

OGRDBstats Report

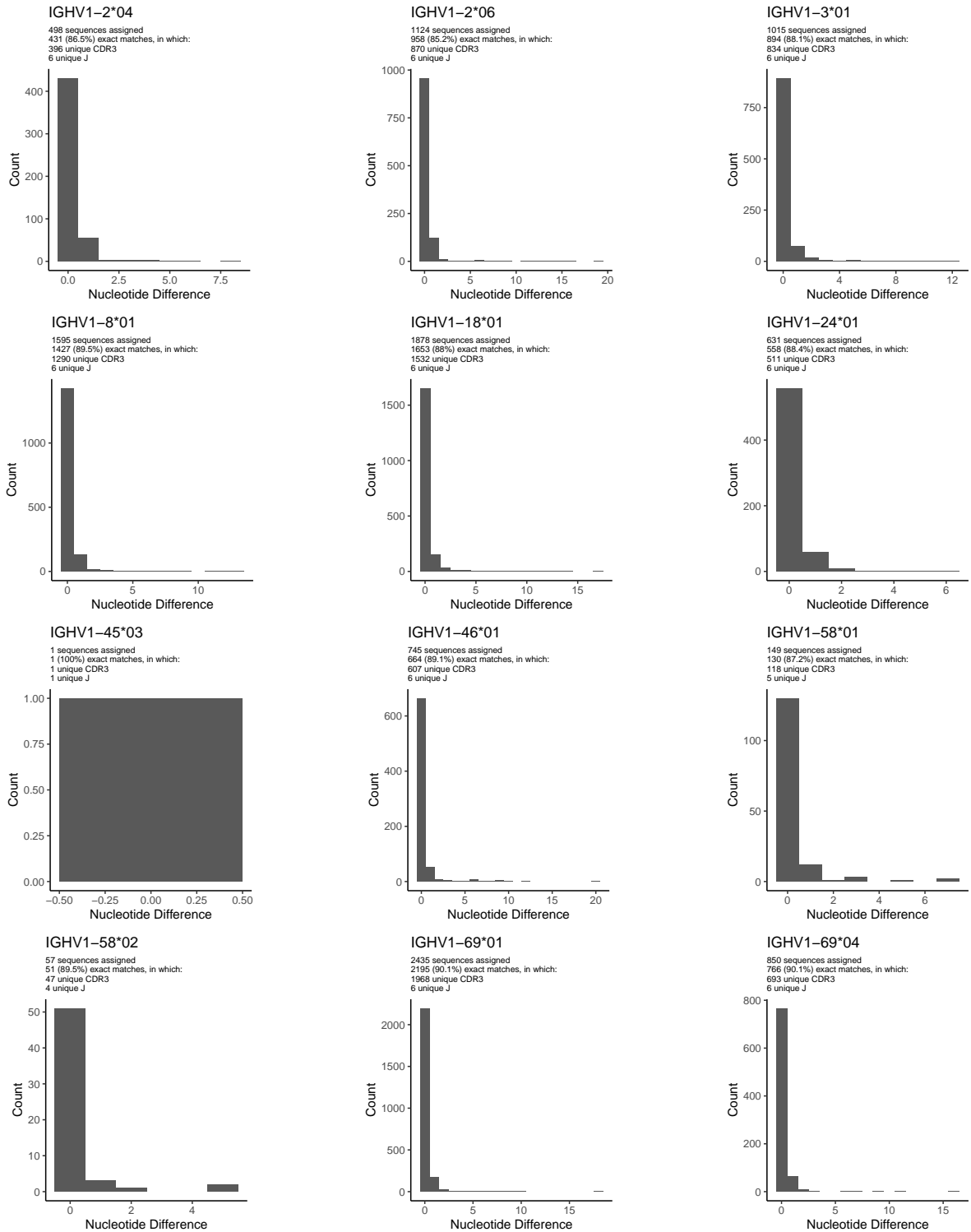
Contents

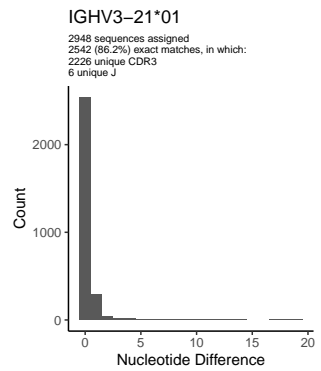
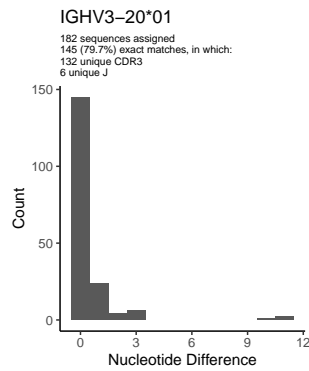
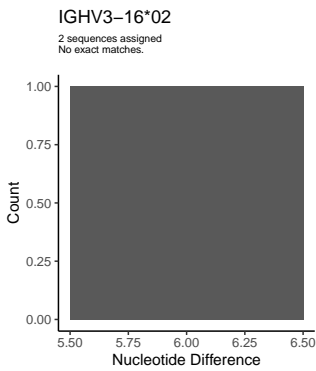
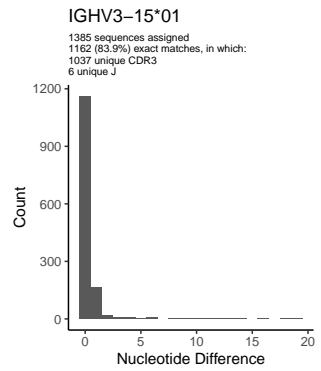
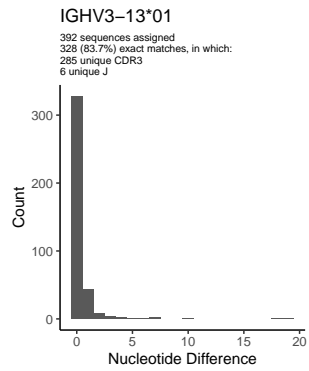
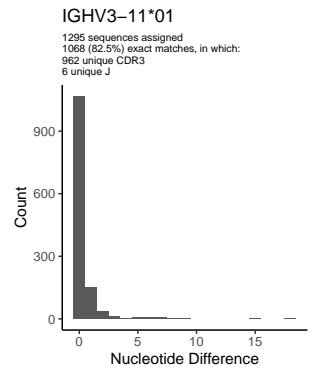
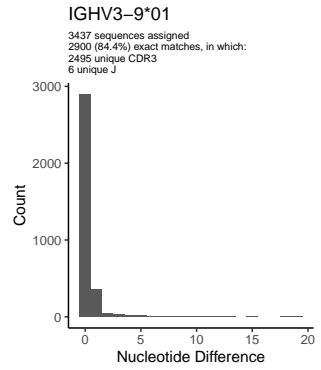
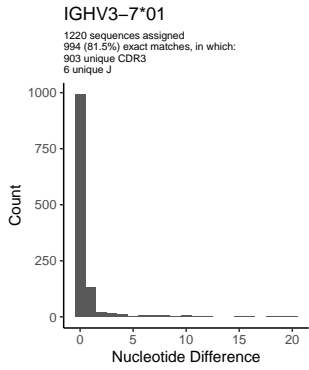
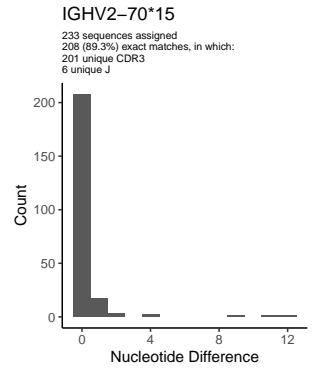
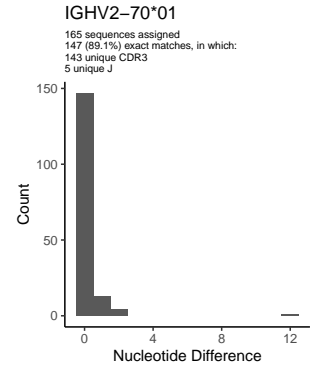
