

Table S2A: Alignment of MUC4-All 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 98 and 100%.

Gene Name	Cell Line	Amplicon size bp	alignment		Gaps
MUC4-All Forward	CCD841	210bp	MUC4-All - CCD841 Amplicon Forward MUC4-All Isoforms	1 10 20 30 40 50 60 70 80 CTGGTCTA-AGCCCCAGAGCGGCTTACCTGCGTGTCCCAAGTGCAGTAGGGGCTACTGTGACCATGGAGGCCAGTGCCAGCACCTGCC 89 16,040 CTGGTCTACAGCCCCAGAGCGGCTTACCTGCGTGTCCCC-GTGCAGTAGGGGCTACTGTGACCATGGAGGCCAGTGCCAGCACCTGCC 16,128 16040 16050 16060 16070 16080 16090 16100 16110 16120	Matrix: DNAFULL Gap open penalty: 10.0 Gap extend penalty: 1.0
			MUC4-All - CCD841 Amplicon Forward MUC4-All Isoforms	90 100 110 120 130 140 150 160 170 CAGTGGGCCCGCTGCAAGCTGTGTCTCTTCTCCATCTACAGGCCCTGGGGCGAGCACTGTGAGCACCTGAGCATGAAACTCGAC 174 16,129 CAGTGGGCCCGCTGCAAGCTGTGTCTCTTCTCCATCTACAGGCCCTGGGGCGAGCACTGTGAGCACCTGAGCATGAAACTCGAC 16,213 16130 16140 16150 16160 16170 16180 16190 16200 16210	Length: 175 Identity: 173 / 175 (98.86%) Gaps: 2 / 175 (1.14%)
MUC4-All Reverse	CCD841	210bp	MUC4-All - CCD841 Amplicon Reverse MUC4-All Isoforms	1 10 20 30 40 50 60 70 80 90 100 GCTTACTTCAGATGCGATGGCTACAAGGGCTACGACCTGGTCTACAGCCCCAGAGCGGCTTACCTGCGTGTCCCAAGTGCAGTAGGGGCTACTGTGACC 100 16,004 GCTTACTTCAGATGCGATGGCTACAAGGGCTACGACCTGGTCTACAGCCCCAGAGCGGCTTACCTGCGTGTCCCAAGTGCAGTAGGGGCTACTGTGACC 16,103 16010 16020 16030 16040 16050 16060 16070 16080 16090 16100	Matrix: DNAFULL Gap open penalty: 10.0 Gap extend penalty: 1.0
			MUC4-All - CCD841 Amplicon Reverse MUC4-All Isoforms	101 110 120 130 140 150 160 170 ATGGAGGCCAGTGCCAGCACCTGCCAGTGGGCCCGCTGCAAGCTGTGTCTCTTCTCCATCTACAGGCCCT 172 16,104 ATGGAGGCCAGTGCCAGCACCTGCCAGTGGGCCCGCTGCAAGCTGTGTCTCTTCTCCATCTACAGGCCCT 16,175 16110 16120 16130 16140 16150 16160 16170	Length: 172 Identity: 171 / 172 (99.42%) Gaps: 0 / 172 (0.00%)
MUC4-All Forward	SW480	210bp	MUC4-All - SW480 Amplicon Forward MUC4-All Isoforms	1 10 20 30 40 50 60 70 80 90 CCCCAGAGCGGCTTACCTGCGTGTCCCGTGCAAGTAGGGGCTACTGTGACCATGGAGGCCAGTGCCAGCACCTGCCAGTGGGCCCGCG 90 16,052 CCCCAGAGCGGCTTACCTGCGTGTCCCGTGCAAGTAGGGGCTACTGTGACCATGGAGGCCAGTGCCAGCACCTGCCAGTGGGCCCGCG 16,141 16060 16070 16080 16090 16100 16110 16120 16130 16140	Matrix: DNAFULL Gap open penalty: 10.0 Gap extend penalty: 1.0
			MUC4-All - SW480 Amplicon Forward MUC4-All Isoforms	91 100 110 120 130 140 150 160 TGCAGCTGTGTCTCTTCTCCATCTACAGGCCCTGGGGCGAGCACTGTGAGCACCTGAGCATGAAACTCGAC 162 16,142 TGCAGCTGTGTCTCTTCTCCATCTACAGGCCCTGGGGCGAGCACTGTGAGCACCTGAGCATGAAACTCGAC 16,213 16150 16160 16170 16180 16190 16200 16210	Length: 162 Identity: 162 / 162 (100.00%) Gaps: 0 / 162 (0.00%)
