

Multiples nucleotide sequence alignment of wtMth212 and Mth212/D151A (clone 4)

	1	10	20	30	40	50	60	70	80	90
Mth212_WT	ATGACCGTGC TAAAAATAATATCTCGAACGCTCAACGGCCTCAGGGCGGTCCACAGGAGGGGGTTCCTTAATGTTTCATGGAGAG									
Mth212D151A_clone4_F	ACCATGGCCGTGC TAAAAATAATATCTCGAACGCTCAACGGCCTCAGGGCGGTCCACAGGAGGGGGTTCCTTAATGTTTCATGGAGAG									
Mth212D151A_clone4_R	ACCATGGCCGTGC TAAAAATAATATCTCGAACGCTCAACGGCCTCAGGGCGGTCCACAGGAGGGGGTTCCTTAATGTTTCATGGAGAG									
Consensus	accATGgCCGTGC TAAAAATAATATCTCGAACGCTCAACGGCCTCAGGGCGGTCCACAGGAGGGGGTTCCTTAATGTTTCATGGAGAG									
	91	100	110	120	130	140	150	160	170	180
Mth212_WT	AAGCCAGACATCCTGTGCTTCAGGAGATAAAGCAGCGCCTGACACGCTCCCGAGGAGCTCAGGCACGTTGAGGGTTACAGAGCTTC									
Mth212D151A_clone4_F	AAGCCAGACATCCTGTGCTTCAGGAGATAAAGCAGCGCCTGACACGCTCCCGAGGAGCTCAGGCACGTTGAGGGTTACAGAGCTTC									
Mth212D151A_clone4_R	AAGCCAGACATCCTGTGCTTCAGGAGATAAAGCAGCGCCTGACACGCTCCCGAGGAGCTCAGGCACGTTGAGGGTTACAGAGCTTC									
Consensus	AAGCCAGACATCCTGTGCTTCAGGAGATAAAGCAGCGCCTGACACGCTCCCGAGGAGCTCAGGCACGTTGAGGGTTACAGAGCTTC									
	181	190	200	210	220	230	240	250	260	270
Mth212_WT	TTCACCCCTGCGGAGAGAAAGGGGTACAGCGGGGTTGCCATGTACACAAAGGTACCCCCCTTCTACTGAGGGAGGGGTTTCGGTGTGGAG									
Mth212D151A_clone4_F	TTCACCCCTGCGGAGAGAAAGGGGTACAGCGGGGTTGCCATGTACACAAAGGTACCCCCCTTCTACTGAGGGAGGGGTTTCGGTGTGGAG									
Mth212D151A_clone4_R	TTCACCCCTGCGGAGAGAAAGGGGTACAGCGGGGTTGCCATGTACACAAAGGTACCCCCCTTCTACTGAGGGAGGGGTTTCGGTGTGGAG									
Consensus	TTCACCCCTGCGGAGAGAAAGGGGTACAGCGGGGTTGCCATGTACACAAAGGTACCCCCCTTCTACTGAGGGAGGGGTTTCGGTGTGGAG									
	271	280	290	300	310	320	330	340	350	360
Mth212_WT	AGATTGCACACCGAGGGTCGGATACAGATCGCAGACTTTGACGACTTCCTCCTCTACACATATACTTCCCAACCGGTAGATGTCAGAG									
Mth212D151A_clone4_F	AGATTGCACACCGAGGGTCGGATACAGATCGCAGACTTTGACGACTTCCTCCTCTACACATATACTTCCCAACCGGTAGATGTCAGAG									
Mth212D151A_clone4_R	AGATTGCACACCGAGGGTCGGATACAGATCGCAGACTTTGACGACTTCCTCCTCTACACATATACTTCCCAACCGGTAGATGTCAGAG									
Consensus	AGATTGCACACCGAGGGTCGGATACAGATCGCAGACTTTGACGACTTCCTCCTCTACACATATACTTCCCAACCGGTAGATGTCAGAG									
	361	370	380	390	400	410	420	430	440	450
Mth212_WT	GAGAGGCTGAAGTATARAATGGAAATTCATGACGCATTCTTGAGGACGTCACCGGGAGAGGGGATTCGGGGAGGAACTGATTATATGT									