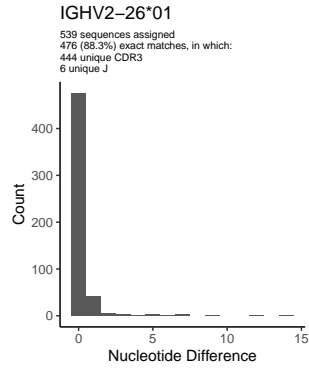
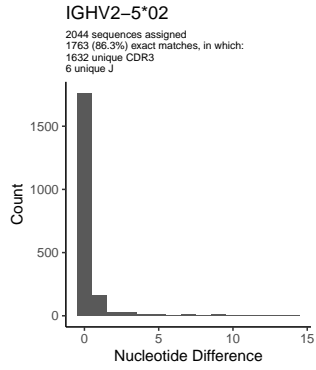
| | | |
|----------|---|-----------|
| 1 | Novel sequence analysis | 2 |
| 1.1 | CDR3 length distribution, in assignments to novel alleles | 2 |
| 2 | Variation from germline, in assignments to each allele | 3 |
| 3 | Allele usage in potential haplotype anchor genes | 8 |
| 4 | Haplotype plots | 9 |
| 5 | Configuration settings | 10 |

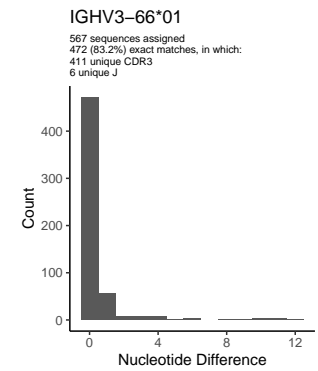
