A

```
       F  E  R  F  I  D  K  N  R  S  D  M  P  D  I  D  L  D  F  D  D  E  L  R  W  K  I  P  A  H  A  R  K
      S  S  S  D  S  S  I  R  I  V  L  I  C  Q  T  L  I  W  T  L  M  M  N  S  A  G  K  F  R  H  T  P  G  R
       L  R  A  I  H  R  *  E  S  F  *  Y  A  R  H  *  S  G  L  *  *  *  T  P  L  E  N  S  G  T  R  Q  E
59501 TCTTCGAGCGATTCATCGATAAGAATCGTTCTGATATGCCAGACATTGATCTGGACTTTGATGATGAACTCCGCTGGAAAATTCCGGCACACGCCAGGAA
      ....:....|....:....|....:....|....:....|....:....|....:....|....:....|....:....|....:....|....:....|
      AGAAGCTCGCTAAGTAGCTATTCTTAGCAAGACTATACGGTCTGTAACTAGACCTGAAACTACTACTTGAGGCGACCTTTTAAGGCCGTGTGCGGTCCTT

       I  Y  G  N  E  N  V  A  N  V  A  N  H  I  T  Y  K  G  K  N  T  L  N  D  I  A  R  A  Y  G  F  A  Q
        F  M  E  M  K  T  S  P  T  S  Q  T  T  S  P  T  K  A  K  T  R  S  T  T  L  P  G  L  T  A  S  H  R
      D  L  W  K  *  K  R  R  Q  R  R  K  P  H  H  L  Q  R  Q  K  H  A  Q  R  H  C  Q  G  L  R  L  R  T  E
59601 GATTTATGGAAATGAAAACGTCGCCAACGTCGCAAACCACATCACCTACAAAGGCAAAAACACGCTCAACGACATTGCCAGGGCTTACGGCTTCGCACAG
      ....:....|....:....|....:....|....:....|....:....|....:....|....:....|....:....|....:....|....:....|
      CTAAATACCTTTACTTTTGCAGCGGTTGCAGCGTTTGGTGTAGTGGATGTTTCCGTTTTTGTGCGAGTTGCTGTAACGGTCCCGAATGCCGAAGCGTGTC

      K  T  F  D  A  I  A  K  R  C  P  D  R  V  E  T  D  T  R  L  G  N  A  I  L  D  V  V  T  A  Y  K  H  H
       K  L  S  T  P  L  L  K  D  V  Q  I  G  W  K  P  T  L  D  L  E  M  Q  F  S  M  L  S  R  R  I  S  I
        N  F  R  R  H  C  *  K  M  S  R  S  G  G  N  R  H  S  T  W  K  C  N  S  R  C  C  H  G  V  *  A  S
59701 AAAACTTTCGACGCCATTGCTAAAAGATGTCCAGATCGGGTGGAAACCGACACTCGACTTGGAAATGCAATTCTCGATGTTGTCACGGCGTATAAGCATC
      ....:....|....:....|....:....|....:....|....:....|....:....|....:....|....:....|....:....|....:....|
      TTTTGAAAGCTGCGGTAACGATTTTCTACAGGTCTAGCCCACCTTTGGCTGTGAGCTGAACCTTTACGTTAAGAGCTACAACAGTGCCGCATATTCGTAG

        P  E  I  S  K  L  L  D  T  Y  G  D  A  I  E  E  A  I  K  L  E  G  N  Q  H  S  M  G  I  H  A  G  G
      I  L  K  F  R  S  C  W  I  H  T  V  M  L  L  R  K  Q  S  N  S  R  E  T  S  I  R  W  E  F  M  L  A  G
       S  *  N  F  E  A  V  G  Y  I  R  *  C  Y  *  G  S  N  Q  T  R  G  K  P  A  F  D  G  N  S  C  W  R
59801 ATCCTGAAATTTCGAAGCTGTTGGATACATACGGTGATGCTATTGAGGAAGCAATCAAACTCGAGGGAAACCAGCATTCGATGGGAATTCATGCTGGCGG
      ....:....|....:....|....:....|....:....|....:....|....:....|....:....|....:....|....:....|....:....|
      TAGGACTTTAAAGCTTCGACAACCTATGTATGCCACTACGATAACTCCTTCGTTAGTTTGAGCTCCCTTTGGTCGTAAGCTACCCTTAAGTACGACCGCC

       F  V  I  A  S  D  P  I  P  E  V  C  P  I  Y  T  K  Y  K  G  Q  G  K  K  R  E  L  A  Q  I  I  P  Y
        S  L  L  L  R  T  L  F  Q  K  C  A  R  F  I  R  N  T  R  D  K  E  R  N  A  N  *  P  K  S  F  R  T
      V  R  Y  C  F  G  P  Y  S  R  S  V  P  D  L  Y  E  I  Q  G  T  R  K  E  T  R  T  S  P  N  H  S  V  R
