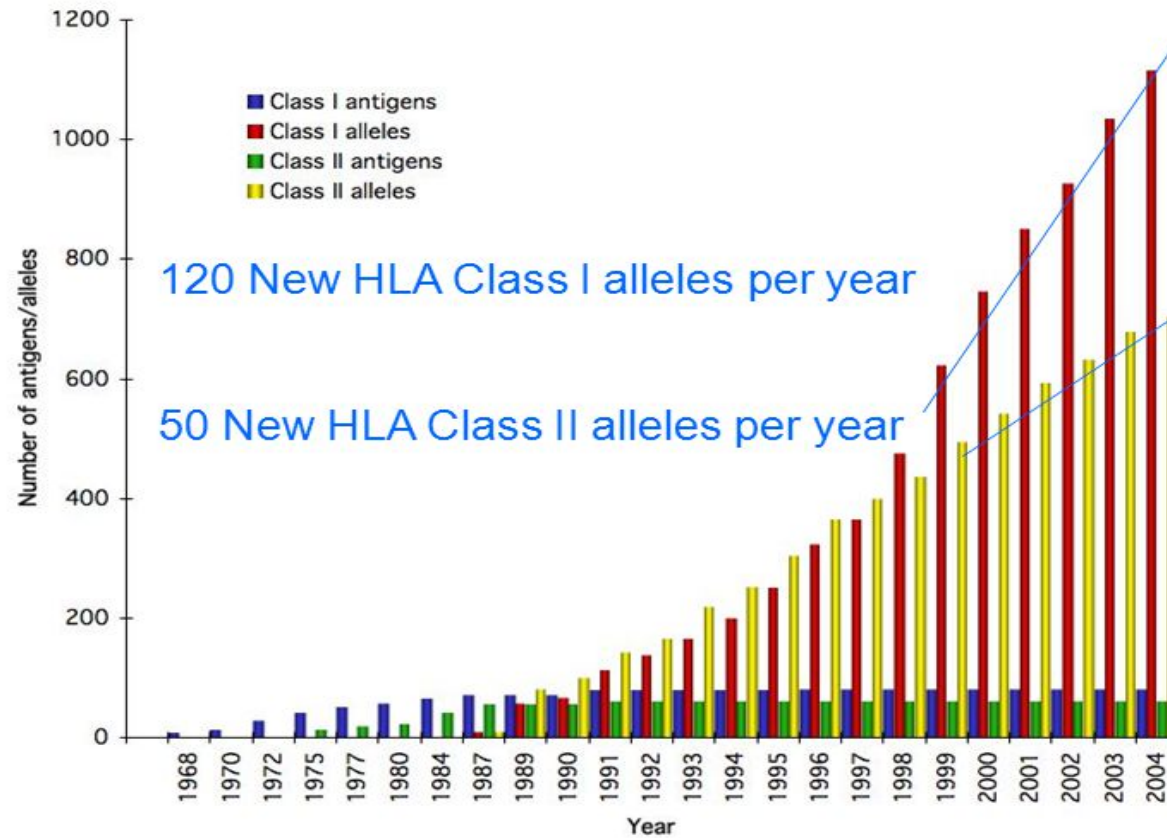


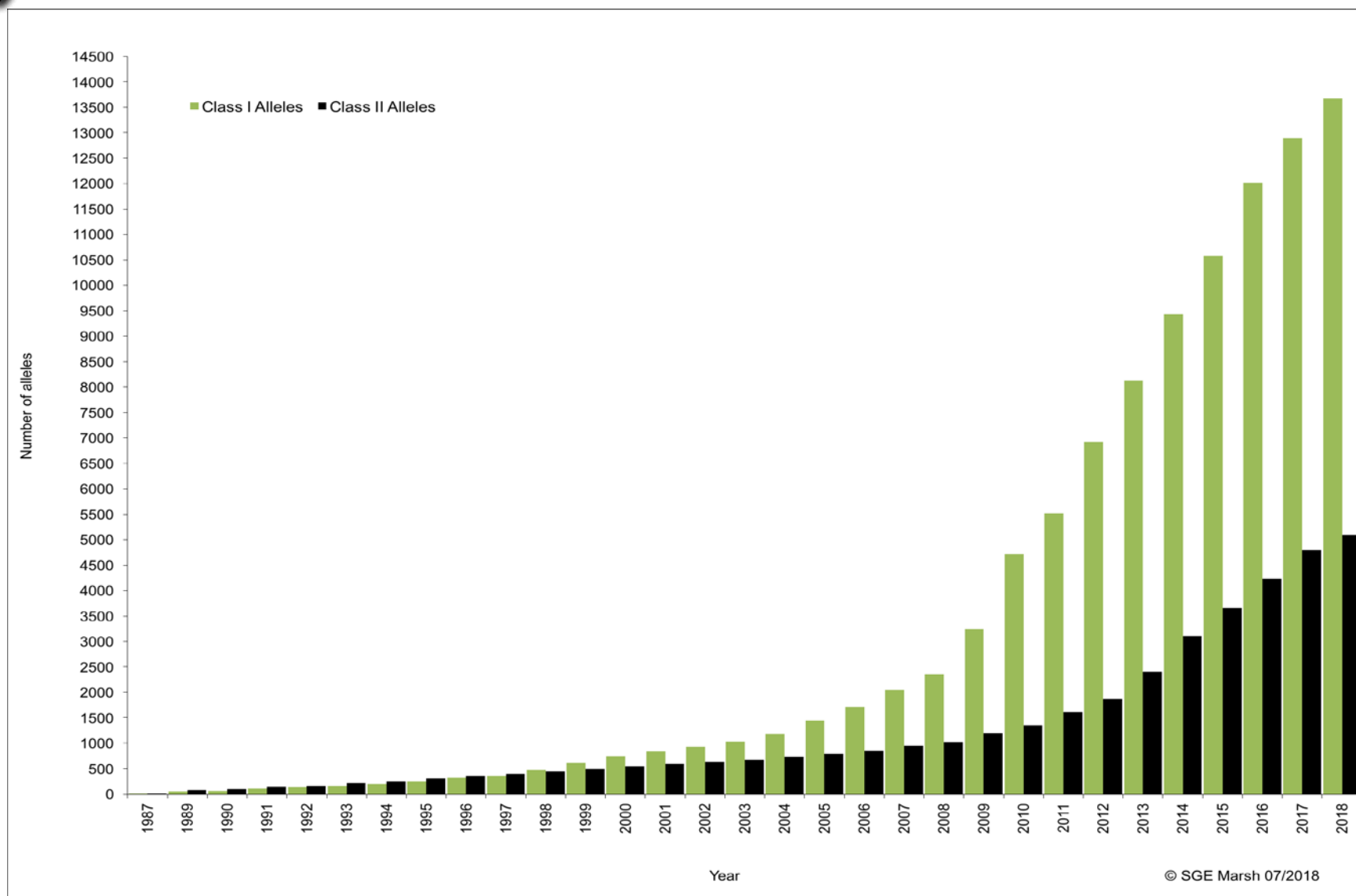
NUOVE VARIANTI HLA

Elena Longhi, 17.09.2018

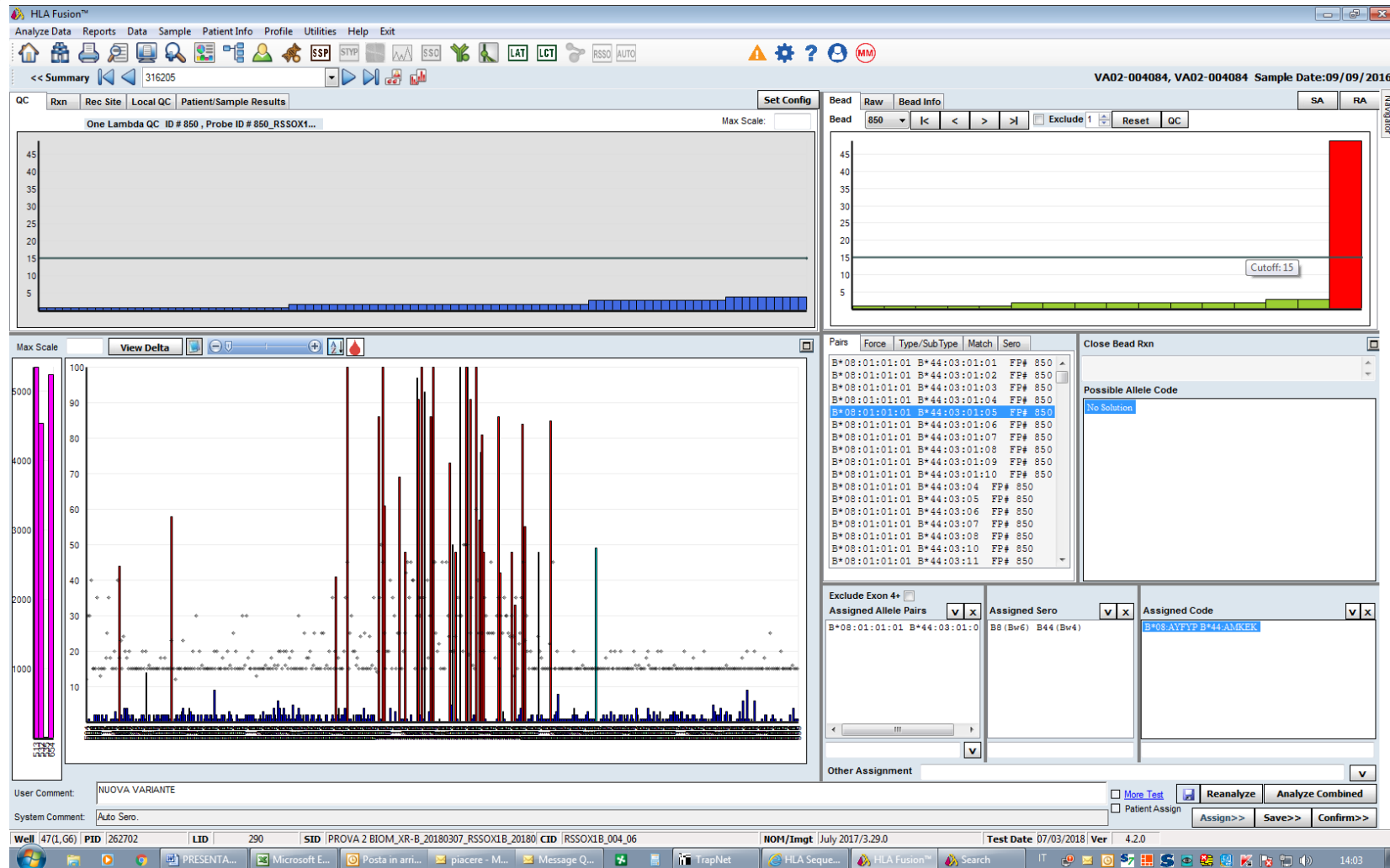
WHO Nomenclature Committee for Factors of the HLA System



