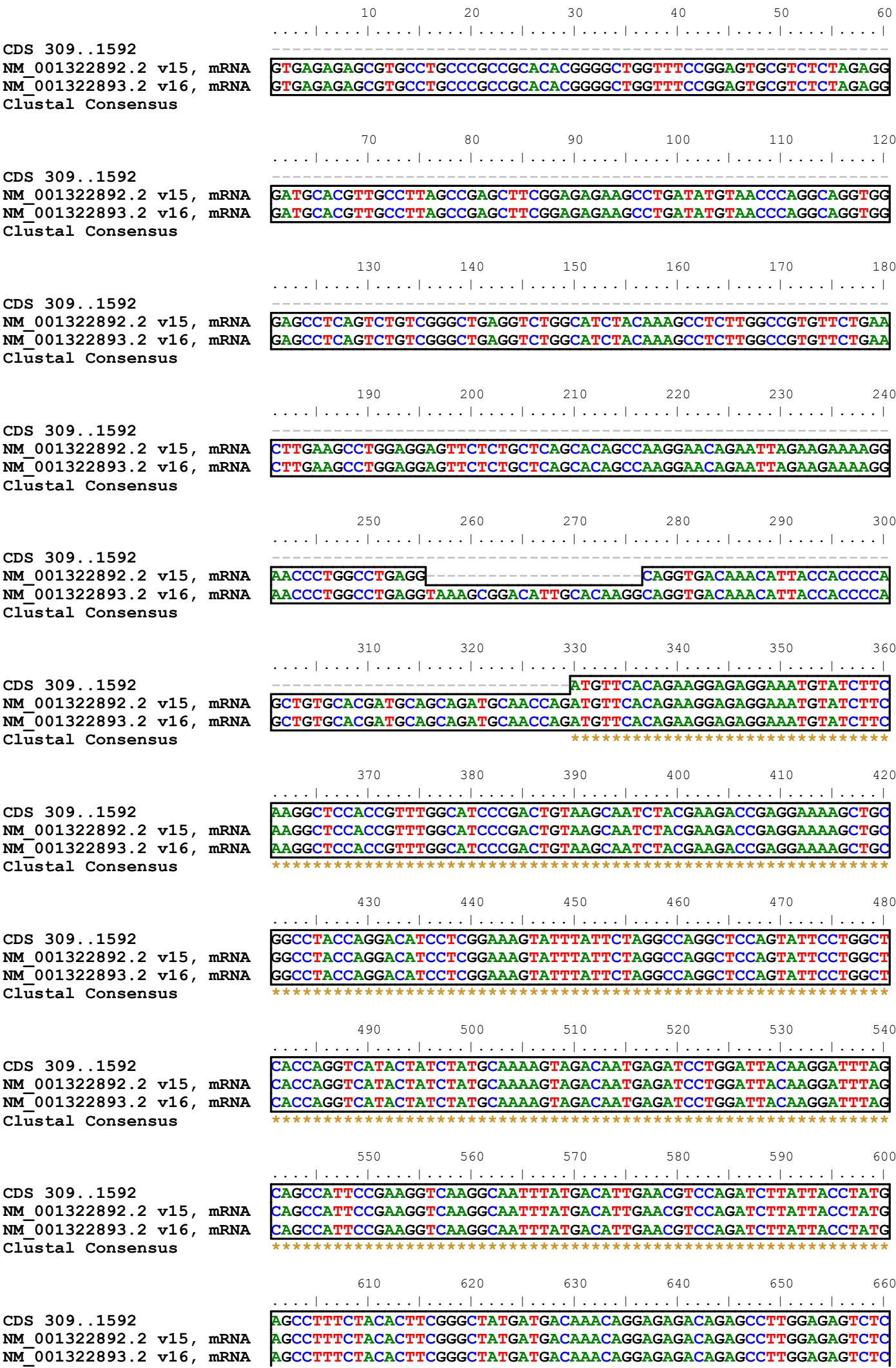




[illegible]

