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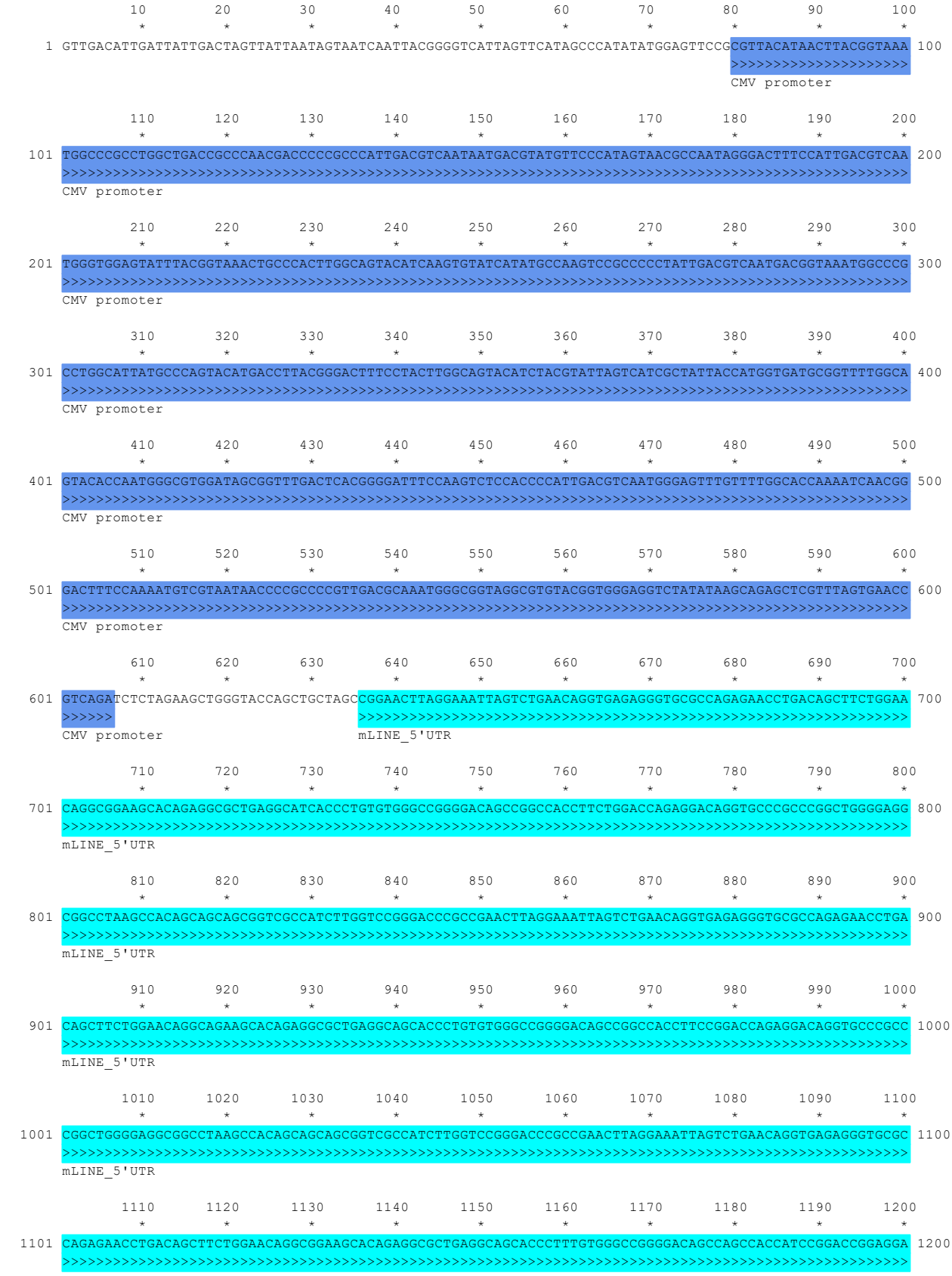

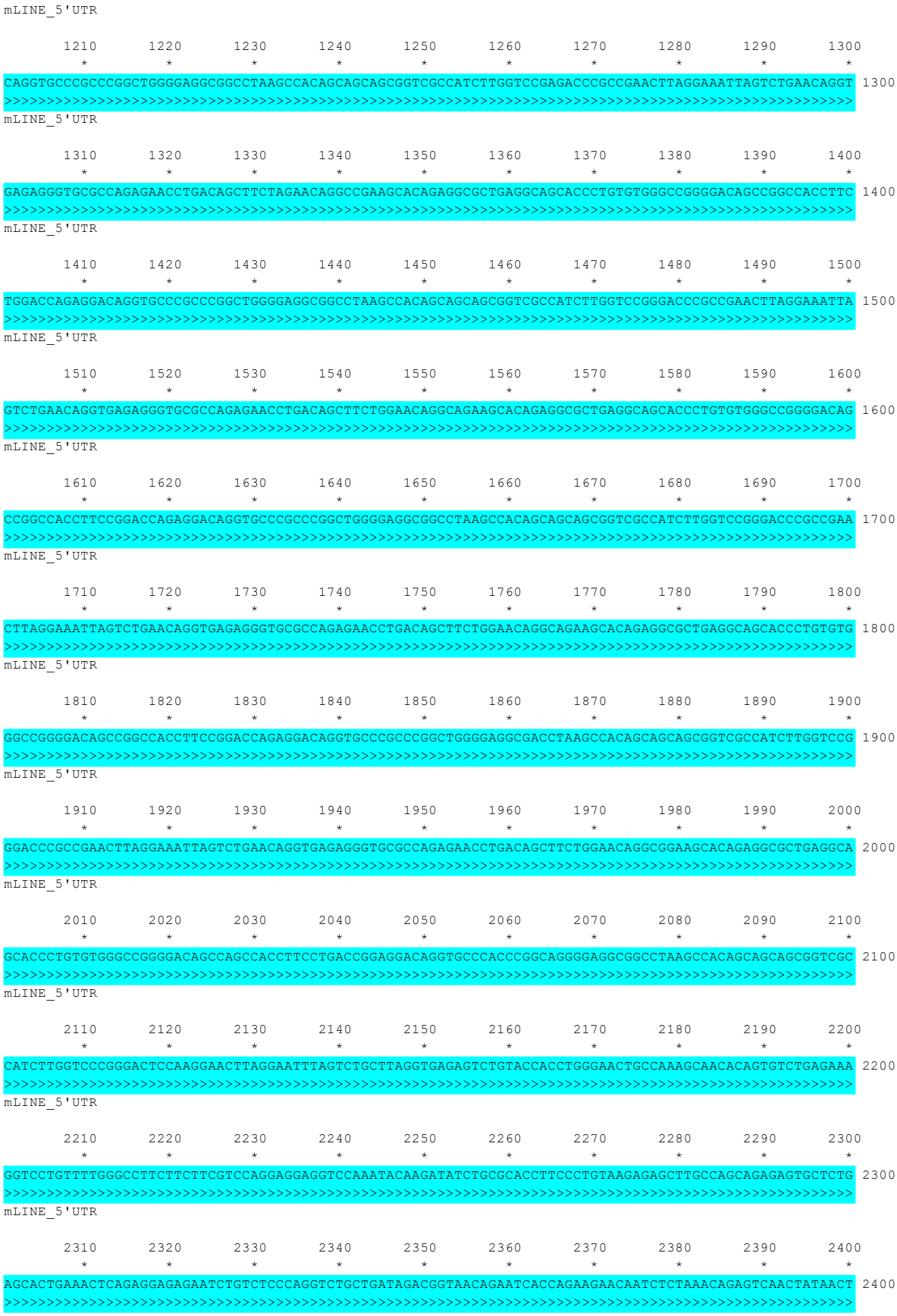
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     mORF1

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      S  L  K  E  I  Q  E  N  T  A  K  E  L  Q  V  L  K  E  K  Q  E  N  T  I  K  Q  V  E  V  L  T  E  K
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     mORF1

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     94
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     mORF1

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       E  I  E  T  L  G  K  K  S  G  T  I  D  L  S  I  S  N  R  I  Q  E  M  E  E  R  I  S  G  A  E  D  S
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     mORF1

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     194
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     mORF1

