

OGRDBstats Report

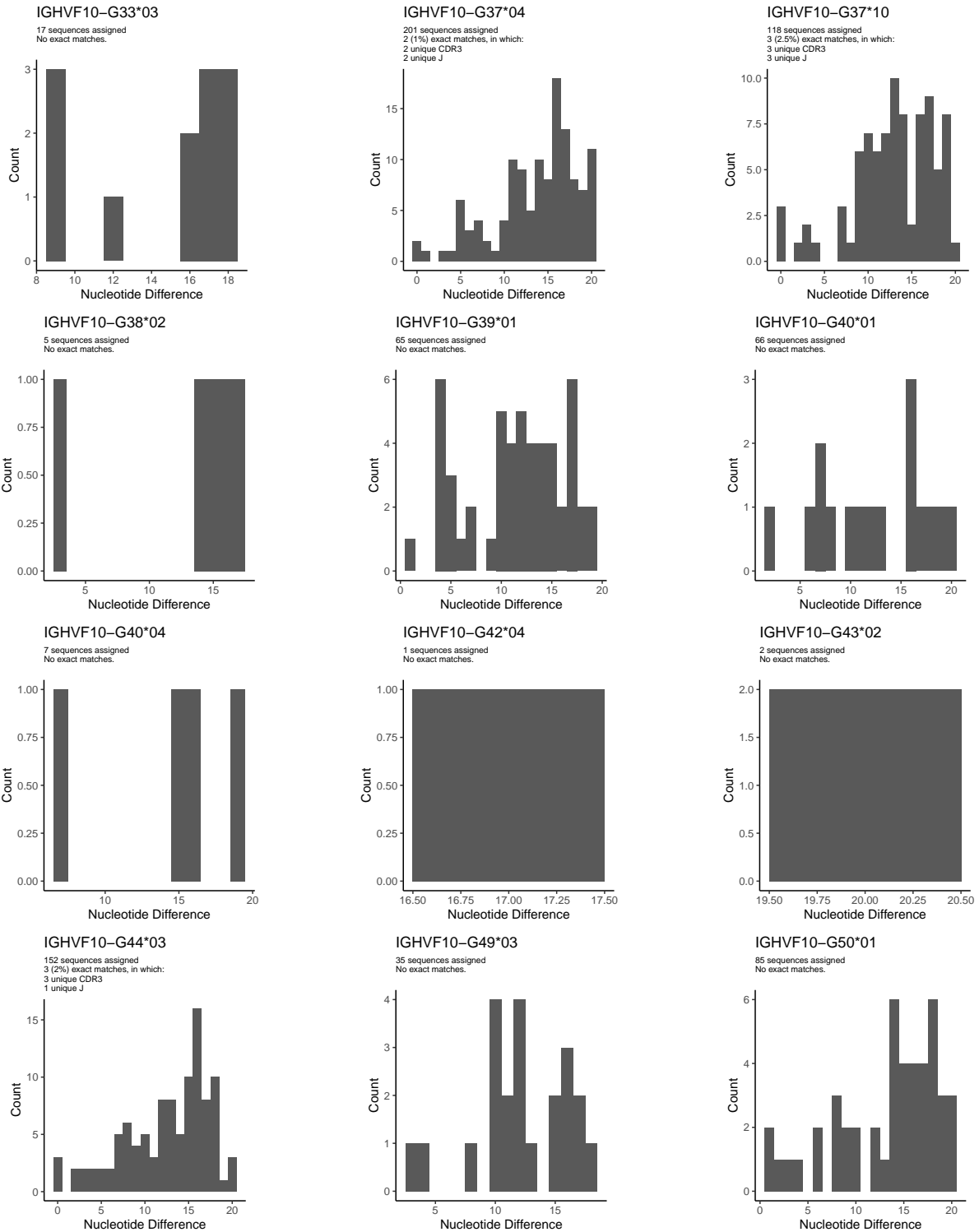
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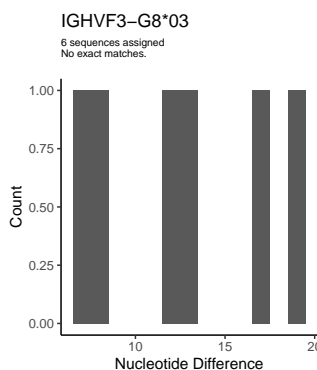
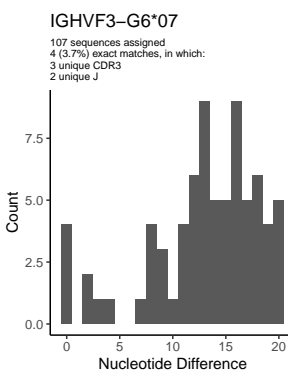
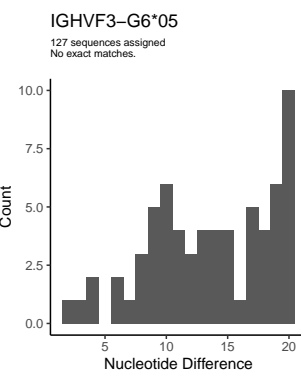
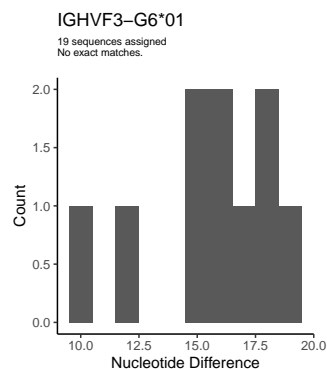
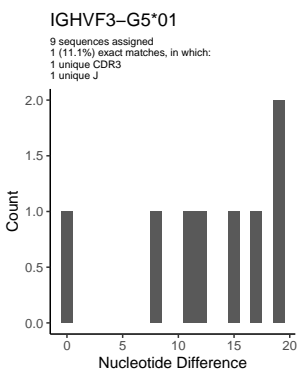
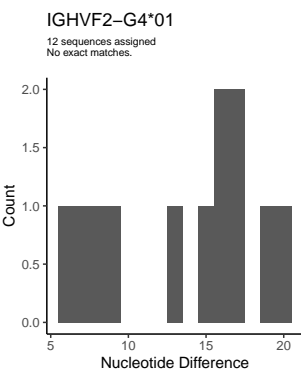
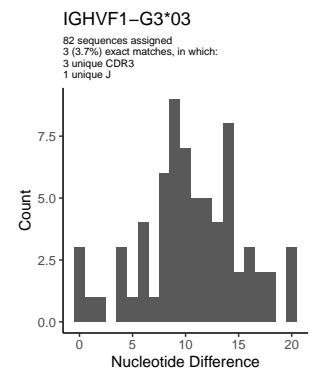
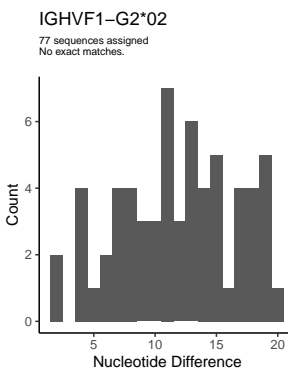
