

Data S1

Worked ConTAMPR Examples

Example	Pages	Sample	Locus	Related to
1	2 - 15	B11	mtCO1	Figure 1, Table 2, Figure S2
2	16-31	B14	28S	Table 2, Figure S3H, Figure S3K
3	32-44	D14	EPIC25	Table 2

Sample: B11

Locus: mtCO1 marker

Hypothesis: DNA from Species A was contaminated with DNA from Species E

1. gi|1005054365|gb|KU860593.1| (A vaga complex sp. A JFF-2016 isolate B11 cytoch...

T T T A T T A T T G G A A T T T G A T C A G G T T T T T A G G T G

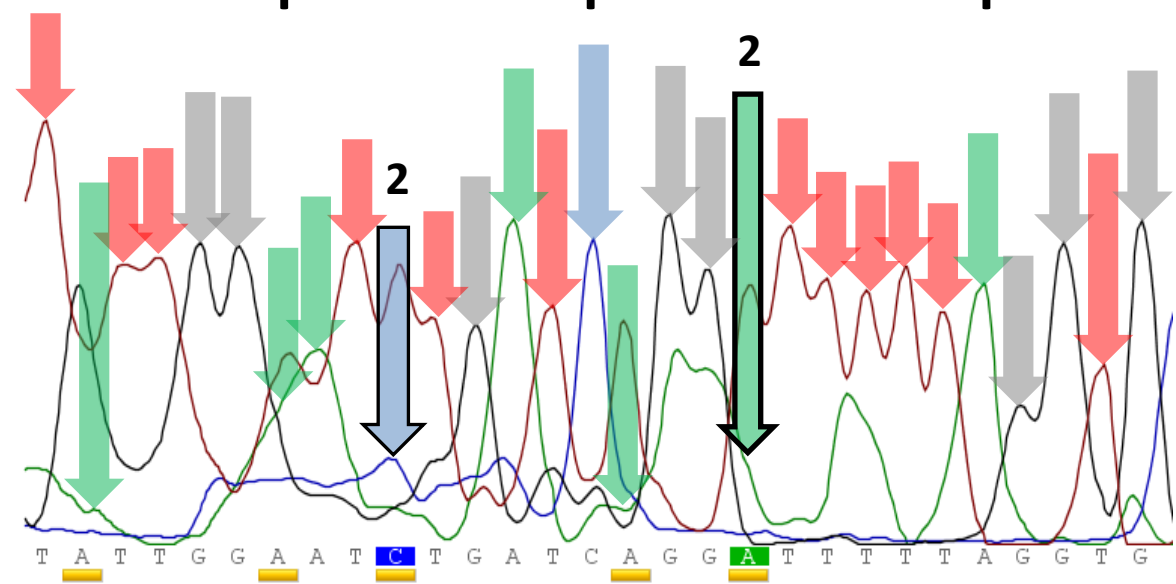


Arrows indicate base calls shared by Hap6 [A] and Hap31 [E]

Numbered arrows show peaks matching Hap31 [E] but not Hap6 [C], with relative height ranks

2. ND_B11-LC01_A01_015.scf

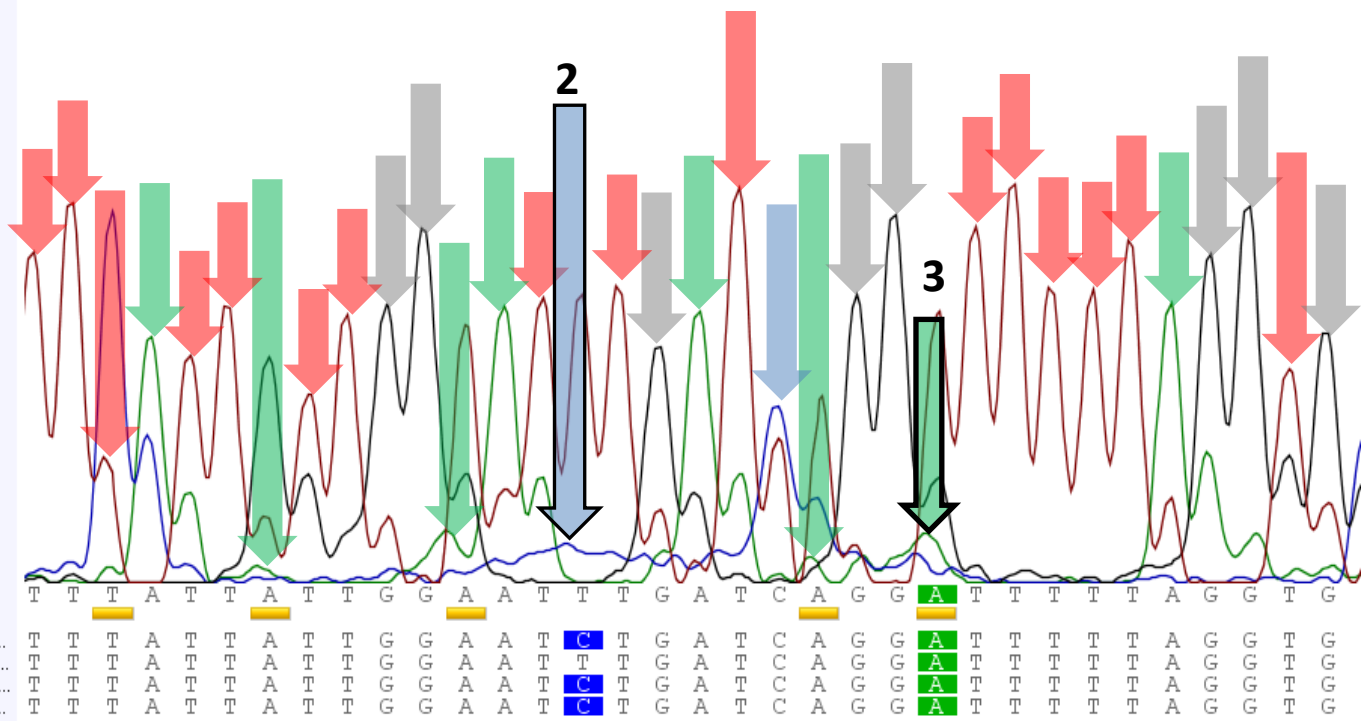
Species A Hap6 shown at top



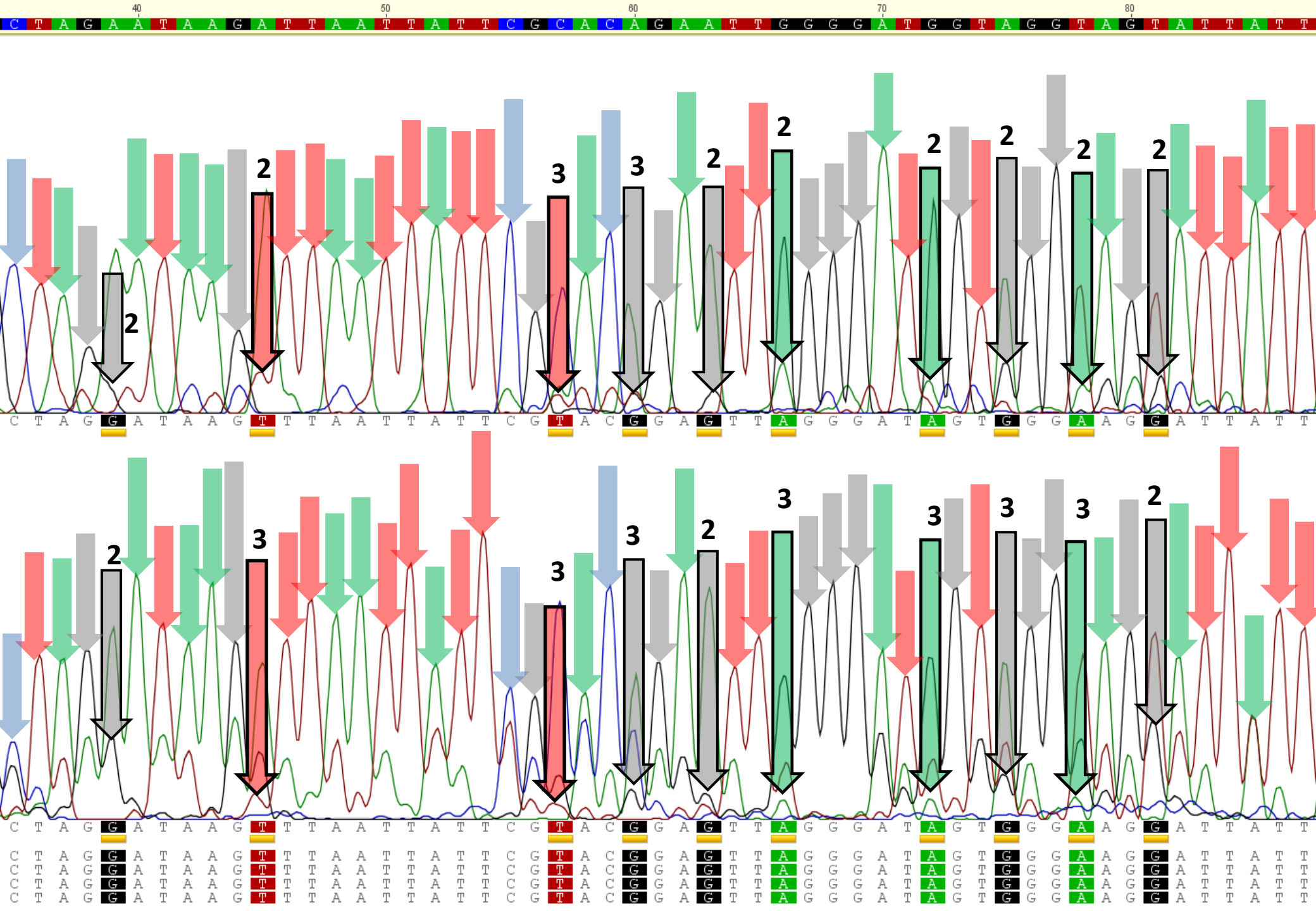
Sample B11 mtCO1 minority peak ranks

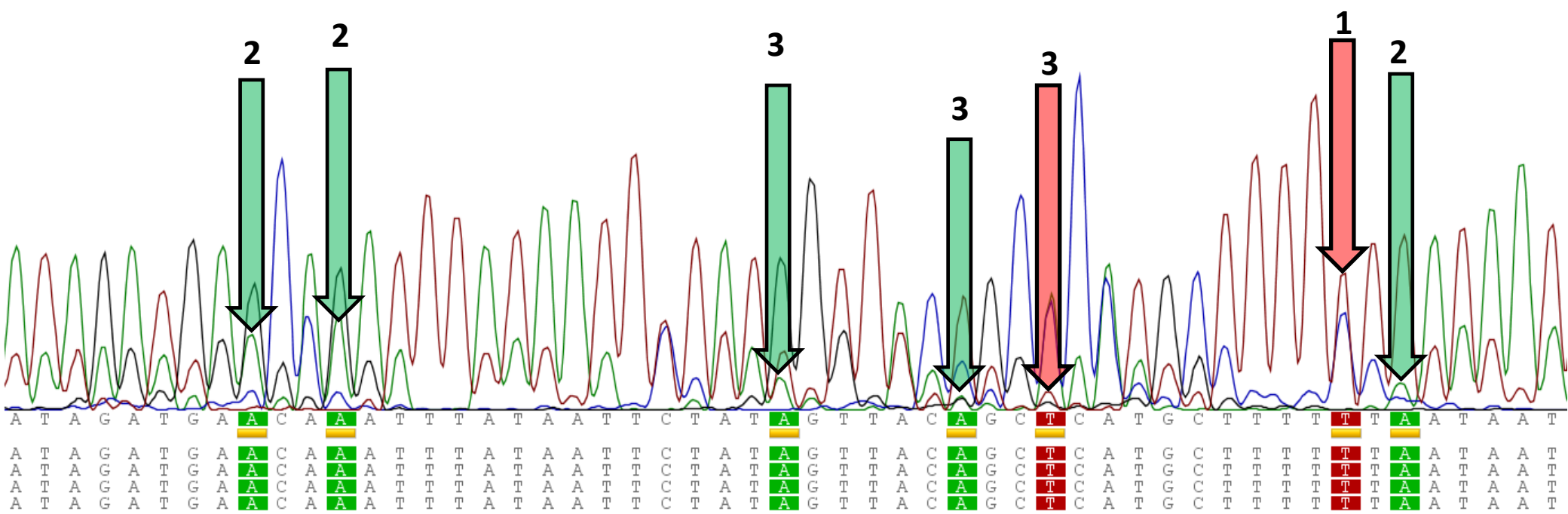
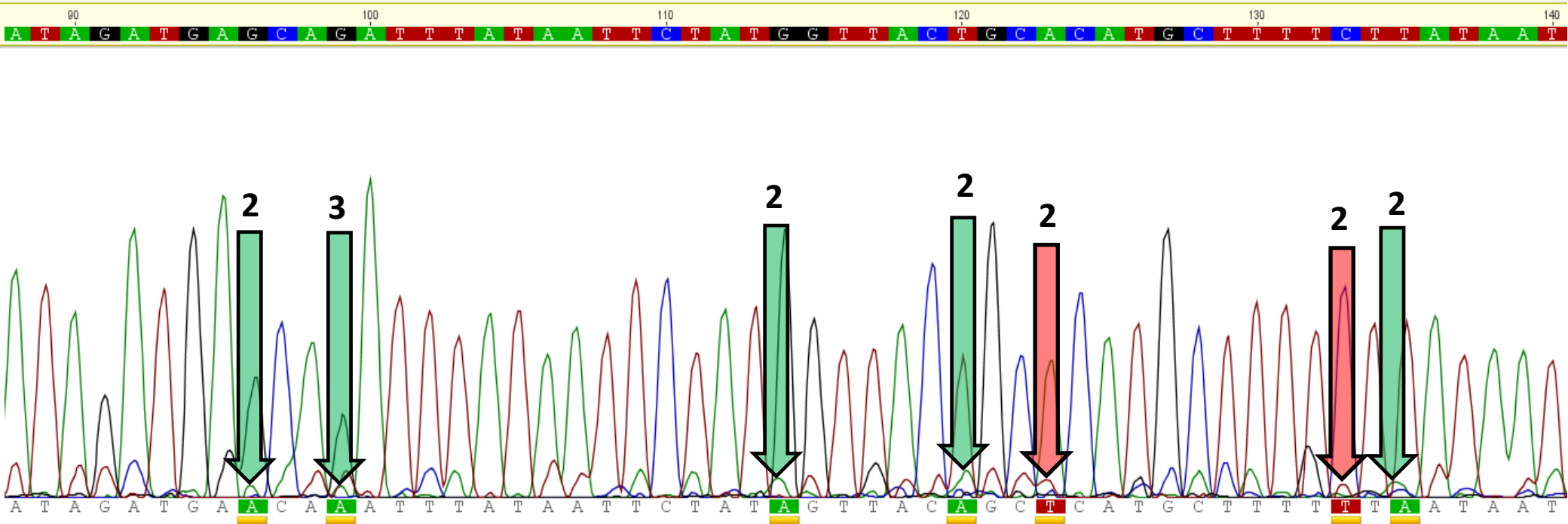
Species E Hap31 (as seen in Individual 81)

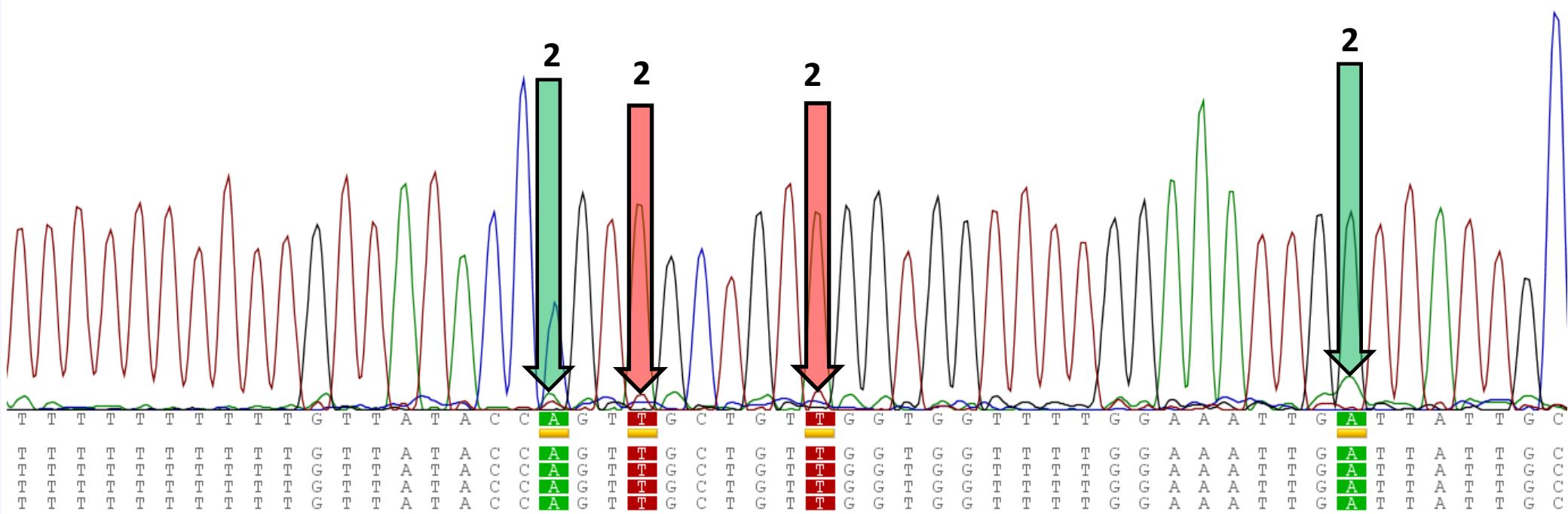
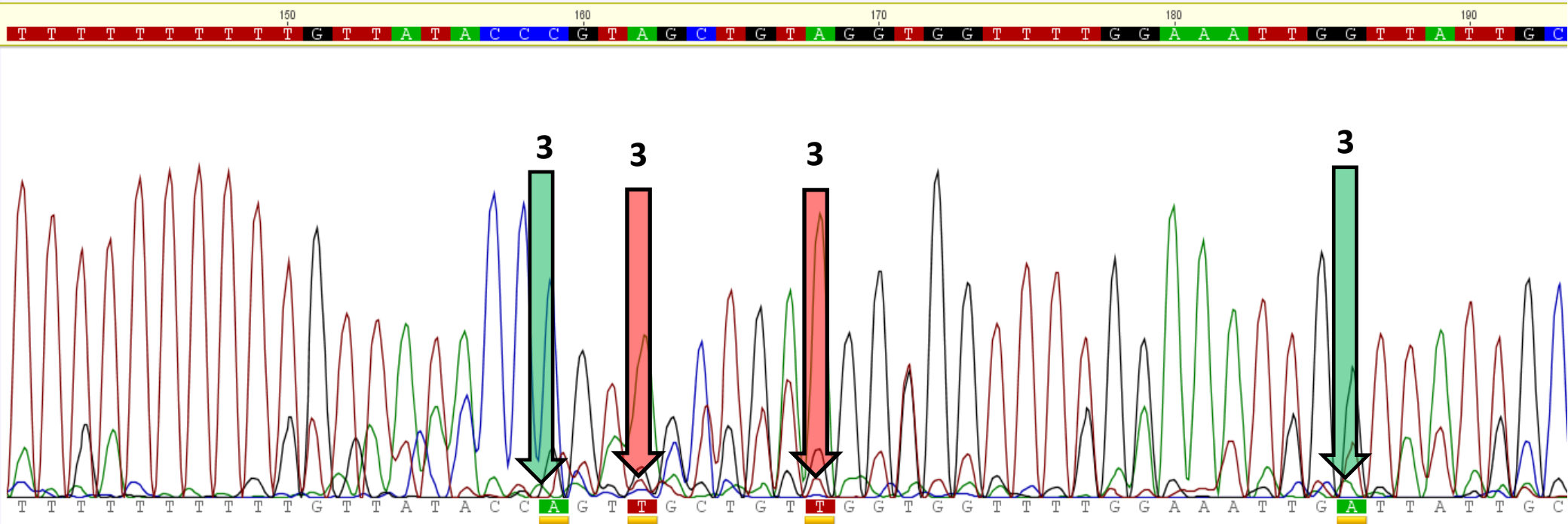
3. ND_B11-HC01_A01_015.scf

