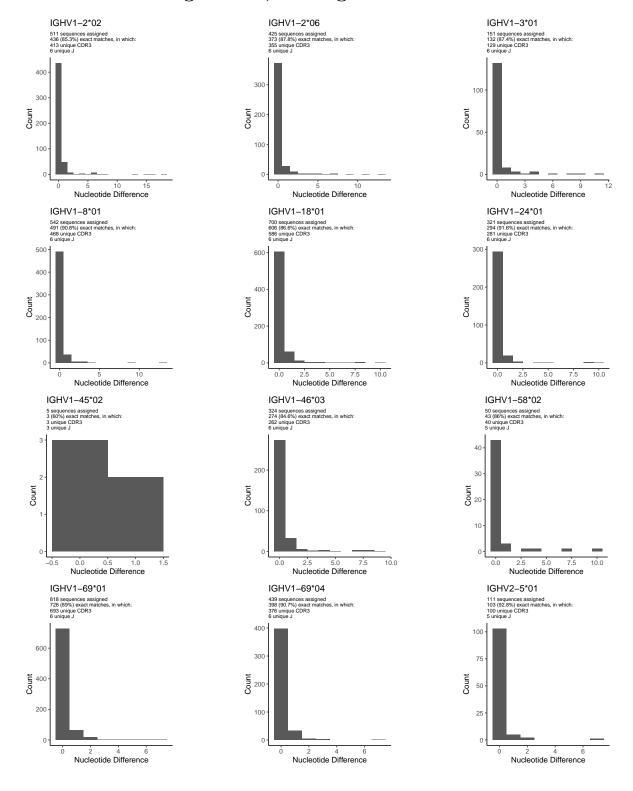
OGRDBstats Report

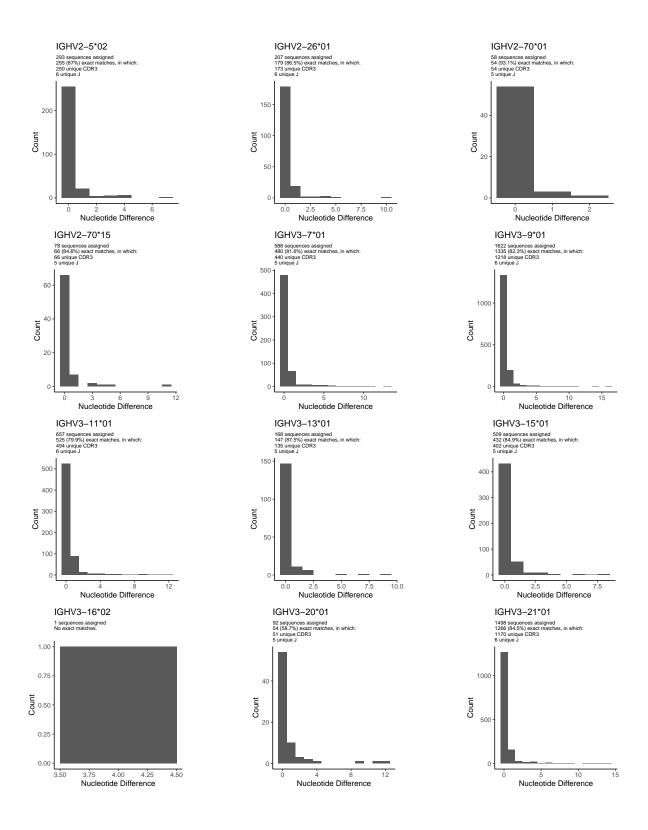
Contents

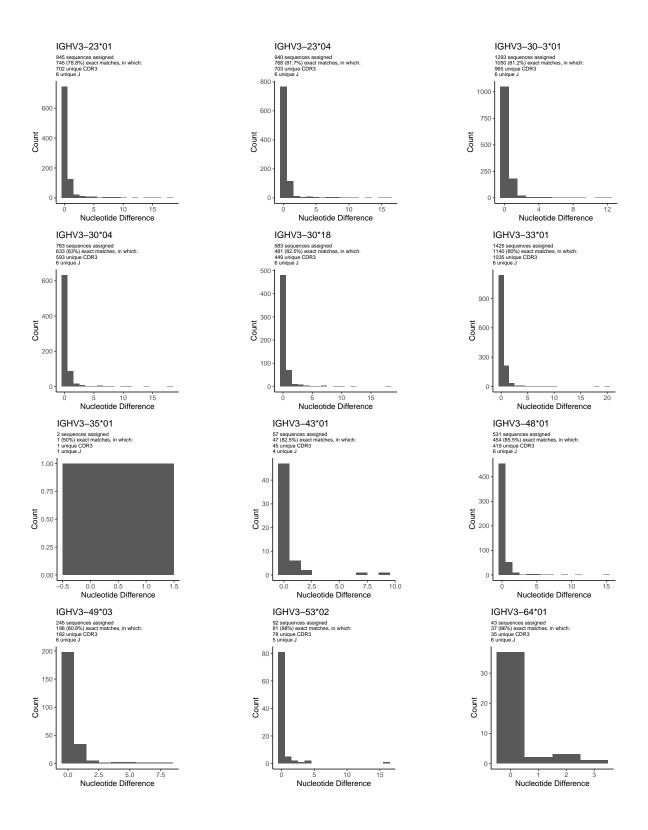
1	Novel sequence analysis 1.1 CDR3 length distribution, in assignments to novel alleles	2 2
2	Variation from germline, in assignments to each allele	3
3	Allele usage in potential haplotype anchor genes	8
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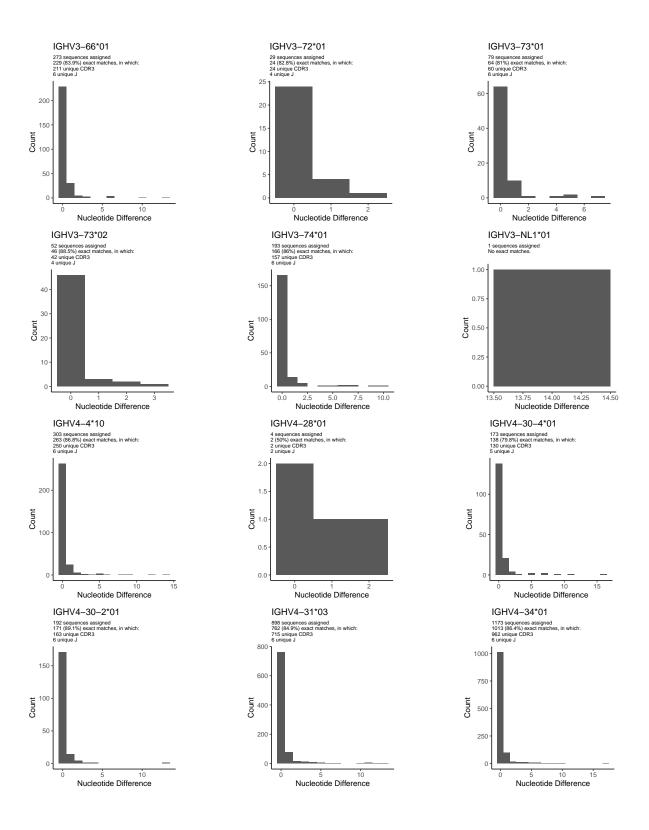
- 1 Novel sequence analysis
- 1.1 CDR3 length distribution, in assignments to novel alleles

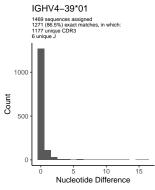
2 Variation from germline, in assignments to each allele





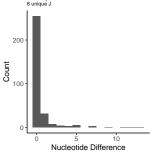






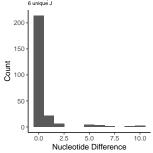
IGHV4-NL1*01

314 sequences assigned 255 (81.2%) exact matches, in which: 245 unique CDR3 6 unique J



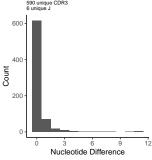
IGHV7-4-1*02

