IMGT®, the international ImMunoGeneTics information system®

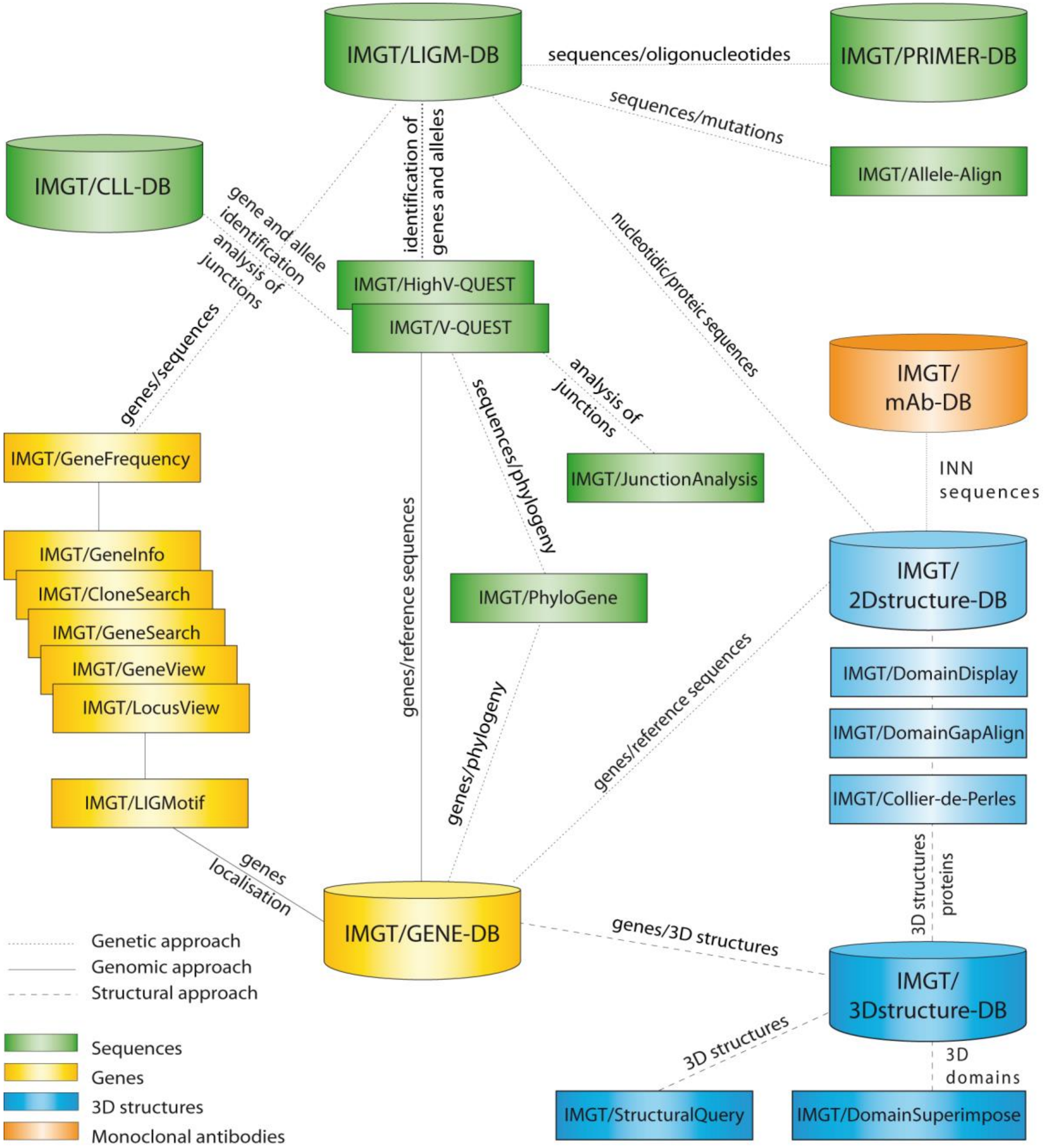
http://www.imgt.org

Marie-Paule Lefranc
IMGT Founder and Director, Professor UM2
and the IMGT team

November 28, 2012

IMGT® in 2012

http://www.imgt.org



IMGT/LIGM-DB
sequences/oligonucleotides
IMGT/PRIMER-DB
sequences/mutations
IMGT/Allele-Align
IMGT/CLL-DB
gene and allele identification
analysis of junctions
identification of genes and alleles
nucleotidic/proteic sequences
IMGT/HighV-QUEST
IMGT/V-QUEST
genes/sequences
analysis of junctions
IMGT/mAb-DB
IMGT/GeneFrequency
sequences/phylogeny
IMGT/JunctionAnalysis
INN sequences
IMGT/GeneInfo
IMGT/CloneSearch
IMGT/GeneSearch
IMGT/GeneView
IMGT/LocusView
genes/reference sequences
IMGT/PhyloGene
IMGT/2Dstructure-DB
IMGT/DomainDisplay
IMGT/DomainGapAlign
IMGT/Collier-de-Perles
genes/phylogeny
genes/reference sequences
IMGT/LIGMotif
genes localisation
IMGT/GENE-DB
genes/3D structures
3D structures
proteins
IMGT/3Dstructure-DB
3D structures
3D domains
IMGT/StructuralQuery
IMGT/DomainSuperimpose

.... Genetic approach
—— Genomic approach
- - - - Structural approach

🟩 Sequences
🟨 Genes
🟦 3D structures
🟧 Monoclonal antibodies

- 7 databases
- 17 online tools

- Sequences
- Genes
- Structures

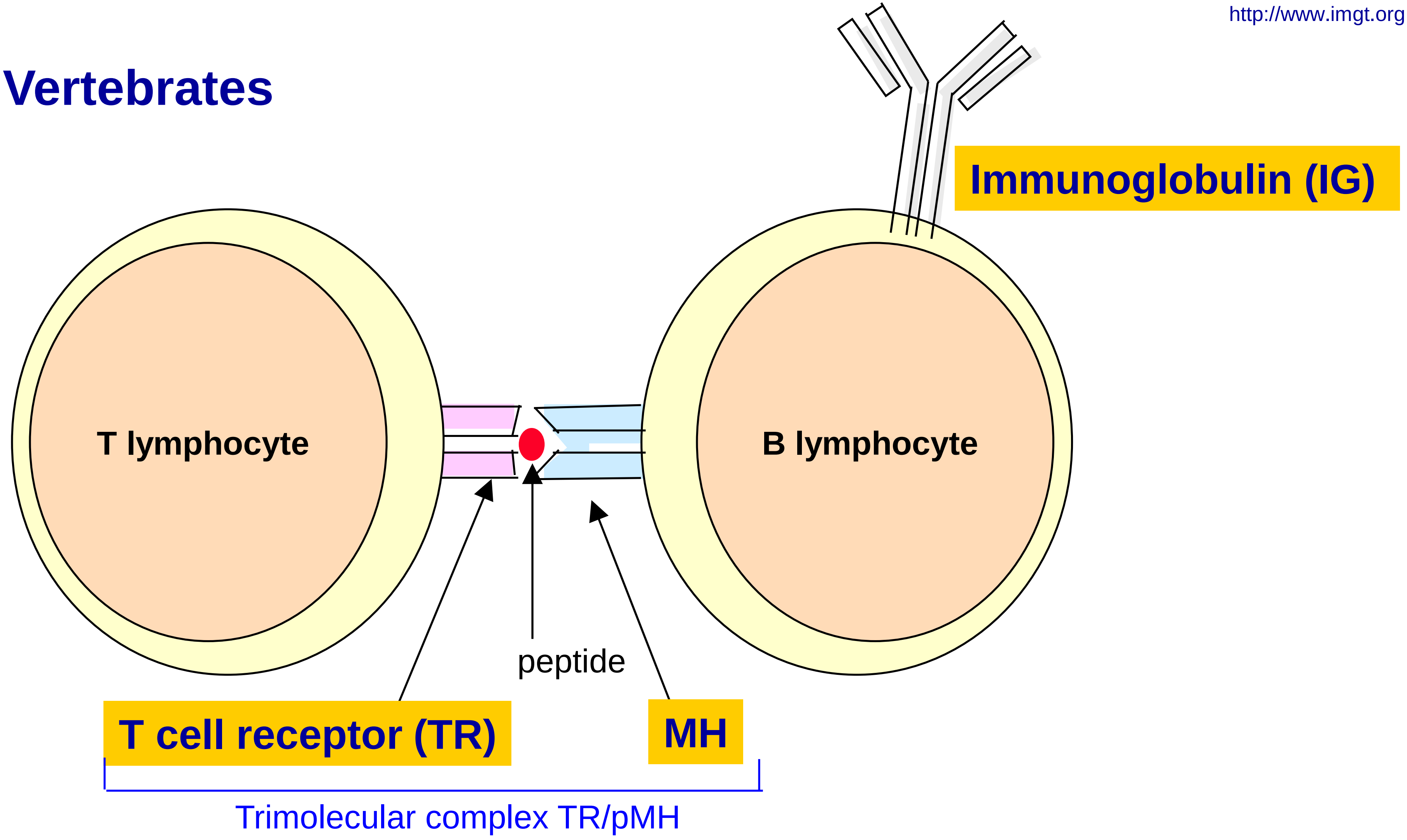
- Immunoglobulins (IG) (or antibodies)
- T cell receptors (TR)
- MH
- IgSF and MhSF

The IMGT® team, Montpellier, France

IMGT®: the adaptive immune response

http://www.imgt.org

Vertebrates



Immunoglobulin (IG)

T lymphocyte

B lymphocyte

peptide

T cell receptor (TR)

