

# OGRDBstats Report

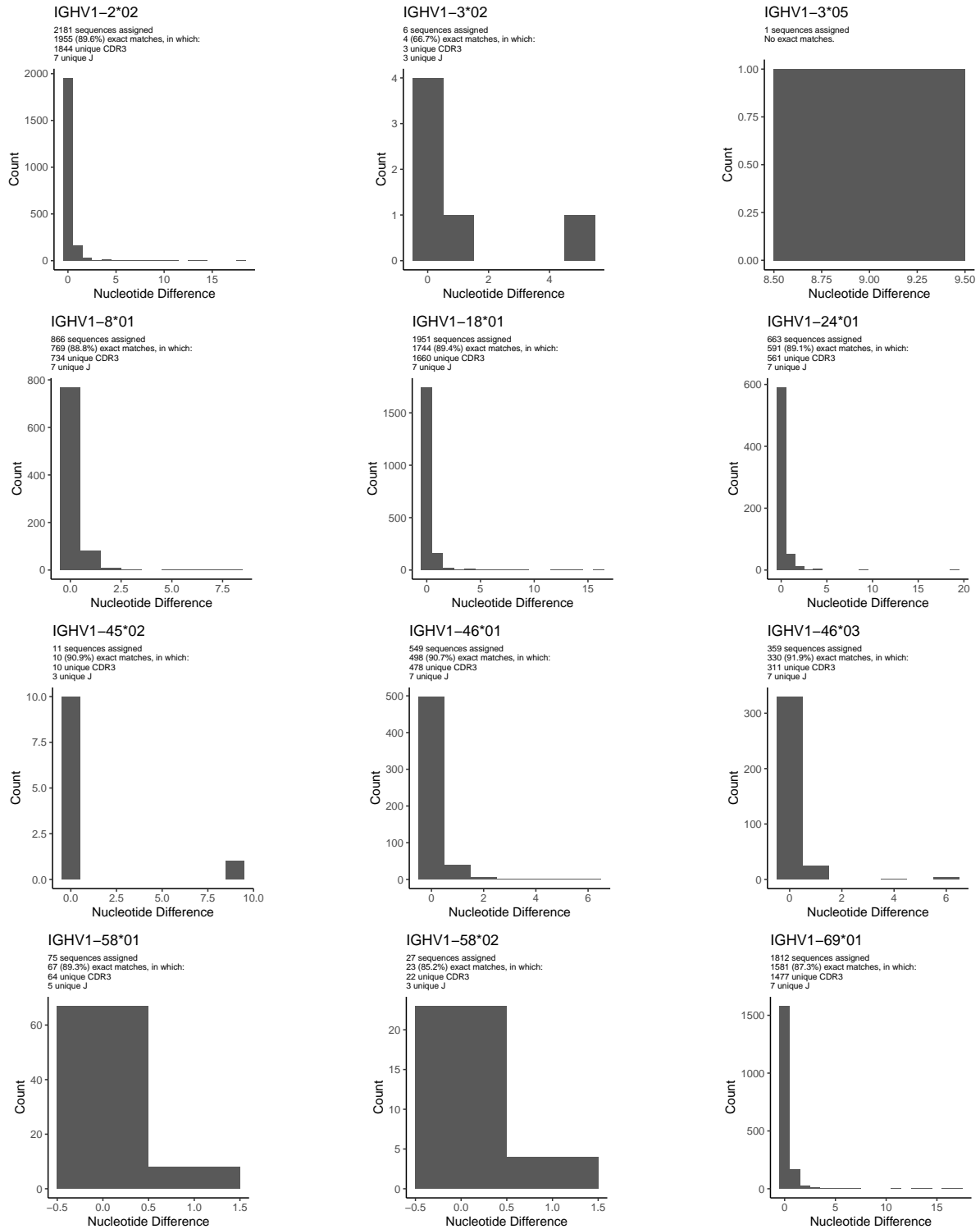
## Contents

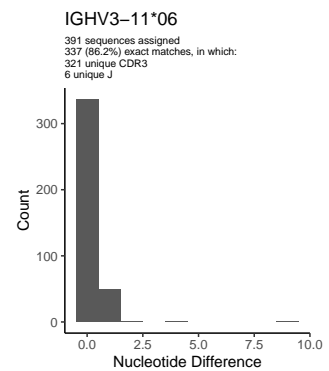
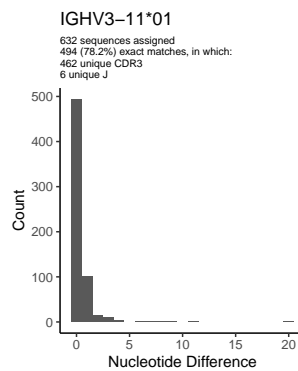
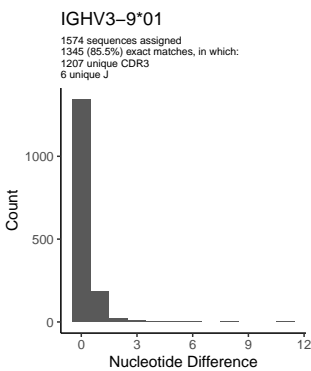
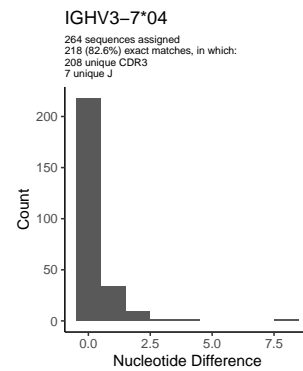
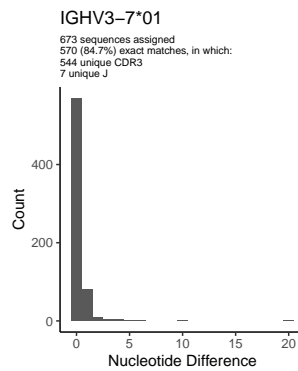
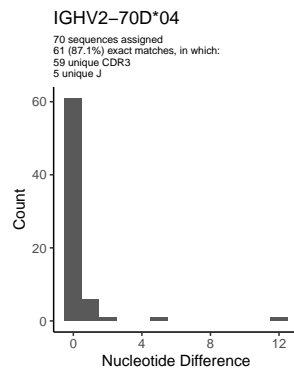
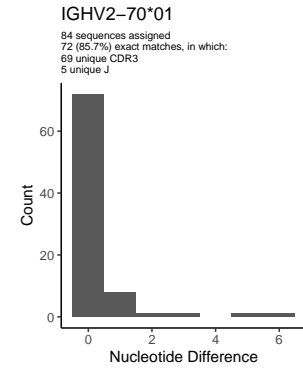
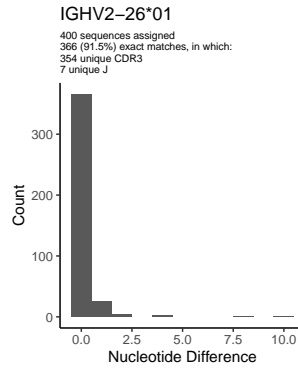
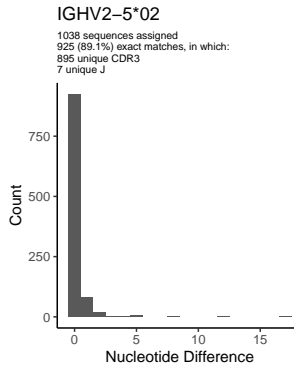
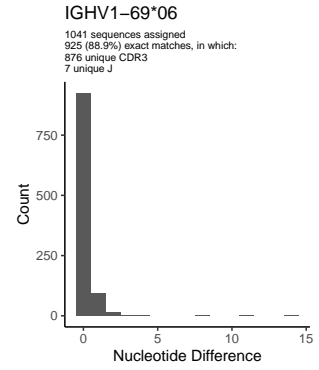
