### Minutes of IARC meeting 117, March 6th, 2023

In attendance: Ayelet Peres, Andrew Collins, Martin Corcoran, William Lees, Corey Watson, Mats Ohlin, James Heather

## 1. Approval of minutes of meeting 116

Approved

### 2. Next meeting

March 20th, 2023 at 10.00 UTC

## 3. Proofreading of novel OGRDB entries

IGHV (AC)

TRBV (JH)

# 4. Discussion of Report of IARC activities to the AIRR-C Executive Sub-committee - Special Meeting with WG/SC Co-leads on March 16, 2023

Discussion. Report accepted for presentation.

Discussion on possibilities for documentation/outreach on best practice in AIRR data analysis.

### 5. Germline reference set manuscript

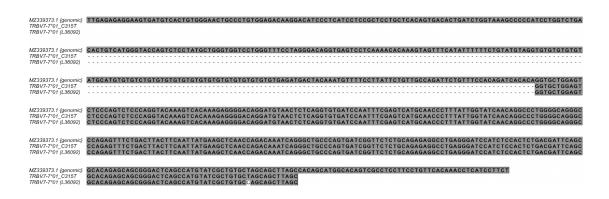
Discussion with a focus on extended IGHV sequences and the need for supplementary conformation of IGHD and IGHJ alleles that has not been a major focus on IARC inference processes. The importance of demonstration / discussion of analysis challenges/errors using databases with incomplete or faulty sequences was discussed.

### 6. Assessment of inference TRBV7-7\*01 C315T in P4 I9 S1 (S00036)

TRBV7-7\*01\_C315T has been inferred in seventeen genotypes in the VDJbase P4 data set, including in VDJbase P4\_I9\_S1, a haplotypable data set (based on heterozygocity in TRBJ1-6). The genotype is also implied to carry TRBV7-7\*01. No other gene apart from IGHV7-6 (alleles of which also carry C315) in the IMGT database is highly similar to these alleles of TRBV7-7. The novel allele is the most expressed allele in the repertoire (58%)

allelic frequency; 0.16% of the total error-free population). It is represented by 37 error-free sequences and 33 unique CDR3s in the error-free set. Haplotyping based on allelic diversity in TRBJ1-6 demonstrates association of TRBV7-7\*01\_C315T with only one of the haplotypes (only few recorded cases; TRBV7-7\*01 was not associated with any allele of TRBJ1-6).

The allele has also been identified as TRBV7-7\*01\_S0326 and Sanger validated (GenBank MZ339373) (Corcoran et al. (2023) Immunity (in press) (10.1016/j.immuni.2023.01.026)). Final decision postponed until next meeting to allow incorporation of genomic validation into our decision process.



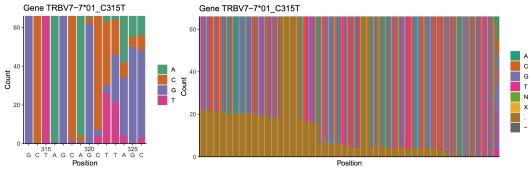
Result summary: TRBV7-7*01_C315T	No rearrangement found				
V-GENE and allele	Homsap TRBV7-7*01 F	score = 1380	identity = 100.00% (276/276 nt)		
FR-IMGT lengths, CDR-IMGT lengths	[5.6.X]				

#### 1. Alignment for V-GENE and allele identification

Closest V-REGIONs (evaluated from the V-REGION first nucleotide to the 2nd-CYS codon)

				Score	Identity	
L36092	Homsap	TRBV7-7*01	F	1380	100.00% (276/276 nt)	
<u>x57607</u>	Homsap	TRBV7-7*02	(F)	1371	99.64% (275/276 nt)	
L36092	Homsap	TRBV7-6*01	F	1281	96.01% (265/276 nt)	
<u>x58806</u>	Homsap	TRBV7-6*02	(F)	1272	95.65% (264/276 nt)	
M11953	Homsap	TRBV7-8*01	F	1119	89.49% (247/276 nt)	

(Note: the difference between TRBV7-7\*01\_C315T and TRBV7-7\*01 is outside of the range assessed by IMGT/V-QUEST)



Consensus plot of 3'-end:

All data:

