Reactive Peptide Maps for *CTL responses to immunodominant regions in HIV*

N. Frahm *et al.*

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Contents

1 Reactive Peptides Mapped on Reference Sequence (B Consensus) 3

1.1 p17 . . . 5

p17 aa 1–100 (1/2) . . . 5

p17 aa 1–100 (2/2) . . . 6

p17 aa 101–132 (1/1) . . . 7

1.2 p24 . . . 8

p24 aa 1–100 (1/2) . . . 8

p24 aa 1–100 (2/2) . . . 9

p24 aa 101–200 (1/2) . . . 10

p24 aa 101–200 (2/2) . . . 11

p24 aa 201–232 (1/1) . . . 12

1.3 p2p7p1p6 . . . 13

p2p7p1p6 aa 1–100 (1/1) . . . 13

p2p7p1p6 aa 101–137 (1/1) . . . 14

1.4 Gag-Pol TF . . . 15

Gag-Pol TF aa 1–56 (1/1) . . . 15

1.5 Protease . . . 16

Protease aa 1–99 (1/1) . . . 16

1.6 RT . . . 17

RT aa 1–100 (1/1) . . . 17

RT aa 101–200 (1/1) . . . 18

RT aa 201–300 (1/1) . . . 19

RT aa 301–400 (1/1) 20
RT aa 401–500 (1/2) 21
RT aa 401–500 (2/2) 22
RT aa 501–560 (1/1) 22
1.7 Integrase 23
Integrase aa 1–100 (1/1) 23
Integrase aa 101–200 (1/2) 24
Integrase aa 101–200 (2/2) 25
Integrase aa 201–288 (1/1) 25
1.8 Vif 26
Vif aa 1–100 (1/1) 26
Vif aa 101–192 (1/1) 27
1.9 Vpr 28
Vpr aa 1–96 (1/2) 28
Vpr aa 1–96 (2/2) 29
1.10 Tat 30
Tat aa 1–100 (1/1) 30
Tat aa 101–102 (1/1) 31
1.11 Rev 32
Rev aa 1–100 (1/1) 32
Rev aa 101–116 (1/1) 33
1.12 Vpu 34
Vpu aa 1–82 (1/1) 34
1.13 gp160 35
gp160 aa 1–100 (1/2) 35
gp160 aa 1–100 (2/2) 36
gp160 aa 101–200 (1/1) 36
gp160 aa 201–300 (1/1) 37
gp160 aa 301–400 (1/1) 38
gp160 aa 401–500 (1/1) 38
gp160 aa 501–600 (1/1) 39
gp160 aa 601–700 (1/1) 40
gp160 aa 701–800 (1/1) 40
gp160 aa 801–856 (1/1) 41

1.14 Nef 42
Nef aa 1–100 (1/4) 42
Nef aa 1–100 (2/4) 43
Nef aa 1–100 (3/4) 44
Nef aa 1–100 (4/4) 45
Nef aa 101–200 (1/4) 46
Nef aa 101–200 (2/4) 47
Nef aa 101–200 (3/4) 48
Nef aa 101–200 (4/4) 49
Nef aa 201–206 (1/1) 49

1 Reactive Peptides Mapped on Reference Sequence (B Consensus)

These are the reactive peptides from the paper *Identification of highly immunodominant regions in HIV by comprehensive CTL screening of ethnically diverse populations*, N Frahm *et al.*, 2003, mapped against the B-clade reference sequence.[1] The B reference sequence is aligned against the HXB2 sequence. The protein labeled *Gag-Pol TF* is the portion of the Pol polyprotein before the start of Protease.

The peptides are labeled with the subject ID's and HLA's. We listed the most common HLA molecules for this set, and color coded them on the map. If appropriate anchor residues were present for these HLA molecules in the protein sequence, for the most common HLA molecules, we color coded the potential epitope on an aligned set of sequences from the map. We just highlighting anchors with spacing for a 9-mer epitope, as the picture gets too busy otherwise.

[1]This is a synthetic sequence based upon the LANL B-consensus sequence.

Table 1: Most reactive HLA's and binding motifs

HLA	**Reactions**	**Motif**	**Color**
C07	1182	xxxxxxxx[YFL]	red
A02	952	x[LM]xxxxxx[VL]	violet
C04	593	x[YPF]xxxxxx[LFM]	orange
B15	580	*undef*†	cyan
B07	533	x[P]xxxxxx[LF]	green
A23	491	*undef*†	magenta
C06	430	x[A]xxxxxx[LIVY]	blue
C03	424	x[A]xxxxxx[LM]	forest
B44	415	x[E]xxxxxx[YF]	
A33	365	xxxxxxxx[R]	
A68	358		
B35	335		
A24	311		
A01	295		
B53	290		
B58	286		
C16	277		
B57	270		
B14	266		

† This serotype does not have a well-defined binding motif.

1.1 p17

Figure 1: p17 aa 1–100 (1/2)

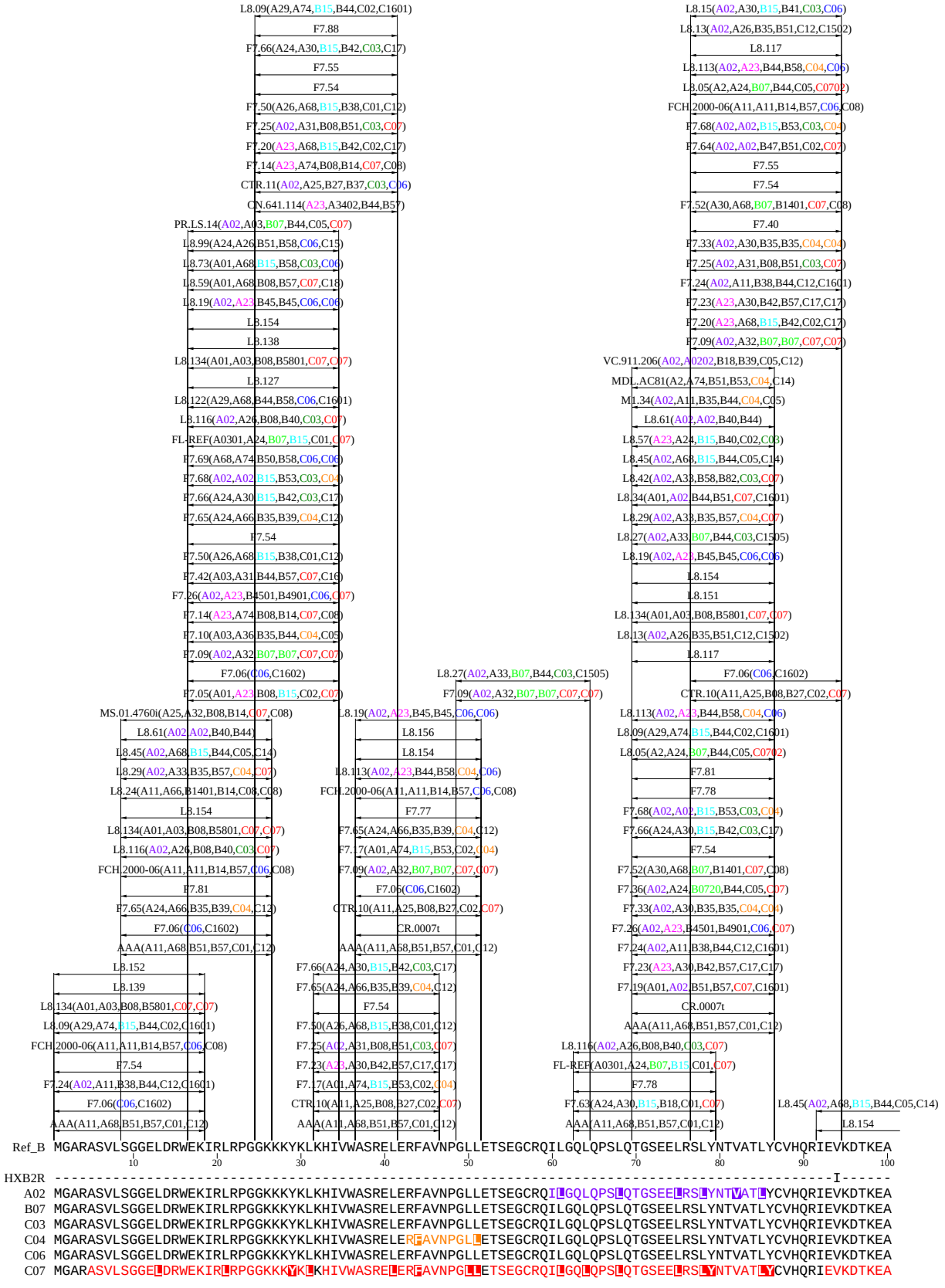


Figure 2: p17 aa 1–100 (2/2)

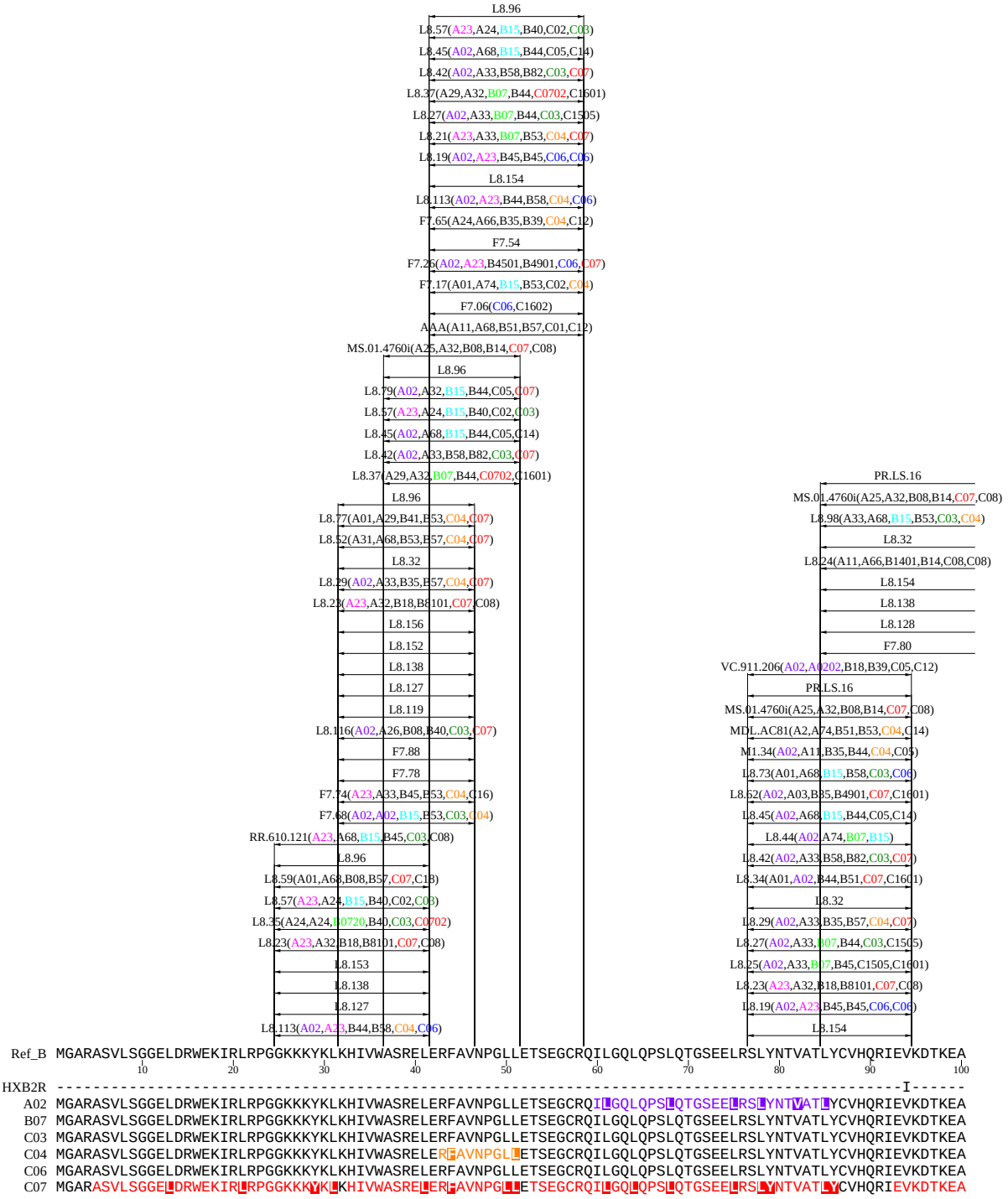
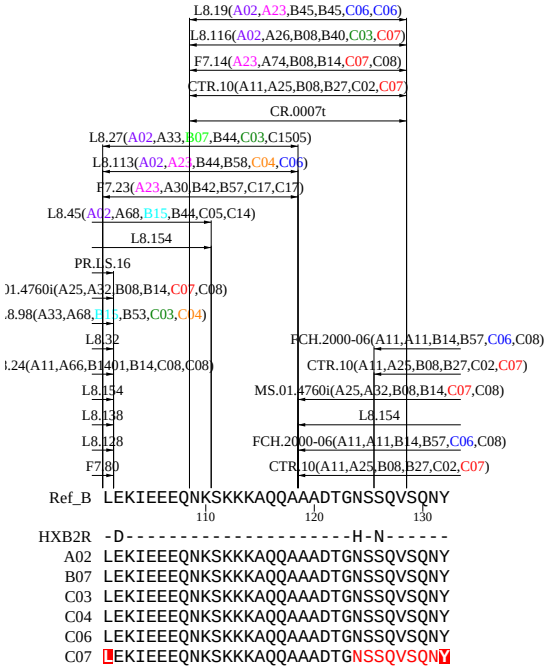


Figure 3: p17 aa 101–132 (1/1)



1.2 p24

Figure 4: p24 aa 1–100 (1/2)

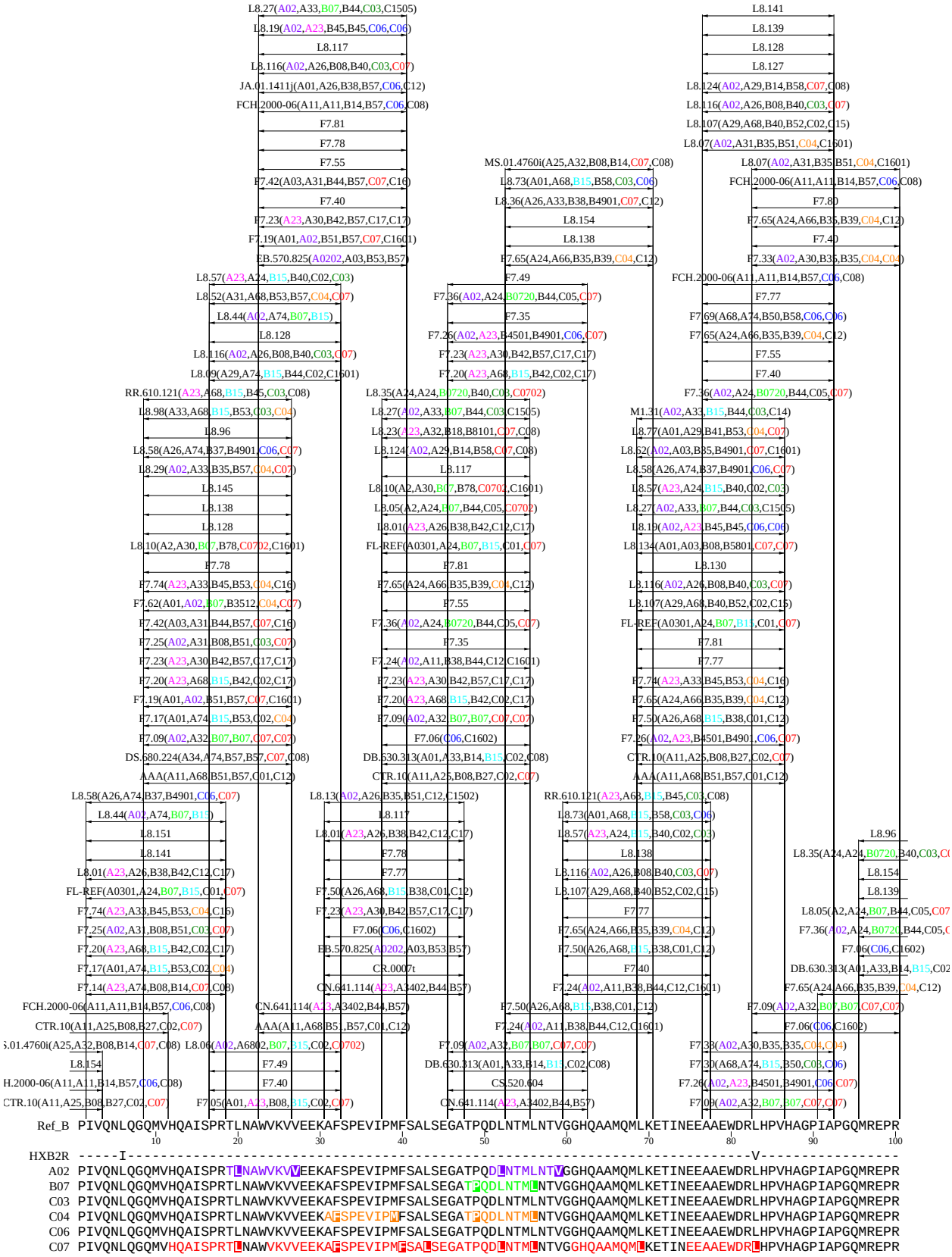


Figure 5: p24 aa 1–100 (2/2)

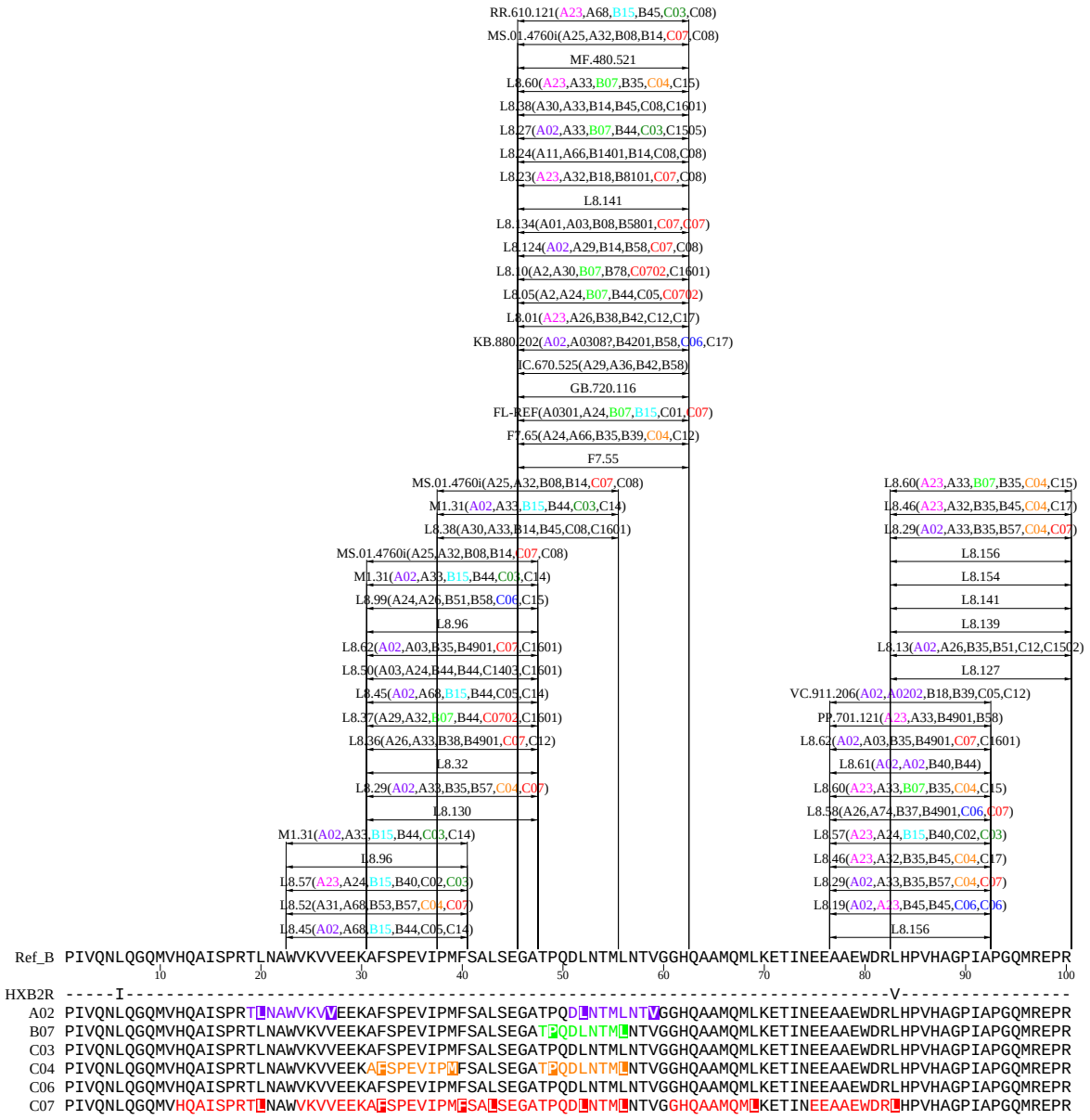


Figure 6: p24 aa 101–200 (1/2)

