

Table S3A: Alignment of MUC4-6 primers using the sample as CCD841, SW480, and SW620 cell lines. Sanger sequencing results were aligned using SnapGene software and NCBI Blast alignment. The confidence scores 80 and 100%.

Gene Name	Cell Line	Amplicon size bp	alignment	Gaps	
MUC4-6 Forward	CCD841	180bp	MUC4-6 - CCD841 Amplicon Forward MUC4-6 Isoform	<pre> 1 CACAGGTGACACACCCCTTCTCTGTACCCGACGCTTCTCTCAGCATCCACAGGTACGCGACCCCTCTCTCTGTACCCGACACTTCTCTCAGCATCCACA 100 6881 CACAGGTGACACACCCCTTCTCTGTACCCGACGCTTCTCTCAGCATCCACAGGTACGCGACCCCTCTCTCTGTACCCGACACTTCTCTCAGCATCCACA 6780 6690 6700 6710 6720 6730 6740 6750 6760 6770 6780 </pre>	<p>Matrix: DNAFULL Gap open penalty: 10.0 Gap extend penalty: 1.0</p> <p>Length: 242 Identity: 227 / 242 (93.80%) Gaps: 0 / 242 (0.00%)</p>
			MUC4-6 - CCD841 Amplicon Forward MUC4-6 Isoform	<pre> 101 GETGACACCCACCCCTTCTCTGTACCCGACGCTTCTCTCAGCATCCACAGGTACGCGACCCCTCTCTCTGTACCCGACACTTCTCTCAGCATCCACA 200 6781 6871 6881 6890 6900 6910 6920 6930 6940 6950 6960 6970 6980 6990 7000 6790 6800 6810 6820 6830 6840 6850 6860 6870 6880 </pre>	
			MUC4-6 - CCD841 Amplicon Forward MUC4-6 Isoform	<pre> 201 AGCCACCCCTTCTCTGTACCCGACACTTCTCTCAGCATCCACA 242 6881 AGCCACCCCTTCTCTGTACCCGACACTTCTCTCAGCATCCACA 6922 6890 6900 6910 6920 </pre>	
MUC4-6 Forward	CCD841	320bp	MUC4-6 - CCD841 Amplicon Forward MUC4-6 Isoform	<pre> 1 ACAGBTGACACACCCCTTCTCTGTACCCGACGCTTCTCTCAGCATCCACAGGTACGCGACCCCTCTCTCTGTACCCGACACTTCTCTCAGCATCCACA 100 9082 ACAGBTGACACACCCCTTCTCTGTACCCGACGCTTCTCTCAGCATCCACAGGTACGCGACCCCTCTCTCTGTACCCGACACTTCTCTCAGCATCCACA 9181 9090 9100 9110 9120 9130 9140 9150 9160 9170 9180 9190 </pre>	<p>Matrix: DNAFULL Gap open penalty: 10.0 Gap extend penalty: 1.0</p> <p>Length: 269 Identity: 256 / 269 (95.17%) Gaps: 0 / 269 (0.00%)</p>
			MUC4-6 - CCD841 Amplicon Forward MUC4-6 Isoform	<pre> 101 GTCAAGCACCCTTCTCTGTACCCGACGCTTCTCTCAGCATCCACAGGTACGCGACCCCTCTCTCTGTACCCGACACTTCTCTCAGCATCCACA 200 9182 9272 9282 9292 9302 9310 9320 9330 9340 9350 9360 9370 9380 9390 9400 9190 9200 9210 9220 9230 9240 9250 9260 9270 9280 </pre>	
			MUC4-6 - CCD841 Amplicon Forward MUC4-6 Isoform	<pre> 201 CGCCACCCCTTCTCTGTACCCGACACTTCTCTCAGCATCCACA 269 9282 CGCCACCCCTTCTCTGTACCCGACACTTCTCTCAGCATCCACA 9399 9290 9300 9310 9320 9330 9340 9350 </pre>	