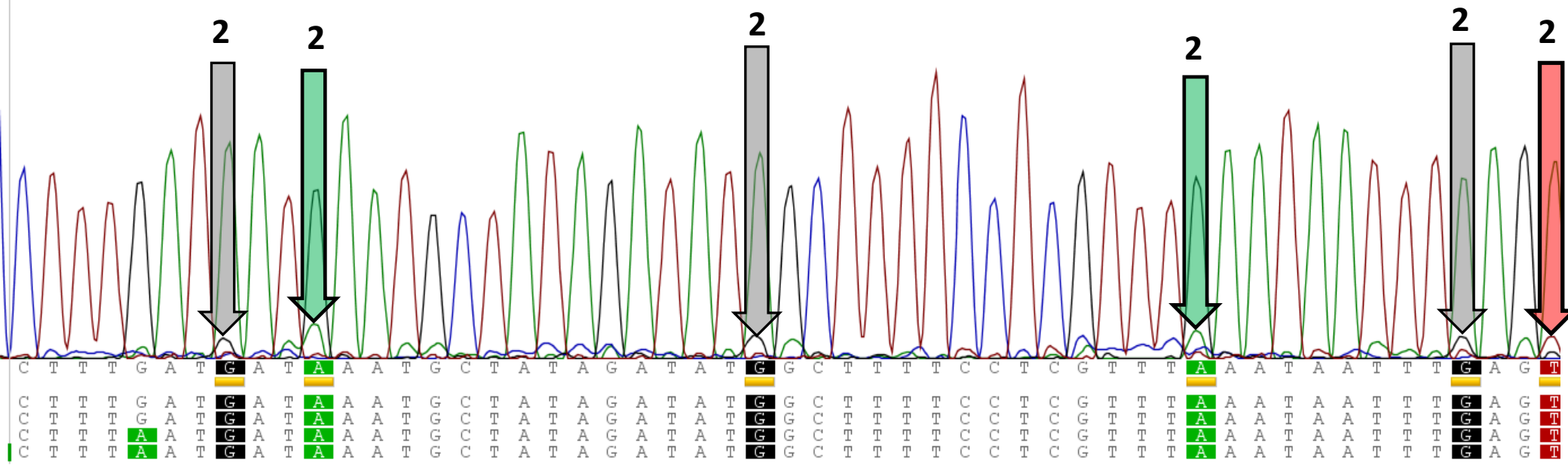
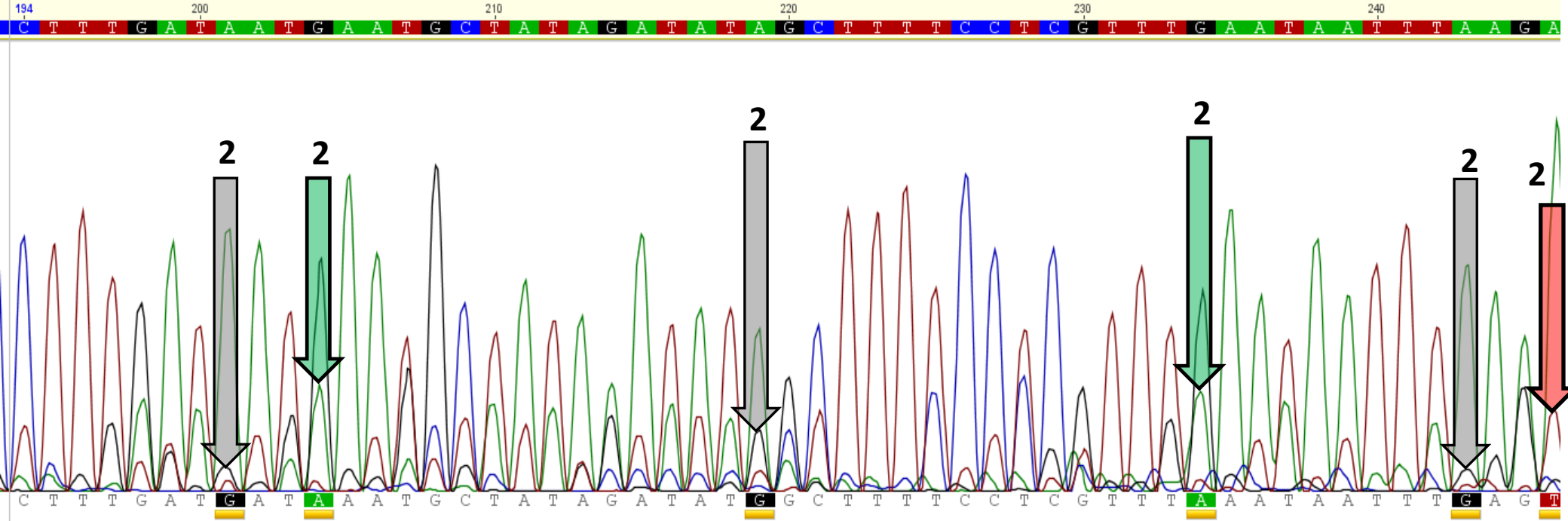


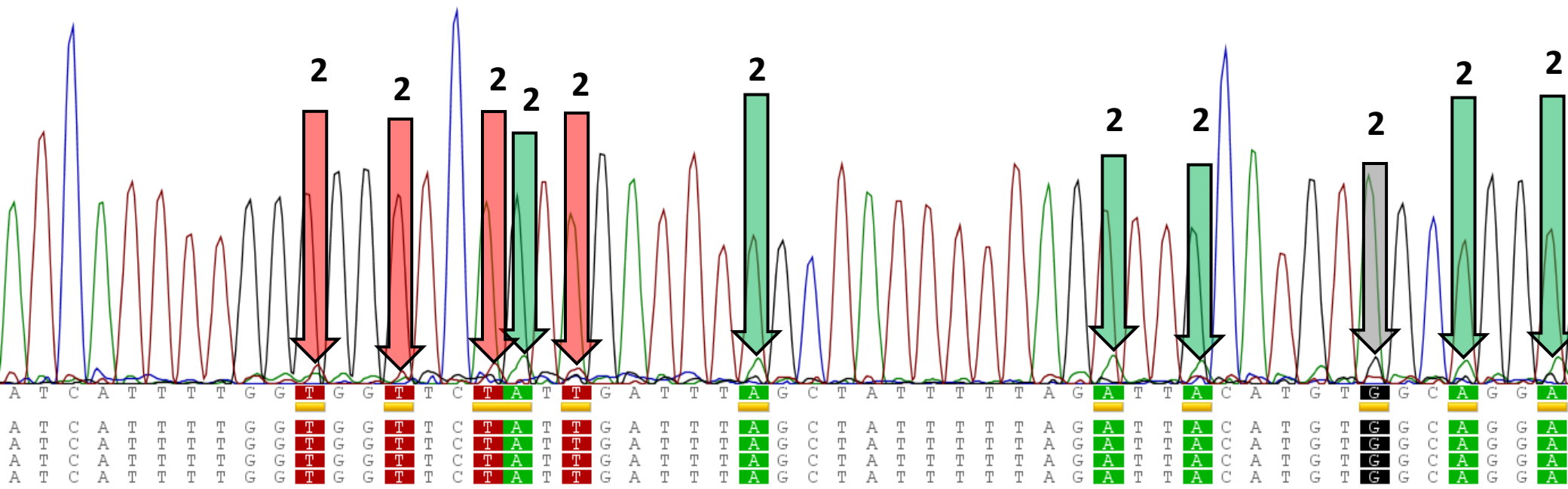
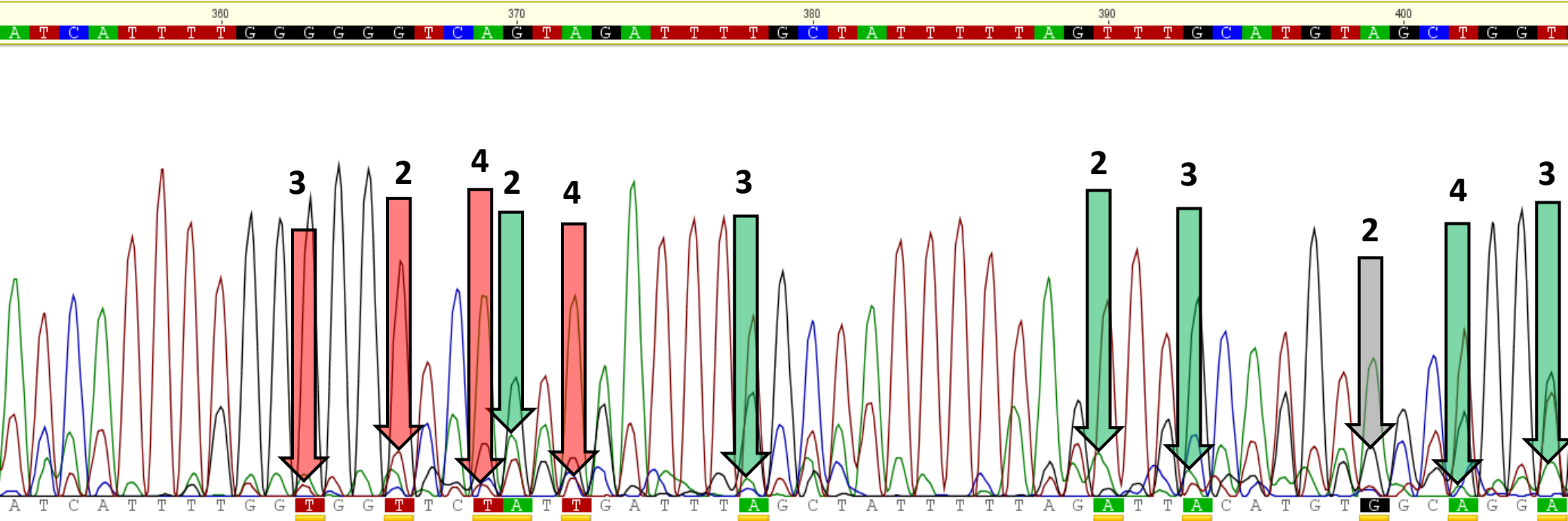
4. gi|1005054467|gb|KU860644.1| (A vaga comp. sp E JFF-2016 isolate Hprim14 ...
 5. gi|1005054361|gb|KU860591.1| (A vaga complex sp. E JFF-2016 isolate A33 cyt...
 6. gi|1005054439|gb|KU860630.1| (A vaga complex sp. E JFF-2016 isolate E3B2 c...
 7. gi|1005054471|gb|KU860646.1| (A vaga comp. sp. E JFF-2016 isolate Hprim16 ...

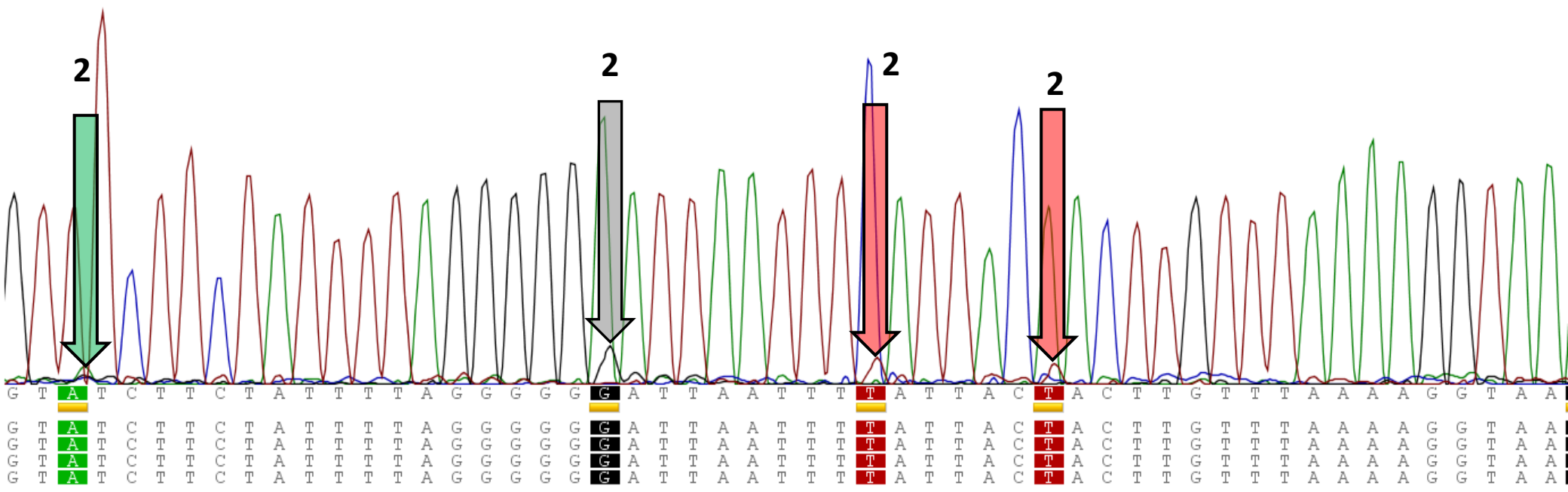
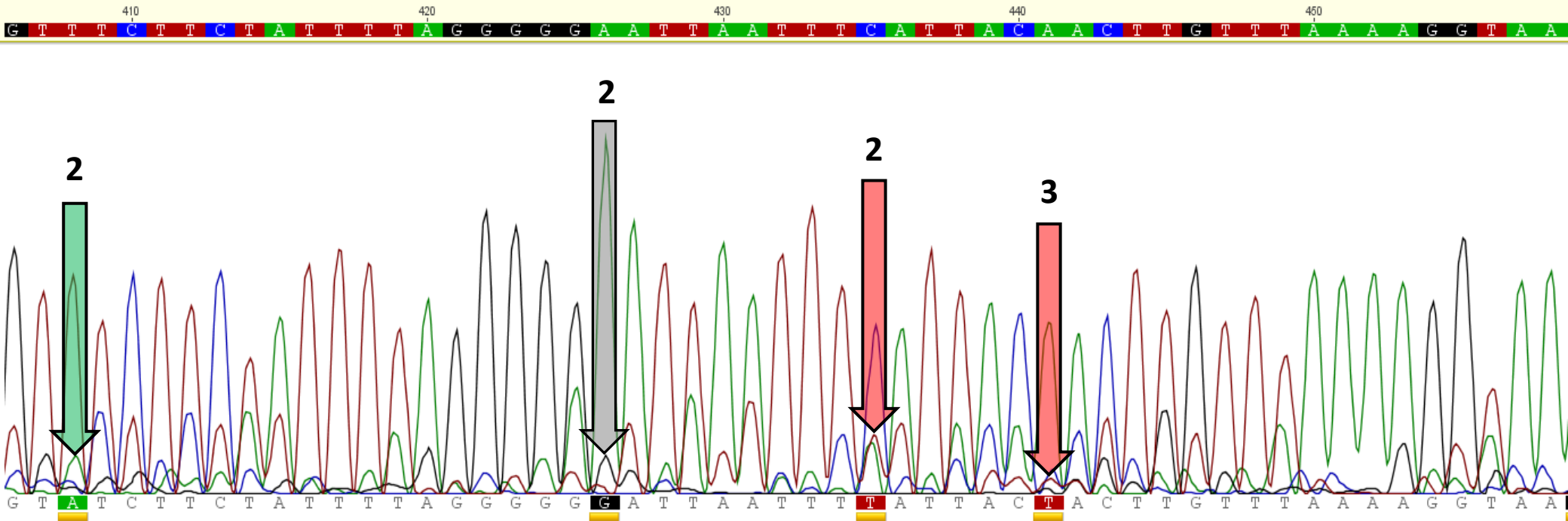


