SUPPLEMENTARY MATERIAL

Figure legends

Figure 1S The synthesis of *vip3aI* gene by successive PCR. Oligonucleotides of ~90 bp were assembled by two-step PCR using 1.5 picomoles of inner primers and 30 picomoles of external primers, which contained suitable restriction cleavage sites for cloning.

Figure 2S The synthesis of *vip3aI* gene by successive PCR. Oligonucleotides of ~90 bp were assembled by single-step PCR using 1.5 picomoles of inner primers and 30 picomoles of external primers, which contained suitable restriction cleavage sites for cloning.

Figure 3S The synthesis of *vip3aI* gene by overlap extension PCR. Oligonucleotides of ~90 bp were assembled by two-step PCR using 1.5 picomoles of inner primers and 30 picomoles of external primers, which contained suitable restriction cleavage sites for cloning.

Figure 4S The synthesis of *vip3aI* gene by overlap extension PCR. Oligonucleotides of ~90 bp were assembled by a single-step PCR.

Figure 5S Comparison of nucleotide sequences of the synthetic *vip3aI* gene and the wild type *vip3a*. The entire open reading-frame sequence encoding for the toxic protein fragment is 2,370 bp. The two genes have 70.5 % homology. All codons were changed according to the preferential codon usage of *Pichia pastoris*.

Figure 6S 60 nt oligonucletide primers designed for the two-step successive PCR (according to Fig.1).

Figure 7S 90 nt oligonucletide primers designed for the two-step successive PCR (according to Fig.1S).

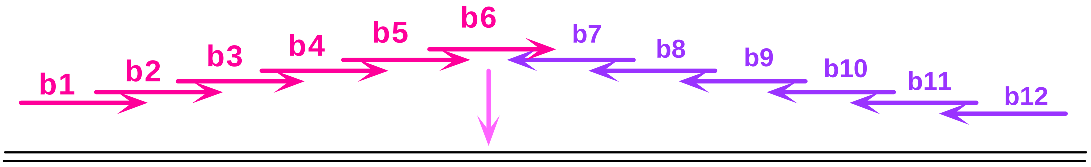
Figure 8S 60 nt oligonucletide primers designed for the two-step successive PCR (according to Fig.2).

Figure 9S 90 nt oligonucletide primers designed for the two-step successive PCR (according to Fig.2S).

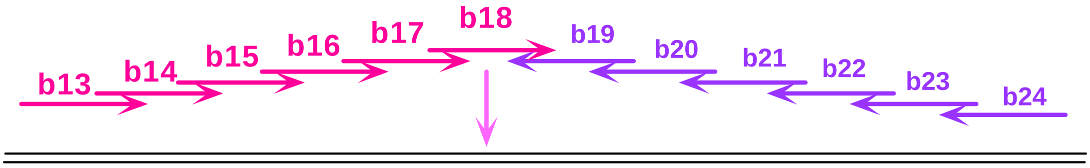
Figure 10S 60 nt oligonucletide primers designed for the two-step verlap extension PCR (according to Fig.3).

Figure 11S 90 nt oligonucletide primers designed for the two-step verlap extension PCR (according to Fig.3S).

Figure 1S



block1 1-860 bp



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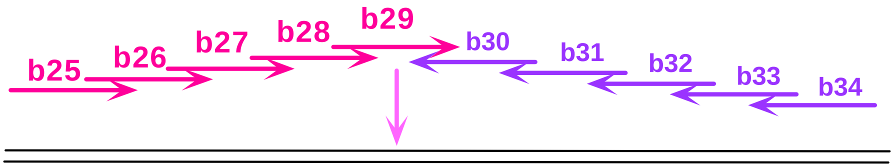
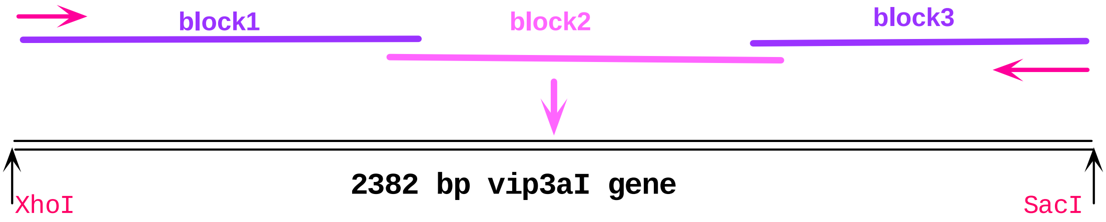


block3 1680-2382 bp



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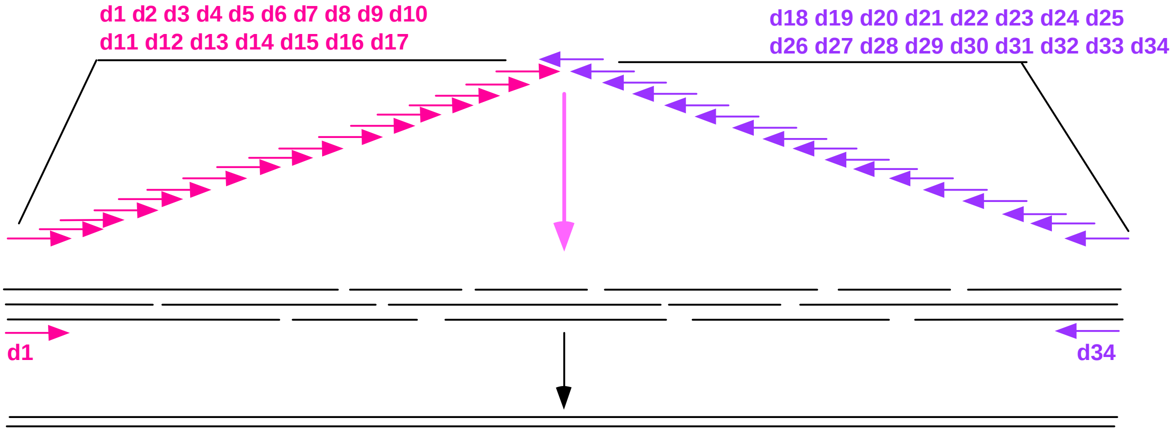
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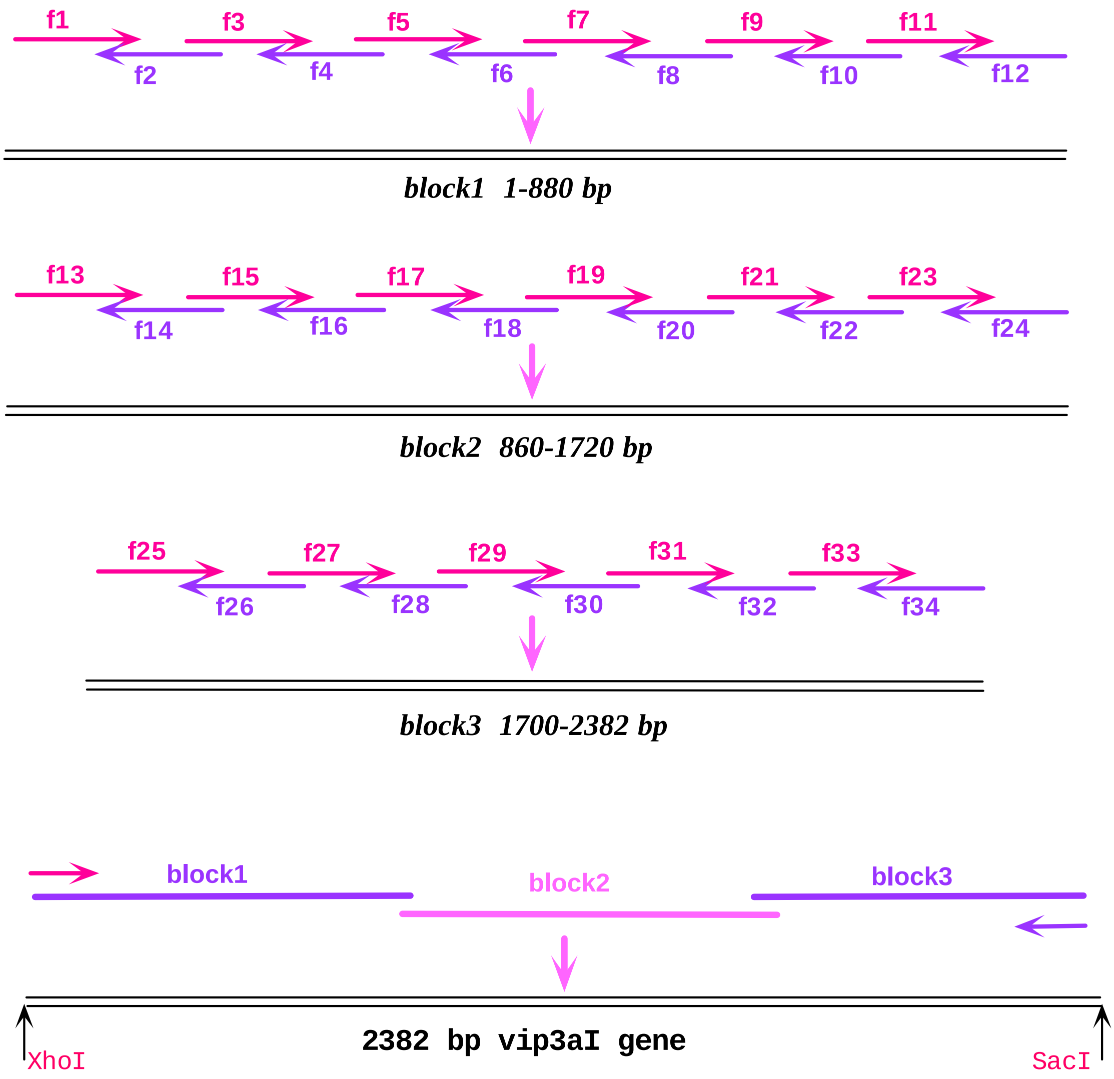
d11 d12 d13 d14 d15 d16 d17
d18 d19 d20 d21 d22 d23 d24 d25
d26 d27 d28 d29 d30 d31 d32 d33 d34
d1
d34

Figure 3S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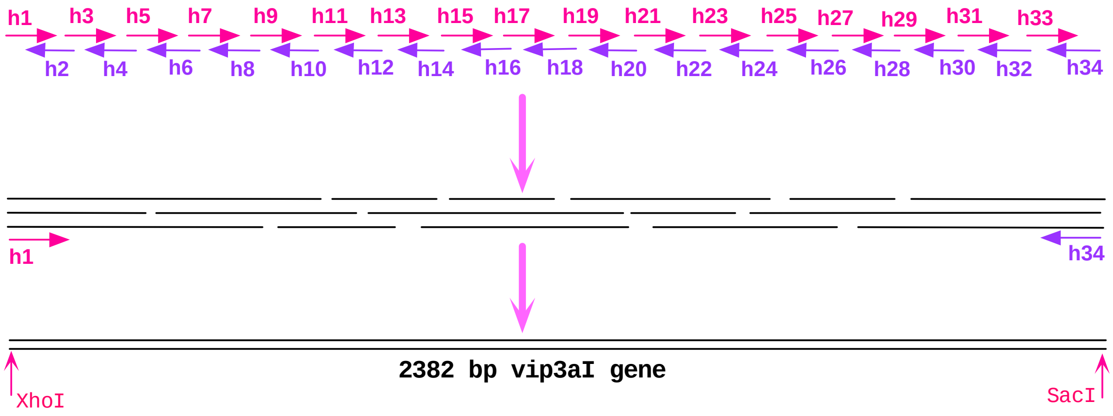
f3
f5
f7
f9
f11
f2
f4
f6
f8
f10
f12
block1 1-880 bp
f13
f15
f17
f19
f21
f23
f14
f16
f18
f20
f22
f24
block2 860-1720 bp
f25
f27
f29
f31
f33
f26
f28
f30
f32
f34
block3 1700-2382 bp
block1
block2
block3
2382 bp vip3aI gene
XhoI
SacI

Figure 4S


h1
h3
h5
h7
h9
h11
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h33
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h4
h6
h8
h10
h12
h14
h16
h18
h20
h22
h24
h26
h28
h30
h32
h34
h1
h34
2382 bp vip3aI gene
XhoI
SacI

