

Exon 13 (ense 00000958566)

```

P1-F 69 -----
P1-R 70 -----GNNNN NNNNNNNNNN NNNNNNTTTT CTTTGGCCAT
P2-F 71 -----
P2-R 72 -----GNNNNN NNNNNNNNNN NNNNTCTTTT CTTTGGCCAT
P3-F 73 -----
P3-R 74 -----GNNNN NNNNNNNNNN NNNNNNTTTT CTTTGGCCAT
P4-F 75 -----GGG GGANGGGGGG GNNNGATNT ANANNTNNAT
P4-R 76 GATTTCACCNT ACNNGAGNGA ATCCAAGTNT GATTNGTCTN NGNNNGAAGG TCTNGGCAA NTGNTCTTTT CTTTGGCCAT
                10      20      30      40      50      60      70      80

```

```

C-C-F 177 tcttctac agGTCTCCTG CAAGCGCAAA ATCTTCTAAC
C-C-R 178 GTCTCCTG CAAGCGCAAA ATCTTCTAAC
P1-F 69 -----GNNNTGGN --AAATGT-T TTTCTTCTAC AGGTCTCCTG CAAGCGCAAA ATCTTCTAAC
P1-R 70 GTGTTTCGAAG AAATCTTTAA TGTTTCTGGA TAACATGT-T TTTCTTCTAC AGGTCTCCTG CAAGCGCAAA ATCTTCTAAC
P2-F 71 -TNTTTGNNN NCNTTCNNA TGTTTCTGGA TAACATGT-T TTTCTTCTAC AGGTCTCCTG CAAGCGCAAA ATCTTCTAAC
P2-R 72 GTGTTTCGAAG AAATCTTTAA TGTTTCTGGA TAACATGT-T TTTCTTNTAC AGGTCTCCTG CAAGCGCAAA ATCTTCTAAC
P3-F 73 -----TTG NNACTTCNNA AGTTTCTGGA -AACATGT-T TTTCTTCTAC AGGTCTCCTG CAAGCGCAAA ATCTTCTAAC
P3-R 74 GTGTTTCGAAG AAATCTTTAA TGTTTCTGGA TAACATGT-T TTTCTTCTAC AGGTCTCCTG CAAGCGCAAA ATCTTNTAAC
P4-F 75 ANNTTC---- --TTCNAAA GCCCNNGGA TAANANGGAN NNNCGGGTAN AGGTCTCCTG CAAGCGCAAA ATCTTCTAAC
P4-R 76 GTGTTTCGAAG AAATCTTTAA TGTTTCTGGA TAACATGT-T TTTCTTCTAC AGGTCTCCTG CAAGCGCAAA ATCTTCTAAC
                90      100     110     120     130     140     150     160

```

```

C-C-F 177 GCAACTACCT CAGCAAAGCC AAGCCAACC- -TCCTACAGT CGCAGCCAAG CATCACCCTC ACCTCCCAGg tcagttttc
C-C-R 178 GCAACTACCT CAGCAAAGCC AAGCCAACC- -TCCTACAGT CGCAGCCAAG CATCACCCTC ACCTCCCAG
P1-F 69 GCAACTACCT CAGCAAAGCC AAGCCAACC- -TCCTACAGT CGCAGCCAAG CATCACCCTC ACCTCCCAGG TCAGTTTTCT
P1-R 70 GCAACTACCT CAGCAAAGCC AAGCCAACC- -TCCTACAGT CGCAGCCAAG CATCACCCTC ACCTCCCAGG TCAGTTTTCT
P2-F 71 GCAACTACCT CAGCAAAGCC AAGCCAACC- -TCCTACAGT CGCAGCCAAG CATCACCCTC ACCTCCCAGG TCAGTTTTCT
P2-R 72 GCAACTACCT CAGCAAAGCC AAGCCAACC- -TCCTACAGT CGCAGCCAAG CATCACCCTC ACCTCCCAGG TCAGTTTTCT
P3-F 73 GCAACTACCT CAGCAAAGCC AAGCCAACC- -TCCTACAGT CGCAGCCAAG CATCACCCTC ACCTCCCAGG TCAGTTTTCT
P3-R 74 GCAACTACCT CAGCAAAGCC AAGCCAACC- -TCCTACAGT CGCAGCCAAG CATCACCCTC ACCTCCCAGG TCAGTTTTNN
P4-F 75 GCAACTACCT CAGCAAAGCC AAGCCANCG GNCTNCTTGT NNNAGCCAAG CNTCACCCTC ACCTCCCAGG TCAGNTTCT
P4-R 76 GCAACTACCT CAGCAAAGCC AAGCCAACC- -TCCTACAGT CGCAGCCAAG CATCACCCTC ACCTCCCAGG TCAGTTTTCT
                170     180     190     200     210     220     230     240

```

```

P1-F 69 TCTATGGGGG CTGCTTTCTC TTATCATATT GTTTGGGGAG ACTTTTGGAN NNNNNNNNNC -----
P1-R 70 TCTA-GGGGG N-GCTTNGN- NGNNAAAA- -----
P2-F 71 TCFATGGGGG CTGCTTTCTC TTATCATATT GTTTGGGGAG ACTTTTGGAN NNNNNNNNNN NNNNNNNNC-
P2-R 72 TCTATGGGGG N-GCTTNGN- NNGNAANA- -----
P3-F 73 TCTATGGGGG CTGCTTTCTC TTATCATATT GTTTGGGGAG ACTTTTGGAN NNNNNNNNNN NNNNNNNN-
P3-R 74 TNNN-NNNGN N-NTNNAAG- GNATCA- -----
P4-F 75 TCTATGGGGG CTGCTTTCTC TTATCATATT GTTTGGGGAG ACTTTTGGAN NTTTANATAA AGNTTATCC ATACAANCCF
P4-R 76 TCTTGGGGGG CTGCNAAAG- TNATCANAA- -----
                250     260     270     280     290     300     310     320

```

```

P1-F 69 ----- 193
P1-R 70 ----- 217
P2-F 71 ----- 225
P2-R 72 ----- 220
P3-F 73 ----- 217
P3-R 74 ----- 215
P4-F 75 TCTTNGCTG CCN 279
P4-R 76 ----- 265
                330

```

Exon 14 (ense 00000958567)

P1-F 77	-----	-----	-----	-----	-GNNACTTGG	ANAAACCTAA	ATATCTCTTC	ACGTGTTTTT
P1-R 78	TNNNNNNNT	TTCCCAAAAT	GTGGCTCTTT	CCTTCAGTTG	TTTACTTGGG	G'FAAACCTAA	ATATCTCTTC	ACGTGTTTTT
P2-F 79	-----	-----	-----	-----	GNNACTTGGG	G'FAAACCTAA	ATATCTCTTC	ACGTGTTTTT
P2-R 80	-NNNNNNNT	TTCCCAAAAT	GTGGCTCTTT	CCTTCAGTTG	TTTACTTGGG	G'FAAACCTAA	ATATCTCTTC	ACGTGTTTTT
P3-F 81	-----	-----	-----	-----	-CN	TNNNNANNNG	N-ATCTCTTC	ACGTGTTTTT
P3-R 82	--NNNNNNNT	TTCCCAAAAT	GTGGCTCTTT	CCTTCAGTTG	TTTACTTGGG	G'FAAACCTAA	ATATCTCTTC	ACGTGTTTTT
P4-F 83	-----	-----	-----	-----	GNNACTTGGG	G'FAAACCTAA	ATATCTCTTC	ACGTGTTTTT
P4-R 84	--NNNNNNNT	TTCCCAANAAT	GTGGCTCTTT	CCTTCAGTTG	TTTACTTGGG	G'FAAACCTAA	ATATCTCTTC	ACGTGTTTTT
	10	20	30	40	50	60	70	80

C-C-F 177		tc	tccaacagCC	AGCAACCCCA	ACACGCACAA	TAGCAGCAAC	CCCAATTCAG	ACACTTCCAC
C-C-R 178			CC	AGCAACCCCA	ACACGCACAA	TAGCAGCAAC	CCCAATTCAG	ACACTTCCAC
P1-F 77	CCTCATTTGT	TTATTCCTTC	TCCAACAGCC	AGCAACCCCA	ACACGCACAA	TAGCAGCAAC	CCCAATTCAG	ACACTTCCAC
P1-R 78	CCTCATTTGT	TTATTCCTTC	TCCAACAGCC	AGCAACCCCA	ACACGCACAA	TAGCAGCAAC	CCCAATTCAG	ACACTTCCAC
P2-F 79	CCTCATTTGT	TTATTCCTTC	TCCAACAGCC	AGCAACCCCA	ACACGCACAA	TAGCAGCAAC	CCCAATTCAG	ACACTTCCAC
P2-R 80	CCTCATTTGT	TTATTCCTTC	TCCAACAGCC	AGCAACCCCA	ACACGCACAA	TAGCAGCAAC	CCCAATTCAG	ACACTTCCAC
P3-F 81	CCTCATTTGT	TTATTCCTTC	TCCAACAGCC	AGCAACCCCA	ACACGCACAA	TAGCAGCAAC	CCCAATTCAG	ACACTTCCAC
P3-R 82	CCTCATTTGT	TTATTCCTTC	TCCAACAGCC	AGCAACCCCA	ACACGCACAA	TAGCAGCAAC	CCCAATTCAG	ACACTTCCAC
P4-F 83	CCTCATTTGT	TTATTCCTTC	TCCAACAGCC	AGCAACCCCA	ACACGCACAA	TAGCAGCAAC	CCCAATTCAG	ACACTTCCAC
P4-R 84	CCTCATTTGT	TTATTCCTTC	TCCAACAGCC	AGCAACCCCA	ACACGCACAA	TAGCAGCAAC	CCCAATTCAG	ACACTTCCAC
	90	100	110	120	130	140	150	160

