

OGRDBstats Report

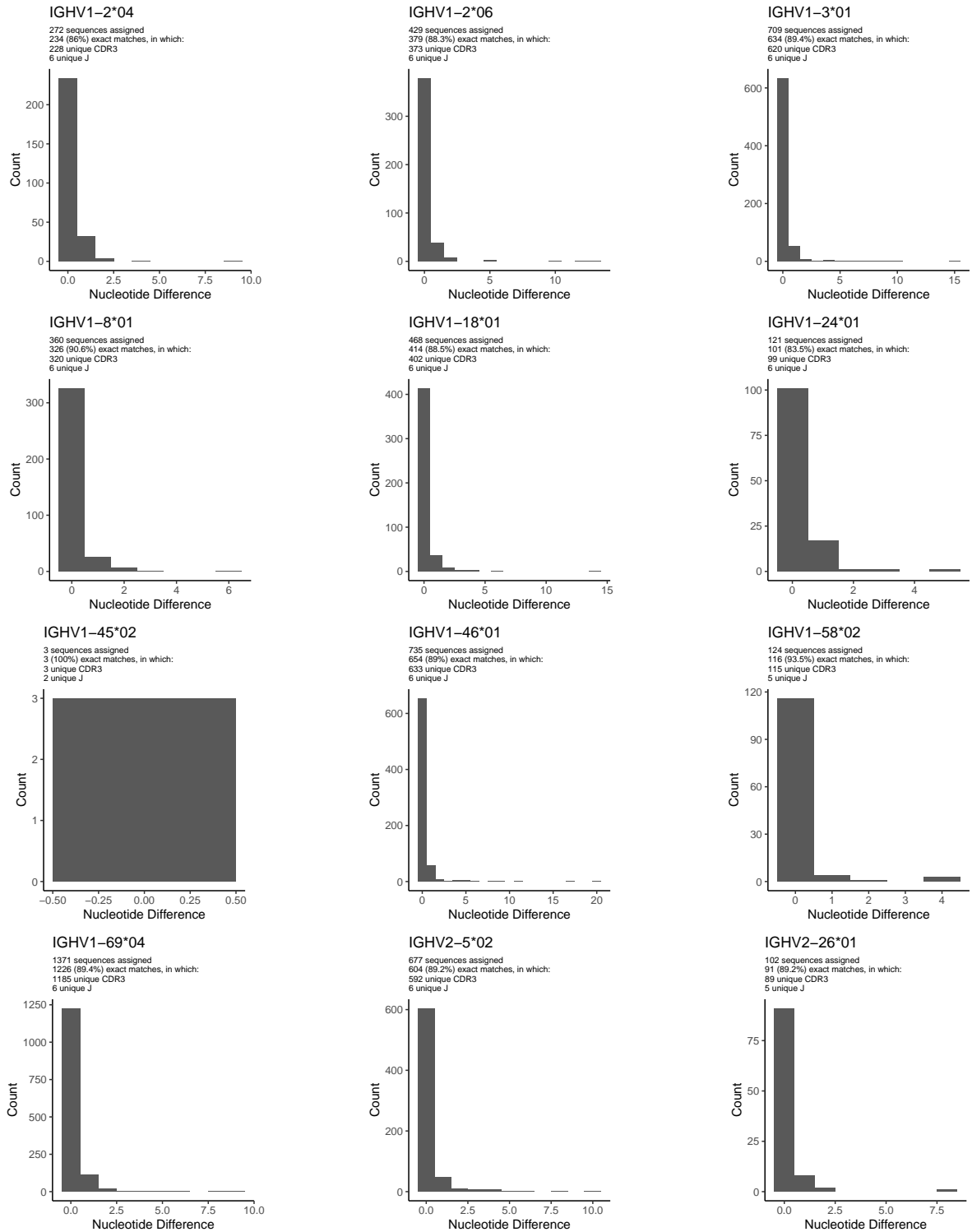
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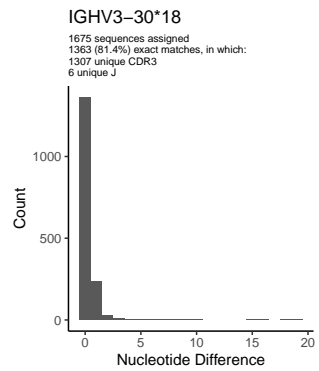
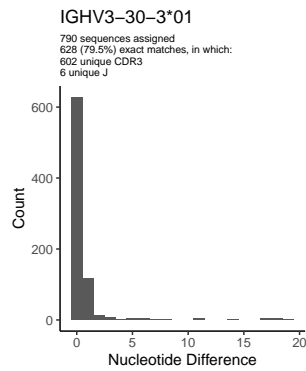
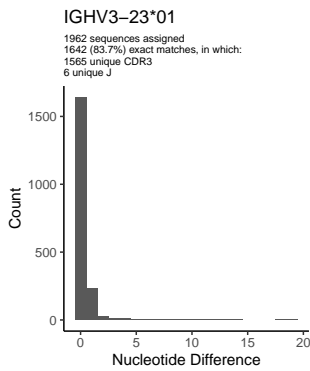
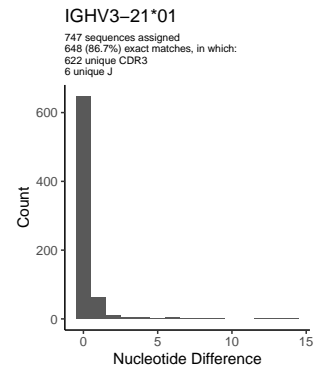
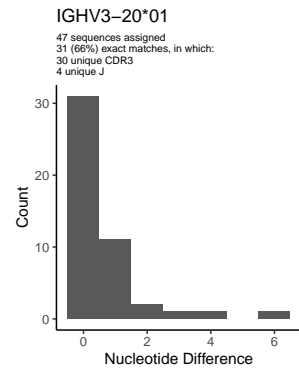
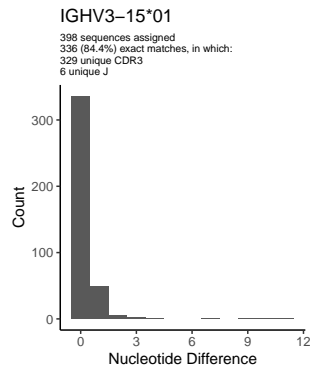
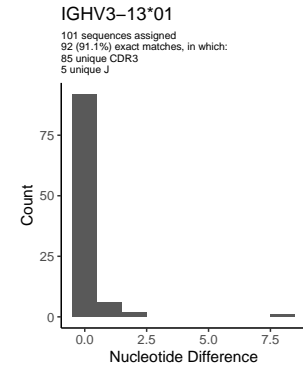
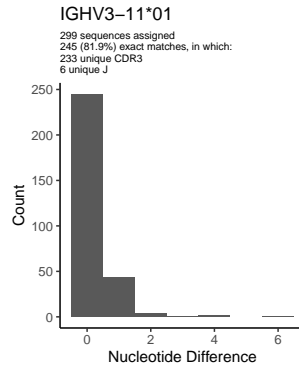
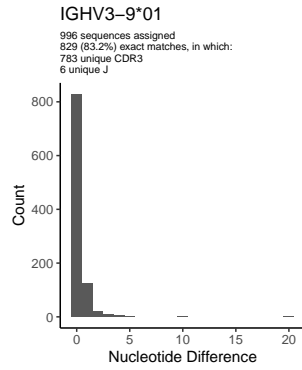