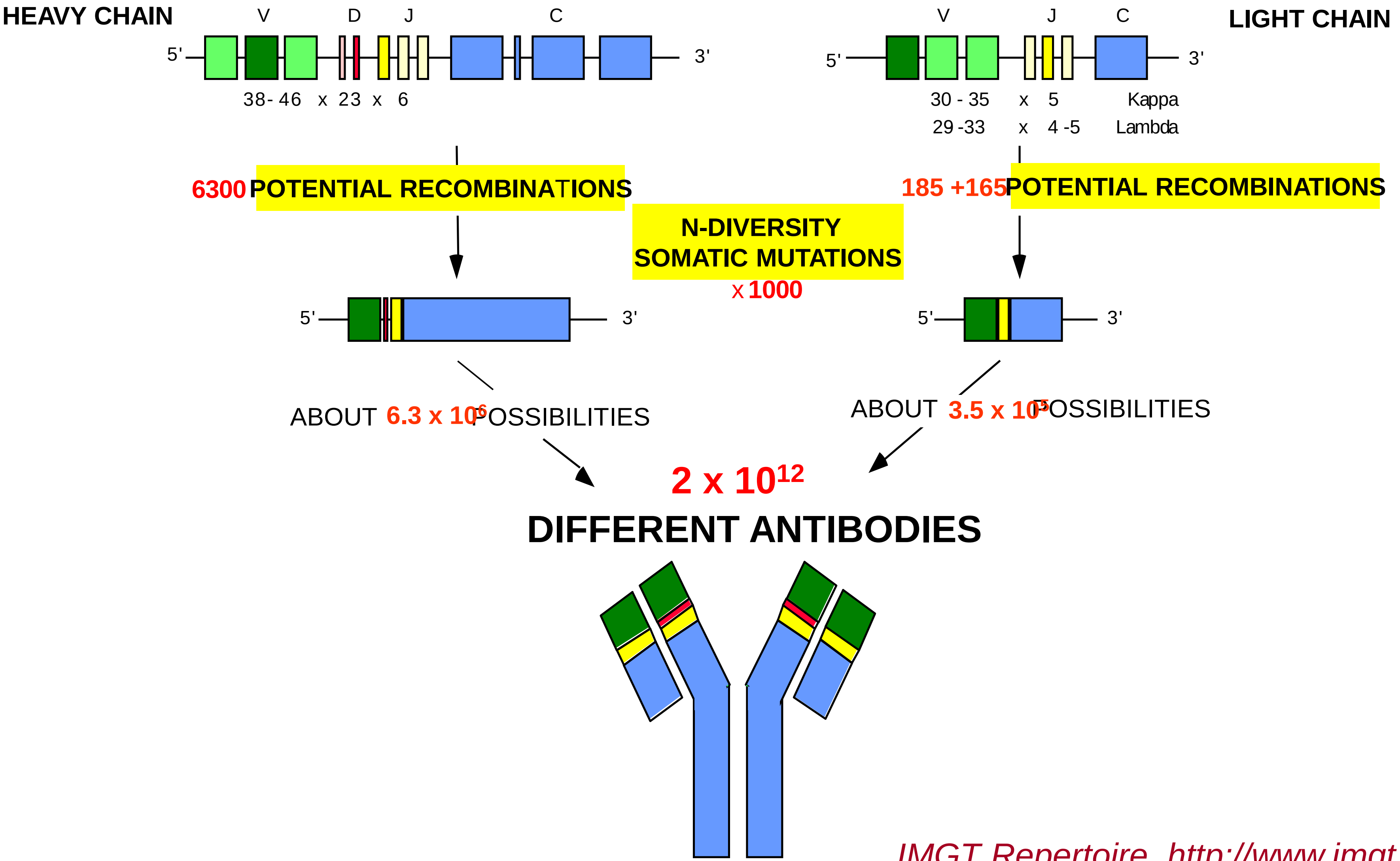
MH

Trimolecular complex TR/pMH

Immunoglobulin (IG) synthesis

http://www.imgt.org

150
FUNCTIONAL IG GENES



6300 POTENTIAL RECOMBINATIONS

185 +165 POTENTIAL RECOMBINATIONS

N-DIVERSITY
SOMATIC MUTATIONS
x 1000

ABOUT **6.3×10^6** POSSIBILITIES

ABOUT **3.5×10^5** POSSIBILITIES

2×10^{12}
DIFFERENT ANTIBODIES

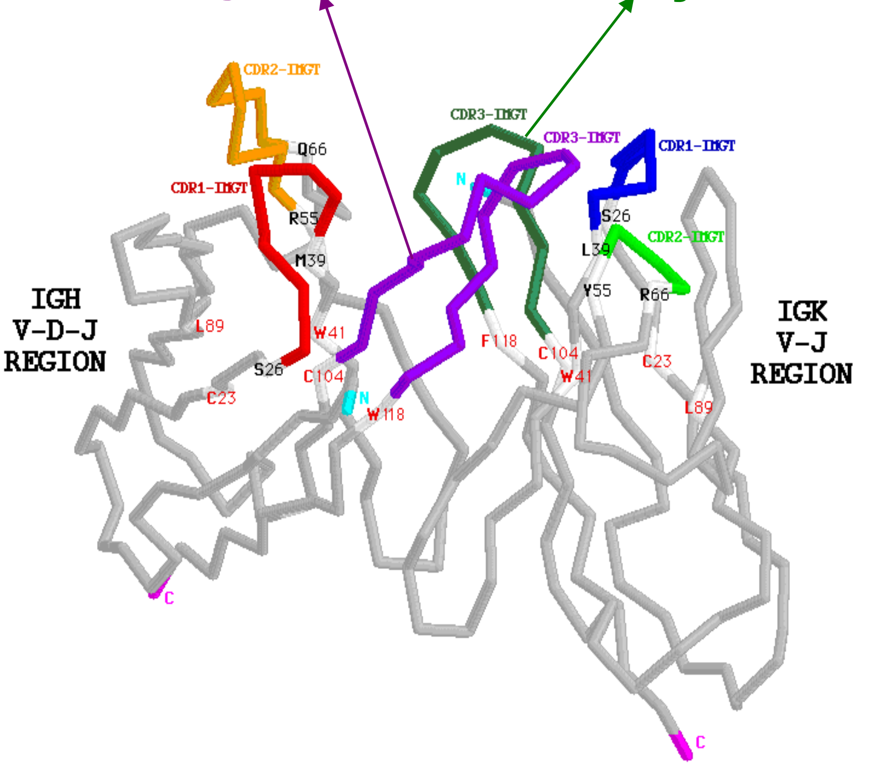
IMGT Repertoire, http://www.imgt.org

V-DOMAIN: VH and V-KAPPA

http://www.imgt.org

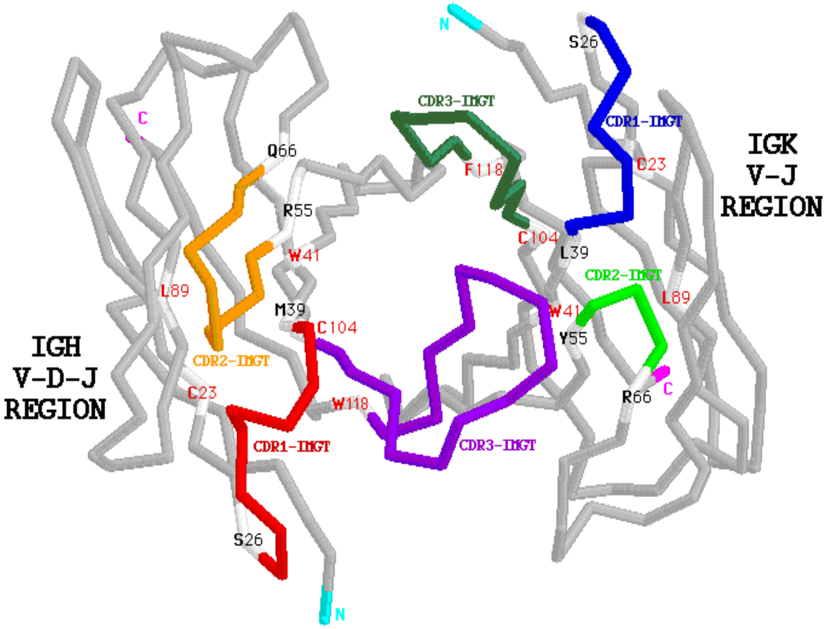
VH **V-KAPPA**

V-D-J junction **V-J junction**



Side view of the V-DOMAIN

VH **V-KAPPA**



View from above the CDR-IMGT

CDR: complementarity determining region
CDR3-IMGT (105-117)
V-D-J junction (104-118), V-J junction (104-118)

IMGT® http://www.imgt.org

Immunoglobulin V-D-J generation of sequence diversity

3’V-REGION N-REGION D-REGION N-REGION 5’J-REGION

tgtgcgaaaga tacc agcatattgtggtggtgactgctattcc gat acaactggttcgactcc**tgg**

JUNCTION

C	**A**	**P**	**Y**	**R**	**G**	**D**	**T**	**Y**	**D**	**Y**	**S**	**W**
tgt	gcg	cca	tac	cgg	ggt	gac	act	tat	gat	tac	**tcc**	**tgg**

IMGT Collier de Perles

Antibody engineering and antibody humanization

http://www.imgt.org

Based on the **IMGT unique numbering** (first one in **1997**)

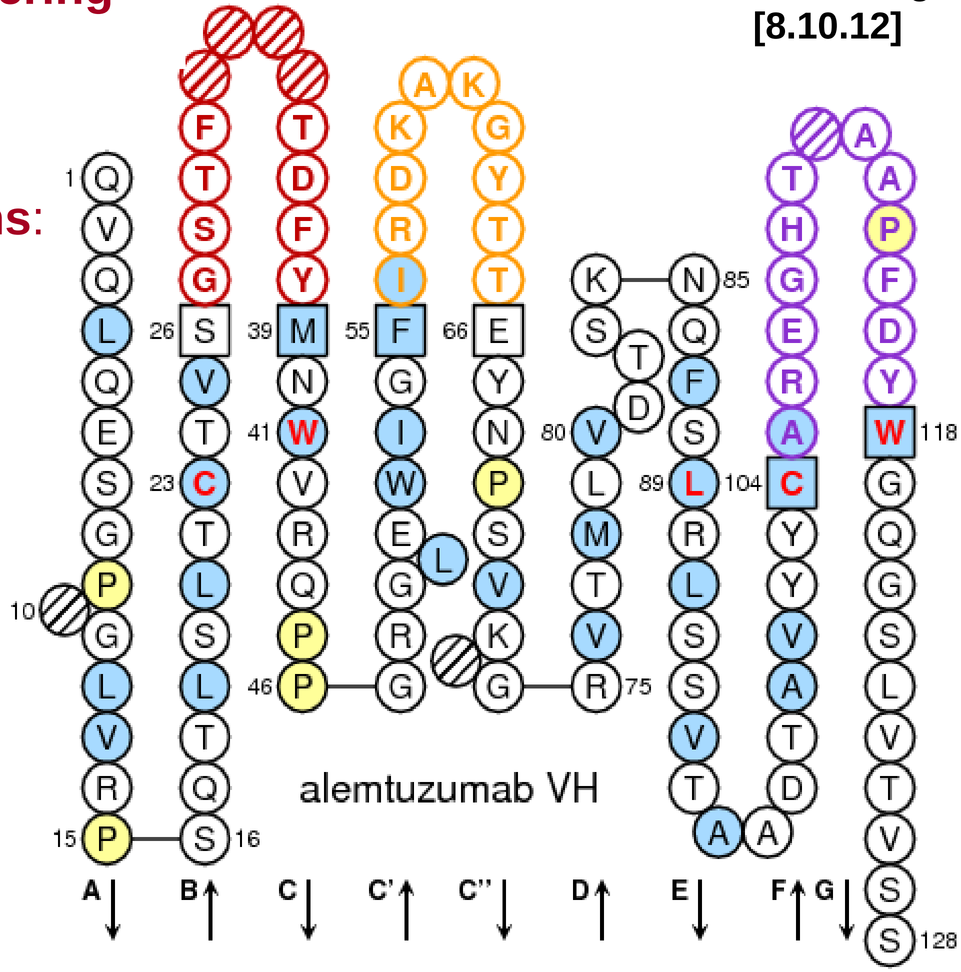
- conserved AA (and codons) are always at the **same positions**:

23	1st-CYS
41	CONSERVED-TRP
89	hydrophobic
104	2nd-CYS
118	J-PHE, J-TRP

- delimitation of the **FR-IMGT** and **CDR-IMGT** is standardized

- **CDR-IMGT lengths** are crucial information

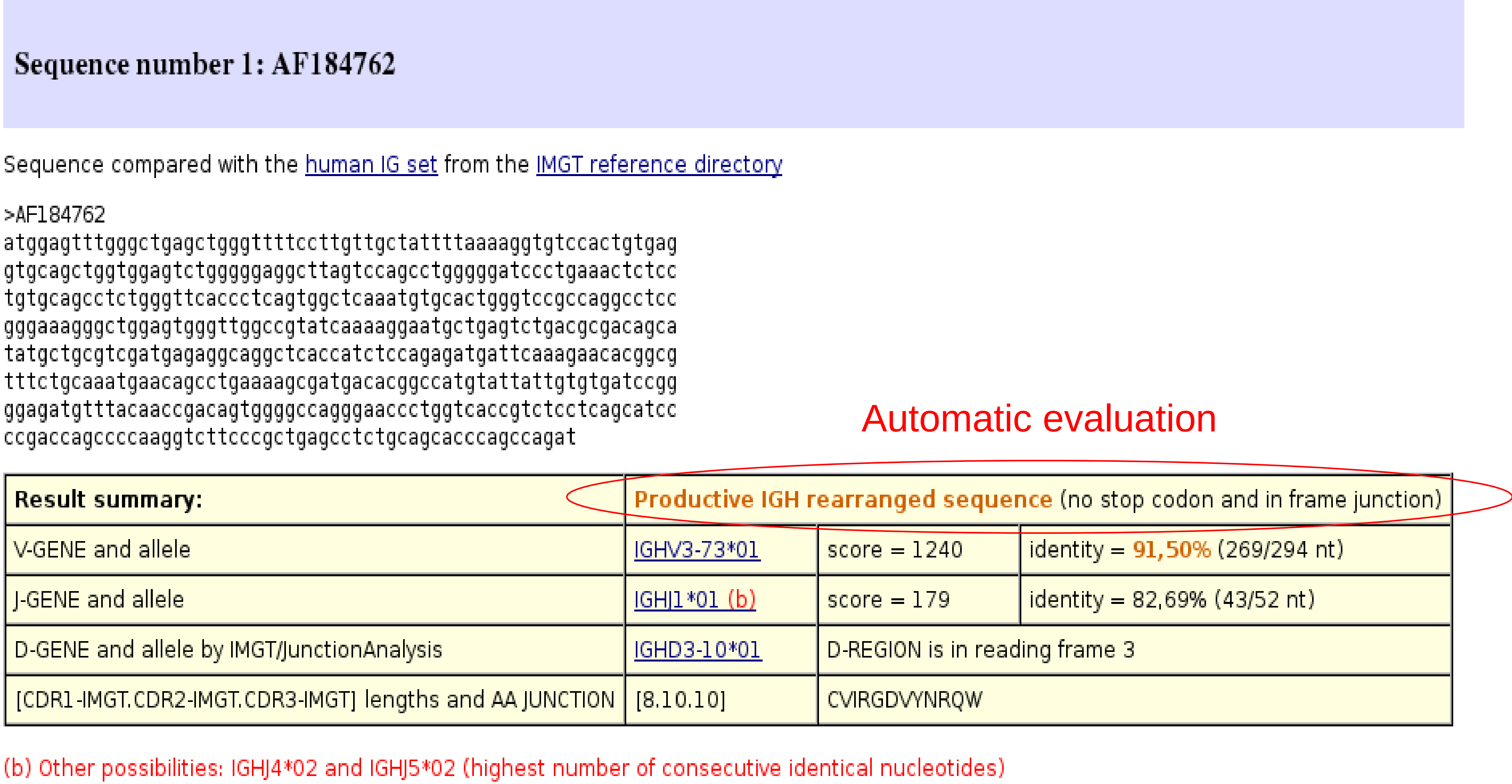
CDR-IMGT lengths [8.10.12]



Lefranc et al. Dev. Comp. Immunol. 27, 55-77 (2003)

IMGT/V-QUEST

Mutation analysis in chronic lymphocytic leukemia (CLL)



Sequence number 1: AF184762

Sequence compared with the human IG set from the IMGT reference directory

```
>AF184762
atggagtttgggctgagctgggttttccttgttgctattttaaaaggtgtccactgtgag
gtgcagctggtggagtctgggggaggcttagtccagcctggggggatccctgaaactctcc
tgtgcagcctctgggttcaccctcagtggctcaaatgtgcactgggtccgccaggcctcc
gggaaagggctggagtgggttggccgtatcaaaaggaatgctgagtctgacgcgacagca
tatgctgcgtcgatgagaggcaggctcaccatctccagagatgattcaaagaacacggcg
tttctgcaaatgaacagcctgaaaagcgatgacacggccatgtattattgtgtgatccgg
ggagatgtttacaaccgacagtggggccagggaaccctggtcaccgtctcctcagcatcc
ccgaccagccccaaggtcttcccgctgagcctctgcagcacccagccagat
```

Automatic evaluation

Result summary:	**Productive IGH rearranged sequence** (no stop codon and in frame junction)		
V-GENE and allele	IGHV3-73*01	score = 1240	identity = **91,50%** (269/294 nt)
J-GENE and allele	IGHJ1*01 (b)	score = 179	identity = 82,69% (43/52 nt)
D-GENE and allele by IMGT/JunctionAnalysis	IGHD3-10*01	D-REGION is in reading frame 3	
[CDR1-IMGT.CDR2-IMGT.CDR3-IMGT] lengths and AA JUNCTION	[8.10.10]	CVIRGDVYNRQW	