Figure 5S

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vip3a  - ATGAACAAGAATAATACTAAATTAAGCACAAGAGCCTTACCAAGTTTTATTGATTATTTT -60
vip3aI - ATGAACAAGAACAACACCAAGTTGTCCACCAGAGCCTTGCCTTCCTTCATCGACTACTTC -60
          M  N  K  N  N  T  K  L  S  T  R  A  L  P  S  F  I  D  Y  F
vip3a  - AATGGCATTTATGGATTTGCCACTGGTATCAAAGACATTATGAACATGATTTTTAAAACG -120
vip3aI - AATGGTATCTACGGATTCGCTACTGGTATCAAGGACATCATGAACATGATCTTCAAGACT -120
          N  G  I  Y  G  F  A  T  G  I  K  D  I  M  N  M  I  F  K  T
vip3a  - GATACAGGTGGTGATCTAACCCTAGACGAAATTTTAAAGAATCAGCAGTTACTAAATGAT -180
vip3aI - GACACTGGTGGTGATCTGACCCTTGACGAGATCTTGAAGAACCAACAACTTCTGAACGAC -180
          D  T  G  G  D  L  T  L  D  E  I  L  K  N  Q  Q  L  L  N  D
vip3a  - ATTTCTGGTAAATTGGATGGGGTGAATGGAAGCTTAAATGATCTTATCGCACAGGGAAAC -240
vip3aI - ATCTCTGGTAAACTTGATGGTGTCAATGGTTCCTTGAACGACCTGATCGCACAGGGTAAC -240
          I  S  G  K  L  D  G  V  N  G  S  L  N  D  L  I  A  Q  G  N
vip3a  - TTAAATACAGAATTATCTAAGGAAATATTAAAAATTGCAAATGAACAAAATCAAGTTTTA -300
vip3aI - CTTAACACAGAACTTTCCAAGGAGATCTTGAAGATCGCTAACGAACAGAACCAAGTCTTG -300
          L  N  T  E  L  S  K  E  I  L  K  I  A  N  E  Q  N  Q  V  L
vip3a  - AATGATGTTAATAACAAACTCGATGCGATAAATACGATGCTTCGGGTATATCTACCTAAA -360
vip3aI - AACGACGTCAACAACAAACTCGATGCTATCAACACCATGTTGAGAGTCTACTTGCCTAAG -360
          N  D  V  N  N  K  L  D  A  I  N  T  M  L  R  V  Y  L  P  K
vip3a  - ATTACCTCTATGTTGAGTGATGTAATGAAACAAAATTATGCGCTAAGTCTGCAAATAGAA -420
vip3aI - ATCACCTCCATGCTTTCCGACGTCATGAAGCAGAACTATGCTTTGTCTCTGCAAATCGAA -420
          I  T  S  M  L  S  D  V  M  K  Q  N  Y  A  L  S  L  Q  I  E
vip3a  - TACTTAAGTAAACAATTGCAAGAGATTTCTGATAAGTTGGATATTATTAATGTAAATGTA -480
vip3aI - TACCTTTCCAAGCAACTTCAAGAGATCTCCGACAAGCTTGACATCATCAACGTCAACGTC -480
          Y  L  S  K  Q  L  Q  E  I  S  D  K  L  D  I  I  N  V  N  V
vip3a  - CTTATTAACTCTACACTTACTGAAATTACACCTGCGTATCAAAGGATTAAATATGTGAAC -540
vip3AI - TTGATCAACTCCACTTTGACCGAGATCACTCCTGCTTACCAGAGAATCAAGTACGTCAAC -540
          L  I  N  S  T  L  T  E  I  T  P  A  Y  Q  R  I  K  Y  V  N
vip3a  - GAAAAATTTGAGGAATTAACTTTTGCTACAGAAACTAGTTCAAAAGTAAAAAAGGATGGC -600
vip3aI - GAGAAGTTCGAGGAGCTTACCTTCGCTACCGAAACCTCCTCCAAGGTCAAGAAGGACGGT -600
          E  K  F  E  E  L  T  F  A  T  E  T  S  S  K  V  K  K  D  G
vip3a  - TCTCCTGCAGATATTCTTGATGAGTTAACTGAGTTAACTGAACTAGCGAAAAGTGTAACA -660
vip3aI - TCTCCTGCTGACATCCTCGACGAGTTGACCGAGTTGACCGAATTGGCTAAGTCCGTCACC -660
          S  P  A  D  I  L  D  E  L  T  E  L  T  E  L  A  K  S  V  T
vip3a  - AAAAATGATGTGGATGGTTTTGAATTTTACCTTAATACATTCCACGATGTAATGGTAGGA -720
vip3aI - AAGAACGACGTCGATGGTTTCGAATTCTACTTGAACACCTTTCATGACGTCATGGTTGGT -720
          K  N  D  V  D  G  F  E  F  Y  L  N  T  F  H  D  V  M  V  G
vip3a  - AATAATTTATTCGGGCGTTCAGCTTTAAAAACTGCATCGGAATTAATTACTAAAGAAAAT -780
vip3aI - AACAACCTTTTCGGTAGATCTGCACTTAAGACTGCTTCTGAACTTATCACCAAGGAGAAC -780
          N  N  L  F  G  R  S  A  L  K  T  A  S  E  L  I  T  K  E  N
vip3a  - GTGAAAACAAGTGGCAGTGAGGTCGGAAATGTTTATAACTTCTTAATTGTATTAACAGCT -840
vip3aI - GTGAAAACCTCTGGTTCCGAGGTTGGTAACGTCTACAACTTCTTGATCGTCTTGACAGCC -840
          V  K  T  S  G  S  E  V  G  N  V  Y  N  F  L  I  V  L  T  A
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vip3a     - CTGCAAGCCCAAGCTTTTCTTACTTTAACAACATGCCGAAAATTATTAGGCTTAGCAGAT -900
vip3aI    - TTGCAAGCTCAAGCTTTCTTGACCTTGACCACCTGTAGAAAGCTTCTTGGTCTTGCTGAC -900
             L  Q  A  Q  A  F  L  T  L  T  T  C  R  K  L  L  G  L  A  D
vip3a     - ATTGATTATACTTCTATTATGAATGAACATTTAAATAAGGAAAAAGAGGAATTTAGAGTA -960
vip3aI    - ATCGACTACACCTCCATCATGAACGAACACCTTAACAAGGAGAAGGAGGAGTTCAGAGTC -960
             I  D  Y  T  S  I  M  N  E  H  L  N  K  E  K  E  E  F  R  V
vip3a     - AACATCCTCCCTACACTTTCTAATACTTTTTCTAATCCTAATTATGCAAAAGTTAAAGGA -1020
vip3aI    - AACATCTTGCCTACTTTGTCCAACACCTTCTCCAACCCTAACTACGCTAAGGTCAAAGGA -1020
             N  I  L  P  T  L  S  N  T  F  S  N  P  N  Y  A  K  V  K  G
vip3a     - AGTGATGAAGATGCAAAGATGATTGTGGAAGCTAAACCAGGACATGCATTGATTGGGTTT -1080
vip3aI    - TCCGACGAAGACGCTAAGATGATCGTTGAAGCTAAACCTGGTCACGCACTTATCGGTTTC -1080
             S  D  E  D  A  K  M  I  V  E  A  K  P  G  H  A  L  I  G  F
vip3a     - GAAATTAGTAATGATTCAATTACAGTATTAAAAGTATATGAGGCTAAGCTAAAACAAAAT -1140
vip3aI    - GAAATCTCCAACGACTCCATCACCGTCCTTAAGGTCTACGAGGCTAAGTTGAAGCAAAAC -1140
             E  I  S  N  D  S  I  T  V  L  K  V  Y  E  A  K  L  K  Q  N
vip3a     - TATCAAGTCGATAAGGATTCCTTATCGGAA TTATTTATGGTGATATGGATAAATTATTG -1200
vip3aI    - TACCAGGTCGACAAGGACTCCCTTTCTGAG TCATCTACGGTGACATGGACAAACTTCTT -1200
             Y  Q  V  D  K  D  S  L  S  E  V  I  Y  G  D  M  D  K  L  L
vip3a     - TGCCCAGATCAATCTGAACAAATCTATTATACAAATAACATAGTATTTCCAAATGAATAT -1260
vip3aI    - TGTCCAGACCAATCCGAACAAATCTACTACACCAACAACATCGTCTTCCCTAACGAGTAC -1260
             C  P  D  Q  S  E  Q  I  Y  Y  T  N  N  I  V  F  P  N  E  Y
vip3a     - GTAATTACTAAAATTGATTTCACTAAAAAAATGAAAACTTTAAGATATGAGGTAACAGCG -1320
vip3aI    - GTCATCACCAAGATCGACTTCACCAAGAAGATGAAGACCCTTAGATACGAGGTCACTGCT -1320
             V  I  T  K  I  D  F  T  K  K  M  K  T  L  R  Y  E  V  T  A
vip3a     - AATTTTTATGATTCTTCTACAGGAGAAATTGACTTAAATAAGAAAAAAGTAGAATCAAGT -1380
vip3aI    - AACTTCTACGACTCCTCCACTGGTGAGATCGATCTTAACAAGAAGAAGGTCGAGTCCTCC -1380
             N  F  Y  D  S  S  T  G  E  I  D  L  N  K  K  K  V  E  S  S
vip3a     - GAAGCGGAGTATAGAACGTTAAGTGCTAATGATGATGGGGTGTATATGCCGTTAGGTGTC -1440
vip3aI    - GAAGCTGAGTACAGAACCCTTTCTGCTAACGACGATGGTGTCTACATGCCTCTTGGTGTC -1440
             E  A  E  Y  R  T  L  S  A  N  D  D  G  V  Y  M  P  L  G  V
vip3a     - ATCAGTGAAACATTTTTGACTCCGATTAATGGGTTTGGCCTCCAAGCTGATGAAAATTCA -1500
vip3aI    - ATCTCCGAGACCTTCCTTACTCCTATCAATGGCTTCGGTTTGCAGGCTGACGAGAACTCC -1500
             I  S  E  T  F  L  T  P  I  N  G  F  G  L  Q  A  D  E  N  S
vip3a     - AGATTAATTACTTTAACATGTAAATCATATTTAAGAGAACTACTGCTAGCAACAGACTTA -1560
vip3aI    - AGACTTATCACCCTTACCTGCAAGTCCTACCTTAGAGAATTGCTCTTGGCTACCGACCTC -1560
             R  L  I  T  L  T  C  K  S  Y  L  R  E  L  L  L  A  T  D  L
vip3a     - AGCAATAAAGAAACTAAATTGATCGTCCCGCCAAGTGGTTTTATTAGCAATATTGTAGAG -1620
vip3aI    - TCTAACAAGGAGACCAAACTCATCGTCCCTCCTTCTGGTTTCATCTCTAACATCGTCGAG -1620
             S  N  K  E  T  K  L  I  V  P  P  S  G  F  I  S  N  I  V  E
vip3a     - AACGGGTCCATAGAAGAGGACAATTTAGAGCCGTGGAAAGCAAATAATAAGAATGCGTAT -1680
vip3aI    - AACGGTTCCATCGAAGAGGACAACCTTGAGCCTTGGAAAGCTAACAACAAGAACGCTTAC -1680
             N  G  S  I  E  E  D  N  L  E  P  W  K  A  N  N  K  N  A  Y
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vip3a    - GTAGATCATACAGGCGGAGTGAATGGAACTAAAGCTTTATATGTTCATAAGGACGGAGGA -1740
vip3aI   - GTCGACCACACTGGTGGTGTCAACGGTACCAAGGCTCTTTACGTCCACAAGGACGGTGGT -1740
            V  D  H  T  G  G  V  N  G  T  K  A  L  Y  V  H  K  D  G  G
vip3a    - ATTTCACAATTTATTGGAGATAAGTTAAAACCGAAAACTGAGTATGTAATCCAATATACT -1800
vip3aI   - ATCTCCCAATTCATCGGAGACAAACTTAAACCTAAAACCGAGTACGTCATCCAATACACC -1800
            I  S  Q  F  I  G  D  K  L  K  P  K  T  E  Y  V  I  Q  Y  T
vip3a    - GTTAAAGGAAAACCTTCTATTCATTTAAAAGATGAAAATACTGGATATATTCATTATGAA -1860
vip3aI   - GTCAAGGGTAAACCTTCCATCCACCTTAAAGACGAAAACACTGGTTACATCCACTACGAA -1860
            V  K  G  K  P  S  I  H  L  K  D  E  N  T  G  Y  I  H  Y  E
vip3a    - GATACAAATAATAATTTAGAAGATTATCAAACTATTAATAAACGTTTTACTACAGGAACT -1920
vip3aI   - GACACCAACAACAACCTTGAAGACTACCAAACCATCAACAAAAGATTCACCACAGGAACC -1920
            D  T  N  N  N  L  E  D  Y  Q  T  I  N  K  R  F  T  T  G  T
vip3a    - GATTTAAAGGGAGTGTATTTAATTTTAAAAAGTCAAAATGGAGATGAAGCTTGGGGAGAT -1980
vip3aI   - GACCTTAAGGGTGTCTACCTTATCCTTAAGTCCCAGAACGGTGACGAGGCTTGGGGTGAC -1980
            D  L  K  G  V  Y  L  I  L  K  S  Q  N  G  D  E  A  W  G  D
vip3a    - AACTTTATTATTTTGGAAATTAGTCCTTCTGAAAAGTTATTAAGTCCAGAATTAATTAAT -2040
vip3aI   - AACTTCATCATCCTTGAGATCTCCCCATCCGAGAAGCTTCTTTCCCCTGAACTTATCAAC -2040
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vip3a    - ACAAATAATTGGACGAGTACGGGATCAACTAATATTAGCGGTAATACACTCACTCTTTAT -2100
vip3aI   - ACCAACAACTGGACCTCCACTGGTTCCACCAACATCTCTGGTAACACCTTGACCTTGTAC -2100
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vip3aI   - CAGGGTGGTAGAGGTATCTTGAAGCAAAACTTGCAACTTGACTCCTTCTCCACCTACAGA -2160
                  Q  G  G  R  G  I  L  K  Q  N  L  Q  L  D  S  F  S  T  Y  R
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vip3aI   - GTCTACTTCTCTGTGTCTGGTGACGCTAACGTCAGAATCAGAAACTCCAGAGAAGTCCTC -2220
            V  Y  F  S  V  S  G  D  A  N  V  R  I  R  N  S  R  E  V  L
vip3a    - TTTGAAAAAAGATATATGAGCGGTGCTAAAGATGTTTCTGAAATGTTCACTACAAAATTT -2280
vip3aI   - TTCGAGAAGAGATACATGTCTGGTGCCAAGGACGTCTCCGAGATGTTCACCACCAAGTTC -2280
            F  E  K  R  Y  M  S  G  A  K  D  V  S  E  M  F  T  T  K  F
vip3a    - GAGAAAGATAACTTTTATATAGAGCTTTCTCAAGGGAATAATTTATATGGTGGTCCTATT -2340
vip3aI   - GAGAAGGACAACTTCTACATCGAGTTGTCCCAAGGTAACAACCTTTACGGTGGTCCTATC -2340
            E  K  D  N  F  Y  I  E  L  S  Q  G  N  N  L  Y  G  G  P  I
vip3a    - GTACATTTTTACGATGTCTCTATTAAGTAA -2370
vip3aI   - GTCCACTTCTATGACGTCTCCATCAAATAA -2370
            V  H  F  Y  D  V  S  I  K  -

