Figure 1:

Mouse RdCVF1 cDNA: SEQ ID NO:1

```
  1 ATCGGATCCCTCTCTGGGTCCCCAGCTCCTTGCATACTGCTACCATGGCA 50
 51 TCTCTCTTCTCTGGACGCATCTTGATCAGGAACAACAGCGACCAGGATGA 100
101 AGTGGAGACAGAGGCAGAGCTGAGCCGTAGGTTAGAGAATCGTCTGGTGT 150
151 TGCTGTTCTTCGGCGCCGGCGCCTGTCCCCAGTGCCAGGCCTTTGCCCCA 200
201 GTCCTCAAAGACTTCTTCGTGCGGCTCACTGACGAGTTCTACGTGCTGCG 250
251 GGCAGCACAGCTGGCCCTGGTCTATGTGTCCCAGGACCCTACAGAGGAGC 300
301 AACAGGACCTCTTCCTCAGGGACATGCCTGAAAAATGGCTCTTCCTGCCG 350
351 TTCCATGATGAACTGAGGAGGTGAGGCCCCAGGGAAGACCAGGGAGGGCT 400
401 TCCTGGAGAAGGCATTTCCCTGGAGGTTTACTGTCCTGGTACTACTTGTG 450
451 CATAAAGAGGTATTCCTC 468
```

Polypeptide : ATG to TGA: SEQ ID NO:2

```
  1 MASLFSGRIL IRNNSDQDEV ETEAELSRRL ENRLVLLFFG AGACPQCQAF
 51 APVLKDFFVR LTDEFYVLRA AQLALVYVSQ DPTEEQQDLF LRDMPEKWLF
101 LPFHDELRR
```

Figure 2:

Mouse RdCVF1L cDNA: SEQ ID NO:3

```
  1 CCCCAGCTCC TTGCATACTG CTACCATGGC ATCTCTCTTC TCTGGACGCA
 51 TCTTGATCAG GAACAACAGC GACCAGGATG AAGTGGAGAC AGAGGCAGAG
101 CTGAGCCGTA GGTTAGAGAA TCGTCTGGTG TTGCTGTTCT TCGGCGCCGG
151 CGCCTGTCCC CAGTGCCAGG CCTTTGCCCC AGTCCTCAAA GACTTCTTCG
201 TGCGGCTCAC TGACGAGTTC TACGTGCTGC GGGCAGCACA GCTGGCCCTG
251 GTCTATGTGT CCCAGGACCC TACAGAGGAG CAACAGGACC TCTTCCTCAG
301 GGACATGCCT GAAAAATGGC TCTTCCTGCC GTTCCATGAT GAACTGAGGA
351 GGGACCTCGG GCGCCAGTTC TCTGTCCGTC AACTGCCAGC GGTTGTGGTA
401 CTTAAGCCTG GTGGGGACGT GCTGACAAGC GACGCCACGG AGGAGATCCA
451 GCGTCTGGGA CCCGCCTGCT TTGCCAACTG GCAGGAGGCC GCAGAGCTCC
501 TGGACCGCAG CTTCCTGCAA CCGGAGGATT TGGATGAGCC TGCGCGGCGC
551 AGCATCACCG AGCCTCTGCG CCGTCGCAAG TACCGAGTAG ACCGGGATGT
601 CGGCGGGAGC GGGGCGAAAC GGCGCGACTC TGGTGAACCC CAGGGGGACG
651 CGGGTACAAG GGCGGAGCTC TGGTGACTCC CAGGGTAGGA GTGGGGACCG
701 GAGCTCTGGT GACACCAAAG TACCGGTGCA CGACCGAGGT TGATGACCCT
751 CCCGAAGGAA CCGG
```

Polypeptide : ATG to TGA: SEQ ID NO:4

```
  1 MASLFSGRIL IRNNSDQDEV ETEAELSRRL ENRLVLLFFG AGACPQCQAF
 51 APVLKDFFVR LTDEFYVLRA AQLALVYVSQ DPTEEQQDLF LRDMPEKWLF
101 LPFHDELRRD LGRQFSVRQL PAVVVLKPGG DVLTSDATEE IQRLGPACFA
151 NWQEAAELLD RSFLQPEDLD EPARRSITEP LRRRKYRVDR DVGGSGAKRR
201 DSGEPQGDAG TRAELW
```

Figure 3:

Human RdCVF1 cDNA: SEQ ID NO:5

```
   1  CCCAGCACCC AACCCAGGTT ACCATGGCCT CCCTGTTCTC TGGCCGCATC
  51  CTGATCCGCA ACAATAGCGA CCAGGACGAG CTGGATACGG AGGCTGAGGT
 101  CAGTCGCAGG CTGGAGAACC GGCTGGTGCT GCTGTTCTTT GGTGCTGGGG
 151  CTTGTCCACA GTGCCAGGCC TTCGTGCCCA TCCTCAAGGA CTTCTTCGTG
 201  CGGCTCACAG ATGAGTTCTA TGTACTGCGG GCGGCTCAGC TGGCCCTGGT
 251  GTACGTGTCC CAGGACTCCA CGGAGGAGCA GCAGGACCTG TTCCTCAAGG
 301  ACATGCCAAA GAAATGGCTT TTCCTGCCCT TTGAGGATGA TCTGAGGAGG
 351  TGA
```

Polypeptide : ATG to TGA: SEQ ID NO:6

```
   1  MASLFSGRIL IRNNSDQDEL DTEAEVSRRL ENRLVLLFFG AGACPQCQAF
  51  VPILKDFFVR LTDEFYVLRA AQLALVYVSQ DSTEEQQDLF LKDMPKKWLF
 101  LPFEDDLRR
```

Figure 4:

Human RdCVF1L cDNA: SEQ ID NO:7

```
   1  CCGGGGACCA CACGCCGCGC TGTCCCCAGC ACCCAACCCA GGTTACCATG
  51  GCCTCCCTGT TCTCTGGCCG CATCCTGATC CGCAACAATA GCGACCAGGA
 101  CGAGCTGGAT ACGGAGGCTG AGGTCAGTCG CAGGCTGGAG AACCGGCTGG
 151  TGCTGCTGTT CTTTGGTGCT GGGGCTTGTC CACAGTGCCA GGCCTTCGTG
 201  CCCATCCTCA AGGACTTCTT CGTGCGGCTC ACAGATGAGT TCTATGTACT
 251  GCGGGCGGCT CAGCTGGCCC TGGTGTACGT GTCCCAGGAC TCCACGGAGG
 301  AGCAGCAGGA CCTGTTCCTC AAGGACATGC CAAAGAAATG GCTTTTCCTG
 351  CCCTTTGAGG ATGATCTGAG GAGGGACCTC GGGCGCCAGT TCTCAGTGGA
 401  GCGCCTGCCG GCGGTCGTGG TGCTCAAGCC GGACGGGGAC GTGCTCACTC
 451  GCGACGGCGC CGACGAGATC CAGCGCCTGG GCACCGCCTG CTTCGCCAAC
 501  TGGCAGGAGG CGGCCGAGGT GCTGGACCGC AACTTCCAGC TGCCAGAGGA
 551  CCTGGAGGAC CAGGAGCCAC GGAGCCTCAC CGAGTGCCTG CGCCGCCACA
 601  AGTACCGCGT GGAAAAGGCG GCGCGAGGCG GGCGCGACCC CGGGGGAGGG
 651  GGTGGGGAGG AGGGCGGGGC CGGGGGGCTG TTCTGA
```

Polypeptide : ATG to TGA: SEQ ID NO:8

```
   1  MASLFSGRIL IRNNSDQDEL DTEAEVSRRL ENRLVLLFFG AGACPQCQAF
  51  VPILKDFFVR LTDEFYVLRA AQLALVYVSQ DSTEEQQDLF LKDMPKKWLF
 101  LPFEDDLRRD LGRQFSVERL PAVVVLKPDG DVLTRDGADE IQRLGTACFA
 151  NWQEAAEVLD RNFQLPEDLE DQEPRSLTEC LRRHKYRVEK AARGGRDPGG
 201  GGGEEGGAGG LF
```

Figure 5:

Mouse RdCVF2 cDNA: SEQ ID NO:9

```
   1  ATAAAATAGA GGGTGGGAGA GGTTGATGGC GTGGCTCTGC TTTTTGGTGC
  51  GGGGCACCCA GCTGTCATCG CTGCTGTCGC AGCTTCTGGA GTGGCCACTG

 101  TGCTCTCTCC TCCCTTCGGC TCAAGGTGAG CTGTTCCAGC AGAAGGCGGG
 151  GCTGAGAGGC GCCTAGTGCT GCGGGAGGCT CAGTGTCATC TTCCAGCTAA
 201  CAGGTGGCCG TGCAGCCCAG GGCTCGTCTC TCCACTGTGT CCTCTTCACG
 251  CCGAGCTCGT GGCGATGGTG GACGTGCTGG GCGGGCGGCG CCTGGTGACC
 301  CGGGAGGGCA CGGTGGTGGA GGCCGAGGTG GCGCTGCAGA ACAAGGTGGT
 351  AGCTTTGTAC TTTGCGGCGG GCCGGTGCTC GCCCAGCCGC GACTTCACGC
 401  CGCTGCTCTG CGACTTCTAC ACGGAGCTGG TGAGCGAGGC GCGGCGGCCC
 451  GCTCCCTTCG AGGTGGTTTT CGTGTCGGCA GACGGCAGTG CGGAGGAGAT
 501  GTTGGACTTC ATGCGCGAGC TGCACGGCTC CTGGCTGGCA TTGCCCTTCC
 551  ACGACCCCTA CCGGCAGTGA GTGGGGACCC AGGGGTCATG GGGCTGGCGC
```

Polypeptide : ATG to TGA: SEQ ID NO:10

```
   1  MVDVLGGRRL VTREGTVVEA EVALQNKVVA LYFAAGRCSP SRDFTPLLCD
  51  FYTELVSEAR RPAPFEVVFV SADGSAEEML DFMRELHGSW LALPFHDPYR
 101  Q
```

Figure 6:

Mouse RdCVF2L cDNA: SEQ ID NO:11

```
   1  TTGACTCTGG TGGGTAGAGA GGGTTTGCAA GGCAGGATAA AATAGAGGGT
  51  GGGAGAGGTT GATGGCGTGG CTCTGCTTTT TGGTGCGGGG CACCAGCTGT
 101  CATCGCTGCT GTCGCAGCTT CTGGAGTGGC CACTGTGCTC TCTCCTCCCT
 151  TCGGCTCAAG GTGAGCTGTT CCAGCAGAAG GCGGGGCTGA GAGGCGCCTA
 201  GTGCTGCGGG AGGCTCAGTG TCATCTTCCA GCTAACAGGT GGCCGTGCAG
 251  CCCAGGGCTC GTCTCTCCAC TGTGTCCTCT TCACGCCGAG CTCGTGGCGA
 301  TGGTGGACGT GCTGGGCGGG CGGCGCCTGG TGACCCGGGA GGGCACGGTG
 351  GTGGAGGCCG AGGTGGCGCT GCAGAACAAG GTGGTAGCTT TGTACTTTGC
 401  GGCGGGCCGG TGCTCGCCCA GCCGCGACTT CACGCCGCTG CTCTGCGACT
 451  TCTACACGGA GCTGGTGAGC GAGGCGCGGC GGCCCGCTCC CTTCGAGGTG
 501  GTTTTCGTGT CGGCAGACGG CAGTGCGGAG GAGATGTTGG ACTTCATGCG
 551  CGAGCTGCAC GGCTCCTGGC TGGCATTGCC CTTCCACGAC CCCTACCGGC
 601  ATGAACTGAA GAAGAGGTAC GAAATCACCG CCATCCCCAA GCTGGTGGTC
 651  ATCAAGCAGA ACGGAGCTGT CATCACCAAC AAAGGGCGGA AGCAGATCCG
 701  AGAGCGCGGG CTAGCTTGCT TTCAGAACTG GGTGGAAGCA GCCGATGTTT
 751  TCCAAAACTT CTCGGGGTGA CCAGGGCAGT TGCTGGAAGT TCAGGGCAAC
 801  TATCTTCAAA AAGGGCTTAG CTGGTTCCCT TCTCTGCTGA GGAATGTCAT
 851  TGTAGAGTCA CCATGCTGTG ACAGAGAGCA TAAACTGCTC AGGAAAGAAC
 901  TACGTCTGCC CCCTGTGGGT CCTAGAGCTC CGTTGAATGT TTATTTCTTA
 951  CACCTTTCTC CACCGGTGCC TAGGATCCAG GACACATCAG CCACGAGTTA
1001  ACAGAACTCT ATGCAAGATG CTCTTTCCTA CAGGAAATTT CTTTGATAAA
1051  TTGACCTATG GAGGTGATAC ATTTTCTGAT GACATTTTTG TGATGCTTTG
1101  GTAAACGTAT TTATTACTCG GGTTTGTAGA CTGTGTAATT TAATAAACCA
1151  ACACTCACAC TTTG
```

