

OGRDBstats Report

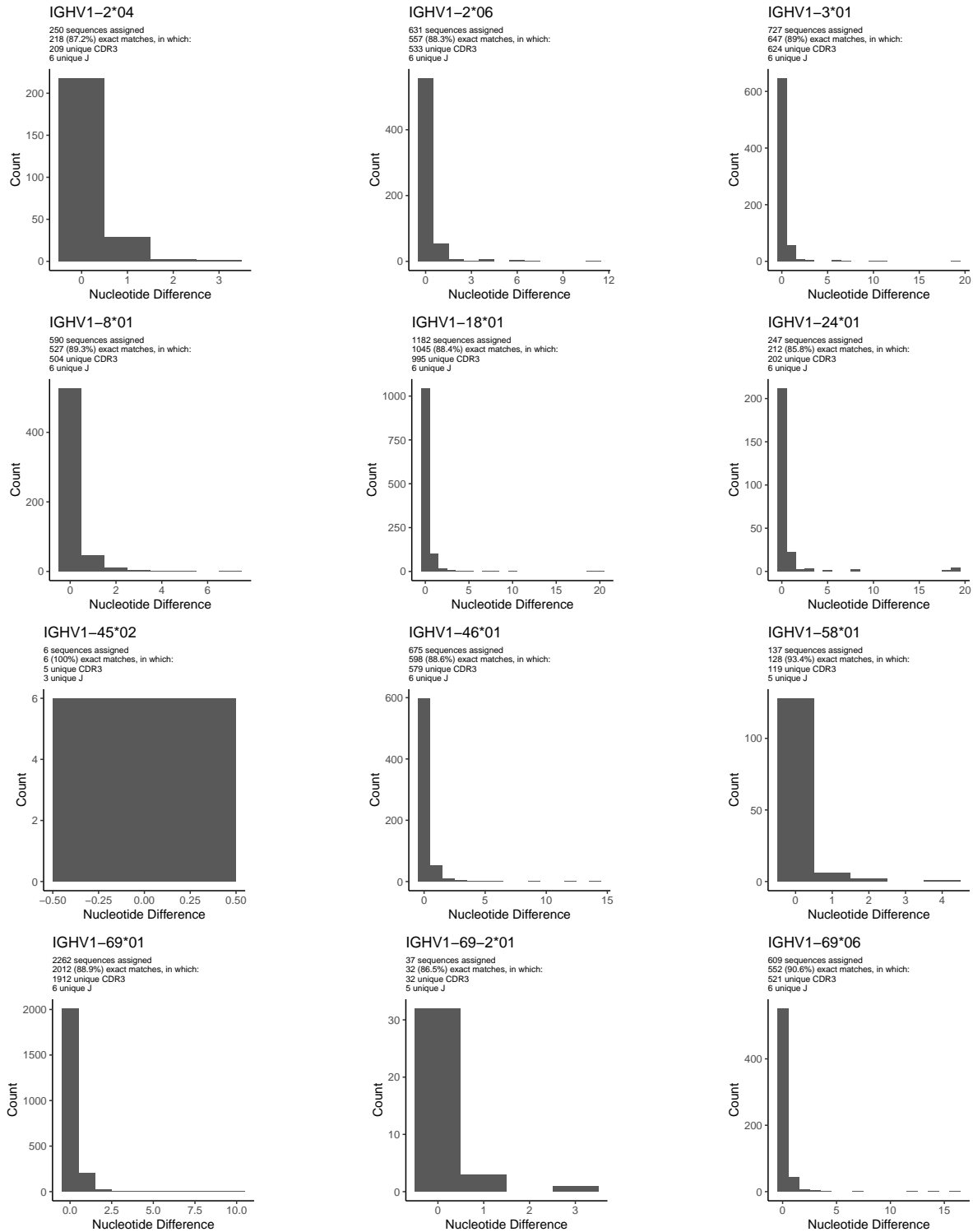
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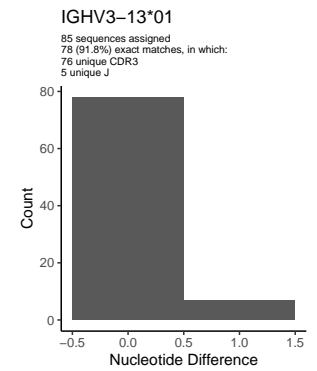
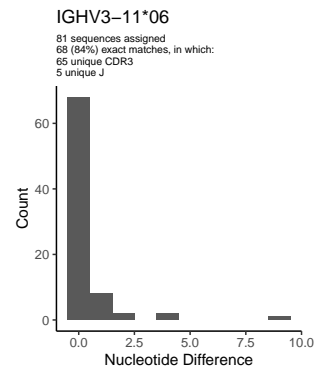
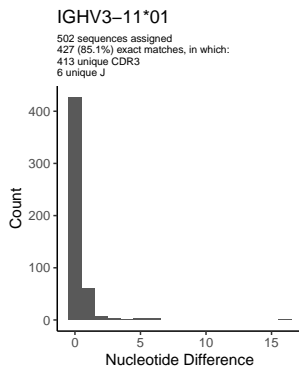
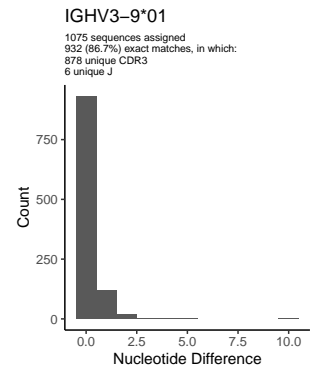
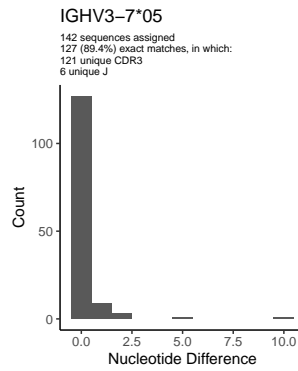
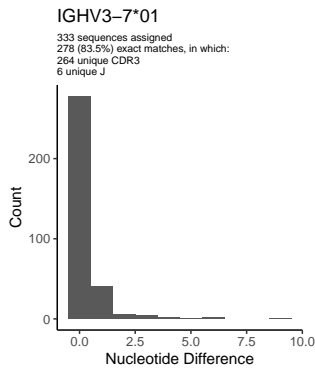
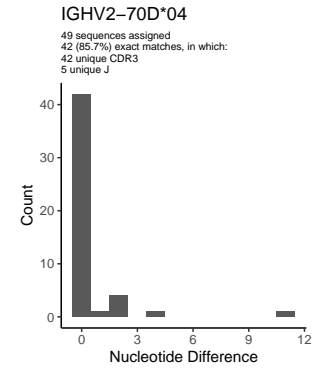
