

OGRDBstats Report

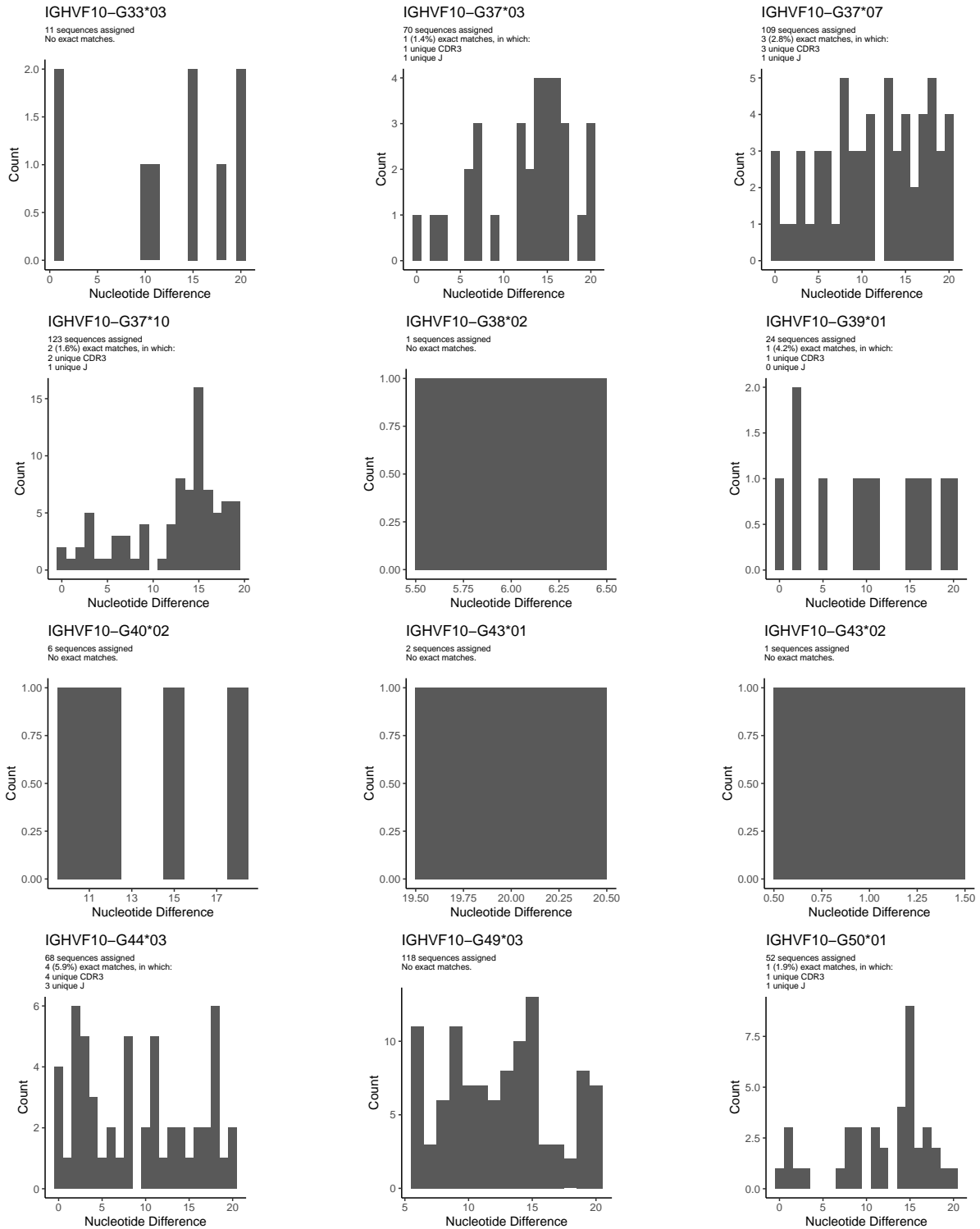
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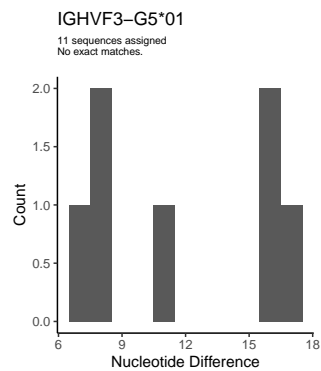
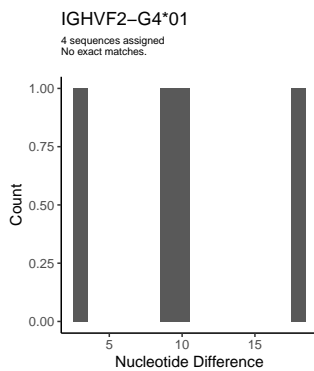
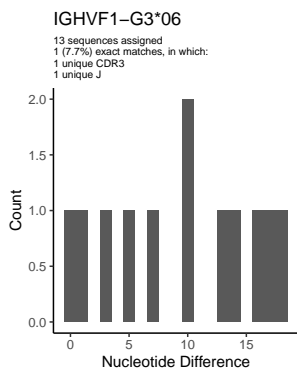
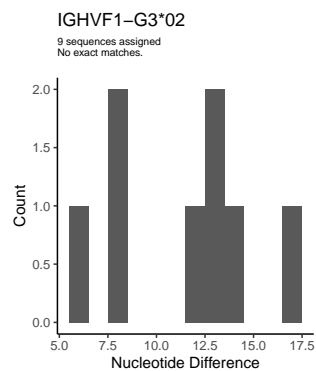
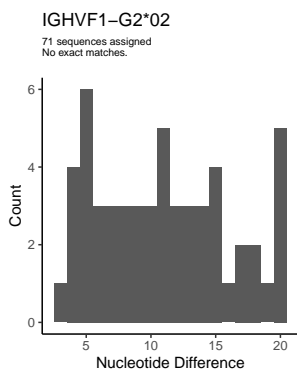
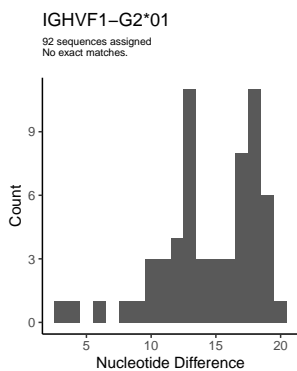
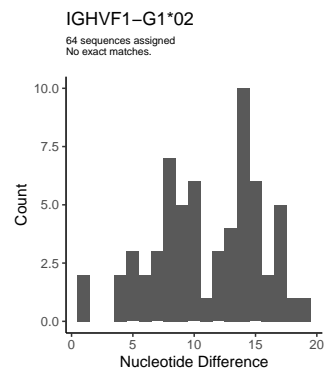
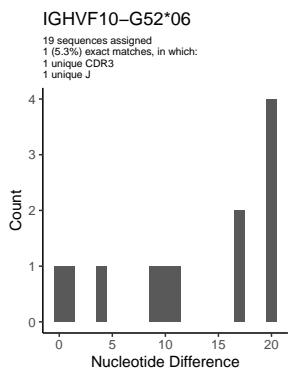
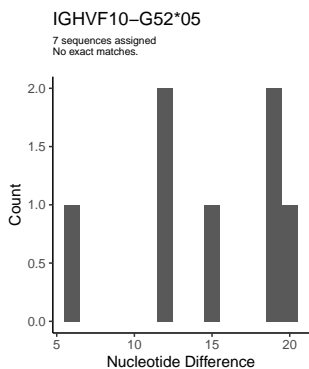
