

# OGRDBstats Report

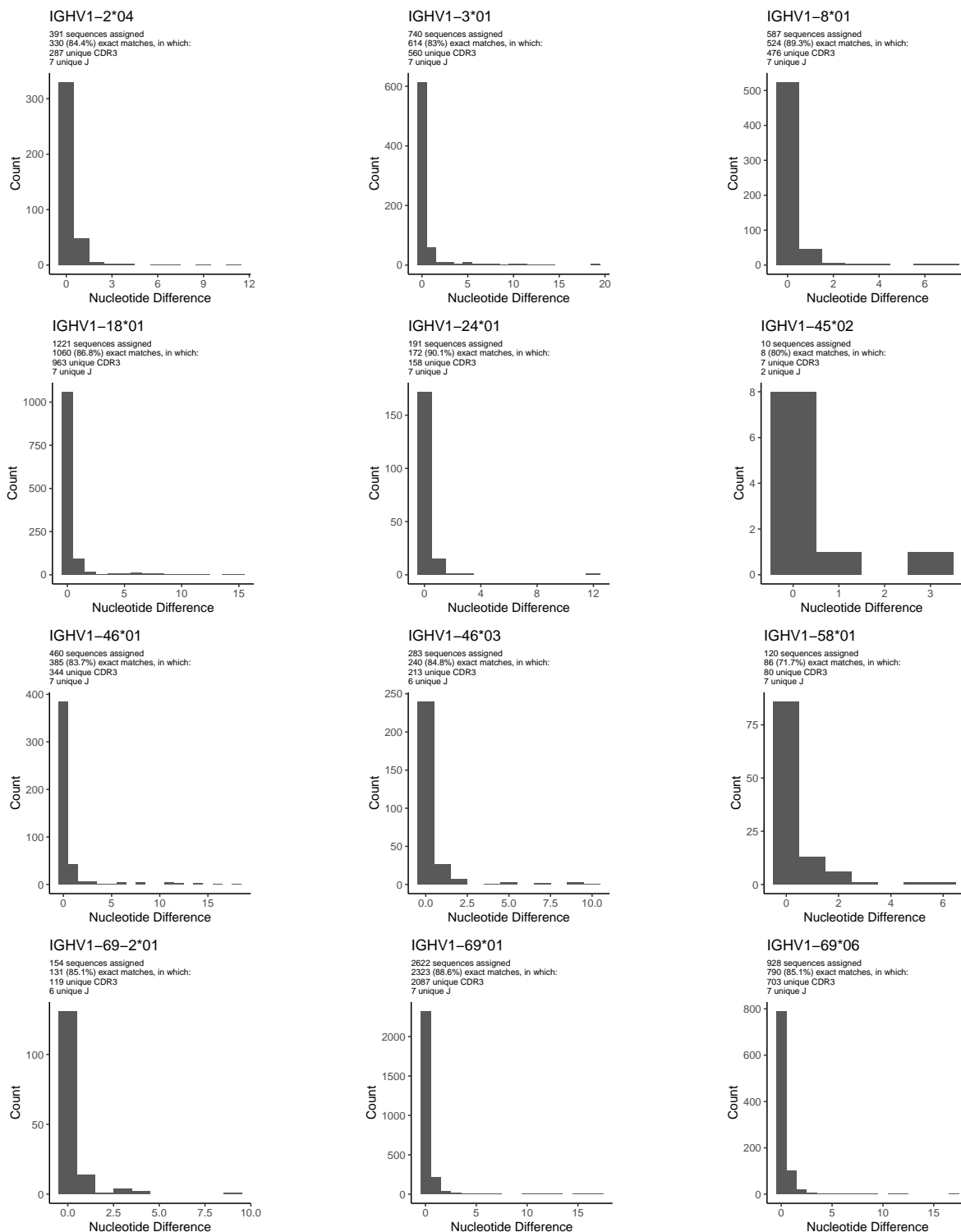
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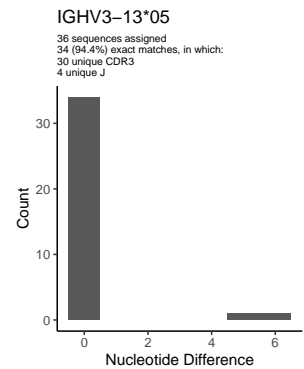
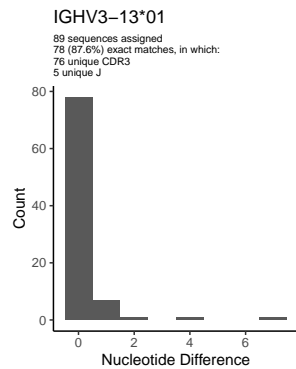
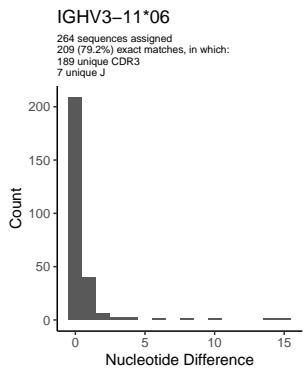
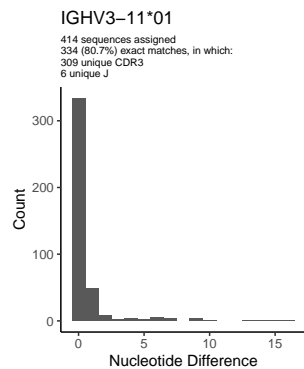
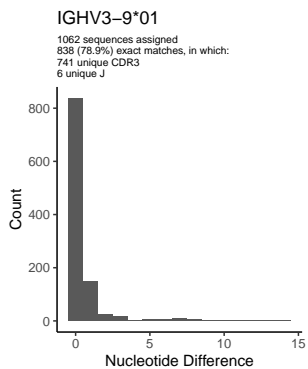
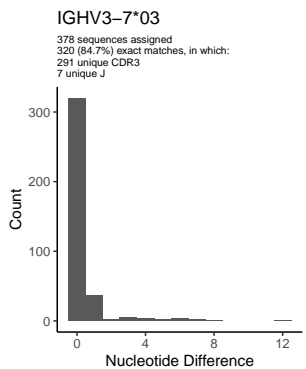
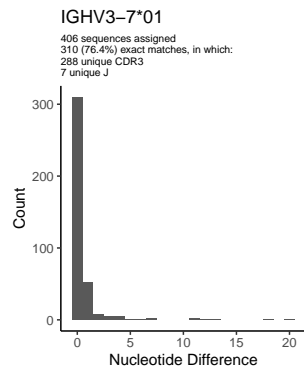