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     mORF1

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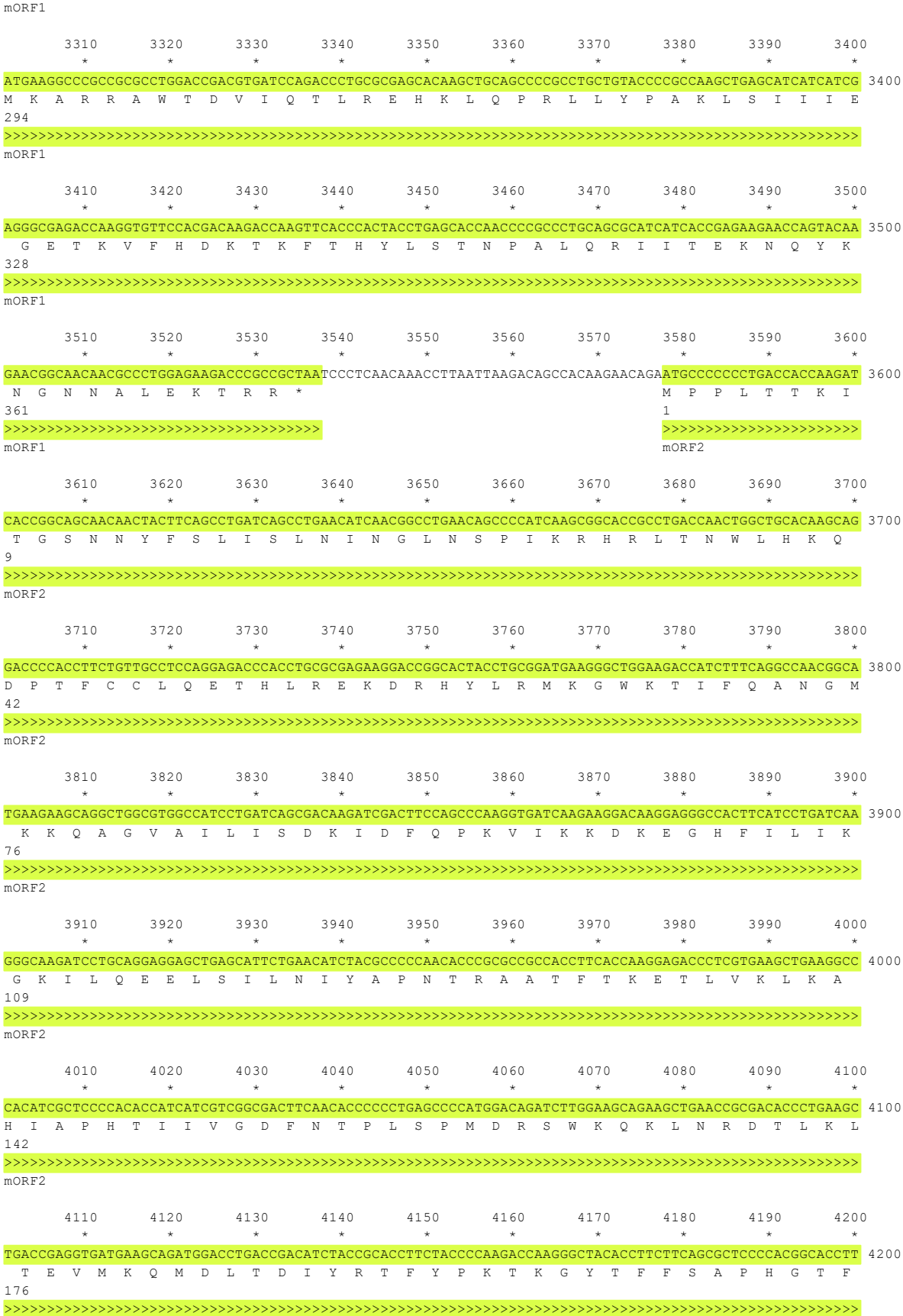
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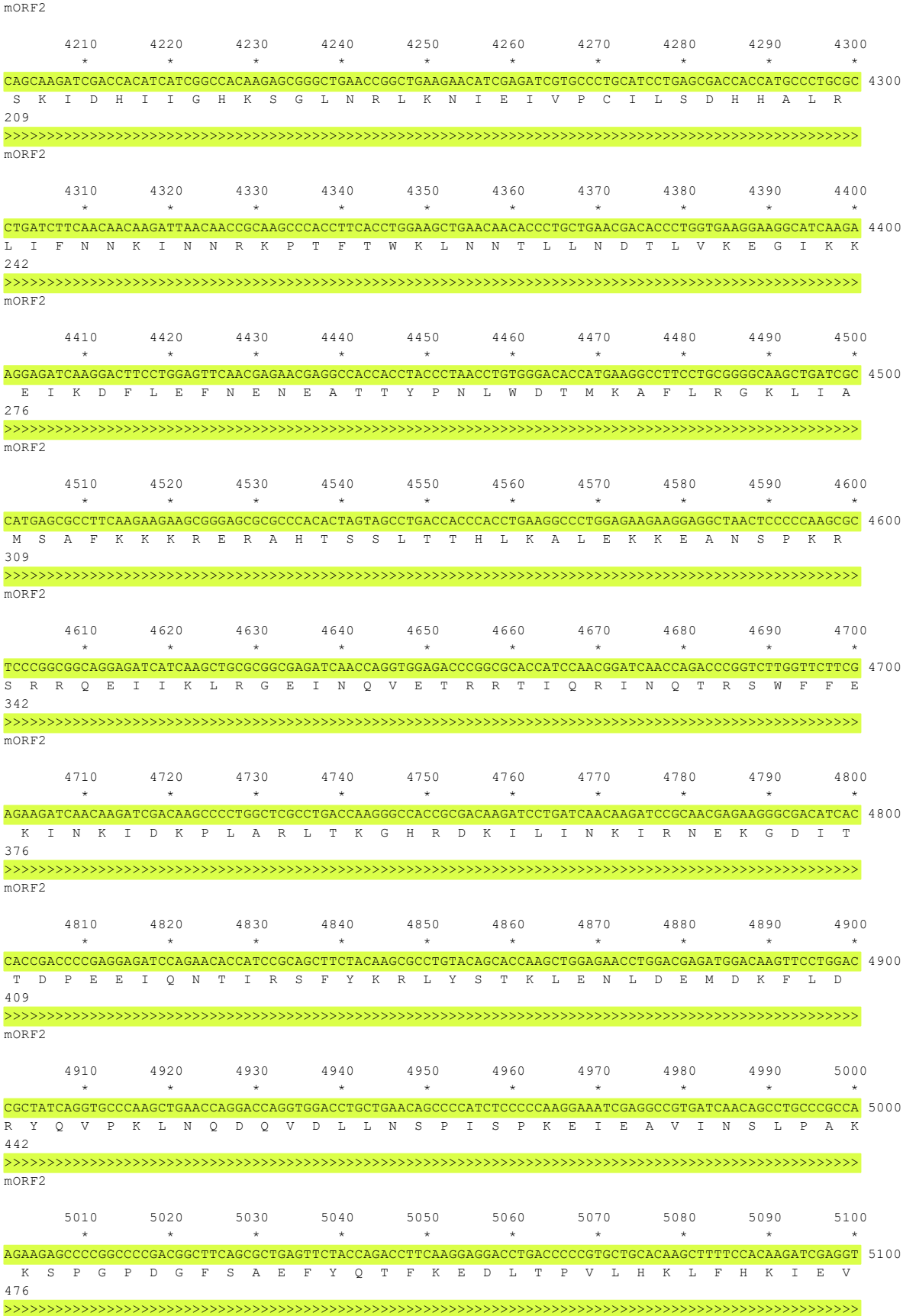
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309
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342
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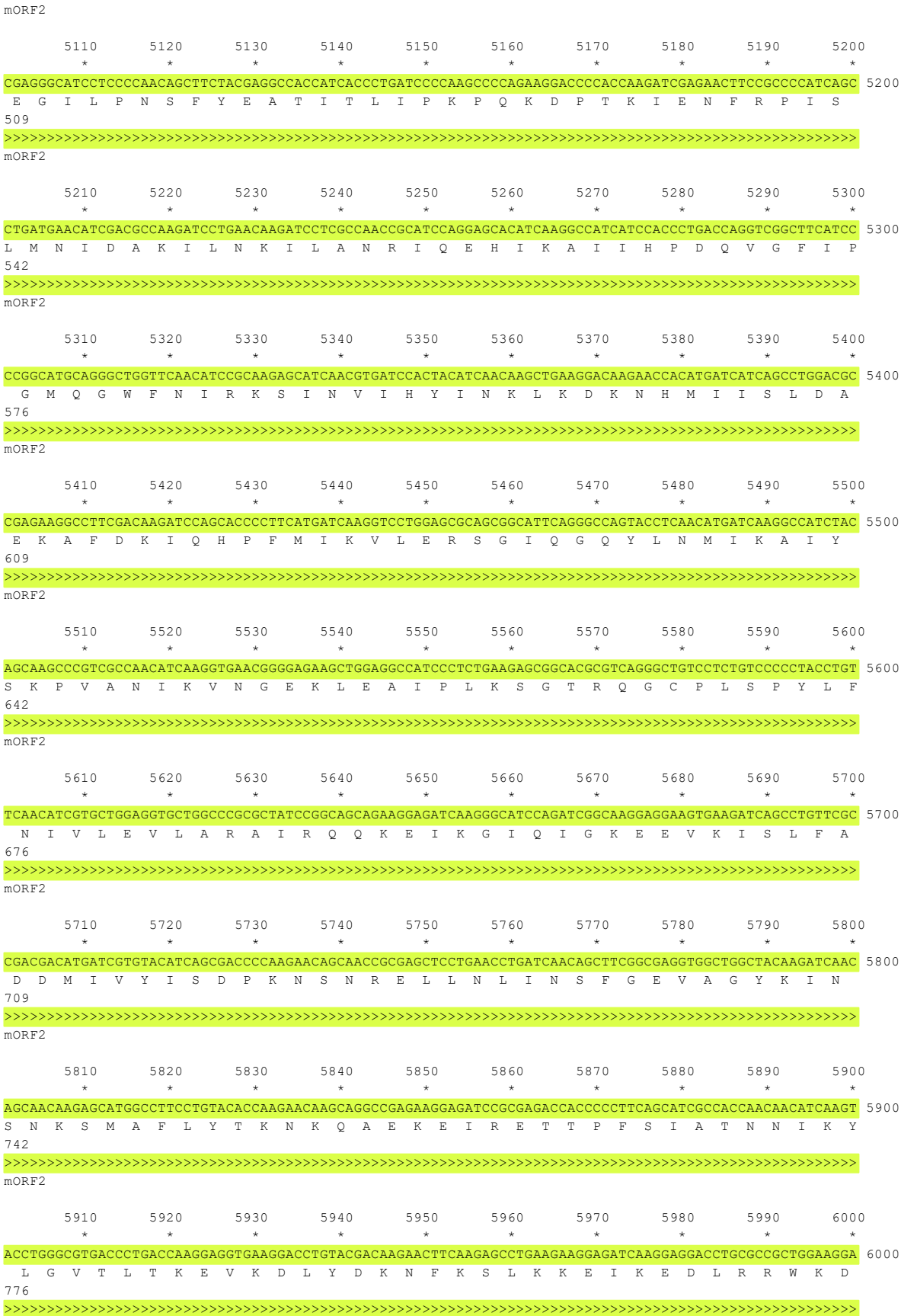
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709
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742
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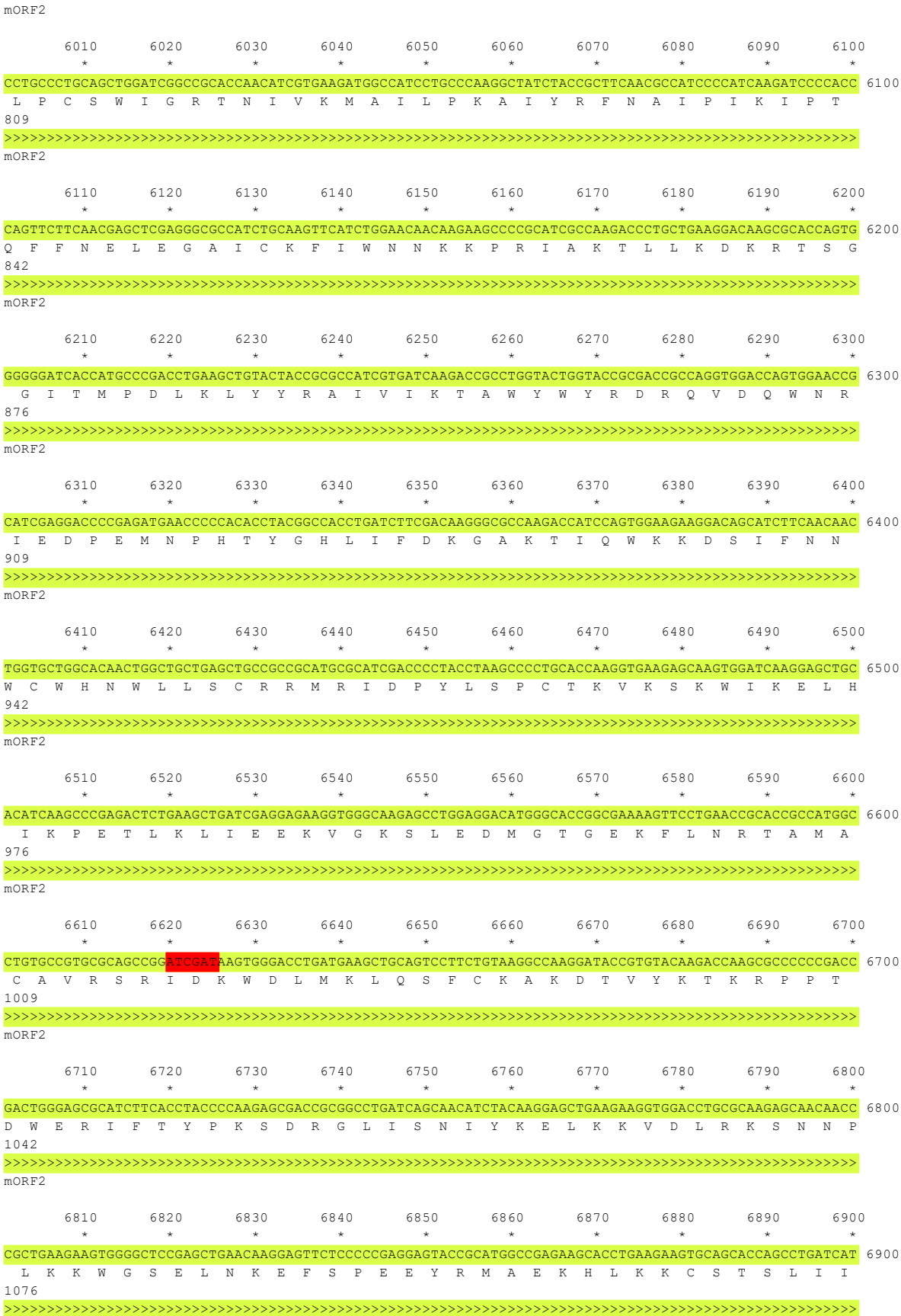
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876
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909
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1042
mORF2
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1076