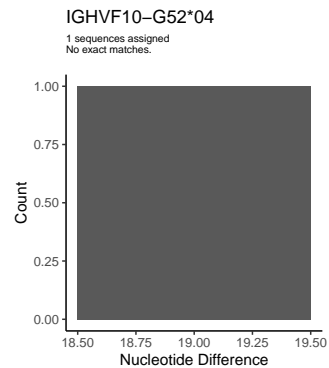
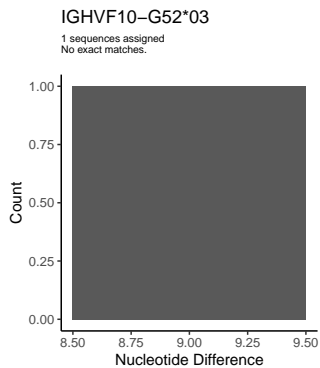
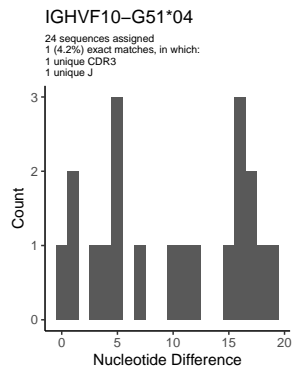
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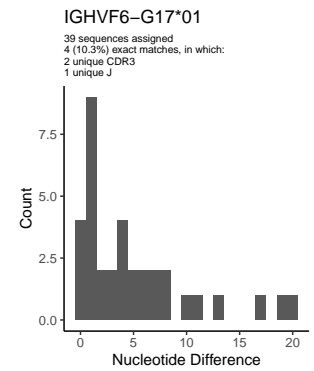
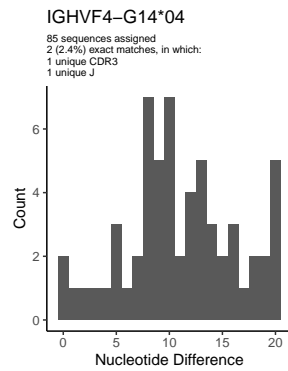
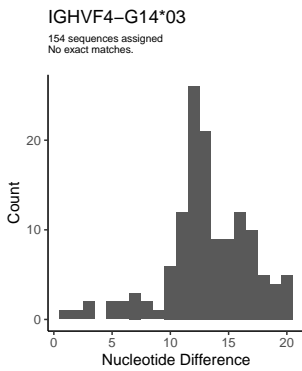
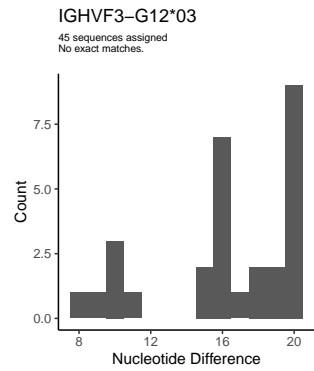
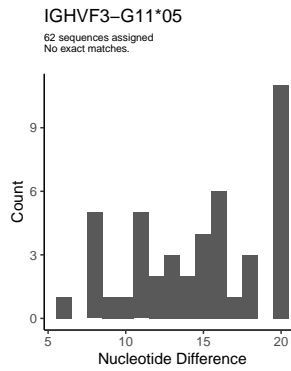
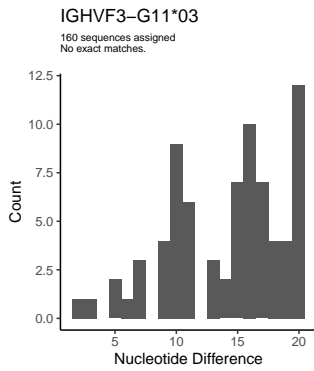
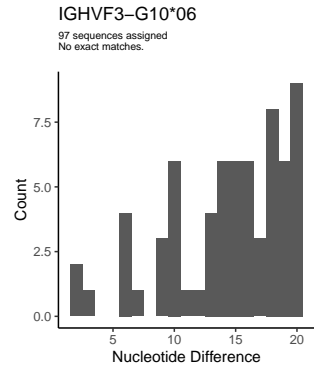
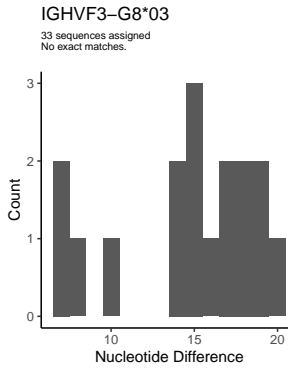
