

# OGRDBstats Report

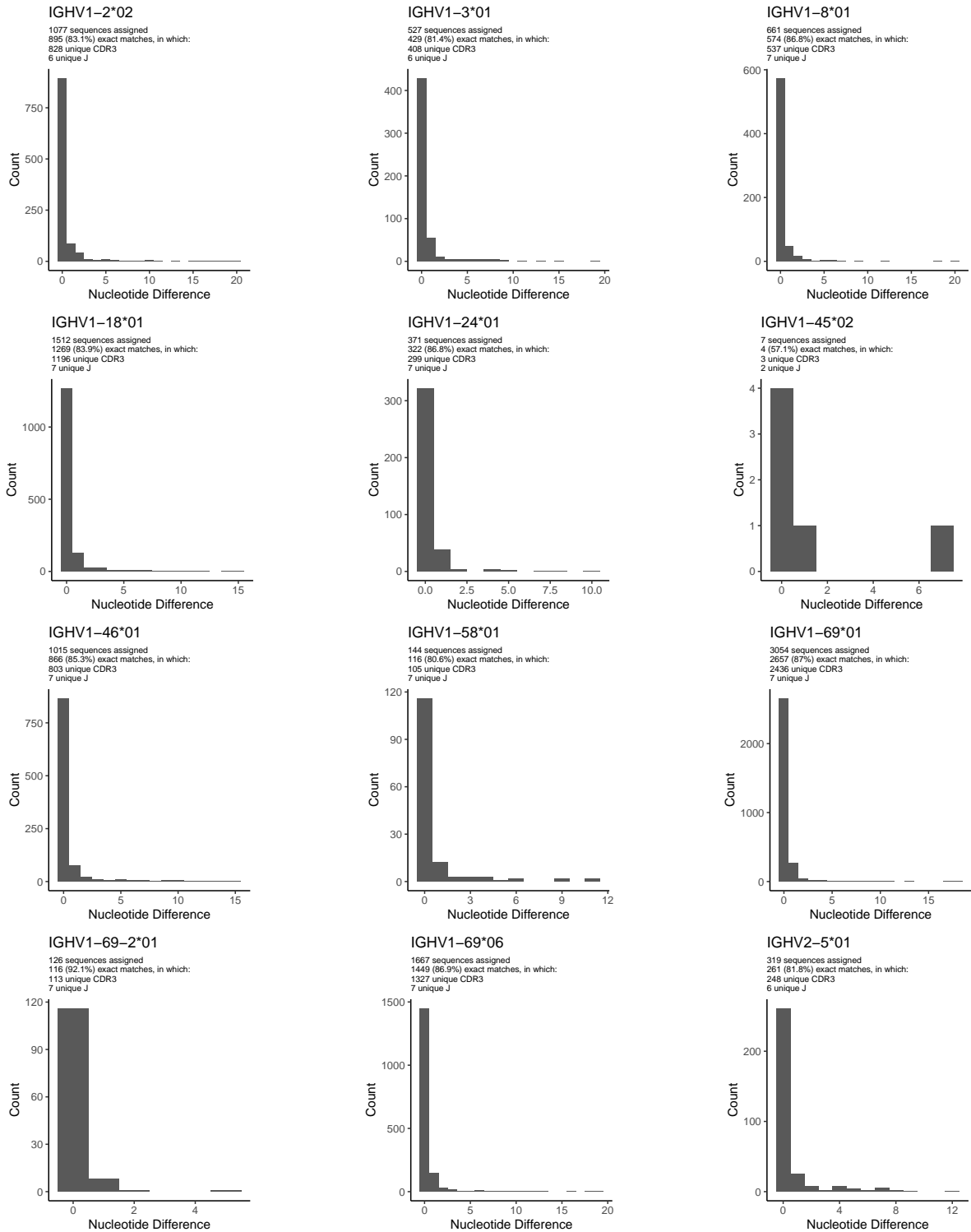
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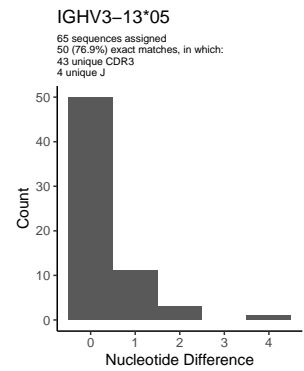
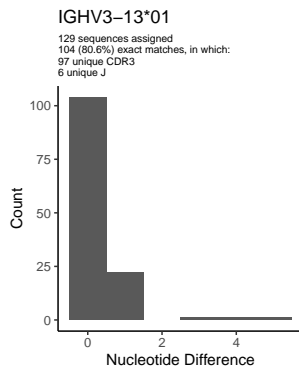
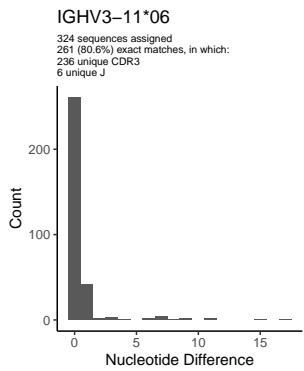
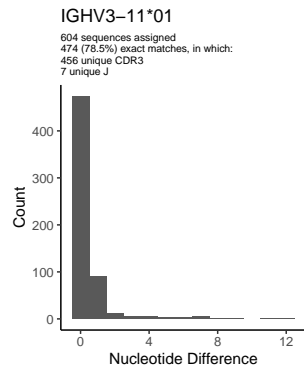
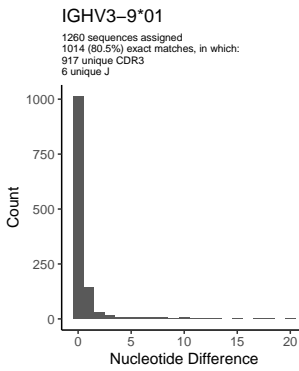
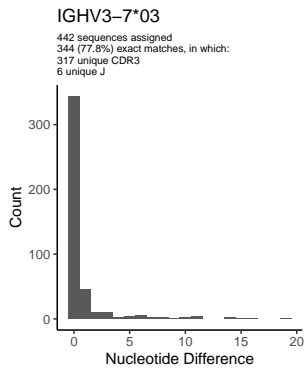
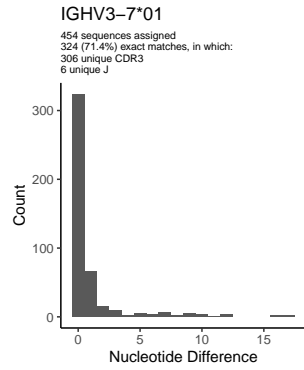
