

A

Gene Name	Cell Line	Amplicon size bp	alignment		Gaps
ADAM12-All Forward	CCD841	198bp	ADAM12-All - CCD841 Amplicon Forward ADAM12-All Isoforms	1 10 20 30 40 50 60 70 80 90 CCATTTCCCATGGTGTTCAGCAGTTGCAGCAGGAAGGACTTGGAGACCAGCCTGGAGAAAGGAATGGGGGTGTGCCTGTTTAACTGCCC 90 1469 CCATTTCCCATGGTGTTCAGCAGTTGCAGCAGGAAGGACTTGGAGACCAGCCTGGAGAAAGGAATGGGGGTGTGCCTGTTTAACTGCCC 1558 1470 1480 1490 1500 1510 1520 1530 1540 1550	Matrix: DNAFULL Gap open penalty: 10.0 Gap extend penalty: 1.0
			ADAM12-All - CCD841 Amplicon Forward ADAM12-All Isoforms	91 100 110 120 130 140 GAAATCAGGGAGTCTTTCGGGGGCCAGAAAGTGTGGGAACAGATTTGTGGA 140 1559 GAAATCAGGGAGTCTTTCGGGGGCCAGAAAGTGTGGGAACAGATTTGTGGA 1608 1560 1570 1580 1590 1600	Length: 140 Identity: 140 / 140 (100.00%) Gaps: 0 / 140 (0.00%)
ADAM12-All Reverse	CCD841	198bp	ADAM12-All - CCD841 Amplicon Reverse ADAM12-All Isoforms	1 10 20 30 40 50 60 70 80 90 GTAGCTGTCAAATGGCGGTTGAGAAAGGAGGCTGCATCATGAACGCTTCCACCGGGTACCCATTTCCCATGGTGTTCAGCAGTTGCAGCA 90 1432 GTAGCTGTCAAATGGCGGTTGAGAAAGGAGGCTGCATCATGAACGCTTCCACCGGGTACCCATTTCCCATGGTGTTCAGCAGTTGCAGCA 1521 1440 1450 1460 1470 1480 1490 1500 1510 1520	Matrix: DNAFULL Gap open penalty: 10.0 Gap extend penalty: 1.0
			ADAM12-All - CCD841 Amplicon Reverse ADAM12-All Isoforms	91 100 110 120 130 140 150 GGAAGGACTTGGAGACCAGCCTGGAGAAAGGAATGGGGGTGTGCCTG-TTAACTGCCGGAAGTCAGG 157 1522 GGAAGGACTTGGAGACCAGCCTGGAGAAAGGAATGGGGGTGTGCCTGTTTAACTGCCGGAAGTCAGG 1589 1530 1540 1550 1560 1570 1580	Length: 158 Identity: 157 / 158 (99.37%) Gaps: 1 / 158 (0.63%)
ADAM12-All Forward	SW480	198bp	ADAM12-All - SW480 Amplicon Forward ADAM12-All Isoforms	1 10 20 30 40 50 60 70 80 ACGCTT-CACCGGGTA-CCATTTCCCATGGTGTTCAGCAGTTGCAGCAGGAAGGACTTGGAGACCAGCCTGGAGAAAGGAATGGGGGTGT 88 1465 ACGCTT-CACCGGGTA-CCATTTCCCATGGTGTTCAGCAGTTGCAGCAGGAAGGACTTGGAGACCAGCCTGGAGAAAGGAATGGGGGTGT 1554 1470 1480 1490 1500 1510 1520 1530 1540 1550	Matrix: DNAFULL Gap open penalty: 10.0 Gap extend penalty: 1.0
			ADAM12-All - SW480 Amplicon Forward ADAM12-All Isoforms	89 90 100 110 120 130 140 150 GCCTGTTTAACTGCCGGAAGTCAGGGAGTCTTTCGGGGGCCAGAAAGTGTGGGAACAGATTTGTGGA 155 1555 GCCTGTTTAACTGCCGGAAGTCAGGGAGTCTTTCGGGGGCCAGAAAGTGTGGGAACAGATTTGTGGA 1621 1560 1570 1580 1590 1600 1610 1620	Length: 157 Identity: 155 / 157 (98.73%) Gaps: 2 / 157 (1.27%)
