

# **Analyse des séquences par les logiciels Multalin et seqscanner**

PCR



PCR-  
Séquençage



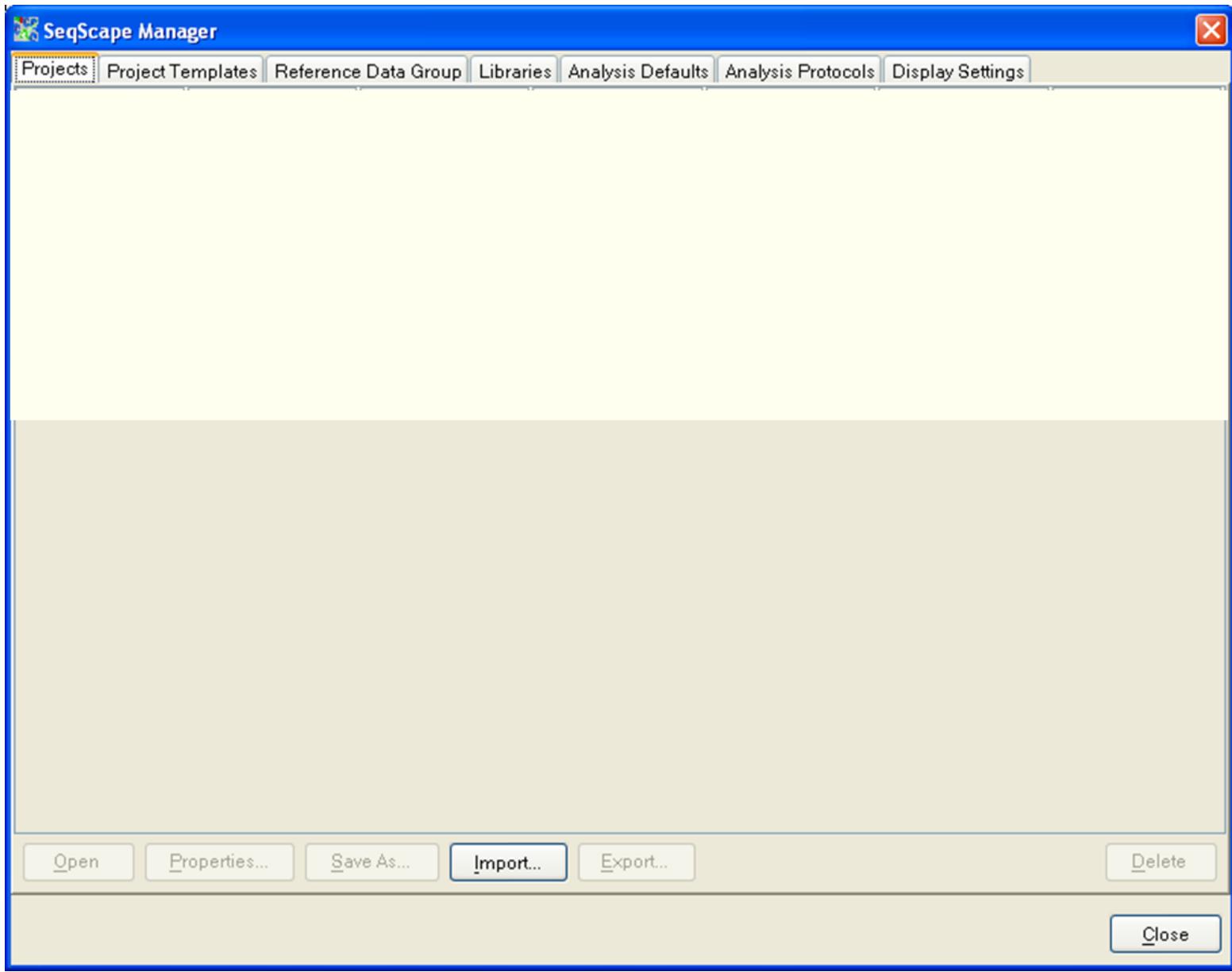
Analyse de  
séquences



Seqscape

Multalin

- 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

Created By: ISABELLE: Isabelle COUPRY

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

Modified By: ISABELLE: isabelle COUPRY

Source: N/A

#### General Settings

Codon Table:

standard



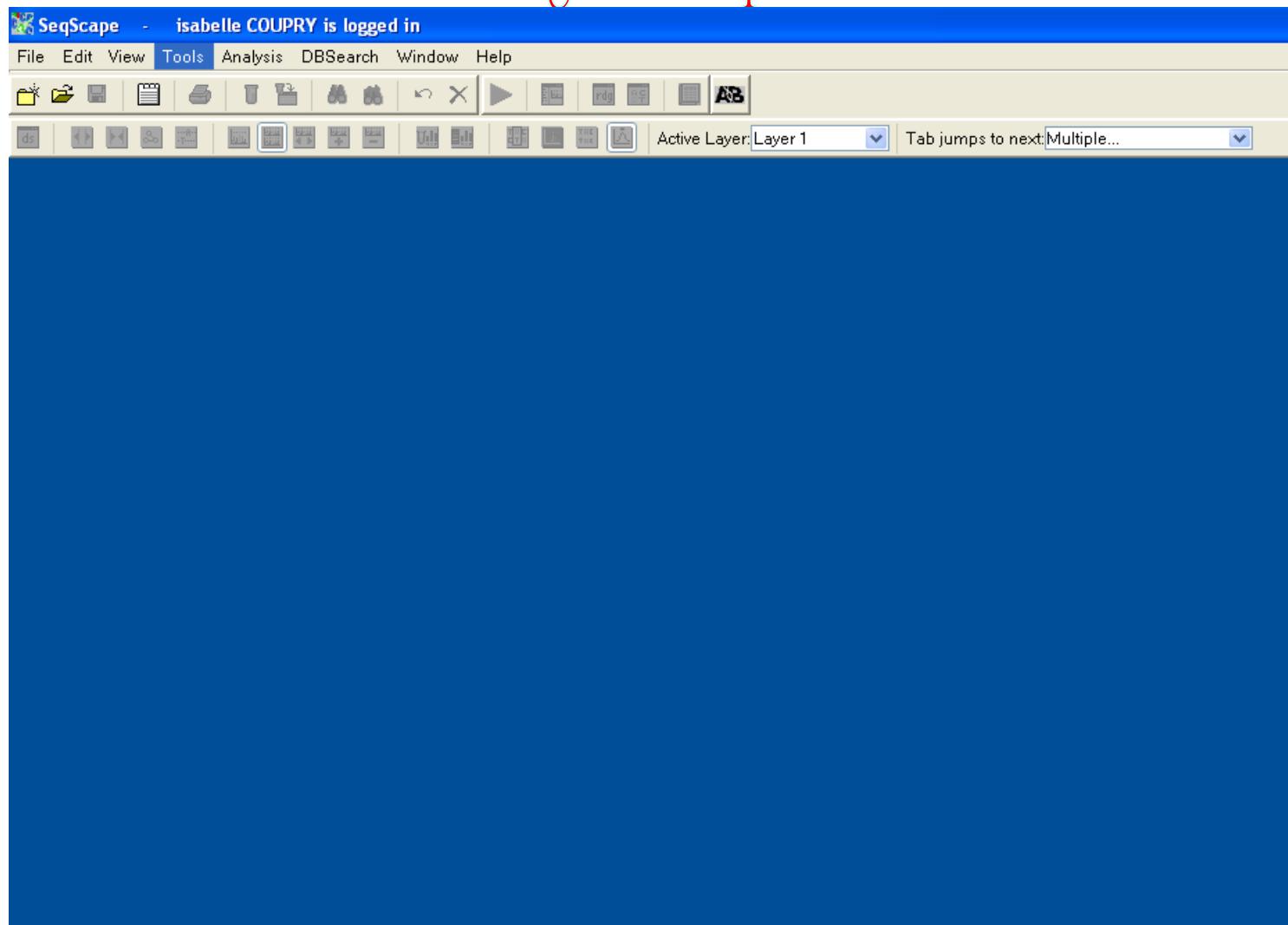
#### Comments

(Large empty text area for comments)