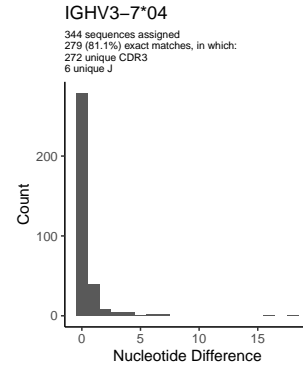
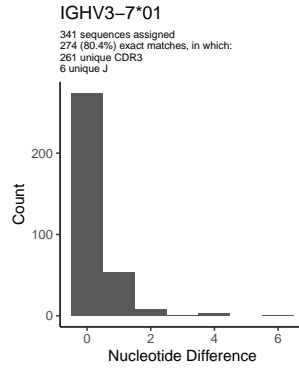
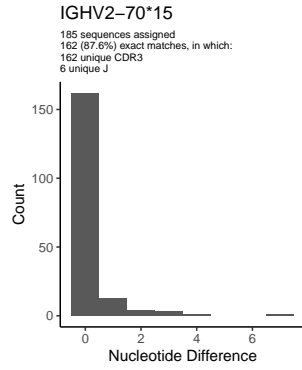
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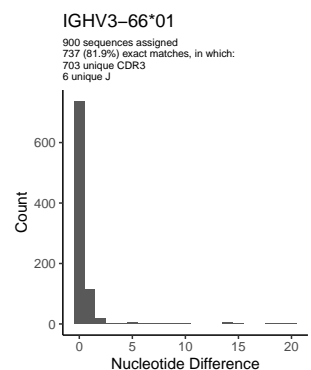
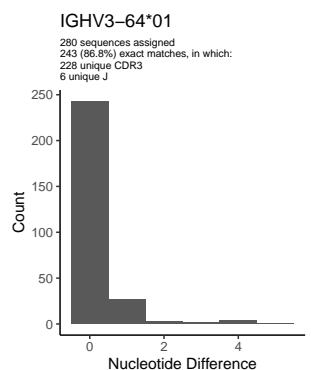
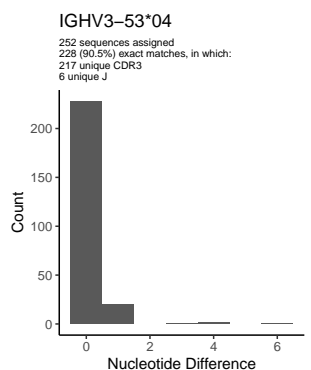
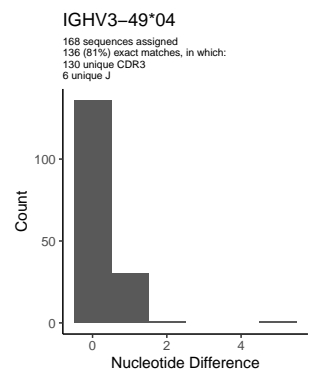
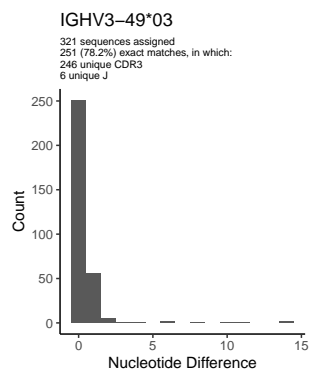
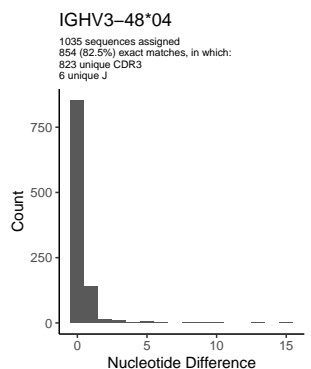
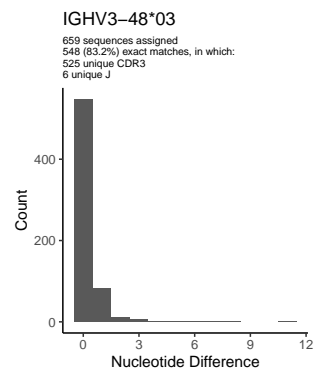
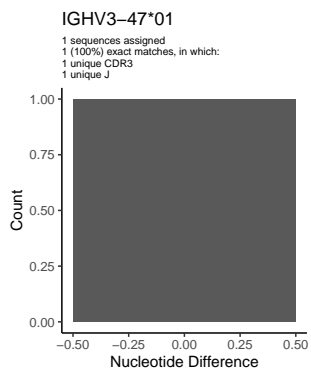
