Minutes of IARC meeting 102, July 26th, 2022

In attendance: Ayelet Peres, Andrew Collins, Gur Yaari (from §4), Martin Corcoran, William Lees, Corey Watson, Mats Ohlin, James Heather (from §4)

1. **Approval of minutes of meeting 101**
   Approved

2. **IGLV7-46*i01**
   IGLV7-46*i01 was previously (IARC meeting 57 on July 7th, 2020, and IARC meeting 58 on July 20th, 2020) affirmed as a level 0 sequence. As it now features in the IMGT database as IGLV7-46*04 with additional, independent genomic support (GenBank: OL352718) it is promoted to level 1 and released into the public domain of OGRDB.

3. **Germline reference set using gene-agnostic naming schema**
   Discussion of the effects of using a gene-agnostic naming schema in IgDiscover / Immcantation and other tools. WL will generate a human reference set using this naming schema for testing of tools.

4. **Assessment of inference TRBV12-4*01_C87T in P4_I24_S1 (S00036)**
   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 heterozygocity 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. The data formed the basis for a discussion of a future best practice for a consolidated approach to allele affirmation (incl. of genes like those of the TRBV locus that undergo extensive 3'-end trimming), gene naming, and reference set generation.

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>TRBV12-4*01_C87T
GATGCTGGAGTTATCCAGTCACCCCGGCACGAGGTGACAGAGATGGGACAAGAAGTG
ACTCTGAGATGTAAACCAATTTCAGGACATGACTACCTTTTCTGGTACAGACAGACC
ATGATGCGGGGACTGGAGTTGCTCATTTACTTTAACAACAACGTTCCGATAGATGAT
TCAGGGATGCCCGAGGATCGATTCTCAGCTAAGATGCCTAATGCATCATTCTCCACT
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CTGAAGATCCAGCCCTCAGAACCCAGGGACTCAGCTGTGTACTTCTGTGCCAGCAGT

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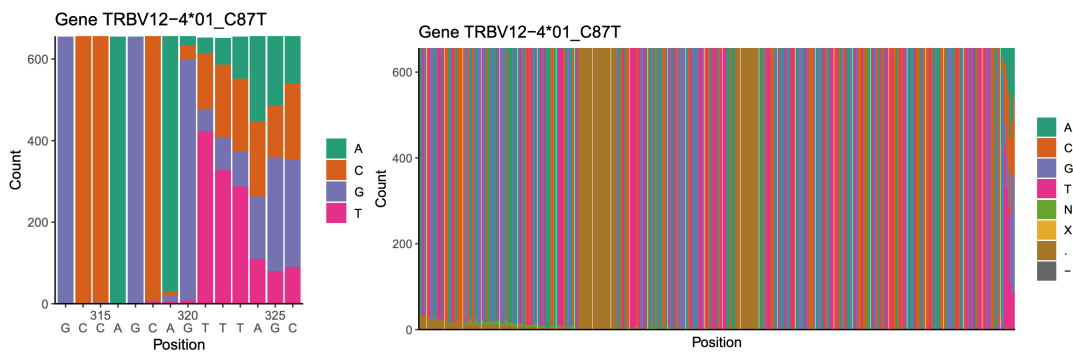
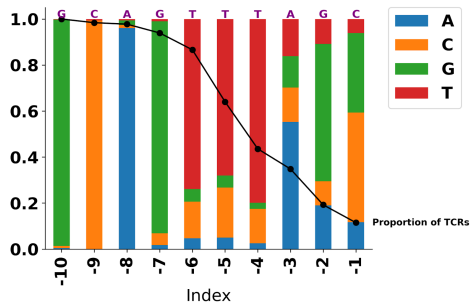| Result summary: **TRBV12-4*01_C87T**	**No rearrangement found**		
V-GENE and allele	Homsap TRBV12-4*01 F, or Homsap TRBV12-4*02 (F)	score = 1371	identity = **99.64%** (275/276 nt)
FR-IMGT lengths, CDR-IMGT lengths	[5.6.X]		

