

Minutes of IARC meeting 108, October 24th, 2022

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

1. Approval of minutes of meeting 107

Approved

2. Report from the AIRR-C Executive Sub-committee - Special Meeting with WG/SC Co-leads on Oct 20, 2022 (WL)

Summary of the discussion at the AIRR-C Executive Sub-committee special meeting.

3. Submission of data for IGLV2-14*i02 (IGLV2-14*04) and of data for additional inferred IGHV P1 sequences in VDJbase that have not yet been affirmed (e.g. IGHV3-30*04 C201T G317A (IGHV3-30*18 G113C C114T) (P1_I70), IGHV3-13*01_G290A_T300C (P1_10), IGHV4-61*01 A41G (P1_I23)) to ENA/GenBank - update

Still awaiting information from ENA/GenBank.

4. IARC - Notes on development of human IGH germline sets that are optimized for use in AIRR-seq analysis.

Discussion. WL and AC will edit the text.

5. Assessment of inference TRBV12-4*01_C87T in P4_I24_S1 (S00036)

Initiated further discussion of this inference and in particular its 3'-end that is subjected to extensive trimming, with a particular focus on how the 3'-end data should be represented, i.e. with a focus on all sequences or with a focus for each position on those clones that have not been trimmed beyond the previous position.

TRBV12-4*01_C87T has been inferred in nine genotypes in the VDJbase P4 data set, including in VDJbase P4_I24_S1, a haplotypable data set (based on heterozygosity in TRBJ1-6). The genotype is also implied to carry TRBV12-4*01. No other gene apart from TRBV12-3 in the IMGT database is closely related to these alleles of TRBV12-4. The novel allele is the most

expressed allele in the repertoire (72% allelic frequency; 1.47% of the total error-free population). It is represented by 499 error-free sequences and 467 unique CDR3s in the error-free set. Haplotyping based on allelic diversity in TRBJ1-6 demonstrates perfect separation from TRBV12-4*01.

>TRBV12-4*01_C87T

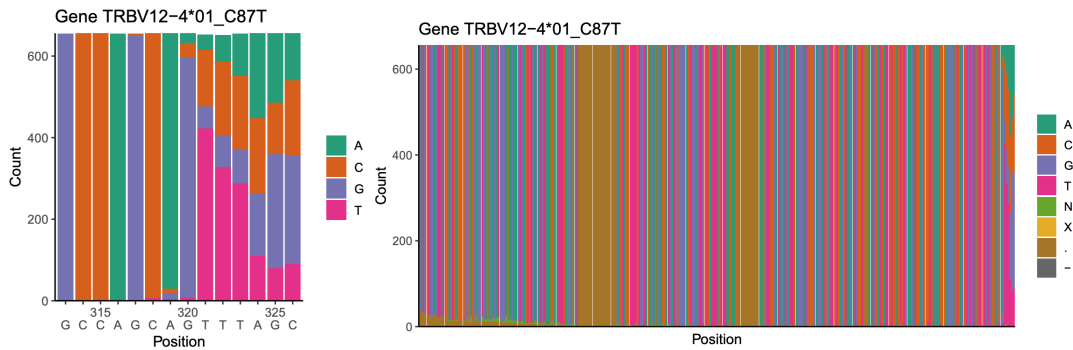
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GATGCTGGAGTTATCCAGTCACCCCGGCACGAGGTGACAGAGATGGGACAAGAAGTG
ACTCTGAGATGTAAACCAATTTTCAGGACATGACTACCTTTTCTGGTACAGACAGACC
ATGATGCGGGGACTGGAGTTGCTCATTTACTTTAACAACAACGTTCCGATAGATGAT
TCAGGGATGCCCCGAGGATCGATTCTCAGCTAAGATGCCTAATGCATCATTCTCCACT
CTGAAGATCCAGCCCTCAGAACCCAGGGACTCAGCTGTGTACTTCTGTGCCAGCAGT
TTAGC
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| | | | |
|---|--|--------------|--------------------------------|
| Result summary: TRBV12-4*01_C87T | No rearrangement found | | |
| V-GENE and allele | Homsap TRBV12-4*01 F , or Homsap TRBV12-4*02 (F) | score = 1371 | identity = 99.64% (275/276 nt) |
| FR-IMGT lengths, CDR-IMGT lengths | [5.6.X] | | |