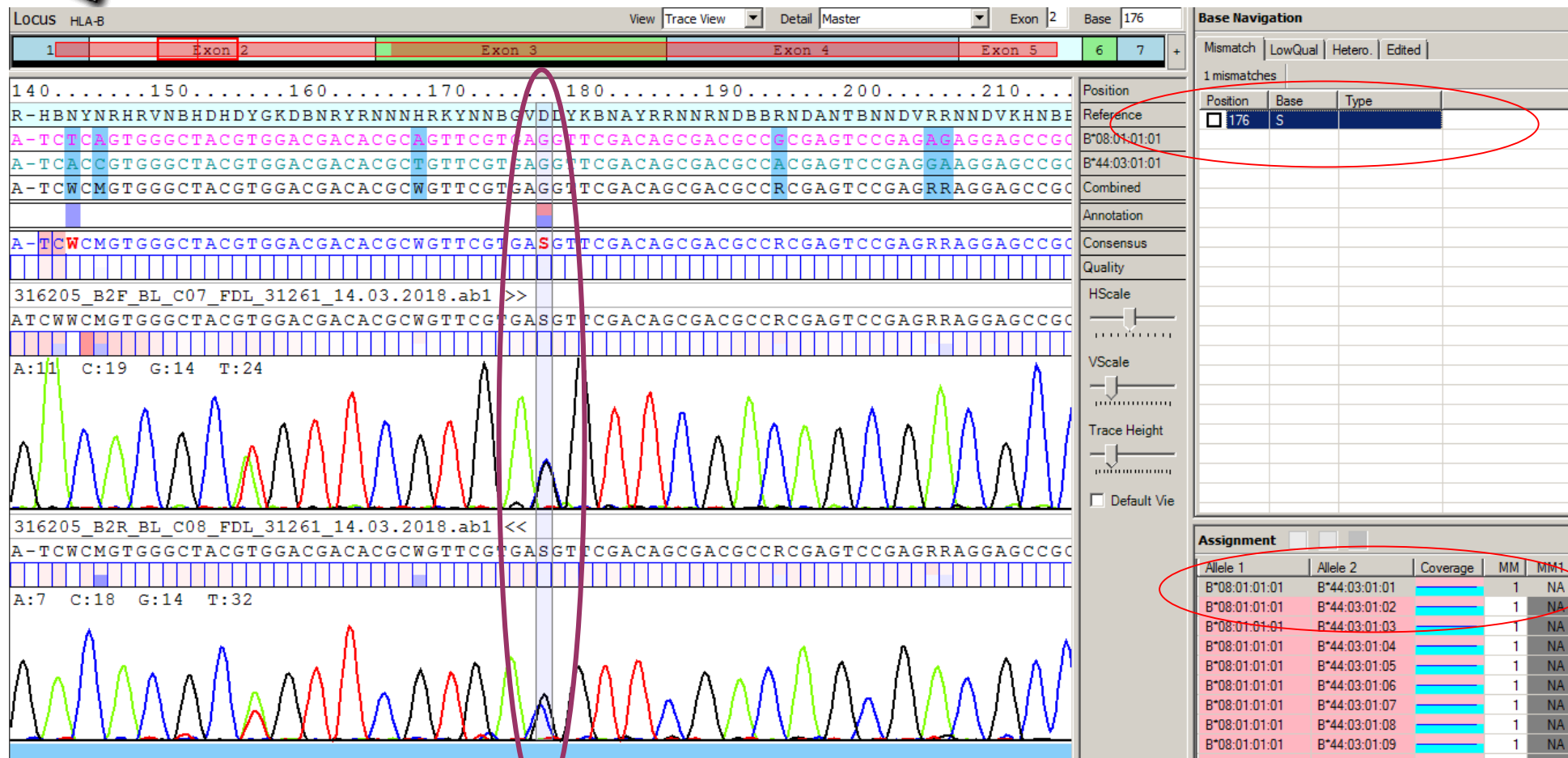
© SGE Marsh 7/2004

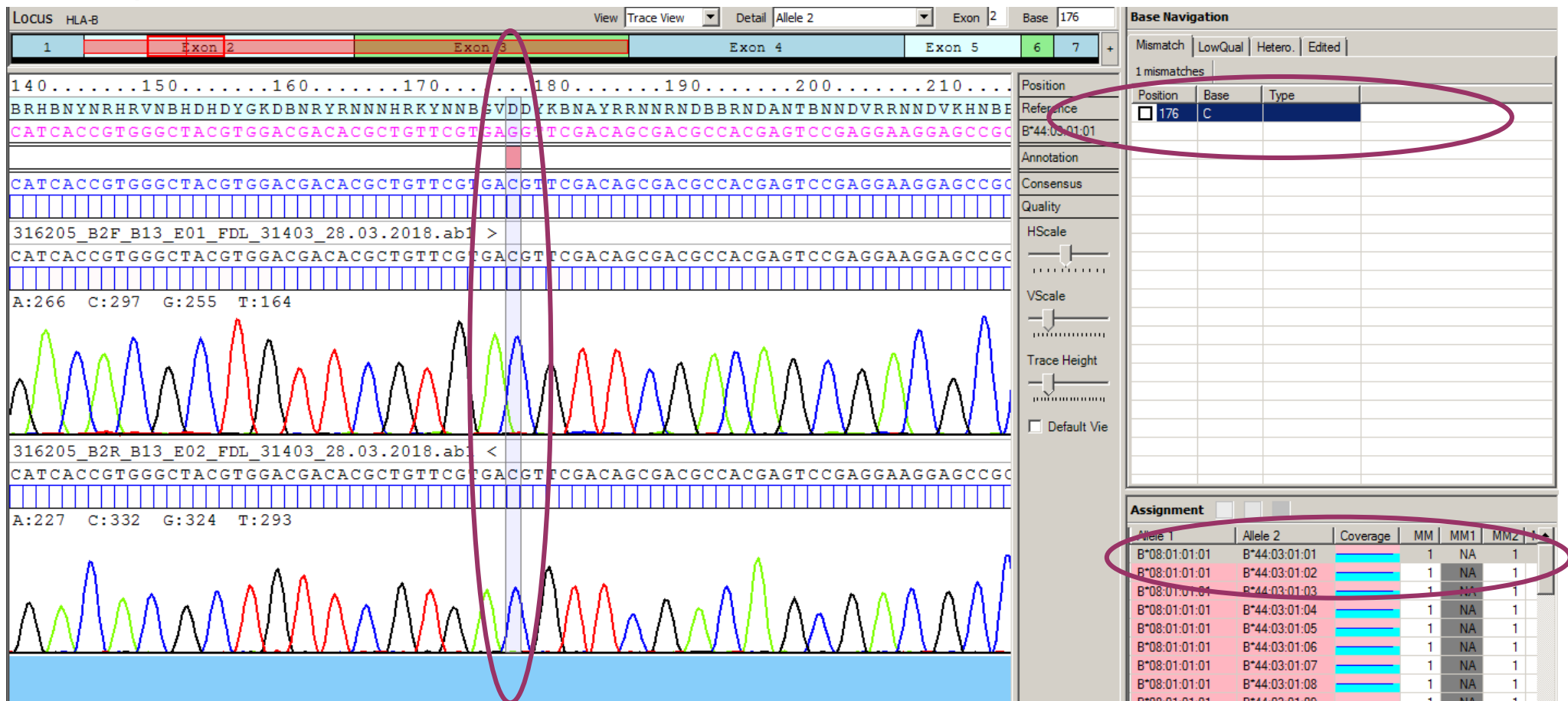


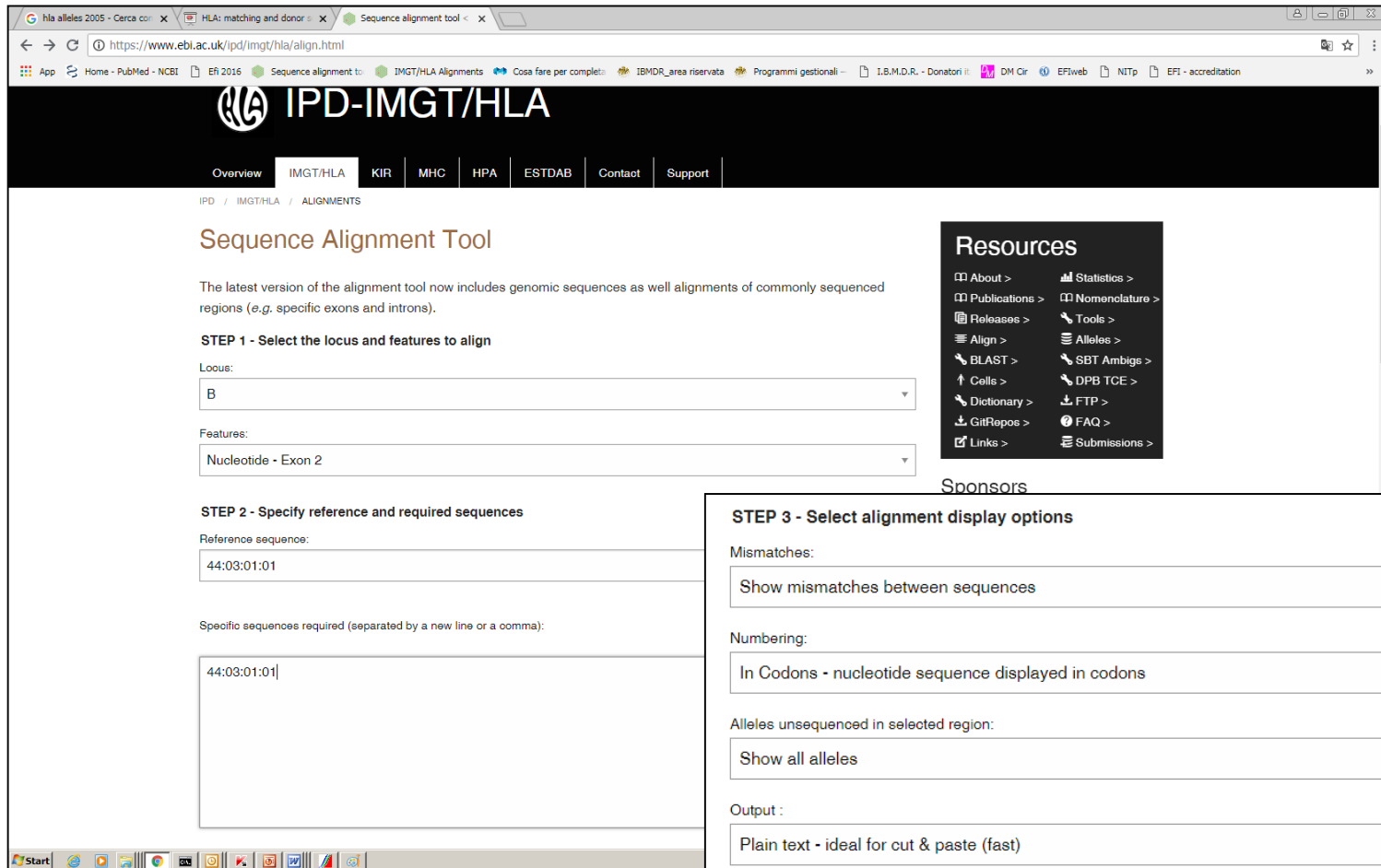
B*44new



TIPIZZAZIONE CONCLUDIBILE SOLO CON SONDA 850 FP
REC SITE SONDA 850: [33--T---38 + 41T-PRK-46]







hla alleles 2005 - Cerca con... x HLA: matching and donor... x Sequence alignment tool < x

https://www.ebi.ac.uk/ipd/imgt/hla/align.html

App Home - PubMed - NCBI EBI 2016 Sequence alignment tool... x IMGT/HLA Alignments Cosa fare per complet... x IBMDR_area riservata Programmi gestionali... x I.B.M.D.R. - Donatori... x DM Cir EBIweb NITp EPI - accreditation

IPD-IMGT/HLA

Overview **IMGT/HLA** KIR MHC HPA ESTDAB Contact Support

IPD / IMGT/HLA / ALIGNMENTS

Sequence Alignment Tool

The latest version of the alignment tool now includes genomic sequences as well alignments of commonly sequenced regions (e.g. specific exons and introns).

STEP 1 - Select the locus and features to align

Locus:

B

Features:

Nucleotide - Exon 2

STEP 2 - Specify reference and required sequences

Reference sequence:

44:03:01:01

Specific sequences required (separated by a new line or a comma):

44:03:01:01

Resources

- About >
- Publications >
- Releases >
- Align >
- BLAST >
- Celle >
- Dictionary >
- GitRepos >
- Links >
- Statistics >
- Nomenclature >
- Tools >
- Alleles >
- SBT Ambigs >
- DPB TCE >
- FTP >
- FAQ >
- Submissions >

Sponsors

STEP 3 - Select alignment display options

Mismatches:

Show mismatches between sequences

Numbering:

In Codons - nucleotide sequence displayed in codons

Alleles unsequenced in selected region:

Show all alleles

Output :

Plain text - ideal for cut & paste (fast)

STEP 4 - Proceed with the alignment

[Align Sequences Now](#)

```

AA Codon      5          10          15          20          25
B*44:03:01:01 GC TCC CAC TCC ATG AGG TAT TTC TAC ACC GCC ATG TCC CGG CCC GGC CGC GGG GAG CCC CGC TTC ATC ACC GTG

AA Codon      30          35          40          45          50
B*44:03:01:01 GGC TAC GTG GAC GAC ACG CTG TTC GTG AGG TTC GAC AGC GAC GCC ACG AGT CCG AGG AAG GAG CCG CGG GCG CCA

AA Codon      55          60          65          70          75
B*44:03:01:01 TGG ATA GAG CAG GAG GGG CCG GAG TAT TGG GAC CGG GAG ACA CAG ATC TCC AAG ACC AAC ACA CAG ACT TAC CGA

AA Codon      80          85          90
B*44:03:01:01 GAG AAC CTG CGC ACC GCG CTC CGC TAC TAC AAC CAG AGC GAG GCC G
  
```

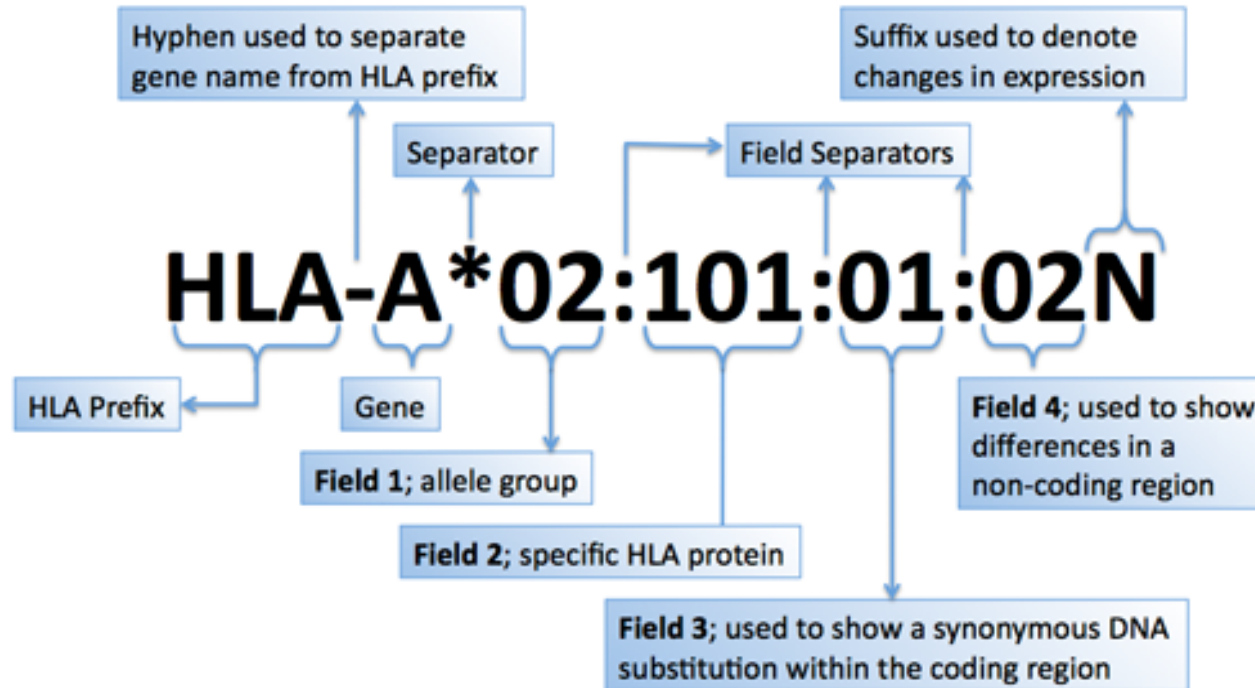
Esone 2

		second base in codon									
		T		C		A		G			
first base in codon	T	TTT	Phe	TCT	Ser	TAT	Tyr	TGT	Cys	T	third base in codon
		TTC	Phe	TCC	Ser	TAC	Tyr	TGC	Cys	C	
		TTA	Leu	TCA	Ser	TAA	stop	TGA	stop	A	
		TTG	Leu	TCG	Ser	TAG	stop	TGG	Trp	G	
	C	CTT	Leu	CCT	Pro	CAT	His	CGT	Arg	T	
		CTC	Leu	CCC	Pro	CAC	His	CGC	Arg	C	
		CTA	Leu	CCA	Pro	CAA	Gln	CGA	Arg	A	
		CTG	Leu	CCG	Pro	CAG	Gln	CGG	Arg	G	
	A	ATT	Ile	ACT	Thr	AAT	Asn	AGT	Ser	T	
		ATC	Ile	ACC	Thr	AAC	Asn	AGC	Ser	C	
		ATA	Ile	ACA	Thr	AAA	Lys	AGA	Arg	A	
		ATG	Met	ACG	Thr	AAG	Lys	AGG	Arg	G	
	G	GTT	Val	GCT	Ala	GAT	Asp	GGT	Gly	T	
		GTC	Val	GCC	Ala	GAC	Asp	GGC	Gly	C	
		GTA	Val	GCA	Ala	GAA	Glu	GGA	Gly	A	
		GTG	Val	GCG	Ala	GAG	Glu	GGG	Gly	G	

