

A

Gene Name	Cell Line	Amplicon size bp	alignment	Gaps
MUC4-6 Forward	CCD841	180bp	MUC4-6 - CCD841 Amplicon Forward MUC4-6 Isoform	<div>Matrix: DNAFULL Gap open penalty: 10.0 Gap extend penalty: 1.0</div> <div>Length: 242 Identity: 227 / 242 (93.80%) Gaps: 0 / 242 (0.00%)</div>
			MUC4-6 - CCD841 Amplicon Forward MUC4-6 Isoform	
			MUC4-6 - CCD841 Amplicon Forward MUC4-6 Isoform	
MUC4-6 Forward	CCD841	320bp	MUC4-6 - CCD841 Amplicon Forward MUC4-6 Isoform	<div>Matrix: DNAFULL Gap open penalty: 10.0 Gap extend penalty: 1.0</div> <div>Length: 269 Identity: 256 / 269 (95.17 %) Gaps: 0 / 269 (0.00%)</div>
			MUC4-6 - CCD841 Amplicon Forward MUC4-6 Isoform	
			MUC4-6 - CCD841 Amplicon Forward MUC4-6 Isoform	
MUC4-6 Forward	SW480	180bp	MUC4-6 - SW480 Amplicon Forward MUC4-6 Isoform	<div>Matrix: DNAFULL Gap open penalty: 10.0 Gap extend penalty: 1.0</div> <div>Length: 145 Identity: 143 / 145 (98.62%) Gaps: 1 / 145 (0.69%)</div>
			MUC4-6 - SW480 Amplicon Forward MUC4-6 Isoform	
			MUC4-6 - SW480 Amplicon Forward MUC4-6 Isoform	
MUC4-6 Forward	SW480	320bp	MUC4-6 - SW480 Amplicon Forward MUC4-6 Isoform	<div>Matrix: DNAFULL Gap open penalty: 10.0 Gap extend penalty: 1.0</div> <div>Length: 245 Identity: 195 / 245 (79.59%) Gaps: 18 / 245 (7.35%)</div>
			MUC4-6 - SW480 Amplicon Forward MUC4-6 Isoform	
			MUC4-6 - SW480 Amplicon Forward MUC4-6 Isoform	
MUC4-6 Forward	SW620	180bp	MUC4-6 - SW620 Amplicon Forward MUC4-6 Isoform	<div>Matrix: DNAFULL Gap open penalty: 10.0 Gap extend penalty: 1.0</div> <div>Length: 228 Identity: 208 / 228 (92.04%) Gaps: 2 / 228 (0.88%)</div>
			MUC4-6 - SW620 Amplicon Forward MUC4-6 Isoform	
			MUC4-6 - SW620 Amplicon Forward MUC4-6 Isoform	
MUC4-6 Reverse	SW620	180bp	MUC4-6 - SW620 Amplicon Reverse MUC4-6 Isoform	<div>Matrix: DNAFULL Gap open penalty: 10.0 Gap extend penalty: 1.0</div> <div>Length: 144 Identity: 139 / 144 (96.53%) Gaps: 0 / 144 (0.00%)</div>
			MUC4-6 - SW620 Amplicon Reverse MUC4-6 Isoform	
			MUC4-6 - SW620 Amplicon Reverse MUC4-6 Isoform	
MUC4-6 Forward	SW620	320bp	MUC4-6 - SW620 Amplicon Forward MUC4-6 Isoform	<div>Matrix: DNAFULL Gap open penalty: 10.0 Gap extend penalty: 1.0</div> <div>Length: 123 Identity: 121 / 123 (98.37%) Gaps: 0 / 123 (0.00%)</div>
			MUC4-6 - SW620 Amplicon Forward MUC4-6 Isoform	
			MUC4-6 - SW620 Amplicon Forward MUC4-6 Isoform	
MUC4-6 Reverse	SW620	320bp	MUC4-6 - SW620 Amplicon Reverse MUC4-6 Isoform	<div>Matrix: DNAFULL Gap open penalty: 10.0 Gap extend penalty: 1.0</div> <div>Length: 139 Identity: 129 / 139 (92.81%) Gaps: 1 / 139 (0.72%)</div>
