

# OGRDBstats Report

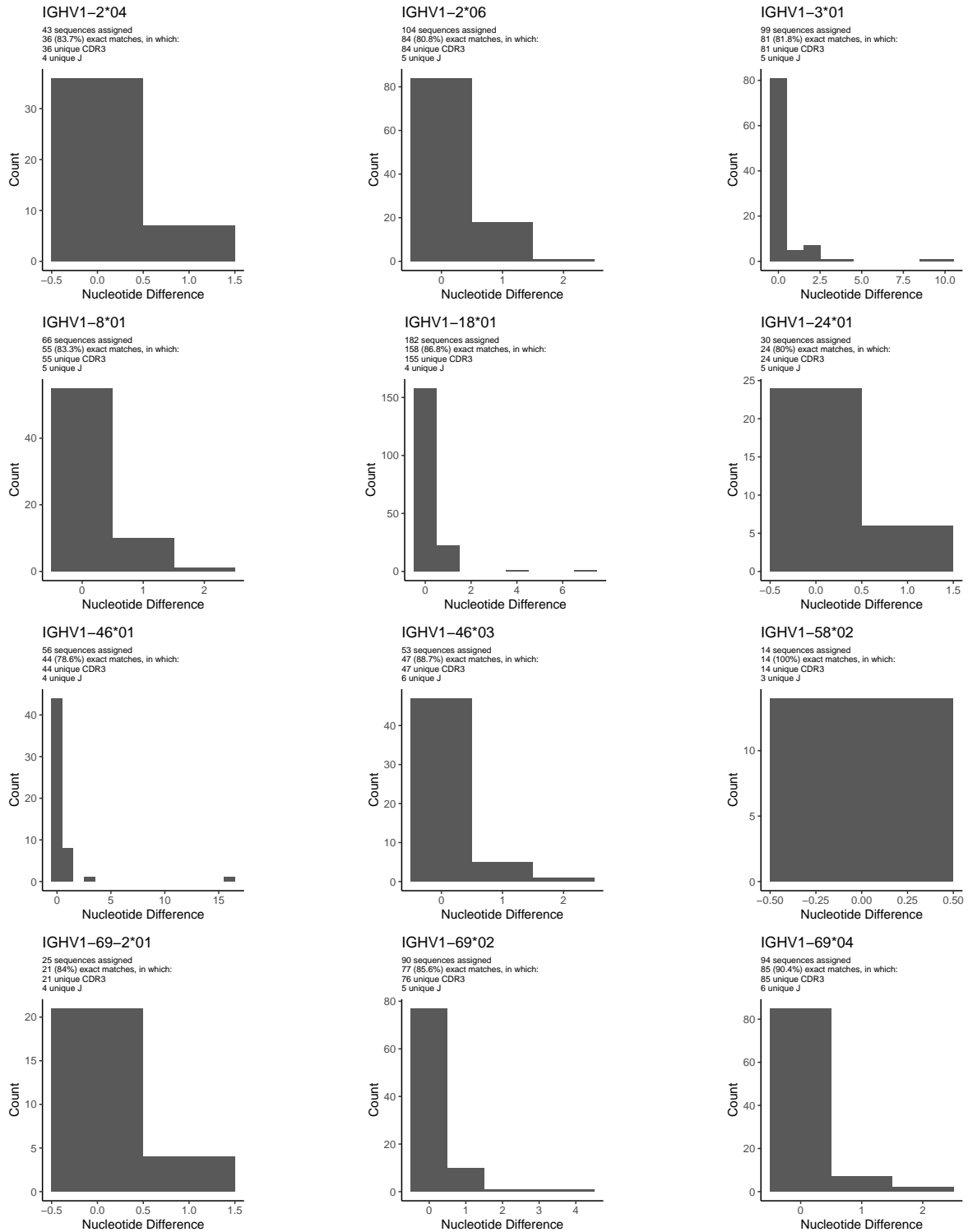
## Contents

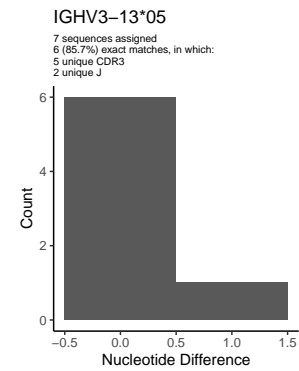
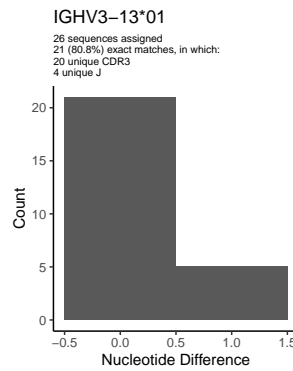
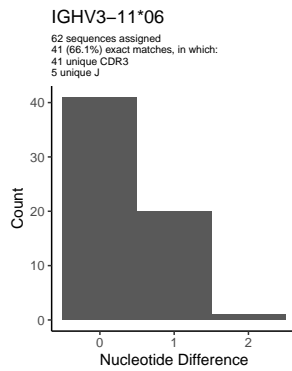
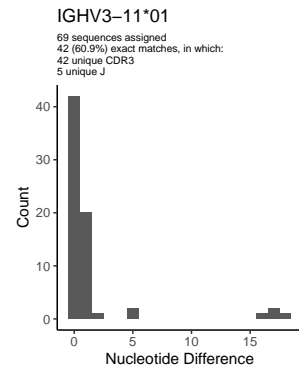
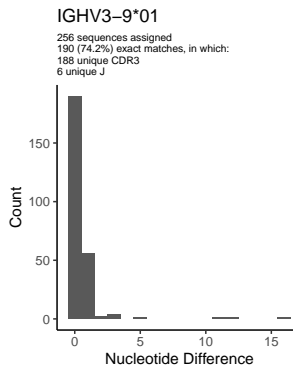
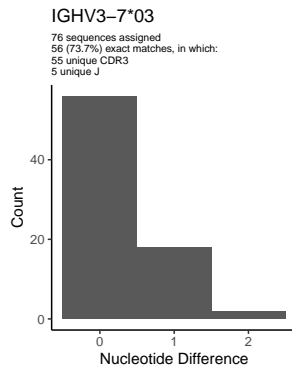
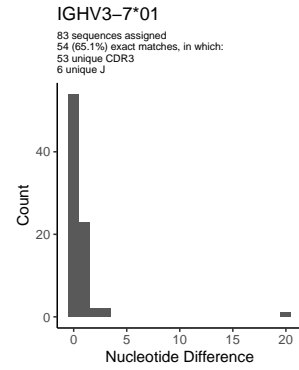
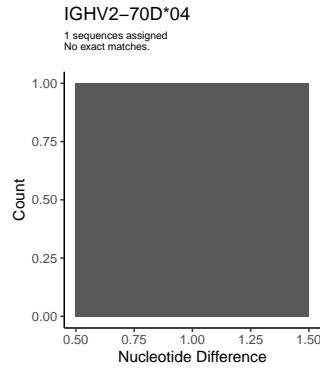
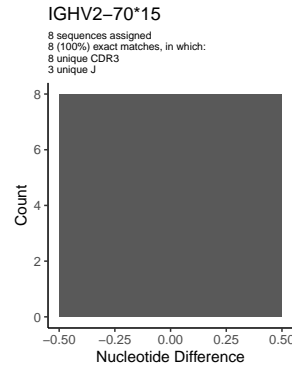