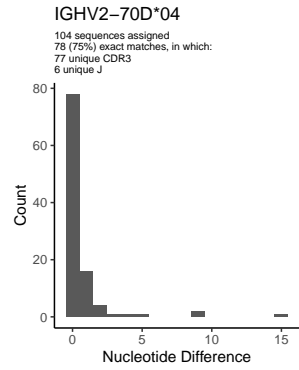
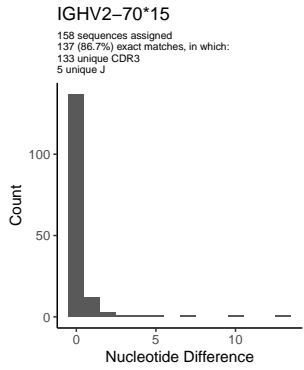
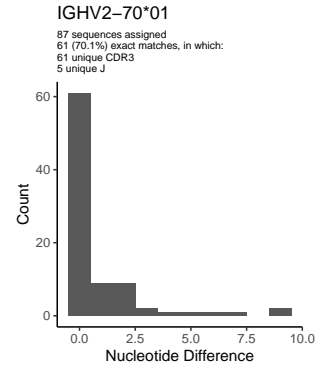
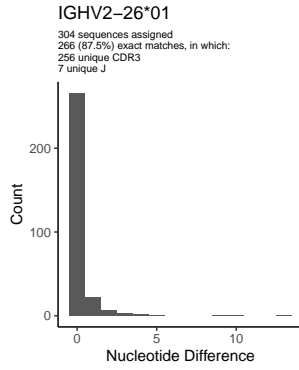
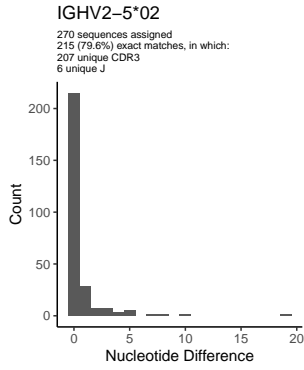
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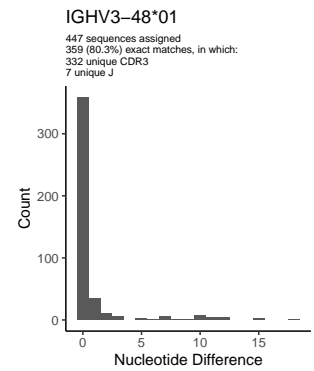
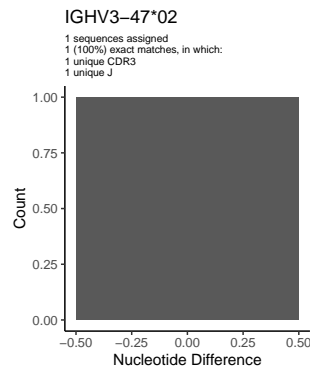
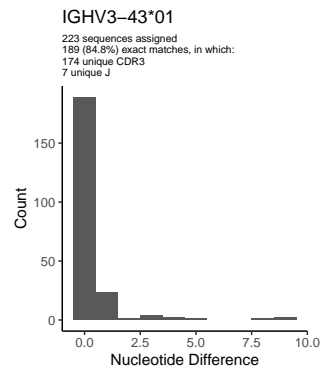
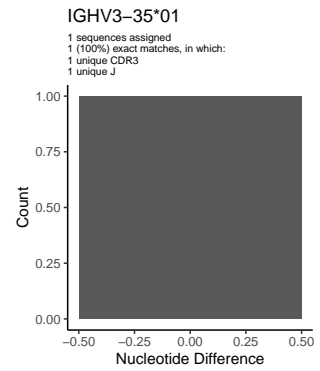
