# IARC Meeting 62: November 3rd 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 61 were accepted, though members were encouraged to continue to review the minutes via email over the coming week.
2. The meeting considered the inference of the variant IGHV3-33*01_g75c in the VDJbase datasets of samples P1_I46_S1 and P1_I93_S1. Similar frequencies were seen in the two samples, and data recorded here comes from the P1_I46 sample. The sequence was seen in 1.94% of all unmutated rearrangements, with 386 sequences including 314 perfect matches to the inferred allele. There was abundant variation in the CDR3 regions of the aligned sequences. IGHV3-33*01 was also present in the genotype, at a similar frequency (2.40% of all unmutated sequences, 466 sequences, 388 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 IGHV3-9*01_t307c, in the VDJbase dataset of sample P1_I86_S1. The sequence was seen in 1.29% of all unmutated rearrangements, with 433 sequences including 368 perfect matches to the inferred allele. There was abundant variation in the CDR3 regions of the aligned sequences. IGHV3-9*01 was also present in the genotype, at a similar frequency (2.25% of all unmutated sequences, 748 sequences, 641 unmutated sequences). Haplotyping data showed almost 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.
4. The meeting considered the inference of the variant IGHV4-30-4*01_a70g_a107g, in the VDJbase dataset of sample P1_I41_S1. The sequence was seen in 0.97% of all unmutated rearrangements, with 360 sequences including 317 perfect matches to the inferred allele. There was abundant variation in the CDR3 regions of the aligned sequences. Haplotyping data clearly showed that the IGHV4-30-4 gene was not present on the alternate chromosome. 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.
5. The meeting considered the inference of the variant IGHV4-39*01_c66g, in the VDJbase dataset of sample P1_I90_S1. The sequence was seen in 2.74% of all unmutated rearrangements, with 1217 sequences including 1098 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 (3.09% of all unmutated sequences,

1360 sequences, 1239 unmutated sequences). Haplotyping data showed almost 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 committee was informed that sequences that were reported to IMGT in early August were still unnamed. AC will raise the matter with IMGT.
7. The committee discussed the future of the IARC and its governance, in the context of preparations for the AIRR-C Meeting V. Members again stated their belief that the current IARC should confine its deliberations to human IG inferences.
8. The next meeting (Meeting 63) will be held on Tuesday November 24th at 10:00 UTC.

The meeting ended at 11:00 UTC.