			MUC4-6 - SW620 Amplicon Reverse MUC4-6 Isoform	
			MUC4-6 - SW620 Amplicon Reverse MUC4-6 Isoform	

B

Gene Name	Cell Line	Amplicon size bp	alignment		Gaps	
MUC4-1 Forward	CCD841	282bp	MUC4-1 - CCD841 Amplicon Forward MUC4-1 Isoform	1 ACACCTTACTGAGCATCCACAGGACACGCCACCTCTCTTCTGTCAACCGACACTTCTCTCAGTTCACACAGGTGACGCCACCCCTCTTCTGTCAACCGACAC 3489 3390 ACACCTTCTCTGAGCATCCACAGGTACGCCACCTCTCTTCTGTCAACCGACACTTCTCTCAGTTCACACAGGTGACGCCACCCCTCTTCTGTCAACCGACAC 3489 3390 3400 3410 3420 3430 3440 3450 3460 3470 3480	Matrix: DNAFULL Gap open penalty: 10.0 Gap extend penalty: 1.0 Length: 166 Identity: 158 / 166 (95.18 %) Gaps: 0 / 166 (0.00 %)	
			MUC4-1 - CCD841 Amplicon Forward MUC4-1 Isoform	101 TTCTCTCAGCATCCACAGGTACGCCACCTCTCTTCTGTCAACCGACACTTCTCTCAGTATGACAGG 166 3490 TTCTCTCAGCATCCACAGGTACGCCACCTCTCTTCTGTCAACCGACACTTCTCTCAGTATGACAGG 3555 3490 3500 3510 3520 3530 3540 3550		
MUC4-1 Forward	CCD841	240bp	MUC4-1 - CCD841 Amplicon Forward MUC4-1 Isoform	1 TCTTTCTGTGA-CGACACTTTCCTCAGTATCCACAGGTACGCCACCTCTCTTCTGTCAACCGACCTTCTCTCAGTGTCCACAGGTGACGCCACCCCTCTT 99 5968 TCTTTCTGTGTCAACCGACTTCTCTCAGTATCCACAGGTACGCCACCTCTCTTCTGTCAACCGACCTTCTCTCAGTGTCCACAGGTGACGCCACCCCTCTT 6067 5970 5980 5990 6000 6010 6020 6030 6040 6050 6060	Matrix: DNAFULL Gap open penalty: 10.0 Gap extend penalty: 1.0 Length: 197 Identity: 191 / 197 (96.95%) Gaps: 1 / 197 (0.51 %)	
			MUC4-1 - CCD841 Amplicon Forward MUC4-1 Isoform	100 CCTGTCAACCGACACTTCTCTCAGTGTCCACAGGTACGCCACCTCTTCCGTGTCAACCGACACTTCTCTCAGTATGTACAGGACAATGCCACCCCTCTTCT 196 6068 CCTGTCAACCGACCTTCTCTCAGTGTCCACAGGTACGCCACCTCTTCCGTGTCAACCGACACTTCTCTCAGTATGTACAGGACAATGCCACCCCTCTTCT 6164 6070 6080 6090 6100 6110 6120 6130 6140 6150 6160		
MUC4-1 Reverse	CCD841	240bp	MUC4-1 - CCD841 Amplicon Reverse MUC4-1 Isoform	1 TCTCTCAGTGTCCACAGGTGACGCCACCTCTCTTCTGTGTACCGACACTTCTCTCAGGTTCACAGGTGACGCCACCTCTCTTCTGTGTACCGACACTTCTCT 100 6563 TCTCTCAGTGTCCACAGGTGACGCCACCTCTCTTCTGTGTACCGACACTTCTCTCAGGTTCACAGGTGACGCCACCTCTCTTCTGTGTACCGACACTTCTCT 6662 6570 6580 6590 6600 6610 6620 6630 6640 6650 6660	Matrix: DNAFULL Gap open penalty: 10.0 Gap extend penalty: 1.0 Length: 186 Identity: 171 / 186 (91.94%) Gaps: 0 / 186 (0.00%)	
			MUC4-1 - CCD841 Amplicon Reverse MUC4-1 Isoform	101 CAGCATCCACAGGTGATGCCACCCCTCTTCTGTGTCAACCGACACTTCTCTCAGGTATCCACAGGTGACGCCACCTCTTCTGTGTACCG 186 6663 CAGCATCCACAGGTGACGCCACCCCTCTTCTGTGTCAACCGACACTTCTCTCAGGTATCCACAGGTGACGCCACCTCTTCTGTGTACCG 6748 6670 6680 6690 6700 6710 6720 6730 6740		