Cod 35 AGG -> ACG

Cod 35 Arg -> Thr

A*01:01,*66:02; B*08:01,*44:284; C*04:01,*07:07; DRB1*03:01,*03:02



Nomenclature	Indicates
HLA	the HLA region and prefix for an HLA gene
<i>HLA-DRB1</i>	a particular HLA locus i.e. DRB1
<i>HLA-DRB1*13</i>	a group of alleles that encode the DR13 antigen or sequence homology to other <i>DRB1*13</i> alleles
<i>HLA-DRB1*13:01</i>	a specific HLA allele
<i>HLA-DRB1*13:01:02</i>	an allele that differs by a synonymous mutation from <i>DRB1*13:01:01</i>
<i>HLA-DRB1*13:01:01:02</i>	an allele which contains a mutation outside the coding region from <i>DRB1*13:01:01:01</i>
<i>HLA-A*24:09N</i>	a 'Null' allele - an allele that is not expressed
<i>HLA-A*30:14L</i>	an allele encoding a protein with significantly reduced or 'Low' cell surface expression
<i>HLA-A*24:02:01:02L</i>	an allele encoding a protein with significantly reduced or 'Low' cell surface expression, where the mutation is found outside the coding region
<i>HLA-B*44:02:01:02S</i>	an allele encoding a protein which is expressed as a 'Secreted' molecule only
<i>HLA-A*32:11Q</i>	an allele which has a mutation that has previously been shown to have a significant effect on cell surface expression, but where this has not been confirmed and its expression remains 'Questionable'



Allele*Frequencies

in Worldwide Populations

Home FAQs Links Publications Automated Access About us Contact EUROSTAM

Menu	The Allele Frequency Net Database
Populations	
HLA	HLA Allele Freq (Classical)
HLA Epitopes (beta)	HLA Allele Freq (Non Classical)
Amino Acid Analysis	Search freqs at lower resolution (New)
KIR	HLA Haplotype Frequency Search
Cytokine	HLA Allele Survey Reports
MIC	HLA Population Standards, World Map
Rare Alleles	HLA Breakdowns
Submit New Data	HLA and Adverse Drug Reactions

- Sponsors
- BAG Health Care
 - Fujirebio Europe
 - Illumina
 - Olerup SSP AB
 - Omixon
 - One Lambda

Does any of this interest you?

- HLA Allele Freq (Classical)
- HLA Allele Freq (Non Classical)
- Search freqs at lower resolution (New)
- HLA Haplotype Frequency Search
- HLA Allele Survey Reports
- HLA Population Standards, World Map
- HLA Breakdowns
- HLA and Adverse Drug Reactions

Browse Genotype Data

common database and can perform database s information already available.

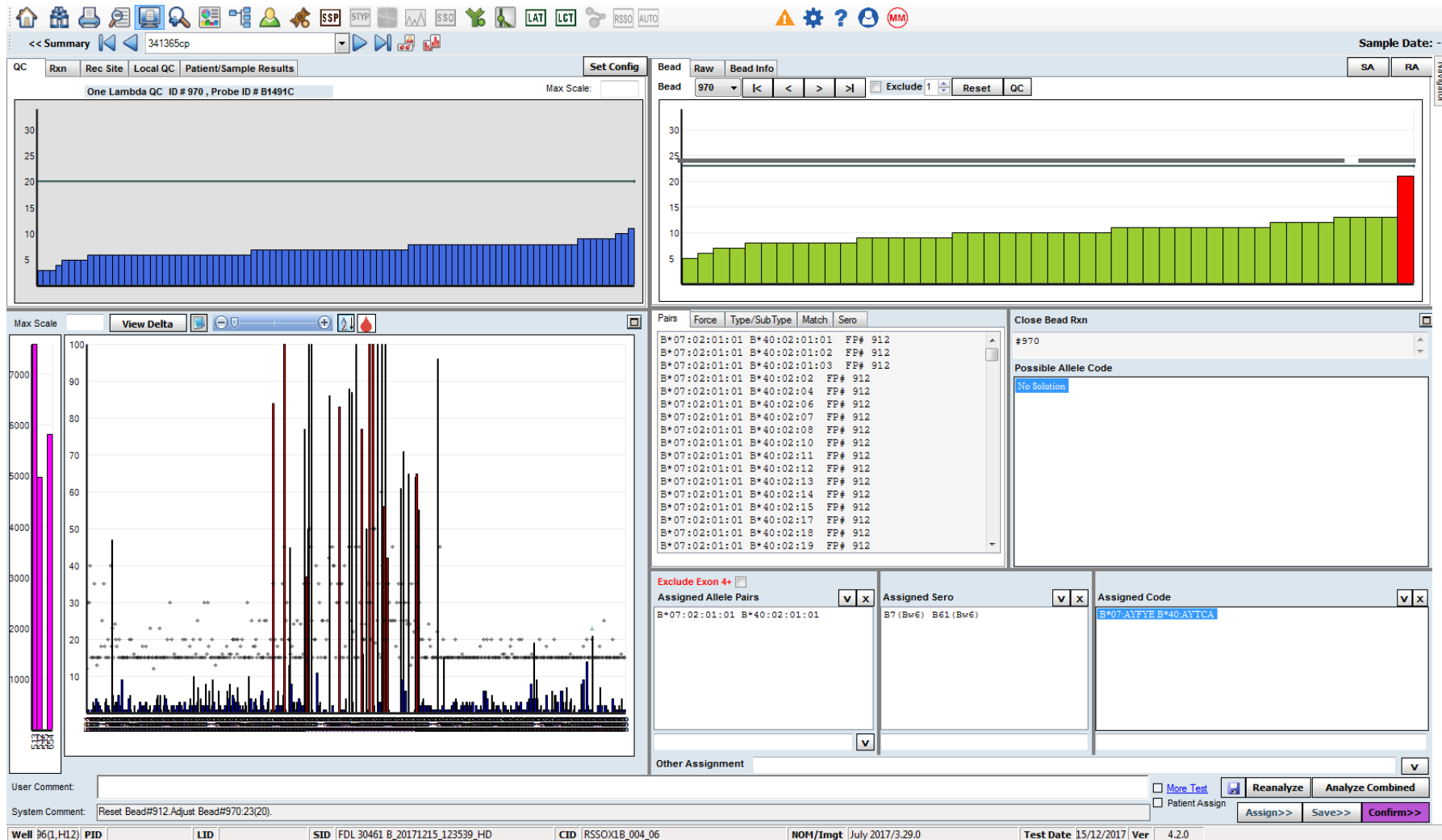
We have currently collected data in allele, haplotyp this website will depend on you to contribute your data.

Please cite this website using our last publication: Allele epitopes, KIR and disease and HLA adverse drug reacti LY, Santos EJ, Kempson F, Maia MH, Silva AL, Silva AL, Middleton D *Nucleic Acid Research* 2015, 28, D784-8. [I

A	B	C	DRB1	DPA1	DPB1	DQA1	DQB1
A*06:02	B*44	Select	Select	Select	Select	Select	Select
Population: All populations Country: All countries Source of dataset: All Sources							
Region: All regions Ethnic Origin: Type of study: Sort by:							
Haplotype							
Sample Size: All Sample Year: All years Loci Tested: Select number							
Displaying 1 to 12 (from 12) records Pages: 1 of 1							
RESET							

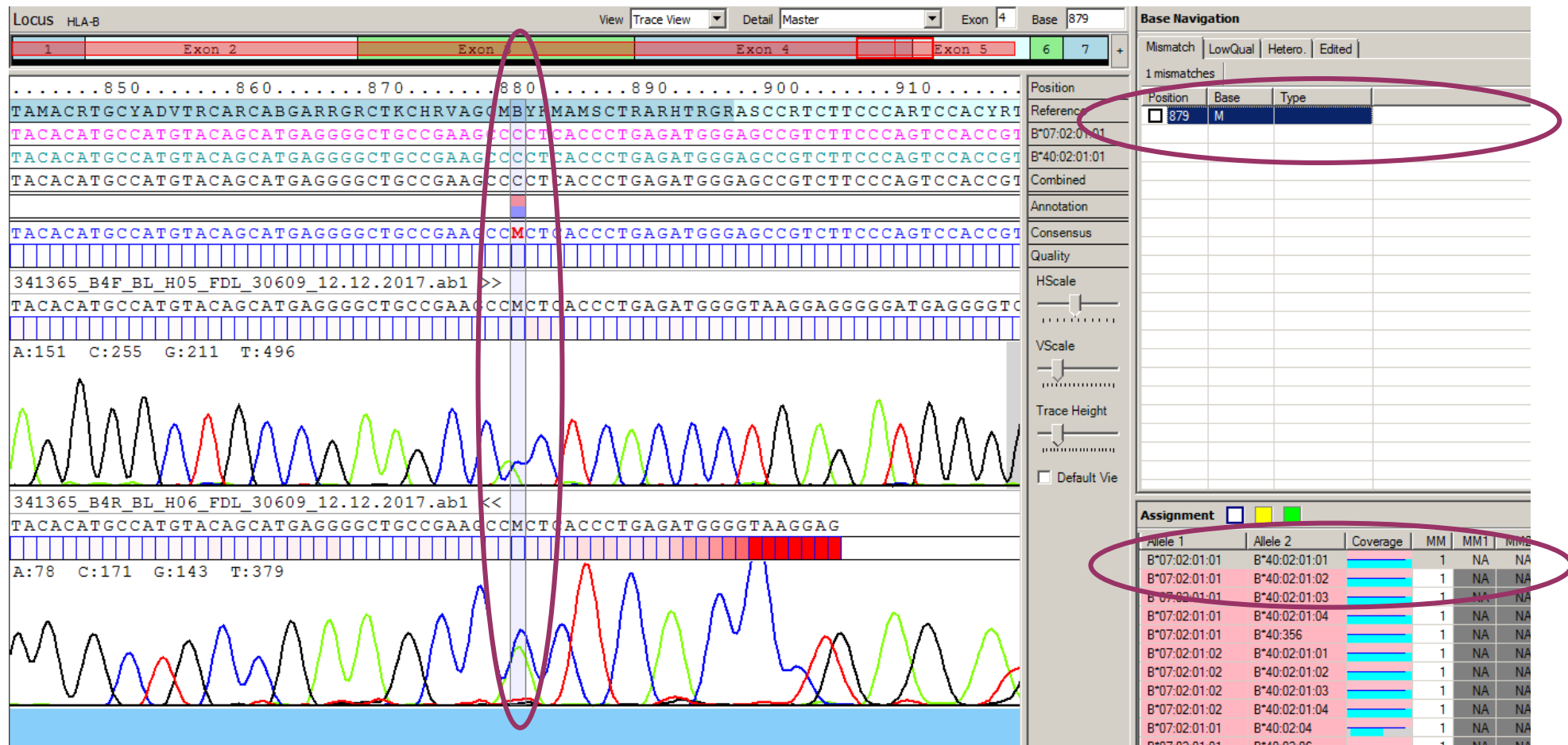
Line	Haplotype	Population	Frequency (%)	Sample Size	Distribution ¹
1	A*66:02-B*44:03	USA African American pop 4	0.0950	2,411	
2	A*66:02-B*44:03-C*04:01-DRB1*04:04-DQB1*03:02	USA African American pop 4	0.0110	2,411	
3	A*66:02-B*44:03-C*04:01-DRB1*07:01-DQB1*02:01	USA African American pop 4	0.0110	2,411	
4	A*66:02-B*44:03-C*04:01-DRB1*12:01-DQB1*05:01	USA African American pop 4	0.0110	2,411	
5	A*66:02-B*44:03-C*04:01-DRB1*13:01-DQB1*05:01	USA African American pop 4	0.0110	2,411	
6	A*66:02-B*44:03-C*06:02-DRB1*10:01-DQB1*05:01	Colombia Bogotá	0.03417636	1,463	
7	A*66:02-B*44:03-C*12:03-DRB1*08:06-DQB1*06:02	USA African American pop 4	0.0440	2,411	
8	A*66:02-B*44:03-C*18:01-DRB1*07:01-DQB1*02:01	USA African American pop 4	0.0440	2,411	
9	A*66:02-B*44:03-DRB1*04:05	Israel Morocco Jews	0.00136	36,718	
10	A*66:02-B*44:10	USA African American pop 4	0.0210	2,411	
11	A*66:02-B*44:18	USA African American pop 4	0.0210	2,411	
12	A*66:02-B*44:18-C*06:02-DRB1*03:01-DQB1*02:01	USA African American pop 4	0.0440	2,411	