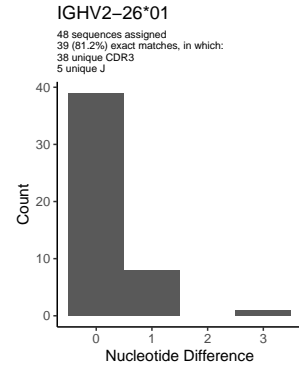
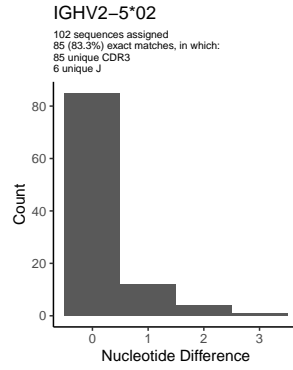
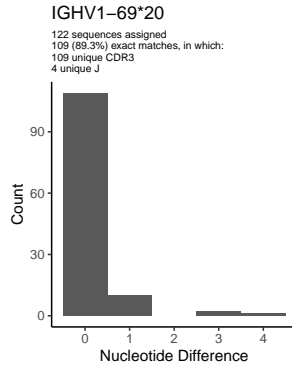
<b>1</b>	<b>Novel sequence analysis</b>	<b>2</b>
1.1	CDR3 length distribution, in assignments to novel alleles . . . . .	2
<b>2</b>	<b>Variation from germline, in assignments to each allele</b>	<b>3</b>
<b>3</b>	<b>Allele usage in potential haplotype anchor genes</b>	<b>9</b>
<b>4</b>	<b>Haplotype plots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