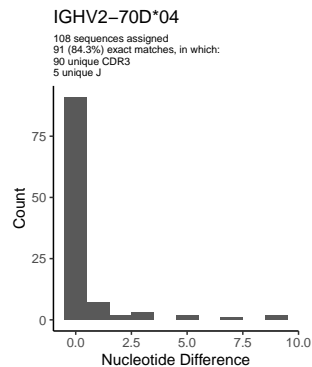
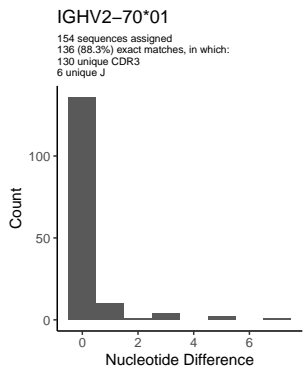
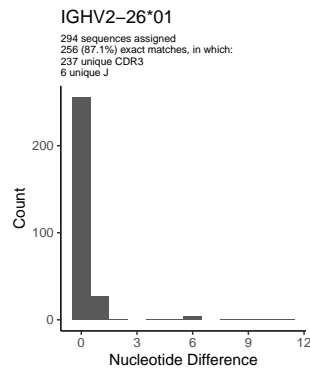
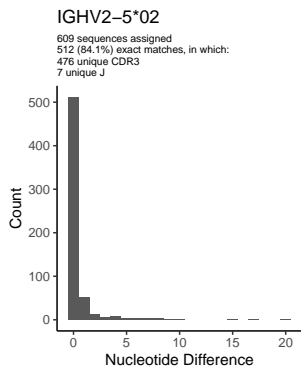
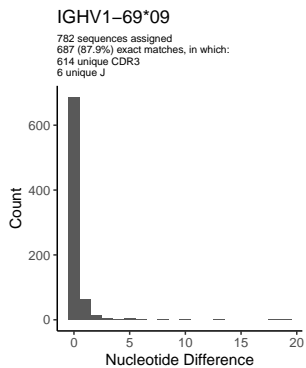
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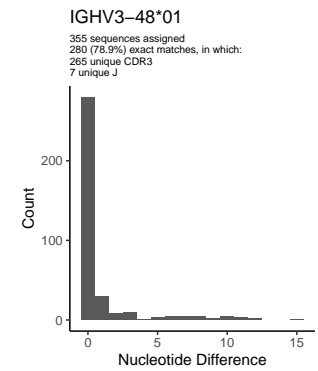
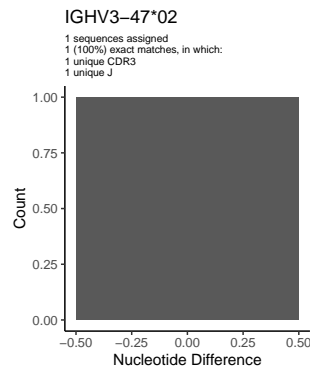
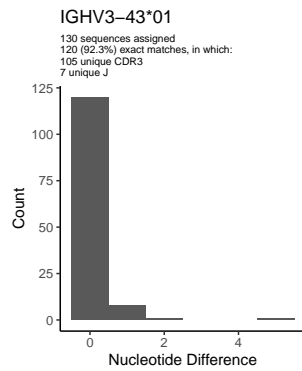
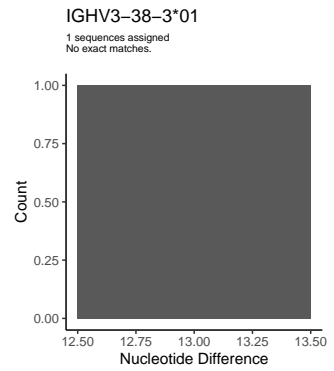