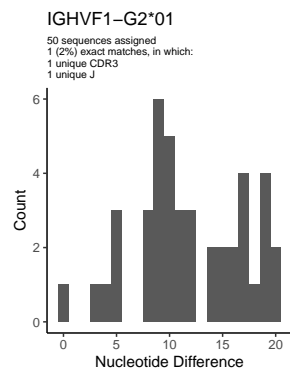
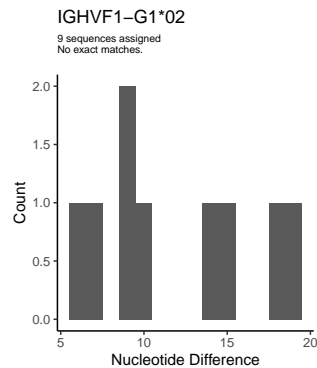
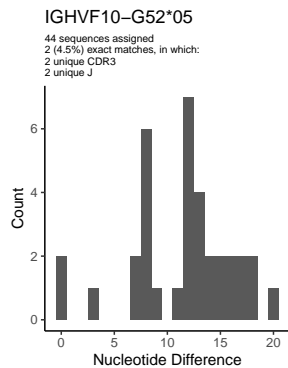
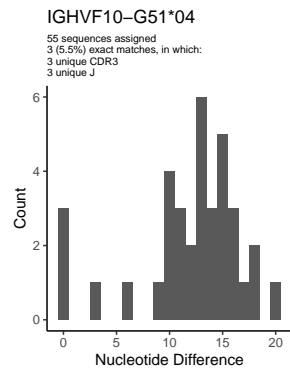
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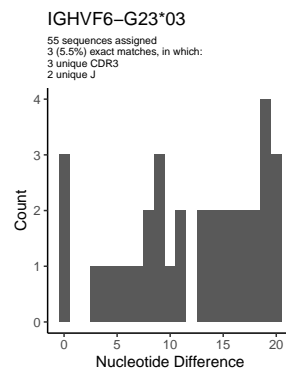
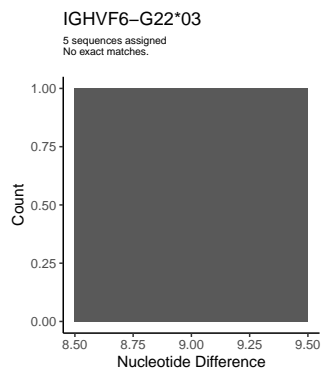
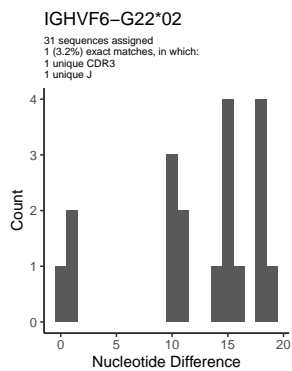
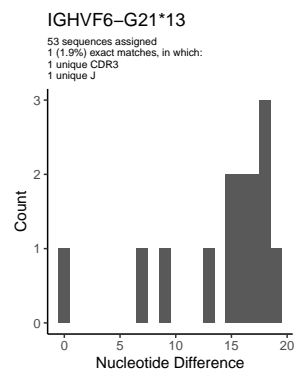
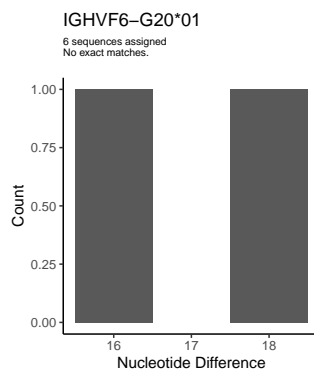
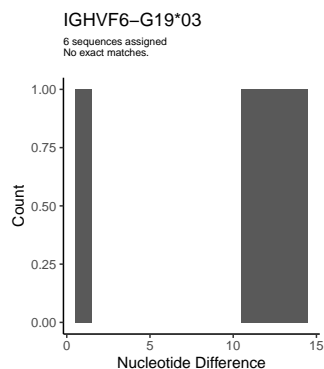