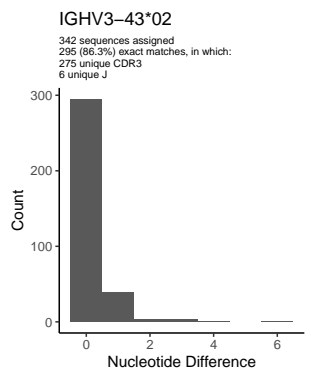
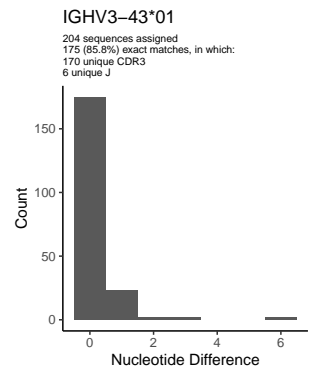
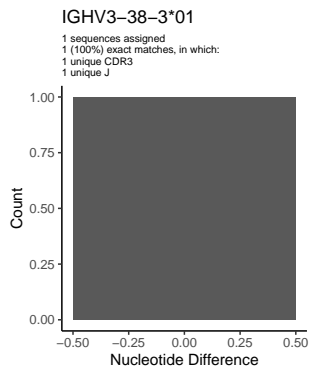
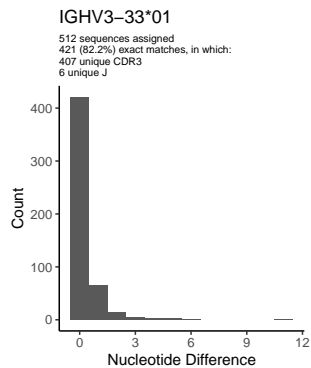
1 Novel sequence analysis

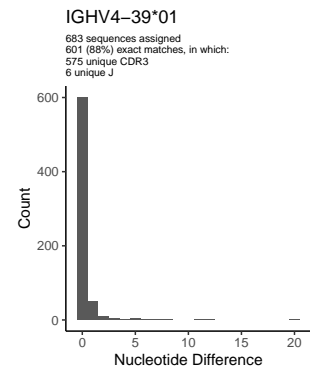
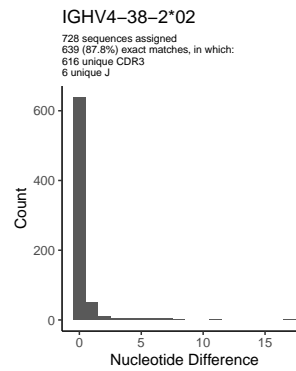
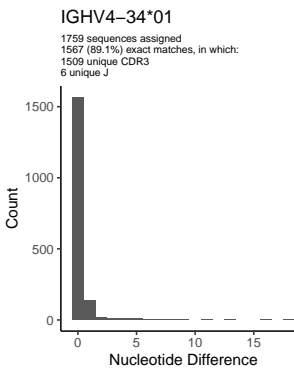
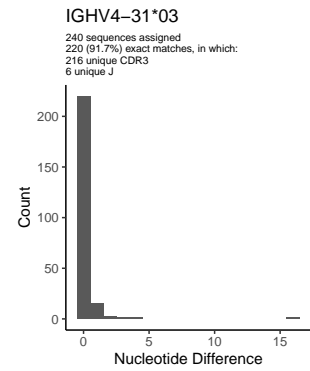
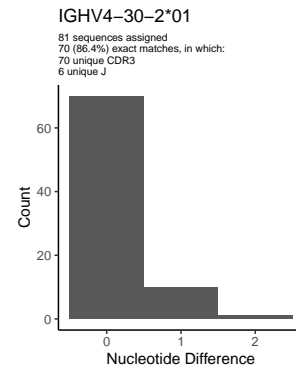
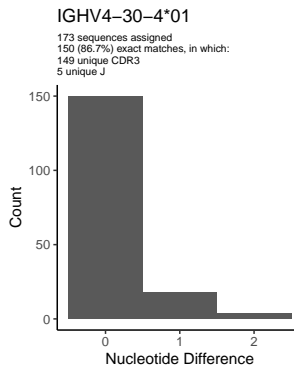
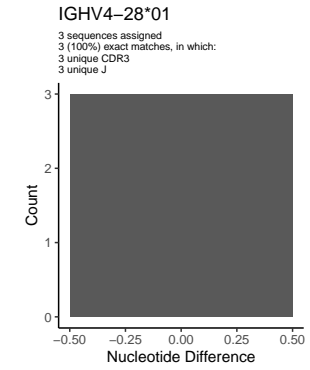
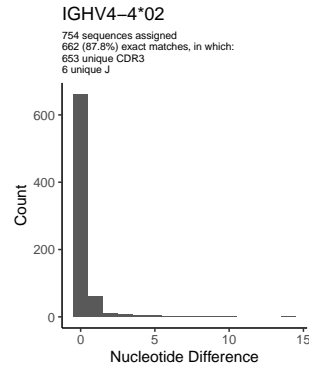
