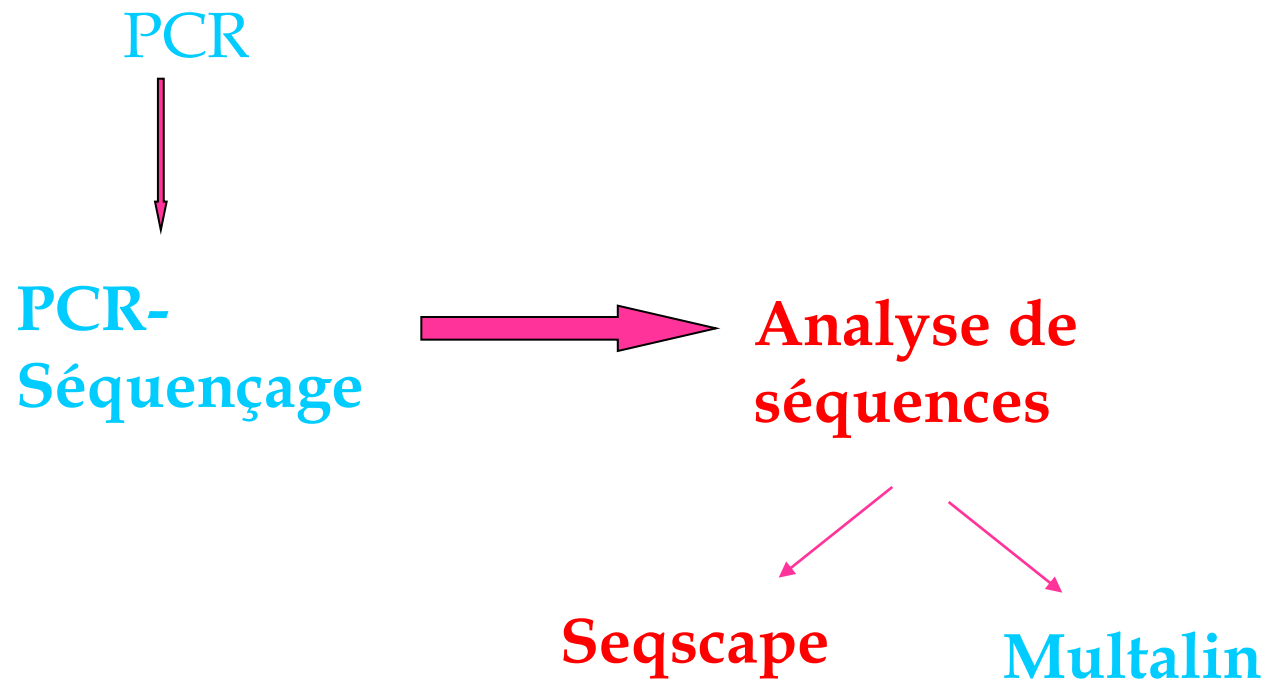
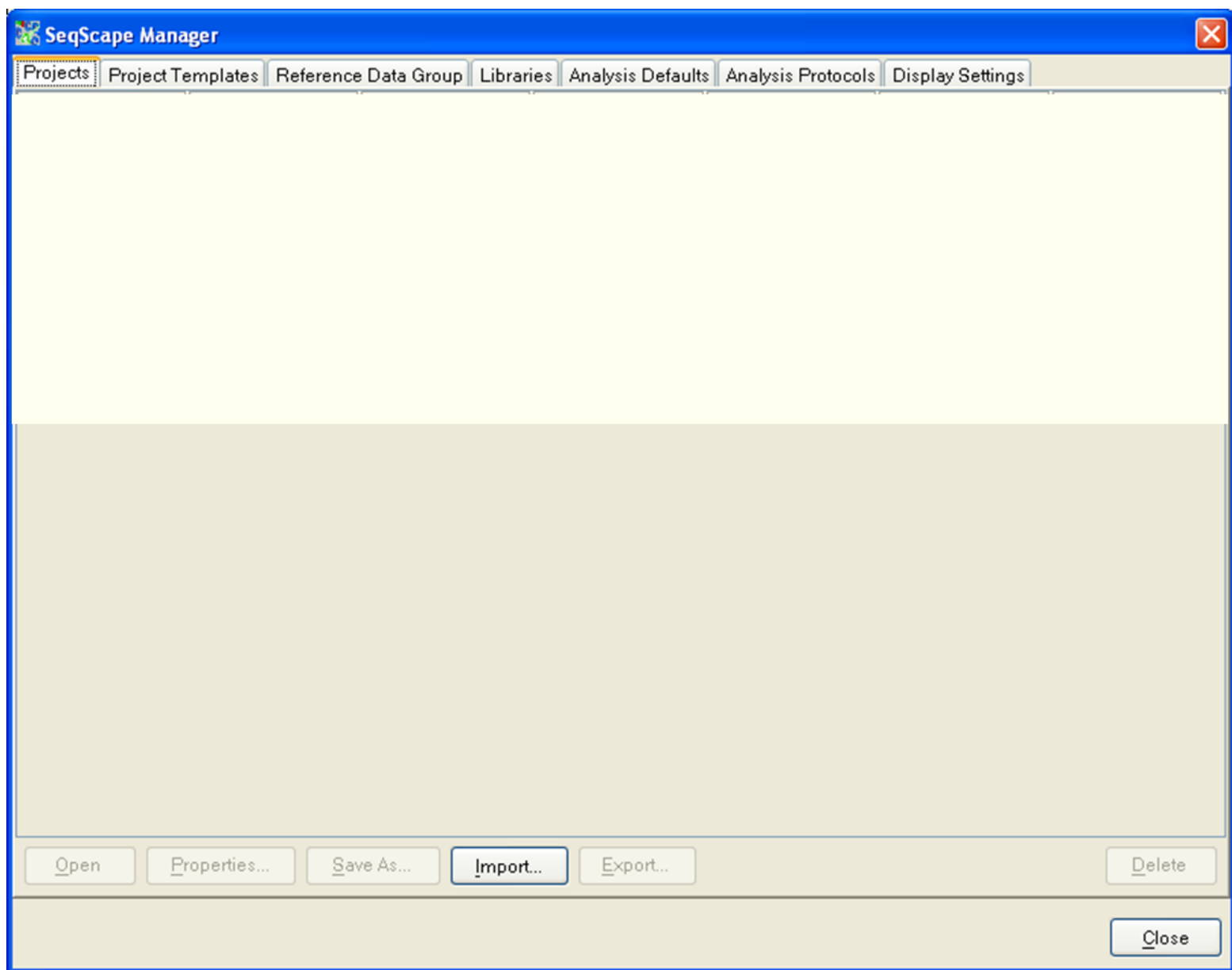


Analyse des séquences par les logiciels Multalin et seqscanner



- A partir de la structure d'un gène, déterminer la séquence codante et en déduire la séquence protéique
 - Trouver des homologies :
 - Au niveau des gènes d'une même famille
 - Au niveau d'un même gène dans différentes espèces
 - Trouver des différences :
 - Polymorphismes
 - Mutations
- → Alignement de séquences (Logiciel SeqScape)