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mORF2

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1109
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mORF2

       7010      7020      7030      7040      7050      7060      7070      7080      7090      7100
         *         *         *         *         *         *         *         *         *         *
7001 GGCGAGCGCGGCACCCTGCTGCACTGCTGGTGGGACTGTCGCCTGGTCCAGCCCCTGTGGAAGAGCGTGTGGCGGTTCCTGCGGAAGCTGGACATCGTGC 7100
G  E  R  G  T  L  L  H  C  W  W  D  C  R  L  V  Q  P  L  W  K  S  V  W  R  F  L  R  K  L  D  I  V  L
1142
>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>
mORF2

       7110      7120      7130      7140      7150      7160      7170      7180      7190      7200
         *         *         *         *         *         *         *         *         *         *
7101 TGCCCGAGGACCCCGCTATCCCCCTGCTGGGCATCTACCCTGAGGAGGCCCCCACCGGCAAGAAGGACACCTGCAGTACCATGTTCATCGCCGCTCTGTT 7200
  P  E  D  P  A  I  P  L  L  G  I  Y  P  E  E  A  P  T  G  K  K  D  T  C  S  T  M  F  I  A  A  L  F
1176
>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>
mORF2

       7210      7220      7230      7240      7250      7260      7270      7280      7290      7300
         *         *         *         *         *         *         *         *         *         *
7201 CATCATCGCCCGCAACTGGAAGGAGCCCCGCTGCCCCAGCACCGAGGAGTGGATTCAGAAGATGTGGTACATCTACACCATGGAGTACTACAGCGCCATC 7300
 I  I  A  R  N  W  K  E  P  R  C  P  S  T  E  E  W  I  Q  K  M  W  Y  I  Y  T  M  E  Y  Y  S  A  I
1209
>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>
mORF2

       7310      7320      7330      7340      7350      7360      7370      7380      7390      7400
         *         *         *         *         *         *         *         *         *         *
7301 AAGAAGAACGAGTTCATGAAGTTCCTGGCCAAGTGGATGGACCTGGAGAGCATCATCCTGAGCGAGGTGACCCAGAGCCAGCGCAACAGCCACAACATGT 7400
K  K  N  E  F  M  K  F  L  A  K  W  M  D  L  E  S  I  I  L  S  E  V  T  Q  S  Q  R  N  S  H  N  M  Y
1242
>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>
mORF2

       7410      7420      7430      7440      7450      7460      7470      7480      7490      7500
         *         *         *         *         *         *         *         *         *         *
7401 ACAGCCTGATCAGCGGCTACTAGCCCAAAACCTAGGATACCCACGATATAAGATACAATTTCCTAAACACATGAAACTCAAGAAAAATGAAGACTGAAGT 7500
  S  L  I  S  G  Y  *
1276
>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>
mORF2                  mLINE 3'UTR upstream for mneol

       7510      7520      7530      7540      7550      7560      7570      7580      7590      7600
         *         *         *         *         *         *         *         *         *         *
7501 GTGGACACTATGCCCCTCCTTAGAAGTGGGAACAAAACACCCATGGAAGGAGTTACAGAAACAAAGTTTGGAGCTGAGATGAAAGGAGGGACCATGTAGA 7600
>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>
mLINE 3'UTR upstream for mneol

       7610      7620      7630      7640      7650      7660      7670      7680      7690      7700
         *         *         *         *         *         *         *         *         *         *
7601 GACTGCCATATCCAGGGATCCACCCCATAATCAGCATCCAAACGCTGACACCATTGCATATACTAGCAAGATTTTATCGAAAGGACCCAGATGTAGCTGT 7700
>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>
mLINE 3'UTR upstream for mneol

       7710      7720      7730      7740      7750      7760      7770      7780      7790      7800
         *         *         *         *         *         *         *         *         *         *
7701 CTCTTGTGAGACTATGCCGGGGCCTAGCAAACACAGAAGTGGATGCTCACAGTCAGCTAATGGATGGATCACAGGGCTCCCAATGGAGGAGCTAGAGAAA 7800
>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>
mLINE 3'UTR upstream for mneol

