

# OGRDBstats Report

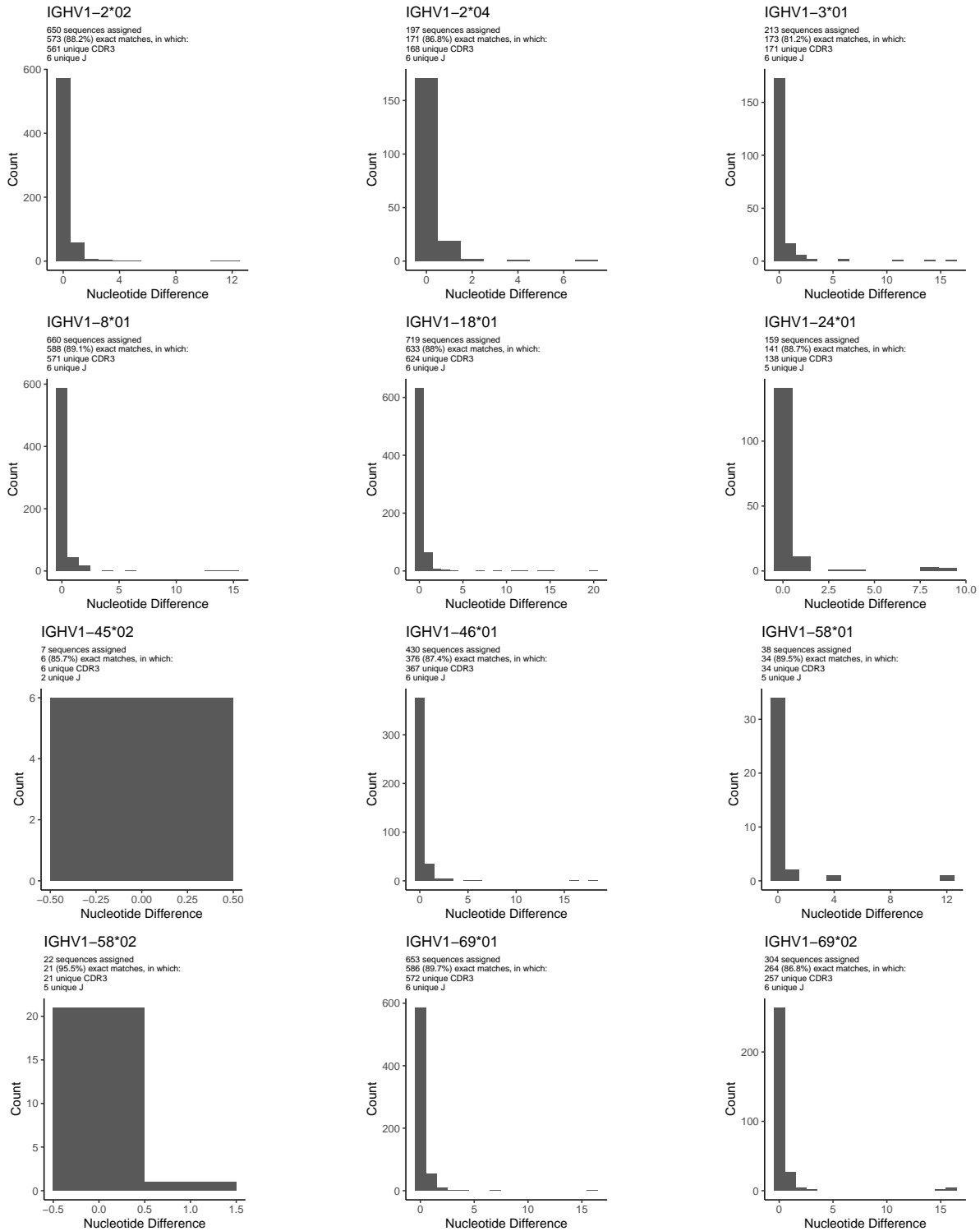
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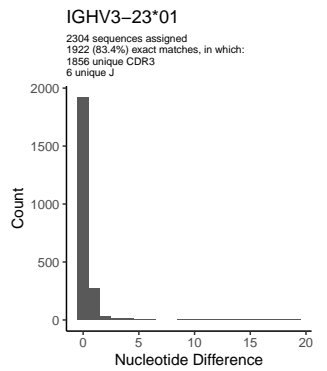
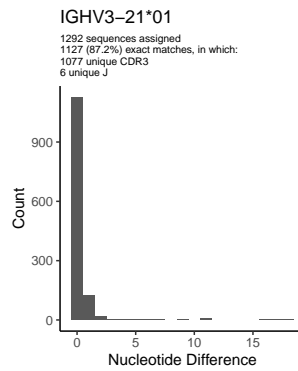
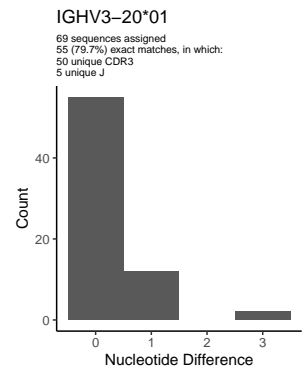
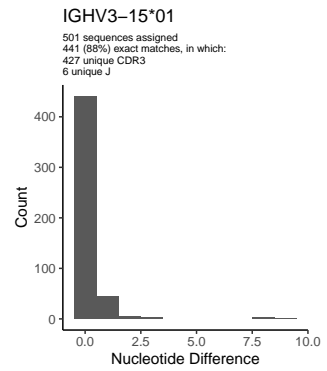
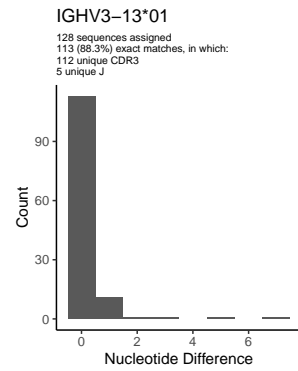
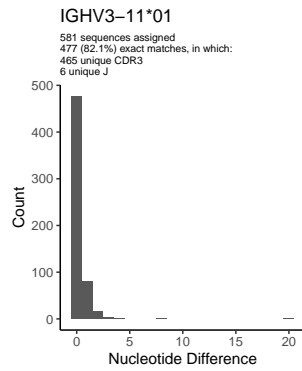
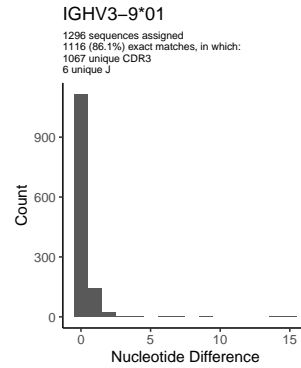
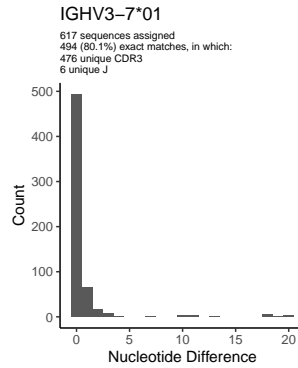
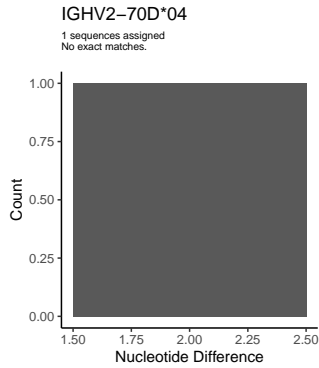
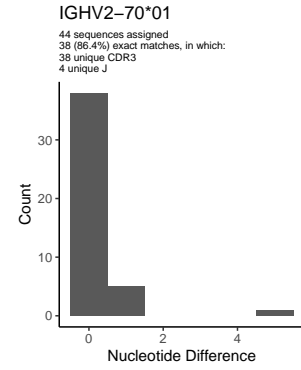
