

OGRDBstats Report

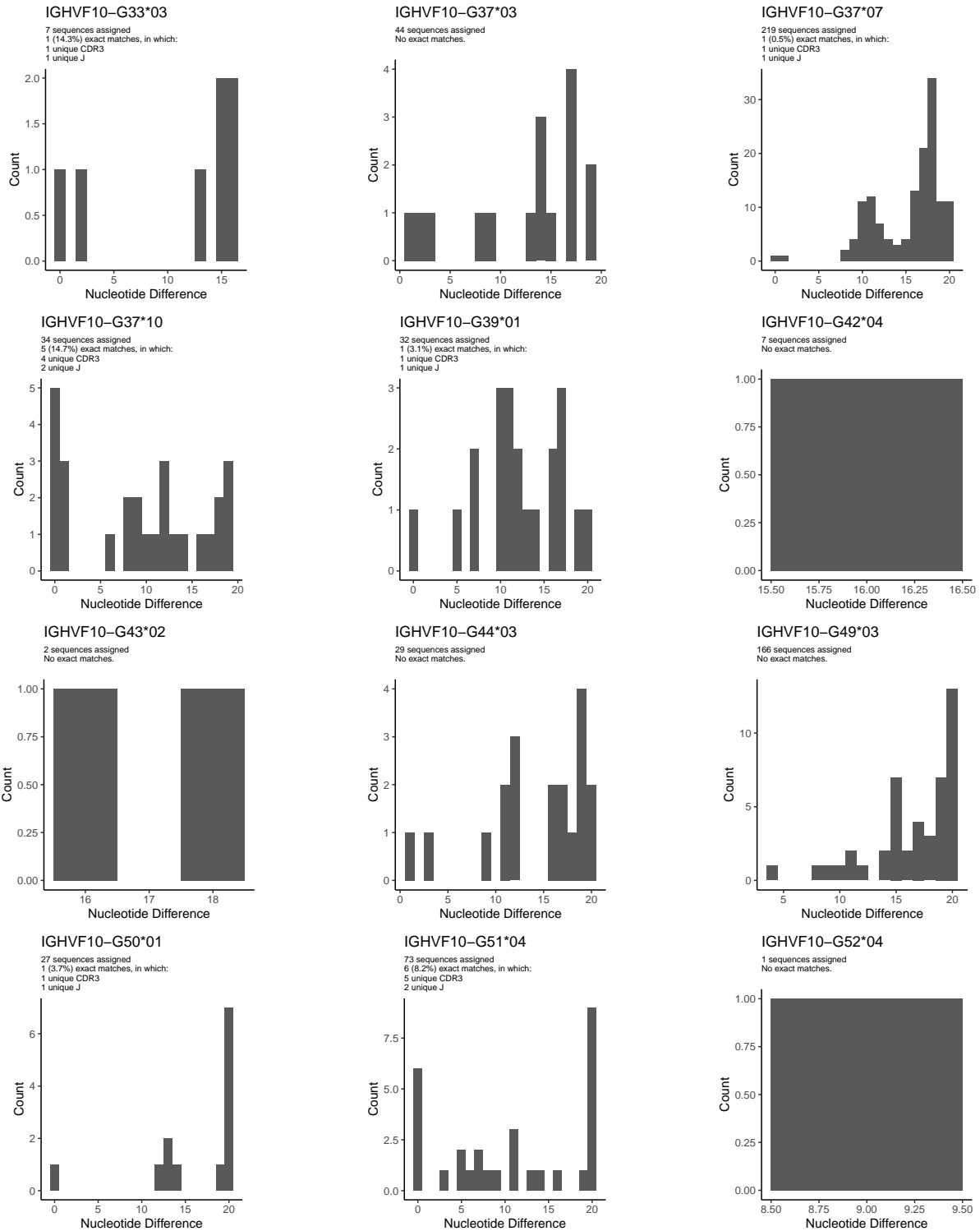
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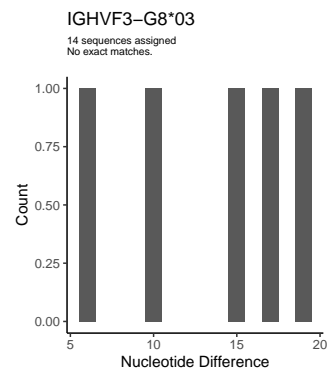
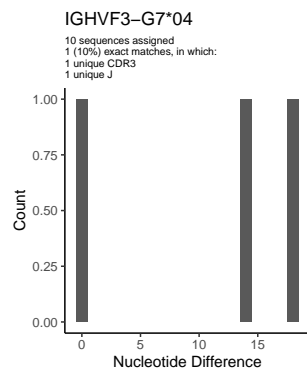
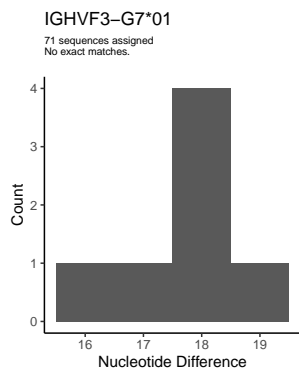
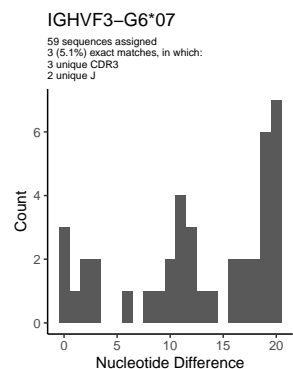
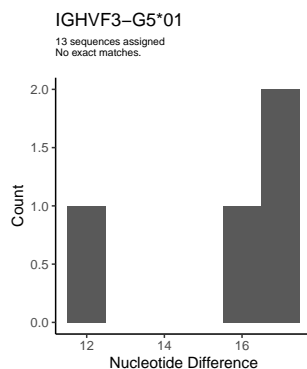
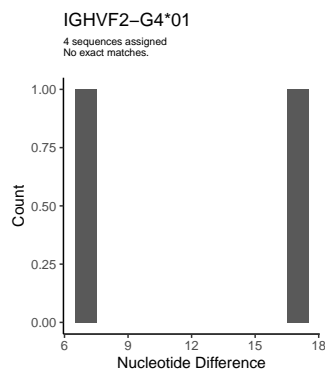
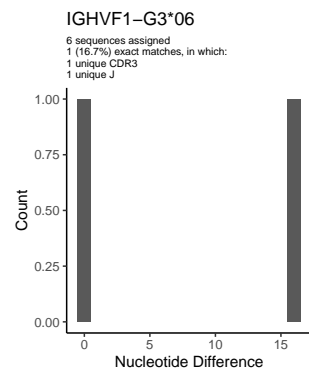
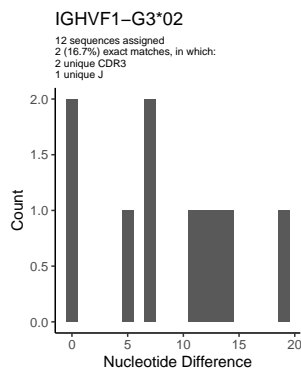
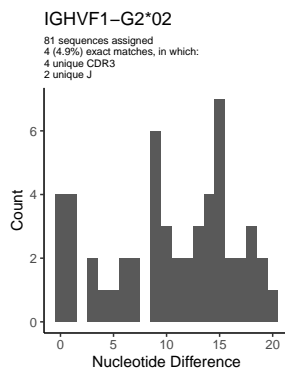
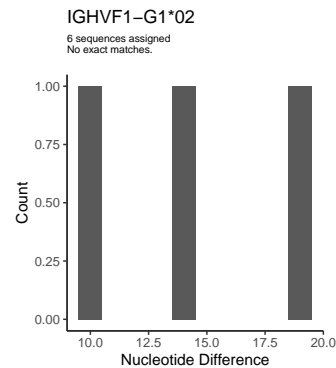