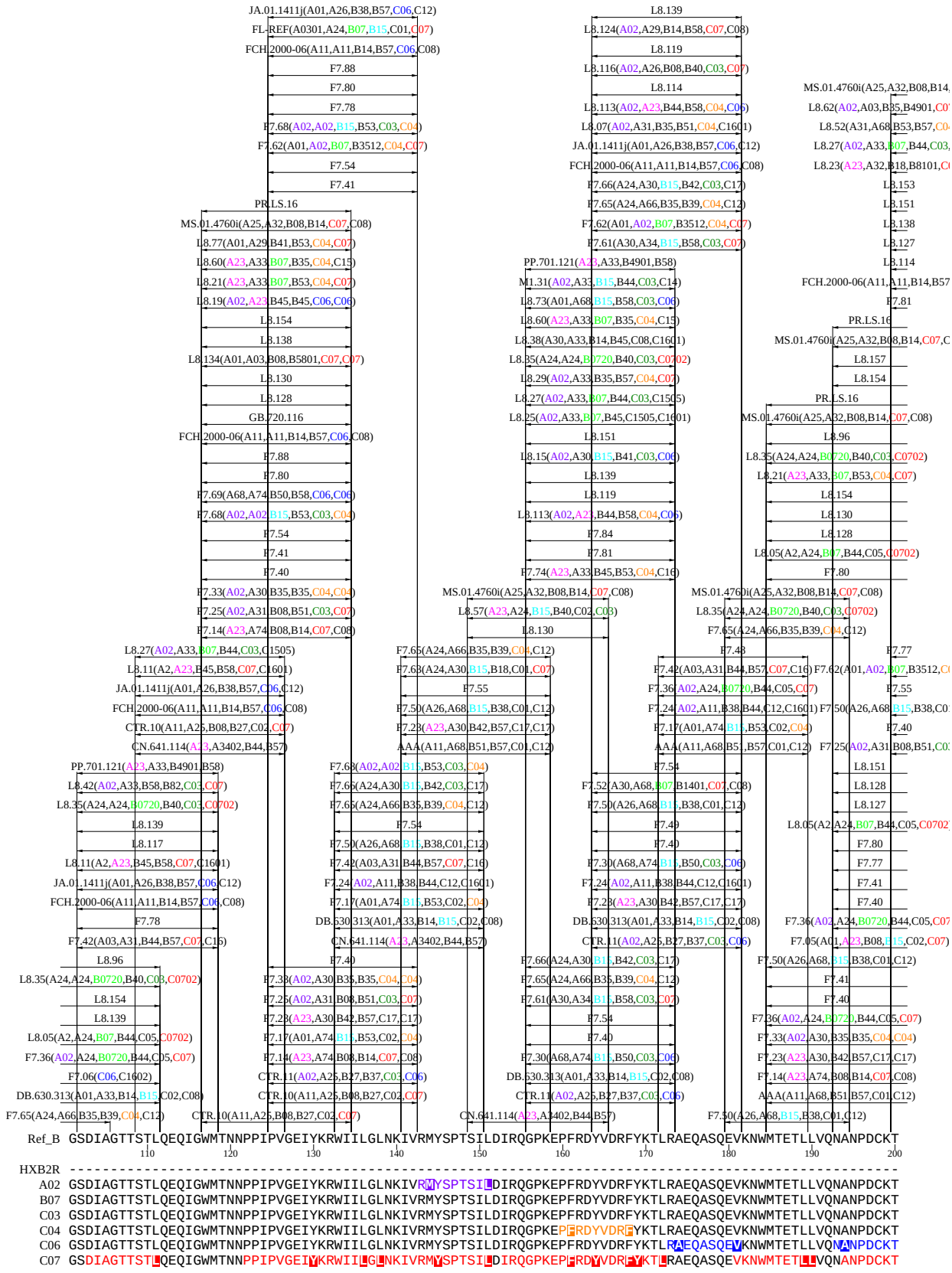


Figure 7: p24 aa 101–200 (2/2)

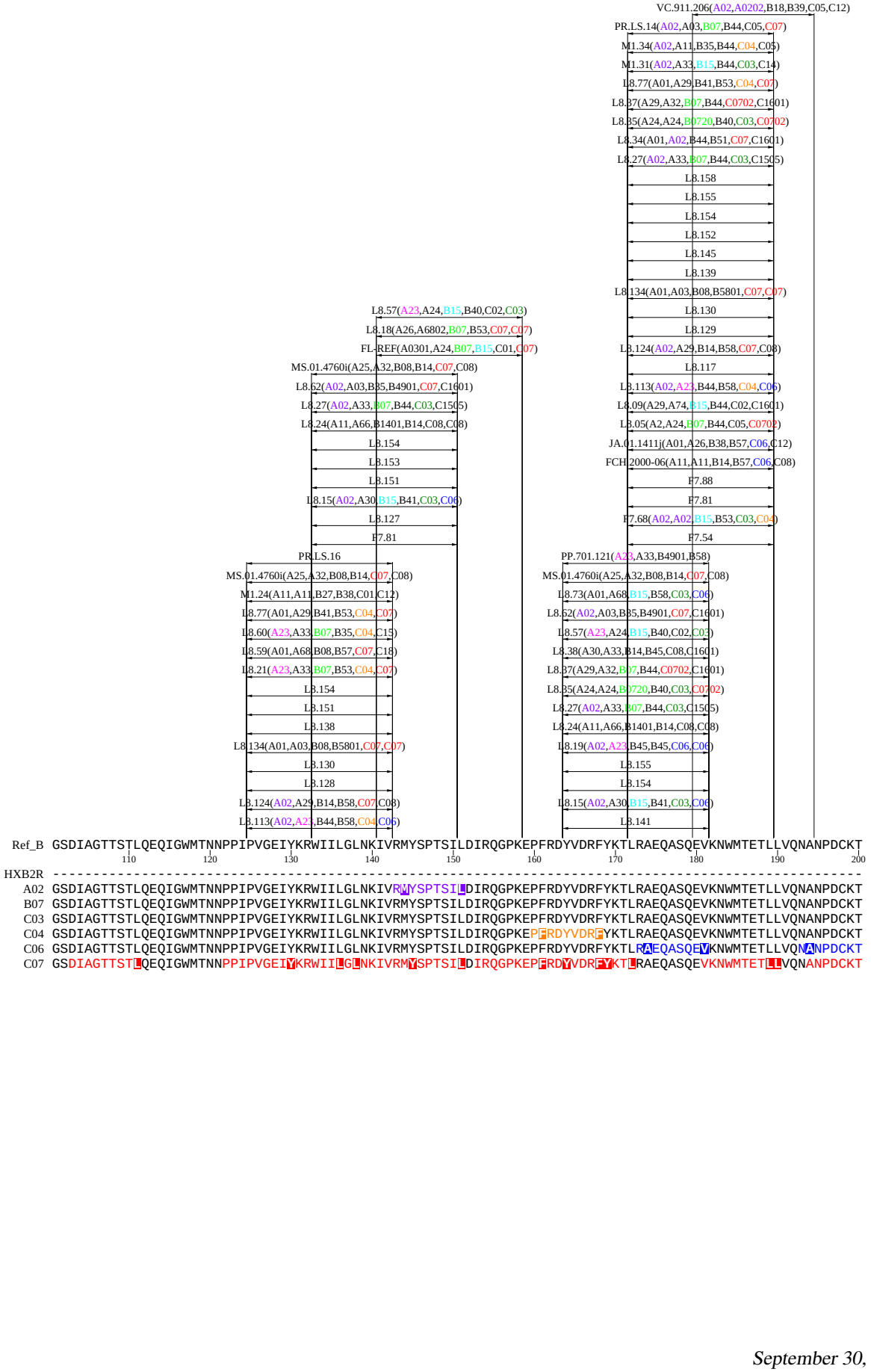
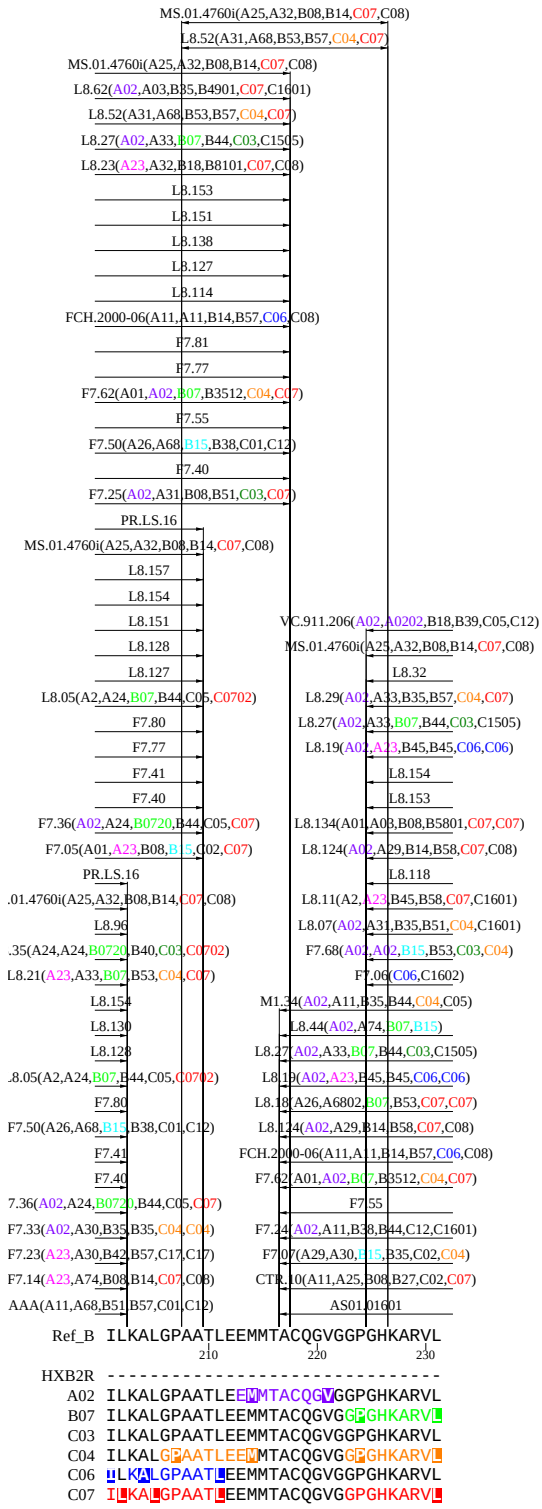


Figure 8: p24 aa 201–232 (1/1)



1.3 p2p7p1p6

Figure 9: p2p7p1p6 aa 1–100 (1/1)

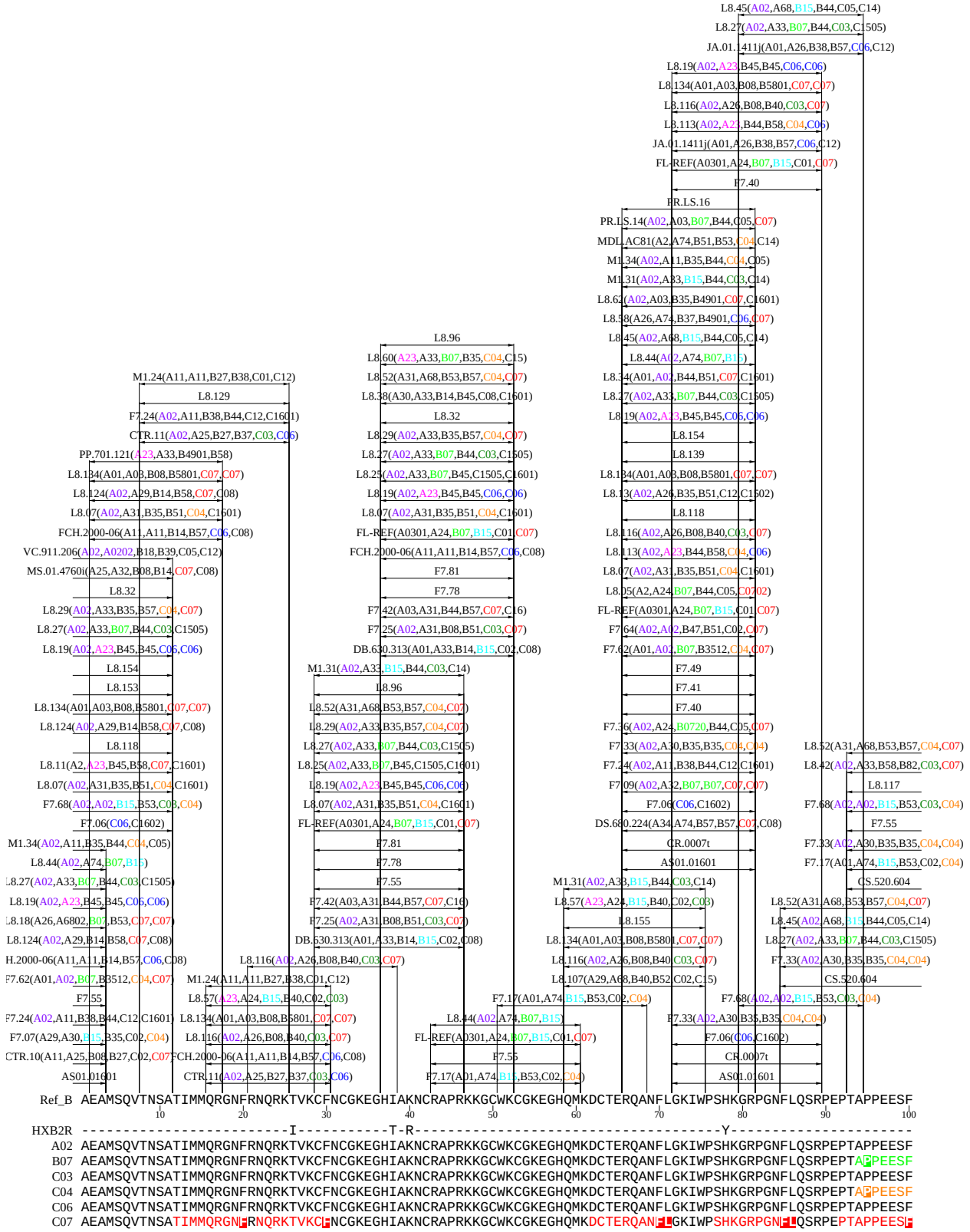
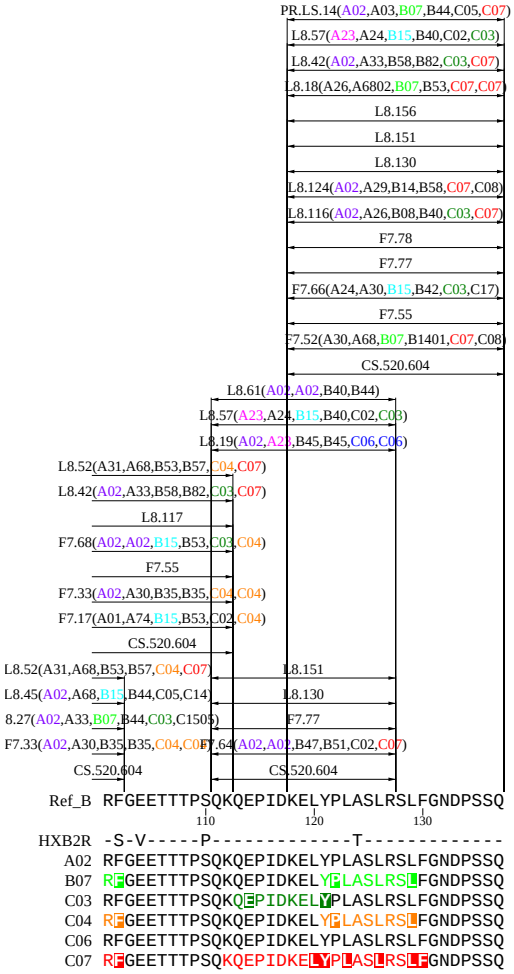
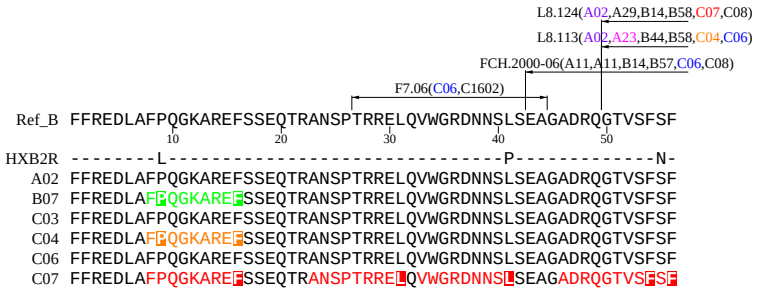


Figure 10: p2p7p1p6 aa 101–137 (1/1)