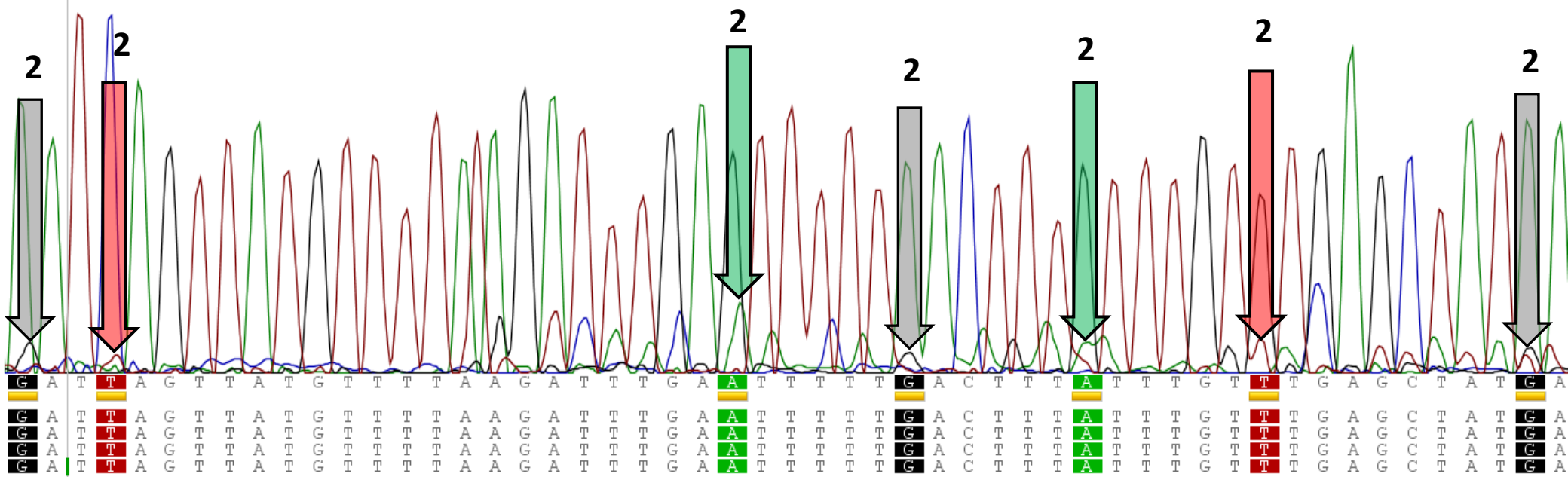
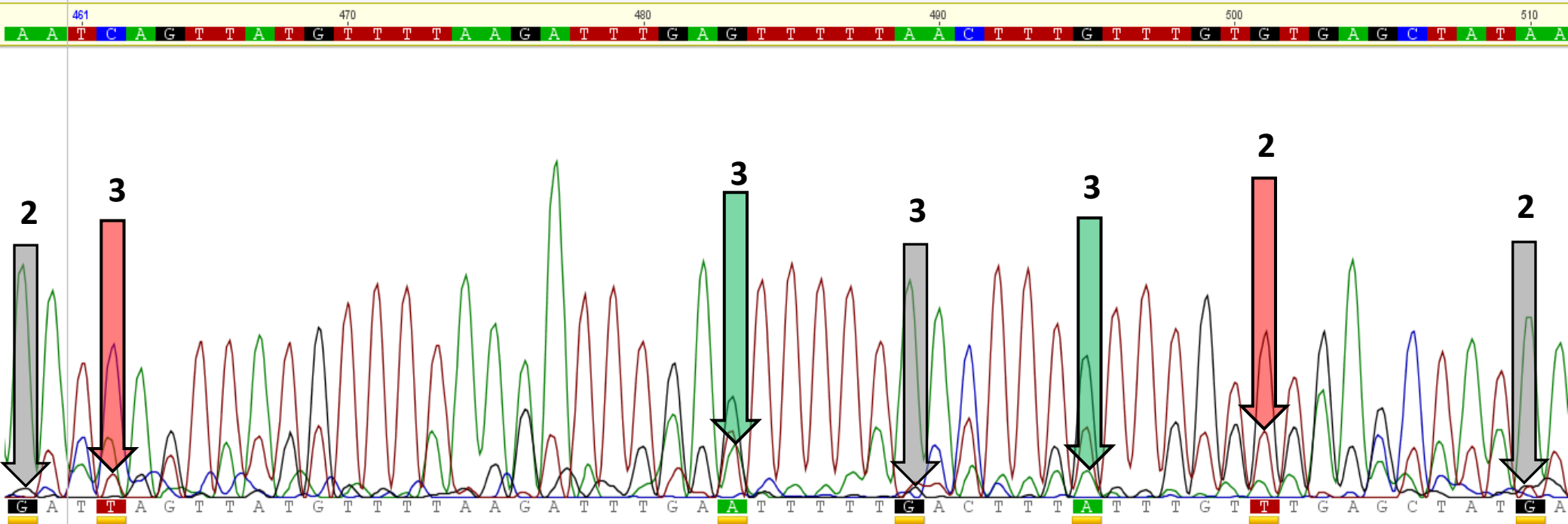


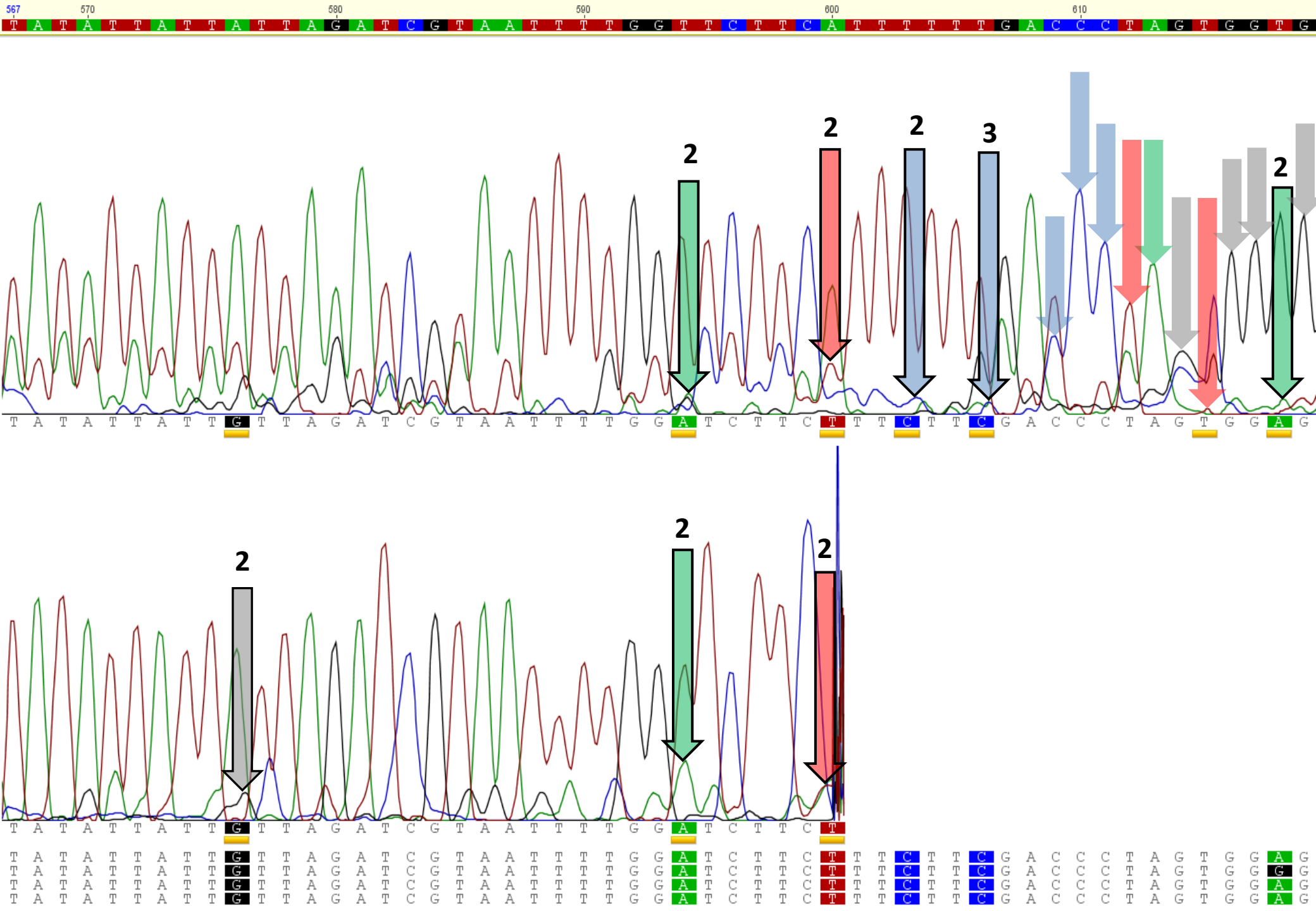


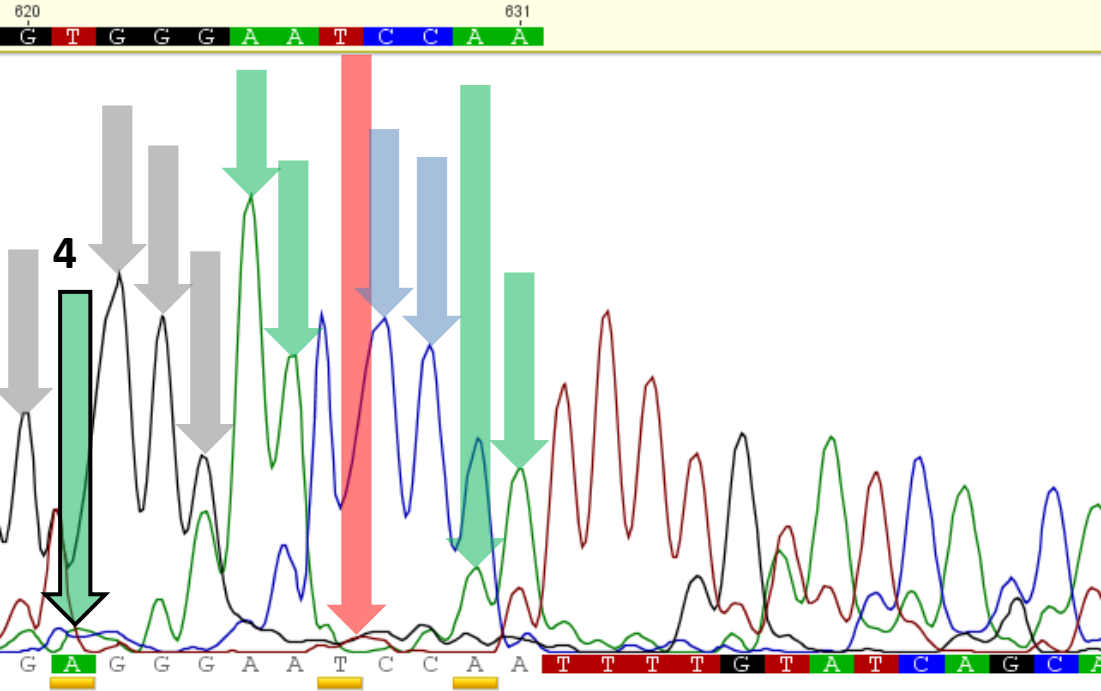












G	A	G	G	G	A	A	T	C	C	A	A
G	A	G	G	G	A	A	T	C	C	A	A
G	A	G	G	G	A	A	T	C	C	A	A
G	A	G	G	G	A	A	T	C	C	A	A

Sample: B14

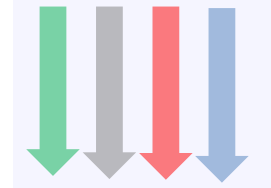
Locus: 28S rDNA (first fragment)

Hypothesis: DNA from Species A was contaminated with DNA from Species E

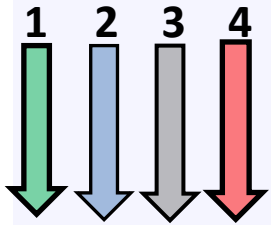
2. *Adineta vaga* complex sp. E JFF-2016 isolate B14 28S rib...

T G C C T T G G A T T C A A T T C G A T C T C T A T A T G A T G G T A A

Species A Hap1 shown at top

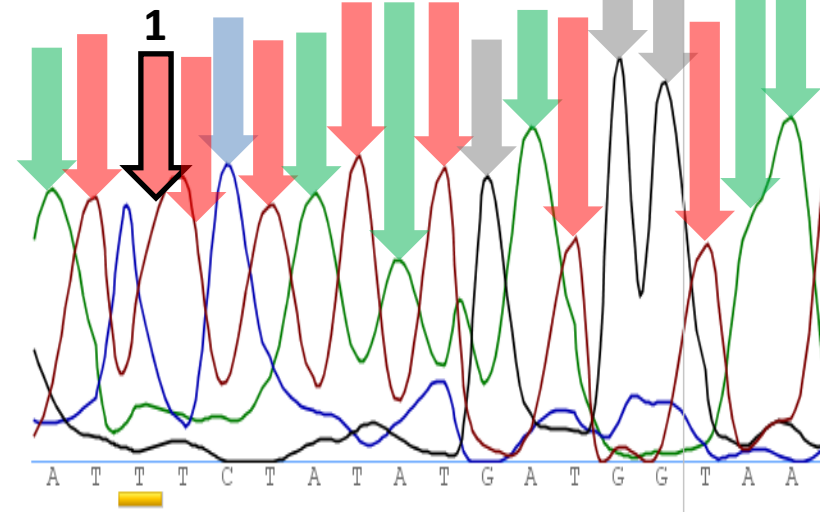


Arrows indicate base calls shared by Hap1 [A] and Hap 16 [E]



Numbered arrows indicate peaks matching Hap 16[E] but not Hap1 [A], with relative height ranks

