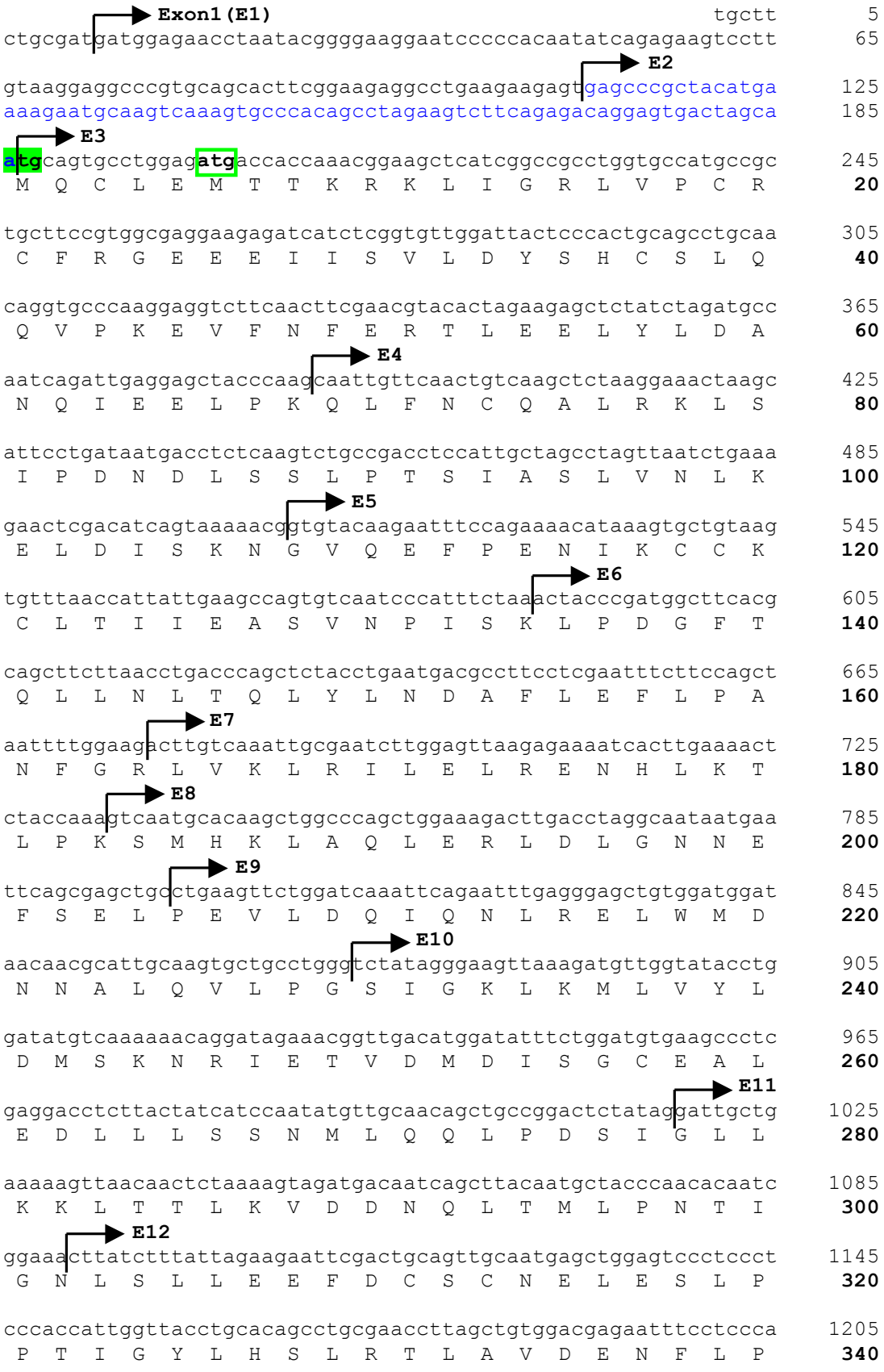
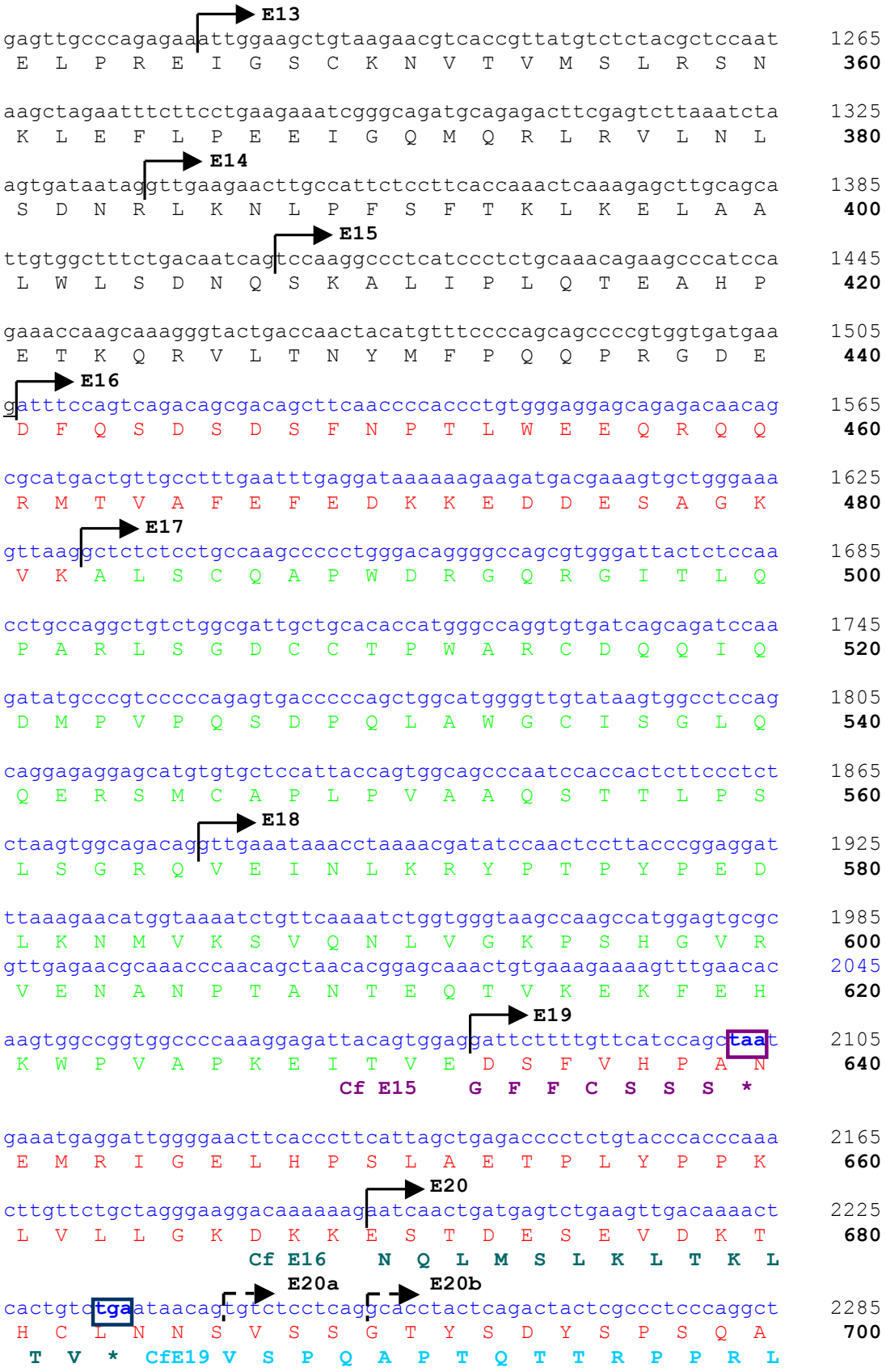
Supplemental Figure for online distribution.