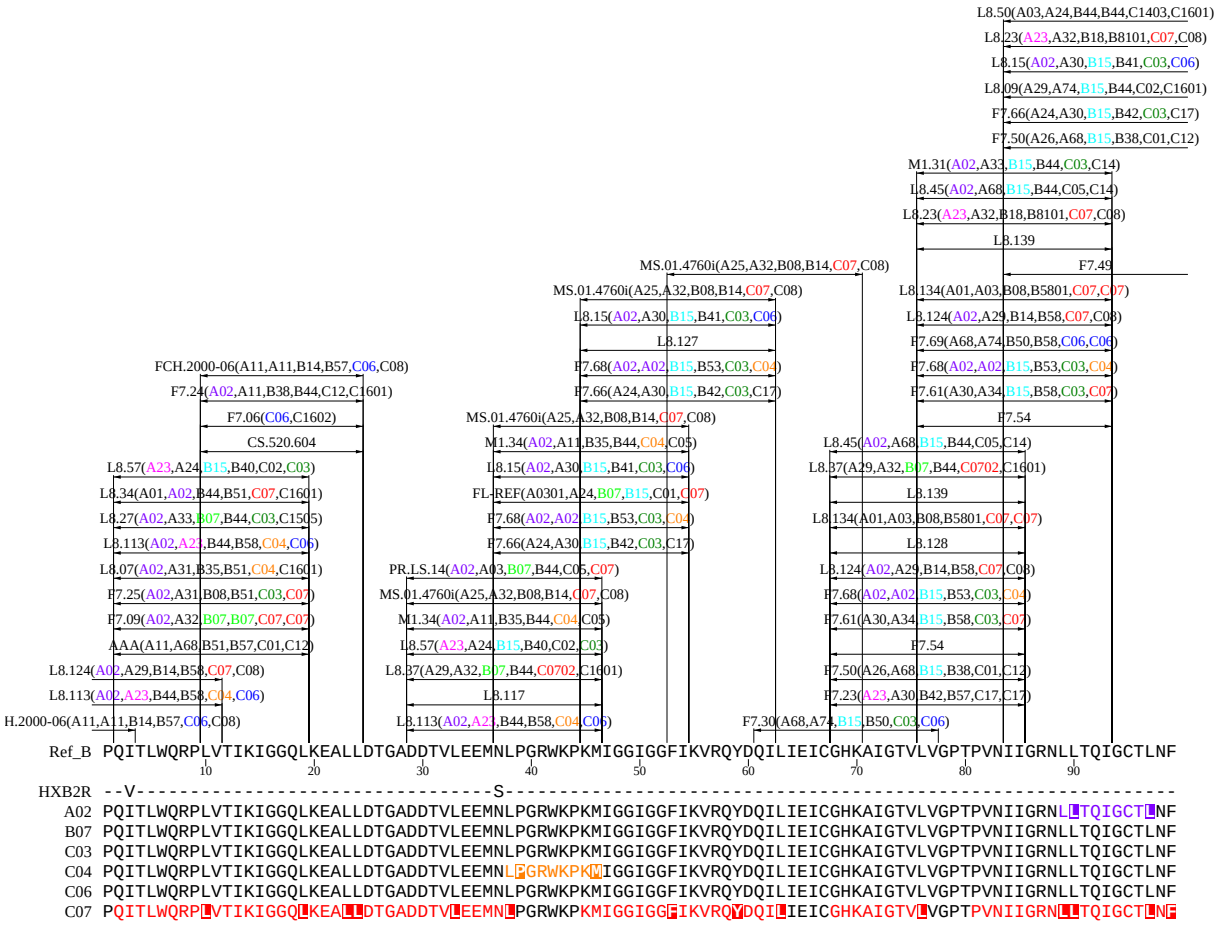
1.4 Gag-Pol TF

Figure 11: Gag-Pol TF aa 1–56 (1/1)



1.5 Protease

Figure 12: Protease aa 1–99 (1/1)



1.6 RT

Figure 13: RT aa 1–100 (1/1)

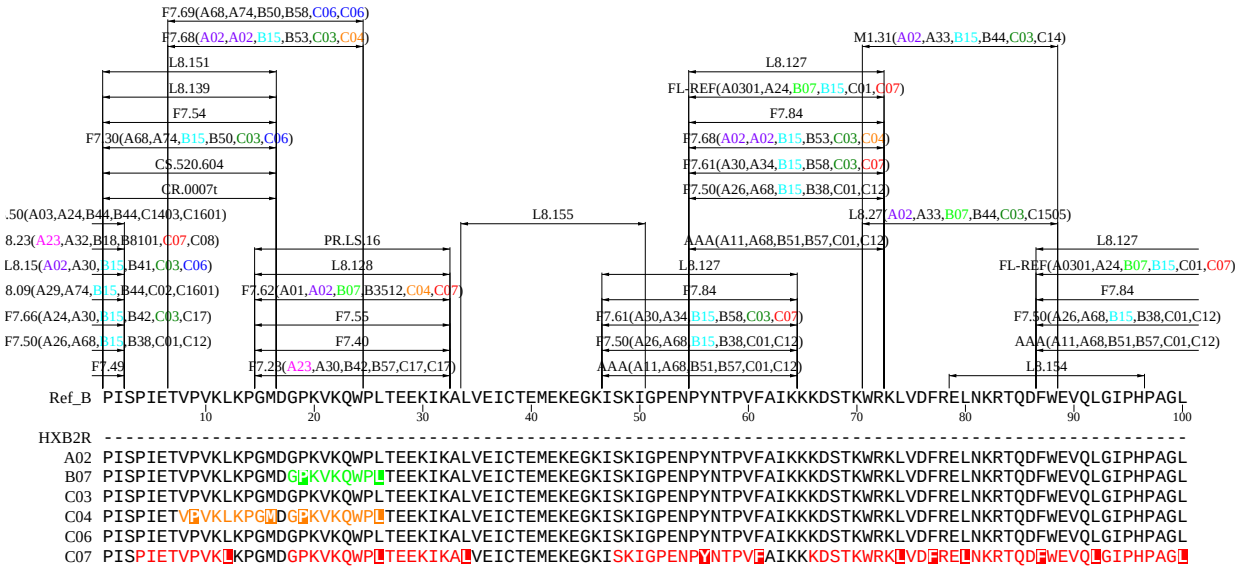


Figure 14: RT aa 101–200 (1/1)

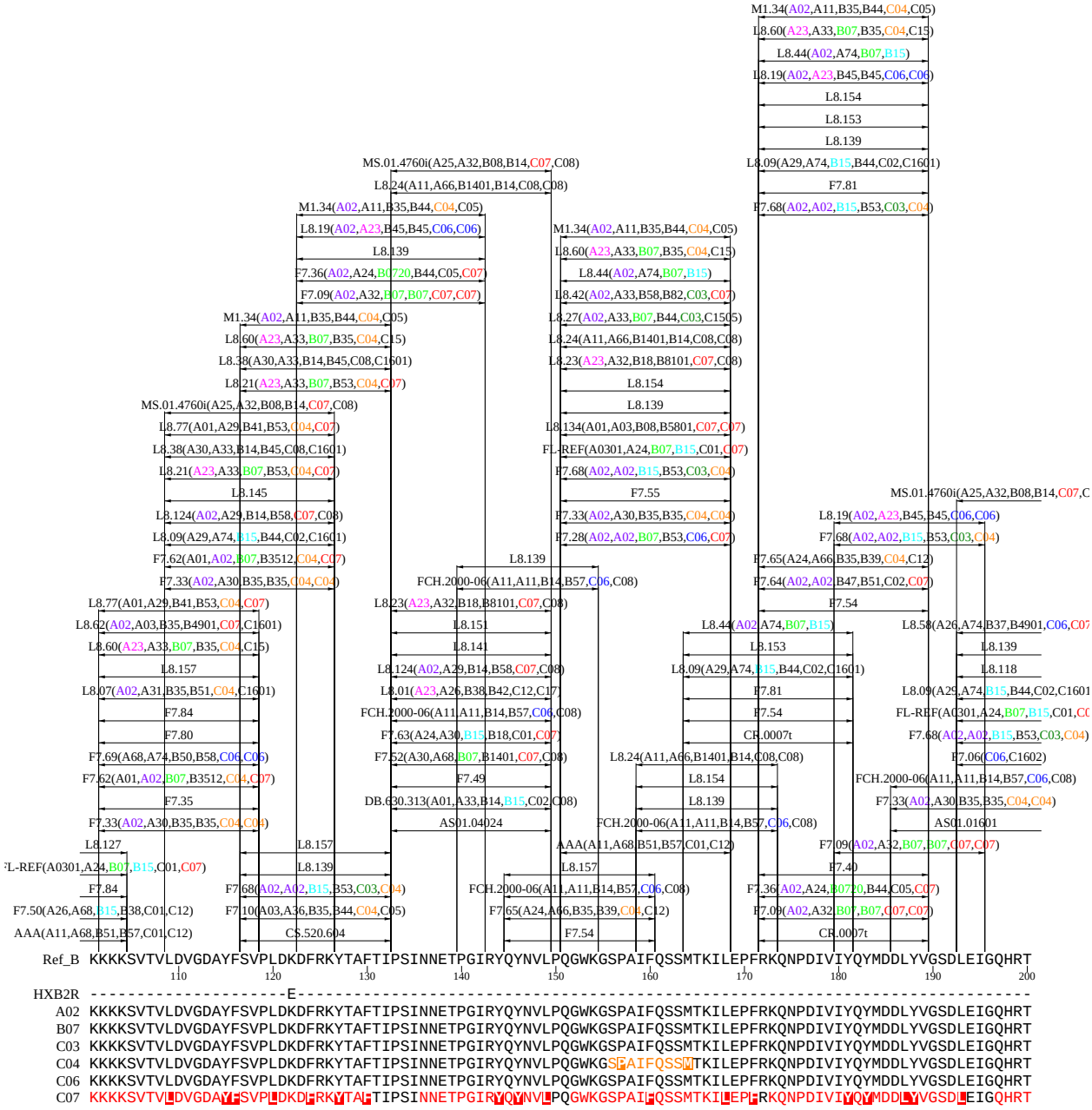


Figure 15: RT aa 201–300 (1/1)

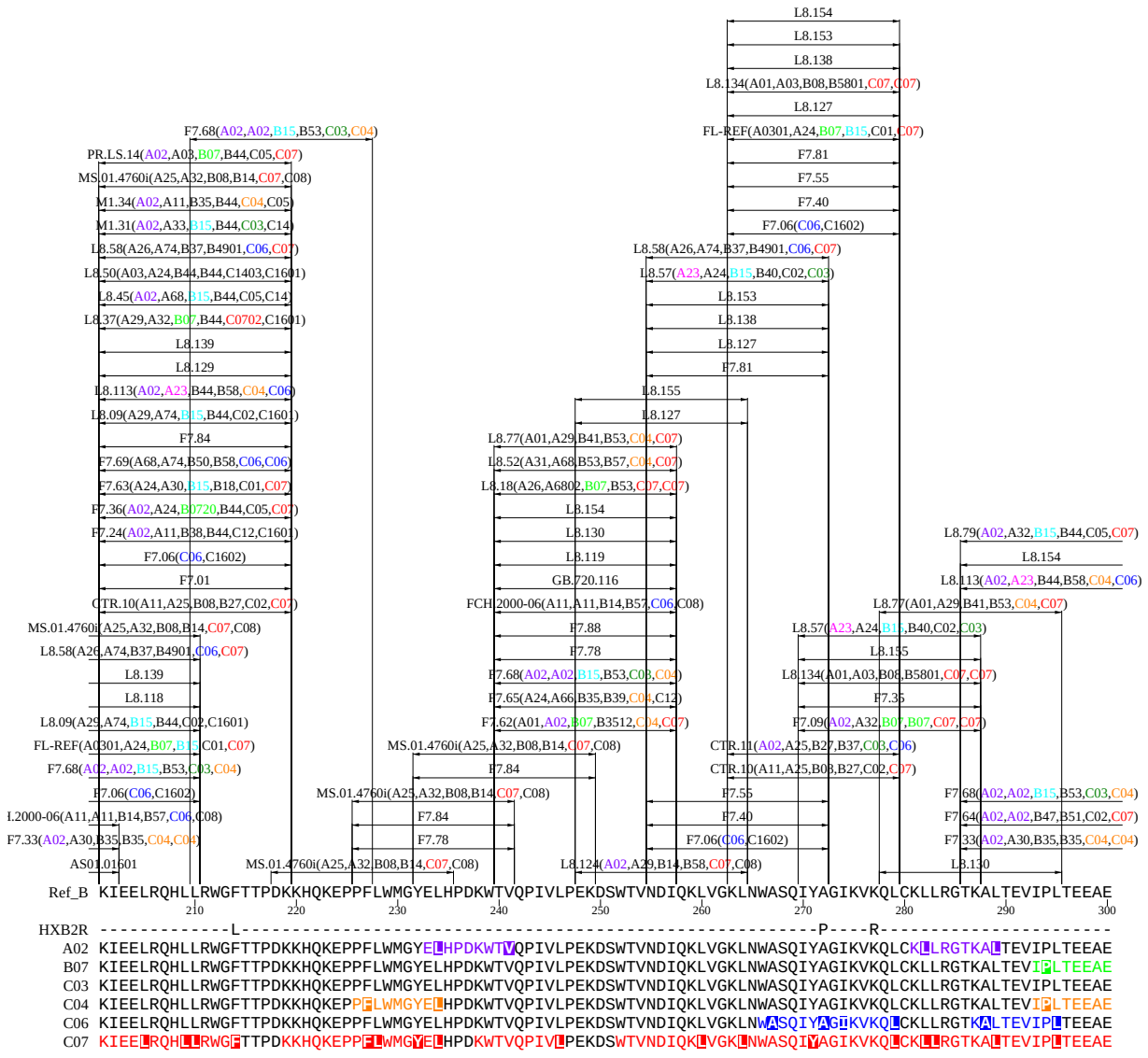


Figure 16: RT aa 301–400 (1/1)

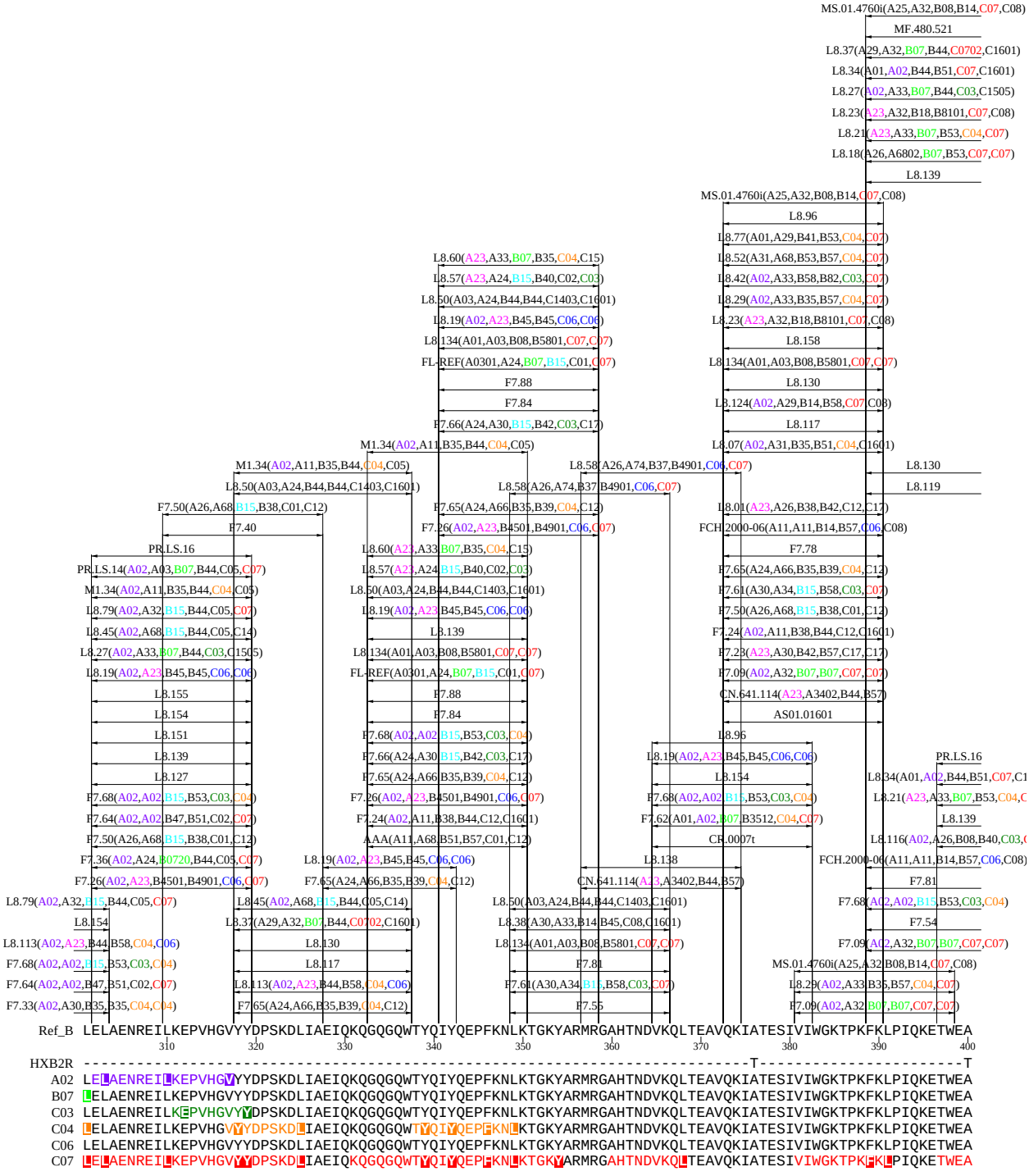


Figure 17: RT aa 401–500 (1/2)