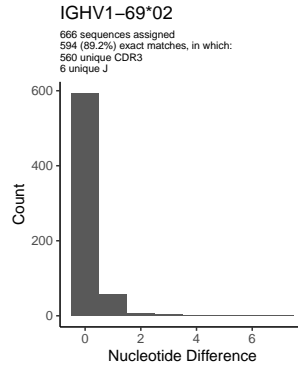
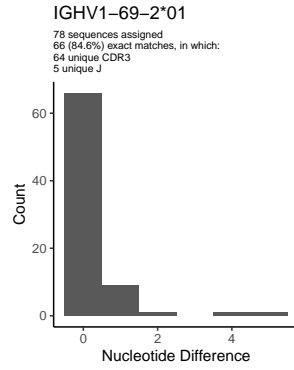
|          |   |           |
|----------|---|-----------|
| <b>1</b> | <b>Novel sequence analysis</b>                                      | <b>2</b>  |
| 1.1      | CDR3 length distribution, in assignments to novel alleles . . . . . | 2         |
| <b>2</b> | <b>Variation from germline, in assignments to each allele</b>       | <b>3</b>  |
| <b>3</b> | <b>Allele usage in potential haplotype anchor genes</b>             | <b>9</b>  |
| <b>4</b> | <b>Haplotype plots</b>  | <b>10</b> |
| <b>5</b> | <b>Configuration settings</b>                                       | <b>11</b> |

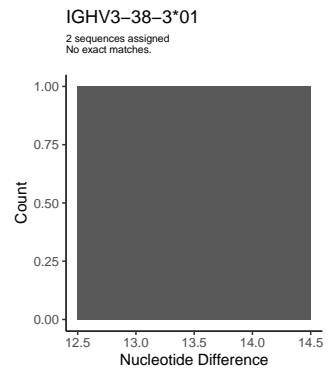
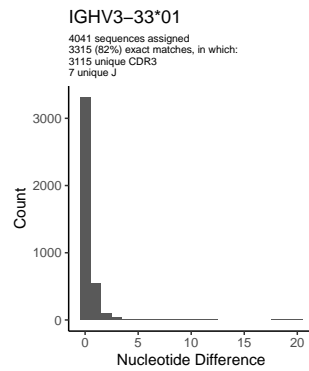
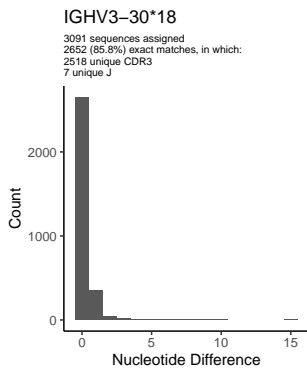
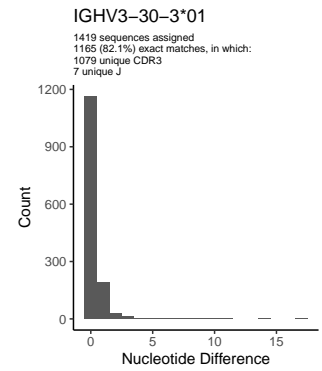
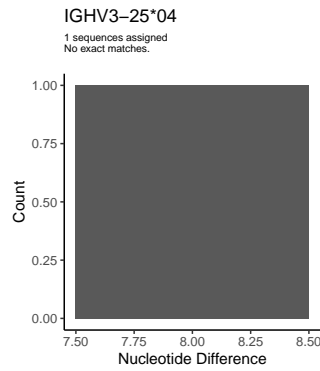
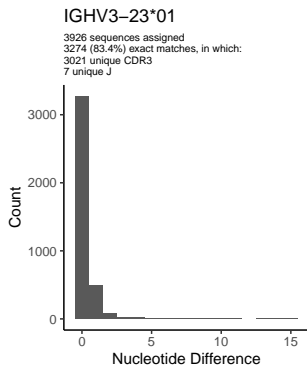