MUC4-All Reverse	SW480	210bp	MUC4-All - SW480 Amplicon Reverse MUC4-All Isoforms	1 10 20 30 40 50 60 70 80 90 100 GCTTACTTCAGATGCGATGGCTACAAGGGCTACGACCTGGTCTACAGCCCCAGAGCGGCTTACCTGCGTGTCCCGTGCAAGTAGGGGCTACTGTGACC 100 16,004 GCTTACTTCAGATGCGATGGCTACAAGGGCTACGACCTGGTCTACAGCCCCAGAGCGGCTTACCTGCGTGTCCCGTGCAAGTAGGGGCTACTGTGACC 16,103 16010 16020 16030 16040 16050 16060 16070 16080 16090 16100	Matrix: DNAFULL Gap open penalty: 10.0 Gap extend penalty: 1.0
			MUC4-All - SW480 Amplicon Reverse MUC4-All Isoforms	101 110 120 130 140 150 160 170 ATGGAGGCCAGTGCCAGCACCTGCCAGTGGGCCCGCTGCAAGCTGTGTCTCTTCTCCATCTACAGGCCCT 172 16,104 ATGGAGGCCAGTGCCAGCACCTGCCAGTGGGCCCGCTGCAAGCTGTGTCTCTTCTCCATCTACAGGCCCT 16,175 16110 16120 16130 16140 16150 16160 16170	Length: 172 Identity: 172 / 172 (100.00%) Gaps: 0 / 172 (0.00%)
MUC4-All Forward	SW620	210bp	MUC4-All - SW620 Amplicon Forward MUC4-All Isoforms	1 10 20 30 40 50 60 70 80 90 100 CCCCAGAGCGGCTTACCTGCGTGTCCCGTGCAAGTAGGGGCTACTGTGACCATGGAGGCCAGTGCCAGCACCTGCCAGTGGGCCCGCTGCAAGCTGT 100 16,051 CCCCAGAGCGGCTTACCTGCGTGTCCCGTGCAAGTAGGGGCTACTGTGACCATGGAGGCCAGTGCCAGCACCTGCCAGTGGGCCCGCTGCAAGCTGT 16,150 16060 16070 16080 16090 16100 16110 16120 16130 16140 16150	Matrix: DNAFULL Gap open penalty: 10.0 Gap extend penalty: 1.0
			MUC4-All - SW620 Amplicon Forward MUC4-All Isoforms	101 110 120 130 140 150 160 GTGTCTTCTCCATCTACAGGCCCTGGGGCGAGCACTGTGAGCACCTGAGCATGAAACTCGAC 163 16,151 GTGTCTTCTCCATCTACAGGCCCTGGGGCGAGCACTGTGAGCACCTGAGCATGAAACTCGAC 16,213 16160 16170 16180 16190 16200 16210	Length: 163 Identity: 163 / 163 (100.00%) Gaps: 0 / 163 (0.00%)
MUC4-All Reverse	SW620	210bp	MUC4-All - SW620 Amplicon Reverse MUC4-All Isoforms	1 10 20 30 40 50 60 70 80 90 100 GCTTACTTCAGATGCGATGGCTACAAGGGCTACGACCTGGTCTACAGCCCCAGAGCGGCTTACCTGCGTGTCCCGTGCAAGTAGGGGCTACTGTGACC 100 16,004 GCTTACTTCAGATGCGATGGCTACAAGGGCTACGACCTGGTCTACAGCCCCAGAGCGGCTTACCTGCGTGTCCCGTGCAAGTAGGGGCTACTGTGACC 16,103 16010 16020 16030 16040 16050 16060 16070 16080 16090 16100	Matrix: DNAFULL Gap open penalty: 10.0 Gap extend penalty: 1.0
			MUC4-All - SW620 Amplicon Reverse MUC4-All Isoforms	101 110 120 130 140 150 160 170 ATGGAGGCCAGTGCCAGCACCTGCCAGTGGGCCCGCTGCAAGCTGTGTCTCTTCTCCATCTACA-CGGCCTGG 175 16,104 ATGGAGGCCAGTGCCAGCACCTGCCAGTGGGCCCGCTGCAAGCTGTGTCTCTTCTCCATCTACA-CGGCCTGG 16,177 16110 16120 16130 16140 16150 16160 16170	Length: 175 Identity: 174 / 175 (99.43%) Gaps: 1 / 175 (0.57%)

Table S2B: Alignment of MUC4-16 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 99 and 100%.

