

Minutes of IARC meeting 110, November 21st, 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 109

Approved

2. A process for incorporation of Sanger-based genomic data in IARC's decision-making process.

The draft created by MC was reviewed. Further discussion at the next meeting.

3. Primers and literature reference of S00036

Information on primer will be updated in OGRDB (AP/WL)

4. Submission of affirmed germline genes to IUIS

The ability of IARC to actually name inferred alleles with reference to specific genes was discussed with particular reference to the complexity and variability of the human IGHV locus involving duplications, deletions, and the presence of some IGHV sequences at more than one locus. MO will prepare a draft of a text to be included in OGRDB in its Notes of inferred alleles of IGHV genes, a text that is also to be reported to IUIS.

5. 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

Submission completed but not yet publicly available. OGRDB submission is pending.

6. A first draft of an IARC germline set - the path forward

Discussion on the complexity of the IGHV locus and the extreme degree of structural variation and allele sharing between different IGHV genes (e.g. IGHV3-30 / IGHV3-30-3 / IGHV3-30-5 / IGHV3-33 and IGHV4-28 / IGHV4-30-2 / IGHV4-30-4 / IGHV4-31) that has been observed in genomic long read sequencing. It was suggested that different approaches will have to be taken in the generation of sets to be used for AIRRseq transcriptome analysis and genomic studies, respectively. This matter is to be considered further in preparation for next meeting.

7. Next meeting

Dec 6th, 2022 at 11.00 UTC