MUC4-6 Forward	SW480	180bp	MUC4-6 - SW480 Amplicon Forward MUC4-6 Isoform	<pre> 1 TATCCACAGGTGACACACCCCTTCTCTGTACCCGACGCTTCTCTCAGCATCCACAGGTACGCGACCCCTCTCTCTGTACCCGACACTTCTCTCAGCAT 100 18,152 TATCCACAGGTGACACACCCCTTCTCTGTACCCGACGCTTCTCTCAGCATCCACAGGTACGCGACCCCTCTCTCTGTACCCGACACTTCTCTCAGCAT 18,250 18160 18170 18180 18190 18200 18210 18220 18230 18240 18250 </pre>	<p>Matrix: DNAFULL Gap open penalty: 10.0 Gap extend penalty: 1.0</p> <p>Length: 145 Identity: 143 / 145 (98.62%) Gaps: 1 / 145 (0.69%)</p>
			MUC4-6 - SW480 Amplicon Forward MUC4-6 Isoform	<pre> 101 CCACAGBTGACACACCCCTTCTCTGTACCCGACGCTTCTCTCAGCATCCACA 145 18,251 CCACAGBTGACACACCCCTTCTCTGTACCCGACGCTTCTCTCAGCATCCACA 18,295 18260 18270 18280 18290 </pre>	
MUC4-6 Forward	SW480	320bp	MUC4-6 - SW480 Amplicon Forward MUC4-6 Isoform	<pre> 1 ACCGGTGACACACCCCTTCTCTGTACCCGACGCTTCTCTCAGCATCCACA 100 4714 ACCGGTGACACACCCCTTCTCTGTACCCGACGCTTCTCTCAGCATCCACA 4812 4720 4730 4740 4750 4760 4770 4780 4790 4800 4810 </pre>	<p>Matrix: DNAFULL Gap open penalty: 10.0 Gap extend penalty: 1.0</p> <p>Length: 245 Identity: 195 / 245 (79.59%) Gaps: 18 / 245 (7.35%)</p>
			MUC4-6 - SW480 Amplicon Forward MUC4-6 Isoform	<pre> 98 GGTGATG-GCCGCTTCTCTGTACCCGACGCTTCTCTCAGCATCCACA 140 4813 GGTGATG-GCCGCTTCTCTGTACCCGACGCTTCTCTCAGCATCCACA 4909 4820 4830 4840 4850 4860 4870 4880 4890 4900 </pre>	
			MUC4-6 - SW480 Amplicon Forward MUC4-6 Isoform	<pre> 191 GTACAGGGC-TTCTCTGTACCCGACGCTTCTCTCAGCATCCACA 233 4910 GT-TTCTCTGTACCCGACGCTTCTCTCAGCATCCACA 4952 4910 4920 4930 4940 4950 </pre>	
MUC4-6 Forward	SW620	180bp	MUC4-6 - SW620 Amplicon Forward MUC4-6 Isoform	<pre> 1 CCTGCTCTGTATCCACAGGTGACACACCCCTTCTCTGTACCCGACGCTTCTCTCAGCATCCACA 100 18,141 CCTGCTCTGTATCCACAGGTGACACACCCCTTCTCTGTACCCGACGCTTCTCTCAGCATCCACA 18,239 18150 18160 18170 18180 18190 18200 18210 18220 18230 </pre>	<p>Matrix: DNAFULL Gap open penalty: 10.0 Gap extend penalty: 1.0</p> <p>Length: 226 Identity: 208 / 226 (92.04%) Gaps: 2 / 226 (0.88%)</p>
			MUC4-6 - SW620 Amplicon Forward MUC4-6 Isoform	<pre> 101 TTCTCAGATCCACAGGTGACACACCCCTTCTCTGTACCCGACGCTTCTCTCAGCATCCACA 200 18,240 TTCTCAGATCCACAGGTGACACACCCCTTCTCTGTACCCGACGCTTCTCTCAGCATCCACA 18,338 18240 18250 18260 18270 18280 18290 18300 18310 18320 18330 </pre>	
			MUC4-6 - SW620 Amplicon Forward MUC4-6 Isoform	<pre> 201 CTCAGATCCACAGGTGACACACCCCTTCTCTGTACCCGACGCTTCTCTCAGCATCCACA 226 18,339 CTCAGATCCACAGGTGACACACCCCTTCTCTGTACCCGACGCTTCTCTCAGCATCCACA 18,384 18340 18350 18360 </pre>	