OK

Cancel

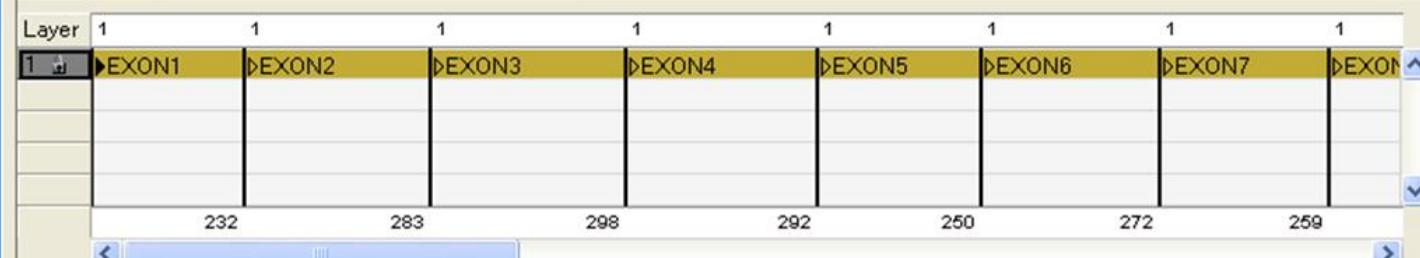
# Fenêtre du logiciel seqscanner



## RDG Properties



General ROI NTV Variants AA Variants Variant Style



## Layer 1 settings

New Layer

Delete Layer

Layer Name

Layer 1

Codon Start Number

1

Orientation



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

- EXON1
- EXON2
- EXON3
- EXON4
- EXON5
- EXON6
- EXON7
- EXON8
- EXON9
- EXON10

1	CGCGCTCTCT	GTTTCTCTGC	AGCCCCGAAG	CTCGCGAATG	40
41	TAGCAGGGCG	CCCAAGCTCG	GTCTCTCAAGA	AGCCATGGCG	80
81	GAATCCAGGG	GCCGTCCTGTA	CCTTTGGATG	TGCTTGGCTG	120
121	CTGCGCTGGC	ATCTTTCCTG	ATGGGATTAA	TGGTGGGTAA	160
161	GTGAACAAAA	CACTCTACCC	CGACTCCGGG	GCTCGTGATT	200
201	CTCTGCAGAG	ATAAAAGGGAG	AAATCCTGGA	GC	232

Add Ref. Segment

Paste Ref. Segment

Split Ref. Segment

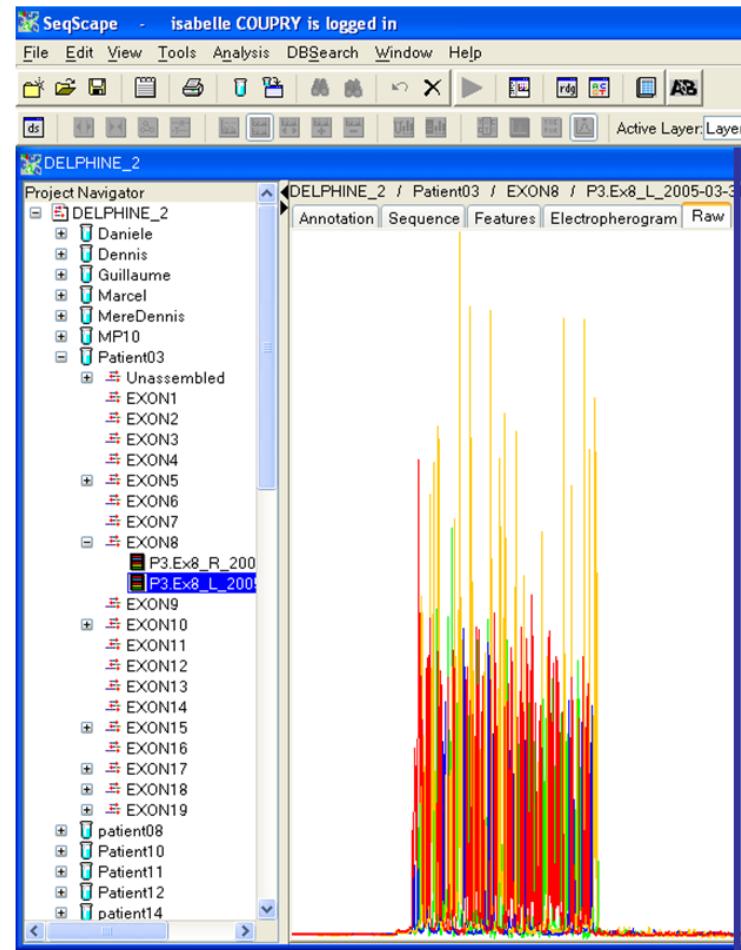
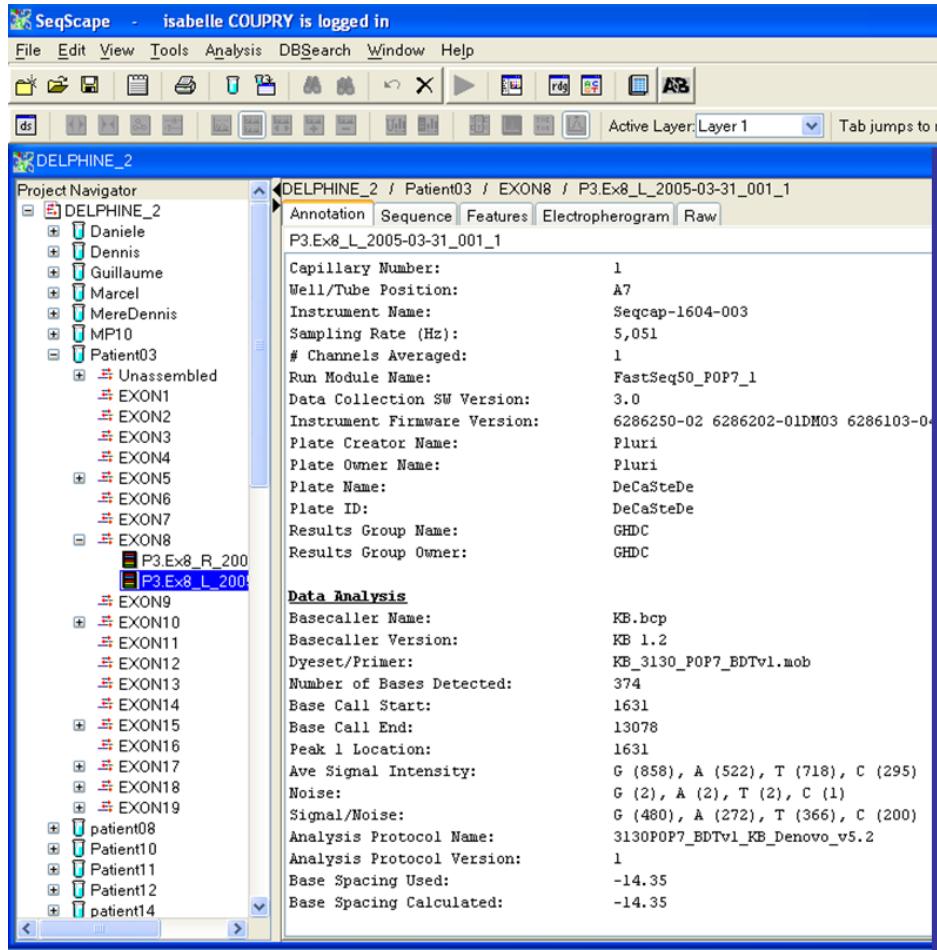
Add Variant