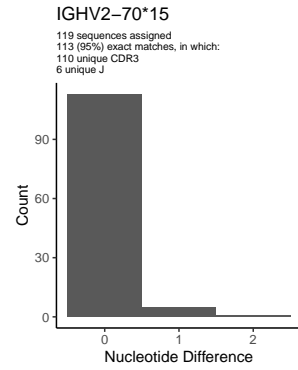
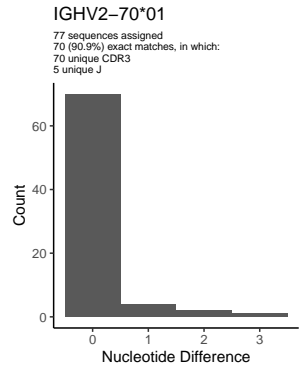
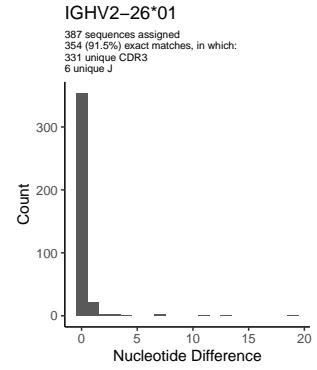
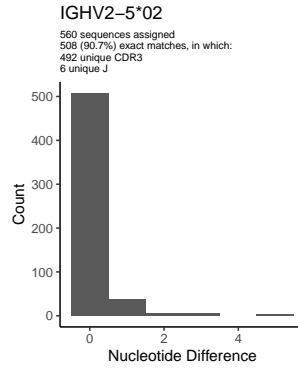
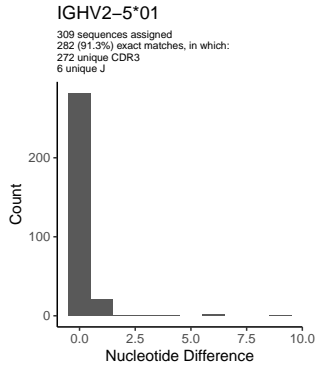
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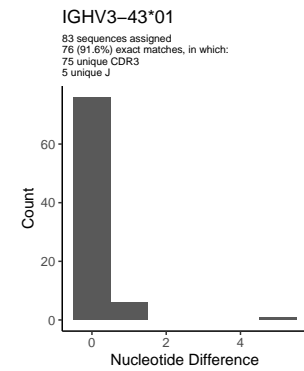
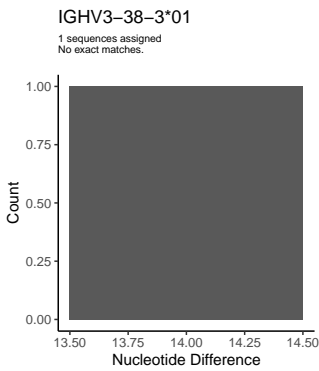
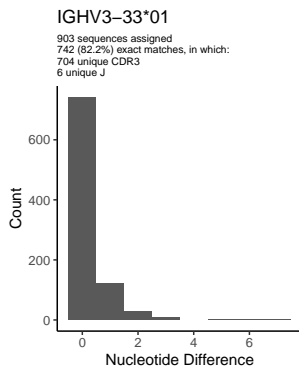
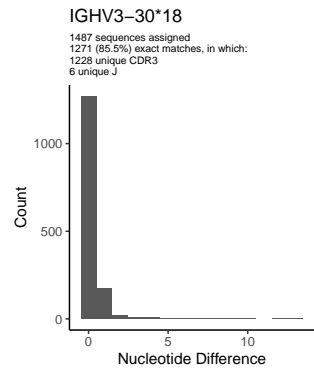
