

OGRDBstats Report

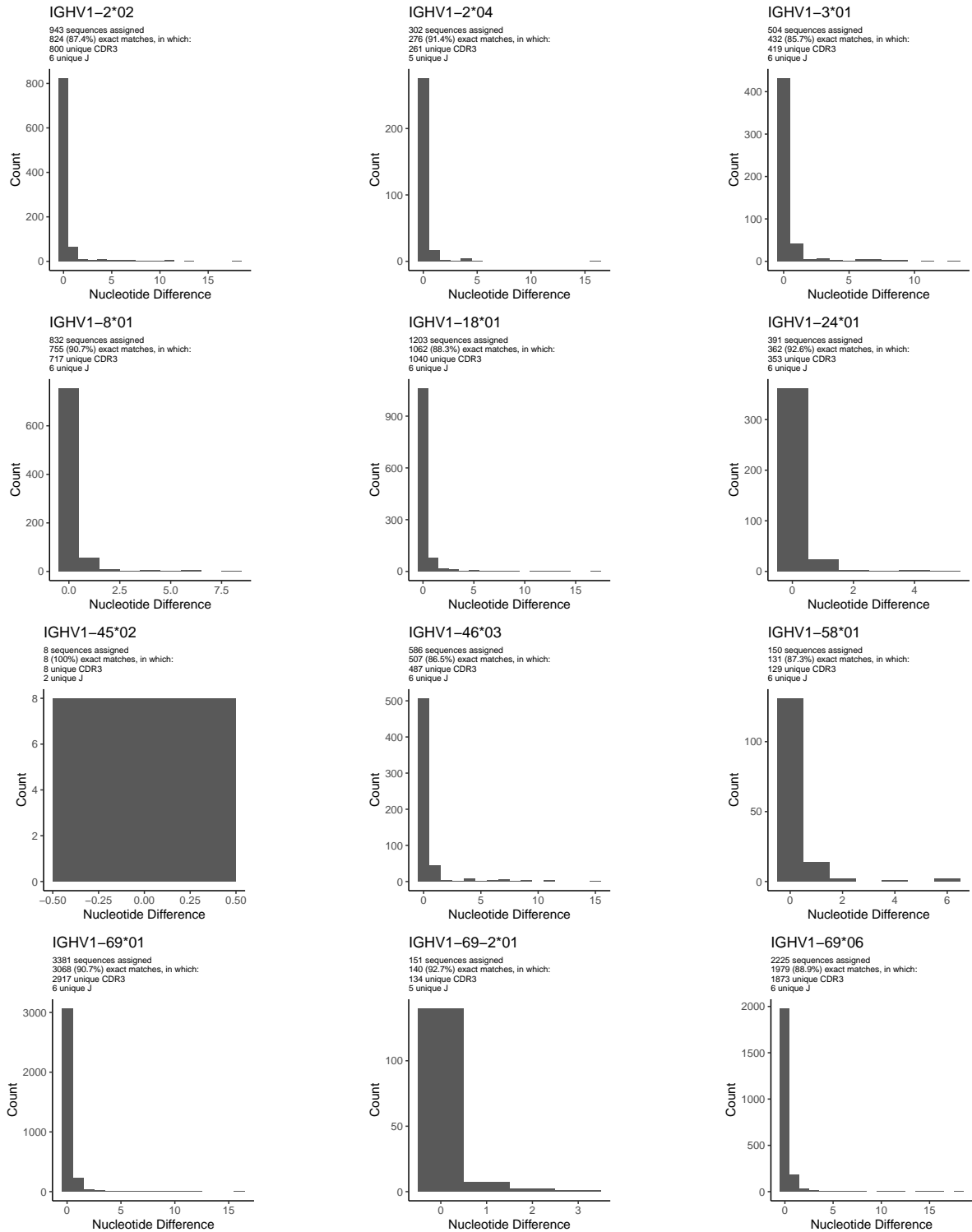
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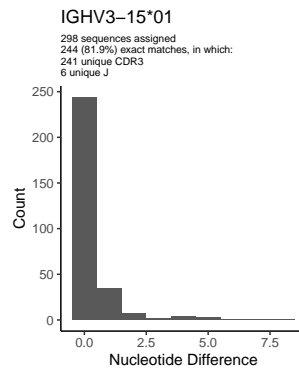
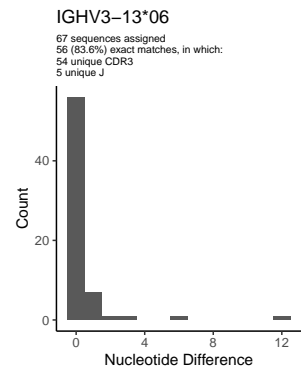
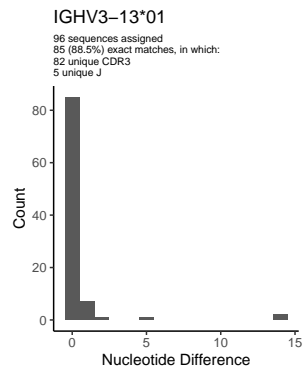
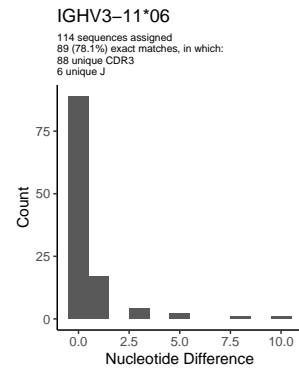
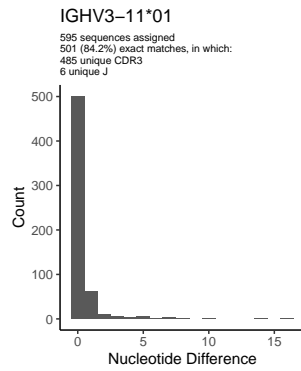
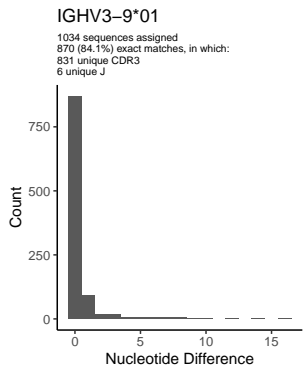
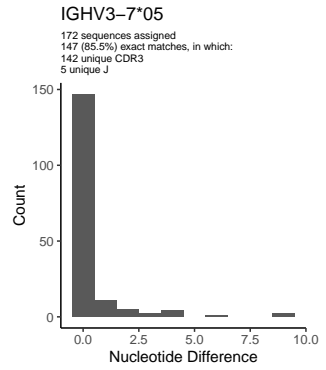
