_clone1_F	CTCTCAGATGTCATGGGCTCAGACCACCTGTCCATAGGACTGGAATAGAACTCTCAGGACACCACCACCACCACCAC									
Mth212D151A_clone1_R	CTCTCAGATGTCATGGGCTCAGACCACCTGTCCATAGGACTGGAATAGAACTCTCAGGACACCACCACCACCACCAC									
Consensus	CTCTCAGATGTCATGGGCTCAGACCACCTGTCCATAGGACTGGAATAGAACTctCgagcaccaccaccaccaccac									