MUC4-6 Reverse	SW620	180bp	MUC4-6 - SW620 Amplicon Reverse MUC4-6 Isoform	<pre> 1 GACGCTTCTCTGTATCCACAGGTGACACACCCCTTCTCTGTACCCGACGCTTCTCTCAGCATCCACA 100 18,189 GACGCTTCTCTGTATCCACAGGTGACACACCCCTTCTCTGTACCCGACGCTTCTCTCAGCATCCACA 18,286 18190 18200 18210 18220 18230 18240 18250 18260 18270 18280 </pre>	<p>Matrix: DNAFULL Gap open penalty: 10.0 Gap extend penalty: 1.0</p> <p>Length: 144 Identity: 139 / 144 (96.53%) Gaps: 0 / 144 (0.00%)</p>
			MUC4-6 - SW620 Amplicon Reverse MUC4-6 Isoform	<pre> 101 CTTCTCAGATCCACAGGTGACACACCCCTTCTCTGTACCCGACGCTTCTCTCAGCATCCACA 144 18,287 CTTCTCAGATCCACAGGTGACACACCCCTTCTCTGTACCCGACGCTTCTCTCAGCATCCACA 18,339 18290 18300 18310 18320 18330 </pre>	
MUC4-6 Forward	SW620	320bp	MUC4-6 - SW620 Amplicon Forward MUC4-6 Isoform	<pre> 1 CACCGACCTTCTCTGTATCCACAGGTGACACACCCCTTCTCTGTACCCGACGCTTCTCTCAGCATCCACA 100 18,189 CACCGACCTTCTCTGTATCCACAGGTGACACACCCCTTCTCTGTACCCGACGCTTCTCTCAGCATCCACA 18,282 18190 18200 18210 18220 18230 18240 18250 18260 18270 18280 </pre>	<p>Matrix: DNAFULL Gap open penalty: 10.0 Gap extend penalty: 1.0</p> <p>Length: 123 Identity: 121 / 123 (98.37%) Gaps: 0 / 123 (0.00%)</p>
			MUC4-6 - SW620 Amplicon Forward MUC4-6 Isoform	<pre> 101 GACGCTTCTCTGTATCCACAGGTGACACACCCCTTCTCTGTACCCGACGCTTCTCTCAGCATCCACA 123 18,283 GACGCTTCTCTGTATCCACAGGTGACACACCCCTTCTCTGTACCCGACGCTTCTCTCAGCATCCACA 18,305 18290 18300 </pre>	
MUC4-6 Reverse	SW620	320bp	MUC4-6 - SW620 Amplicon Reverse MUC4-6 Isoform	<pre> 1 CCACCCCTTCTCTGTATCCACAGGTGACACACCCCTTCTCTGTACCCGACGCTTCTCTCAGCATCCACA 99 4772 CCACCCCTTCTCTGTATCCACAGGTGACACACCCCTTCTCTGTACCCGACGCTTCTCTCAGCATCCACA 4871 4780 4790 4800 4810 4820 4830 4840 4850 4860 4870 </pre>	<p>Matrix: DNAFULL Gap open penalty: 10.0 Gap extend penalty: 1.0</p> <p>Length: 139 Identity: 129 / 139 (92.81%) Gaps: 1 / 139 (0.72%)</p>
			MUC4-6 - SW620 Amplicon Reverse MUC4-6 Isoform	<pre> 100 CCTCTCTGTATCCACAGGTGACACACCCCTTCTCTGTACCCGACGCTTCTCTCAGCATCCACA 138 4872 CCTCTCTGTATCCACAGGTGACACACCCCTTCTCTGTACCCGACGCTTCTCTCAGCATCCACA 4910 4880 4890 4900 4910 </pre>	

Table S3B: Alignment of MUC4-1 primers using the sample as CCD841, SW480, and SW620 cell lines. Sanger sequencing results were aligned using SnapGene software and NCBI Blast alignment. The confidence scores 91 and 100%.

