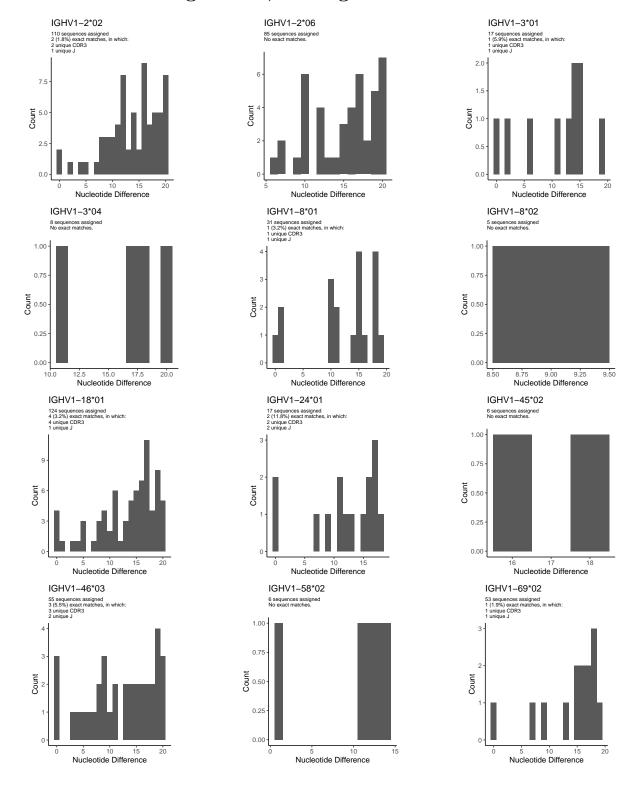
OGRDBstats Report

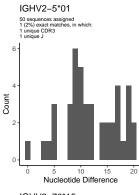
Contents

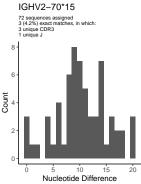
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2	Variation from germline, in assignments to each allele	3
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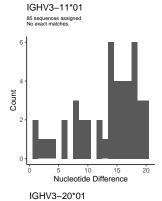
- 1 Novel sequence analysis
- 1.1 CDR3 length distribution, in assignments to novel alleles

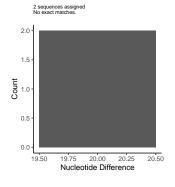
2 Variation from germline, in assignments to each allele

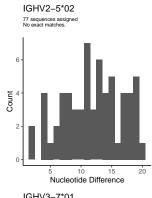


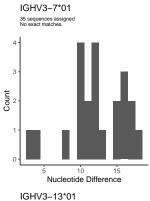


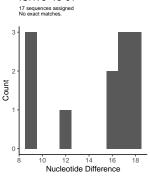


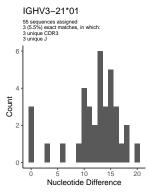


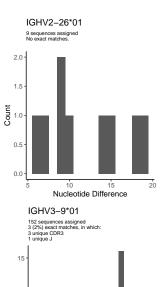


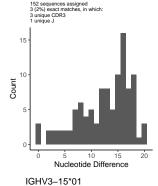


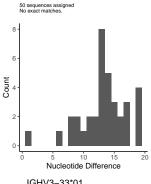


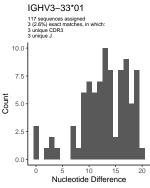


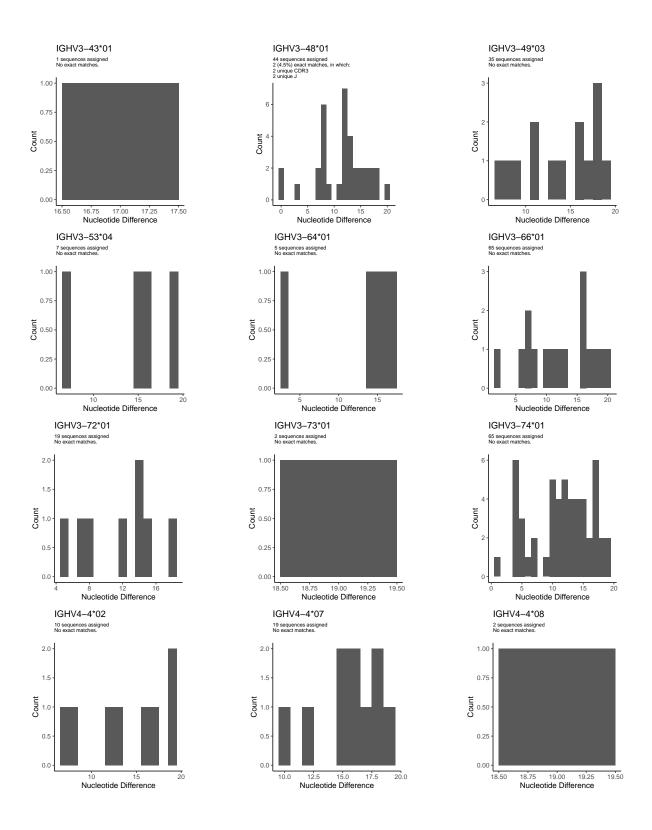


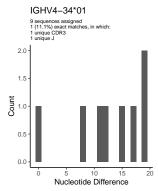






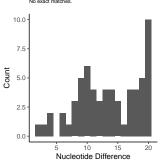




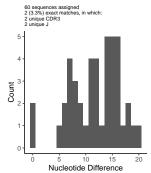


IGHV4-NL1*01

123 sequences assigned No exact matches.

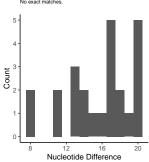


IGHV7-4-1*02

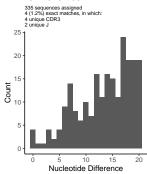




70 sequences assigned No exact matches.

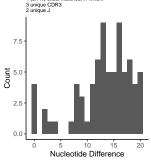


IGHV5-51*03



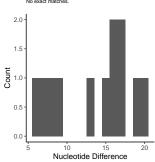
IGHV4-59*01

107 sequences assigned 4 (3.7%) exact matches, in which: 3 unique CDR3 2 unique J

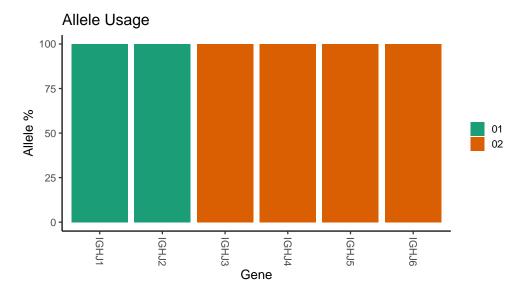


IGHV6-1*01

12 sequences assigned No exact matches.



3 Allele usage in potential haplotype anchor genes



4 Haplotype plots

5 Configuration settings

```
## Repertoire file: /misc/work/jenkins/PRJNA248475/M4/M4_cln/M4_cln/M4_cln/25/050d79ea1e1841bf2b161f24a
##
## Germline reference file: /misc/work/jenkins/PRJNA248475/M4/M4_cln/M4_cln/M4_cln/00/3c6b53ac41fdb25ba
##
## Novel allele file:
##
## Species: Homosapiens
##
## Chain: IGHV
##
## Segment: V
##
## Warning no inferred sequences found.
```