ADAM12-All Reverse	SW480	198bp	ADAM12-All - Sw480 Amplicon Reverse ADAM12-All Isoforms	1 10 20 30 40 50 60 70 80 90 TGTAGCTGTCAAATGGCGGTTGAGAAAGGAGGCTGCATCATGAACGCTTCCACCGGGTACCCATTTCCCATGGTGTTCAGCAGTTGCAGC 90 1431 TGTAGCTGTCAAATGGCGGTTGAGAAAGGAGGCTGCATCATGAACGCTTCCACCGGGTACCCATTTCCCATGGTGTTCAGCAGTTGCAGC 1520 1440 1450 1460 1470 1480 1490 1500 1510 1520	Matrix: DNAFULL Gap open penalty: 10.0 Gap extend penalty: 1.0
			ADAM12-All - Sw480 Amplicon Reverse ADAM12-All Isoforms	91 100 110 120 130 140 150 160 AGGAAGGACTTGGAGACCAGCCTGGAGAAAGGAATGGGGGTGTGCCTGTTTAACTGCCGGAAGTCAGGGAG 162 1521 AGGAAGGACTTGGAGACCAGCCTGGAGAAAGGAATGGGGGTGTGCCTGTTTAACTGCCGGAAGTCAGGGAG 1592 1530 1540 1550 1560 1570 1580 1590	Length: 162 Identity: 162 / 162 (100.00%) Gaps: 0 / 162 (0.00%)
ADAM12-All Forward	SW620	198bp	ADAM12-All - SW620 Amplicon Forward ADAM12-All Isoforms	1 10 20 30 40 50 60 70 80 90 CACCGGTACCCATTTCCCATGGTGTTCAGCAGTTGCAGCAGGAAGGACTTGGAGACCAGCCTGGAGAAAGGAATGGGGGTGTGCCTGTT 90 1481 CACCGGTACCCATTTCCCATGGTGTTCAGCAGTTGCAGCAGGAAGGACTTGGAGACCAGCCTGGAGAAAGGAATGGGGGTGTGCCTGTT 1570 1490 1500 1510 1520 1530 1540 1550 1560 1570	Matrix: DNAFULL Gap open penalty: 10.0 Gap extend penalty: 1.0
			ADAM12-All - SW620 Amplicon Forward ADAM12-All Isoforms	91 100 110 120 130 140 TAACTGCCGGAAGTCAGGGAGTCTTTCGGGGGCCAGAAAGTGTGGGAACAGATTTGTGG 149 1571 TAACTGCCGGAAGTCAGGGAGTCTTTCGGGGGCCAGAAAGTGTGGGAACAGATTTGTGG 1629 1580 1590 1600 1610 1620	Length: 149 Identity: 149 / 149 (100.00%) Gaps: 0 / 149 (0.00%)
ADAM12-All Reverse	SW620	198bp	ADAM12-All - SW620 Amplicon Reverse ADAM12-All Isoforms	1 10 20 30 40 50 60 70 80 90 GTAGCTGTCAAATGGCGGTTGAGAAAGGAGGCTGCATCATGAACGCTTCCACCGGGTACCCATTTCCCATGGTGTTCAGCAGTTGCAGCA 90 1432 GTAGCTGTCAAATGGCGGTTGAGAAAGGAGGCTGCATCATGAACGCTTCCACCGGGTACCCATTTCCCATGGTGTTCAGCAGTTGCAGCA 1521 1440 1450 1460 1470 1480 1490 1500 1510 1520	Matrix: DNAFULL Gap open penalty: 10.0 Gap extend penalty: 1.0
			ADAM12-All - SW620 Amplicon Reverse ADAM12-All Isoforms	91 100 110 120 130 140 150 GGAAGGACTTGGAGACCAGCCTGGAGAAAGGAATGGGGGTGTGCCTG-TTAACTGCCGGAAGTCA 155 1522 GGAAGGACTTGGAGACCAGCCTGGAGAAAGGAATGGGGGTGTGCCTGTTTAACTGCCGGAAGTCA 1587 1530 1540 1550 1560 1570 1580	Length: 156 Identity: 155 / 156 (99.36%) Gaps: 1 / 156 (0.64%)

B

Gene Name	Cell Line	Amplicon size bp	alignment		Gaps