253 sequences assigned 214 (84.6%) exact matches, in which: 205 unique CDR3 6 unique J



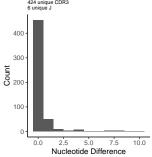
IGHV4-59*01

733 sequences assigned 616 (84%) exact matches, in which: 590 unique CDR3 6 unique J



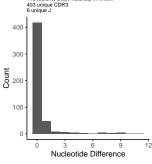
IGHV5-51*03

538 sequences assigned 454 (84.4%) exact matches, in which: 424 unique CDR3 6 unique J

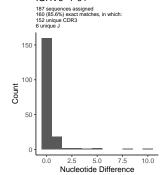


IGHV4-61*11

502 sequences assigned 418 (83.3%) exact matches, in which: 403 unique CDR3 6 unique J



IGHV6-1*01



3 Allele usage in potential haplotype anchor genes



4 Haplotype plots

5 Configuration settings

```
## Repertoire file: /misc/work/jenkins/PRJEB26509/S39/S39/42/42/cc/866f693137eb180d1607ec52e7b2c1/42_Fir
## ## Germline reference file: /misc/work/jenkins/PRJEB26509/S39/S39/42/42/6a/78f975f6a7d48e79a87e3fe270ef
## Novel allele file:
## Species: Homosapiens
## ## Chain: IGHV
## ## Segment: V
## ## Warning no inferred sequences found.
```