

OGRDBstats Report

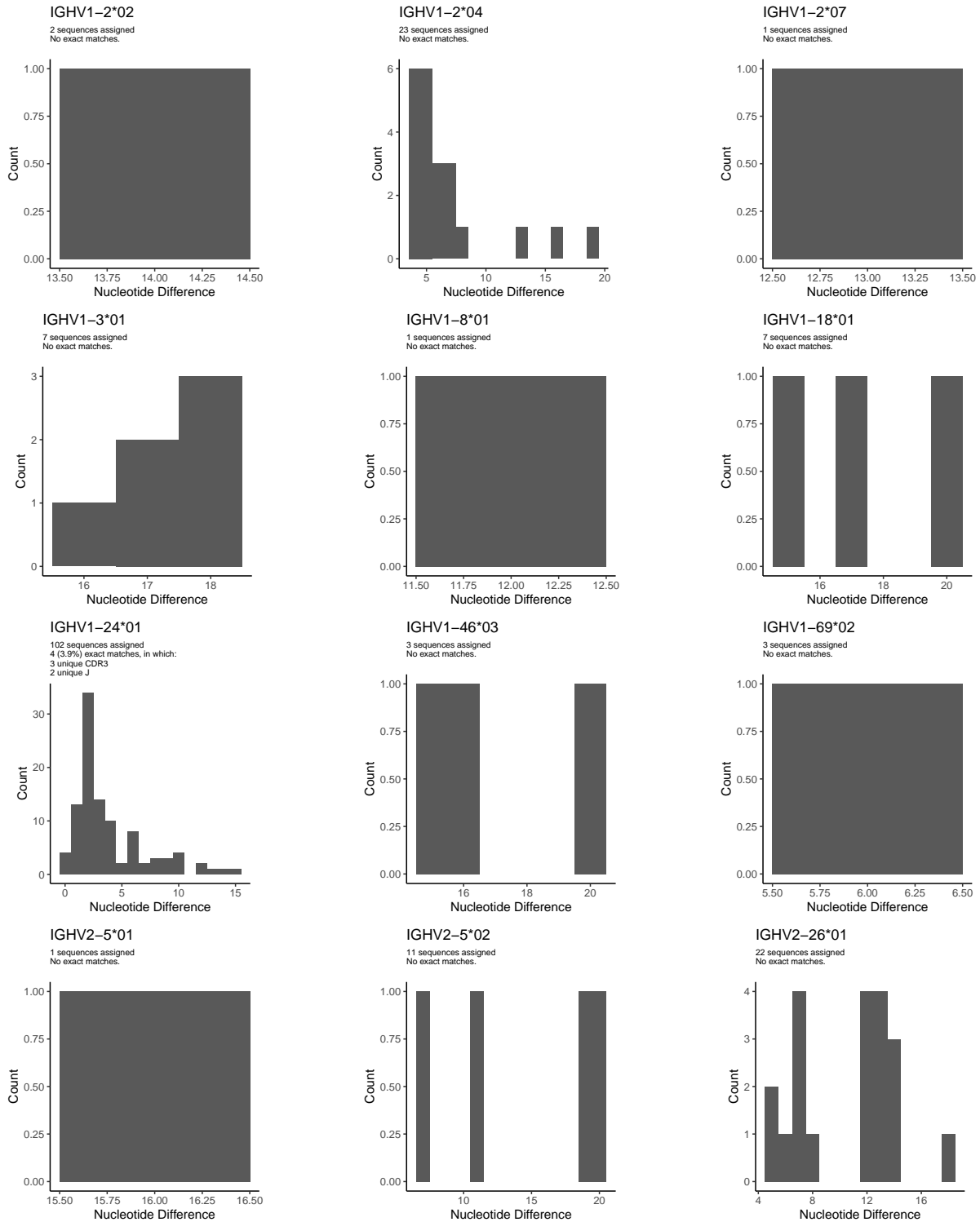
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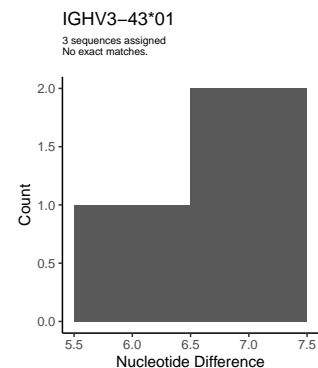
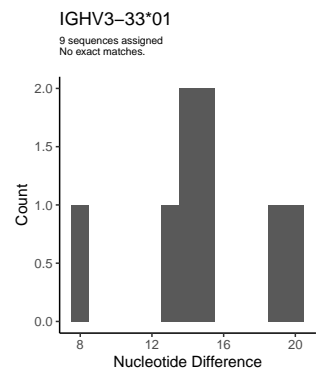
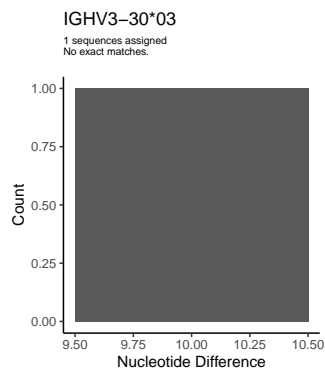
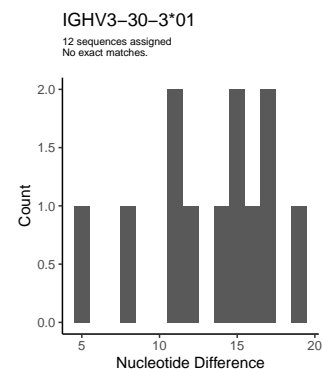
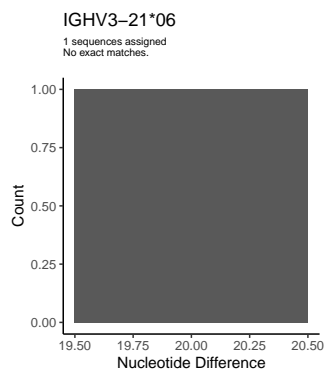
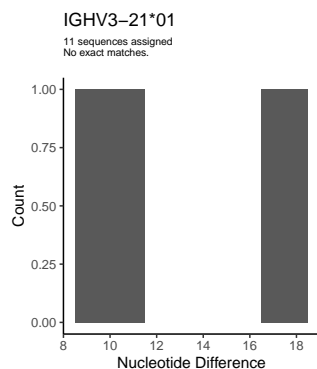
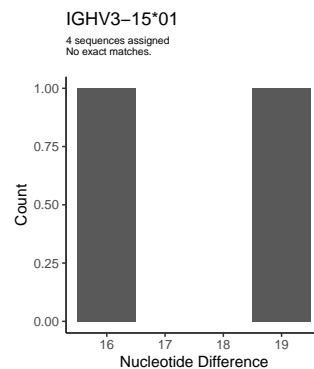