RDG Properties

General

ROI

NT Variants

AA Variants

Variant Style

Reference Data Group Description

Reference Data Group Name: NAALADASE

Created: 17 déc. 2004 at 15:08:26 CET

Modified: 17 déc. 2004 at 15:18:46 CET

Source: N/A

Created By: ISABELLE: Isabelle COUPRY

Modified By: ISABELLE: isabelle COUPRY

General Settings

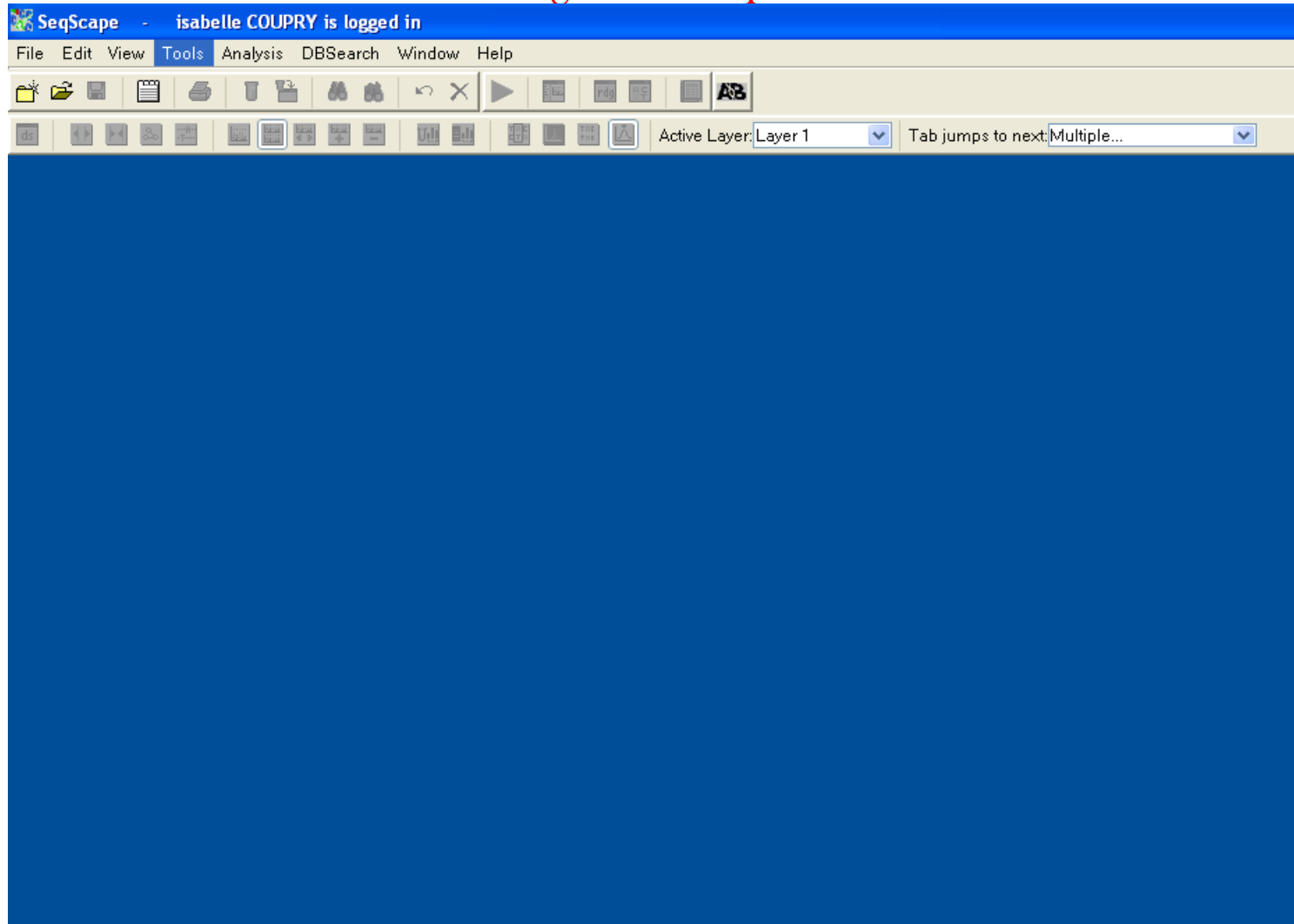
Codon Table: standard

Comments

OK

Cancel

Fenêtre du logiciel seqscanner



Genomic browser view of the HNF1A gene structure. The top track shows the gene structure with exons labeled EXON1 through EXON8. The bottom track shows the genomic coordinates from 232 to 259. The HNF1A gene is located on chromosome 12p13.3.

Delete Layer

Layer Name	Layer 1
------------	---------

Codon Start Number

Orientation

Library:

Translation Frame 1

Right ▾

	ROI Name	Segment	Seg. Start	Seg. End	ROI Start	ROI Length	Translation	Color	on Layer 1
1	EXON1	EXON1	1	232	1	232	<input checked="" type="checkbox"/>		<input checked="" type="checkbox"/>
2	EXON2	EXON2	1	283	1	283	<input checked="" type="checkbox"/>		<input checked="" type="checkbox"/>
3	EXON3	EXON3	1	298	1	298	<input checked="" type="checkbox"/>		<input checked="" type="checkbox"/>
4	EXON4	EXON4	1	292	1	292	<input checked="" type="checkbox"/>		<input checked="" type="checkbox"/>
5	EXON5	EXON5	1	250	1	250	<input checked="" type="checkbox"/>		<input checked="" type="checkbox"/>

Reference Sequence		CGCGCTCTCT	GTTTCTCTGC	AGCCCCGAAG	CTCGCGAATG	40
EXON1	41	TAGCAGGCGC	CCCAAGCTCG	GTCCTCAAGA	AGCCATGGCG	80
EXON2	81	GAATCCAGGG	GCCGTCTGTA	CCTTTGGATG	TGCTTGGCTG	120
EXON3	121	CTGCGCTGGC	ATCTTTCTGT	ATGGGATTTA	TGGTGGGTAA	160
EXON4	161	GTGAACAAAA	CACTCTACCC	CGACTCCGGG	GCTCGTGATT	200
EXON5	201	CTCTGCAGAG	ATAAAGGGAG	AAATCTTGGA	GC	232
EXON6						
EXON7						
EXON8						
EXON9						

Paste Ref. Segment

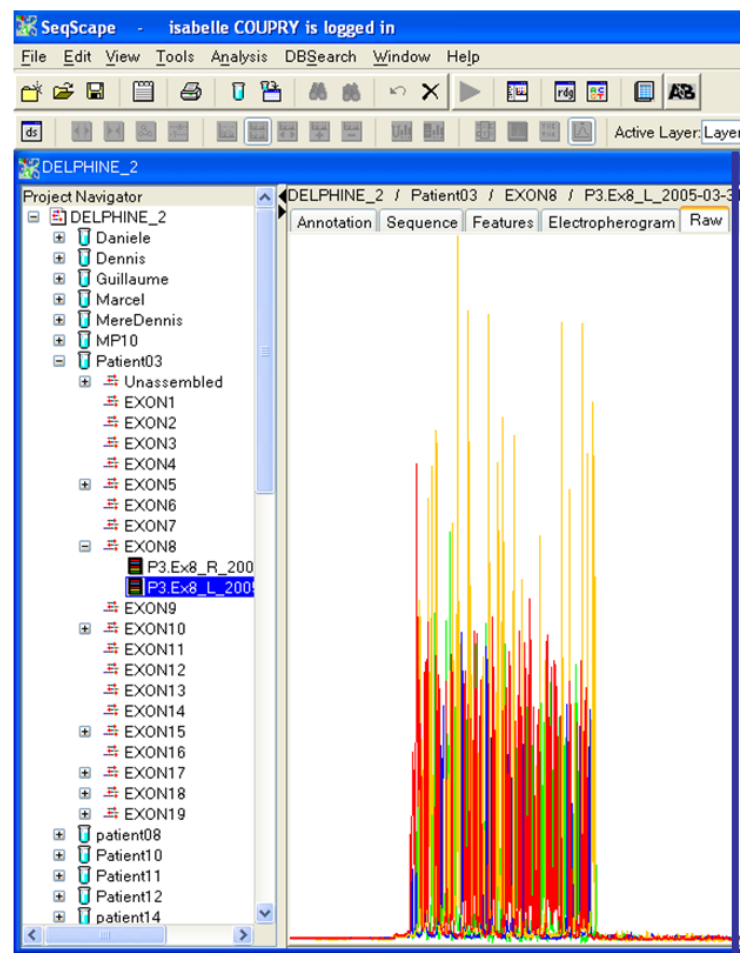
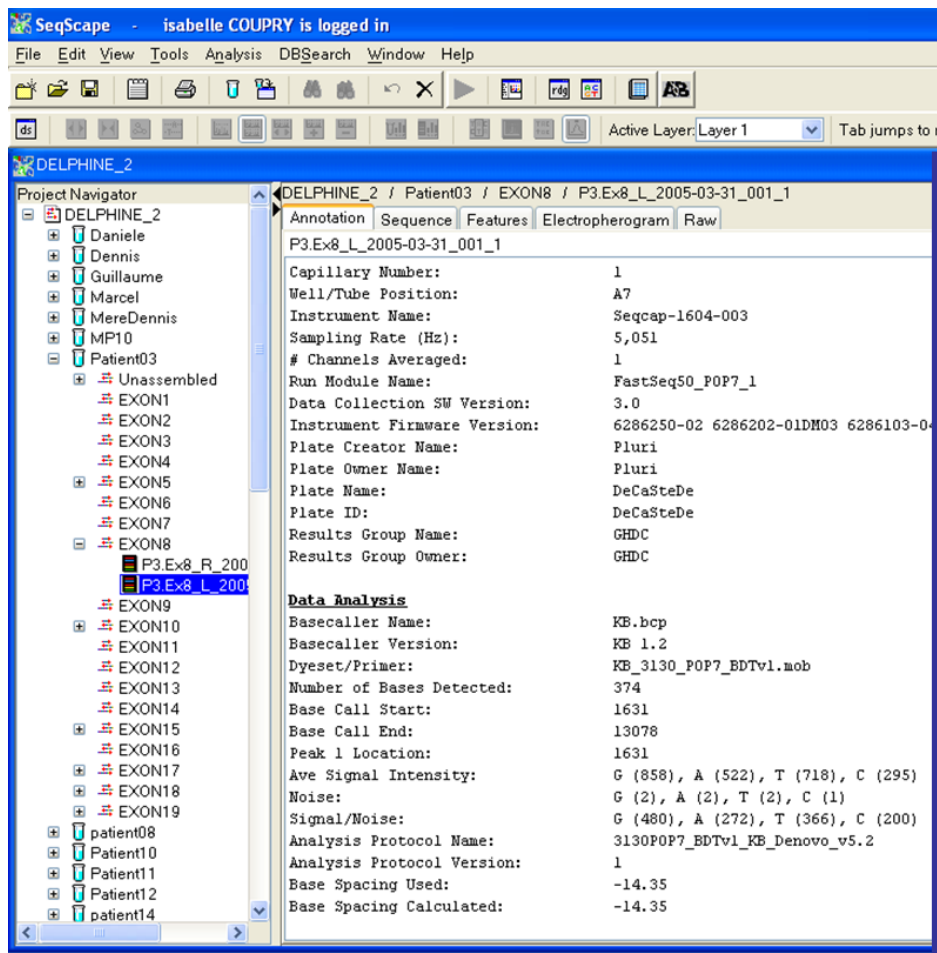
Add Variant