730 740 750 760 770 780

TCCATCGGTCCACGAGCCAGGGCTCCATCAACTCCCCTGTTGTACAGCCGCCACAGCTACA
TCCATCGGTCCACGAGCCAGGGCTCCATCAACTCCCCTGTTGTACAGCCGCCACAGCTACA
TCCATCGGTCCACGAGCCAGGGCTCCATCAACTCCCCTGTTGTACAGCCGCCACAGCTACA

790 800 810 820 830 840

CTCCAAACCGTCCCGCTCTCCCCAGCATTTCCACAGACCTGATCAAGGAATCAACATTT
CTCCAAACCGTCCCGCTCTCCCCAGCATTTCCACAGACCTGATCAAGGAATCAACATTT
CTCCAAACCGTCCCGCTCTCCCCAGCATTTCCACAGACCTGATCAAGGAATCAACATTT

850 860 870 880 890 900

ACCGAAAGCCACCCATCTACAAACAGCATGCTGCCTTGGCAGCCCAGAGCAAGTCCCTCAG
ACCGAAAGCCACCCATCTACAAACAGCATGCTGCCTTGGCAGCCCAGAGCAAGTCCCTCAG
ACCGAAAGCCACCCATCTACAAACAGCATGCTGCCTTGGCAGCCCAGAGCAAGTCCCTCAG

910 920 930 940 950 960

AAGATATCATCAAGTTTTCCAAGTTCCTCCAGCAGCCCAGGCCACCAGACCCCAGCGAGACAC
AAGATATCATCAAGTTTTCCAAGTTCCTCCAGCAGCCCAGGCCACCAGACCCCAGCGAGACAC
AAGATATCATCAAGTTTTCCAAGTTCCTCCAGCAGCCCAGGCCACCAGACCCCAGCGAGACAC

970 980 990 1000 1010 1020

C A A A G A T T G A G A C G G A C C A C T G G C C T G G T C C C C C C T C A T T T G C T G T C G T A G G A C C T G A C A
C A A A G A T T G A G A C G G A C C A C T G G C C T G G T C C C C C C T C A T T T G C T G T C G T A G G A C C T G A C A
C A A A G A T T G A G A C G G A C C A C T G G C C T G G T C C C C C C T C A T T T G C T G T C G T A G G A C C T G A C A

1030 1040 1050 1060 1070 1080

TGAAACGCAGATCTAGTGGCAGAGAGGAAGATGATGAGGAACTTCTGAGACGTCGGCAGC
TGAAACGCAGATCTAGTGGCAGAGAGGAAGATGATGAGGAACTTCTGAGACGTCGGCAGC
TGAAACGCAGATCTAGTGGCAGAGAGGAAGATGATGAGGAACTTCTGAGACGTCGGCAGC

1090 1100 1110 1120 1130 1140

TTCAAGAGAGCAATTAAATGAAGCTTAACTCAGGCCCTGGGACAGTTGATCTTGAAAGAAG
TTCAAGAGAGAGCAATTAAATGAAGCTTAACTCAGGCCCTGGGACAGTTGATCTTGAAAGAAG
TTCAAGAGAGAGCAATTAAATGAAGCTTAACTCAGGCCCTGGGACAGTTGATCTTGAAAGAAG

1150 1160 1170 1180 1190 1200

AGATGGAGAAAGAGAGCCGGGAAAGGTCATCTCTGTAGCCAGTCGCTACGATTCTCCCA
AGATGGAGAAAGAGAGCCGGGAAAGGTCATCTCTGTAGCCAGTCGCTACGATTCTCCCA
AGATGGAGAAAGAGAGCCGGGAAAGGTCATCTCTGTAGCCAGTCGCTACGATTCTCCCA

[illegible]

1270 1280 1290 1300 1310 1320
 . . . | . . . | . . . | . . . | . . . | . . . | . . . | . . . |
 ATGGGCTTCACCGGCGTGTTCCTACCGACTTCGCTCAGTATAACAGCTATGGGGATGTCA