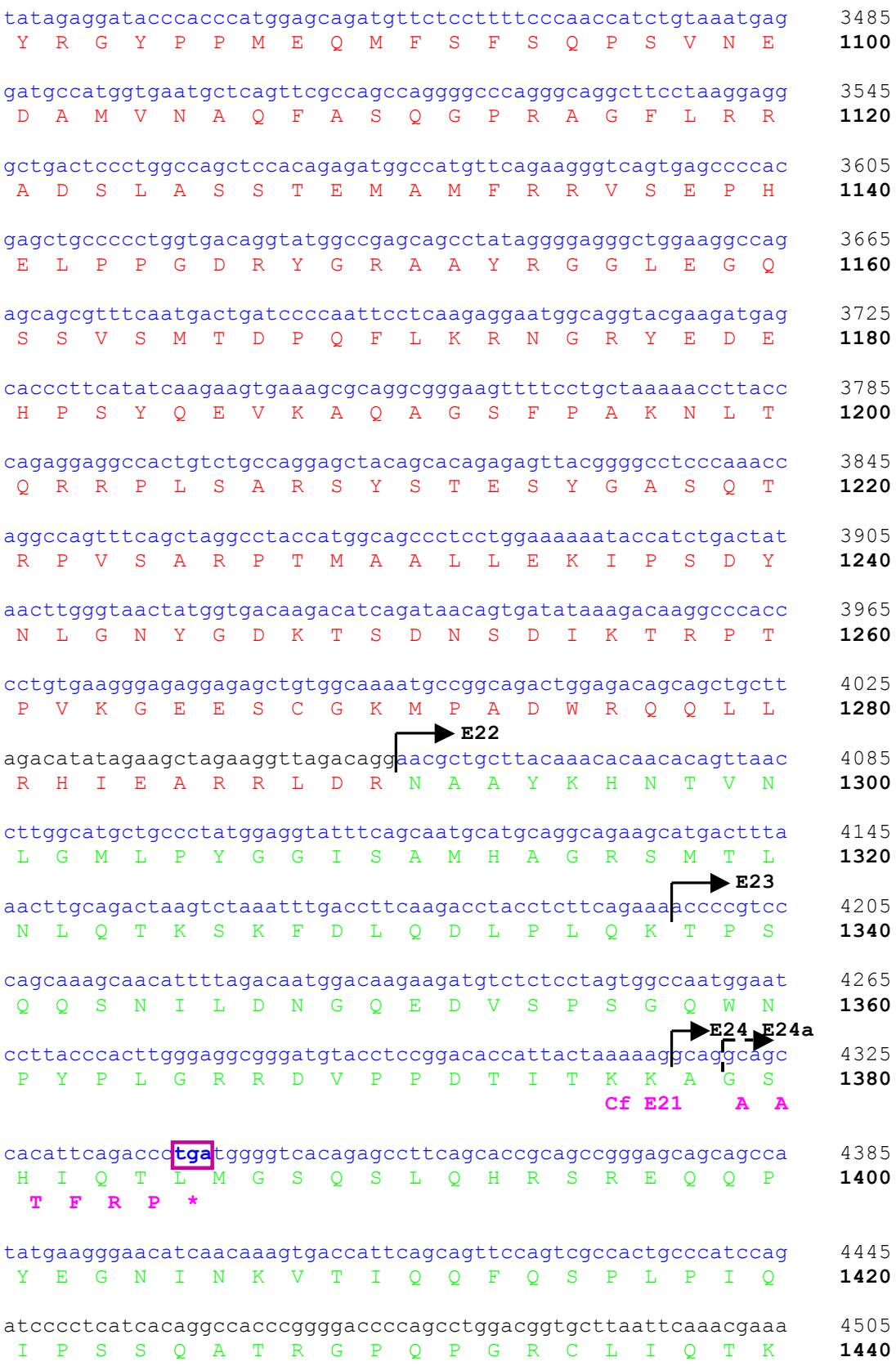


Supplemental Figure for online distribution.