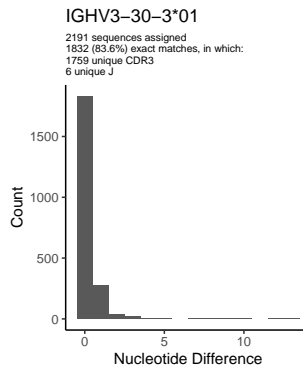
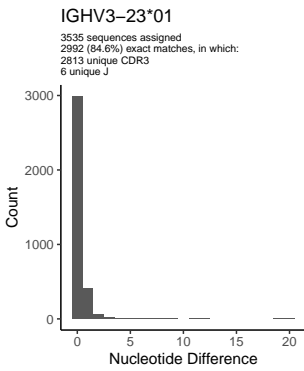
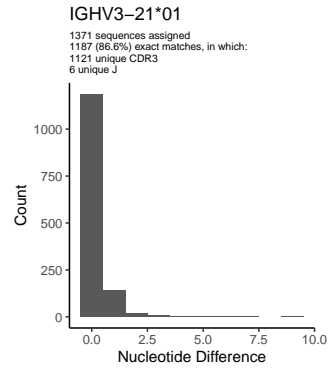
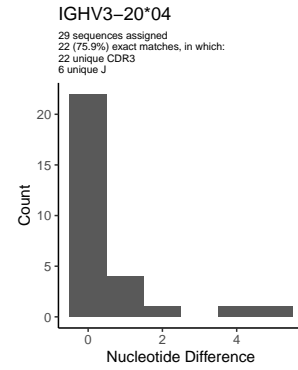
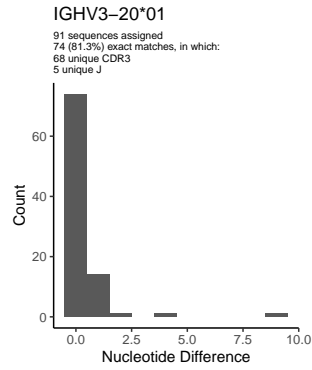
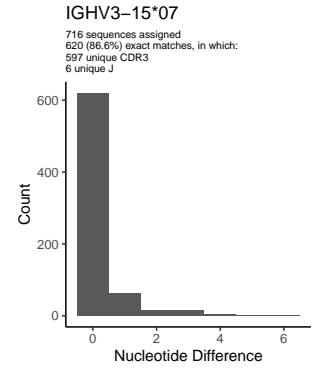
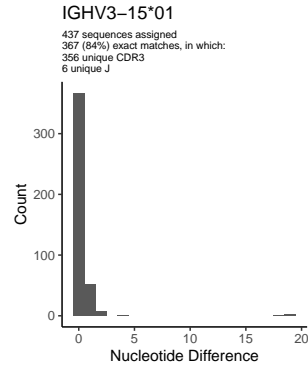
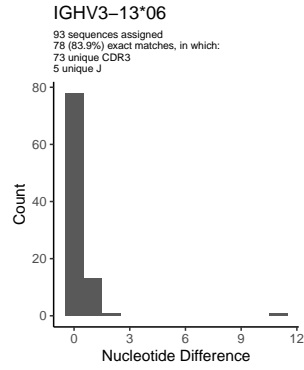
1 Novel sequence analysis

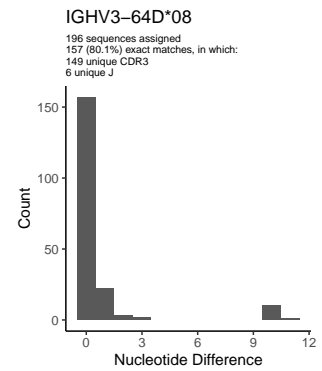
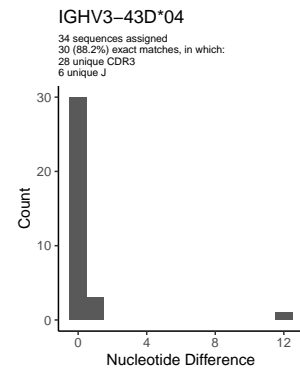