Gene Name	Cell Line	Amplicon size bp	alignment										Gaps		
MUC4-16 Forward	CCD841	223bp	MUC4-16 - CCD841 Amplicon Forward MUC4-16 Isoforms	<div>1 ATAAAAACGGCCACATCCCCATCTTCTTCCACCTATGCTGGATAGACACACATCAACAACAAATTACAACGGCCACCATCAACAACATCATTTCAACAATACATT 100</div> <div>1880 ATAAAAACGGCCACATCCCCATCTTCTTCCACCTATGCTGGATAGACACACATCCAACAACAAATTACAACGGCCACCATCAACAACATCATTTCAACAATACATT 1779</div> <div>1880 1890 1900 1910 1920 1930 1940 1950 1960 1970 1980 1990</div>										Matrix:	DNAFULL
			MUC4-16 - CCD841 Amplicon Forward MUC4-16 Isoforms	<div>101 CCACAAGCACCTCTCTCAGGAATCACCAGCTGTTTCCCAAAGGGGTCACACTCAAGCCCCGCAGACCACACAAGAATC 179</div> <div>1980 CCACAAGCACCTCTCTCAGGAATCACCAGCTGTTTCCCAAAGGGGTCACACTCAAGCCCCGCAGACCACACAAGAATC 2058</div> <div>1980 1990 2000 2010 2020 2030 2040 2050</div>										Gap open penalty:	10.0
MUC4-16 Reverse	CCD841	223bp	MUC4-16 - CCD841 Amplicon Reverse MUC4-16 Isoforms	<div>1 TGGAGAGGCTCTTCTCAGCAGCCCAAGCTACAGTGTGACTCAGATGATAAAAACGGCCACATCCCCATCTTCTTCCACCTATGCTGGATAGACACACATCA 100</div> <div>1834 TGGAGAGGCTCTTCTCAGCAGCCCAAGCTACAGTGTGACTCAGATGATAAAAACGGCCACATCCCCATCTTCTTCCACCTATGCTGGATAGACACACATCC 1933</div> <div>1840 1850 1860 1870 1880 1890 1900 1910 1920 1930</div>										Matrix:	DNAFULL
			MUC4-16 - CCD841 Amplicon Reverse MUC4-16 Isoforms	<div>101 CAACAAATTACAACGGCACCATTCAACAATCATTTCAACAATACATTTCCACAAGCACCTCTCTCAGGAATCACCAGCTG 179</div> <div>1934 CAACAAATTACAACGGCACCATTCAACAATCATTTCAACAATACATTTCCACAAGCACCTCTCTCAGGAATCACCAGCTG 2012</div> <div>1940 1950 1960 1970 1980 1990 2000 2010</div>										Gap open penalty:	10.0
MUC4-16 Forward	SW480	223bp	MUC4-16 - SW480 Amplicon Forward MUC4-16 Isoforms	<div>1 AAAACGGCCACATCCCCATCTTCTTCCACCTATGCTGGATAGACACACATCAACAACAAATTACAACGGCACCATTCAACAACATCATTTCAACAATACATTCCA 100</div> <div>1883 AAAACGGCCACATCCCCATCTTCTTCCACCTATGCTGGATAGACACACATCCAACAACAAATTACAACGGCACCATTCAACAACATCATTTCAACAATACATTCCA 1982</div> <div>1890 1900 1910 1920 1930 1940 1950 1960 1970 1980</div>										Matrix:	DNAFULL
			MUC4-16 - SW480 Amplicon Forward MUC4-16 Isoforms	<div>101 CAAGCACCTCTCTCTCAGGAATCACCAGCTGTTTCCCAAAGGGGTCACACTCAAGCCCCGCAGACCACACAAGAAT 175</div> <div>1983 CAAGCACCTCTCTCTCAGGAATCACCAGCTGTTTCCCAAAGGGGTCACACTCAAGCCCCGCAGACCACACAAGAAT 2057</div> <div>1990 2000 2010 2020 2030 2040 2050</div>										Gap open penalty:	10.0