MUC4-1 Forward	SW480	240bp	MUC4-1 - SW480 Amplicon Forward MUC4-1 Isoform	1 TCTTCTGTGTGA-CGACACTTTCCTCAGTATCCACAGGTACGCCACCTCTCTTCTGTGTACCGACCTTCTCTCAGTGTCCACAGGTGACGCCACCCCTCTT 99 5968 TCTTCTGTGTGAACCGACTTCTCTCAGTATCCACAGGTACGCCACCTCTCTTCTGTGTACCGACCTTCTCTCAGTGTCCACAGGTGACGCCACCCCTCTT 6067 5970 5980 5990 6000 6010 6020 6030 6040 6050 6060	Matrix: DNAFULL Gap open penalty: 10.0 Gap extend penalty: 1.0 Length: 197 Identity: 191 / 197 (96.95%) Gaps: 1 / 197 (0.51 %)	
			MUC4-1 - SW480 Amplicon Forward MUC4-1 Isoform	100 CCTGTCAACCGACACTTCTCTCAGTGTCCACAGGTACGCCACCCCTCTTCTGTGTCAACCGACACTTCTCTCAGTATGTACAGGACAATGCCACCCCTCTTCT 196 6068 CCTGTCAACCGACCTTCTCTCAGTGTCCACAGGTACGCCACCCCTCTTCTGTGTCAACCGACACTTCTCTCAGTATGTACAGGACAATGCCACCCCTCTTCT 6164 6070 6080 6090 6100 6110 6120 6130 6140 6150 6160		
MUC4-1 Forward	SW480	282bp	MUC4-1 - SW480 Amplicon Forward MUC4-1 Isoform	1 TCCACAGGTGACGCCACCCCTCTTCTGTGTACCGACACTTCTCTCAGTATCCACAGGTGATGCCACCTCTCTTCTGTGTCAACCGACACTTCTCTCAGTATCCA 100 3356 TCCACAGGTGACGCCACCCCTCTTCTGTGTACCGACACTTCTCTCAGTATCCACAGGTGATGCCACCTCTCTTCTGTGTCAACCGACACTTCTCTCAGTATCCA 3455 3360 3370 3380 3390 3400 3410 3420 3430 3440 3450	Matrix: DNAFULL Gap open penalty: 10.0 Gap extend penalty: 1.0 Length: 221 Identity: 206 / 221 (93.21 %) Gaps: 0 / 221 (0.00%)	
			MUC4-1 - SW480 Amplicon Forward MUC4-1 Isoform	101 CAGGACATGCCACCCCTCTTCAATGTCAACCGACACTTCTCTCAGTATCCACAGGTGATGCCACCTCTCTTCTGTGTCAACCGACACTTCTCTCAGTATCCA 200 3456 CAGGTGACGCCACCCCTCTTCTGTGTCAACCGACACTTCTCTCAGTATCCACAGGTGATGCCACCTCTCTTCTGTGTCAACCGACACTTCTCTCAGTATCCA 3555 3460 3470 3480 3490 3500 3510 3520 3530 3540 3550		
MUC4-1 Forward	SW480	282bp	MUC4-1 - SW480 Amplicon Forward MUC4-1 Isoform	201 ACACACACCCCTCTTCTATGT 221 3556 TACACACCCCTCTTCTATGT 3576 3560 3570		
MUC4-1 Reverse	SW620	282bp	MUC4-1 - SW620 Amplicon Forward MUC4-1 Isoform	1 TTCTCTCAGATCCACAGGTGACGCCACCCCTCTTCTGTGTACCGACACTTCTCTCAGTATCCACAGGTGACGCCACCTCTCTTCTGTGTACCGACACTTCT 100 8914 TTCTCTCAGATCCACAGGTGACGCCACCCCTCTTCTGTGTACCGACACTTCTCTCAGTATCCACAGGTGACGCCACCTCTCTTCTGTGTACCGACACTTCT 9013 8920 8930 8940 8950 8960 8970 8980 8990 9000 9010	Matrix: DNAFULL Gap open penalty: 10.0 Gap extend penalty: 1.0 Length: 379 Identity: 354 / 379 (93.40%) Gaps: 0 / 379 (0.00%)	
			MUC4-1 - SW620 Amplicon Forward MUC4-1 Isoform	101 TCAGCATCCACAGGTGACGCCACCCCTCTTCTGTGTCAACCGACACTTCTCTCAGTATCCACAGGTGATGCCACCCCTCTTCTGTGTCAACCGACACTTCTCTCAG 200 9014 TCAGCATCCACAGGTGACGCCACCCCTCTTCTGTGTCAACCGACACTTCTCTCAGTATCCACAGGTGATGCCACCCCTCTTCTGTGTCAACCGACACTTCTCTCAG 9113 9020 9030 9040 9050 9060 9070 9080 9090 9100 9110		
MUC4-1 Reverse	SW620	282bp	MUC4-1 - SW620 Amplicon Forward MUC4-1 Isoform	201 CATCCACAGGACATGCCACCCCTCTTCTGTGTCAACCGACACTTCTCTCAGTATCCACAGGTGATGCCACCCCTCTTCTGTGTCAACCGACACTTCTCTCAGCATC 300 9114 CATCCATAGGTGACGCCACCTCTTCTGTGTCAACCGACACTTCTCTCAGTATCCACAGGTGATGCCACCCCTCTTCTGTGTCAACCGACACTTCTCTCAGCATC 9213 9120 9130 9140 9150 9160 9170 9180 9190 9200 9210		