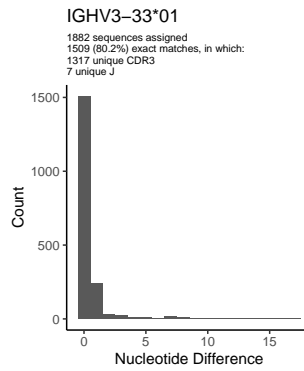
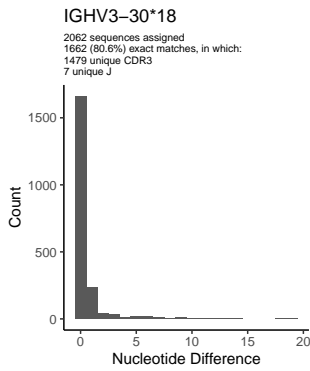
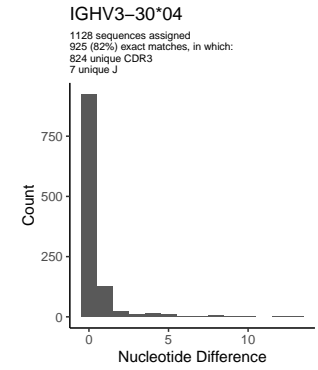
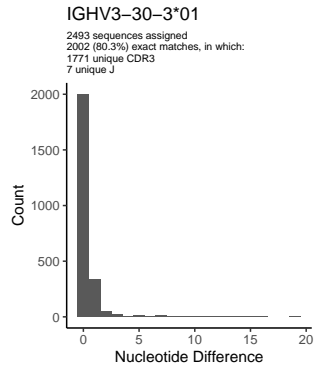
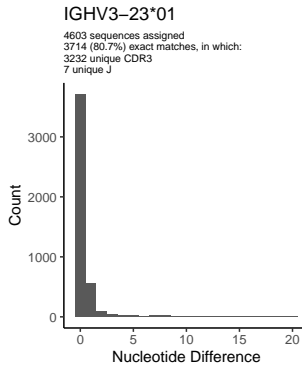
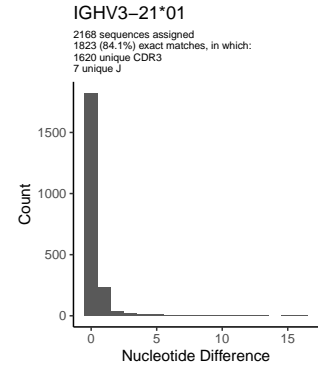
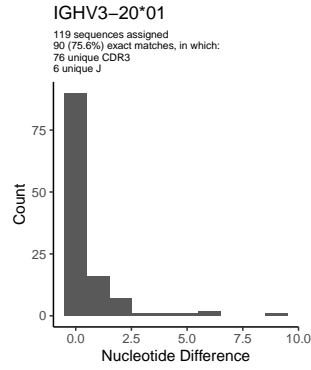
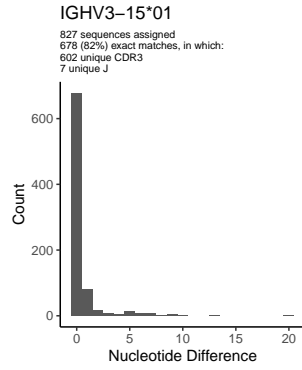
# 1 Novel sequence analysis

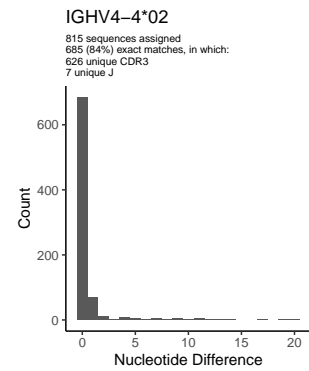
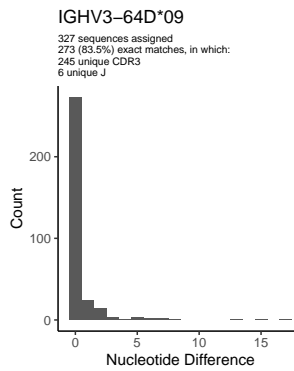