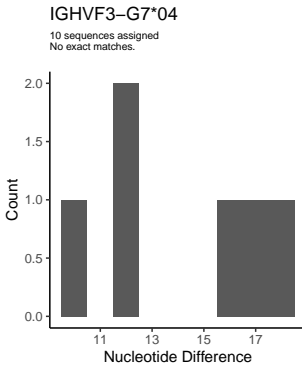
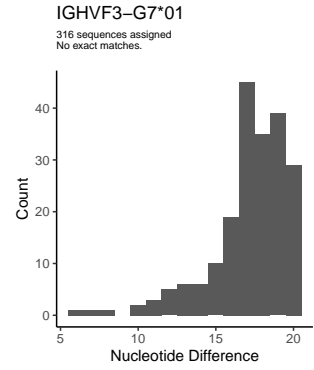
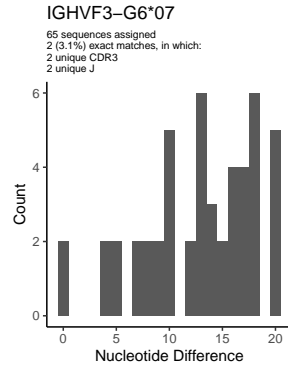
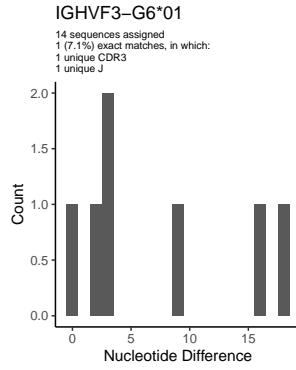
1 Novel sequence analysis

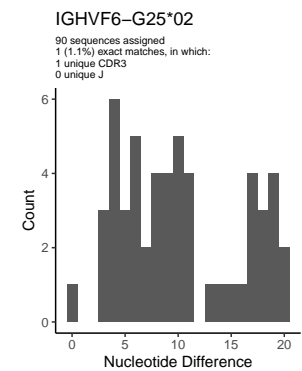
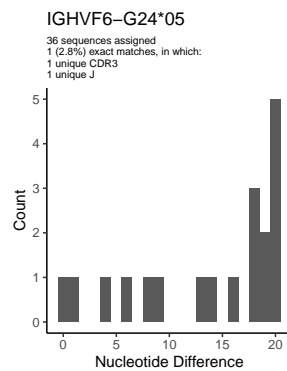
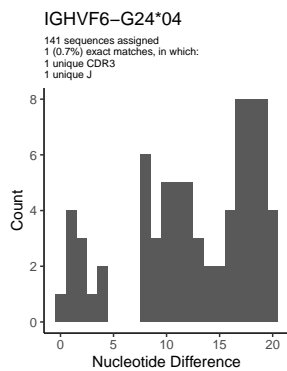
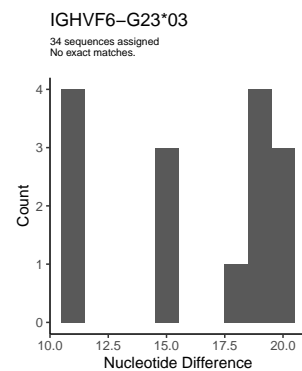
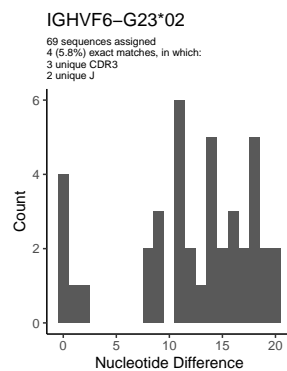
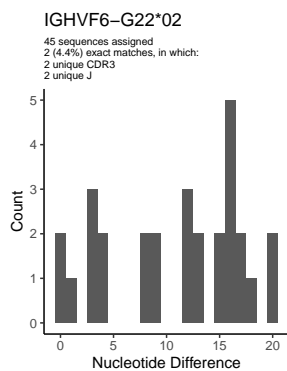
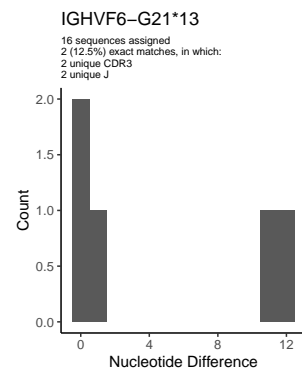