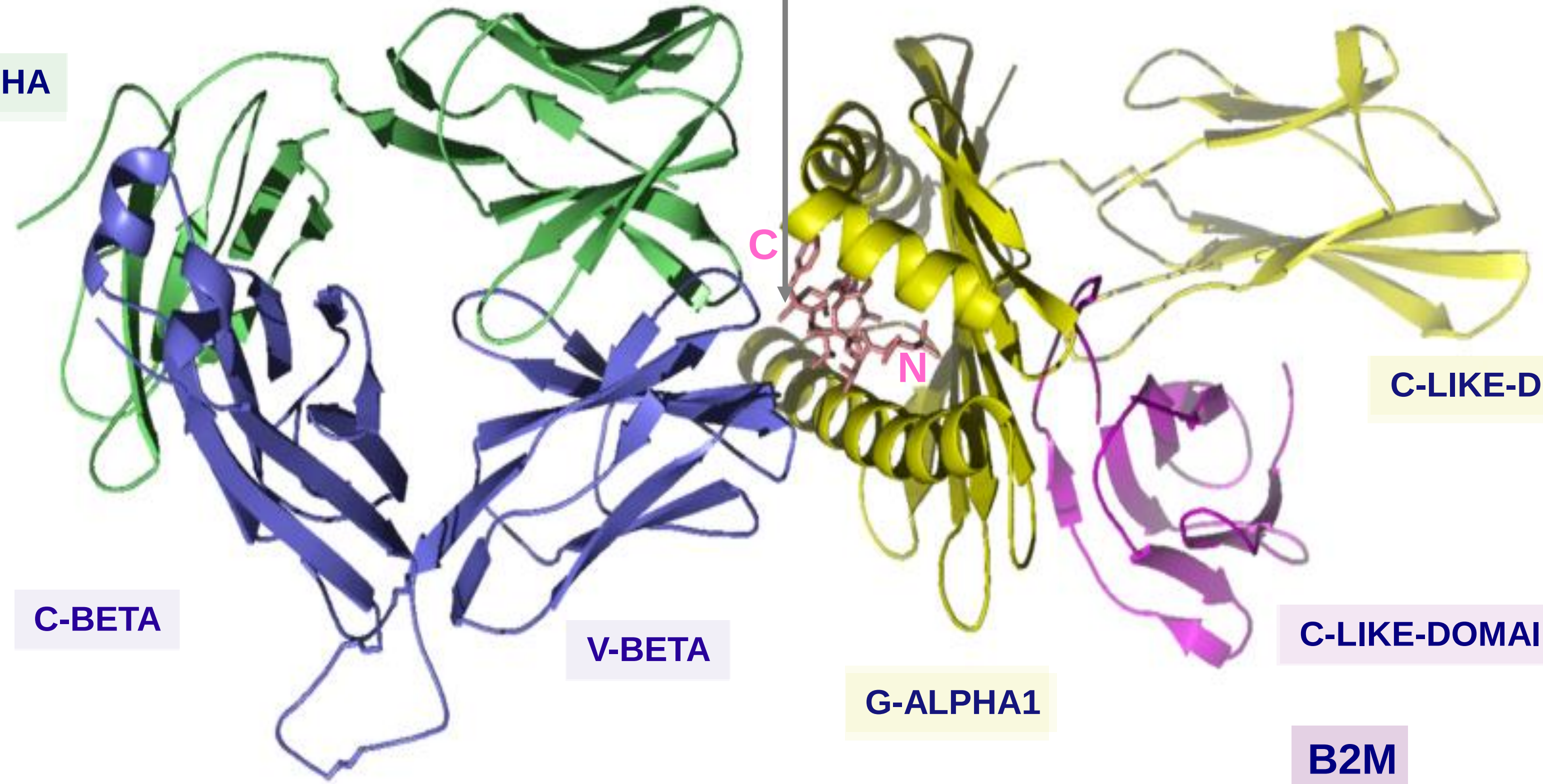
(b) Other possibilities: IGHJ4*02 and IGHJ5*02 (highest number of consecutive identical nucleotides)

IMGT/V-QUEST provides **22 different output results** (analysis of IG nucleotide sequences and of their translation)

TR repertoire analysis

ImMunoGeneTics Information system®
http://www.imgt.org

T cell receptor (TR) Peptide MH1



TR-ALPHA

V-ALPHA

C-ALPHA

C-BETA

V-BETA

TR-BETA

G-ALPHA2

I-ALPHA

C-LIKE-DOMAIN

C-LIKE-DOMAIN

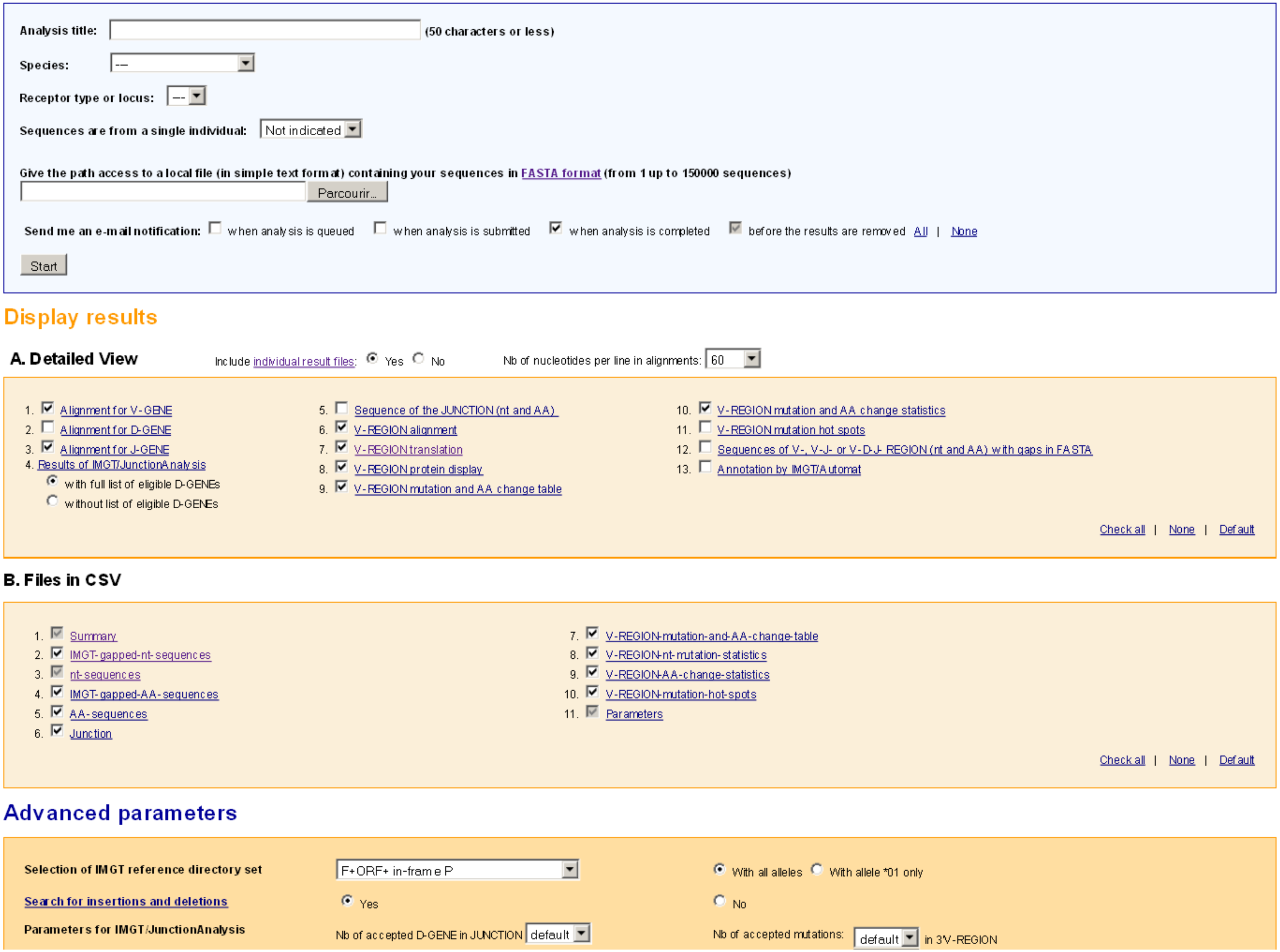
G-ALPHA1

B2M

IMGT/HighV-QUEST submission page

Interface for submission very similar to IMGT/V-QUEST online

http://www.imgt.org



Analysis title: (50 characters or less)

Species: ---

Receptor type or locus: ---

Sequences are from a single individual: Not indicated

Give the path access to a local file (in simple text format) containing your sequences in FASTA format (from 1 up to 150000 sequences)

Send me an e-mail notification: ☐ when analysis is queued ☐ when analysis is submitted ☑ when analysis is completed ☑ before the results are removed All | None

Display results

A. Detailed View

Include individual result files: ● Yes ○ No

Nb of nucleotides per line in alignments: 60

1. ☑ Alignment for V-GENE
2. ☐ Alignment for D-GENE
3. ☑ Alignment for J-GENE
4. Results of IMGT/JunctionAnalysis
   - ● with full list of eligible D-GENEs
   - ○ without list of eligible D-GENEs
5. ☐ Sequence of the JUNCTION (nt and AA)
6. ☑ V-REGION alignment
7. ☑ V-REGION translation
8. ☑ V-REGION protein display
9. ☑ V-REGION mutation and AA change table
10. ☑ V-REGION mutation and AA change statistics
11. ☐ V-REGION mutation hot spots
12. ☐ Sequences of V-, V-J- or V-D-J- REGION (nt and AA) with gaps in FASTA
13. ☐ Annotation by IMGT/Automat

Check all | None | Default

B. Files in CSV

1. ☑ Summary
2. ☑ IMGT-gapped-nt-sequences
3. ☑ nt-sequences
4. ☑ IMGT-gapped-AA-sequences
5. ☑ AA-sequences
6. ☑ Junction
7. ☑ V-REGION-mutation-and-AA-change-table
8. ☑ V-REGION-nt-mutation-statistics
9. ☑ V-REGION-AA-change-statistics
10. ☑ V-REGION-mutation-hot-spots
11. ☑ Parameters

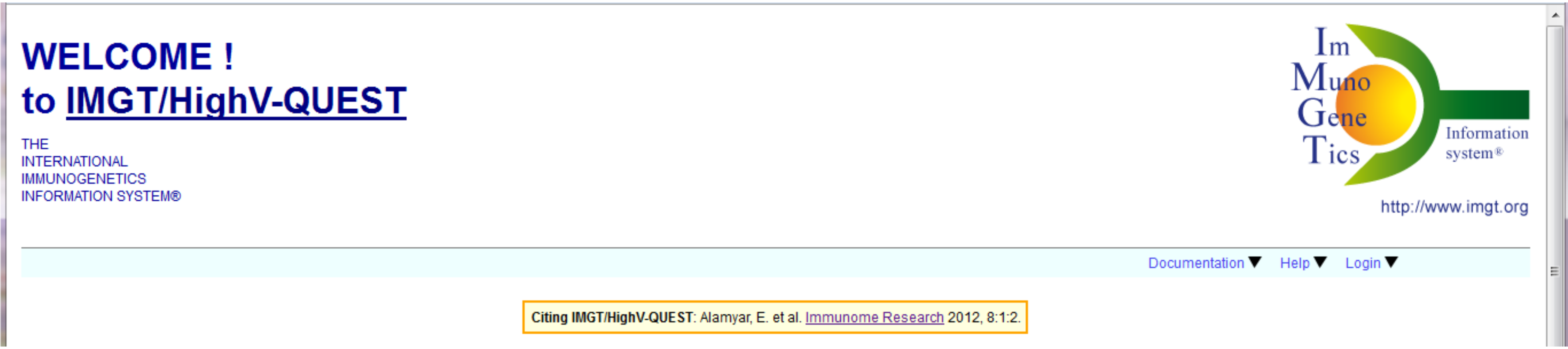
Check all | None | Default

Advanced parameters

Selection of IMGT reference directory set F+ORF+ in-frame P ● With all alleles ○ With allele *01 only

Search for insertions and deletions ● Yes ○ No

Parameters for IMGT/JunctionAnalysis Nb of accepted D-GENE in JUNCTION default Nb of accepted mutations: default in 3'V-REGION

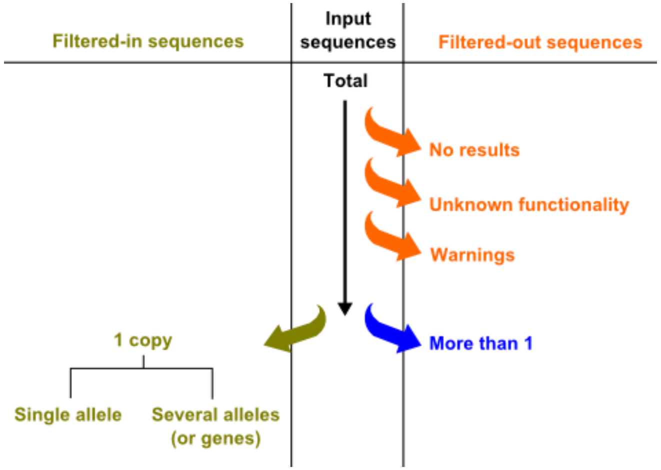


WELCOME !
to IMGT/HighV-QUEST

THE
INTERNATIONAL
IMMUNOGENETICS
INFORMATION SYSTEM®

Citing IMGT/HighV-QUEST: Alamyar, E. et al. Immunome Research 2012, 8:1:2.