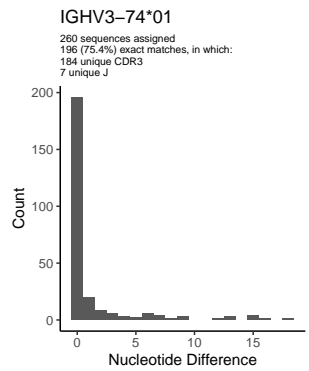
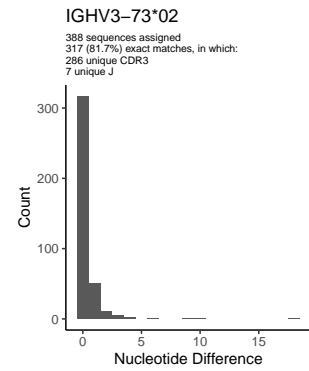
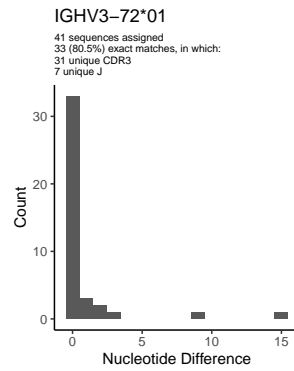
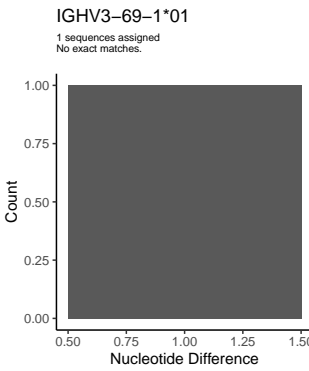
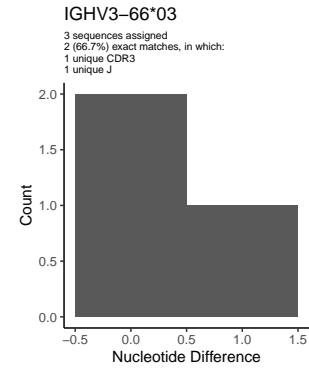
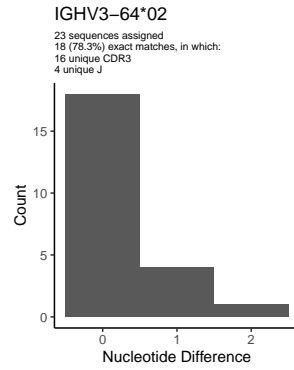
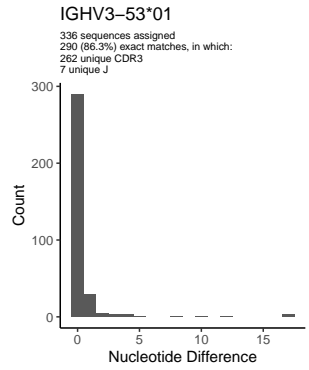
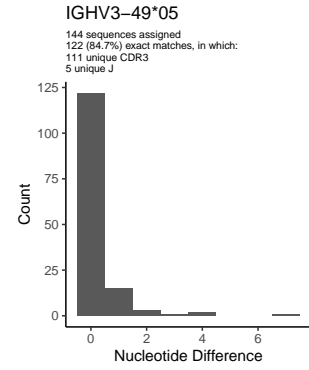
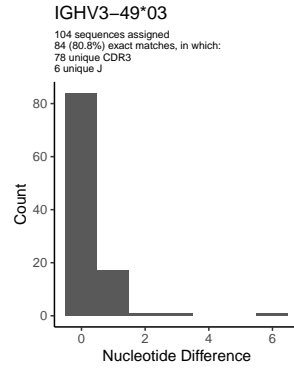
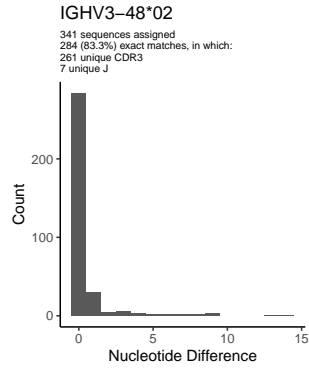