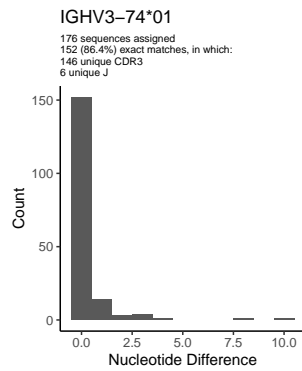
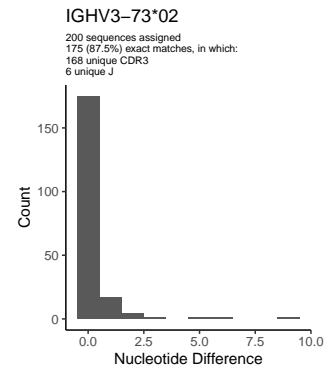
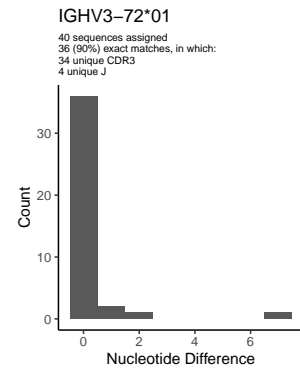
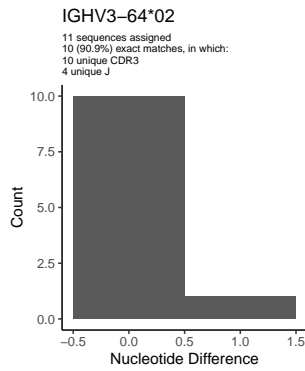
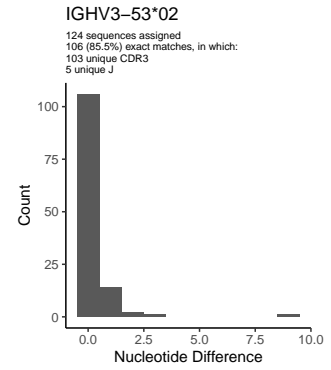
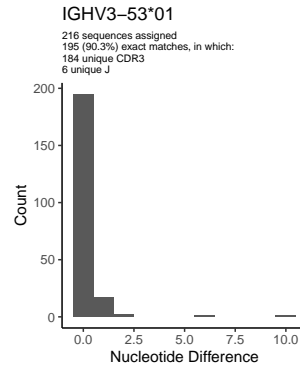
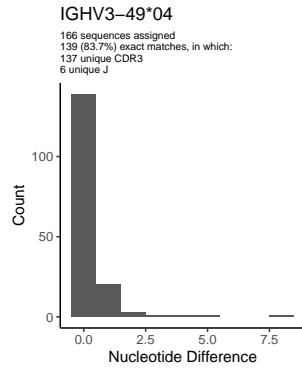
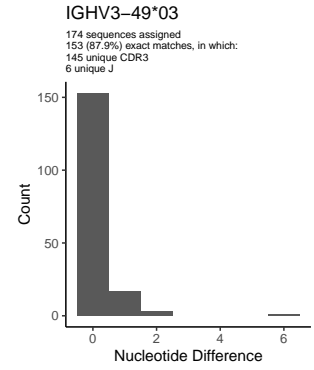
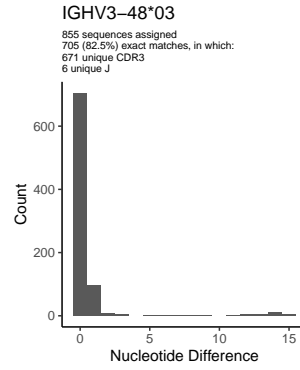
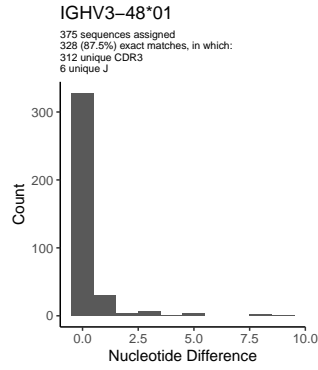