Identity  : 1672 ( 70.5%)
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Figure 6S

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  1 CTCGAGATGA ACAAGAACAA CACCAAGTTG TCCACCAGAG CCTTGCCTTC CTTCATCGAC a1
    GAGCTCTACT TGTTCTTGTT GTGGTTCAAC AGGTGGTCTC GGAACGGAAG GAAGTAGCTG

 61 TACTTCAATG GTATCTACGG ATTCGCTACT GGTATCAAGG ACATCATGAA CATGATCTTC a2
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121 AAGACTGACA CTGGTGGTGA TCTGACCCTT GACGAGATCT TGAAGAACCA ACAACTTCTG a3a4
    TTCTGACTGT GACCACCACT AGACTGGGAA CTGCTCTAGA ACTTCTTGGT TGTTGAAGAC

181 AACGACATCT CTGGTAAACT TGATGGTGTC AATGGTTCCT TGAACGACCT GATCGCACAG a5
    TTGCTGTAGA GACCATTTGA ACTACCACAG TTACCAAGGA ACTTGCTGGA CTAGCGTGTC

241 GGTAACCTTA ACACAGAACT TTCCAAGGAG ATCTTGAAGA TCGCTAACGA ACAGAACCAA a6
    CCATTGGAAT TGTGTCTTGA AAGGTTCCTC TAGAACTTCT AGCGATTGCT TGTCTTGGTT a7a8

301 GTCTTGAACG ACGTCAACAA CAAACTCGAT GCTATCAACA CCATGTTGAG AGTCTACTTG
    CAGAACTTGC TGCAGTTGTT GTTTGAGCTA CGATAGTTGT GGTACAACTC TCAGATGAAC a9

361 CCTAAGATCA CCTCCATGCT TTCCGACGTC ATGAAGCAGA ACTATGCTTT GTCTCTGCAA e9
    GGATTCTAGT GGAGGTACGA AAGGCTGCAG TACTTCGTCT TGATACGAAA CAGAGACGTT a10a11

421 ATCGAATACC TTTCCAAGCA ACTTCAAGAG ATCTCCGACA AGCTTGACAT CATCAACGTC
    TAGCTTATGG AAAGGTTCGT TGAAGTTCTC TAGAGGCTGT TCGAACTGTA GTAGTTGCAG a12

481 AACGTCTTGA TCAACTCCAC TTTGACCGAG ATCACTCCTG CTTACCAGAG AATCAAGTAC a13
    TTGCAGAACT AGTTGAGGTG AAACTGGCTC TAGTGAGGAC GAATGGTCTC TTAGTTCATG
block1
541 GTCAACGAGA AGTTCGAGGA GCTTACCTTC GCTACCGAAA CCTCCTCCAA GGTCAAGAAG a14
    CAGTTGCTCT TCAAGCTCCT CGAATGGAAG CGATGGCTTT GGAGGAGGTT CCAGTTCTTC

601 GACGGTTCTC CTGCTGACAT CCTCGACGAG TTGACCGAGT TGACCGAATT GGCTAAGTCC a15a16
    CTGCCAAGAG GACGACTGTA GGAGCTGCTC AACTGGCTCA ACTGGCTTAA CCGATTCAGG

661 GTCACCAAGA ACGACGTCGA TGGTTTCGAA TTCTACTTGA ACACCTTTCA TGACGTCATG a17
    CAGTGGTTCT TGCTGCAGCT ACCAAAGCTT AAGATGAACT TGTGGAAAGT ACTGCAGTAC

721 GTTGGTAACA ACCTTTTCGG TAGATCTGCA CTTAAGACTG CTTCTGAACT TATCACCAAG a18
    CAACCATTGT TGGAAAAGCC ATCTAGACGT GAATTCTGAC GAAGACTTGA ATAGTGGTTC a19a20

781 GAGAACGTGA AAACCTCTGG TTCCGAGGTT GGTAACGTCT ACAACTTCTT GATCGTCTTG
    CTCTTGCACT TTTGGAGACC AAGGCTCCAA CCATTGCAGA TGTTGAAGAA CTAGCAGAAC a21
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 841 ACAGCCTTGC AAGCTCAAGC TTTCTTGACC TTGACCACCT GTAGAAAGCT TCTTGGTCTT
     TGTCGGAACG TTCGAGTTCG AAAGAACTGG AACTGGTGGA CATCTTTCGA AGAACCAGAA a22a23

 901 GCTGACATCG ACTACACCTC CATCATGAAC GAACACCTTA ACAAGGAGAA GGAGGAGTTC
     CGACTGTAGC TGATGTGGAG GTAGTACTTG CTTGTGGAAT TGTTCCTCTT CCTCCTCAAG a24

 961 AGAGTCAACA TCTTGCCTAC TTTGTCCAAC ACCTTCTCCA ACCCTAACTA CGCTAAGGTC a245
     TCTCAGTTGT AGAACGGATG AAACAGGTTG TGGAAGAGGT TGGGATTGAT GCGATTCCAG
block2
1021 AAAGGATCCG ACGAAGACGC TAAGATGATC GTTGAAGCTA AACCTGGTCA CGCACTTATC a26
     TTTCCTAGGC TGCTTCTGCG ATTCTACTAG CAACTTCGAT TTGGACCAGT GCGTGAATAG

1081 GGTTTCGAAA TCTCCAACGA CTCCATCACC GTCCTTAAGG TCTACGAGGC TAAGTTGAAG a27a28
     CCAAAGCTTT AGAGGTTGCT GAGGTAGTGG CAGGAATTCC AGATGCTCCG ATTCAACTTC

1141 CAAAACTACC AGGTCGACAA GGACTCCCTT TCTGAGGTCA TCTACGGTGA CATGGACAAA a29
     GTTTTGATGG TCCAGCTGTT CCTGAGGGAA AGACTCCAGT AGATGCCACT GTACCTGTTT

1201 CTTCTTTGTC CAGACCAATC CGAACAAATC TACTACACCA ACAACATCGT CTTCCCTAAC a30
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1261 GAGTACGTCA TCACCAAGAT CGACTTCACC AAGAAGATGA AGACCCTTAG ATACGAGGTC
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1321 ACTGCTAACT TCTACGACTC CTCCACTGGT GAGATCGATC TTAACAAGAA GAAGGTCGAG
     TGACGATTGA AGATGCTGAG GAGGTGACCA CTCTAGCTAG AATTGTTCTT CTTCCAGCTC a34a35

1381 TCCTCCGAAG CTGAGTACAG AACCCTTTCT GCTAACGACG ATGGTGTCTA CATGCCTCTT
     AGGAGGCTTC GACTCATGTC TTGGGAAAGA CGATTGCTGC TACCACAGAT GTACGGAGAA a36

1441 GGTGTCATCT CCGAGACCTT CCTTACTCCT ATCAATGGCT TCGGTTTGCA GGCTGACGAG a37
     CCACAGTAGA GGCTCTGGAA GGAATGAGGA TAGTTACCGA AGCCAAACGT CCGACTGCTC
block3
1501 AACTCCAGAC TTATCACCCT TACCTGCAAG TCCTACCTTA GAGAATTGCT CTTGGCTACC a38
    TTGAGGTCTG AATAGTGGGA ATGGACGTTC AGGATGGAAT CTCTTAACGA GAACCGATGG

1561 GACCTCTCTA ACAAGGAGAC CAAACTCATC GTCCCTCCTT CTGGTTTCAT CTCTAACATC a39a40
     CTGGAGAGAT TGTTCCTCTG GTTTGAGTAG CAGGGAGGAA GACCAAAGTA GAGATTGTAG

1621 GTCGAGAACG GTTCCATCGA AGAGGACAAC CTTGAGCCTT GGAAAGCTAA CAACAAGAAC a41
     CAGCTCTTGC CAAGGTAGCT TCTCCTGTTG GAACTCGGAA CCTTTCGATT GTTGTTCTTG
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1681  GCTTACGTCG ACCACACTGG TGGTGTCAAC GGTACCAAGG CTCTTTACGT CCACAAGGAC a42
      CGAATGCAGC TGGTGTGACC ACCACAGTTG CCATGGTTCC GAGAAATGCA GGTGTTCCTG a43a44

 1741 GGTGGTATCT CCCAATTCAT CGGAGACAAA CTTAAACCTA AAACCGAGTA CGTCATCCAA
      CCACCATAGA GGGTTAAGTA GCCTCTGTTT GAATTTGGAT TTTGGCTCAT GCAGTAGGTT a45

 1801 TACACCGTCA AGGGTAAACC TTCCATCCAC CTTAAAGACG AAAACACTGG TTACATCCAC
      ATGTGGCAGT TCCCATTTGG AAGGTAGGTG GAATTTCTGC TTTTGTGACC AATGTAGGTG a46a47

 1861 TACGAAGACA CCAACAACAA CCTTGAAGAC TACCAAACCA TCAACAAAAG ATTCACCACA
      ATGCTTCTGT GGTTGTTGTT GGAACTTCTG ATGGTTTGGT AGTTGTTTTC TAAGTGGTGT a48