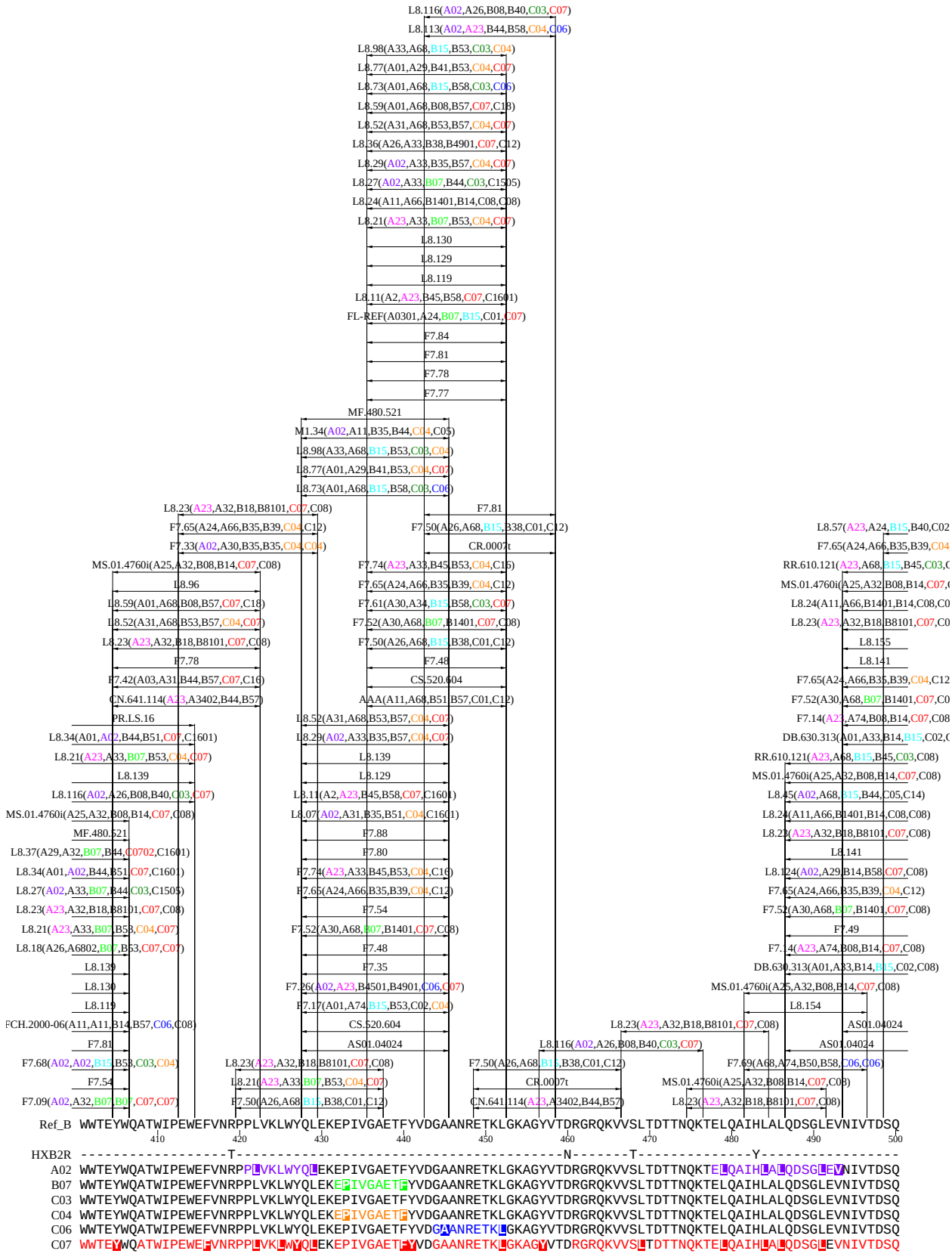
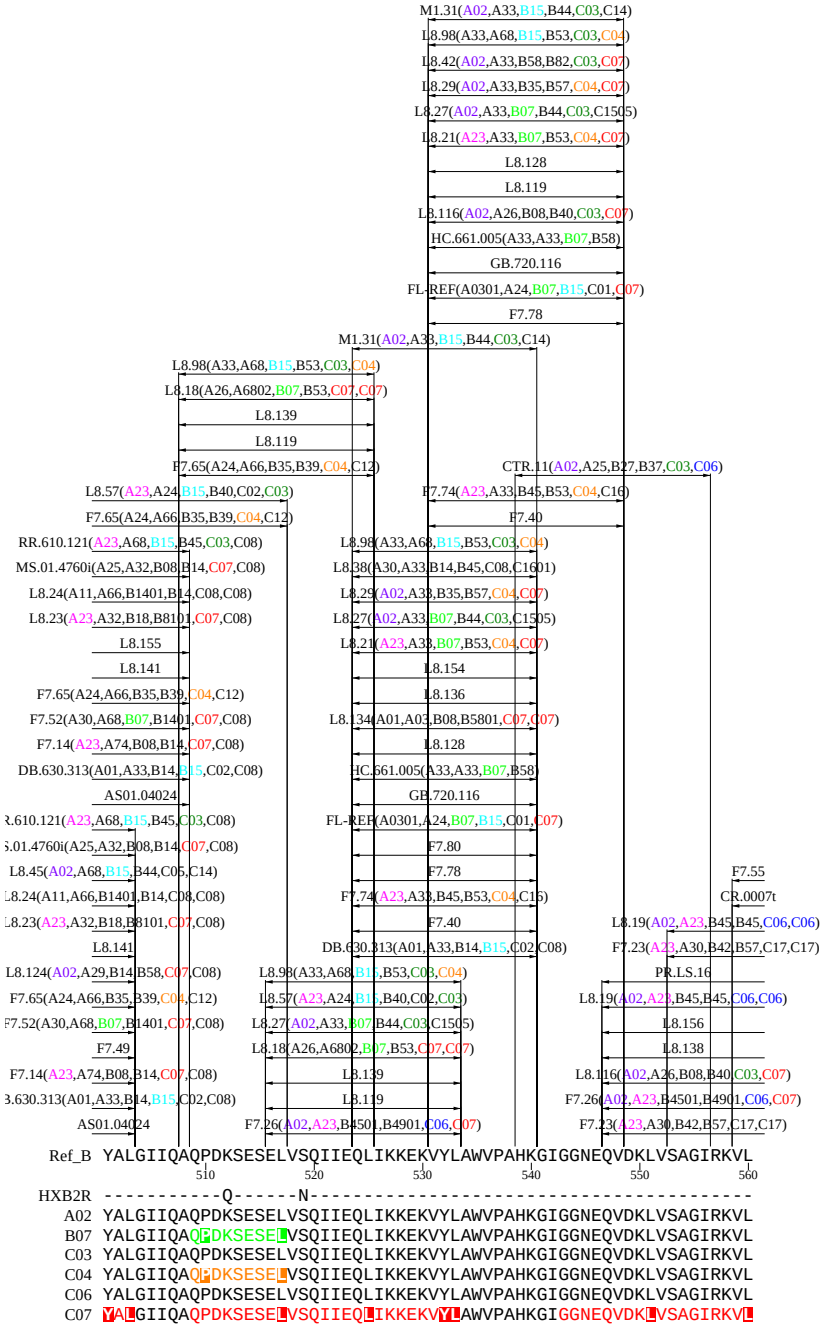


Figure 18: RT aa 401–500 (2/2)

Figure 19: RT aa 501–560 (1/1)



1.7 Integrase

Figure 20: Integrase aa 1–100 (1/1)

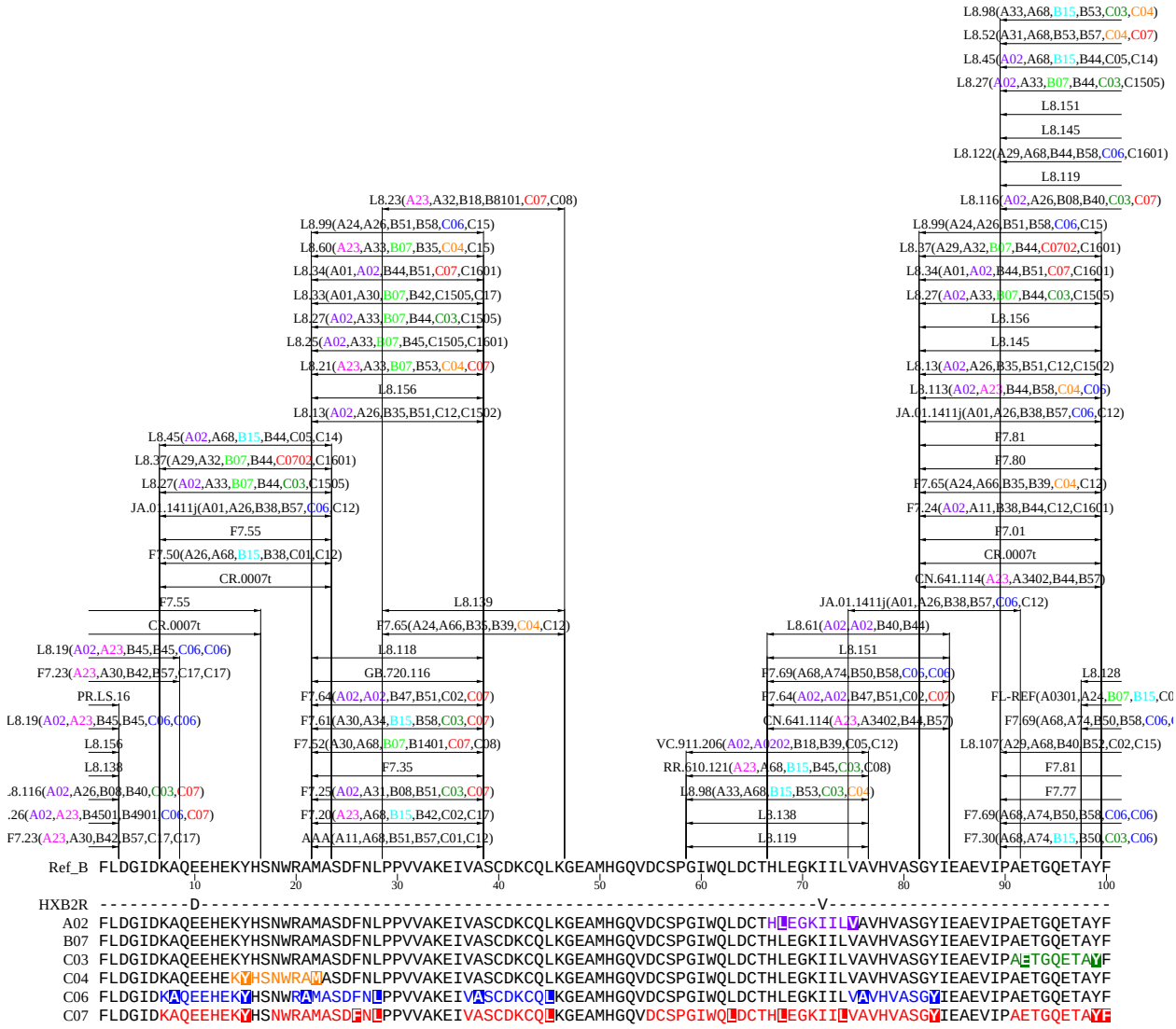


Figure 21: Integrase aa 101–200 (1/2)

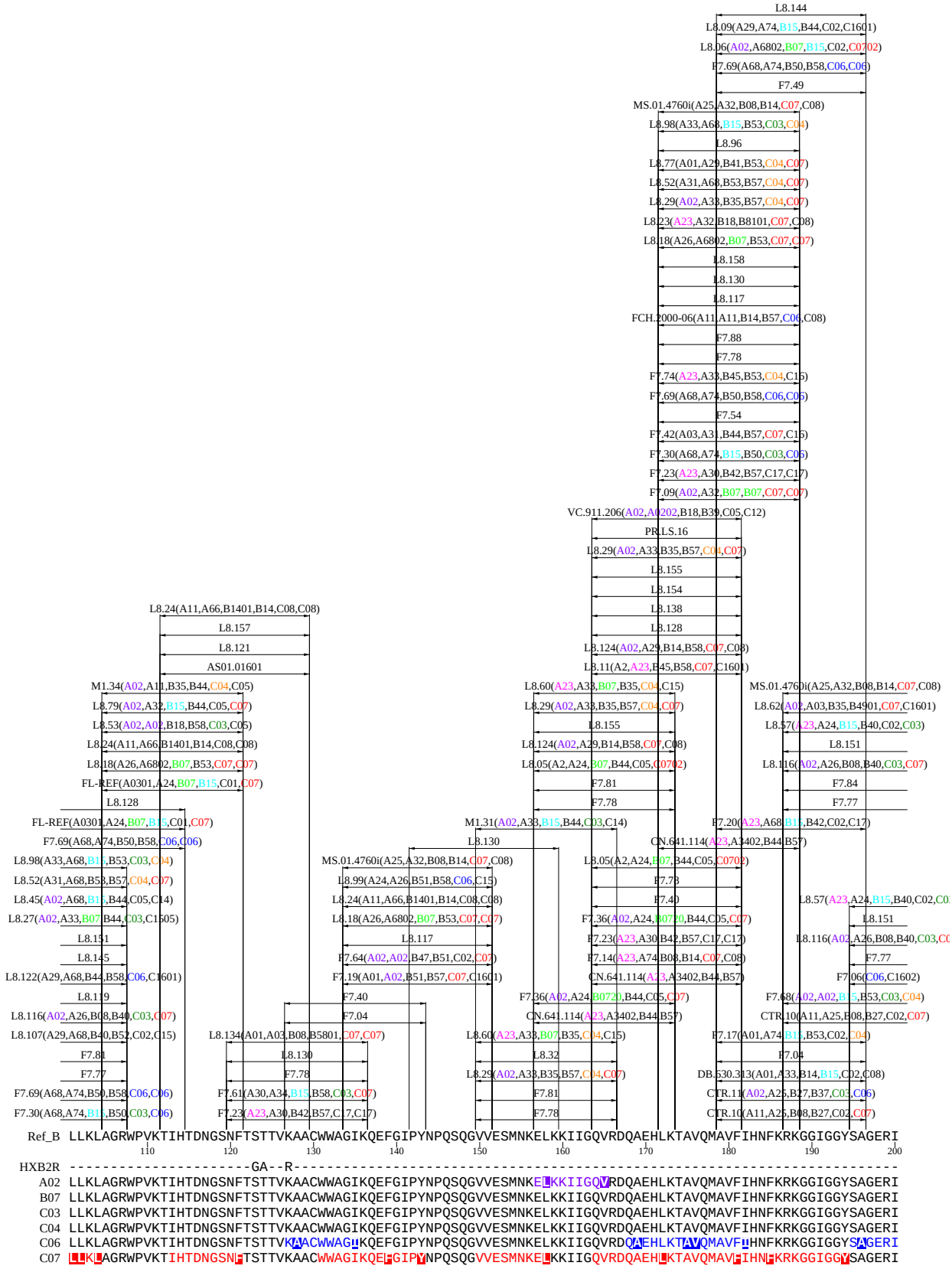


Figure 22: Integrase aa 101–200 (2/2)

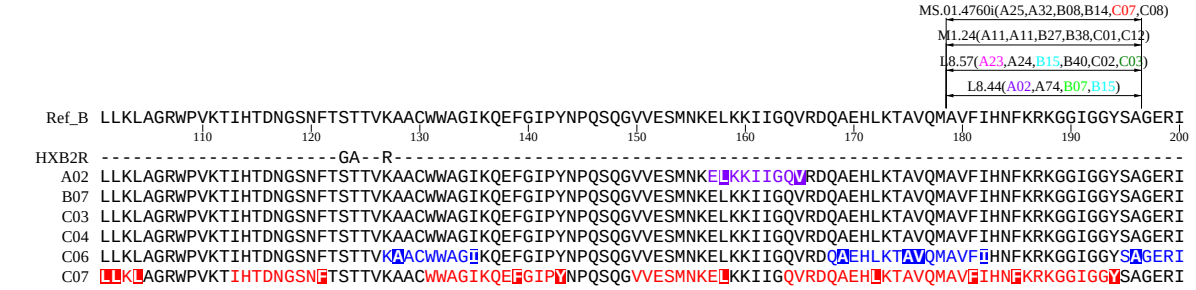
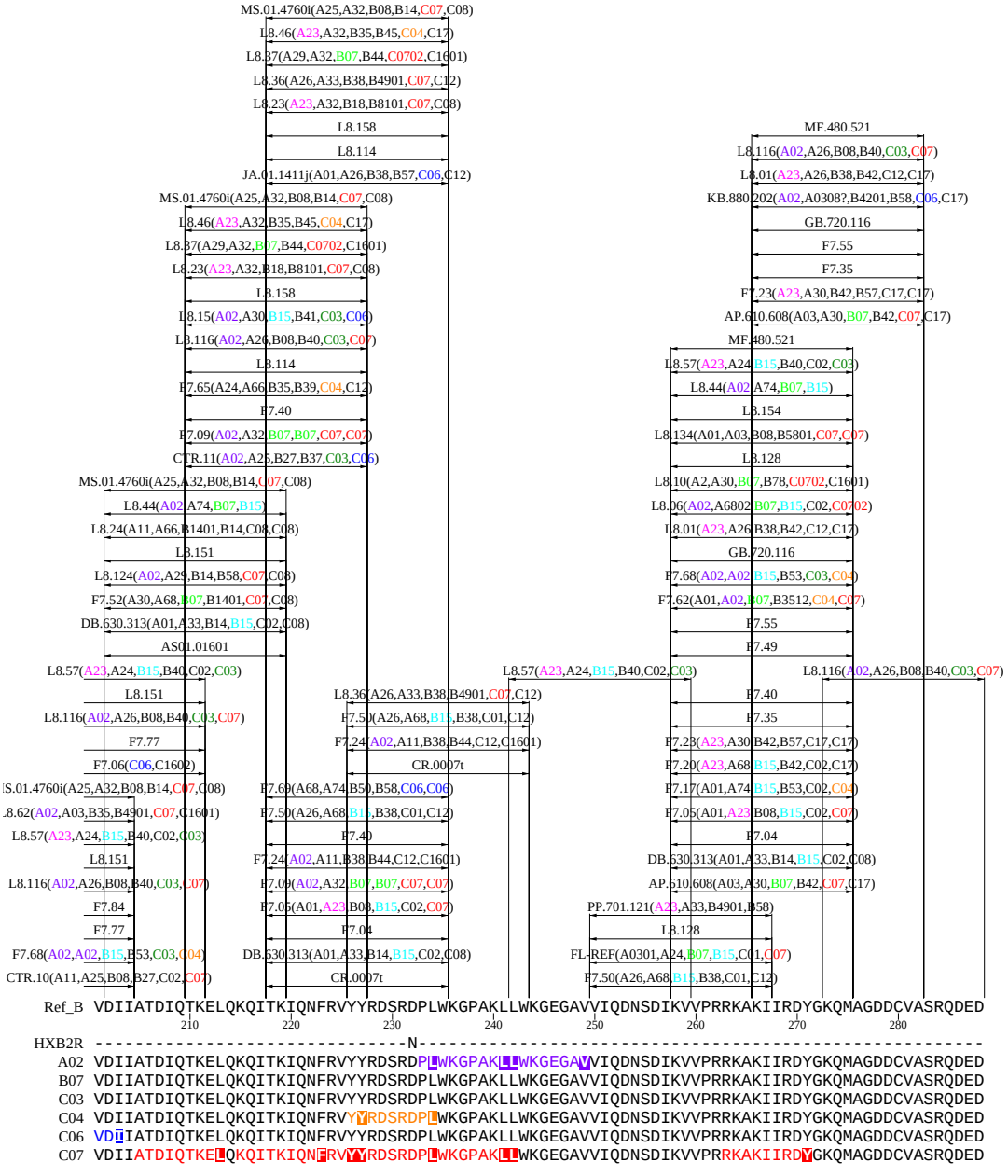


Figure 23: Integrase aa 201–288 (1/1)



1.8 Vif

Figure 24: Vif aa 1–100 (1/1)

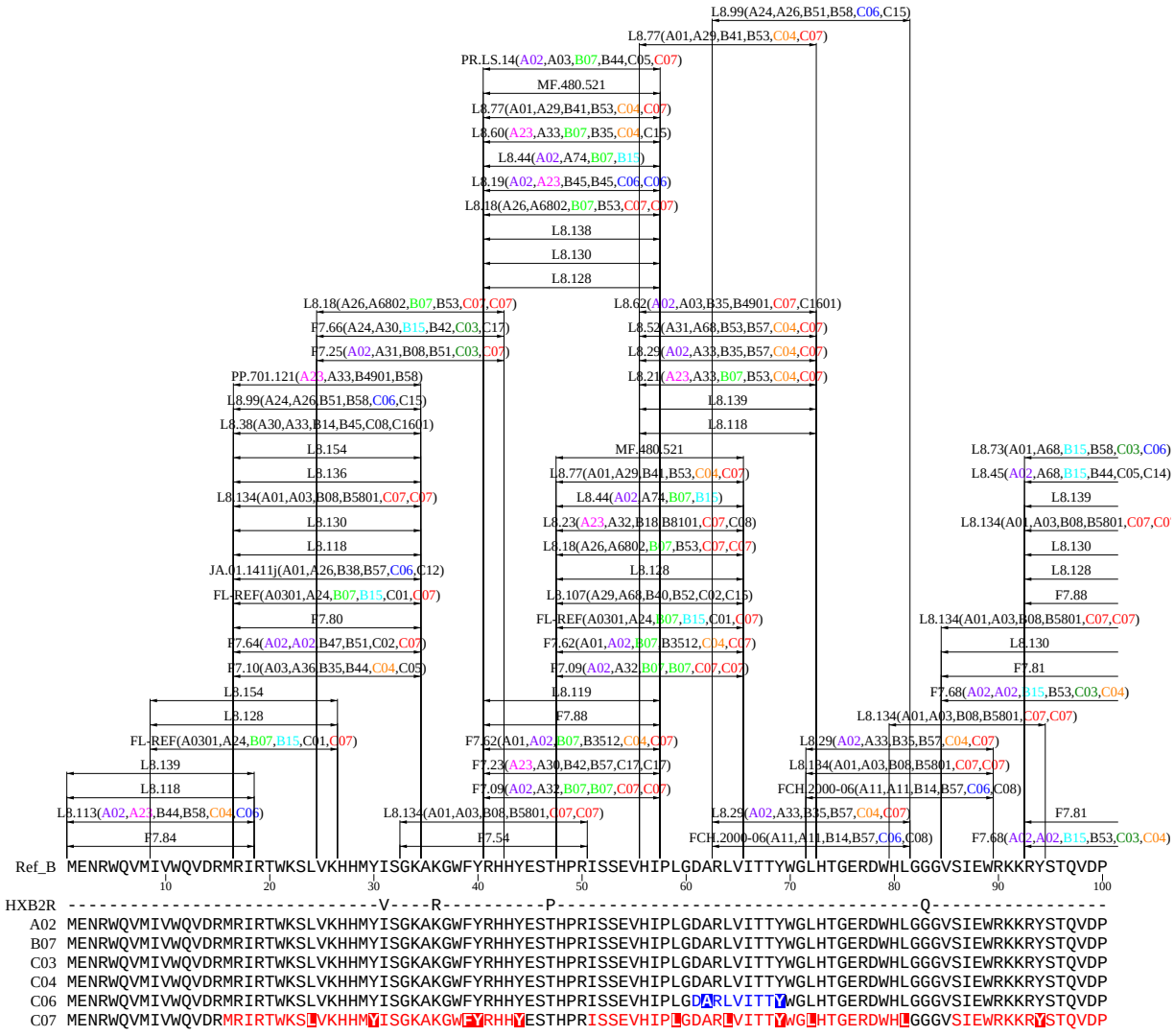


Figure 25: Vif aa 101–192 (1/1)