59901 GTTCGTTATTGCTTCGGACCCTATTCCAGAAGTGTGCCCGATTTATACGAAATACAAGGGACAAGGAAAGAAACGCGAACTAGCCCAAATCATTCCGTAC
      ....:....|....:....|....:....|....:....|....:....|....:....|....:....|....:....|....:....|....:....|
      CAAGCAATAACGAAGCCTGGGATAAGGTCTTCACACGGGCTAAATATGCTTTATGTTCCCTGTTCCTTTCTTTGCGCTTGATCGGGTTTAGTAAGGCATG

      E  K  R  D  A  E  H  L  G  M  L  K  M  D  F  L  G  L  S  T  M  G  M  I  G  K  I  R  G  W  L  R  M  P
       K  N  E  M  Q  N  I  S  E  C  S  R  W  T  F  S  V  C  Q  Q  W  A  *  S  G  R  F  V  V  G  F  G  C
        K  T  R  C  R  T  S  R  N  A  Q  D  G  L  S  R  S  V  N  N  G  H  D  R  E  D  S  W  L  A  S  D  A
60001 GAAAAACGAGATGCAGAACATCTCGGAATGCTCAAGATGGACTTTCTCGGTCTGTCAACAATGGGCATGATCGGGAAGATTCGTGGTTGGCTTCGGATGC
      ....:....|....:....|....:....|....:....|....:....|....:....|....:....|....:....|....:....|....:....|
      CTTTTTGCTCTACGTCTTGTAGAGCCTTACGAGTTCTACCTGAAAGAGCCAGACAGTTGTTACCCGTACTAGCCCTTCTAAGCACCAACCGAAGCCTACG
```

B

```
        G  S  *  V  T  S  P  T  P  H  D  R  A  D  D  Y  M  E  L  R  K  R  W  L  N  R  Y  A  R  V  Q  A  Q
      E  A  H  K  *  L  V  L  P  L  M  I  A  Q  T  I  T  W  S  L  E  N  D  G  *  T  D  T  H  G  F  R  L  R
       R  L  I  S  D  *  S  Y  P  S  *  S  R  R  R  L  H  G  A  *  K  T  M  V  E  Q  I  R  T  G  S  G  S
11501 GAGGCTCATAAGTGACTAGTCCTACCCCTCATGATCGCGCAGACGATTACATGGAGCTTAGAAAACGATGGTTGAACAGATACGCACGGGTTCAGGCTCA
      ....:....|....:....|....:....|....:....|....:....|....:....|....:....|....:....|....:....|....:....|
      CTCCGAGTATTCACTGATCAGGATGGGGAGTACTAGCGCGTCTGCTAATGTACCTCGAATCTTTTGCTACCAACTTGTCTATGCGTGCCCAAGTCCGAGT

       A  D  K  K  L  R  D  A  L  I  Q  A  A  E  D  A  Y  K  Q  L  I  S  E  T  S  K  S  T  F  S  A  H  V
        P  T  R  N  S  G  M  L  L  F  K  Q  R  K  M  R  T  N  N  *  Y  R  R  L  Q  K  A  R  F  R  H  M  *
      G  R  Q  E  T  P  G  C  S  Y  S  S  S  G  R  C  V  Q  T  I  D  I  G  D  F  K  K  H  V  F  G  T  C  E
11601 GGCCGACAAGAAACTCCGGGATGCTCTTATTCAAGCAGCGGAAGATGCGTACAAACAATTGATATCGGAGACTTCAAAAAGCACGTTTTCGGCACATGTG
      ....:....|....:....|....:....|....:....|....:....|....:....|....:....|....:....|....:....|....:....|
      CCGGCTGTTCTTTGAGGCCCTACGAGAATAAGTTCGTCGCCTTCTACGCATGTTTGTTAACTATAGCCTCTGAAGTTTTTCGTGCAAAAGCCGTGTACAC

      K  S  A  Q  I  R  I  L  L  K  E  I  R  G  I  L  D  D  L  F  G  E  E  L  K  I  I  H  L  G  Q  S  D  A
       K  V  P  K  S  A  S  C  *  R  K  L  G  V  S  L  M  T  S  S  E  K  N  S  K  L  S  I  L  D  N  Q  T
        K  C  P  N  P  H  P  A  K  G  N  *  G  Y  P  *  *  P  L  R  R  R  T  Q  N  Y  P  S  W  T  I  R  R
11701 AAAAGTGCCCAAATCCGCATCCTGCTAAAGGAAATTAGGGGTATCCTTGATGACCTCTTCGGAGAAGAACTCAAAATTATCCATCTTGGACAATCAGACG
      ....:....|....:....|....:....|....:....|....:....|....:....|....:....|....:....|....:....|....:....|
      TTTTCACGGGTTTAGGCGTAGGACGATTTCCTTTAATCCCCATAGGAACTACTGGAGAAGCCTCTTCTTGAGTTTTAATAGGTAGAACCTGTTAGTCTGC
```

Figure S1