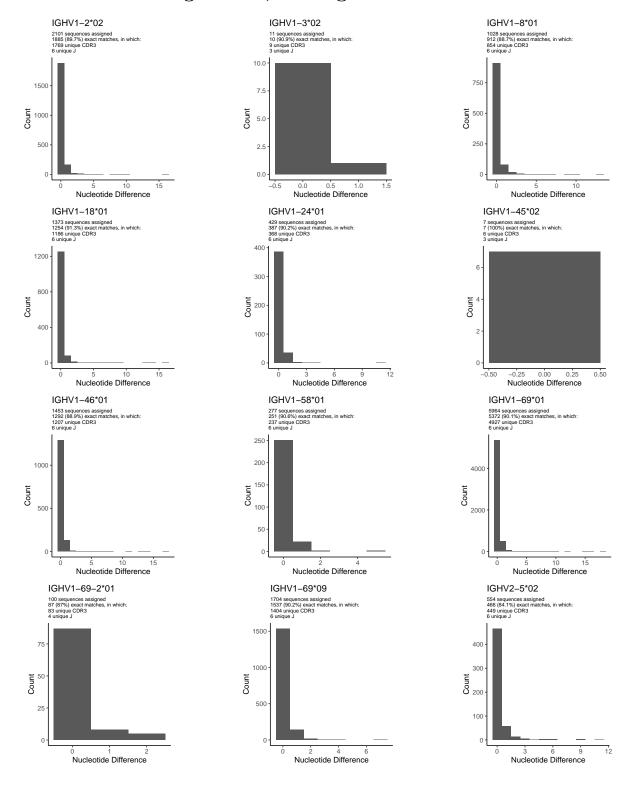
OGRDBstats Report

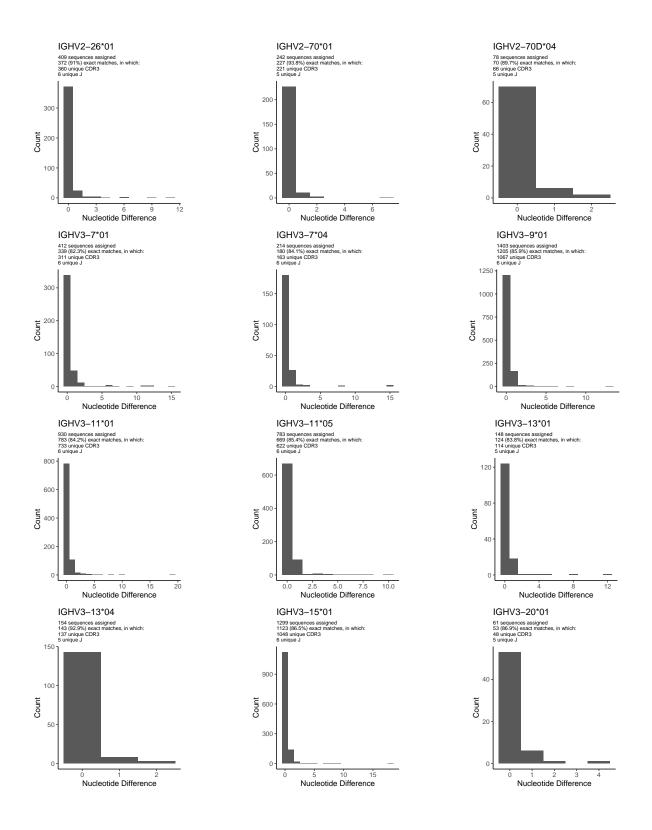
Contents

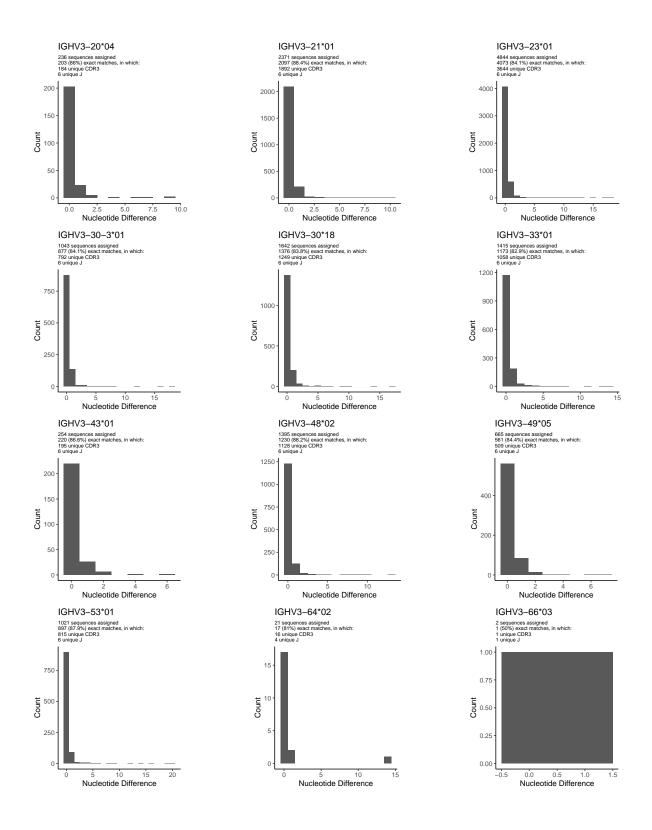
| 1 | Novel sequence analysis 1.1 CDR3 length distribution, in assignments to novel alleles | 2 2 |
|---|---|------------|
| 2 | Variation from germline, in assignments to each allele | 3 |
| 3 | Allele usage in potential haplotype anchor genes | 8 |
| 4 | Haplotype plots | 9 |
| 5 | Configuration settings | 10 |

