

Table S1A: Alignment of ADAM12-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 99 and 100%.

Gene Name	Cell Line	Amplicon size bp	alignment		Gaps
ADAM12- All Forward	CCD841	198bp	ADAM12-All - CCD841 Amplicon Forward ADAM12-All Isoforms	<div>102030405060708090</div> <div>1CCATTTCCCATGGTGTTCAGCAGTTGCAGCAGGAAGGACTTTGGAGACCAGCCTGGAGAAAGGAATGGGGGTGTGCCTGTTTAACCTGCCG90</div> <div>1469CCATTTCCCATGGTGTTCAGCAGTTGCAGCAGGAAGGACTTTGGAGACCAGCCTGGAGAAAGGAATGGGGGTGTGCCTGTTTAACCTGCCG1558</div> <div>147014801490150015101520153015401550</div>	Matrix: DNAFULL Gap open penalty: 10.0 Gap extend penalty: 1.0
			ADAM12-All - CCD841 Amplicon Forward ADAM12-All Isoforms	<div>100110120130140</div> <div>91GAAGTCAGGGAAGTCTTTCCGGGGCCAGAAAGTGTGGGAACAGATTTGTGGA140</div> <div>1559GAAGTCAGGGAAGTCTTTCCGGGGCCAGAAAGTGTGGGAACAGATTTGTGGA1608</div> <div>15601570158015901600</div>	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	<div>102030405060708090</div> <div>1GTAGCTGTCAAATGGCGGTGAGAAAGGAGGCTGCATCATGAACGCTTCCACCGGGTACCCATTTCCCATGGTGTTCAGCAGTTGCAGCA90</div> <div>1432GTAGCTGTCAAATGGCGGTGAGAAAGGAGGCTGCATCATGAACGCTTCCACCGGGTACCCATTTCCCATGGTGTTCAGCAGTTGCAGCA1521</div> <div>144014501460147014801490150015101520</div>	Matrix: DNAFULL Gap open penalty: 10.0 Gap extend penalty: 1.0
			ADAM12-All - CCD841 Amplicon Reverse ADAM12-All Isoforms	<div>100110120130140150</div> <div>91GGAAGGACTTTGGAGACCAGCCTGGAGAAAGGAATGGGGGTGTGCCTGTTAACCTGCCGGAAGTCAGG157</div> <div>1522GGAAGGACTTTGGAGACCAGCCTGGAGAAAGGAATGGGGGTGTGCCTGTTAACCTGCCGGAAGTCAGG1589</div> <div>153015401550156015701580</div>	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	<div>1020304050607080</div> <div>1ACGCTT-CACCGGGTA-CCATTTCCCATGGTGTTCAGCAGTTGCAGCAGGAAGGACTTTGGAGACCAGCCTGGAGAAAGGAATGGGGGTGT88</div> <div>1465ACGCTTCCACCGGGTACCATTTCCCATGGTGTTCAGCAGTTGCAGCAGGAAGGACTTTGGAGACCAGCCTGGAGAAAGGAATGGGGGTGT1554</div> <div>147014801490150015101520153015401550</div>	Matrix: DNAFULL Gap open penalty: 10.0 Gap extend penalty: 1.0
			ADAM12-All - SW480 Amplicon Forward ADAM12-All Isoforms	<div>90100110120130140150</div> <div>89GCCTGTTTAACCTGCCGGAAGTCAGGGAGTCTTTCCGGGGCCAGAAAGTGTGGGAACAGATTTGTGGA155</div> <div>1555GCCTGTTTAACCTGCCGGAAGTCAGGGAGTCTTTCCGGGGCCAGAAAGTGTGGGAACAGATTTGTGGA1621</div> <div>1560157015801590160016101620</div>	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	<div>102030405060708090</div> <div>1TGTAGCTGTCAAATGGCGGTGAGAAAGGAGGCTGCATCATGAACGCTTCCACCGGGTACCCATTTCCCATGGTGTTCAGCAGTTGCAGC90</div> <div>1431TGTAGCTGTCAAATGGCGGTGAGAAAGGAGGCTGCATCATGAACGCTTCCACCGGGTACCCATTTCCCATGGTGTTCAGCAGTTGCAGC1520</div> <div>144014501460147014801490150015101520</div>	Matrix: DNAFULL Gap open penalty: 10.0 Gap extend penalty: 1.0