 1921 GGAACCGACC TTAAGGGTGT CTACCTTATC CTTAAGTCCC AGAACGGTGA CGAGGCTTGG a49
      CCTTGGCTGG AATTCCCACA GATGGAATAG GAATTCAGGG TCTTGCCACT GCTCCGAACC
Block4
 1981 GGTGACAACT TCATCATCCT TGAGATCTCC CCATCCGAGA AGCTTCTTTC CCCTGAACTT a50
      CCACTGTTGA AGTAGTAGGA ACTCTAGAGG GGTAGGCTCT TCGAAGAAAG GGGACTTGAA

 2041 ATCAACACCA ACAACTGGAC CTCCACTGGT TCCACCAACA TCTCTGGTAA CACCTTGACC a51a52
      TAGTTGTGGT TGTTGACCTG GAGGTGACCA AGGTGGTTGT AGAGACCATT GTGGAACTGG

 2101 TTGTACCAGG GTGGTAGAGG TATCTTGAAG CAAAACTTGC AACTTGACTC CTTCTCCACC a53
      AACATGGTCC CACCATCTCC ATAGAACTTC GTTTTGAACG TTGAACTGAG GAAGAGGTGG

 2161 TACAGAGTCT ACTTCTCTGT GTCTGGTGAC GCTAACGTCA GAATCAGAAA CTCCAGAGAA a54
      ATGTCTCAGA TGAAGAGACA CAGACCACTG CGATTGCAGT CTTAGTCTTT GAGGTCTCTT a55a56

 2221 GTCCTCTTCG AGAAGAGATA CATGTCTGGT GCCAAGGACG TCTCCGAGAT GTTCACCACC
      CAGGAGAAGC TCTTCTCTAT GTACAGACCA CGGTTCCTGC AGAGGCTCTA CAAGTGGTGG a57

 2281 AAGTTCGAGA AGGACAACTT CTACATCGAG TTGTCCCAAG GTAACAACCT TTACGGTGGT
      TTCAAGCTCT TCCTGTTGAA GATGTAGCTC AACAGGGTTC CATTGTTGGA AATGCCACCA a58a59

 2341 CCTATCGTCC ACTTCTATGA CGTCTCCATC AAATAAGAGC TC                    a60
      GGATAGCAGG TGAAGATACT GCAGAGGTAG TTTATTCTCG AG
```

Total number of bases is: 2382.

DNA sequence composition: 685 A; 665 C; 455 G; 577 T; 0 OTHER;

Figure 7S

```
           10         20         30         40         50         60
  1 CTCGAGATGA ACAAGAACAA CACCAAGTTG TCCACCAGAG CCTTGCCTTC CTTCATCGAC
    GAGCTCTACT TGTTCTTGTT GTGGTTCAAC AGGTGGTCTC GGAACGGAAG GAAGTAGCTG

 61 TACTTCAATG GTATCTACGG ATTCGCTACT GGTATCAAGG ACATCATGAA CATGATCTTC b1
    ATGAAGTTAC CATAGATGCC TAAGCGATGA CCATAGTTCC TGTAGTACTT GTACTAGAAG

121 AAGACTGACA CTGGTGGTGA TCTGACCCTT GACGAGATCT TGAAGAACCA ACAACTTCTG b2
    TTCTGACTGT GACCACCACT AGACTGGGAA CTGCTCTAGA ACTTCTTGGT TGTTGAAGAC

181 AACGACATCT CTGGTAAACT TGATGGTGTC AATGGTTCCT TGAACGACCT GATCGCACAG b3
    TTGCTGTAGA GACCATTTGA ACTACCACAG TTACCAAGGA ACTTGCTGGA CTAGCGTGTC

241 GGTAACCTTA ACACAGAACT TTCCAAGGAG ATCTTGAAGA TCGCTAACGA ACAGAACCAA b4
    CCATTGGAAT TGTGTCTTGA AAGGTTCCTC TAGAACTTCT AGCGATTGCT TGTCTTGGTT

301 GTCTTGAACG ACGTCAACAA CAAACTCGAT GCTATCAACA CCATGTTGAG AGTCTACTTG
    CAGAACTTGC TGCAGTTGTT GTTTGAGCTA CGATAGTTGT GGTACAACTC TCAGATGAAC

361 CCTAAGATCA CCTCCATGCT TTCCGACGTC ATGAAGCAGA ACTATGCTTT GTCTCTGCAA b5
    GGATTCTAGT GGAGGTACGA AAGGCTGCAG TACTTCGTCT TGATACGAAA CAGAGACGTT

421 ATCGAATACC TTTCCAAGCA ACTTCAAGAG ATCTCCGACA AGCTTGACAT CATCAACGTC b6
    TAGCTTATGG AAAGGTTCGT TGAAGTTCTC TAGAGGCTGT TCGAACTGTA GTAGTTGCAG b7

481 AACGTCTTGA TCAACTCCAC TTTGACCGAG ATCACTCCTG CTTACCAGAG AATCAAGTAC
    TTGCAGAACT AGTTGAGGTG AAACTGGCTC TAGTGAGGAC GAATGGTCTC TTAGTTCATG b8

541 GTCAACGAGA AGTTCGAGGA GCTTACCTTC GCTACCGAAA CCTCCTCCAA GGTCAAGAAG
    CAGTTGCTCT TCAAGCTCCT CGAATGGAAG CGATGGCTTT GGAGGAGGTT CCAGTTCTTC b9

601 GACGGTTCTC CTGCTGACAT CCTCGACGAG TTGACCGAGT TGACCGAATT GGCTAAGTCC
    CTGCCAAGAG GACGACTGTA GGAGCTGCTC AACTGGCTCA ACTGGCTTAA CCGATTCAGG b10

661 GTCACCAAGA ACGACGTCGA TGGTTTCGAA TTCTACTTGA ACACCTTTCA TGACGTCATG
    CAGTGGTTCT TGCTGCAGCT ACCAAAGCTT AAGATGAACT TGTGGAAAGT ACTGCAGTAC b11

721 GTTGGTAACA ACCTTTTCGG TAGATCTGCA CTTAAGACTG CTTCTGAACT TATCACCAAG
    CAACCATTGT TGGAAAAGCC ATCTAGACGT GAATTCTGAC GAAGACTTGA ATAGTGGTTC b12

781 GAGAACGTGA AACCTCTGGG TTCCGAGGTT GGTAACGTCT ACAACTTCTT GATCGTCTTG
    CTCTTGCACT TTTGGAGACC AAGGCTCCAA CCATTGCAGA TGTTGAAGAA CTAGCAGAAC
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 841 ACAGCCTTGC AAGCTCAAGC TTTCTTGACC TTGACCACCT GTAGAAAGCT TCTTGGTCTT
     TGTCGGAACG TTCGAGTTCG AAAGAACTGG AACTGGTGGA CATCTTTCGA AGAACCAGAA
block1
 901 GCTGACATCG ACTACACCTC CATCATGAAC GAACACCTTA ACAAGGAGAA GGAGGAGTTC b13
     CGACTGTAGC TGATGTGGAG GTAGTACTTG CTTGTGGAAT TGTTCCTCTT CCTCCTCAAG

 961 AGAGTCAACA TCTTGCCTAC TTTGTCCAAC ACCTTCTCCA ACCCTAACTA CGCTAAGGTC b14
     TCTCAGTTGT AGAACGGATG AAACAGGTTG TGGAAGAGGT TGGGATTGAT GCGATTCCAG

1021 AAAGGATCCG ACGAAGACGC TAAGATGATC GTTGAAGCTA AACCTGGTCA CGCACTTATC b15
     TTTCCTAGGC TGCTTCTGCG ATTCTACTAG CAACTTCGAT TTGGACCAGT GCGTGAATAG

1081 GGTTTCGAAA TCTCCAACGA CTCCATCACC GTCCTTAAGG TCTACGAGGC TAAGTTGAAG b16
     CCAAAGCTTT AGAGGTTGCT GAGGTAGTGG CAGGAATTCC AGATGCTCCG ATTCAACTTC

1141 CAAAACTACC AGGTCGACAA GGACTCCCTT TCTGAGGTCA TCTACGGTGA CATGGACAAA
     GTTTTGATGG TCCAGCTGTT CCTGAGGGAA AGACTCCAGT AGATGCCACT GTACCTGTTT

1201 CTTCTTTGTC CAGACCAATC CGAACAAATC TACTACACCA ACAACATCGT CTTCCCTAAC b17
     GAAGAAACAG GTCTGGTTAG GCTTGTTTAG ATGATGTGGT TGTTGTAGCA GAAGGGATTG

1261 GAGTACGTCA TCACCAAGAT CGACTTCACC AAGAAGATGA AGACCCTTAG ATACGAGGTC b18
     CTCATGCAGT AGTGGTTCTA GCTGAAGTGG TTCTTCTACT TCTGGGAATC TATGCTCCAG b19

1321 ACTGCTAACT TCTACGACTC CTCCACTGGT GAGATCGATC TTAACAAGAA GAAGGTCGAG
     TGACGATTGA AGATGCTGAG GAGGTGACCA CTCTAGCTAG AATTGTTCTT CTTCCAGCTC b20

1381 TCCTCCGAAG CTGAGTACAG AACCCTTTCT GCTAACGACG ATGGTGTCTA CATGCCTCTT
     AGGAGGCTTC GACTCATGTC TTGGGAAAGA CGATTGCTGC TACCACAGAT GTACGGAGAA b21

1441 GGTGTCATCT CCGAGACCTT CCTTACTCCT ATCAATGGCT TCGGTTTGCA GGCTGACGAG
     CCACAGTAGA GGCTCTGGAA GGAATGAGGA TAGTTACCGA AGCCAAACGT CCGACTGCTC b22

1501 AACTCCAGAC TTATCACCCT TACCTGCAAG TCCTACCTTA GAGAATTGCT CTTGGCTACC
    TTGAGGTCTG AATAGTGGGA ATGGACGTTC AGGATGGAAT CTCTTAACGA GAACCGATGG b23

1561 GACCTCTCTA ACAAGGAGAC CAAACTCATC GTCCCTCCTT CTGGTTTCAT CTCTAACATC
     CTGGAGAGAT TGTTCCTCTG GTTTGAGTAG CAGGGAGGAA GACCAAAGTA GAGATTGTAG b24

1621 GTCGAGAACG GTTCCATCGA AGAGGACAAC CTTGAGCCTT GGAAAGCTAA CAACAAGAAC
     CAGCTCTTGC CAAGGTAGCT TCTCCTGTTG GAACTCGGAA CCTTTCGATT GTTGTTCTTG
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   1681 GCTTACGTCG ACCACACTGG TGGTGTCAAC GGTACCAAGG CTCTTTACGT CCACAAGGAC
        CGAATGCAGC TGGTGTGACC ACCACAGTTG CCATGGTTCC GAGAAATGCA GGTGTTCCTG
Block2
   1741 GGTGGTATCT CCCAATTCAT CGGAGACAAA CTTAAACCTA AAACCGAGTA CGTCATCCAA b25
       CCACCATAGA GGGTTAAGTA GCCTCTGTTT GAATTTGGAT TTTGGCTCAT GCAGTAGGTT

   1801 TACACCGTCA AGGGTAAACC TTCCATCCAC CTTAAAGACG AAAACACTGG TTACATCCAC b26
       ATGTGGCAGT TCCCATTTGG AAGGTAGGTG GAATTTCTGC TTTTGTGACC AATGTAGGTG

   1861 TACGAAGACA CCAACAACAA CCTTGAAGAC TACCAAACCA TCAACAAAAG ATTCACCACA b27
       ATGCTTCTGT GGTTGTTGTT GGAACTTCTG ATGGTTTGGT AGTTGTTTTC TAAGTGGTGT

   1921 GGAACCGACC TTAAGGGTGT CTACCTTATC CTTAAGTCCC AGAACGGTGA CGAGGCTTGG b28
       CCTTGGCTGG AATTCCCACA GATGGAATAG GAATTCAGGG TCTTGCCACT GCTCCGAACC

   1981 GGTGACAACT TCATCATCCT TGAGATCTCC CCATCCGAGA AGCTTCTTTC CCCTGAACTT
       CCACTGTTGA AGTAGTAGGA ACTCTAGAGG GGTAGGCTCT TCGAAGAAAG GGGACTTGAA b30