       7810      7820      7830      7840      7850      7860      7870      7880      7890      7900
         *         *         *         *         *         *         *         *         *         *
7801 GTACCCAAGGAGCTAAAGGGATCTGCAACCCTATAGGTGGAACAACATTATGAACTAACCAGTACCCCTGAGCTCTTGACTCTAGCTGCATATGTATCAA 7900
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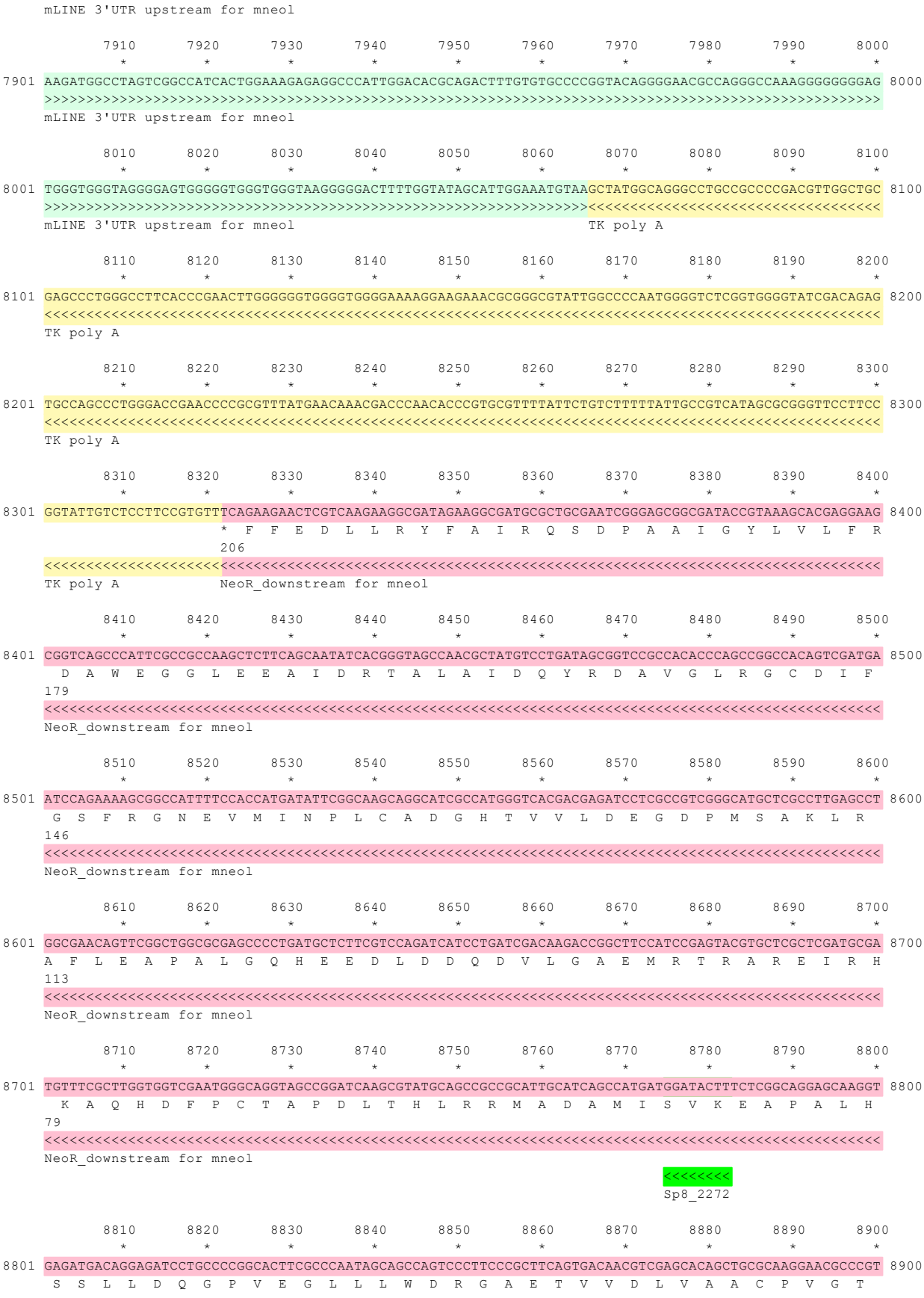
mLINE 3'UTR upstream for mneol
7910 7920 7930 7940 7950 7960 7970 7980 7990 8000
7901 AAGATGGCCTAGTCGGCCATCACTGGAAAGAGAGGCCCATTGGACACGCAGACTTTGTGTGCCCCGGTACAGGGGAACGCCAGGGCCAAAGGGGGGGGAG 8000
mLINE 3'UTR upstream for mneol
8010 8020 8030 8040 8050 8060 8070 8080 8090 8100
8001 TGGGTGGGTAGGGGAGTGGGGGTGGGTGGGTAAGGGGGACTTTTGGTATAGCATTGGAAATGTAAGCTATGGCAGGGCCTGCCGCCCCGACGTTGGCTGC 8100
mLINE 3'UTR upstream for mneol
TK poly A
8110 8120 8130 8140 8150 8160 8170 8180 8190 8200
8101 GAGCCCTGGGCCTTCACCCGAACTTGGGGGGTGGGGTGGGGAAAAGGAAGAAACGCGGGCGTATTGGCCCCAATGGGGTCTCGGTGGGGTATCGACAGAG 8200
TK poly A
8210 8220 8230 8240 8250 8260 8270 8280 8290 8300
8201 TGCCAGCCCTGGGACCGAACCCCGCGTTTATGAACAAACGACCCAACACCCGTGCGTTTTATTCTGTCTTTTTATTGCCGTCATAGCGCGGGTTCCTTCC 8300
TK poly A
8310 8320 8330 8340 8350 8360 8370 8380 8390 8400
8301 GGTATTGTCTCCTTCCGTGTTTCAGAAGAACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAATCGGGAGCGGCGATACCGTAAAGCACGAGGAAG 8400
* F F E D L L R Y F A I R Q S D P A A I G Y L V L F R
206
TK poly A
NeoR_downstream for mneol
8410 8420 8430 8440 8450 8460 8470 8480 8490 8500
8401 CGGTCAGCCCATTCGCCGCCAAGCTCTTCAGCAATATCACGGGTAGCCAACGCTATGTCCTGATAGCGGTCCGCCACACCCAGCCGGCCACAGTCGATGA 8500
D A W E G G L E E A I D R T A L A I D Q Y R D A V G L R G C D I F
179
NeoR_downstream for mneol
8510 8520 8530 8540 8550 8560 8570 8580 8590 8600
8501 ATCCAGAAAAGCGGCCATTTTCCACCATGATATTCGGCAAGCAGGCATCGCCATGGGTCACGACGAGATCCTCGCCGTCGGGCATGCTCGCCTTGAGCCT 8600
G S F R G N E V M I N P L C A D G H T V V L D E G D P M S A K L R
146
NeoR_downstream for mneol
8610 8620 8630 8640 8650 8660 8670 8680 8690 8700
8601 GGCGAACAGTTCGGCTGGCGCGAGCCCCTGATGCTCTTCGTCCAGATCATCCTGATCGACAAGACCGGCTTCCATCCGAGTACGTGCTCGCTCGATGCGA 8700
A F L E A P A L G Q H E E D L D D Q D V L G A E M R T R A R E I R H
113
NeoR_downstream for mneol
8710 8720 8730 8740 8750 8760 8770 8780 8790 8800
8701 TGTTTCGCTTGGTGGTCGAATGGGCAGGTAGCCGGATCAAGCGTATGCAGCCGCCGCATTGCATCAGCCATGATGGATACTTTCTCGGCAGGAGCAAGGT 8800
K A Q H D F P C T A P D L T H L R R M A D A M I S V K E A P A L H
79
NeoR_downstream for mneol
Sp8_2272
8810 8820 8830 8840 8850 8860 8870 8880 8890 8900
8801 GAGATGACAGGAGATCCTGCCCCGGCACTTCGCCCAATAGCAGCCAGTCCCTTCCCGCTTCAGTGACAACGTCGAGCACAGCTGCGCAAGGAACGCCCGT 8900
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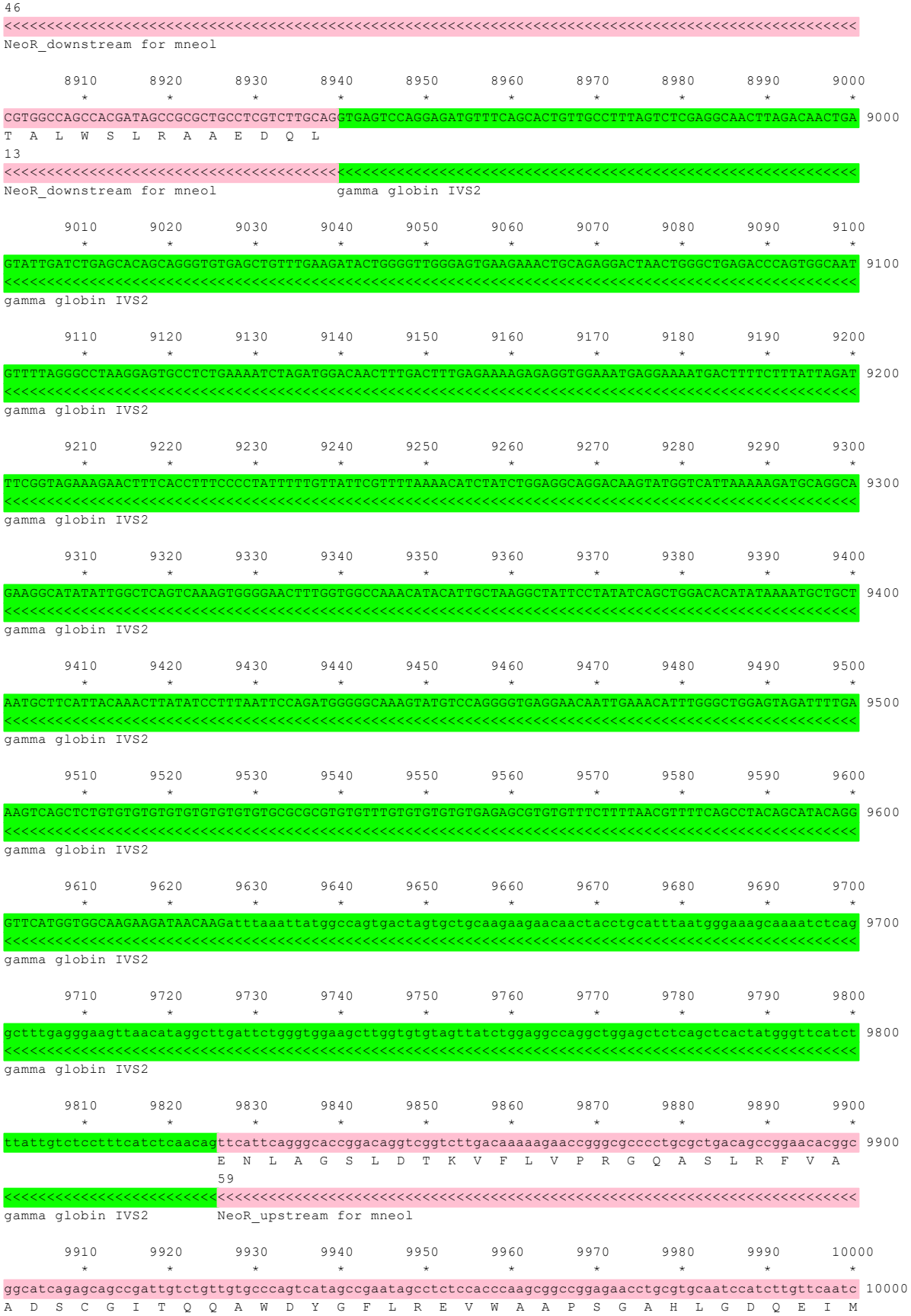
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NeoR_downstream for mneol
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T A L W S L R A A E D Q L
13
NeoR_downstream for mneol
gamma globin IVS2
9010 9020 9030 9040 9050 9060 9070 9080 9090 9100
9001 GTATTGATCTGAGCACAGCAGGGTGTGAGCTGTTTGAAGATACTGGGGTTGGGAGTGAAGAAACTGCAGAGGACTAACTGGGCTGAGACCCAGTGGCAAT 9100
gamma globin IVS2
9110 9120 9130 9140 9150 9160 9170 9180 9190 9200
9101 GTTTTAGGGCCTAAGGAGTGCCTCTGAAAATCTAGATGGACAACTTTGACTTTGAGAAAAGAGAGGTGGAAATGAGGAAAATGACTTTTCTTTATTAGAT 9200
gamma globin IVS2
9210 9220 9230 9240 9250 9260 9270 9280 9290 9300
9201 TTCGGTAGAAAGAACTTTCACCTTTCCCCTATTTTTGTTATTCGTTTTAAAACATCTATCTGGAGGCAGGACAAGTATGGTCATTAAAAAGATGCAGGCA 9300
gamma globin IVS2
9310 9320 9330 9340 9350 9360 9370 9380 9390 9400
9301 GAAGGCATATATTGGCTCAGTCAAAGTGGGGAACTTTGGTGGCCAAACATACATTGCTAAGGCTATTCCTATATCAGCTGGACACATATAAAATGCTGCT 9400
gamma globin IVS2
9410 9420 9430 9440 9450 9460 9470 9480 9490 9500
9401 AATGCTTCATTACAAACTTATATCCTTTAATTCCAGATGGGGGCAAAGTATGTCCAGGGGTGAGGAACAATTGAAACATTTGGGCTGGAGTAGATTTTGA 9500
gamma globin IVS2
9510 9520 9530 9540 9550 9560 9570 9580 9590 9600
9501 AAGTCAGCTCTGTGTGTGTGTGTGTGTGTGTGCGCGCGTGTGTTTGTGTGTGTGTGAGAGCGTGTGTTTCTTTTAACGTTTTCAGCCTACAGCATACAGG 9600
gamma globin IVS2
9610 9620 9630 9640 9650 9660 9670 9680 9690 9700
9601 GTTCATGGTGGCAAGAAGATAACAAGatttaaattatggccagtgactagtgctgcaagaagaacaactacctgcatttaatgggaaagcaaaatctcag 9700
gamma globin IVS2
9710 9720 9730 9740 9750 9760 9770 9780 9790 9800
9701 gctttgagggaagttaacataggcttgattctgggtggaagcttggtgtgtagttatctggaggccaggctggagctctcagctcactatgggttcatct 9800
gamma globin IVS2
9810 9820 9830 9840 9850 9860 9870 9880 9890 9900
9801 ttattgtctcctttcatctcaacagttcattcagggcaccggacaggtcggtcttgacaaaaagaaccgggcgcccctgcgctgacagccggaacacggc 9900
E N L A G S L D T K V F L V P R G Q A S L R F V A
59
gamma globin IVS2
NeoR_upstream for mneol
9910 9920 9930 9940 9950 9960 9970 9980 9990 10000
9901 ggcatcagagcagccgattgtctgttgtgcccagtcatagccgaatagcctctccacccaagcggccggagaacctgcgtgcaatccatcttgttcaatc 10000
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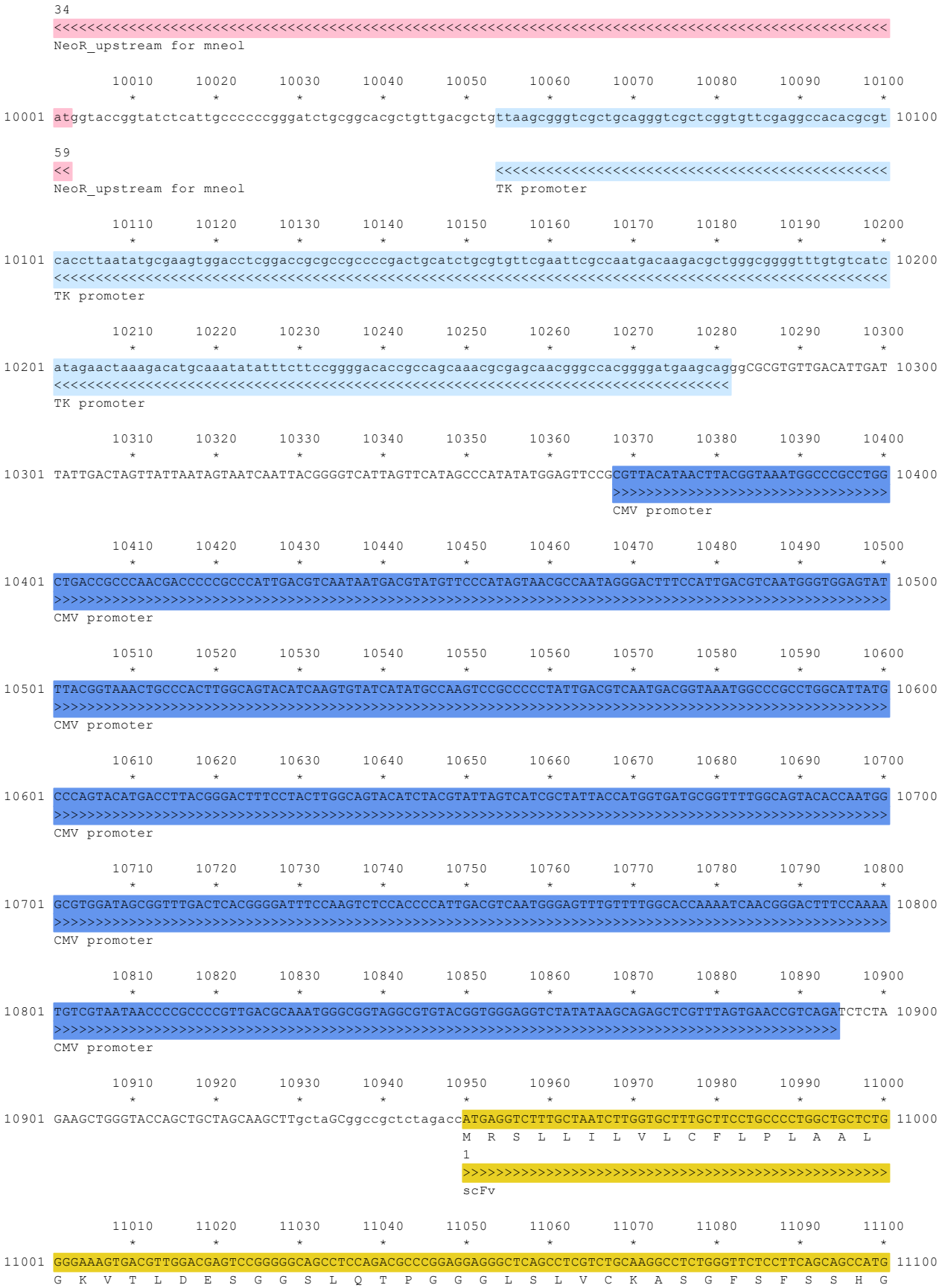
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10001 atggtaccggtatctcattgccccccgggatctgcggcacgctgttgacgctgttaagcgggtcgctgcagggtcgctcggtgttcgaggccacacgcgt 10100
59
NeoR_upstream for mneol
TK promoter
10110 10120 10130 10140 10150 10160 10170 10180 10190 10200
10101 caccttaatatgcgaagtggacctcggaccgcgccgccccgactgcatctgcgtgttcgaattcgccaatgacaagacgctgggcggggtttgtgtcatc 10200
TK promoter
10210 10220 10230 10240 10250 10260 10270 10280 10290 10300
10201 atagaactaaagacatgcaaatatatttcttccggggacaccgccagcaaacgcgagcaacgggccacggggatgaagcaggCGCGTGTTGACATTGAT 10300
TK promoter
10310 10320 10330 10340 10350 10360 10370 10380 10390 10400
10301 TATTGACTAGTTATTAATAGTAATCAATTACGGGGTCATTAGTTCATAGCCCATATATGGAGTTCCGCGTTACATAACTTACGGTAAATGGCCCGCCTGG 10400
CMV promoter
10410 10420 10430 10440 10450 10460 10470 10480 10490 10500
10401 CTGACCGCCCAACGACCCCCGCCCATTGACGTCAATAATGACGTATGTTCCCATAGTAACGCCAATAGGGACTTTCCATTGACGTCAATGGGTGGAGTAT 10500
CMV promoter
10510 10520 10530 10540 10550 10560 10570 10580 10590 10600
10501 TTACGGTAAACTGCCCACTTGGCAGTACATCAAGTGTATCATATGCCAAGTCCGCCCCCTATTGACGTCAATGACGGTAAATGGCCCGCCTGGCATTATG 10600
CMV promoter
10610 10620 10630 10640 10650 10660 10670 10680 10690 10700
10601 CCCAGTACATGACCTTACGGGACTTTCCTACTTGGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGATGCGGTTTTGGCAGTACACCAATGG 10700
CMV promoter
10710 10720 10730 10740 10750 10760 10770 10780 10790 10800
10701 GCGTGGATAGCGGTTTGACTCACGGGGATTTCCAAGTCTCCACCCCATTGACGTCAATGGGAGTTTGTTTTGGCACCAAAATCAACGGGACTTTCCAAAA 10800
CMV promoter
10810 10820 10830 10840 10850 10860 10870 10880 10890 10900
10801 TGTCGTAATAACCCCGCCCCGTTGACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGCAGAGCTCGTTTAGTGAACCGTCAGATCTCTA 10900
CMV promoter
10910 10920 10930 10940 10950 10960 10970 10980 10990 11000
10901 GAAGCTGGGTACCAGCTGCTAGCAAGCTTgctaGCggccgctctagaccATGAGGTCTTTGCTAATCTTGGTGCTTTGCTTCCTGCCCCTGGCTGCTCTG 11000
M R S L L I L V L C F L P L A A L
1
scFv
11010 11020 11030 11040 11050 11060 11070 11080 11090 11100
11001 GGGAAAGTGACGTTGGACGAGTCCGGGGGCAGCCTCCAGACGCCCGGAGGAGGGCTCAGCCTCGTCTGCAAGGCCTCTGGGTTCTCCTTCAGCAGCCATG 11100
G K V T L D E S G G G S L Q T P G G G L S L V C K A S G F S F S S H G