NM_001322892.2 v15, mRNA ATGGGGCTTCACCGGCCTGTTTCTACCGACTTCGCTCAGTATAACAGCTATGGGGATGTCA
NM_001322893.2 v16, mRNA ATGGGGCTTCACCGGCCTGTTTCTACCGACTTCGCTCAGTATAACAGCTATGGGGATGTCA
Clustal Consensus *****

1330 1340 1350 1360 1370 1380
....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|

CDS 309..1592 GCGGGGGAGTGCAGATTACCAGACACTCCCAGATGGCCACATGCCTGCAATGAGAATGG
NM_001322892.2 v15, mRNA GCGGGGGAGTGCAGATTACCAGACACTCCCAGATGGCCACATGCCTGCAATGAGAATGG
NM_001322893.2 v16, mRNA GCGGGGGAGTGCAGATTACCAGACACTCCCAGATGGCCACATGCCTGCAATGAGAATGG
Clustal Consensus *****

1390 1400 1410 1420 1430 1440
....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|

CDS 309..1592 ACCGAGGAGTGTCATGCCAACATGTTGGAACCAAGATATTTCCATATGAAATGCTCA
NM_001322892.2 v15, mRNA ACCGAGGAGTGTCATGCCAACATGTTGGAACCAAGATATTTCCATATGAAATGCTCA
NM_001322893.2 v16, mRNA ACCGAGGAGTGTCATGCCAACATGTTGGAACCAAGATATTTCCATATGAAATGCTCA
Clustal Consensus *****

1450 1460 1470 1480 1490 1500
....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|

CDS 309..1592 TGGTGACCAACAGAGGGCGAAACAAAATCCTCAGAGAGGTGGACAGAACCAGGCTGGAGC
NM_001322892.2 v15, mRNA TGGTGACCAACAGAGGGCGAAACAAAATCCTCAGAGAGGTGGACAGAACCAGGCTGGAGC
NM_001322893.2 v16, mRNA TGGTGACCAACAGAGGGCGAAACAAAATCCTCAGAGAGGTGGACAGAACCAGGCTGGAGC
Clustal Consensus *****

1510 1520 1530 1540 1550 1560
....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|

CDS 309..1592 GCCACTTAGCCCCTGAAGTGTTTCGGGAAATCTTTGGAATGTCCATACAGGAGTTTGACA
NM_001322892.2 v15, mRNA GCCACTTAGCCCCTGAAGTGTTTCGGGAAATCTTTGGAATGTCCATACAGGAGTTTGACA
NM_001322893.2 v16, mRNA GCCACTTAGCCCCTGAAGTGTTTCGGGAAATCTTTGGAATGTCCATACAGGAGTTTGACA
Clustal Consensus *****

1570 1580 1590 1600 1610 1620
....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|

CDS 309..1592 GGTTACCTCTTTTGGAGACGCAACGACATGAAGAAAAAAGCAAACTCTTCTAA
NM_001322892.2 v15, mRNA GGTTACCTCTTTTGGAGACGCAACGACATGAAGAAAAAAGCAAACTCTTCTAAGTCCAC
NM_001322893.2 v16, mRNA GGTTACCTCTTTTGGAGACGCAACGACATGAAGAAAAAAGCAAACTCTTCTAAGTCCAC
Clustal Consensus *****

1630 1640 1650 1660 1670 1680
....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|

CDS 309..1592 TCGTGAATGGCAATTAGAGAAAGGACTGACAGTGGCGGTGCCCCATAGGATGTCATATTG
NM_001322892.2 v15, mRNA TCGTGAATGGCAATTAGAGAAAGGACTGACAGTGGCGGTGCCCCATAGGATGTCATATTG
NM_001322893.2 v16, mRNA TCGTGAATGGCAATTAGAGAAAGGACTGACAGTGGCGGTGCCCCATAGGATGTCATATTG
Clustal Consensus -----

1690 1700 1710 1720 1730 1740
....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|