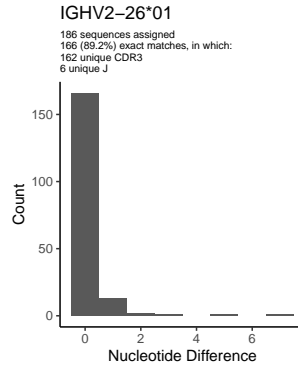
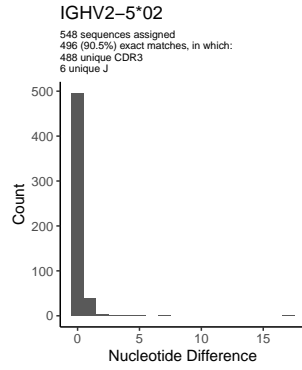
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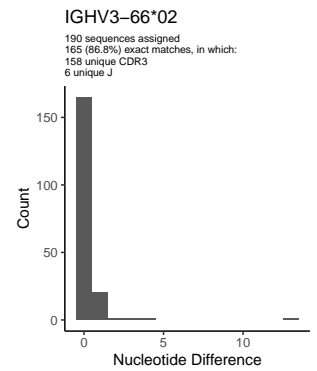
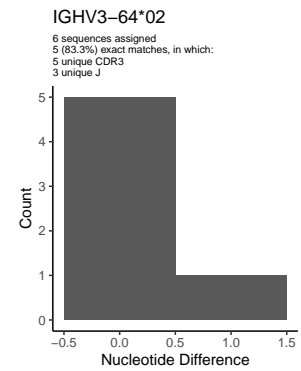
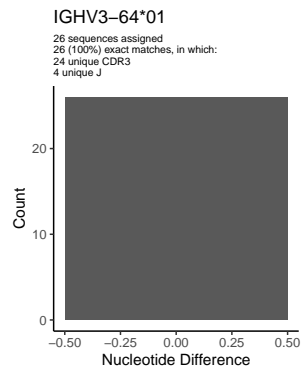
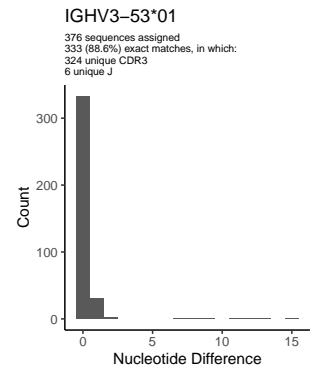
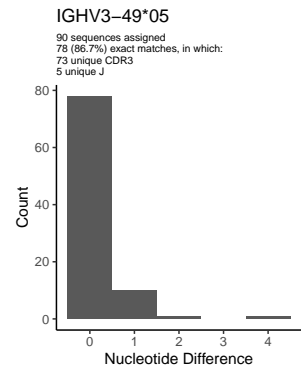
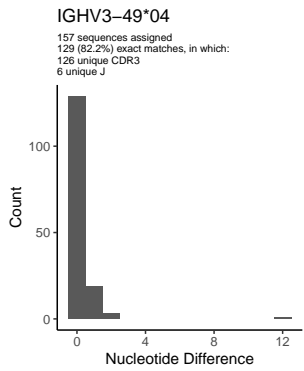
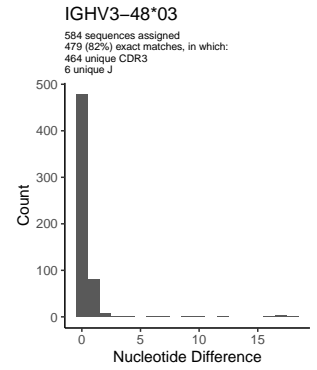
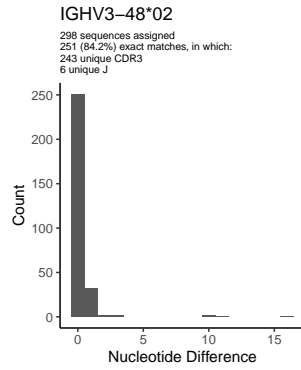
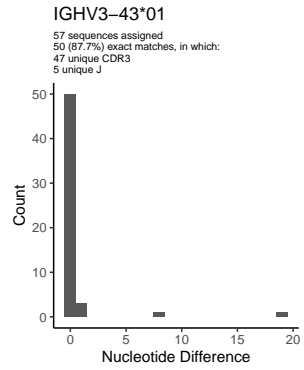
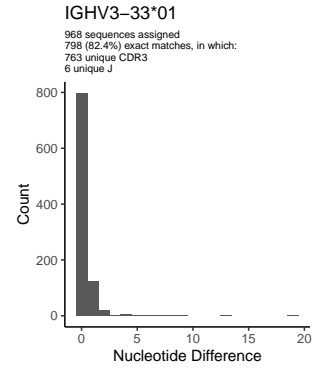
