

# OGRDBstats Report

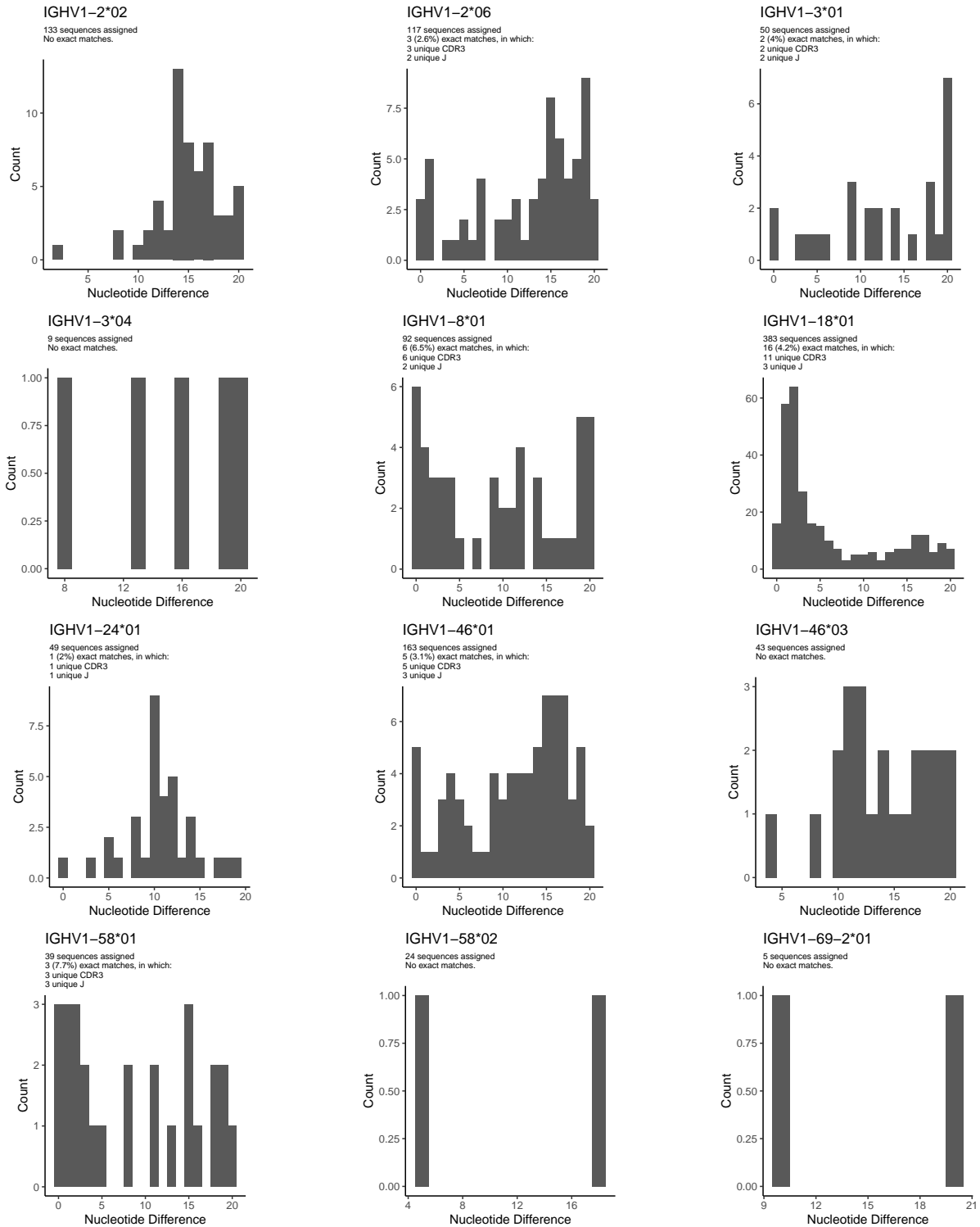
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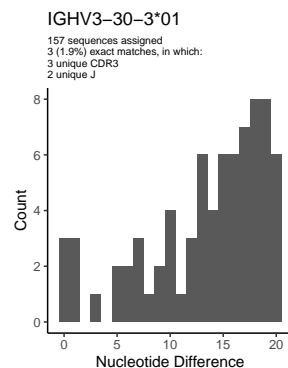
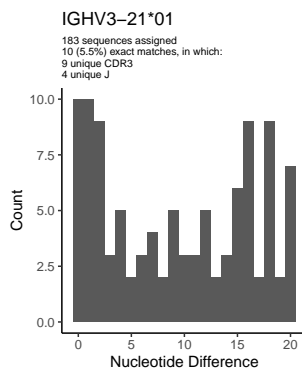
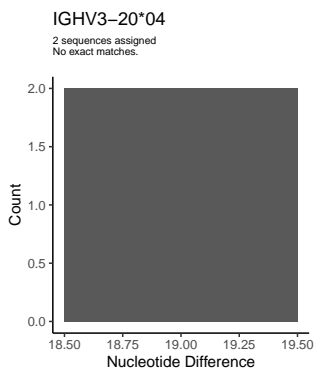
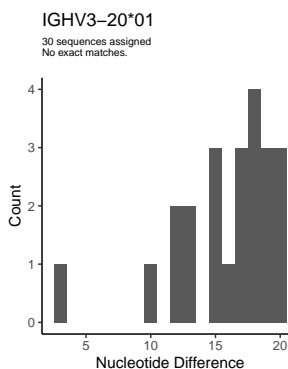
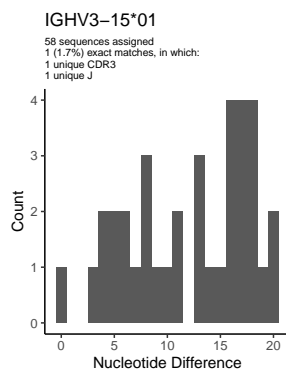
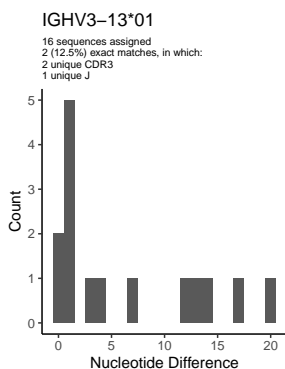
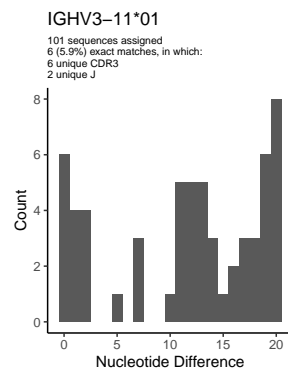
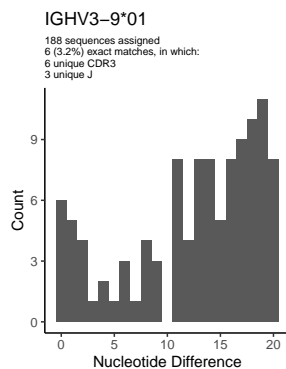
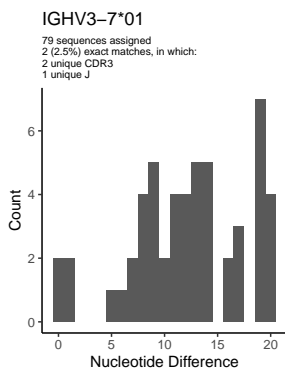