CDS 309..1592 AGGCCCCAAACTTGATTGGAGAATTTGCAAACCTACCGTCGCTCAGCAACACCAAAAAGAGA
NM_001322892.2 v15, mRNA AGGCCCCAAACTTGATTGGAGAATTTGCAAACCTACCGTCGCTCAGCAACACCAAAAAGAGA
NM_001322893.2 v16, mRNA AGGCCCCAAACTTGATTGGAGAATTTGCAAACCTACCGTCGCTCAGCAACACCAAAAAGAGA
Clustal Consensus -----

1750 1760 1770 1780 1790 1800
....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|

CDS 309..1592 AAGTCTGGTTAAACACCATGAGTCAAATGTCGGGCCAGCCAACAGTAACACTTGCCAAG
NM_001322892.2 v15, mRNA AAGTCTGGTTAAACACCATGAGTCAAATGTCGGGCCAGCCAACAGTAACACTTGCCAAG
NM_001322893.2 v16, mRNA AAGTCTGGTTAAACACCATGAGTCAAATGTCGGGCCAGCCAACAGTAACACTTGCCAAG
Clustal Consensus -----

1810 1820 1830 1840 1850 1860
....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|

CDS 309..1592 AAGCATGGCGTAGAAATTTCTATGTTCCGAAACACAGAGTAGTGTCACATGTGAGCTTT
NM_001322892.2 v15, mRNA AAGCATGGCGTAGAAATTTCTATGTTCCGAAACACAGAGTAGTGTCACATGTGAGCTTT
NM_001322893.2 v16, mRNA AAGCATGGCGTAGAAATTTCTATGTTCCGAAACACAGAGTAGTGTCACATGTGAGCTTT
Clustal Consensus -----

1870 1880 1890 1900 1910 1920
....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|

CDS 309..1592 TCACATTACCTTATGTATACAACAGGAGCTGCGTTGTTTTCTTCTTTTCTTTTCTTTTCTTTA
NM_001322892.2 v15, mRNA TCACATTACCTTATGTATACAACAGGAGCTGCGTTGTTTTCTTCTTTTCTTTTCTTTTCTTTA
NM_001322893.2 v16, mRNA TCACATTACCTTATGTATACAACAGGAGCTGCGTTGTTTTCTTCTTTTCTTTTCTTTTCTTTA
Clustal Consensus -----

1930 1940 1950 1960 1970 1980

[illegible]

TCTGTTGTCCAACAACAGTGCTGACTGTCCGGATAAGAGCTGGCAAGTGCCCTTAGGATG
TCTGTTGTCCAACAACAGTGCTGACTGTCCGGATAAGAGCTGGCAAGTGCCCTTAGGATG

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CCGCA TGGGAAAAATCGGTTATCATAAATTCAAAGTATAAATATATTTATTAAAGTAGCGC

CCGCATGGGAAAAATCGGTTATCATAAATTCAAAGTATAAAATATATTTTATTAAGTAGCGC
CCGCATGGGAAAAATCGGTTATCATAAATTCAAAGTATAAAATATATTTTATTAAGTAGCGC

[illegible]

TGCGGCTAAGAAGGAAGAGTGAGGGGTCTGTCCATGGGGTGGCAGTGATTTACACCCGC

TGCGGCCTAAGAAAGGAAGAGTGAGGGGTCTGTCCATGGGGTGGCAGTGATTTTCAACCCGCTGCGGCCTAAGAAAGGAAGAGTGAGGGGTCTGTCCATGGGGTGGCAGTGATTTTCAACCCGCT

. . . | . . . | . . . | . . . | . . . | . . . | . . . | . . . | . . . | . . . | . . . |

CTTTCTTGAA TGGCTTCGTGTTACTCAGCCGTGCCCTGGCAGGAATGGA ACTCCATCAGG

CTTTCTTGAATGGCTTCGTGTTACTCAGCCGTGCCCTGGCAGGAATGGAATCCATCAGG
CTTTCTTGAATGGCTTCGTGTTACTCAGCCGTGCCCTGGCAGGAATGGAATCCATCAGG

. . . | . . . | . . . | . . . | . . . | . . . | . . . | . . . | . . . | . . . | . . . |