Polypeptide : ATG to TGA: SEQ ID NO:12

```
   1  MVDVLGGRRL VTREGTVVEA EVALQNKVVA LYFAAGRCSP SRDFTPLLCD
```

```
  51  FYTELVSEAR RPAPFEVVFV SADGSAEEML DFMRELHGSW LALPFHDPYR
 101  HELKKRYEIT AIPKLVVIKQ NGAVITNKGR KQIRERGLAC FQNWVEAADV
 151  FQNFSG
```

Figure 7:

Human RdCVF2 cDNA: SEQ ID NO:13

```
   1  GTGTGGGCGG GGCGCAGTTG GGGGAGGGTG CAGAGACCTG AGGGCTTGAG
  51  GTTGCCTGGC TGGCCCCGCT CCCAGAGGCG GGTGCCGCGC TGTCGCCCAG
 101  GTATCTGGGG TCTCTGGTGT CTGAGTGTCT CATTGTCGGC GCGAACACAA
 151  TTGCTCCAGC CACAGGCGAG GCCTGGCCAA GGTGTGGGCG CATCTAGGGC
 201  AGGTCTTGAG AGGTCCAGCG CCCGGTGGTG CGGACAGAGG CGGGGCACCG
 251  CGGCGCTCGC CGCCGCCTCC CCGCAGGTGA TCATCCTCCT GCAGGTGTCC
 301  TCGGGTCTCA GGTGGCTGCG TGTCTGCGCC ATGGTTGACA TTCTGGGCGA
 351  GCGGCACCTG GTGACCTGTA AGGGCGCGAC GGTGGAGGCC GAGGCGGCGC
 401  TGCAGAACAA GGTGGTGGCA CTGTACTTCG CGGCGGCCCG GTGCGCGCCG
 451  AGCCGCGACT TCACGCCGCT GCTCTGCGAC TTCTATACGG CGCTGGTGGC
 501  CGAGGCGCGG CGGCCCGCGC CCTTCGAAGT GGTCTTCGTG TCAGCCGACG
 551  GCAGCTGCCA GGAGATGCTG GACTTCATGC GCGAGCTGCA TGGCGCCTGG
 601  CTGGCGCTGC CCTTCCACGA CCCCTACCGG CAACGGAGTC TCGCTCTGTT
 651  GCCCAGGCTG GAGTGCAGTG GCGTGATCTT AGCTCACTGC AACCTTTGCC
 701  TCCTGGGTTC AAGTGATTCT CTAGCCTTAG CCTCCTGAGC ATCTGGGACT
 751  ACAGCCATTG CTGTGAATTA CGTGAGGGAA AGATATTGAA GAGGAGTTGG
 801  ACACTCCGAG AGTGCAGCTG TTCTCCCCCC GCACCATCCG TGTCCTGCAT
 851  TCTGCGAGTC TGTGCTCATT AACAATGTGC TGTGACCATG TGACTCAGCA
 901  ATCCTGCTGC TGGGTATATA CCCGAAAGAA AGGAAAAGGA AGCCAGTATA
 951  TTGAAGAGGT ATCTGCACCC CCATGTTTAT TGCAGCACTG TTCACAACAG
1001  CCAAGATTTG GAAGCAACCT AAGTGTCCAT CAACAGATGA ATGGATAAAG
1051  AAAACGTGGT ACATATACAC AATGGAGTAC TCTTCAGCCA TTAAAAAAAT
1101  GAGATTCTGT CATTTGCAAT AATATAGATG GAAAAGGAGG CCCTTATGTG
1151  AAGTGAAATA AGCCAGGCAC AGAAAGACAA ACATCACATG TTCTCACTTA
1201  TTTGTGGGAT CTAATGATCA AAACAATTGA ACTCTTGGAC ATAGAGAGTA
1251  GAAGGTTGGT TACCAGAAGC TGGAAAGGAA AGTGGGGTTG GGAGGAAGGT
1301  GGGAATGGTT AATAGGTACA AAAAAATACA AAGAATAAAT AAGACCTAAT
1351  ATTTGATAGC ACAACAGTGT GACTACTGTC AATAATCATT TAATTGTACA
1401  TTTAAAAATA ACTATAATTG CATTGTTTGT AACACAAAAG ATAAATGCTT
1451  GAGGAGAAAA AAAAAAAAAA AA
```

Polypeptide : ATG to TGA : SEQ ID NO:14

```
   1  MVDILGERHL VTCKGATVEA EAALQNKVVA LYFAAARCAP SRDFTPLLCD
  51  FYTALVAEAR RPAPFEVVFV SADGSCQEML DFMRELHGAW LALPFHDPYR
 101  QRSLALLPRL ECSGVILAHC NLCLLGSSDS LALAS
```

Figure 8:

Pileup short sequences :

```
         1                                                  50
mRdCVF1  MASLFSGRIL IRNNSDQDEV ETEAELSRRL ENRLVLLFFG AGACPQCQAF
hRdCVF1  MASLFSGRIL IRNNSDQDEL DTEAEVSRRL ENRLVLLFFG AGACPQCQAF
mRdCVF2  MVDVLGGRRL VTREG....T VVEAEVA..L QNKVVALYFA AGRCSPSRDF
hRdCVF2  MVDILGERHL VTCKG....A TVEAEAA..L QNKVVALYFA AARCAPSRDF
```

```
          51                                                        100
mRdCVF1   APVLKDFFVR LTDEFYVLRA AQLALVYVSQ DPTEEQQDLF LRDMPEKWLF
hRdCVF1   VPILKDFFVR LTDEFYVLRA AQLALVYVSQ DSTEEQQDLF LKDMPKKWLF
mRdCVF2   TPLLCDFYTE LVSE..ARRP APFEVVFVSA DGSAEEMLDF MRELHGSWLA
hRdCVF2   TPLLCDFYTA LVAE..ARRP APFEVVFVSA DGSCQEMLDF MRELHGAWLA

          101                                                143
mRdCVF1   LPFHDELRR
hRdCVF1   LPFEDDLRR
mRdCVF2   LPFHDPYRQ
hRdCVF2   LPFHDPYRQR SLALLPRLEC SGVILAHCNL CLLGSSDSLA LAS
```

Pileup long sequences :

```
          1                                                          50
mRdCVF1L  MASLFSGRIL IRNNSDQDEV ETEAELSRRL ENRLVLLFFG AGACPQCQAF
hRdCVF1L  MASLFSGRIL IRNNSDQDEL DTEAEVSRRL ENRLVLLFFG AGACPQCQAF
mRdCVF2L  MVDVLGGRRL VTREG....T VVEAEVA..L QNKVVALYFA AGRCSPSRDF
 hRdCVF2  MVDILGERHL VTCKG....A TVEAEAA..L QNKVVALYFA AARCAPSRDF

          51                                                        100
mRdCVF1L  APVLKDFFVR LTDEFYVLRA AQLALVYVSQ DPTEEQQDLF LRDMPEKWLF
hRdCVF1L  VPILKDFFVR LTDEFYVLRA AQLALVYVSQ DSTEEQQDLF LKDMPKKWLF
mRdCVF2L  TPLLCDFYTE LVSE..ARRP APFEVVFVSA DGSAEEMLDF MRELHGSWLA
 hRdCVF2  TPLLCDFYTA LVAE..ARRP APFEVVFVSA DGSCQEMLDF MRELHGAWLA

          101                                                       150
mRdCVF1L  LPFHDELRRD ...LGRQFSV RQLPAVVVLK PGGDVLTSDA TEEIQRLGPA
hRdCVF1L  LPFEDDLRRD ...LGRQFSV ERLPAVVVLK PDGDVLTRDG ADEIQRLGTA
mRdCVF2L  LPFHDPYRHE ...LKKRYEI TAIPKLVVIK QNGAVITNKG RKQIRERGLA
 hRdCVF2  LPFHDPYRQR SLALLPRLEC SGV...ILAH CNLCLLGSSD SLALAS

          151                                                       200
mRdCVF1L  CFANWQEAAE LLDRSFLQPE DLDEPARRSI TEPLRRRKYR VDRDVGGSGA
hRdCVF1L  CFANWQEAAE VLDRNFQLPE DLEDQEPRSL TECLRRHKYR VEKAARGG..
mRdCVF2L  CFQNWVEAAD VFQNFSG
 hRdCVF2

          201              219
mRdCVF1L  KRRDSGEPQG DAGTRAELW
hRdCVF1L  ..RDPGGGGG EEGGAGGLF
mRdCVF2L
 hRdCVF2
```

Figure 9:

SEQ ID NO: 26: 5' cgggatccATGGCATCTCTCTTCTCTGGACGC 3'

SEQ ID NO: 27: 5' ggaattcTCACCTCCTCAGTTCATCATGGAA 3'

Figure 10:

```
          1                                                        50
RdCVF1    MASLFSGRIL IRNNSDQDEV ETEAELSRRL ENRLVLLFFG AGACPQCQAF
RdCVF2    MVDVLGGRRL V....TREGT VVEAEVA..L QNKVVALYFA AGRCSPSRDF

          51                                                       100
RdCVF1    APVLKDFFVR LTDEFYVLRA AQLALVYVSQ DPTEEQQDLF LRDMPEKWLF
RdCVF2    TPLLCDFYTE LVSE..ARRP APFEVVFVSA DGSAEEMLDF MRELHGSWLA

          101
RdCVF1    LPFHDELRR
RdCVF2    LPFHDPYRQ
```

Figure 11:

```
bc016199          mouse RdCVF2
bg707818          human RdCVF2

          1                                                        50
bc016199  MVDVLGGRRL VTREGTVVEA EVALQNKVVA LYFAAGRCSP SRDFTPLLCD
bg707818  MVDILGERHL VTCKGATVEA EAALQNKVVA LYFAAARCAP SRDFTPLLCD

          51                                                       100
bc016199  FYTELVSEAR RPAPFEVVFV SADGSAEEML DFMRELHGSW LALPFHDPYR
bg707818  FYTALVAEAR RPAPFEVVFV SADGSCQEML DFMRELHGAW LALPFHEPYR

          101               120
bc016199  Q*
bg707818  QRSLALLPRL ECSGVILAH*
```