- Analysis of IG and TR sequences from high throughput sequencing (HTS)
- Submission of 150.000 HTS sequences (from 454) per job
- Output: text for Excel (same results as IMGT/V-QUEST online).
- Statistical analysis on 450.000 sequences (‘1 copy’, ‘Single allele’)



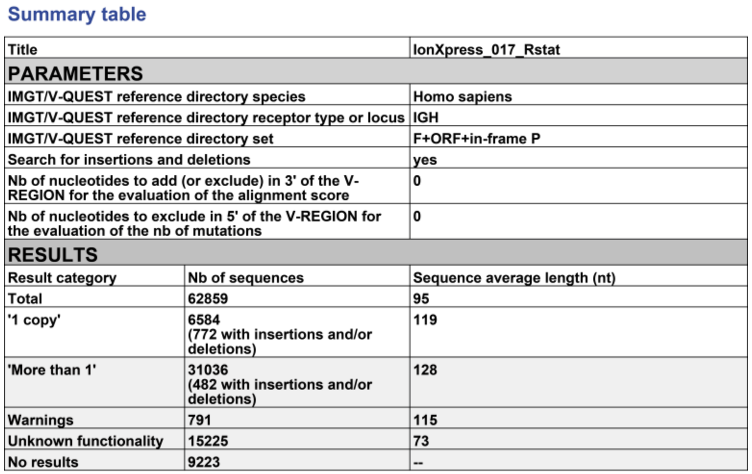
1_IMGT_report__MPL_IGH_180511_20110803__all.pdf
2_IMGT_report__MPL_IGH_180511_20110803__summary.pdf
3_IMGT_report__MPL_IGH_180511_20110803__1copy_single-allele.pdf
4_IMGT_report__MPL_IGH_180511_20110803__1copy_several-alleles.pdf
5_IMGT_report__MPL_IGH_180511_20110803__CDR3-IMGT.pdf
6_IMGT_report__MPL_IGH_180511_20110803__filtered-out_sequences.pdf
MPL_IGH_180511_20110803_IGHD_Homsap_positions_1.png
MPL_IGH_180511_20110803_IGHJ_Homsap_positions_1.png
MPL_IGH_180511_20110803_IGHV-J-CDR3-IMGT_1copy_several-alleles.png
MPL_IGH_180511_20110803_IGHV-J_CDR3-IMGT_1copy_single-allele.png
MPL_IGH_180511_20110803_IGHV-J_CDR3-IMGT_1copy_single-and-several-alleles.png
MPL_IGH_180511_20110803_IGHV_Homsap_positions_1.png
MPL_IGH_180511_20110803_IGHV_Homsap_unmapped.png
MPL_IGH_180511_20110803_IGH_1copy_several-alleles.png
MPL_IGH_180511_20110803_IGH_1copy_single-allele.png

Alamyar et al. Immunome Res. (2012)

IMGT/HighV-QUEST

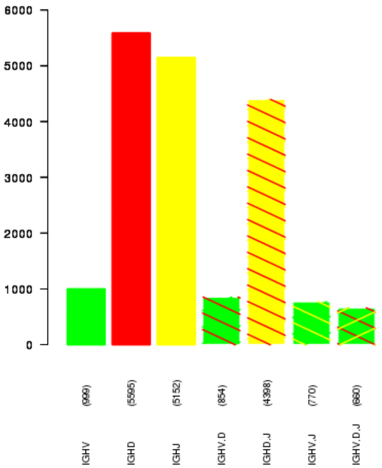
http://www.imgt.org

Example of experiment from Ion torrent

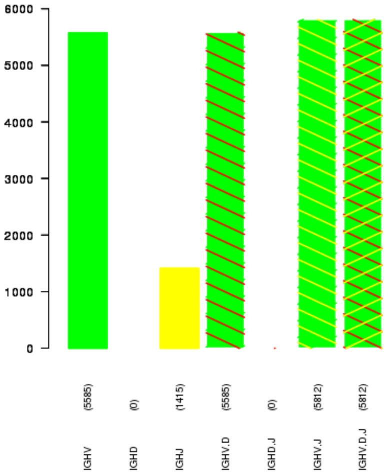


Summary table

Title	IonXpress_017_Rstat	
PARAMETERS		
IMGT/V-QUEST reference directory species	Homo sapiens	
IMGT/V-QUEST reference directory receptor type or locus	IGH	
IMGT/V-QUEST reference directory set	F+ORF+in-frame P	
Search for insertions and deletions	yes	
Nb of nucleotides to add (or exclude) in 3' of the V-REGION for the evaluation of the alignment score	0	
Nb of nucleotides to exclude in 5' of the V-REGION for the evaluation of the nb of mutations	0	
RESULTS		
Result category	Nb of sequences	Sequence average length (nt)
Total	62859	95
'1 copy'	6584 (772 with insertions and/or deletions)	119
'More than 1'	31036 (482 with insertions and/or deletions)	128
Warnings	791	115
Unknown functionality	15225	73
No results	9223	--

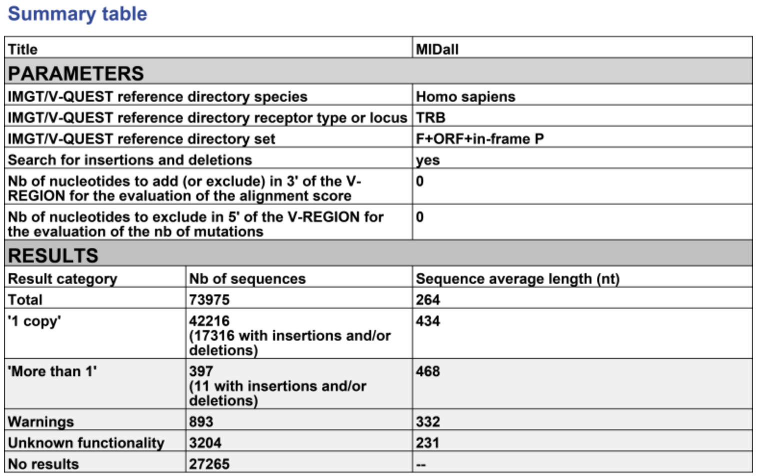


Sequences: '1 copy' with 'single allele' for IGH



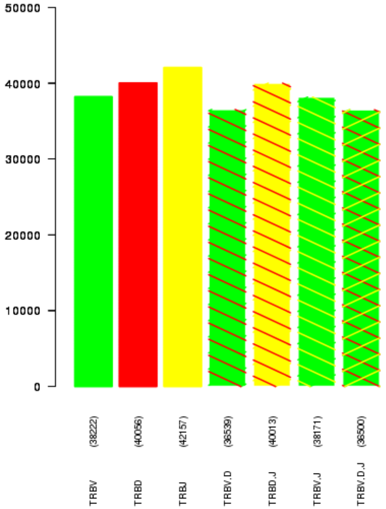
Sequences: '1 copy' with 'several alleles (or genes)' for IGH

Example of experiment from 454

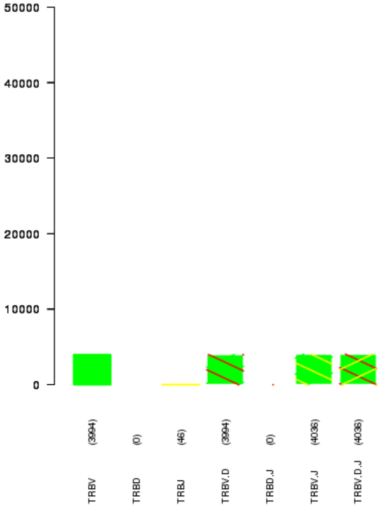


Summary table

Title	MIDall	
PARAMETERS		
IMGT/V-QUEST reference directory species	Homo sapiens	
IMGT/V-QUEST reference directory receptor type or locus	TRB	
IMGT/V-QUEST reference directory set	F+ORF+in-frame P	
Search for insertions and deletions	yes	
Nb of nucleotides to add (or exclude) in 3' of the V-REGION for the evaluation of the alignment score	0	
Nb of nucleotides to exclude in 5' of the V-REGION for the evaluation of the nb of mutations	0	
RESULTS		
Result category	Nb of sequences	Sequence average length (nt)
Total	73975	264
'1 copy'	42216 (17316 with insertions and/or deletions)	434
'More than 1'	397 (11 with insertions and/or deletions)	468
Warnings	893	332
Unknown functionality	3204	231
No results	27265	--



Sequences: '1 copy' with 'single allele' for TRB



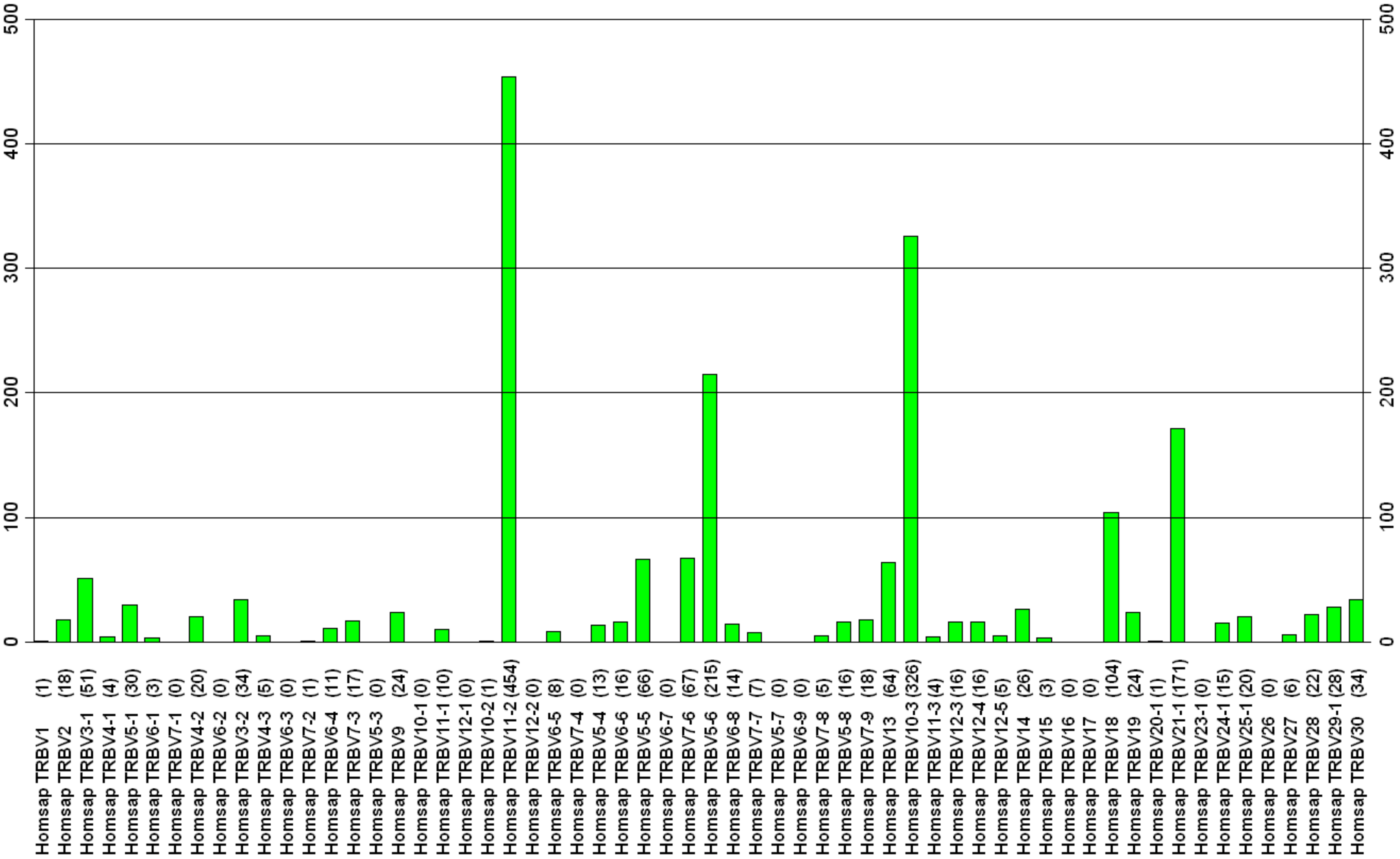
Sequences: '1 copy' with 'several alleles (or genes)' for TRB

Alamyar et al. Immunome Res. (2012)