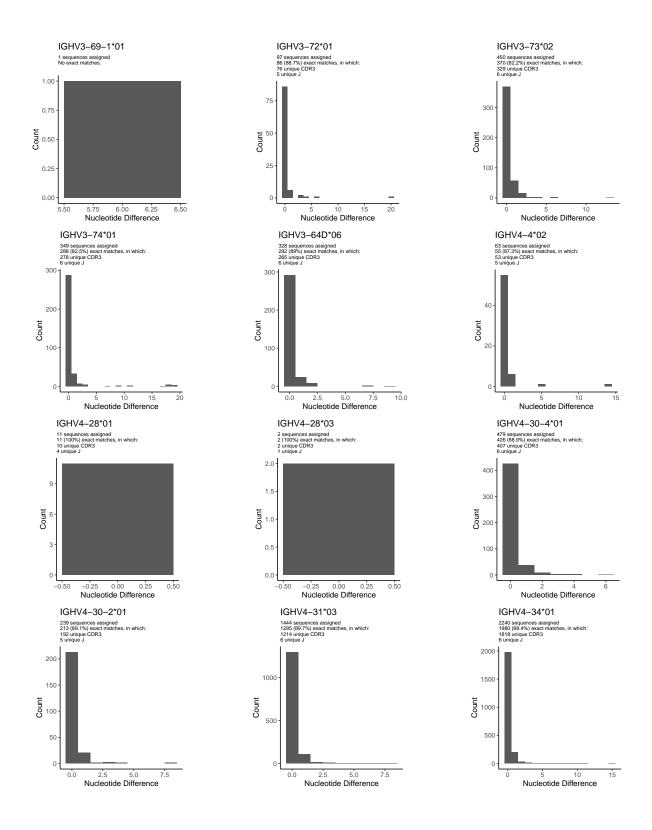
- 1 Novel sequence analysis
- 1.1 CDR3 length distribution, in assignments to novel alleles

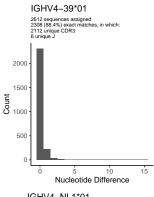
2 Variation from germline, in assignments to each allele





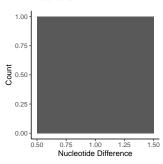






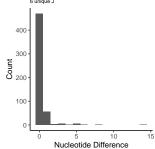
IGHV4-NL1*01

1 sequences assigned No exact matches.



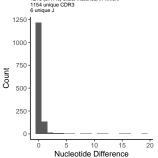
IGHV6-1*01

546 sequences assigned 470 (86.1%) exact matches, in which: 431 unique CDR3 6 unique J

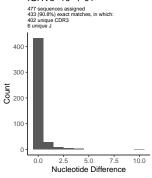


IGHV4-59*01

1398 sequences assigned 1218 (87.1%) exact matches, in which: 1154 unique CDR3 6 unique J

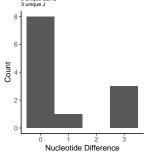


IGHV5-10-1*01



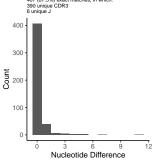
IGHV7-4-1*01

12 sequences assigned 8 (66.7%) exact matches, in which: 8 unique CDR3 3 unique J

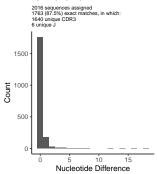


IGHV4-61*01

465 sequences assigned 407 (87.5%) exact matches, in which: 390 unique CDR3 6 unique J



IGHV5-51*01



3 Allele usage in potential haplotype anchor genes



4 Haplotype plots

5 Configuration settings

```
## Repertoire file: /misc/work/jenkins/PRJEB26509/S8/S8/8/06/97740a921a1b220fa924752283541b/8_Finale_
##
## Germline reference file: /misc/work/jenkins/PRJEB26509/S8/S8/8/03/dc29c3561c82e1aa84b8d0f727b7b5/r
##
## Novel allele file:
##
## Species: Homosapiens
##
## Chain: IGHV
##
## Segment: V
##
## Warning no inferred sequences found.
```