			ADAM12-All - Sw480 Amplicon Reverse ADAM12-All Isoforms	<div>100110120130140150160</div> <div>91AGGAAGGACTTTGGAGACCAGCCTGGAGAAAGGAATGGGGGTGTGCCTGTTTAACCTGCCGGAAGTCAGGGAG162</div> <div>1521AGGAAGGACTTTGGAGACCAGCCTGGAGAAAGGAATGGGGGTGTGCCTGTTTAACCTGCCGGAAGTCAGGGAG1592</div> <div>1530154015501560157015801590</div>	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	<div>102030405060708090</div> <div>1CACCGGGTACCCATTTCCCATGGTGTTCAGCAGTTGCAGCAGGAAGGACTTTGGAGACCAGCCTGGAGAAAGGAATGGGGGTGTGCCTGTT90</div> <div>1481CACCGGGTACCCATTTCCCATGGTGTTCAGCAGTTGCAGCAGGAAGGACTTTGGAGACCAGCCTGGAGAAAGGAATGGGGGTGTGCCTGTT1570</div> <div>149015001510152015301540155015601570</div>	Matrix: DNAFULL Gap open penalty: 10.0 Gap extend penalty: 1.0
			ADAM12-All - SW620 Amplicon Forward ADAM12-All Isoforms	<div>100110120130140</div> <div>91TAACCTGCCGGAAGTCAGGGAGTCTTTCCGGGGCCAGAAAGTGTGGGAACAGATTTGTGG149</div> <div>1571TAACCTGCCGGAAGTCAGGGAGTCTTTCCGGGGCCAGAAAGTGTGGGAACAGATTTGTGG1629</div> <div>15801590160016101620</div>	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	<div>102030405060708090</div> <div>1GTAGCTGTCAAATGGCGGTGAGAAAGGAGGCTGCATCATGAACGCTTCCACCGGGTACCCATTTCCCATGGTGTTCAGCAGTTGCAGCA90</div> <div>1432GTAGCTGTCAAATGGCGGTGAGAAAGGAGGCTGCATCATGAACGCTTCCACCGGGTACCCATTTCCCATGGTGTTCAGCAGTTGCAGCA1521</div> <div>144014501460147014801490150015101520</div>	Matrix: DNAFULL Gap open penalty: 10.0 Gap extend penalty: 1.0
			ADAM12-All - SW620 Amplicon Reverse ADAM12-All Isoforms	<div>100110120130140150</div> <div>91GGAAGGACTTTGGAGACCAGCCTGGAGAAAGGAATGGGGGTGTGCCTGTTAACCTGCCGGAAGTCA155</div> <div>1522GGAAGGACTTTGGAGACCAGCCTGGAGAAAGGAATGGGGGTGTGCCTGTTAACCTGCCGGAAGTCA1587</div> <div>153015401550156015701580</div>	Length: 156 Identity: 155 / 156 (99.36%) Gaps: 1 / 156 (0.64%)

Table S1B: Alignment of ADAM12-245 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
ADAM12-245 Forward	CCD841	205bp	ADAM12-245 - CCD841 Amplicon Forward ADAM12-245 Isoforms	<div>102030405060708090100</div> <div>1A6GAGGAAGGAGCTCAAAAGTCTGGCTTTTCACTGAGCCCCCACAGCAGTGGGGGAGAAGCAAGGGTTGGGCCCAAGTGTCCCCTTTCCCCAGTGACACC100</div> <div>2847A6GAGGAAGGAGCTCAAAAGTCTGGCTTTTCACTGAGCCTCCACAGCAGTGGGGGAGAAGCAAGGGTTGGGCCCAAGTGTCCCCTTTCCCCAGTGACACC2946</div> <div>2850286028702880289029002910292029302940</div>	Matrix: DNAFULL Gap open penalty: 10.0 Gap extend penalty: 1.0
			ADAM12-245 - CCD841 Amplicon Forward ADAM12-245 Isoforms	<div>110120130140150</div> <div>101TCAGCCTTGGCAGCCCTGATGACTGGTCTCTGGCTGCAACTTAATGCTCTGA152</div> <div>2947TCAGCCTTGGCAGCCCTGATGACTGGTCTCTGGCTGCAACTTAATGCTCTGA2998</div> <div>29502960297029802990</div>	Length: 152 Identity: 151 / 152 (99.34%) Gaps: 0 / 152 (0.00%)