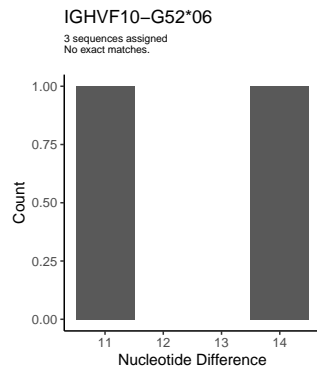
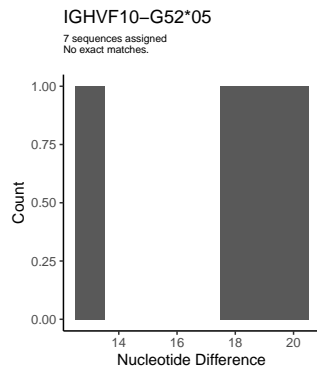
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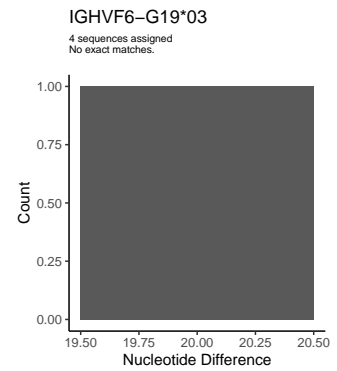
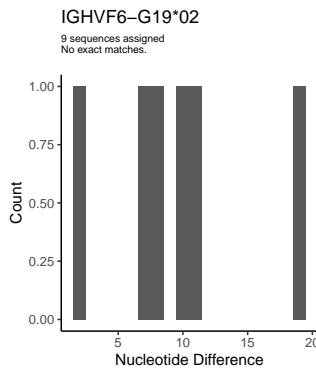
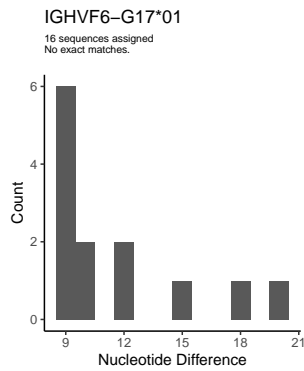
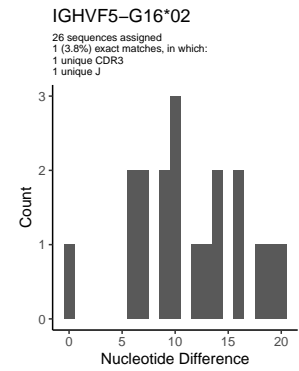
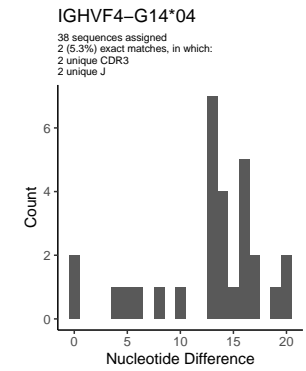
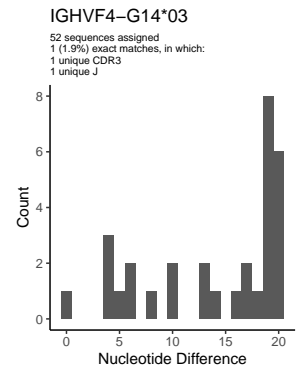
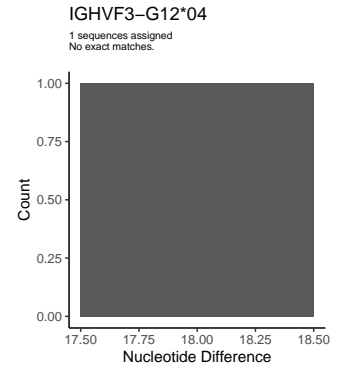
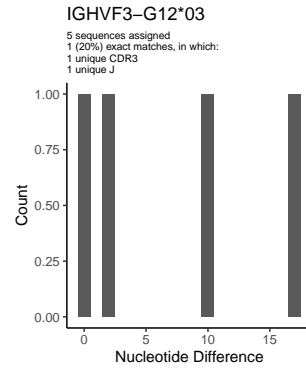
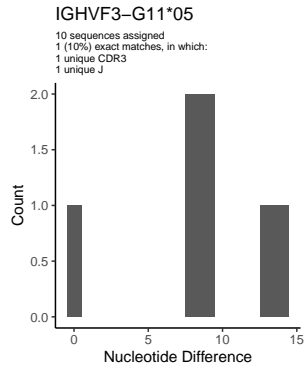