Gene Name	Cell Line	Amplicon size bp	alignment	Gaps
MUC4-1 Forward	CCD841	282bp	MUC4-1 - CCD841 Amplicon Forward MUC4-1 Isoform 1 ACACCTTACTGAGCATCCACAGGACAGCCACCCTCTTCTTCCGTACCCGACACTTCTCCAGGTCACAGGTCACGCCACCCCTCTTCTGTCACCGACAC 100 3390 ACACCTTCTGATCCACAGGTACGCCACCTCTTCTTCCGTACCCGACACTTCTCCAGGTCACAGGTCACGCCACCCCTCTTCTGTCACCGACAC 3489	Matrix: DNAFULL Gap open penalty: 10.0 Gap extend penalty: 1.0
			MUC4-1 - CCD841 Amplicon Forward MUC4-1 Isoform 101 TTCTTCAGCATCCACAGGTACGCCACCCCTCTTCTTCCGTACCCGACACTTCTCCAGGTCACAGGTCACGCCACCCCTCTTCTGTCACCGACAC 166 3490 TTCTTCAGCATCCACAGGTACGCCACCCCTCTTCTTCCGTACCCGACACTTCTCCAGGTCACAGGTCACGCCACCCCTCTTCTGTCACCGACAC 3555	Length: 166 Identity: 158 / 166 (95.18 %) Gaps: 0 / 166 (0.00 %)
MUC4-1 Forward	CCD841	240bp	MUC4-1 - CCD841 Amplicon Forward MUC4-1 Isoform 1 TCTTCTGTGCA-CGACACTTCTCAGTATCCACAGGTACGCCACCCCTCTTCTTCCGTACCCGACACTTCTCCAGGTCACAGGTCACGCCACCCCTCTT 99 5968 TCTTCTGTGCA-CGACACTTCTCAGTATCCACAGGTACGCCACCCCTCTTCTTCCGTACCCGACACTTCTCCAGGTCACAGGTCACGCCACCCCTCTT 6067	Matrix: DNAFULL Gap open penalty: 10.0 Gap extend penalty: 1.0
			MUC4-1 - CCD841 Amplicon Forward MUC4-1 Isoform 100 CCTGTACCCGACCTTCTCAGTATCCACAGGTACGCCACCCCTCTTCCGTACCCGACACTTCTCCAGGTCACAGGTCACGCCACCCCTCTTCTT 196 6068 CCTGTACCCGACCTTCTCAGTATCCACAGGTACGCCACCCCTCTTCCGTACCCGACACTTCTCCAGGTCACAGGTCACGCCACCCCTCTTCTT 6164	Length: 197 Identity: 191 / 197 (96.95 %) Gaps: 1 / 197 (0.51 %)
MUC4-1 Reverse	CCD841	240bp	MUC4-1 - CCD841 Amplicon Reverse MUC4-1 Isoform 1 TCTCAGTGTCCACAGGTCACGCCACCCCTCTTCTTCCGTACCCGACACTTCTCCAGGTCACAGGTCACGCCACCCCTCTTCTTCTGTCACCGACAC 100 6563 TCTCAGTGTCCACAGGTCACGCCACCCCTCTTCTTCCGTACCCGACACTTCTCCAGGTCACAGGTCACGCCACCCCTCTTCTTCTGTCACCGACAC 6662	Matrix: DNAFULL Gap open penalty: 10.0 Gap extend penalty: 1.0
			MUC4-1 - CCD841 Amplicon Reverse MUC4-1 Isoform 101 CAGCATCCACAGGTACGCCACCCCTCTTCTTCCGTACCCGACACTTCTCCAGGTCACAGGTCACGCCACCCCTCTTCTTCTGTCACCGACAC 186 6663 CAGCATCCACAGGTACGCCACCCCTCTTCTTCCGTACCCGACACTTCTCCAGGTCACAGGTCACGCCACCCCTCTTCTTCTGTCACCGACAC 6748	Length: 186 Identity: 171 / 186 (91.94 %) Gaps: 0 / 186 (0.00 %)