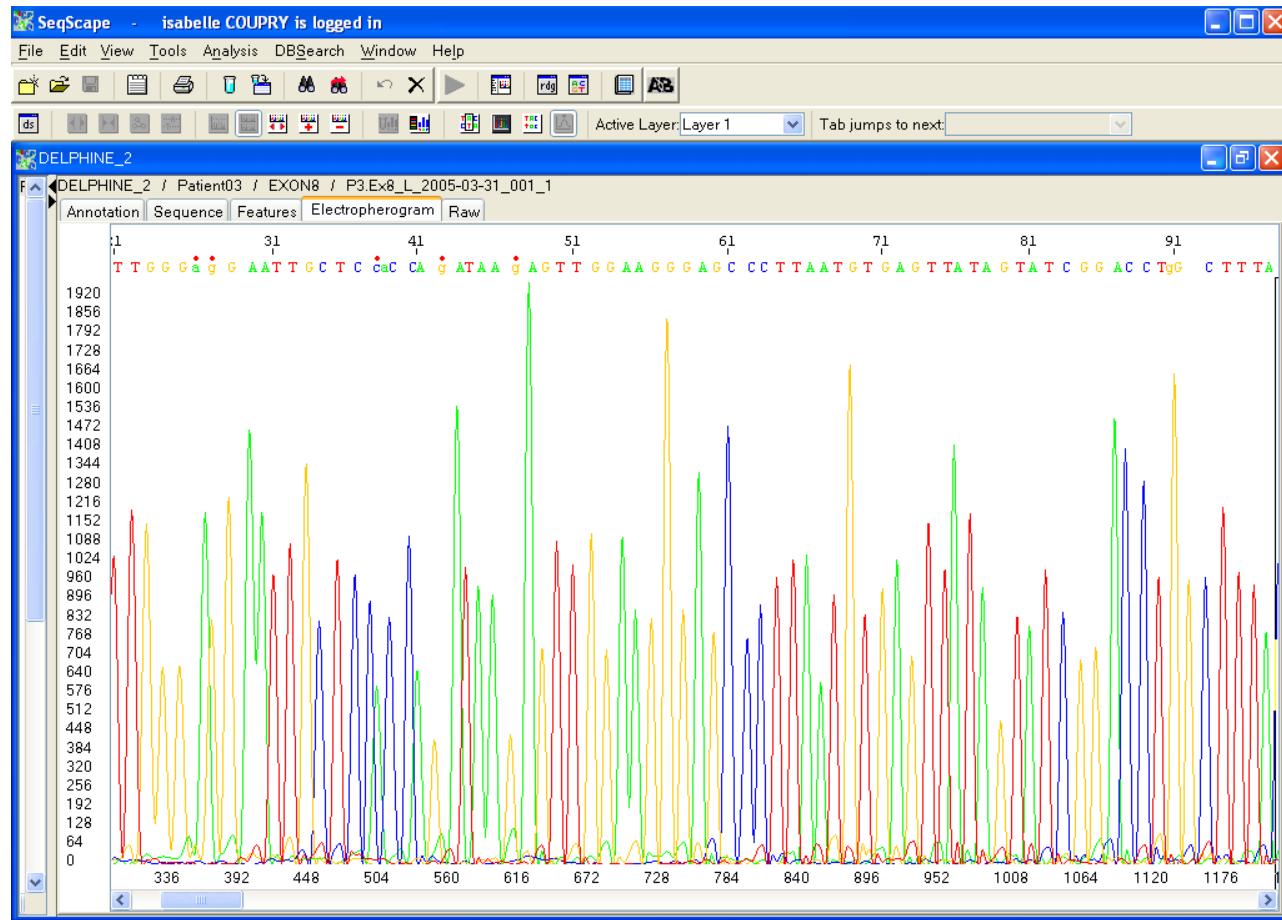
Add ROI

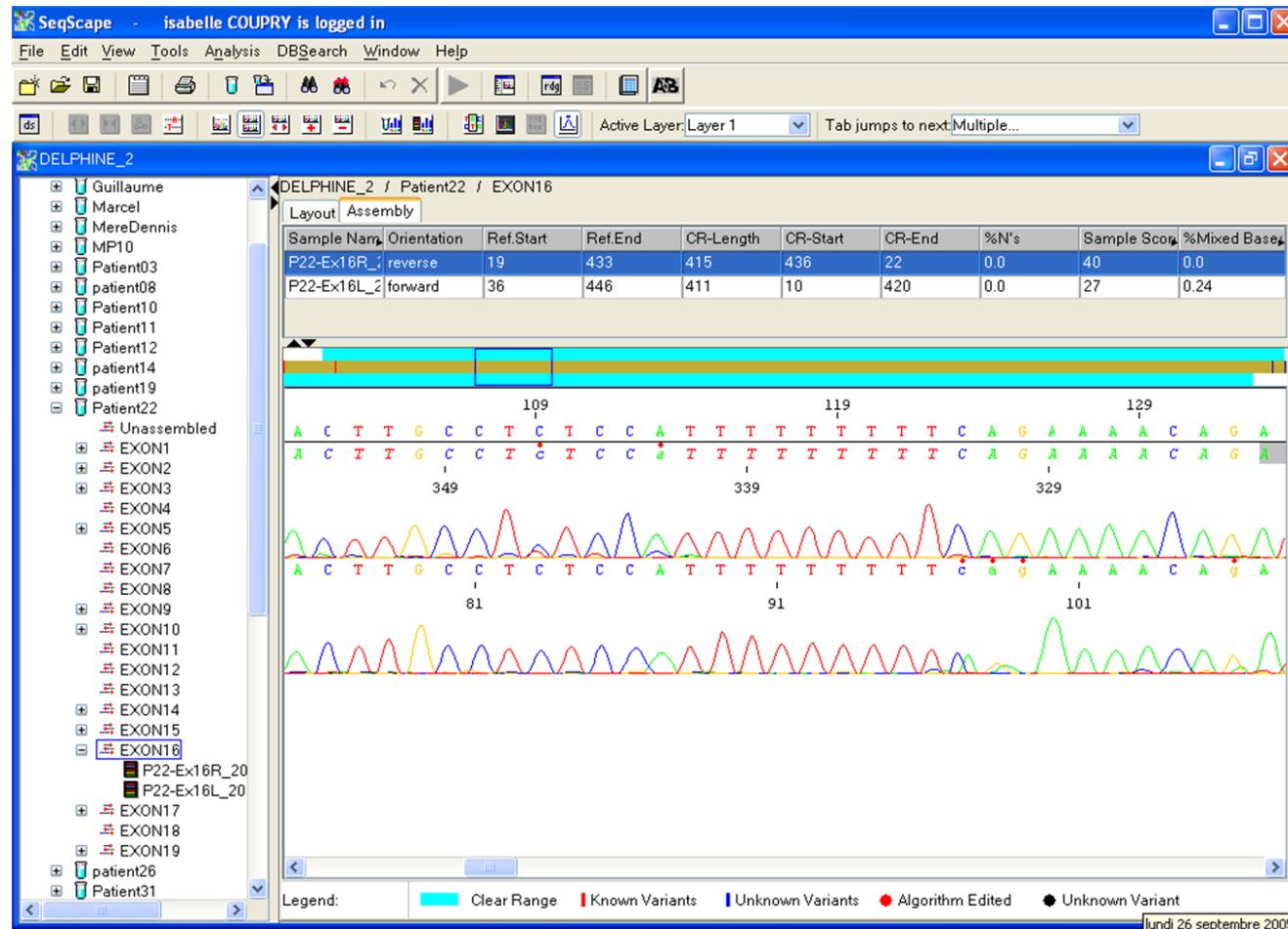
Info

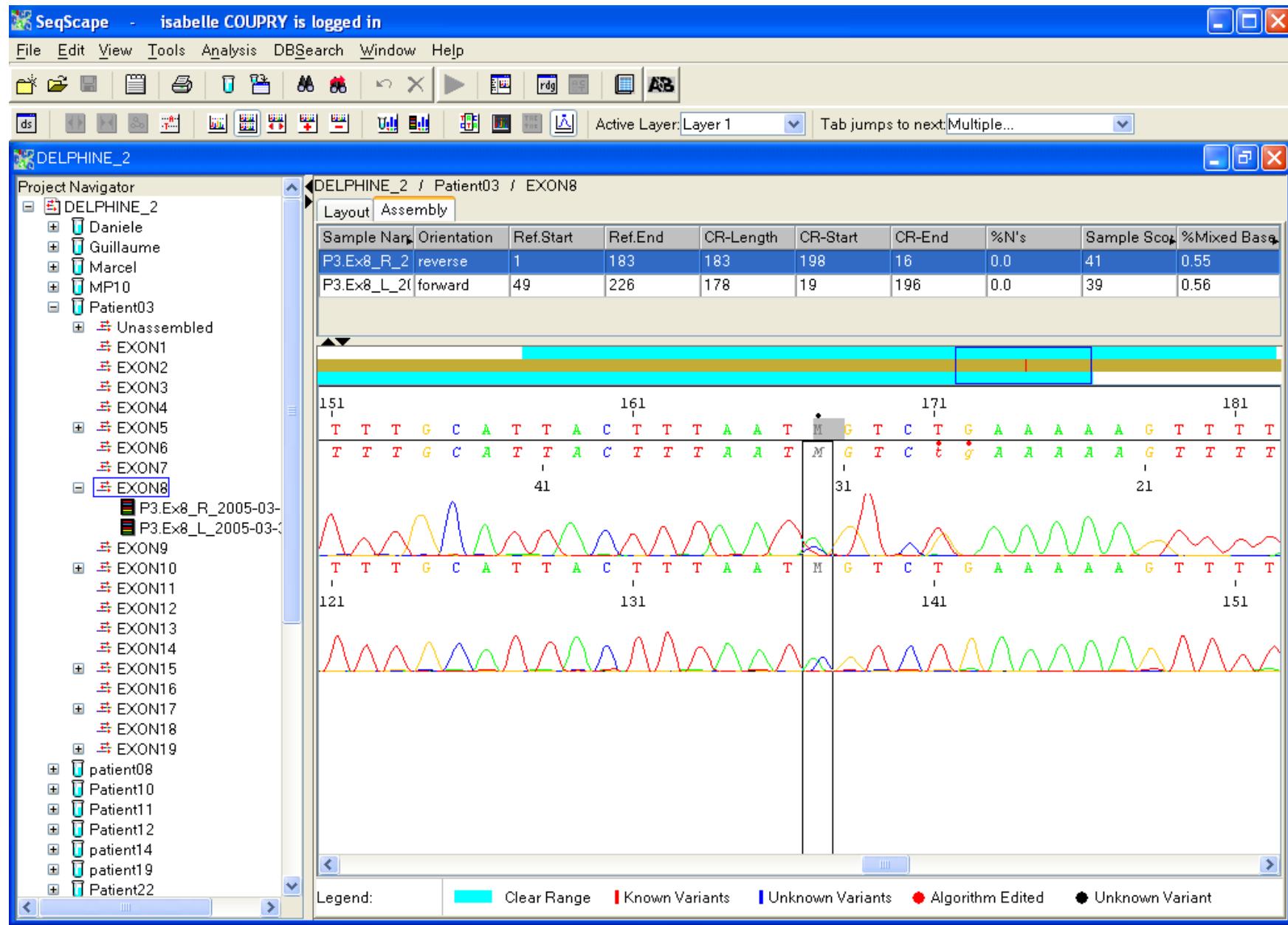
OK

Cancel