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          18
          >>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>
          scFv

                 11110      11120      11130      11140      11150      11160      11170      11180      11190      11200
                     *          *          *          *          *          *          *          *          *          *
    11101 GCATGGGCTGGGTGCGCCAGGCGCCTGGCAGAGGGCTGGAGTGGGTCGGTCTTATTAGCGGTGCTGGTAGTAGCACAAGATACGGGTCGGCGGTGCAGGG 11200
            M  G  W  V  R  Q  A  P  G  R  G  L  E  W  V  G  L  I  S  G  A  G  S  S  T  R  Y  G  S  A  V  Q  G
          52
          >>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>
          scFv

                 11210      11220      11230      11240      11250      11260      11270      11280      11290      11300
                     *          *          *          *          *          *          *          *          *          *
    11201 CCGTGCCACCATCTCGAGGGACAACGGGCAGAGCACAGTGAGGCTGCAGCTGAACAACCTCAGGGCTGAGGACACCGGCACCTACTACTGCGCCAAAGCT 11300
           R  A  T  I  S  R  D  N  G  Q  S  T  V  R  L  Q  L  N  N  L  R  A  E  D  T  G  T  Y  Y  C  A  K  A
          85
          >>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>
          scFv

                 11310      11320      11330      11340      11350      11360      11370      11380      11390      11400
                     *          *          *          *          *          *          *          *          *          *
    11301 GCTGATACTGTTTACGATGATGATGATACTTATATAAGTGCTGATAATATCGACACGTGGGGCCACGGGACCGAAGTCATCGTGTCGACAGGTGGAGGCG 11400
          A  D  T  V  Y  D  D  D  D  T  Y  I  S  A  D  N  I  D  T  W  G  H  G  T  E  V  I  V  S  T  G  G  G  G
          118
          >>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>
          scFv

                 11410      11420      11430      11440      11450      11460      11470      11480      11490      11500
                     *          *          *          *          *          *          *          *          *          *
    11401 GCTCTGGTGGCGGTGGCAGTGGCGGCGGAGGTTCTGACGTCGCGCTGACTCAGCCGGCCTCGGTGTCAGCAAACCTGGGAGGAACCGTCGAGATCACCTG 11500
            S  G  G  G  G  S  G  G  G  G  S  D  V  A  L  T  Q  P  A  S  V  S  A  N  L  G  G  T  V  E  I  T  C
          152
          >>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>
          scFv

                 11510      11520      11530      11540      11550      11560      11570      11580      11590      11600
                     *          *          *          *          *          *          *          *          *          *
    11501 CTCCGGGGGCAGCTACTATGGCTGGTACCAGCAGAAGTCTCCTGGCAGTGCCCTTGTCACTGTGATCTATGAAGACACCAAGAGACCCTCGAACATCCCT 11600
           S  G  G  S  Y  Y  G  W  Y  Q  Q  K  S  P  G  S  A  L  V  T  V  I  Y  E  D  T  K  R  P  S  N  I  P
          185
          >>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>
          scFv

                 11610      11620      11630      11640      11650      11660      11670      11680      11690      11700
                     *          *          *          *          *          *          *          *          *          *
    11601 TCACGATTCTCCGGTTCCACATCCGGCTCCACAAGCACATTAACCATCACTGGGGTCCAAGCCGAGGACGAGGCTGTCTATTTCTGTGGGAGCTACGACA 11700
          S  R  F  S  G  S  T  S  G  S  T  S  T  L  T  I  T  G  V  Q  A  E  D  E  A  V  Y  F  C  G  S  Y  D  I
          218
          >>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>
          scFv