ADAM12-245 Forward	CCD841	205bp	ADAM12-245 - CCD841 Amplicon Forward ADAM12-245 Isoforms	<div>102030405060708090100</div> <div>1AGGAGGAAAGAGGACTCAAAAGTCTGGCCTTTCACTGAGCC</div> <div>2847AGGAGGAAAGAGGACTCAAAAGTCTGGCCTTTCACTGAGCC</div> <div>28502860287028802890290029102920293029402946</div>	Matrix: DNAFULL Gap open penalty: 10.0 Gap extend penalty: 1.0 Length: 152 Identity: 151 / 152 (99.34%) Gaps: 0 / 152 (0.00%)
			ADAM12-245 - CCD841 Amplicon Forward ADAM12-245 Isoforms	<div>110120130140150</div> <div>101TCAGCCTTGGCAGCCCTGATGACTGGTCTCTGGCTGCAACTTAATGCTCTGA</div> <div>2947TCAGCCTTGGCAGCCCTGATGACTGGTCTCTGGCTGCAACTTAATGCTCTGA</div> <div>295029602970298029902998</div>	
ADAM12-245 Reverse	CCD841	205bp	ADAM12-245 - CCD841 Amplicon Reverse ADAM12-245 Isoforms	<div>102030405060708090100</div> <div>1CTGCTCCTGAGAGAGTAGCAGGTTACCACCTCTGGCAGGCCCCAGCCCTGCAGCAAGGAGGAAAGAGGACTCAAAAGTCTGGCCTTTCACTGAGCCTCCACA</div> <div>2793CTGCTCCTGAGAGAGTAGCAGGTTACCACCTCTGGCAGGCCCCAGCCCTGCAGCAAGGAGGAAAGAGGACTCAAAAGTCTGGCCTTTCACTGAGCCTCCACA</div> <div>28002810282028302840285028602870288028902892</div>	Matrix: DNAFULL Gap open penalty: 10.0 Gap extend penalty: 1.0 Length: 161 Identity: 161 / 161 (100.00%) Gaps: 0 / 161 (0.00%)
			ADAM12-245 - CCD841 Amplicon Reverse ADAM12-245 Isoforms	<div>110120130140150160</div> <div>101GCAGTGGGGGAGAAAGCAAGGGTTGGGCCCAAGTGTCCTTTCCCAAGTGACACCTCAGCCT</div> <div>2893GCAGTGGGGGAGAAAGCAAGGGTTGGGCCCAAGTGTCCTTTCCCAAGTGACACCTCAGCCT</div> <div>2900291029202930294029502953</div>	
ADAM12-245 Forward	SW480	205bp	ADAM12-245 - SW480 Amplicon Forward ADAM12-245 Isoforms	<div>102030405060708090100</div> <div>1CCAGCCCTGCAGCAAGGAGGAAGAGGACTCAAAAGTCTGGCCTTTCACTGAGCCTCCACAGCAGTGGGGGAGAAAGCAAGGGTTGGGCCCAAGTGTCCTTT</div> <div>2833CCAGCCCTGCAGCAAGGAGGAAGAGGACTCAAAAGTCTGGCCTTTCACTGAGCCTCCACAGCAGTGGGGGAGAAAGCAAGGGTTGGGCCCAAGTGTCCTTT</div> <div>28402850286028702880289029002910292029302932</div>	Matrix: DNAFULL Gap open penalty: 10.0 Gap extend penalty: 1.0 Length: 166 Identity: 166 / 166 (100.00%) Gaps: 0 / 166 (0.00%)
			ADAM12-245 - SW480 Amplicon Forward ADAM12-245 Isoforms	<div>110120130140150160</div> <div>101TCCCCAGTGACACCTCAGCCTTGGCAGCCCTGATGACTGGTCTCTGGCTGCAACTTAATGCTCTGA</div> <div>2933TCCCCAGTGACACCTCAGCCTTGGCAGCCCTGATGACTGGTCTCTGGCTGCAACTTAATGCTCTGA</div> <div>2940295029602970298029902998</div>	