C-C-F 177	AGAGCCAGTC	AACACCAAAG	CGAATTGATA	CTCCCAGCTT	GGAGGAGCCC	AGTGACCTTG	AGGAGCTTGA	GCAGTTTGCC
C-C-R 178	AGAGCCAGTC	AACACCAAAG	CGAATTGATA	CTCCCAGCTT	GGAGGAGCCC	AGTGACCTTG	AGGAGCTTGA	GCAGTTTGCC
P1-F 77	AGAGCCAGTC	AACACCAAAG	CGAATTGATA	CTCCCAGCTT	GGAGGAGCCC	AGTGACCTTG	AGGAGCTTGA	GCAGTTTGCC
P1-R 78	AGAGCCAGTC	AACACCAAAG	CGAATTGATA	CTCCCAGCTT	GGAGGAGCCC	AGTGACCTTG	AGGAGCTTGA	GCAGTTTGCC
P2-F 79	AGAGCCAGTC	AACACCAAAG	CGAATTGATA	CTCCCAGCTT	GGAGGAGCCC	AGTGACCTTG	AGGAGCTTGA	GCAGTTTGCC
P2-R 80	AGAGCCAGTC	AACACCAAAG	CGAATTGATA	CTCCCAGCTT	GGAGGAGCCC	AGTGACCTTG	AGGAGCTTGA	GCAGTTTGCC
P3-F 81	AGAGCCAGTC	AACACCAAAG	CGAATTGATA	CTCCCAGCTT	GGAGGAGCCC	AGTGACCTTG	AGGAGCTTGA	GCAGTTTGCC
P3-R 82	AGAGCCAGTC	AACACCAAAG	CGAATTGATA	CTCCCAGCTT	GGAGGAGCCC	AGTGACCTTG	AGGAGCTTGA	GCAGTTTGCC
P4-F 83	AGAGCCAGTC	AACACCAAAG	CGAATTGATA	CTCCCAGCTT	GGAGGAGCCC	AGTGACCTTG	AGGAGCTTGA	GCAGTTTGCC
P4-R 84	AGAGCCAGTC	AACACCAAAG	CGAATTGATA	CTCCCAGCTT	GGAGGAGCCC	AGTGACCTTG	AGGAGCTTGA	GCAGTTTGCC
	170	180	190	200	210	220	230	240

C-C-F 177	AAGACCTTCA	AACAAAAGCG	AATCAAACCTT	GGATTCACCTC	AGgtagggtg	aa		
C-C-R 178	AAGACCTTCA	AACAAAAGCG	AATCAAACCTT	GGATTCACCTC	AG			
P1-F 77	AAGACCTTCA	AACAAAAGCG	AATCAAACCTT	GGATTCACCTC	AGGTAGGGTG	AATTGGCCTT	ACATTGATTC	CCCTCCTTGG
P1-R 78	AAGACCTTCA	AACAAAAGCG	AATCAAACCTT	GGATTCACCTC	AGGTAGGGTG	AATTGGCCTT	ACATTGATTC	CCCTCCTTGG
P2-F 79	AAGACCTTCA	AACAAAAGCG	AATCAAACCTT	GGATTCACCTC	AGGTAGGGTG	AATTGGCCTT	ACATTGATTC	CCCTCCTTGG
P2-R 80	AAGACCTTCA	AACAAAAGCG	AATCAAACCTT	GGATTCACCTC	AGGTAGGGTG	AATTGGCCTT	ACATTGATTC	CCCTCCTTGG
P3-F 81	AAGACCTTCA	AACAAAAGCG	AATCAAACCTT	GGATTCACCTC	AGGTAGGGTG	AATTGGCCTT	ACATTGATTC	CCCTCCTTGG
P3-R 82	AAGACCTTCA	AACAAAAGCG	AATCAAACCTT	GGATTCACCTC	AGGTAGGGTG	AAT-GGCCCTT	ACATTNATTC	CCCTCCTTGG
P4-F 83	AAGACCTTCA	AACAAAAGCG	AATCAAACCTT	GGATTCACCTC	AGGTAGGGTG	AATTGGCCTT	ACATTGATTC	CCCTCCTTGG
P4-R 84	AAGACCTTCA	AACAAAAGCG	AATCAAACCTT	GGATTCACCTC	AGGTAGGGTG	AATTGGCCTT	ACATTGATTC	CCCTCCTTGG
	250	260	270	280	290	300	310	320

P1-F 77	CTGGGTCCAA	ATACAGTTGG	CTCTCTGTAT	TCATGGATNC	CACANANNNN	NNNN-----	-----	333
P1-R 78	-CGGGTCCAA	ATACAGTTGG	NNNCAA----	-----	-----	-----	-----	345
P2-F 79	CTGGGTCCAA	ATACAGTTGG	CTCTCTGTAT	TCATGGATCC	NACAAANNNN	NNN-----	-----	333
P2-R 80	-CGGGTCCAA	A-NCAGAGN	NANAA----	-----	-----	-----	-----	341
P3-F 81	CTGGGTCCAA	ATACAGTTGG	CTCTCTGTAT	TCATGGATNC	CACANANNNN	NNNNNNNNNN	NNNNNNNNNN	350
P3-R 82	-CGGG-CCAN	N-ACNGNGGN	NA-----	-----	-----	-----	-----	335
P4-F 83	CTGGGTCCAA	ATACAGTTGG	CTCTCTGTAT	TCATGG-TNC	CACAAAANNN	NNNNNNNNNN	NNNNNNNNNN	347
P4-R 84	-CGGGTCCAA	A-ACAGNNG-	-----	-----	-----	-----	-----	334
	330	340	350	360	370	380		

Exon 15 (ense 00000958568)

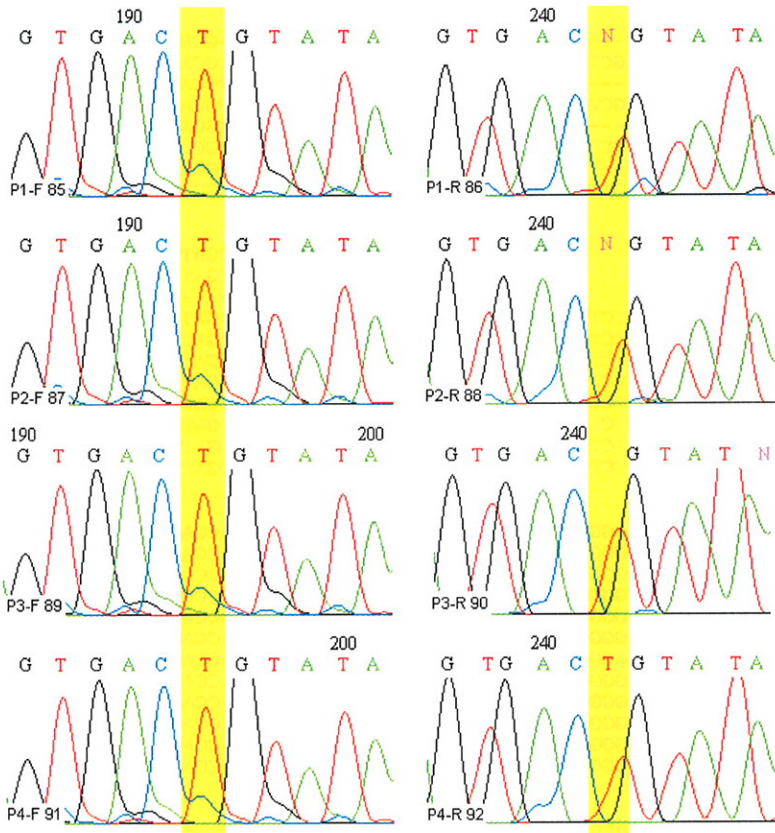
P1-F 85	-----	-----	-----	-----	-----	GTCTTTCCCTC	TCCTCTTCTC	CTGCTCTGTA	
P1-R 86	GNNNNNNNNN	NNNNNNNNNC	NTAGGCTTTA	AGCACTGGTG	AGATAACTCT	GTCTTTCCCTC	TCCTCTTCTC	CTGCTCTGTA	
P2-F 87	-----	-----	-----	-----	-----	GTCTTTCCCTC	TCCTCTTCTC	CTGCTCTGTA	
P2-R 88	NNNNNNNNNN	NNNNNNNNNC	NTAGGCTTTA	AGCACTGGTG	AGATAACTCT	GTCTTTCCCTC	TCCTCTTCTC	CTGCTCTGTA	
P3-F 89	-----	-----	-----	-----	-----C	NGNNNNNNNTC	TCCTCTTCTC	CTGCTCTGTA	
P3-R 90	NNNNNNNNNN	NNNNNNNNNT	TTAGGCNT-A	AGCACTGGTG	AGATAACTCT	GTCTTTCCCTC	TCCTCTTCTC	CTGCTCTGTA	
P4-F 91	-----	-----	-----	-----	-----C	TCCTCTTCTC	TCCTCTTCTC	CTGCTCTGTA	
P4-R 92	NNNNNNNNNN	NNNNNNNNCN	TTAGGCTTTA	AGCACTGGTG	AGATAACTCT	GTCTTTCCCTC	TCCTCTTCTC	CTGCTCTGTA	
		10	20	30	40	50	60	70	80

	ttgtgtgtgag	GGTGATGTTG	GGCT-CGCTA	TGGGG-AAAC	TATATGGAAA	TGACTTCAGC	CAAAC'TACCA	TCTCTCGATT	
C-C-F 177		GGTGATGTTG	GGCTTCNCTA	TGGGGAAAC	TATATGGNAA	TGACTTCAGC	CAAAC'TACCN	TCTTTTGATT	
C-C-R 178		GGTGATGTTG	GGCT-CGCTA	TGGGG-AAAC	TATATGGAAA	TGACTTCAGC	CAAAC'TACCA	TCTCTCGATT	
P1-F 85	TTGTGTGTAG	GGTGATGTTG	GGCT-CGCTA	TGGGG-AAAC	TATATGGAAA	TGACTTCAGC	CAAAC'TACCA	TCTCTCGATT	
P1-R 86	TTGTGTGTAG	GGTGATGTTG	GGCT-CGCTA	TGGGG-AAAC	TATATGGAAA	TGACTTCAGC	CAAAC'TACCA	TCTCTCGATT	
P2-F 87	TTGTGTGTAG	GGTGATGTTG	GGCT-CGCTA	TGGGG-AAAC	TATATGGAAA	TGACTTCAGC	CAAAC'TACCA	TCTCTCGATT	
P2-R 88	TTGTGTGTAG	GGTGATGTTG	GGCT-CGCTA	TGGGG-AAAC	TATATGGAAA	TGACTTCAGC	CAAAC'TACCA	TCTCTCGATT	
P3-F 89	TTGTGTGTAG	GGTGATGTTG	GGCT-CGCTA	TGGGG-AAAC	TATATGGAAA	TGACTTCAGC	CAAAC'TACCA	TCTCTCGATT	
P3-R 90	TTGTGTGTAG	GGTGATGTTG	GGCT-CGCTA	TGGGG-AAAC	TATATGGAAA	TGACTTCAGC	CAAAC'TACCA	TCTCTCGATT	
P4-F 91	TTGTGTGTAG	GGTGATGTTG	GGCT-CGCTA	TGGGG-AAAC	TATATGGAAA	TGACTTCAGC	CAAAC'TACCA	TCTCTCGATT	
P4-R 92	TTGTGTGTAG	GGTGATGTTG	GGCT-CGCTA	TGGGG-AAAC	TATATGGAAA	TGACTTCAGC	CAAAC'TACCA	TCTCTCGATT	
		90	100	110	120	130	140	150	160

