

OGRDBstats Report

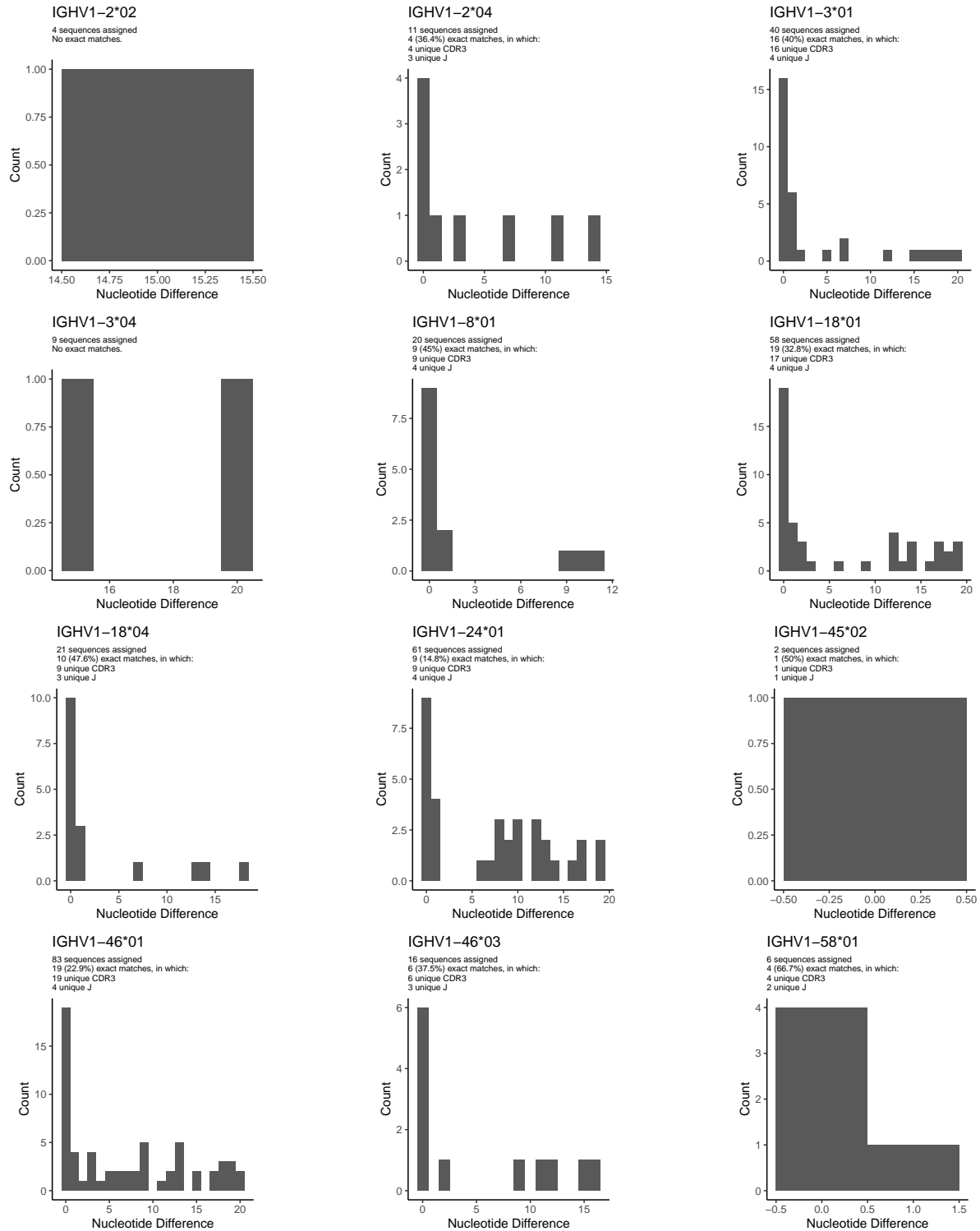
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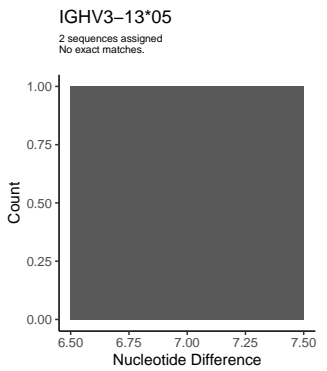
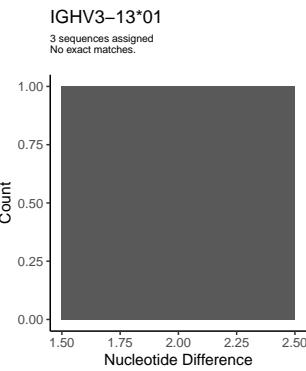
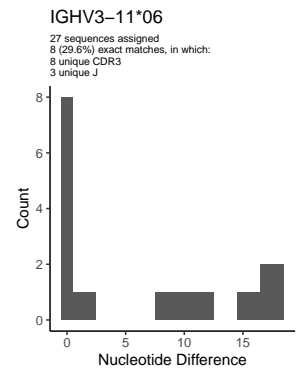
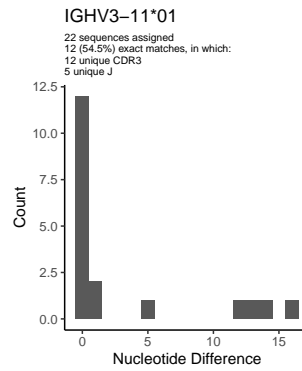
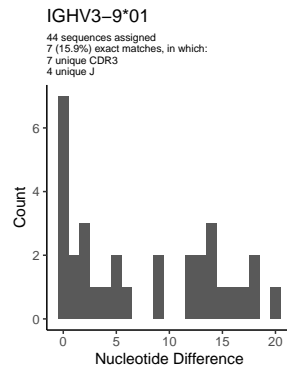
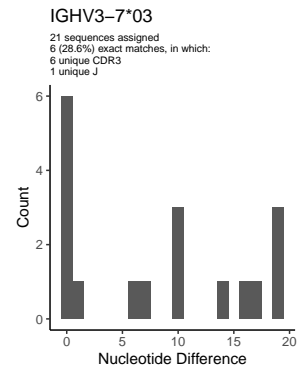
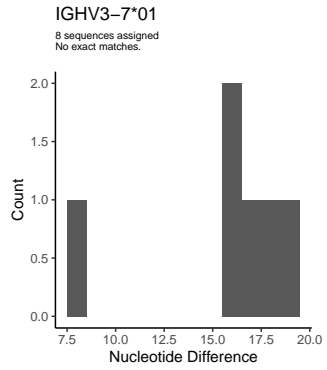
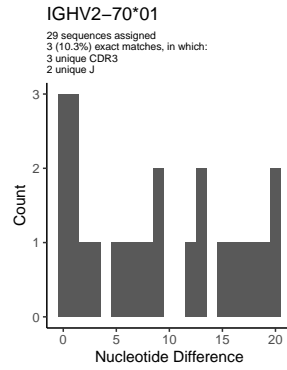
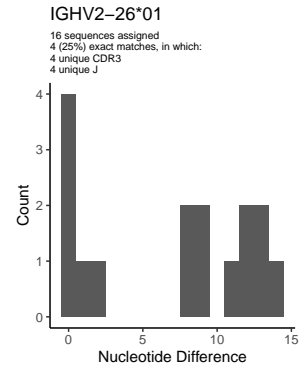