ADAM12-245 Reverse	SW480	205bp	ADAM12-245 - SW480 Amplicon Reverse ADAM12-245 Isoforms	<div>102030405060708090100</div> <div>1CTGCTCCTGAGAGAGTAGCAGGTTACCACCTCTGGCAGGCCCCAGCCCTGCAGCAAGGAGGAAGAGGACTCAAAAGTCTGGCCTTTCACTGAGCCTCCACA</div> <div>2793CTGCTCCTGAGAGAGTAGCAGGTTACCACCTCTGGCAGGCCCCAGCCCTGCAGCAAGGAGGAAGAGGACTCAAAAGTCTGGCCTTTCACTGAGCCTCCACA</div> <div>28002810282028302840285028602870288028902892</div>	Matrix: DNAFULL Gap open penalty: 10.0 Gap extend penalty: 1.0 Length: 160 Identity: 160 / 160 (100.00%) Gaps: 0 / 160 (0.00%)
			ADAM12-245 - SW480 Amplicon Reverse ADAM12-245 Isoforms	<div>110120130140150160</div> <div>101AAGAGGACTCAAAAGTCTGGCCTTTCACTGAGCCTCCACAGCAGTGGGGGAGAAAGCAAGG</div> <div>2893AAGAGGACTCAAAAGTCTGGCCTTTCACTGAGCCTCCACAGCAGTGGGGGAGAAAGCAAGG</div> <div>2900291029202930294029502952</div>	
ADAM12-245 Forward	SW620	205bp	ADAM12-245 - SW620 Amplicon Forward ADAM12-245 Isoforms	<div>102030405060708090</div> <div>1CCAGCCCTGCAGC-AGGAGGAAGAGGACTCAAAAGTCTGGCCTTTCACTGAGCCTCCACAGCAGTGGGGGAGAAAGCAAGGGTTGGGCCCAAGTGTCCTTT</div> <div>2833CCAGCCCTGCAGCAAGGAGGAAGAGGACTCAAAAGTCTGGCCTTTCACTGAGCCTCCACAGCAGTGGGGGAGAAAGCAAGGGTTGGGCCCAAGTGTCCTTT</div> <div>28402850286028702880289029002910292029302932</div>	Matrix: DNAFULL Gap open penalty: 10.0 Gap extend penalty: 1.0 Length: 166 Identity: 165 / 166 (99.40%) Gaps: 1 / 166 (0.60%)
			ADAM12-245 - SW620 Amplicon Forward ADAM12-245 Isoforms	<div>100110120130140150160</div> <div>100TCCCCAGTGACACCTCAGCCTTGGCAGCCCTGATGACTGGTCTCTGGCTGCAACTTAATGCTCTGA</div> <div>2933TCCCCAGTGACACCTCAGCCTTGGCAGCCCTGATGACTGGTCTCTGGCTGCAACTTAATGCTCTGA</div> <div>2940295029602970298029902998</div>	
ADAM12-245 Reverse	SW620	205bp	ADAM12-245 - SW620 Amplicon Reverse ADAM12-245 Isoforms	<div>102030405060708090100</div> <div>1CTGCTCCTGAGAGAGTAGCAGGTTACCACCTCTGGCAGGCCCCAGCCCTGCAGCAAGGAGGAAGAGGACTCAAAAGTCTGGCCTTTCACTGAGCCTCCACA</div> <div>2793CTGCTCCTGAGAGAGTAGCAGGTTACCACCTCTGGCAGGCCCCAGCCCTGCAGCAAGGAGGAAGAGGACTCAAAAGTCTGGCCTTTCACTGAGCCTCCACA</div> <div>28002810282028302840285028602870288028902892</div>	Matrix: DNAFULL Gap open penalty: 10.0 Gap extend penalty: 1.0 Length: 160 Identity: 160 / 160 (100.00%) Gaps: 0 / 160 (0.00%)
			ADAM12-245 - SW620 Amplicon Reverse ADAM12-245 Isoforms	<div>110120130140150160</div> <div>101GCAGTGGGGGAGAAAGCAAGGGTTGGGCCCAAGTGTCCTTTCCCAAGTGACACCTCAGCC</div> <div>2893GCAGTGGGGGAGAAAGCAAGGGTTGGGCCCAAGTGTCCTTTCCCAAGTGACACCTCAGCC</div> <div>2900291029202930294029502952</div>	