GAACAGGGCAGCTCTGTTTGAATGGGGTGAAAAACAGCAAAATTAAATTCCTTAGCAAGCTC

GAACAGGGG CAGCTCTGTTTGAATGGGGTGAAAAACAGCAAAATTAAATTCCTTAGCAAGCTC
GAACAGGGG CAGCTCTGTTTGAATGGGGTGAAAAACAGCAAAATTAAATTCCTTAGCAAGCTC

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CTTGTTCTCTACTGTTCAACGGGACCTGGCTGGCAAATGACTTAGCTATTAGTATATTTA

CTTGGTTCTCTACTGTTCAACCGGGACCTGGCTGGCAAATGACTTAGCTATTAGTATATTTA
CTTGGTTCTCTACTGTTCAACCGGGACCTGGCTGGCAAATGACTTAGCTATTAGTATATTTA

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AAAC TGT CAAA GCAA AGGA AGCA GGA TGA AGG AAC CTT CCT TAA CTCT

AAAAAC**TGTT**CAAAAGCAAAAGAGAGGAACAGGAAT**G**AAAGGAAAC**CTT**CC**CTT**AAC**TCT**
 AAAAC**TGTT**CAAAAGCAAAAGAGAGGAACAGGAAT**G**AAAGGAAAC**CTT**CC**CTT**AAC**TCT**

. . . | . . . | . . . | . . . | . . . | . . . | . . . | . . . | . . . | . . . | . . . |

TTCTGCTTCCCATAGCAGGTCTGGTTCCTGCTCCCCGCCTAGGACAGGAGCTGTCTGGAG

TTCTGCTTCCCATAGCAGGTCTGGTTCCTGCTCCCCGCTAGGACAGGAGCTGTC TGGAGAG
TTCTGCTTCCCATAGCAGGTCTGGTTCCTGCTCCCCGCTAGGACAGGAGCTGTC TGGAGAG

. . . | . . . | . . . | . . . | . . . | . . . | . . . | . . . | . . . | . . . | . . . |

CTCCACCTTTGCAAAGAAAGGAAAAACACAAATTGCCCCAGATTGGCCAGTGGCATGC

CTCCACCTTTGCAAGGAAAGGAAAAACACAAATTGCCCCAGATTGGCCCAGTGGCATGCTC
CTCCACCTTTGCAAGGAAAGGAAAAACACAAATTGCCCCAGATTGGCCCAGTGGCATGCTC

[illegible]

CA TTAGGTGA TTTTGCA TAGGGGCCA TATCA TTCATGGCC AAAAAAAAA CCA AAAAGCAA

CATTAGGTGATTTTGCATAGGGGCCATATCATTATGGCCAAAAAAACCAAAAAGCAAA
CATTAGGTGATTTTGCATAGGGGCCATATCATTATGGCCAAAAAAACCAAAAAGCAAA

.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|

AAACAAAAACAAGTCCCATGTCCCTACTGACTCTAGTTCTTCCAGTCGTTATCCTCTGCTG

AAACAAAAACAAGTCCCATGTCCCTACTGACTCTAGTTCTTCCAGTCGTTATCCCTCGCTG
AAACAAAAACAAGTCCCATGTCCCTACTGACTCTAGTTCTTCCAGTCGTTATCCCTCGCTG

[illegible]

CDS 309..1592		
NM_001322892.2 v15, mRNA	TGGTGCATTTCCAGTGCTTCCTTACCTGTCAATAACAATGGTGGCCACCTGGGTCCCAGC	
NM_001322893.2 v16, mRNA	TGGTGCATTTCCAGTGCTTCCTTACCTGTCAATAACAATGGTGGCCACCTGGGTCCCAGC	
Clustal Consensus		
	391039203930394039503960	
		
CDS 309..1592		
NM_001322892.2 v15, mRNA	ACTTGCGCTGGTGGAGAGATTGTTTTTCATTATGGAGCTAATAAAGGGTCCCTACGTTTTAC	
NM_001322893.2 v16, mRNA	ACTTGGBCTGGTGGAGAGAATTTTTTTCATTATGGAGCTAATAAAGGGTCCCTACGTTTTAC	
Clustal Consensus		
	397039803990400040104020	
		