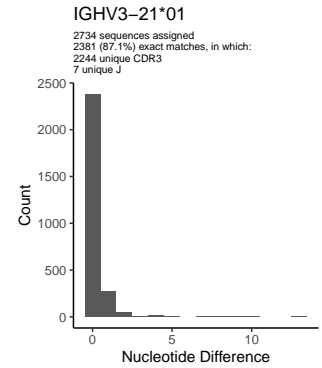
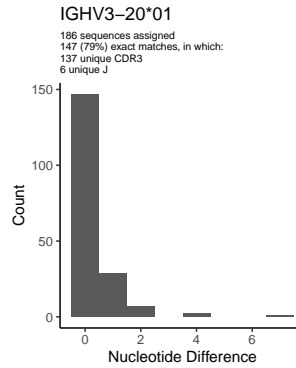
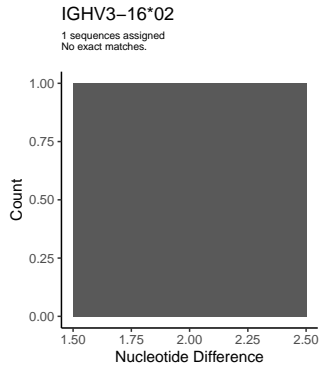
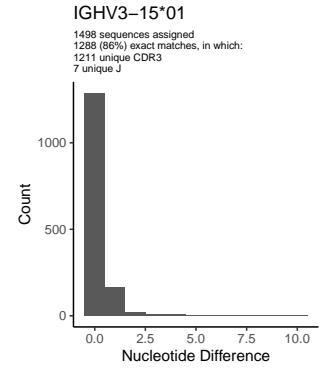
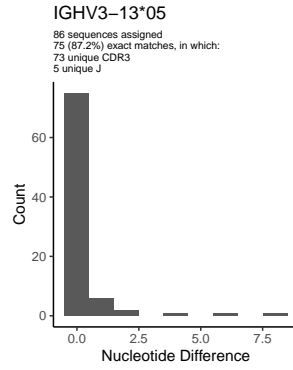
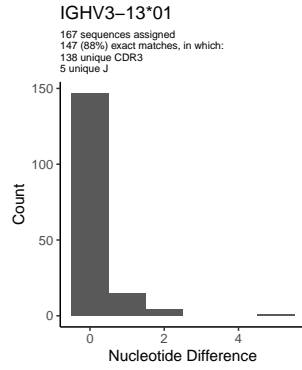
# 1 Novel sequence analysis

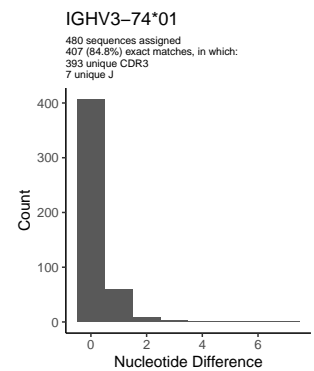
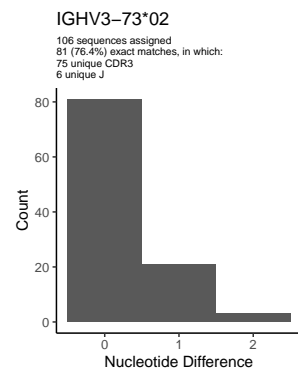
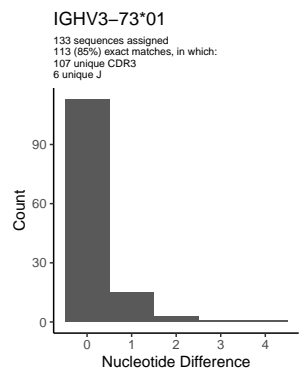
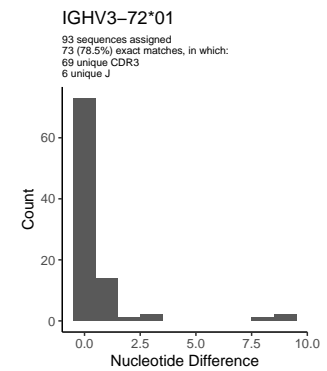
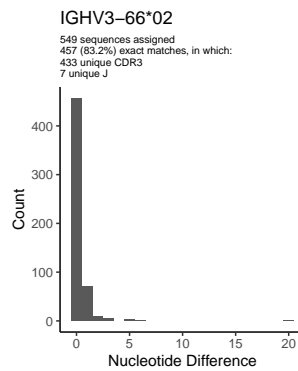