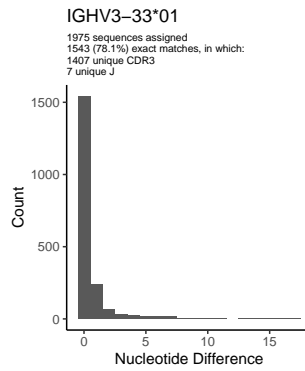
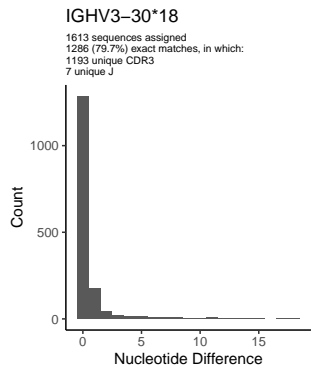
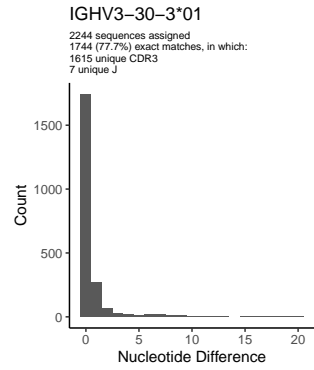
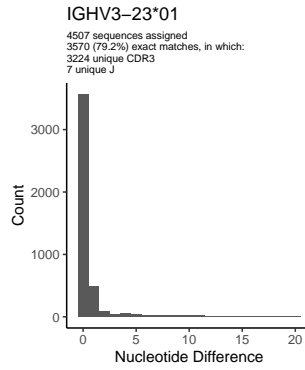
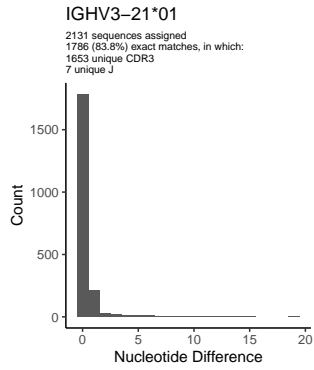
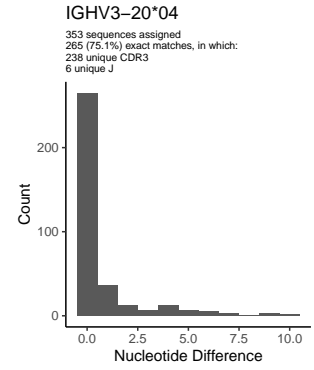
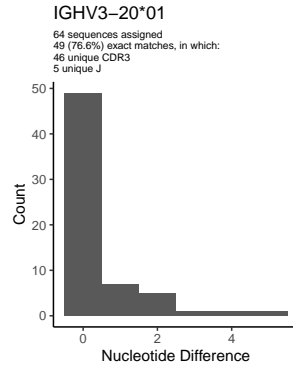
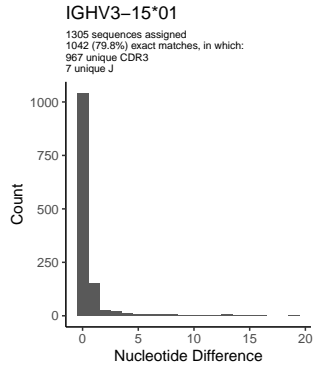
# 1 Novel sequence analysis

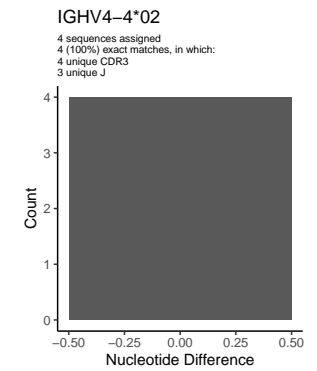
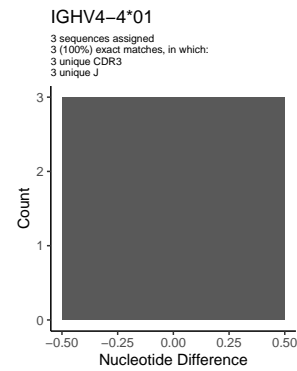
