

Multiples nucleotide sequence alignment of wtMth212 and Mth212/D151S (clone 1)

	1	10	20	30	40	50	60	70	80	90
Mth212_WT	ATGACCGTGC TAAAAATAATATCTCGGACGTCACGGCCTCAGGGCGGTCCACAGGAAGGGGTTCCCTTAATGGTTTCATGGAGAG									
Mth212D151S_clone1_F	ACCATGCGCGTGC TAAAAATAATATCTCGGACGTCACGGCCTCAGGGCGGTCCACAGGAAGGGGTTCCCTTAATGGTTTCATGGAGAG									
Mth212D151S_clone1_R	ACCATGCGCGTGC TAAAAATAATATCTCGGACGTCACGGCCTCAGGGCGGTCCACAGGAAGGGGTTCCCTTAATGGTTTCATGGAGAG									
Consensus	accATGgCCGTGCTAAAAATAATATCTCGGACGTCACGGCCTCAGGGCGGTCCACAGGAAGGGGTTCCCTTAATGGTTTCATGGAGAG									
	91	100	110	120	130	140	150	160	170	180
Mth212_WT	AAGCCAGACATCCTGTGCTTCAGGAGATAAAGCAGCGCCTGACACAGCTCCCGAGGAGCTCAGGCACGTTGAGGGTTACAGAACTTC									
Mth212D151S_clone1_F	AAGCCAGACATCCTGTGCTTCAGGAGATAAAGCAGCGCCTGACACAGCTCCCGAGGAGCTCAGGCACGTTGAGGGTTACAGAACTTC									
Mth212D151S_clone1_R	AAGCCAGACATCCTGTGCTTCAGGAGATAAAGCAGCGCCTGACACAGCTCCCGAGGAGCTCAGGCACGTTGAGGGTTACAGAACTTC									
Consensus	AAGCCAGACATCCTGTGCTTCAGGAGATAAAGCAGCGCCTGACACAGCTCCCGAGGAGCTCAGGCACGTTGAGGGTTACAGAACTTC									
	181	190	200	210	220	230	240	250	260	270
Mth212_WT	TTCACCCCTCGGGAGAGAAAGGGGTACAGCGGGGTTGCCATGTACACAAAGGTACCCCCCTTCTACTGAGGGAGGGGTTTCGGTGTGGAG									
Mth212D151S_clone1_F	TTCACCCCTCGGGAGAGAAAGGGGTACAGCGGGGTTGCCATGTACACAAAGGTACCCCCCTTCTACTGAGGGAGGGGTTTCGGTGTGGAG									
Mth212D151S_clone1_R	TTCACCCCTCGGGAGAGAAAGGGGTACAGCGGGGTTGCCATGTACACAAAGGTACCCCCCTTCTACTGAGGGAGGGGTTTCGGTGTGGAG									
Consensus	TTCACCCCTCGGGAGAGAAAGGGGTACAGCGGGGTTGCCATGTACACAAAGGTACCCCCCTTCTACTGAGGGAGGGGTTTCGGTGTGGAG									
	271	280	290	300	310	320	330	340	350	360
Mth212_WT	AGATTTCGACACCGAGGGTCGGATACAGATCGCAGACTTTGACGACTTCCTCCTCTACACATATACTTCCACACGGTAGATGTCAGAG									
Mth212D151S_clone1_F	AGATTTCGACACCGAGGGTCGGATACAGATCGCAGACTTTGACGACTTCCTCCTCTACACATATACTTCCACACGGTAGATGTCAGAG									
Mth212D151S_clone1_R	AGATTTCGACACCGAGGGTCGGATACAGATCGCAGACTTTGACGACTTCCTCCTCTACACATATACTTCCACACGGTAGATGTCAGAG									
Consensus	AGATTTCGACACCGAGGGTCGGATACAGATCGCAGACTTTGACGACTTCCTCCTCTACACATATACTTCCACACGGTAGATGTCAGAG									
	361	370	380	390	400	410	420	430	440	450
Mth212_WT	GAGAGGCTGAAGTATARAAC TGGAAATTCATGACGATTCTTGAGGACGTCACCGGAGAGGGGATTCTGGGGAGGAACTGATTATATGT									