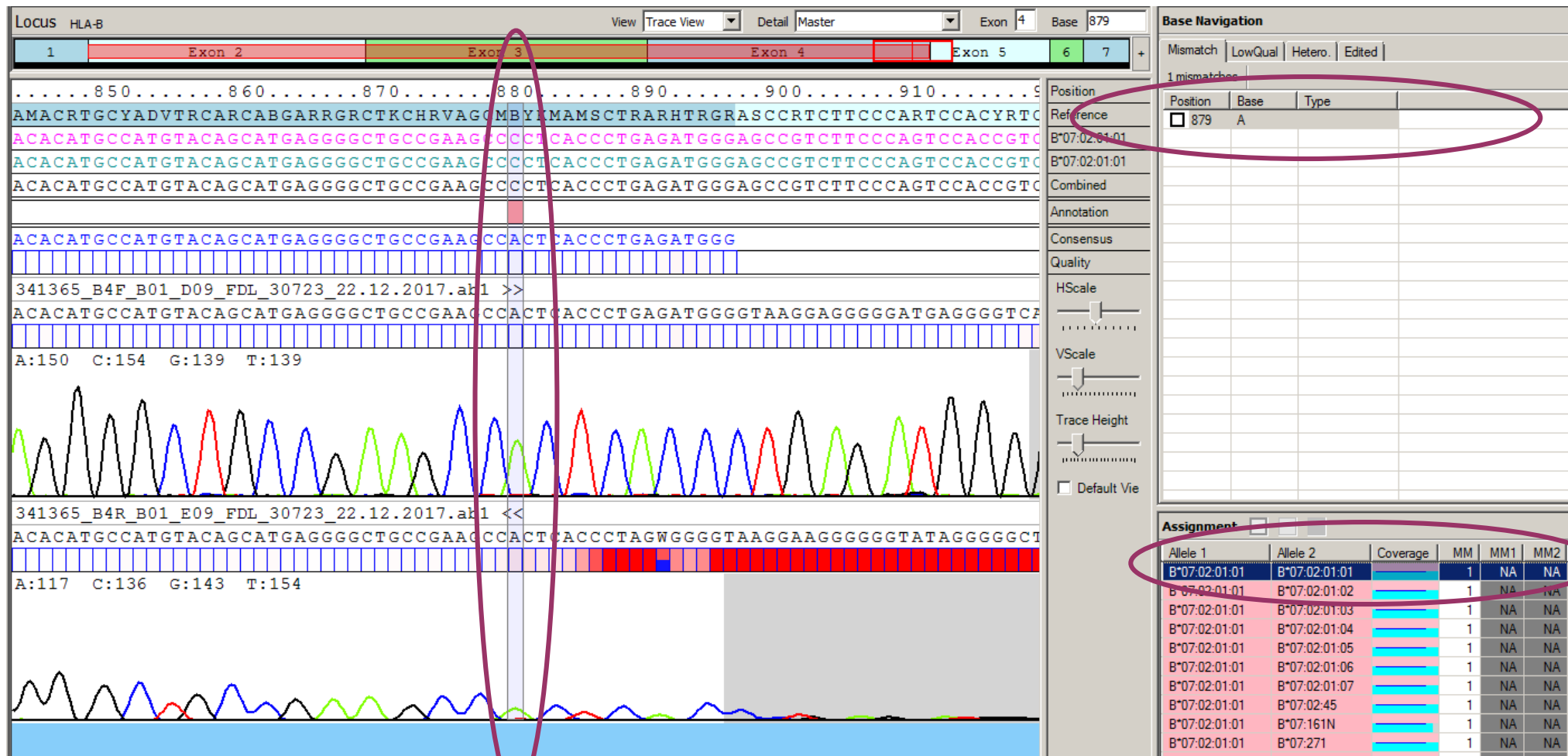
B*07new



TIPIZZAZIONE CONCLUDIBILE SOLO CON SONDA 912 negativa

Rec site: [205--C--209 + 223-----227] / [258-----264 + 270---S--275] / 256-----I----265





AA Codon	185	190	195	200	205
B*07:02:01:01	AC CCC CCA AAG ACA CAC GTG ACC CAC CAC CCC ATC TCT GAC CAT GAG GCC ACC CTG AGG TGC TGG GCC CTG GGT				
AA Codon	210	215	220	225	230
B*07:02:01:01	TTC TAC CCT GCG GAG ATC ACA CTG ACC TGG CAG CGG GAT GGC GAG GAC CAA ACT CAG GAC ACT GAG CTT GTG GAG				
AA Codon	235	240	245	250	255
B*07:02:01:01	ACC AGA CCA GCA GGA GAT AGA ACC TTC CAG AAG TGG GCA GCT GTG GTG GTG CCT TCT GGA GAA GAG CAG AGA TAC				
AA Codon	260	265	270		
B*07:02:01:01	ACA TGC CAT GTA CAG CAT GAG GGG CTG CCG AAG CCC CTC ACC CTG AGA TGG G				

Esone 4

second base in codon

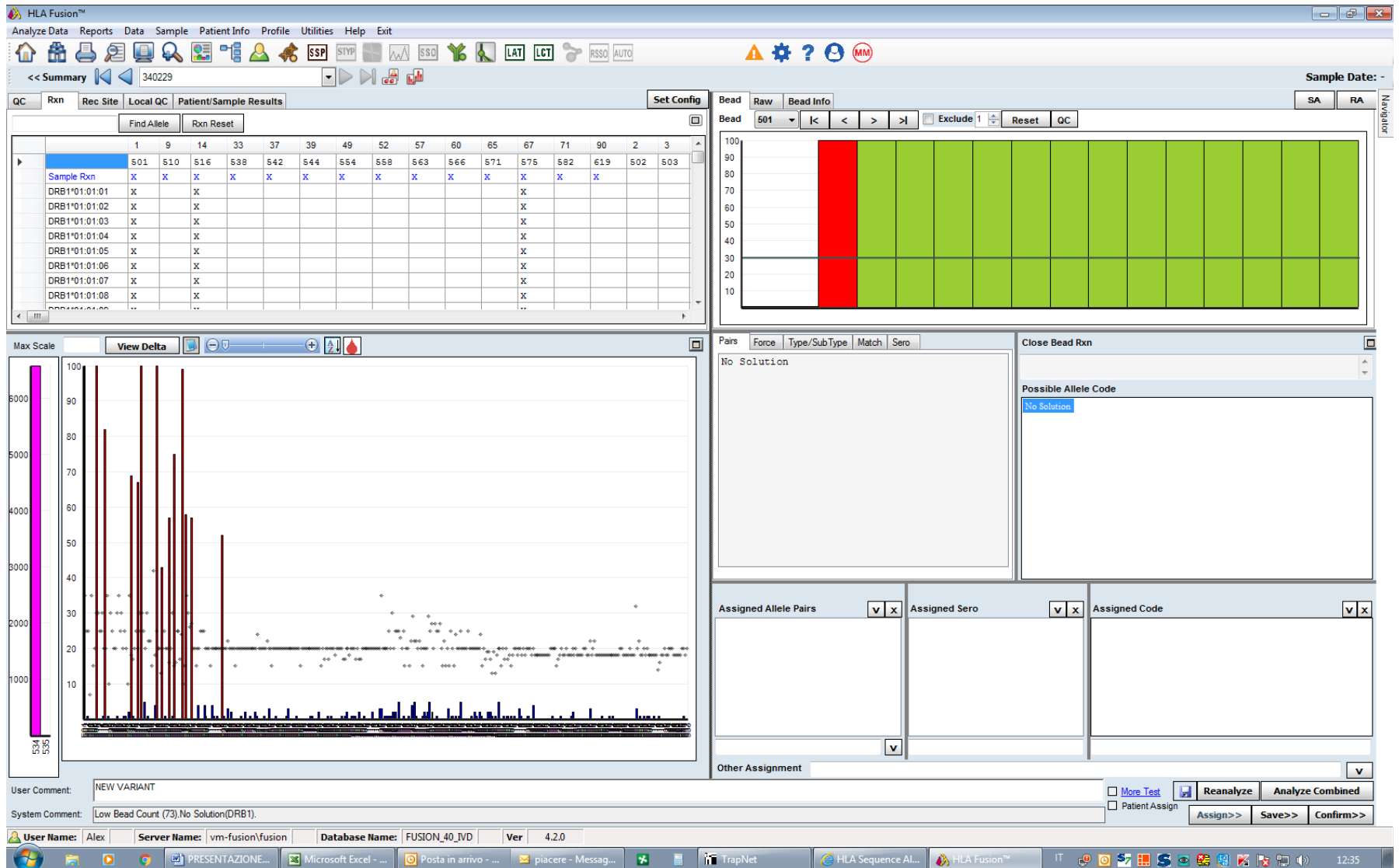
	T	C	A	G	
T	TTT Phe	TCT Ser	TAT Tyr	TGT Cys	T
	TTC Phe	TCC Ser	TAC Tyr	TGC Cys	C
	TTA Leu	TCA Ser	TAA stop	TGA stop	A
	TTG Leu	TCG Ser	TAG stop	TGG Trp	G
C	CTT Leu	CCT Pro	CAT His	CGT Arg	T
	CTC Leu	CCC Pro	CAC His	CGC Arg	C
	CTA Leu	CCA Pro	CAA Gln	CGA Arg	A
	CTG Leu	CCG Pro	CAG Gln	CGG Arg	G
A	ATT Ile	ACT Thr	AAT Asn	AGT Ser	T
	ATC Ile	ACC Thr	AAC Asn	AGC Ser	C
	ATA Ile	ACA Thr	AAA Lys	AGA Arg	A
	ATG Met	ACG Thr	AAG Lys	AGG Arg	G
G	GTT Val	GCT Ala	GAT Asp	GGT Gly	T
	GTC Val	GCC Ala	GAC Asp	GGC Gly	C
	GTA Val	GCA Ala	GAA Glu	GGA Gly	A
	GTG Val	GCG Ala	GAG Glu	GGG Gly	G