	TGAAGCC-TT	GAACCT-CAG	CTTTAAGAAC	ATGTG-CAAG	TTGAAGCCAC	TTTT--AGAG	AAGTGG--CT	AAATGAT-GC	
C-C-F 177	TGAAGNCCTT	GAACCTCAN	CTTAAAAAAC	ATGGGGCAAG	TTNAACCCNT	CTTTTAAGAG	GAGTGGNNTT	AAATGANTGC	
C-C-R 178	TGAAGCC-TT	GAACCT-CAG	CTTTAAGAAC	ATGTG-CAAG	TTGAAGCCAC	TTTT--AGAG	AAGTGG--CT	AAATGAT-GC	
P1-F 85	TGAAGCC-TT	GAACCT-CAG	CTTTAAGAAC	ATGTG-CAAG	TTGAAGCCAC	TTTT--AGAG	AAGTGG--CT	AAATGAT-GC	
P1-R 86	TGAAGCC-TT	GAACCT-CAG	CTTTAAGAAC	ATGTG-CAAG	TTGAAGCCAC	TTTT--AGAG	AAGTGG--CT	AAATGAT-GC	
P2-F 87	TGAAGCC-TT	GAACCT-CAG	CTTTAAGAAC	ATGTG-CAAG	TTGAAGCCAC	TTTT--AGAG	AAGTGG--CT	AAATGAT-GC	
P2-R 88	TGAAGCC-TT	GAACCT-CAG	CTTTAAGAAC	ATGTG-CAAG	TTGAAGCCAC	TTTT--AGAG	AAGTGG--CT	AAATGAT-GC	
P3-F 89	TGAAGCC-TT	GAACCT-CAG	CTTTAAGAAC	ATGTG-CAAG	TTGAAGCCAC	TTTT--AGAG	AAGTGG--CT	AAATGAT-GC	
P3-R 90	TGAAGCC-TT	GAACCT-CAG	CTTTAAGAAC	ATGTG-CAAG	TTGAAGCCAC	TTTT--AGAG	AAGTGG--CT	AAATGAT-GC	
P4-F 91	TGAAGCC-TT	GAACCT-CAG	CTTTAAGAAC	ATGTG-CAAG	TTGAAGCCAC	TTTT--AGAG	AAGTGG--CT	AAATGAT-GC	
P4-R 92	TGAAGCC-TT	GAACCT-CAG	CTTTAAGAAC	ATGTG-CAAG	TTGAAGCCAC	TTTT--AGAG	AAGTGG--CT	AAATGAT-GC	
		170	180	190	200	210	220	230	240

	AGgtaagtga	ct							
C-C-F 177	AA								
C-C-R 178	AG								
P1-F 85	AGGTAAAGTGA	CTGTATAAGA	CATTTCTTTG	TCATTCATTG	GAATTTTACA	TGGGGATTGT	TATATAAATT	GGANNNNNNN	
P1-R 86	AGGTAAAGTGA	CNGTATAAGA	CATTTNNTNT	C-----	-----	-----	-----	-----	
P2-F 87	AGGTAAAGTGA	CTGTATAAGA	CATTTCTTTG	TCATTCATTG	GAATTTTACA	TGGGGATTGT	TATATAAATT	GGANNNNNNN	
P2-R 88	AGGTAAAGTGA	CNGTATAAGA	CATTTNNTNT	C-----	-----	-----	-----	-----	
P3-F 89	AGGTAAAGTGA	CTGTATAAGA	CATTTCTTTG	TCATTCATTG	GAATTTTACA	TGGGGATTGT	TATATAAATT	GGANNNNNNN	
P3-R 90	AGGTAAAGTGA	C-GTATN-GA	C-----	-----	-----	-----	-----	-----	
P4-F 91	AGGTAAAGTGA	CTGTATAAGA	CATTTCTTTG	TCATTCATTG	GAATTTTACA	TGGGGATTGT	TATATAAATT	GANNNAANNNN	
P4-R 92	AGGTAAAGTGA	CTGTATAAGA	CATTTNNTNT	C-----	-----	-----	-----	-----	
		250	260	270	280	290	300	310	320

P1-F 85	NNNNNNNNNN	N	271
P1-R 86	-----	-	261
P2-F 87	NNNNNNNNNN	N	271
P2-R 88	-----	-	261
P3-F 89	NNNNNNNNNN	N	274
P3-R 90	-----	-	248
P4-F 91	NNNNNNNNNN	-	274
P4-R 92	-----	-	261



Exon 16 (ense 00000958569)

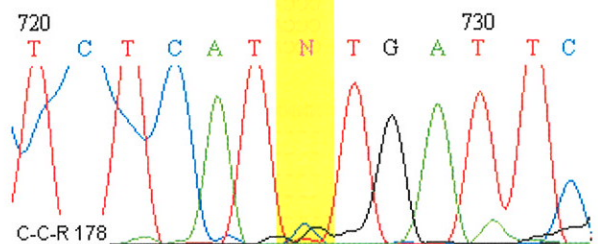
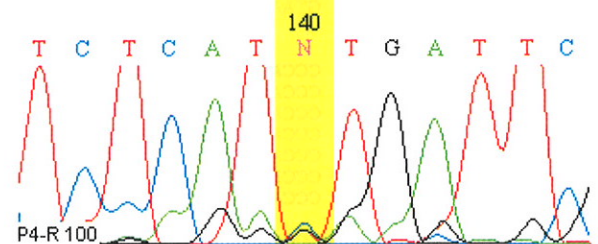
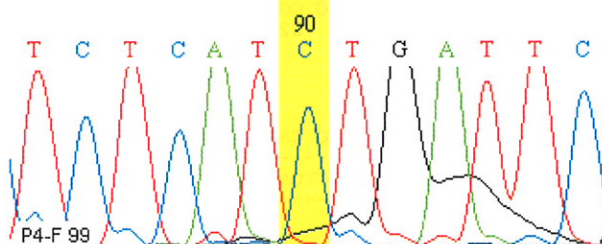
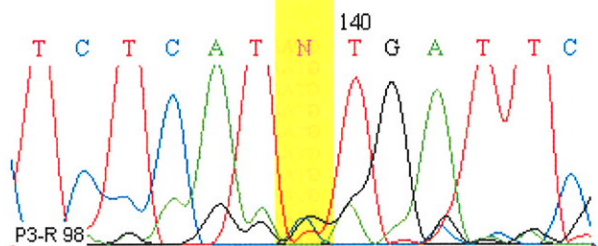
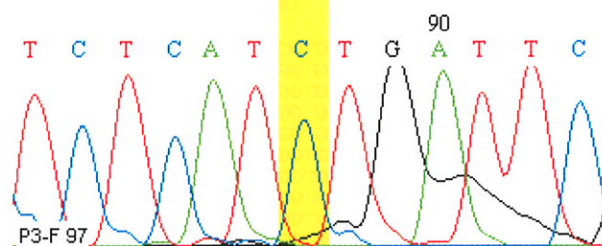
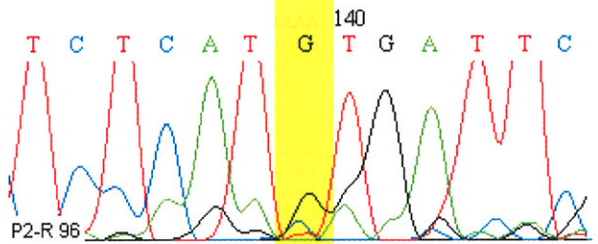
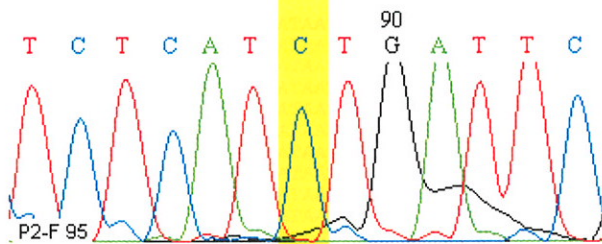
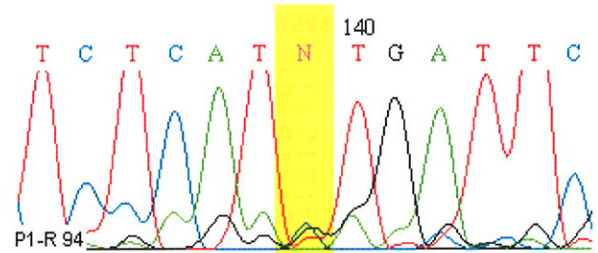
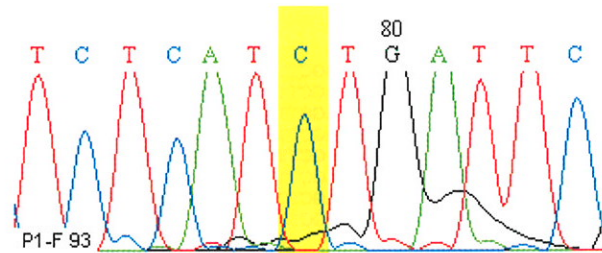
P1-F 93 -----  
P1-R 94 -NNNNNNNNNN NNNNNNNNNN NCC<sup>TT</sup>GNATG TAG<sup>CTT</sup>ATTTT TGT<sup>CAG</sup>TTTT GTT<sup>GTT</sup>TAATA TGCATATTAT GCACATGAAT  
P2-F 95 -----  
P2-R 96 -NNNNNNNNNN NNNNNNNNN<sup>T</sup> TCC<sup>TT</sup>TGGATG TAG<sup>CTT</sup>ATTTT TGT<sup>CAG</sup>TTTT GTT<sup>GTT</sup>TAATA TGCATATTAT GCACATGAAT  
P3-F 97 -----  
P3-R 98 -GNNNNNNNNN NNNNNNNNN<sup>T</sup> TCC<sup>TT</sup>TGGATG TAG<sup>CTT</sup>ATTTT TGT<sup>CAG</sup>TTTT GTT<sup>GTT</sup>TAATA TGCATATTAT GCACATGAAT  
P4-F 99 -----  
P4-R 100 NNNNNNN<sup>TAA</sup> NNNNNNN<sup>ANN</sup>T TCT<sup>TT</sup>GGGATG TAG<sup>CTT</sup>ATTTT TGT<sup>CAG</sup>TTTT GTT<sup>GTT</sup>TAATA TGCATATTAT GCACATGAAT  
10 20 30 40 50 60 70 80

att cttacagAGA ACCTCTCATC TGATTCGTCC CTCTCCAGCC  
C-C-R 178 AGA ACCTCTCATN TGATTCGTCC CTCTCCAGCC  
C-D-F 179 -----  
P1-F 93 CACTGTGCTC AGCTAATTTT ATTTCTGTAT TTTCTTCATT CTTACAGAGA ACCTCTCATC TGATTCGTCC CTCTCCAGCC  
P1-R 94 CACTGTGCTC AGCTAATTTT ATTTCTGTAT TTTCTTCATT CTTACAGAGA ACCTCTCATN TGATTCGTCC CTCTCCAGCC  
P2-F 95 CACTGTGCTN AGCTAATTTT ATTTCTGTAT TTTCTTCATT CTTACAGAGA ACCTCTCATC TGATTCGTCC CTCTCCAGCC  
P2-R 96 CACTGTGCTC AGCTAATTTT ATTTCTGTAT TTTCTTCATT CTTACAGAGA ACCTCTCATG TGATTCGTCC CTCTCCAGCC  
P3-F 97 CACTGTGCTC AGCTAATTTT ATTTCTGTAT TTTCTTCATT CTTACAGAGA ACCTCTCATC TGATTCGTCC CTCTCCAGCC  
P3-R 98 CACTGTGCTC AGCTAATTTT ATTTCTGTAT TTTCTTCATT CTTACAGAGA ACCTCTCATN TGATTCGTCC CTCTCCAGCC  
P4-F 99 CACTGTGCTN AGCTAATTTT ATTTCTGTAT TTTCTTCATT CTTACAGAGA ACCTCTCATC TGATTCGTCC CTCTCCAGCC  
P4-R 100 CACTGTGCTC AGCTAATTTT ATTTCTGTAT TTTCTTCATT CTTACAGAGA ACCTCTCATN TGATTCGTCC CTCTCCAGCC  
90 100 110 120 130 140 150 160