                 11710      11720      11730      11740      11750      11760      11770      11780      11790      11800
                     *          *          *          *          *          *          *          *          *          *
    11701 TCAGTAGTTATGCTGATCTCTTTGGGGCCGGGACAACCCTGACCGTCCTTAAGCGCGgatccGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACC 11800
            S  S  Y  A  D  L  F  G  A  G  T  T  L  T  V  L  K  R        E  P  K  S  C  D  K  T  H  T  C  P  P
          252                                                         1
          >>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>       >>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>
          scFv                                                        Fc derived from human IgG1

                 11810      11820      11830      11840      11850      11860      11870      11880      11890      11900
                     *          *          *          *          *          *          *          *          *          *
    11801 GTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGC 11900
           C  P  A  P  E  L  L  G  G  P  S  V  F  L  F  P  P  K  P  K  D  T  L  M  I  S  R  T  P  E  V  T  C
          14
          >>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>
          Fc derived from human IgG1

                 11910      11920      11930      11940      11950      11960      11970      11980      11990      12000
                     *          *          *          *          *          *          *          *          *          *
    11901 GTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 12000
          V  V  V  D  V  S  H  E  D  P  E  V  K  F  N  W  Y  V  D  G  V  E  V  H  N  A  K  T  K  P  R  E  E  Q
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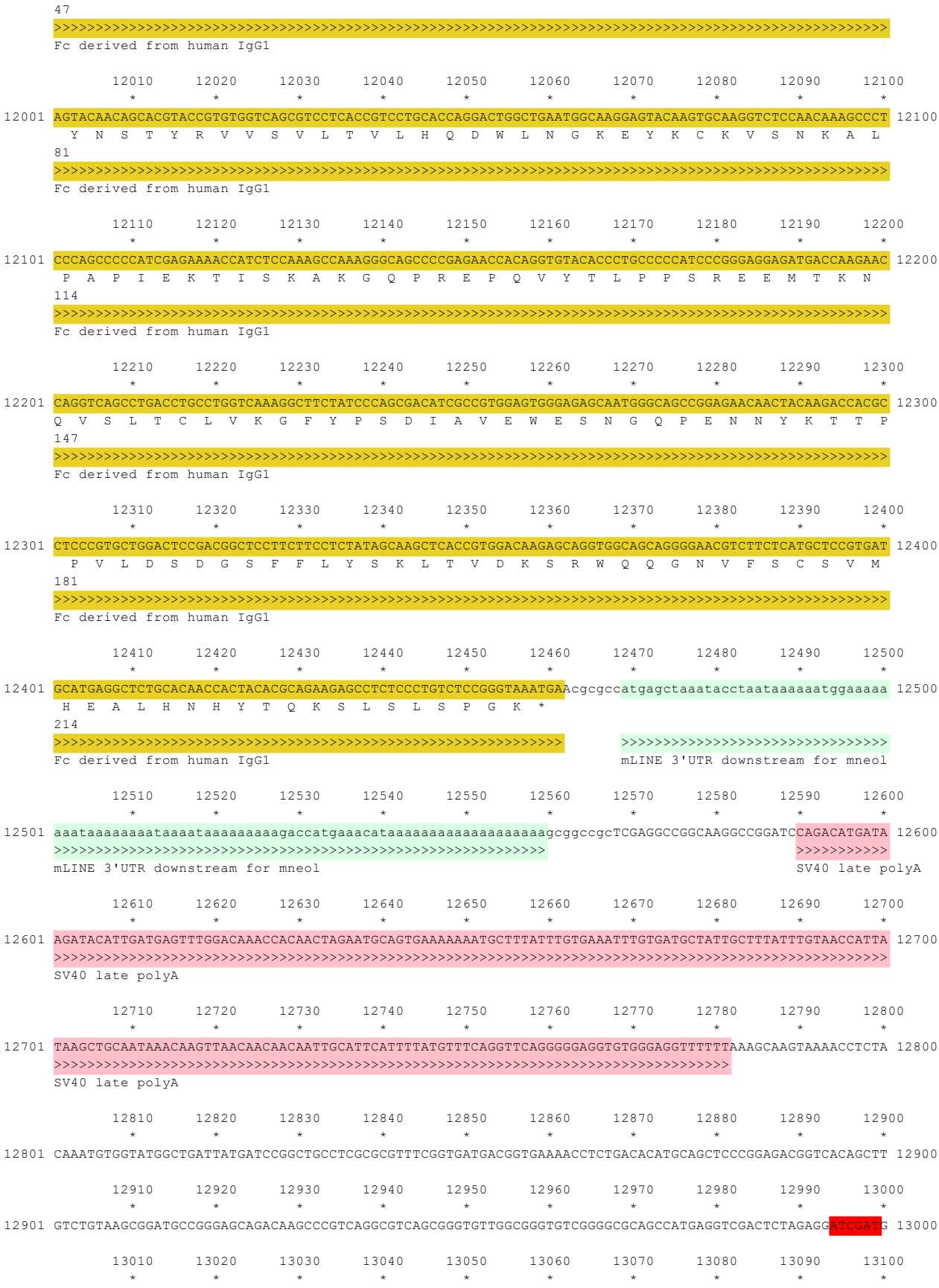
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Fc derived from human IgG1
12001 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCT 12100
Y N S T Y R V V S V L T V L H Q D W L N G K E Y K C K V S N K A L
81
Fc derived from human IgG1
12101 CCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAAC 12200
P A P I E K T I S K A K G Q P R E P Q V Y T L P P S R E E M T K N
114
Fc derived from human IgG1
12201 CAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 12300
Q V S L T C L V K G F Y P S D I A V E W E S N G Q P E N N Y K T T P
147
Fc derived from human IgG1
12301 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGAT 12400
P V L D S D G S F F L Y S K L T V D K S R W Q Q G N V F S C S V M
181
Fc derived from human IgG1
12401 GCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGAAcgcgccatgagctaaatacctaataaaaaatggaaaaa 12500
H E A L H N H Y T Q K S L S L S P G K *
214
Fc derived from human IgG1
mLINE 3'UTR downstream for mneol
12501 aaataaaaaaaaataaaataaaaaaaaaagaccatgaaacataaaaaaaaaaaaaaaaaaaagcggccgcTCGAGGCCGGCAAGGCCGGATCCAGACATGATA 12600
mLINE 3'UTR downstream for mneol
SV40 late polyA
12601 AGATACATTGATGAGTTTGGACAAACCACAACTAGAATGCAGTGAAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTA 12700
SV40 late polyA
12701 TAAGCTGCAATAAACAAGTTAACAACAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAGCAAGTAAAACCTCTA 12800
SV40 late polyA
12801 CAAATGTGGTATGGCTGATTATGATCCGGCTGCCTCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTCCCGGAGACGGTCACAGCTT 12900
12901 GTCTGTAAGCGGATGCCGGGAGCAGACAAGCCCGTCAGGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCGCAGCCATGAGGTCGACTCTAGAGGATCGATG 13000

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13001 ATAAGCTGTCAAACATGAGAATTCTTGAAGACGAAAGGGCCTCGTGATACGCCTATTTTTATAGGTTAATGTCATGATAATAATGGTTTCTTAGACGTCA 13100

        13110     13120     13130     13140     13150     13160     13170     13180     13190     13200
          *         *         *         *         *         *         *         *         *         *
13101 GGTGGCACTTTTCGGGGAAATGTGCGCGGAACCCCTATTTGTTTATTTTTCTAAATACATTCAAATATGTATCCGCTCATGAGACAATAACCCTGATAAA 13200
                                      >>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>
                                      beta-lactamase promoter

        13210     13220     13230     13240     13250     13260     13270     13280     13290     13300
          *         *         *         *         *         *         *         *         *         *
13201 TGCTTCAATAATATTGAAAAAGGAAGAGTATGAGTATTCAACATTTCCGTGTCGCCCTTATTCCCTTTTTTGCGGCATTTTGCCTTCCTGTTTTTGCTCA 13300
      >>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>
      beta-lactamase promoter

        13310     13320     13330     13340     13350     13360     13370     13380     13390     13400
          *         *         *         *         *         *         *         *         *         *
13301 CCCAGAAACGCTGGTGAAAGTAAAAGATGCTGAAGATCAGTTGGGTGCACGAGTGGGTTACATCGAACTGGATCTCAACAGCGGTAAGATCCTTGAGAGT 13400

        13410     13420     13430     13440     13450     13460     13470     13480     13490     13500
          *         *         *         *         *         *         *         *         *         *
13401 TTTCGCCCCGAAGAACGTTTTCCAATGATGAGCACTTTTAAAGTTCTGCTATGTGGCGCGGTATTATCCCGTGTTGACGCCGGGCAAGAGCAACTCGGTC 13500
                              M  S  T  F  K  V  L  L  C  G  A  V  L  S  R  V  D  A  G  Q  E  Q  L  G  R
                              1
                              >>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>
                              AmpR

        13510     13520     13530     13540     13550     13560     13570     13580     13590     13600
          *         *         *         *         *         *         *         *         *         *
13501 GCCGCATACACTATTCTCAGAATGACTTGGTTGAGTACTCACCAGTCACAGAAAAGCATCTTACGGATGGCATGACAGTAAGAGAATTATGCAGTGCTGC 13600
        R  I  H  Y  S  Q  N  D  L  V  E  Y  S  P  V  T  E  K  H  L  T  D  G  M  T  V  R  E  L  C  S  A  A
      26
      >>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>
      AmpR

        13610     13620     13630     13640     13650     13660     13670     13680     13690     13700
          *         *         *         *         *         *         *         *         *         *
13601 CATAACCATGAGTGATAACACTGCGGCCAACTTACTTCTGACAACGATCGGAGGACCGAAGGAGCTAACCGCTTTTTTGCACAACATGGGGGATCATGTA 13700
       I  T  M  S  D  N  T  A  A  N  L  L  L  T  T  I  G  G  P  K  E  L  T  A  F  L  H  N  M  G  D  H  V
      59
      >>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>
      AmpR

        13710     13720     13730     13740     13750     13760     13770     13780     13790     13800
          *         *         *         *         *         *         *         *         *         *
13701 ACTCGCCTTGATCGTTGGGAACCGGAGCTGAATGAAGCCATACCAAACGACGAGCGTGACACCACGATGCCTGCAGCAATGGCAACAACGTTGCGCAAAC 13800
      T  R  L  D  R  W  E  P  E  L  N  E  A  I  P  N  D  E  R  D  T  T  M  P  A  A  M  A  T  T  L  R  K  L
      92
      >>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>
      AmpR

        13810     13820     13830     13840     13850     13860     13870     13880     13890     13900
          *         *         *         *         *         *         *         *         *         *
13801 TATTAACTGGCGAACTACTTACTCTAGCTTCCCGGCAACAATTAATAGACTGGATGGAGGCGGATAAAGTTGCAGGACCACTTCTGCGCTCGGCCCTTCC 13900
        L  T  G  E  L  L  T  L  A  S  R  Q  Q  L  I  D  W  M  E  A  D  K  V  A  G  P  L  L  R  S  A  L  P
      126
      >>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>
      AmpR