1.9 Vpr

Figure 26: Vpr aa 1–96 (1/2)

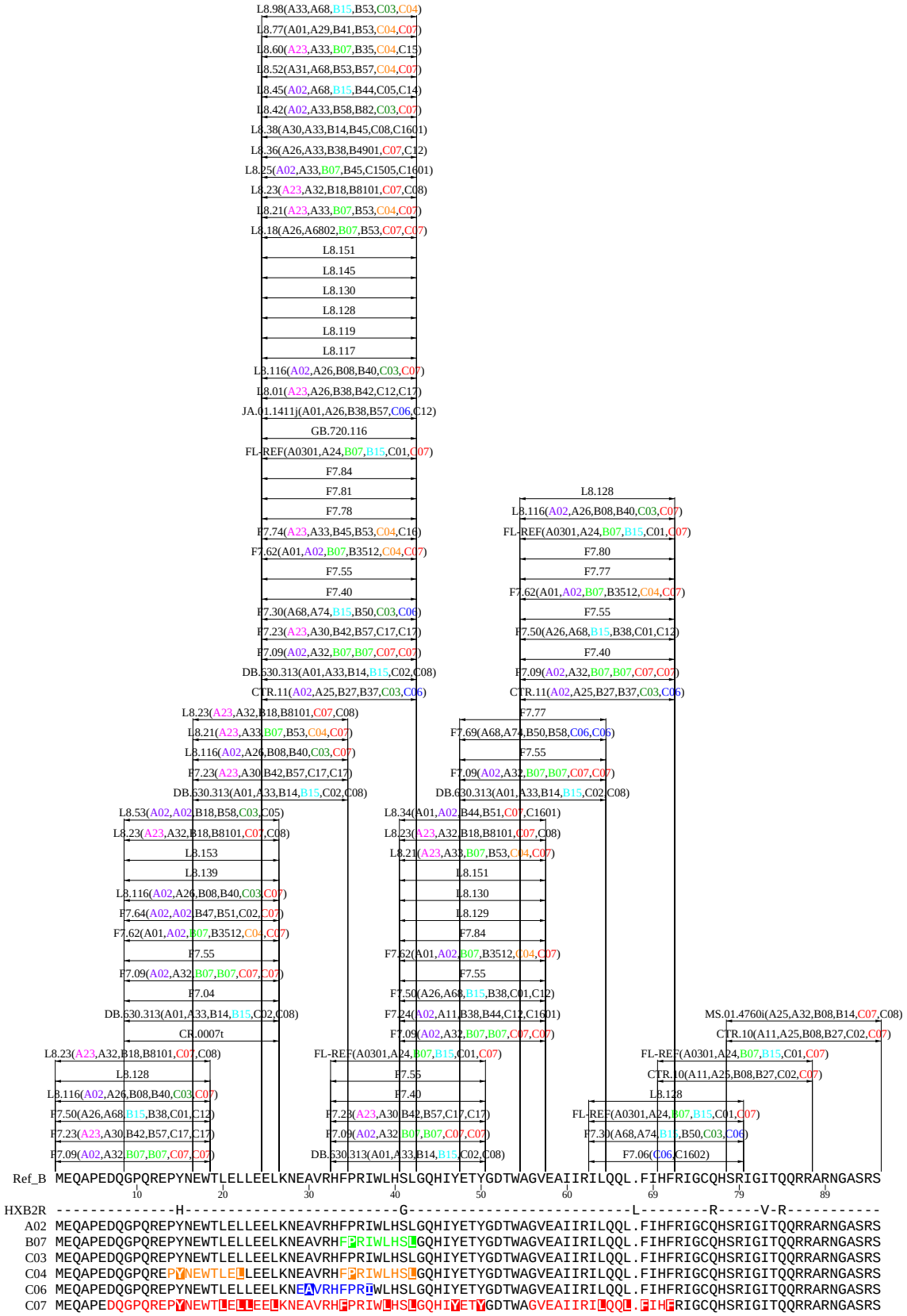
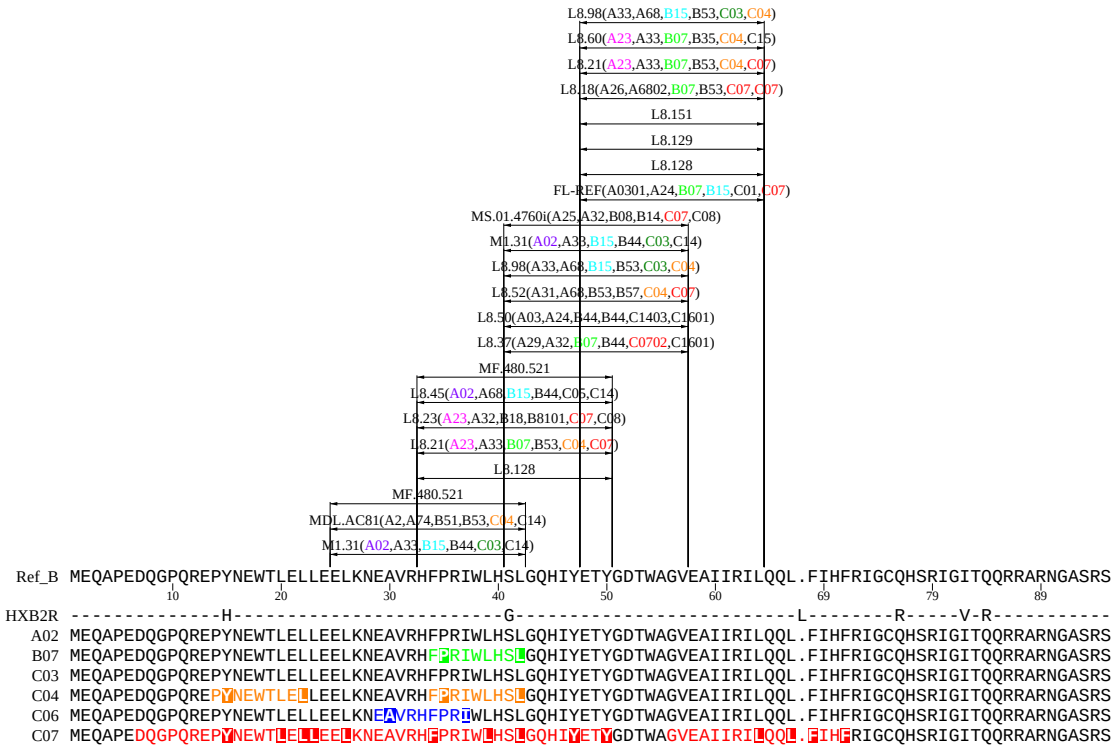


Figure 27: Vpr aa 1–96 (2/2)



1.10 Tat

Figure 28: Tat aa 1–100 (1/1)

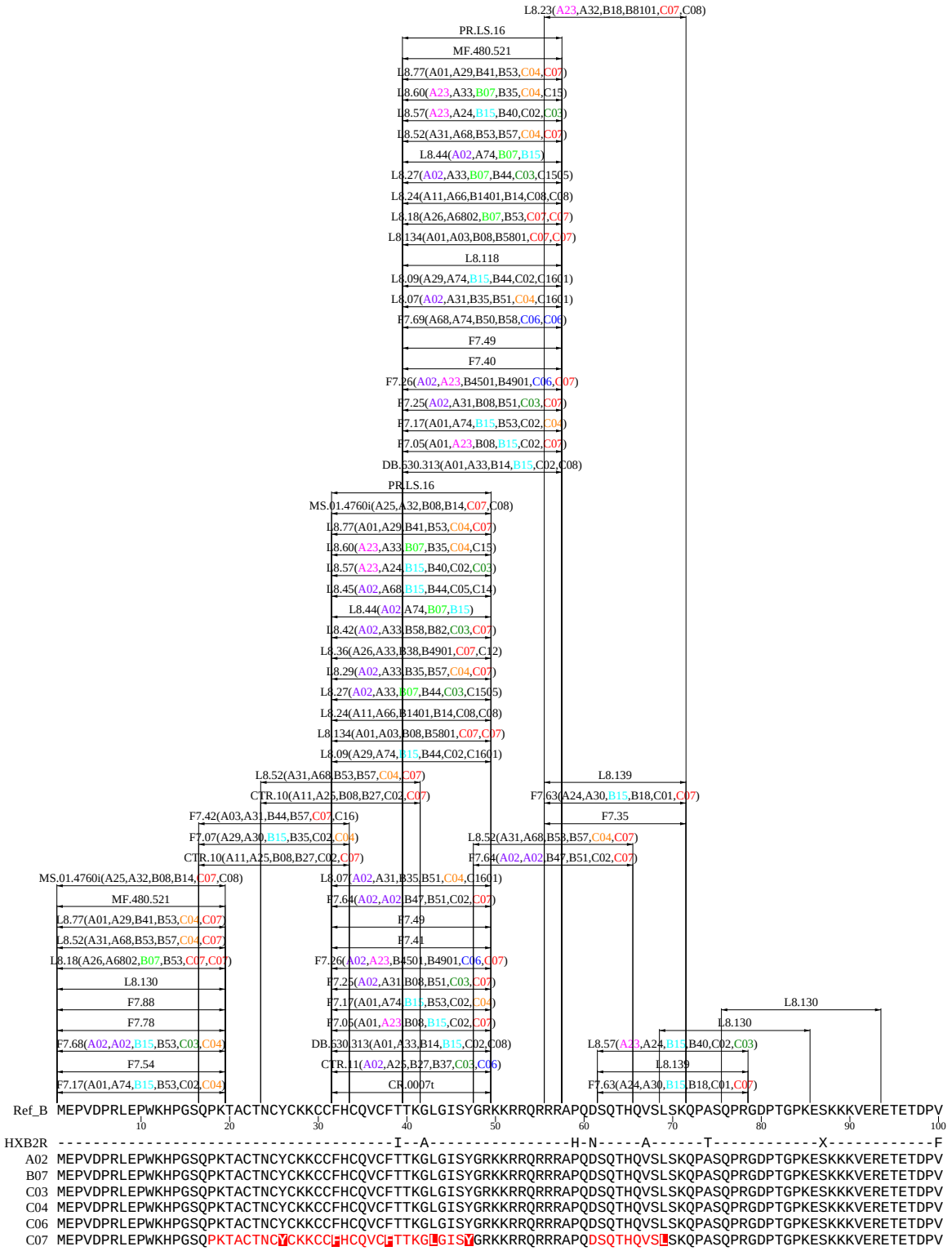


Figure 29: Tat aa 101–102 (1/1)

```
Ref_B  DQ
       102
HXB2R  -.
  A02  DQ
  B07  DQ
  C03  DQ
  C04  DQ
  C06  DQ
  C07  DQ
```

1.11 Rev

Figure 30: Rev aa 1–100 (1/1)

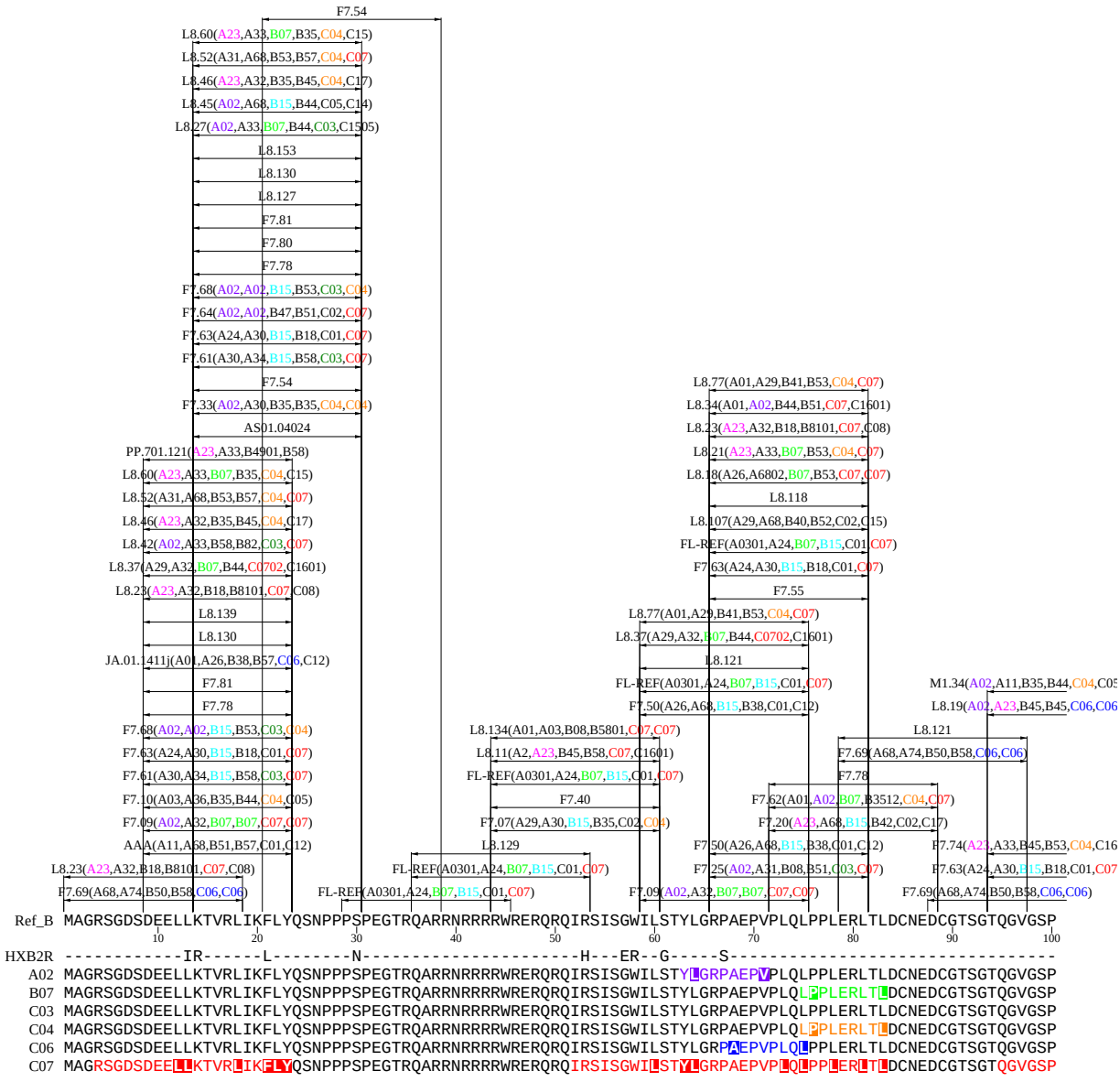
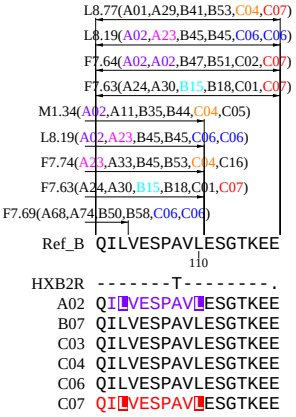
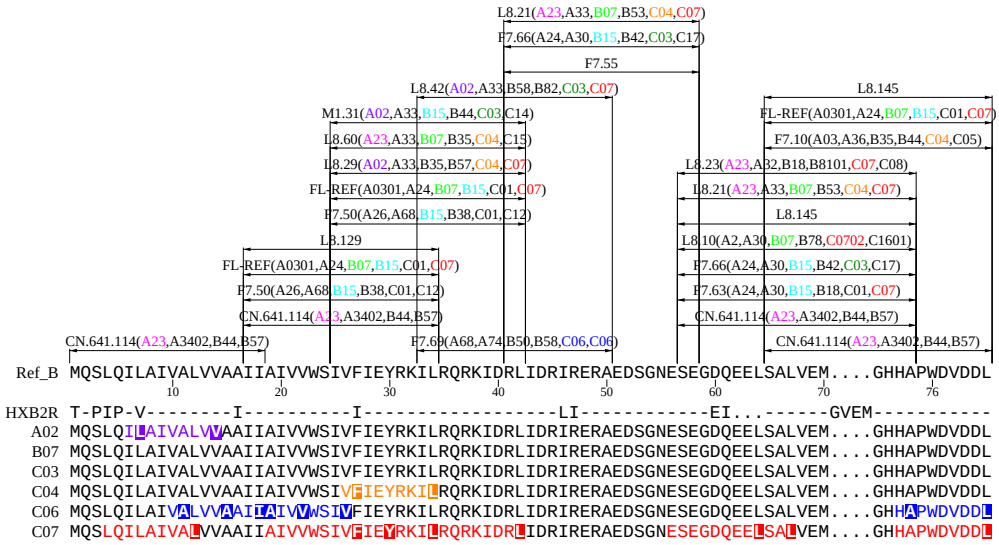


Figure 31: Rev aa 101–116 (1/1)



1.12 Vpu

Figure 32: Vpu aa 1–82 (1/1)



1.13 gp160

Figure 33: gp160 aa 1–100 (1/2)

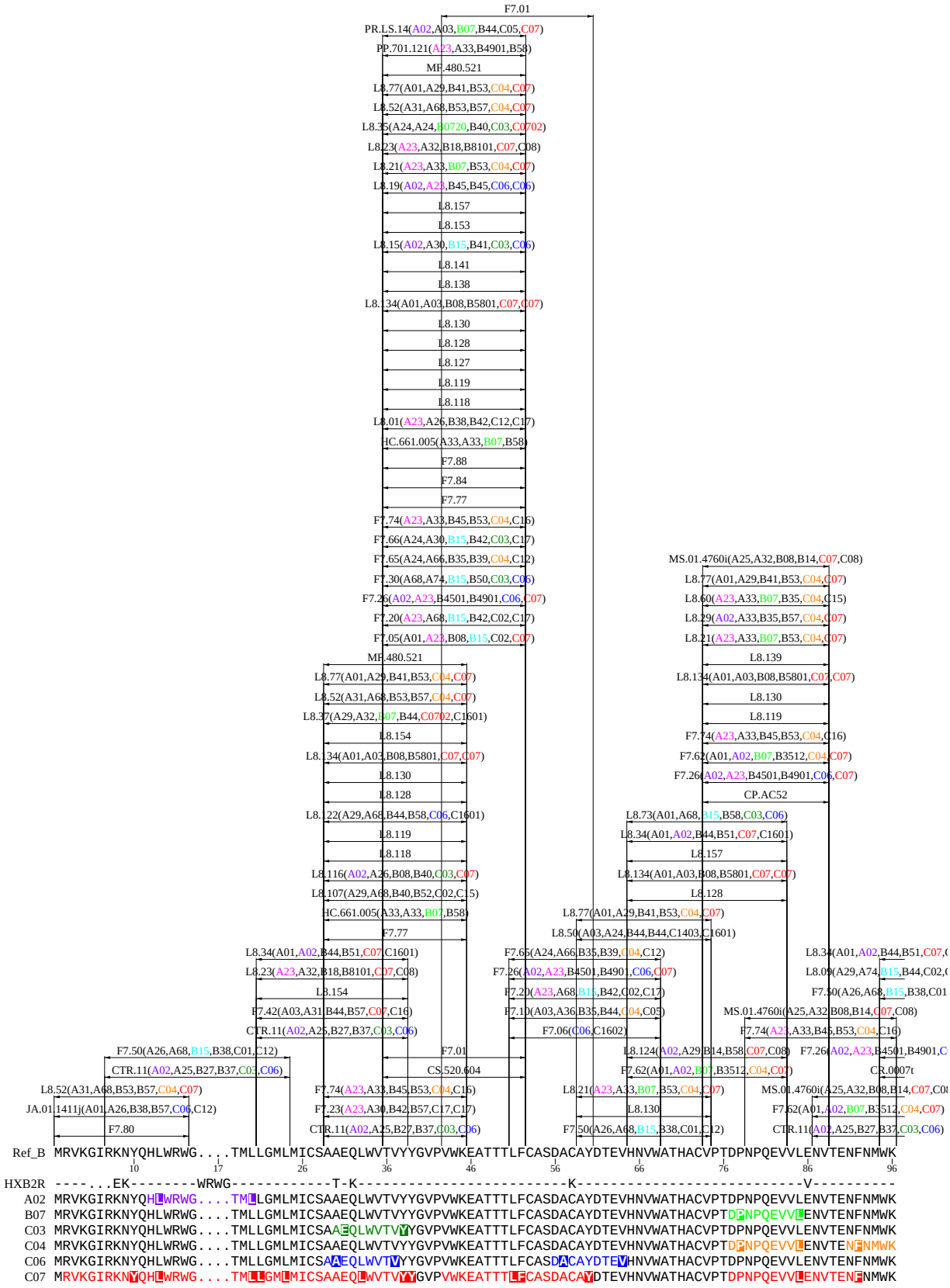


Figure 34: gp160 aa 1–100 (2/2)