ADAM12-245 Reverse	CCD841	205bp	ADAM12-245 - CCD841 Amplicon Reverse ADAM12-245 Isoforms	<div>102030405060708090100</div> <div>1CTGCTCCTGAGAGAGTAGCAGGTTACCACTCTGGCAGGCCCCAGCCCTGCAGCAAGGAGGAAGAGGACTCAAAAGTCTGGCCTTTTCACTGAGCCTCCACA100</div> <div>2793CTGCTCCTGAGAGAGTAGCAGGTTACCACTCTGGCAGGCCCCAGCCCTGCAGCAAGGAGGAAGAGGACTCAAAAGTCTGGCCTTTTCACTGAGCCTCCACA2892</div> <div>2800281028202830284028502860287028802890</div>	Matrix: DNAFULL Gap open penalty: 10.0 Gap extend penalty: 1.0
			ADAM12-245 - CCD841 Amplicon Reverse ADAM12-245 Isoforms	<div>110120130140150160</div> <div>101GCAGTGGGGGAGAAGCAAGGGTTGGGCCCAAGTGTCCCCTTTCCCAAGTGACACCTCAGCCT161</div> <div>2893GCAGTGGGGGAGAAGCAAGGGTTGGGCCCAAGTGTCCCCTTTCCCAAGTGACACCTCAGCCT2953</div> <div>290029102920293029402950</div>	Length: 161 Identity: 161 / 161 (100.00%) Gaps: 0 / 161 (0.00%)
ADAM12-245 Forward	SW480	205bp	ADAM12-245 - SW480 Amplicon Forward ADAM12-245 Isoforms	<div>102030405060708090100</div> <div>1CCAGCCCTGCAGCAAGGAGGAAGAGGACTCAAAAGTCTGGCCTTTTCACTGAGCCTCCACAGCAGTGGGGGAGAAGCAAGGGTTGGGCCCAAGTGTCCCCTT100</div> <div>2833CCAGCCCTGCAGCAAGGAGGAAGAGGACTCAAAAGTCTGGCCTTTTCACTGAGCCTCCACAGCAGTGGGGGAGAAGCAAGGGTTGGGCCCAAGTGTCCCCTT2932</div> <div>2840285028602870288028902900291029202930</div>	Matrix: DNAFULL Gap open penalty: 10.0 Gap extend penalty: 1.0
			ADAM12-245 - SW480 Amplicon Forward ADAM12-245 Isoforms	<div>110120130140150160</div> <div>101TCCCAAGTGACACCTCAGCCTTGGCAGCCCTGATGACTGGTCTCTGGCTGCAACTTAATGCTCTGA166</div> <div>2933TCCCAAGTGACACCTCAGCCTTGGCAGCCCTGATGACTGGTCTCTGGCTGCAACTTAATGCTCTGA2998</div> <div>294029502960297029802990</div>	Length: 166 Identity: 166 / 166 (100.00%) Gaps: 0 / 166 (0.00%)
ADAM12-245 Reverse	SW480	205bp	ADAM12-245 - SW480 Amplicon Reverse ADAM12-245 Isoforms	<div>102030405060708090100</div> <div>1CTGCTCCTGAGAGAGTAGCAGGTTACCACTCTGGCAGGCCCCAGCCCTGCAGCAAGGAGGAAGAGGACTCAAAAGTCTGGCCTTTTCACTGAGCCTCCACA100</div> <div>2793CTGCTCCTGAGAGAGTAGCAGGTTACCACTCTGGCAGGCCCCAGCCCTGCAGCAAGGAGGAAGAGGACTCAAAAGTCTGGCCTTTTCACTGAGCCTCCACA2892</div> <div>2800281028202830284028502860287028802890</div>	Matrix: DNAFULL Gap open penalty: 10.0 Gap extend penalty: 1.0
			ADAM12-245 - SW480 Amplicon Reverse ADAM12-245 Isoforms	<div>110120130140150160</div> <div>101AAGAGGACTCAAAAGTCTGGCCTTTTCACTGAGCCTCCACAGCAAGTGGGGGAGAAGCAAGG160</div> <div>2893AAGAGGACTCAAAAGTCTGGCCTTTTCACTGAGCCTCCACAGCAAGTGGGGGAGAAGCAAGG2952</div> <div>290029102920293029402950</div>	Length: 160 Identity: 160 / 160 (100.00%) Gaps: 0 / 160 (0.00%)
ADAM12-245 Forward	SW620	205bp	ADAM12-245 - SW620 Amplicon Forward ADAM12-245 Isoforms	<div>102030405060708090</div> <div>1CCAGCCCTGCAGC-A6GAGGAAGAGGACTCAAAAGTCTGGCCTTTTCACTGAGCCTCCACAGCAGTGGGGGAGAAGCAAGGGTTGGGCCCAAGTGTCCCCTT99</div> <div>2833CCAGCCCTGCAGCAGGAGGAAGAGGACTCAAAAGTCTGGCCTTTTCACTGAGCCTCCACAGCAGTGGGGGAGAAGCAAGGGTTGGGCCCAAGTGTCCCCTT2932</div> <div>2840285028602870288028902900291029202930</div>	Matrix: DNAFULL Gap open penalty: 10.0 Gap extend penalty: 1.0