CDS 309..1592		
NM_001322892.2 v15, mRNA	ATTGATTAAATGAATTATCACCCAGACATGTGCAGATGAAATGTCAATATAAGAAAAATCA	
NM_001322893.2 v16, mRNA	ATTGATTAAATGAATTATCACCCAGACATGTGCAGATGAAATGTCAATATAAGAAAAATCA	
Clustal Consensus		
	403040404050406040704080	
		
CDS 309..1592		
NM_001322892.2 v15, mRNA	AGGTATTTGGGAAACATGGGCATAATCAGGTAGTTTTTGCTAAAATTCCTCTTCCTTGGTC	
NM_001322893.2 v16, mRNA	AGGTATTTGGGAAACATGGGCATAATCAGGTAGTTTTTGCTAAAATTCCTCTTCCTTGGTC	
Clustal Consensus		
	409041004110412041304140	
		
CDS 309..1592		
NM_001322892.2 v15, mRNA	TACATAAAGAAGACATGGGTCTGT CATAG AATGGGGACATTAGACTGAAAAC TGGGACAA	
NM_001322893.2 v16, mRNA	TACATAAAGAAGACATGGGTCTGT CATAG AATGGGGACATTAGACTGAAAAC TGGGACAA	
Clustal Consensus		
	415041604170418041904200	
		
CDS 309..1592		
NM_001322892.2 v15, mRNA	CCCCCTTCCTTAATTTTATAGAGACTAGGAGTTAAGGGGCCTGCCTAAGATTGCAGTGATA	
NM_001322893.2 v16, mRNA	CCCCCTTCCTTAATTTTATAGAGACTAGGAGTTAAGGGGCCTGCCTAAGATTGCAGTGATA	
Clustal Consensus		
	421042204230424042504260	
		
CDS 309..1592		
NM_001322892.2 v15, mRNA	AAGAACTGAACCCCTAAATCAGCTCCC ACTA ATGAAACCCTGCTTTCCTTGATCTTTTAA	
NM_001322893.2 v16, mRNA	AAGAACTGAACCCCTAAATCAGCTCCC ACTA ATGAAACCCTGCTTTCCTTGATCTTTTAA	
Clustal Consensus		
	427042804290430043104320	
		
CDS 309..1592		
NM_001322892.2 v15, mRNA	ACTCAGTTC TG CATCCA AC TTGAGAAGAAAAA AGCTTCCTTTCCATATCAAGT ACCATAT	
NM_001322893.2 v16, mRNA	ACTCAGTTC TG CATCCA AC TTGAGAAGAAAAA AGCTTCCTTTCCATATCAAGT ACCATAT	
Clustal Consensus		
	433043404350436043704380	
		
CDS 309..1592		
NM_001322892.2 v15, mRNA	GAGTTCATTTAAACTGCACCTTGCAGAAATGCATTGCCAGAAAGCACCAGTAGCCTCCTA	
NM_001322893.2 v16, mRNA	GAGTTCATTTAAACTGCACCTTGCAGAAATGCATTGCCAGAAAGCACCAGTAGCCTCCTA	
Clustal Consensus		
	439044004410442044304440	
		
CDS 309..1592		
NM_001322892.2 v15, mRNA	TCTGCAAGCAGAGTAGTGCTCTGCTCTGGGGAGGGGTCAATTGGAACCATAATGCAGAGT	
NM_001322893.2 v16, mRNA	TCTGCAAGCAGAGTAGTGCTCTGCTCTGGGGAGGGGTCAATTGGAACCATAATGCAGAGT	
Clustal Consensus		
	445044604470448044904500	
		
CDS 309..1592		
NM_001322892.2 v15, mRNA	GGGCCCCCTACTCCATTTCCCAGCAAAGGGCTCCAGCTGGAGGGATGGGTTGTGGGGCAA	
NM_001322893.2 v16, mRNA	GGGCCCCCTACTCCATTTCCCAGCAAAGGGCTCCAGCTGGAGGGATGGGTTGTGGGGCAA	
Clustal Consensus		