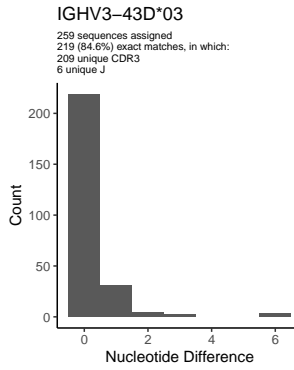
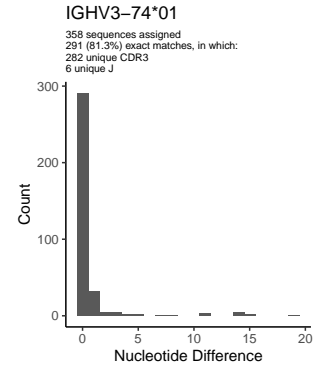
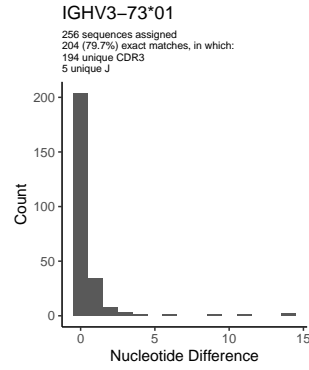
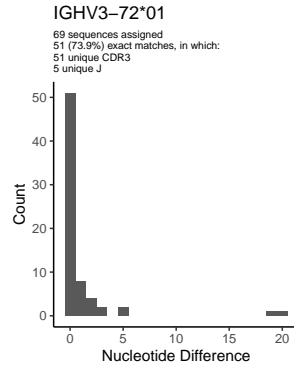
1.1 CDR3 length distribution, in assignments to novel alleles

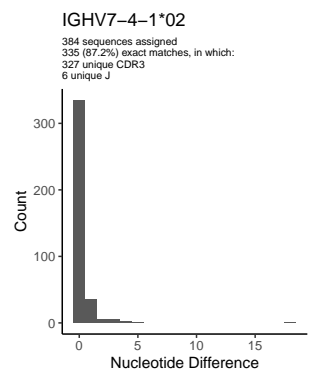
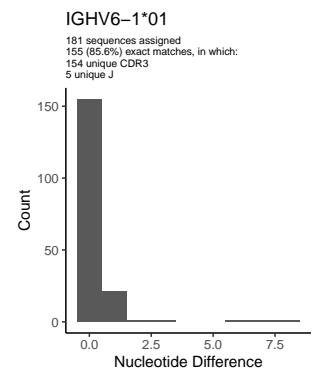
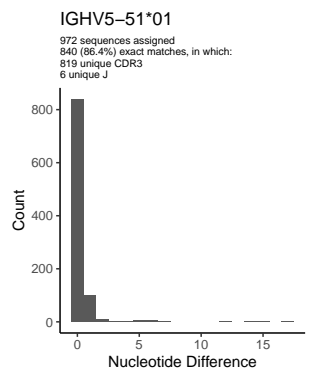
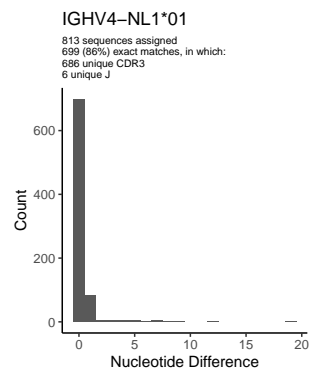
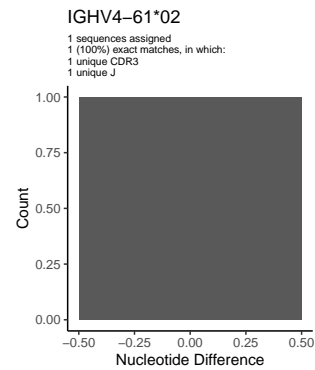
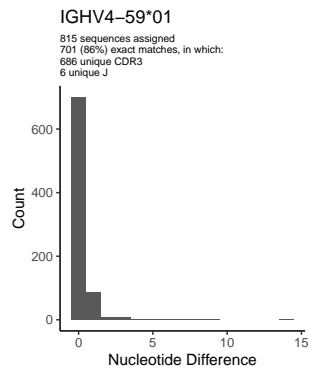
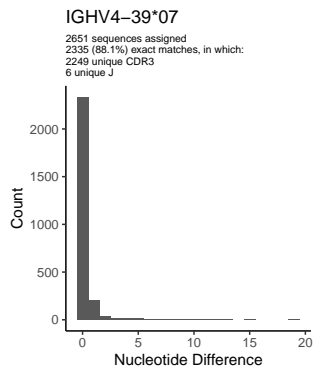
2 Variation from germline, in assignments to each allele











3 Allele usage in potential haplotype anchor genes



4 Haplotype plots

5 Configuration settings

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##  
## Germline reference file: /work/jenkins/PRJEB26509/S30/S30/30/30/5d/4bb2f5fdd10b094146bf2ce1a46985/re  
##  
## Novel allele file:  
##  
## Species: Homosapiens  
##  
## Chain: IGHV  
##  
## Segment: V  
##  
## Warning    no inferred sequences found.
```