C

Gene Name	Cell Line	Amplicon size bp	alignment		Gaps
ADAM12-13 Forward	CCD841	197bp	ADAM12-13 - CCD841 Amplicon Forward ADAM12-13 Isoforms	<pre> 10 20 30 40 50 60 70 80 90 100 1 AATGTAAGCCATGCTGGAAAAATAACTGCTGAGATACATACAGAATTACTGTAAC TGATTACACTTGGTAATTGTACTAAAGCCAAACATATATATAC 100 4855 AATGTAAGCCATGCTGGAAAAATAACTGCTGAGATACATACAGAATTACTGTAAC TGATTACACTTGGTAATTGTACTAAAGCCAAACATATATATAC 4954 4860 4870 4880 4890 4900 4910 4920 4930 4940 4950 </pre>	Matrix: DNAFULL Gap open penalty: 10.0 Gap extend penalty: 1.0
			ADAM12-13 - CCD841 Amplicon Forward ADAM12-13 Isoforms	<pre> 110 120 130 140 101 TATTA AAAAGGTTTACAGAATTTTATGGTGCATTACGTGGGCATTG 146 4955 TATTA AAAAGGTTTACAGAATTTTATGGTGCATTACGTGGGCATTG 5000 4960 4970 4980 4990 5000 </pre>	Length: 146 Identity: 146 / 146 (100.00%) Gaps: 0 / 146 (0.00%)
ADAM12-13 Reverse	CCD841	197bp	ADAM12-13 - CCD841 Amplicon Reverse ADAM12-13 Isoforms	<pre> 10 20 30 40 50 60 70 80 90 100 1 TCCAAC TCGTATAGCATGCATCTGTTTATTCTATAGTTATTAAGTTCTTTAAAA TGTAAGCCATGCTGGAAAAATAACTGCTGAGATACATACAGAAT 100 4803 TCCAAC TCGTATAGCATGCATCTGTTTATTCTATAGTTATTAAGTTCTTTAAAA TGTAAGCCATGCTGGAAAAATAACTGCTGAGATACATACAGAAT 4902 4810 4820 4830 4840 4850 4860 4870 4880 4890 4900 </pre>	Matrix: DNAFULL Gap open penalty: 10.0 Gap extend penalty: 1.0
			ADAM12-13 - CCD841 Amplicon Reverse ADAM12-13 Isoforms	<pre> 110 120 130 140 150 160 101 TACTGTAACTGATTACACTTGGTAATTGTACTAAAGCCAAACATATATATACTAT AAAAAAGGTT 165 4903 TACTGTAACTGATTACACTTGGTAATTGTACTAAAGCCAAACATATATATACTAT AAAAAAGGTT 4967 4910 4920 4930 4940 4950 4960 </pre>	Length: 165 Identity: 164 / 165 (99.39%) Gaps: 0 / 165 (0.00%)
ADAM12-13 Forward	SW480	197bp	ADAM12-13 - SW480 Amplicon Forward ADAM12-13 Isoforms	<pre> 10 20 30 40 50 60 70 80 90 100 1 AAATGTAAGCCATGCTGGAAAAATAACTGCTGAGATACATACAGAATTACTGTAAC TGATTACACTTGGTAATTGTACTAAAGCCAAACATATATATA 100 4854 AAATGTAAGCCATGCTGGAAAAATAACTGCTGAGATACATACAGAATTACTGTAAC TGATTACACTTGGTAATTGTACTAAAGCCAAACATATATATA 4953 4860 4870 4880 4890 4900 4910 4920 4930 4940 4950 </pre>	Matrix: DNAFULL Gap open penalty: 10.0 Gap extend penalty: 1.0
			ADAM12-13 - SW480 Amplicon Forward ADAM12-13 Isoforms	<pre> 110 120 130 140 101 CTATTA AAAAGGTTTACAGAATTTTATGGTGCATTACGTGGGCATTG 147 4954 CTATTA AAAAGGTTTACAGAATTTTATGGTGCATTACGTGGGCATTG 5000 4960 4970 4980 4990 5000 </pre>	Length: 147 Identity: 147 / 147 (100.00%) Gaps: 0 / 147 (0.00%)