CAAGTG-CCC TGAATTCT-- CCAGGAATTG A-GGGCTTGA GCCGTAGGAG GAAGAAACGC ACCAGCATAG AGA-CCAACA  
C-C-R 178 CAAGTG-CCC TGAATTCT-- CCAGGAATTG A-GGGCTTGA GCCGTAGGAG GAAGAAACGC ACCAGCATAG AGN-CNNNA  
C-D-F 179 NNNNCN-NNN NGAATTC-- CN-GGAATTG A-GGGCTTGA GCCGTAGGAG GAAGAAACGC ACCAGCATAG AGA-CCAACA  
C-D-R 180 CAAGNGGCC NNAANTNTTT CCAGAAAANN ANGGGCTTNN ACCNTAGGGG NAAAAAACGC CCCCNCATAG AGNNCCCACN  
P1-F 93 CAAGTG-CCC TGAATTCT-- CCAGGAATTG A-GGGCTTGA GCCGTAGGAG GAAGAAACGC ACCAGCATAG AGA-CCAACA  
P1-R 94 CAAGTG-CCC TGAATTNT-- CCAGGAATTG A-GGGCTTGA GCCGTAGGAG GAAGAAACGC ACCAGCATAG AGA-CCAACA  
P2-F 95 CAAGTG-CCC TGAATTCT-- CCAGGAATTG A-GGGCTTGA GCCGTAGGAG GAAGAAACGC ACCAGCATAG AGA-CCAACA  
P2-R 96 CAAGTG-CCC TGAATTNT-- CCAGGAATTG A-GGGCTTGA GCCGTAGGAG GAAGAAACGC ACCAGCATAG AGA-CCAACA  
P3-F 97 CAAGTG-CCC TGAATTCT-- CCAGGAATTG A-GGGCTTGA GCCGTAGGAG GAAGAAACGC ACCAGCATAG AGA-CCAACA  
P3-R 98 CAAGTG-CCC TGAATTNT-- CCAGGAATTG A-GGGCTTGA NCCGTAGGAG GAAGAAACGC ACCAGCATAG AGA-CCAACA  
P4-F 99 CAAGTG-CCC TGAATTCT-- CCAGGAATTG A-GGGCTTGA GCCGTAGGAG GAAGAAACGC ACCAGCATAG AGA-CCAACA  
P4-R 100 CAAGTG-CCC TGAATTCT-- CCAGGAATTG A-GGGCTTGA GCCGTAGGAG GAAGAAACGC ACCAGCATAG AGA-CCAACA  
170 180 190 200 210 220 230 240

TCCGTGTGGC CTTAGAGAAG AGTTTCTTGG AGgtcagtga gg  
C-C-R 178 NA-----  
C-D-F 179 TCCGTGTGGC CTTAGAGAAG AGNTTCTTGG AG  
C-D-R 180 TCCGTGTGGC NTTAAAGAAG AGTTTCTTGG AG  
P1-F 93 TCCGTGTGGC CTTAGAGAAG AGTTTCTTGG AGGTCAGTGA GGATTTTACT TTTCTGTACA TGGGATTGTC TGTGTAGTCC  
P1-R 94 TCCGTGTGGC CTTAGAGAAG AGTTTCTGG- AGGTCAG--  
P2-F 95 TCCGTGTGGC CTTAGAGAAG AGTTTCTTGG AGGTCAGTGA GGATTTTACT TTTCTGTACA TGGGATTGTC TGTGTAGTCT  
P2-R 96 TCCGTGTGGC CTTAGAGAAG AGTTTCTNG- AGGTCAGTN- GGATTNACNN NNNGTNNNA  
P3-F 97 TCCGTGTGGC CTTAGAGAAG AGTTTCTTGG AGGTCAGTGA GGATTTTACT TTTCTGTACA TGGGATTGTC TGTGTAGTCT  
P3-R 98 TCCGTGTGGC CTTAGAGAAG AGTTTCTTN- AGGTCANTNN NNNNNNNNNN NGTNG-----  
P4-F 99 TCCGTGTGGC CTTAGAGAAG AGTTTCTTGG AGGTCAGTGA GGATTTTACT TTTCTGTACA TGGGATTGTC TGTGTAGTCC  
P4-R 100 TCCGTGTGGC CTTAGAGAAG AGTTTCTNNG AGGTCAGTGA GGATTTTACT TNCNGTNGNN AA-----  
250 260 270 280 290 300 310 320

P1-F 93 TTA<sup>AAAA</sup>NNN NNNNNNNNN NNN 276  
P1-R 94 ----- --- 270  
P2-F 95 TTA<sup>AAAA</sup>NNN NNNNNNNNN NNN 286  
P2-R 96 ----- --- 292  
P3-F 97 NT<sup>AAAA</sup>NNNN NNNNNNNNN NN- 284  
P3-R 98 ----- --- 288  
P4-F 99 TTA<sup>AAAA</sup>NNN NNNNNNNNN NNN 288  
P4-R 100 ----- --- 297  
330 340



Exon 17 (ense 00000958570)

P1-F 101	-----	-----	-----	-----	---TTTGTGAA	GGATAGCTTT	TGGAAATACA	TCTTTTCACC	cacc
P1-R 102	---NNNNNTC	C+GCCC+GAT	TATGCCAGTA	GTTCAAAAAG	TTATTTGCAA	GGATAGCTTT	TGGAAATACA	TCTTTTCACC	
P2-F 103	-----	-----	-----	-----	-----	---TAGCTTT	TGGAAATACA	TCTTTTCACC	
P2-R 104	-NNNNNTTTC	C+GA-G+GAT	TATGCCAGTA	GTTCAAAAAG	TTATTTGCAA	GGATAGCTTT	TGGAAATACA	TCTTTTCACC	
P3-F 105	-----	-----	-----	-----	-----	-----GCCTTT	TGGAAATACA	TCTTTTCACC	
P3-R 106	NNNNNNCCFTC	C+GACC+GAT	TATGCCAGTA	GTTCAAAAAG	TTATTTGCAA	GGATAGCTTT	TGGAAATACA	TCTTTTCACC	
P4-F 107	-----	-----	-----	-----	---TTTGCAAA	GGATAGCTTT	TGGAAATACA	TCTTTTCACC	
P4-R 108	-NNNNNTTTC	C+GA-G+GAT	TATGCCAGTA	GTTCAAAAAG	TTATTTGCAA	GGATAGCTTT	TGGAAATACA	TCTTTTCACC	
		10	20	30	40	50	60	70	80
ctgcagAATC AAAA-GCCTA CCTCGGAAGA GATCACTATG ATTGCTGATC AGCTCAATAT GGAAAAAGAG GTGATTCGTG									
C-D-F 179	ATTC	AAAA-GCCTA	CCTCGGAAGA	GATCACTATG	ATTGCTGATC	AGCTCAATAT	GGAAAAAGAG	GTGATTCGTG	
C-D-R 180	ATTC	AAAA-GCCTA	CCTCGGAAGA	GATCACTATG	ATTGCTGATC	AGCTCAATAT	GGAAAAAGAG	GTGATTCGTG	
P1-F 101	C+GCAG+ATC	AAAA-GCCTA	CCTCGGAAGA	GATCACTATG	ATTGCTGATC	AGCTCAATAT	GGAAAAAGAG	GTGATTCGTG	
P1-R 102	C+GCAG+ATC	AAAA-GCCTA	CCTCGGAAGA	GATCACTATG	ATTGCTGATC	AGCTCAATAT	GGAAAAAGAG	GTGATTCGTG	
P2-F 103	C+GCAG+ATC	AAAA-GCCTA	CCTCGGAAGA	GATCACTATG	ATTGCTGATC	AGCTCAATAT	GGAAAAAGAG	GTGATTCGTG	
P2-R 104	C+GCAG+ATC	AAAA-GCCTA	CCTCGGAAGA	GATCACTATG	ATTGCTGATC	AGCTCAATAT	GGAAAAAGAG	GTGATTCGTG	
P3-F 105	C+GCAG+ATC	AAAA-GCCTA	CCTCGGAAGA	GATCACTATG	ATTGCTGATC	AGCTCAATAT	GGAAAAAGAG	GTGATTCGTG	
P3-R 106	C+GCAG+ATC	AAAA-GCCTA	CCTCGGAAGA	GATCACTATG	ATTGCTGATC	AGCTCAATAT	GGAAAAAGAG	GTGATTCGTG	
P4-F 107	C+GCAG+ATC	AAAA-GCCTA	CCTCGGAAGA	GATCACTATG	ATTGCTGATC	AGCTCAATAT	GGAAAAAGAG	GTGATTCGTG	
P4-R 108	C+GCAG+ATC	AAAA-GCCTA	CCTCGGAAGA	GATCACTATG	ATTGCTGATC	AGCTCAATAT	GGAAAAAGAG	GTGATTCGTG	
		90	100	110	120	130	140	150	160
TTTGGTTC-T GTAACCGCCG CCAGAAAGAA AAAAGAATCA ACCCACCAG CAGTGGTGGG ACCAGCAGCT CACCTATTAA									
C-D-F 179	TTTGGTTC-T	GTAACCGCCG	CCAGAAAGAA	AAAAGAATCA	ACCCACCAG	CAGTGGTGGG	ACCAGCAGCT	CACCTATTAA	
C-D-R 180	TTTGGTTC-T	GTAACCGCCG	CCAGAAAGAA	AAAAGAATCA	ACCCACCAG	CAGTGGTGGG	ACCAGCAGCT	CACCTATTAA	
P1-F 101	TTTGGTTC-T	GTAACCGCCG	CCAGAAAGAA	AAAAGAATCA	ACCCACCAG	CAGTGGTGGG	ACCAGCAGCT	CACCTATTAA	
P1-R 102	TTTGGTTC-T	GTAACCGCCG	CCAGAAAGAA	AAAAGAATCA	ACCCACCAG	CAGTGGTGGG	ACCAGCAGCT	CACCTATTAA	
P2-F 103	TTTGGTTC-T	GTAACCGCCG	CCAGAAAGAA	AAAAGAATCA	ACCCACCAG	CAGTGGTGGG	ACCAGCAGCT	CACCTATTAA	
P2-R 104	TTTGGTTC-T	GTAACCGCCG	CCAGAAAGAA	AAAAGAATCA	ACCCACCAG	CAGTGGTGGG	ACCAGCAGCT	CACCTATTAA	
P3-F 105	TTTGGTTC-T	GTAACCGCCG	CCAGAAAGAA	AAAAGAATCA	ACCCACCAG	CAGTGGTGGG	ACCAGCAGCT	CACCTATTAA	
P3-R 106	TTTGGTTC-T	GTAACCGCCG	CCAGAAAGAA	AAAAGAATCA	ACCCACCAG	CAGTGGTGGG	ACCAGCAGCT	CACCTATTAA	
P4-F 107	TTTGGTTC-T	GTAACCGCCG	CCAGAAAGAA	AAAAGAATCA	ACCCACCAG	CAGTGGTGGG	ACCAGCAGCT	CACCTATTAA	
P4-R 108	TTTGGTTC-T	GTAACCGCCG	CCAGAAAGAA	AAAAGAATCA	ACCCACCAG	CAGTGGTGGG	ACCAGCAGCT	CACCTATTAA	
		170	180	190	200	210	220	230	240
AGCAATTTTC CCCAGCCCAA CTTCACTGgt aagaataa									
C-D-F 179	AGCAATTTTC	CCCAGCCCAA	CTTCACTGgt	aagaataa					
C-D-R 180	AGCAATTTTC	CCCAGCCCAA	CTTCACTGgt	aagaataa					
P1-F 101	AGCAATTTTC	CCCAGCCCAA	CTTCACTGgt	aagaataa					
P1-R 102	AGCAATTTTC	CCCAGCCCAA	CTTCACTGgt	aagaataa					
P2-F 103	AGCAATTTTC	CCCAGCCCAA	CTTCACTGgt	aagaataa					
P2-R 104	AGCAATTTTC	CCCAGCCCAA	CTTCACTGgt	aagaataa					
P3-F 105	AGCAATTTTC	CCCAGCCCAA	CTTCACTGgt	aagaataa					
P3-R 106	AGCAATTTTC	CCCAGCCCAA	CTTCACTGgt	aagaataa					
P4-F 107	AGCAATTTTC	CCCAGCCCAA	CTTCACTGgt	aagaataa					
P4-R 108	AGCAATTTTC	CCCAGCCCAA	CTTCACTGgt	aagaataa					
		250	260	270	280	290	300	310	320
P1-F 101	N NNNNNNNN	NNNNNNNNNN	NNN	299					
P1-R 102	-----	-----	---	264					
P2-F 103	N NNNN---	-----	---	272					
P2-R 104	-----	-----	---	269					
P3-F 105	-N NNNN---	-----	---	270					
P3-R 106	-----	-----	---	280					
P4-F 107	N NNNN---	-----	---	282					
P4-R 108	-----	-----	---	276					
		330	340						