1.1 CDR3 length distribution, in assignments to novel alleles

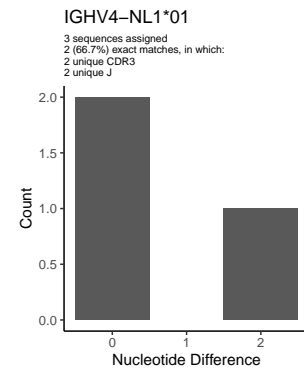
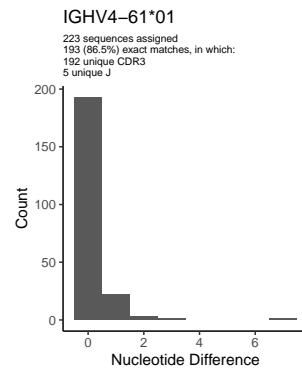
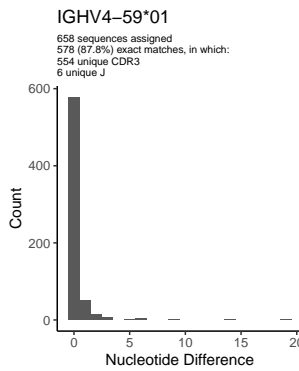
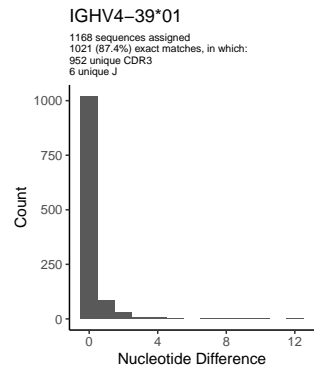
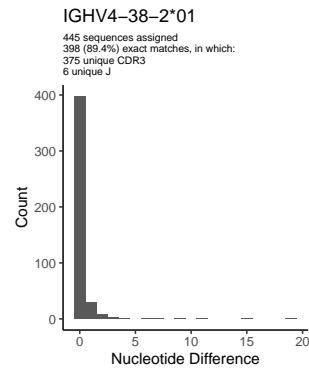
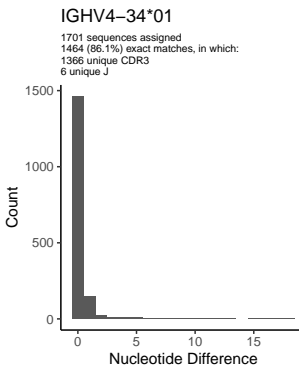
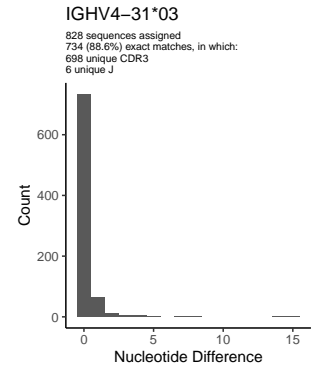
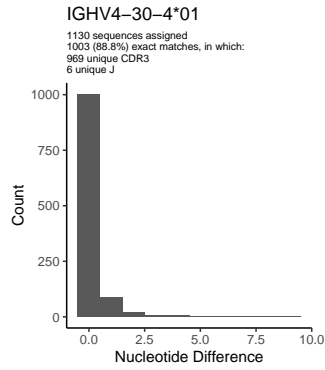
