

OGRDBstats Report

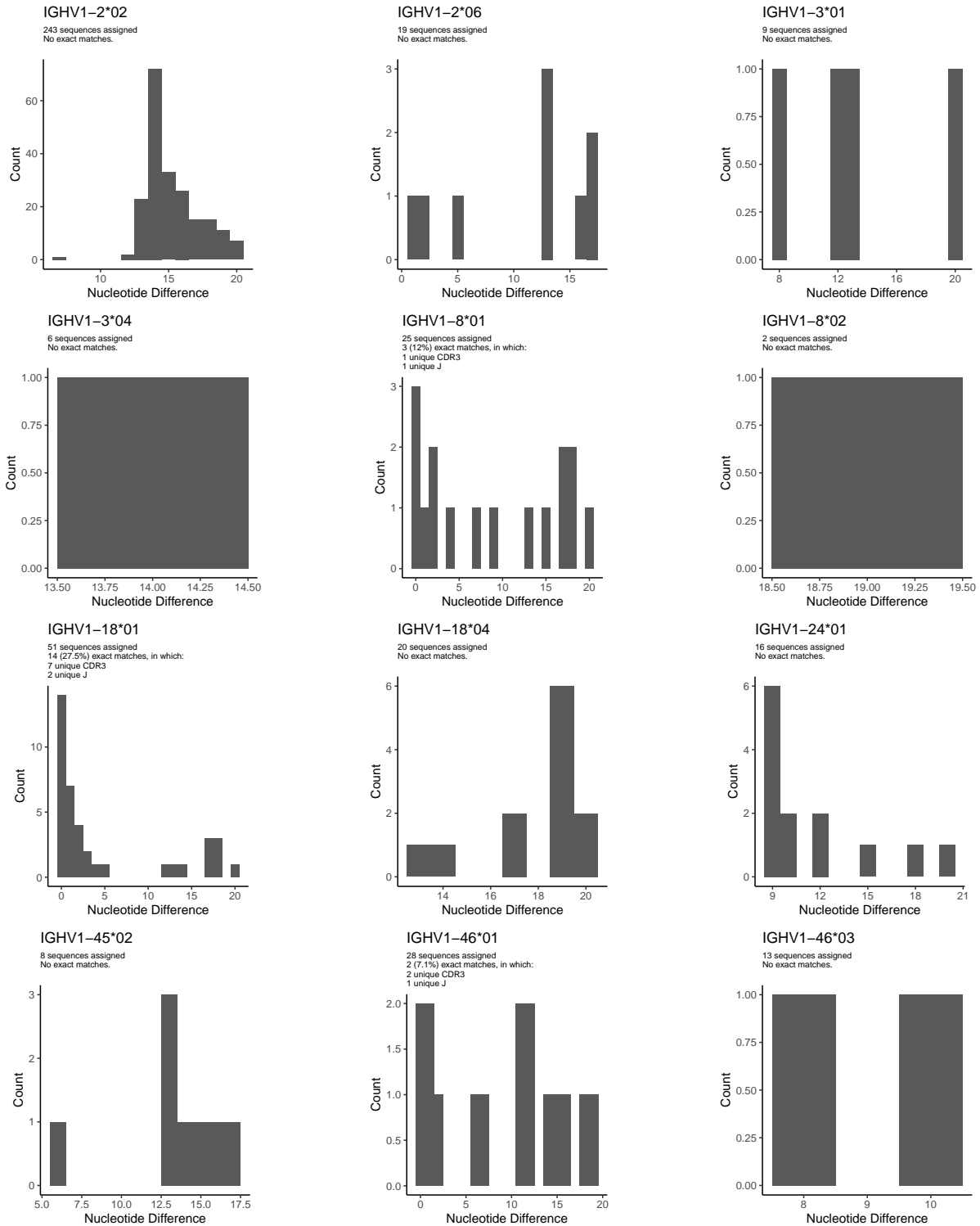
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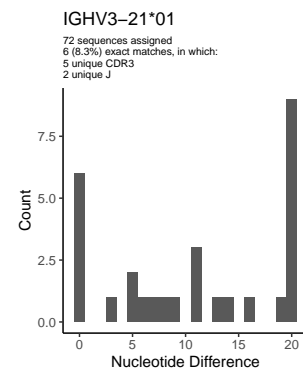
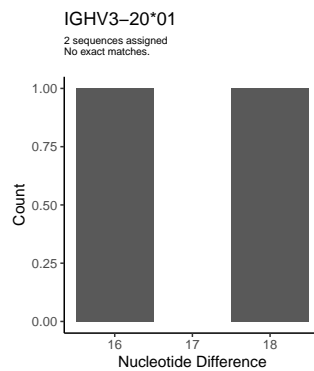
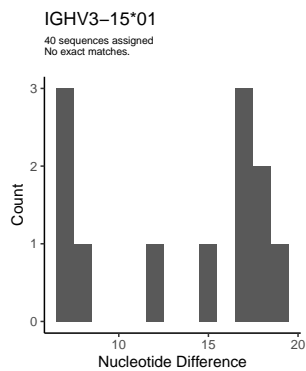
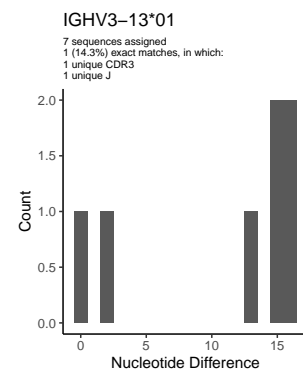
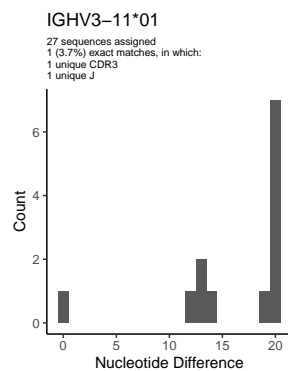
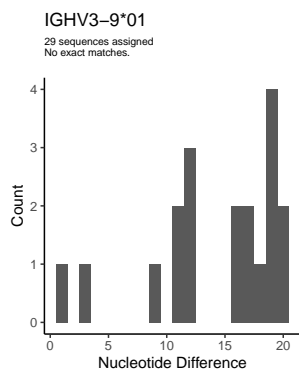
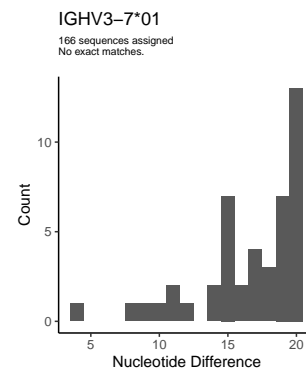
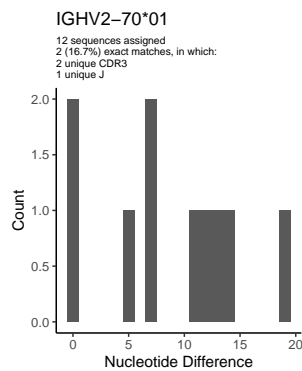
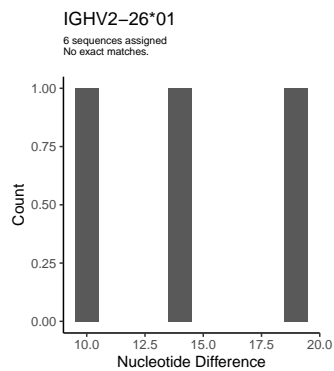
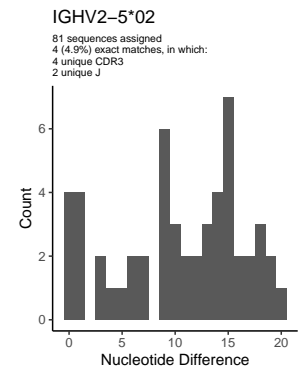
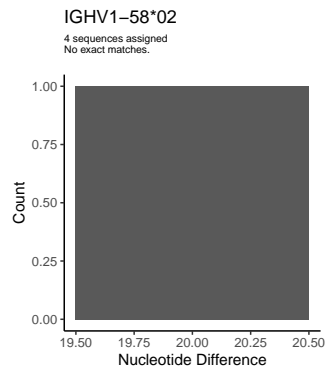
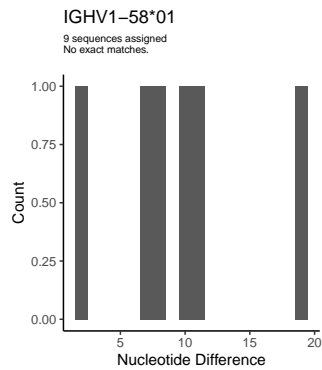
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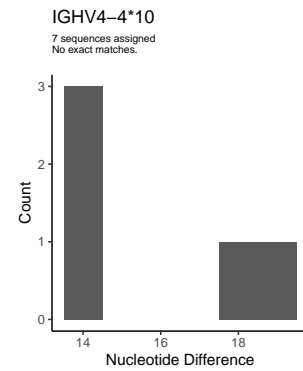
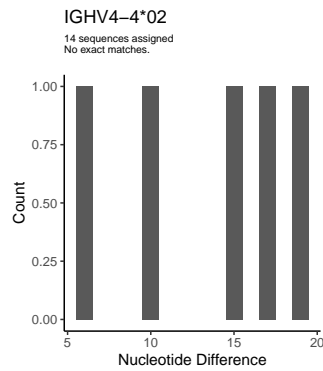
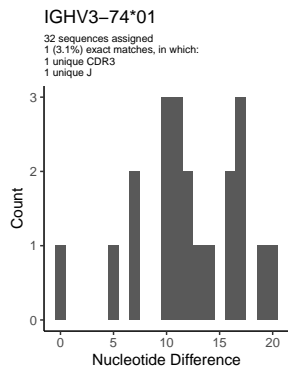
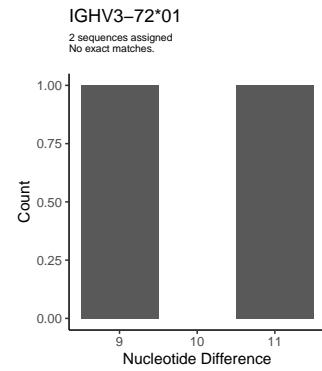
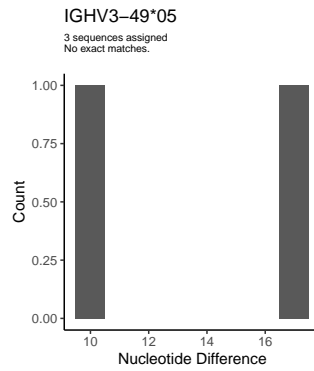
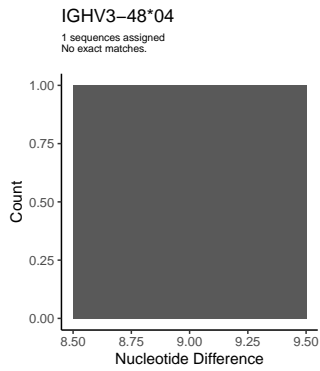