ND_1_B14-0FCT_G11_083.scf

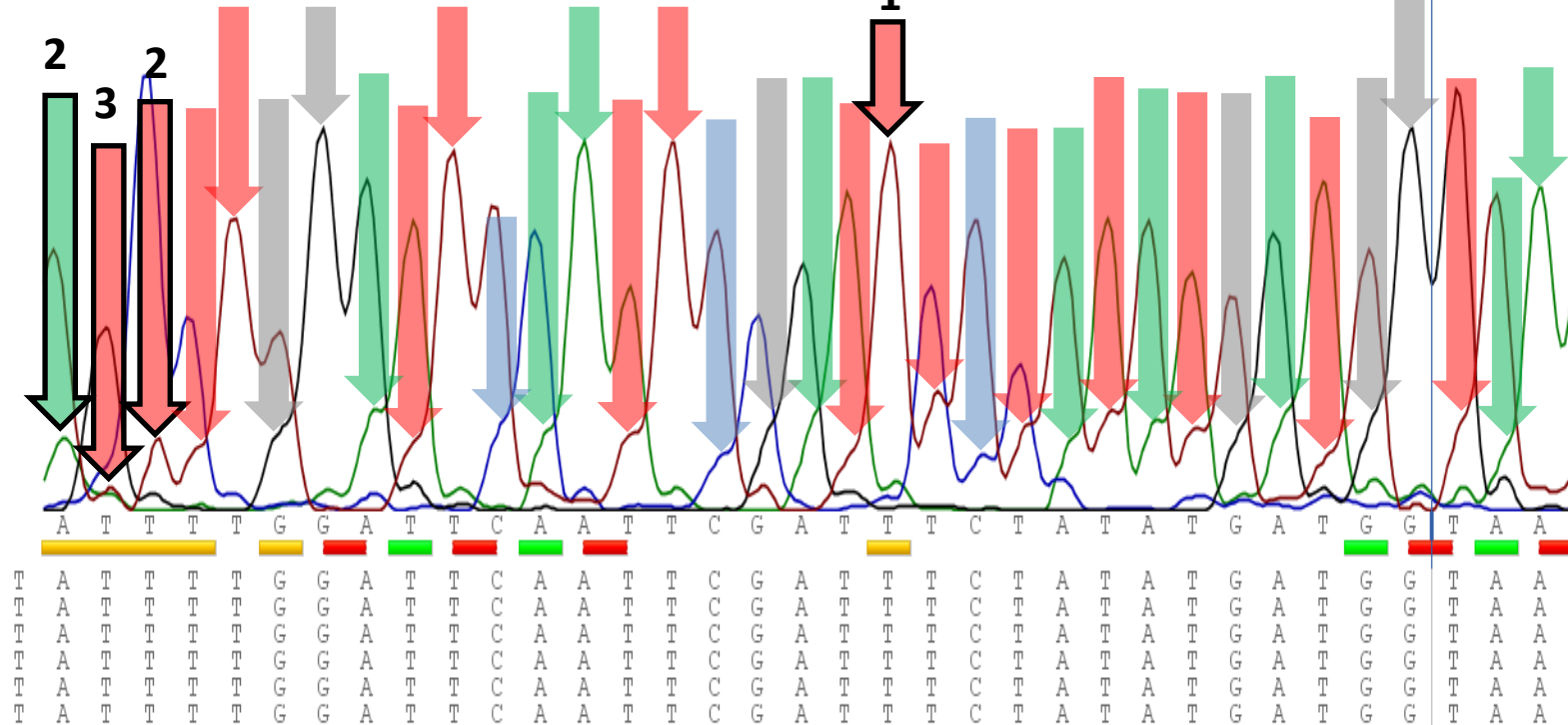


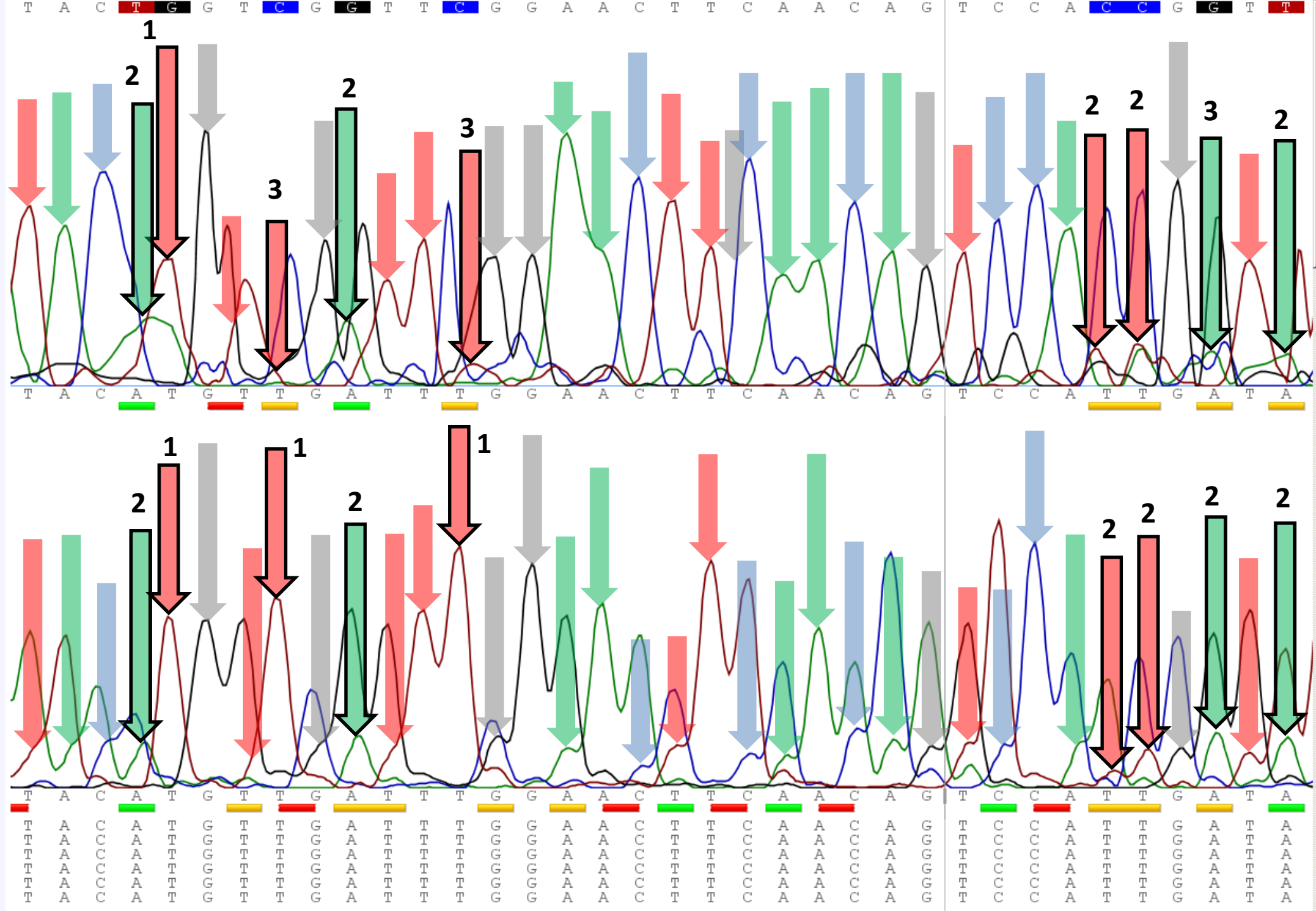
Sample B14 28S minority peak ranks

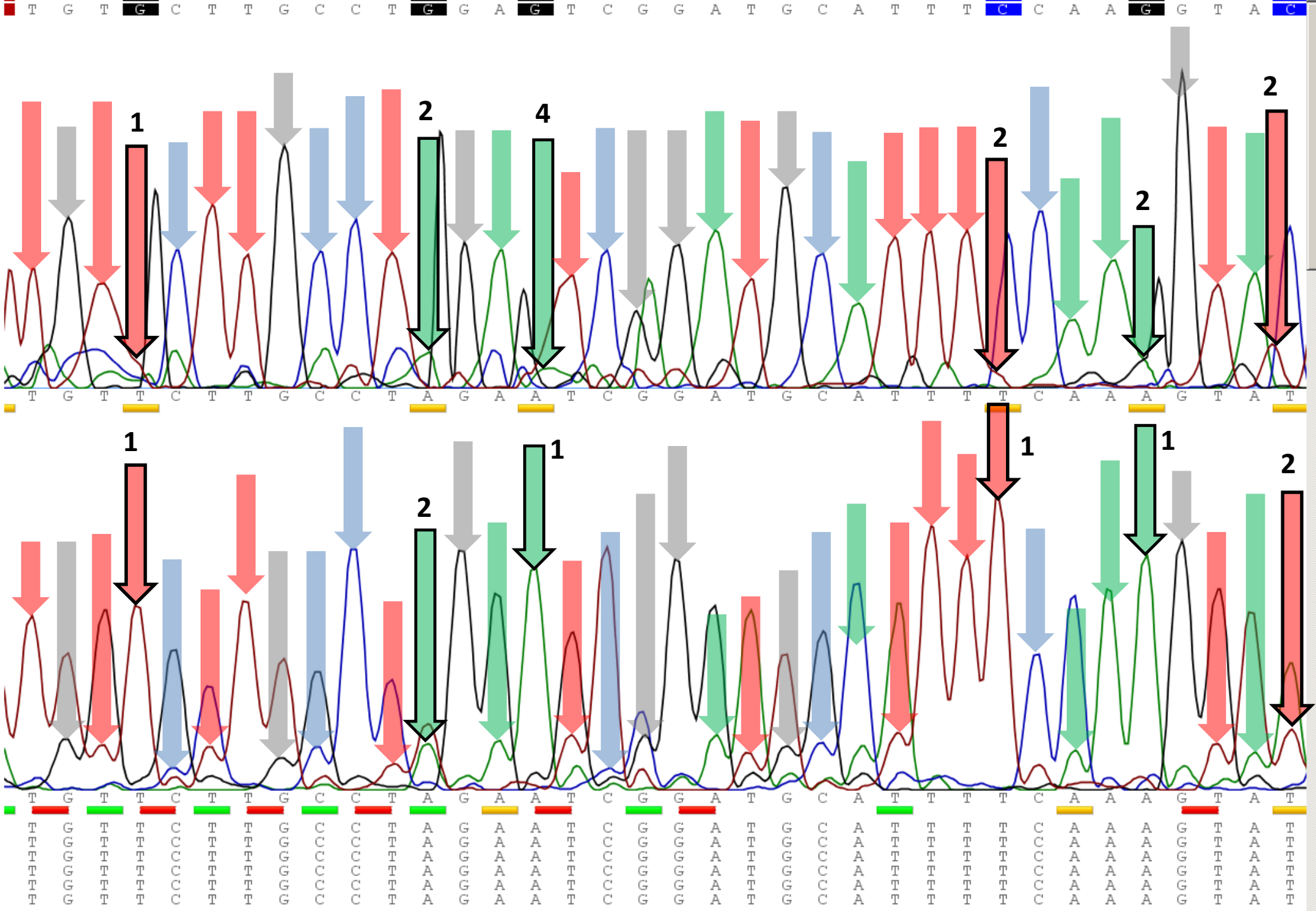
Species E Hap16
(as seen in Individual 70)

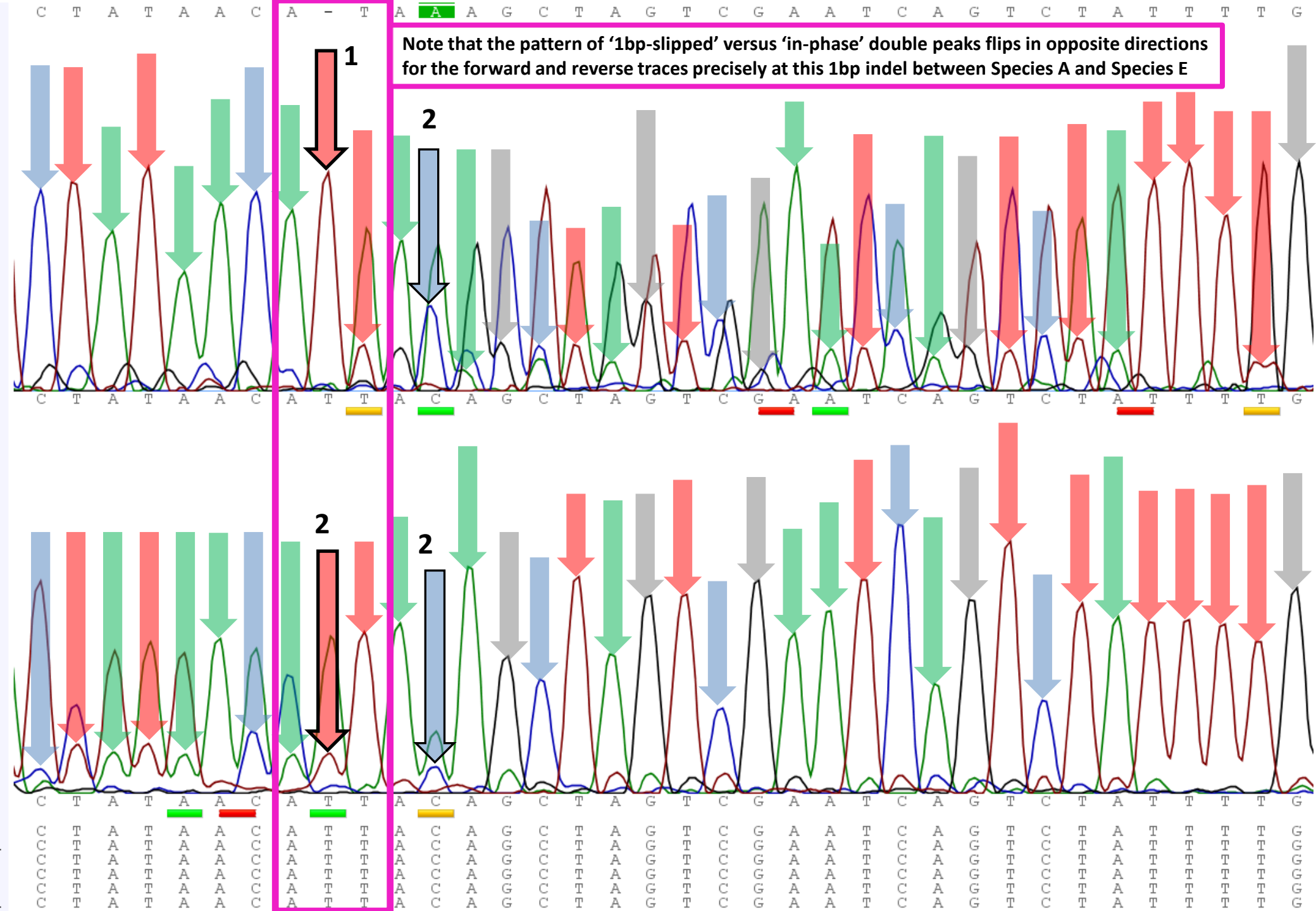
ND_1_B14-1RCT_G11_083.scf

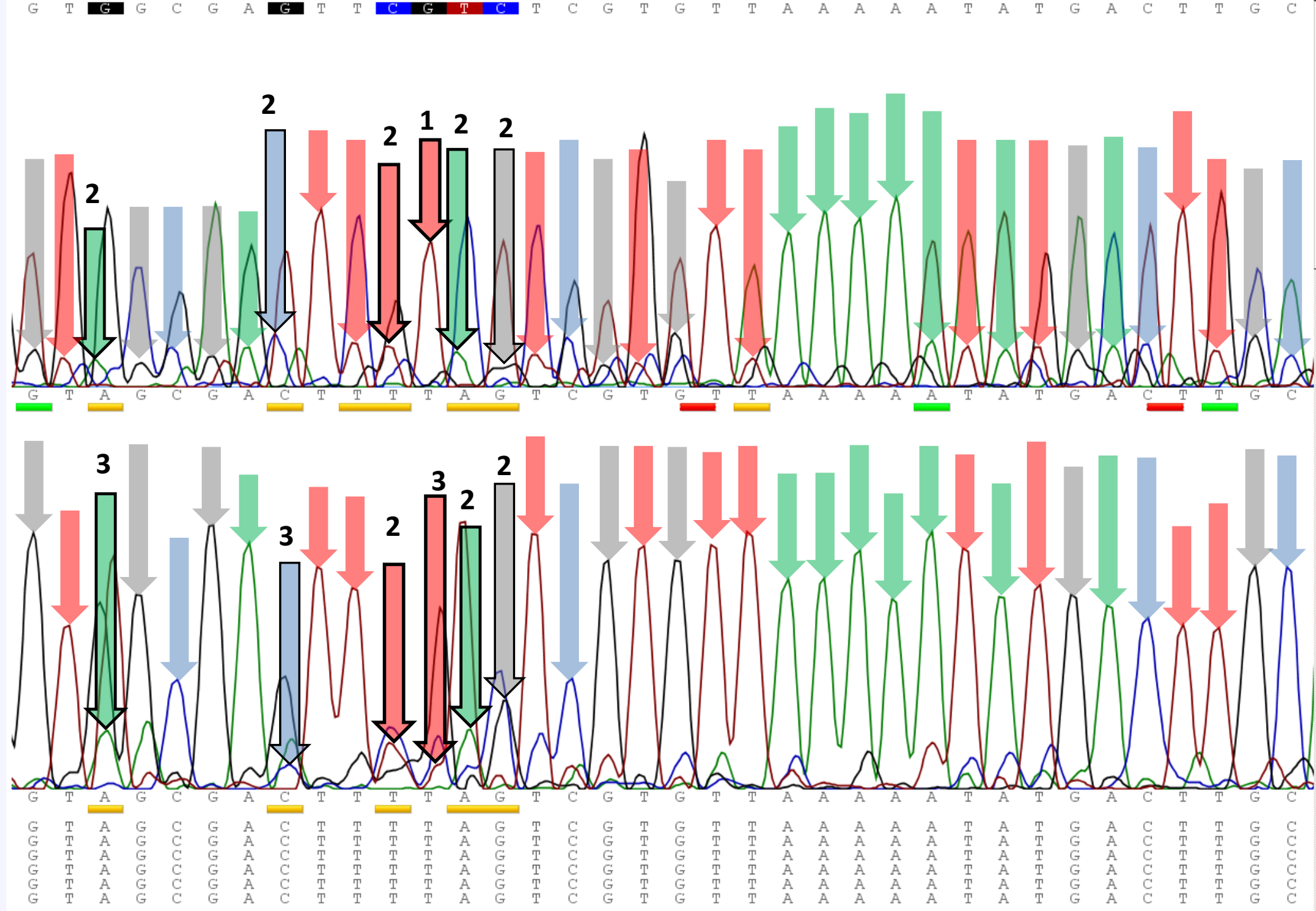
- 5. *Adineta vaga* complex sp. E JFF-2016 isolate A21 28S rib...
- 6. *Adineta vaga* complex sp. E JFF-2016 isolate E3B2b 28S ri...
- 7. *Adineta vaga* complex sp. E JFF-2016 isolate E3T1 28S ri...
- 8. *Adineta vaga* complex sp. E JFF-2016 isolate B39b 28S ri...
- 9. *Adineta vaga* complex sp. E JFF-2016 isolate B38b 28S ri...
- 10. *Adineta vaga* complex sp. E JFF-2016 isolate Hprim14b ...