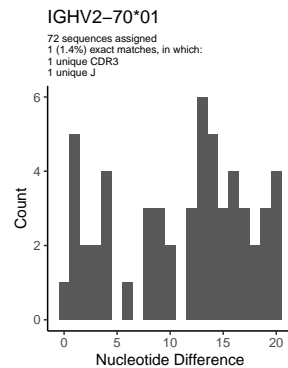
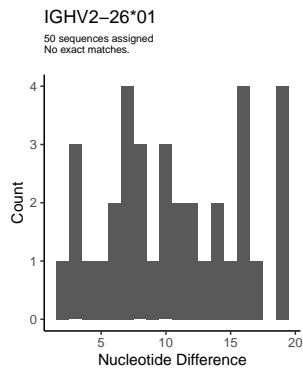
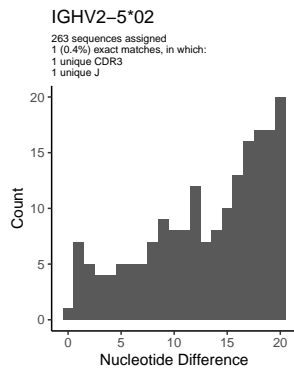
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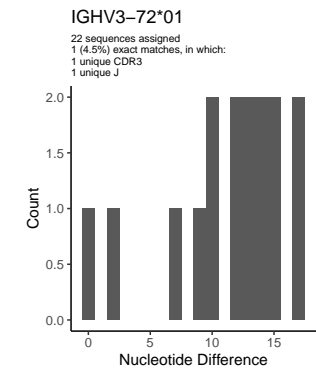
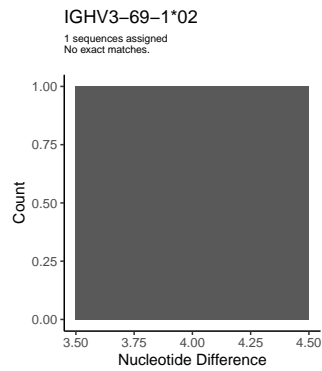
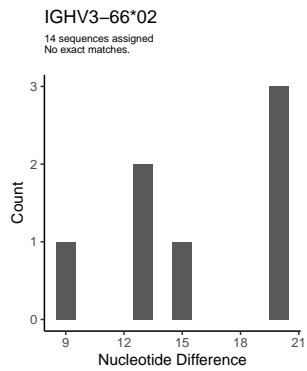
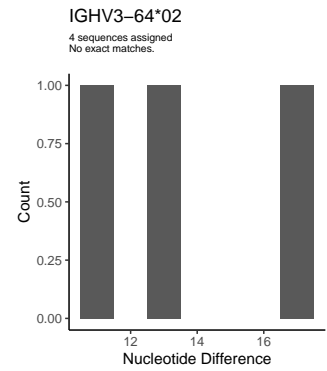
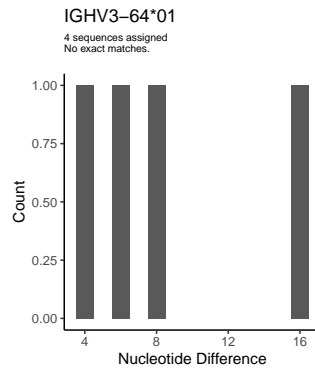
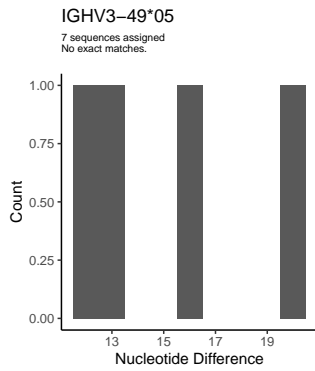
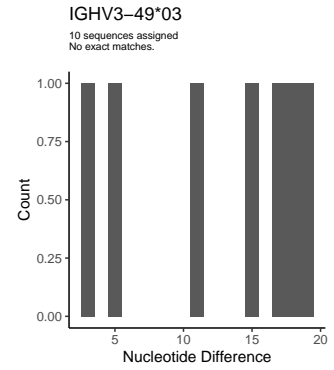
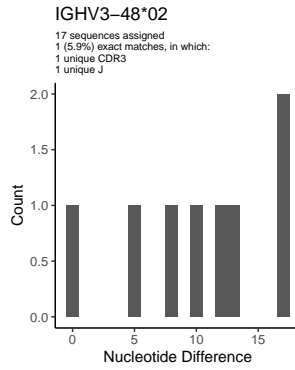