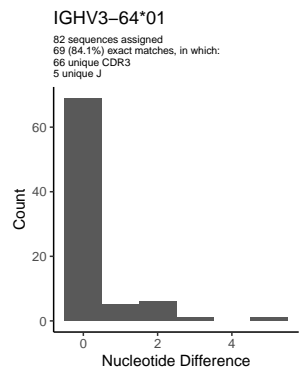
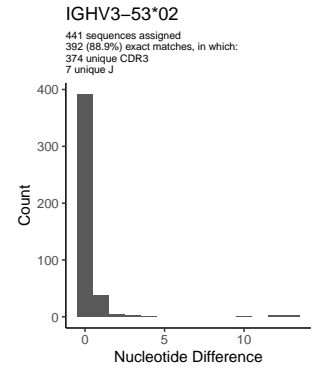
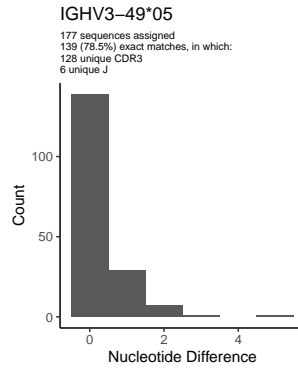
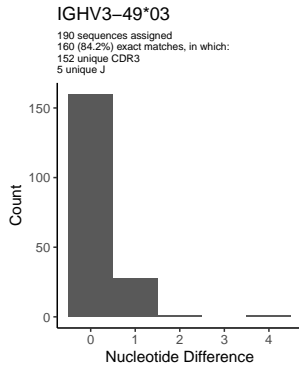
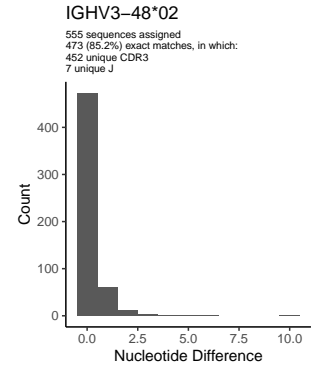
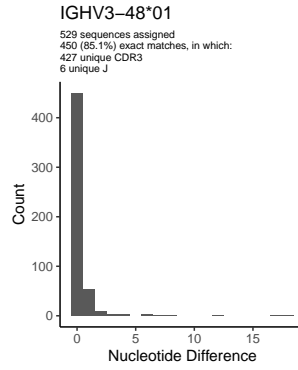
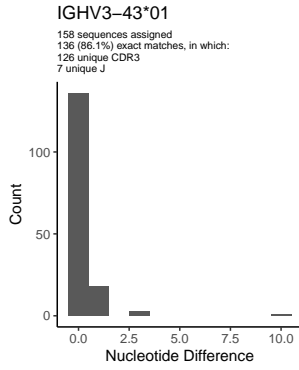
## 1.1 CDR3 length distribution, in assignments to novel alleles

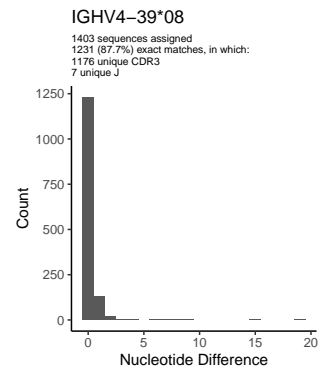
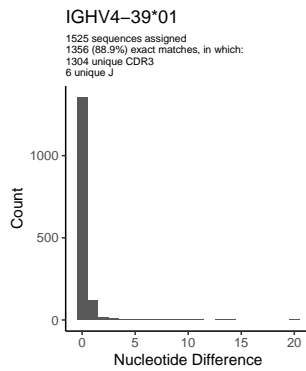