1. Alignment for V-GENE and allele identification

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

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                                    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)
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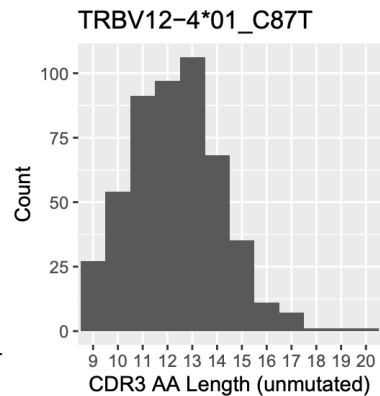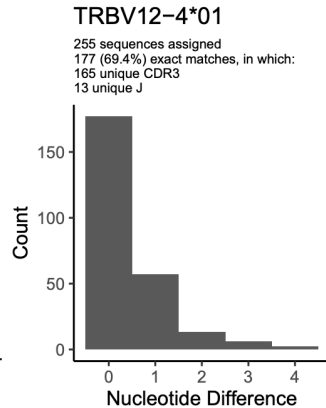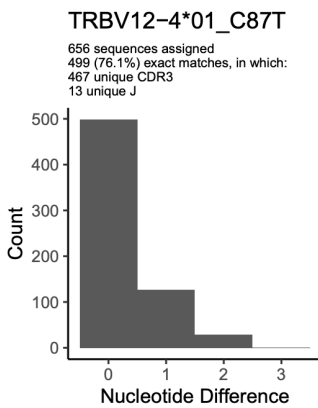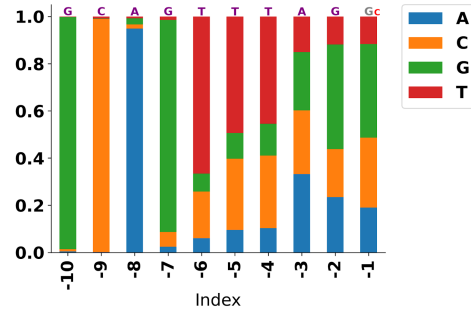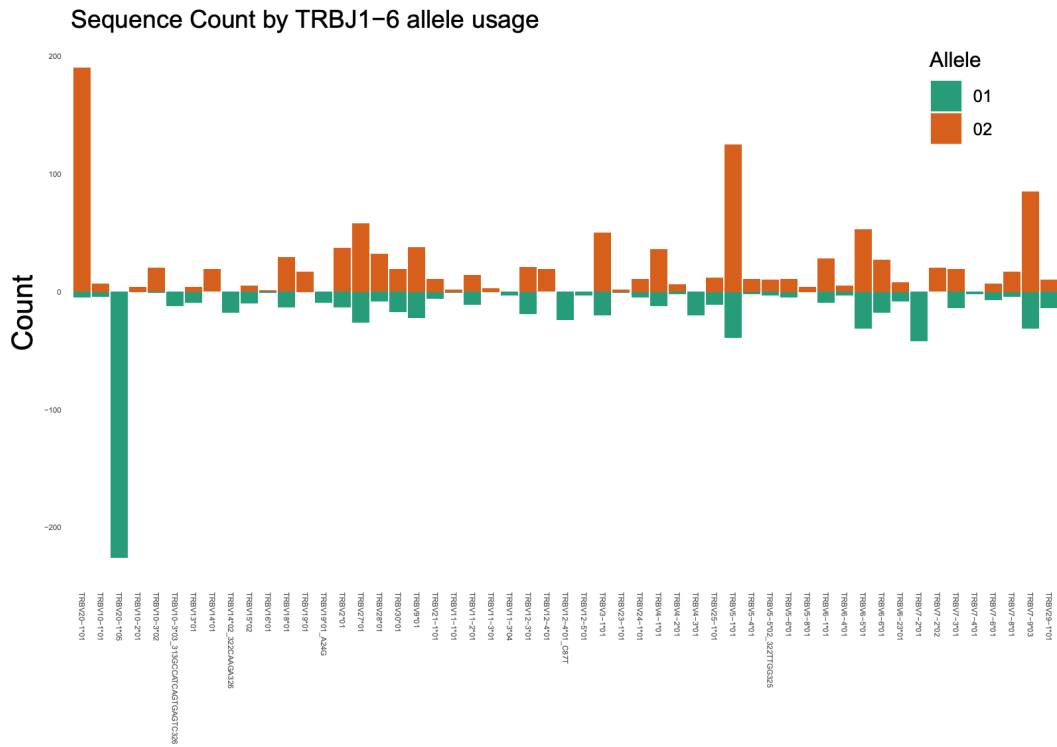

Gene TRBV12−4*01_C87T

Gene TRBV12−4*01_C87T

Consensus plot of 3'-end:

All data:

TRBV12−4*01_C87T

656 sequences assigned
499 (76.1%) exact matches, in which:
467 unique CDR3
13 unique J

TRBV12−4*01

255 sequences assigned
177 (69.4%) exact matches, in which:
165 unique CDR3
13 unique J

TRBV12−4*01_C87T

Sequence Count by TRBJ1−6 allele usage

5. Definition of priorities for future IARC efforts
WL will create a document to collect ideas in preparation of a discussion of IARC's future priorities and activities.

6. Next meeting
August 15th, 2022 at 10 UTC.