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



### New NT Variant

Type:

ROI:

Position (bp):  To

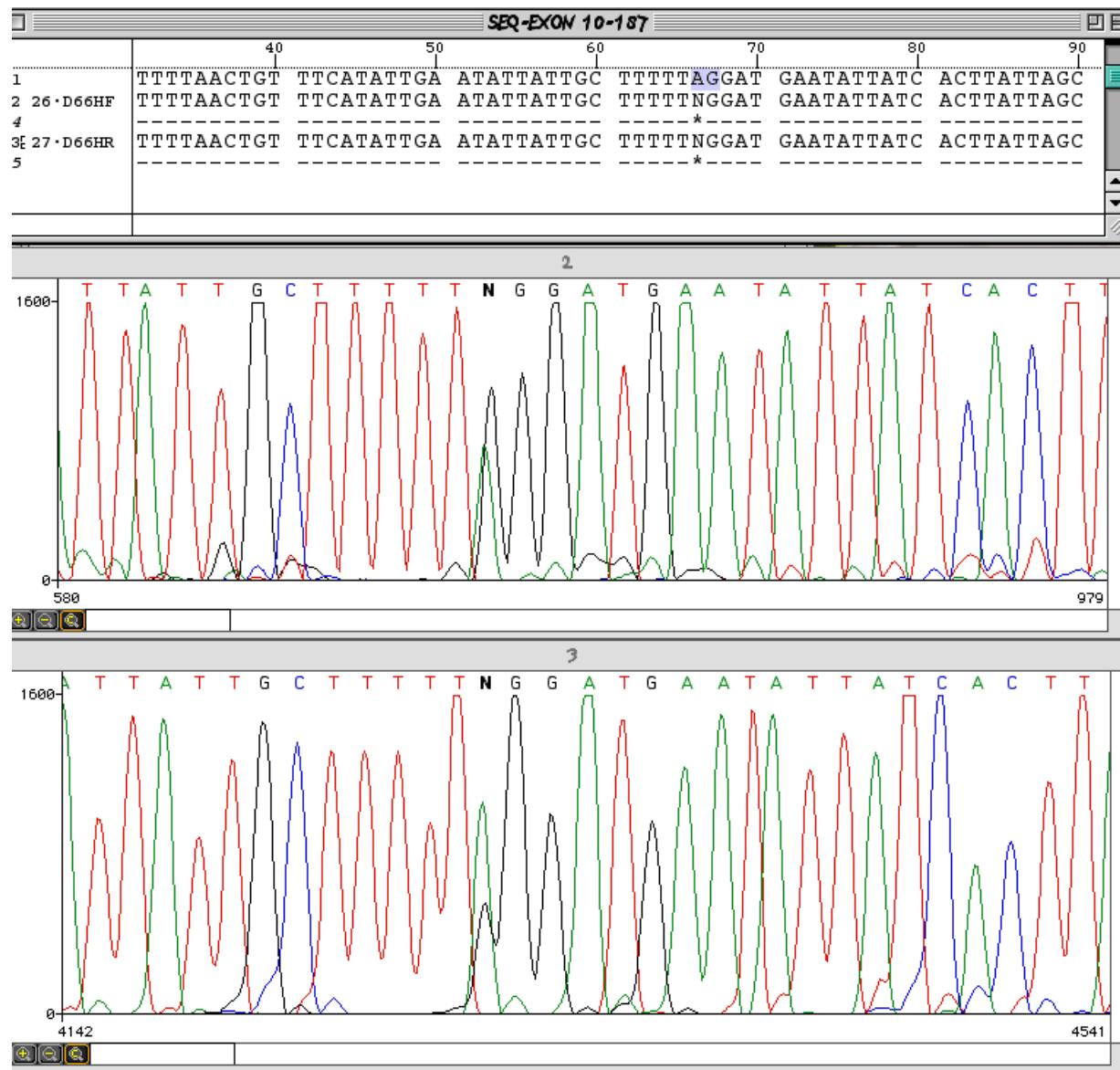
Reference base(s):