   2041 ATCAACACCA ACAACTGGAC CTCCACTGGT TCCACCAACA TCTCTGGTAA CACCTTGACC b29
        TAGTTGTGGT TGTTGACCTG GAGGTGACCA AGGTGGTTGT AGAGACCATT GTGGAACTGG

   2101 TTGTACCAGG GTGGTAGAGG TATCTTGAAG CAAAACTTGC AACTTGACTC CTTCTCCACC
        AACATGGTCC CACCATCTCC ATAGAACTTC GTTTTGAACG TTGAACTGAG GAAGAGGTGG b31

   2161 TACAGAGTCT ACTTCTCTGT GTCTGGTGAC GCTAACGTCA GAATCAGAAA CTCCAGAGAA
        ATGTCTCAGA TGAAGAGACA CAGACCACTG CGATTGCAGT CTTAGTCTTT GAGGTCTCTT b32

   2221 GTCCTCTTCG AGAAGAGATA CATGTCTGGT GCCAAGGACG TCTCCGAGAT GTTCACCACC
       CAGGAGAAGC TCTTCTCTAT GTACAGACCA CGGTTCCTGC AGAGGCTCTA CAAGTGGTGG b33

   2281 AAGTTCGAGA AGGACAACTT CTACATCGAG TTGTCCCAAG GTAACAACCT TTACGGTGGT
        TTCAAGCTCT TCCTGTTGAA GATGTAGCTC AACAGGGTTC CATTGTTGGA AATGCCACCA b34

   2341 CCTATCGTCC ACTTCTATGA CGTCTCCATC AAATAAGAGC TC
        GGATAGCAGG TGAAGATACT GCAGAGGTAG TTTATTCTCG AG
Block3
```

Total number of bases is: 2382.

DNA sequence composition: 685 A; 665 C; 455 G; 577 T; 0 OTHER;

Figure 8S

```
           10         20         30         40         50         60
  1 CTCGAGATGA ACAAGAACAA CACCAAGTTG TCCACCAGAG CCTTGCCTTC CTTCATCGAC c1
    GAGCTCTACT TGTTCTTGTT GTGGTTCAAC AGGTGGTCTC GGAACGGAAG GAAGTAGCTG

 61 TACTTCAATG GTATCTACGG ATTCGCTACT GGTATCAAGG ACATCATGAA CATGATCTTC c2
    ATGAAGTTAC CATAGATGCC TAAGCGATGA CCATAGTTCC TGTAGTACTT GTACTAGAAG

121 AAGACTGACA CTGGTGGTGA TCTGACCCTT GACGAGATCT TGAAGAACCA ACAACTTCTG c3 c4
    TTCTGACTGT GACCACCACT AGACTGGGAA CTGCTCTAGA ACTTCTTGGT TGTTGAAGAC

181 AACGACATCT CTGGTAAACT TGATGGTGTC AATGGTTCCT TGAACGACCT GATCGCACAG c5
    TTGCTGTAGA GACCATTTGA ACTACCACAG TTACCAAGGA ACTTGCTGGA CTAGCGTGTC

241 GGTAACCTTA ACACAGAACT TTCCAAGGAG ATCTTGAAGA TCGCTAACGA ACAGAACCAA c6 c7
    CCATTGGAAT TGTGTCTTGA AAGGTTCCTC TAGAACTTCT AGCGATTGCT TGTCTTGGTT

301 GTCTTGAACG ACGTCAACAA CAAACTCGAT GCTATCAACA CCATGTTGAG AGTCTACTTG c8
    CAGAACTTGC TGCAGTTGTT GTTTGAGCTA CGATAGTTGT GGTACAACTC TCAGATGAAC

361 CCTAAGATCA CCTCCATGCT TTCCGACGTC ATGAAGCAGA ACTATGCTTT GTCTCTGCAA c9 c10
    GGATTCTAGT GGAGGTACGA AAGGCTGCAG TACTTCGTCT TGATACGAAA CAGAGACGTT

421 ATCGAATACC TTTCCAAGCA ACTTCAAGAG ATCTCCGACA AGCTTGACAT CATCAACGTC c11
    TAGCTTATGG AAAGGTTCGT TGAAGTTCTC TAGAGGCTGT TCGAACTGTA GTAGTTGCAG

481 AACGTCTTGA TCAACTCCAC TTTGACCGAG ATCACTCCTG CTTACCAGAG AATCAAGTAC c12 c13
    TTGCAGAACT AGTTGAGGTG AAACTGGCTC TAGTGAGGAC GAATGGTCTC TTAGTTCATG

541 GTCAACGAGA AGTTCGAGGA GCTTACCTTC GCTACCGAAA CCTCCTCCAA GGTCAAGAAG c14
    CAGTTGCTCT TCAAGCTCCT CGAATGGAAG CGATGGCTTT GGAGGAGGTT CCAGTTCTTC

601 GACGGTTCTC CTGCTGACAT CCTCGACGAG TTGACCGAGT TGACCGAATT GGCTAAGTCC c15c16
    CTGCCAAGAG GACGACTGTA GGAGCTGCTC AACTGGCTCA ACTGGCTTAA CCGATTCAGG

661 GTCACCAAGA ACGACGTCGA TGGTTTCGAA TTCTACTTGA ACACCTTTCA TGACGTCATG c17
    CAGTGGTTCT TGCTGCAGCT ACCAAAGCTT AAGATGAACT TGTGGAAAGT ACTGCAGTAC

721 GTTGGTAACA ACCTTTTCGG TAGATCTGCA CTTAAGACTG CTTCTGAACT TATCACCAAG c18c19
    CAACCATTGT TGGAAAAGCC ATCTAGACGT GAATTCTGAC GAAGACTTGA ATAGTGGTTC

781 GAGAACGTGA AAACCTCTGG TTCCGAGGTT GGTAACGTCT ACAACTTCTT GATCGTCTTG c20
    CTCTTGCACT TTTGGAGACC AAGGCTCCAA CCATTGCAGA TGTTGAAGAA CTAGCAGAAC
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 841 ACAGCCTTGC AAGCTCAAGC TTTCTTGACC TTGACCACCT GTAGAAAGCT TCTTGGTCTT c21c22
     TGTCGGAACG TTCGAGTTCG AAAGAACTGG AACTGGTGGA CATCTTTCGA AGAACCAGAA

 901 GCTGACATCG ACTACACCTC CATCATGAAC GAACACCTTA ACAAGGAGAA GGAGGAGTTC c23
     CGACTGTAGC TGATGTGGAG GTAGTACTTG CTTGTGGAAT TGTTCCTCTT CCTCCTCAAG

 961 AGAGTCAACA TCTTGCCTAC TTTGTCCAAC ACCTTCTCCA ACCCTAACTA CGCTAAGGTC c24c25
     TCTCAGTTGT AGAACGGATG AAACAGGTTG TGGAAGAGGT TGGGATTGAT GCGATTCCAG

1021 AAAGGATCCG ACGAAGACGC TAAGATGATC GTTGAAGCTA AACCTGGTCA CGCACTTATC c26
     TTTCCTAGGC TGCTTCTGCG ATTCTACTAG CAACTTCGAT TTGGACCAGT GCGTGAATAG

1081 GGTTTCGAAA TCTCCAACGA CTCCATCACC GTCCTTAAGG TCTACGAGGC TAAGTTGAAG c27c28
     CCAAAGCTTT AGAGGTTGCT GAGGTAGTGG CAGGAATTCC AGATGCTCCG ATTCAACTTC

1141 CAAAACTACC AGGTCGACAA GGACTCCCTT TCTGAGGTCA TCTACGGTGA CATGGACAAA c29
     GTTTTGATGG TCCAGCTGTT CCTGAGGGAA AGACTCCAGT AGATGCCACT GTACCTGTTT

1201 CTTCTTTGTC CAGACCAATC CGAACAAATC TACTACACCA ACAACATCGT CTTCCCTAAC c30
     GAAGAAACAG GTCTGGTTAG GCTTGTTTAG ATGATGTGGT TGTTGTAGCA GAAGGGATTG c31c32

1261 GAGTACGTCA TCACCAAGAT CGACTTCACC AAGAAGATGA AGACCCTTAG ATACGAGGTC
     CTCATGCAGT AGTGGTTCTA GCTGAAGTGG TTCTTCTACT TCTGGGAATC TATGCTCCAG c33

1321 ACTGCTAACT TCTACGACTC CTCCACTGGT GAGATCGATC TTAACAAGAA GAAGGTCGAG
     TGACGATTGA AGATGCTGAG GAGGTGACCA CTCTAGCTAG AATTGTTCTT CTTCCAGCTC c34c35

1381 TCCTCCGAAG CTGAGTACAG AACCCTTTCT GCTAACGACG ATGGTGTCTA CATGCCTCTT
     AGGAGGCTTC GACTCATGTC TTGGGAAAGA CGATTGCTGC TACCACAGAT GTACGGAGAA c36

1441 GGTGTCATCT CCGAGACCTT CCTTACTCCT ATCAATGGCT TCGGTTTGCA GGCTGACGAG
     CCACAGTAGA GGCTCTGGAA GGAATGAGGA TAGTTACCGA AGCCAAACGT CCGACTGCTC c37c38

1501 AACTCCAGAC TTATCACCCT TACCTGCAAG TCCTACCTTA GAGAATTGCT CTTGGCTACC
     TTGAGGTCTG AATAGTGGGA ATGGACGTTC AGGATGGAAT CTCTTAACGA GAACCGATGG c39

1561 GACCTCTCTA ACAAGGAGAC CAAACTCATC GTCCCTCCTT CTGGTTTCAT CTCTAACATC
     CTGGAGAGAT TGTTCCTCTG GTTTGAGTAG CAGGGAGGAA GACCAAAGTA GAGATTGTAG c40c41

1621 GTCGAGAACG GTTCCATCGA AGAGGACAAC CTTGAGCCTT GGAAAGCTAA CAACAAGAAC
     CAGCTCTTGC CAAGGTAGCT TCTCCTGTTG GAACTCGGAA CCTTTCGATT GTTGTTCTTG c42

1681 GCTTACGTCG ACCACACTGG TGGTGTCAAC GGTACCAAGG CTCTTTACGT CCACAAGGAC
     CGAATGCAGC TGGTGTGACC ACCACAGTTG CCATGGTTCC GAGAAATGCA GGTGTTCCTG c43c44
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1741 GGTGGTATCT CCCAATTCAT CGGAGACAAA CTTAAACCTA AAACCGAGTA CGTCATCCAA
     CCACCATAGA GGGTTAAGTA GCCTCTGTTT GAATTTGGAT TTTGGCTCAT GCAGTAGGTT c45
                           ◄────────────────────

1801 TACACCGTCA AGGGTAAACC TTCCATCCAC CTTAAAGACG AAAACACTGG TTACATCCAC
     ATGTGGCAGT TCCCATTTGG AAGGTAGGTG GAATTTCTGC TTTTGTGACC AATGTAGGTG c46c47
     ◄────────────────────                       ◄────────────────────

1861 TACGAAGACA CCAACAACAA CCTTGAAGAC TACCAAACCA TCAACAAAAG ATTCACCACA
     ATGCTTCTGT GGTTGTTGTT GGAACTTCTG ATGGTTTGGT AGTTGTTTTC TAAGTGGTGT c47
                           ◄────────────────────

1921 GGAACCGACC TTAAGGGTGT CTACCTTATC CTTAAGTCCC AGAACGGTGA CGAGGCTTGG
     CCTTGGCTGG AATTCCCACA GATGGAATAG GAATTCAGGG TCTTGCCACT GCTCCGAACC c48c50
     ◄────────────────────                       ◄────────────────────

1981 GGTGACAACT TCATCATCCT TGAGATCTCC CCATCCGAGA AGCTTCTTTC CCCTGAACTT
     CCACTGTTGA AGTAGTAGGA ACTCTAGAGG GGTAGGCTCT TCGAAGAAAG GGGACTTGAA c51
                           ◄────────────────────

2041 ATCAACACCA ACAACTGGAC CTCCACTGGT TCCACCAACA TCTCTGGTAA CACCTTGACC
     TAGTTGTGGT TGTTGACCTG GAGGTGACCA AGGTGGTTGT AGAGACCATT GTGGAACTGG c52c53
     ◄────────────────────                       ◄────────────────────

