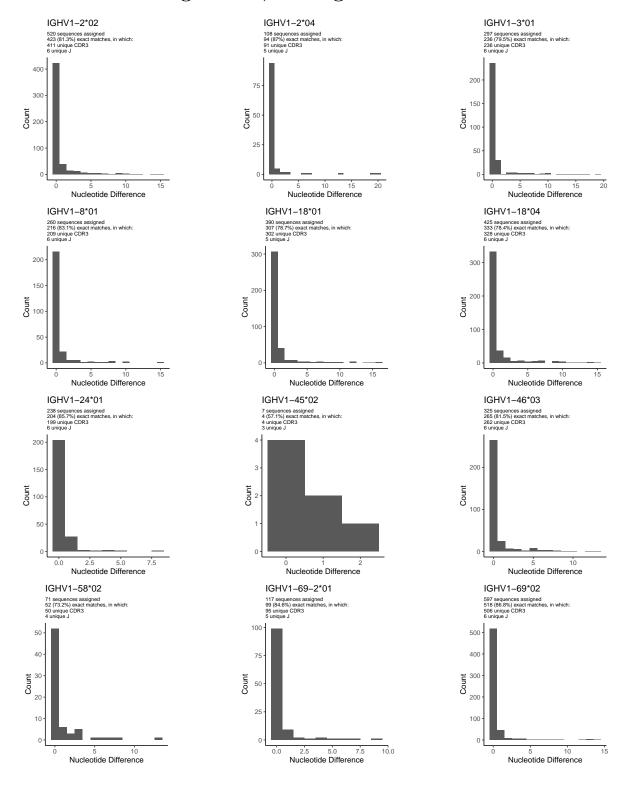
OGRDBstats Report

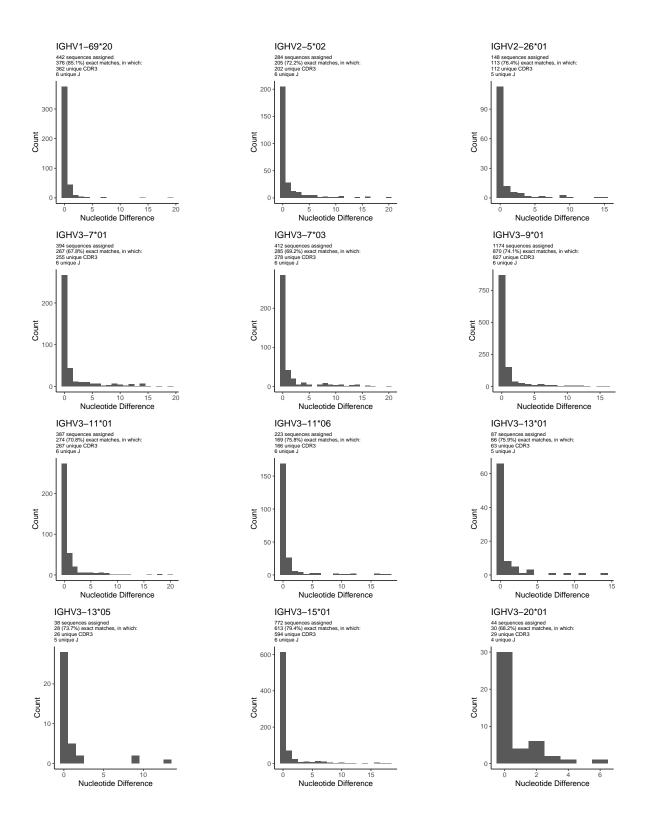
Contents

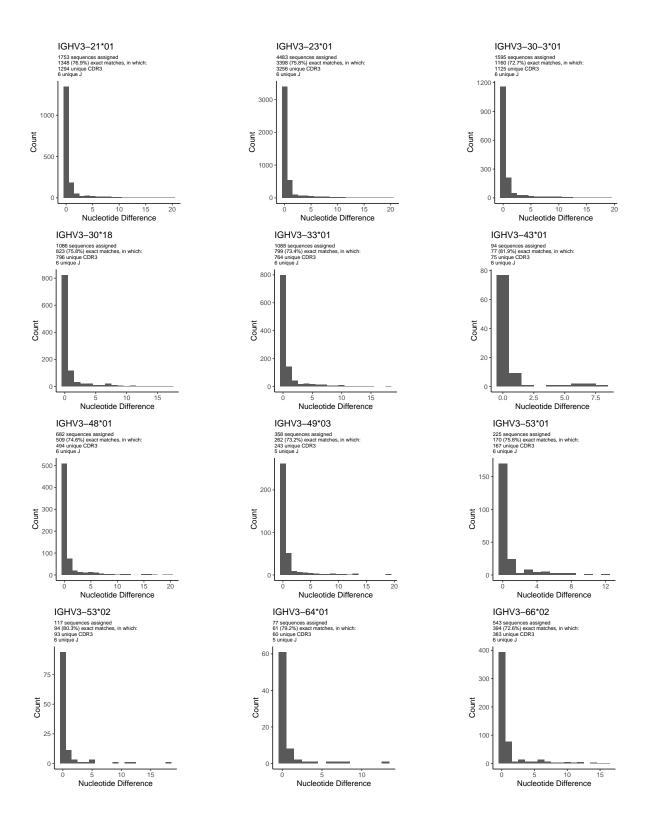
1	Novel sequence analysis 1.1 CDR3 length distribution, in assignments to novel alleles	2 2
2	Variation from germline, in assignments to each allele	3
3	Allele usage in potential haplotype anchor genes	8
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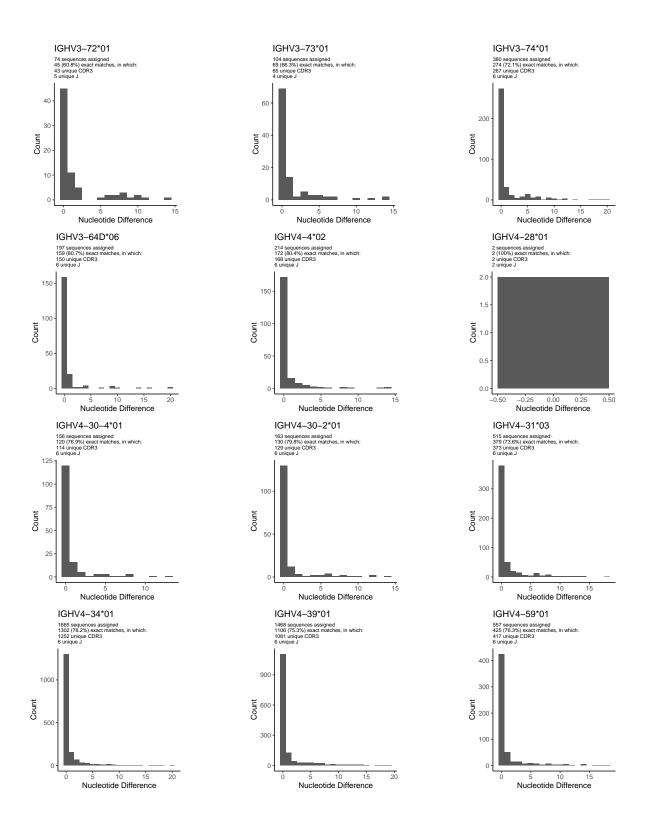
- 1 Novel sequence analysis
- 1.1 CDR3 length distribution, in assignments to novel alleles

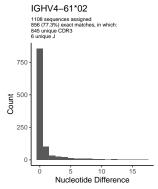
2 Variation from germline, in assignments to each allele





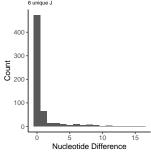






IGHV5-51*03

616 sequences assigned 473 (76.8%) exact matches, in which: 465 unique CDR3 6 unique J

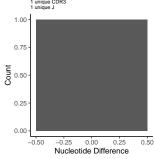


IGHV7-81*01

1 sequences assigned 1 (100%) exact matches, in which: 1 unique CDR3 1 unique J 1.00 0.75 Conut 0.50 0.25 0.00 -0.25 0.00 0.25 Nucleotide Difference 0.50