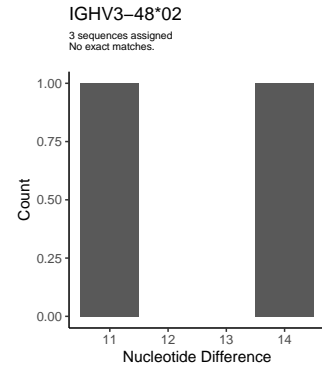
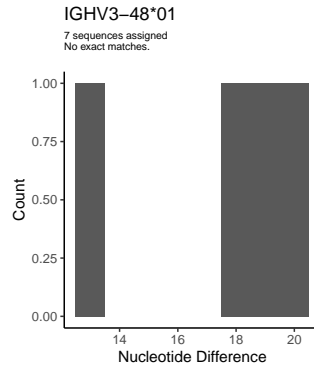
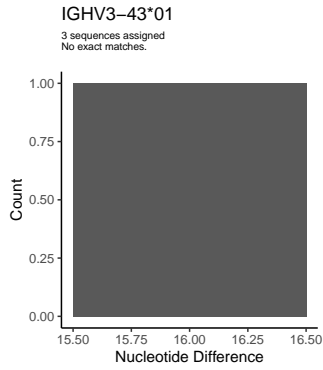
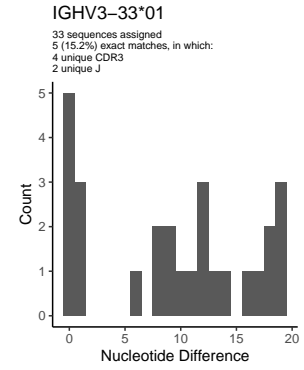
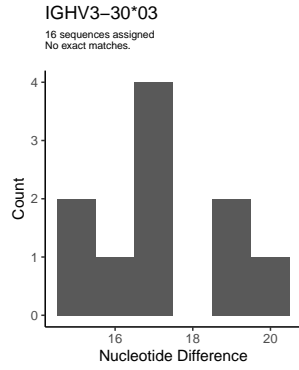
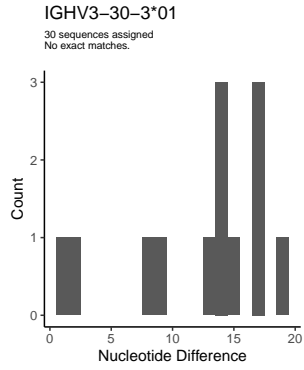
1 Novel sequence analysis

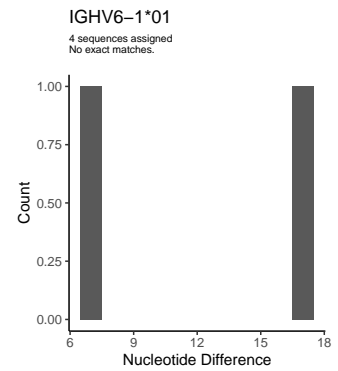
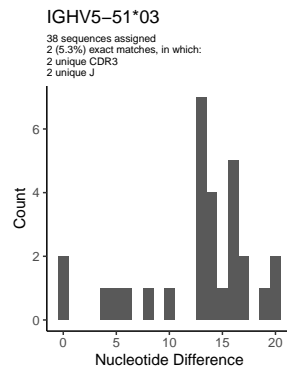
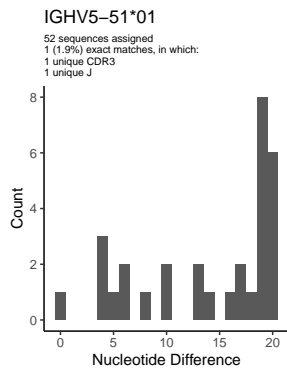
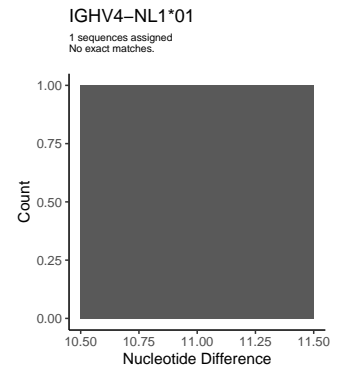