Exon 18 (ense 00001157574)

P1-F 109 -----TT CCAGATCAA GAAAGACTGT AAAATCATTT  
P1-R 110 -NNNNNTCCG AAAACAGCTT TCCAACATAG GATGTCAGGT GTCTCAATTC CAAGATCAA GAAAGACTGT AAAATCATTT  
P2-F 111 -----TT  
P2-R 112 NNNNNNTCCG AAAACAGCTT TCCAACATAG GATGTCAGGT GTCTCAATTC CAAGATCAA GAAAGACTGT AAAATCATTT  
P3-F 113 -----TT  
P3-R 114 --NNNNCCG AAAACAGCTT TCCAACATAG GATGTCAGGT GTCTCAATTC CAAGATCAA GAAAGACTGT AAAATCATTT  
P4-F 115 -----TNA AGAAAGACTG TAAATCATTT  
P4-R 116 NNNNNTCCGA AAAACAGCTT TCCAACATAG GATGTCAGGT GTCTCAATTC CAAGATCAA GAAAGACTGT AAAATCATTT  
10 20 30 40 50 60 70 80

tgac ctcaagGTGG CGACCACACC AAGCCTTGTG  
C-D-F 179 GTGG CGACCACACC AAGCCTTGTG  
C-D-R 180 GTGG CGACCACACC AAGCCTTGTG  
P1-F 109 CCTCTTTAAG TTTTGATTTT AAGTGCTTTG TCCATGTTTT CATTTCTGAC CTC AAGGTGG CGACCACACC AAGCCTTGTG  
P1-R 110 CCTCTTTAAG TTTTGATTTT AAGTGCTTTG TCCATGTTTT CATTTCTGAC CTC AAGGTGG CGACCACACC AAGCCTTGTG  
P2-F 111 -----TTNNG TTTTGATTTT NANTGCTTTG TCCATGTTTT CATTTCTGAC CTC ANGGNGG CGACCACACC NAGCCTTGTG  
P2-R 112 CCTCTTTAAG TTTTGATTTT AAGTGCTTTG TCCATGTTTT CATTTCTGAC CTC AAGGTGG CGACCACACC AAGCCTTGTG  
P3-F 113 -----AG TTTTNATTTN A-GTGCTTTG TCCATGTTTT CATTTCTGAC CTC AAGGTGG CGACCACACC AAGCCTTGTG  
P3-R 114 CCTCTTTAAG TTTTGATTTT AAGTGCTTTG TCCATGTTTT CATTTCTGAC CTC AAGGTGG CGACCACACC AAGCCTTGTG  
P4-F 115 CCTCTTTAAG TTTTGATTTT AAGTGCTTTG TCCATGTTTT CATTTCTGAC CTC AAGGTGG CGACCACACC AAGCCTTGTG  
P4-R 116 CCTCTTTAAG TTTTGATTTT AAGTGCTTTG TCCATGTTTT CATTTCTGAC CTC AAGGTGG CGACCACACC AAGCCTTGTG  
90 100 110 120 130 140 150 160

ACTAGCAGTG CAGCAACTAC CCTCAGTCC AGCCCTGTCC TCCCTCTGAC CAGTGCCTGTG GTGACGAATC TTTCAGTTAC  
C-D-F 179 ACTAGCAGTG CAGCAACTAC CCTCAGTCC AGCCCTGTCC TCCCTCTGAC CAGTGCCTGTG GTGACGAATC TTTCAGTTAC  
C-D-R 180 ACTAGCAGTG CAGCAACTAC CCTCAGTCC AGCCCTGTCC TCCCTCTGAC CAGTGCCTGTG GTGACGAATC TTTCAGTTAC  
P1-F 109 ACTAGCAGTG CAGCAACTAC CCTCAGTCC AGCCCTGTCC TCCCTCTGAC CAGTGCCTGTG GTGACGAATC TTTCAGTTAC  
P1-R 110 ACTAGCAGTG CAGCAACTAC CCTCAGTCC AGCCCTGTCC TCCCTCTGAC CAGTGCCTGTG GTGACGAATC TTTCAGTTAC  
P2-F 111 ACTAGCAGTG CAN-----  
P2-R 112 ACTAGCAGTG CAGCAACTAC CCTCAGTCC AGCCCTGTCC TCCCTCTGAC CAGTGCCTGTG GTGACGAATC TTTCAGTTAC  
P3-F 113 ACTAGCAGTG CAGCAACTAC CCTCAGTCC AGCCCTGTCC TCCCTCTGAC CAGTGCCTGTG GTGACGAATC TTTCAGTTAC  
P3-R 114 ACTAGCAGTG CAGCAACTAC CCTCAGTCC AGCCCTGTCC TCCCTCTGAC CAGTGCCTGTG GTGACGAATC TTTCAGTTAC  
P4-F 115 ACTAGCAGTG CAGCAACTAC CCTCAGTCC AGCCCTGTCC TCCCTCTGAC CAGTGCCTGTG GTGACGAATC TTTCAGTTAC  
P4-R 116 ACTAGCAGTG CAGCAACTAC CCTCAGTCC AGCCCTGTCC TCCCTCTGAC CAGTGCCTGTG GTGACGAATC TTTCAGTTAC  
170 180 190 200 210 220 230 240

AGGtaagcag ct  
C-D-F 179 AG  
C-D-R 180 AG  
P1-F 109 AGGTAAAGCAG CTGCCAGGCC ATGCACCTGC TGAGCACATG GGAGGCCCGT TTTGGGTTAT TATAANAGTC TACCATTAAA  
P1-R 110 AGGTAAAGCAG CTGCCAGGCC ATGCACCTGC TGAGCACATG GGAGGCCCGT TTTGGGTTAT TATAANAGTC TACCATTAAA  
P2-F 111 -----  
P2-R 112 AGGTAAAGCAG CTGCCAGGCC ATGCACCTGC TGAGCACATG GGAGGCCCGT TTTGGGTTAT TATAANAGTC TACCATTAAA  
P3-F 113 AGGTAAAGCAG CTGCCAGGCC ATGCACCTGC TGAGCACATG GGAGGCCCGT TTTGGGTTAT TATAANAGTC TACCATTAAA  
P3-R 114 AGGTAAAGCAG CTGCCAGGCC ATGCACCTGC TGAGCACATG GGAGGCCCGT TTTGGGTTAT TATAANAGTC TACCATTAAA  
P4-F 115 AGGTAAAGCAG CTGCCAGGCC ATGCACCTGC TGAGCACATG GGAGGCCCGT TTTGGGTTAT TATAANAGTC TACCATTAAA  
P4-R 116 AGGTAAAGCAG CTGCCAGGCC ATGCACCTG-----  
250 260 270 280 290 300 310 320

P1-F 109 TTGTGAATTA AGGCCCTACN TAAAAANNNN- 301  
P1-R 110 ----- 298  
P2-F 111 ----- 88  
P2-R 112 ----- 278  
P3-F 113 TTGTGAATTA AGGCCCTACC TAANANNNN- 260  
P3-R 114 ----- 276  
P4-F 115 TTGTGAATTA AGGCCCTNCC TAAAAANNNN 293  
P4-R 116 ----- 269  
330 340 350