Figure 12:

```
 Name: mRdCVF2          mouse sequence bc016199
 Name: be552141         homo sapiens
 Name: bi517442         homo sapiens
 Name: bg707818         homo sapiens
 Name: bi603812         homo sapiens

mRdCVF2                                                ATGGT GGACGTGCTG
be552141  TGTCCTCGGG TCTCAGGTGG CTGCGTGTCT GCGCCATGGT TGACATTCTG
bi517442  TGTCCTCGGG TCTCAGGTGG CTGCGTGTCT GCGCCATGGT TGACATTCTG
bg707818  TGTCCTCGGG TCTCAGGTGG CTGCGTGTCT GCGCCATGGT TGACATTCTG
bi603812  TGTCCTCGGG TCTCAGGTGG CTGCGTGTCT GCGCCATGGT TGACATTCTG

mRdCVF2   GGCGGGCGGC GCCTGGTGAC CCGGGAGGGC ACGGTGGTGG AGGCCGAGGT
be552141  GGCGAGCGGC ACCTGGTGAC CTGTAAGGGC GCGACGGTGG AGGCCGAGGC
bi517442  GGCGAGCGGC ACCTGGTGAC CTGTAAGGGC GCGACGGTGG AGGCCGAGGC
bg707818  GGCGAGCGGC ACCTGGTGAC CTGTAAGGGC GCGACGGTGG AGGCCGAGGC
bi603812  GGCGAGCGGC ACCTGGTGAC CTGTAAGGGC GCGACGGTGG AGGCCGAGGC

mRdCVF2   GGCGCTGCAG AACAAGGTGG TAGCTTTGTA CTTTGCGGCG GGCCGGTGCT
be552141  GGCGCTGCAG AACAAGGTGG TGGCACTGTA CTTCGCGGCG GCCCGGTGCG
bi517442  GGCGCTGCAG AACAAGGTGG TGGCACTGTA CTTCGCGGCG G.CCGGTGCG
bg707818  GGCGCTGCAG AACAAGGTGG TGGCACTGTA CTTCGCGGCG GCCCGGTGCG
bi603812  GGCGCTGCAG AACAAGGTGG TGGCACTGTA CTTCGCGGCG GCCCGGTGCG
```

```
mRdCVF2    CGCCCAGCCG CGACTTCACG CCGCTGCTCT GCGACTTCTA CACGGAGCTG
be552141   CGCCGAGCCG CGACTTCACG CCGCTGCTCT GCGACTTCTA TACGGCGCTG
bi517442   CGCCGAGCCG CGA.TTCACG CCGCTGCTCT GCGACTTCTA TACGGCGCTG
bg707818   CGCCGAGCCG CGACTTCACG CCGCTGCTCT GCGACTTCTA TACGGCGCTG
bi603812   CGCCGAGCCG CGACTTCACG CCGCTGCTCT GCGACTTCTA TACGGCGCTG

mRdCVF2    GTGAGCGAGG CGCGGCGGCC CGCTCCCTTC GAGGTGGTTT TCGTGTCGGC
be552141   GTGGCCGAGG CGCGGCGGCC CGCGCCCTTC GAAGTGGTCT TCGTGTCAGC
bi517442   GTGGCCGAG. ...CGCGGGG CCGCGCCTTC GAAGTGGTCT TCGTGTCAGC
bg707818   GTGGCCGAGG CGCGGCGGCC CGCGCCCTTC GAAGTGGTCT TCGTGTCAGC
bi603812   GTGGCCGAGG CGCGGCGGCC CGCGCCCTTC GAAGTGGTCT TCGTGTCAGC

mRdCVF2    AGACGGCAGT GCGGAGGAGA TGT.TGGACT TCATGCGCGA GCTGCACGGC
be552141   CGACGGCAGC TCCCAGGAGA TGC.TGGACT TCATGCGCGA GCTGCATGGC
bi517442   CGACGGCAGC TCCCAGGAGA TGC.TGGACT TCATGCGCGA GCTG.ATGGC
bg707818   CGACGGCAGC TGCCAGGAGA TGC.TGGACT TCATGCGCGA GCTGCATGGC
bi603812   CGACGGCAGC TGCCAGGAGA TGCTTGGACT TCATGCGCGA GCTGCATTGC

mRdCVF2    TCCTGGC.TG GCATTGCCCT TCCACGACCC CTACCGGCAG TGA
be552141   GCCTGGC.TG GCGCTGCCCT TCCACGACCC CTACCGGCAC CATTGCTGTG
bi517442   GCCTGGC.TG GCGCTG.CCT TCCACGACCC CTACCGGCAC AGCCGGAGCC
bg707818   GCCTGGC.TG GCGCTGCCCT TCCACGAACC CTACCGGCAA CGGAGTCTCG
bi603812   GCCTGGCTTG GCGCTGCCCT TCCACGACCC CTACCGGCAA CGGAGTCTCG
```

Figure 13:

```
pileup

                GapWeight: 5
          GapLengthWeight: 1

 Name: RdCVF1
 Name: bg299078
 Name: ai716631
 Name: bg294111
 Name: be108041              Rev
 Name: bg395178

          1                                                    50
  RdCVF1  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
bg299078  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ --ATCGGATC CTCTCTGGGT
ai716631  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~CG GCCGCTTAAT SINE
bg294111  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
be108041  ACGAGGTCAA CCTTGGCTAC ACAGGGAGTC TGAGGACAGC ATGGGNTACA
bg395178  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~A CGCCGCGCTG

          51                                                   100
  RdCVF1  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~ATGGC ATCTCTCTTC TCTGGACGCA
bg299078  CCCCAGCTCC TTGCATACTG CTACCATGGC ATCTCTCTTC TCTGGACGCA
ai716631  TAAGACGGAT CCCCGACTAC GTAGTCGGGA ATTCGGCACG AGGGGCCGCA
bg294111  ~~~CAGCTCC TTGCATACTG CTACCATGGC ATCTCTCTTC TCTGGACGCA
be108041  AGAAACCCTC TCTCAAAACC AAACAAGGCC TGGCAGTACT AGTGCACTTG
bg395178  TCCCCAGCAC CCAACCCAGG TTACCATGGC CTCCCTGTTC TCTGGCCGCA

          101                                                  150
  RdCVF1  TCTTGATCAG GAACAACAGC GACCAGGATG AAGTGGAGAC AGAGGCAGAG
bg299078  TCTTGATCAG GAACAACAGC GACCAGGATG AAGTGGAGAC AGAGGCAGAG
```

```
ai716631  TCTTGATCAG GAACAACAGC GACCAGGATG AAGTGGAGAC AGAGGCAGAG
bg294111  TCTTGATCAG GAACAACAGC GACCAGGATG AAGTGGAGAC AGAGGCAGAG
be108041  GGAGGCAGAG GAACAACAGC GACCAGGATG AAGTGGAGAC AGAGGCAGAG
bg395178  TCCTGATCCG CAACAATAGC GACCAGGACG AGCTGGATAC GGAGGCTGAG

          151                                                 200
  RdCVF1  CTGAGCCGTA GGTTAGAGAA TCGTCTGGTG TTGCTGTTCT TCGGCGCCGG
bg299078  CTGAGCCGTA GGTTAGAGAA TCGTCTGGTG TTGCTGTTCT TCGGCGCCGG
ai716631  CTGAGCCGCC GGTTAGAGAA TCGTCTTGTG CTACTGTTCT TCGGTGCTGG
bg294111  CTGAGCCGTA GGTTAGAGAA TCGTCTGGTG .TGCTGTTCT TCGGCGCCGG
be108041  CTGAGCCGCC GGTTAGAGAA TCGTCTTGTG CTACTGTTCT TCGGTGCTGG
bg395178  GTCAGTCGCA GGCTGGAGAA CCGGCTGGTG CTGCTGTTCT TTGGTGCTGG

          201                                                 250
  RdCVF1  CGCCTGTCCC CAGTGCCAGG CCTTTGCCCC AGTCCTCAAA GACTTCTTCG
bg299078  CGCCTGTCCC CAGTGCCAGG CC.TTGCCCC AGTCCTCAAA GACTTCTTCG
ai716631  GGCCTGTCCC CAGTGCCAGG CCTTCGCCCC AGTCCTCAAA GACTTCTTCG
bg294111  CGCCTGTCCC CAGTGCCAGG CC.TTGCCCC AGTCCTCAAA GACTTCTTCG
be108041  GGCCTGTCCC CAGTGCCAGG CCTTCGCCCC AGTCCTCAAA GACTTCTTCG
bg395178  GGCTTGTCCA CAGTGCCAGG CCTTCGTGCC CATCCTCAAG GACTTCTTCG

          251                                                 300
  RdCVF1  TGCGGCTCAC TGACGAGTTC TACGTGCTGC GGGCAGCACA GCTGGCCCTG
bg299078  TGCGGCTCAC TGACGAGTTC TACGTGCTGC GGGCAGCACA GCTGGCCCTG
ai716631  TGCGGCTCAC TGATGAGTTC TACGTGCTAC GGGCAGCACA GCTGGCCCTG
bg294111  TGCGGCTCAC TGACGAGTTC TACGTGCTGC GGGCAGCACA GCTGGCCCTG
be108041  TGCGGCTCAC TGATGAGTTC TACGTGCTAC GGGCAGCACA GCTGGCCCTG
bg395178  TGCGGCTCAC AGATGAGTTC TATGTACTGC GGGCGGCTCA GCTGGCCCTG

          301                                                 350
  RdCVF1  GTCTATGTGT CCCAGGACCC TACAGAGGAG CAACAGGACC TCTTCCTCAG
bg299078  GTCTATGTGT CCCAGGACCC TACAGAGGAG CAACAGGACC TCTTCCTCAG
ai716631  GTCTATGTGT CCCAGGACCC TACAGAGGAG CAACAGGACC TGTTCCTCCG
bg294111  GTCTATGTGT CCCAGGACCC TACAGAGGAG CAACAGGACC TCTTCCTCAG
be108041  GTCTATGTGT CCCAGGACCC TACAGAGGAG CAACAGGACC TGTTCCTCCG
bg395178  GTGTACGTGT CCCAGGACTC CACGGAGGAG CAGCAGGACC TGTTCCTCAA

          351                                                 400
  RdCVF1  GGACATGCCT GAAAAATGGC TCTTCCTGCC GTTCCA.TGA TGAACTGAGG
bg299078  GGACATGCCT GAAAAATGGC TCTTCCTGCC GTCCCACTGA TGAACTGAGG
ai716631  GGACATGCCT GAAAAGTGGC TCTTCCTGCC GTTCCA.TGA TGACCTGAGG
bg294111  GGACATGCCT GAAAAATGGC TCTTCCTGCC GTTCCA.TGA TGAACTGAGG
be108041  GGACATGCCT GAAAAGTGGC TCTTCCTGCC GTTCCA.TGA TGACCTGAGG
bg395178  GGACATGCCA AAGAAATGGC TTTTCCTGCC CTTTGA.GGA TGATCTGAGG

          401                                                 450
  RdCVF1  AGGTGA---- ---------- ---------- ---------- ----------
bg299078  AGGTGAGGCC CCAGGGAAGA CCAGGGAGGG CTTCCTGGAG AAGGCATTTC
ai716631  AGAGACCTCG GGCGCCAGTT CTCCGT---- ---------- ----------
bg294111  AGGGACCTCG GGCGCCAGTT CTCTGTCCGT CAACTGCCAG CGGTTGTGGT
be108041  AGTAATAAAA ATTAGAGGTT GTGGCTCAAA AAAAAAAAAA AAAA------
bg395178  AGGGACCTCG GGCGCCAGTT CTCAGTGGAG CGCCTGCCGG CGGTCGTGGT

          451                                                 500
  RdCVF1  ---------- ---------- ---------- ---------- ----------
bg299078  CCTGGAGGTT TACTGTCCTG GTACTACTTG TGCACTAAAG AGGTATTCCT
ai716631  ---------- ---------- ---------- ---------- ----------
bg294111  ACTTAAGCCT GGTGGGGACG TGCTGACAAG CGACGCCACG GAGGAGATCC
be108041  ---------- ---------- ---------- ---------- ----------
bg395178  GCTCAAGCCG GACGGGGACG TGCTCACTCG CGACGGCGCC GACGAGATCC
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          501                                                  550
  RdCVF1  ---------- ---------- ---------- ---------- ----------
bg299078  CCACACCAAC CACAGGCGAC AACAACACAC AAGAGGTGTC CCATCCGCTC
ai716631  ---------- ---------- ---------- ---------- ----------
bg294111  AGCGTCTGGG ACCCGCCTGC TTTGCCAACT GGCAGGAGGC CGCAGAGCTC
be108041  ---------- ---------- ---------- ---------- ----------
bg395178  AGCGCCTGGG CACCGCCTGC TTCGCCAACT GGCAGGAGGC GGCCGAGGTG

          551                                                  600
  RdCVF1  ---------- ---------- ---------- ---------- ----------
bg299078  TTCCATCACA GCCCACTGAC GCCAGACAGC ATCGCGACGC TCACGGCTCA
ai716631  ---------- ---------- ---------- ---------- ----------
bg294111  CTGGACCGCA GCTTCCTGCA ACCGGAGGAT TTGGATGAGC CTGCGCGGCG
be108041  ---------- ---------- ---------- ---------- ----------
bg395178  CTGGACCGCA ACTTCCAGCT GCCAGAGGAC CTGGAGGACC AGGAGCCACG

          601                                                  650
  RdCVF1  ---------- ---------- ---------- ---------- ----------
bg299078  GAAAAACACA GGTAGTCTCA CAGGCCTGCC ATCCTAATAC TGGCCACCCT
ai716631  ---------- ---------- ---------- ---------- ----------
bg294111  CAGCATCACC GAGCCTCTGC GCCGTCGCAA GTACCGAGTA GACCGGGATG
be108041  ---------- ---------- ---------- ---------- ----------
bg395178  GAGCCTCACC GAGTGCCTGC GCCGCCACAA GTACCGCGTG GAAAAGGCGG

          651                                                  700
  RdCVF1  ---------- ---------- ---------- ---------- ----------
bg299078  GAGCACAAGA GCGATGGCTA CAAGCCTCAA GGCTAGAATC TAAAACCACG
ai716631  ---------- ---------- ---------- ---------- ----------
bg294111  TCGGCGGGAG CGGGGCGAAA CGGCGCGACT CTGGTGAACC CCAGGGGGAC
be108041  ---------- ---------- ---------- ---------- ----------
bg395178  CGCGAGGCGG CGCGACCCGG GGGAGGGGCT GGGGACGGAG GCCGGGGCCC

          701                                                  750
  RdCVF1  ---------- ---------- ---------- ---------- ----------
bg299078  AGGTGGGGAC CGTAGGCCCC ACTCCCCGGG AGCGC----- ----------
ai716631  ---------- ---------- ---------- ---------- ----------
bg294111  GCGGGTACAA GGGCGGAGCT CTGGTGACTC CCAGGGTAGG AGTGGGGACC
be108041  ---------- ---------- ---------- ---------- ----------
bg395178  GGGGGGCTGT ACTGACCGCT GGGTGGAGCA GAGGGAGGGG GATTGGTGGA

          751                                                  800
  RdCVF1  ---------- ---------- ---------- ---------- ----------
bg299078  ---------- ---------- ---------- ---------- ----------
ai716631  ---------- ---------- ---------- ---------- ----------
bg294111  GGAGCTCTGG TGACACCAAA GTACCGGTGC ACGACCGAGG TTGATGACCC
be108041  ---------- ---------- ---------- ---------- ----------
bg395178  AGAACAACAA CCACACGCAG CCAGCACCAG GTATCCCGAC TAGGGGAGAC

          801                                                  850
  RdCVF1  ---------- ---------- ---------- ---------- ----------
bg299078  ---------- ---------- ---------- ---------- ----------
ai716631  ---------- ---------- ---------- ---------- ----------
bg294111  TCCCGAAGGA ACCGG----- ---------- ---------- ----------
be108041  ---------- ---------- ---------- ---------- ----------
bg395178  AGGGCGAAGA CCTGACCCAA AGCACAACCA CCGGGGACAC TAAACGACTC

          851                                                  900
  RdCVF1  ---------- ---------- ---------- ---------- ----------
bg299078  ---------- ---------- ---------- ---------- ----------
ai716631  ---------- ---------- ---------- ---------- ----------
bg294111  ---------- ---------- ---------- ---------- ----------
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be108041  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
bg395178  AACTCAATCC TGTGGGCACC AGGACACCGC AAAAAAAAAC AAAAAAAGCA

          901                          929
  RdCVF1  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~
bg299078  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~
ai716631  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~
bg294111  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~
be108041  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~
bg395178  AAATGCAAAA AAAGACAGGA CATACGACG
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Figure 14:

BG299078