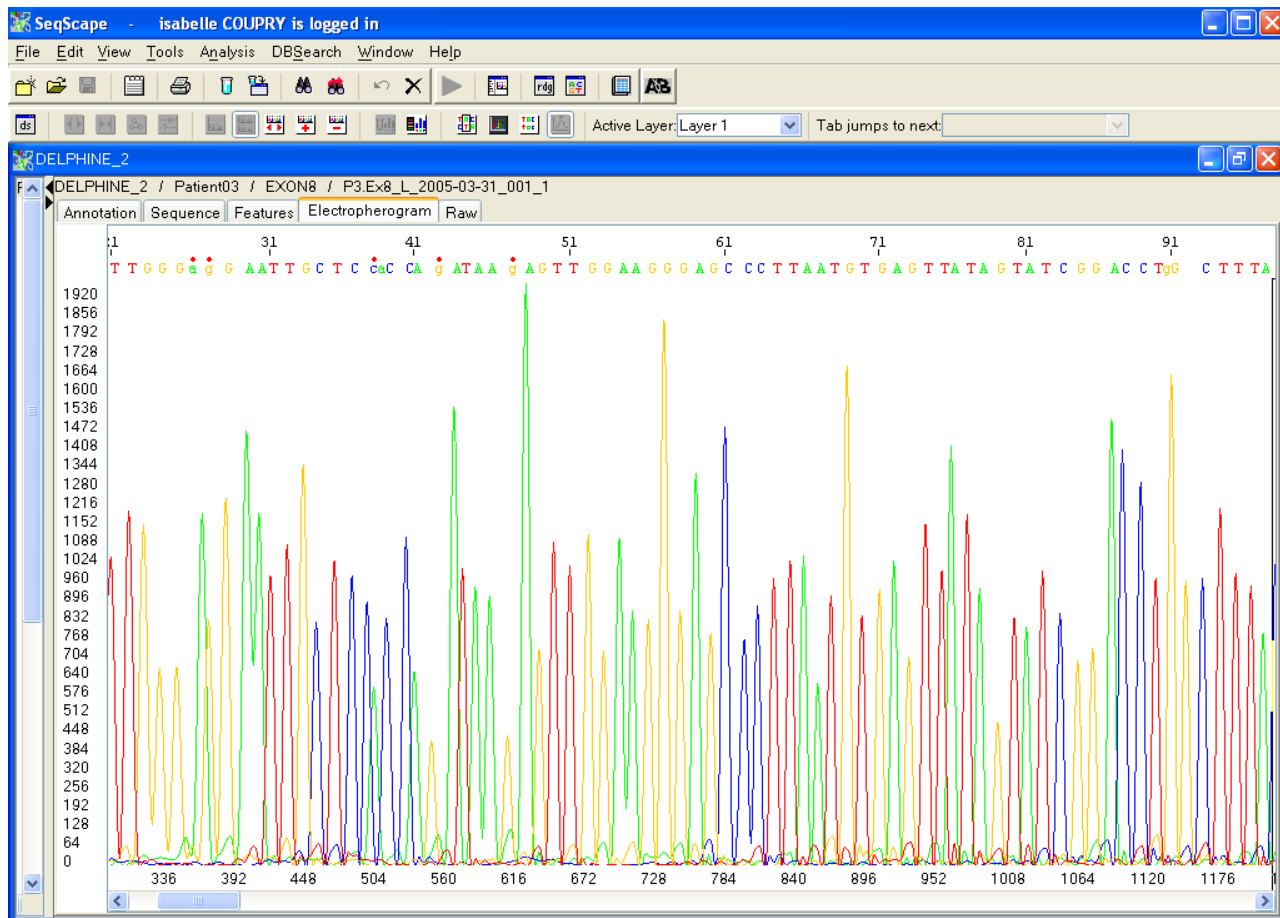
Add ROI

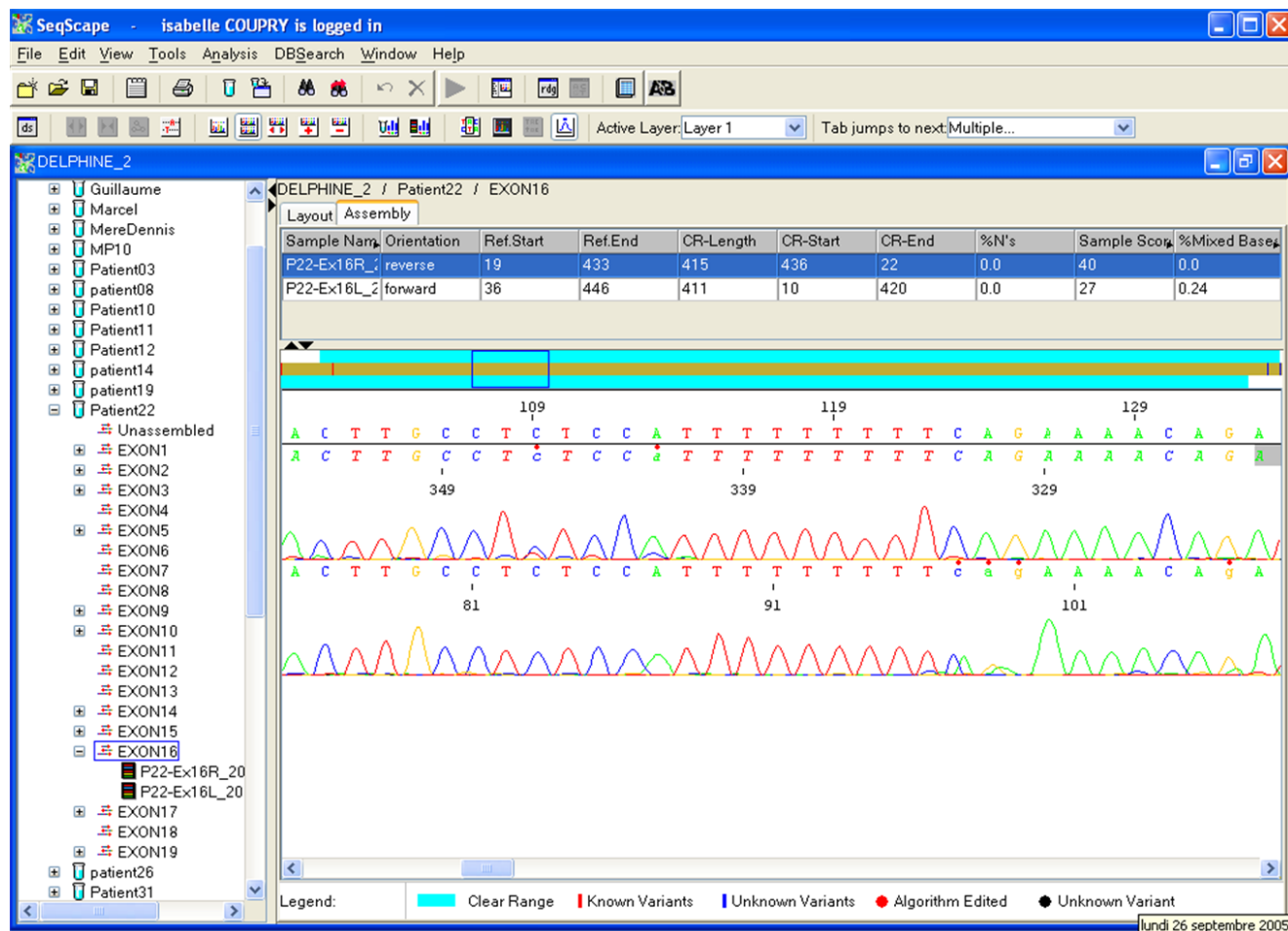
Info

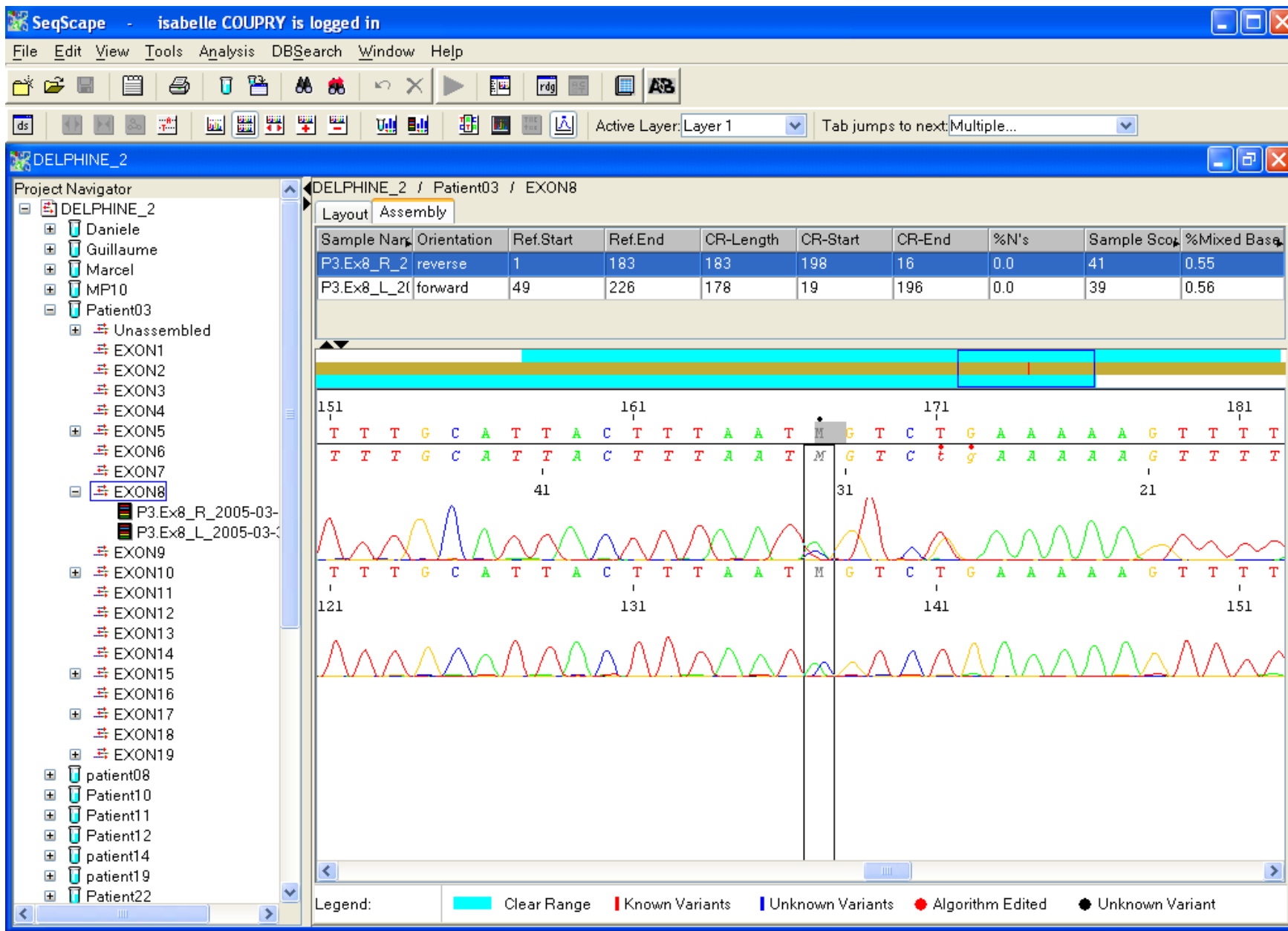
OK

Cancel









Symbole ²	Description	Bases représentées					
A	adénine	A				1	
C	cytosine		C				
G	guanine			G			
T	thymine				T		
U	uracile				U		
W	<i>weak</i>	A			T	2	
S	<i>strong</i>		C	G			
M	amino	A	C				
K	keto			G	T		
R	purine	A		G			