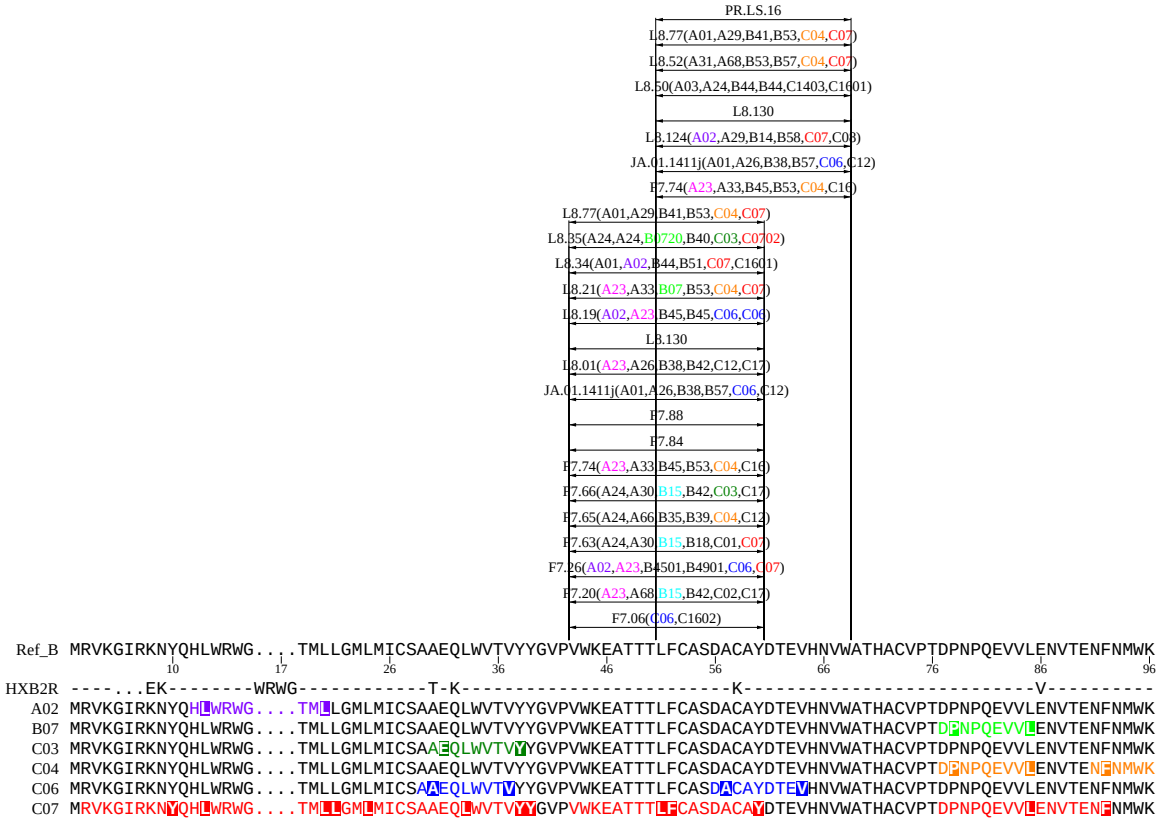


Figure 35: gp160 aa 101–200 (1/1)

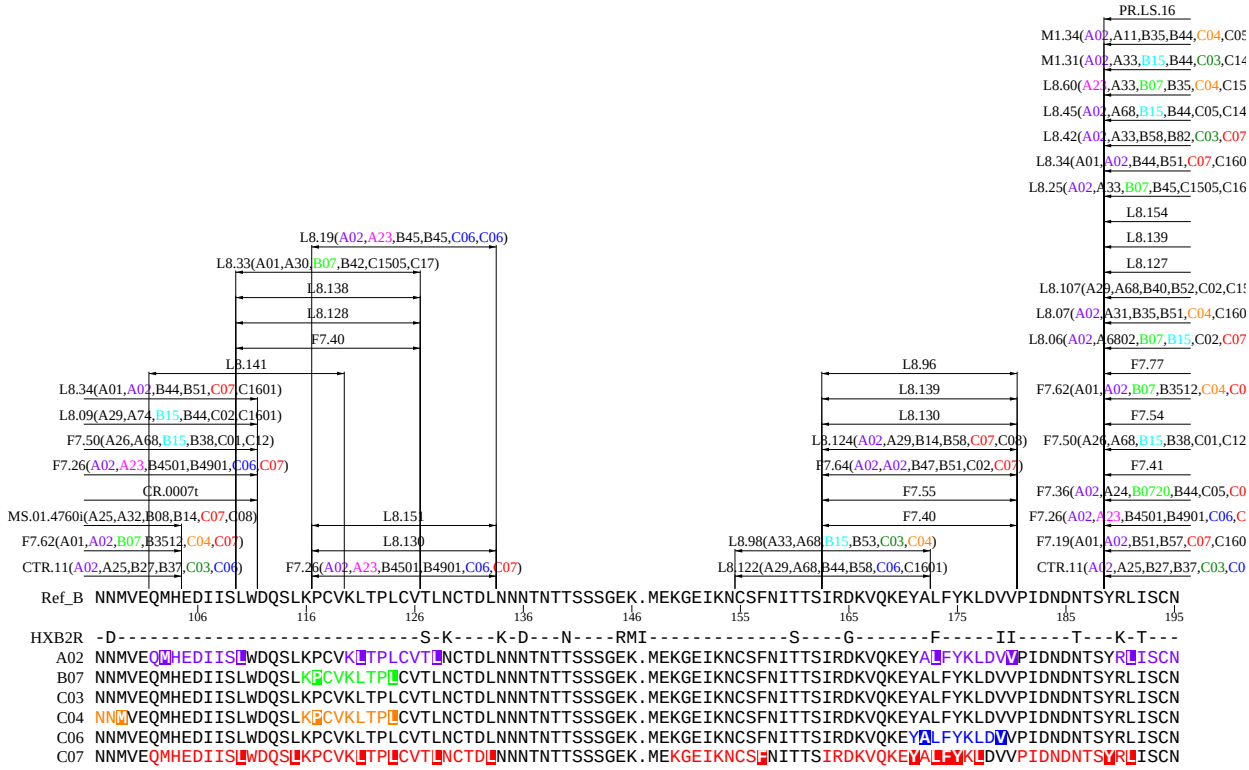


Figure 36: gp160 aa 201–300 (1/1)

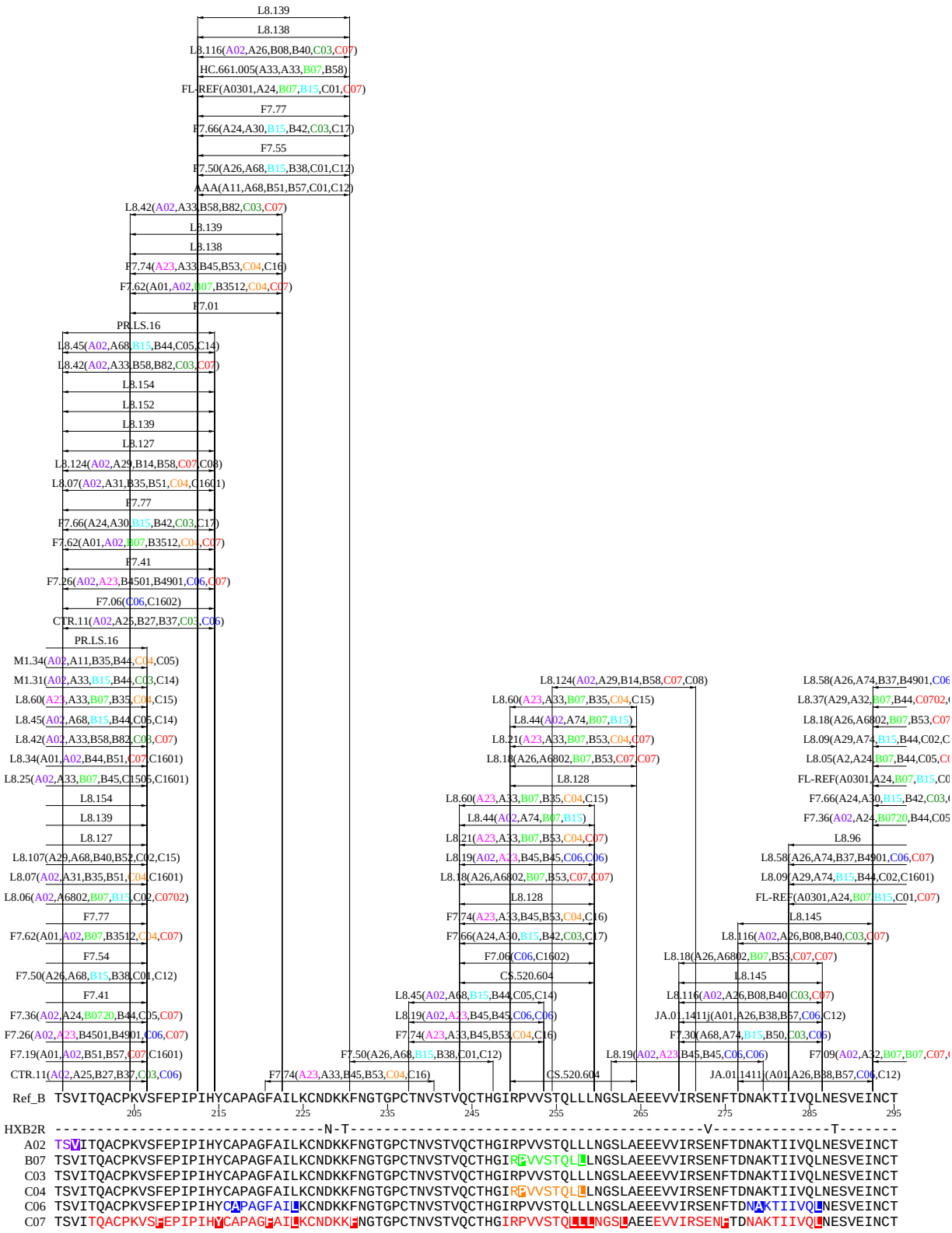


Figure 37: gp160 aa 301–400 (1/1)

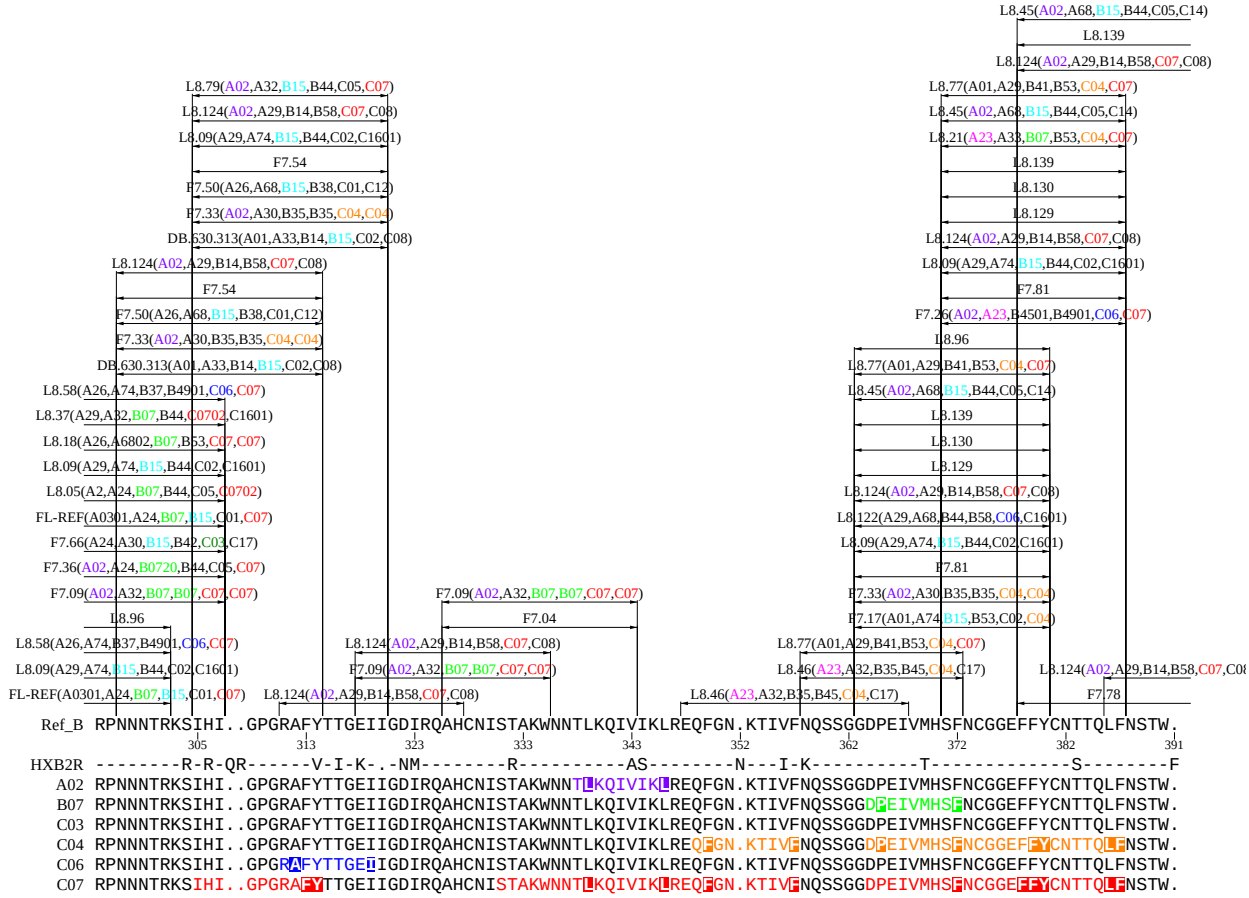


Figure 38: gp160 aa 401–500 (1/1)

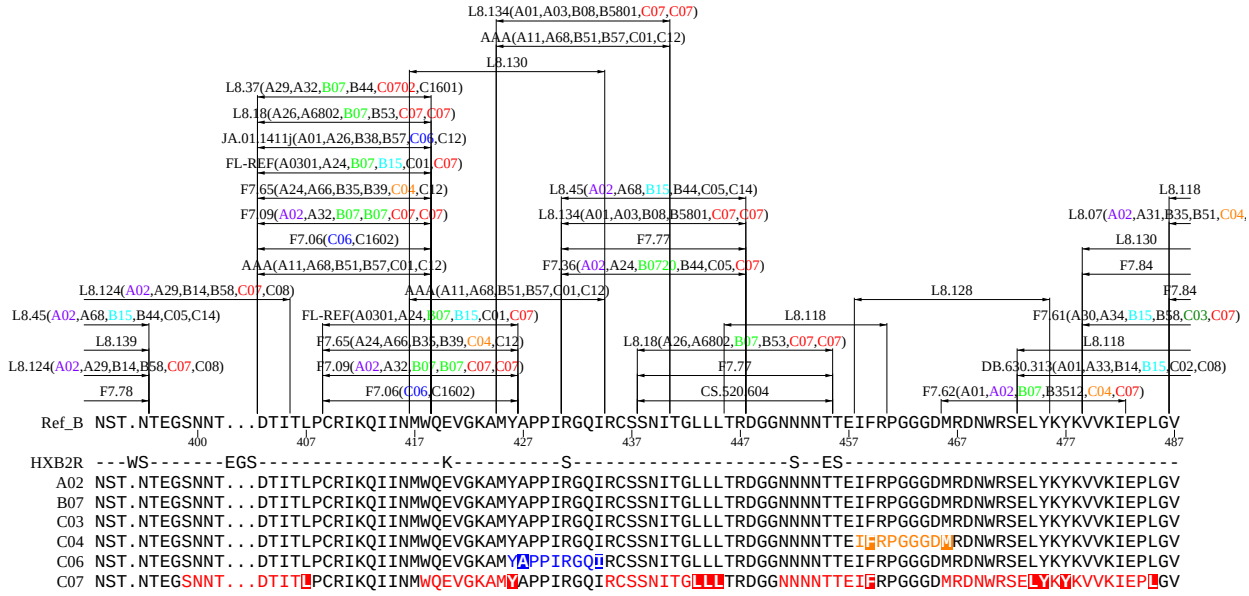


Figure 39: gp160 aa 501–600 (1/1)