Mth212D151A_clone4_F	GAGAGGCTGAAGTATARAATGGAAATTCATGACGCATTCTTGAGGACGTCACCGGGAGAGGGGATTCGGGGAGGAACTGATTATATGT									
Mth212D151A_clone4_R	GAGAGGCTGAAGTATARAATGGAAATTCATGACGCATTCTTGAGGACGTCACCGGGAGAGGGGATTCGGGGAGGAACTGATTATATGT									
Consensus	GAGAGGCTGAAGTATARAATGGAAATTCATGACGCATTCTTGAGGACGTCACCGGGAGAGGGGATTCGGGGAGGAACTGATTATATGT									
	451	460	470	480	490	500	510	520	530	540
Mth212_WT	GGGGAC TTCAACACAGCCACAGGGAGATAGACCTTGCAGGGCCAAAGGAAACAGCAGCTATCAGGTTTCCTTCCCGTTGAGAGGGCC									
Mth212D151A_clone4_F	GGGGCATTCAACACAGCCACAGGGAGATAGACCTTGCAGGGCCAAAGGAAACAGCAGCTATCAGGTTTCCTTCCCGTTGAGAGGGCC									
Mth212D151A_clone4_R	GGGGCATTCAACACAGCCACAGGGAGATAGACCTTGCAGGGCCAAAGGAAACAGCAGCTATCAGGTTTCCTTCCCGTTGAGAGGGCC									
Consensus	GGGGcaTTCAACACAGCCACAGGGAGATAGACCTTGCAGGGCCAAAGGAAACAGCAGCTATCAGGTTTCCTTCCCGTTGAGAGGGCC									
	541	550	560	570	580	590	600	610	620	630
Mth212_WT	TGGATCGATAAATTTATTGAAATGGGTACGTGGACACCTTCAGGATGTTCAACAGTGACCCGGACAGTACACATGGTGGAGCTACAGG									
Mth212D151A_clone4_F	TGGATCGATAAATTTATTGAAATGGGTACGTGGACACCTTCAGGATGTTCAACAGTGACCCGGACAGTACACATGGTGGAGCTACAGG									
Mth212D151A_clone4_R	TGGATCGATAAATTTATTGAAATGGGTACGTGGACACCTTCAGGATGTTCAACAGTGACCCGGACAGTACACATGGTGGAGCTACAGG									
Consensus	TGGATCGATAAATTTATTGAAATGGGTACGTGGACACCTTCAGGATGTTCAACAGTGACCCGGACAGTACACATGGTGGAGCTACAGG									
	631	640	650	660	670	680	690	700	710	720
Mth212_WT	ACAGGGGCCCGTGAGAGGAGACGTCGCTGGAGACTCGACTACTTCTTTGTAACGAGGAGTTCAAGGGGAGGTTAAAGGTCCTGGATA									
Mth212D151A_clone4_F	ACAGGGGCCCGTGAGAGGAGACGTCGCTGGAGACTCGACTACTTCTTTGTAACGAGGAGTTCAAGGGGAGGTTAAAGGTCCTGGATA									
Mth212D151A_clone4_R	ACAGGGGCCCGTGAGAGGAGACGTCGCTGGAGACTCGACTACTTCTTTGTAACGAGGAGTTCAAGGGGAGGTTAAAGGTCCTGGATA									
Consensus	ACAGGGGCCCGTGAGAGGAGACGTCGCTGGAGACTCGACTACTTCTTTGTAACGAGGAGTTCAAGGGGAGGTTAAAGGTCCTGGATA									
	721	730	740	750	760	770	780	790	798	
Mth212_WT	CTCTCAGATGTCATGGGCTCAGACCACTGTCCATAGGACTGGAATAGACTATTA									
Mth212D151A_clone4_F	CTCTCAGATGTCATGGGCTCAGACCACTGTCCATAGGACTGGAATAGACTATCTCAGACCAACCAACCAACCAAC									
Mth212D151A_clone4_R	CTCTCAGATGTCATGGGCTCAGACCACTGTCCATAGGACTGGAATAGACTATCTCAGACCAACCAACCAACCAAC									
Consensus	CTCTCAGATGTCATGGGCTCAGACCACTGTCCATAGGACTGGAATAGACTctcagacacacacacacacacac									