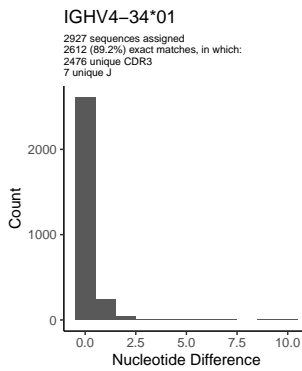
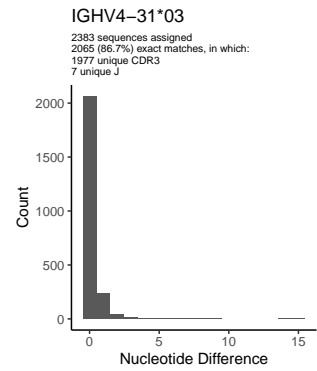
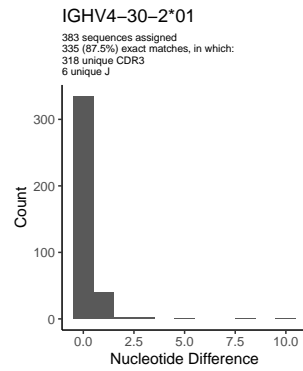
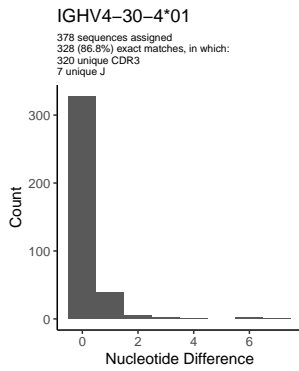
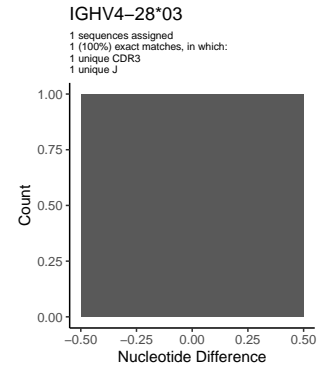
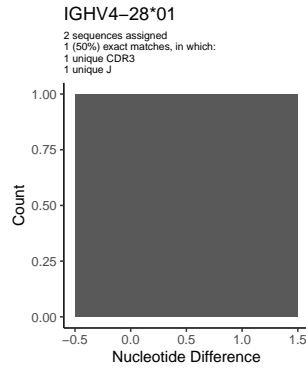
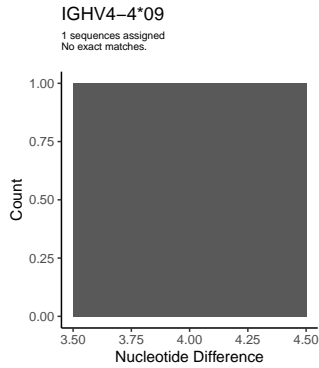
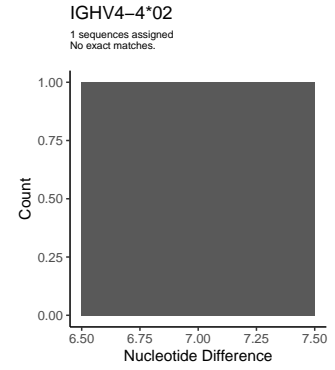
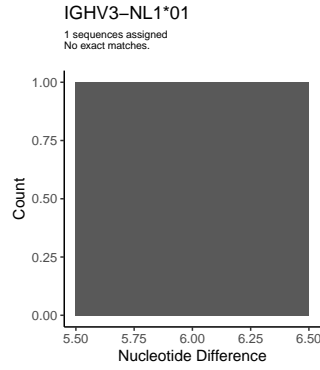
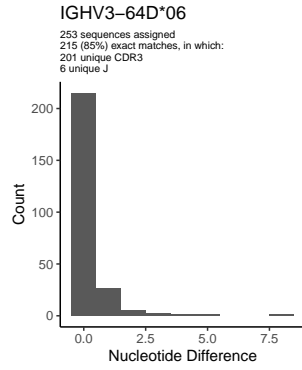
## 2 Variation from germline, in assignments to each allele

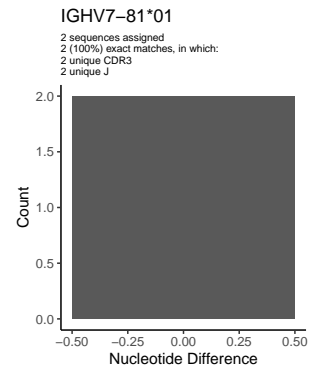