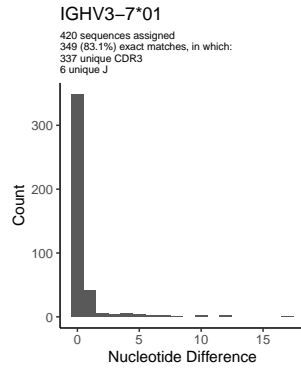
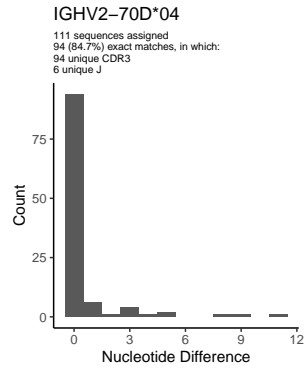
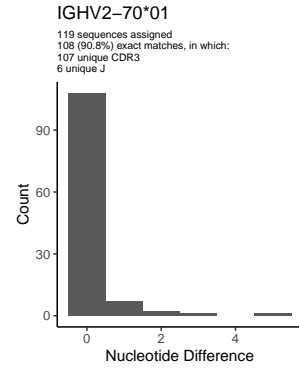
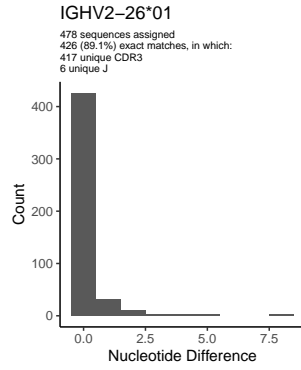
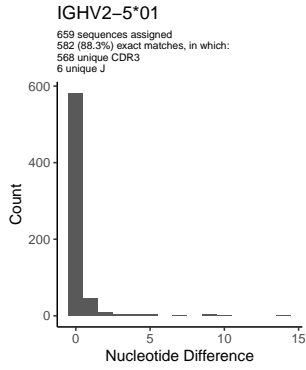
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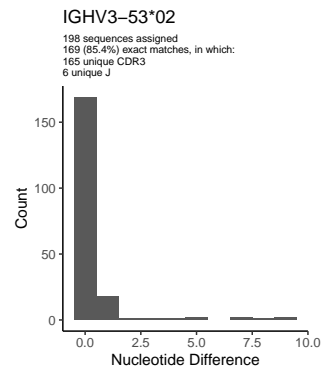
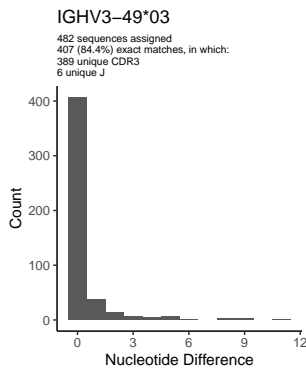
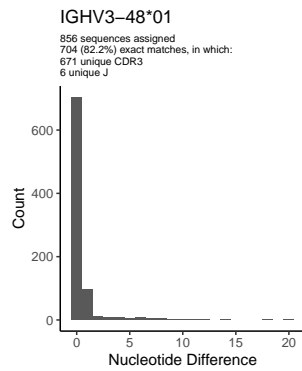