ADAM12-13 Reverse	SW480	197bp	ADAM12-13 - SW480 Amplicon Reverse ADAM12-13 Isoforms	<pre> 10 20 30 40 50 60 70 80 90 100 1 TCCAAC TCGTATAGCATGCATCTGTTTATTCTATAGTTATTAAGTTCTTTAAAA TGTAAGCCATGCTGGAAAAATAACTGCTGAGATACATACAGAAT 100 4803 TCCAAC TCGTATAGCATGCATCTGTTTATTCTATAGTTATTAAGTTCTTTAAAA TGTAAGCCATGCTGGAAAAATAACTGCTGAGATACATACAGAAT 4902 4810 4820 4830 4840 4850 4860 4870 4880 4890 4900 </pre>	Matrix: DNAFULL Gap open penalty: 10.0 Gap extend penalty: 1.0
			ADAM12-13 - SW480 Amplicon Reverse ADAM12-13 Isoforms	<pre> 110 120 130 140 150 101 TACTGTAACTGATTACACTTGGTAATTGTACTAAAGCCAAACATATATATACT 153 4903 TACTGTAACTGATTACACTTGGTAATTGTACTAAAGCCAAACATATATATACT 4955 4910 4920 4930 4940 4950 </pre>	Length: 153 Identity: 153 / 153 (100.00%) Gaps: 0 / 153 (0.00%)
ADAM12-13 Forward	SW620	197bp	ADAM12-13 - SW620 Amplicon Forward ADAM12-13 Isoforms	<pre> 10 20 30 40 50 60 70 80 90 100 1 AATGTAAGCCATGCTGGAAAAATAACTGCTGAGATACATACAGAATTACTGTAAC TGATTACACTTGGTAATTGTACTAAAGCCAAACATATATATAC 100 4855 AATGTAAGCCATGCTGGAAAAATAACTGCTGAGATACATACAGAATTACTGTAAC TGATTACACTTGGTAATTGTACTAAAGCCAAACATATATATAC 4954 4860 4870 4880 4890 4900 4910 4920 4930 4940 4950 </pre>	Matrix: DNAFULL Gap open penalty: 10.0 Gap extend penalty: 1.0
			ADAM12-13 - SW620 Amplicon Forward ADAM12-13 Isoforms	<pre> 110 120 130 140 101 TATTA AAAAGGTTTACAGAATTTTATGGTGCATTACGTGGGCATT 145 4955 TATTA AAAAGGTTTACAGAATTTTATGGTGCATTACGTGGGCATT 4999 4960 4970 4980 4990 </pre>	Length: 145 Identity: 145 / 145 (100.00%) Gaps: 0 / 145 (0.00%)
ADAM12-13 Reverse	SW620	197bp	ADAM12-13 - SW620 Amplicon Reverse ADAM12-13 Isoforms	<pre> 10 20 30 40 50 60 70 80 90 100 1 TCCAAC TCGTATAGCATGCATCTGTTTATTCTATAGTTATTAAGTTCTTTAAAA TGTAAGCCATGCTGGAAAAATAACTGCTGAGATACATACAGAAT 100 4803 TCCAAC TCGTATAGCATGCATCTGTTTATTCTATAGTTATTAAGTTCTTTAAAA TGTAAGCCATGCTGGAAAAATAACTGCTGAGATACATACAGAAT 4902 4810 4820 4830 4840 4850 4860 4870 4880 4890 4900 </pre>	Matrix: DNAFULL Gap open penalty: 10.0 Gap extend penalty: 1.0
			ADAM12-13 - SW620 Amplicon Reverse ADAM12-13 Isoforms	<pre> 110 120 130 140 150 101 TACTGTAACTGATTACACTTGGTAATTGTACTAAAGCCAAACATATATATACTAT 155 4903 TACTGTAACTGATTACACTTGGTAATTGTACTAAAGCCAAACATATATATACTAT 4957 4910 4920 4930 4940 4950 </pre>	Length: 155 Identity: 155 / 155 (100.00%) Gaps: 0 / 155 (0.00%)