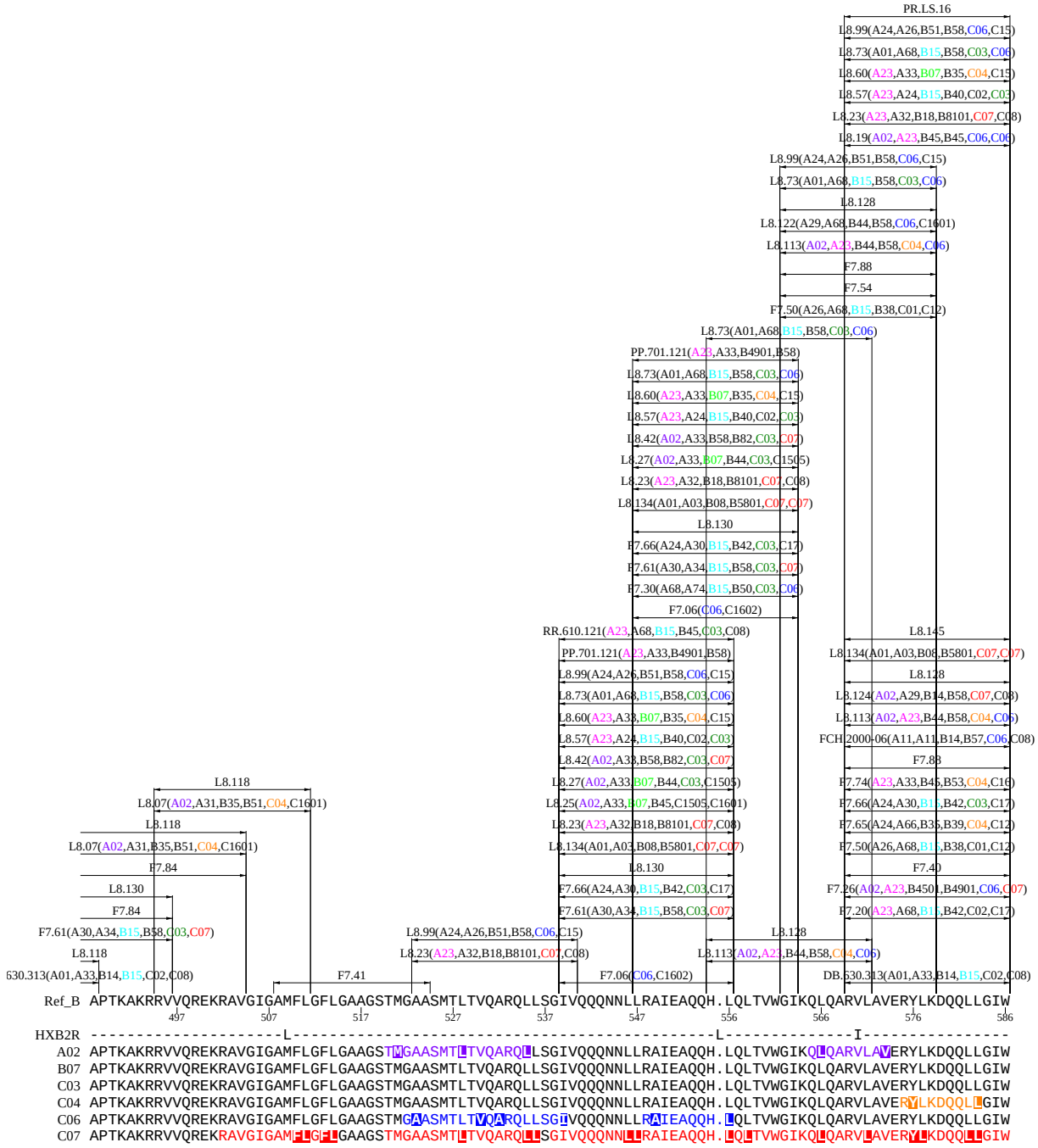


Figure 40: gp160 aa 601–700 (1/1)

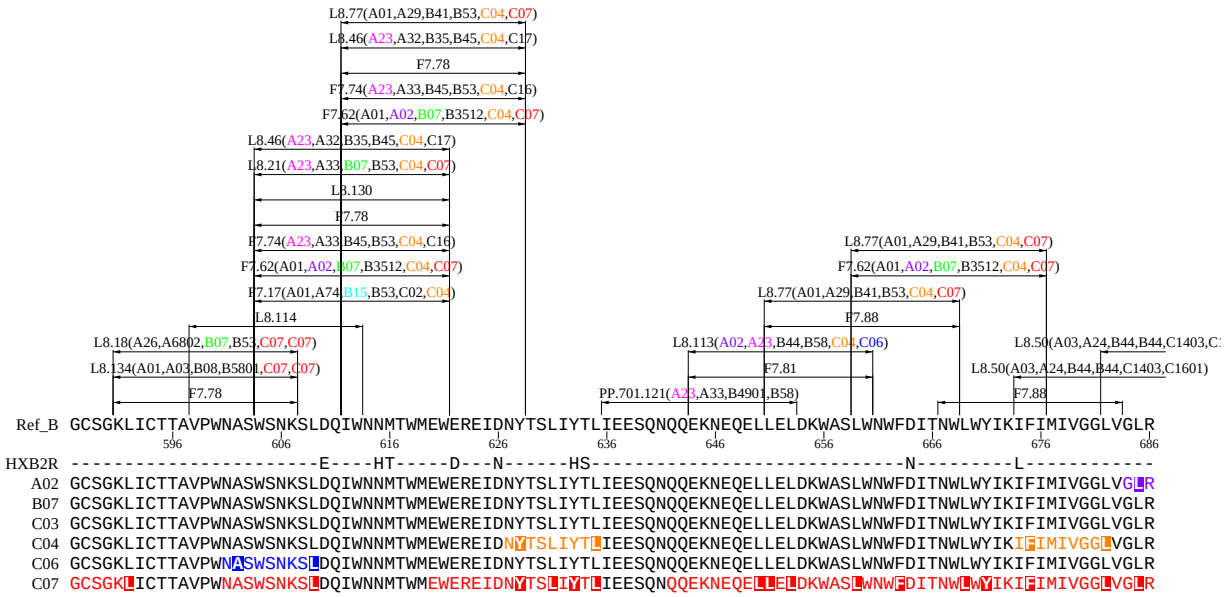


Figure 41: gp160 aa 701–800 (1/1)

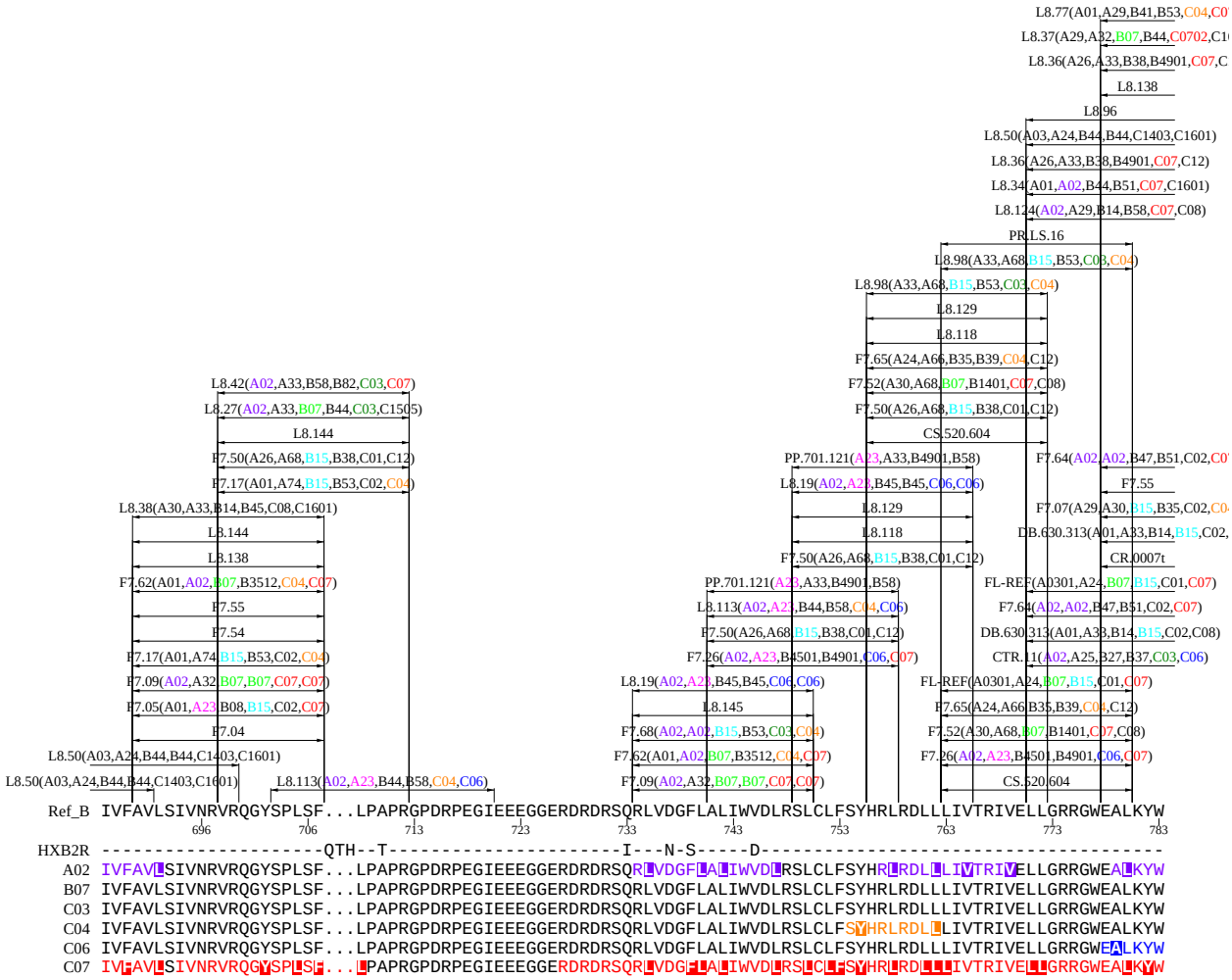
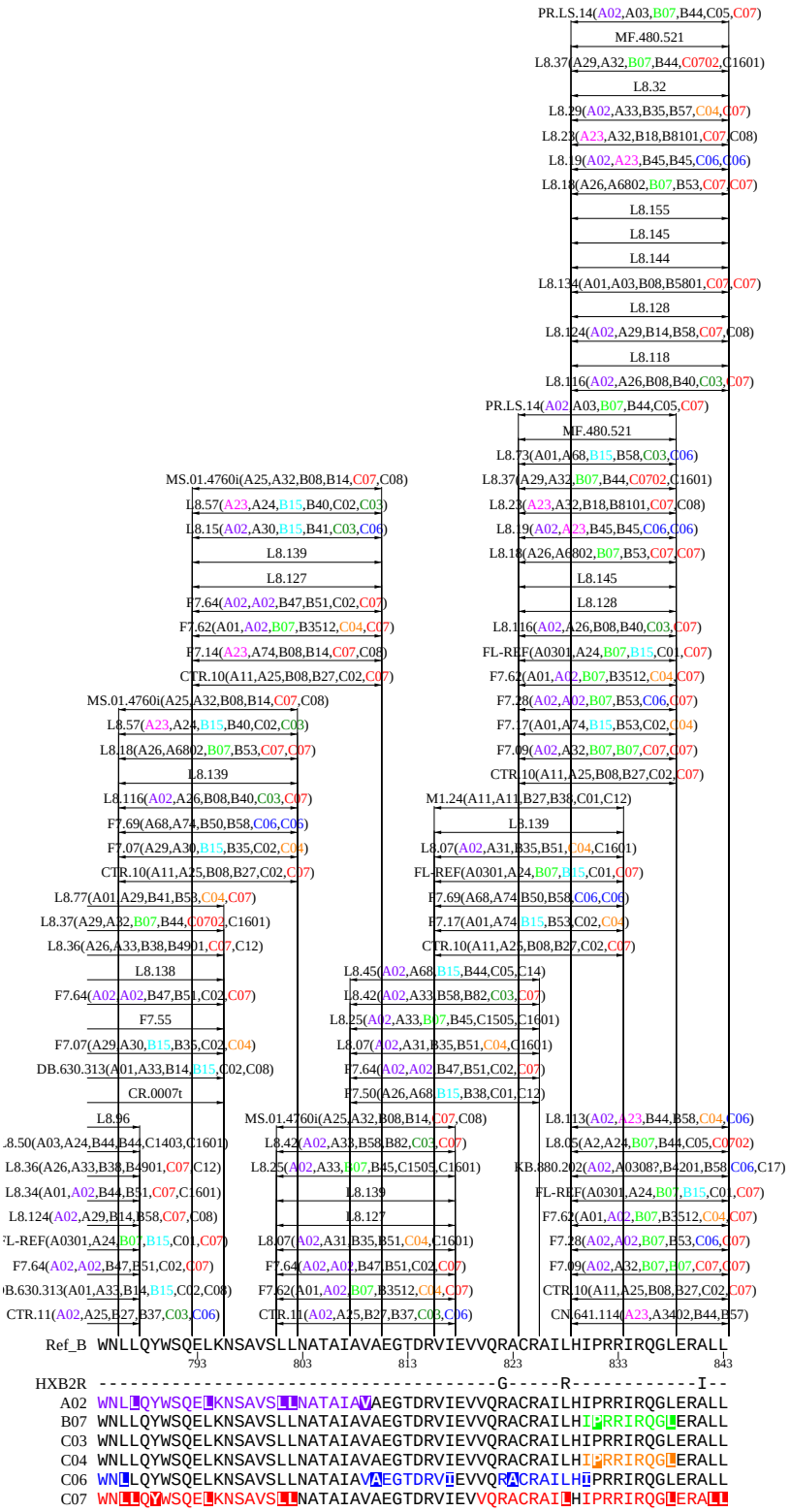


Figure 42: gp160 aa 801–856 (1/1)



1.14 Nef

Figure 43: Nef aa 1–100 (1/4)

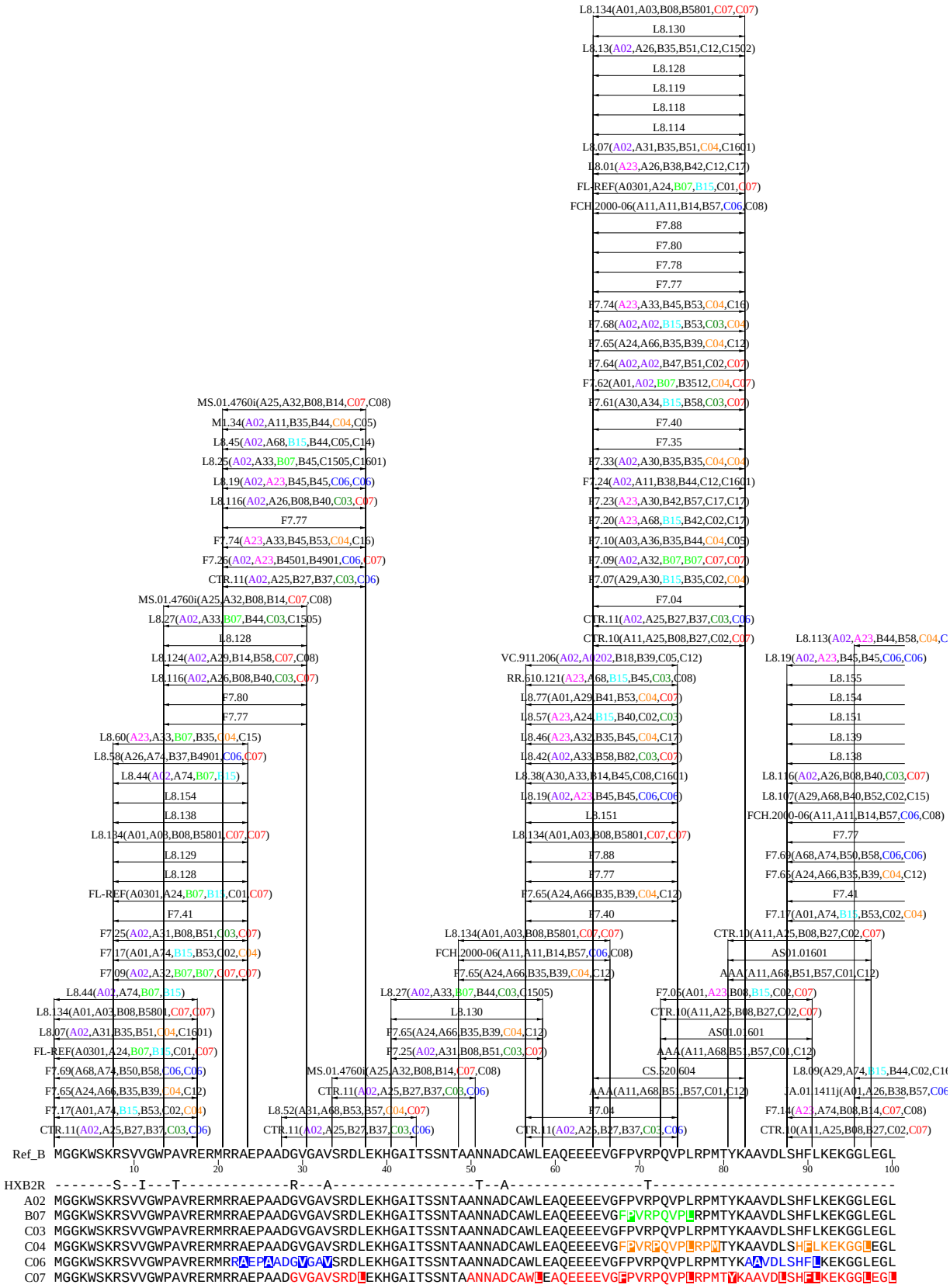


Figure 44: Nef aa 1–100 (2/4)

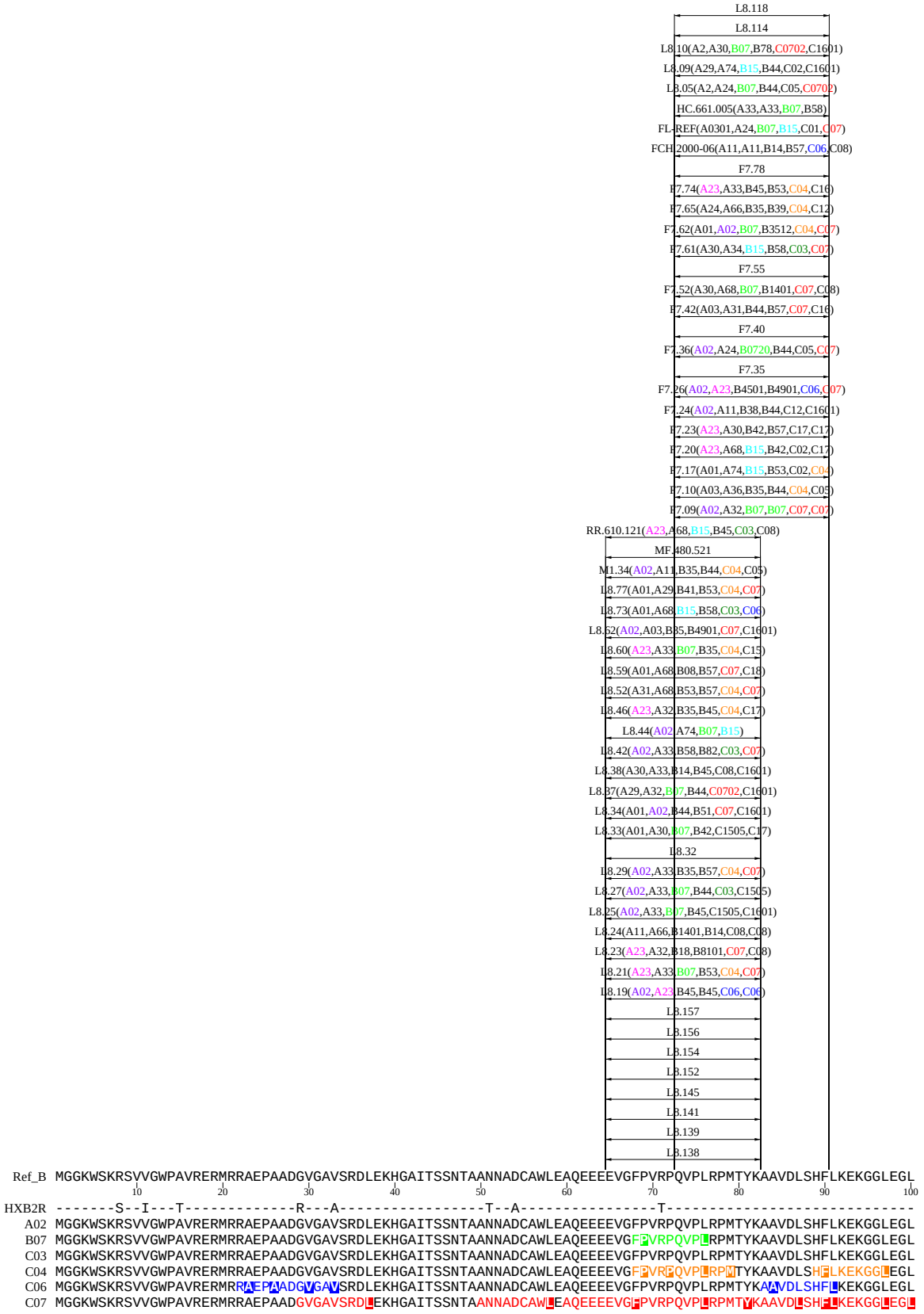


Figure 45: Nef aa 1–100 (3/4)