Cod 269 CCC -> CCA

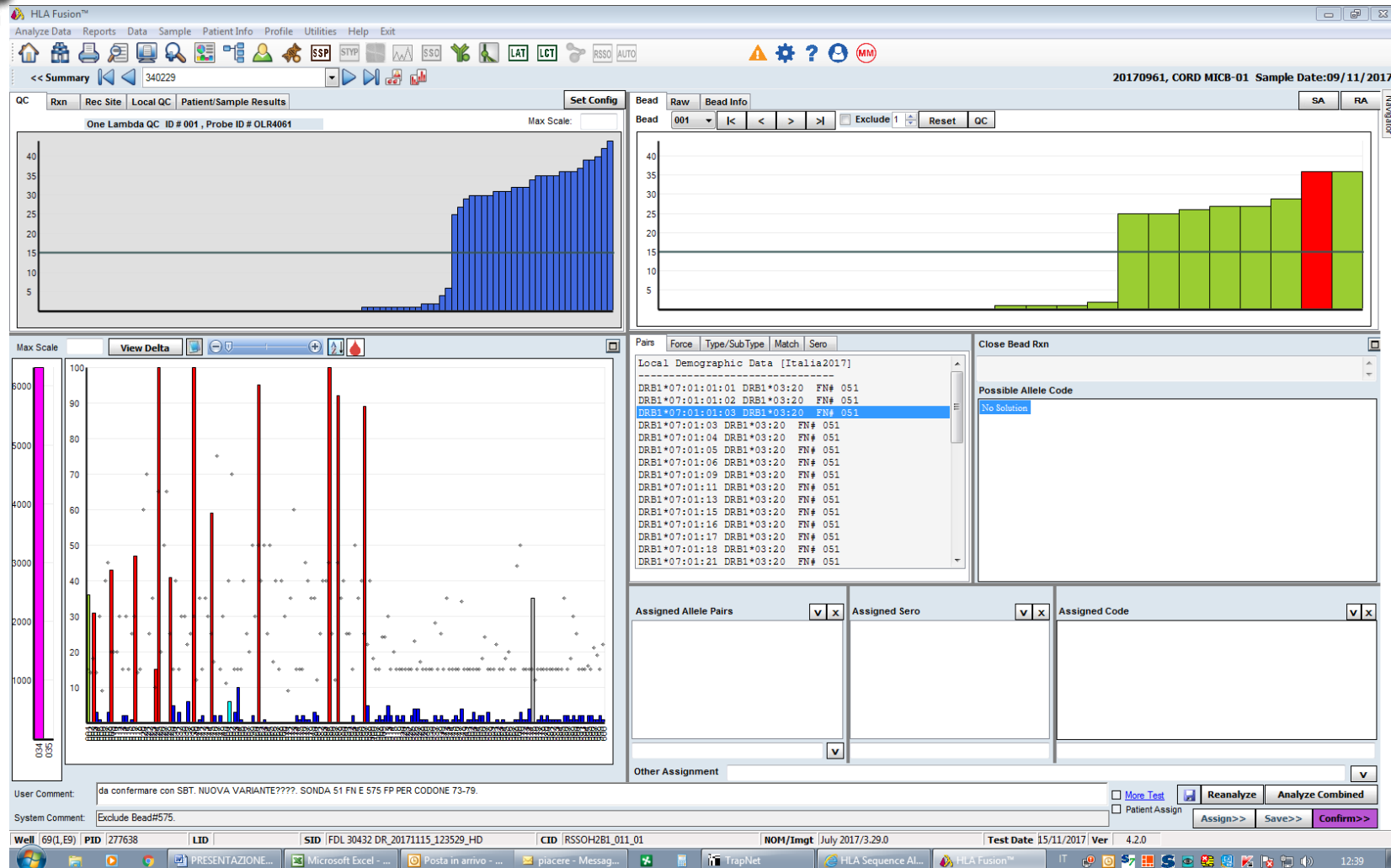
Cod 269 Pro -> Pro

A*03:01,*32:01; B*07:02:55,*40:02; C*02:02,*07:02; DRB1*15:02,*16:01

DRB1*03:145



LUMINEX KIT XR NON CONCLUDIBILE

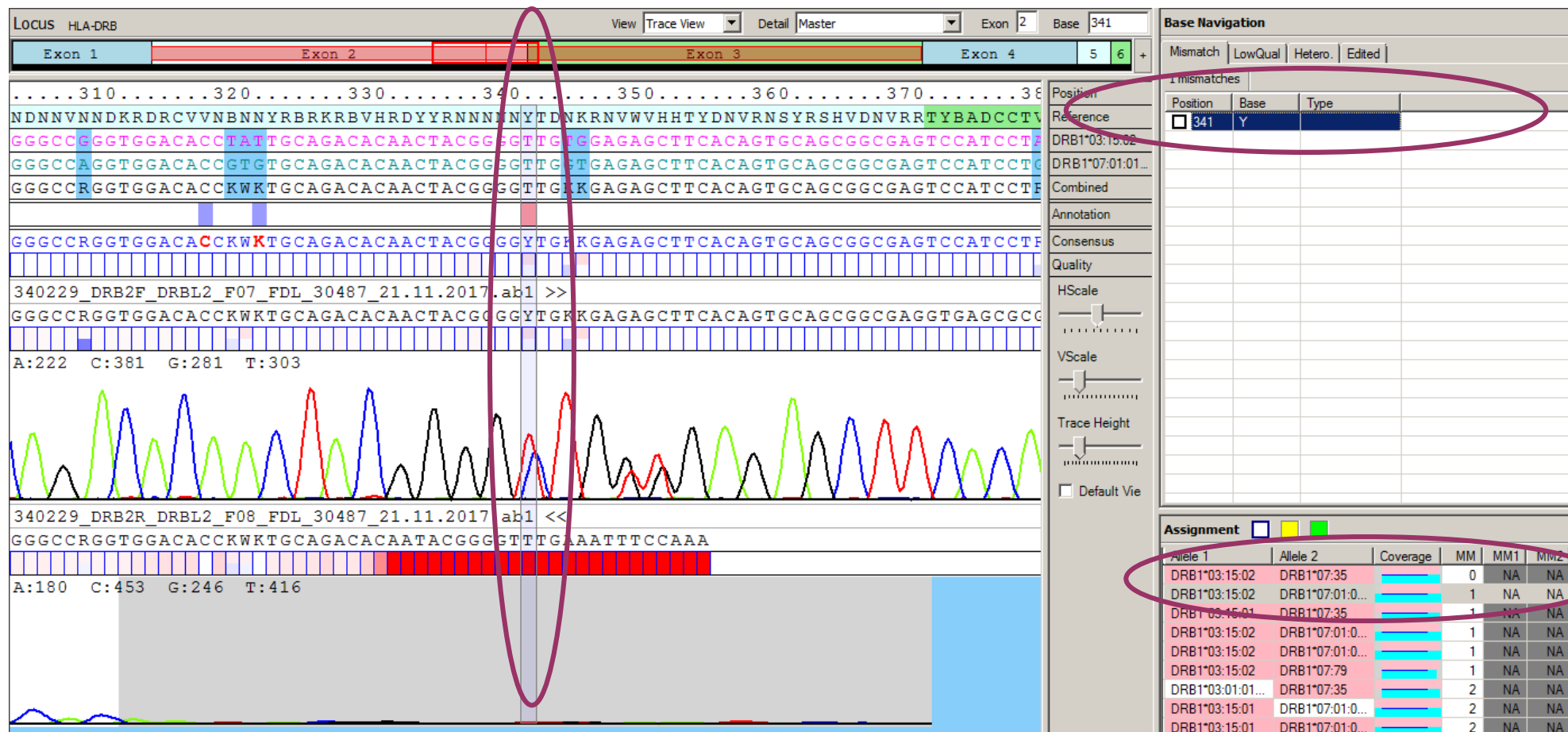


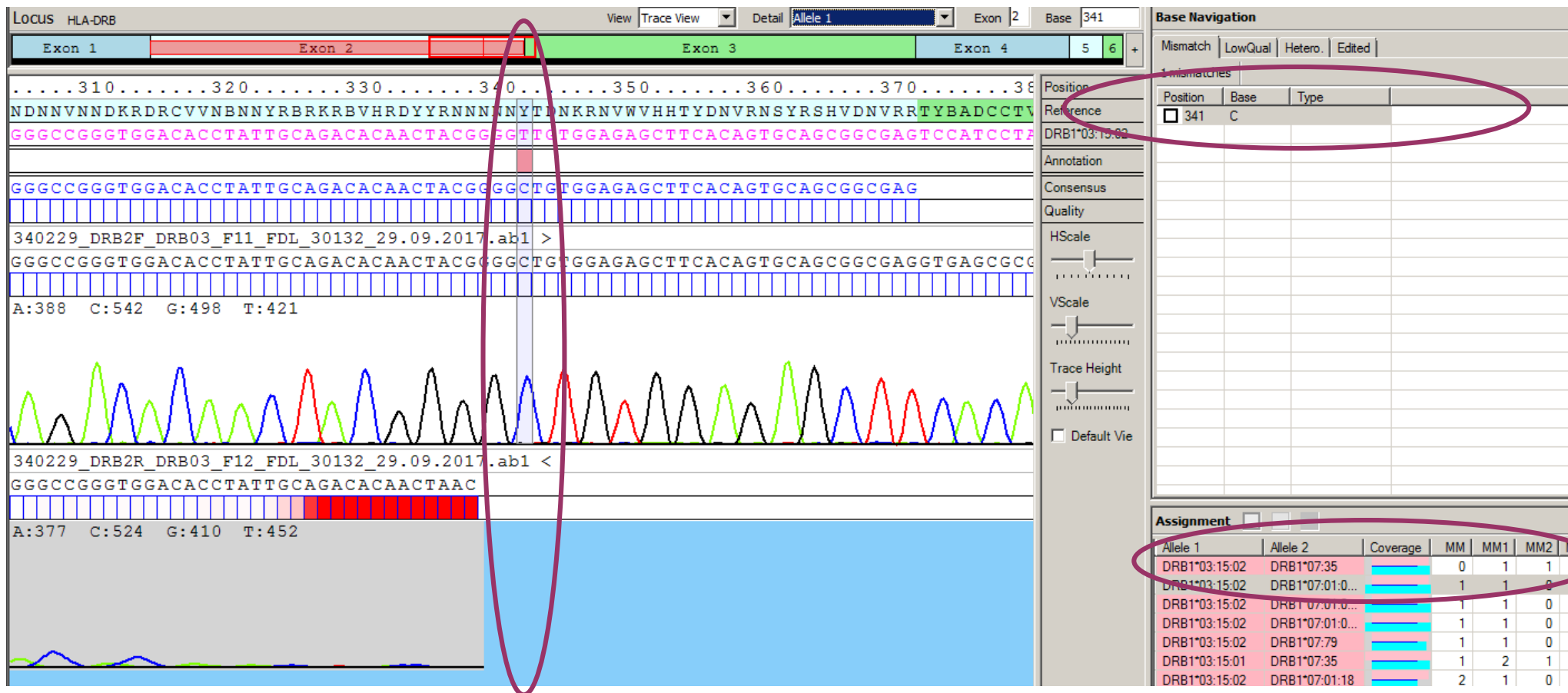
LUMINEX KIT XR:

SE SONTA 575 FP E 51 FN DRB1*07:01:01:01 DRB1*03:20

REC SITE SONTA 51: 73GR--N-78

REC SITE SONTA 575: 73SE--76 / 73---N--78 / 73GR-----79





AA Codon	10	15	20	25	
DRB1*03:15:02	CA CGT TTC TTG GAG TAC TCT ACG TCT GAG TGT CAT TTC TTC AAT GGG ACG GAG CGG GTG CGG TAC CTG GAC AGA				
AA Codon	30	35	40	45	50
DRB1*03:15:02	TAC TTC CAT AAC CAG GAG GAG AAC GTG CGC TTC GAC AGC GAC GTG GGG GAG TTC CGG GCG GTG ACG GAG CTG GGG				
AA Codon	55	60	65	70	75
DRB1*03:15:02	CGG CCT GAT GCC GAG TAC TGG AAC AGC CAG AAG GAC CTC CTG GAG CAG AAG CGG GGC CGG GTG GAC ACC TAT TGC				
AA Codon	80	85	90		
DRB1*03:15:02	AGA CAC AAC TAC GGG GTT GTG GAG AGC TTC ACA GTG CAG CGG CGA G				

Esone 2

Cod 85 GTT -> GCT

Cod 85 Val -> Ala

		second base in codon					
		T	C	A	G		
first base in codon	T	TTT Phe	TCT Ser	TAT Tyr	TGT Cys	T	third base in codon
		TTC Phe	TCC Ser	TAC Tyr	TGC Cys	C	
		TTA Leu	TCA Ser	TAA stop	TGA stop	A	
		TTG Leu	TCG Ser	TAG stop	TGG Trp	G	
C		CTT Leu	CCT Pro	CAT His	CGT Arg	T	
		CTC Leu	CCC Pro	CAC His	CGC Arg	C	
		CTA Leu	CCA Pro	CAA Gln	CGA Arg	A	
		CTG Leu	CCG Pro	CAG Gln	CGG Arg	G	
A		ATT Ile	ACT Thr	AAT Asn	AGT Ser	T	
		ATC Ile	ACC Thr	AAC Asn	AGC Ser	C	
		ATA Ile	ACA Thr	AAA Lys	AGA Arg	A	
		ATG Met	ACG Thr	AAG Lys	AGG Arg	G	
G		GTT Val	GCT Ala	GAT Asp	GGT Gly	T	
		GTC Val	GCC Ala	GAC Asp	GGC Gly	C	
		GTA Val	GCA Ala	GAA Glu	GGA Gly	A	
		GTG Val	GCG Ala	GAG Glu	GGG Gly	G	

Cord Blood

A*01:01,*29:02; B*08:01,*50:01;DRB1*03:145,*07:01

Mother

A*01:01,*03:01; B*08:01,*15:16;DRB1*03:145,*04:05

Allele*Frequencies

in Worldwide Populations



HLA > Haplotype Frequency Search

Please specify your search by selecting options from boxes. Then, click "Search" to find HLA Haplotype frequencies that match your criteria. **Remember at least one option must be selected.**

A	B	C	DRB1	DPA1	DPB1	DQA1	DQB1
A*01:01	B*08:01	Select	DRB1*03	Select	Select	Select	Select

Population: Country: Source of dataset:

Region: Ethnic Origin: Type of study: Sort by:

Sample Size: Sample Year: Loci Tested:

Displaying 1 to 100 (from 111) records Pages: 1 2 of 2

Line	Haplotype	Population	Frequency (%)	Sample Size	Distribution ¹
1	A*01:01:01-B*08:01-C*07:01-DRB1*03:01	 South Africa Caucasians	8.8900	102	
2	A*01:01:01-B*08:01-DRB1*03:01:01	 Madeira	2.4000	185	
3	A*01:01:01-B*08:01-DRB1*03:01:01	 Portugal North	2.2000	46	
4	A*01:01:01-B*08:01-DRB1*03:01:01	 Portugal Center	3.0000	50	
5	A*01:01-B*08:01-C*04:01-DRB1*03:01	 Poland DKMS	0.0024	20,653	
6	A*01:01-B*08:01-C*05:01-DRB1*03:01-DQB1*02:01	 Germany DKMS - Turkey minority	0.0100	4,856	
7	A*01:01-B*08:01-C*05:01-DRB1*03:01-DQB1*02:01-DPB1*01:01	 Russians from Karelia	0.05620504	1,075	
8	A*01:01-B*08:01-C*06:02-DRB1*03:01-DQB1*02:01	 India Tamil Nadu	0.0200723	2,492	
9	A*01:01-B*08:01-C*07:01-DRB1*03:01	 Brazil Vale do Ribeira Quilombos	0.6944	144	
10	A*01:01-B*08:01-C*07:01-DRB1*03:01	 Germany DKMS - Netherlands minority	6.7000	1,374	
11	A*01:01-B*08:01-C*07:01-DRB1*03:01	 Germany DKMS - Portugal minority	3.8430	1,176	
12	A*01:01-B*08:01-C*07:01-DRB1*03:01	 Germany DKMS - Romania minority	5.7550	1,234	
13	A*01:01-B*08:01-C*07:01-DRB1*03:01	 Germany DKMS - Greece minority	2.4470	1,894	
14	A*01:01-B*08:01-C*07:01-DRB1*03:01	 Germany DKMS - Croatia minority	4.7620	2,057	
15	A*01:01-B*08:01-C*07:01-DRB1*03:01	 Germany DKMS - Austria minority	5.2170	1,698	
16	A*01:01-B*08:01-C*07:01-DRB1*03:01	 Germany DKMS - Bosnia and Herzegovina minority	5.3070	1,028	

38	A*01:01-B*08:01-C*07:01-DRB1*03:01-DQB1*02:01	 Ireland South	11.5000	250	
39	A*01:01-B*08:01-C*07:01-DRB1*03:01-DQB1*02:01	 Italy pop 5	4.6500	975	
40	A*01:01-B*08:01-C*07:01-DRB1*03:01-DQB1*02:01	 Poland	4.0000	200	
41	A*01:01-B*08:01-C*07:01-DRB1*03:01-DQB1*02:01	 USA African American pop 4	1.3910	2,411	

DRB1*13:new

SureTyper (CE-IVD) Session 356967

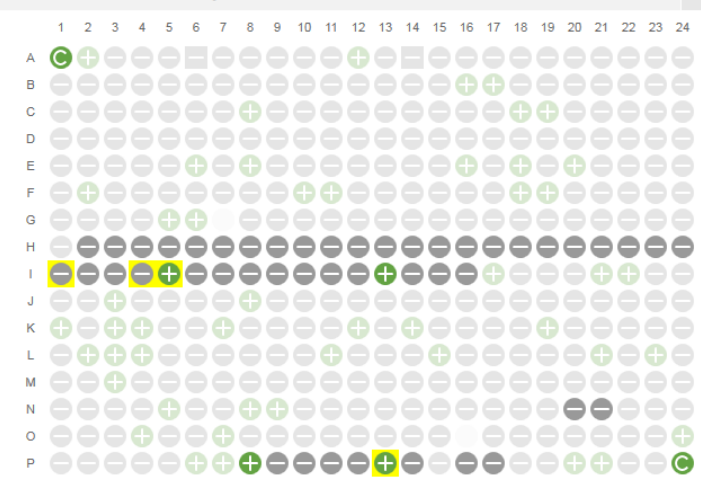
Sample ID — 356967 | Patient ID — MOD 290...