2101 TTGTACCAGG GTGGTAGAGG TATCTTGAAG CAAAACTTGC AACTTGACTC CTTCTCCACC
     AACATGGTCC CACCATCTCC ATAGAACTTC GTTTTGAACG TTGAACTGAG GAAGAGGTGG c54
                           ◄────────────────────

2161 TACAGAGTCT ACTTCTCTGT GTCTGGTGAC GCTAACGTCA GAATCAGAAA CTCCAGAGAA
     ATGTCTCAGA TGAAGAGACA CAGACCACTG CGATTGCAGT CTTAGTCTTT GAGGTCTCTT c55c56
     ◄────────────────────                       ◄────────────────────

2221 GTCCTCTTCG AGAAGAGATA CATGTCTGGT GCCAAGGACG TCTCCGAGAT GTTCACCACC
     CAGGAGAAGC TCTTCTCTAT GTACAGACCA CGGTTCCTGC AGAGGCTCTA CAAGTGGTGG c57
                           ◄────────────────────

2281 AAGTTCGAGA AGGACAACTT CTACATCGAG TTGTCCCAAG GTAACAACCT TTACGGTGGT
     TTCAAGCTCT TCCTGTTGAA GATGTAGCTC AACAGGGTTC CATTGTTGGA AATGCCACCA c58c59
     ◄────────────────────                       ◄────────────────────

2341 CCTATCGTCC ACTTCTATGA CGTCTCCATC AAATAAGAGC TC
     GGATAGCAGG TGAAGATACT GCAGAGGTAG TTTATTCTCG AG


Total number of bases is: 2382.
DNA sequence composition:   685 A;   665 C;   455 G;   577 T; 0 OTHER;
```

Figure 9S

```
          10         20         30         40         50         60
  1 CTCGAGATGA ACAAGAACAA CACCAAGTTG TCCACCAGAG CCTTGCCTTC CTTCATCGAC
    GAGCTCTACT TGTTCTTGTT GTGGTTCAAC AGGTGGTCTC GGAACGGAAG GAAGTAGCTG

 61 TACTTCAATG GTATCTACGG ATTCGCTACT GGTATCAAGG ACATCATGAA CATGATCTTC  d1
    ATGAAGTTAC CATAGATGCC TAAGCGATGA CCATAGTTCC TGTAGTACTT GTACTAGAAG

121 AAGACTGACA CTGGTGGTGA TCTGACCCTT GACGAGATCT TGAAGAACCA ACAACTTCTG  d2
    TTCTGACTGT GACCACCACT AGACTGGGAA CTGCTCTAGA ACTTCTTGGT TGTTGAAGAC

181 AACGACATCT CTGGTAAACT TGATGGTGTC AATGGTTCCT TGAACGACCT GATCGCACAG  d3
    TTGCTGTAGA GACCATTTGA ACTACCACAG TTACCAAGGA ACTTGCTGGA CTAGCGTGTC

241 GGTAACCTTA ACACAGAACT TTCCAAGGAG ATCTTGAAGA TCGCTAACGA ACAGAACCAA  d4
    CCATTGGAAT TGTGTCTTGA AAGGTTCCTC TAGAACTTCT AGCGATTGCT TGTCTTGGTT

301 GTCTTGAACG ACGTCAACAA CAAACTCGAT GCTATCAACA CCATGTTGAG AGTCTACTTG
    CAGAACTTGC TGCAGTTGTT GTTTGAGCTA CGATAGTTGT GGTACAACTC TCAGATGAAC

361 CCTAAGATCA CCTCCATGCT TTCCGACGTC ATGAAGCAGA ACTATGCTTT GTCTCTGCAA d5
    GGATTCTAGT GGAGGTACGA AAGGCTGCAG TACTTCGTCT TGATACGAAA CAGAGACGTT

421 ATCGAATACC TTTCCAAGCA ACTTCAAGAG ATCTCCGACA AGCTTGACAT CATCAACGTC d6
    TAGCTTATGG AAAGGTTCGT TGAAGTTCTC TAGAGGCTGT TCGAACTGTA GTAGTTGCAG

481 AACGTCTTGA TCAACTCCAC TTTGACCGAG ATCACTCCTG CTTACCAGAG AATCAAGTAC d7
    TTGCAGAACT AGTTGAGGTG AAACTGGCTC TAGTGAGGAC GAATGGTCTC TTAGTTCATG

541 GTCAACGAGA AGTTCGAGGA GCTTACCTTC GCTACCGAAA CCTCCTCCAA GGTCAAGAAG d8
    CAGTTGCTCT TCAAGCTCCT CGAATGGAAG CGATGGCTTT GGAGGAGGTT CCAGTTCTTC

601 GACGGTTCTC CTGCTGACAT CCTCGACGAG TTGACCGAGT TGACCGAATT GGCTAAGTCC d9
    CTGCCAAGAG GACGACTGTA GGAGCTGCTC AACTGGCTCA ACTGGCTTAA CCGATTCAGG

661 GTCACCAAGA ACGACGTCGA TGGTTTCGAA TTCTACTTGA ACACCTTTCA TGACGTCATG d10
    CAGTGGTTCT TGCTGCAGCT ACCAAAGCTT AAGATGAACT TGTGGAAAGT ACTGCAGTAC

721 GTTGGTAACA ACCTTTTCGG TAGATCTGCA CTTAAGACTG CTTCTGAACT TATCACCAAG
    CAACCATTGT TGGAAAAGCC ATCTAGACGT GAATTCTGAC GAAGACTTGA ATAGTGGTTC

781 GAGAACGTGA AAACCTCTGG TTCCGAGGTT GGTAACGTCT ACAACTTCTT GATCGTCTTG d11
    CTCTTGCACT TTTGGAGACC AAGGCTCCAA CCATTGCAGA TGTTGAAGAA CTAGCAGAAC
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 841 ACAGCCTTGC AAGCTCAAGC TTTCTTGACC TTGACCACCT GTAGAAAGCT TCTTGGTCTT d12
     TGTCGGAACG TTCGAGTTCG AAAGAACTGG AACTGGTGGA CATCTTTCGA AGAACCAGAA

 901 GCTGACATCG ACTACACCTC CATCATGAAC GAACACCTTA ACAAGGAGAA GGAGGAGTTC d13
     CGACTGTAGC TGATGTGGAG GTAGTACTTG CTTGTGGAAT TGTTCCTCTT CCTCCTCAAG

 961 AGAGTCAACA TCTTGCCTAC TTTGTCCAAC ACCTTCTCCA ACCCTAACTA CGCTAAGGTC d14
     TCTCAGTTGT AGAACGGATG AAACAGGTTG TGGAAGAGGT TGGGATTGAT GCGATTCCAG

1021 AAAGGATCCG ACGAAGACGC TAAGATGATC GTTGAAGCTA AACCTGGTCA CGCACTTATC d15
     TTTCCTAGGC TGCTTCTGCG ATTCTACTAG CAACTTCGAT TTGGACCAGT GCGTGAATAG

1081 GGTTTCGAAA TCTCCAACGA CTCCATCACC GTCCTTAAGG TCTACGAGGC TAAGTTGAAG d16
     CCAAAGCTTT AGAGGTTGCT GAGGTAGTGG CAGGAATTCC AGATGCTCCG ATTCAACTTC

1141 CAAAACTACC AGGTCGACAA GGACTCCCTT TCTGAGGTCA TCTACGGTGA CATGGACAAA
     GTTTTGATGG TCCAGCTGTT CCTGAGGGAA AGACTCCAGT AGATGCCACT GTACCTGTTT d18

1201 CTTCTTTGTC CAGACCAATC CGAACAAATC TACTACACCA ACAACATCGT CTTCCCTAAC d17
     GAAGAAACAG GTCTGGTTAG GCTTGTTTAG ATGATGTGGT TGTTGTAGCA GAAGGGATTG d19

1261 GAGTACGTCA TCACCAAGAT CGACTTCACC AAGAAGATGA AGACCCTTAG ATACGAGGTC
     CTCATGCAGT AGTGGTTCTA GCTGAAGTGG TTCTTCTACT TCTGGGAATC TATGCTCCAG d20

1321 ACTGCTAACT TCTACGACTC CTCCACTGGT GAGATCGATC TTAACAAGAA GAAGGTCGAG
     TGACGATTGA AGATGCTGAG GAGGTGACCA CTCTAGCTAG AATTGTTCTT CTTCCAGCTC

1381 TCCTCCGAAG CTGAGTACAG AACCCTTTCT GCTAACGACG ATGGTGTCTA CATGCCTCTT
     AGGAGGCTTC GACTCATGTC TTGGGAAAGA CGATTGCTGC TACCACAGAT GTACGGAGAA d21

1441 GGTGTCATCT CCGAGACCTT CCTTACTCCT ATCAATGGCT TCGGTTTGCA GGCTGACGAG
     CCACAGTAGA GGCTCTGGAA GGAATGAGGA TAGTTACCGA AGCCAAACGT CCGACTGCTC d22

1501 AACTCCAGAC TTATCACCCT TACCTGCAAG TCCTACCTTA GAGAATTGCT CTTGGCTACC
     TTGAGGTCTG AATAGTGGGA ATGGACGTTC AGGATGGAAT CTCTTAACGA GAACCGATGG d23

1561 GACCTCTCTA ACAAGGAGAC CAAACTCATC GTCCCTCCTT CTGGTTTCAT CTCTAACATC
     CTGGAGAGAT TGTTCCTCTG GTTTGAGTAG CAGGGAGGAA GACCAAAGTA GAGATTGTAG d24

1621 GTCGAGAACG GTTCCATCGA AGAGGACAAC CTTGAGCCTT GGAAAGCTAA CAACAAGAAC
     CAGCTCTTGC CAAGGTAGCT TCTCCTGTTG GAACTCGGAA CCTTTCGATT GTTGTTCTTG d25
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1681 GCTTACGTCG ACCACACTGG TGGTGTCAAC GGTACCAAGG CTCTTTACGT CCACAAGGAC
     CGAATGCAGC TGGTGTGACC ACCACAGTTG CCATGGTTCC GAGAAATGCA GGTGTTCCTG d26

1741 GGTGGTATCT CCCAATTCAT CGGAGACAAA CTTAAACCTA AAACCGAGTA CGTCATCCAA
     CCACCATAGA GGGTTAAGTA GCCTCTGTTT GAATTTGGAT TTTGGCTCAT GCAGTAGGTT

1801 TACACCGTCA AGGGTAAACC TTCCATCCAC CTTAAAGACG AAAACACTGG TTACATCCAC
     ATGTGGCAGT TCCCATTTGG AAGGTAGGTG GAATTTCTGC TTTTGTGACC AATGTAGGTG d27

1861 TACGAAGACA CCAACAACAA CCTTGAAGAC TACCAAACCA TCAACAAAAG ATTCACCACA
     ATGCTTCTGT GGTTGTTGTT GGAACTTCTG ATGGTTTGGT AGTTGTTTTC TAAGTGGTGT  d28

1921 GGAACCGACC TTAAGGGTGT CTACCTTATC CTTAAGTCCC AGAACGGTGA CGAGGCTTGG
     CCTTGGCTGG AATTCCCACA GATGGAATAG GAATTCAGGG TCTTGCCACT GCTCCGAACC d29

1981 GGTGACAACT TCATCATCCT TGAGATCTCC CCATCCGAGA AGCTTCTTTC CCCTGAACTT
     CCACTGTTGA AGTAGTAGGA ACTCTAGAGG GGTAGGCTCT TCGAAGAAAG GGGACTTGAA d30

2041 ATCAACACCA ACAACTGGAC CTCCACTGGT TCCACCAACA TCTCTGGTAA CACCTTGACC
     TAGTTGTGGT TGTTGACCTG GAGGTGACCA AGGTGGTTGT AGAGACCATT GTGGAACTGG d31

2101 TTGTACCAGG GTGGTAGAGG TATCTTGAAG CAAAACTTGC AACTTGACTC CTTCTCCACC
     AACATGGTCC CACCATCTCC ATAGAACTTC GTTTTGAACG TTGAACTGAG GAAGAGGTGG

2161 TACAGAGTCT ACTTCTCTGT GTCTGGTGAC GCTAACGTCA GAATCAGAAA CTCCAGAGAA
     ATGTCTCAGA TGAAGAGACA CAGACCACTG CGATTGCAGT CTTAGTCTTT GAGGTCTCTT d32

