

IARC Meeting 63: November 24th 2020: minutes

The meeting commenced at 10:00 UTC. AC, MC, MO, CS and WL were in attendance. Corey Watson and Gur Yaari were also present.

1. The minutes of meeting 62 were accepted.
2. The meeting considered the inference of the variant IGHV4-39*07_c288a in the VDJbase datasets of sample P1_I29_S1. (It was present in two other VDJbase samples). The sequence was seen in 4.61% of all unmutated rearrangements, with 1201 sequences including 1068 perfect matches to the inferred allele. There was abundant variation in the CDR3 regions of the aligned sequences. IGHV4-39*01 was also present in the genotype, at a similar frequency (4.35% of all unmutated sequences, 1135 sequences, 1009 unmutated sequences). Plots of the final 3' nucleotides were unavailable. Haplotyping data strongly supported the inference. The sequence was tentatively affirmed as a Level 1 sequence, and the final 3' nucleotides will be considered at a later date, when terminal nucleotide plots become available, at which time the affirmed sequence will be noted in the IARC minutes.
3. The meeting considered the inference of the variant IGHV4-4*02_a106g, in the VDJbase dataset of sample P1_I42_S1. The sequence was seen in 1.27% of all unmutated rearrangements, with 268 sequences including 234 perfect matches to the inferred allele. There was abundant variation in the CDR3 regions of the aligned sequences. IGHV4-4*07 was also present in the genotype, at a lower frequency (0.73% of all unmutated sequences, 157 sequences, 135 unmutated sequences). Haplotyping data was not available. Plots of the final 3' nucleotides of the inference were also unavailable. In light of the low sequence counts and the lack of haplotyping, the inferred sequence was affirmed as a Level 0 sequence. The final 3' nucleotides will be considered at a later date, at which time the affirmed sequence will be noted in the IARC minutes.
4. The meeting considered the inference of the variant IGHV4-61*01_a41g, in the VDJbase dataset of sample P1_I23_S1. The sequence was seen in 0.33% of all unmutated rearrangements, with 95 sequences including 90 perfect matches to the inferred allele. IGHV4-61*01 was also present in the genotype, at a similar frequency (0.41% of all unmutated sequences, 123 sequences, 112 unmutated sequences). Haplotyping data showed fairly good separation of the chromosomes (7:93; 100:0). There was abundant variation in the CDR3 regions of the aligned sequences. Plots of the final 3' nucleotides of the inference were unavailable. The low frequencies seen are typical for IGHV4-61*01, but in light of the low counts, the inferred sequence was affirmed as a Level 0 sequence. The final 3' nucleotides will be considered at a later date, at which time the affirmed sequence will be noted in the IARC minutes. The meeting supported the continued collection of data on allele expression levels.
5. The meeting considered the inference of the variant IGHV4-61*02_a234g, in the VDJbase dataset of sample P1_I86_S1. The sequence was seen in ten samples, including 4 P1 samples. The meeting focused on sample P1_I86_S1, in which the inferences was seen in 1.82% of all unmutated rearrangements, with 592 sequences including 519 perfect matches

to the inferred allele. There was abundant variation in the CDR3 regions of the aligned sequences. IGHV4-61*01 was also present in the genotype, at a lower frequency (0.38% of all unmutated sequences, 116 sequences, 107 unmutated sequences). Haplotyping data showed perfect separation of the assigned alleles. Plots of the final 3' nucleotides of the inference were unavailable. The inferred sequence was tentatively affirmed as a Level 1 sequence. The final 3' nucleotides will be considered at a later date, at which time the affirmed sequence will be noted in the IARC minutes.

6. The next meeting (Meeting 64) will be scheduled via email after the AIRR Community Meeting V..

The meeting ended at 11:04 UTC.