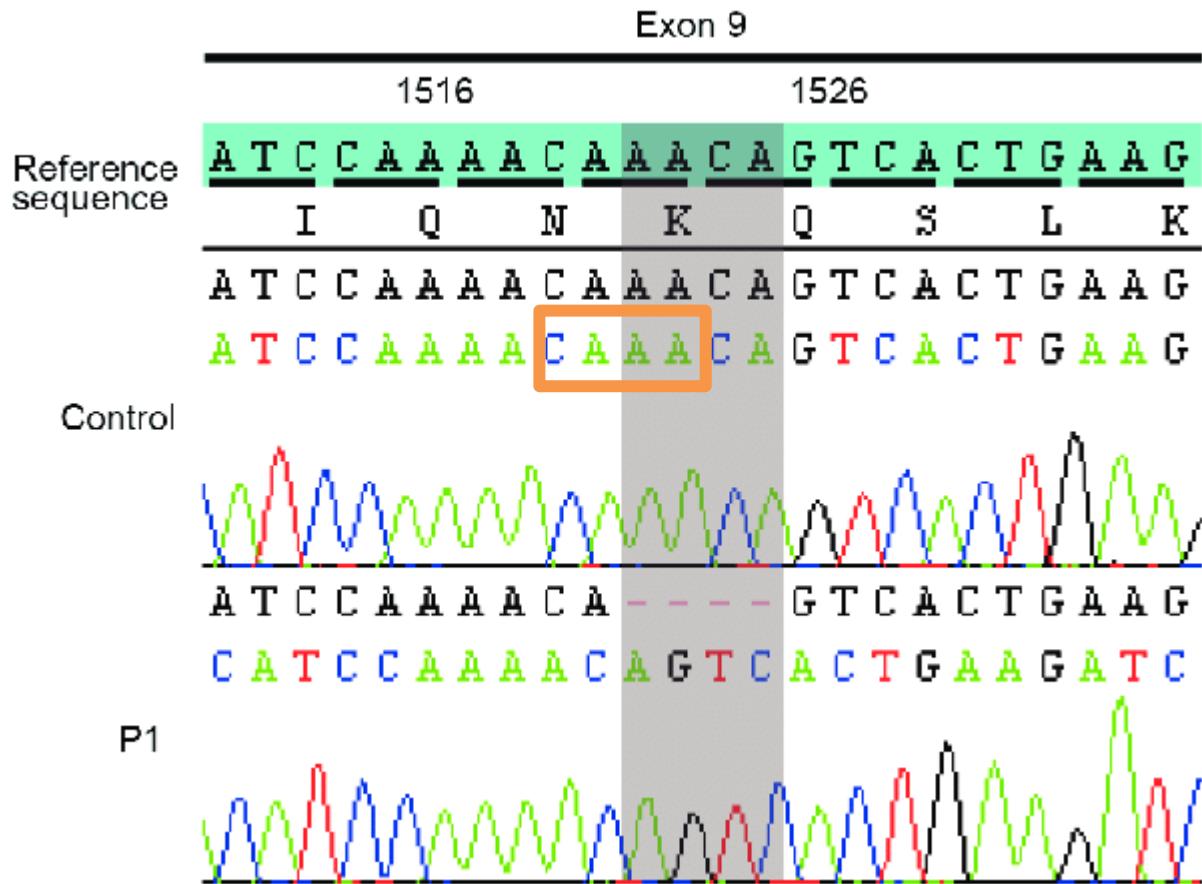
Variant base(s):

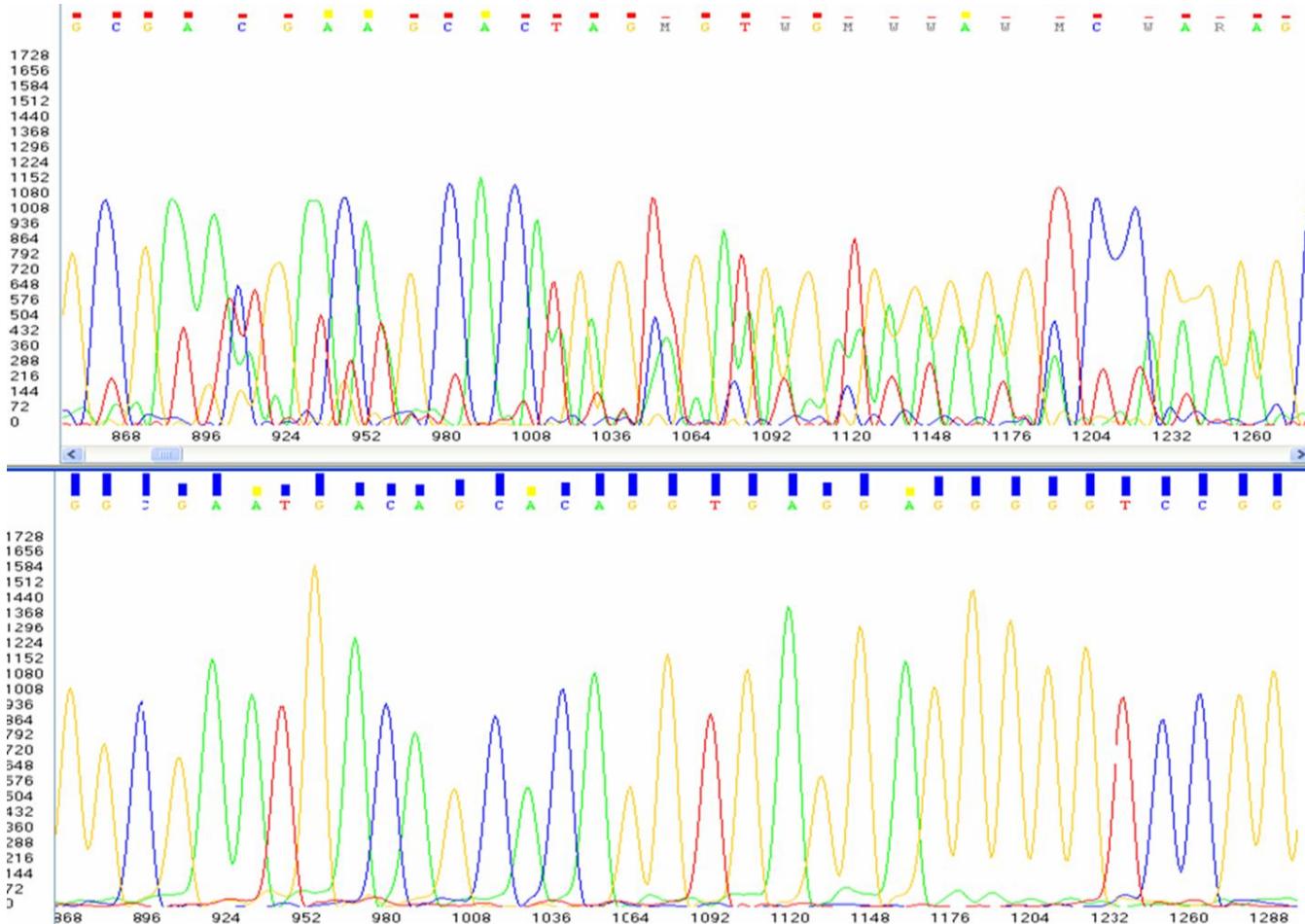
Style:

Description:

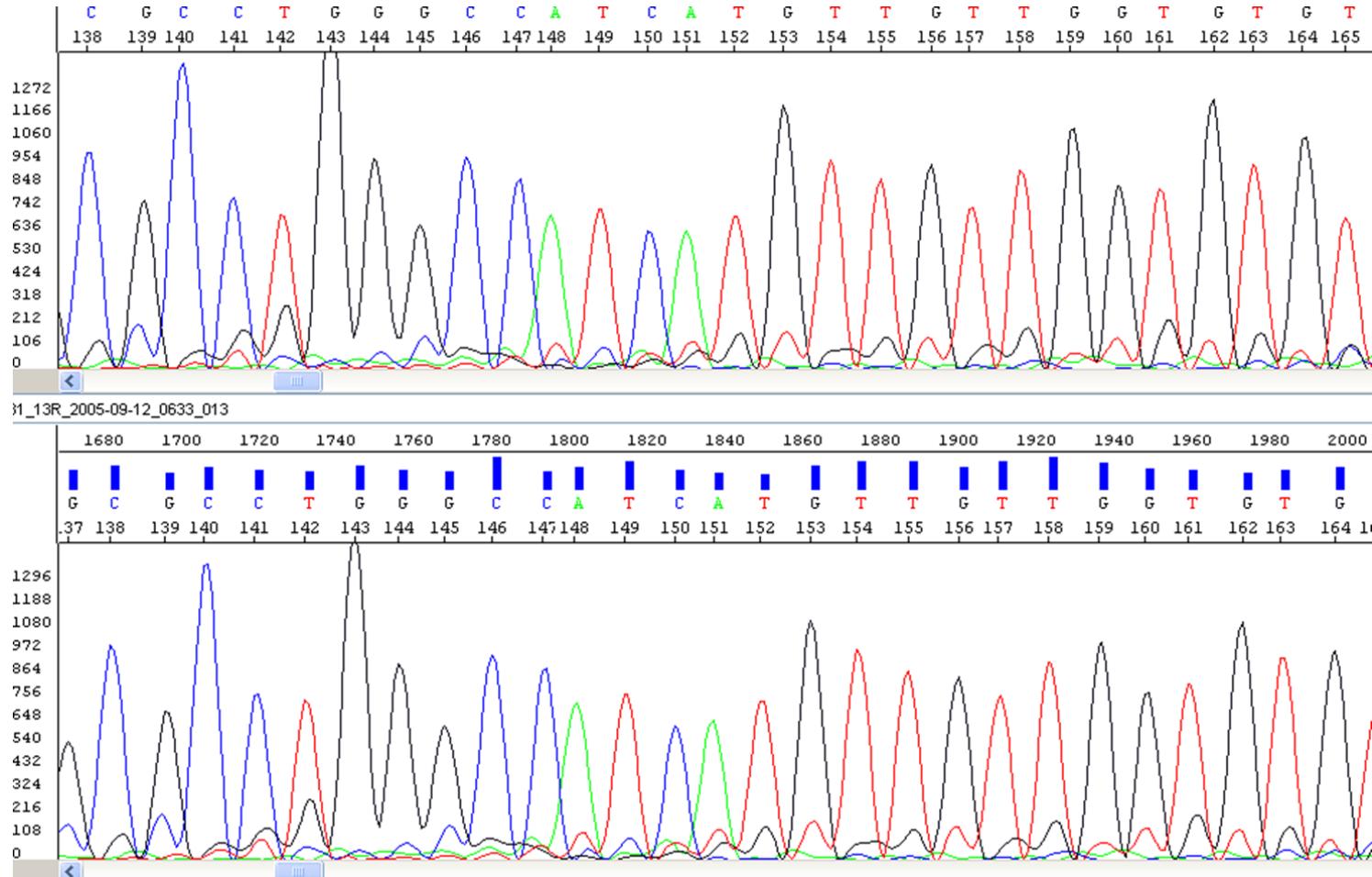
Used by all ROIs



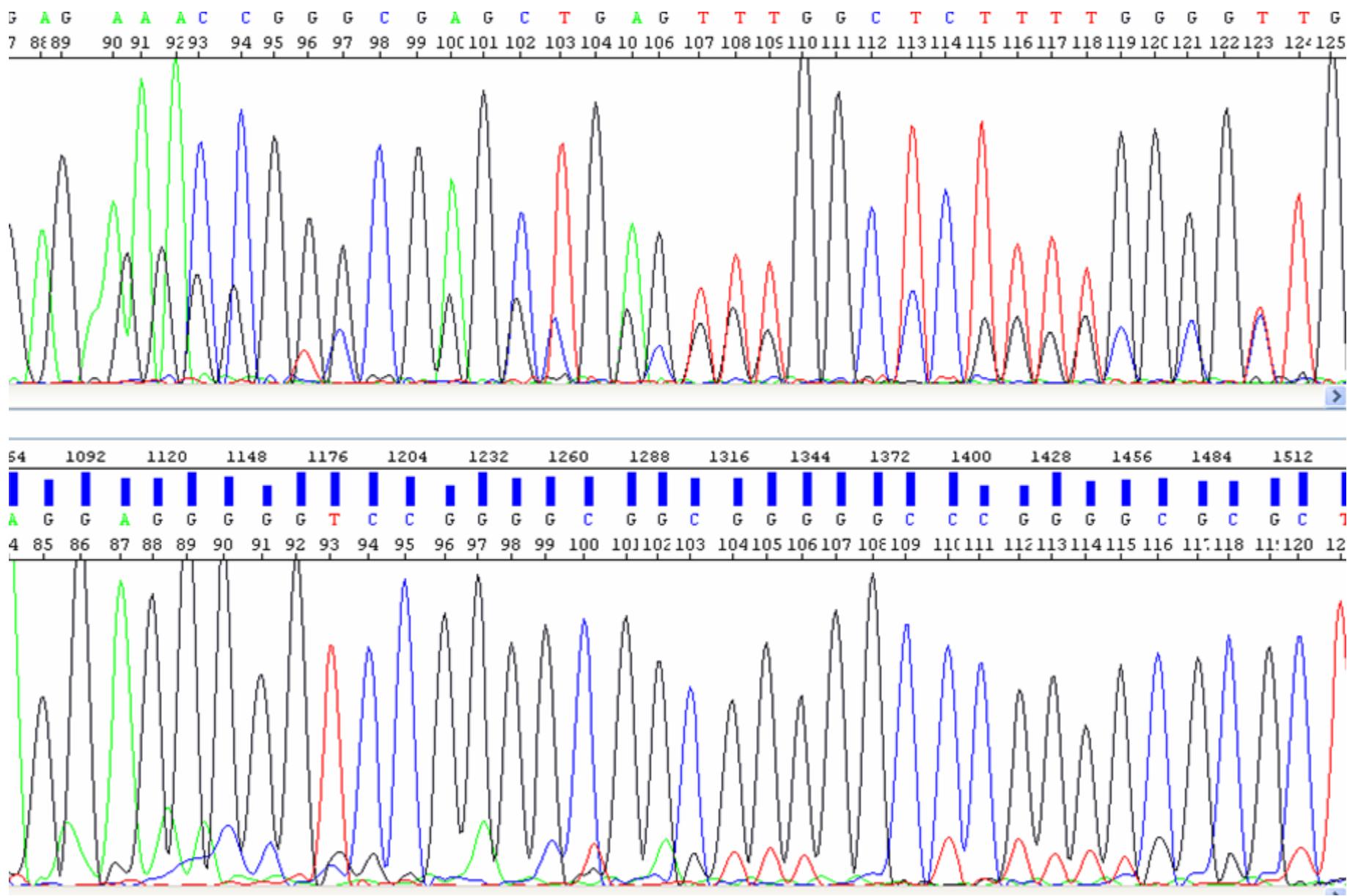




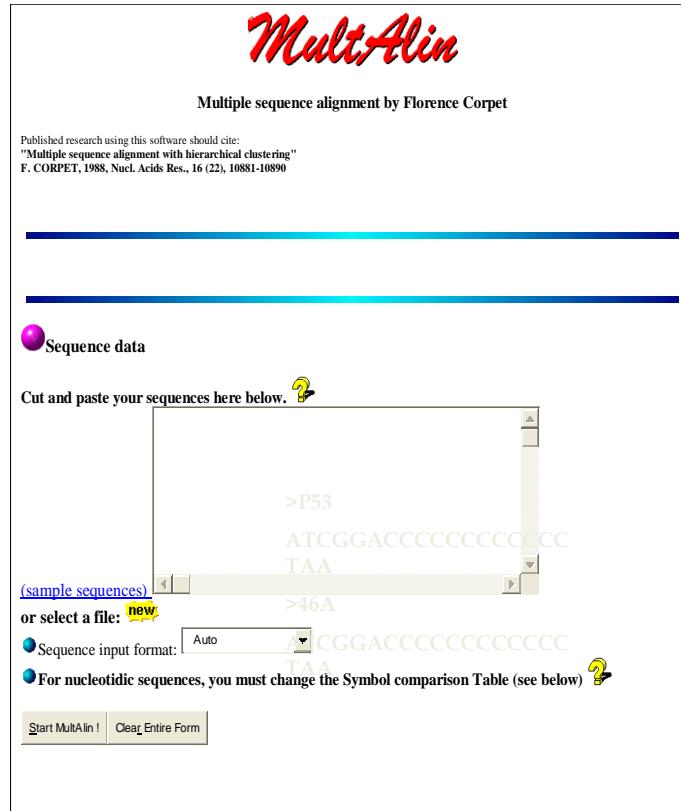
Diminution du temps d'injection



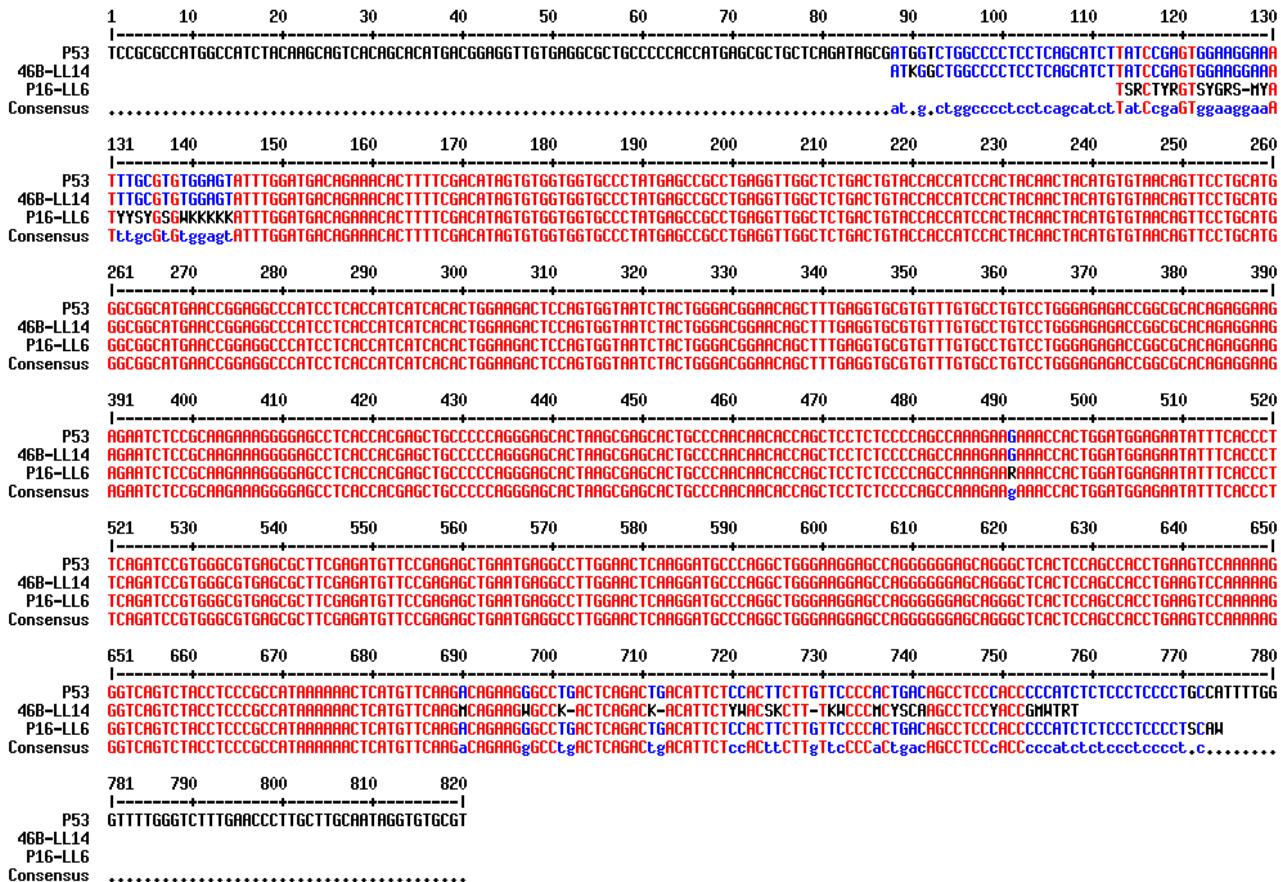
amorce partiellement dégradée

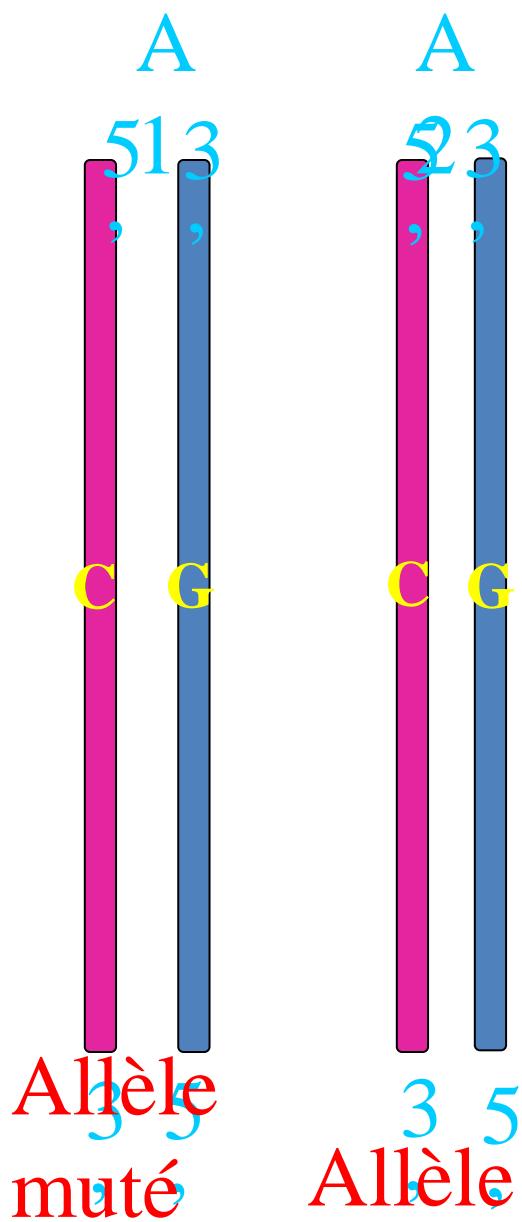


# Fenêtre du logiciel "Mulalin"

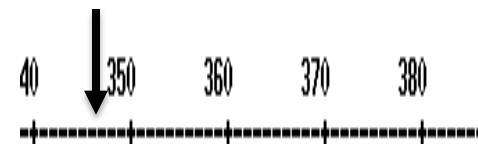