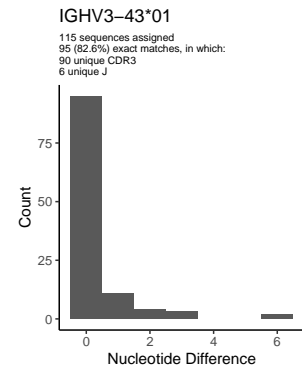
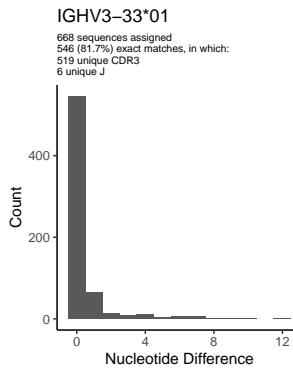
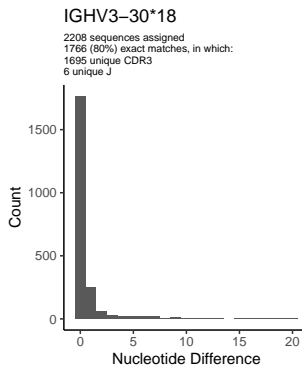
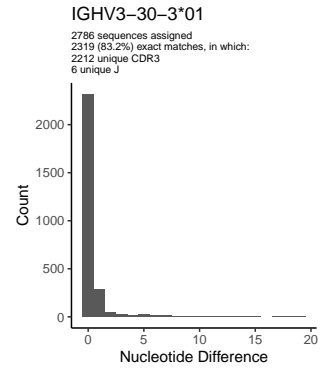
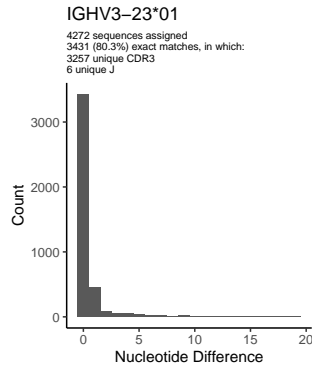
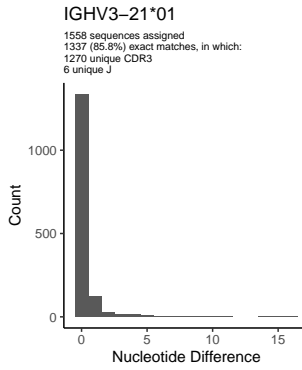
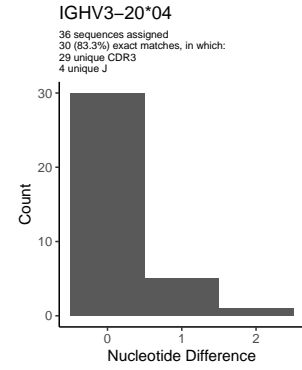
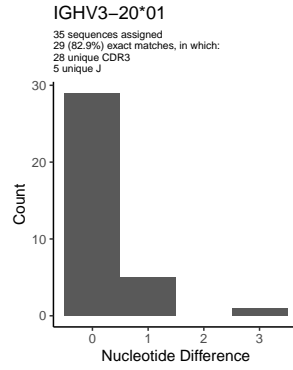
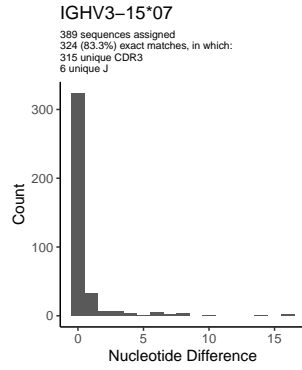
1 Novel sequence analysis