			ADAM12-245 - SW620 Amplicon Forward ADAM12-245 Isoforms	<div>100110120130140150160</div> <div>100TCCCCAGTGACACCTCAGCCTTGGCAGCCCTGATGACTGGTCTCTGGCTGCAACTTAATGCTCTGA165</div> <div>2933TCCCCAGTGACACCTCAGCCTTGGCAGCCCTGATGACTGGTCTCTGGCTGCAACTTAATGCTCTGA2998</div> <div>294029502960297029802990</div>	Length: 166 Identity: 165 / 166 (99.40%) Gaps: 1 / 166 (0.60%)
ADAM12-245 Reverse	SW620	205bp	ADAM12-245 - SW620 Amplicon Reverse ADAM12-245 Isoforms	<div>102030405060708090100</div> <div>1CTGCTCCTGAGAGAGTAGCAGGTTACCACTCTGGCAGGCCCCAGCCCTGCAGCAAGGAGGAAGAGGACTCAAAAGTCTGGCCTTTTCACTGAGCCTCCACA100</div> <div>2793CTGCTCCTGAGAGAGTAGCAGGTTACCACTCTGGCAGGCCCCAGCCCTGCAGCAAGGAGGAAGAGGACTCAAAAGTCTGGCCTTTTCACTGAGCCTCCACA2892</div> <div>2800281028202830284028502860287028802890</div>	Matrix: DNAFULL Gap open penalty: 10.0 Gap extend penalty: 1.0
			ADAM12-245 - SW620 Amplicon Reverse ADAM12-245 Isoforms	<div>110120130140150160</div> <div>101GCAGTGGGGGAGAAGCAAGGGTTGGGCCCAAGTGTCCCCTTTCCCAAGTGACACCTCAGCC160</div> <div>2893GCAGTGGGGGAGAAGCAAGGGTTGGGCCCAAGTGTCCCCTTTCCCAAGTGACACCTCAGCC2952</div> <div>290029102920293029402950</div>	Length: 160 Identity: 160 / 160 (100.00%) Gaps: 0 / 160 (0.00%)

Table S1C: Alignment of ADAM12-245 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
ADAM12-13 Forward	CCD841	197bp	ADAM12-13 - CCD841 Amplicon Forward ADAM12-13 Isoforms	<div><div>1020405060708090100</div><div>1AATGTAAGCCATGCTGGAAAAATAACTGCTGAGATACATACAGAATTACTGTAAC TGATTACACTTGGTAATTGTACTAAAGCCAAACATATATATAC100</div><div>4855AATGTAAGCCATGCTGGAAAAATAACTGCTGAGATACATACAGAATTACTGTAAC TGATTACACTTGGTAATTGTACTAAAGCCAAACATATATATAC4954</div><div>4860487048804890490049104920493049404950</div></div>	Matrix: DNAFULL Gap open penalty: 10.0 Gap extend penalty: 1.0
			ADAM12-13 - CCD841 Amplicon Forward ADAM12-13 Isoforms	<div><div>110120130140</div><div>101TATTA AAAAGGTTTACAGAATTTTATGGTGCA TTACGTGGGCATTG146</div><div>4955TATTA AAAAGGTTTACAGAATTTTATGGTGCA TTACGTGGGCATTG5000</div><div>49604970498049905000</div></div>	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	<div><div>102030405060708090100</div><div>1TCCAAC TCGTATAGCATGCATCTGTTTATTC TATAGTTATTAAGTTC TTTAA AATGTAAGCCATGCTGGAAAAATAACTGCTGAGATACATACAGAAT100</div><div>4803TCCAAC TCGTATAGCATGCATCTGTTTATTC TATAGTTATTAAGTTC TTTAA AATGTAAGCCATGCTGGAAAAATAACTGCTGAGATACATACAGAAT4902</div><div>4810482048304840485048604870488048904900</div></div>	Matrix: DNAFULL Gap open penalty: 10.0 Gap extend penalty: 1.0
			ADAM12-13 - CCD841 Amplicon Reverse ADAM12-13 Isoforms	<div><div>110120130140150160</div><div>101TACTGTAACTGATTACACTTGGTAATTGTACTAAAGCCAAACATATATATACTATAAAAAGGTT165</div><div>4903TACTGTAACTGATTACACTTGGTAATTGTACTAAAGCCAAACATATATATACTATAAAAAGGTT4967</div><div>491049204930494049504960</div></div>	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	<div><div>102030405060708090100</div><div>1AAATGTAAGCCATGCTGGAAAAATAACTGCTGAGATACATACAGAATTACTGTAAC TGATTACACTTGGTAATTGTACTAAAGCCAAACATATATATA100</div><div>4854AAATGTAAGCCATGCTGGAAAAATAACTGCTGAGATACATACAGAATTACTGTAAC TGATTACACTTGGTAATTGTACTAAAGCCAAACATATATATA4953</div><div>4860487048804890490049104920493049404950</div></div>	Matrix: DNAFULL Gap open penalty: 10.0 Gap extend penalty: 1.0