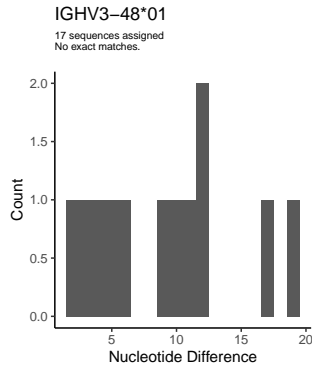
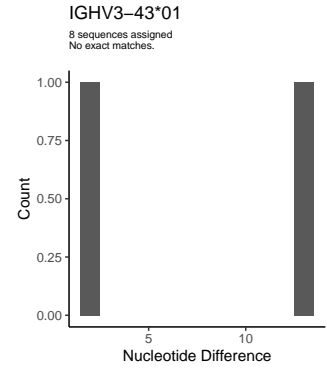
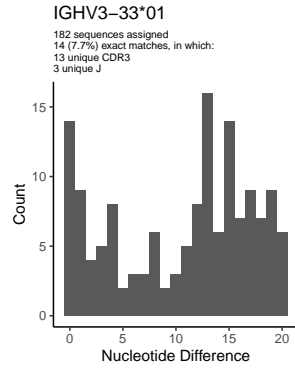
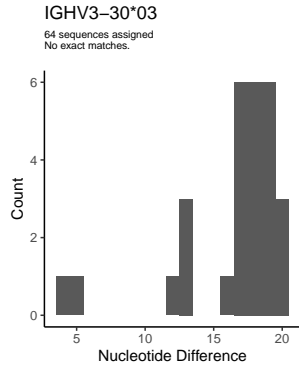
# 1 Novel sequence analysis

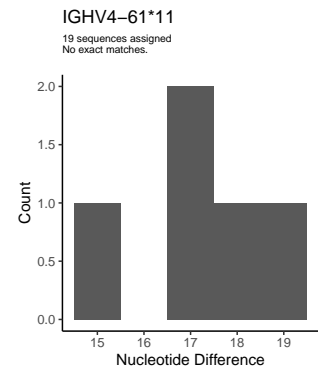
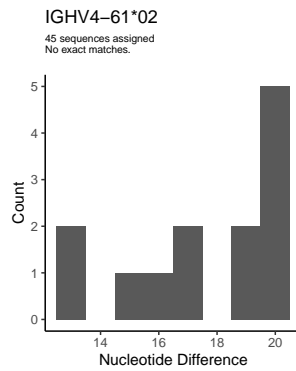
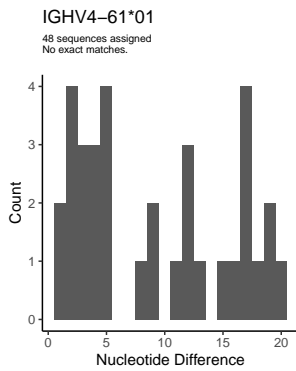
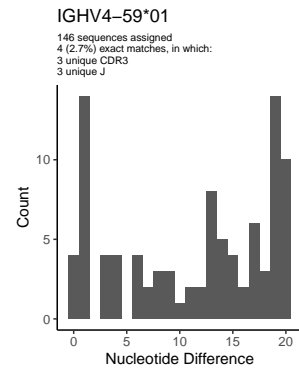
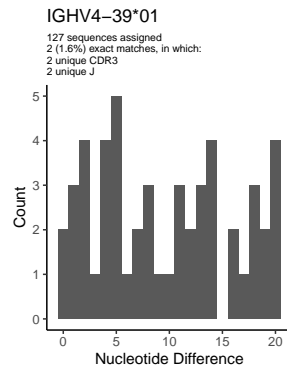
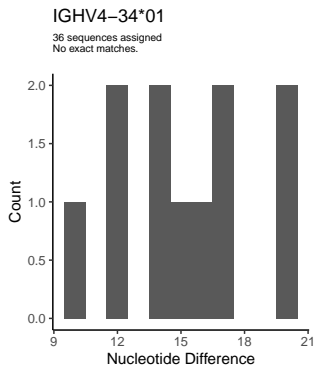
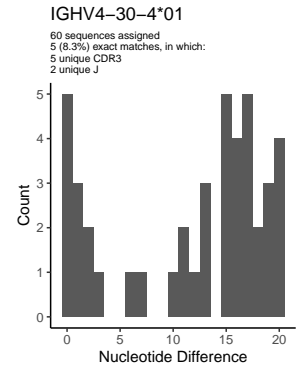