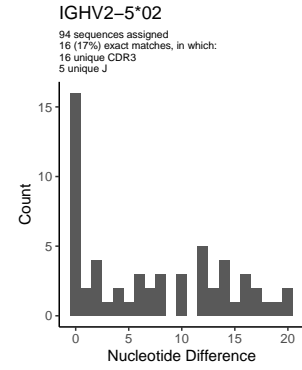
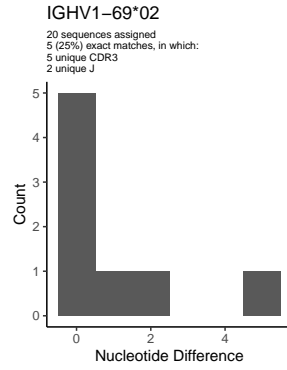
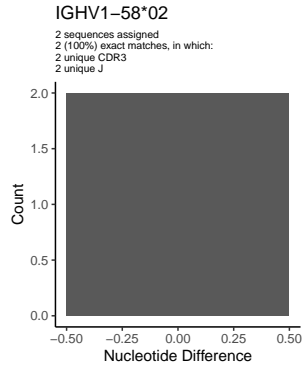
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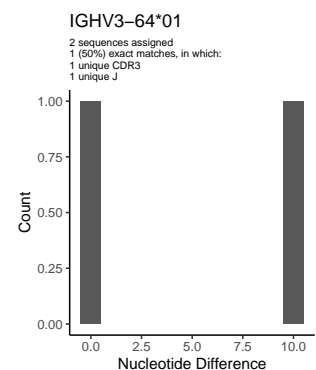
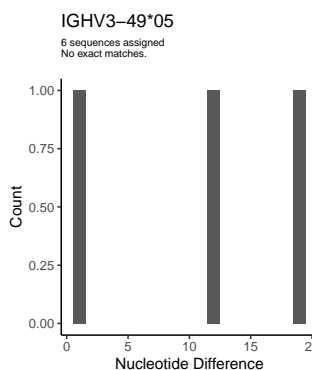
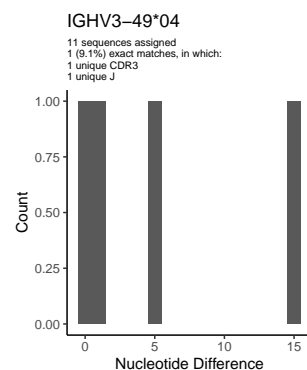
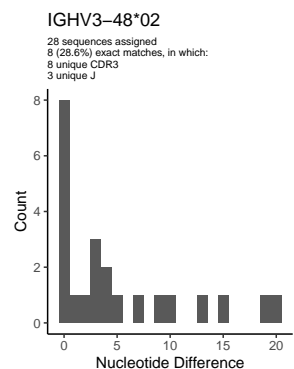
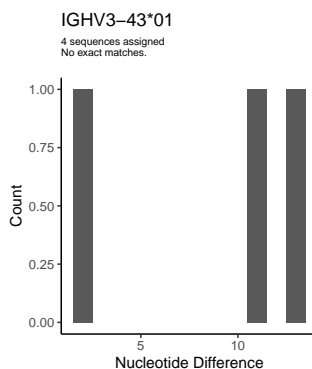
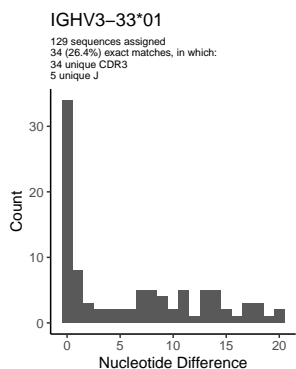
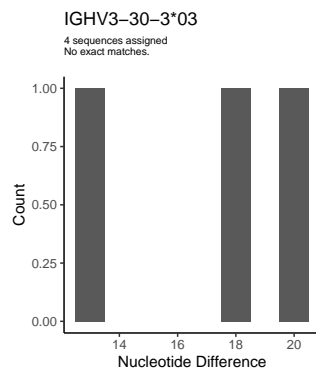
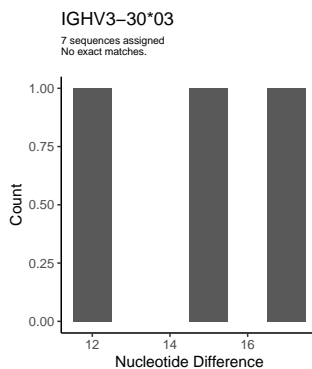