Exon 19 (ense 00001157566)

gtct tttcagGCAC

C-D-F 179  
C-D-R 180  
P1-F 125  
P1-R 126 NNNNGGGGNT TTTAAAAAGC ACATTCCTCC AAAACCATT T ACAAAAGGTC ATCTTCTAAT CTGTTTGTCT TTT-AGGCAC  
P2-F 127  
P2-R 128 ---NNNGNT NTTTAAAAAG CCATTCCTCC AAAACCATT T ACAAAAGGTC ATCTTCTAAT CTGTTTGTCT TTT-AGGCAC  
P2-F 185  
P3-F 129  
P3-R 130 --NNNGGGT TTTAANAN-C ACATTCCTCC AAAACCATT T ACAAAAGGTC ATCTTCTAAT CTGTTTGTCT TTT-AGGCAC  
P4-F 131  
P4-R 132 --NNNNNGG TTTAAAAAGC ACATTCCTCC AAAACCATT T ACAAAAGGTC ATCTTCTAAT CTGTTTGTCT TTT-AGGCAC  
P4-F 187  
P4-R 188 --NNNNGGGN NNTAAAAAN ACATTCCTCC AAAACCATT T ACAAAAGGTC ATCTTCTAAT CTGTTTGTCT TTT-AGGCAC

10 20 30 40 50 60 70 80

TTCAGACACC ACCTCCAACA ACACAGCAAC CGTGATTTCC ACAGCGCCTC C-AGCTTCCT CAGCAGTCAC GTCCCCCTCT  
C-D-F 179 TTCAGACACC ACCTCCAACA ACACAGCAAC CGTGATTTCC ACAGCGCCTC C-AGCTTCCT CAGCAGTCAC GTCCCCCTCT  
C-D-R 180 TTCAGACACC ACCTCCAACA ACACAGCAAC CGTGATTTCC ACAGCGCCTC C-AGCTTCCT CAGCAGTCAC GTCCCCCTCT  
C-E-F 181  
C-E-R 182  
P1-F 125 TTCAGACACC ACCTCCAACA ACACAGCAAC ANC CGT-NTTNC ANAGNGCCTC CNAGTTTCTT CAGCAGTNAN GTCCCCCTTT  
P1-R 126 TTCAGACACC ACCTCCAACA ACACAGCAAC CGTGATTTCC ACAGCGCCTC C-AGCTTCCT -GTTTGTCT TTT-AGGCAC  
P2-F 127 TTCAGACACC ACCTCCAACA ACACAGCAAC CGTGATTTCC ACAGCGCCTC C-AGCTTCCT CANCAGTCAC GTCCCCCTCT  
P2-R 128 TTCAGACACC ACCTCCAACA ACACAGCAAC CGTGATTTCC ACAGCGCCTC C-AGCTTCCT CAGCAGTCAC GTCCCCCTCT  
P2-F 185 ---AAC CGTGATTTCC ACANCGCCTC C-GGGGNC-T CANCAGTCAC GTCCCCCTCT  
P3-F 129 TTCAGACACC ACCTCCAACA ACACAGCAAC CGTGATTTCC ACAGCGCCTC C-AGCTTCCT CAGCAGTCAC GTCCCCCTCT  
P3-R 130 TTCAGACACC ACCTCCAACA ACACAGCAAC CGTGATTTCC ACAGCGCCTC C-AGCTTCCT CAGCAGTCAC GTCCCCCTCT  
P4-F 131  
P4-R 132 TTCAGACACC ACCTCCAACA ACACAGCAAC CGTGATTTCC ACAGCGCCTC C-AGCTTCCT CAGCAGTCAC GTCCCCCTCT  
P4-F 187 TT-AGACACC ACCTCCAACA ACACAGCAAC CGTGATTTCC ACAGCGCCTC C-AGCTTCCT CAGCAGTCAC GTCCCCCTCT  
P4-R 188 TTCAGACACC ACCTCCAACA ACACAGCAAC CGTGATTTCC ACAGCGCCTC C-AGCTTCCT CAGCAGTCAC GTCCCCCTCT

90 100 110 120 130 140 150 160

CTGAGTCCCT CCCCTTCTGC CTCAGCCTCC ACCTCCGAGG CATCCAGTGC CAGTGAGACC AG-CACAACA CAGACCACCT  
C-D-F 179 CTGAGTCCCT CCCCTTCTGC CTCAGCCTCC ACCTCCGAGG CATCCAGTGC CAGTGAGACC AGGCAACA CAGACCACCT  
C-D-R 180 CTGAGTCCCT CCCCTTCTGC CTCAGCCTCC ACCTCCGAGG CATCCAGTGC CAGTGAGACC AG-CACAACA CAGACCACCT  
C-E-F 181 TNNNGNNNT NNNNNNTNNN NNNNNN-TNN NNNTNNNNN NNTNNNGNG GGGTGAGACC AG-CACAACA CAGACCACCT  
C-E-R 182 TTGAGTCCCT CCCCTTCTGC CTCAGCCTCC ACNTCCGAGG CATCCAGTGC CAGTGAGACC AG-CACAACA CAGACCACCT  
P1-F 125 CTGAGTCCCT CCCCTTCTGC CTCAGCCTCC ACCTCCGAGG CATCCAGTGC CAGTGAGACC AG-CACAACA CAGACCACCT  
P1-R 126 CTGAGTCCCT CCCCTTCTGC CTCAGCCTCC ACCTCCGAGG CATCCAGTGC CAGTGAGACC AG-CACAACA CAGACCACCT  
P2-F 127 CTGANTCCCT CCCCTTCTGC CTCAGCCTCC ACCTCCGAGG CATCCAGTGC CAGTGAGACC AG-CACAACA CAGACCACCT  
P2-R 128 NTGAGTCCCT CCCCTTCTGC CTCAGCCTCC ACCTCCGAGG CATCCAGTGC CAGTGAGACC AG-CACAACA CAGACCACCT  
P2-F 185 NTGAGTCCCT CNNTTNTGN NNTNNNNNTNN NNNTNNNNNG NATNNNGTGC CAGTGAGACC AG-CACAACA CAGACCACCT  
P3-F 129 CTGAGTCCCT CCCCTTCTGC CTCAGCCTCC ACCTCCGAGG CATCCAGTGC CAGTGAGACC AG-CACAACA CAGACCACCT  
P3-R 130 NTGAGTCCCT CCCCTTCTGC CTCAGCCTCC ACCTCCGAGG CATCCAGTGC CAGTGAGACC AG-CACAACA CAGACCACCT  
P4-F 131  
P4-R 132 CTGAGTCCCT CCCCTTCTGC CTCAGCCTCC ACCTCCGAGG CATCCAGTGC CAGTGAGACC AG-CACAACA CAGACCACCT  
P4-F 187 CTGAGTCCCT CCCCTTCTGC CTCAGCCTCC ACCTCCGAGG CATCCAGTGC CAGTGAGACC AG-CACAACA CAGACCACCT  
P4-R 188 CTGAGTCCCT CCCCTTCTGC CTCAGCCTCC ACCTCCGAGG CATCCAGTGC CAGTGAGACC AG-CACAACA CAGACCACCT

170 180 190 200 210 220 230 240

CCACTCCFTT GTCTCCCTT CTTGGGACCA GCCAGGTGAT GGTGACAGCA TCAGGTTTGC AAACAGCAGC AGCTGCTGCC  
C-D-F 179 CCACTCCFTT GTCTCCCTT CTTGGGACCA GCCAGGTGAT GGTGACAGCA TCAGGTTTGC AAACAGCAGC AGCTGCTGCC  
C-D-R 180 CCACTCCFTT GTCTCCCTT CTTGGGACCA GCCAGGTGAT GGTGACAGCA TCAGGTTTGC AAACAGCAGC AGCTGCTGCC  
C-E-F 181 CCACTCCFTT GTCTCCCTT NPTGGGACCA GCCAGGTGAT GGTGACAACN TCAGGTTTGC AAACAGCAGC AGCTGCTGCC  
C-E-R 182 CCANTCTFTT GTCTCCCTT CTTGGGACCA GCCAGGTGAT GGTGACAGCA TCAGGTTTGC AAACAGCA-C AGCTGCTGCC  
P1-F 125 CCACTCCFTT GTCTCCCTT CTTGGGACCA GCCAGGTGAT GGTGACAGCA TCAGGTTTGC AAACAGCAGC AGCTGCTGCC  
P1-R 126 CCACTCCFTT GTCTCCCTT CTTGGGACCA GCCAGGTGAT GGTGACAGCA TCAGGTTTGC AAACAGCAGC AGCTGCTGCC  
P2-F 127 CCACTCCFTT GTCTCCCTT CTTGGGACCA GCCAGGTGAT GGTGACAGCA TCAGGTTTGC AAACAGCAGC AGCTGCTGCC  
P2-R 128 CCACTCCFTT GTCTCCCTT CTTGGGACCA GCCAGGTGAT GGTGACAGCA TCAGGTTTGC AAACAGCAGC AGCTGCTGCC  
P2-F 185 CCACTCCFTT GTCTCCCTT TPTGGGACCA GCCAGGTGAT GGTGACAGCA TCAGGTTTGC AAACAGCAGC AGCTGCTGCC  
P3-F 129 CCACTCCFTT GTCTCCCTT CTTGGGACCA GCCAGGTGAT GGTGACAGCA TCAGGTTTGC AAACAGCAGC AGCTGCTGCC  
P3-R 130 CCACTCCFTT GTCTCCCTT CTTGGGACCA GCCAGGTGAT GGTGACAGCA TCAGGTTTGC AAACAGCAGC AGCTGCTGCC  
P4-F 131  
P4-R 132 CCACTCCFTT GTCTCCCTT CTTGGGACCA GCCAGGTGAT GGTGACAGCA TCAGGTTTGC AAACAGCAGC AGCTGCTGCC  
P4-F 187 CCACTCCFTT GTCTCCCTT CTTGGGACCA GCCAGGTGAT GGTGACAGCA TCAGGTTTGC AAACAGCAGC AGCTGCTGCC  
P4-R 188 CCACTCCFTT GTCTCCCTT CTTGGGACCA GCCAGGTGAT GGTGACAGCA TCAGGTTTGC AAACAGCAGC AGCTGCTGCC

