

# OGRDBstats Report

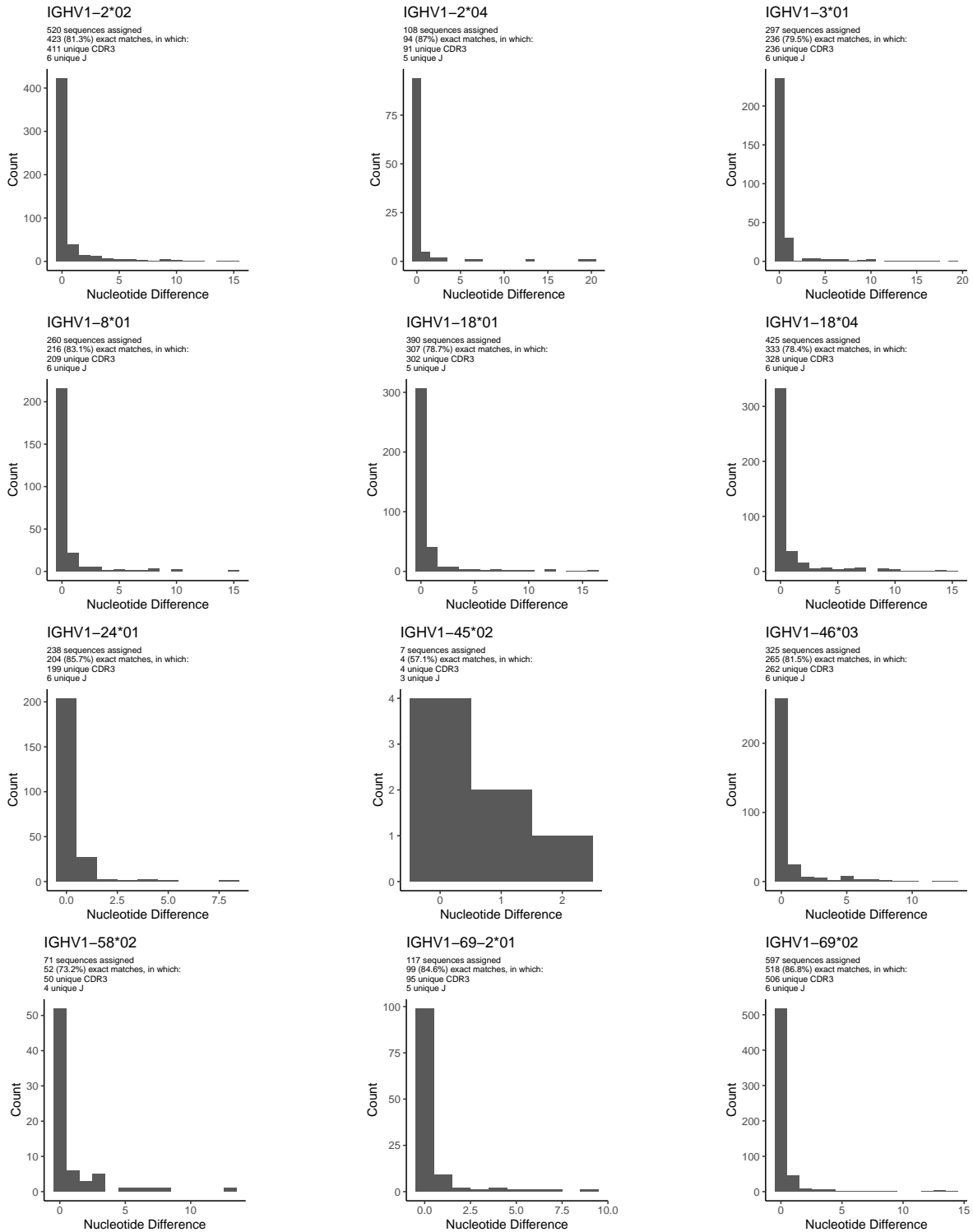
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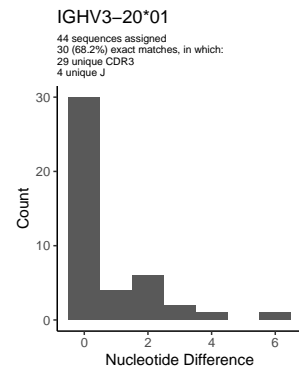
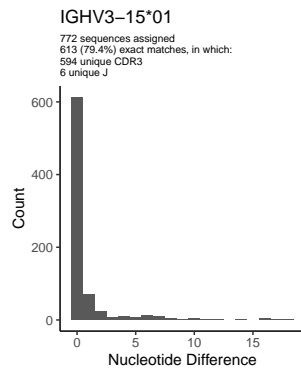
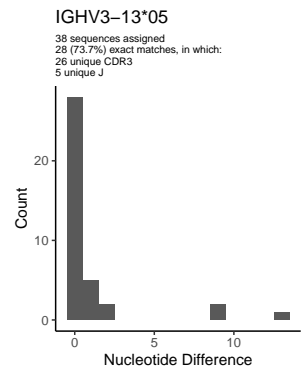
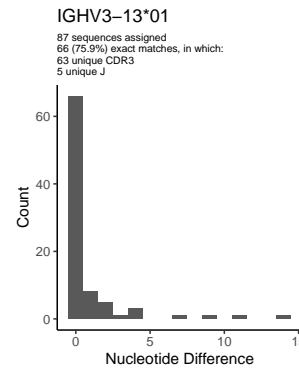
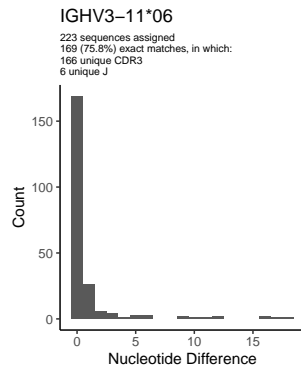
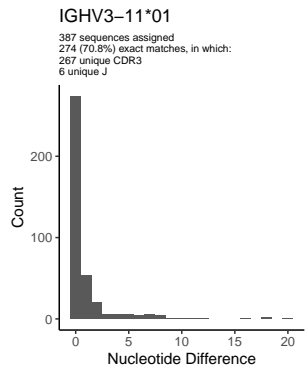
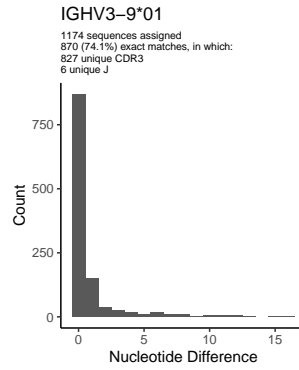
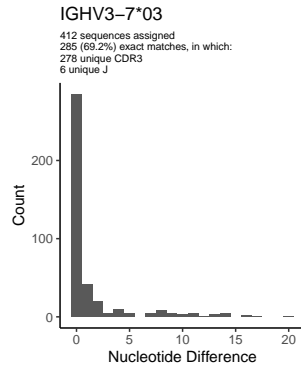
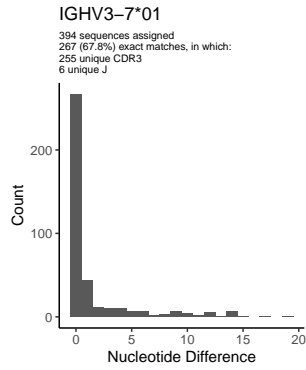
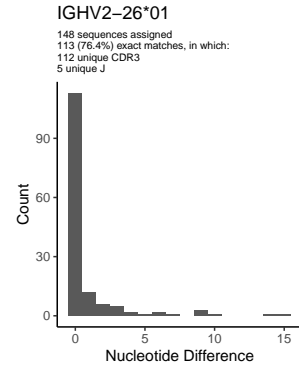