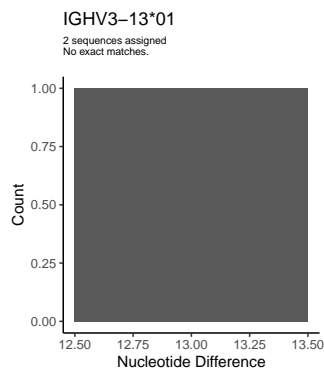
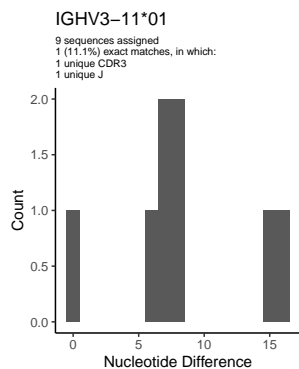
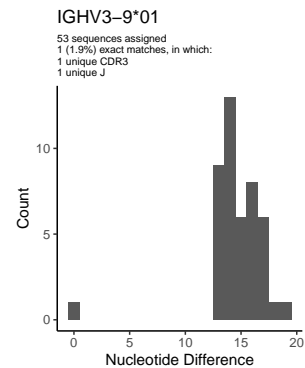
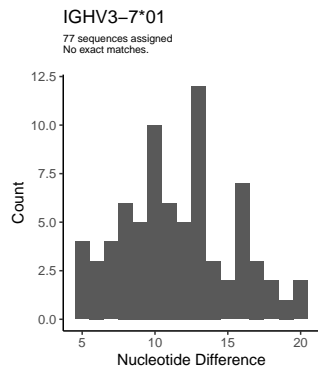
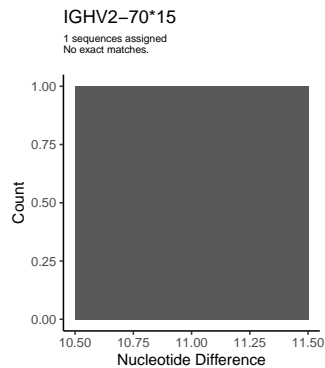
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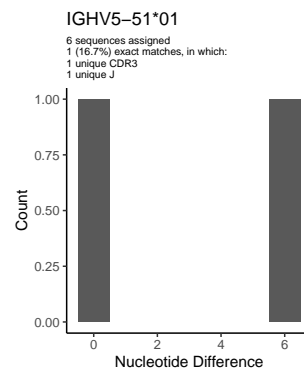
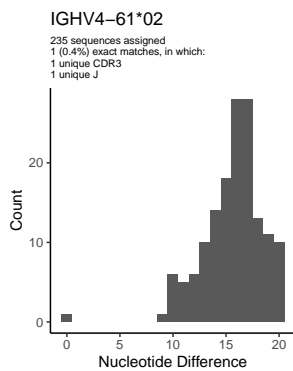
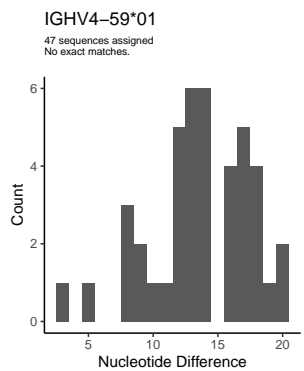