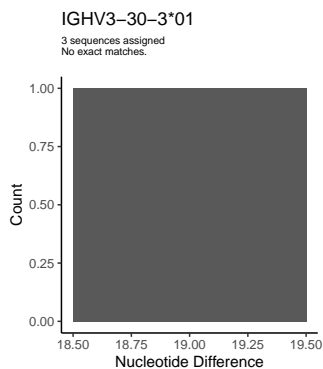
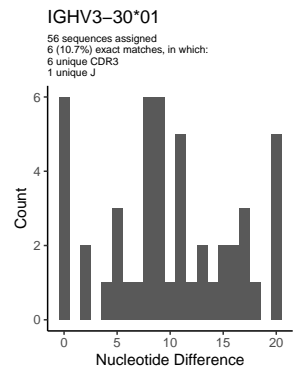
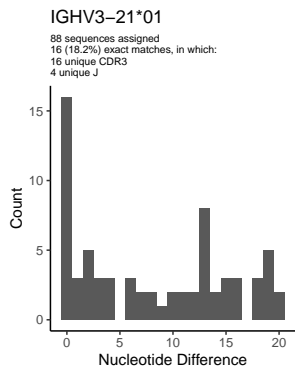
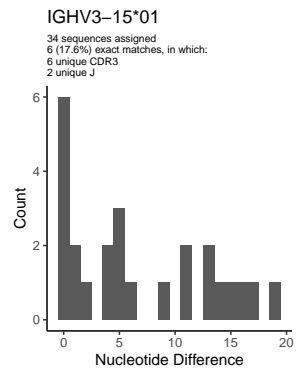
1 Novel sequence analysis

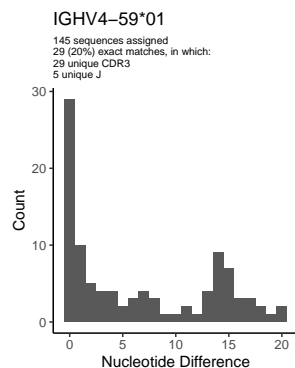
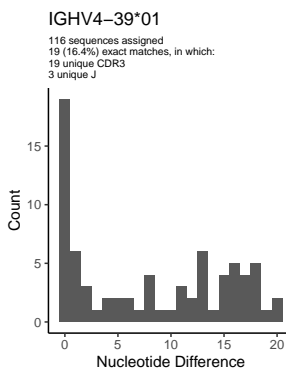
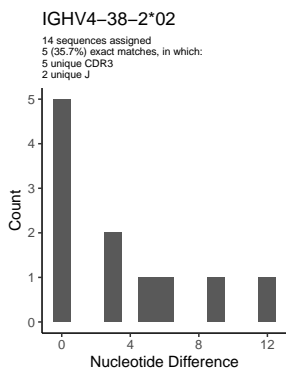
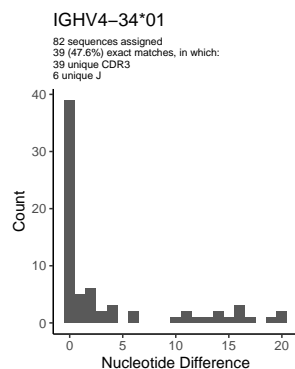
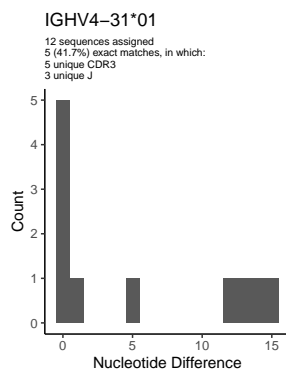
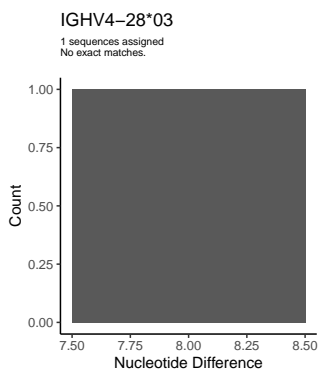
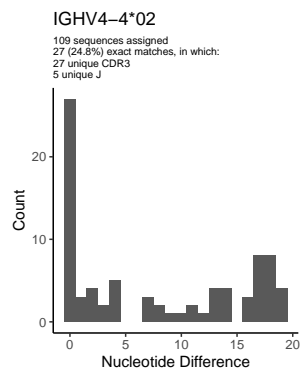
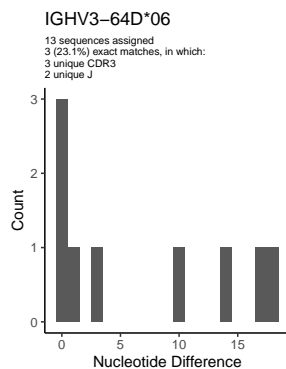