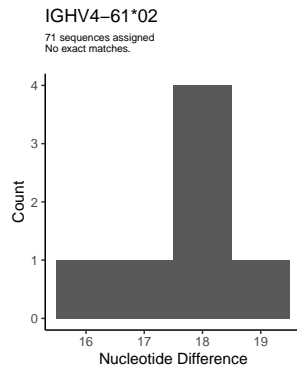
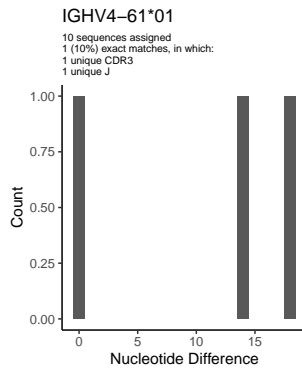
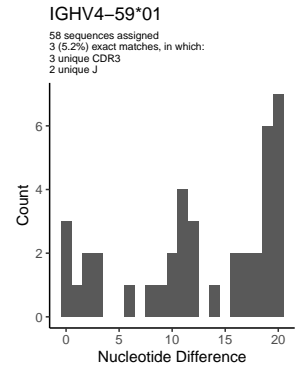
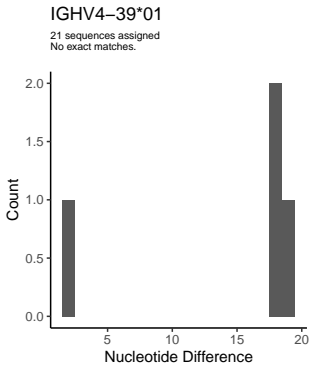
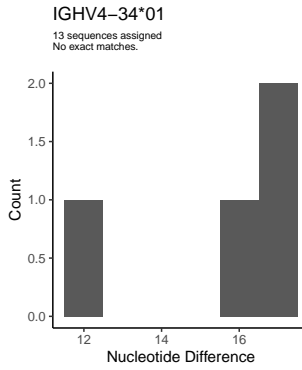
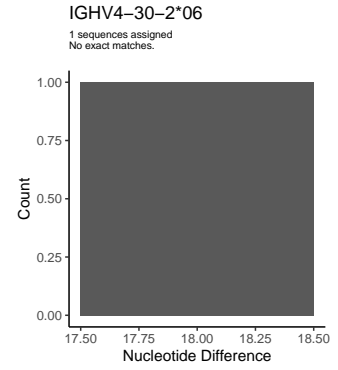
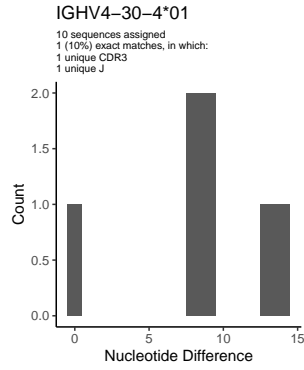
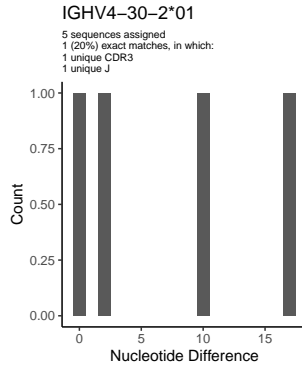
1.1 CDR3 length distribution, in assignments to novel alleles

2 Variation from germline, in assignments to each allele



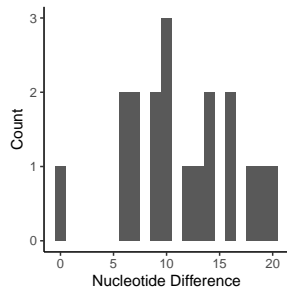






IGHV7-4-1*02

26 sequences assigned
1 (3.8%) exact matches, in which:
1 unique CDR3
1 unique J



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/8d/e8f4647efe454c02
##
## Germline reference file: /misc/work/jenkins/PRJNA248475/M5/M5_lesion/M5_lesion/M5_lesion/38/acf53a2b
##
## Novel allele file:
##
## Species: Homosapiens
##
## Chain: IGHV
##
## Segment: V
##
## Warning   no inferred sequences found.
```