MUC4-16 Reverse	SW480	223bp	MUC4-16 - SW480 Amplicon Reverse MUC4-16 Isoforms	<div>1 TGGAGAGGCTCTTCTCAGCAGCCCAAGCTACAGTGTGACTCAGATGATAAAAACGGCCACATCCCCATCTTCTTCCACCTATGCTGGATAGACACACATCA 100</div> <div>1834 TGGAGAGGCTCTTCTCAGCAGCCCAAGCTACAGTGTGACTCAGATGATAAAAACGGCCACATCCCCATCTTCTTCCACCTATGCTGGATAGACACACATCC 1933</div> <div>1840 1850 1860 1870 1880 1890 1900 1910 1920 1930</div>										Matrix:	DNAFULL
			MUC4-16 - SW480 Amplicon Reverse MUC4-16 Isoforms	<div>101 CAACAAATTACAACGGCACCATTCAACAATCATTTCAACAATACATTTCCACAAGCACCTCTCTCTCAGG 167</div> <div>1934 CAACAAATTACAACGGCACCATTCAACAATCATTTCCACAAGCACCTCTCTCTCAGG 2000</div> <div>1940 1950 1960 1970 1980 1990 2000</div>										Gap open penalty:	10.0
MUC4-16 Forward	SW620	223bp	MUC4-16 - SW620 Amplicon Forward MUC4-16 Isoforms	<div>9 TGACTCAGATGATAAAAACGGCCACATCCCCATCTTCTTCCACCTATGCTGGATAGACACACATCAACAACAAATTACAACGGCACCATTCAACAACATCATTT 108</div> <div>1869 TGACTCAGATGATAAAAACGGCCACATCCCCATCTTCTTCCACCTATGCTGGATAGACACACATCCAACAACAAATTACAACGGCACCATTCAACAACATCATTT 1968</div> <div>1870 1880 1890 1900 1910 1920 1930 1940 1950 1960</div>										Matrix:	DNAFULL
			MUC4-16 - SW620 Amplicon Forward MUC4-16 Isoforms	<div>109 CAAATCATTTCAACAATACATTTCCACAAGCACCTCTCTCTCAGGAATCACCAGCTGTTTCCCAAAGGGGTCACACTCAAGCCCCGCAGACCA 198</div> <div>1969 CAAATCATTTCAACAATACATTTCCACAAGCACCTCTCTCTCAGGAATCACCAGCTGTTTCCCAAAGGGGTCACACTCAAGCCCCGCAGACCA 2058</div> <div>1970 1980 1990 2000 2010 2020 2030 2040 2050</div>										Gap open penalty:	10.0
MUC4-16 Reverse	SW620	223bp	MUC4-16 - SW620 Amplicon Reverse MUC4-16 Isoforms	<div>1 TGGAGAGGCTCTTCTCAGCAGCCCAAGCTACAGTGTGACTCAGATGATAAAAACGGCCACATCCCCATCTTCTTCCACCTATGCTGGATAGACACACATCA 100</div> <div>1834 TGGAGAGGCTCTTCTCAGCAGCCCAAGCTACAGTGTGACTCAGATGATAAAAACGGCCACATCCCCATCTTCTTCCACCTATGCTGGATAGACACACATCC 1933</div> <div>1840 1850 1860 1870 1880 1890 1900 1910 1920 1930</div>										Matrix:	DNAFULL
			MUC4-16 - SW620 Amplicon Reverse MUC4-16 Isoforms	<div>101 CAACAAATTACAACGGCACCATTCAACAATCATTTCAACAATACATTTCCACAAGCACCTCTCTCTCAGGAATCACCAGCTG 179</div> <div>1934 CAACAAATTACAACGGCACCATTCAACAATCATTTCAACAATACATTTCCACAAGCACCTCTCTCTCAGGAATCACCAGCTG 2012</div> <div>1940 1950 1960 1970 1980 1990 2000 2010</div>										Gap open penalty:	10.0

Table S2C: Alignment of MUC4-16 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 95 and 100%.