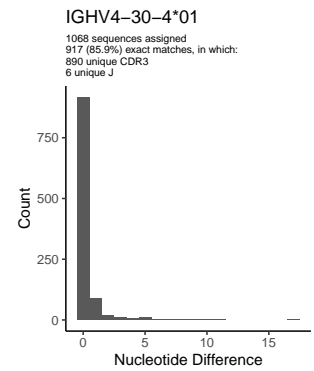
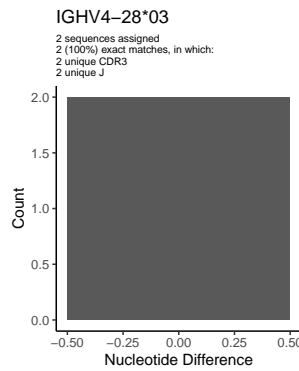
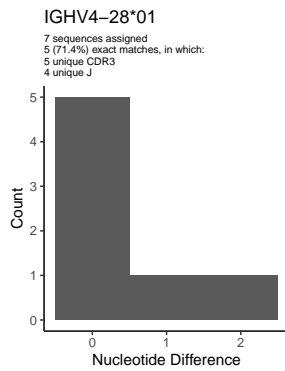
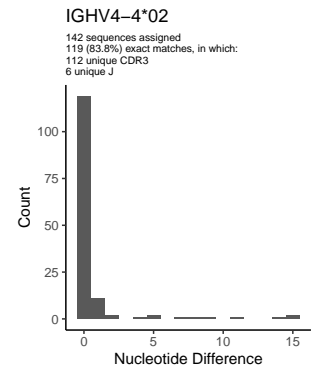
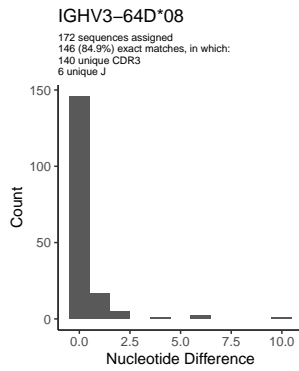
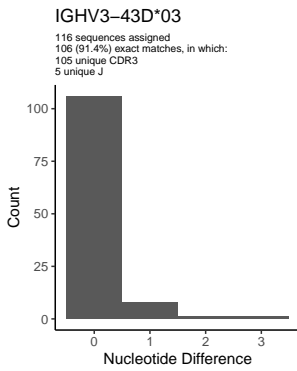
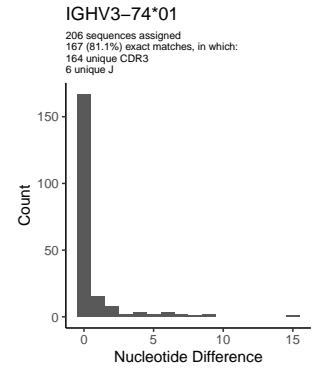
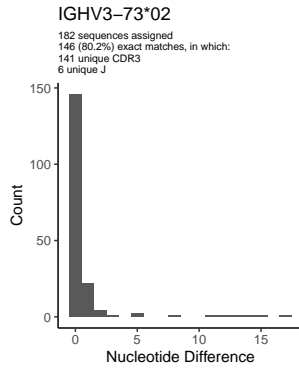
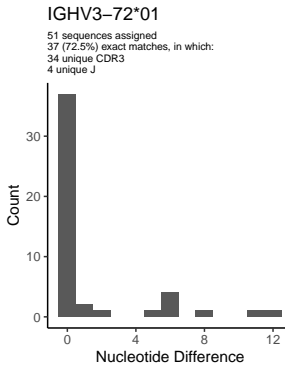
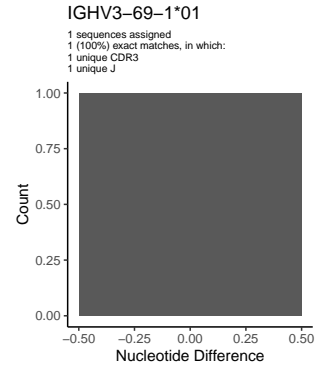
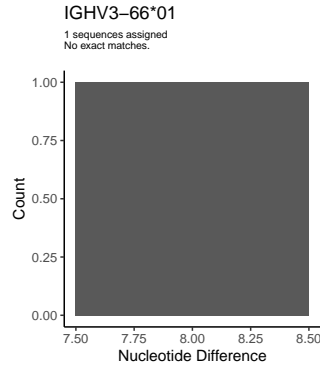
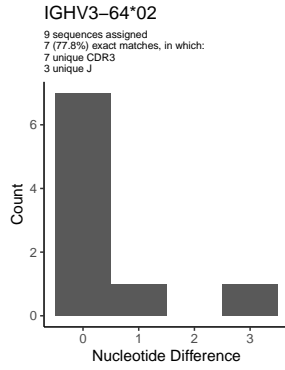
1.1 CDR3 length distribution, in assignments to novel alleles