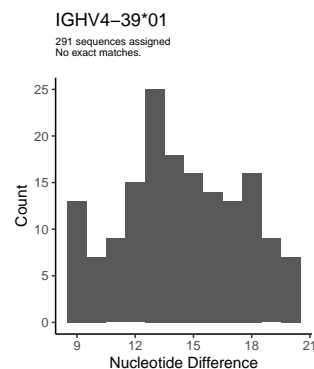
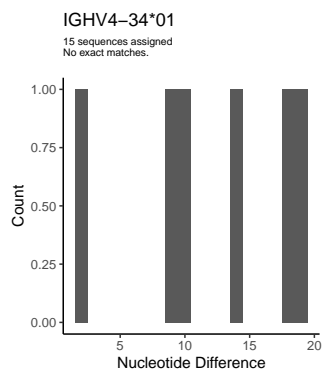
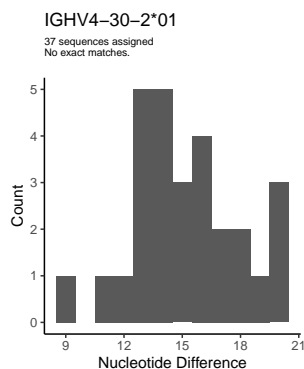
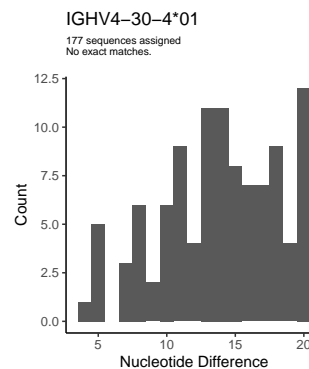
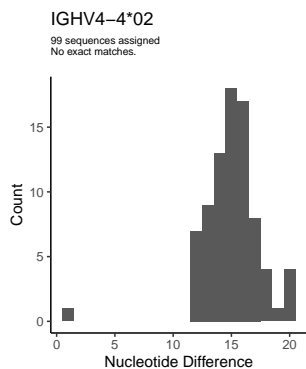
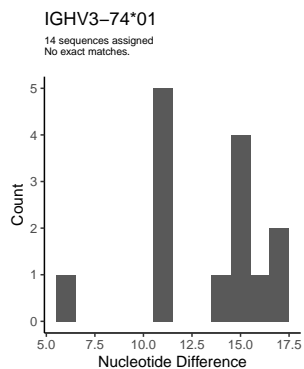
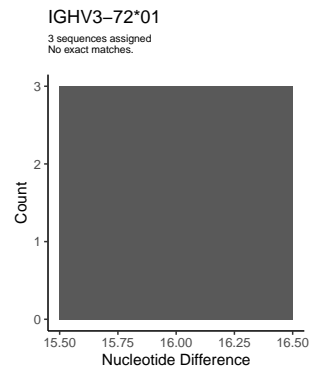
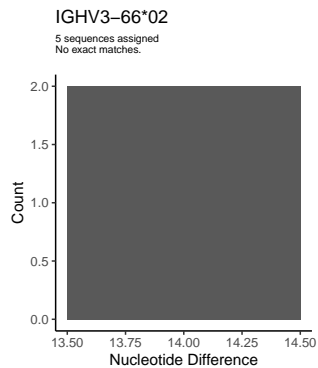
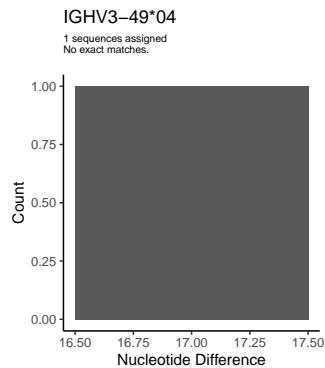
1 Novel sequence analysis