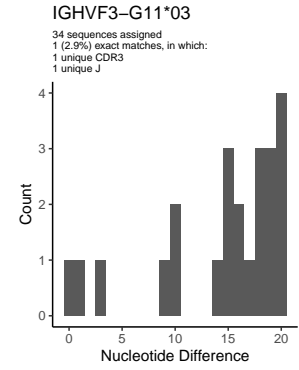
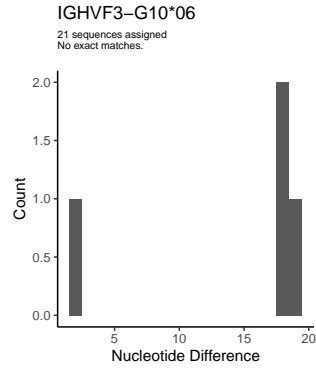
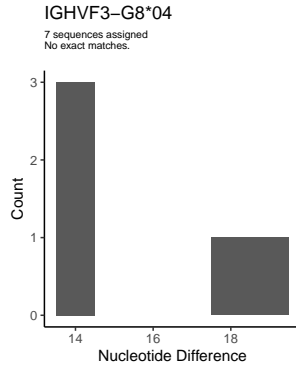
1 Novel sequence analysis

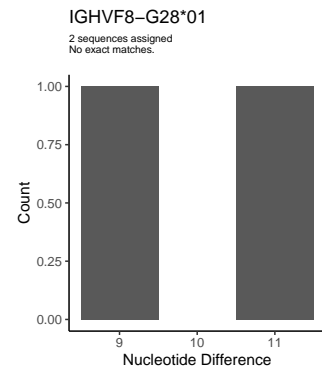
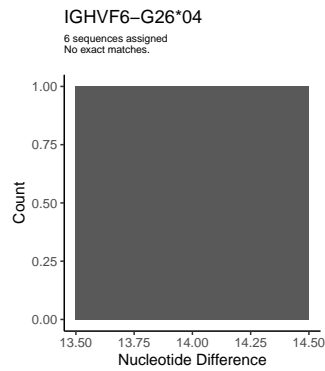
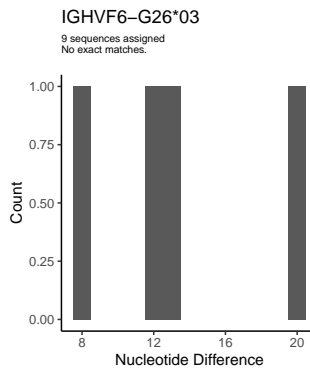
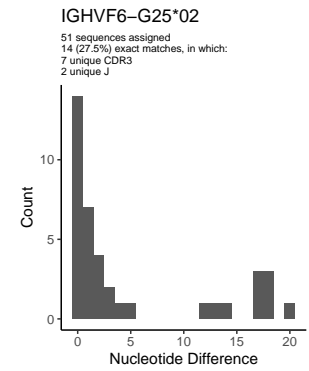
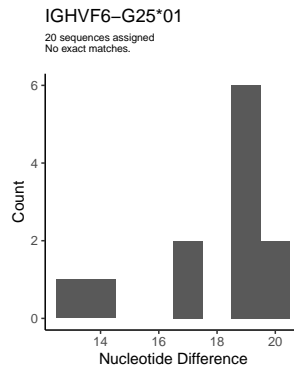
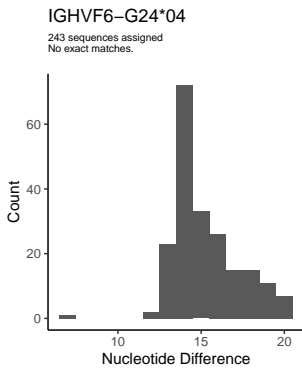
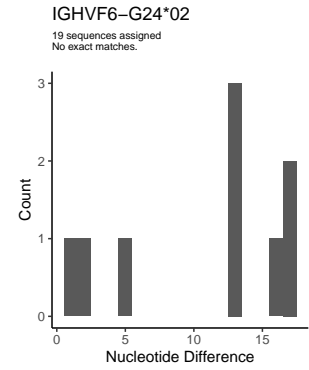
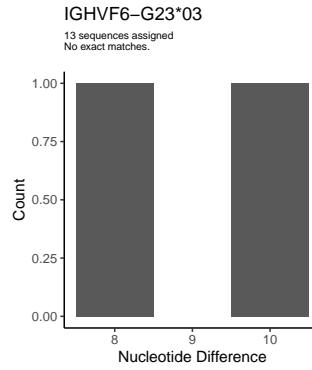
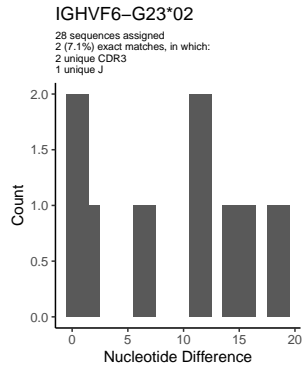