			4510	4520	4530	4540	4550	4560
								
CDS 309..1592								
NM_001322892.2 v15, mRNA			CCTGGTTCC	TGCTAACTGCCAGATTGAATGTGTGGGCTAGAATGCCTGCACATTTAGTTA				
NM_001322893.2 v16, mRNA			CCTGGTTCC	TGCTAACTGCCAGATTGAATGTGTGGGCTAGAATGCCTGCACATTTAGTTA				
Clustal Consensus								
			4570	4580	4590	4600	4610	4620
								
CDS 309..1592								
NM_001322892.2 v15, mRNA			AACTGGGCTCAGCATGCTTGTCCTCAAAATGTCCATCCTGGTCACAGCACACAAGATGGC					
NM_001322893.2 v16, mRNA			AACTGGGCTCAGCATGCTTGTCCTCAAAATGTCCATCCTGGTCACAGCACACAAGATGGC					
Clustal Consensus								
			4630	4640	4650	4660	4670	4680
								
CDS 309..1592								
NM_001322892.2 v15, mRNA			TATTGGTCTGCTTTTACCC	TACCCGTGACTATACATGAAAATTCAGTTATTAACACACT				
NM_001322893.2 v16, mRNA			TATTGGTCTGCTTTTACCC	TACCCGTGACTATACATGAAAATTCAGTTATTAACACACT				
Clustal Consensus								
			4690	4700	4710	4720	4730	4740
								
CDS 309..1592								
NM_001322892.2 v15, mRNA			CAAAC	TGGTGGAGCTTGTTACCC	TAGGAAGGGGATTGTATATATGGCAGGCTTCCCTGG			
NM_001322893.2 v16, mRNA			CAAAC	TGGTGGAGCTTGTTACCC	TAGGAAGGGGATTGTATATATGGCAGGCTTCCCTGG			
Clustal Consensus								
			4750	4760	4770	4780	4790	4800
								
CDS 309..1592								
NM_001322892.2 v15, mRNA			TGCCGATGTAAAGGGCTACATTTGGGAACATTTGACTTCCTTGGGACTCTTAAGTGCATA					
NM_001322893.2 v16, mRNA			TGCCGATGTAAAGGGCTACATTTGGGAACATTTGACTTCCTTGGGACTCTTAAGTGCATA					
Clustal Consensus								
			4810	4820	4830	4840	4850	4860
								
CDS 309..1592								
NM_001322892.2 v15, mRNA			ATGATGGCATGAAGTAAAAGGGG	CCCTCAATGATGATAGGAAAATCAGTTCTTTTAAATTT				
NM_001322893.2 v16, mRNA			ATGATGGCATGAAGTAAAAGGGG	CCCTCAATGATGATAGGAAAATCAGTTCTTTTAAATTT				
Clustal Consensus								
			4870	4880	4890	4900	4910	4920
								
CDS 309..1592								
NM_001322892.2 v15, mRNA			TC	TTCAAGAAAATCCAGGCTATCACATAGTCTTTCTGTGTGACTTATTAGGAGATAGGAA				
NM_001322893.2 v16, mRNA			TC	TTCAAGAAAATCCAGGCTATCACATAGTCTTTCTGTGTGACTTATTAGGAGATAGGAA				
Clustal Consensus								
			4930	4940	4950	4960	4970	4980
								
CDS 309..1592								
NM_001322892.2 v15, mRNA			GAGCATTTGGGAAACTTGCACAGCTAGCTATGCATCTACATTTTGGTTTGGGGTTAGTTAT					
NM_001322893.2 v16, mRNA			GAGCATTTGGGAAACTTGCACAGCTAGCTATGCATCTACATTTTGGTTTGGGGTTAGTTAT					
Clustal Consensus								
			4990	5000	5010	5020	5030	5040
								