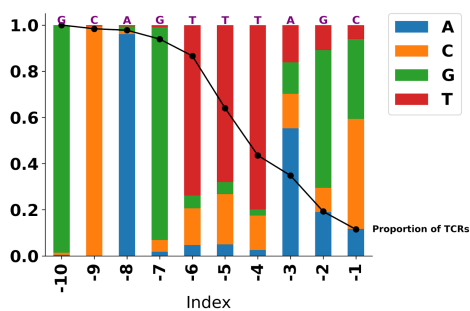
1. Alignment for V-GENE and allele identification

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

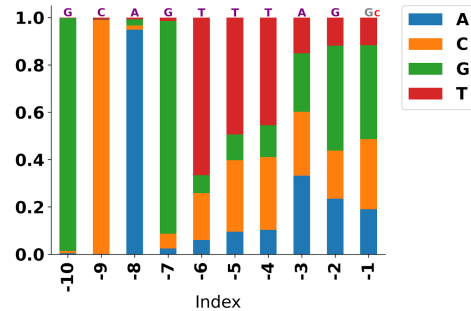
| | | Score | Identity |
|------------------------|------------------------|-------|---------------------|
| K02546 | Homsap TRBV12-4*01 F | 1371 | 99.64% (275/276 nt) |
| M14264 | Homsap TRBV12-4*02 (F) | 1371 | 99.64% (275/276 nt) |
| X07192 | Homsap TRBV12-3*01 F | 1326 | 97.83% (270/276 nt) |
| X07223 | Homsap TRBV12-5*01 F | 957 | 82.97% (229/276 nt) |
| X07224 | Homsap TRBV12-1*01 P | 867 | 79.35% (219/276 nt) |

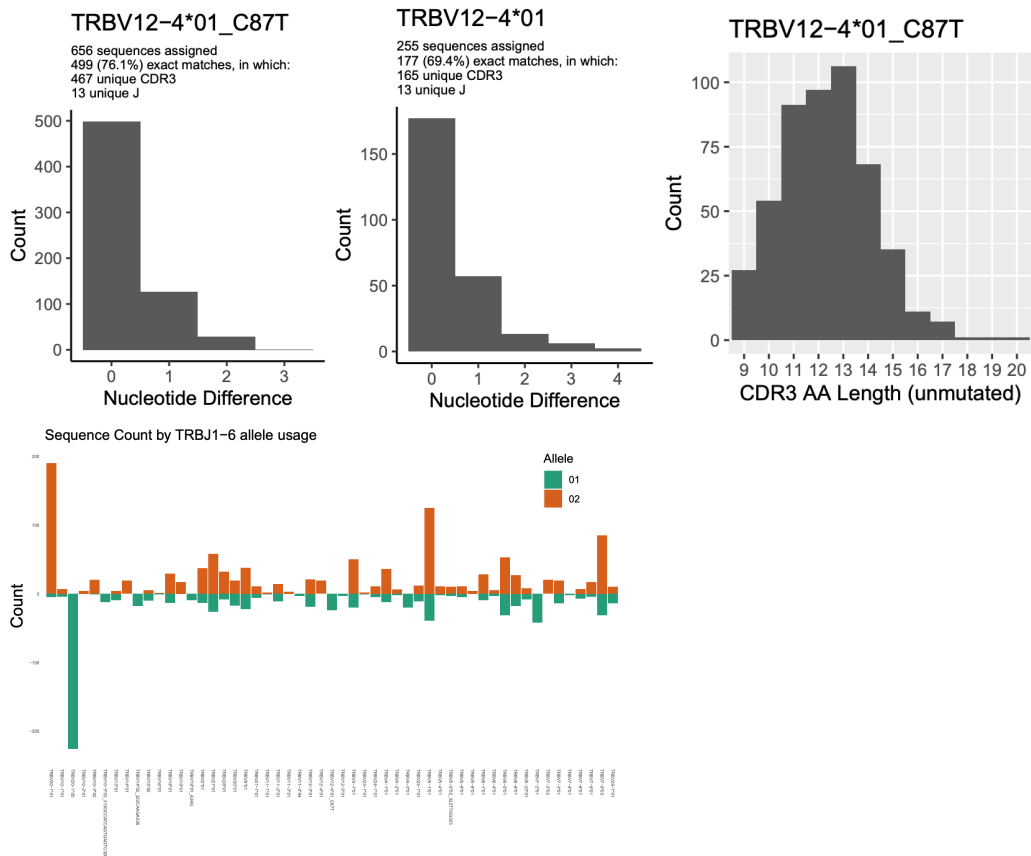


Consensus plot of 3'-end:



All data:





6. Next meeting
 November 7th, 2022 at 11.00 UTC.