IMGT/HighV-QUEST

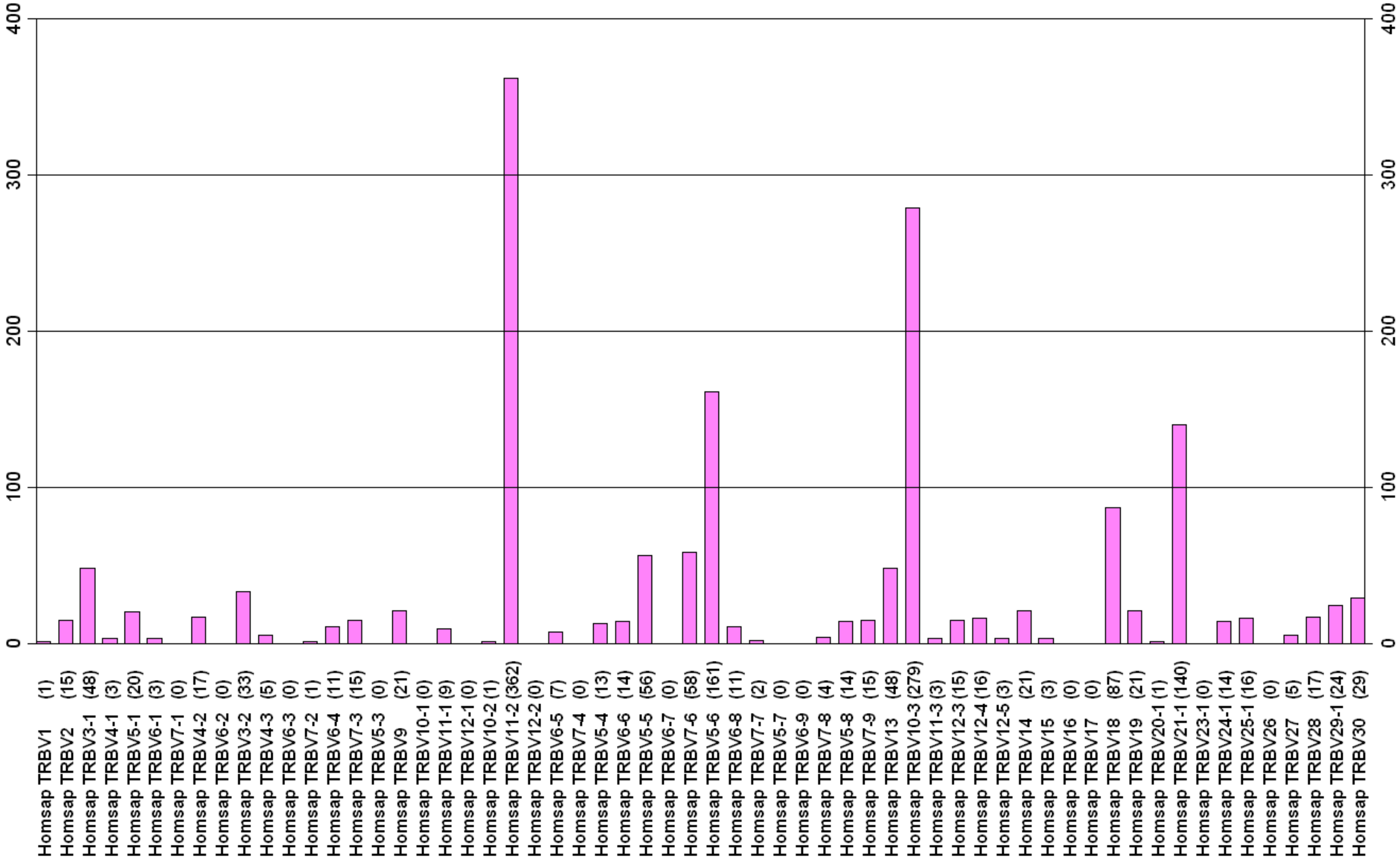
Nb of sequences per TRBV gene: expressed repertoire

‘1 copy’ + ‘More than 1’ (in-frame) C104, F118

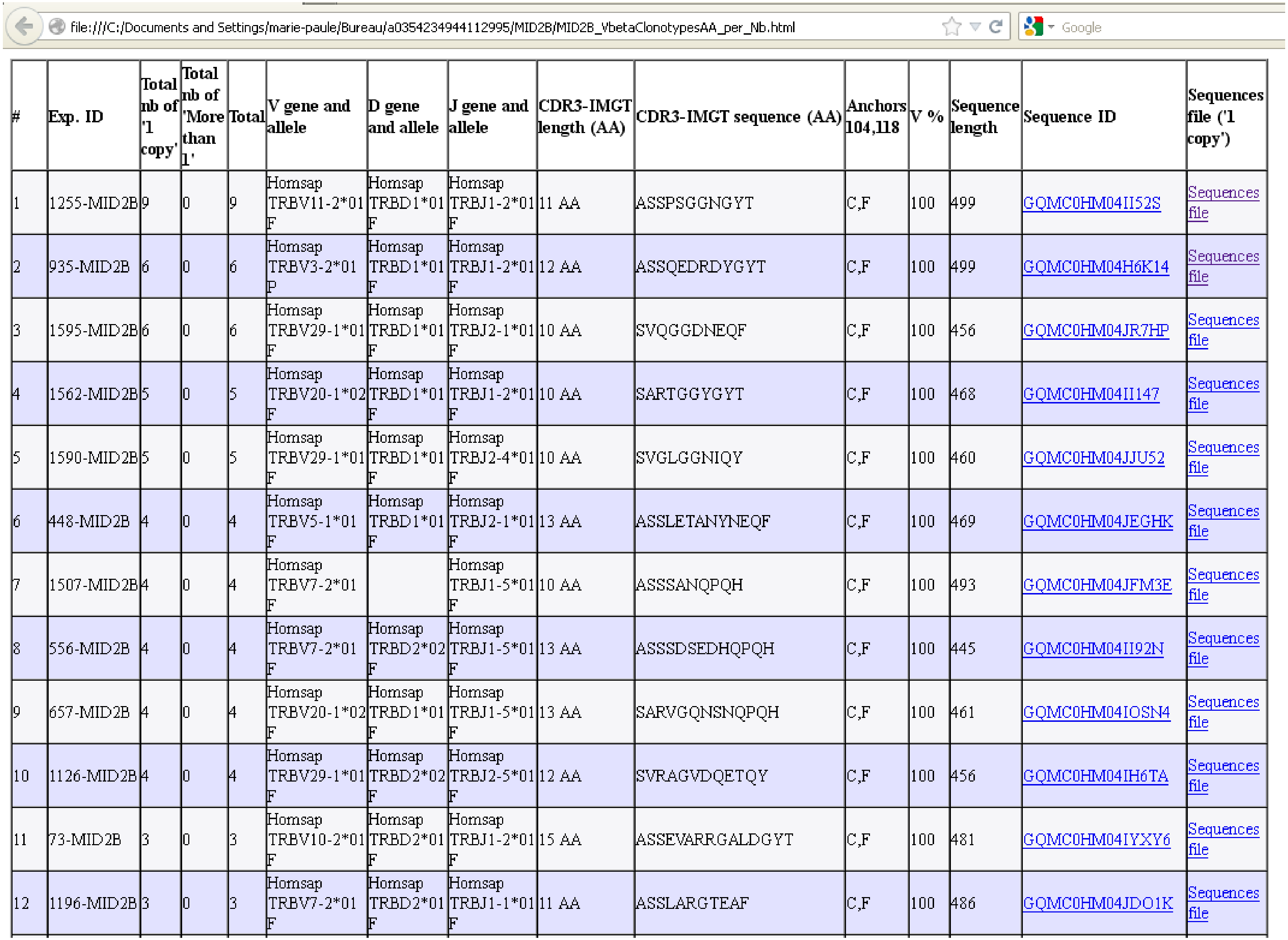


IMGT/HighV-QUEST

Nb of different clonotypes per TRBV gene



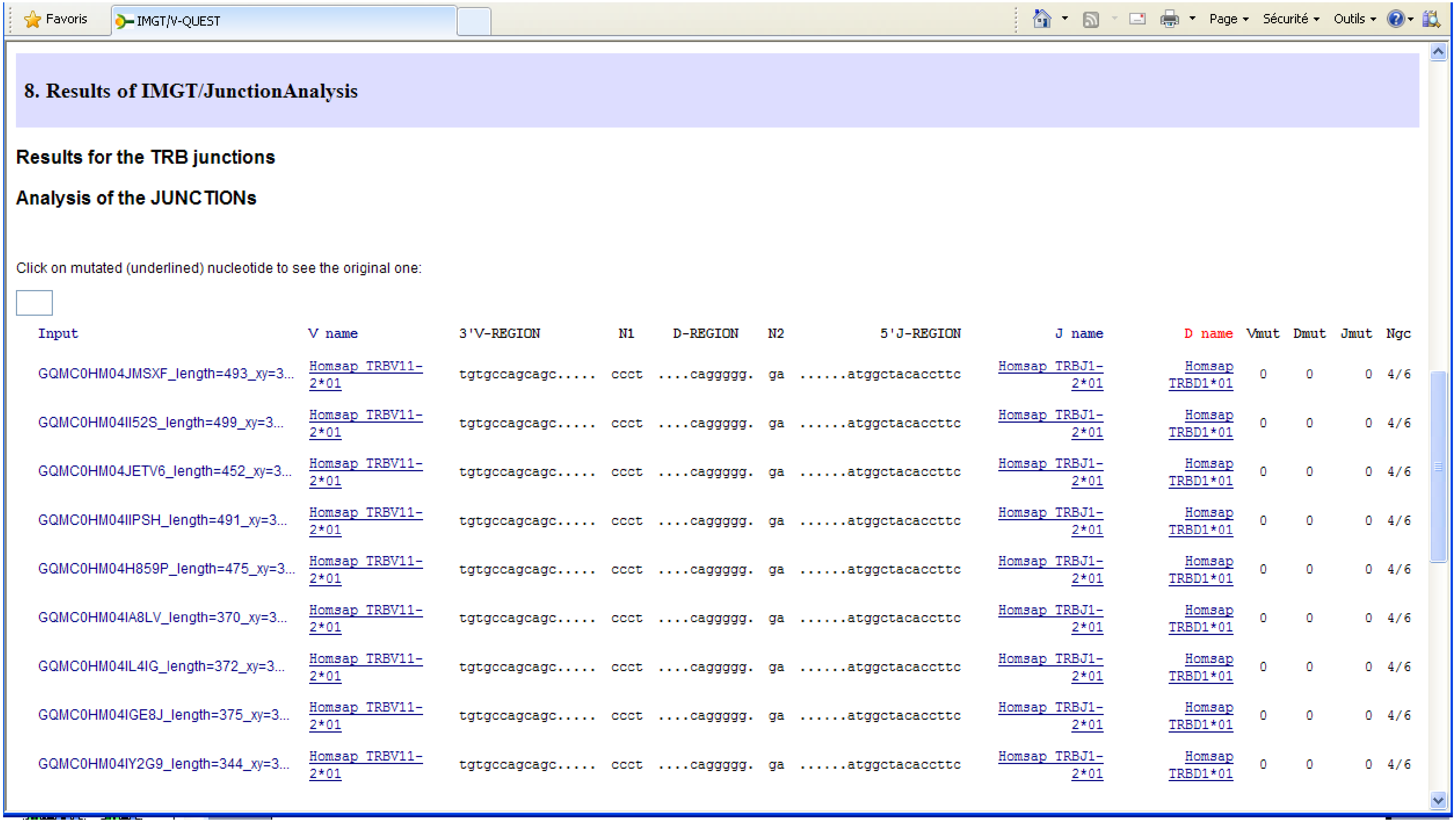
V-beta clonotypes (AA)



file:///C:/Documents and Settings/marie-paule/Bureau/a0354234944112995/MID2B/MID2B_VbetaClonotypesAA_per_Nb.html

#	Exp. ID	Total nb of '1 copy'	Total nb of 'More than 1'	Total	V gene and allele	D gene and allele	J gene and allele	CDR3-IMGT length (AA)	CDR3-IMGT sequence (AA)	Anchors 104,118	V %	Sequence length	Sequence ID	Sequences file ('1 copy')
1	1255-MID2B	9	0	9	Homsap TRBV11-2*01 F	Homsap TRBD1*01 F	Homsap TRBJ1-2*01 F	11 AA	ASSPSGGNGYT	C,F	100	499	GQMC0HM04II52S	Sequences file
2	935-MID2B	6	0	6	Homsap TRBV3-2*01 P	Homsap TRBD1*01 F	Homsap TRBJ1-2*01 F	12 AA	ASSQEDRDYGYT	C,F	100	499	GQMC0HM04H6K14	Sequences file
3	1595-MID2B	6	0	6	Homsap TRBV29-1*01 F	Homsap TRBD1*01 F	Homsap TRBJ2-1*01 F	10 AA	SVQGGDNEQF	C,F	100	456	GQMC0HM04JR7HP	Sequences file
4	1562-MID2B	5	0	5	Homsap TRBV20-1*02 F	Homsap TRBD1*01 F	Homsap TRBJ1-2*01 F	10 AA	SARTGGYGYT	C,F	100	468	GQMC0HM04II147	Sequences file
5	1590-MID2B	5	0	5	Homsap TRBV29-1*01 F	Homsap TRBD1*01 F	Homsap TRBJ2-4*01 F	10 AA	SVGLGGNIQY	C,F	100	460	GQMC0HM04JJU52	Sequences file
6	448-MID2B	4	0	4	Homsap TRBV5-1*01 F	Homsap TRBD1*01 F	Homsap TRBJ2-1*01 F	13 AA	ASSLETANYNEQF	C,F	100	469	GQMC0HM04JEGHK	Sequences file
7	1507-MID2B	4	0	4	Homsap TRBV7-2*01 F		Homsap TRBJ1-5*01 F	10 AA	ASSSANQPQH	C,F	100	493	GQMC0HM04JFM3E	Sequences file
8	556-MID2B	4	0	4	Homsap TRBV7-2*01 F	Homsap TRBD2*02 F	Homsap TRBJ1-5*01 F	13 AA	ASSSDSEDHQPQH	C,F	100	445	GQMC0HM04II92N	Sequences file
9	657-MID2B	4	0	4	Homsap TRBV20-1*02 F	Homsap TRBD1*01 F	Homsap TRBJ1-5*01 F	13 AA	SARVGQNSNQPQH	C,F	100	461	GQMC0HM04IOSN4	Sequences file
10	1126-MID2B	4	0	4	Homsap TRBV29-1*01 F	Homsap TRBD2*02 F	Homsap TRBJ2-5*01 F	12 AA	SVRAGVDQETQY	C,F	100	456	GQMC0HM04IH6TA	Sequences file
11	73-MID2B	3	0	3	Homsap TRBV10-2*01 F	Homsap TRBD2*01 F	Homsap TRBJ1-2*01 F	15 AA	ASSEVARRGALDGYT	C,F	100	481	GQMC0HM04IYXY6	Sequences file
12	1196-MID2B	3	0	3	Homsap TRBV7-2*01 F	Homsap TRBD2*01 F	Homsap TRBJ1-1*01 F	11 AA	ASSLARGTEAF	C,F	100	486	GQMC0HM04JDO1K	Sequences file