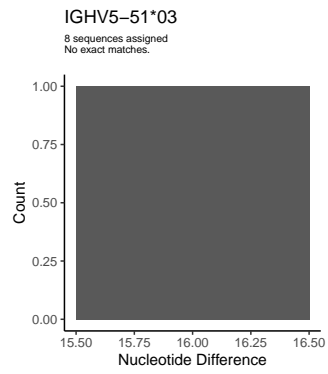
1.1 CDR3 length distribution, in assignments to novel alleles

2 Variation from germline, in assignments to each allele

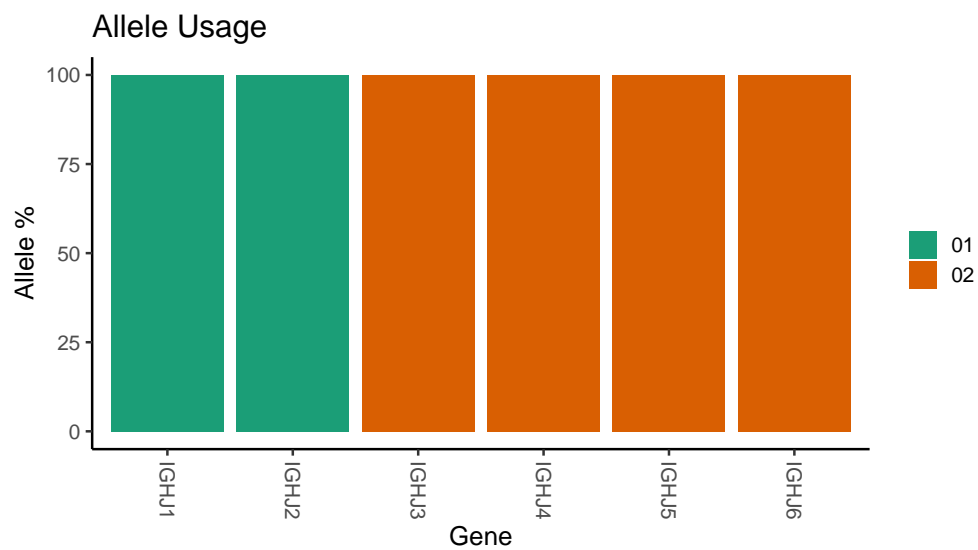








3 Allele usage in potential haplotype anchor genes



4 Haplotype plots

5 Configuration settings

```
## Repertoire file: /work/jenkins/PRJNA248475/M3/M3_lesion/M3_lesion/M3_lesion/c9/43cf7ed2f0df1c0e2cf90
##
## Germline reference file: /work/jenkins/PRJNA248475/M3/M3_lesion/M3_lesion/M3_lesion/a1/b337df4380d4a
##
## Novel allele file:
##
## Species: Homosapiens
##
## Chain: IGHV
##
## Segment: V
##
## Warning    no inferred sequences found.
```