```
  ATCGGATCCTCTCTGGGTCCCCAGCTCCTTGCATACTGCTACCATGGCATCTCTCTTCTC
1 ---------+---------+---------+---------+---------+---------+ 60
  TAGCCTAGGAGAGACCCAGGGGTCGAGGAACGTATGACGATGGTACCGTAGAGAGAAGAG

    TGGACGCATCTTGATCAGGAACAACAGCGACCAGGATGAAGTGGAGACAGAGGCAGAGCT
61  ---------+---------+---------+---------+---------+---------+ 120
    ACCTGCGTAGAACTAGTCCTTGTTGTCGCTGGTCCTACTTCACCTCTGTCTCCGTCTCGA

    GAGCCGTAGGTTAGAGAATCGTCTGGTGTTGCTGTTCTTCGGCGCCGGCGCCTGTCCCCA
121 ---------+---------+---------+---------+---------+---------+ 180
    CTCGGCATCCAATCTCTTAGCAGACCACAACGACAAGAAGCCGCGGCCGCGGACAGGGGT
             +T
    GTGCCAGGCCTTGCCCCAGTCCTCAAAGACTTCTTCGTGCGGCTCACTGACGAGTTCTAC
181 ---------+---------+---------+---------+---------+---------+ 240
    CACGGTCCGGAACGGGGTCAGGAGTTTCTGAAGAAGCACGCCGAGTGACTGCTCAAGATG

    GTGCTGCGGGCAGCACAGCTGGCCCTGGTCTATGTGTCCCAGGACCCTACAGAGGAGCAA
241 ---------+---------+---------+---------+---------+---------+ 300
    CACGACGCCCGTCGTGTCGACCGGGACCAGATACACAGGGTCCTGGGATGTCTCCTCGTT
                                                  removed
    CAGGACCTCTTCCTCAGGGACATGCCTGAAAAATGGCTCTTCCTGCCGTCCCACTGATGA
301 ---------+---------+---------+---------+---------+---------+ 360
    GTCCTGGAGAAGGAGTCCCTGTACGGACTTTTTACCGAGAAGGACGGCAGGGTGACTACT

    ACTGAGGAGGTGAGGCCCCAGGGAAGACCAGGGAGGGCTTCCTGGAGAAGGCATTTCCCT
361 ---------+---------+---------+---------+---------+---------+ 420
    TGACTCCTCCACTCCGGGGTCCCTTCTGGTCCCTCCCGAAGGACCTCTTCCGTAAAGGGA

    GGAGGTTTACTGTCCTGGTACTACTTGTGCACTAAAGAGGTATTCCTCCACACCAACCAC
421 ---------+---------+---------+---------+---------+---------+ 480
    CCTCCAAATGACAGGACCATGATGAACACGTGATTTCTCCATAAGGAGGTGTGGTTGGTG

    AGGCGACAACAACACACAAGAGGTGTCCCATCCGCTCTTCCATCACAGCCCACTGACGCC
481 ---------+---------+---------+---------+---------+---------+ 540
    TCCGCTGTTGTTGTGTGTTCTCCACAGGGTAGGCGAGAAGGTAGTGTCGGGTGACTGCGG

    AGACAGCATCGCGACGCTCACGGCTCAGAAAAACACAGGTAGTCTCACAGGCCTGCCATC
541 ---------+---------+---------+---------+---------+---------+ 600
    TCTGTCGTAGCGCTGCGAGTGCCGAGTCTTTTTGTGTCCATCAGAGTGTCCGGACGGTAG

    CTAATACTGGCCACCCTGAGCACAAGAGCGATGGCTACAAGCCTCAAGGCTAGAATCTAA
601 ---------+---------+---------+---------+---------+---------+ 660
    GATTATGACCGGTGGGACTCGTGTTCTCGCTACCGATGTTCGGAGTTCCGATCTTAGATT
```

```
    AACCACGAGGTGGGGACCGTAGGCCCCACTCCCCGGGAGCGC
661 ---------+---------+---------+---------+-- 702
    TTGGTGCTCCACCCCTGGCATCCGGGGTGAGGGGCCCTCGCG
```

Figure 15:

BG294111

```
  CAGCTCCTTGCATACTGCTACCATGGCATCTCTCTTCTCTGGACGCATCTTGATCAGGAA
1 ---------+---------+---------+---------+---------+---------+ 60
  GTCGAGGAACGTATGACGATGGTACCGTAGAGAGAAGAGACCTGCGTAGAACTAGTCCTT

   CAACAGCGACCAGGATGAAGTGGAGACAGAGGCAGAGCTGAGCCGTAGGTTAGAGAATCG
61 ---------+---------+---------+---------+---------+---------+ 120
   GTTGTCGCTGGTCCTACTTCACCTCTGTCTCCGTCTCGACTCGGCATCCAATCTCTTAGC
         +T                                              +T
   TCTGGTGTGCTGTTCTTCGGCGCCGGCGCCTGTCCCCAGTGCCAGGCCTTGCCCCAGTCC
121 ---------+---------+---------+---------+---------+---------+ 180
    AGACCACACGACAAGAAGCCGCGGCCGCGGACAGGGGTCACGGTCCGGAACGGGGTCAGG

    TCAAAGACTTCTTCGTGCGGCTCACTGACGAGTTCTACGTGCTGCGGGCAGCACAGCTGG
181 ---------+---------+---------+---------+---------+---------+ 240
    AGTTTCTGAAGAAGCACGCCGAGTGACTGCTCAAGATGCACGACGCCCGTCGTGTCGACC

    CCCTGGTCTATGTGTCCCAGGACCCTACAGAGGAGCAACAGGACCTCTTCCTCAGGGACA
241 ---------+---------+---------+---------+---------+---------+ 300
    GGGACCAGATACACAGGGTCCTGGGATGTCTCCTCGTTGTCCTGGAGAAGGAGTCCCTGT

    TGCCTGAAAAATGGCTCTTCCTGCCGTTCCATGATGAACTGAGGAGGGACCTCGGGCGCC
301 ---------+---------+---------+---------+---------+---------+ 360
    ACGGACTTTTTACCGAGAAGGACGGCAAGGTACTACTTGACTCCTCCCTGGAGCCCGCGG

    AGTTCTCTGTCCGTCAACTGCCAGCGGTTGTGGTACTTAAGCCTGGTGGGGACGTGCTGA
361 ---------+---------+---------+---------+---------+---------+ 420
    TCAAGAGACAGGCAGTTGACGGTCGCCAACACCATGAATTCGGACCACCCCTGCACGACT