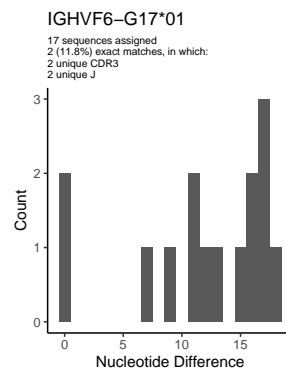
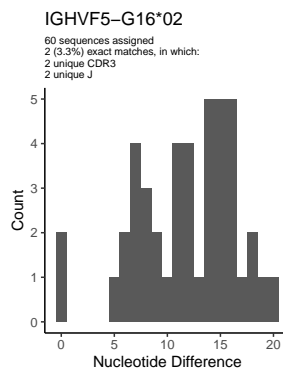
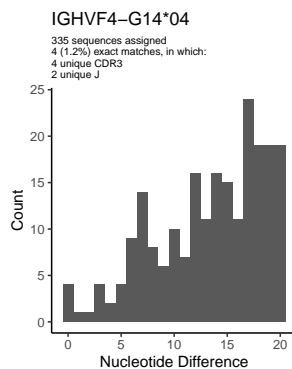
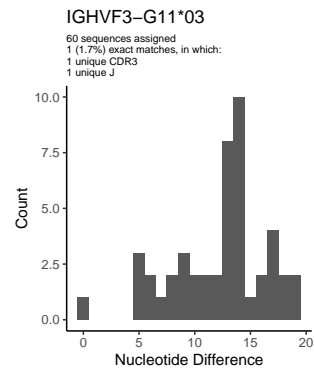
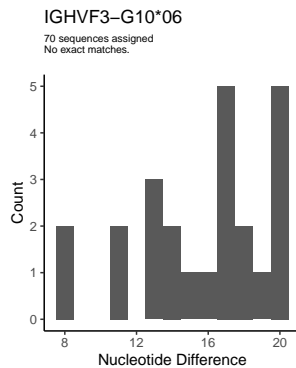
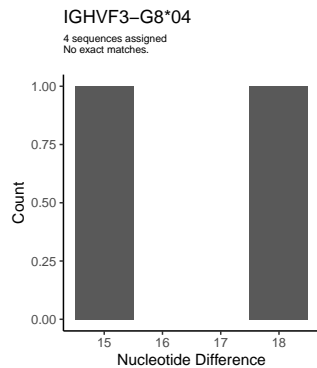
1 Novel sequence analysis

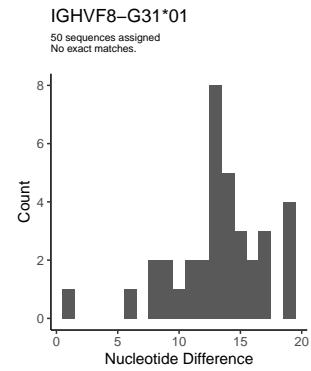
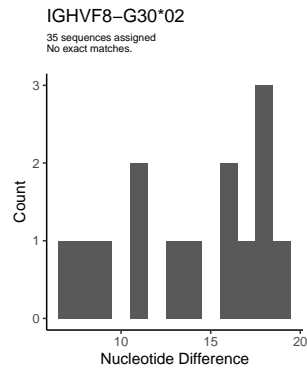
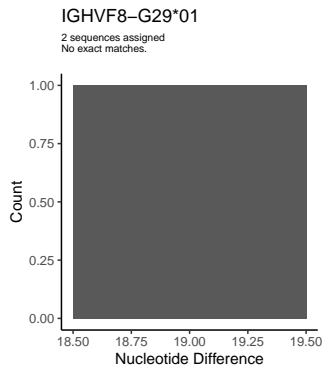
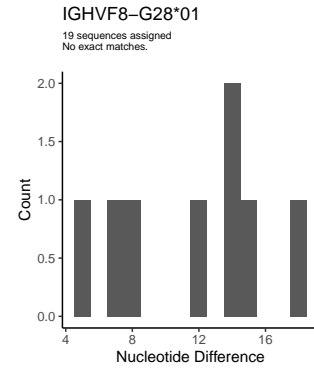