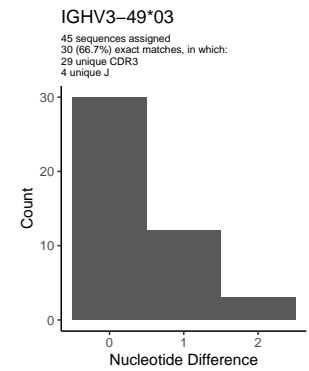
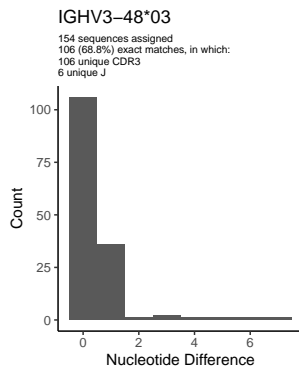
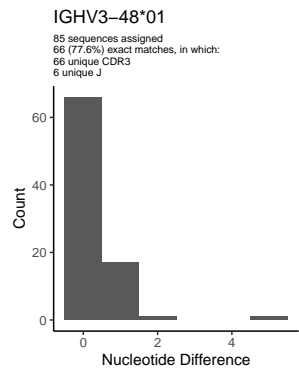
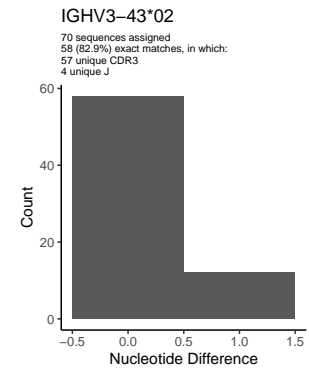
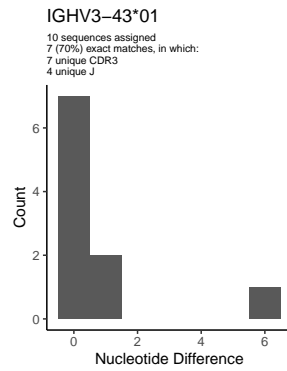
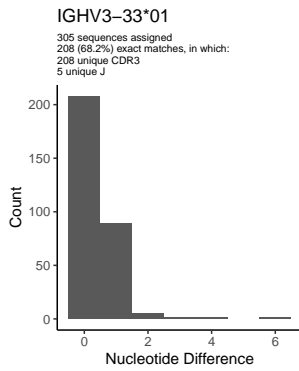
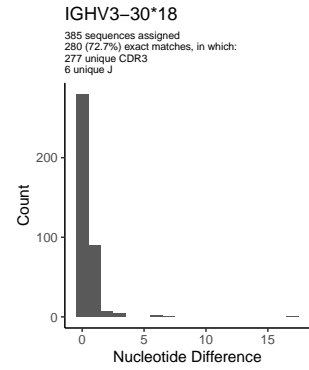
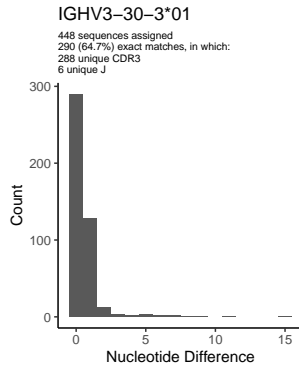
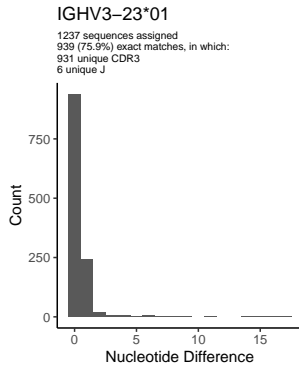
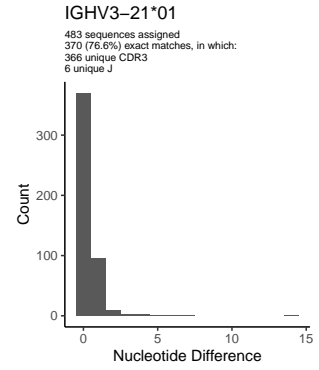