        13910     13920     13930     13940     13950     13960     13970     13980     13990     14000
          *         *         *         *         *         *         *         *         *         *
13901 GGCTGGCTGGTTTATTGCTGATAAATCTGGAGCCGGTGAGCGTGGGTCTCGCGGTATCATTGCAGCACTGGGGCCAGATGGTAAGCCCTCCCGTATCGTA 14000
       A  G  W  F  I  A  D  K  S  G  A  G  E  R  G  S  R  G  I  I  A  A  L  G  P  D  G  K  P  S  R  I  V
      159
      >>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>
      AmpR

        14010     14020     14030     14040     14050     14060     14070     14080     14090     14100
          *         *         *         *         *         *         *         *         *         *
14001 GTTATCTACACGACGGGGAGTCAGGCAACTATGGATGAACGAAATAGACAGATCGCTGAGATAGGTGCCTCACTGATTAAGCATTGGTAACTGTCAGACC 14100
      V  I  Y  T  T  G  S  Q  A  T  M  D  E  R  N  R  Q  I  A  E  I  G  A  S  L  I  K  H  W
      192
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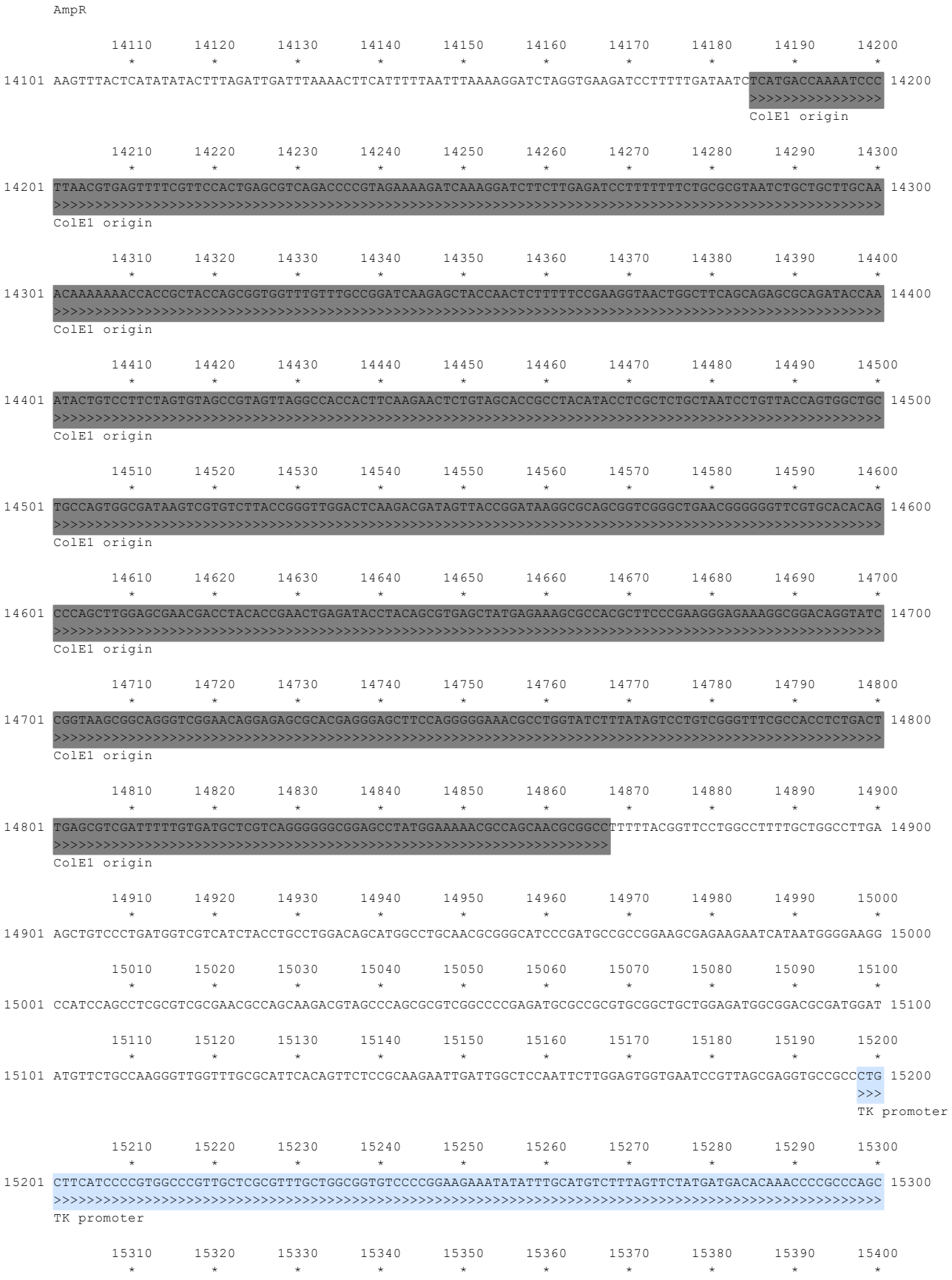
AmpR
14110 14120 14130 14140 14150 14160 14170 14180 14190 14200
14101 AAGTTTACTCATATATACTTTAGATTGATTTAAAACTTCATTTTTAATTTAAAAGGATCTAGGTGAAGATCCTTTTTGATAATCTCATGACCAAAATCCC 14200
ColE1 origin
14210 14220 14230 14240 14250 14260 14270 14280 14290 14300
14201 TTAACGTGAGTTTTCGTTCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAAGGATCTTCTTGAGATCCTTTTTTTCTGCGCGTAATCTGCTGCTTGCAA 14300
ColE1 origin
14310 14320 14330 14340 14350 14360 14370 14380 14390 14400
14301 ACAAAAAAACCACCGCTACCAGCGGTGGTTTGTTTGCCGGATCAAGAGCTACCAACTCTTTTTCCGAAGGTAACTGGCTTCAGCAGAGCGCAGATACCAA 14400
ColE1 origin
14410 14420 14430 14440 14450 14460 14470 14480 14490 14500
14401 ATACTGTCCTTCTAGTGTAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCACCGCCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGC 14500
ColE1 origin
14510 14520 14530 14540 14550 14560 14570 14580 14590 14600
14501 TGCCAGTGGCGATAAGTCGTGTCTTACCGGGTTGGACTCAAGACGATAGTTACCGGATAAGGCGCAGCGGTCGGGCTGAACGGGGGGTTCGTGCACACAG 14600
ColE1 origin
14610 14620 14630 14640 14650 14660 14670 14680 14690 14700
14601 CCCAGCTTGGAGCGAACGACCTACACCGAACTGAGATACCTACAGCGTGAGCTATGAGAAAGCGCCACGCTTCCCGAAGGGAGAAAGGCGGACAGGTATC 14700
ColE1 origin
14710 14720 14730 14740 14750 14760 14770 14780 14790 14800
14701 CGGTAAGCGGCAGGGTCGGAACAGGAGAGCGCACGAGGGAGCTTCCAGGGGGAAACGCCTGGTATCTTTATAGTCCTGTCGGGTTTCGCCACCTCTGACT 14800
ColE1 origin
14810 14820 14830 14840 14850 14860 14870 14880 14890 14900
14801 TGAGCGTCGATTTTTGTGATGCTCGTCAGGGGGGCGGAGCCTATGGAAAAACGCCAGCAACGCGGCCTTTTTACGGTTCCTGGCCTTTTGCTGGCCTTGA 14900
ColE1 origin
14910 14920 14930 14940 14950 14960 14970 14980 14990 15000
14901 AGCTGTCCCTGATGGTCGTCATCTACCTGCCTGGACAGCATGGCCTGCAACGCGGGCATCCCGATGCCGCCGGAAGCGAGAAGAATCATAATGGGGAAGG 15000
15010 15020 15030 15040 15050 15060 15070 15080 15090 15100
15001 CCATCCAGCCTCGCGTCGCGAACGCCAGCAAGACGTAGCCCAGCGCGTCGGCCCCGAGATGCGCCGCGTGCGGCTGCTGGAGATGGCGGACGCGATGGAT 15100
15110 15120 15130 15140 15150 15160 15170 15180 15190 15200
15101 ATGTTCTGCCAAGGGTTGGTTTGCGCATTCACAGTTCTCCGCAAGAATTGATTGGCTCCAATTCTTGGAGTGGTGAATCCGTTAGCGAGGTGCCGCCCTG 15200
TK promoter
15210 15220 15230 15240 15250 15260 15270 15280 15290 15300
15201 CTTCATCCCCGTGGCCCGTTGCTCGCGTTTGCTGGCGGTGTCCCCGGAAGAAATATATTTGCATGTCTTTAGTTCTATGATGACACAAACCCCGCCCAGC 15300
TK promoter
15310 15320 15330 15340 15350 15360 15370 15380 15390 15400

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15301 GTCTTGTCATTGGCGAATTCGAACACGCAGATGCAGTCGGGGCGGCGCGGTCCGAGGTCCACTTCGCATATTAAGGTGACGCGTGTGGCCTCGAACACCG 15400
      >>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>
      TK promoter

             15410     15420     15430     15440     15450     15460     15470     15480     15490     15500
               *         *         *         *         *         *         *         *         *         *
15401 AGCGACCCTGCAGCGACCCGCTTAACAGCGTCAACAGCGTGCCGCAGATCCCGGGGGCAATGAGATATGAAAAAGCCTGAACTCACCGCGACGTCTGTC 15500
                                                                         M  K  K  P  E  L  T  A  T  S  V
                                                                         1
      >>>>>>>>>>>>>>>>>>>>>>>>>                                          >>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>
      TK promoter                                                        HygR

             15510     15520     15530     15540     15550     15560     15570     15580     15590     15600
               *         *         *         *         *         *         *         *         *         *
15501 GAGAAGTTTCTGATCGAAAAGTTCGACAGCGTCTCCGACCTGATGCAGCTCTCGGAGGGCGAAGAATCTCGTGCTTTCAGCTTCGATGTAGGAGGGCGTG 15600
      E  K  F  L  I  E  K  F  D  S  V  S  D  L  M  Q  L  S  E  G  E  E  S  R  A  F  S  F  D  V  G  G  R  G
      12
      >>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>
      HygR