			ADAM12-13 - SW480 Amplicon Forward ADAM12-13 Isoforms	<div><div>110120130140</div><div>101CTATTA AAAAGGTTTACAGAATTTTATGGTGCA TTACGTGGGCATTG147</div><div>4954CTATTA AAAAGGTTTACAGAATTTTATGGTGCA TTACGTGGGCATTG5000</div><div>49604970498049905000</div></div>	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	<div><div>102030405060708090100</div><div>1TCCAAC TCGTATAGCATGCATCTGTTTATTC TATAGTTATTAAGTTC TTTAA AATGTAAGCCATGCTGGAAAAATAACTGCTGAGATACATACAGAAT100</div><div>4803TCCAAC TCGTATAGCATGCATCTGTTTATTC TATAGTTATTAAGTTC TTTAA AATGTAAGCCATGCTGGAAAAATAACTGCTGAGATACATACAGAAT4902</div><div>4810482048304840485048604870488048904900</div></div>	Matrix: DNAFULL Gap open penalty: 10.0 Gap extend penalty: 1.0
			ADAM12-13 - SW480 Amplicon Reverse ADAM12-13 Isoforms	<div><div>110120130140150</div><div>101TACTGTAACTGATTACACTTGGTAATTGTACTAAAGCCAAACATATATACT153</div><div>4903TACTGTAACTGATTACACTTGGTAATTGTACTAAAGCCAAACATATATACT4955</div><div>49104920493049404950</div></div>	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	<div><div>102030405060708090100</div><div>1AATGTAAGCCATGCTGGAAAAATAACTGCTGAGATACATACAGAATTACTGTAAC TGATTACACTTGGTAATTGTACTAAAGCCAAACATATATATAC100</div><div>4855AATGTAAGCCATGCTGGAAAAATAACTGCTGAGATACATACAGAATTACTGTAAC TGATTACACTTGGTAATTGTACTAAAGCCAAACATATATATAC4954</div><div>4860487048804890490049104920493049404950</div></div>	Matrix: DNAFULL Gap open penalty: 10.0 Gap extend penalty: 1.0
			ADAM12-13 - SW620 Amplicon Forward ADAM12-13 Isoforms	<div><div>110120130140</div><div>101TATTA AAAAGGTTTACAGAATTTTATGGTGCA TTACGTGGGCATT145</div><div>4955TATTA AAAAGGTTTACAGAATTTTATGGTGCA TTACGTGGGCATT4999</div><div>4960497049804990</div></div>	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	<div><div>102030405060708090100</div><div>1TCCAAC TCGTATAGCATGCATCTGTTTATTC TATAGTTATTAAGTTC TTTAA AATGTAAGCCATGCTGGAAAAATAACTGCTGAGATACATACAGAAT100</div><div>4803TCCAAC TCGTATAGCATGCATCTGTTTATTC TATAGTTATTAAGTTC TTTAA AATGTAAGCCATGCTGGAAAAATAACTGCTGAGATACATACAGAAT4902</div><div>4810482048304840485048604870488048904900</div></div>	Matrix: DNAFULL Gap open penalty: 10.0 Gap extend penalty: 1.0
			ADAM12-13 - SW620 Amplicon Reverse ADAM12-13 Isoforms	<div><div>110120130140150</div><div>101TACTGTAACTGATTACACTTGGTAATTGTACTAAAGCCAAACATATATACTAT155</div><div>4903TACTGTAACTGATTACACTTGGTAATTGTACTAAAGCCAAACATATATACTAT4957</div><div>49104920493049404950</div></div>	Length: 155 Identity: 155 / 155 (100.00%) Gaps: 0 / 155 (0.00%)