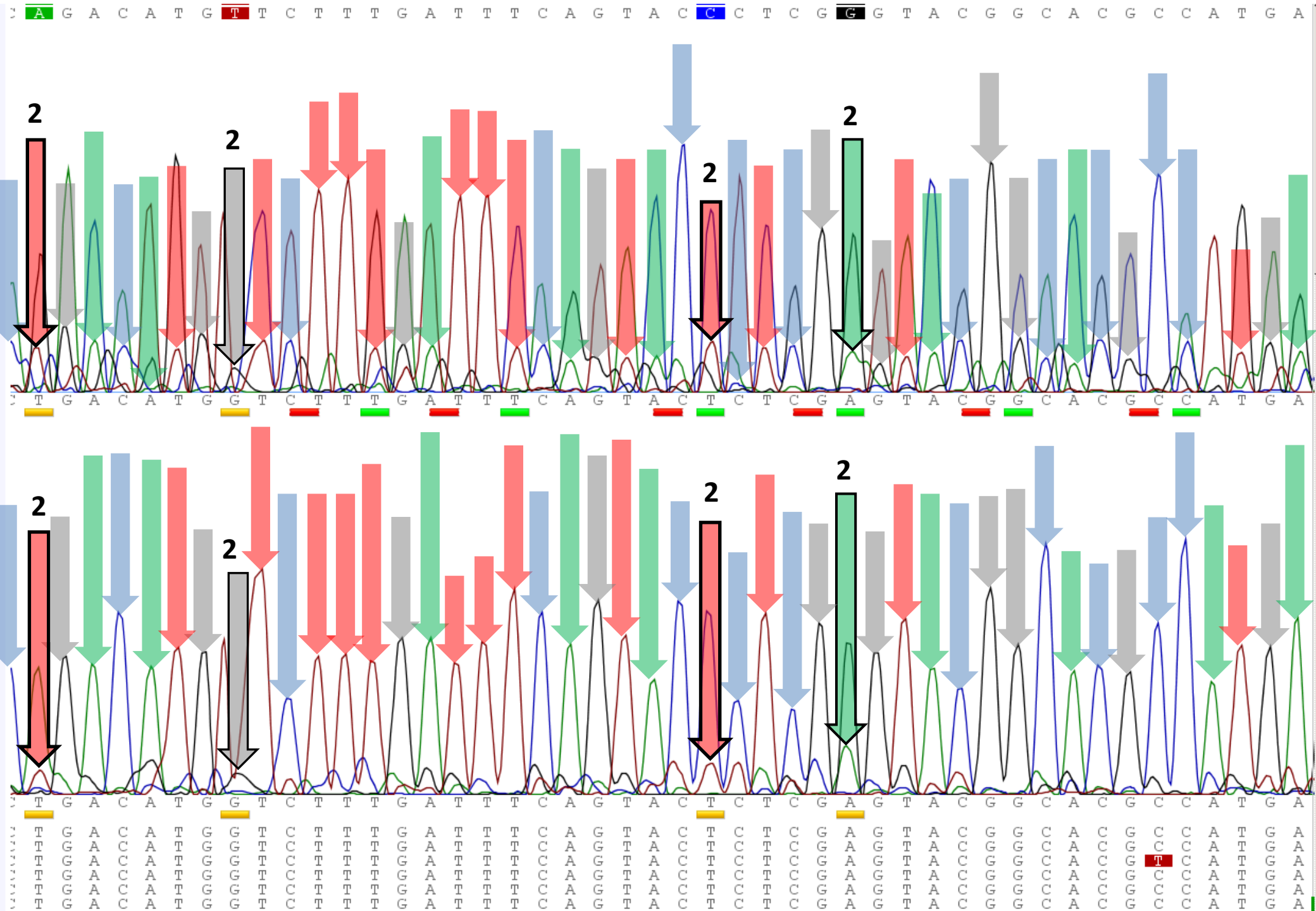


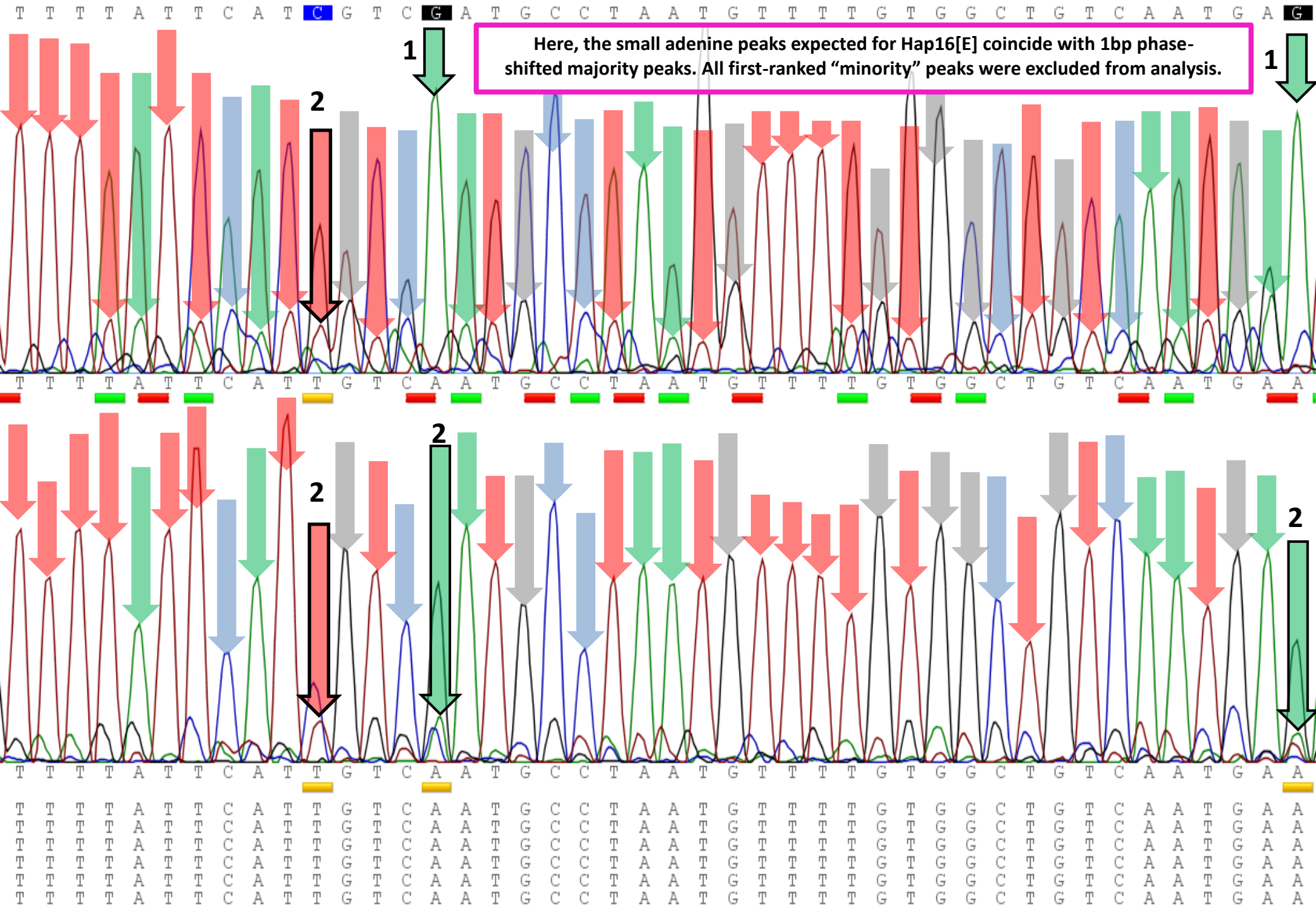


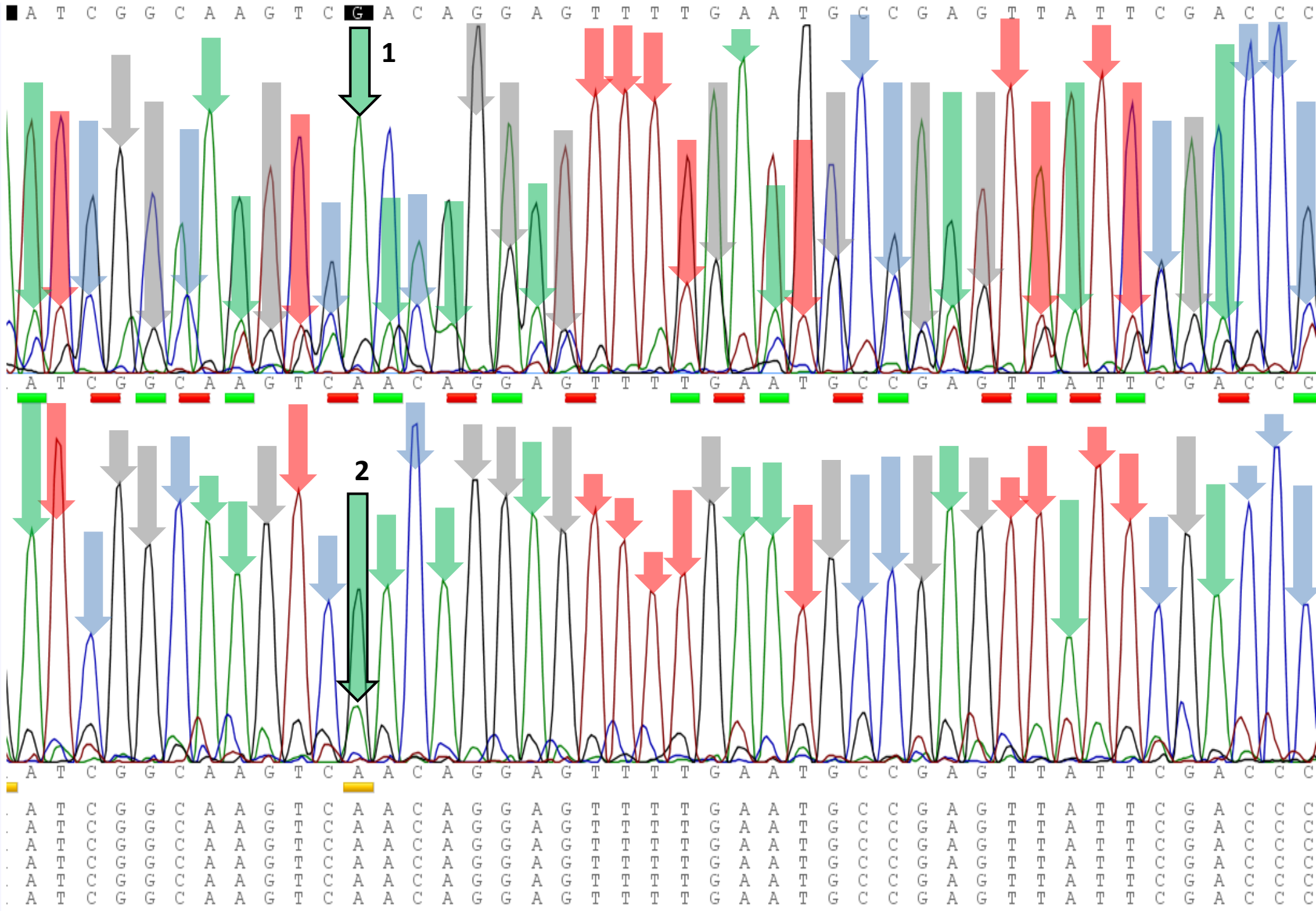


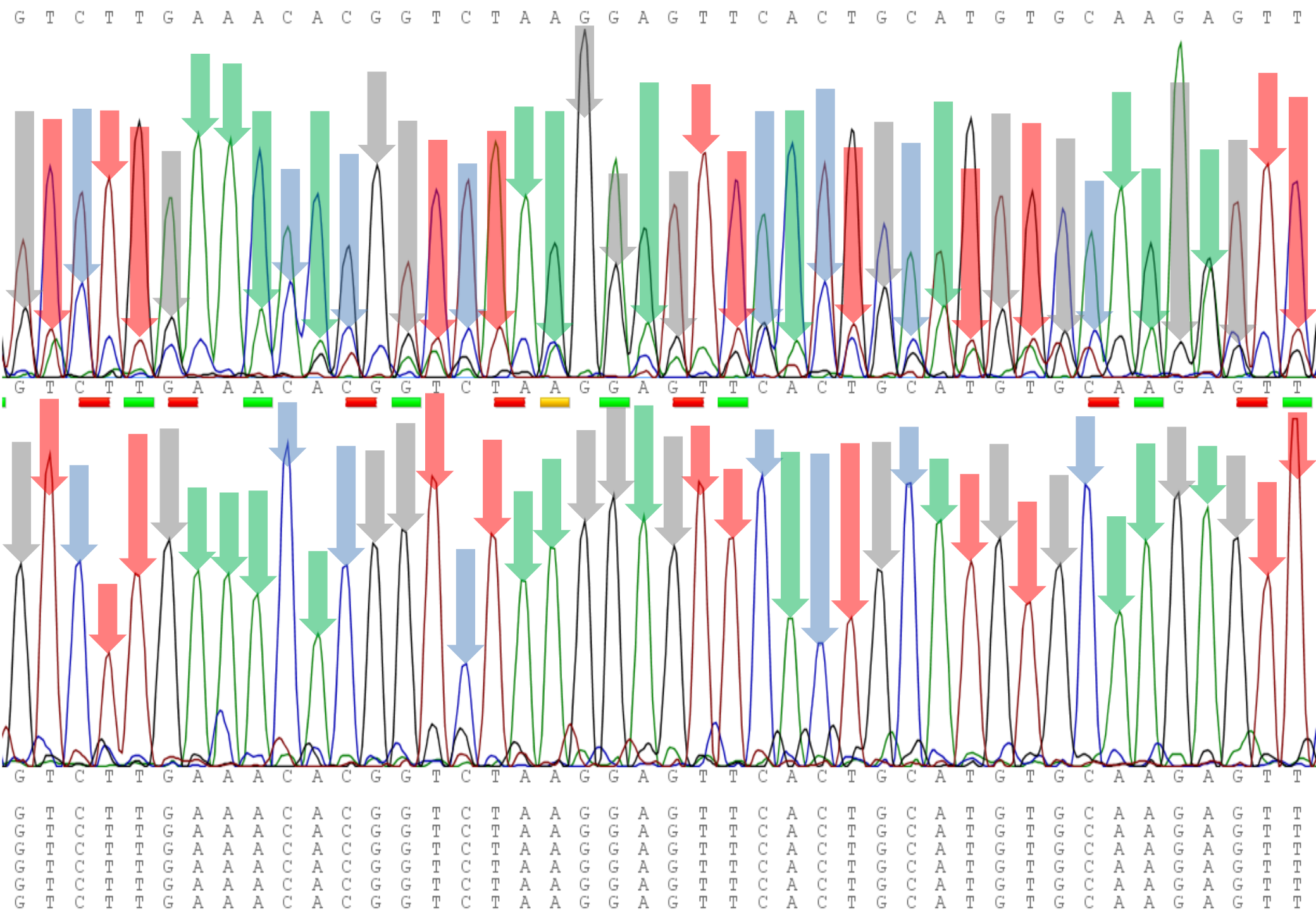


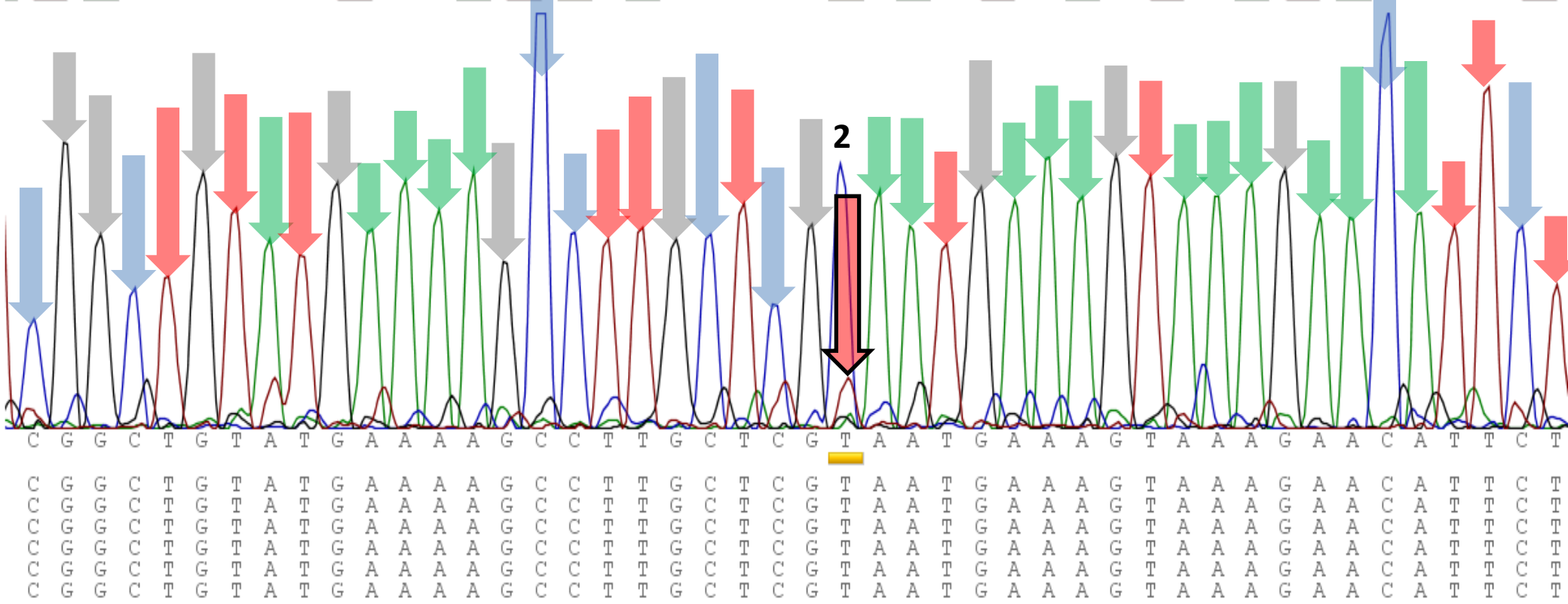
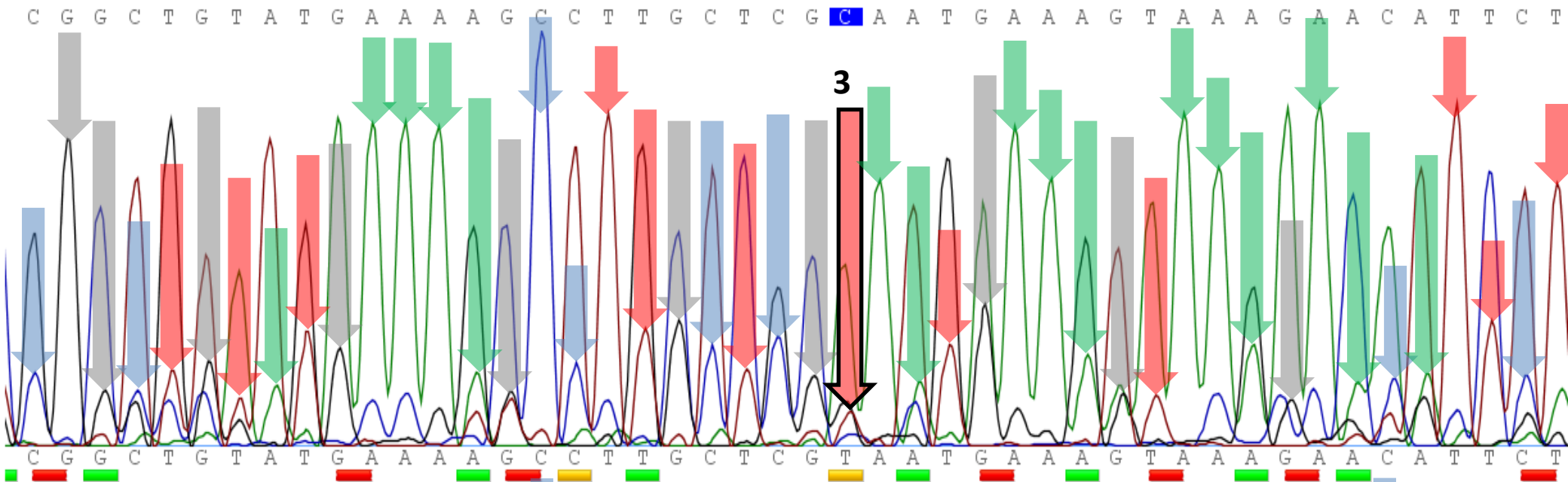