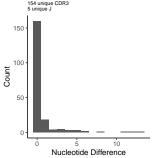


1 sequences assigned 1 (100%) exact matches, in which: 1 unique CDR3 1 unique J



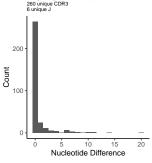
IGHV6-1*01

199 sequences assigned 160 (80.4%) exact matches, in which: 154 unique CDR3 5 unique J



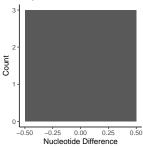
IGHV5-10-1*03

328 sequences assigned 264 (80.5%) exact matches, in which: 260 unique CDR3 6 unique J



IGHV7-4-1*01

3 sequences assigned 3 (100%) exact matches, in which: 2 unique CDR3 2 unique J



3 Allele usage in potential haplotype anchor genes



4 Haplotype plots

5 Configuration settings

```
## Repertoire file: /misc/work/jenkins/PRJEB26509/S73/S73/77/77/e8/Oaf59d43d1bc8aebfd7073800739ba/77_Fir
##
## Germline reference file: /misc/work/jenkins/PRJEB26509/S73/S73/77/77/f6/7c1dbaaf5240ab6a6e59a5b1cedef#
## Novel allele file:
##
## Species: Homosapiens
##
## Chain: IGHV
##
## Segment: V
##
## Warning no inferred sequences found.
```