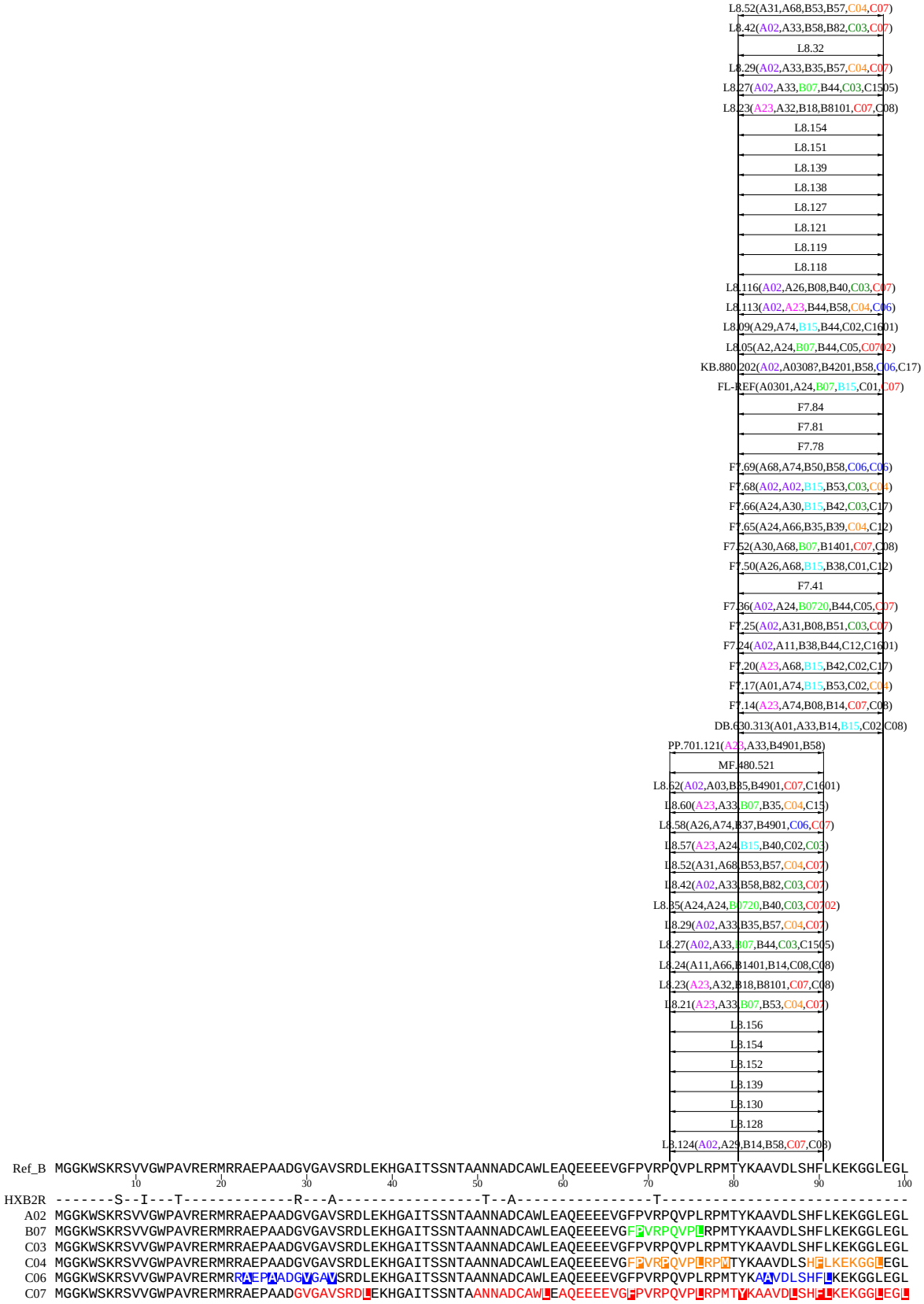


Figure 46: Nef aa 1–100 (4/4)

Figure 47: Nef aa 101–200 (1/4)

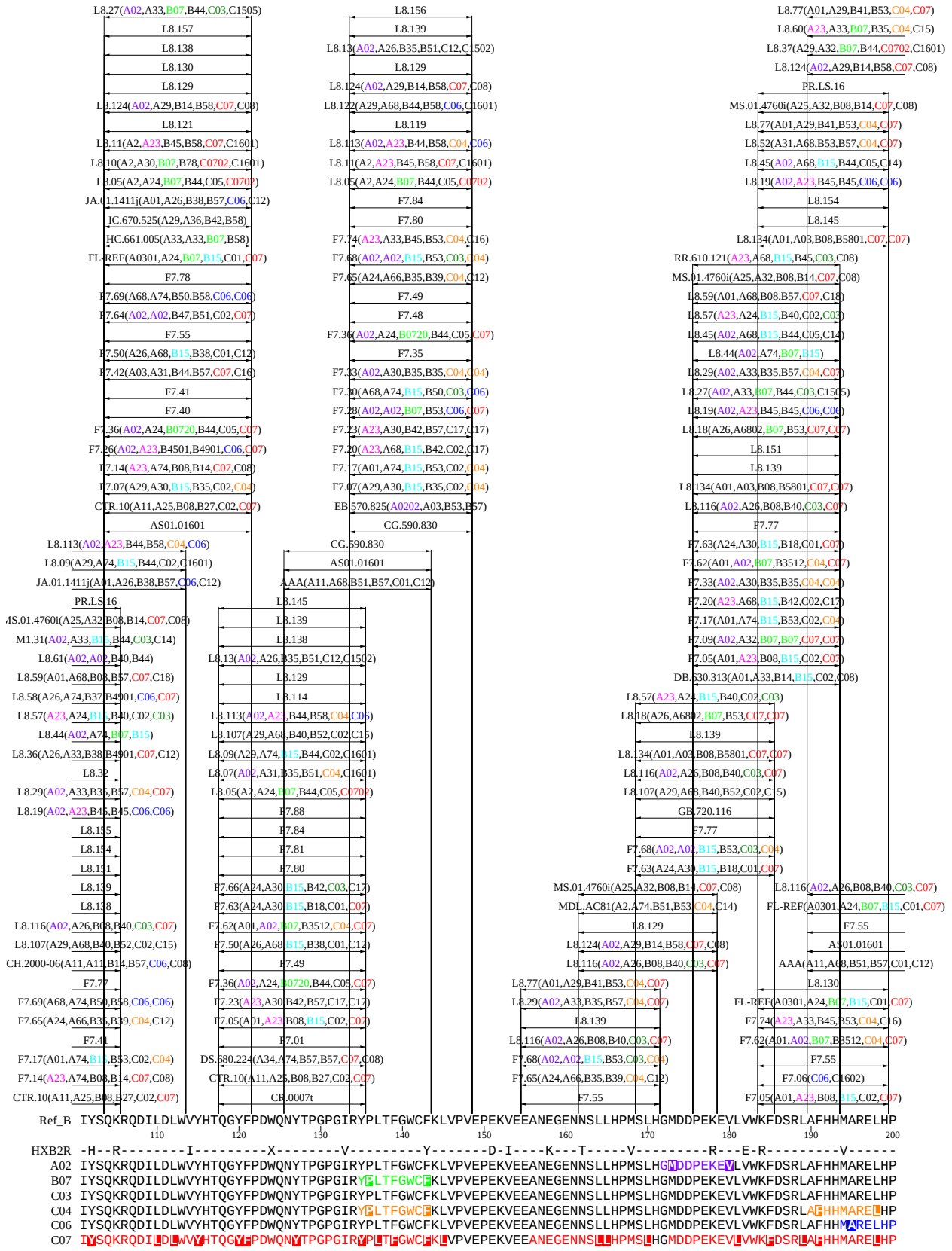


Figure 48: Nef aa 101–200 (2/4)

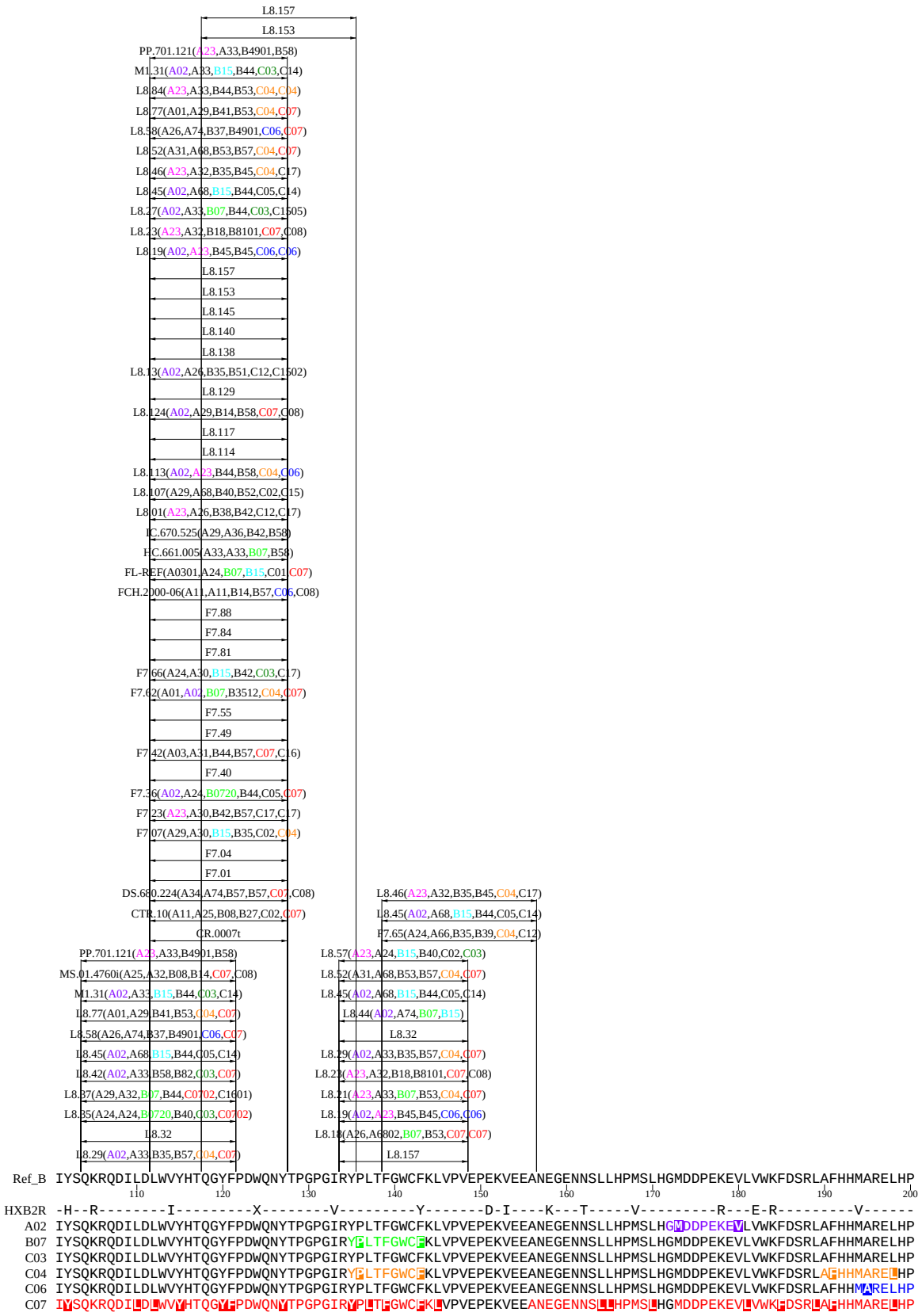


Figure 49: Nef aa 101–200 (3/4)

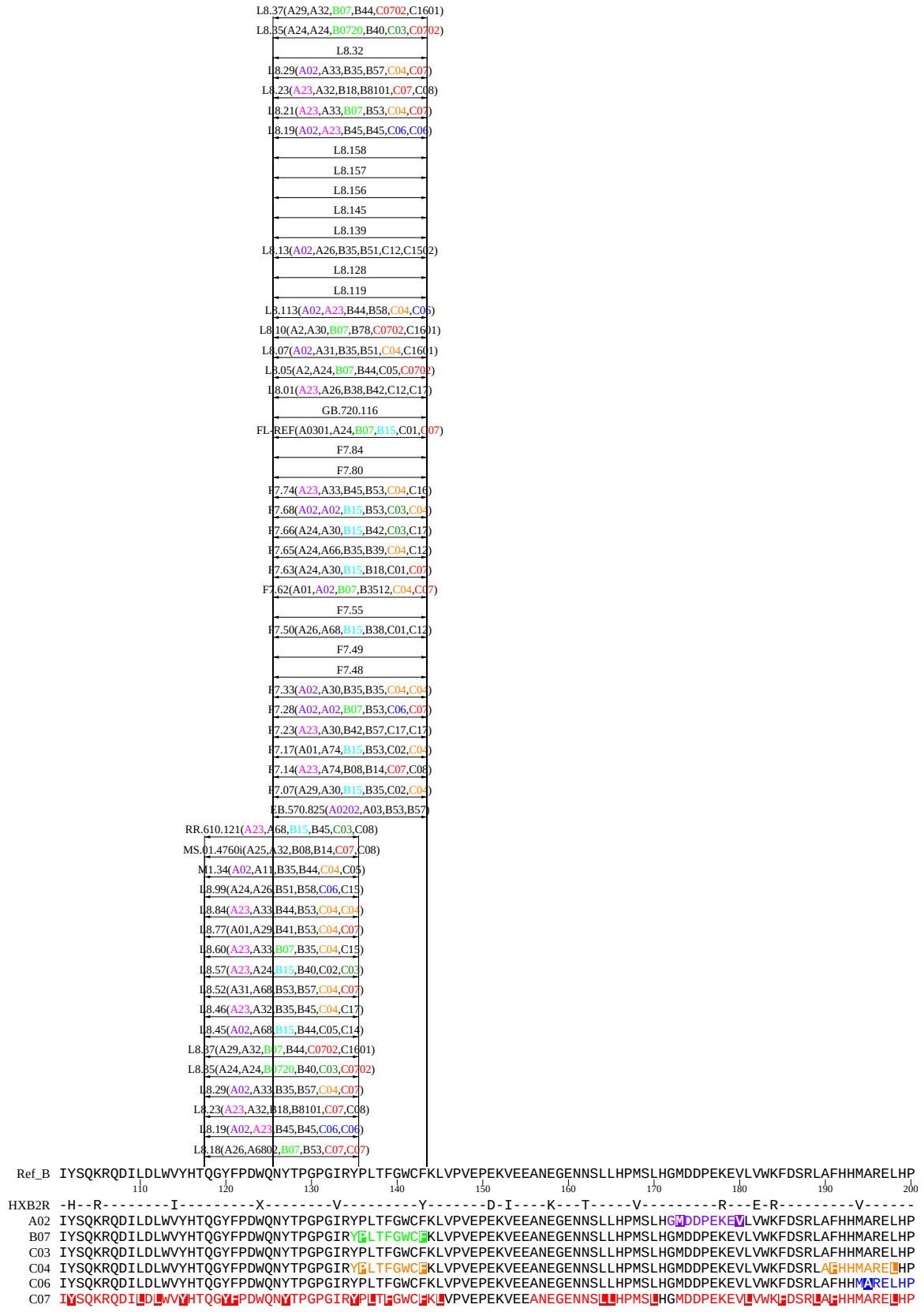


Figure 50: Nef aa 101–200 (4/4)

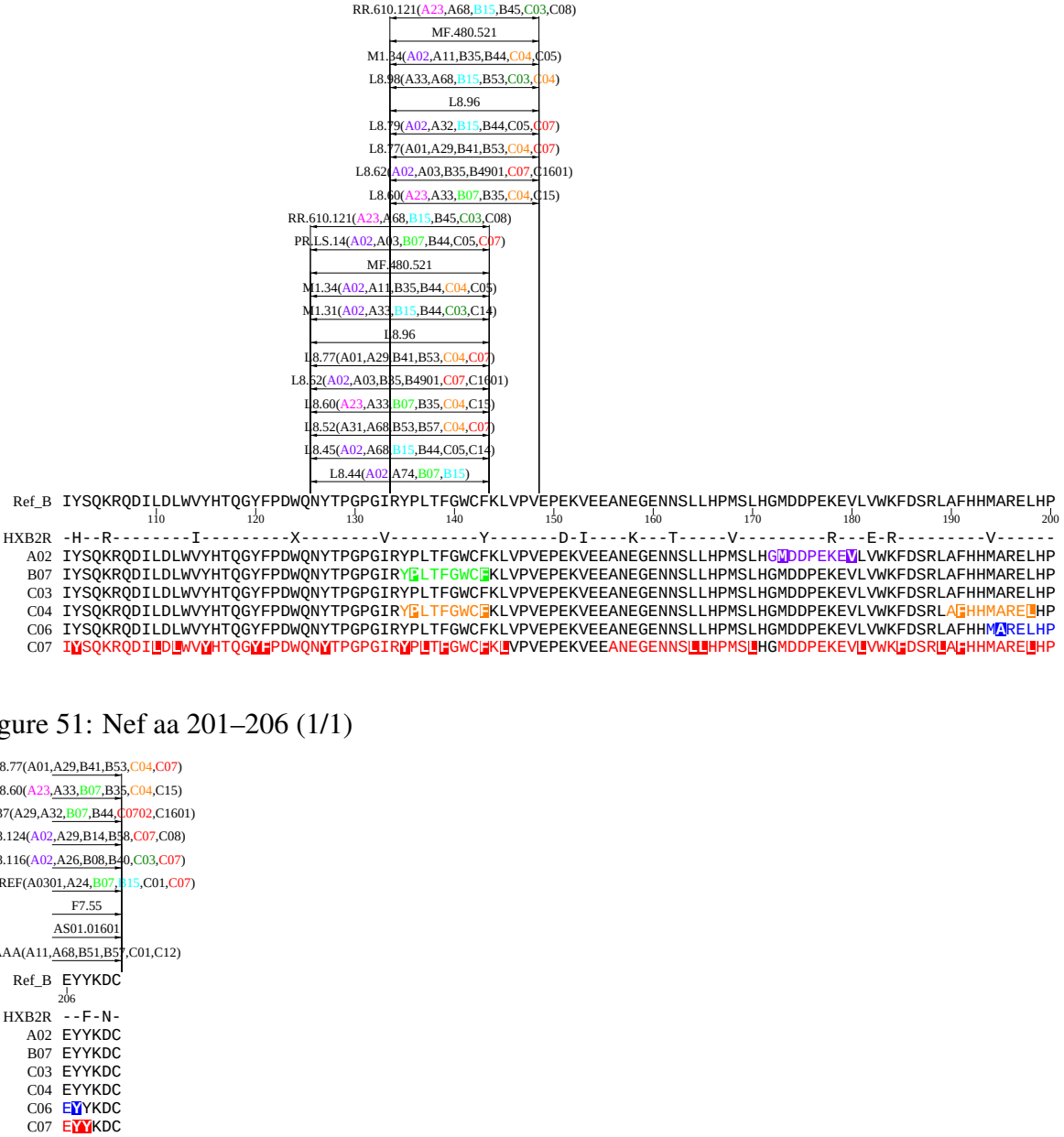
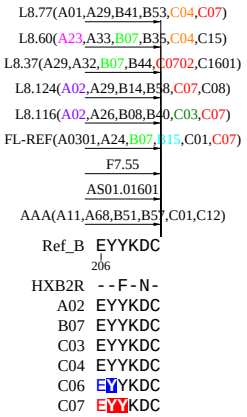



Figure 51: Nef aa 201–206 (1/1)