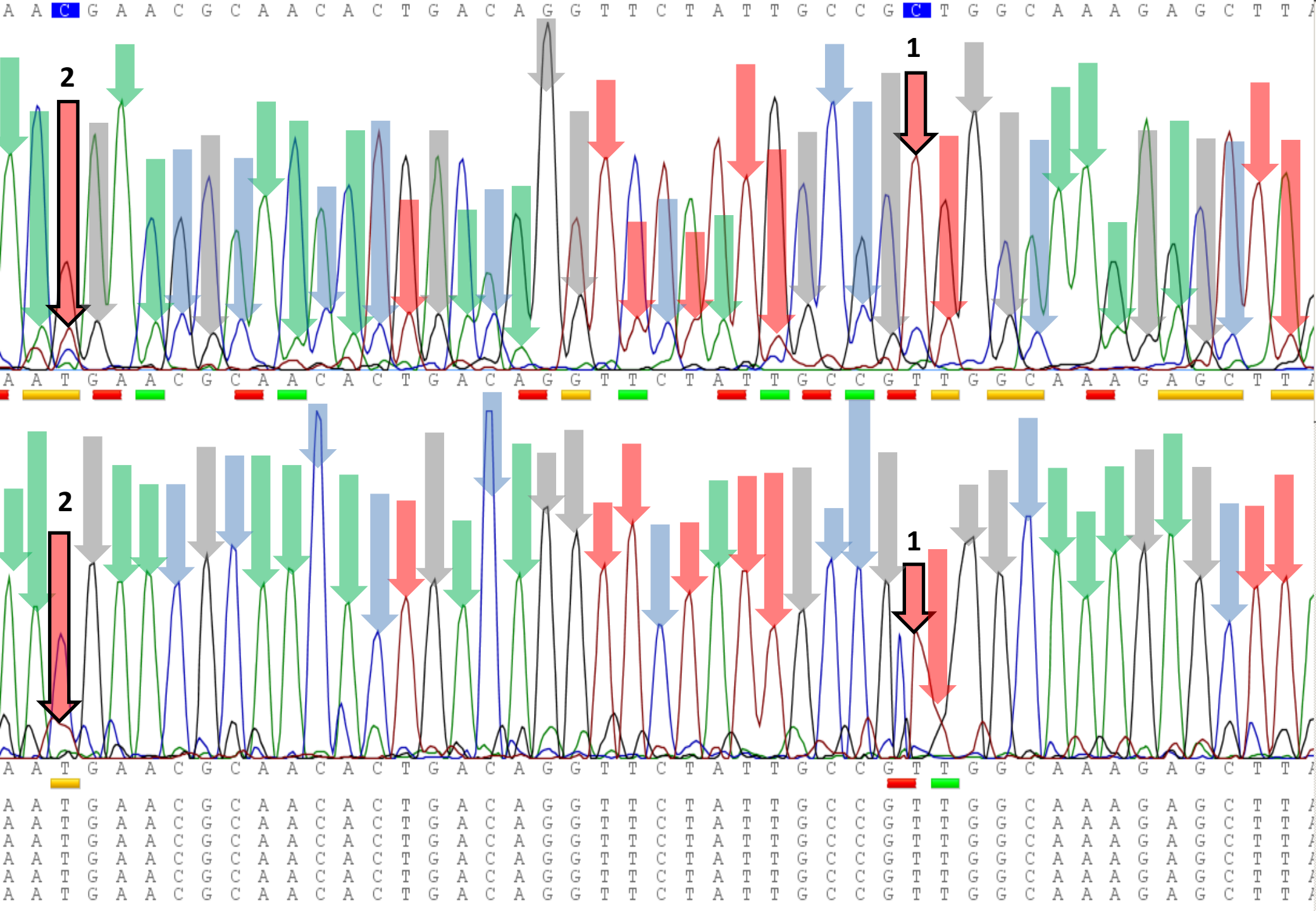


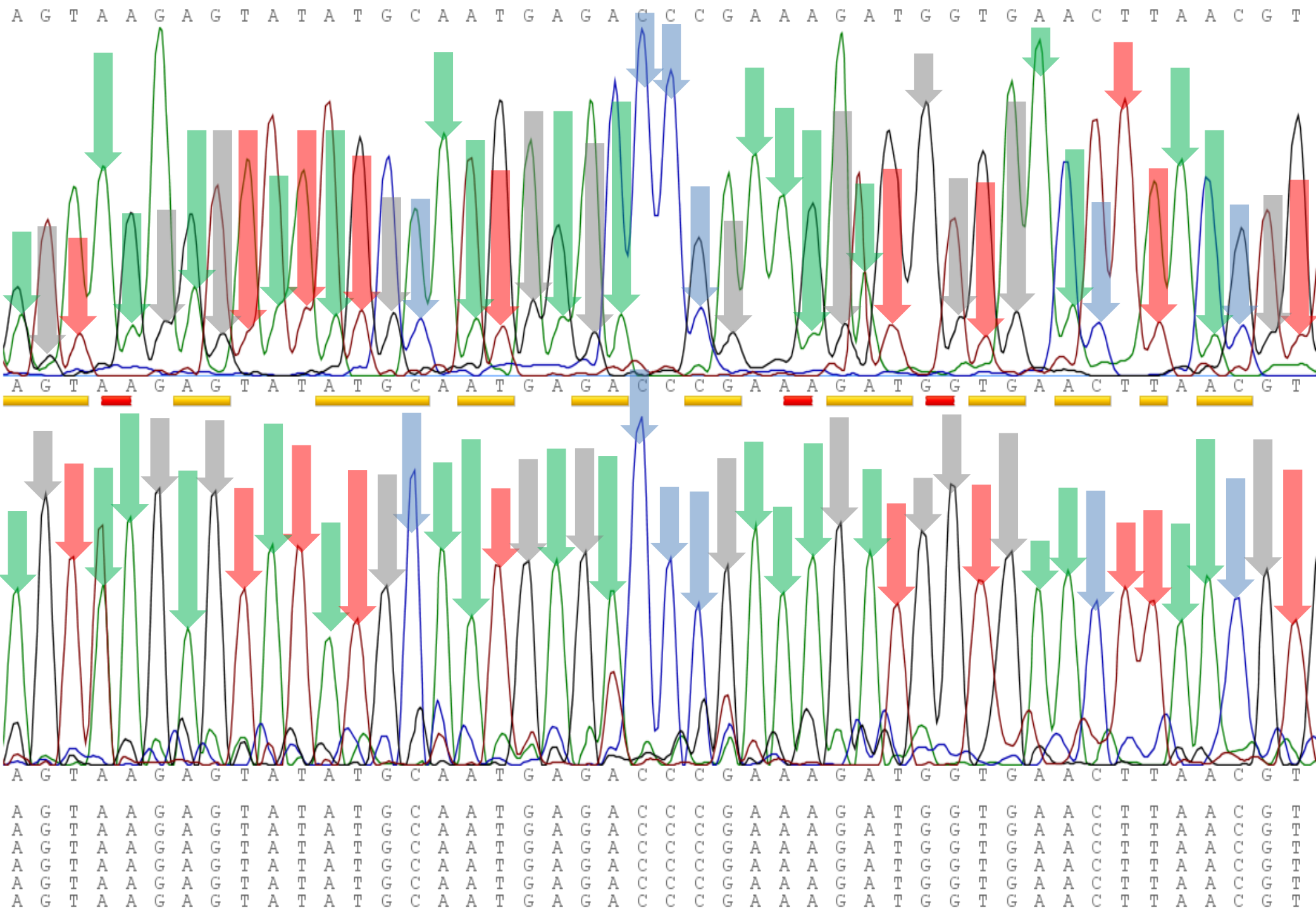










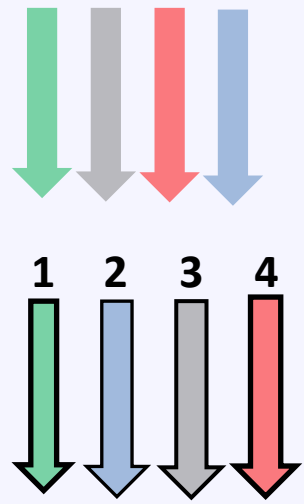


Sample: D14

Locus: EPIC25 marker

Hypothesis: congruent DNA from Species A
is present as expected; incongruent DNA
from Species C is contamination

Species C Hap10 shown at top



NB: Owing to alignment difficulties caused by indels such as this one, the minority and majority peaks are almost never superimposed, but shifted by different amounts in different sections

FJUD 4. ND_25_D14-25SPER_C05_043.scf

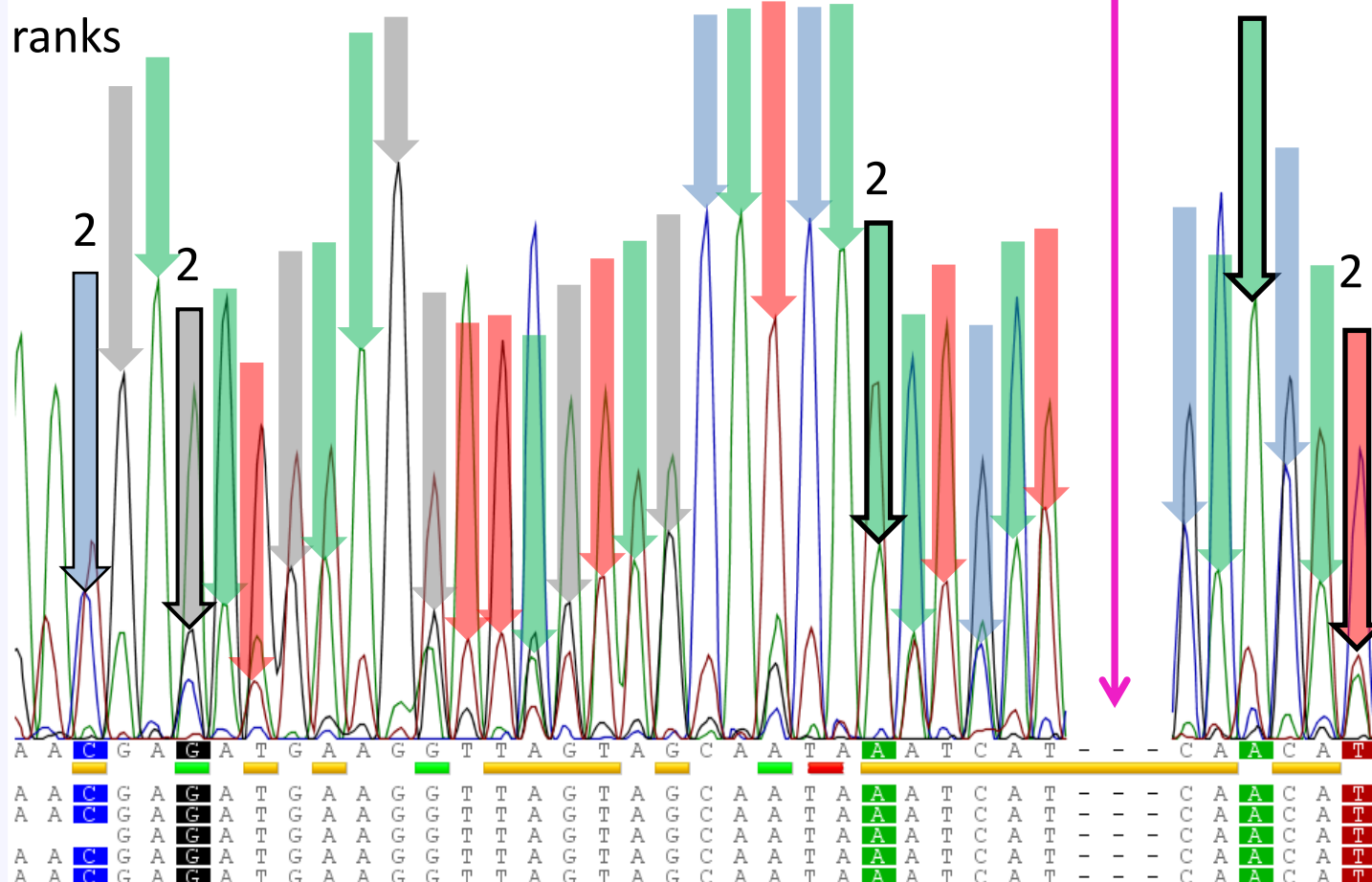
Sample D14 EPIC25 minority peak ranks (first PCR)

NB: The EPIC25 reference haplotypes appear to have been uploaded to GenBank in the 3' to 5' direction, so the sequence from the forward primer (EPIC25F) is shown in reverse complement here.

Species A Hap4 [A], as seen in Individual 12

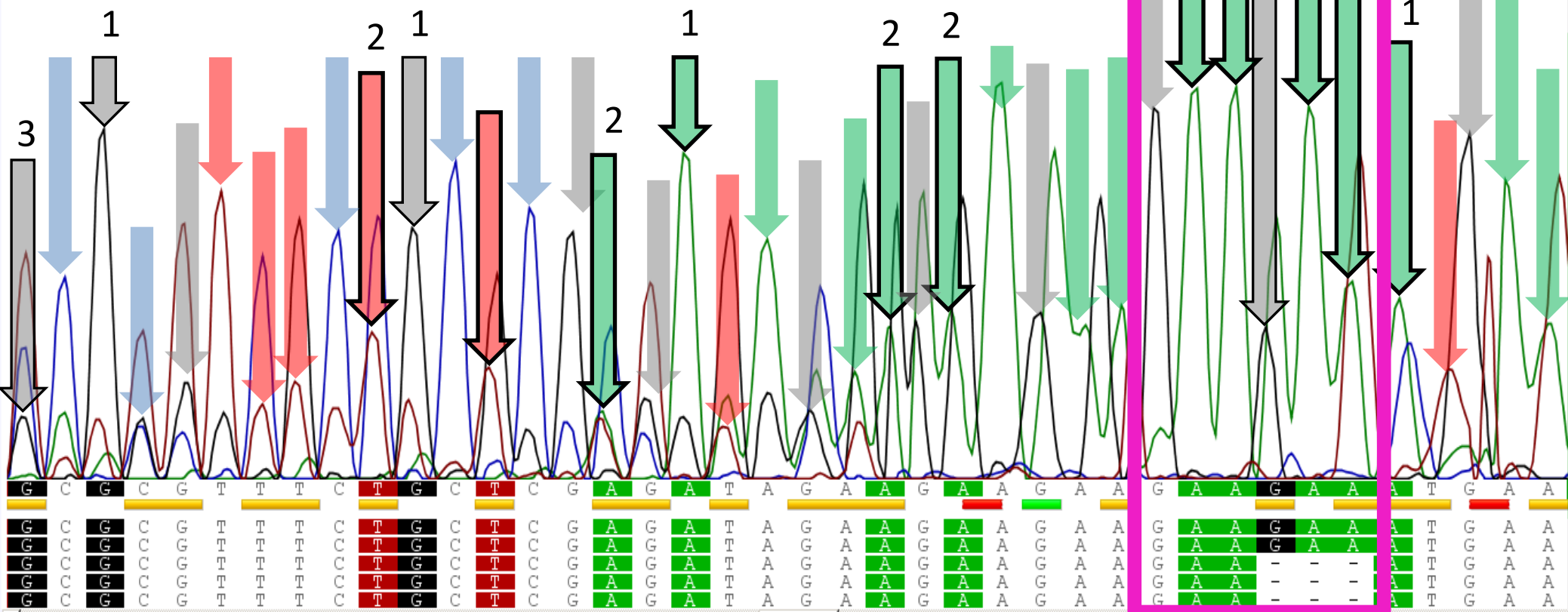
REV 5. ND_25_D14-25SPEF_C05_043.scf

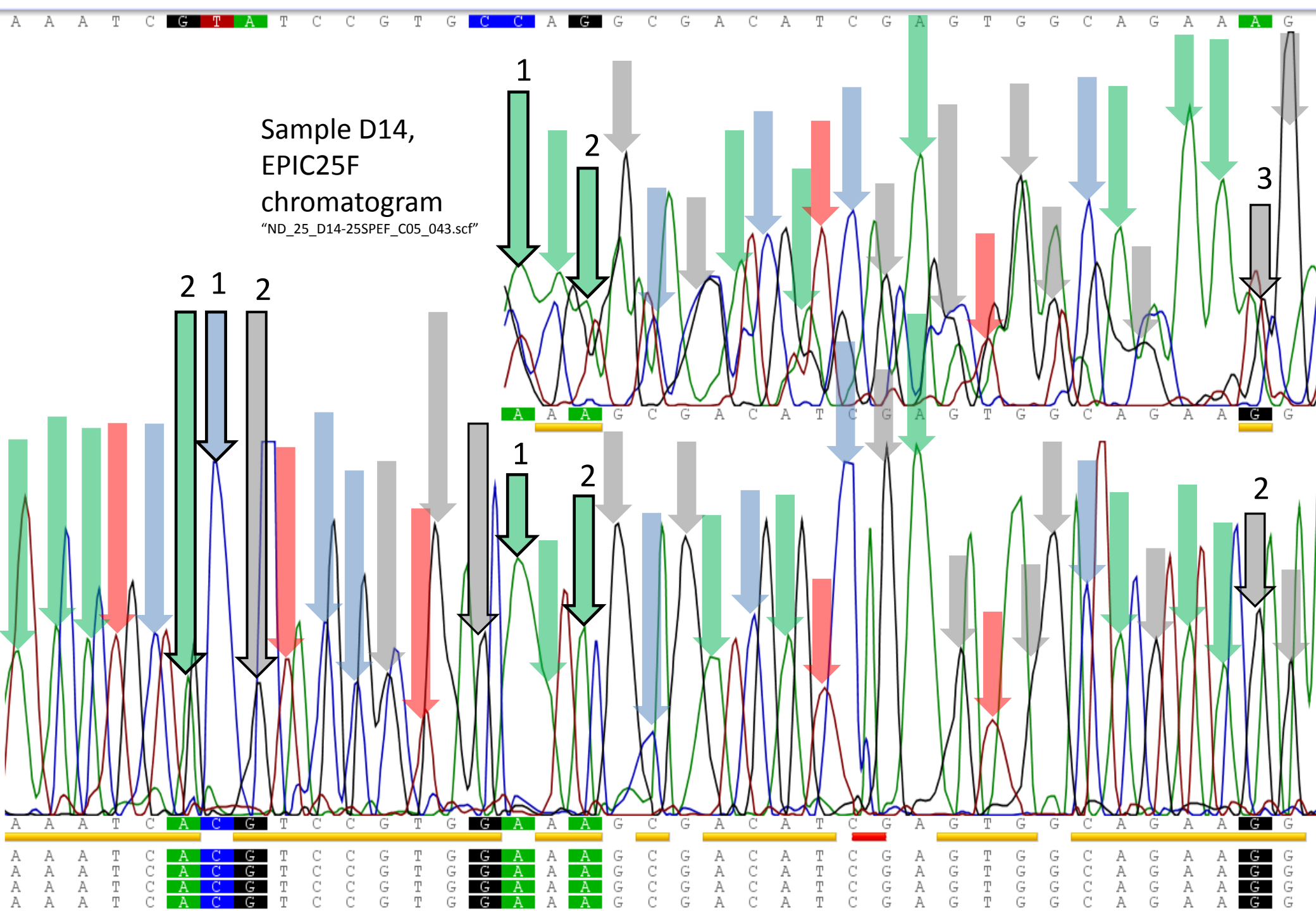
FJUD 6. Hap3[A]: Adineta vaga complex sp. A JFF-2016 isolate H3-04a MTSS1-like p...
 FJUD 7. Hap4 [A]: Adineta vaga complex sp. A JFF-2016 isolate H3-04a MTS...
 FJUD 8. Hap1[A]: Adineta vaga complex sp. A JFF-2016 isolate C3T3 MTSS1...
 FJUD 9. Hap5[A]: Adineta vaga complex sp. A JFF-2016 isolate E31b MTSS1...
 FJUD 10. Adineta vaga complex sp. A JFF-2016 isolate H3-04b MTSS1-like p...