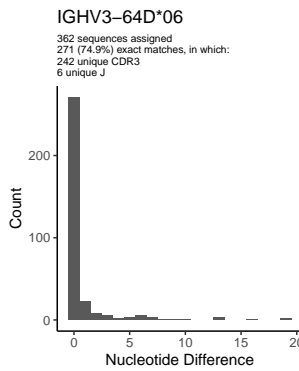
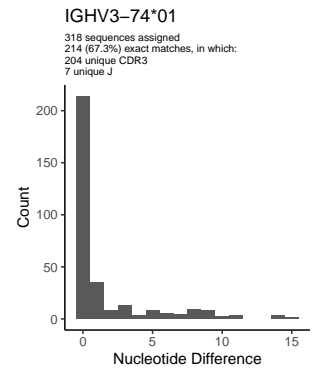
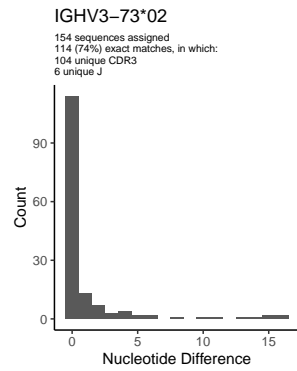
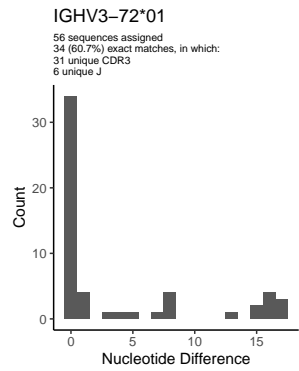
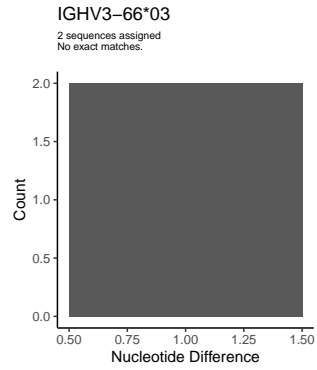
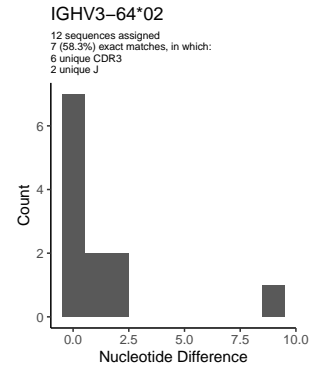
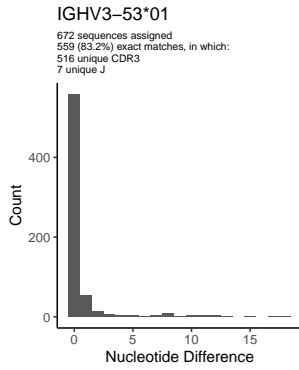
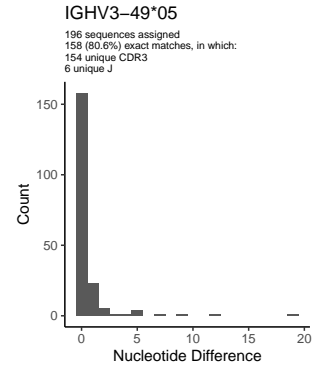
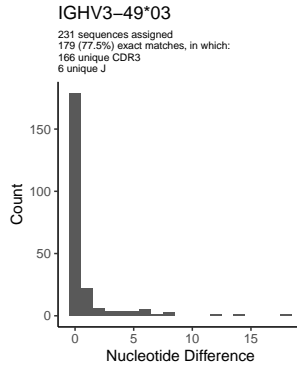
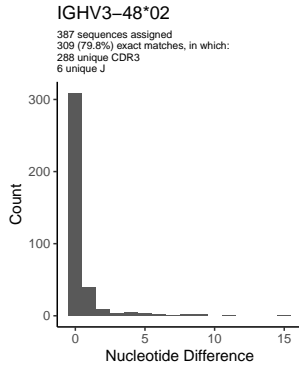