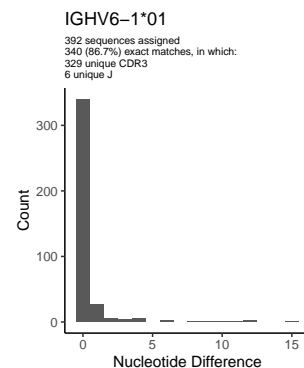
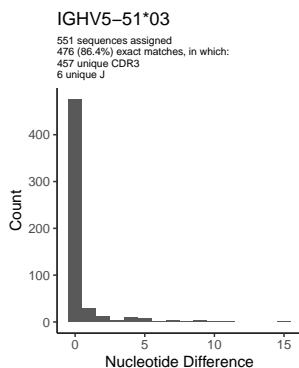
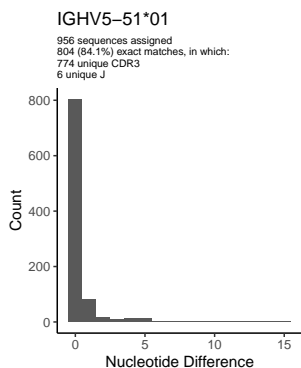
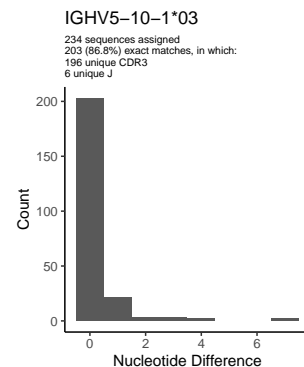
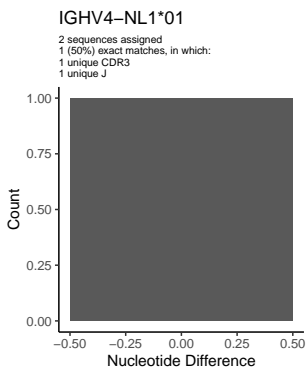
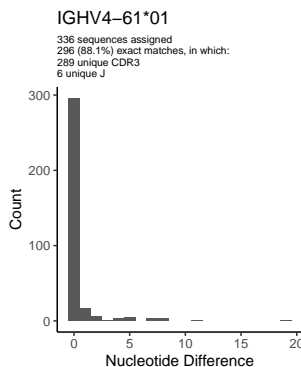
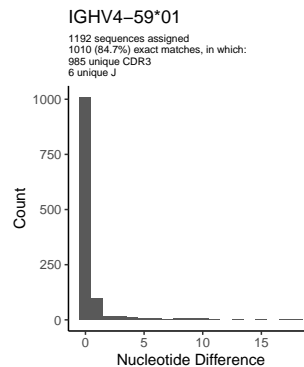
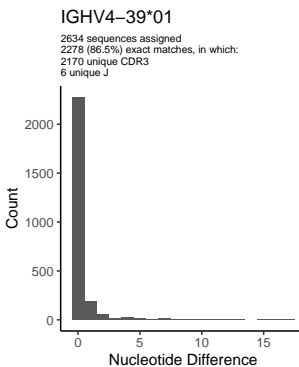
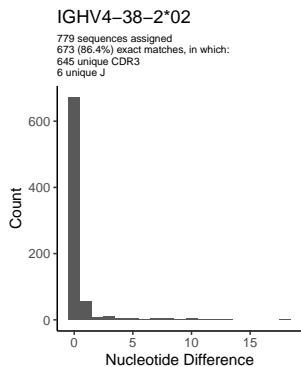
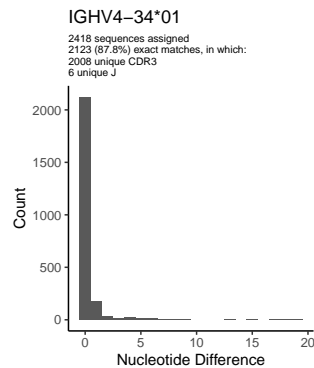
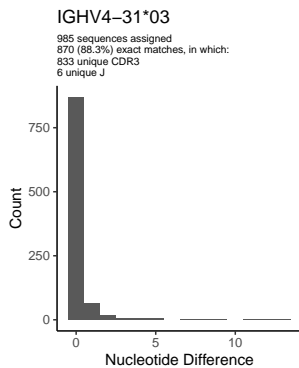
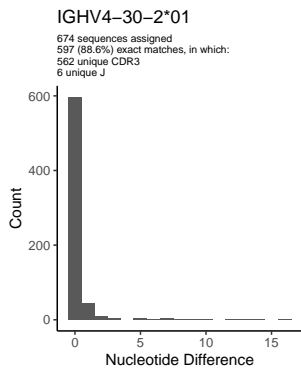
2 Variation from germline, in assignments to each allele