## 1.1 CDR3 length distribution, in assignments to novel alleles

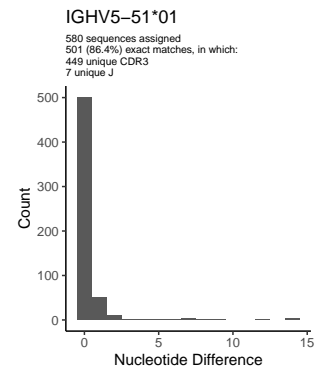
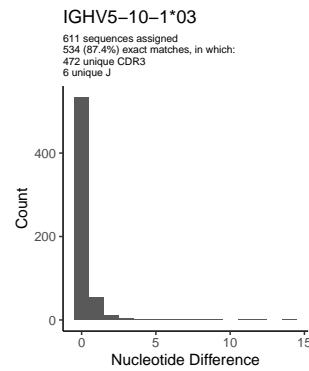
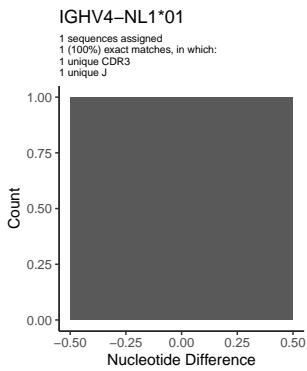
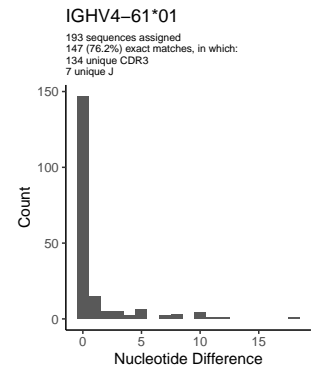
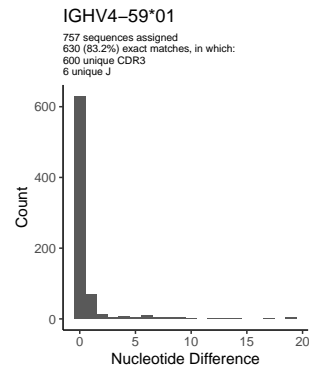
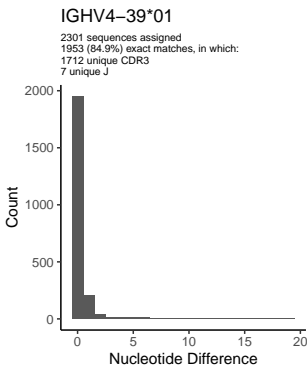
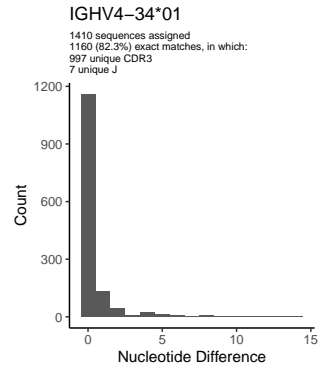
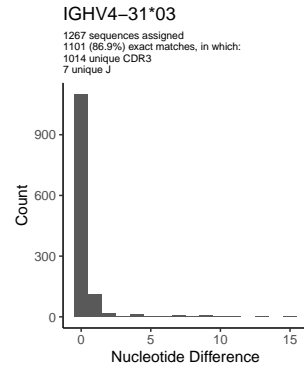
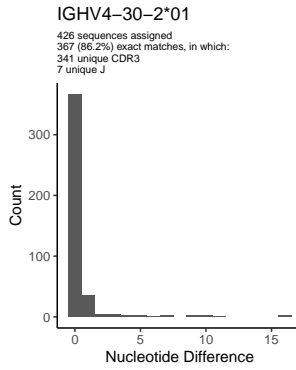