IMGT/JunctionAnalysis



8. Results of IMGT/JunctionAnalysis

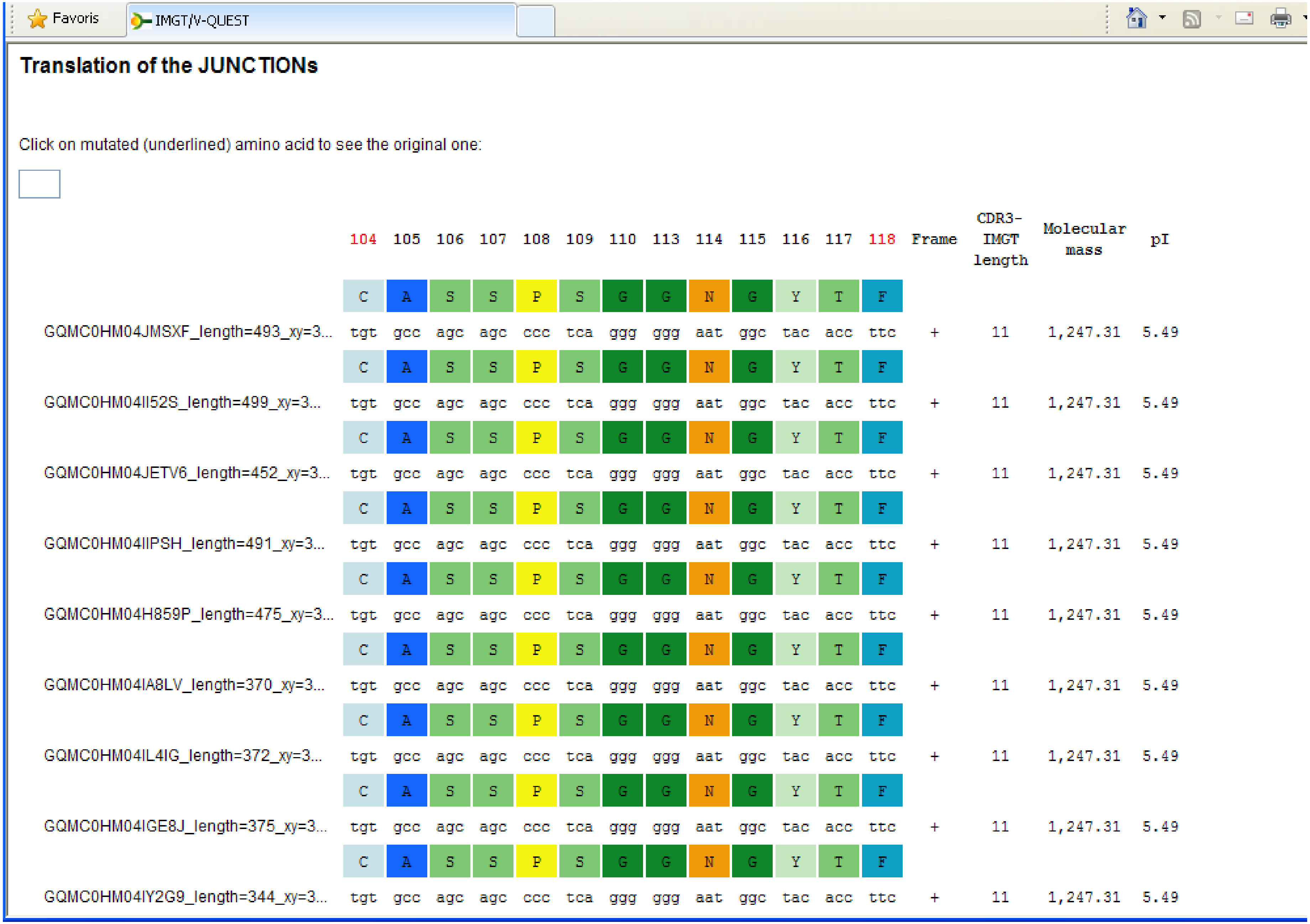
Results for the TRB junctions

Analysis of the JUNCTIONs

Click on mutated (underlined) nucleotide to see the original one:

Input	V name	3'V-REGION	N1	D-REGION	N2	5'J-REGION	J name	D name	Vmut	Dmut	Jmut	Ngc
GQMC0HM04JMSXF_length=493_xy=3...	Homsap TRBV11-2*01	tgtgccagcagc.....	ccct	....caggggg.	ga	......atggctacaccttc	Homsap TRBJ1-2*01	Homsap TRBD1*01	0	0	0	4/6
GQMC0HM04II52S_length=499_xy=3...	Homsap TRBV11-2*01	tgtgccagcagc.....	ccct	....caggggg.	ga	......atggctacaccttc	Homsap TRBJ1-2*01	Homsap TRBD1*01	0	0	0	4/6
GQMC0HM04JETV6_length=452_xy=3...	Homsap TRBV11-2*01	tgtgccagcagc.....	ccct	....caggggg.	ga	......atggctacaccttc	Homsap TRBJ1-2*01	Homsap TRBD1*01	0	0	0	4/6
GQMC0HM04IIPSH_length=491_xy=3...	Homsap TRBV11-2*01	tgtgccagcagc.....	ccct	....caggggg.	ga	......atggctacaccttc	Homsap TRBJ1-2*01	Homsap TRBD1*01	0	0	0	4/6
GQMC0HM04H859P_length=475_xy=3...	Homsap TRBV11-2*01	tgtgccagcagc.....	ccct	....caggggg.	ga	......atggctacaccttc	Homsap TRBJ1-2*01	Homsap TRBD1*01	0	0	0	4/6
GQMC0HM04IA8LV_length=370_xy=3...	Homsap TRBV11-2*01	tgtgccagcagc.....	ccct	....caggggg.	ga	......atggctacaccttc	Homsap TRBJ1-2*01	Homsap TRBD1*01	0	0	0	4/6
GQMC0HM04IL4IG_length=372_xy=3...	Homsap TRBV11-2*01	tgtgccagcagc.....	ccct	....caggggg.	ga	......atggctacaccttc	Homsap TRBJ1-2*01	Homsap TRBD1*01	0	0	0	4/6
GQMC0HM04IGE8J_length=375_xy=3...	Homsap TRBV11-2*01	tgtgccagcagc.....	ccct	....caggggg.	ga	......atggctacaccttc	Homsap TRBJ1-2*01	Homsap TRBD1*01	0	0	0	4/6
GQMC0HM04IY2G9_length=344_xy=3...	Homsap TRBV11-2*01	tgtgccagcagc.....	ccct	....caggggg.	ga	......atggctacaccttc	Homsap TRBJ1-2*01	Homsap TRBD1*01	0	0	0	4/6

IMGT/JunctionAnalysis



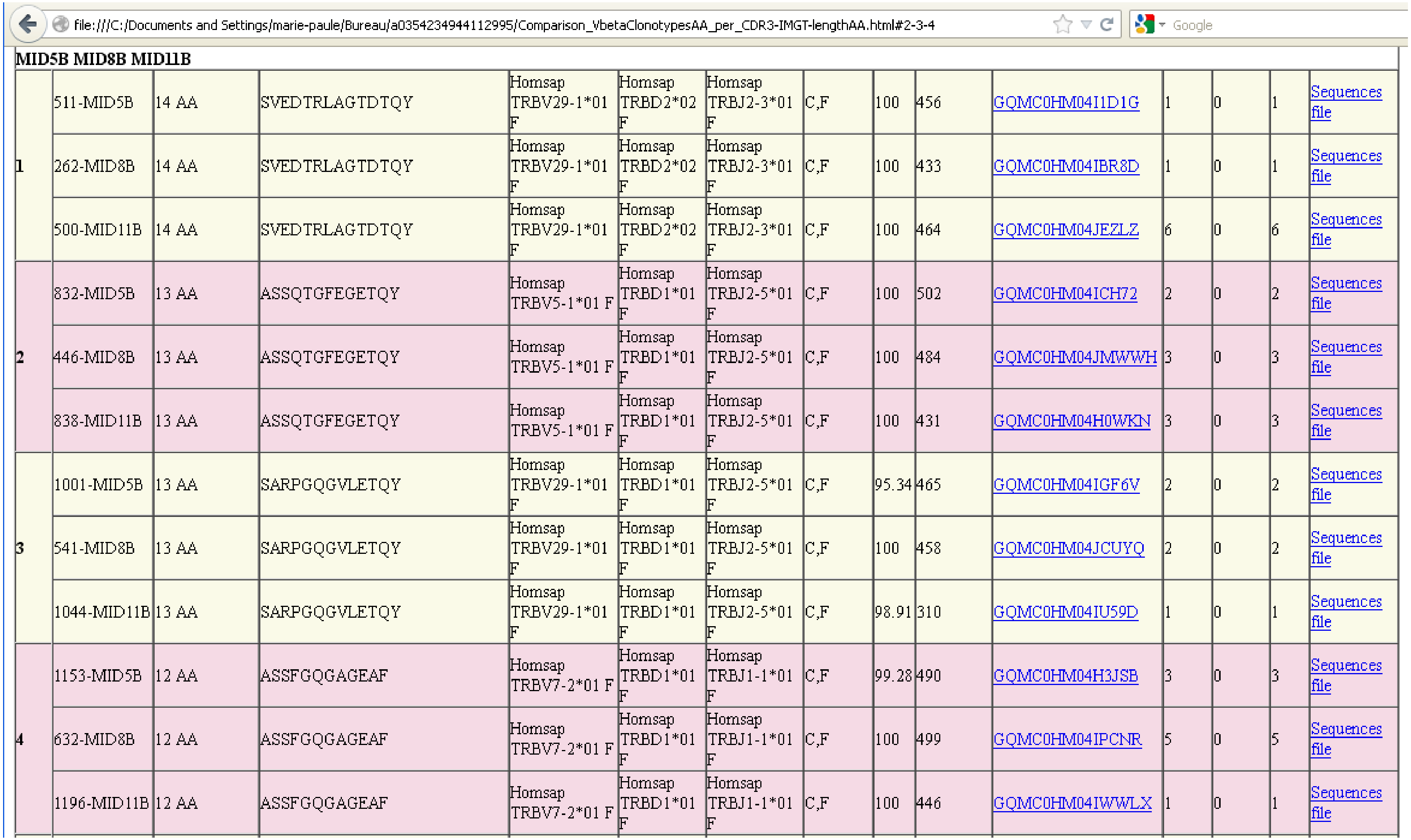
Translation of the JUNCTIONs

Click on mutated (underlined) amino acid to see the original one:

	104	105	106	107	108	109	110	113	114	115	116	117	118	Frame	CDR3-IMGT length	Molecular mass	pI
	C	A	S	S	P	S	G	G	N	G	Y	T	F				
GQMC0HM04JMSXF_length=493_xy=3...	tgt	gcc	agc	agc	ccc	tca	ggg	ggg	aat	ggc	tac	acc	ttc	+	11	1,247.31	5.49
	C	A	S	S	P	S	G	G	N	G	Y	T	F				
GQMC0HM04II52S_length=499_xy=3...	tgt	gcc	agc	agc	ccc	tca	ggg	ggg	aat	ggc	tac	acc	ttc	+	11	1,247.31	5.49
	C	A	S	S	P	S	G	G	N	G	Y	T	F				
GQMC0HM04JETV6_length=452_xy=3...	tgt	gcc	agc	agc	ccc	tca	ggg	ggg	aat	ggc	tac	acc	ttc	+	11	1,247.31	5.49
	C	A	S	S	P	S	G	G	N	G	Y	T	F				
GQMC0HM04IIPSH_length=491_xy=3...	tgt	gcc	agc	agc	ccc	tca	ggg	ggg	aat	ggc	tac	acc	ttc	+	11	1,247.31	5.49
	C	A	S	S	P	S	G	G	N	G	Y	T	F				
GQMC0HM04H859P_length=475_xy=3...	tgt	gcc	agc	agc	ccc	tca	ggg	ggg	aat	ggc	tac	acc	ttc	+	11	1,247.31	5.49
	C	A	S	S	P	S	G	G	N	G	Y	T	F				
GQMC0HM04IA8LV_length=370_xy=3...	tgt	gcc	agc	agc	ccc	tca	ggg	ggg	aat	ggc	tac	acc	ttc	+	11	1,247.31	5.49
	C	A	S	S	P	S	G	G	N	G	Y	T	F				
GQMC0HM04IL4IG_length=372_xy=3...	tgt	gcc	agc	agc	ccc	tca	ggg	ggg	aat	ggc	tac	acc	ttc	+	11	1,247.31	5.49
	C	A	S	S	P	S	G	G	N	G	Y	T	F				
GQMC0HM04IGE8J_length=375_xy=3...	tgt	gcc	agc	agc	ccc	tca	ggg	ggg	aat	ggc	tac	acc	ttc	+	11	1,247.31	5.49
	C	A	S	S	P	S	G	G	N	G	Y	T	F				
GQMC0HM04IY2G9_length=344_xy=3...	tgt	gcc	agc	agc	ccc	tca	ggg	ggg	aat	ggc	tac	acc	ttc	+	11	1,247.31	5.49

Comparison between 4 sets: pre- and post-vaccination H1N1

V beta clonotypes (AA) only present post-vaccination



file:///C:/Documents and Settings/marie-paule/Bureau/a0354234944112995/Comparison_VbetaClonotypesAA_per_CDR3-IMGT-lengthAA.html#2-3-4