250 260 270 280 290 300 310 320

CTTCAAGGAG CTGCACAGTT GCCAGCAAAAT GCCAGTCTTG CTGCCATGGC AGCTGCTGCA GGACTAAAACC CAAGCCTGAT  
C-D-F 179 TTTNAAGGAG CTGCACAGTT GCCAANAAT GCCATCTTG CTGCCNTGGC ANTTGCTGCA GGANTAAACC CNGGGGGGG  
C-D-R 180 CTTCAAGGAG CTGCACAGTT GCCAGCAAAAT GCCAGTCTTG CTGCCA-GGC AGCNGCGNNC AAAATATTNA ATATNG---  
C-E-F 181 CTTNAAGGAG CTGCACAGTT GCCANAAAT GCCANTCTTG CTGCCATGGN ANCTGCTGCA CAAACCTGAT  
C-E-R 182 CTTCAAGGAG CTGCACAGTT GCCAGCAAAAT GCCAGTCTTG CTGCCATGGC AGCTGCTGCA GGACTAAAACC CAAGCCTGAT  
P1-F 125 CTTCAAGGAG CTGCACAGTT GCCAGCAAAAT GCCAGTCTTG CTGCCATGGC AGCTGCTGCA GGACTAAAACC CAAGCCTGAT  
P1-R 126 CTTCAAGGAG CTGCACAGTT GCCAGCAAAAT GCCAGTCTTG CTGCCATGGC AGCTGCTGCA GGACTAAAACC CAAGCCTGAT  
P2-F 127 CTTCAAGGAG CTGCACAGTT GCCAGCAAAAT GCCAGTCTTG CTGCCATGGC AGCTGCTGCA GGACTAAAACC CAAGCCTGAT  
P2-R 128 CTTCAAGGAG CTGCACAGTT GCCAGCAAAAT GCCAGTCTTG CTGCCATGGC AGCTGCTGCA GGACTAAAACC CAAGCCTGAT  
P2-F 185 CTTCAAGGAG CTGCACAGTT GCCAGCAAAAT GCCAGTCTTG CTGCCATGGC AGCTGCTGCA GGACTAAAACC CAAGCCTGAT  
P3-F 129 CTTCAAGGAG CTGCACAGTT GCCAGCAAAAT GCCAGTCTTG CTGCCATGGC AGCTGCTGCA GGACTAAAACC CAAGCCTGAT  
P3-R 130 CTTCAAGGAG CTGCACAGTT GCCAGCAAAAT GCCAGTCTTG CTGCCATGGC AGCTGCTGCA GGACTAAAACC CAAGCCTGAT  
P4-F 131  
P4-R 132 CTTCAAGGAG CTGCACAGTT GCCAGCAAAAT GCCAGTCTTG CTGCCATGGC AGCTGCTGCA GGACTAAAACC CAAGCCTGAT  
P4-F 187 CTTCAAGGAG CTGCACAGTT GCCAGCAAAAT GCCAGTCTTG CTGCCATGGC AGCTGCTGCA GGACTAAAACC CAAGCCTGAT  
P4-R 188 CTTCAAGGAG CTGCACAGTT GCCAGCAAAAT GCCAGTCTTG CTGCCATGGC AGCTGCTGCA GGACTAAAACC CAAGCCTGAT

	330	340	350	360	370	380	390	400
C-D-F 179	GGCACCCCTCA	CAGTTTGCGG	CTGGGtaagg	cgct				
C-D-R 180	-----	-----	759					
C-E-F 181	GGCACCCCTCA	CAGTTTGCGG	CTGG					
C-E-R 182	GGCACCCCTCA	CAGTTTGCGG	CTGG					
P1-F 125	GGCACCCCTCA	CAGTTTGCGG	CTGGGTAAGG	CGCATTTCACA	TCTCATTCAC	GTCAGAGGTG	GANNITCCCC	AANNCCCCCN
P1-R 126	GGCACCCCTCA	CAGTTTGCGG	CTGG-----	-----	-----	-----	-----	-----
P2-F 127	GGCACCCCTCA	CAGTTTGCGG	CTGGGTAAGG	CGCATTTCACA	TCTCATTCAC	GTCAGAGGTG	GAGNITCCA	ANGNNCCCN
P2-R 128	GGCACCCCTCA	CAGTTTGCGG	CTGGGTAAGG	CGCATTTCACA	-----	-----	-----	-----
P2-F 185	GGCACCCCTCA	CAGTTTGCGG	CTGGGTAAGG	CGCATTTCACA	TCTCATTCAC	GTCAGAGGTG	AGANNCCCC	AANNCCCN
P3-F 129	GGCACCCCTCA	CAGTTTGCGG	CTGGGTAAGG	CGCATTTCACA	TCTCATTCAC	GTCAGAGGTG	GAGNITNCC	AANNCCCN
P3-R 130	GGCACCCCTCA	CAGTTTGCGG	CTGGGTAAGG	CGCATTTCACN	NTCANNAA	-----	-----	-----
P4-F 131	-----	-----	-----	-----	-----	-----	-----	-----
P4-R 132	GGCACCCCTCA	CAGTTTGCGG	CTGGGTAAGG	CGCATTTCACA	TCTCAGNANN	NA-----	-----	-----
P4-F 187	GGCACCCCTCA	CAGTTTGCGG	CTGGGTAAGG	CGCATTTCACA	TCTCATTCAC	GTCAGAGGTG	GAGITGCCCC	AANNCCCN
P4-R 188	GGCACCCCTCA	CAGTTTGCGG	CTGGGTAAGG	CGCATTTCACA	TNTCAGNNNN	NA-----	-----	-----
	410	420	430	440	450	460	470	480
P1-F 125	NN----	419						
P1-R 126	-----	422						
P2-F 127	-----	427						
P2-R 128	-----	434						
P2-F 185	NNNNN-	375						
P3-F 129	-----	418						
P3-R 130	-----	442						
P4-F 131	-----	7						
P4-R 132	-----	448						
P4-F 187	NNNNNN	421						
P4-R 188	-----	449						

Exon 20 (ense 00000958573)

```

                                                    ggact tgcagAGGTG
C-E-F 181
C-E-R 182
P1-F 117 ----- --TNNTTT GATGNCNNAA AGTGACNCCT CTTTGGACT TGCAGAGGTG
P1-R 118 ----- ---NNNTTT AAAATNAGAC NNGCGTGTGC ATGGTAATAA AGTGACTCCT CTTTGGACN TGCAGAGGTG
P2-F 191 ----- ---NNNTTT AAAATNAGAC NNGCGTGTGC ATGGTAATAA AGTGACTCCT CTTTGGACT TGCAGAGGTG
P2-F 199 ----- ---TT NTNGGCNTAA AGTGACTCCT CTTTGGACT TGCAGAGGTG
P3-F 121 ----- ---TT NTGTCNNNTAA AGTGACTCCT CTTTGGACT TGCAGAGGTG
P3-F 193 ----- ---T NNNGGCNNAA AGTGACTCCT CTTTGGACT TGCAGAGGTG
P3-F 201 ----- ---T NNNGGCNNAA AGTGACTCCT CTTTGGACT TGCAGAGGTG
P4-F 195 ----- ---T TNTNCCNNNA AGTGACTCCT CTTTGGACT TGCAGAGGTG
P4-R 196 NNNNNNNNNN NNNNNNNNTTT AAAATNAGAC CTGCGTCTGC ATGGTAATAA AGTGACTCCT CTTTGGACT TGCAGAGGTG
                10          20          30          40          50          60          70          80

```

```

CCTTACTCAG TCTGAATCCA GGGACCCCTGA GCGGTGCTCT CAGC-CCAGC TCTAATGAGC AACAGTACAC T-GGCAACTA
C-E-F 181 CCTTACTCAG TCTGAANCCA GGGACCCCTGA GCGGTGCTCT CAGCACCNC TCTAATGAGC AAAAGTACAC T-GGNAACTA
C-E-R 182 CCTTACTCAG TCTGAATCCA GGGACCCCTGA GCGGTGCTCT CAGC-CCAGC TCTAATGAGC AACAGTACAC TTGGCAACTA
P1-F 117 CCTTACTCAG TCTGAATCCA GGGACCCCTGA GCGGTGCTCT CAGC-CCAGC TCTAATGAGC AACAGTACAC T-GGCAACTA
P1-R 118 CCTTACTCAG TCTGAATCCA GGGACCCCTGA GCGGTGCTCT CAGC-CCAGC TCTAATGAGC AACAGTACAC T-GGCAACTA
P2-F 191 CCTTACTCAG TCTGAATCCA GGGACCCCTGA GCGGTGCTCT CAGC-CCAGC TCTAATGAGC AACAGTACAC T-GGCAACTA
P2-F 199 CCTTACTCAG TCTGAATCCA GGGACCCCTGA GCGGTGCTCT CAGC-CCAGC TCTAATGAGC NANAGTACAC T-GGCAACTA
P3-F 121 CCTTACTCAG TCTGAATCCA GGGACCCCTGA GCGGTGCTCT CAGC-CCAGC TCTAATGAGC AACAGTACAC T-GGCAACTA
P3-F 193 CCTTACTCAG TCTGAATCCA GGGACCCCTGA GCGGTGCTCT CAGC-CCAGC TCTAATGAGC AACAGTACAC T-GGCAACTA
P3-F 201 CCTTACTCAG TCTGAATCCA GGGACCCCTGA GCGGTGCTCT CAGC-CCAGC TCTAATGAGC AACAGTACAC T-GGCAACTA
P4-F 195 CCTTACTCAG TCTGAATCCA GGGACCCCTGA GCGGTGCTCT CAGC-CCAGC TCTAATGAGC AACAGTACAC T-GGCAACTA
P4-R 196 CCTTACTCAG TCTGAATCCA GGGACCCCTGA GCGGTGCTCT CAGC-CCAGC TCTAATGAGC AACAGTACAC T-GGCAACTA
                90          100          110          120          130          140          150          160

```

```

TTCAAGgtca gtagaa
C-E-F 181 NTNAAG
C-E-R 182 TTCAAG
P1-F 117 TTCAAGGTCA GTANAANCCT TTTTCPTAAT TTGGTGGCAT GCACGTGTGT GTGAGTGTGT GTGTGTGTGT GTGTGTGTGN
P1-R 118 TTCAAGGTCA GTAGAAGCCT TTTTNTTAAT TTGGTGGCAT GCACGTGTGT GTGAGTGTGT GTGTGTGTGT GTGTGTGCNT
P2-F 191 TTCAAGGTCA GTANAAGCCT TTTTCPTANT TTGGTGGCAT GCACGTGTGT GTGAGTGTGT GTGTGTGTGT GTGTGTGCNT
P2-F 199 TTCAAGGTCA GTAAAAGCCT TTTTCPTANT TTGGTGGCAT GCACGTGTGT GTGAGTGTGT GTGTGTGTGT GTGTGTGCNT
P3-F 121 TTCAAGGTCA GTANAAGCCT TTTTCPTANT TTGGTGGCAT GCACGTGTGT GTGAGTGTGT GTGTGTGTGT GTGTGTGCNT
P3-F 193 TTCAAGGTCA GTANAAGCCT TTTTCPTANT TTGGTGGCAT GCACGTGTGT GTGAGTGTGT GTGTGTGTGT GTGTGTGCNT
P3-F 201 TTCAAGGTCA GTANAAGCCT TTTTCPTACT TTGGTGGCAT GCACGTGTGT GTGAGTGTGT GTGTGTGTGT GTGTGTGCNT
P4-F 195 TTCAAGGTCA GTANAAGCCT TTTTCPTACT TTGGTGGCAT GCACGTGTGT GTGAGTGTGT GTGTGTGTGT GTGTGTGCNT
P4-R 196 TTCAAGGTCA GTAGAAGCCT TTTTCPTACT TTGGTGGCAT GCACGTGTGT GTGAG-----
                170          180          190          200          210          220          230          240