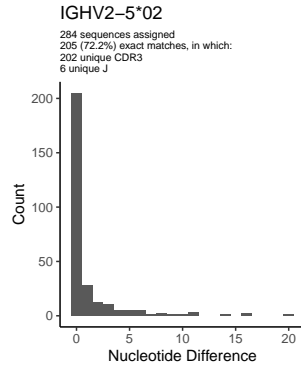
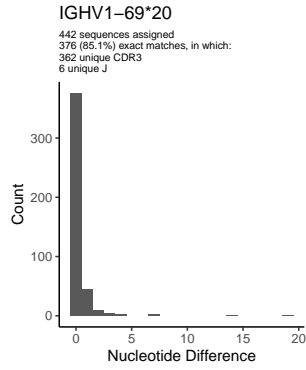
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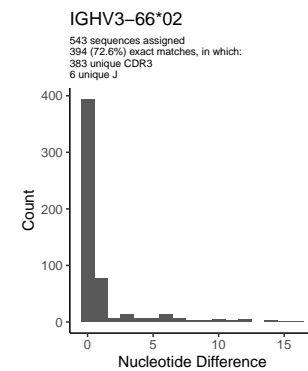
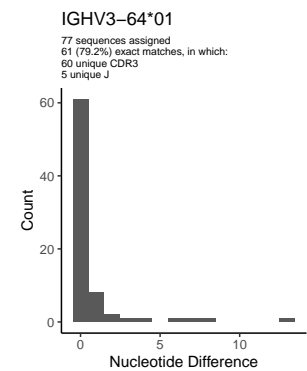
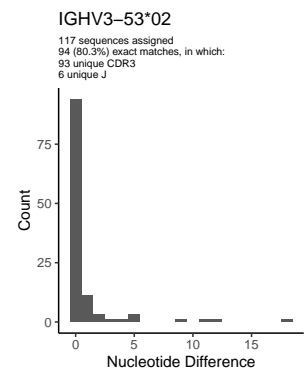
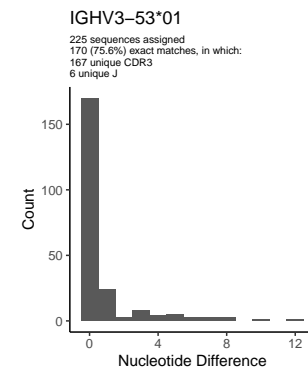
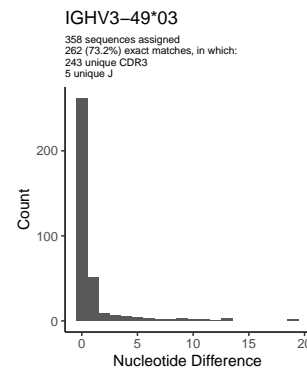
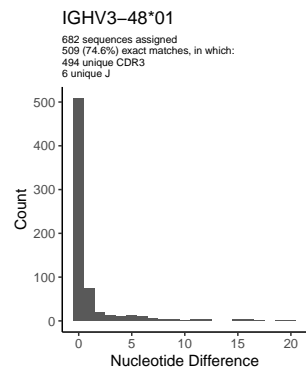
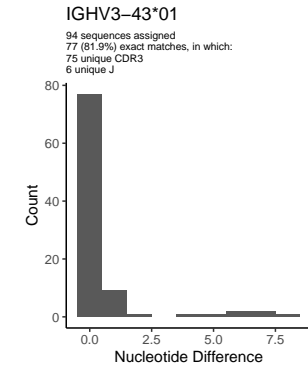
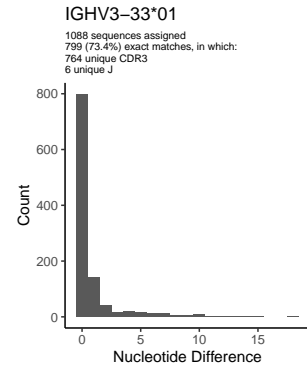
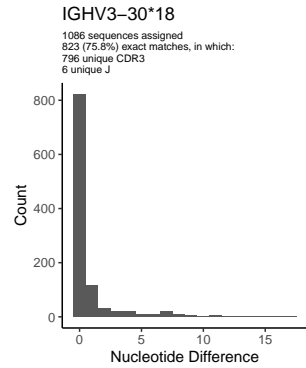