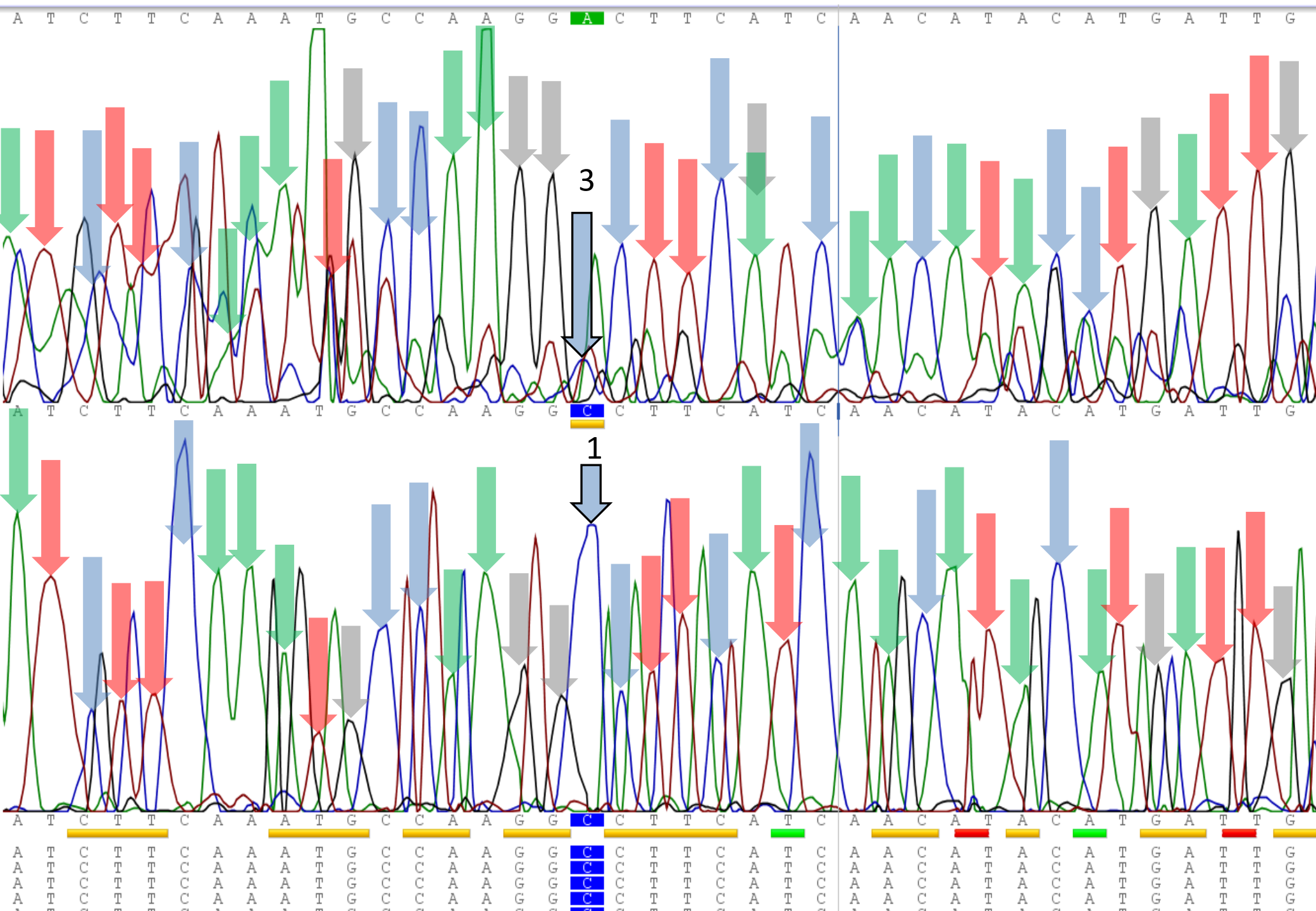


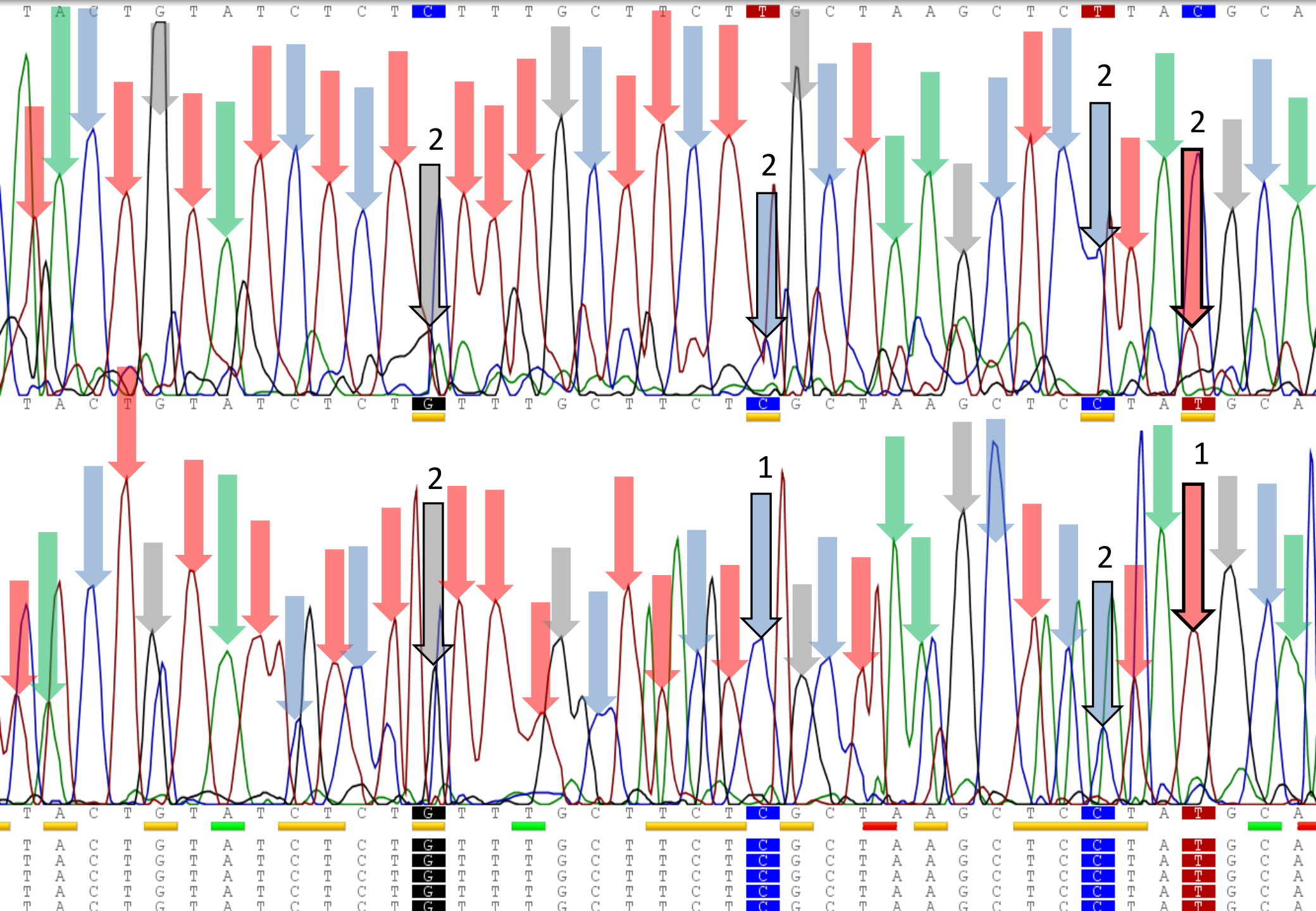
T C T C G T T T C G C C G C G C T A G A C G G A G A A G - - - - - T G A A

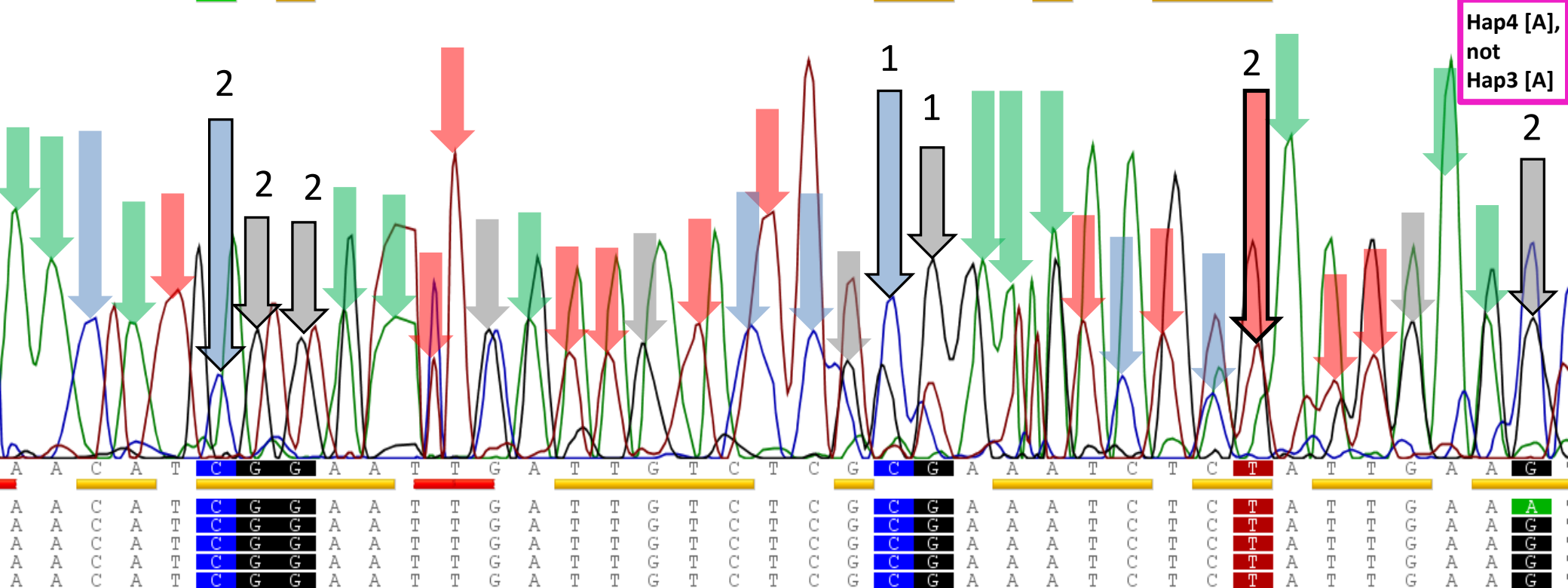
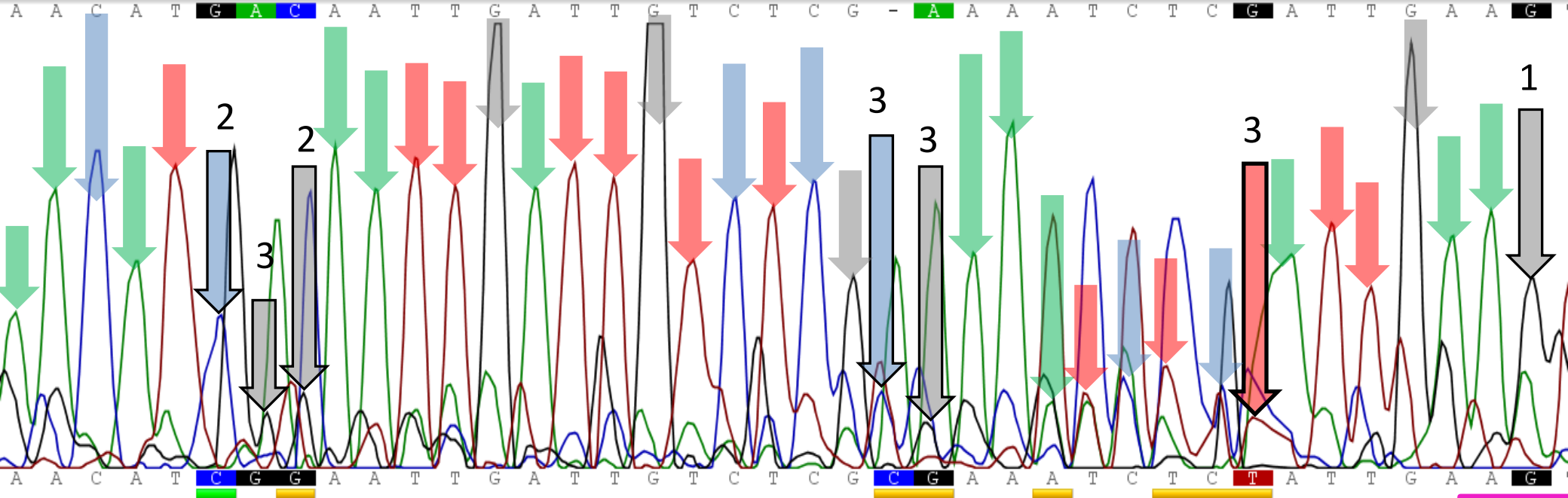
Here, we can determine how many variable copy GAA tandem repeats the native Species A haplotype had. The answer is GAA₅, not GAA₄, which indicates EPIC25 Hap4 [A], not Hap1 [A]. Species C Hap10 does not have any GAA tandem repeats here at all. NB: these correspond to TTC repeats on the coding strand, as discussed by Debortoli et al. [S1].

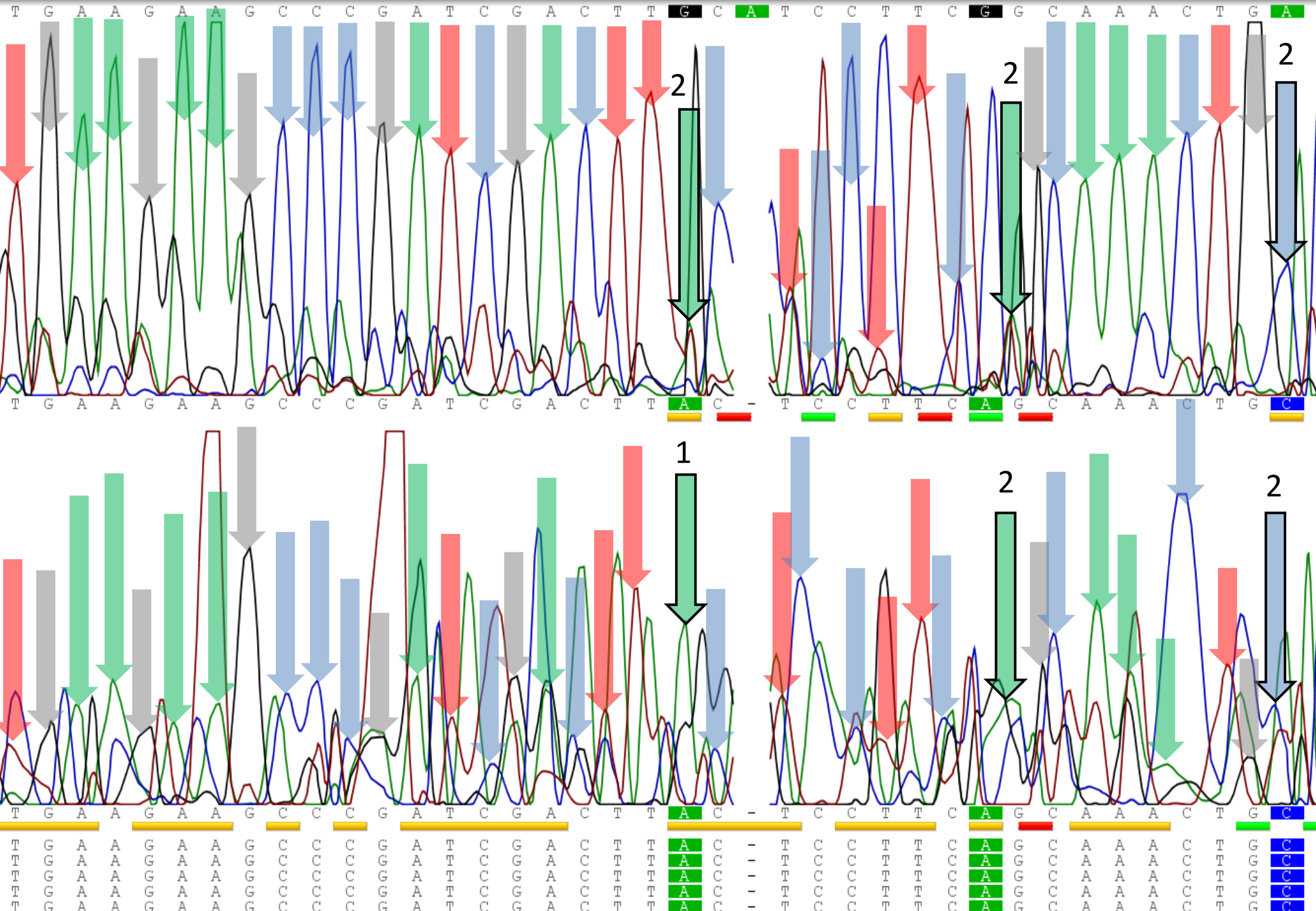


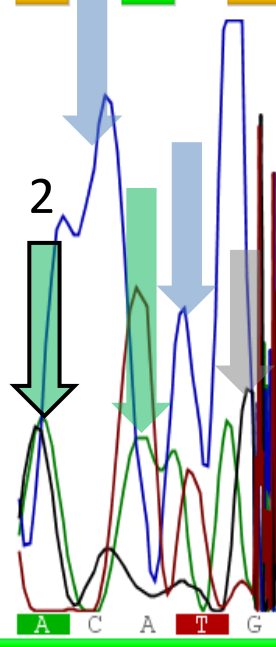
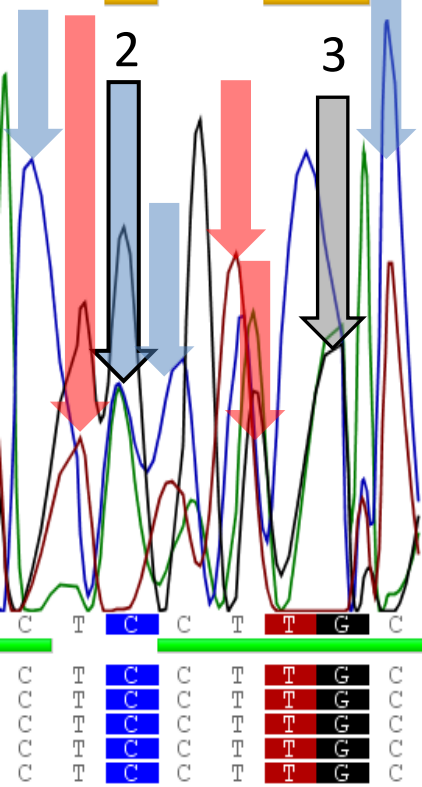