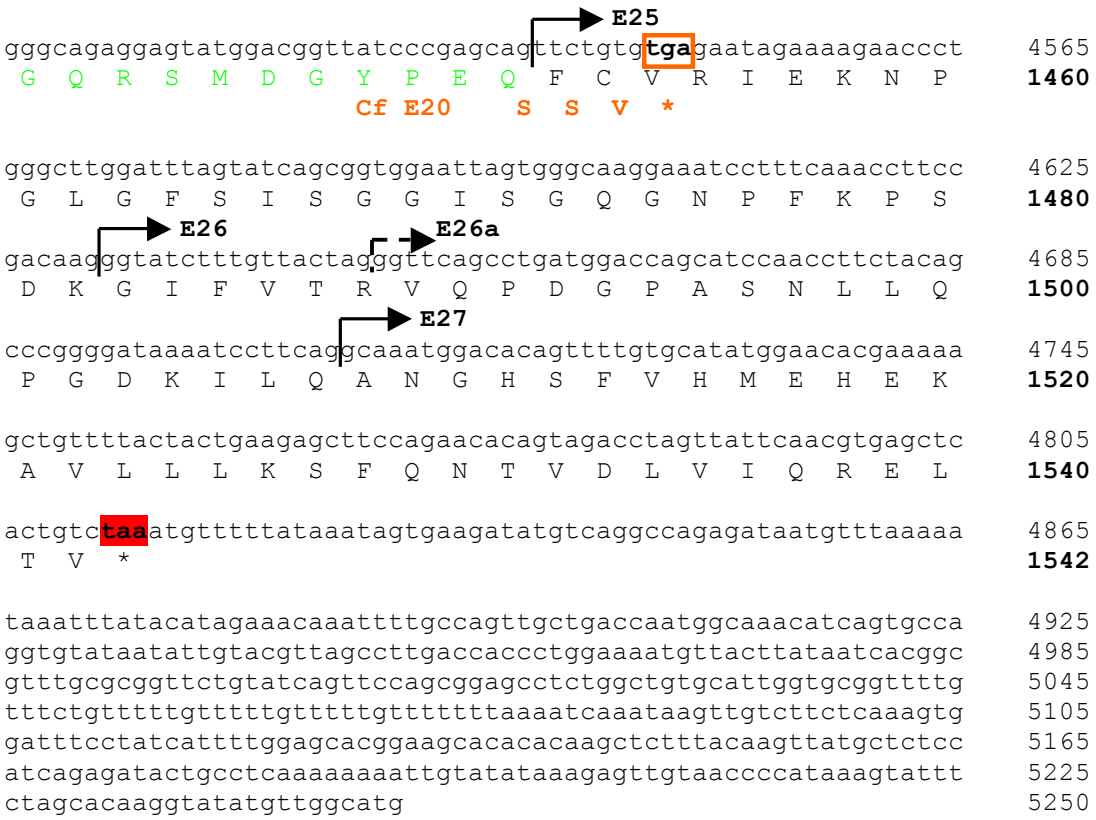


Supplemental Figure for online distribution.

```
tcctcagcatcctccaacacccgggtgaaagtggggtccttgcagccaacaactaaagat    2345
 S  S  A  S  S  N  T  R  V  K  V  G  S  L  Q  P  T  T  K  D     720
   P  Q  H  P  P  T  P  G  *

                                    E21
gccgtgcataactctttgtggggtaacaggattgcaccacctttcccacagcctctagat    2405
 A  V  H  N  S  L  W  G  N  R  I  A  P  P  F  P  Q  P  L  D     740

caaagccattactcacccaacgggaggctgtccctccagggaacctcccccagcgtcct    2465
 A  K  P  L  L  T  Q  R  E  A  V  P  P  G  N  L  P  Q  R  P     760

gatcggctgccaatgagtgatgctttccctgacaactggaccgatggctcccattacgat    2525
 D  R  L  P  M  S  D  A  F  P  D  N  W  T  D  G  S  H  Y  D     780

aacacaggttttgtctccgaggaagccacaggcgagaatgccaacaataaccctctctta    2585
 N  T  G  F  V  S  E  E  A  T  G  E  N  A  N  N  N  P  L  L     800

agctccaaggctagaagcgtacctgctcatgggcgcaggcctttaatcaggcaagaaagg    2645
 S  S  K  A  R  S  V  P  A  H  G  R  R  P  L  I  R  Q  E  R     820

attgtcggtgttcccctggaactggagcagtccacccacagacacacaccagaaacagaa    2705
 I  V  G  V  P  L  E  L  E  Q  S  T  H  R  H  T  P  E  T  E     840

gtgcctccttccaatccctggcagaattggaccagaacccccagtccatttgaggacagg    2765
 V  P  P  S  N  P  W  Q  N  W  T  R  T  P  S  P  F  E  D  R     860

actgcttttccctccaaattagaaacaacccctactaccagtcccttgcctgaaagaaaa    2825
 T  A  F  P  S  K  L  E  T  T  P  T  T  S  P  L  P  E  R  K     880