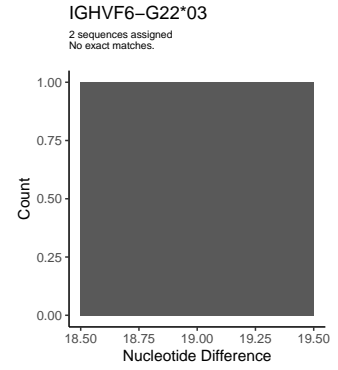
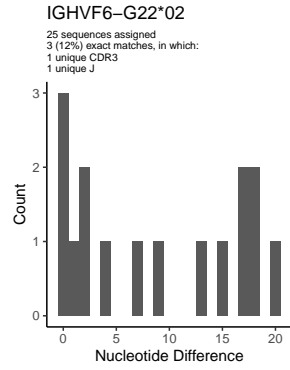
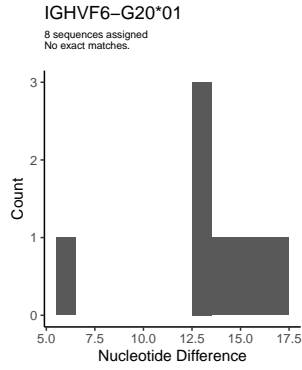
1.1 CDR3 length distribution, in assignments to novel alleles

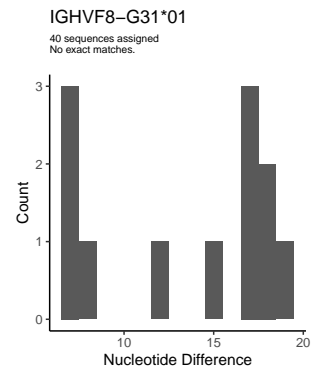
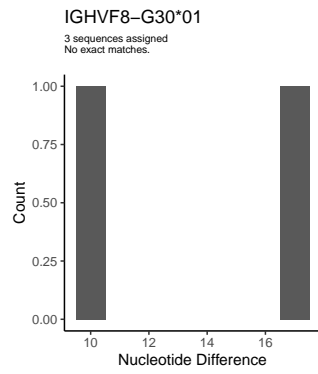
2 Variation from germline, in assignments to each allele











3 Allele usage in potential haplotype anchor genes



4 Haplotype plots

5 Configuration settings

```
## Repertoire file: /misc/work/jenkins/PRJNA248475/M5/M5_lesion/M5_lesion/M5_lesion/e4/a9ed3fb2d1cd4eb1
##
## Germline reference file: /misc/work/jenkins/PRJNA248475/M5/M5_lesion/M5_lesion/M5_lesion/e4/a9ed3fb2
##
## Novel allele file: /misc/work/jenkins/PRJNA248475/M5/M5_lesion/M5_lesion/M5_lesion/e4/a9ed3fb2d1cd4e
##
## Species: Homosapiens
##
## Chain: IGHV
##
## Segment: V
##
## Novel sequence(s) IGHVF3 G9 04_A319G are not listed in the genotype and will be ignored.
##
##
## No sequences found for IGHVF3 G9 04_A319G(check SEQUENCE_IMGT in input file)
```