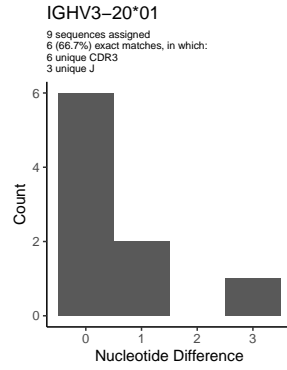
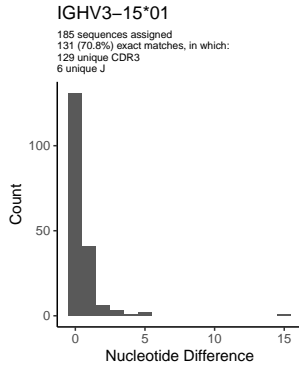
# 1 Novel sequence analysis

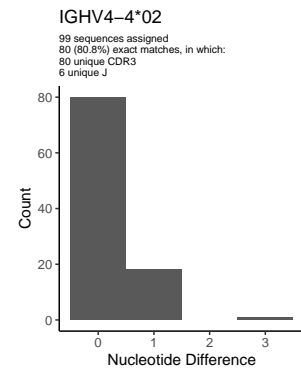
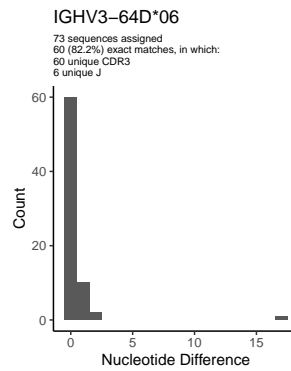
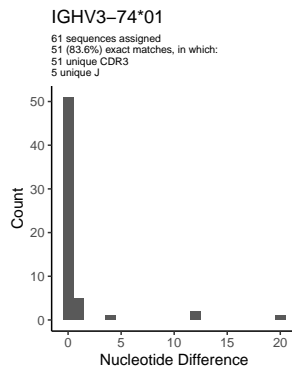
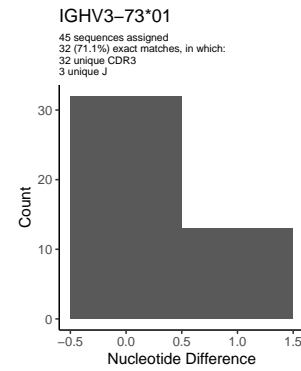
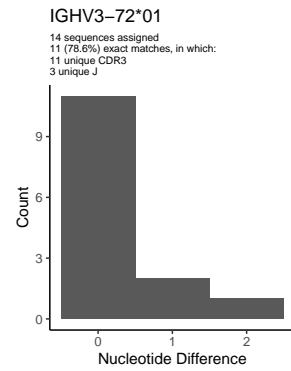
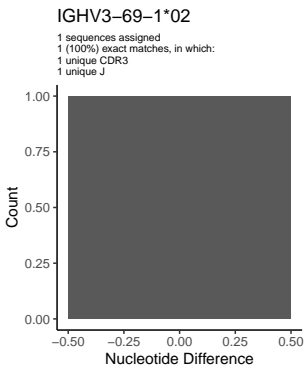
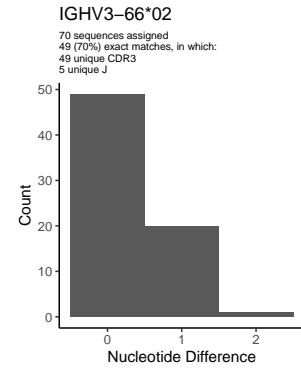
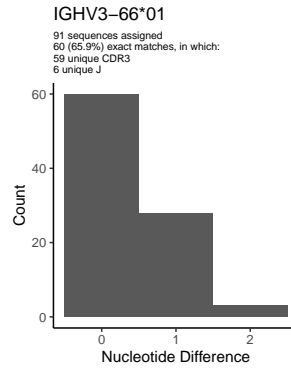