## 1.1 CDR3 length distribution, in assignments to novel alleles

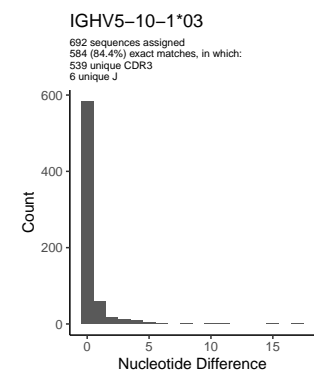
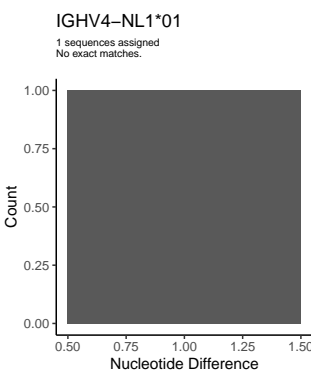
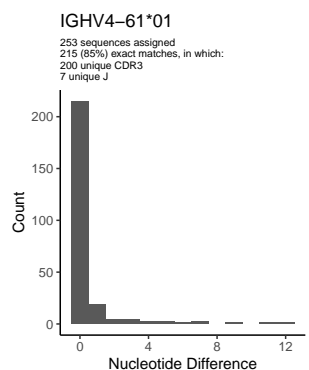
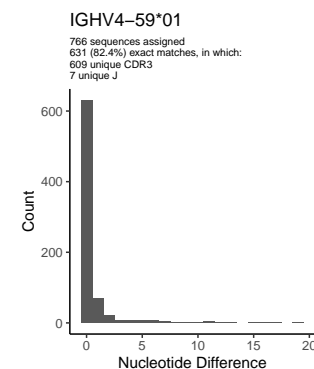
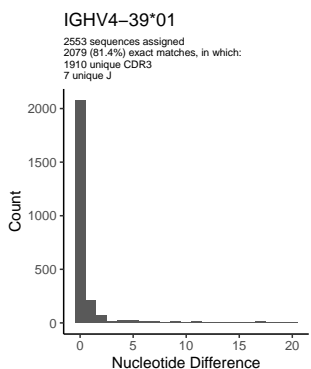
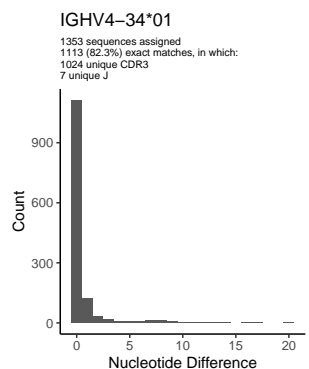
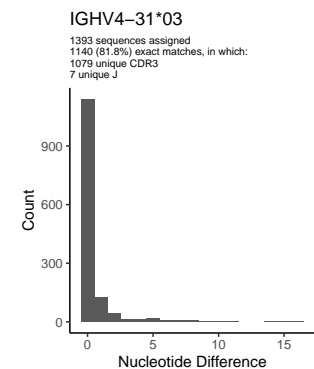
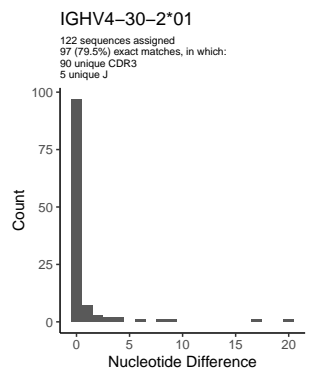
