

Multiples nucleotide sequence alignment of wtMth212 and Mth212/D151A (clone 3)

	1	10	20	30	40	50	60	70	80	90
Mth212_UT	----- ----- ----- ----- ----- ----- ----- ----- ----- -----									
Mth212D151A_clone3_F	ATGACCGTGTCTAAAAATAATATCTCTGGACGCTCAACGGCCTCAGGGCGGTCCACAGGAAGGGGTTCTTAATAGGTTTCATGGAAGAG									
Mth212D151A_clone3_R	ACCATGCGCGTGTCTAAAAATAATATCTCTGGACGCTCAACGGCCTCAGGGCGGTCCACAGGAAGGGGTTCTTAATAGGTTTCATGGAAGAG									
Consensus	accATgCGCGTGTCTAAAAATAATATCTCTGGACGCTCAACGGCCTCAGGGCGGTCCACAGGAAGGGGTTCTTAATAGGTTTCATGGAAGAG									
	91	100	110	120	130	140	150	160	170	180
Mth212_UT	----- ----- ----- ----- ----- ----- ----- ----- ----- -----									
Mth212D151A_clone3_F	AAGCCAGACATCTCTGTGCCCTCAGGAGATAAAGCAGCGCCTGACAGCTCCCCAGGAAGCTCAGGCACGTTGAGGGTTACAGAGCTTC									
Mth212D151A_clone3_R	AAGCCAGACATCTCTGTGCCCTCAGGAGATAAAGCAGCGCCTGACAGCTCCCCAGGAAGCTCAGGCACGTTGAGGGTTACAGAGCTTC									
Consensus	AAGCCAGACATCTCTGTGCCCTCAGGAGATAAAGCAGCGCCTGACAGCTCCCCAGGAAGCTCAGGCACGTTGAGGGTTACAGAGCTTC									
	181	190	200	210	220	230	240	250	260	270
Mth212_UT	----- ----- ----- ----- ----- ----- ----- ----- ----- -----									
Mth212D151A_clone3_F	TTCACCCCTGCGGAGAGAAAGGGGTACAGCGGGGTTGCCATGTACACAAAGGTACCCCCCTCTTCACTGAGGGAGGGTTCCGGTGTGGAG									
Mth212D151A_clone3_R	TTCACCCCTGCGGAGAGAAAGGGGTACAGCGGGGTTGCCATGTACACAAAGGTACCCCCCTCTTCACTGAGGGAGGGTTCCGGTGTGGAG									
Consensus	TTCACCCCTGCGGAGAGAAAGGGGTACAGCGGGGTTGCCATGTACACAAAGGTACCCCCCTCTTCACTGAGGGAGGGTTCCGGTGTGGAG									
	271	280	290	300	310	320	330	340	350	360
Mth212_UT	----- ----- ----- ----- ----- ----- ----- ----- ----- -----									
Mth212D151A_clone3_F	AGATTTCGACACCGAGGGTCGGATACAGATCGCAGACTTTGACGACTTCCTCCTTACACATATACTTCCCCAACGGTAGAGTGTACAGAG									
Mth212D151A_clone3_R	AGATTTCGACACCGAGGGTCGGATACAGATCGCAGACTTTGACGACTTCCTCCTTACACATATACTTCCCCAACGGTAGAGTGTACAGAG									
Consensus	AGATTTCGACACCGAGGGTCGGATACAGATCGCAGACTTTGACGACTTCCTCCTTACACATATACTTCCCCAACGGTAGAGTGTACAGAG									
	361	370	380	390	400	410	420	430	440	450
Mth212_UT	----- ----- ----- ----- ----- ----- ----- ----- ----- -----									
Mth212D151A_clone3_F	GAGAGGCTGAGGTATTAAC TGGAA TTTCTATGACGCATTCTT TGAGGACGCTCAACCGGGAGAGGGATTTCGGGGAGGAGACGTGATTATATGT									
Mth212D151A_clone3_R	GAGAGGCTGAGGTATTAAC TGGAA TTTCTATGACGCATTCTT TGAGGACGCTCAACCGGGAGAGGGATTTCGGGGAGGAGACGTGATTATATGT									
Consensus	GAGAGGCTGAGGTATTAAC TGGAA TTTCTATGACGCATTCTT TGAGGACGCTCAACCGGGAGAGGGATTTCGGGGAGGAGACGTGATTATATGT									
	451	460	470	480	490	500	510	520	530	540
Mth212_UT	----- ----- ----- ----- ----- ----- ----- ----- ----- -----									
Mth212D151A_clone3_F	GGGGAC TTTCAACACAGCCACAGGGAGATAGACCTTGCAAGGCCAAGGAAACAGCACGATACAGGTTCTCTCCCGTTGAGAGGGCC									
Mth212D151A_clone3_R	GGGGCA TTTCAACACAGCCACAGGGAGATAGACCTTGCAAGGCCAAGGAAACAGCACGATACAGGTTCTCTCCCGTTGAGAGGGCC									
Consensus	GGGGCa TTTCAACACAGCCACAGGGAGATAGACCTTGCAAGGCCAAGGAAACAGCACGATACAGGTTCTCTCCCGTTGAGAGGGCC									
	541	550	560	570	580	590	600	610	620	630
Mth212_UT	----- ----- ----- ----- ----- ----- ----- ----- ----- -----									
Mth212D151A_clone3_F	TGGATCGATAAATTTATTGAAATGGGTACGTGGACACCTTCAGGATGTTCAACAGTGACCCCGGACAGTACACATGGTGGAGCTACAGG									
Mth212D151A_clone3_R	TGGATCGATAAATTTATTGAAATGGGTACGTGGACACCTTCAGGATGTTCAACAGTGACCCCGGACAGTACACATGGTGGAGCTACAGG									
Consensus	TGGATCGATAAATTTATTGAAATGGGTACGTGGACACCTTCAGGATGTTCAACAGTGACCCCGGACAGTACACATGGTGGAGCTACAGG									
	631	640	650	660	670	680	690	700	710	720
Mth212_UT	----- ----- ----- ----- ----- ----- ----- ----- ----- -----									
Mth212D151A_clone3_F	ACAGGGGCCCGTGAGAGGAGACGTCCGCTGGAGACTCGACTACTCTTTGTAAACAGGAGGTTCAAGGGGAGGTTAAAGGTCCTGGATA									
Mth212D151A_clone3_R	ACAGGGGCCCGTGAGAGGAGACGTCCGCTGGAGACTCGACTACTCTTTGTAAACAGGAGGTTCAAGGGGAGGTTAAAGGTCCTGGATA									
Consensus	ACAGGGGCCCGTGAGAGGAGACGTCCGCTGGAGACTCGACTACTCTTTGTAAACAGGAGGTTCAAGGGGAGGTTAAAGGTCCTGGATA									
	721	730	740	750	760	770	780	790	798	
Mth212_UT	----- ----- ----- ----- ----- ----- ----- ----- ----- -----									
Mth212D151A_clone3_F	CTCTCAGATGTCATGGGCTCAGACCACTGTCCCATAGGACTGGAATAGAACTACTCGAGCACCCACCACCACCACCAC									
Mth212D151A_clone3_R	CTCTCAGATGTCATGGGCTCAGACCACTGTCCCATAGGACTGGAATAGAACTACTCGAGCACCCACCACCACCACCAC									
Consensus	CTCTCAGATGTCATGGGCTCAGACCACTGTCCCATAGGACTGGAATAGAACTActcgagcaccaccaccaccaccac									