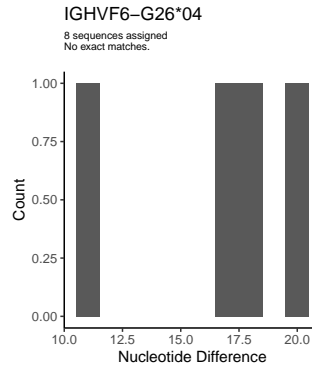
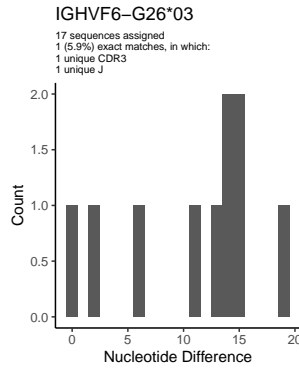
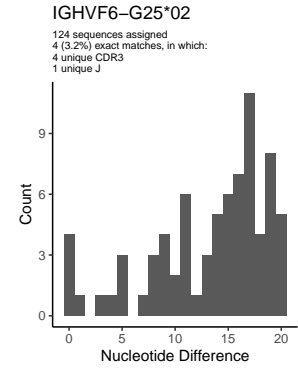
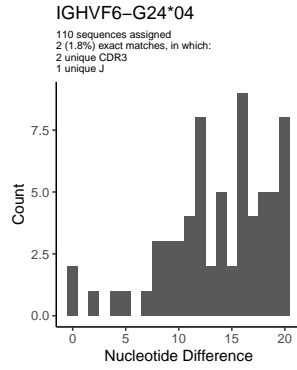
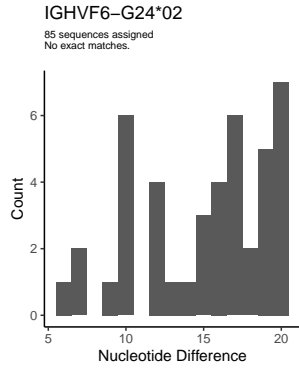
1.1 CDR3 length distribution, in assignments to novel alleles

2 Variation from germline, in assignments to each allele

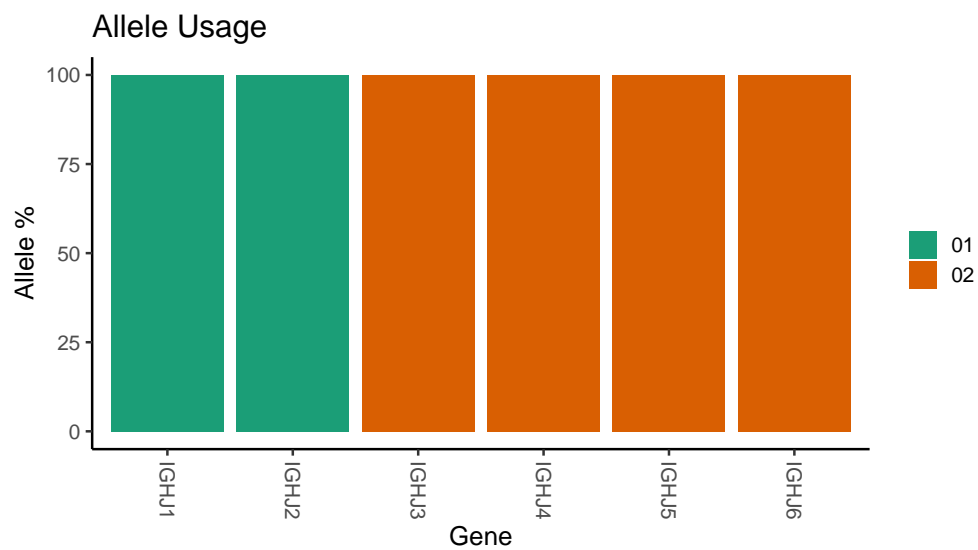








3 Allele usage in potential haplotype anchor genes



4 Haplotype plots

5 Configuration settings

```
## Repertoire file: /work/jenkins/PRJNA248475/M4/M4_cln/M4_cln/M4_cln/36/8de7a1d92114de6de6baa9b3c075b0,
##
## Germline reference file: /work/jenkins/PRJNA248475/M4/M4_cln/M4_cln/M4_cln/36/8de7a1d92114de6de6baa9b3c075b0,
##
## Novel allele file: /work/jenkins/PRJNA248475/M4/M4_cln/M4_cln/M4_cln/36/8de7a1d92114de6de6baa9b3c075b0,
##
## 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)
```