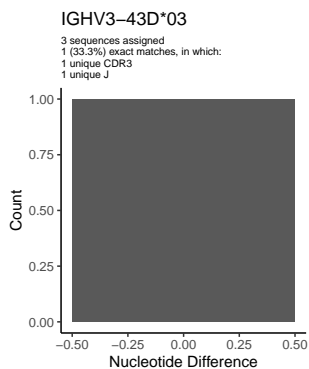
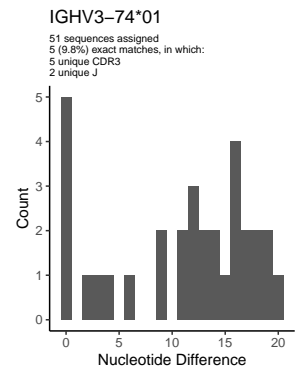
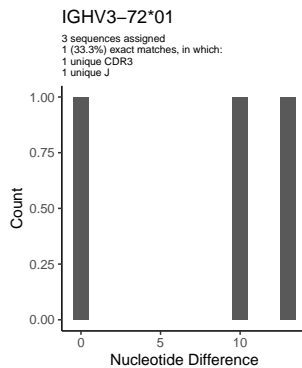
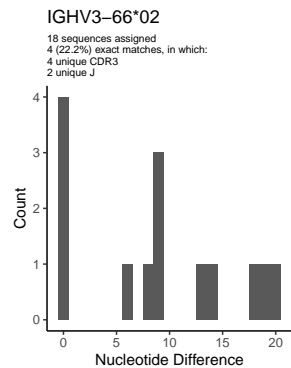
1.1 CDR3 length distribution, in assignments to novel alleles

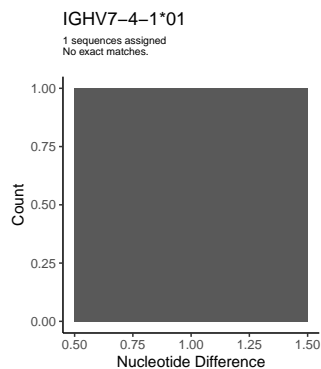
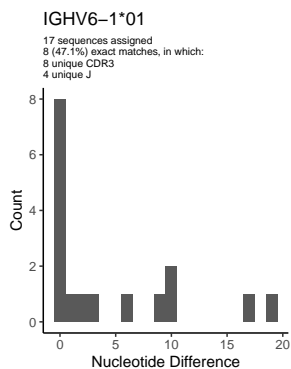
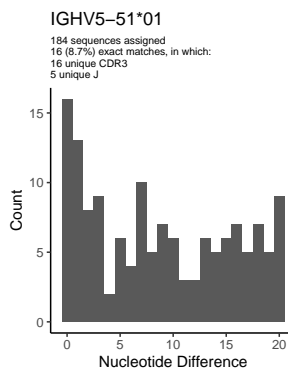
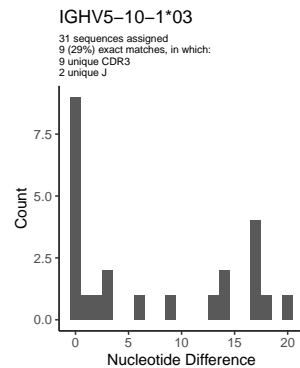
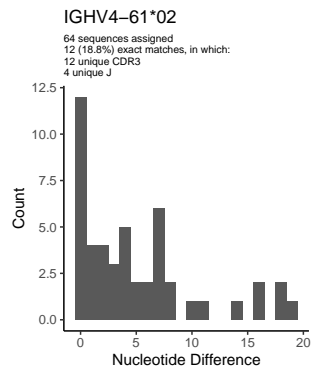
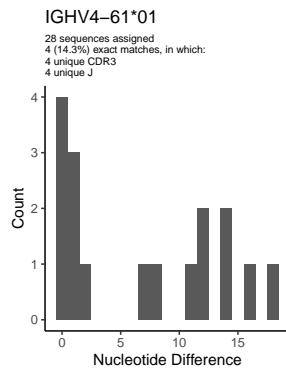
2 Variation from germline, in assignments to each allele











3 Allele usage in potential haplotype anchor genes



4 Haplotype plots

5 Configuration settings

```
## Repertoire file: /misc/work/jenkins/PRJNA248475/M2/M2_cln/M2_cln/M2_cln/f3/7869268f4446ff5edf434078e
##
## Germline reference file: /misc/work/jenkins/PRJNA248475/M2/M2_cln/M2_cln/M2_cln/2b/02f581163356937fa
##
## Novel allele file:
##
## Species: Homosapiens
##
## Chain: IGHV
##
## Segment: V
##
## Warning    no inferred sequences found.
```