MID5B MID8B MID11B

1	511-MID5B	14 AA	SVEDTRLAGTDTQY	Homsap TRBV29-1*01 F	Homsap TRBD2*02 F	Homsap TRBJ2-3*01 F	C,F	100	456	GQMC0HM04I1D1G	1	0	1	Sequences file
	262-MID8B	14 AA	SVEDTRLAGTDTQY	Homsap TRBV29-1*01 F	Homsap TRBD2*02 F	Homsap TRBJ2-3*01 F	C,F	100	433	GQMC0HM04IBR8D	1	0	1	Sequences file
	500-MID11B	14 AA	SVEDTRLAGTDTQY	Homsap TRBV29-1*01 F	Homsap TRBD2*02 F	Homsap TRBJ2-3*01 F	C,F	100	464	GQMC0HM04JEZLZ	6	0	6	Sequences file
2	832-MID5B	13 AA	ASSQTGFEGETQY	Homsap TRBV5-1*01 F	Homsap TRBD1*01 F	Homsap TRBJ2-5*01 F	C,F	100	502	GQMC0HM04ICH72	2	0	2	Sequences file
	446-MID8B	13 AA	ASSQTGFEGETQY	Homsap TRBV5-1*01 F	Homsap TRBD1*01 F	Homsap TRBJ2-5*01 F	C,F	100	484	GQMC0HM04JMWWH	3	0	3	Sequences file
	838-MID11B	13 AA	ASSQTGFEGETQY	Homsap TRBV5-1*01 F	Homsap TRBD1*01 F	Homsap TRBJ2-5*01 F	C,F	100	431	GQMC0HM04H0WKN	3	0	3	Sequences file
3	1001-MID5B	13 AA	SARPGQGVLETQY	Homsap TRBV29-1*01 F	Homsap TRBD1*01 F	Homsap TRBJ2-5*01 F	C,F	95.34	465	GQMC0HM04IGF6V	2	0	2	Sequences file
	541-MID8B	13 AA	SARPGQGVLETQY	Homsap TRBV29-1*01 F	Homsap TRBD1*01 F	Homsap TRBJ2-5*01 F	C,F	100	458	GQMC0HM04JCUYQ	2	0	2	Sequences file
	1044-MID11B	13 AA	SARPGQGVLETQY	Homsap TRBV29-1*01 F	Homsap TRBD1*01 F	Homsap TRBJ2-5*01 F	C,F	98.91	310	GQMC0HM04IU59D	1	0	1	Sequences file
4	1153-MID5B	12 AA	ASSFGQGAGEAF	Homsap TRBV7-2*01 F	Homsap TRBD1*01 F	Homsap TRBJ1-1*01 F	C,F	99.28	490	GQMC0HM04H3JSB	3	0	3	Sequences file
	632-MID8B	12 AA	ASSFGQGAGEAF	Homsap TRBV7-2*01 F	Homsap TRBD1*01 F	Homsap TRBJ1-1*01 F	C,F	100	499	GQMC0HM04IPCNR	5	0	5	Sequences file
	1196-MID11B	12 AA	ASSFGQGAGEAF	Homsap TRBV7-2*01 F	Homsap TRBD1*01 F	Homsap TRBJ1-1*01 F	C,F	100	446	GQMC0HM04IWWLX	1	0	1	Sequences file

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1. **IMGT® est la référence mondiale en immunogénétique et immunoinformatique**.

- Encyclopedia of Systems Biology (61 entrées, 2013)
- Cold Spring Harbor Protocols (11 publications, 2011)
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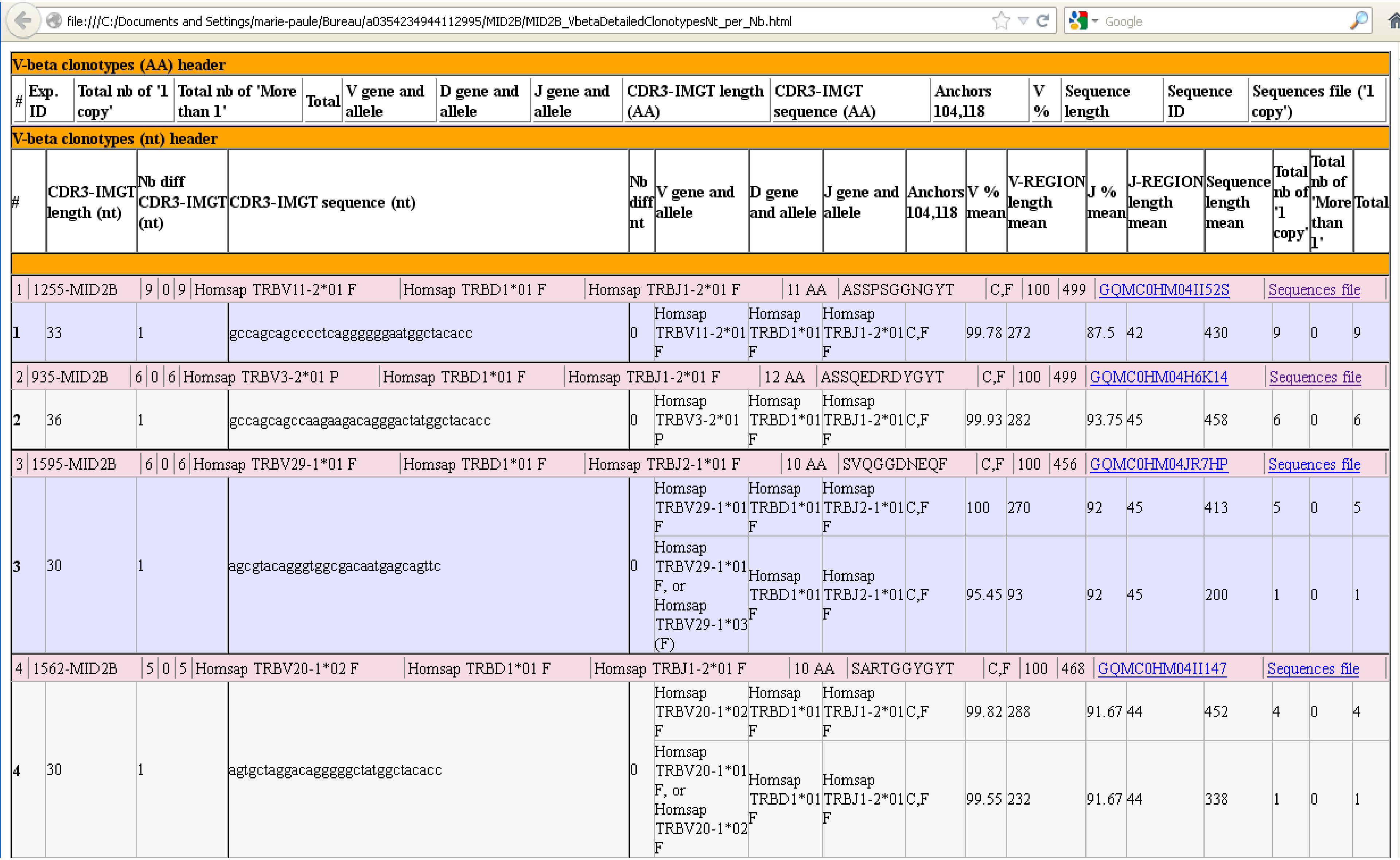


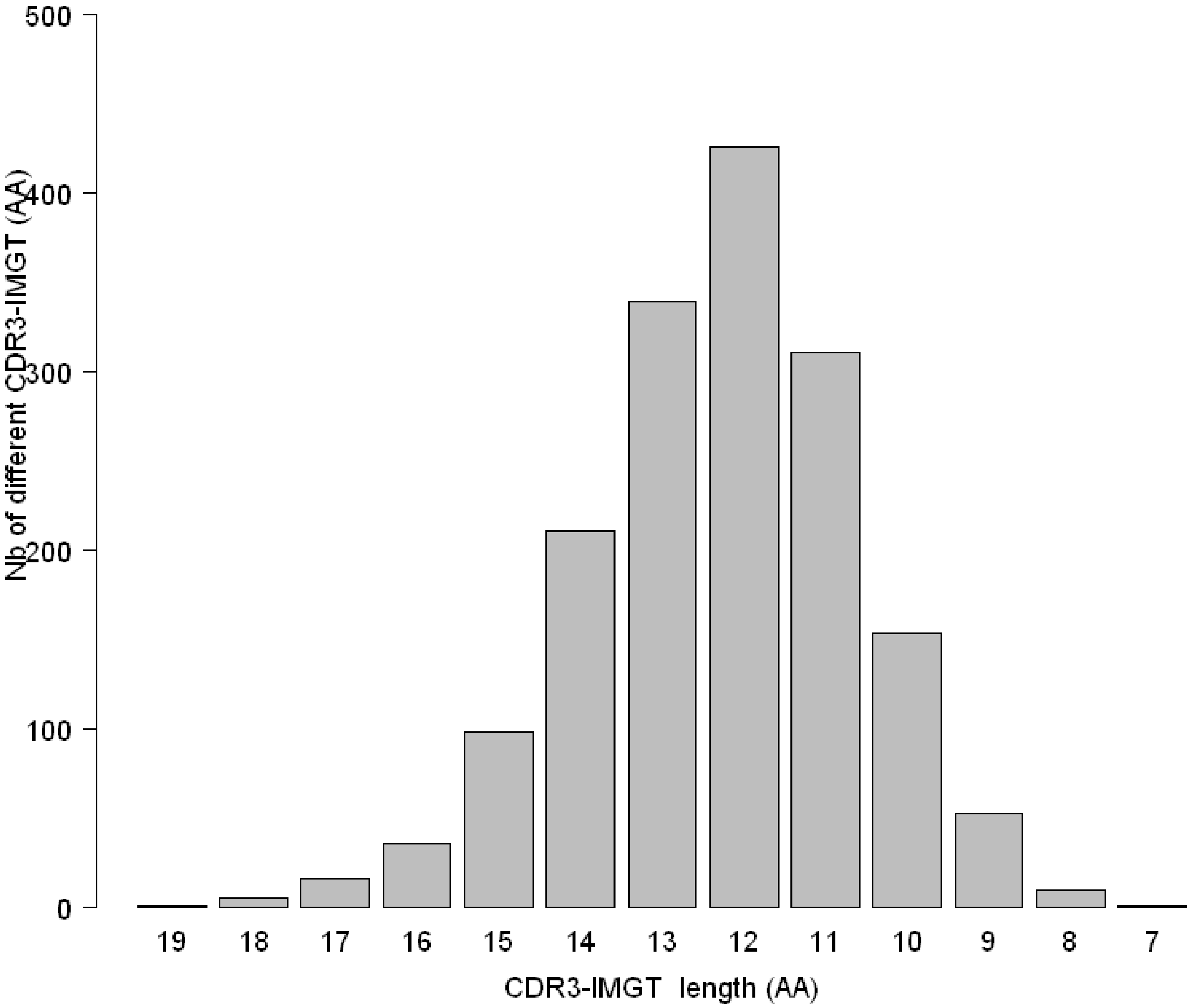
V-beta clonotypes (AA) header

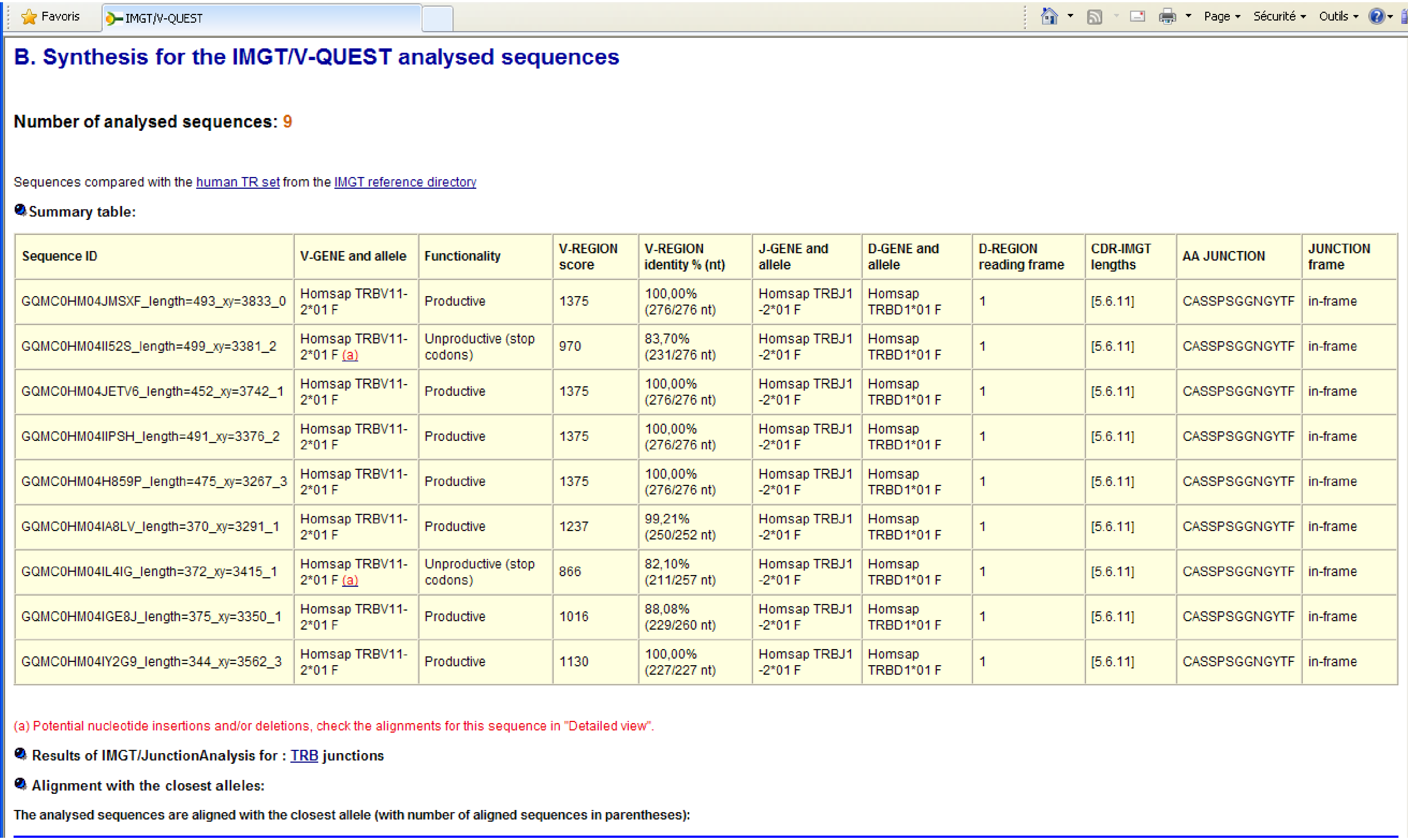
#	Exp. ID	Total nb of '1 copy'	Total nb of 'More than 1'	Total	V gene and allele	D gene and allele	J gene and allele	CDR3-IMGT length (AA)	CDR3-IMGT sequence (AA)	Anchors 104,118	V %	Sequence length	Sequence ID	Sequences file ('1 copy')
1	1255-MID2B	9	0	9	Homsap TRBV11-2*01 F	Homsap TRBD1*01 F	Homsap TRBJ1-2*01 F	11 AA	ASSPSGGNGYT	C,F	100	499	GQMC0HM04II52S	Sequences file
2	935-MID2B	6	0	6	Homsap TRBV3-2*01 P	Homsap TRBD1*01 F	Homsap TRBJ1-2*01 F	12 AA	ASSQEDRDYGYT	C,F	100	499	GQMC0HM04H6K14	Sequences file
3	1595-MID2B	6	0	6	Homsap TRBV29-1*01 F	Homsap TRBD1*01 F	Homsap TRBJ2-1*01 F	10 AA	SVQGGDNEQF	C,F	100	456	GQMC0HM04JR7HP	Sequences file
4	1562-MID2B	5	0	5	Homsap TRBV20-1*02 F	Homsap TRBD1*01 F	Homsap TRBJ1-2*01 F	10 AA	SARTGGYGYT	C,F	100	468	GQMC0HM04II147	Sequences file