2221 GTCCTCTTCG AGAAGAGATA CATGTCTGGT GCCAAGGACG TCTCCGAGAT GTTCACCACC
     CAGGAGAAGC TCTTCTCTAT GTACAGACCA CGGTTCCTGC AGAGGCTCTA CAAGTGGTGG d33

2281 AAGTTCGAGA AGGACAACTT CTACATCGAG TTGTCCCAAG GTAACAACCT TTACGGTGGT
     TTCAAGCTCT TCCTGTTGAA GATGTAGCTC AACAGGGTTC CATTGTTGGA AATGCCACCA d34

2341 CCTATCGTCC ACTTCTATGA CGTCTCCATC AAATAAGAGC TC
     GGATAGCAGG TGAAGATACT GCAGAGGTAG TTTATTCTCG AG


Total number of bases is: 2382.
DNA sequence composition:   685 A;   665 C;   455 G;   577 T; 0 OTHER;
```

Figure 10S

```
            10         20         30         40         50         60
  1 CTCGAGATGA ACAAGAACAA CACCAAGTTG TCCACCAGAG CCTTGCCTTC CTTCATCGAC e1
    GAGCTCTACT TGTTCTTGTT GTGGTTCAAC AGGTGGTCTC GGAACGGAAG GAAGTAGCTG e2

 61 TACTTCAATG GTATCTACGG ATTCGCTACT GGTATCAAGG ACATCATGAA CATGATCTTC
    ATGAAGTTAC CATAGATGCC TAAGCGATGA CCATAGTTCC TGTAGTACTT GTACTAGAAG

121 AAGACTGACA CTGGTGGTGA TCTGACCCTT GACGAGATCT TGAAGAACCA ACAACTTCTG e3
    TTCTGACTGT GACCACCACT AGACTGGGAA CTGCTCTAGA ACTTCTTGGT TGTTGAAGAC e4

181 AACGACATCT CTGGTAAACT TGATGGTGTC AATGGTTCCT TGAACGACCT GATCGCACAG e5
    TTGCTGTAGA GACCATTTGA ACTACCACAG TTACCAAGGA ACTTGCTGGA CTAGCGTGTC e6

241 GGTAACCTTA ACACAGAACT TTCCAAGGAG ATCTTGAAGA TCGCTAACGA ACAGAACCAA e7
    CCATTGGAAT TGTGTCTTGA AAGGTTCCTC TAGAACTTCT AGCGATTGCT TGTCTTGGTT e8

301 GTCTTGAACG ACGTCAACAA CAAACTCGAT GCTATCAACA CCATGTTGAG AGTCTACTTG
    CAGAACTTGC TGCAGTTGTT GTTTGAGCTA CGATAGTTGT GGTACAACTC TCAGATGAAC

361 CCTAAGATCA CCTCCATGCT TTCCGACGTC ATGAAGCAGA ACTATGCTTT GTCTCTGCAA e9
    GGATTCTAGT GGAGGTACGA AAGGCTGCAG TACTTCGTCT TGATACGAAA CAGAGACGTT e10

421 ATCGAATACC TTTCCAAGCA ACTTCAAGAG ATCTCCGACA AGCTTGACAT CATCAACGTC e11
    TAGCTTATGG AAAGGTTCGT TGAAGTTCTC TAGAGGCTGT TCGAACTGTA GTAGTTGCAG e12

481 AACGTCTTGA TCAACTCCAC TTTGACCGAG ATCACTCCTG CTTACCAGAG AATCAAGTAC e13
    TTGCAGAACT AGTTGAGGTG AAACTGGCTC TAGTGAGGAC GAATGGTCTC TTAGTTCATG e14
block1
541 GTCAACGAGA AGTTCGAGGA GCTTACCTTC GCTACCGAAA CCTCCTCCAA GGTCAAGAAG
    CAGTTGCTCT TCAAGCTCCT CGAATGGAAG CGATGGCTTT GGAGGAGGTT CCAGTTCTTC

601 GACGGTTCTC CTGCTGACAT CCTCGACGAG TTGACCGAGT TGACCGAATT GGCTAAGTCC e15
    CTGCCAAGAG GACGACTGTA GGAGCTGCTC AACTGGCTCA ACTGGCTTAA CCGATTCAGG e16

661 GTCACCAAGA ACGACGTCGA TGGTTTCGAA TTCTACTTGA ACACCTTTCA TGACGTCATG e17
    CAGTGGTTCT TGCTGCAGCT ACCAAAGCTT AAGATGAACT TGTGGAAAGT ACTGCAGTAC e18

721 GTTGGTAACA ACCTTTTCGG TAGATCTGCA CTTAAGACTG CTTCTGAACT TATCACCAAG e19
    CAACCATTGT TGGAAAAGCC ATCTAGACGT GAATTCTGAC GAAGACTTGA ATAGTGGTTC e20

781 GAGAACGTGA AAACCTCTGG TTCCGAGGTT GGTAACGTCT ACAACTTCTT GATCGTCTTG
    CTCTTGCACT TTTGGAGACC AAGGCTCCAA CCATTGCAGA TGTTGAAGAA CTAGCAGAAC
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 841 ACAGCCTTGC AAGCTCAAGC TTTCTTGACC TTGACCACCT GTAGAAAGCT TCTTGGTCTT e21
     TGTCGGAACG TTCGAGTTCG AAAGAACTGG AACTGGTGGA CATCTTTCGA AGAACCAGAA e22

 901 GCTGACATCG ACTACACCTC CATCATGAAC GAACACCTTA ACAAGGAGAA GGAGGAGTTC e23
     CGACTGTAGC TGATGTGGAG GTAGTACTTG CTTGTGGAAT TGTTCCTCTT CCTCCTCAAG e24

 961 AGAGTCAACA TCTTGCCTAC TTTGTCCAAC ACCTTCTCCA ACCCTAACTA CGCTAAGGTC e25
     TCTCAGTTGT AGAACGGATG AAACAGGTTG TGGAAGAGGT TGGGATTGAT GCGATTCCAG e26
block2
1021 AAAGGATCCG ACGAAGACGC TAAGATGATC GTTGAAGCTA AACCTGGTCA CGCACTTATC
     TTTCCTAGGC TGCTTCTGCG ATTCTACTAG CAACTTCGAT TTGGACCAGT GCGTGAATAG

1081 GGTTTCGAAA TCTCCAACGA CTCCATCACC GTCCTTAAGG TCTACGAGGC TAAGTTGAAG e27
     CCAAAGCTTT AGAGGTTGCT GAGGTAGTGG CAGGAATTCC AGATGCTCCG ATTCAACTTC e28

1141 CAAAACTACC AGGTCGACAA GGACTCCCTT TCTGAGGTCA TCTACGGTGA CATGGACAAA e29
     GTTTTGATGG TCCAGCTGTT CCTGAGGGAA AGACTCCAGT AGATGCCACT GTACCTGTTT e30

1201 CTTCTTTGTC CAGACCAATC CGAACAAATC TACTACACCA ACAACATCGT CTTCCCTAAC e31
     GAAGAAACAG GTCTGGTTAG GCTTGTTTAG ATGATGTGGT TGTTGTAGCA GAAGGGATTG e32

1261 GAGTACGTCA TCACCAAGAT CGACTTCACC AAGAAGATGA AGACCCTTAG ATACGAGGTC
     CTCATGCAGT AGTGGTTCTA GCTGAAGTGG TTCTTCTACT TCTGGGAATC TATGCTCCAG

1321 ACTGCTAACT TCTACGACTC CTCCACTGGT GAGATCGATC TTAACAAGAA GAAGGTCGAG e33
     TGACGATTGA AGATGCTGAG GAGGTGACCA CTCTAGCTAG AATTGTTCTT CTTCCAGCTC e34

1381 TCCTCCGAAG CTGAGTACAG AACCCTTTCT GCTAACGACG ATGGTGTCTA CATGCCTCTT e35
     AGGAGGCTTC GACTCATGTC TTGGGAAAGA CGATTGCTGC TACCACAGAT GTACGGAGAA e36

1441 GGTGTCATCT CCGAGACCTT CCTTACTCCT ATCAATGGCT TCGGTTTGCA GGCTGACGAG e37
     CCACAGTAGA GGCTCTGGAA GGAATGAGGA TAGTTACCGA AGCCAAACGT CCGACTGCTC e38
block3
1501 AACTCCAGAC TTATCACCCT TACCTGCAAG TCCTACCTTA GAGAATTGCT CTTGGCTACC
     TTGAGGTCTG AATAGTGGGA ATGGACGTTC AGGATGGAAT CTCTTAACGA GAACCGATGG

1561 GACCTCTCTA ACAAGGAGAC CAAACTCATC GTCCCTCCTT CTGGTTTCAT CTCTAACATC e39
     CTGGAGAGAT TGTTCCTCTG GTTTGAGTAG CAGGGAGGAA GACCAAAGTA GAGATTGTAG e40

1621 GTCGAGAACG GTTCCATCGA AGAGGACAAC CTTGAGCCTT GGAAAGCTAA CAACAAGAAC e41
     CAGCTCTTGC CAAGGTAGCT TCTCCTGTTG GAACTCGGAA CCTTTCGATT GTTGTTCTTG e42
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    1681 GCTTACGTCG ACCACACTGG TGGTGTCAAC GGTACCAAGG CTCTTTACGT CCACAAGGAC e43
         CGAATGCAGC TGGTGTGACC ACCACAGTTG CCATGGTTCC GAGAAATGCA GGTGTTCCTG e44

    1741 GGTGGTATCT CCCAATTCAT CGGAGACAAA CTTAAACCTA AAACCGAGTA CGTCATCCAA
         CCACCATAGA GGGTTAAGTA GCCTCTGTTT GAATTTGGAT TTTGGCTCAT GCAGTAGGTT

    1801 TACACCGTCA AGGGTAAACC TTCCATCCAC CTTAAAGACG AAAACACTGG TTACATCCAC e45
         ATGTGGCAGT TCCCATTTGG AAGGTAGGTG GAATTTCTGC TTTTGTGACC AATGTAGGTG e46

    1861 TACGAAGACA CCAACAACAA CCTTGAAGAC TACCAAACCA TCAACAAAAG ATTCACCACA e47
         ATGCTTCTGT GGTTGTTGTT GGAACTTCTG ATGGTTTGGT AGTTGTTTTC TAAGTGGTGT e48

    1921 GGAACCGACC TTAAGGGTGT CTACCTTATC CTTAAGTCCC AGAACGGTGA CGAGGCTTGG e49
         CCTTGGCTGG AATTCCCACA GATGGAATAG GAATTCAGGG TCTTGCCACT GCTCCGAACC e50
Block4
    1981 GGTGACAACT TCATCATCCT TGAGATCTCC CCATCCGAGA AGCTTCTTTC CCCTGAACTT
         CCACTGTTGA AGTAGTAGGA ACTCTAGAGG GGTAGGCTCT TCGAAGAAAG GGGACTTGAA

    2041 ATCAACACCA ACAACTGGAC CTCCACTGGT TCCACCAACA TCTCTGGTAA CACCTTGACC e51
         TAGTTGTGGT TGTTGACCTG GAGGTGACCA AGGTGGTTGT AGAGACCATT GTGGAACTGG e52

    2101 TTGTACCAGG GTGGTAGAGG TATCTTGAAG CAAAACTTGC AACTTGACTC CTTCTCCACC e53
         AACATGGTCC CACCATCTCC ATAGAACTTC GTTTTGAACG TTGAACTGAG GAAGAGGTGG e54

    2161 TACAGAGTCT ACTTCTCTGT GTCTGGTGAC GCTAACGTCA GAATCAGAAA CTCCAGAGAA e55
         ATGTCTCAGA TGAAGAGACA CAGACCACTG CGATTGCAGT CTTAGTCTTT GAGGTCTCTT e56

    2221 GTCCTCTTCG AGAAGAGATA CATGTCTGGT GCCAAGGACG TCTCCGAGAT GTTCACCACC
         CAGGAGAAGC TCTTCTCTAT GTACAGACCA CGGTTCCTGC AGAGGCTCTA CAAGTGGTGG

    2281 AAGTTCGAGA AGGACAACTT CTACATCGAG TTGTCCCAAG GTAACAACCT TTACGGTGGT e57
         TTCAAGCTCT TCCTGTTGAA GATGTAGCTC AACAGGGTTC CATTGTTGGA AATGCCACCA e58