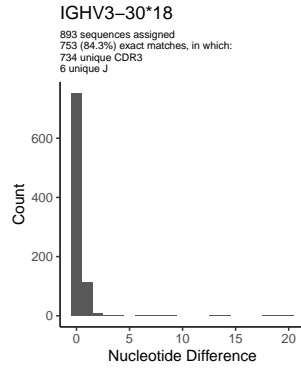
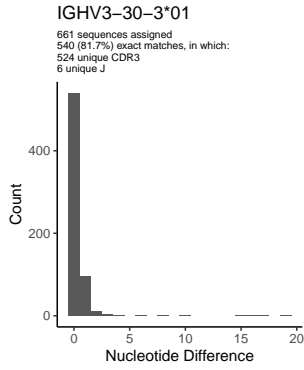
# 1 Novel sequence analysis

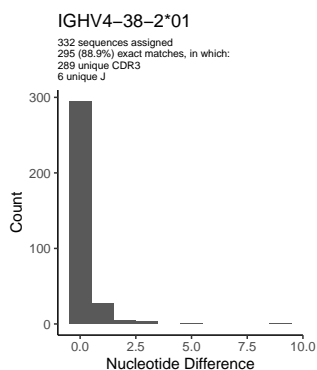
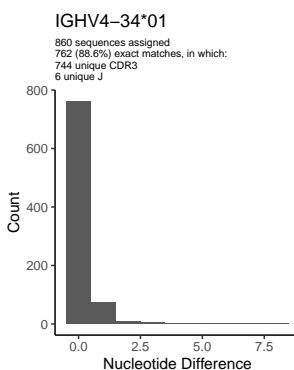
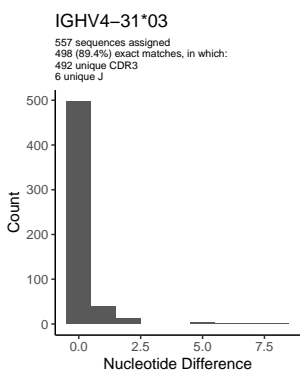
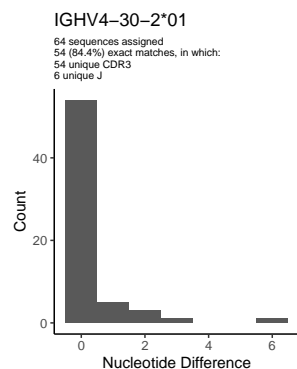
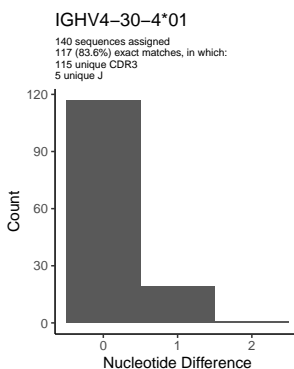
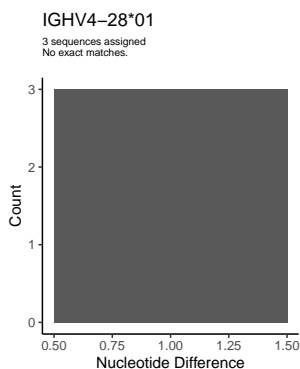
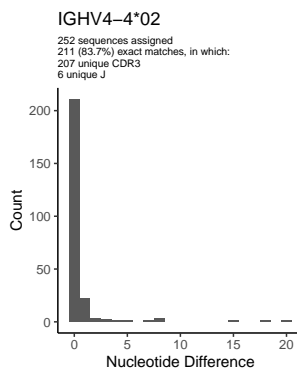
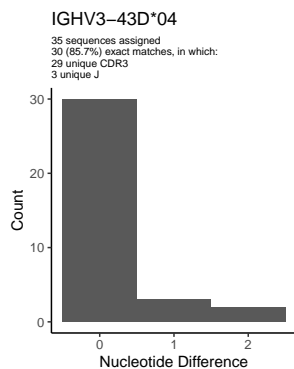
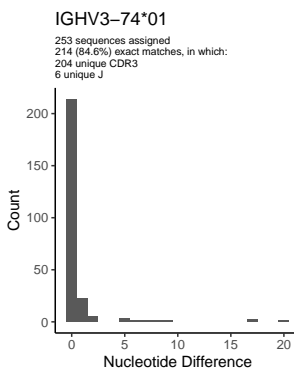
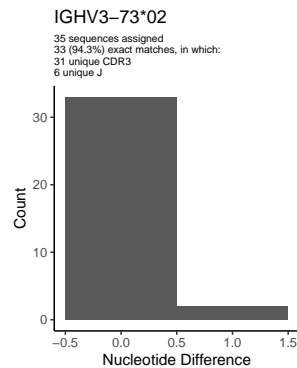