V-beta clonotypes (nt) header

#	CDR3-IMGT length (nt)	Nb diff CDR3-IMGT (nt)	CDR3-IMGT sequence (nt)	Nb diff nt	V gene and allele	D gene and allele	J gene and allele	Anchors 104,118	V % mean	V-REGION length mean	J % mean	J-REGION length mean	Sequence length mean	Total nb of '1 copy'	Total nb of 'More than 1'	Total
1	33	1	gccagcagcccctcagggggggaatggctacacc	0	Homsap TRBV11-2*01 F	Homsap TRBD1*01 F	Homsap TRBJ1-2*01 F	C,F	99.78	272	87.5	42	430	9	0	9
2	36	1	gccagcagccaagaagacagggactatggctacacc	0	Homsap TRBV3-2*01 P	Homsap TRBD1*01 F	Homsap TRBJ1-2*01 F	C,F	99.93	282	93.75	45	458	6	0	6
3	30	1	agcgtacagggtggcgacaatgagcagttc	0	Homsap TRBV29-1*01 F	Homsap TRBD1*01 F	Homsap TRBJ2-1*01 F	C,F	100	270	92	45	413	5	0	5
					Homsap TRBV29-1*01 F, or Homsap TRBV29-1*03 (F)	Homsap TRBD1*01 F	Homsap TRBJ2-1*01 F	C,F	95.45	93	92	45	200	1	0	1
4	30	1	agtgctaggacagggggctatggctacacc	0	Homsap TRBV20-1*02 F	Homsap TRBD1*01 F	Homsap TRBJ1-2*01 F	C,F	99.82	288	91.67	44	452	4	0	4
					Homsap TRBV20-1*01 F, or Homsap TRBV20-1*02 F	Homsap TRBD1*01 F	Homsap TRBJ1-2*01 F	C,F	99.55	232	91.67	44	338	1	0	1

Nb of different CDR3-IMGT (AA) per CDR3-IMGT length





B. Synthesis for the IMGT/V-QUEST analysed sequences

Number of analysed sequences: 9

Sequences compared with the human TR set from the IMGT reference directory

Summary table:

Sequence ID	V-GENE and allele	Functionality	V-REGION score	V-REGION identity % (nt)	J-GENE and allele	D-GENE and allele	D-REGION reading frame	CDR-IMGT lengths	AA JUNCTION	JUNCTION frame
GQMC0HM04JMSXF_length=493_xy=3833_0	Homsap TRBV11-2*01 F	Productive	1375	100,00% (276/276 nt)	Homsap TRBJ1-2*01 F	Homsap TRBD1*01 F	1	[5.6.11]	CASSPSGGNGYTF	in-frame
GQMC0HM04II52S_length=499_xy=3381_2	Homsap TRBV11-2*01 F (a)	Unproductive (stop codons)	970	83,70% (231/276 nt)	Homsap TRBJ1-2*01 F	Homsap TRBD1*01 F	1	[5.6.11]	CASSPSGGNGYTF	in-frame
GQMC0HM04JETV6_length=452_xy=3742_1	Homsap TRBV11-2*01 F	Productive	1375	100,00% (276/276 nt)	Homsap TRBJ1-2*01 F	Homsap TRBD1*01 F	1	[5.6.11]	CASSPSGGNGYTF	in-frame
GQMC0HM04IIPSH_length=491_xy=3376_2	Homsap TRBV11-2*01 F	Productive	1375	100,00% (276/276 nt)	Homsap TRBJ1-2*01 F	Homsap TRBD1*01 F	1	[5.6.11]	CASSPSGGNGYTF	in-frame
GQMC0HM04H859P_length=475_xy=3267_3	Homsap TRBV11-2*01 F	Productive	1375	100,00% (276/276 nt)	Homsap TRBJ1-2*01 F	Homsap TRBD1*01 F	1	[5.6.11]	CASSPSGGNGYTF	in-frame
GQMC0HM04IA8LV_length=370_xy=3291_1	Homsap TRBV11-2*01 F	Productive	1237	99,21% (250/252 nt)	Homsap TRBJ1-2*01 F	Homsap TRBD1*01 F	1	[5.6.11]	CASSPSGGNGYTF	in-frame
GQMC0HM04IL4IG_length=372_xy=3415_1	Homsap TRBV11-2*01 F (a)	Unproductive (stop codons)	866	82,10% (211/257 nt)	Homsap TRBJ1-2*01 F	Homsap TRBD1*01 F	1	[5.6.11]	CASSPSGGNGYTF	in-frame
GQMC0HM04IGE8J_length=375_xy=3350_1	Homsap TRBV11-2*01 F	Productive	1016	88,08% (229/260 nt)	Homsap TRBJ1-2*01 F	Homsap TRBD1*01 F	1	[5.6.11]	CASSPSGGNGYTF	in-frame
GQMC0HM04IY2G9_length=344_xy=3562_3	Homsap TRBV11-2*01 F	Productive	1130	100,00% (227/227 nt)	Homsap TRBJ1-2*01 F	Homsap TRBD1*01 F	1	[5.6.11]	CASSPSGGNGYTF	in-frame

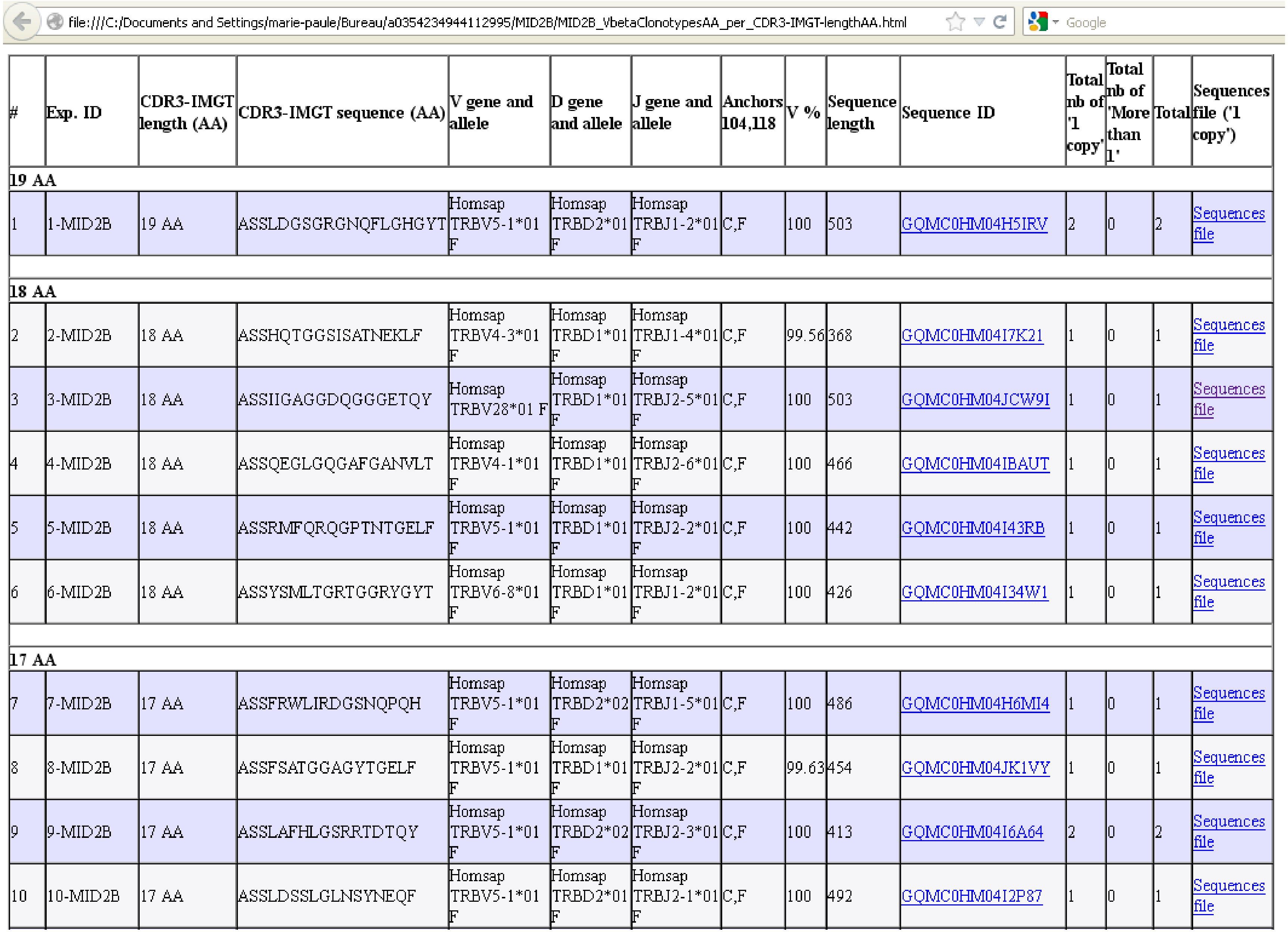
(a) Potential nucleotide insertions and/or deletions, check the alignments for this sequence in "Detailed view".

Results of IMGT/JunctionAnalysis for : TRB junctions

Alignment with the closest alleles:

The analysed sequences are aligned with the closest allele (with number of aligned sequences in parentheses):

V beta clonotypes (AA) per CDR3-IMGT length



#	Exp. ID	CDR3-IMGT length (AA)	CDR3-IMGT sequence (AA)	V gene and allele	D gene and allele	J gene and allele	Anchors 104,118	V %	Sequence length	Sequence ID	Total nb of '1 copy'	Total nb of 'More than 1'	Total	Sequences file ('1 copy')
19 AA														
1	1-MID2B	19 AA	ASSLDGSGRGNQFLGHGYT	Homsap TRBV5-1*01 F	Homsap TRBD2*01 F	Homsap TRBJ1-2*01 F	C,F	100	503	GQMC0HM04H5IRV	2	0	2	Sequences file
18 AA														
2	2-MID2B	18 AA	ASSHQTGGSISATNEKLF	Homsap TRBV4-3*01 F	Homsap TRBD1*01 F	Homsap TRBJ1-4*01 F	C,F	99.56	368	GQMC0HM04I7K21	1	0	1	Sequences file
3	3-MID2B	18 AA	ASSIIGAGGDQGGGETQY	Homsap TRBV28*01 F	Homsap TRBD1*01 F	Homsap TRBJ2-5*01 F	C,F	100	503	GQMC0HM04JCW9I	1	0	1	Sequences file
4	4-MID2B	18 AA	ASSQEGLGQGAFGANVLT	Homsap TRBV4-1*01 F	Homsap TRBD1*01 F	Homsap TRBJ2-6*01 F	C,F	100	466	GQMC0HM04IBAUT	1	0	1	Sequences file
5	5-MID2B	18 AA	ASSRMFQRQGPTNTGELF	Homsap TRBV5-1*01 F	Homsap TRBD1*01 F	Homsap TRBJ2-2*01 F	C,F	100	442	GQMC0HM04I43RB	1	0	1	Sequences file
6	6-MID2B	18 AA	ASSYSMLTGRTGGRYGYT	Homsap TRBV6-8*01 F	Homsap TRBD1*01 F	Homsap TRBJ1-2*01 F	C,F	100	426	GQMC0HM04I34W1	1	0	1	Sequences file
17 AA														
7	7-MID2B	17 AA	ASSFRWLIRDGSNQPQH	Homsap TRBV5-1*01 F	Homsap TRBD2*02 F	Homsap TRBJ1-5*01 F	C,F	100	486	GQMC0HM04H6MI4	1	0	1	Sequences file
8	8-MID2B	17 AA	ASSFSATGGAGYTGELF	Homsap TRBV5-1*01 F	Homsap TRBD1*01 F	Homsap TRBJ2-2*01 F	C,F	99.63	454	GQMC0HM04JK1VY	1	0	1	Sequences file
9	9-MID2B	17 AA	ASSLAFHLGSRRTDTQY	Homsap TRBV5-1*01 F	Homsap TRBD2*02 F	Homsap TRBJ2-3*01 F	C,F	100	413	GQMC0HM04I6A64	2	0	2	Sequences file
10	10-MID2B	17 AA	ASSLDSSLGLNSYNEQF	Homsap TRBV5-1*01 F	Homsap TRBD2*01 F	Homsap TRBJ2-1*01 F	C,F	100	492	GQMC0HM04I2P87	1	0	1	Sequences file