gaccacatgaaggagcctacagagacaccaggtccctttttctccgggagtgccatgggag    2885
 D  H  M  K  E  P  T  E  T  P  G  P  F  S  P  G  V  P  W  E     900

taccacgaccccacccccaaccggagtctcggtaatgtcttttctcaaatccactgccgc    2945
 Y  H  D  P  T  P  N  R  S  L  G  N  V  F  S  Q  I  H  C  R     920

ccagattcgtctaaaggtgttattgcaattagcaaaagcacggagaggctttccccgctc    3005
 P  D  S  S  K  G  V  I  A  I  S  K  S  T  E  R  L  S  P  L     940

atgaaagatataaagtccaacaagttcaaaaagtcccagagtattgatgagattgacgtc    3065
 M  K  D  I  K  S  N  K  F  K  K  S  Q  S  I  D  E  I  D  V     960

ggtacctacaaggtctataacattccactggaaaactatgcctctggaagcgatcactta    3125
 G  T  Y  K  V  Y  N  I  P  L  E  N  Y  A  S  G  S  D  H  L     980

ggaagccacgagcggccagacaagttcttgggaccagagcacggcatgtccagtatgtcc    3185
 G  S  H  E  R  P  D  K  F  L  G  P  E  H  G  M  S  S  M  S    1000

aggagccagtcggtacccatgctggatgacgaaatgctcatgtacggaagtagtaaaggc    3245
 R  S  Q  S  V  P  M  L  D  D  E  M  L  M  Y  G  S  S  K  G    1020

ccaccccaacaaaaagcatctatgactaagaaggtctatcagtttgaccaaagcttcaat    3305
 P  P  Q  Q  K  A  S  M  T  K  K  V  Y  Q  F  D  Q  S  F  N    1040

ccacaaggagcggtggaagtaaaagcagagaagaggatcccacccccttttgcacacaat    3365
 P  Q  G  A  V  E  V  K  A  E  K  R  I  P  P  P  F  A  H  N    1060

tctgagtatgtacaacagcccggtaaaaacatcgccaaggatctcgtcagccccagagcc    3425
 S  E  Y  V  Q  Q  P  G  K  N  I  A  K  D  L  V  S  P  R  A    1080
```