			MUC4-1 - SW620 Amplicon Forward MUC4-1 Isoform	301 CACAGGTGACGCCACCCCTCTTCTGTGTCAACCGACACTTCTCTCAGTATCCACAGGTGATGCCACCCCTCTTCTGTGTCAACCGACACTTCTCTCAGCATC 379 9214 CACGGTCAACCGACCCCTCTTCTGTGTCAACCGACACTTCTCTCAGTATCCACAGGTGATGCCACCCCTCTTCTGTGTCAACCGACACTTCTCTCAGCATC 9292 9220 9230 9240 9250 9260 9270 9280 9290		
MUC4-1 Reverse	SW620	282bp	MUC4-1 - SW620 Amplicon Reverse MUC4-1 Isoform	1 CACCACCTCTTCTGTGTGTGACCATCTCCTCTCTCAGTATCCACAGGTGACGCCACCCCTCTTCTGTGTGACCATCTCCTCTCTCAGTATCCACAGGTGACGCCAC 100 8839 CACCACCTCTTCTGTGTGTGACCATCTCCTCTCTCAGTATCCACAGGTGACGCCACCCCTCTTCTGTGTGACCATCTCCTCTCTCAGTATCCACAGGTGACGCCAC 8938 8840 8850 8860 8870 8880 8890 8900 8910 8920 8930	Matrix: DNAFULL Gap open penalty: 10.0 Gap extend penalty: 1.0 Length: 268 Identity: 249 / 268 (92.91 %) Gaps: 1 / 268 (0.37 %)	
			MUC4-1 - SW620 Amplicon Reverse MUC4-1 Isoform	101 ACCCTCTTCTGTGTGACCAACCTTCTCTCAGTATCCACAGGTGACGCCACCTCTTCTGTGTGACCAACCTTCTCTCAGTATCCACAGGTGACGCCACCC 200 8939 ACCCTCTTCTGTGTGACCAACCTTCTCTCAGTATCCACAGGTGACGCCACCTCTTCTGTGTGACCAACCTTCTCTCAGTATCCACAGGTGACGCCACCC 9038 8940 8950 8960 8970 8980 8990 9000 9010 9020 9030		
MUC4-1 Reverse	SW620	240bp	MUC4-1 - SW620 Amplicon Reverse MUC4-1 Isoform	201 CTCTTCTGTGTGACCAACCTTCTCTCAGTATCCACAGGTGACGCCACCTCTCTCTGTGTGTGACCAACCTTCTCTCAGTATCCACAGGTGACGCCACCTCTCTCTGTGTGACCAACCT 267 9039 CTCTTCTGTGTGACCAACCTTCTCTCAGTATCCACAGGTGACGCCACCTCTCTCTGTGTGTGACCAACCTTCTCTCAGTATCCACAGGTGACGCCACCTCTCTCTGTGTGACCAACCT 9106 9040 9050 9060 9070 9080 9090 9100	Matrix: DNAFULL Gap open penalty: 10.0 Gap extend penalty: 1.0 Length: 198 Identity: 190 / 198 (95.96%) Gaps: 2 / 198 (1.01 %)	
			MUC4-1 - SW620 Amplicon Reverse MUC4-1 Isoform	1 CCATCCCTTCTCTCAGTATCCACAGGTGACACCATGCTCTTCTGTGTGTGACCAACCTTCTCTCAGTATCCACAGGTGACGCCACCCCTCTCTGTGTGTGACCAACCT 100 11,643 CCATCCCTTCTCTCAGTATCCACAGGTGACACCATGCTCTTCTGTGTGTGACCAACCTTCTCTCAGTATCCACAGGTGACGCCACCCCTCTCTGTGTGTGACCAACCT 11,742 11650 11670 11680 11690 11700 11710 11720 11730 11740		
MUC4-1 Reverse	SW620	240bp	MUC4-1 - SW620 Amplicon Reverse MUC4-1 Isoform	101 CTTTCTCTCAGTATCCACAGGTGACACCCCTCTTCTGTGTGACCAACCTTCTCTCAGTATCCACAGGTGACGCCACCCCTCTCTCTGTGTGACCAACCTTCTCTCAGTATCCACAGGTGACGCCACCCCTCTCTCTGTGTGACCAACCT 196 11,743 CTTTCTCTCAGTATCCACAGGTGACACCCCTCTTCTGTGTGACCAACCTTCTCTCAGTATCCACAGGTGACGCCACCCCTCTCTCTGTGTGACCAACCTTCTCTCAGTATCCACAGGTGACGCCACCCCTCTCTCTGTGTGACCAACCT 11,840 11750 11760 11770 11780 11790 11800 11810 11820 11830 11840		