Gene Name	Cell Line	Amplicon size bp	alignment		Gaps
MUC4-4 Forward	CCD841	158bp	MUC4-4 - CCD841 Amplicon Forward MUC4-4 Isoform	<div>1020114</div> <div>120130140150160170180190200</div> <div>1 TGAAGGGGGCATGCTGGACGTGGGTCCCTGGGTGTCCCTGAGCTGCCTGTGTCTCTGCCTCCTCCGCATGTGGTCCCAGGAATCA 87</div> <div>114 TGAAGGGGGGCACTGCTGGAGGAGGGTCCCTGGGTGTCCCTGAGCTGCCTGTGTCTCTGCCTCCTCCGCATGTGGTCCCAGGAATGA 200</div>	<div>Matrix: DNAFULL</div> <div>Gap open penalty: 10.0</div> <div>Gap extend penalty: 1.0</div> <div>Length: 87</div> <div>Identity: 83 / 87 (95.40%)</div> <div>Gaps: 0 / 87 (0.00%)</div>
MUC4-4 Reverse	CCD841	158bp	MUC4-4 - CCD841 Amplicon Reverse MUC4-4 Isoform MUC4-4 - CCD841 Amplicon Reverse MUC4-4 Isoform	<div>102030405060708090100</div> <div>41 GTCTGCTCCTCACACTGCAAGCTGCTGGGCCGTGGAGCTTCCCTAGGGAGCCAGGGGGACTTTTGCCGACGCCATGAAGGGGGGCACGCTGGAGGAGGGTCC 100</div> <div>41 GTCTGCTCCTCACACTGCAAGCTGCTGGGCCGTGGAGCTTCCCTAGGGAGCCAGGGGGACTTTTGCCGACGCCATGAAGGGGGGCACGCTGGAGGAGGGTCC 140</div> <div>110120</div> <div>101 CCTGGGTGTCCCTGAGCTGCCTG 123</div> <div>141 CCTGGGTGTCCCTGAGCTGCCTG 163</div> <div>150160</div>	<div>Matrix: DNAFULL</div> <div>Gap open penalty: 10.0</div> <div>Gap extend penalty: 1.0</div> <div>Length: 123</div> <div>Identity: 122 / 123 (99.19%)</div> <div>Gaps: 0 / 123 (0.00%)</div>
MUC4-4 Forward	SW480	158bp	MUC4-4 - SW480 Amplicon Forward MUC4-4 Isoform MUC4-4 - SW480 Amplicon Forward MUC4-4 Isoform	<div>102030405060708090100</div> <div>1 CCCAGGGAGCCAGGGGGACTTTTGCCGACGCCATGAAGGGGGGCACGCTGGAGGAGGGTCCCTGGGTGTCCCTGAGCTGCCTGTGTCTCTGCCTCCTTCC 100</div> <div>81 CCCAGGGAGCCAGGGGGACTTTTGCCGACGCCATGAAGGGGGGCACGCTGGAGGAGGGTCCCTGGGTGTCCCTGAGCTGCCTGTGTCTCTGCCTCCTTCC 180</div> <div>90100110120130140150160170180</div> <div>110</div> <div>101 GCATGTGTGCCAGGAAT 118</div> <div>181 GCATGTGTGCCAGGAAT 198</div> <div>190</div>	<div>Matrix: DNAFULL</div> <div>Gap open penalty: 10.0</div> <div>Gap extend penalty: 1.0</div> <div>Length: 118</div> <div>Identity: 118 / 118 (100.00%)</div> <div>Gaps: 0 / 118 (0.00%)</div>