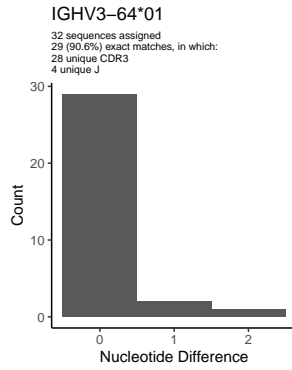
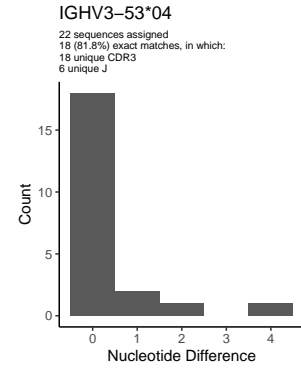
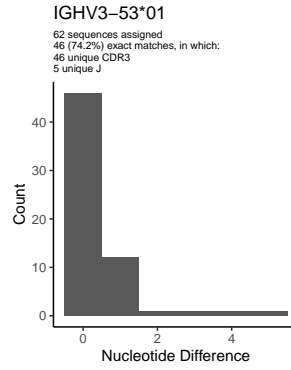
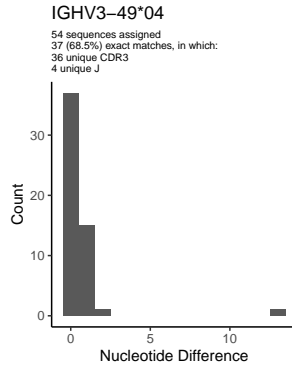
## 1.1 CDR3 length distribution, in assignments to novel alleles

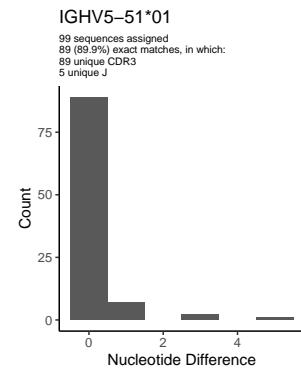
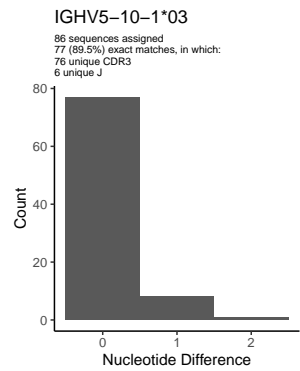
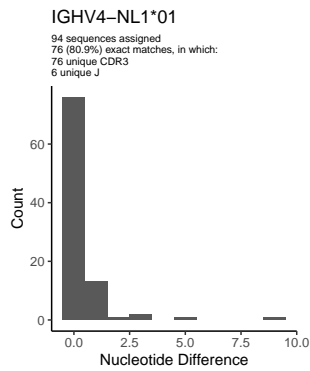
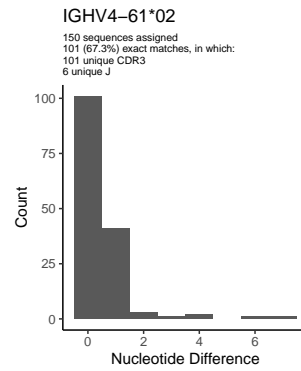
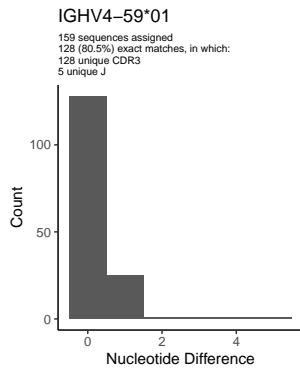
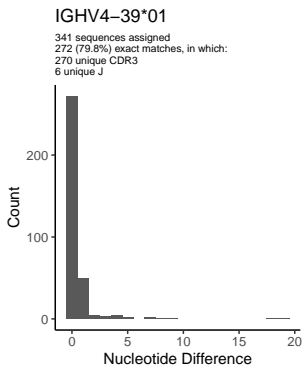