```

```

P1-F 117 GCTNGAN--- ----- 211
P1-R 118 ----- 212
P2-F 191 GANACAAANA AAAANNNNNN NNNNNNNNNN 230
P2-F 199 GNCACAAANA AAAANNNNNN NNNNNNNNNC 230
P3-F 121 GANANAAAANA AAAANNNN-- ----- 195
P3-F 193 GANACAAANA AAAANNNNNN NNNNNNNNNN 230
P3-F 201 GNNACAAANA AAAANNNNNN NNNNNNNNNN 229
P4-F 195 GANACANAAA NNNNNNNNNN NNNNNNN--- 226
P4-R 196 ----- 213
                250          260          270

```



Exon 21 (ense 00001218941)

P1-F 133 ----- --TTNNTGA- AGACTTTTGA TGTGTTATTT GGCFTCTCCA GGATGATGTT AATGTTTTCA  
P2-R 136 -----G ATTNCCTGAT AGACGTTTGA TGTGTTATTT GGCFTCTCCA GGATGATGTT AATGTTTTCA  
P3-F 137 -----TGAT AGACTTTTGA TGTGTTATTT GGCFTCTCCA GGATGATGTT AATGTTTTCA  
P3-R 138 NNNNNCCCC TTGCGTTGTA GGAAAATGAT AGACTTTTGA TGTGTTATTT GGCFTCTCCA GGATGATGTT AATGTTTTCA  
P4-F 139 -----TTNNTGAT AGACTTTTGA TGTGTTATTT GGCFTCTCCA GGATGATGTT AATGTTTTCA  
P4-R 140 NNNNCNCCCC CNGCGGTGTA GGAAAATGAT AGACTTTTGA TGTGTTATTT GGCFTCTCCA GGATGATGTT AATGTTTTCA  
10 20 30 40 50 60 70 80

ttgtctg tagCTCTTGC TTCTGGTGGC TCTCTTCCAA TAACATCACT TGATGCAACT  
C-E-R 182 CTCTTGC TTCTGGTGGC TCTCTTCCAA TAACATCACT TGATGCAACT  
P1-F 133 TTCCCTGCCTG TTTTGGGGGG TTTTGTCTG TAGCTCTTGC TTCTGGTGGC TCTCTTCCAA TAACATCACT TGATGCAACT  
P2-R 136 TTCCCTGCCTG TTTTGGGGGG TTTTGTCTG TAGCTCTTGC TTCTGGTGGC TCTCTTCCAA TAACATCACT TGATGCAACT  
P3-F 137 TTCCCTGCCTG TTTTGGGGGG TTTTGTCTG TAGCTCTTGC TTCTGGTGGC TCTCTTCCAA TAACATCACT TGATGCAACT  
P3-R 138 TTCCCTGCCTG TTTTGGGGGG TTTTGTCTG TAGCTCTTGC TTCTGGTGGC TCTCTTCCAA TAACATCACT TGATGCAACT  
P4-F 139 TTCCCTGCCTG TTTTGGGGGG TTTTGTCTG TAGCTCTTGC TTCTGGTGGC TCTCTTCCAA TAACATCACT TGATGCAACT  
P4-R 140 TTCCCTGCCTG TTTTGGGGGG TTTTGTCTG TAGCTCTTGC TTCTGGTGGC TCTCTTCCAA TAACATCACT TGATGCAACT  
90 100 110 120 130 140 150 160

GGGAACCTGG TATTTGCCAA TCGGGGAGGA GCCCCCAACA TCGTGACTGC CCCTCTGTTT CTGAACCTC AGAACCTCTC  
C-E-R 182 GGGAACTGG TATTTGCCAA TCGGGGAGGA GCCCCCAACA TCGTGACTGC CCCTCTGTTT CTGAACCTC AGAACCTCTC  
P1-F 133 GGGAACTGG TATTTGCCAA TCGGGGAGGA GCCCCCAACA TCGTGACTGC CCCTCTGTTT CTGAACCTC AGAACCTCTC  
P2-R 136 GGGAACTGG TATTTGCCAA TCGGGGAGGA GCCCCCAACA TCGTGACTGC CCCTCTGTTT CTGAACCTC AGAACCTCTC  
P3-F 137 GGGAACTGG TATTTGCCAA TCGGGGAGGA GCCCCCAACA TCGTGACTGC CCCTCTGTTT CTGAACCTC AGAACCTCTC  
P3-R 138 GGGAACTGG TATTTGCCAA TCGGGGAGGA GCCCCCAACA TCGTGACTGC CCCTCTGTTT CTGAACCTC AGAACCTCTC  
P4-F 139 GGGAACTGG TATTTGCCAA TCGGGGAGGA GCCCCCAACA TCGTGACTGC CCCTCTGTTT CTGAACCTC AGAACCTCTC  
P4-R 140 GGGAACTGG TATTTGCCAA TCGGGGAGGA GCCCCCAACA TCGTGACTGC CCCTCTGTTT CTGAACCTC AGAACCTCTC  
170 180 190 200 210 220 230 240

TCTGCTCACC AGCAACCTG TTAGCTTGGT CTC TGCCGCC GCAGCATCTG CAGGGAATC TGCACCTGTA GCCAGCCTTC  
C-E-R 182 TGTGCTCACC AGCAACCTG TTAGCTTGGT CTC TGCCGCC GCAGCATCTG CAGGGAATC TGCACCTGTA GCCAGCCTTC  
P1-F 133 TGTGCTCACC AGCAACCTG TTAGCTTGGT CTC TGCCGCC GCAGCATCTG CAGGGAATC TGCACCTGTA GCCAGCCTTC  
P2-R 136 TGTGCTCACC AGCAACCTG TTAGCTTGGT CTC TGCCGCC GCAGCATCTG CAGGGAATC TGCACCTGTA GCCAGCCTTC  
P3-F 137 TGTGCTCACC AGCAACCTG TTAGCTTGGT CTC TGCCGCC GCAGCATCTG CAGGGAATC TGCACCTGTA GCCAGCCTTC  
P3-R 138 TGTGCTCACC AGCAACCTG TTAGCTTGGT CTC TGCCGCC GCAGCATCTG CAGGGAATC TGCACCTGTA GCCAGCCTTC  
P4-F 139 TGTGCTCACC AGCAACCTG TTAGCTTGGT CTC TGCCGCC GCAGCATCTG CAGGGAATC TGCACCTGTA GCCAGCCTTC  
P4-R 140 TGTGCTCACC AGCAACCTG TTAGCTTGGT CTC TGCCGCC GCAGCATCTG CAGGGAATC TGCACCTGTA GCCAGCCTTC  
250 260 270 280 290 300 310 320

ACGCCACCTC CACCTCTGCT GAGTCCATCC AGAACTCTCT CTTACAGTG GCCTCTGCCA GCGGGGTGC GTCCACCACC  
C-E-R 182 ACGCCACCTC CACCTCTGCT GAGTCCATCC AGAACTCTCT CTTACAGTG GCCTCTGCCA GCGGGGTGC GTCCACCACC  
P1-F 133 ACGCCACCTC CACCTCTGCT GAGTCCATCC AGAACTCTCT CTTACAGTG GCCTCTGCCA GCGGGGTGC GTCCACCACC  
P2-R 136 ACGCCACCTC CACCTCTGCT GAGTCCATCC AGAACTCTCT CTTACAGTG GCCTCTGCCA GCGGGGTGC GTCCACCACC  
P3-F 137 ACGCCACCTC CACCTCTGCT GAGTCCATCC AGAACTCTCT CTTACAGTG GCCTCTGCCA GCGGGGTGC GTCCACCACC  
P3-R 138 ACGCCACCTC CACCTCTGCT GAGTCCATCC AGAACTCTCT CTTACAGTG GCCTCTGCCA GCGGGGTGC GTCCACCACC  
P4-F 139 ACGCCACCTC CACCTCTGCT GAGTCCATCC AGAACTCTCT CTTACAGTG GCCTCTGCCA GCGGGGTGC GTCCACCACC  
P4-R 140 ACGCCACCTC CACCTCTGCT GAGTCCATCC AGAACTCTCT CTTACAGTG GCCTCTGCCA GCGGGGTGC GTCCACCACC  
330 340 350 360 370 380 390 400

ACCACCGCCT CCAAGGCACA GTGAgctggg cagagctggg ctgccagaag cctttttcac tctgcagtgt gattggactg  
C-E-R 182 ACCNCCCCCT NNAAGGCACA NNGAGCNGGG C-----  
P1-F 133 ACCACCGCCT CCAAGGCACA GTGAGCTGGG CAGAGCTGGG CTGCCAGAAG CCTTTTTCAC TCTGCAGTGT GATTGGACGC  
P2-R 136 ACCACCGCCT CCAAGGCACA GTGAGCTGGG CAGAGCTGGG CTGCCAGAAN CCTTTTTCAC TCTGCANIGT GATTGGATCC  
P3-F 137 ACCACCGCCT CCAAGGCACA GTGAGCTGGG CAGAGCTGGG CTGCCAGAAG CCTTTTTCAC TCTGCAGTGT GATTGGCGGN  
P3-R 138 ACCACCGCCT CCAAGGCACA GTGAGCTGGG CAGAGCTGGG CTGCCAGAAG CCTTTTTC-----  
P4-F 139 ACCACCGCCT CCAAGGCACA GTGAGCTGGG CAGAGCTGGG CTGCCAGAAG CCTTTTTCAC TCTGCAGTGT GATTGGATGC  
P4-R 140 ACCACCGCCT CCAAGGCACA GTGAGCTGGG CAGAGCTGGG CTGCCAGAAG CCTTTTTC-----  
410 420 430 440 450 460 470 480

caggtaata aactgaaaaa tgtga.....  
C-E-R 182 -----  
P1-F 133 CCNCAANNNN 467  
P2-R 136 NNCAACCNNN 471  
P3-F 137 CNCAANNN-- 462  
P3-R 138 ----- 457  
P4-F 139 CCCCNCNNNN 468  
P4-R 140 ----- 459  
490

Lower case letters at 3'end indicate the untranslated region (UTR)