MUC4-4 Reverse	SW480	158bp	MUC4-4 - SW480 Amplicon Reverse MUC4-4 Isoform MUC4-4 - SW480 Amplicon Reverse MUC4-4 Isoform	<div>102030405060708090100</div> <div>1 GTCTGCTCCTCACACTGCAAGCTGCTGGGCCGTGGAGCTTCCCAAGGGAGCCAGGGGGACTTTTGCCGACGCCATGAAGGGGGGCACGCTGGAGGAGGGTCC 100</div> <div>41 GTCTGCTCCTCACACTGCAAGCTGCTGGGCCGTGGAGCTTCCCAAGGGAGCCAGGGGGACTTTTGCCGACGCCATGAAGGGGGGCACGCTGGAGGAGGGTCC 140</div> <div>5060708090100110120130140</div> <div>110120</div> <div>101 CCTGGGTGTCCCTGAGCTGC 120</div> <div>141 CCTGGGTGTCCCTGAGCTGC 160</div> <div>150160</div>	<div>Matrix: DNAFULL</div> <div>Gap open penalty: 10.0</div> <div>Gap extend penalty: 1.0</div> <div>Length: 120</div> <div>Identity: 120 / 120 (100.00%)</div> <div>Gaps: 0 / 120 (0.00%)</div>
MUC4-4 Forward	SW620	158bp	MUC4-4 - SW620 Amplicon Forward MUC4-4 Isoform MUC4-4 - SW620 Amplicon Forward MUC4-4 Isoform	<div>102030405060708090100</div> <div>1 AGGGAGCCAGGGGGACTTTTGCCGACGCCATGAAGGGGGGCACGCTGGAGGAGGGTCCCTGGGTGTCCCTGAGCTGCCTGTGTCTCTGCCTCCTTCCGCA 100</div> <div>84 AGGGAGCCAGGGGGACTTTTGCCGACGCCATGAAGGGGGGCACGCTGGAGGAGGGTCCCTGGGTGTCCCTGAGCTGCCTGTGTCTCTGCCTCCTTCCGCA 183</div> <div>90100110120130140150160170180</div> <div>110</div> <div>101 TGTGGTCCCAGGAAT 115</div> <div>184 TGTGGTCCCAGGAAT 198</div> <div>190</div>	<div>Matrix: DNAFULL</div> <div>Gap open penalty: 10.0</div> <div>Gap extend penalty: 1.0</div> <div>Length: 115</div> <div>Identity: 115 / 115 (100.00%)</div> <div>Gaps: 0 / 115 (0.00%)</div>
MUC4-4 Reverse	SW620	158bp	MUC4-4 - SW620 Amplicon Reverse MUC4-4 Isoform MUC4-4 - SW620 Amplicon Reverse MUC4-4 Isoform	<div>102030405060708090100</div> <div>1 GTCTGCTCCTCACACTGCAAGCTGCTGGGCCGTGGAGCTTCCCAAGGGAGCCAGGGGGACTTTTGCCGACGCCATGAAGGGGGGCACGCTGGAGGAGGGTCC 100</div> <div>41 GTCTGCTCCTCACACTGCAAGCTGCTGGGCCGTGGAGCTTCCCAAGGGAGCCAGGGGGACTTTTGCCGACGCCATGAAGGGGGGCACGCTGGAGGAGGGTCC 140</div> <div>5060708090100110120130140</div> <div>110120</div> <div>101 CCTGGGTGTCCCTGAGCTGCC 121</div> <div>141 CCTGGGTGTCCCTGAGCTGCC 161</div> <div>150160</div>	<div>Matrix: DNAFULL</div> <div>Gap open penalty: 10.0</div> <div>Gap extend penalty: 1.0</div> <div>Length: 121</div> <div>Identity: 121 / 121 (100.00%)</div> <div>Gaps: 0 / 121 (0.00%)</div>