Tray 1 — Plate SX241727-DFK

TEST	GENOTYPE	PHENOTYPE	TEST	GENOTYPE	PHENOTYPE
HLA-A auto-dropout	A*01 A*68	A1 A68	HLA-C	C*03 C*07	Cw9 Cw7
HLA-B	B*15 B*55	B63 B55	Bw		Bw4 Bw6
HLA-DRB1 rare-manual	DRB1*13 DRB1*16	Undefined DR16	HLA-DRB345	DRB3*03 DRB5*02	DR52 DR51
HLA-DQA1	DQA1*01 DQA1*01	DQA01 DQA01	HLA-DQB1 auto	DQB1*05 DQB1*06	DQ5 DQ6
HLA-DPA1	DPA1*02 DPA1*02	DPA02 DPA02	HLA-DPB1 auto		EDP10 EDP10

Session Info Catalog # 1575C | Kit Lot # K3552 | Kit Name: LinkSeq HLA ABCDRDQDP+ | Report Info
Alleles Info Database Version: IMGT/HLA release: version 3.31.0 - Jan 2018 | Considered Rare Allele If Labeled: d, e, f or u

Tray Viewer



SureTyper Test Result Details

TEST RESULT FOR HLA-DRB1

Genotype — DRB1*13 DRB1*16 | Phenotype — Undefined DR16

This genotype was manually chosen.

More than one genotype can explain the reaction pattern.

Possibilities to consider:

ALLELE GROUP	ALLELES	P GROUP	ANTIGEN
DRB1*13	DRB1* 13:103e, 13:121e, 13:160e, 13:173e, 13:200Ne, 13:218e	-	-
DRB1*16	DRB1* 16:01:01, 16:02:04:01, DRB1* 16:03:01d, DRB1* 16:01:03e-16:01:14e, 16:02:01:02e-16:02:01:03e, 16:02:03e-16:02:07e, 16:05:02e	16:01P, 16:02P, 16:05P	DR16
	DRB1* 16:38e	16:38P	-
	DRB1* 16:07, DRB1* 16:12d, DRB1* 16:08e, 16:11e, 16:13Ne-16:15e, 16:17e, 16:19e-16:26e, 16:28e-16:32e, 16:34e-16:37e, 16:39e-16:47e	-	-

One side of this genotype requires a RARE allele, which makes this call less likely. This genotype was MANUALLY chosen.

Undo This Chosen Test Call

OR

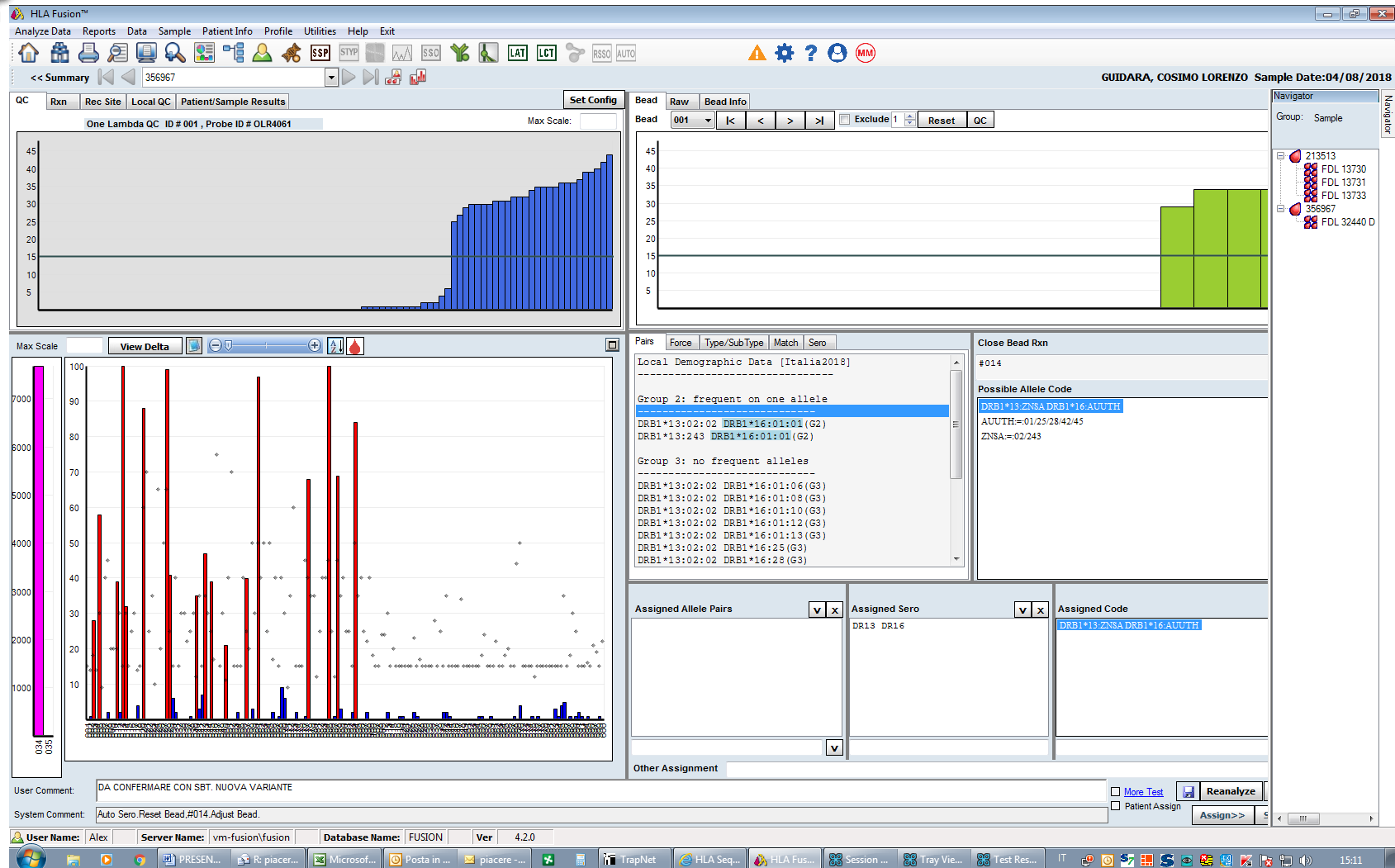
ALLELE GROUP	ALLELES	P GROUP	ANTIGEN
DRB1*13	DRB1* 13:103e, 13:121e, 13:160e, 13:173e, 13:200Ne, 13:218e	-	-
DRB1*15	DRB1* 15:115Ne	-	-

Both sides of this genotype require RARE alleles, which makes this call less likely.

ALLELES BY GROUP

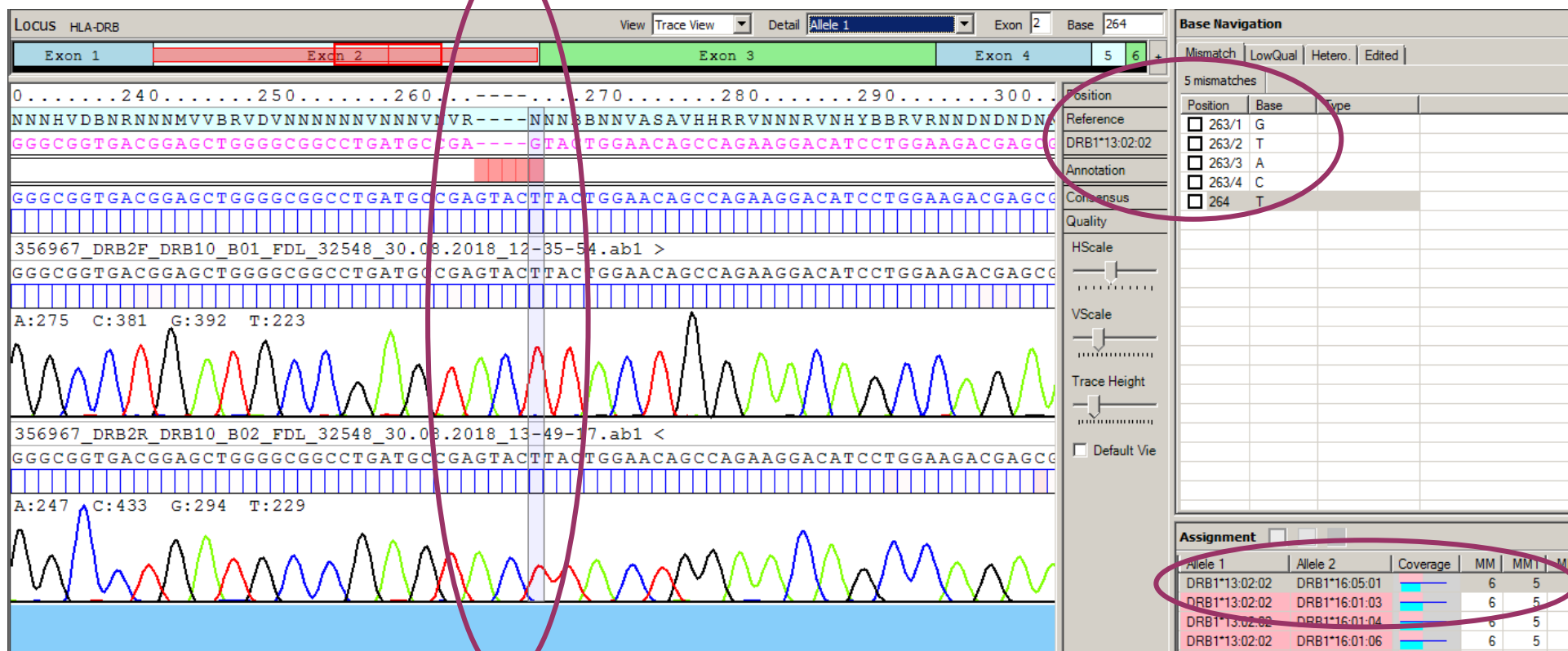
GROUP	ALLELES
DRB1*13	DRB1* 13:103e, 13:121e, 13:160e, 13:173e, 13:200Ne, 13:218e

LINKSEQ TIPIZZAZIONE DRB1*13 RARA. MIX I1 E I4 NEG PER DRB1*13:01



TIPIZZ LUMINEX CONFERMA LA PRESENZA D'UN ALLELE RARO MA NON PRESENTE NEL ELENCO DI POSSIBILITA' FORNITE DAL LINKSEQ.





AA Codon	10	15	20	25	
DRB1*13:02:02	CA CGT TTC TTG GAG TAC TCT ACG TCT GAG TGT CAT TTC TTC AAT GGG ACG GAG CGG GTG CGG TTC CTG GAC AGA				
AA Codon	30	35	40	45	50
DRB1*13:02:02	TAC TTC CAT AAC CAG GAG GAG AAC GTG CGC TTC GAC AGC GAC GTG GGG GAG TTC CGG GCG GTG ACG GAG CTG GGG				
AA Codon	55	60	65	70	75
DRB1*13:02:02	CGG CCT GAT GCC GAG TAC TGG AAC AGC CAG AAG GAC ATC CTG GAA GAC GAG CGC GCC GCG GTG GAC ACC TAC TGC				
AA Codon	80	85	90		
DRB1*13:02:02	AGA CAC AAC TAC GGG GTT GGT GAG AGC TTC ACA GTG CAG CGG CGA G				

DRB1*13new

CA CGT TTC TTG GAG TAC TCT ACG TCT GAG TGT CAT TTC TTC AAT GGG ACG GAG CGG GTG CGG TTC CTG GAC AGA TAC TTC
 CAT AAC CAG GAG GAG AAC GTG CGC TTC GAC AGC GAC GTG GGG GAG TTC CGG GCG GTG ACG GAG CTG GGG CGG CCT GAT GCC
 GAG TAC **TTA** **CTG** GAA CAG CCA GAA GGA CAT CCT GGA AGA CGA GCG CGC CGC GGT GGA CAC CTA CTG CAG ACA CAA CTA CGG
 GGT TGG **TGA** GAG CTT CAC AGT GCA GCG GCG AG