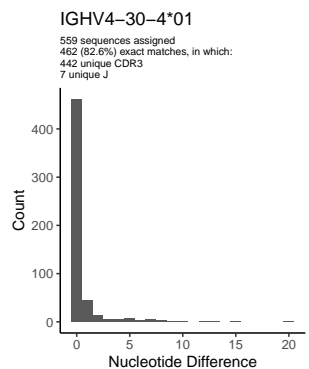
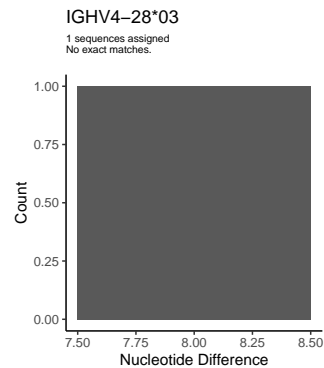
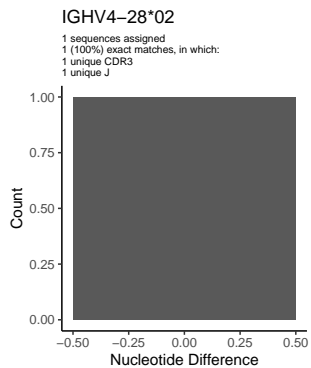
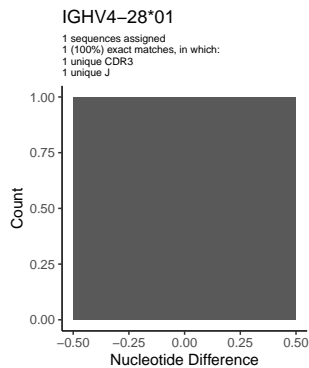
## 2 Variation from germline, in assignments to each allele

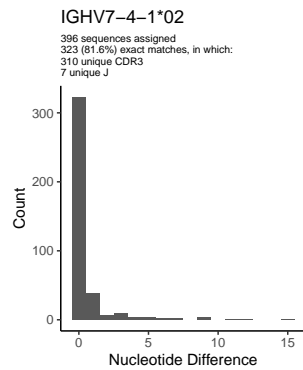
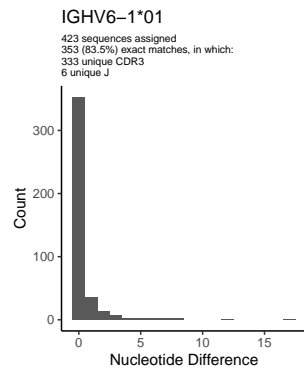
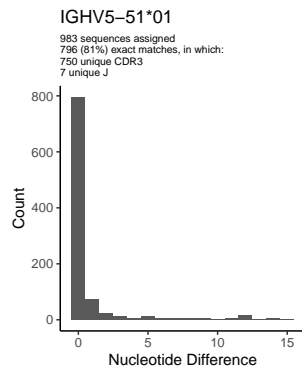






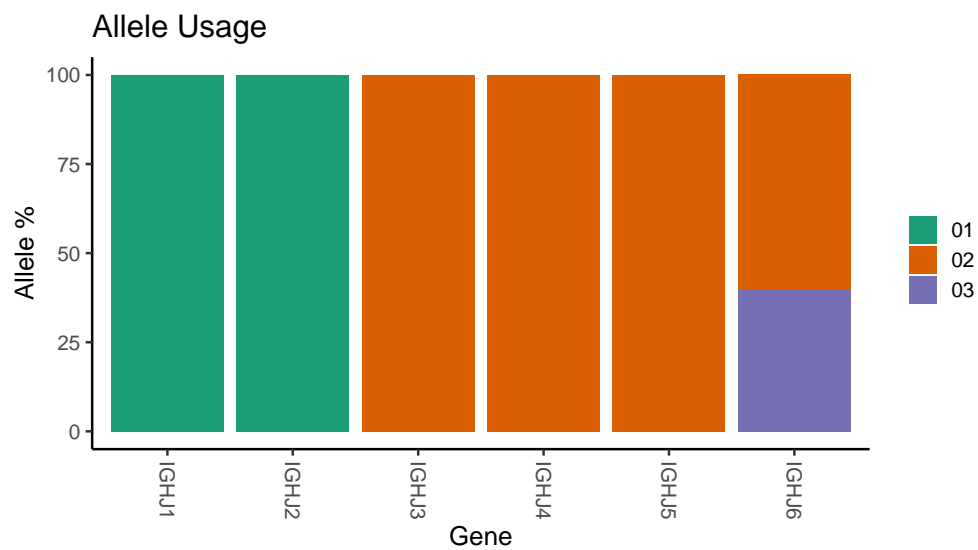




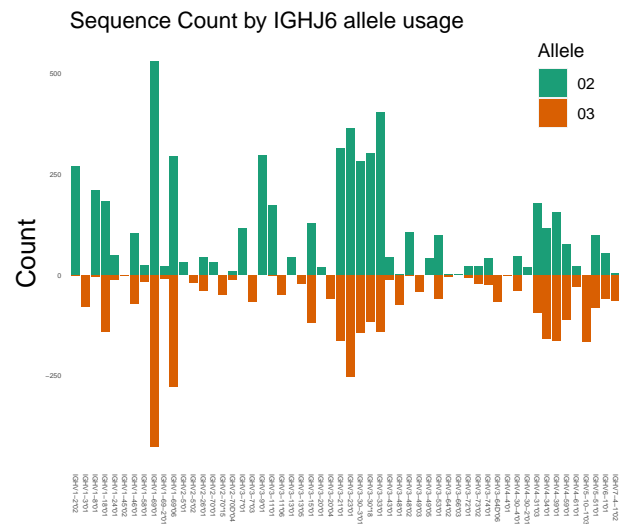




### 3 Allele usage in potential haplotype anchor genes



## 4 Haplotype plots



## 5 Configuration settings

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##
## Germline reference file: /misc/work/jenkins/PRJEB26509/S54/S54/57/57/4e/b3df23d504e091397f6a0d6a4152
##
## Novel allele file:
##
## Species: Homosapiens
##
## Chain: IGHV
##
## Segment: V
##
## Warning    no inferred sequences found.
```