    CAAGCGACGCCACGGAGGAGATCCAGCGTCTGGGACCCGCCTGCTTTGCCAACTGGCAGG
421 ---------+---------+---------+---------+---------+---------+ 480
    GTTCGCTGCGGTGCCTCCTCTAGGTCGCAGACCCTGGGCGGACGAAACGGTTGACCGTCC

    AGGCCGCAGAGCTCCTGGACCGCAGCTTCCTGCAACCGGAGGATTTGGATGAGCCTGCGC
481 ---------+---------+---------+---------+---------+---------+ 540
    TCCGGCGTCTCGAGGACCTGGCGTCGAAGGACGTTGGCCTCCTAAACCTACTCGGACGCG

    GGCGCAGCATCACCGAGCCTCTGCGCCGTCGCAAGTACCGAGTAGACCGGGATGTCGGCG
541 ---------+---------+---------+---------+---------+---------+ 600
    CCGCGTCGTAGTGGCTCGGAGACGCGGCAGCGTTCATGGCTCATCTGGCCCTACAGCCGC

    GGAGCGGGGCGAAACGGCGCGACTCTGGTGAACCCCAGGGGGACGCGGGTACAAGGGCGG
601 ---------+---------+---------+---------+---------+---------+ 660
    CCTCGCCCCGCTTTGCCGCGCTGAGACCACTTGGGGTCCCCCTGCGCCCATGTTCCCGCC

    AGCTCTGGTGACTCCCAGGGTAGGAGTGGGGACCGGAGCTCTGGTGACACCAAAGTACCG
661 ---------+---------+---------+---------+---------+---------+ 720
    TCGAGACCACTGAGGGTCCCATCCTCACCCCTGGCCTCGAGACCACTGTGGTTTCATGGC

    GTGCACGACCGAGGTTGATGACCCTCCCGAAGGAACCGG
721 ---------+---------+---------+--------- 759
    CACGTGCTGGCTCCAACTACTGGGAGGGCTTCCTTGGCC
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Figure 16:

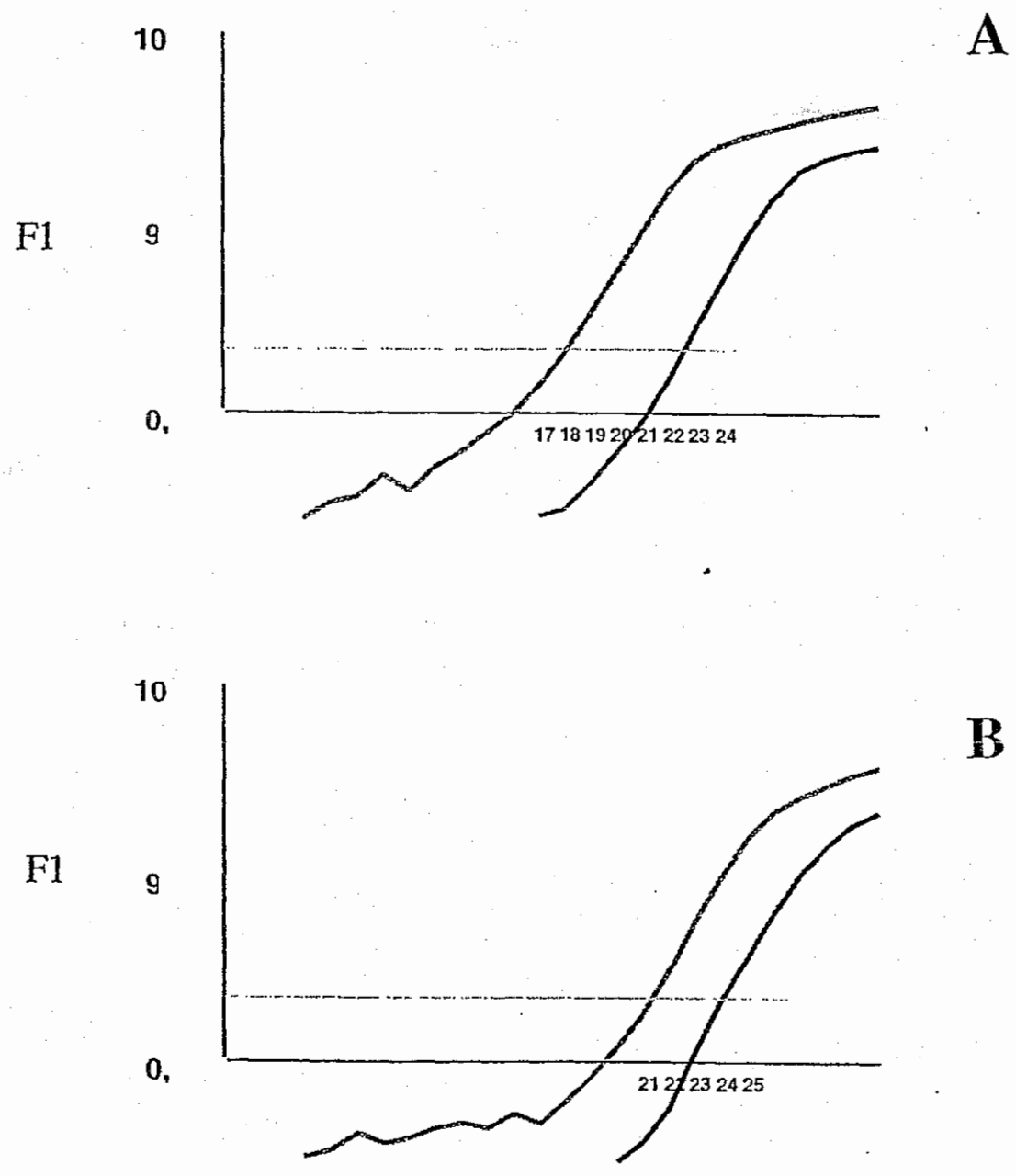


Figure 17:

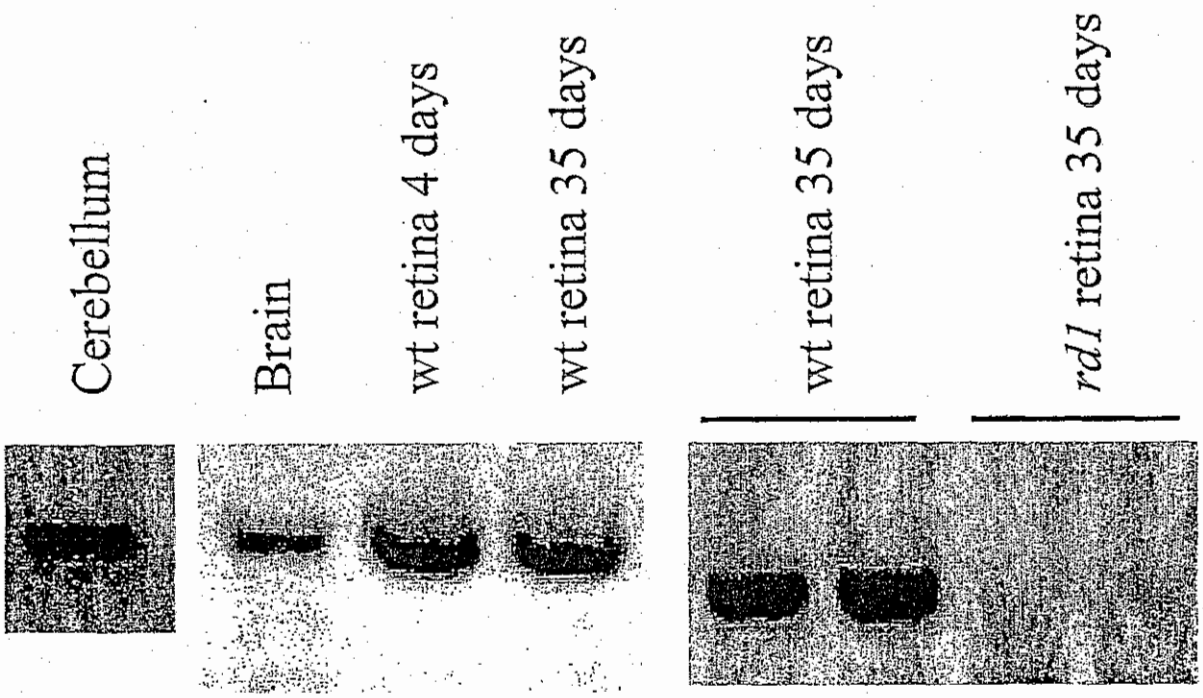
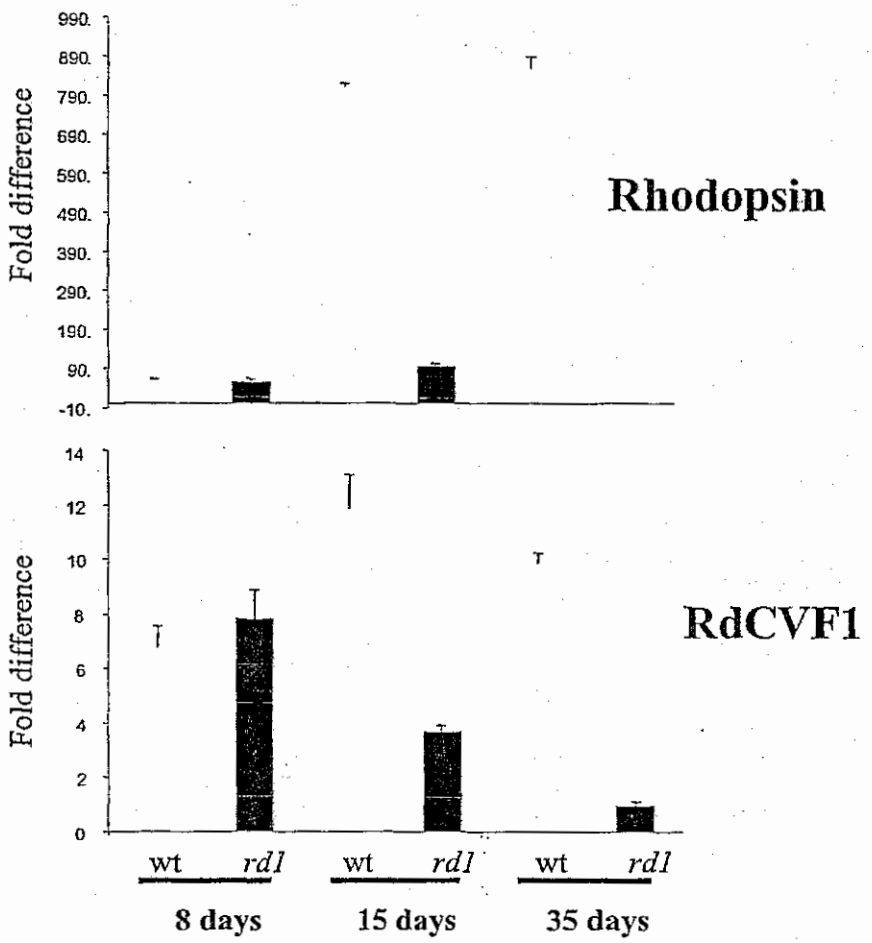
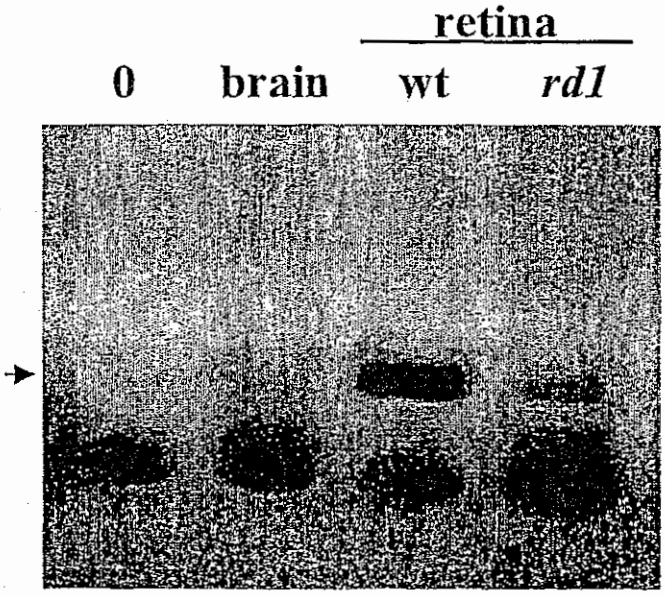