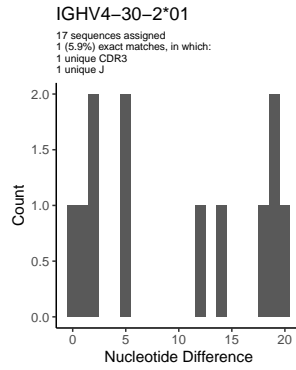
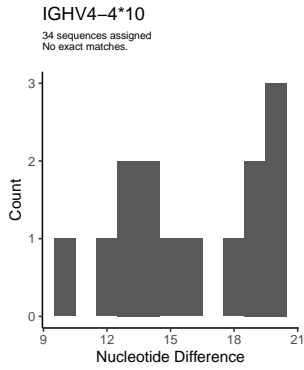
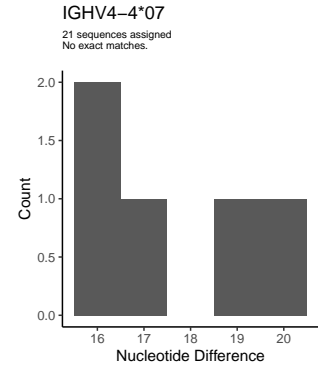
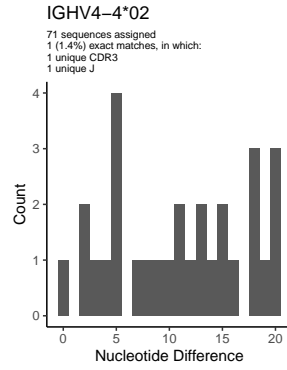
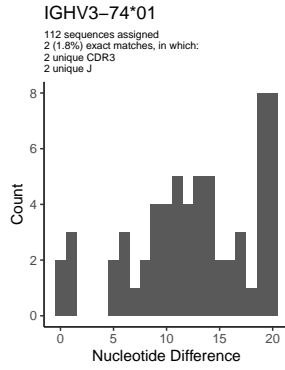
## 1.1 CDR3 length distribution, in assignments to novel alleles

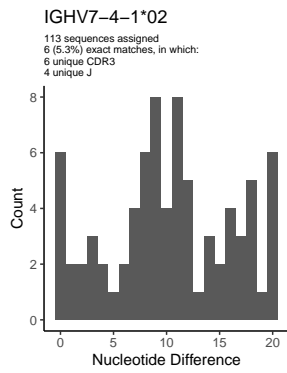
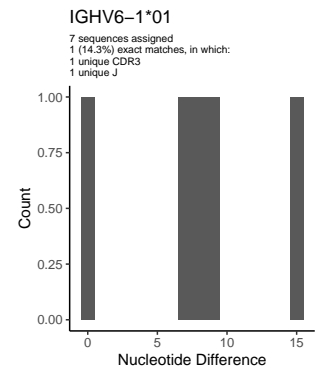
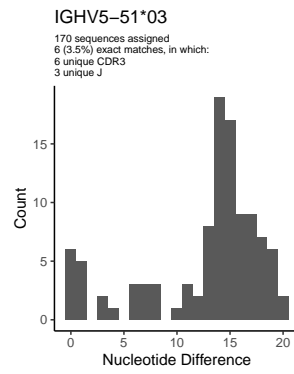
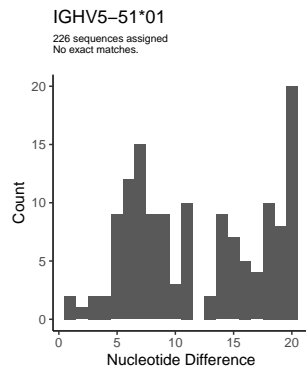
## 2 Variation from germline, in assignments to each allele











### 3 Allele usage in potential haplotype anchor genes





## 4 Haplotype plots

## 5 Configuration settings

```
## Repertoire file: /misc/work/jenkins/PRJNA248475/M5/M5_cln/M5_cln/M5_cln/84/079cb3ba7eecba1e33d7bcb37a
##
## Germline reference file: /misc/work/jenkins/PRJNA248475/M5/M5_cln/M5_cln/M5_cln/79/8bebc3dd7919508d8
##
## Novel allele file:
##
## Species: Homosapiens
##
## Chain: IGHV
##
## Segment: V
##
## Warning   no inferred sequences found.
```