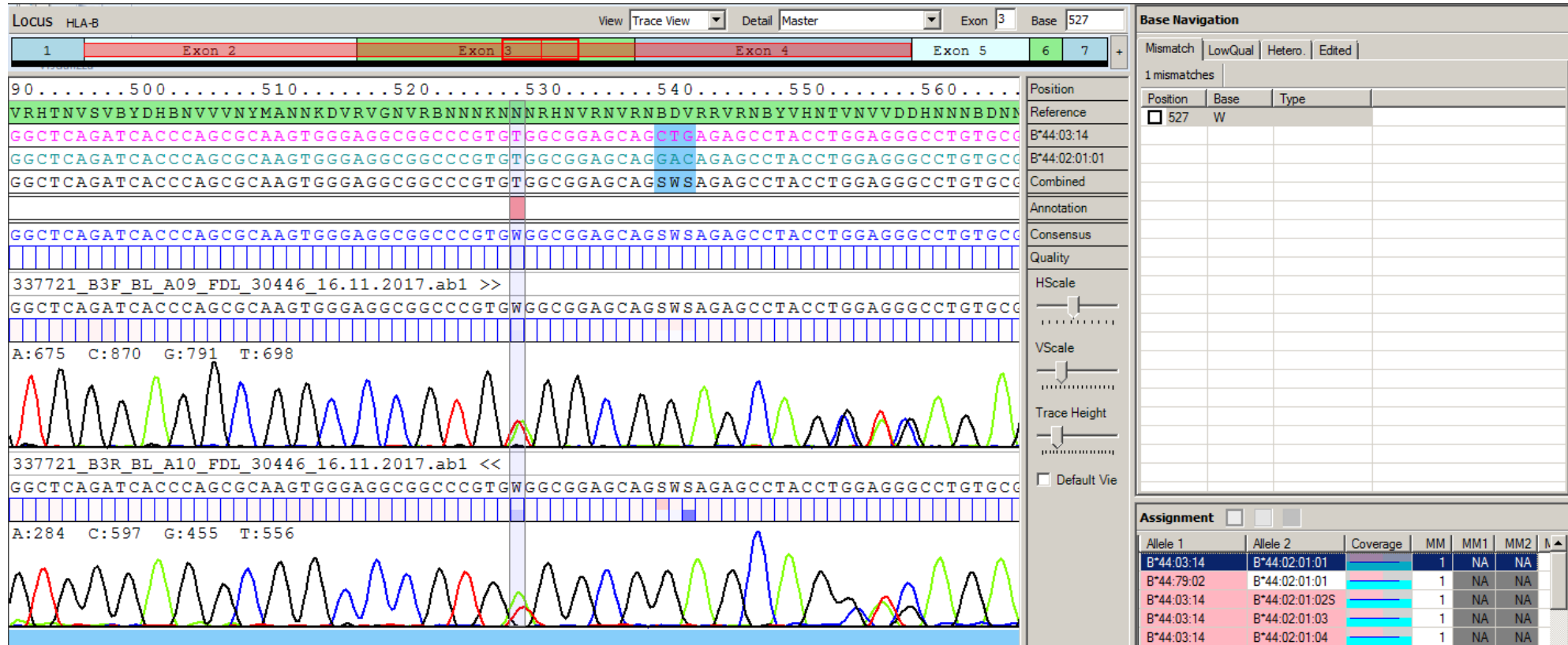
second base in codon

	T	C	A	G	
first base in codon	T	TTT Phe TTC Phe TTA Leu TTG Leu	TCT Ser TCC Ser TCA Ser TCG Ser	TAT Tyr TAC Tyr TAA stop TAG stop	TGT Cys TGC Cys TGA stop TGG Trp
	C	CTT Leu CTC Leu CTA Leu CTG Leu	CCT Pro CCC Pro CCA Pro CCG Pro	CAT His CAC His CAA Gln CAG Gln	CGT Arg CGC Arg CGA Arg CGG Arg
	A	ATT Ile ATC Ile ATA Ile ATG Met	ACT Thr ACC Thr ACA Thr ACG Thr	AAT Asn AAC Asn AAA Lys AAG Lys	AGT Ser AGC Ser AGA Arg AGG Arg
	G	GTT Val GTC Val GTA Val GTG Val	GCT Ala GCC Ala GCA Ala GCG Ala	GAT Asp GAC Asp GAA Glu GAG Glu	GGT Gly GGC Gly GGA Gly GGG Gly
					third base in codon
					T C A G T C A G T C A G

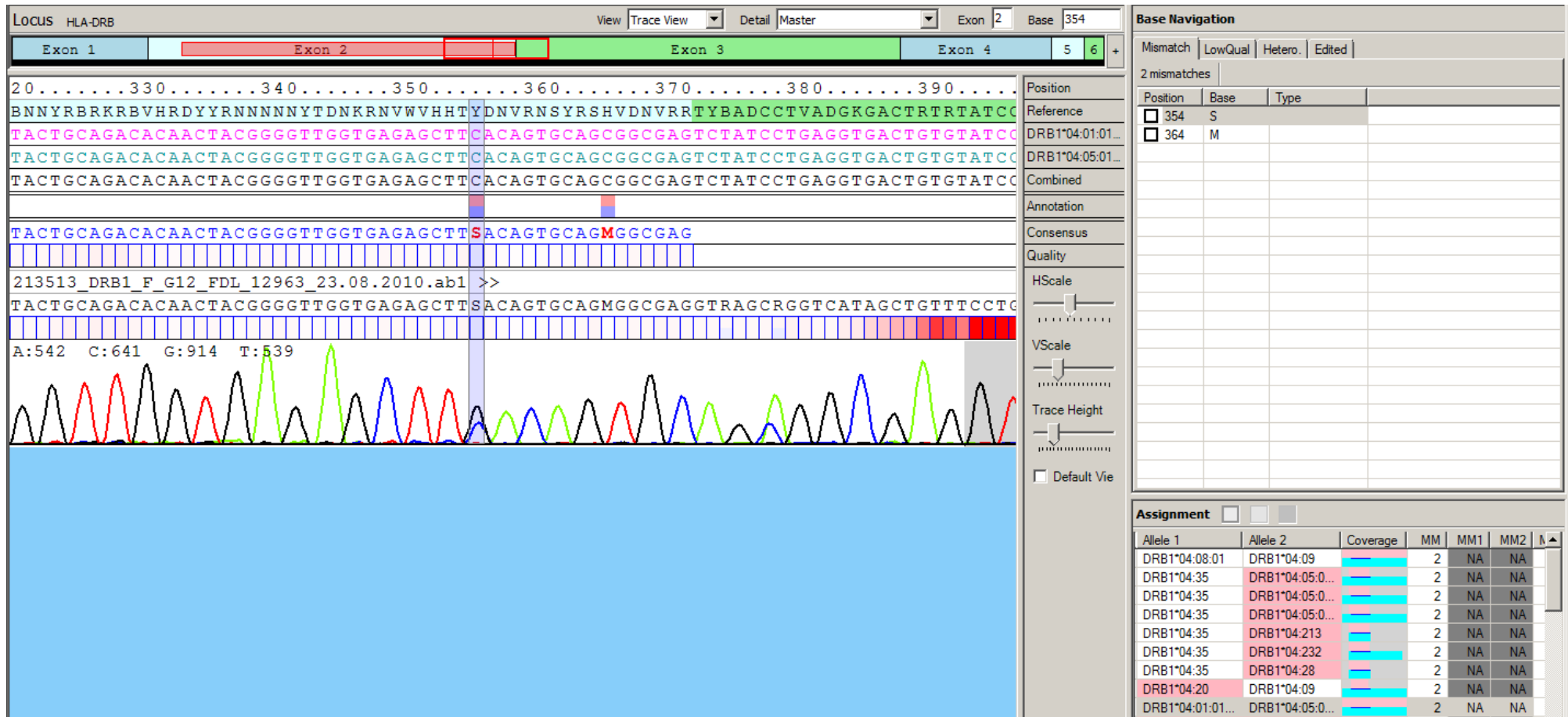


DRB1*13new = *13Null ?

B*44,*44



DRB1*04,*04



TypeStream™ Visual (For Research Use Only)

Analyze Data Reports Data Sample Patient Info Profile Utilities About Exit

Home Settings Help Search Data Sample Patient Info Profile Utilities About Exit

<< Summary 337721 Show Read Coverage

Locus	Allele Pair	[K/N/I] 1	[K/N/I] 2	#B	#G
A	A*29:02:01:01 A*68:01:02:02	[0/0/0]	[0/0/0]	0	1
B	B*44:02:01:01 B*44	[0/0/0]	[1/0*/0*]	0	1
C	C*02:02:02:01 C*16:01:01:01	[0/0/0]	[0/0/0]	1	1
DRB34	DRB4*01:01:01 DRB5*02:06	[0/0/1]	[0/0*/0*]	1	1
DRB1	DRB1*07:01:01:01 DRB1*16:01:01	[0/0/0]	[0/0/0]	1	1
DQA1	DQA1*01:02:02:02 DQA1*02:01:01	[0/0/0*]	[0/0/1]	0	1
DQB1	DQB1*02:02:01:01 DQB1*05:02:01	[0/0/0]	[0/0/1]	0	1
DPA1	DPA1*01:03:01:01 DPA1*01:03:01:02	[0/0/0*]	[0/0/0]	2	1
DPB1	DPB1*02:01:02 DPB1*04:01:01	[0/0/3]	[0/0/1]	2	1

Allele 1 Allele 2

B*44:02:01:01 B*44

G Allele 1 Allele 2

G2 B*44:02:01:01 B*44:03:14

G2 B*44:02:01:01 B*44:79:02

Allele 1 Allele 2

[0/0/0] B*44:02:01:01 [1/0*/0*] B*44:03:14

[K/N/I]	Allele	Position	Ref	Cons
[1/0*/0*]	B*44:03:14	E3-850	C	C
		E3-900	T	A
[1/0*/0*]	B*44:79:02	E3-850	G	C
		E3-900	A	A

Locus User Comments :

Locus System Comments :

Missed health metric: Mismatches in an exon

Final Allele Code

Final Sero Assignment

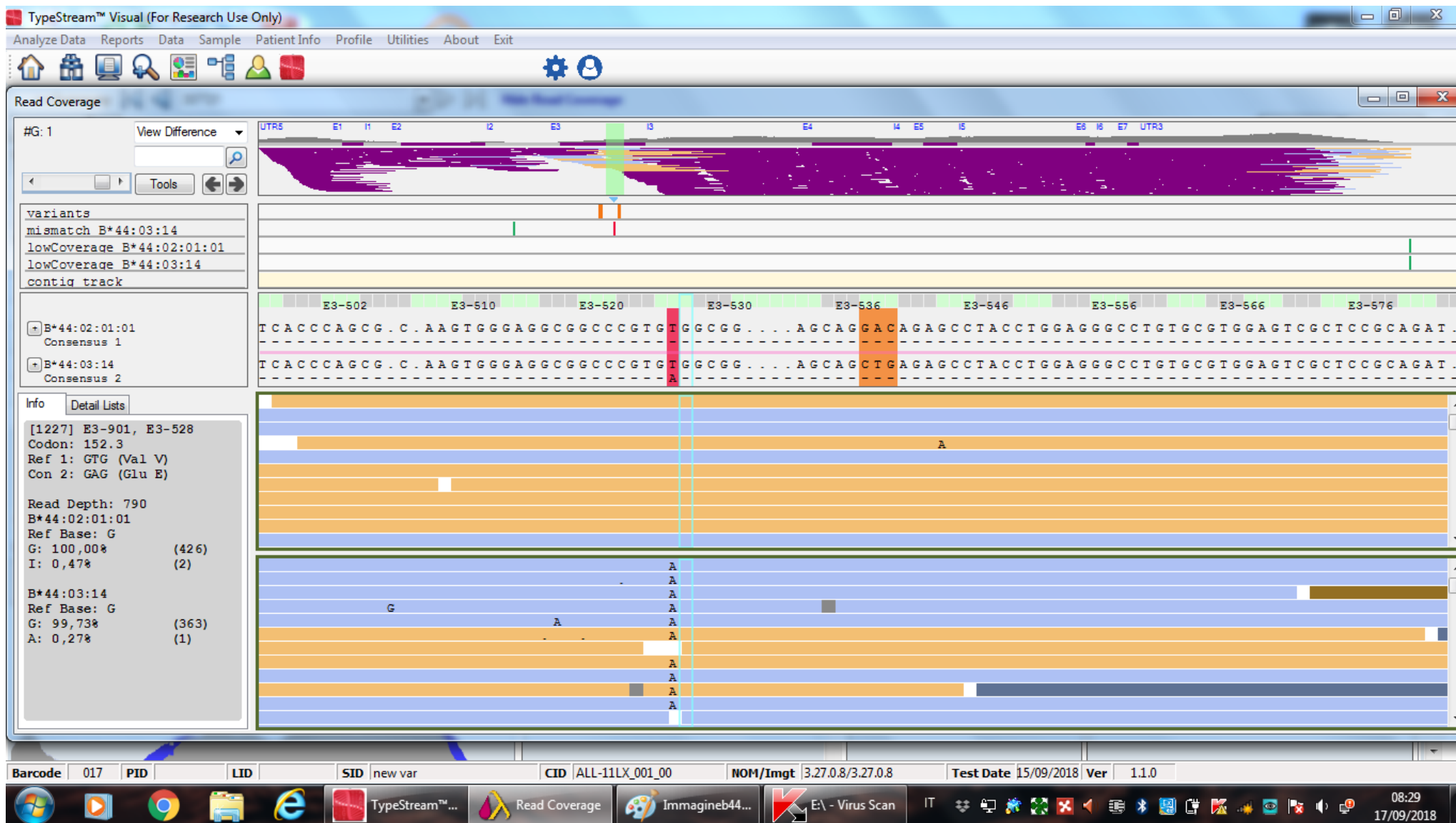
B44 B44

Final 1 Final 2

2 3 4 fields 2 3 4 fields

Barcode 017 PID LID SID new var CID ALL-11LX_001_00 NOM/Imgt 3.27.0.8/3.27.0.8 Test Date 15/09/2018 Ver 1.1.0

20:15 15/09/2018



Analyze Data Reports Data Sample Patient Info Profile Utilities About Exit



<< Summary < 213513 > >> Show Read Coverage

Set Config Analysis Parameter

☐ More Test ☐ Patient Assign ☒ Allele Pair ☐ Allele Code

Save

Confirm

User Comments:

System Comments: Auto Ser.