    2341 CCTATCGTCC ACTTCTATGA CGTCTCCATC AAATAAGAGC TC   e59
         GGATAGCAGG TGAAGATACT GCAGAGGTAG TTTATTCTCG AG   e60
Block5

Total number of bases is: 2382.
DNA sequence composition:   685 A;   665 C;   455 G;   577 T; 0 OTHER;
```

Figure 11S

```
           10         20         30         40         50         60
1   CTCGAGATGA ACAAGAACAA CACCAAGTTG TCCACCAGAG CCTTGCCTTC CTTCATCGAC
    GAGCTCTACT TGTTCTTGTT GTGGTTCAAC AGGTGGTCTC GGAACGGAAG GAAGTAGCTG

               ------------------->
61  TACTTCAATG GTATCTACGG ATTCGCTACT GGTATCAAGG ACATCATGAA CATGATCTTC e1
    ATGAAGTTAC CATAGATGCC TAAGCGATGA CCATAGTTCC TGTAGTACTT GTACTAGAAG e2
               <-------------------

121 AAGACTGACA CTGGTGGTGA TCTGACCCTT GACGAGATCT TGAAGAACCA ACAACTTCTG
    TTCTGACTGT GACCACCACT AGACTGGGAA CTGCTCTAGA ACTTCTTGGT TGTTGAAGAC

                                     ------------------->
181 AACGACATCT CTGGTAAACT TGATGGTGTC AATGGTTCCT TGAACGACCT GATCGCACAG e3
    TTGCTGTAGA GACCATTTGA ACTACCACAG TTACCAAGGA ACTTGCTGGA CTAGCGTGTC e4
                                     <-------------------

241 GGTAACCTTA ACACAGAACT TTCCAAGGAG ATCTTGAAGA TCGCTAACGA ACAGAACCAA
    CCATTGGAAT TGTGTCTTGA AAGGTTCCTC TAGAACTTCT AGCGATTGCT TGTCTTGGTT

                                                           ----------
301 GTCTTGAACG ACGTCAACAA CAAACTCGAT GCTATCAACA CCATGTTGAG AGTCTACTTG
    CAGAACTTGC TGCAGTTGTT GTTTGAGCTA CGATAGTTGT GGTACAACTC TCAGATGAAC  e6
                                                           <---------

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361 CCTAAGATCA CCTCCATGCT TTCCGACGTC ATGAAGCAGA ACTATGCTTT GTCTCTGCAA e5
    GGATTCTAGT GGAGGTACGA AAGGCTGCAG TACTTCGTCT TGATACGAAA CAGAGACGTT
    ----------

421 ATCGAATACC TTTCCAAGCA ACTTCAAGAG ATCTCCGACA AGCTTGACAT CATCAACGTC
    TAGCTTATGG AAAGGTTCGT TGAAGTTCTC TAGAGGCTGT TCGAACTGTA GTAGTTGCAG

                          ------------------->
481 AACGTCTTGA TCAACTCCAC TTTGACCGAG ATCACTCCTG CTTACCAGAG AATCAAGTAC e7
    TTGCAGAACT AGTTGAGGTG AAACTGGCTC TAGTGAGGAC GAATGGTCTC TTAGTTCATG e8
                          <-------------------

541 GTCAACGAGA AGTTCGAGGA GCTTACCTTC GCTACCGAAA CCTCCTCCAA GGTCAAGAAG
    CAGTTGCTCT TCAAGCTCCT CGAATGGAAG CGATGGCTTT GGAGGAGGTT CCAGTTCTTC

                                                ------------------->
601 GACGGTTCTC CTGCTGACAT CCTCGACGAG TTGACCGAGT TGACCGAATT GGCTAAGTCC e9
    CTGCCAAGAG GACGACTGTA GGAGCTGCTC AACTGGCTCA ACTGGCTTAA CCGATTCAGG e10
                                                <-------------------

661 GTCACCAAGA ACGACGTCGA TGGTTTCGAA TTCTACTTGA ACACCTTTCA TGACGTCATG
    CAGTGGTTCT TGCTGCAGCT ACCAAAGCTT AAGATGAACT TGTGGAAAGT ACTGCAGTAC

721 GTTGGTAACA ACCTTTTCGG TAGATCTGCA CTTAAGACTG CTTCTGAACT TATCACCAAG
    CAACCATTGT TGGAAAAGCC ATCTAGACGT GAATTCTGAC GAAGACTTGA ATAGTGGTTC

               ------------------->
781 GAGAACGTGA AAACCTCTGG TTCCGAGGTT GGTAACGTCT ACAACTTCTT GATCGTCTTG e11
    CTCTTGCACT TTTGGAGACC AAGGCTCCAA CCATTGCAGA TGTTGAAGAA CTAGCAGAAC e12
               <-------------------
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 841 ACAGCCTTGC AAGCTCAAGC TTTCTTGACC TTGACCACCT GTAGAAAGCT TCTTGGTCTT
     TGTCGGAACG TTCGAGTTCG AAAGAACTGG AACTGGTGGA CATCTTTCGA AGAACCAGAA
block 1
 901 GCTGACATCG ACTACACCTC CATCATGAAC GAACACCTTA ACAAGGAGAA GGAGGAGTTC e13
     CGACTGTAGC TGATGTGGAG GTAGTACTTG CTTGTGGAAT TGTTCCTCTT CCTCCTCAAG e14

 961 AGAGTCAACA TCTTGCCTAC TTTGTCCAAC ACCTTCTCCA ACCCTAACTA CGCTAAGGTC
     TCTCAGTTGT AGAACGGATG AAACAGGTTG TGGAAGAGGT TGGGATTGAT GCGATTCCAG

1021 AAAGGATCCG ACGAAGACGC TAAGATGATC GTTGAAGCTA AACCTGGTCA CGCACTTATC
     TTTCCTAGGC TGCTTCTGCG ATTCTACTAG CAACTTCGAT TTGGACCAGT GCGTGAATAG e16

1081 GGTTTCGAAA TCTCCAACGA CTCCATCACC GTCCTTAAGG TCTACGAGGC TAAGTTGAAG e15
     CCAAAGCTTT AGAGGTTGCT GAGGTAGTGG CAGGAATTCC AGATGCTCCG ATTCAACTTC

1141 CAAAACTACC AGGTCGACAA GGACTCCCTT TCTGAGGTCA TCTACGGTGA CATGGACAAA
     GTTTTGATGG TCCAGCTGTT CCTGAGGGAA AGACTCCAGT AGATGCCACT GTACCTGTTT

1201 CTTCTTTGTC CAGACCAATC CGAACAAATC TACTACACCA ACAACATCGT CTTCCCTAAC e17
     GAAGAAACAG GTCTGGTTAG GCTTGTTTAG ATGATGTGGT TGTTGTAGCA GAAGGGATTG e18

1261 GAGTACGTCA TCACCAAGAT CGACTTCACC AAGAAGATGA AGACCCTTAG ATACGAGGTC
     CTCATGCAGT AGTGGTTCTA GCTGAAGTGG TTCTTCTACT TCTGGGAATC TATGCTCCAG

1321 ACTGCTAACT TCTACGACTC CTCCACTGGT GAGATCGATC TTAACAAGAA GAAGGTCGAG e19
     TGACGATTGA AGATGCTGAG GAGGTGACCA CTCTAGCTAG AATTGTTCTT CTTCCAGCTC e20

1381 TCCTCCGAAG CTGAGTACAG AACCCTTTCT GCTAACGACG ATGGTGTCTA CATGCCTCTT
     AGGAGGCTTC GACTCATGTC TTGGGAAAGA CGATTGCTGC TACCACAGAT GTACGGAGAA

1441 GGTGTCATCT CCGAGACCTT CCTTACTCCT ATCAATGGCT TCGGTTTGCA GGCTGACGAG
     CCACAGTAGA GGCTCTGGAA GGAATGAGGA TAGTTACCGA AGCCAAACGT CCGACTGCTC e22

1501 AACTCCAGAC TTATCACCCT TACCTGCAAG TCCTACCTTA GAGAATTGCT CTTGGCTACC e21
     TTGAGGTCTG AATAGTGGGA ATGGACGTTC AGGATGGAAT CTCTTAACGA GAACCGATGG

1561 GACCTCTCTA ACAAGGAGAC CAAACTCATC GTCCCTCCTT CTGGTTTCAT CTCTAACATC
     CTGGAGAGAT TGTTCCTCTG GTTTGAGTAG CAGGGAGGAA GACCAAAGTA GAGATTGTAG

1621 GTCGAGAACG GTTCCATCGA AGAGGACAAC CTTGAGCCTT GGAAAGCTAA CAACAAGAAC e23
     CAGCTCTTGC CAAGGTAGCT TCTCCTGTTG GAACTCGGAA CCTTTCGATT GTTGTTCTTG e24
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   1681 GCTTACGTCG ACCACACTGG TGGTGTCAAC GGTACCAAGG CTCTTTACGT CCACAAGGAC
        CGAATGCAGC TGGTGTGACC ACCACAGTTG CCATGGTTCC GAGAAATGCA GGTGTTCCTG
block 2
   1741 GGTGGTATCT CCCAATTCAT CGGAGACAAA CTTAAACCTA AAACCGAGTA CGTCATCCAA e25
        CCACCATAGA GGGTTAAGTA GCCTCTGTTT GAATTTGGAT TTTGGCTCAT GCAGTAGGTT e26

   1801 TACACCGTCA AGGGTAAACC TTCCATCCAC CTTAAAGACG AAAACACTGG TTACATCCAC
        ATGTGGCAGT TCCCATTTGG AAGGTAGGTG GAATTTCTGC TTTTGTGACC AATGTAGGTG

   1861 TACGAAGACA CCAACAACAA CCTTGAAGAC TACCAAACCA TCAACAAAAG ATTCACCACA
        ATGCTTCTGT GGTTGTTGTT GGAACTTCTG ATGGTTTGGT AGTTGTTTTC TAAGTGGTGT e28

   1921 GGAACCGACC TTAAGGGTGT CTACCTTATC CTTAAGTCCC AGAACGGTGA CGAGGCTTGG e27
        CCTTGGCTGG AATTCCCACA GATGGAATAG GAATTCAGGG TCTTGCCACT GCTCCGAACC

   1981 GGTGACAACT TCATCATCCT TGAGATCTCC CCATCCGAGA AGCTTCTTTC CCCTGAACTT
        CCACTGTTGA AGTAGTAGGA ACTCTAGAGG GGTAGGCTCT TCGAAGAAAG GGGACTTGAA

   2041 ATCAACACCA ACAACTGGAC CTCCACTGGT TCCACCAACA TCTCTGGTAA CACCTTGACC e29
        TAGTTGTGGT TGTTGACCTG GAGGTGACCA AGGTGGTTGT AGAGACCATT GTGGAACTGG e30

   2101 TTGTACCAGG GTGGTAGAGG TATCTTGAAG CAAAACTTGC AACTTGACTC CTTCTCCACC
        AACATGGTCC CACCATCTCC ATAGAACTTC GTTTTGAACG TTGAACTGAG GAAGAGGTGG

   2161 TACAGAGTCT ACTTCTCTGT GTCTGGTGAC GCTAACGTCA GAATCAGAAA CTCCAGAGAA e31
        ATGTCTCAGA TGAAGAGACA CAGACCACTG CGATTGCAGT CTTAGTCTTT GAGGTCTCTT e32

   2221 GTCCTCTTCG AGAAGAGATA CATGTCTGGT GCCAAGGACG TCTCCGAGAT GTTCACCACC
        CAGGAGAAGC TCTTCTCTAT GTACAGACCA CGGTTCCTGC AGAGGCTCTA CAAGTGGTGG

   2281 AAGTTCGAGA AGGACAACTT CTACATCGAG TTGTCCCAAG GTAACAACCT TTACGGTGGT
        TTCAAGCTCT TCCTGTTGAA GATGTAGCTC AACAGGGTTC CATTGTTGGA AATGCCACCA e34

   2341 CCTATCGTCC ACTTCTATGA CGTCTCCATC AAATAAGAGC TC    e33
        GGATAGCAGG TGAAGATACT GCAGAGGTAG TTTATTCTCG AG
block3

Total number of bases is: 2382.
DNA sequence composition:    685 A;   665 C;   455 G;   577 T; 0 OTHER;
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