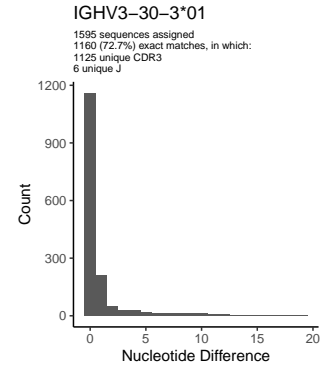
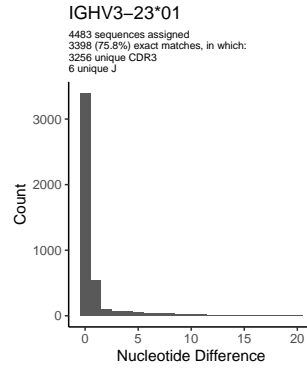
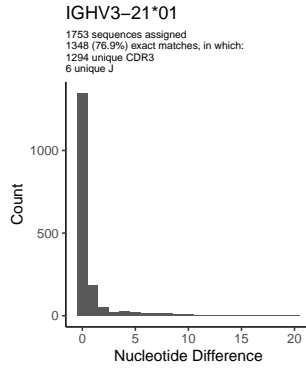
# 1 Novel sequence analysis

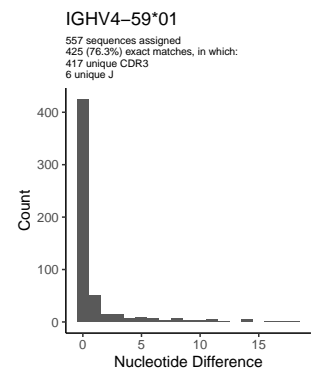
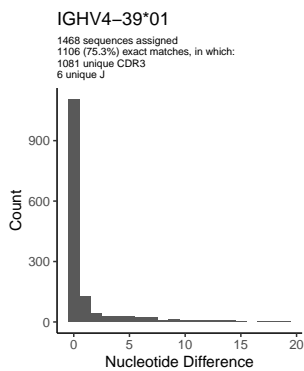
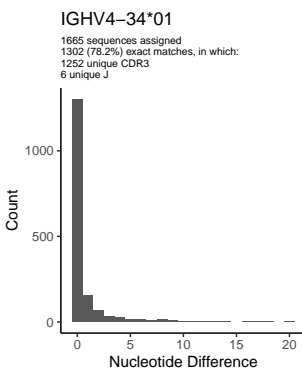
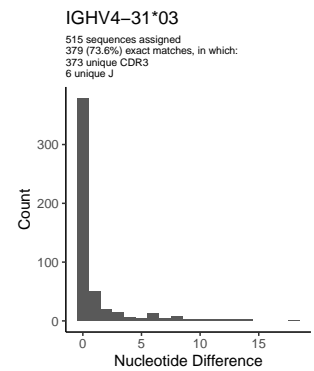
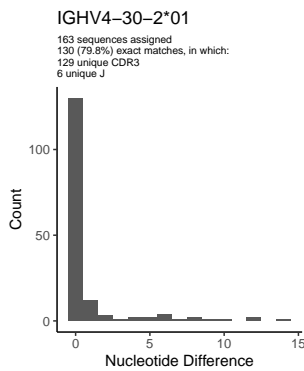
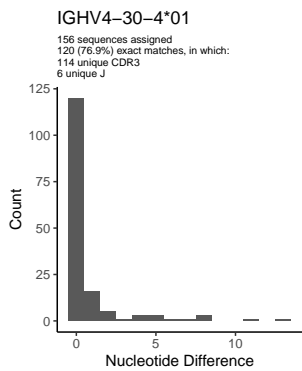
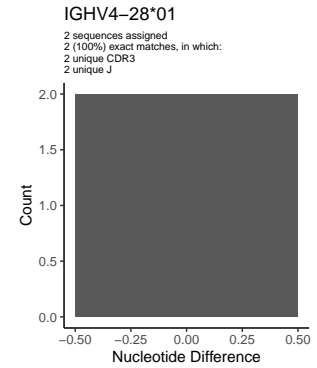
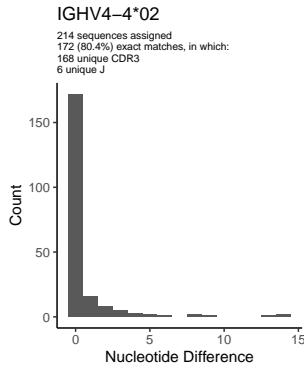
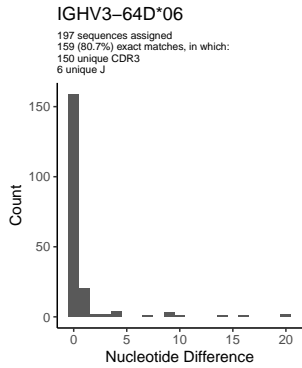