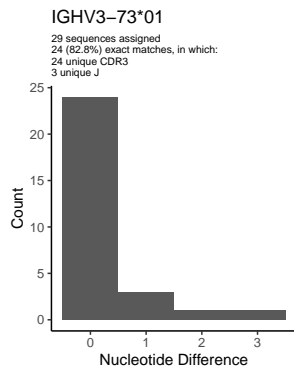
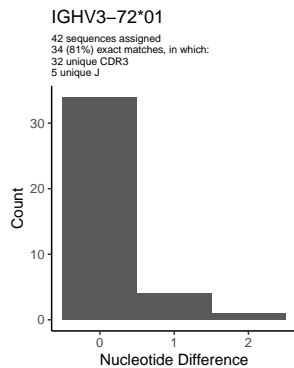
## 1.1 CDR3 length distribution, in assignments to novel alleles

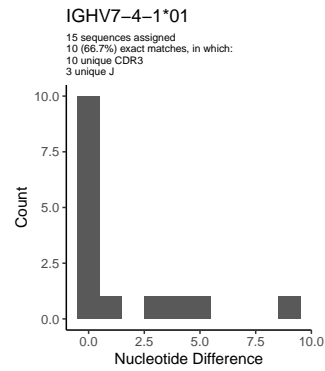
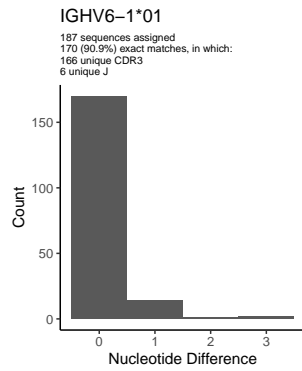
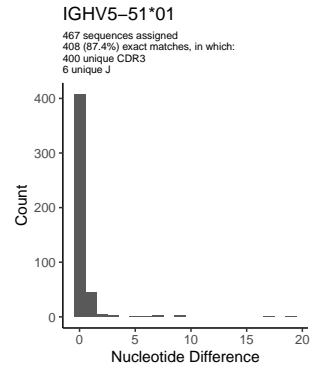
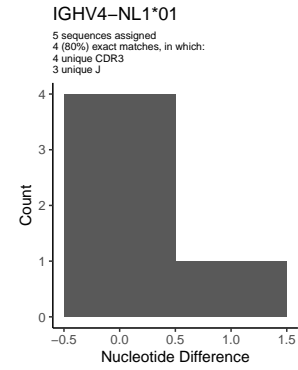
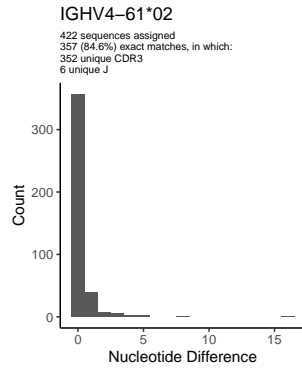
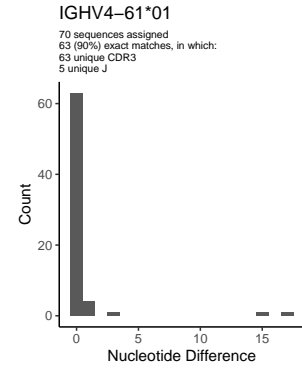
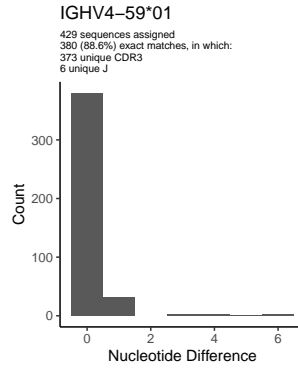
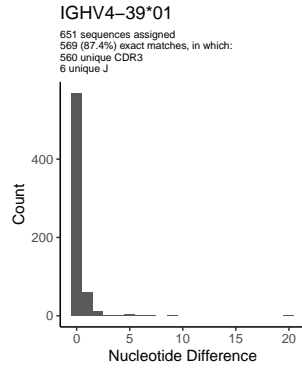
## 2 Variation from germline, in assignments to each allele











### 3 Allele usage in potential haplotype anchor genes





## 4 Haplotype plots

## 5 Configuration settings

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## Repertoire file: /misc/work/jenkins/PRJEB26509/S20/S20/20/20/90/045eb8a7e3d22d5ad97d34295f8f41/20_Fi
##
## Germline reference file: /misc/work/jenkins/PRJEB26509/S20/S20/20/20/06/79639998794c50dfc2b7e343b2a3
##
## Novel allele file:
##
## Species: Homosapiens
##
## Chain: IGHV
##
## Segment: V
##
## Warning    no inferred sequences found.
```