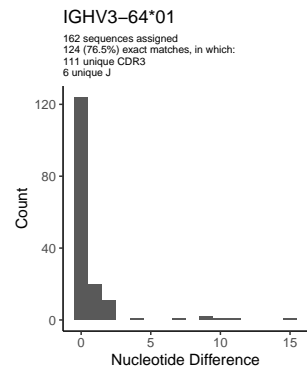
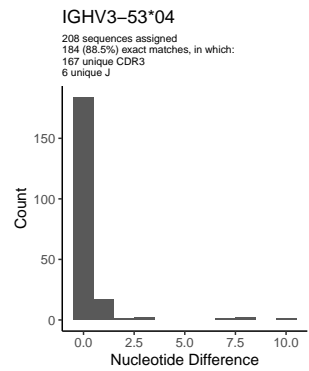
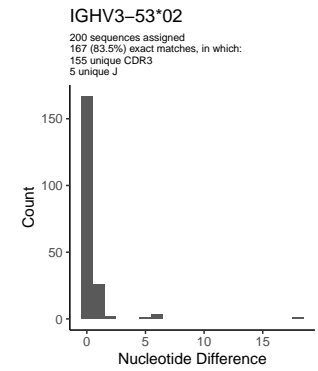
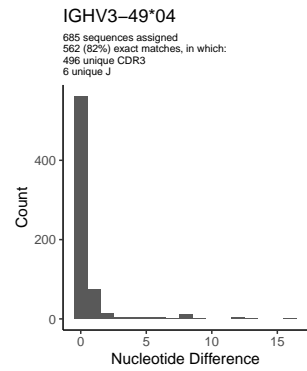
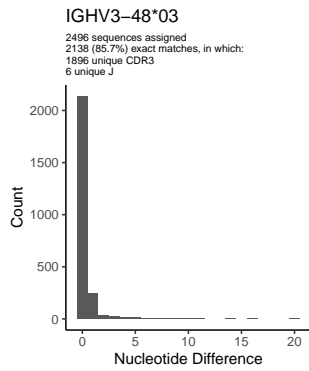
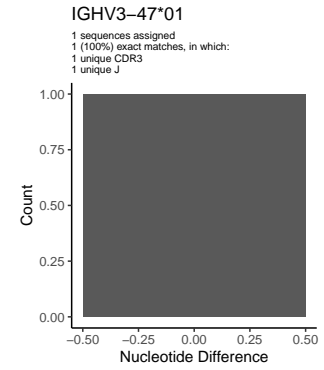
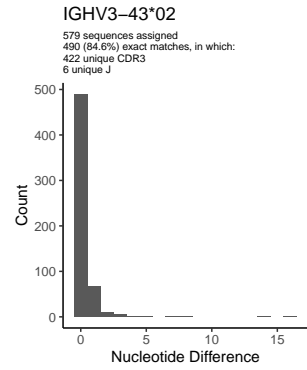
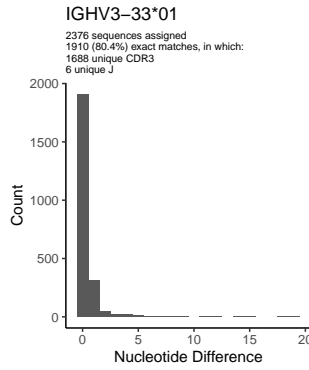
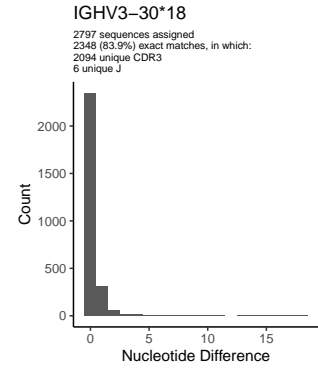
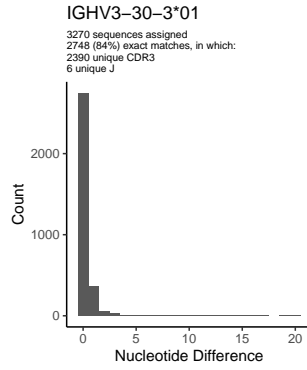
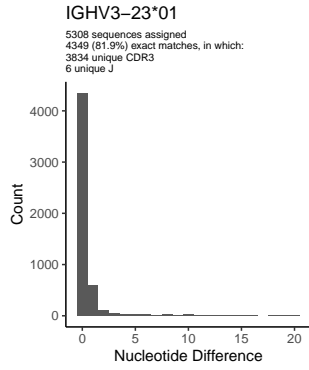
1 Novel sequence analysis