Y	pyrimidine		C		T	3	
B	pas A (B vient après A)		C	G	T		
D	pas C (D vient après C)	A		G	T		
H	pas G (H vient après G)	A	C		T		
V	pas T (V vient après T et U)	A	C	G		4	
N ou -	<i>any base</i>	A	C	G	T		



New NT Variant

Type:

ROI:

Position (bp): To

Reference base(s):

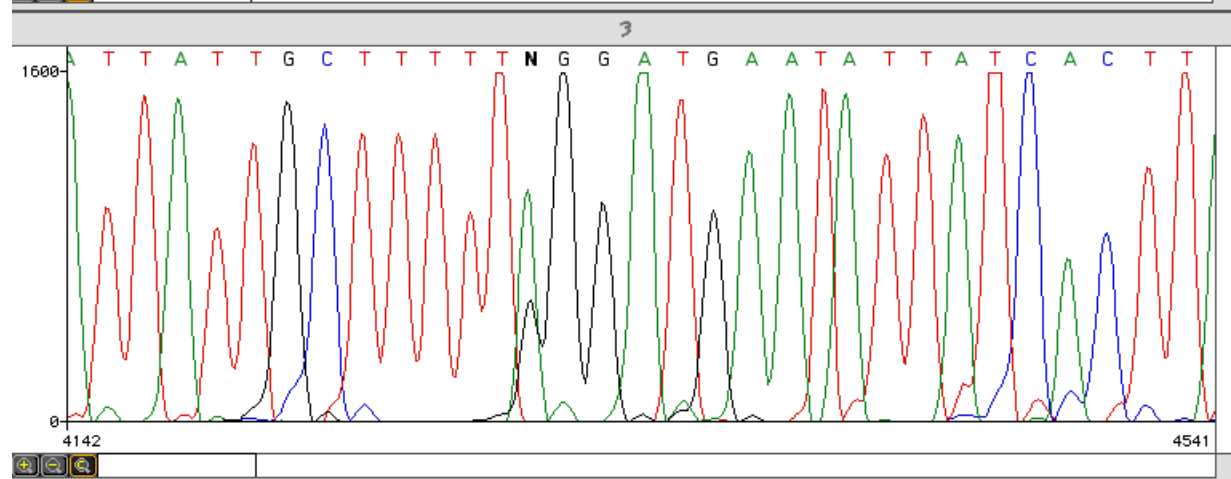
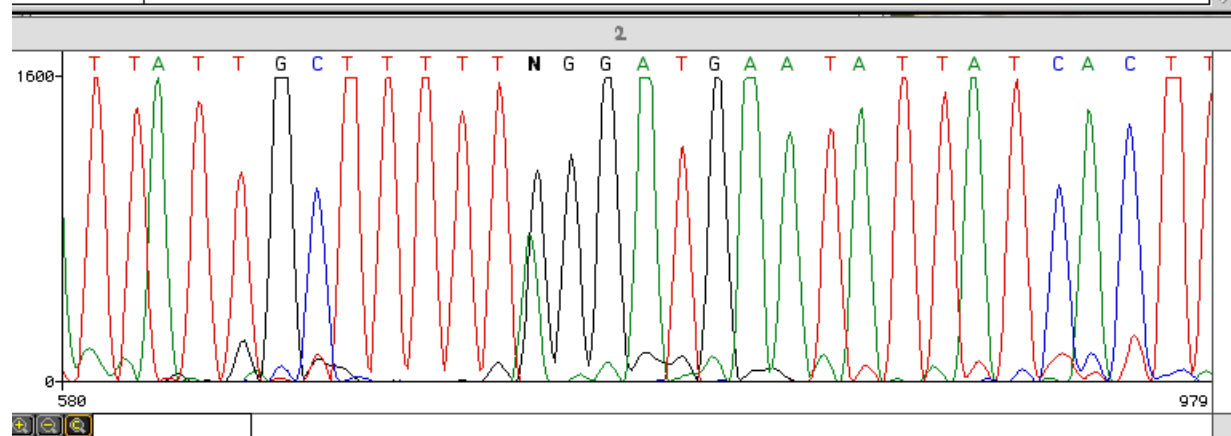
Variant base(s):