CDS 309..1592								
NM_001322892.2 v15, mRNA			GAAATGTTCTTAAATATGACGTGTTCAATAA	CTTTCACATAAACTTCCGTGTTCTCCAAAACC				
NM_001322893.2 v16, mRNA			GAAATGTTCTTAAATATGACGTGTTCAATAA	CTTTCACATAAACTTCCGTGTTCTCCAAAACC				
Clustal Consensus								
			5050	5060	5070	5080	5090	5100
								
CDS 309..1592								
NM_001322892.2 v15, mRNA			TC	AAAGAGATAGAGTTAATGAGTTGTTGTTTTTTTTTAAATGGGGGTAGTTTTCTATCTG				

CDS 309..1592

5770	5780	5790	5800	5810	5820
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TTTGT CAGTATGCCCAAAAGCTTGCTCTTTTGTGCTCCCTTTTGAATAACTTTCTATCCA
TTTGT CAGTATGCCCAAAAGCTTGCTCTTTTGTGCTCCCTTTTGAATAACTTTCTATCCA

GAAAAAGAGATTATTTGGGACTTGAGATTTGCAGTGATACCAACTTATAGCAATGATGTA
GAAAAAGAGATTATTTGGGACTTGAGATTTGCAGTGATACCAACTTATAGCAATGATGTA

CTTTAAGGGAACTACCCAACTATGTTGTGATAGAAGAAAGAGAAACCTTCACTTTGGCAT
CTTTAAGGGAACTACCCAACTATGTTGTGATAGAAGAAAGAGAAACCTTCACTTTGGCAT

TTTTTTTTTAACTACTGTTTATTTTCTGTTTGCGGCCAGGAAGCAGTGGGAGGTGGTGG
TTTTTTTTTAACTACTGTTTATTTTCTGTTTGCGGCCAGGAAGCAGTGGGAGGTGGTGG

CAGATATGCTTTGCATATGGATTGTTATGTTTTTATTTGGGCAGTTTAAATCATGGAAAA
CAGATATGCTTTGCATATGGATTGTTATGTTTTTATTTGGGCAGTTTAAATCATGGAAAA

CTCAAAAAAGAGGGGGGAAATGGTCAAGTTTAAGCCAAAAGAACTTTCTAAACAATGTAT
CTCAAAAAAGAGGGGGGAAATGGTCAAGTTTAAGCCAAAAGAACTTTCTAAACAATGTAT

AGGTACACAGCAAAATTAAACAAATCCAACAAATTTCTGAAGCTTAGTGTAATTGAGTGGT
AGGTACACAGCAAAATTAAACAAATCCAACAAATTTCTGAAGCTTAGTGTAATTGAGTGGT

GGTTGTTATTCAATAAAATTATTCCC AAAAGTGTTTCTCCTAAGAGTG CAGTTC CCA TGA
GGTTGTTATTCAATAAAATTATTCCC AAAAGTGTTTCTCCTAAGAGTG CAGTTC CCA TGA

GTCAC TTCC TGAACCCATTGACCAAAGGTGGG CAGAGACAA TCCTGTAGACCTTGACATT
GTCAC TTCC TGAACCCATTGACCAAAGGTGGG CAGAGACAA TCCTGTAGACCTTGACATT

CAGAAAGATGTGAGCTGCTTACTGATCATATATGCATACGTTTCTTTACAGCAGAGGAAA
CAGAAAGATGTGAGCTGCTTACTGATCATATATGCATACGTTTCTTTACAGCAGAGGAAA

CCATTGTCACAAAAC TGATGTTCTTTTGGGGTTTATGTACAGACTTGTCCAATCATGT
CCATTGTCACAAAAC TGATGTTCTTTTGGGGTTTATGTACAGACTTGTCCAATCATGT

G T G T G G T T C C T G C G A G T T G C T G A T G A C T C C G C A T T G A A G C T C T C T G A G T T C T T T G A T T T T
G T G T G G T T C C T G C G A G T T G C T G A T G A C T C C G C A T T G A A G C T C T C T G A G T T C T T T G A T T T T