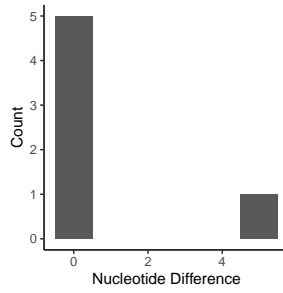




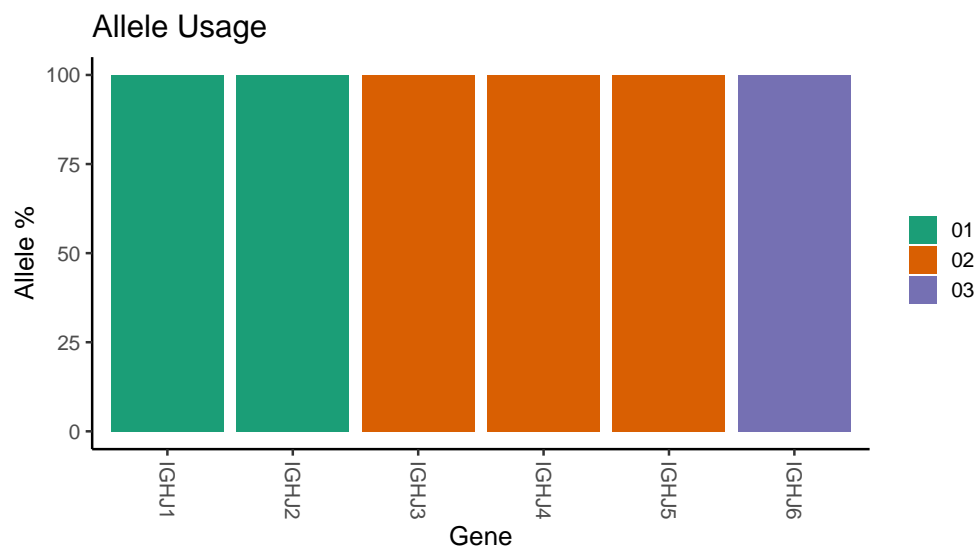


IGHV7-4-1*01

6 sequences assigned
5 (83.3%) exact matches, in which:
5 unique CDR3
2 unique J



3 Allele usage in potential haplotype anchor genes



4 Haplotype plots

5 Configuration settings

```
## Repertoire file: /work/jenkins/PRJEB26509/S7/S7/7/7/91/03be57af8e1aad129054dee760486a/7_Finale_genot  
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## Germline reference file: /work/jenkins/PRJEB26509/S7/S7/7/7/23/7a501c90def9ed313e27d56bfb049c/referen  
##  
## Novel allele file:  
##  
## Species: Homosapiens  
##  
## Chain: IGHV  
##  
## Segment: V  
##  
## Warning    no inferred sequences found.
```