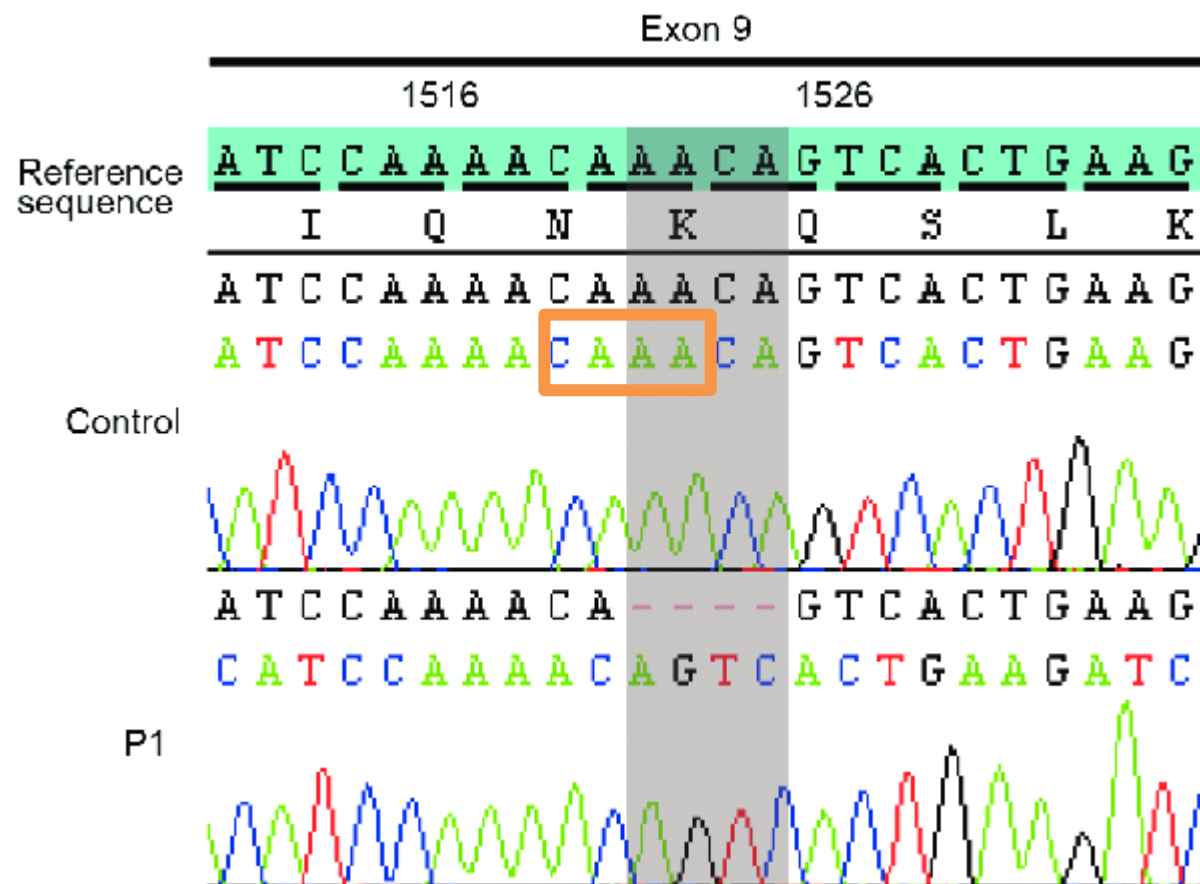
Style:

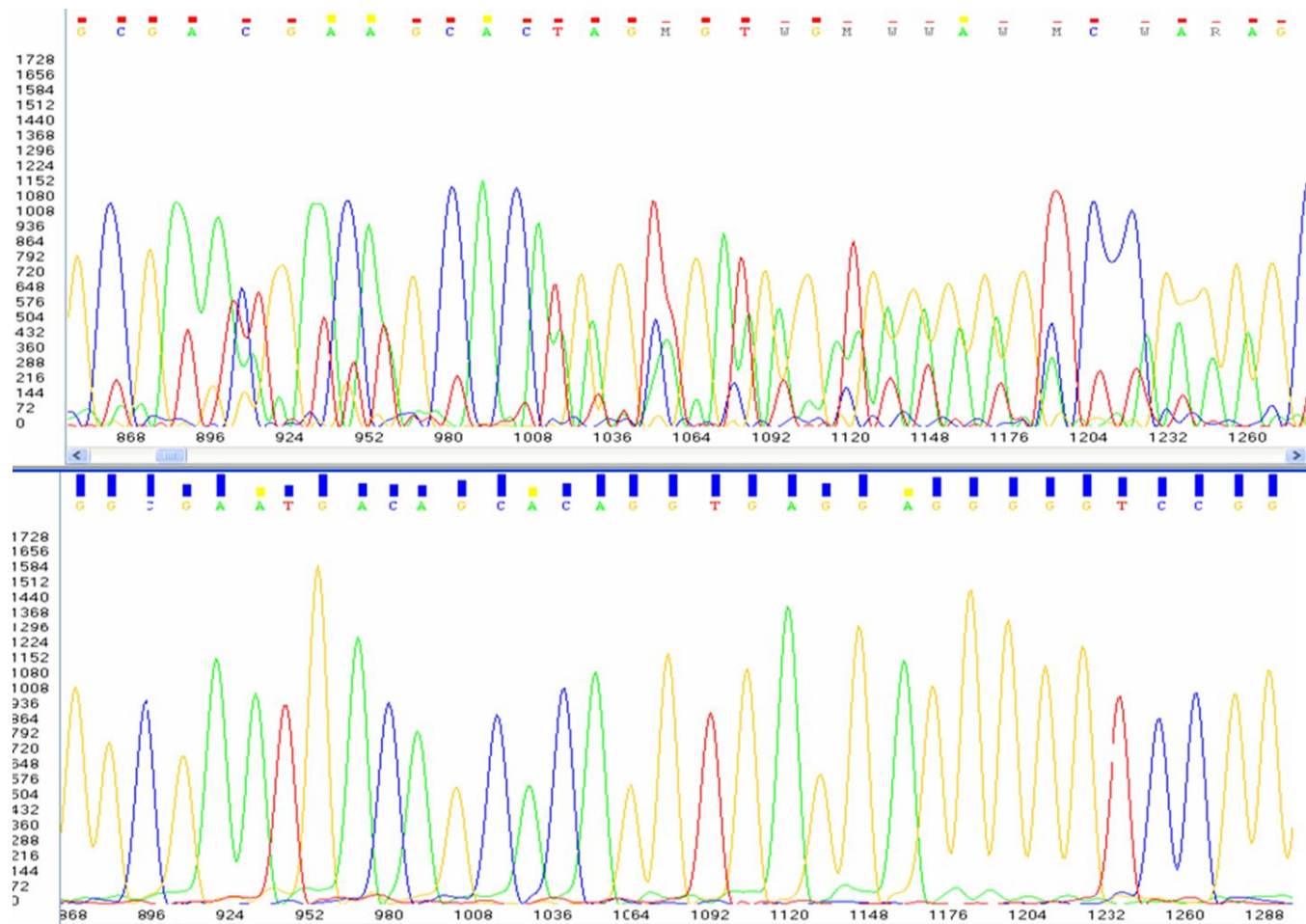
Description:

☒ Used by all ROIs

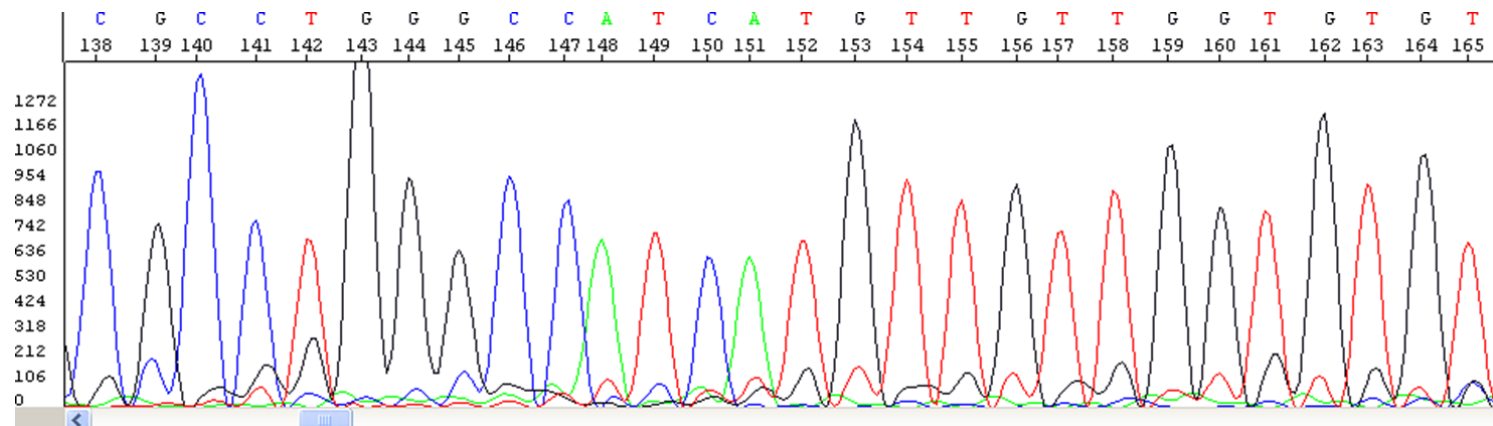
SEQ-EXON 10-187							
		40	50	60	70	80	90
1		TTTTAACTGT	TTCATATTGA	ATATTATTGC	TTTTTTAGGAT	GAATATTATC	ACTTATTAGC
2 26·D66HF		TTTTAACTGT	TTCATATTGA	ATATTATTGC	TTTTTTGGGAT	GAATATTATC	ACTTATTAGC
4		-----	-----	-----	-----*	-----	-----
3 27·D66HR		TTTTAACTGT	TTCATATTGA	ATATTATTGC	TTTTTTGGGAT	GAATATTATC	ACTTATTAGC
5		-----	-----	-----	-----*	-----	-----



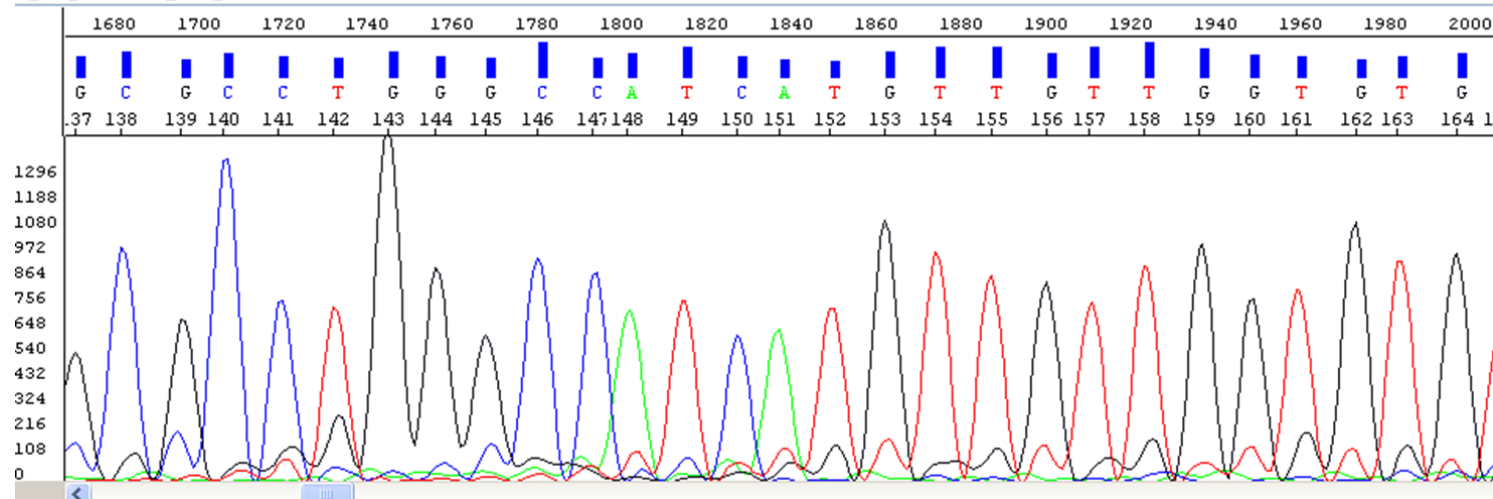




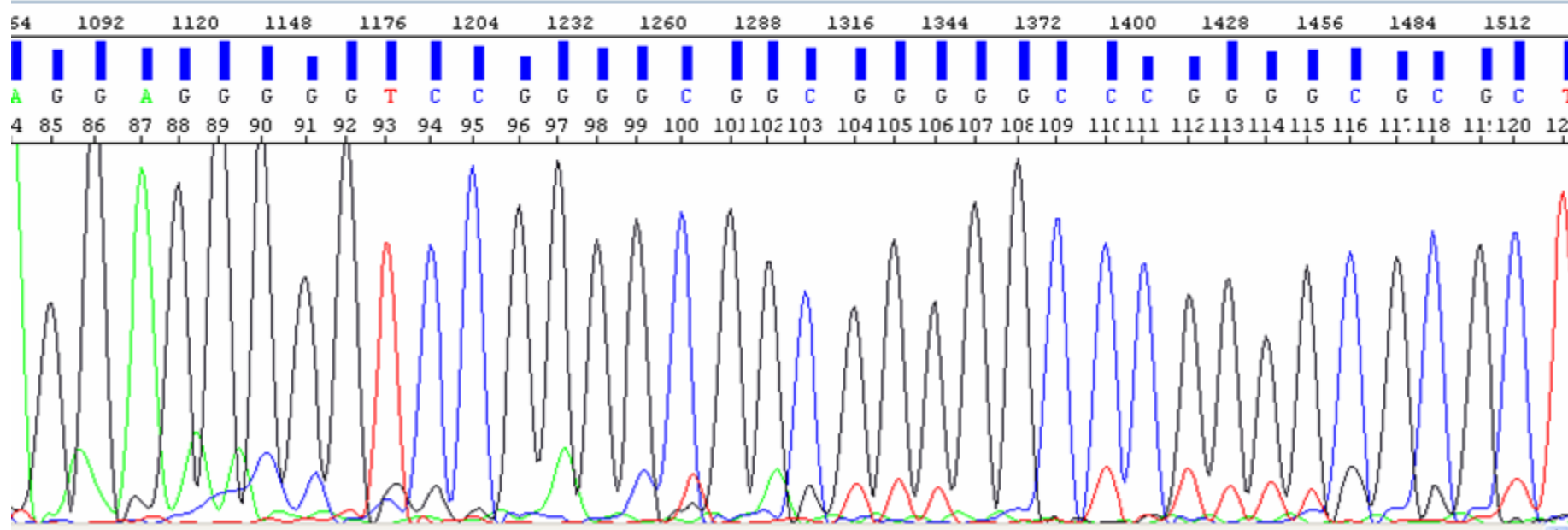
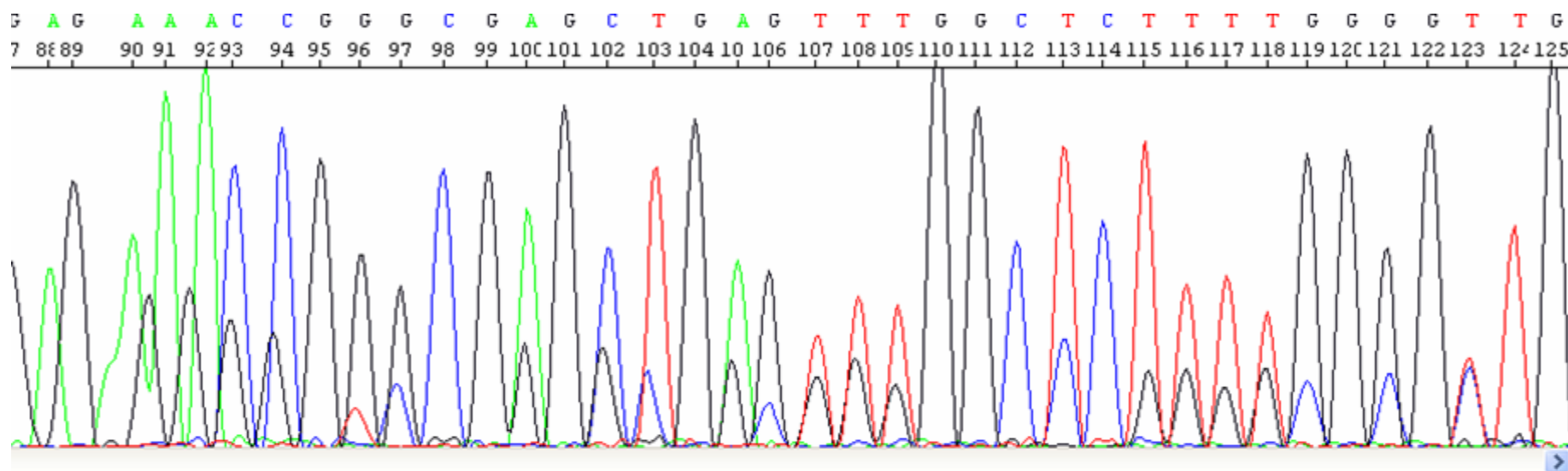
Diminution du temps d'injection