Cerebellum
Brain
wt retina 4 days
wt retina 35 days
wt retina 35 days
rd1 retina 35 days

Figure 18:


Fold difference
990.
890.
790.
690.
590.
490.
390.
290.
190.
90.
-10.
Rhodopsin
Fold difference
14
12
10
8
6
4
2
0
RdCVF1
wt
rd1
wt
rd1
wt
rd1
8 days
15 days
35 days


retina
0
brain
wt
rd1

New Seq RdCVF.ST25.txt
SEQUENCE LISTING

<110> UNIVERSITE LOUIS PASTEUR/ NOVARTIS AG

<120> Disease associated protein

<130> 4-31883

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Phe Ser Gly Arg Ile Leu Ile Arg Asn Asn Ser Asp Gln Asp Glu Val
5                   10                  15                  20

gag aca gag gca gag ctg agc cgt agg tta gag aat cgt ctg gtg ttg      152
Glu Thr Glu Ala Glu Leu Ser Arg Arg Leu Glu Asn Arg Leu Val Leu
                25                  30                  35

ctg ttc ttc ggc gcc ggc gcc tgt ccc cag tgc cag gcc ttt gcc cca      200
Leu Phe Phe Gly Ala Gly Ala Cys Pro Gln Cys Gln Ala Phe Ala Pro
            40                  45                  50

gtc ctc aaa gac ttc ttc gtg cgg ctc act gac gag ttc tac gtg ctg      248
Val Leu Lys Asp Phe Phe Val Arg Leu Thr Asp Glu Phe Tyr Val Leu
        55                  60                  65

cgg gca gca cag ctg gcc ctg gtc tat gtg tcc cag gac cct aca gag      296
Arg Ala Ala Gln Leu Ala Leu Val Tyr Val Ser Gln Asp Pro Thr Glu
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70 75 80

gag caa cag gac ctc ttc ctc agg gac atg cct gaa aaa tgg ctc ttc 344
Glu Gln Gln Asp Leu Phe Leu Arg Asp Met Pro Glu Lys Trp Leu Phe
85 90 95 100

ctg ccg ttc cat gat gaa ctg agg agg tga ggccccaggg aagaccaggg 394
Leu Pro Phe His Asp Glu Leu Arg Arg
105

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aagaggtatt cctc 468

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20 25 30

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35 40 45

Ala Phe Ala Pro Val Leu Lys Asp Phe Phe Val Arg Leu Thr Asp Glu
50 55 60

Phe Tyr Val Leu Arg Ala Ala Gln Leu Ala Leu Val Tyr Val Ser Gln
65 70 75 80

Asp Pro Thr Glu Glu Gln Gln Asp Leu Phe Leu Arg Asp Met Pro Glu
85 90 95

Lys Trp Leu Phe Leu Pro Phe His Asp Glu Leu Arg Arg
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Leu Ile Arg Asn Asn Ser Asp Gln Asp Glu Val Glu Thr Glu Ala Glu
10                  15                  20                  25

ctg agc cgt agg tta gag aat cgt ctg gtg ttg ctg ttc ttc ggc gcc       148
Leu Ser Arg Arg Leu Glu Asn Arg Leu Val Leu Leu Phe Phe Gly Ala
                30                  35                  40

ggc gcc tgt ccc cag tgc cag gcc ttt gcc cca gtc ctc aaa gac ttc       196
Gly Ala Cys Pro Gln Cys Gln Ala Phe Ala Pro Val Leu Lys Asp Phe
            45                  50                  55

ttc gtg cgg ctc act gac gag ttc tac gtg ctg cgg gca gca cag ctg       244
Phe Val Arg Leu Thr Asp Glu Phe Tyr Val Leu Arg Ala Ala Gln Leu
        60                  65                  70

gcc ctg gtc tat gtg tcc cag gac cct aca gag gag caa cag gac ctc       292
Ala Leu Val Tyr Val Ser Gln Asp Pro Thr Glu Glu Gln Gln Asp Leu
    75                  80                  85

ttc ctc agg gac atg cct gaa aaa tgg ctc ttc ctg ccg ttc cat gat       340
Phe Leu Arg Asp Met Pro Glu Lys Trp Leu Phe Leu Pro Phe His Asp
90                  95                  100                 105

gaa ctg agg agg gac ctc ggg cgc cag ttc tct gtc cgt caa ctg cca       388
Glu Leu Arg Arg Asp Leu Gly Arg Gln Phe Ser Val Arg Gln Leu Pro
                110                 115                 120

gcg gtt gtg gta ctt aag cct ggt ggg gac gtg ctg aca agc gac gcc       436
Ala Val Val Val Leu Lys Pro Gly Gly Asp Val Leu Thr Ser Asp Ala
            125                 130                 135

acg gag gag atc cag cgt ctg gga ccc gcc tgc ttt gcc aac tgg cag       484
Thr Glu Glu Ile Gln Arg Leu Gly Pro Ala Cys Phe Ala Asn Trp Gln
        140                 145                 150

gag gcc gca gag ctc ctg gac cgc agc ttc ctg caa ccg gag gat ttg       532
Glu Ala Ala Glu Leu Leu Asp Arg Ser Phe Leu Gln Pro Glu Asp Leu
    155                 160                 165

gat gag cct gcg cgg cgc agc atc acc gag cct ctg cgc cgt cgc aag       580
Asp Glu Pro Ala Arg Arg Ser Ile Thr Glu Pro Leu Arg Arg Arg Lys
170                 175                 180                 185

tac cga gta gac cgg gat gtc ggc ggg agc ggg gcg aaa cgg cgc gac       628
Tyr Arg Val Asp Arg Asp Val Gly Gly Ser Gly Ala Lys Arg Arg Asp
                190                 195                 200

tct ggt gaa ccc cag ggg gac gcg ggt aca agg gcg gag ctc tgg tga       676
Ser Gly Glu Pro Gln Gly Asp Ala Gly Thr Arg Ala Glu Leu Trp
            205                 210                 215

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Arg Leu Val Leu Leu Phe Phe Gly Ala Gly Ala Cys Pro Gln Cys Gln
35 40 45

Ala Phe Ala Pro Val Leu Lys Asp Phe Phe Val Arg Leu Thr Asp Glu
50 55 60

Phe Tyr Val Leu Arg Ala Ala Gln Leu Ala Leu Val Tyr Val Ser Gln
65 70 75 80

Asp Pro Thr Glu Glu Gln Gln Asp Leu Phe Leu Arg Asp Met Pro Glu
85 90 95

Lys Trp Leu Phe Leu Pro Phe His Asp Glu Leu Arg Arg Asp Leu Gly
100 105 110

Arg Gln Phe Ser Val Arg Gln Leu Pro Ala Val Val Val Leu Lys Pro
115 120 125

Gly Gly Asp Val Leu Thr Ser Asp Ala Thr Glu Glu Ile Gln Arg Leu
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Gly Pro Ala Cys Phe Ala Asn Trp Gln Glu Ala Ala Glu Leu Leu Asp
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Arg Ser Phe Leu Gln Pro Glu Asp Leu Asp Glu Pro Ala Arg Arg Ser
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Ile Thr Glu Pro Leu Arg Arg Arg Lys Tyr Arg Val Asp Arg Asp Val
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                        1               5                   10

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Ile Arg Asn Asn Ser Asp Gln Asp Glu Leu Asp Thr Glu Ala Glu Val
                15                  20                  25

agt cgc agg ctg gag aac cgg ctg gtg ctg ctg ttc ttt ggt gct ggg      149
Ser Arg Arg Leu Glu Asn Arg Leu Val Leu Leu Phe Phe Gly Ala Gly
            30                  35                  40

gct tgt cca cag tgc cag gcc ttc gtg ccc atc ctc aag gac ttc ttc      197
Ala Cys Pro Gln Cys Gln Ala Phe Val Pro Ile Leu Lys Asp Phe Phe
        45                  50                  55

gtg cgg ctc aca gat gag ttc tat gta ctg cgg gcg gct cag ctg gcc      245
Val Arg Leu Thr Asp Glu Phe Tyr Val Leu Arg Ala Ala Gln Leu Ala
    60                  65                  70

ctg gtg tac gtg tcc cag gac tcc acg gag gag cag cag gac ctg ttc      293
Leu Val Tyr Val Ser Gln Asp Ser Thr Glu Glu Gln Gln Asp Leu Phe
75                  80                  85                  90

ctc aag gac atg cca aag aaa tgg ctt ttc ctg ccc ttt gag gat gat      341
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20 25 30

Arg Leu Val Leu Leu Phe Phe Gly Ala Gly Ala Cys Pro Gln Cys Gln
35 40 45

Ala Phe Val Pro Ile Leu Lys Asp Phe Phe Val Arg Leu Thr Asp Glu
50 55 60

Phe Tyr Val Leu Arg Ala Ala Gln Leu Ala Leu Val Tyr Val Ser Gln
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20 25 30 35

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Leu Leu Phe Phe Gly Ala Gly Ala Cys Pro Gln Cys Gln Ala Phe Val
40 45 50

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Pro Ile Leu Lys Asp Phe Phe Val Arg Leu Thr Asp Glu Phe Tyr Val
            55                  60                  65

ctg cgg gcg gct cag ctg gcc ctg gtg tac gtg tcc cag gac tcc acg      296
Leu Arg Ala Ala Gln Leu Ala Leu Val Tyr Val Ser Gln Asp Ser Thr
        70                  75                  80

gag gag cag cag gac ctg ttc ctc aag gac atg cca aag aaa tgg ctt      344
Glu Glu Gln Gln Asp Leu Phe Leu Lys Asp Met Pro Lys Lys Trp Leu
    85                  90                  95

ttc ctg ccc ttt gag gat gat ctg agg agg gac ctc ggg cgc cag ttc      392
Phe Leu Pro Phe Glu Asp Asp Leu Arg Arg Asp Leu Gly Arg Gln Phe
100                 105                 110                 115

tca gtg gag cgc ctg ccg gcg gtc gtg gtg ctc aag ccg gac ggg gac      440
Ser Val Glu Arg Leu Pro Ala Val Val Val Leu Lys Pro Asp Gly Asp
                120                 125                 130

gtg ctc act cgc gac ggc gcc gac gag atc cag cgc ctg ggc acc gcc      488
Val Leu Thr Arg Asp Gly Ala Asp Glu Ile Gln Arg Leu Gly Thr Ala
            135                 140                 145

tgc ttc gcc aac tgg cag gag gcg gcc gag gtg ctg gac cgc aac ttc      536
Cys Phe Ala Asn Trp Gln Glu Ala Ala Glu Val Leu Asp Arg Asn Phe
        150                 155                 160

cag ctg cca gag gac ctg gag gac cag gag cca cgg agc ctc acc gag      584
Gln Leu Pro Glu Asp Leu Glu Asp Gln Glu Pro Arg Ser Leu Thr Glu
    165                 170                 175

tgc ctg cgc cgc cac aag tac cgc gtg gaa aag gcg gcg cga ggc ggg      632
Cys Leu Arg Arg His Lys Tyr Arg Val Glu Lys Ala Ala Arg Gly Gly
180                 185                 190                 195

cgc gac ccc ggg gga ggg ggt ggg gag gag ggc ggg gcc ggg ggg ctg      680
Arg Asp Pro Gly Gly Gly Gly Gly Glu Glu Gly Gly Ala Gly Gly Leu
                200                 205                 210

ttc tga                                                             686
Phe
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<210> 8