Mth212D151S_clone1_F	GAGAGGCTGAAGTATARAAC TGGAAATTCATGACGATTCTTGAGGACGTCACCGGAGAGGGGATTCTGGGGAGGAACTGATTATATGT									
Mth212D151S_clone1_R	GAGAGGCTGAAGTATARAAC TGGAAATTCATGACGATTCTTGAGGACGTCACCGGAGAGGGGATTCTGGGGAGGAACTGATTATATGT									
Consensus	GAGAGGCTGAAGTATARAAC TGGAAATTCATGACGATTCTTGAGGACGTCACCGGAGAGGGGATTCTGGGGAGGAACTGATTATATGT									
	451	460	470	480	490	500	510	520	530	540
Mth212_WT	GGGAGCTTCACACAGCCACAGGGAGATAGACCTTGCAGGCGCAAGGGAACAGCAGCTATCAGGTTTCCTCCCGTTGAGAGGGGCC									
Mth212D151S_clone1_F	GGGAGCTTCACACAGCCACAGGGAGATAGACCTTGCAGGCGCAAGGGAACAGCAGCTATCAGGTTTCCTCCCGTTGAGAGGGGCC									
Mth212D151S_clone1_R	GGGAGCTTCACACAGCCACAGGGAGATAGACCTTGCAGGCGCAAGGGAACAGCAGCTATCAGGTTTCCTCCCGTTGAGAGGGGCC									
Consensus	GGGAGCTTCACACAGCCACAGGGAGATAGACCTTGCAGGCGCAAGGGAACAGCAGCTATCAGGTTTCCTCCCGTTGAGAGGGGCC									
	541	550	560	570	580	590	600	610	620	630
Mth212_WT	TGGATCGATAAATTTATTGAAATGGGTACGTGGACACCTTCAGGATGTTCAACAGTGACCCCGGACAGTACACATGGTGGAGCTACAGG									
Mth212D151S_clone1_F	TGGATCGATAAATTTATTGAAATGGGTACGTGGACACCTTCAGGATGTTCAACAGTGACCCCGGACAGTACACATGGTGGAGCTACAGG									
Mth212D151S_clone1_R	TGGATCGATAAATTTATTGAAATGGGTACGTGGACACCTTCAGGATGTTCAACAGTGACCCCGGACAGTACACATGGTGGAGCTACAGG									
Consensus	TGGATCGATAAATTTATTGAAATGGGTACGTGGACACCTTCAGGATGTTCAACAGTGACCCCGGACAGTACACATGGTGGAGCTACAGG									
	631	640	650	660	670	680	690	700	710	720
Mth212_WT	ACAGGGGCCCGTGAGAGGAGACGTCGGCTGGAGACTCGACTACTTCTTTGTAAACAGGAGGTTCAAGGGAGAGGTTAAAGGCTCCTGGATA									
Mth212D151S_clone1_F	ACAGGGGCCCGTGAGAGGAGACGTCGGCTGGAGACTCGACTACTTCTTTGTAAACAGGAGGTTCAAGGGAGAGGTTAAAGGCTCCTGGATA									
Mth212D151S_clone1_R	ACAGGGGCCCGTGAGAGGAGACGTCGGCTGGAGACTCGACTACTTCTTTGTAAACAGGAGGTTCAAGGGAGAGGTTAAAGGCTCCTGGATA									
Consensus	ACAGGGGCCCGTGAGAGGAGACGTCGGCTGGAGACTCGACTACTTCTTTGTAAACAGGAGGTTCAAGGGAGAGGTTAAAGGCTCCTGGATA									
	721	730	740	750	760	770	780	790	798	
Mth212_WT	CTCTCAGATGTCATGGGCTCAGACCACTGTCCCATAGGACTGGAATAGACTATTA									
Mth212D151S_clone1_F	CTCTCAGATGTCATGGGCTCAGACCACTGTCCCATAGGACTGGAATAGACTATCTCAGGACCAACCAACCAACCAAC									
Mth212D151S_clone1_R	CTCTCAGATGTCATGGGCTCAGACCACTGTCCCATAGGACTGGAATAGACTATCTCAGGACCAACCAACCAACCAAC									
Consensus	CTCTCAGATGTCATGGGCTCAGACCACTGTCCCATAGGACTGGAATAGACTATctcagaccaccaccaccaccaccac									