11_13R_2005-09-12_0633_013



amorce partiellement dégradée



contaminé par les amorces PCR

Fenêtre du logiciel "Mulalin"

MultAlin

Multiple sequence alignment by Florence Corpet

Published research using this software should cite:
"Multiple sequence alignment with hierarchical clustering"
F. CORPET, 1988, Nucl. Acids Res., 16 (22), 10881-10890

Sequence data

Cut and paste your sequences here below. ?

(sample sequences)

>P53
ATCGGACCCCCCCCCC
TAA
>46A
CGGACCCCCCCCCC
TAA

or select a file: [new](#)

Sequence input format:

For nucleotidic sequences, you must change the Symbol comparison Table (see below) ?

Exemple de séquence analysée par Multalin

1 10 20 30 40 50 60 70 80 90 100 110 120 130

P53 TCCGCGCCATGCCATCTACAGCAGTCACAGACATGACGAGGTTGTGAGGCGCTGCCCCACCATGAGCGTGCTCAGATAGCGATGGTGGTGGCCCTCTCAGCATCTTATCCGAGTGGAGAGGAA

46B-LL14 ATKGCGTGGCCCTCTCAGCATCTTATCCGAGTGGAGAGGAA

P16-LL6 TSCRTYRGTSYGRS-HYA TSCRTYRGTSYGRS-HYA

Consensusat.g.ctggccctcctcagcatct.TatCcgatggaaggaa

131 140 150 160 170 180 190 200 210 220 230 240 250 260

P53 TTGCGGTGGAGATTGGATGACGAAACACCTTTTCACATAGTGTGGTGGTGCCTATGAGCGGCTGAGGTTGGCTTGACTGTACACCATCCACTACACTACATGTGTACAGTCTCTGCAATG

46B-LL14 TTGCGGTGGAGATTGGATGACGAAACACCTTTTCACATAGTGTGGTGGTGCCTATGAGCGGCTGAGGTTGGCTTGACTGTACACCATCCACTACACTACATGTGTACAGTCTCTGCAATG

P16-LL6 TTYSYSGWKKKKATTGGATGACGAAACACCTTTTCACATAGTGTGGTGGTGCCTATGAGCGGCTGAGGTTGGCTTGACTGTACACCATCCACTACACTACATGTGTACAGTCTCTGCAATG

Consensus Tttgcgtgtggagattttggatgacgaaacaccttttcacatagtgtgggtgggtgccctatgagcggctgaggttggcttgactgtaccaccatccactacactacatgtgtacagttcttgcagt

261 270 280 290 300 310 320 330 340 350 360 370 380 390

P53 GCGGCGATGACCGGAGGCCATCTCCACATCATCACTGGAGACTCCAGTGGTATCTACTGGGACGGARAGCTTTGAGGTGCGTGTTTGTGCTGTCTTGGGAGAGACGGCGCACAGAGGAG

46B-LL14 GCGGCGATGACCGGAGGCCATCTCCACATCATCACTGGAGACTCCAGTGGTATCTACTGGGACGGARAGCTTTGAGGTGCGTGTTTGTGCTGTCTTGGGAGAGACGGCGCACAGAGGAG

P16-LL6 GCGGCGATGACCGGAGGCCATCTCCACATCATCACTGGAGACTCCAGTGGTATCTACTGGGACGGARAGCTTTGAGGTGCGTGTTTGTGCTGTCTTGGGAGAGACGGCGCACAGAGGAG

Consensus GCGGCGATGACCGGAGGCCATCTCCACATCATCACTGGAGACTCCAGTGGTATCTACTGGGACGGARAGCTTTGAGGTGCGTGTTTGTGCTGTCTTGGGAGAGACGGCGCACAGAGGAG

391 400 410 420 430 440 450 460 470 480 490 500 510 520

P53 AGAATCTCCGCAAGAGGGGAGCCTCACACGAGCTGCCCGAGGAGCACTAAGCGAGCACTGCCACACACCCAGCTCTCTCCCGAGCCAAAGAGAACCACTGGATGGAGATATTTACCCCT

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P16-LL6 AGAATCTCCGCAAGAGGGGAGCCTCACACGAGCTGCCCGAGGAGCACTAAGCGAGCACTGCCACACACCCAGCTCTCTCCCGAGCCAAAGAGAACCACTGGATGGAGATATTTACCCCT

Consensus AGAATCTCCGCAAGAGGGGAGCCTCACACGAGCTGCCCGAGGAGCACTAAGCGAGCACTGCCACACACCCAGCTCTCTCCCGAGCCAAAGAGAACCACTGGATGGAGATATTTACCCCT

521 530 540 550 560 570 580 590 600 610 620 630 640 650

P53 TCAGATCCGTGGGCGTGAGCGCTTCGAGATGTTCCGAGAGCTGATGAGGCCCTTGGAATCAGGATGCCAGGCTGGGAGGAGCCAGGGGGAGCAGGGCTCACTCCAGCCACCTGAGTCCAAAAG

46B-LL14 TCAGATCCGTGGGCGTGAGCGCTTCGAGATGTTCCGAGAGCTGATGAGGCCCTTGGAATCAGGATGCCAGGCTGGGAGGAGCCAGGGGGAGCAGGGCTCACTCCAGCCACCTGAGTCCAAAAG

P16-LL6 TCAGATCCGTGGGCGTGAGCGCTTCGAGATGTTCCGAGAGCTGATGAGGCCCTTGGAATCAGGATGCCAGGCTGGGAGGAGCCAGGGGGAGCAGGGCTCACTCCAGCCACCTGAGTCCAAAAG

Consensus TCAGATCCGTGGGCGTGAGCGCTTCGAGATGTTCCGAGAGCTGATGAGGCCCTTGGAATCAGGATGCCAGGCTGGGAGGAGCCAGGGGGAGCAGGGCTCACTCCAGCCACCTGAGTCCAAAAG