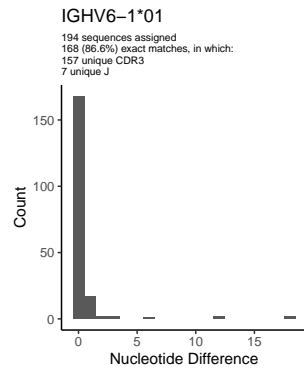
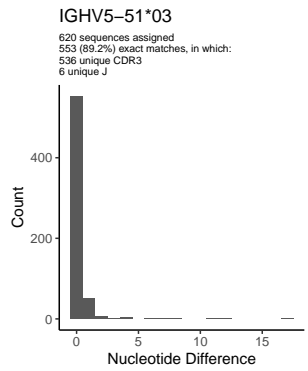
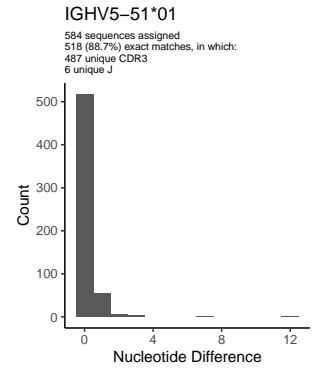
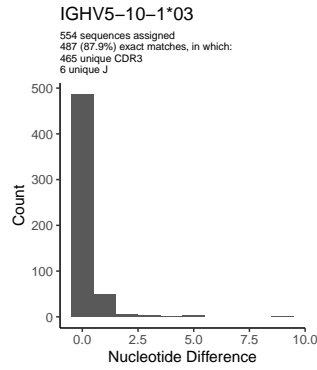
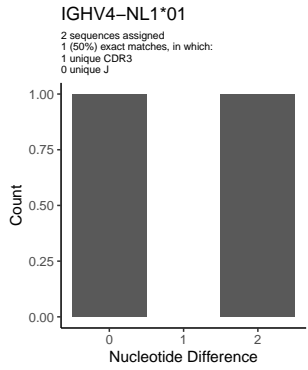
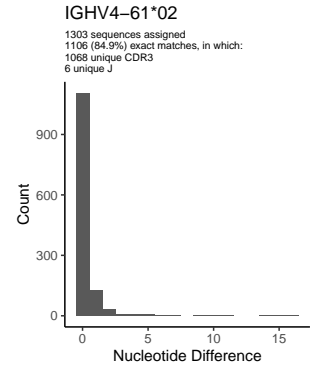
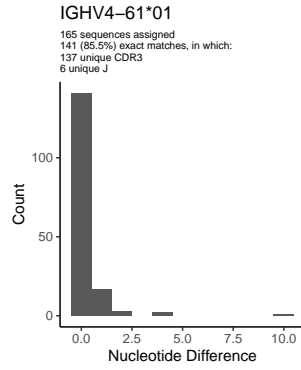
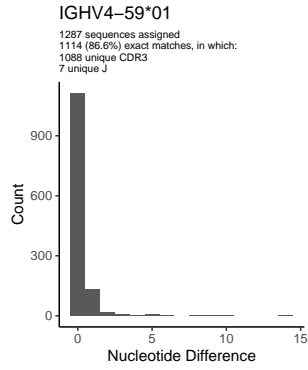






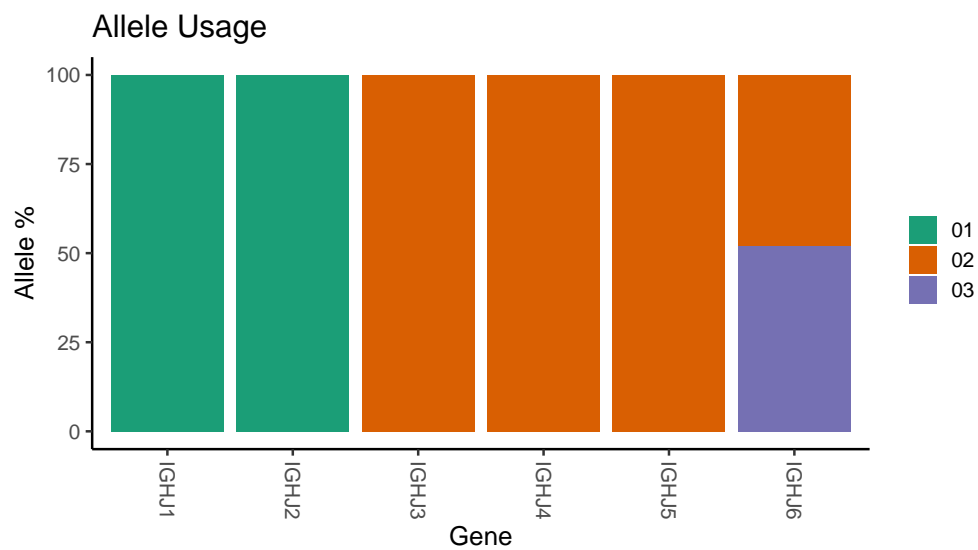




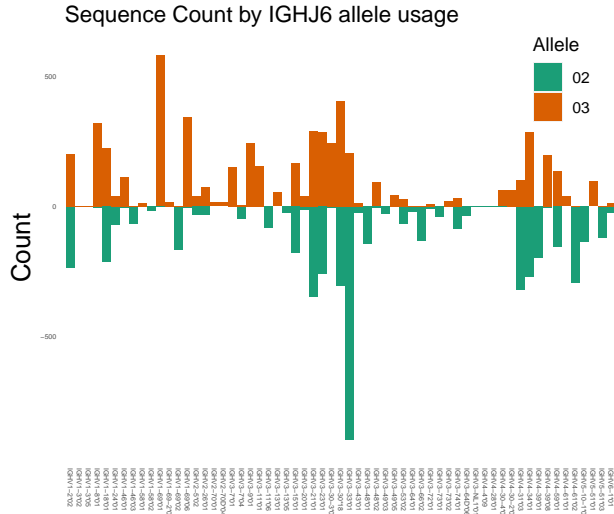




### 3 Allele usage in potential haplotype anchor genes



# 4 Haplotype plots



## 5 Configuration settings

```
## Repertoire file: /work/jenkins/PRJEB26509/S86/S86/90/90/88/8f62a91cf1c052778a2b55f4f6f498/90_Finale_  
##  
## Germline reference file: /work/jenkins/PRJEB26509/S86/S86/90/90/9e/48c20addffa2aba24f3fc7c1f1376f/re  
##  
## Novel allele file:  
##  
## Species: Homosapiens  
##  
## Chain: IGHV  
##  
## Segment: V  
##  
## Warning    no inferred sequences found.
```