Locus	Allele Pair	[K/N/I] 1	[K/N/I] 2	#B	#G
A	A*02:01:01:01 A*24:02:01	[0/0/0]	[0/0/1]	0	1
B	B*18:01:01 B*49:01:01	[0/0/1]	[0/0/0]	4	1
C	C*07:01:01:01 C*07:01:01:01	[0/0/0]	[0/0/0]	0	1
DRB1	DRB1*04:01:01 DRB1*04	[0/0/3]	[1/0/0*]	0	1
DRB34	DRB4*01:03:01 DRB4*01:03:01	[0/0/1]	[0/0/1]	0	1
DQA1	DQA1*03:03:01:01 DQA1*03:03:01:01	[0/0/0]	[0/0/0]	0	1
DQB1	DQB1*03:01:01 DQB1*03:02:01	[0/0/1]	[0/0/1]	0	1
DPA1	DPA1*01:03:01 DPA1*01:03:01	[0/0/1]	[0/0/1]	0	1
DPB1	DPB1*02:01:02 DPB1*04:01:01	[0/0/4]	[0/0/1]	1	1

Allele 1	Allele 2
DRB1*04:01:01	DRB1*04
G	Allele 1
G1	DRB1*04:01:01:01
	Allele 2
	DRB1*04:05:01

Allele Code Serology Resolving Positions Close Match List

Allele 1		Allele 2				
[0/0/3]	DRB1*04:01:01:01	[1/0/0*]	DRB1*04:05:01			
[K/N/I]	Allele	[K/N/I]	Allele	Position	Ref	Con
[0/0/3]	DRB1*04:01:01:01	[1/0/0*]	DRB1*04:05:01	E2-5626	C	G

Read Coverage

#G: 1

View Difference

UTRS E1 I1

E2 I2

E3 I3

E4 I4

E5 I5

E6 I6

E7 I7

E8 I8

UTR

variants
mismatch DRB1*04:01:01:01
highBackground DRB1*04:01:01:01
mismatch DRB1*04:05:01
highBackground DRB1*04:05:01
lowCoverage DRB1*04:01:01:01
lowCoverage DRB1*04:05:01
contig track

DRB1*04:01:01:01
Consensus 1

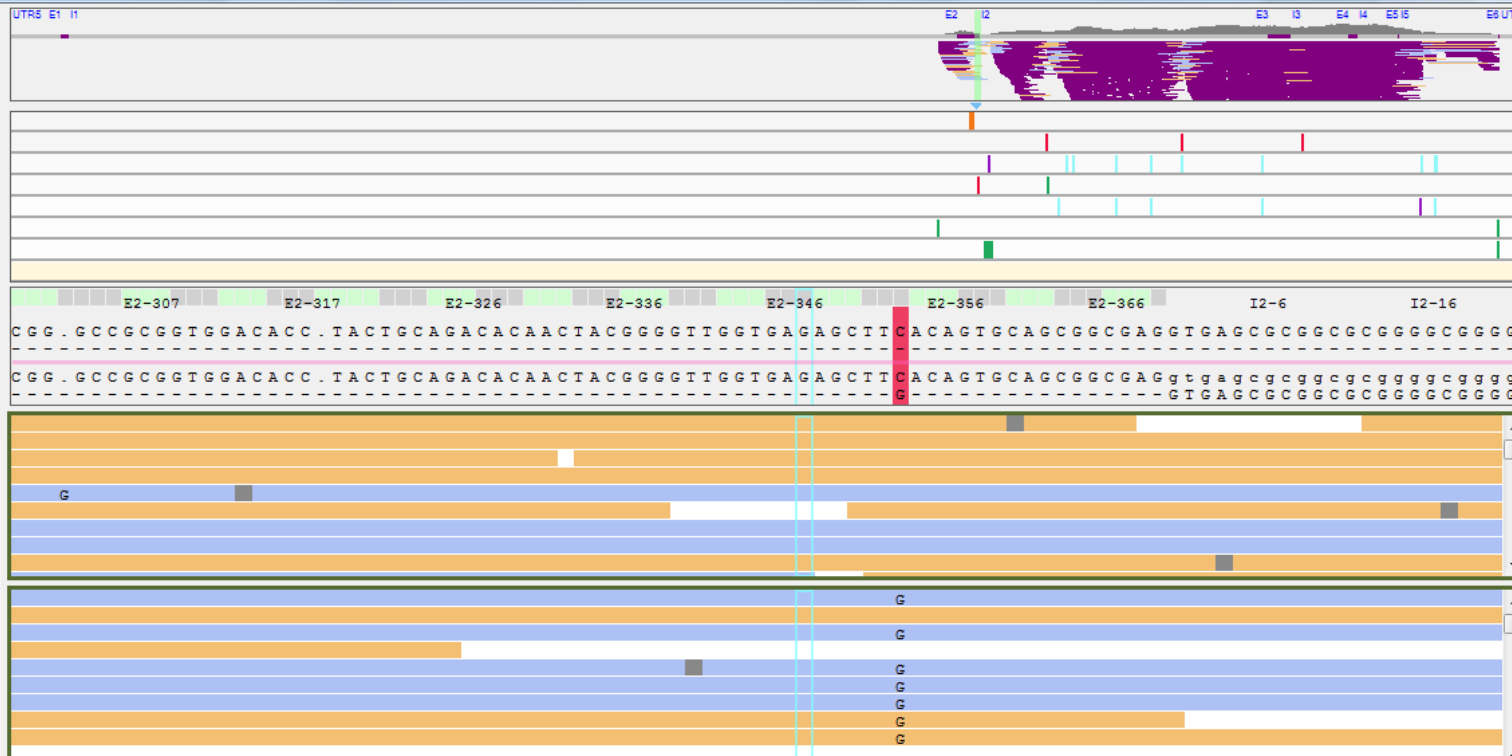
DRB1*04:05:01
Consensus 2

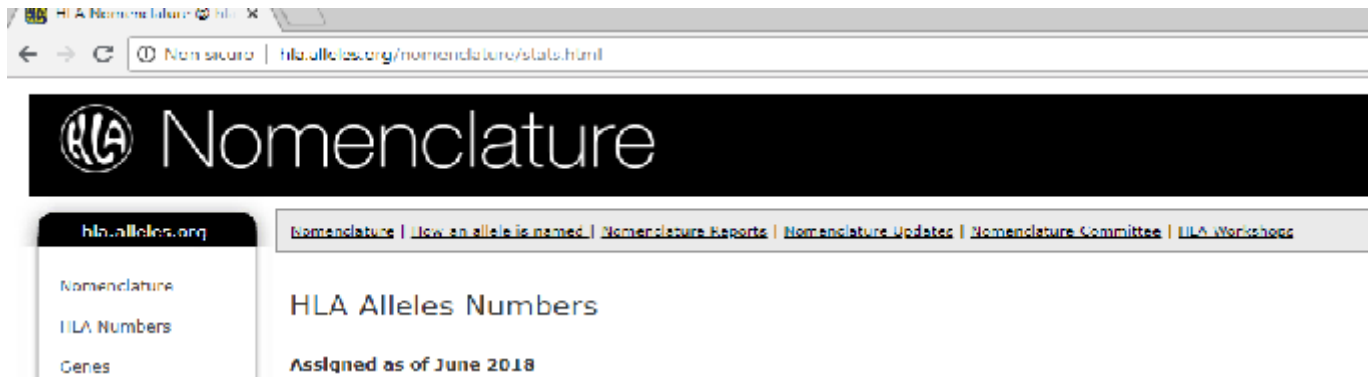
Info Detail Lists

[11821] E2-5620, E2-348
Codon: 87.3
Ref 1: GAG (Glu E)
Ref 2: GAG (Glu E)

Read Depth: 260
DRB1*04:01:01:01
Ref Base: G
G: 99,38% (161)
C: 0,62% (1)

DRB1*04:05:01
Ref Base: G
G: 100,00% (98)
I: 1,02% (1)





HLA Nomenclature

hla.alleles.org

Nomenclature | How an allele is named | Nomenclature Reports | Nomenclature Updates | Nomenclature Committee | HLA Workshops

Nomenclature
HLA Numbers
Genes

HLA Alleles Numbers

Assigned as of June 2018

In association with

IPD Database

HLA Informatics Group



Numbers of HLA Alleles

HLA Class I Alleles	13,680
HLA Class II Alleles	5,091
HLA Alleles	18,771
Other non-HLA Alleles	184
Number of Confidential Alleles	6

HLA Class I

Gene	A	B	C	E	F	G
Alleles	4,340	5,212	3,930	27	31	61
Proteins	2,980	3,700	2,661	8	6	19
Nulls	206	154	147	1	0	3

- ✓ Gli alleli HLA noti sono oltre 18.000
- ✓ Le proteine HLA note sono meno di 13.000

HLA Class II

Gene	DRA	DRB	DQA1	DQB1	DPA1	DPA2	DPB1
Alleles	7	2,593	95	1,259	67	5	1,014
Proteins	2	1,878	35	838	29	2	692
Nulls	0	81	3	35	0	0	27

- ✓ Le biglie Luminex per la ricerca di anticorpi sono attualmente circa 200

HLA Class II - DRB Alleles

Gene	DRB1	DRB2	DRB3	DRB4	DRB5	DRB6	DRB7
Alleles	2,268	1	171	80	61	3	2
Proteins	1,622	0	140	62	54	0	0
Nulls	61	0	6	10	4	0	0

**QUALE IL SIGNIFICATO
TRAPIANTOLOGICO DI TUTTI
QUESTI NUOVI ALLELI?**



- hla.alleles.org
- Nomenclature
- HLA Numbers
- Genes
- Alleles
- Proteins
- Antigens
- Dictionary
- WMDA

[Alignments](#) | [Class I Alleles](#) | [Class II Alleles](#) | [Other Alleles](#) | [Null and Alternatively Expressed Alleles](#) | [Deleted Alleles](#) | [G Groups](#) | [P Groups](#) | [Heat maps](#)

Nomenclature for Factors of the HLA System

P Codes For Reporting of Ambiguous Allele Typings

This file contains details of all HLA Sequences having the same antigen binding domains. This analysis is performed on the protein sequence, and for HLA Class I alleles, identity in the 'antigen binding domains' is based on identical protein sequences as encoded by exons 2 and 3. For HLA Class II alleles this is based on identical protein sequences as encoded by exon 2. HLA alleles having nucleotide sequences that encode the same protein sequence for the peptide binding domains (exon 2 and 3 for HLA class I and exon 2 only for HLA class II alleles) will be designated by an upper case 'P' which follows the 2 field allele designation of the lowest numbered allele in the group. The group designation will contain a minimum of four digits. A computer readable file of these codes, [hla_nom_p.txt](#), is available to download, please see the [WMDA](#) section for further details.

Group Designation	Alleles Within Group
A*01:01P	A*01.01.01.01/A*01.01.01.03/A*01.01.01.04/A*01.01.01.05/A*01.01.01.06/A*01.01.01.07/A*01.01.01.08/A*01.01.01.09/A*01.01.01.10/A*01.01.01.11/A*01.01.01.12/ A*01.01.01.13/A*01.01.01.14/A*01.01.01.15/A*01.01.01.16/A*01.01.01.17/A*01.01.01.18/A*01.01.02/A*01.01.03/A*01.01.04/A*01.01.05/A*01.01.06/A*01.01.07/ A*01.01.08/A*01.01.09/A*01.01.10/A*01.01.11/A*01.01.12/A*01.01.13/A*01.01.14/A*01.01.15/A*01.01.16/A*01.01.17/A*01.01.18/A*01.01.19/A*01.01.20/A*01.01.21/ A*01.01.22/A*01.01.23/A*01.01.24/A*01.01.25/A*01.01.26/A*01.01.27/A*01.01.28/A*01.01.29/A*01.01.30/A*01.01.31/A*01.01.32/A*01.01.33/A*01.01.34/A*01.01.35/ A*01.01.36/A*01.01.37/A*01.01.38/A*01.01.39/A*01.01.40/A*01.01.41/A*01.01.42/A*01.01.43/A*01.01.44/A*01.01.45/A*01.01.46/A*01.01.47/A*01.01.48/A*01.01.49/ A*01.01.50/A*01.01.51/A*01.01.52/A*01.01.53/A*01.01.54/A*01.01.55/A*01.01.56/A*01.01.57/A*01.01.58/A*01.01.59/A*01.01.60/A*01.01.61/A*01.01.62/A*01.01.63/ A*01.01.64/A*01.01.65/A*01.01.66/A*01.01.67/A*01.01.68/A*01.01.69/A*01.01.70/A*01.01.71/A*01.01.72/A*01.01.73/A*01.01.74/A*01.01.75/A*01.01.76/A*01.01.77/ A*01.01.78/A*01.01.79/A*01.01.80/A*01.01.81/A*01.01.82/A*01.01.83/A*01.01.84/A*01.01.85/A*01.01.86/A*01.01.87/A*01.01.88/A*01.01.89/A*01.01.92/A*01.01.93/A*01.01.94/ A*01.81/A*01.103/A*01.107/A*01.109/A*01.132/A*01.141/A*01.142/A*01.155/A*01.177/A*01.212/A*01.217/A*01.234/A*01.237/A*01.246/A*01.248Q/A*01.249/A*01.251/ A*01.252/A*01.253/A*01.261
A*01:03P	A*01.03.01.01/A*01.03.01.02
A*01:09P	A*01.09.01.01/A*01.09.01.02/A*01.09.02
A*01:67P	A*01.67.01/A*01.67.02
A*01:69P	A*01.69.01/A*01.69.02
A*01:83P	A*01.83.01/A*01.83.02
A*01:88P	A*01.88.01/A*01.88.02/A*01.88.03
A*02:01P	A*02.01.01.01/A*02.01.01.02L/A*02.01.01.03/A*02.01.01.04/A*02.01.01.05/A*02.01.01.06/A*02.01.01.07/A*02.01.01.08/A*02.01.01.09/A*02.01.01.10/A*02.01.01.11/ A*02.01.01.12/A*02.01.01.13/A*02.01.01.14/A*02.01.01.15/A*02.01.01.16/A*02.01.01.17/A*02.01.01.18/A*02.01.01.19/A*02.01.01.20/A*02.01.01.21/A*02.01.01.22/ A*02.01.01.23/A*02.01.01.24/A*02.01.01.25/A*02.01.01.26/A*02.01.01.27/A*02.01.01.28/A*02.01.01.29/A*02.01.01.30/A*02.01.01.31/A*02.01.01.32/A*02.01.01.33/ A*02.01.01.34/A*02.01.01.35/A*02.01.01.36/A*02.01.01.37/A*02.01.01.38/A*02.01.01.39/A*02.01.01.40/A*02.01.01.41/A*02.01.02/A*02.01.03/A*02.01.04/A*02.01.05/ A*02.01.06/A*02.01.07/A*02.01.08/A*02.01.09/A*02.01.10/A*02.01.100/A*02.01.101/A*02.01.102/A*02.01.103/A*02.01.104/A*02.01.105/A*02.01.106/A*02.01.107/ A*02.01.108/A*02.01.109/A*02.01.11/A*02.01.110/A*02.01.111/A*02.01.112/A*02.01.113/A*02.01.114/A*02.01.115/A*02.01.116/A*02.01.117/A*02.01.118/A*02.01.119/

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