             15610     15620     15630     15640     15650     15660     15670     15680     15690     15700
               *         *         *         *         *         *         *         *         *         *
15601 GATATGTCCTGCGGGTAAATAGCTGCGCCGATGGTTTCTACAAAGATCGTTATGTTTATCGGCACTTTGCATCGGCCGCGCTCCCGATTCCGGAAGTGCT 15700
       Y  V  L  R  V  N  S  C  A  D  G  F  Y  K  D  R  Y  V  Y  R  H  F  A  S  A  A  L  P  I  P  E  V  L
      46
      >>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>
      HygR

             15710     15720     15730     15740     15750     15760     15770     15780     15790     15800
               *         *         *         *         *         *         *         *         *         *
15701 TGACATTGGGGAATTCAGCGAGAGCCTGACCTATTGCATCTCCCGCCGTGCACAGGGTGTCACGTTGCAAGACCTGCCTGAAACCGAACTGCCCGCTGTT 15800
       D  I  G  E  F  S  E  S  L  T  Y  C  I  S  R  R  A  Q  G  V  T  L  Q  D  L  P  E  T  E  L  P  A  V
      79
      >>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>
      HygR

             15810     15820     15830     15840     15850     15860     15870     15880     15890     15900
               *         *         *         *         *         *         *         *         *         *
15801 CTGCAGCCGGTCGCGGAGGCCATGGATGCGATCGCTGCGGCCGATCTTAGCCAGACGAGCGGGTTCGGCCCATTCGGACCGCAAGGAATCGGTCAATACA 15900
      L  Q  P  V  A  E  A  M  D  A  I  A  A  A  D  L  S  Q  T  S  G  F  G  P  F  G  P  Q  G  I  G  Q  Y  T
      112
      >>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>
      HygR

             15910     15920     15930     15940     15950     15960     15970     15980     15990     16000
               *         *         *         *         *         *         *         *         *         *
15901 CTACATGGCGTGATTTCATATGCGCGATTGCTGATCCCCATGTGTATCACTGGCAAACTGTGATGGACGACACCGTCAGTGCGTCCGTCGCGCAGGCTCT 16000
       T  W  R  D  F  I  C  A  I  A  D  P  H  V  Y  H  W  Q  T  V  M  D  D  T  V  S  A  S  V  A  Q  A  L
      146
      >>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>
      HygR

             16010     16020     16030     16040     16050     16060     16070     16080     16090     16100
               *         *         *         *         *         *         *         *         *         *
16001 CGATGAGCTGATGCTTTGGGCCGAGGACTGCCCCGAAGTCCGGCACCTCGTGCACGCGGATTTCGGCTCCAACAATGTCCTGACGGACAATGGCCGCATA 16100
       D  E  L  M  L  W  A  E  D  C  P  E  V  R  H  L  V  H  A  D  F  G  S  N  N  V  L  T  D  N  G  R  I
      179
      >>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>
      HygR

             16110     16120     16130     16140     16150     16160     16170     16180     16190     16200
               *         *         *         *         *         *         *         *         *         *
16101 ACAGCGGTCATTGACTGGAGCGAGGCGATGTTCGGGGATTCCCAATACGAGGTCGCCAACATCTTCTTCTGGAGGCCGTGGTTGGCTTGTATGGAGCAGC 16200
      T  A  V  I  D  W  S  E  A  M  F  G  D  S  Q  Y  E  V  A  N  I  F  F  W  R  P  W  L  A  C  M  E  Q  Q
      212
      >>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>
      HygR

             16210     16220     16230     16240     16250     16260     16270     16280     16290     16300
               *         *         *         *         *         *         *         *         *         *
16201 AGACGCGCTACTTCGAGCGGAGGCATCCGGAGCTTGCAGGATCGCCGCGGCTCCGGGCGTATATGCTCCGCATTGGTCTTGACCAACTCTATCAGAGCTT 16300
       T  R  Y  F  E  R  R  H  P  E  L  A  G  S  P  R  L  R  A  Y  M  L  R  I  G  L  D  Q  L  Y  Q  S  L
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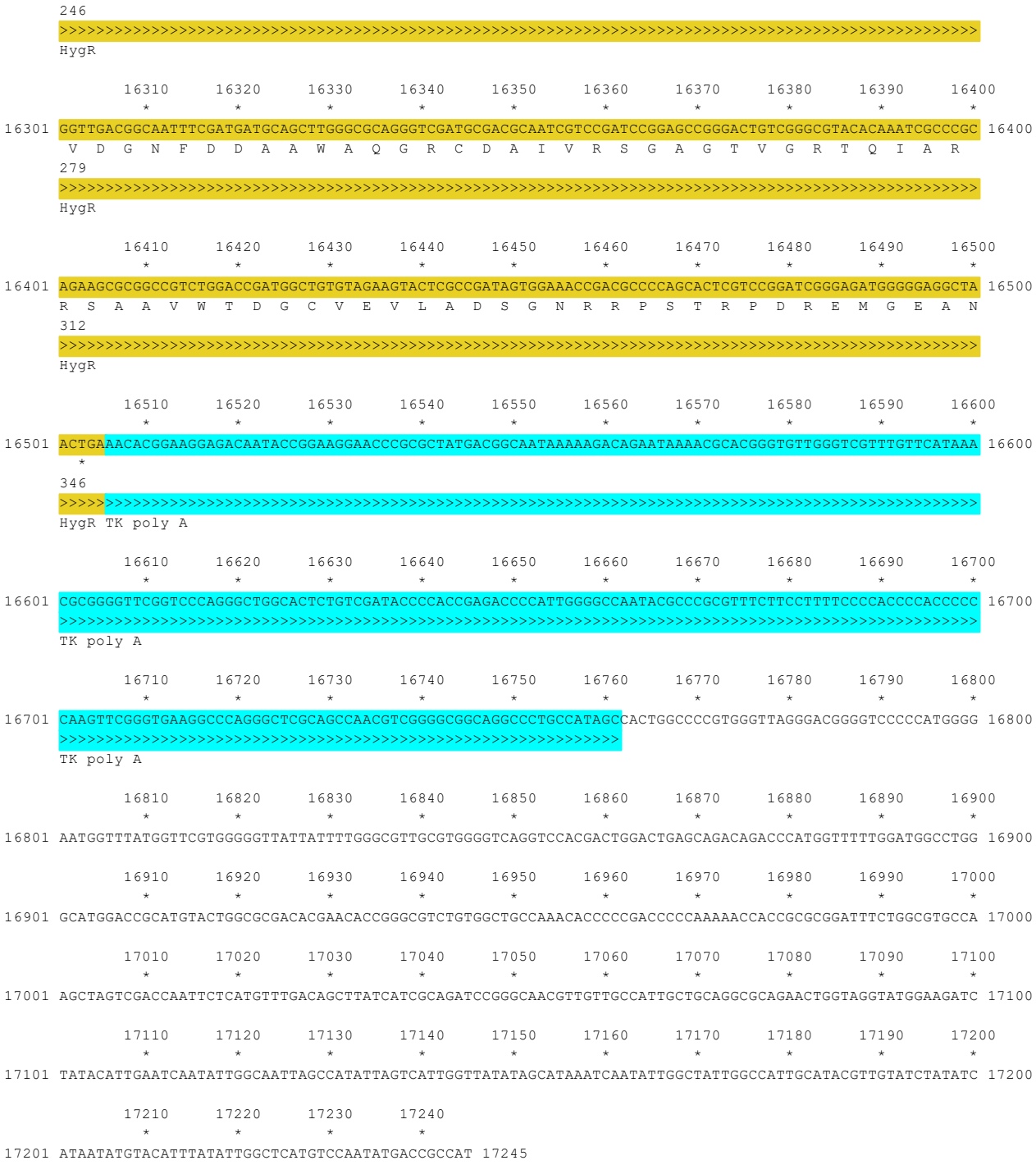
246
HygR
16310 16320 16330 16340 16350 16360 16370 16380 16390 16400
16301 GGTTGACGGCAATTTCGATGATGCAGCTTGGGCGCAGGGTCGATGCGACGCAATCGTCCGATCCGGAGCCGGGACTGTCGGGCGTACACAAATCGCCCGC 16400
V D G N F D D A A W A Q G R C D A I V R S G A G T V G R T Q I A R
279
HygR
16410 16420 16430 16440 16450 16460 16470 16480 16490 16500
16401 AGAAGCGCGGCCGTCTGGACCGATGGCTGTGTAGAAGTACTCGCCGATAGTGGAAACCGACGCCCCAGCACTCGTCCGGATCGGGAGATGGGGGAGGCTA 16500
R S A A V W T D G C V E V L A D S G N R R P S T R P D R E M G E A N
312
HygR
16510 16520 16530 16540 16550 16560 16570 16580 16590 16600
16501 ACTGAAACACGGAAGGAGACAATACCGGAAGGAACCCGCGCTATGACGGCAATAAAAAGACAGAATAAAACGCACGGGTGTTGGGTCGTTTGTTCATAAA 16600
346
HygR TK poly A
16610 16620 16630 16640 16650 16660 16670 16680 16690 16700
16601 CGCGGGGTTCGGTCCCAGGGCTGGCACTCTGTCGATACCCCACCGAGACCCCATTGGGGCCAATACGCCCGCGTTTCTTCCTTTTCCCCACCCCACCCCC 16700
TK poly A
16710 16720 16730 16740 16750 16760 16770 16780 16790 16800
16701 CAAGTTCGGGTGAAGGCCCAGGGCTCGCAGCCAACGTCGGGGCGGCAGGCCCTGCCATAGCCACTGGCCCCGTGGGTTAGGGACGGGGTCCCCCATGGGG 16800
TK poly A
16810 16820 16830 16840 16850 16860 16870 16880 16890 16900
16801 AATGGTTTATGGTTCGTGGGGGTTATTATTTTGGGCGTTGCGTGGGGTCAGGTCCACGACTGGACTGAGCAGACAGACCCATGGTTTTTGGATGGCCTGG 16900
16910 16920 16930 16940 16950 16960 16970 16980 16990 17000
16901 GCATGGACCGCATGTACTGGCGCGACACGAACACCGGGCGTCTGTGGCTGCCAAACACCCCCGACCCCCAAAAACCACCGCGCGGATTTCTGGCGTGCCA 17000
17010 17020 17030 17040 17050 17060 17070 17080 17090 17100
17001 AGCTAGTCGACCAATTCTCATGTTTGACAGCTTATCATCGCAGATCCGGGCAACGTTGTTGCCATTGCTGCAGGCGCAGAACTGGTAGGTATGGAAGATC 17100
17110 17120 17130 17140 17150 17160 17170 17180 17190 17200
17101 TATACATTGAATCAATATTGGCAATTAGCCATATTAGTCATTGGTTATATAGCATAAATCAATATTGGCTATTGGCCATTGCATACGTTGTATCTATATC 17200
17210 17220 17230 17240
17201 ATAATATGTACATTTATATTGGCTCATGTCCAATATGACCGCCAT 17245