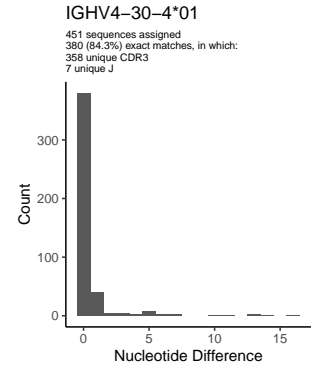
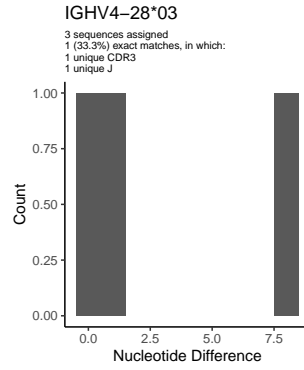
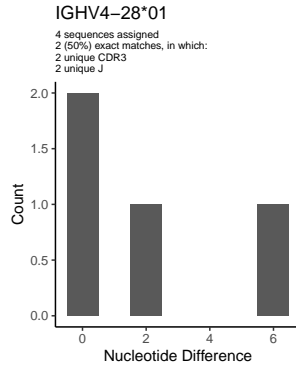
## 2 Variation from germline, in assignments to each allele

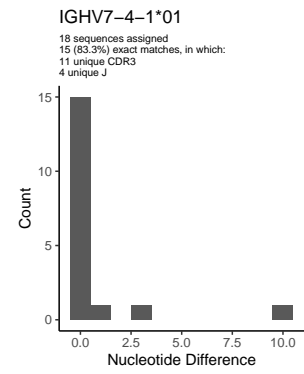
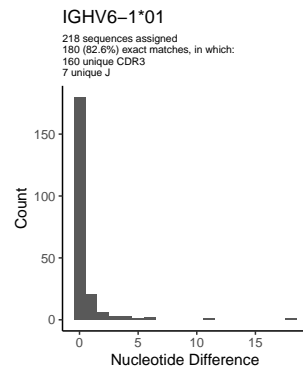
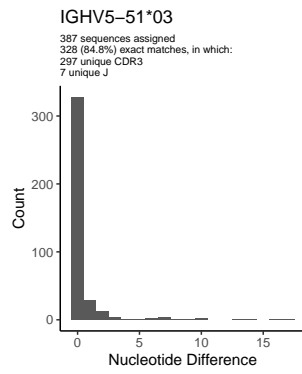






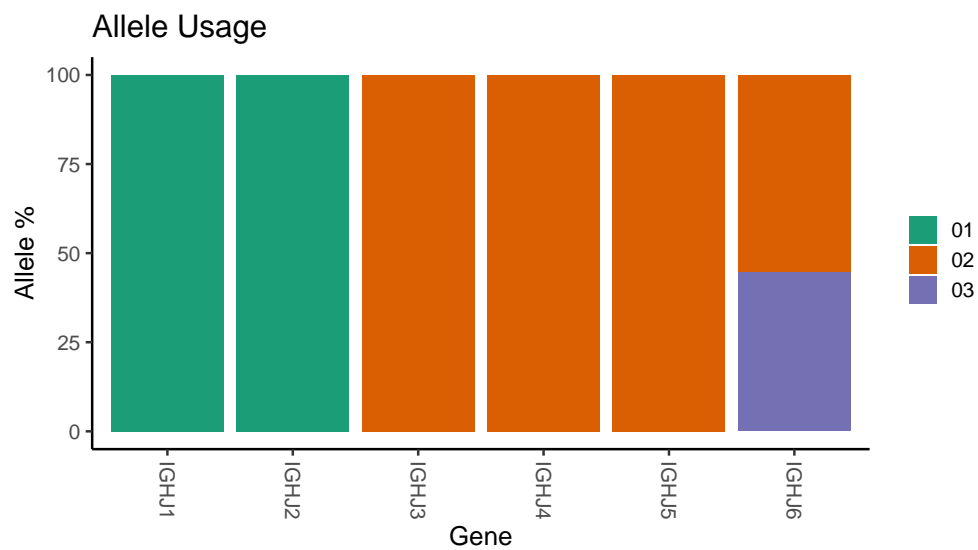




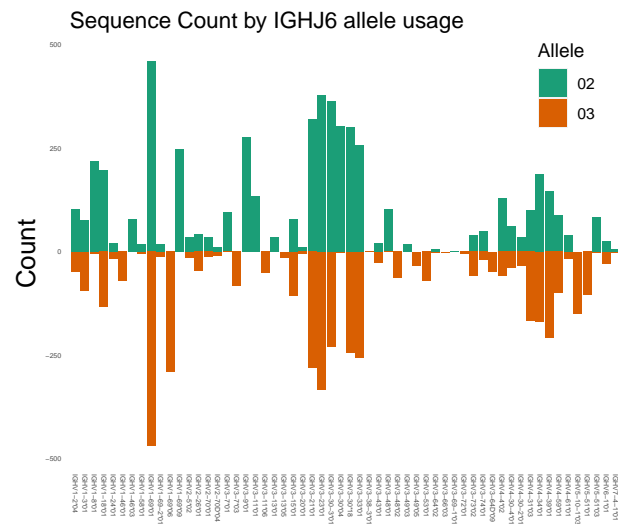




### 3 Allele usage in potential haplotype anchor genes



## 4 Haplotype plots



## 5 Configuration settings

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## Germline reference file: /work/jenkins/PRJEB26509/S77/S77/81/81/c5/f2b8719d9d0694e5ba49a719021589/re  
##  
## Novel allele file:  
##  
## Species: Homosapiens  
##  
## Chain: IGHV  
##  
## Segment: V  
##  
## Warning    no inferred sequences found.
```