MUC4-1 Forward	SW480	240bp	MUC4-1 - SW480 Amplicon Forward MUC4-1 Isoform 1 TCTTCTGTGCA-CGACACTTCTCAGTATCCACAGGTACGCCACCCCTCTTCTTCCGTACCCGACACTTCTCCAGGTCACAGGTCACGCCACCCCTCTT 99 5968 TCTTCTGTGCA-CGACACTTCTCAGTATCCACAGGTACGCCACCCCTCTTCTTCCGTACCCGACACTTCTCCAGGTCACAGGTCACGCCACCCCTCTT 6067	Matrix: DNAFULL Gap open penalty: 10.0 Gap extend penalty: 1.0
			MUC4-1 - SW480 Amplicon Forward MUC4-1 Isoform 100 CCTGTACCCGACCTTCTCAGTATCCACAGGTACGCCACCCCTCTTCCGTACCCGACACTTCTCCAGGTCACAGGTCACGCCACCCCTCTTCTT 196 6068 CCTGTACCCGACCTTCTCAGTATCCACAGGTACGCCACCCCTCTTCCGTACCCGACACTTCTCCAGGTCACAGGTCACGCCACCCCTCTTCTT 6164	Length: 197 Identity: 191 / 197 (96.95 %) Gaps: 1 / 197 (0.51 %)
MUC4-1 Forward	SW480	282bp	MUC4-1 - SW480 Amplicon Forward MUC4-1 Isoform 1 TCCACAGGTACGCCACCCCTCTTCTTCCGTACCCGACACTTCTCCAGGTCACAGGTCACGCCACCCCTCTTCTTCTGTCACCGACACATCCA 100 3356 TCCACAGGTACGCCACCCCTCTTCTTCCGTACCCGACACTTCTCCAGGTCACAGGTCACGCCACCCCTCTTCTTCTGTCACCGACACATCCA 3455	Matrix: DNAFULL Gap open penalty: 10.0 Gap extend penalty: 1.0
			MUC4-1 - SW480 Amplicon Forward MUC4-1 Isoform 101 CAGGACATCCACAGGTACGCCACCCCTCTTCTTCCGTACCCGACACTTCTCCAGGTCACAGGTCACGCCACCCCTCTTCTTCTGTCACCGACAC 200 3456 CAGGACATCCACAGGTACGCCACCCCTCTTCTTCCGTACCCGACACTTCTCCAGGTCACAGGTCACGCCACCCCTCTTCTTCTGTCACCGACAC 3555	Length: 221 Identity: 206 / 221 (93.21 %) Gaps: 0 / 221 (0.00 %)
			MUC4-1 - SW480 Amplicon Forward MUC4-1 Isoform 201 ACACACCACCCCTCTTCTATGT 221 3556 TACACACCACCCCTCTTCTATGT 3576	
MUC4-1 Reverse	SW620	282bp	MUC4-1 - SW620 Amplicon Forward MUC4-1 Isoform 1 TTCTCAGTATCCACAGGTACGCCACCCCTCTTCTTCCGTACCCGACACTTCTCCAGGTCACAGGTCACGCCACCCCTCTTCTTCTGTCACCGACAC 100 8914 TTCTCAGTATCCACAGGTACGCCACCCCTCTTCTTCCGTACCCGACACTTCTCCAGGTCACAGGTCACGCCACCCCTCTTCTTCTGTCACCGACAC 9013	Matrix: DNAFULL Gap open penalty: 10.0 Gap extend penalty: 1.0
			MUC4-1 - SW620 Amplicon Forward MUC4-1 Isoform 101 TCAGCATCCACAGGTACGCCACCCCTCTTCTTCCGTACCCGACACTTCTCCAGGTCACAGGTCACGCCACCCCTCTTCTTCTGTCACCGACAC 200 9014 TCAGCATCCACAGGTACGCCACCCCTCTTCTTCCGTACCCGACACTTCTCCAGGTCACAGGTCACGCCACCCCTCTTCTTCTGTCACCGACAC 9113	Length: 379 Identity: 354 / 379 (93.40 %) Gaps: 0 / 379 (0.00 %)