651 660 670 680 690 700 710 720 730 740 750 760 770 780

P53 GGTCACTCTACCTCCCGCATAAAAACTCATGTTCAAGACAGAGGGCTGACTCAGACTGACATTTCCACTTCTGTTCCCACTGACAGCTCCACCCCATCTCTCCCTCCCTGCCATTTTGG

46B-LL14 GGTCACTCTACCTCCCGCATAAAAACTCATGTTCAAGACAGAGGGCTGACTCAGACTGACATTTCCACTTCTGTTCCCACTGACAGCTCCACCCCATCTCTCCCTCCCTGCCATTTTGG

P16-LL6 GGTCACTCTACCTCCCGCATAAAAACTCATGTTCAAGACAGAGGGCTGACTCAGACTGACATTTCCACTTCTGTTCCCACTGACAGCTCCACCCCATCTCTCTCCCTCCCTGCCATTTTGG

Consensus GGTCACTCTACCTCCCGCATAAAAACTCATGTTCAAGACAGAGGGCTGACTCAGACTGACATTTCCACTTCTGTTCCCACTGACAGCTCCACCCCATCTCTCTCCCTCCCTGCCATTTTGG

781 790 800 810 820

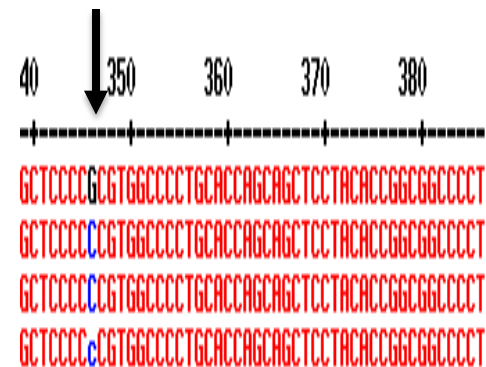
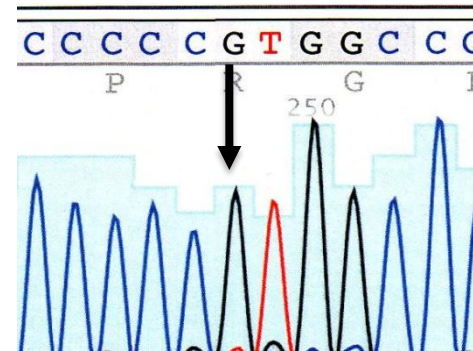
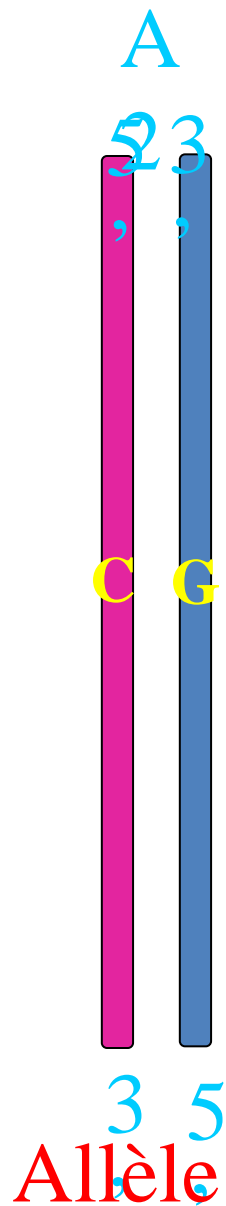
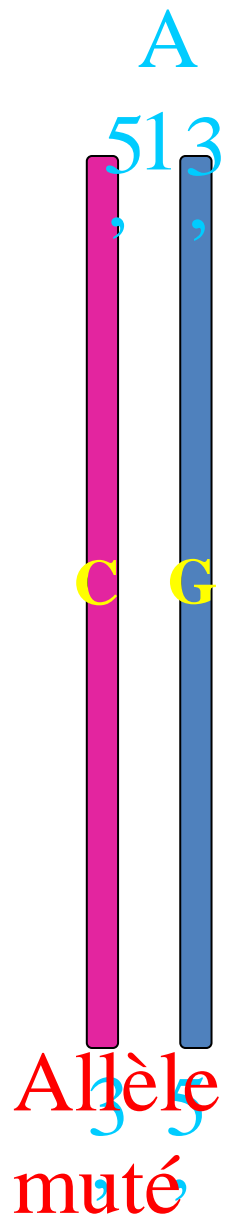
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46B-LL14 GTTTTGGGTCTTTGACCCCTTGCTTGCATAGGTGTGCGT

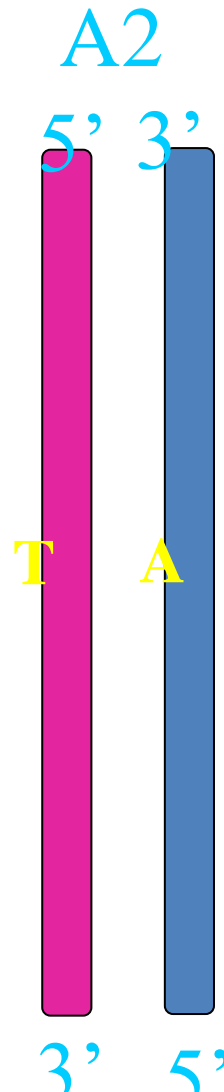
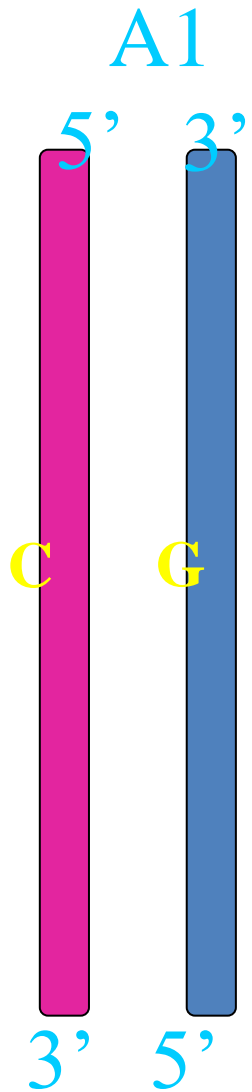
P16-LL6 GTTTTGGGTCTTTGACCCCTTGCTTGCATAGGTGTGCGT

Consensus

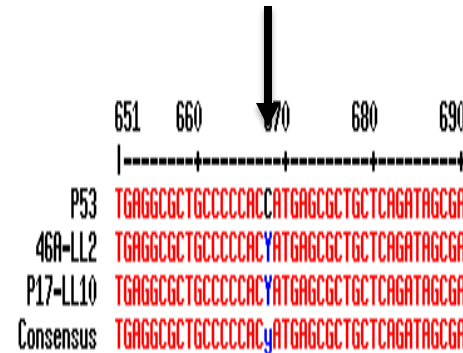
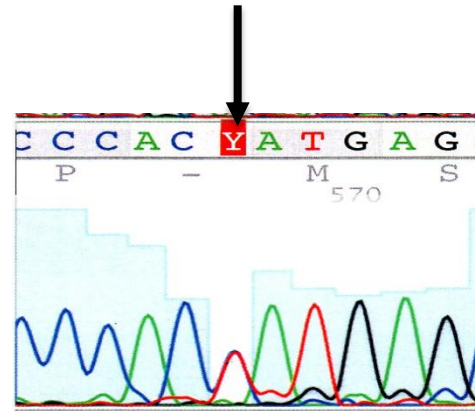
EX : Substitution G
vers C
À l'état
homozygote



EX : Substitution C vers T À l'état hétérozygote



Allèle normal Allèle muté



Homo sapiens TAS2R38_PAV.adn
 Pan paniscus TAS2R38.adn
 Gorilla gorilla TAS2R38.adn
 Pan troglodytes TAS2R38.adn
 Pongo pygmaeus TAS2R38.adn
 Macaca mulatta TAS2R38.adn
 Hylobates klossii TAS2R38.adn
 Papio hamadryas TAS2R38.adn
 Rattus norvegicus TAS2R38.adn

* * * * * : * * * * * : * * * * * : * : * * : : : * * * * *																													
5					10					15					20					25					30				
A	T	G	T	T	G	A	C	T	C	T	A	A	C	T	C	G	C	A	T	C	C	G	C	A	C	T	G	T	G
A	T	G	T	T	G	A	C	T	C	T	A	A	C	T	C	G	C	A	T	C	C	A	C	A	C	T	G	T	G
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