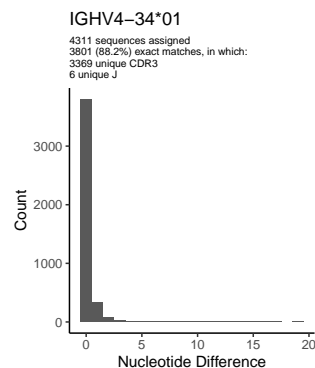
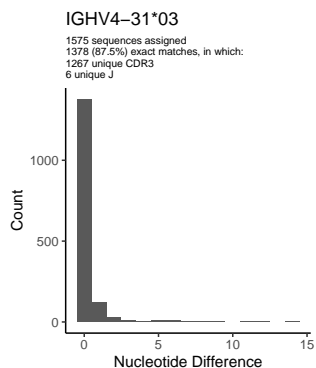
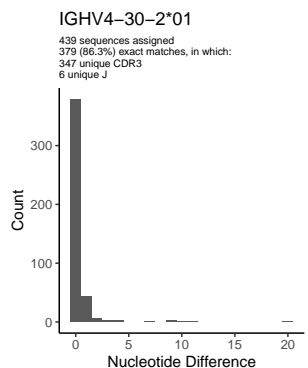
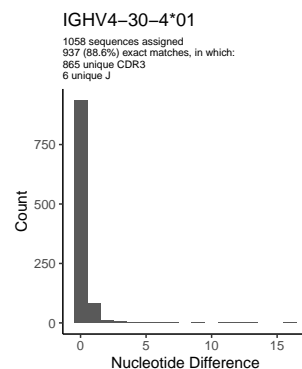
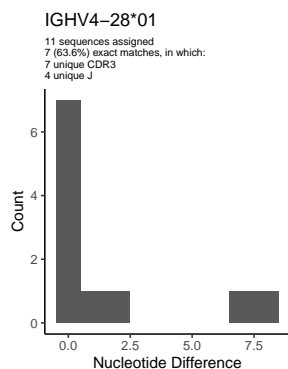
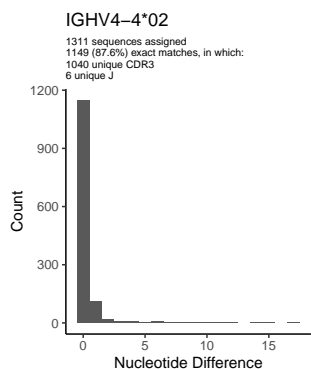
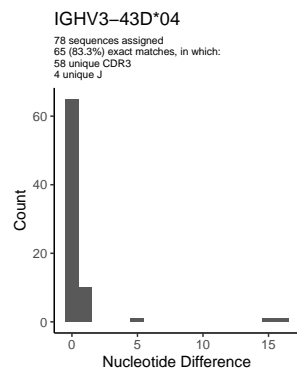
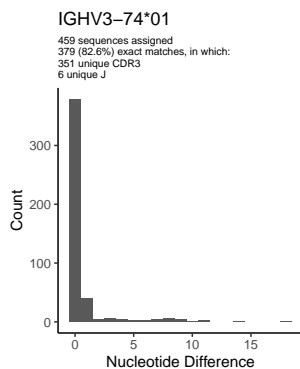
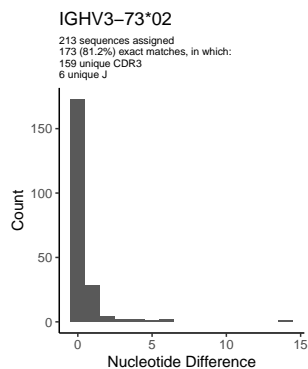
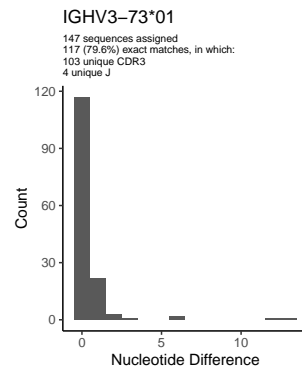
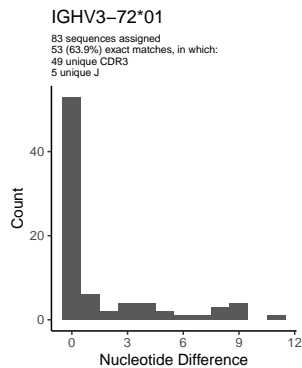