<211> 212

<212> PRT

<213> Homo sapiens

<400> 8

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Met Ala Ser Leu Phe Ser Gly Arg Ile Leu Ile Arg Asn Asn Ser Asp
1               5                   10                  15

Gln Asp Glu Leu Asp Thr Glu Ala Glu Val Ser Arg Arg Leu Glu Asn
            20                  25                  30

Arg Leu Val Leu Leu Phe Phe Gly Ala Gly Ala Cys Pro Gln Cys Gln
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35 40 45

Ala Phe Val Pro Ile Leu Lys Asp Phe Phe Val Arg Leu Thr Asp Glu
50 55 60

Phe Tyr Val Leu Arg Ala Ala Gln Leu Ala Leu Val Tyr Val Ser Gln
65 70 75 80

Asp Ser Thr Glu Glu Gln Gln Asp Leu Phe Leu Lys Asp Met Pro Lys
85 90 95

Lys Trp Leu Phe Leu Pro Phe Glu Asp Asp Leu Arg Arg Asp Leu Gly
100 105 110

Arg Gln Phe Ser Val Glu Arg Leu Pro Ala Val Val Val Leu Lys Pro
115 120 125

Asp Gly Asp Val Leu Thr Arg Asp Gly Ala Asp Glu Ile Gln Arg Leu
130 135 140

Gly Thr Ala Cys Phe Ala Asn Trp Gln Glu Ala Ala Glu Val Leu Asp
145 150 155 160

Arg Asn Phe Gln Leu Pro Glu Asp Leu Glu Asp Gln Glu Pro Arg Ser
165 170 175

Leu Thr Glu Cys Leu Arg Arg His Lys Tyr Arg Val Glu Lys Ala Ala
180 185 190

Arg Gly Gly Arg Asp Pro Gly Gly Gly Gly Gly Glu Glu Gly Gly Ala
195 200 205

Gly Gly Leu Phe
210

<210> 9

<211> 600

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (265)..(570)

<223>

<400> 9

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gctgtcatcg ctgctgtcgc agcttctgga gtggccactg tgctctctcc tcccttcggc 120

tcaaggtgag ctgttccagc agaaggcggg gctgagaggc gcctagtgct gcgggaggct 180

cagtgtcatc ttccagctaa caggtggccg tgcagcccag ggctcgtctc tccactgtgt 240

cctcttcacg ccgagctcgt ggcg atg gtg gac gtg ctg ggc ggg cgg cgc 291
Met Val Asp Val Leu Gly Gly Arg Arg
1 5

ctg gtg acc cgg gag ggc acg gtg gtg gag gcc gag gtg gcg ctg cag 339
Leu Val Thr Arg Glu Gly Thr Val Val Glu Ala Glu Val Ala Leu Gln
10 15 20 25

aac aag gtg gta gct ttg tac ttt gcg gcg ggc cgg tgc tcg ccc agc 387
Asn Lys Val Val Ala Leu Tyr Phe Ala Ala Gly Arg Cys Ser Pro Ser
30 35 40

cgc gac ttc acg ccg ctg ctc tgc gac ttc tac acg gag ctg gtg agc 435
Arg Asp Phe Thr Pro Leu Leu Cys Asp Phe Tyr Thr Glu Leu Val Ser
45 50 55

gag gcg cgg cgg ccc gct ccc ttc gag gtg gtt ttc gtg tcg gca gac 483
Glu Ala Arg Arg Pro Ala Pro Phe Glu Val Val Phe Val Ser Ala Asp
60 65 70

ggc agt gcg gag gag atg ttg gac ttc atg cgc gag ctg cac ggc tcc 531
Gly Ser Ala Glu Glu Met Leu Asp Phe Met Arg Glu Leu His Gly Ser
75 80 85

tgg ctg gca ttg ccc ttc cac gac ccc tac cgg cag tga gtggggaccc 580
Trp Leu Ala Leu Pro Phe His Asp Pro Tyr Arg Gln
90 95 100

aggggtcatg gggctggcgc 600

<210> 10

<211> 101

<212> PRT

<213> Mus musculus

<400> 10

Met Val Asp Val Leu Gly Gly Arg Arg Leu Val Thr Arg Glu Gly Thr
1 5 10 15

Val Val Glu Ala Glu Val Ala Leu Gln Asn Lys Val Val Ala Leu Tyr
20 25 30

Phe Ala Ala Gly Arg Cys Ser Pro Ser Arg Asp Phe Thr Pro Leu Leu
35 40 45

Cys Asp Phe Tyr Thr Glu Leu Val Ser Glu Ala Arg Arg Pro Ala Pro
50 55 60

Phe Glu Val Val Phe Val Ser Ala Asp Gly Ser Ala Glu Glu Met Leu
65 70 75 80

Asp Phe Met Arg Glu Leu His Gly Ser Trp Leu Ala Leu Pro Phe His
85 90 95

Asp Pro Tyr Arg Gln
100

<210> 11

<211> 1164

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (300)..(770)

<223>

<400> 11

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ctggagtggc cactgtgctc tctcctccct tcggctcaag gtgagctgtt ccagcagaag 180

gcggggctga gaggcgccta gtgctgcggg aggctcagtg tcatcttcca gctaacaggt 240

ggccgtgcag cccagggctc gtctctccac tgtgtcctct tcacgccgag ctcgtggcg 299

atg gtg gac gtg ctg ggc ggg cgg cgc ctg gtg acc cgg gag ggc acg 347
Met Val Asp Val Leu Gly Gly Arg Arg Leu Val Thr Arg Glu Gly Thr
1 5 10 15

gtg gtg gag gcc gag gtg gcg ctg cag aac aag gtg gta gct ttg tac 395
Val Val Glu Ala Glu Val Ala Leu Gln Asn Lys Val Val Ala Leu Tyr
20 25 30

ttt gcg gcg ggc cgg tgc tcg ccc agc cgc gac ttc acg ccg ctg ctc 443
Phe Ala Ala Gly Arg Cys Ser Pro Ser Arg Asp Phe Thr Pro Leu Leu
35 40 45

tgc gac ttc tac acg gag ctg gtg agc gag gcg cgg cgg ccc gct ccc 491
Cys Asp Phe Tyr Thr Glu Leu Val Ser Glu Ala Arg Arg Pro Ala Pro
50 55 60

ttc gag gtg gtt ttc gtg tcg gca gac ggc agt gcg gag gag atg ttg 539
Phe Glu Val Val Phe Val Ser Ala Asp Gly Ser Ala Glu Glu Met Leu
65 70 75 80

gac ttc atg cgc gag ctg cac ggc tcc tgg ctg gca ttg ccc ttc cac 587
Asp Phe Met Arg Glu Leu His Gly Ser Trp Leu Ala Leu Pro Phe His
85 90 95

gac ccc tac cgg cat gaa ctg aag aag agg tac gaa atc acc gcc atc 635
Asp Pro Tyr Arg His Glu Leu Lys Lys Arg Tyr Glu Ile Thr Ala Ile
100 105 110

ccc aag ctg gtg gtc atc aag cag aac gga gct gtc atc acc aac aaa 683
Pro Lys Leu Val Val Ile Lys Gln Asn Gly Ala Val Ile Thr Asn Lys
115 120 125

ggg cgg aag cag atc cga gag cgc ggg cta gct tgc ttt cag aac tgg 731
Gly Arg Lys Gln Ile Arg Glu Arg Gly Leu Ala Cys Phe Gln Asn Trp
130 135 140

gtg gaa gca gcc gat gtt ttc caa aac ttc tcg ggg tga ccagggcagt 780
Val Glu Ala Ala Asp Val Phe Gln Asn Phe Ser Gly
145 150 155