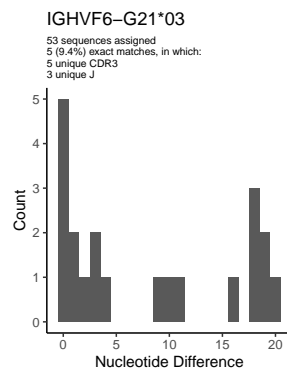
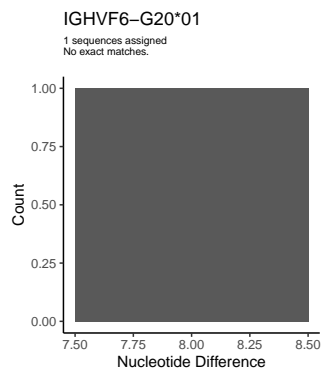
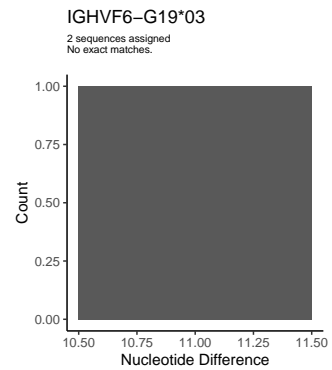
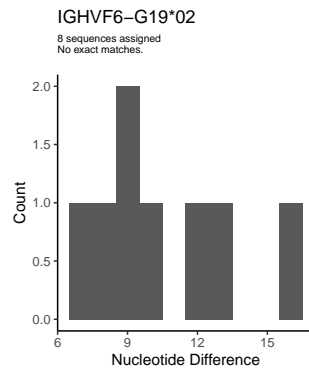
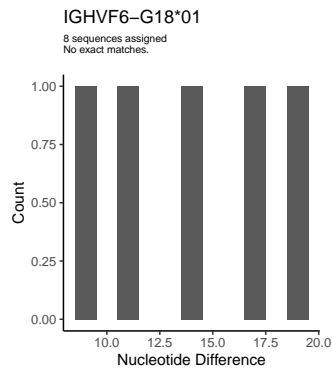
1.1 CDR3 length distribution, in assignments to novel alleles

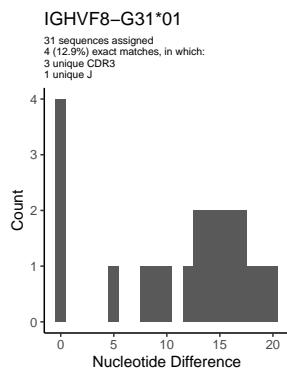
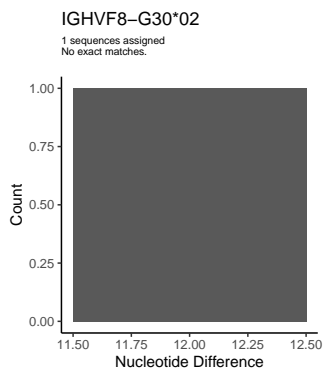
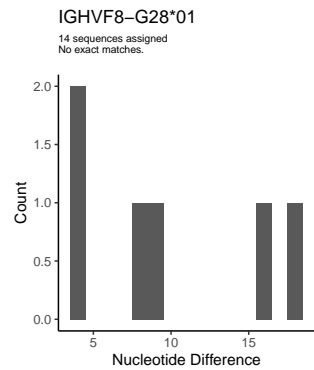
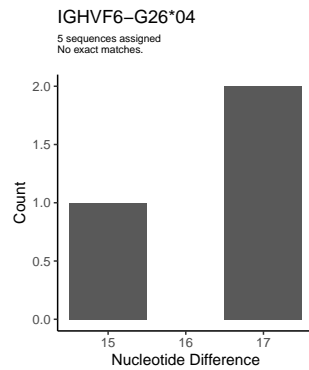
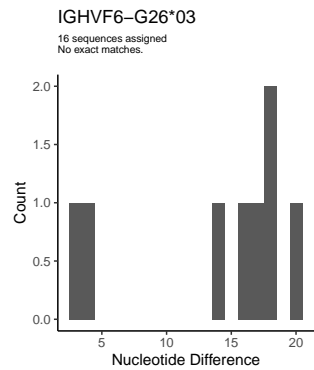
2 Variation from germline, in assignments to each allele











3 Allele usage in potential haplotype anchor genes



4 Haplotype plots

5 Configuration settings

```
## Repertoire file: /misc/work/jenkins/PRJNA248475/M3/M3_cln/M3_cln/M3_cln/24/a209f81cb8d29fbb334cd10c1
##
## Germline reference file: /misc/work/jenkins/PRJNA248475/M3/M3_cln/M3_cln/M3_cln/54/1efbe6c92217f71bd
##
## Novel allele file:
##
## Species: Homosapiens
##
## Chain: IGHV
##
## Segment: V
##
## Warning    no inferred sequences found.
```