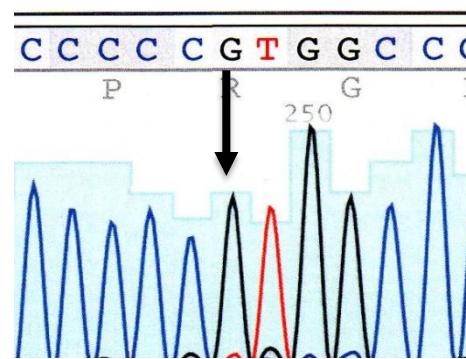


# Exemple de séquence analysée par Multalin



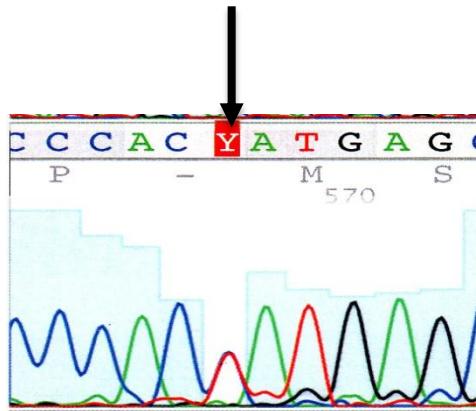
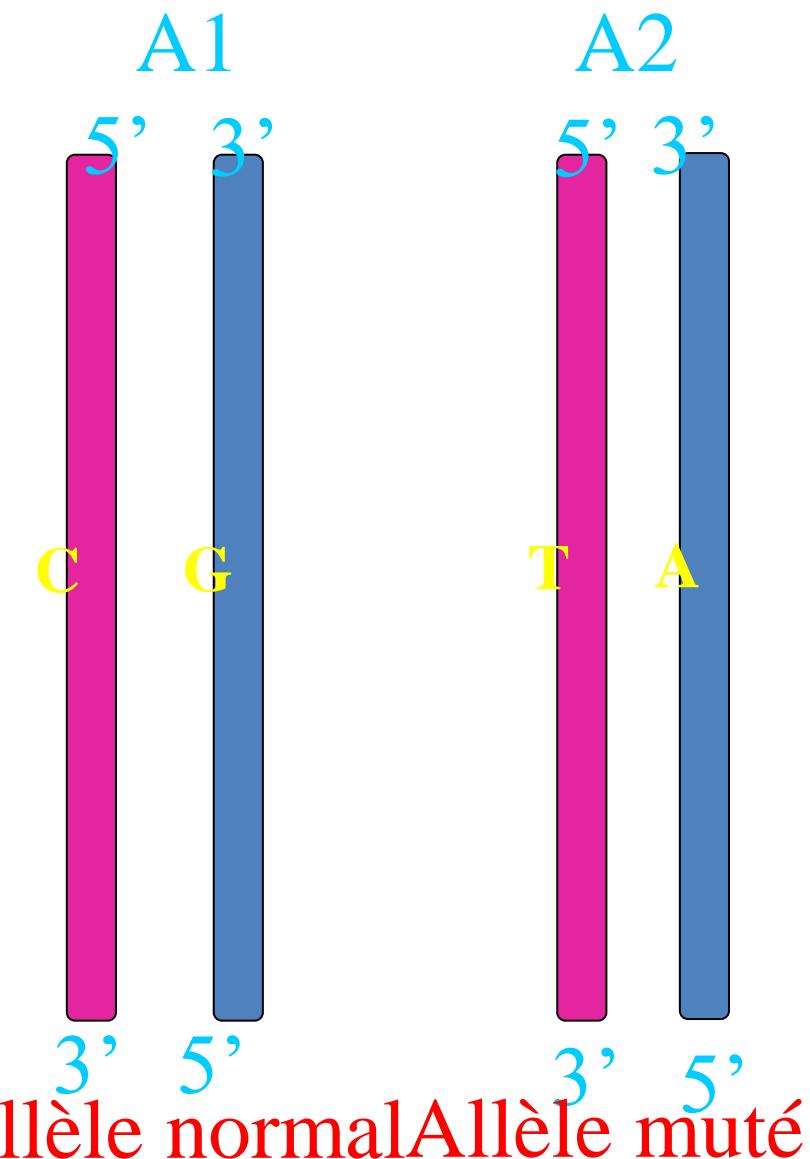


EX : Substitution G  
vers C  
À l'état  
homozygote



GCTCCCCCGTGGCCCTGACCCAGCTCTACACGGGGCCCT  
GCTCCCCCGTGGCCCTGACCCAGCTCTACACGGGGCCCT  
GCTCCCCCGTGGCCCTGACCCAGCTCTACACGGGGCCCT  
GCTCCCCCGTGGCCCTGACCCAGCTCTACACGGGGCCCT

## EX : Substitution C vers T À l'état hétérozygote



651     660     670     680     690

P53    TGAGGGGCTGCCCTACCAATGAGGCCTGCTCAGATAGGCAT

d6A-LL2 TGAGGGGCTGCCCTACCYATGAGGCCTGCTCAGATAGGCAT

P17-LL10 TGAGGGGCTGCCCTACRYATGAGGCCTGCTCAGATAGGCAT

Consensus TGAGGGGCTGCCCTACyATGAGGCCTGCTCAGATAGGCAT