tgctggaagt tcagggcaac tatcttcaaa aagggcttag ctggttccct tctctgctga 840

ggaatgtcat tgtagagtca ccatgctgtg acagagagca taaactgctc aggaaagaac 900

tacgtctgcc ccctgtgggt cctagagctc cgttgaatgt ttatttctta caccttctc 960

caccggtgcc taggatccag gacacatcag ccacgagtta acagaactct atgcaagatg 1020

ctctttccta caggaaattt ctttgataaa ttgacctatg gaggtgatac attttctgat 1080

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<210> 12

<211> 156

<212> PRT

<213> Mus musculus

<400> 12

Met Val Asp Val Leu Gly Gly Arg Arg Leu Val Thr Arg Glu Gly Thr
1 5 10 15

Val Val Glu Ala Glu Val Ala Leu Gln Asn Lys Val Val Ala Leu Tyr
20 25 30

Phe Ala Ala Gly Arg Cys Ser Pro Ser Arg Asp Phe Thr Pro Leu Leu
35 40 45

Cys Asp Phe Tyr Thr Glu Leu Val Ser Glu Ala Arg Arg Pro Ala Pro
50 55 60

Phe Glu Val Val Phe Val Ser Ala Asp Gly Ser Ala Glu Glu Met Leu
65 70 75 80

Asp Phe Met Arg Glu Leu His Gly Ser Trp Leu Ala Leu Pro Phe His
85 90 95

```
Asp Pro Tyr Arg His Glu Leu Lys Lys Arg Tyr Glu Ile Thr Ala Ile
            100                 105                 110

Pro Lys Leu Val Val Ile Lys Gln Asn Gly Ala Val Ile Thr Asn Lys
        115                 120                 125

Gly Arg Lys Gln Ile Arg Glu Arg Gly Leu Ala Cys Phe Gln Asn Trp
    130                 135                 140

Val Glu Ala Ala Asp Val Phe Gln Asn Phe Ser Gly
145                 150                 155
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<210> 13

<211> 1472

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (331)..(738)

<223>

<400> 13

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ctgagtgtct cattgtcggc gcgaacacaa ttgctccagc cacaggcgag gcctggccaa    180

ggtgtgggcg catctagggc aggtcttgag aggtccagcg cccggtggtg cggacagagg    240

cggggcaccg cggcgctcgc cgccgcctcc ccgcaggtga tcatcctcct gcaggtgtcc    300

tcgggtctca ggtggctgcg tgtctgcgcc atg gtt gac att ctg ggc gag cgg     354
                                Met Val Asp Ile Leu Gly Glu Arg
                                1               5

cac ctg gtg acc tgt aag ggc gcg acg gtg gag gcc gag gcg gcg ctg      402
His Leu Val Thr Cys Lys Gly Ala Thr Val Glu Ala Glu Ala Ala Leu
    10                  15                  20

cag aac aag gtg gtg gca ctg tac ttc gcg gcg gcc cgg tgc gcg ccg      450
Gln Asn Lys Val Val Ala Leu Tyr Phe Ala Ala Ala Arg Cys Ala Pro
25                  30                  35                  40

agc cgc gac ttc acg ccg ctg ctc tgc gac ttc tat acg gcg ctg gtg      498
Ser Arg Asp Phe Thr Pro Leu Leu Cys Asp Phe Tyr Thr Ala Leu Val
                45                  50                  55

gcc gag gcg cgg cgg ccc gcg ccc ttc gaa gtg gtc ttc gtg tca gcc      546
Ala Glu Ala Arg Arg Pro Ala Pro Phe Glu Val Val Phe Val Ser Ala
            60                  65                  70
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gac ggc agc tgc cag gag atg ctg gac ttc atg cgc gag ctg cat ggc 594
Asp Gly Ser Cys Gln Glu Met Leu Asp Phe Met Arg Glu Leu His Gly
75 80 85

gcc tgg ctg gcg ctg ccc ttc cac gac ccc tac cgg caa cgg agt ctc 642
Ala Trp Leu Ala Leu Pro Phe His Asp Pro Tyr Arg Gln Arg Ser Leu
90 95 100

gct ctg ttg ccc agg ctg gag tgc agt ggc gtg atc tta gct cac tgc 690
Ala Leu Leu Pro Arg Leu Glu Cys Ser Gly Val Ile Leu Ala His Cys
105 110 115 120

aac ctt tgc ctc ctg ggt tca agt gat tct cta gcc tta gcc tcc tga 738
Asn Leu Cys Leu Leu Gly Ser Ser Asp Ser Leu Ala Leu Ala Ser
125 130 135

gcatctggga ctacagccat tgctgtgaat tacgtgaggg aaagatattg aagaggagtt 798

ggacactccg agagtgcagc tgttctcccc ccgcaccatc cgtgtcctgc attctgcgag 858

tctgtgctca ttaacaatgt gctgtgacca tgtgactcag caatcctgct gctgggtata 918

tacccgaaag aaaggaaaag gaagccagta tattgaagag gtatctgcac ccccatgttt 978

attgcagcac tgttcacaac agccaagatt tggaagcaac ctaagtgtcc atcaacagat 1038

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caaaacaatt gaactcttgg acatagagag tagaaggttg gttaccagaa gctggaaagg 1278

aaagtggggt tgggaggaag gtgggaatgg ttaataggta caaaaaaata caaagaataa 1338

ataagaccta atatttgata gcacaacagt gtgactactg tcaataatca tttaattgta 1398

catttaaaaa taactataat tgcattgttt gtaacacaaa agataaatgc ttgaggagaa 1458

aaaaaaaaaa aaaa 1472

<210> 14

<211> 135

<212> PRT

<213> Homo sapiens

<400> 14

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1 5 10 15

Thr Val Glu Ala Glu Ala Ala Leu Gln Asn Lys Val Val Ala Leu Tyr
20 25 30

Phe Ala Ala Ala Arg Cys Ala Pro Ser Arg Asp Phe Thr Pro Leu Leu
35 40 45

Cys Asp Phe Tyr Thr Ala Leu Val Ala Glu Ala Arg Arg Pro Ala Pro
50 55 60

Phe Glu Val Val Phe Val Ser Ala Asp Gly Ser Cys Gln Glu Met Leu
65 70 75 80

Asp Phe Met Arg Glu Leu His Gly Ala Trp Leu Ala Leu Pro Phe His
85 90 95

Asp Pro Tyr Arg Gln Arg Ser Leu Ala Leu Leu Pro Arg Leu Glu Cys
100 105 110

Ser Gly Val Ile Leu Ala His Cys Asn Leu Cys Leu Leu Gly Ser Ser
115 120 125

Asp Ser Leu Ala Leu Ala Ser
130 135

<210> 15

<211> 702

<212> DNA

<213> Mus musculus

<400> 15
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tggacgcatc ttgatcagga acaacagcga ccaggatgaa gtggagacag aggcagagct 120

gagccgtagg ttagagaatc gtctggtgtt gctgttcttc ggcgccggcg cctgtcccca 180

gtgccaggcc ttgccccagt cctcaaagac ttcttcgtgc ggctcactga cgagttctac 240

gtgctgcggg cagcacagct ggccctggtc tatgtgtccc aggaccctac agaggagcaa 300

caggacctct tcctcaggga catgcctgaa aaatggctct tcctgccgtc ccactgatga 360

actgaggagg tgaggcccca gggaagacca gggagggctt cctggagaag gcatttccct 420

ggaggtttac tgtcctggta ctacttgtgc actaaagagg tattcctcca caccaaccac 480

aggcgacaac aacacacaag aggtgtccca tccgctcttc catcacagcc cactgacgcc 540

agacagcatc gcgacgctca cggctcagaa aaacacaggt agtctcacag gcctgccatc 600

ctaatactgg ccaccctgag cacaagagcg atggctacaa gcctcaaggc tagaatctaa 660

aaccacgagg tggggaccgt aggccccact ccccgggagc gc 702

<210> 16

<211> 387

<212> DNA

<213> Rattus norvegicus

<400> 16
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catcttgatc aggaacaaca gcgaccagga tgaagtggag acagaggcag agctgagccg 120
ccggttagag aatcgtcttg tgctactgtt cttcggtgct ggggcctgtc cccagtgcca 180
ggccttcgcc ccagtcctca aagacttctt cgtgcggctc actgatgagt tctacgtgct 240
acgggcagca cagctggccc tggtctatgt gtcccaggac cctacagagg agcaacagga 300
cctgttcctc cgggacatgc ctgaaaagtg gctcttcctg ccgttccatg atgacctgag 360
gagagacctc gggcgccagt tctccgt 387

<210> 17
<211> 759
<212> DNA
<213> Mus musculus

<400> 17
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caacagcgac caggatgaag tggagacaga ggcagagctg agccgtaggt tagagaatcg 120
tctggtgtgc tgttcttcgg cgccggcgcc tgtccccagt gccaggcctt gccccagtcc 180
tcaaagactt cttcgtgcgg ctcactgacg agttctacgt gctgcgggca gcacagctgg 240
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tgcctgaaaa atggctcttc ctgccgttcc atgatgaact gaggagggac ctcgggcgcc 360
agttctctgt ccgtcaactg ccagcggttg tggtacttaa gcctggtggg gacgtgctga 420
caagcgacgc cacggaggag atccagcgtc tgggacccgc ctgctttgcc aactggcagg 480
aggccgcaga gctcctggac cgcagcttcc tgcaaccgga ggatttggat gagcctgcgc 540
ggcgcagcat caccgagcct ctgcgccgtc gcaagtaccg agtagaccgg gatgtcggcg 600
ggagcggggc gaaacggcgc gactctggtg aaccccaggg ggacgcgggt acaagggcgg 660
agctctggtg actcccaggg taggagtggg gaccggagct ctggtgacac caaagtaccg 720
gtgcacgacc gaggttgatg accctcccga aggaaccgg 759

<210> 18
<211> 443
<212> DNA
<213> Rattus norvegicus

<220>

<221> misc_feature

<222> (46)..(46)

<223> any nucleotide

<400> 18

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tctcaaaacc aaacaaggcc tggcagtact agtgcacttg ggaggcagag gaacaacagc 120

gaccaggatg aagtggagac agaggcagag ctgagccgcc ggttagagaa tcgtcttgtg 180

ctactgttct tcggtgctgg ggcctgtccc cagtgccagg ccttcgcccc agtcctcaaa 240

gacttcttcg tgcggctcac tgatgagttc tacgtgctac gggcagcaca gctggccctg 300

gtctatgtgt cccaggaccc tacagaggag caacaggacc tgttcctccg ggacatgcct 360

gaaaagtggc tcttcctgcc gttccatgat gacctgagga gtaataaaaa ttagaggttg 420

tggctcaaaa aaaaaaaaaa aaa 443

<210> 19

<211> 889

<212> DNA

<213> Homo sapiens

<400> 19

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atcctgatcc gcaacaatag cgaccaggac gagctggata cggaggctga ggtcagtcgc 120

aggctggaga accggctggt gctgctgttc tttggtgctg gggcttgtcc acagtgccag 180

gccttcgtgc ccatcctcaa ggacttcttc gtgcggctca cagatgagtt ctatgtactg 240

cgggcggctc agctggccct ggtgtacgtg tcccaggact ccacggagga gcagcaggac 300

ctgttcctca aggacatgcc aaagaaatgg cttttcctgc cctttgagga tgatctgagg 360

agggacctcg ggcgccagtt ctcagtggag cgcctgccgg cggtcgtggt gctcaagccg 420

gacggggacg tgctcactcg cgacggcgcc gacgagatcc agcgcctggg caccgcctgc 480

ttcgccaact ggcaggaggc ggccgaggtg ctggaccgca acttccagct gccagaggac 540

ctggaggacc aggagccacg gagcctcacc gagtgcctgc gccgccacaa gtaccgcgtg 600

gaaaaggcgg cgcgaggcgg cgcgacccgg gggaggggct ggggacggag gccggggccc 660

gggggctgt actgaccgct gggtggagca gagggagggg gattggtgga agaacaacaa 720

ccacacgcag ccagcaccag gtatcccgac taggggagac agggcgaaga cctgacccaa 780

agcacaacca ccggggacac taaacgactc aactcaatcc tgtgggcacc aggacaccgc 840

aaaaaaaaac aaaaaaagca aaatgcaaaa aaagacagga catacgacg 889

<210> 20

<211> 348

<212> DNA

<213> Homo sapiens

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acctggtgac ctgtaagggc gcgacggtgg aggccgaggc ggcgctgcag aacaaggtgg 120

tggcactgta cttcgcggcg gcccggtgcg cgccgagccg cgacttcacg ccgctgctct 180

gcgacttcta tacggcgctg gtggccgagg cgcggcggcc cgcgcccttc gaagtggtct 240

tcgtgtcagc cgacggcagc tcccaggaga tgctggactt catgcgcgag ctgcatggcg 300

cctggctggc gctgcccttc cacgacccct accggcacca ttgctgtg 348

<210> 21

<211> 340

<212> DNA

<213> Homo sapiens

<400> 21
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acctggtgac ctgtaagggc gcgacggtgg aggccgaggc ggcgctgcag aacaaggtgg 120

tggcactgta cttcgcggcg gccggtgcgc gccgagccgc gattcacgcc gctgctctgc 180

gacttctata cggcgctggt ggccgagcgc ggggccgcgc cttcgaagtg gtcttcgtgt 240

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ggcgctgcct tccacgaccc ctaccggcac agccggagcc 340

<210> 22

<211> 348

<212> DNA

<213> Homo sapiens

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acctggtgac ctgtaagggc gcgacggtgg aggccgaggc ggcgctgcag aacaaggtgg 120

tggcactgta cttcgcggcg gcccggtgcg cgccgagccg cgacttcacg ccgctgctct 180

gcgacttcta tacggcgctg gtggccgagg cgcggcggcc cgcgcccttc gaagtggtct 240

tcgtgtcagc cgacggcagc tgccaggaga tgctggactt catgcgcgag ctgcatggcg 300

cctggctggc gctgcccttc cacgaaccct accggcaacg gagtctcg 348

<210> 23

<211> 350

<212> DNA

<213> Homo sapiens

<400> 23

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acctggtgac ctgtaagggc gcgacggtgg aggccgaggc ggcgctgcag aacaaggtgg 120

tggcactgta cttcgcggcg gcccggtgcg cgccgagccg cgacttcacg ccgctgctct 180

gcgacttcta tacggcgctg gtggccgagg cgcggcggcc cgcgcccttc gaagtggtct 240

tcgtgtcagc cgacggcagc tgccaggaga tgcttggact tcatgcgcga gctgcattgc 300

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<210> 24

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 24

tctatgtgtc ccaggaccct acag 24

<210> 25

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 25

tttatgcaca agtagtacca ggacag 26

<210> 26

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 26
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<210> 27

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 27
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<210> 28

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Adaptor

<400> 28
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<210> 29

<211> 14

<212> DNA

<213> Artificial Sequence

<220>

<223> Adaptor

<400> 29
aattcggcac gagg 14

<210> 30

<211> 10

<212> DNA

<213> Artificial Sequence

<220>

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