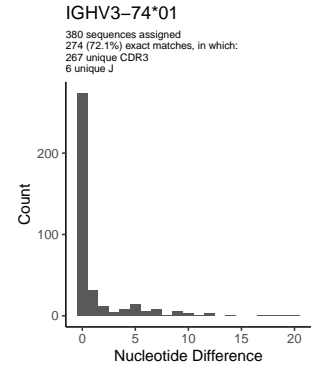
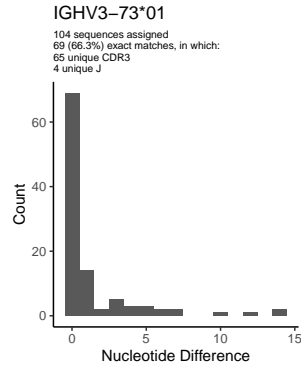
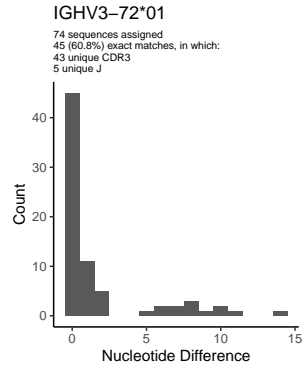
## 1.1 CDR3 length distribution, in assignments to novel alleles

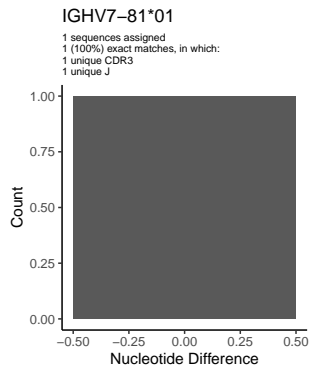
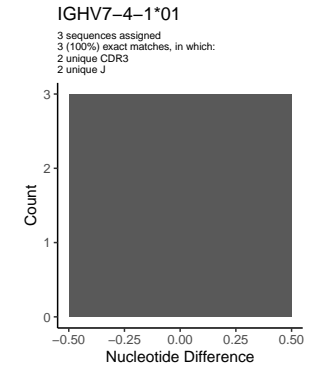
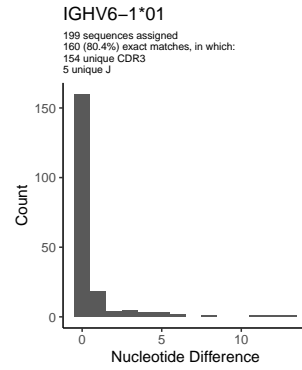
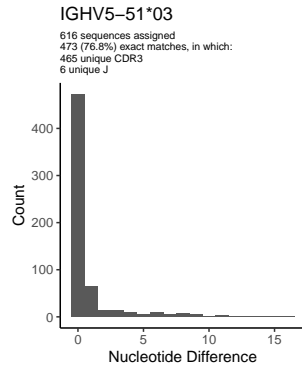
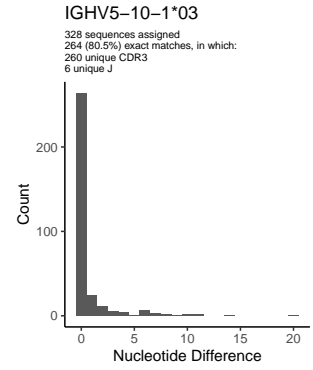
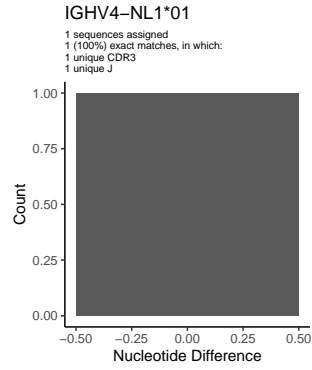
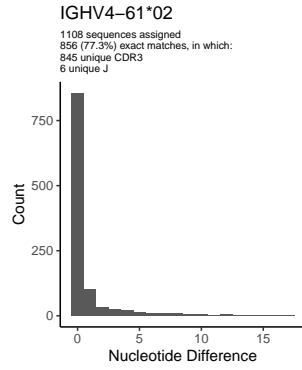
## 2 Variation from germline, in assignments to each allele











### 3 Allele usage in potential haplotype anchor genes





## 4 Haplotype plots

## 5 Configuration settings

```
## Repertoire file: /misc/work/jenkins/PRJEB26509/S73/S73/77/77/e8/0af59d43d1bc8aebfd7073800739ba/77_Fi
##
## Germline reference file: /misc/work/jenkins/PRJEB26509/S73/S73/77/77/f6/7c1dbaaf5240ab6a6e59a5b1ced
##
## Novel allele file:
##
## Species: Homosapiens
##
## Chain: IGHV
##
## Segment: V
##
## Warning   no inferred sequences found.
```