			MUC4-1 - SW620 Amplicon Forward MUC4-1 Isoform 201 CATCCACAGGACATCCACAGGTACGCCACCCCTCTTCTTCCGTACCCGACACTTCTCCAGGTCACAGGTCACGCCACCCCTCTTCTTCTGTCACCGACAC 300 9114 CATCCACAGGACATCCACAGGTACGCCACCCCTCTTCTTCCGTACCCGACACTTCTCCAGGTCACAGGTCACGCCACCCCTCTTCTTCTGTCACCGACAC 9213	
MUC4-1 - SW620 Amplicon Forward MUC4-1 Isoform 301 CACAGGTACGCCACCCCTCTTCTTCCGTACCCGACACTTCTCCAGGTCACAGGTCACGCCACCCCTCTTCTTCTGTCACCGACAC 379 9214 CACAGGTACGCCACCCCTCTTCTTCCGTACCCGACACTTCTCCAGGTCACAGGTCACGCCACCCCTCTTCTTCTGTCACCGACAC 9292				
MUC4-1 Reverse	SW620	282bp	MUC4-1 - SW620 Amplicon Reverse MUC4-1 Isoform 1 CACCACCTTCTTCTGTCACCGACACTTCTCCAGGTCACAGGTCACGCCACCCCTCTTCTTCCGTACCCGACACTTCTCCAGGTCACAGGTCACGCCACCCCTCTT 100 8840 CACCACCTTCTTCTGTCACCGACACTTCTCCAGGTCACAGGTCACGCCACCCCTCTTCTTCCGTACCCGACACTTCTCCAGGTCACAGGTCACGCCACCCCTCTT 8938	Matrix: DNAFULL Gap open penalty: 10.0 Gap extend penalty: 1.0
			MUC4-1 - SW620 Amplicon Reverse MUC4-1 Isoform 101 ACCCCCTTCTTCTGTCACCGACACTTCTCCAGGTCACAGGTCACGCCACCCCTCTTCTTCCGTACCCGACACTTCTCCAGGTCACAGGTCACGCCACCCCTCTT 200 8939 ACCCCCTTCTTCTGTCACCGACACTTCTCCAGGTCACAGGTCACGCCACCCCTCTTCTTCCGTACCCGACACTTCTCCAGGTCACAGGTCACGCCACCCCTCTT 9038	Length: 268 Identity: 249 / 268 (92.91 %) Gaps: 1 / 268 (0.37 %)
			MUC4-1 - SW620 Amplicon Reverse MUC4-1 Isoform 201 CTCTTCTGTCACCGACACTTCTCCAGGTCACAGGTCACGCCACCCCTCTTCTTCCGTACCCGACACTTCTCCAGGTCACAGGTCACGCCACCCCTCTTCTT 267 9039 CTCTTCTGTCACCGACACTTCTCCAGGTCACAGGTCACGCCACCCCTCTTCTTCCGTACCCGACACTTCTCCAGGTCACAGGTCACGCCACCCCTCTTCTT 9106	
MUC4-1 Reverse	SW620	240bp	MUC4-1 - SW620 Amplicon Reverse MUC4-1 Isoform 1 CCATCCCTTCTCAGTATCCACAGGTACACCACCTCTTCTTCCGTACCCGACACTTCTCCAGGTCACAGGTCACGCCACCCCTCTTCTTCTGTCACCGACAC 100 11,643 CCATCCCTTCTCAGTATCCACAGGTACACCACCTCTTCTTCCGTACCCGACACTTCTCCAGGTCACAGGTCACGCCACCCCTCTTCTTCTGTCACCGACAC 11,742	Matrix: DNAFULL Gap open penalty: 10.0 Gap extend penalty: 1.0
			MUC4-1 - SW620 Amplicon Reverse MUC4-1 Isoform 101 CTTTCTGTCACCGACACTTCTCCAGGTCACAGGTCACGCCACCCCTCTTCTTCCGTACCCGACACTTCTCCAGGTCACAGGTCACGCCACCCCTCTTCTT 196 11,743 CTTTCTGTCACCGACACTTCTCCAGGTCACAGGTCACGCCACCCCTCTTCTTCCGTACCCGACACTTCTCCAGGTCACAGGTCACGCCACCCCTCTTCTT 11,840	Length: 198 Identity: 190 / 198 (95.96 %) Gaps: 2 / 198 (1.01 %)