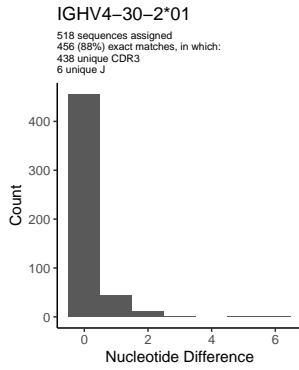
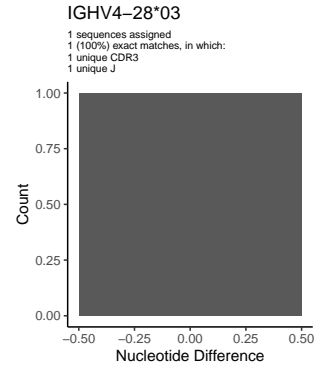
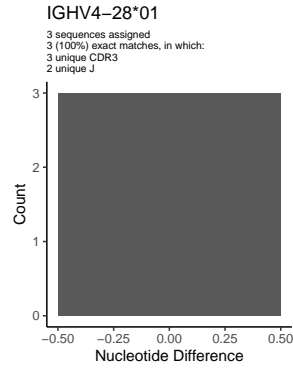
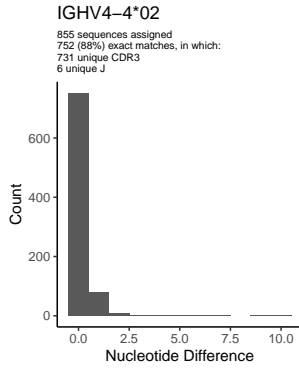
2 Variation from germline, in assignments to each allele

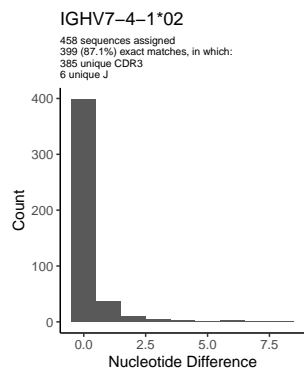
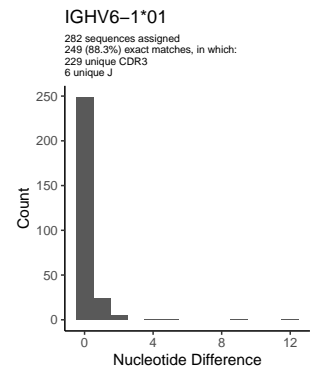
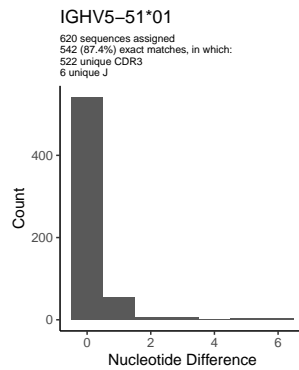
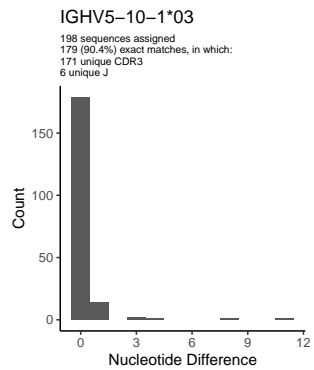




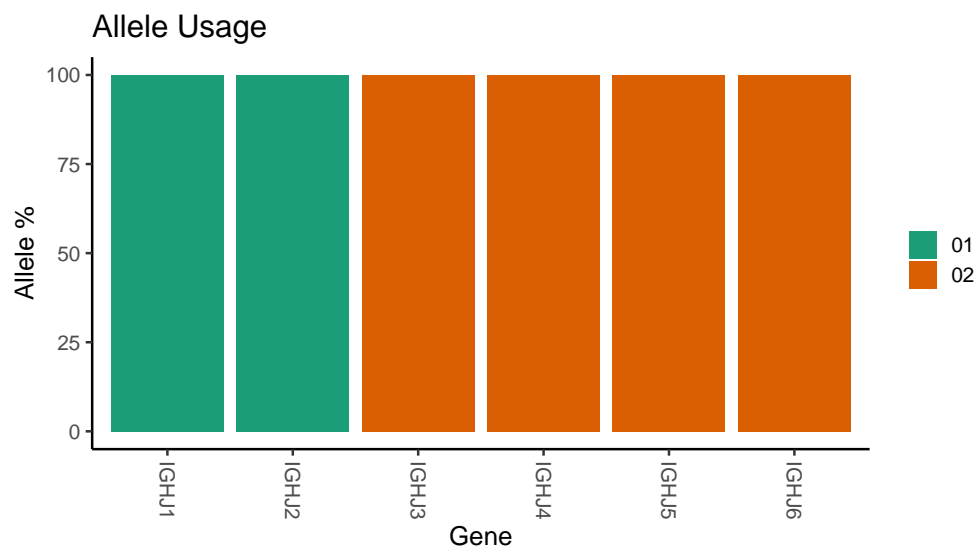








3 Allele usage in potential haplotype anchor genes



4 Haplotype plots

5 Configuration settings

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## Germline reference file: /misc/work/jenkins/PRJEB26509/S9/S9/9/9/c6/c1ce35780db55cf30acbb1d5c38548/r  
##  
## Novel allele file:  
##  
## Species: Homosapiens  
##  
## Chain: IGHV  
##  
## Segment: V  
##  
## Warning    no inferred sequences found.
```