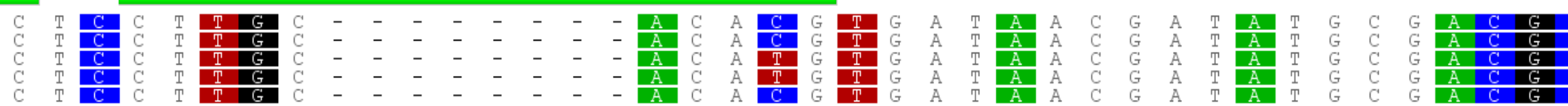


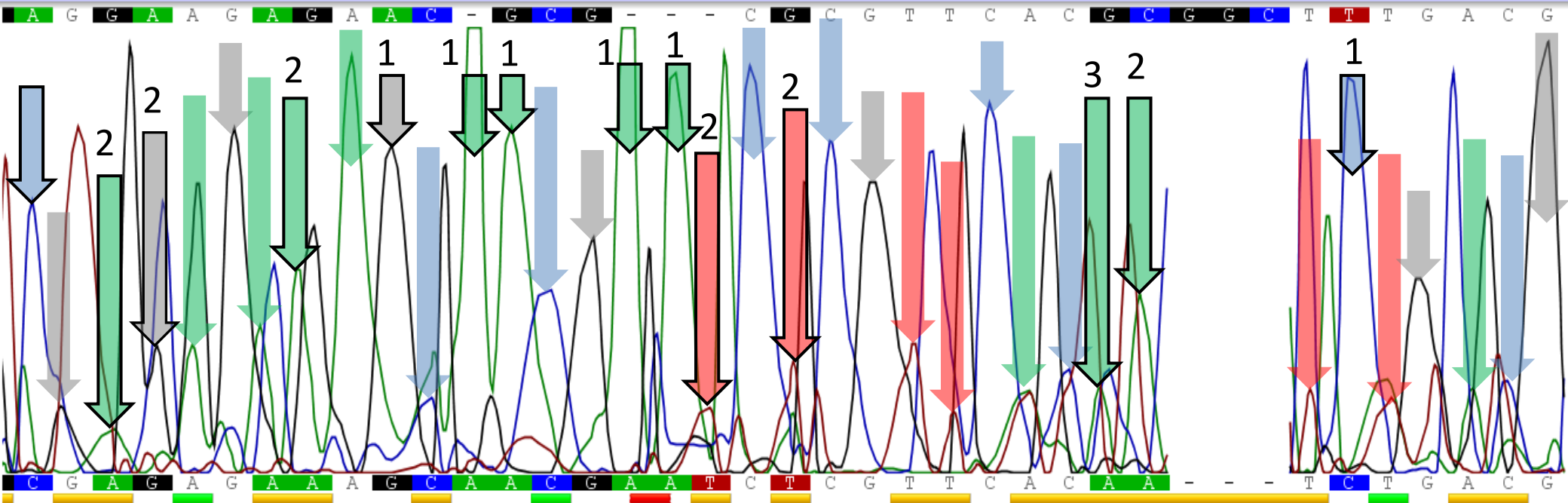




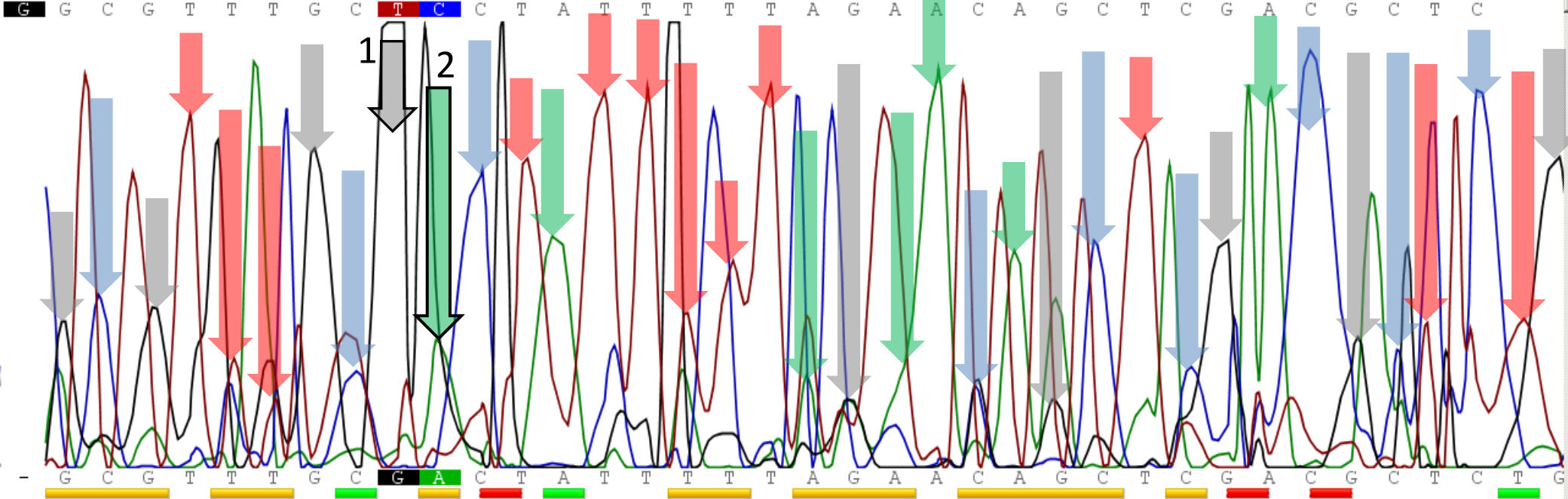


End of readable sequence from forward chromatogram. The last indel between Hap 10 (C) and Hap 4 (A) creates so much noise that bases can no longer be reliably read after this point.

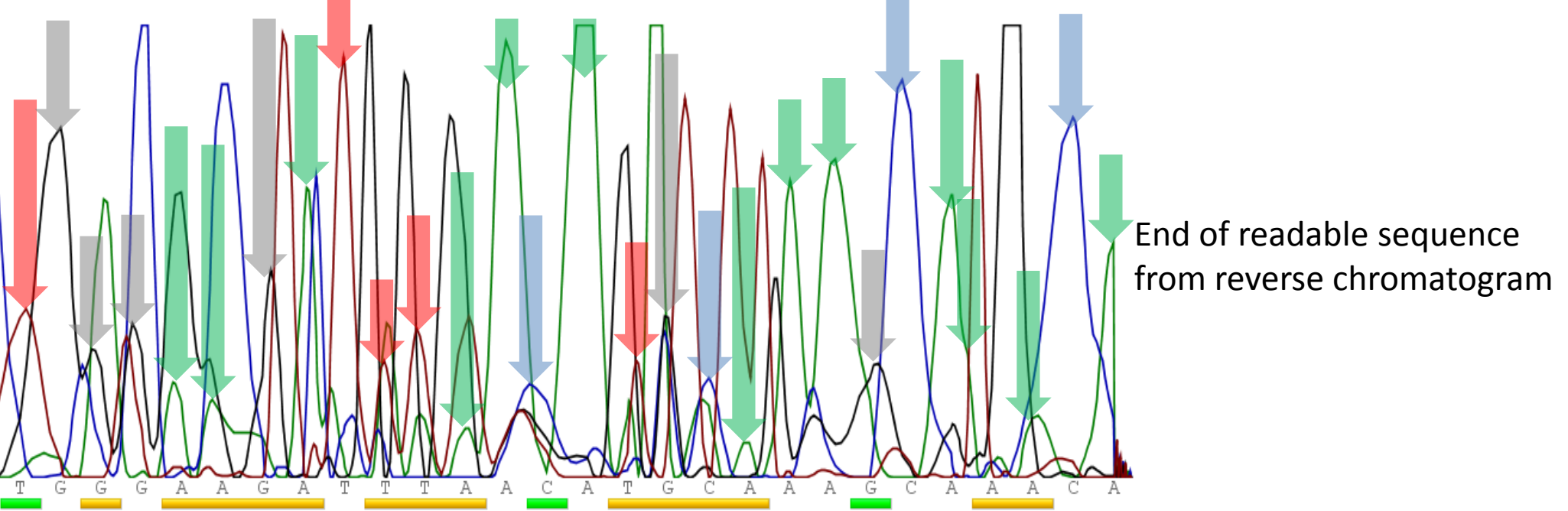




C	G	A	G	A	G	A	A	A	G	C	A	A	C	G	A	A	T	C	T	C	G	T	T	T	C	A	C	A	A	-	-	-	T	C	T	G	A	C	G
C	G	A	G	A	G	A	A	A	G	C	A	A	C	G	A	A	T	C	T	C	G	T	T	T	C	A	C	A	A	-	-	-	T	C	T	G	A	C	G
C	G	A	G	A	G	A	A	A	G	C	A	A	C	G	A	A	T	C	T	C	G	T	T	T	C	A	C	A	A	-	-	-	T	C	T	G	A	C	G
C	G	A	G	A	G	A	A	A	G	C	A	A	C	G	A	A	T	C	T	C	G	T	T	T	C	A	C	A	A	-	-	-	T	C	T	G	A	C	G



-	G	C	G	T	T	T	G	C	G	A	C	T	A	T	T	T	T	T	A	G	A	A	C	A	G	C	T	C	G	A	C	G	C	T	C	T	G
-	G	C	G	T	T	T	G	C	G	A	C	T	A	T	T	T	T	T	A	G	A	A	C	A	G	C	T	C	G	A	C	G	C	T	C	T	G
-	G	C	G	T	T	T	G	C	G	A	C	T	A	T	T	T	T	T	A	G	A	A	C	A	G	C	T	C	G	A	C	G	C	T	C	T	G
-	G	C	G	T	T	T	G	C	G	A	C	T	A	T	T	T	T	T	A	G	A	A	C	A	G	C	T	C	G	A	C	G	C	T	C	T	G
-	G	C	G	T	T	T	G	C	G	A	C	T	A	T	T	T	T	T	A	G	A	A	C	A	G	C	T	C	G	A	C	G	C	T	C	T	G



This is the end of Hap10 [C], but Hap4 [A] can be read along the chromatogram a little further, since Individual 12 was one of the samples where Debortoli et al. [S1] sequenced additional flanking regions.

T	G	G	G	A	A	G	A	T	T	T	A	A	C	A	T	G	C	A	A	A	G	C	A	A	A	C	A
T	G	G	G	A	A	G	A	T	T	T	A	A	C	A	T	G	C	A	A	A	G	C	A	A	A	C	A

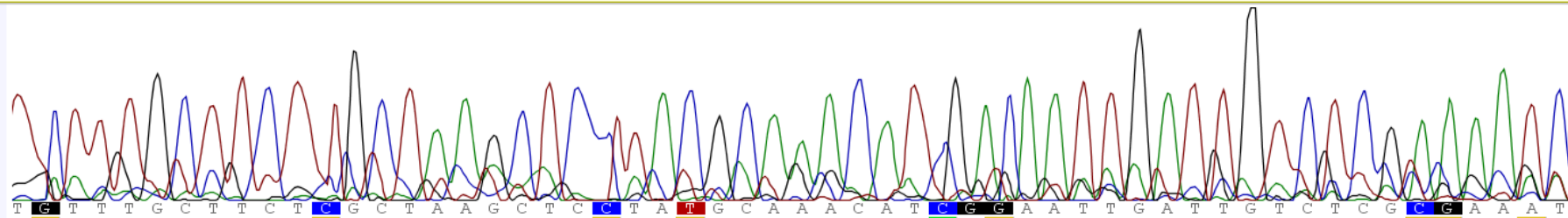
Comparison of chromatograms from two replicate PCRs using Sample D14

The files from the first amplification (labelled 'C05') show strong peaks in both directions corresponding precisely to EPIC25 Hap4 [A], as shown previously. However, a second PCR from the same tube of template ('B02' files, below) showed almost no evidence of Hap4 [A]. If the 'B02' chromatograms had been examined alone, contamination might have been missed, and it would have been less easy to reject the hypothesis that Hap10 [C] had replaced Hap4 [A].

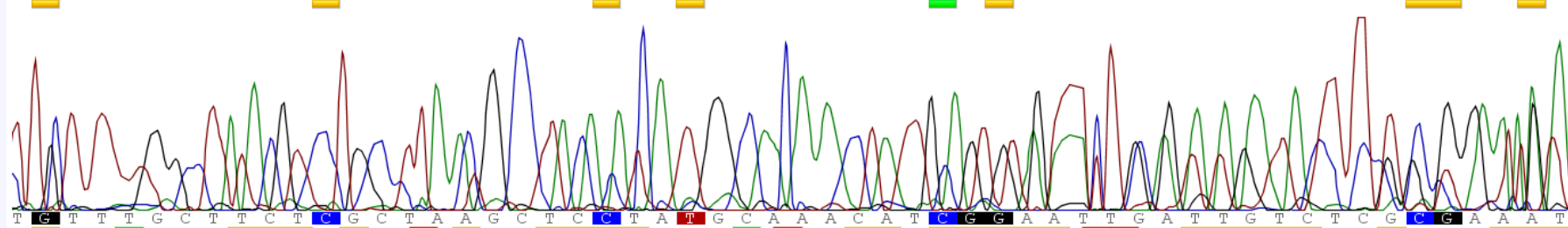
Adineta vaga complex sp. C Hap10 JF...

T C T T T G C T T C T T G C T A A G C T C T T A C G C A A A C A T G A C A A T T G A T T G T C T C G - A A A A A T

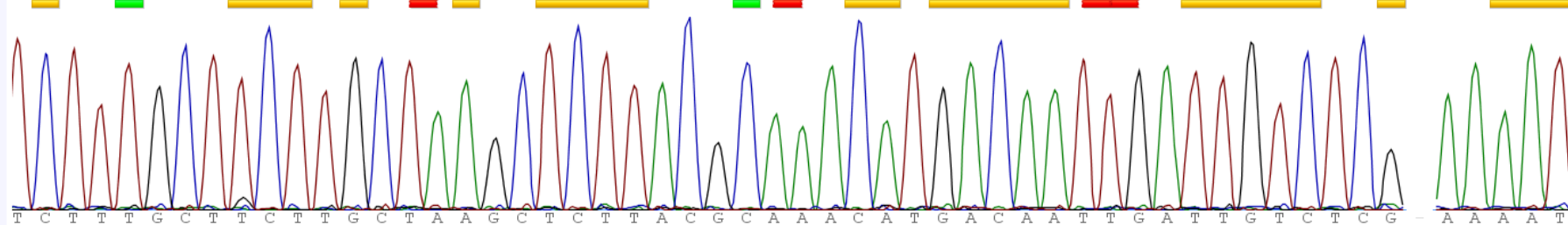
ND_25_D14-25SPER_C05_043.scf



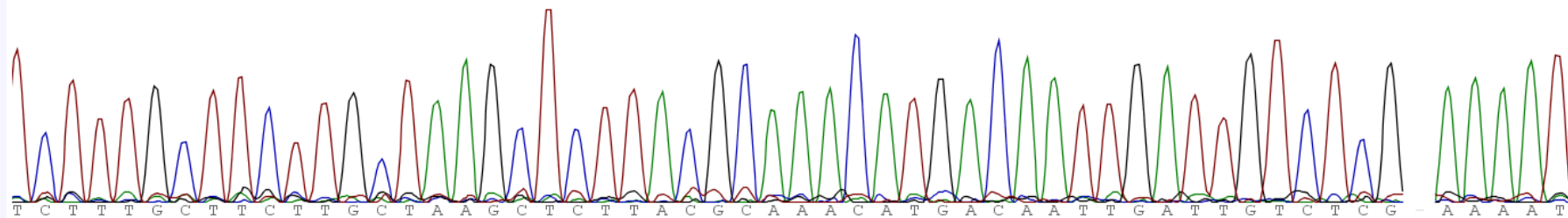
ND_25_D14-25SPEF_C05_043.scf



ND_25_D14-25SPER_B02_032.scf



ND_25_D14-25SPEF_B02_032.scf



Hap4 [A]: Adineta vaga complex sp. AJ...

T C T T T G C T T C T T G C T A A G C T C T T A C G C A A A C A T G A C A A T T G A T T G T C T C G - A A A A A T