tatagaggatacccacccatggagcagatgttctccttttcccaaccatctgtaaatgag 3485
Y R G Y P P M E Q M F S F S Q P S V N E 1100
gatgccatggtgaatgctcagttcgccagccaggggcccagggcaggcttcctaaggagg 3545
D A M V N A Q F A S Q G P R A G F L R R 1120
gctgactccctggccagctccacagagatggccatgttcagaagggtcagtgagccccac 3605
A D S L A S S T E M A M F R R V S E P H 1140
gagctgccccctggtgacaggtatggccgagcagcctatagggagggctggaaggccag 3665
E L P P G D R Y G R A A Y R G G L E G Q 1160
agcagcgtttcaatgactgatccccaattcctcaagaggaatggcaggtacgaagatgag 3725
S S V S M T D P Q F L K R N G R Y E D E 1180
cacccttcatatcaagaagtgaaagcgcaggcgggaagttttcctgctaaaaaccttacc 3785
H P S Y Q E V K A Q A G S F P A K N L T 1200
cagaggaggccactgtctgccaggagctacagcacagagagttacggggcctcccaaacc 3845
Q R R P L S A R S Y S T E S Y G A S Q T 1220
aggccagtttcagctaggcctaccatggcagccctcctggaaaaaataccatctgactat 3905
R P V S A R P T M A A L L E K I P S D Y 1240
aacttgggtaactatggtgacaagacatcagataacagtgatataaagacaaggcccacc 3965
N L G N Y G D K T S D N S D I K T R P T 1260
cctgtgaagggagaggagagctgtggcaaaatgccggcagactggagacagcagctgctt 4025
P V K G E E S C G K M P A D W R Q Q L L 1280
E22
agacatatagaagctagaaggttagacaggaacgctgcttacaaacacaacacagttaac 4085
R H I E A R R L D R N A A Y K H N T V N 1300
cttggcatgctgccctatggaggtatttcagcaatgcatgcaggcagaagcatgacttta 4145
L G M L P Y G G I S A M H A G R S M T L 1320
E23
aacttgcagactaagtctaaatttgaccttcaagacctacctcttcagaaaaccccgtcc 4205
N L Q T K S K F D L Q D L P L Q K T P S 1340
cagcaaagcaacattttagacaatggacaagaagatgtctctcctagtggccaatggaat 4265
Q Q S N I L D N G Q E D V S P S G Q W N 1360
E24 E24a
ccttacccacttgggaggcgggatgtacctccggacaccattactaaaaaggcaggcagc 4325
P Y P L G R R D V P P D T I T K K A G S 1380
Cf E21 A A
cacattcagaccctgatggggtcacagagccttcagcaccgcagccgggagcagcagcca 4385
H I Q T L M G S Q S L Q H R S R E Q Q P 1400
T F R P *
tatgaagggaacatcaacaaagtgaccattcagcagttccagtcgccactgcccatccag 4445
Y E G N I N K V T I Q Q F Q S P L P I Q 1420
atcccctcatcacaggccacccggggacccccagcctggacggtgcttaattcaaacgaaa 4505
I P S S Q A T R G P Q P G R C L I Q T K 1440

Supplemental Figure for online distribution.



Notes:

1) The nucleotide sequence of the predicted longest mRNA variant of densin is shown along with the resulting amino acid sequence below. Nucleotides and amino acids are numbered at the right in normal and bold font, respectively, based on the longest theoretical sequence.

2) The beginning of each exon is indicated with a solid arrow and cryptic starts are indicated as dashed arrows. Each star site is labeled with the corresponding exon number (E#). The splice donor exon for the alternative splicing events is indicated by "Cf" (continues from).

3) Nucleotide sequences of exons that are known to be alternatively spliced are indicated in blue. The corresponding amino acid sequences are in red if skipping of the exon would shift the reading frame and in green if the reading frame remains the same.

4) The conventional start and stop codons for the longest variant are highlighted in solid green and red boxes, respectively. An alternative start codons due to frame shift splicing is indicated by an open green box. Novel stop codons created by frame shift splicing are indicated by open colored boxes to match a second line of colored amino acid sequence showing the novel downstream residues underneath the “normal” residues. [For the skipping of Exon21-24 (CfE20), the first novel amino acid is Ser which is encoded by the last two bases in E20 and the first base in E25: for simplicity, this Ser is shown under E25, along with the rest of the novel C-terminal domain.)