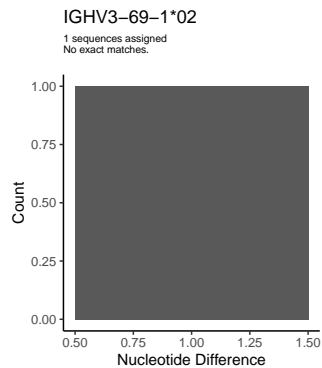
1.1 CDR3 length distribution, in assignments to novel alleles

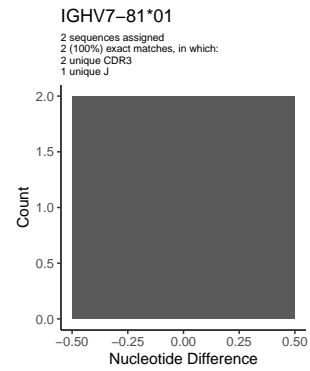
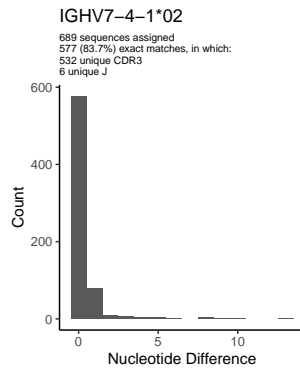
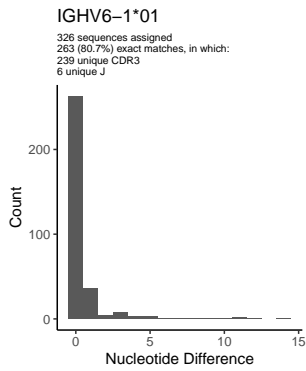
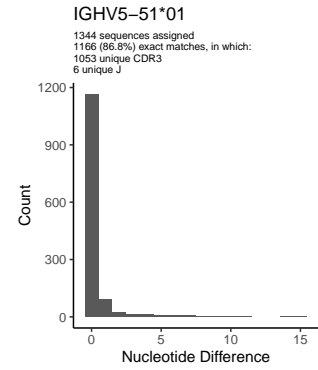
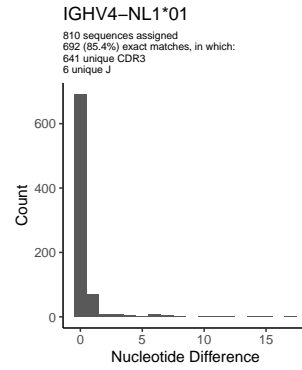
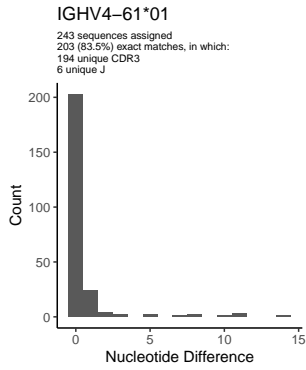
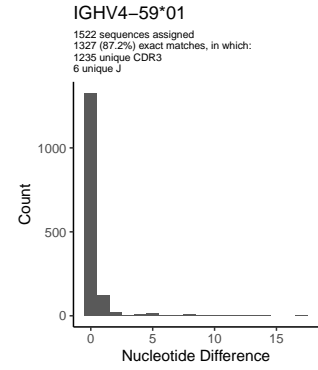
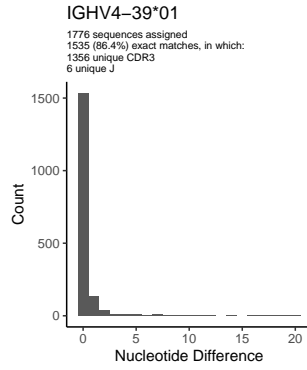
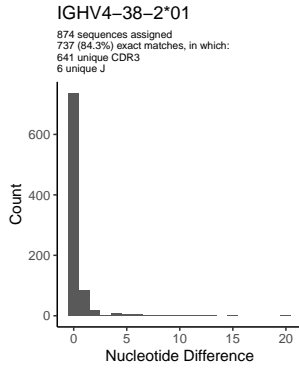
2 Variation from germline, in assignments to each allele











3 Allele usage in potential haplotype anchor genes



4 Haplotype plots

5 Configuration settings

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## Germline reference file: /work/jenkins/PRJEB26509/S64/S64/68/68/25/af8fcd7fd1195322d63bdd08a27bb8/re  
##  
## Novel allele file:  
##  
## Species: Homosapiens  
##  
## Chain: IGHV  
##  
## Segment: V  
##  
## Warning    no inferred sequences found.
```