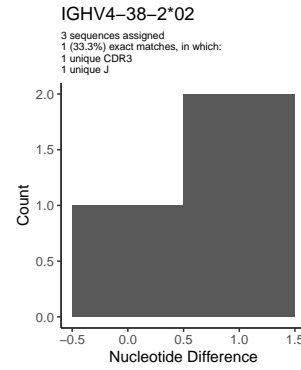
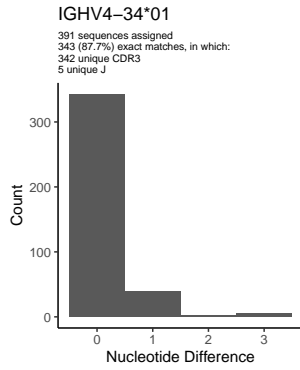
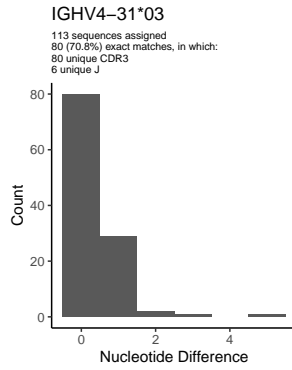
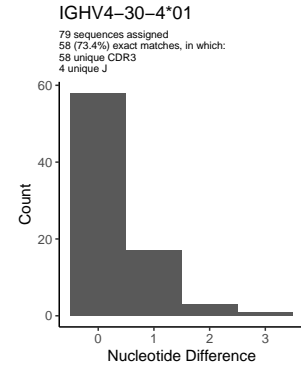
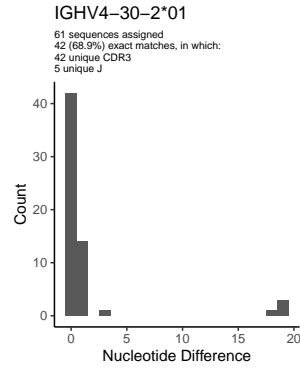
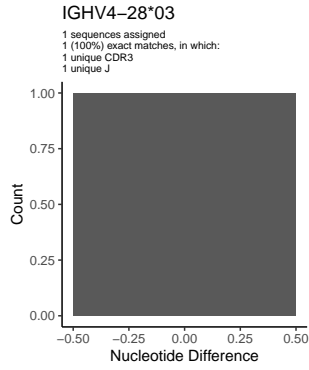
## 2 Variation from germline, in assignments to each allele

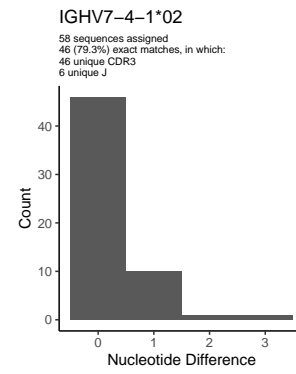
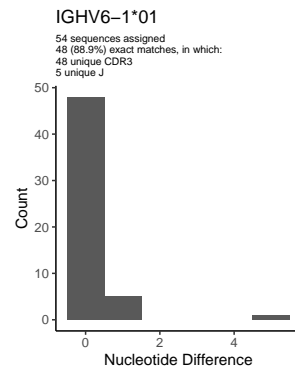
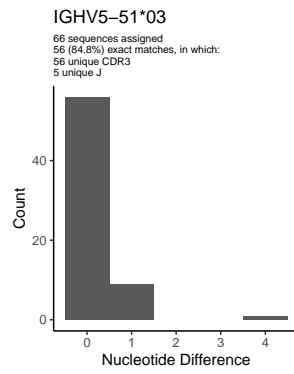






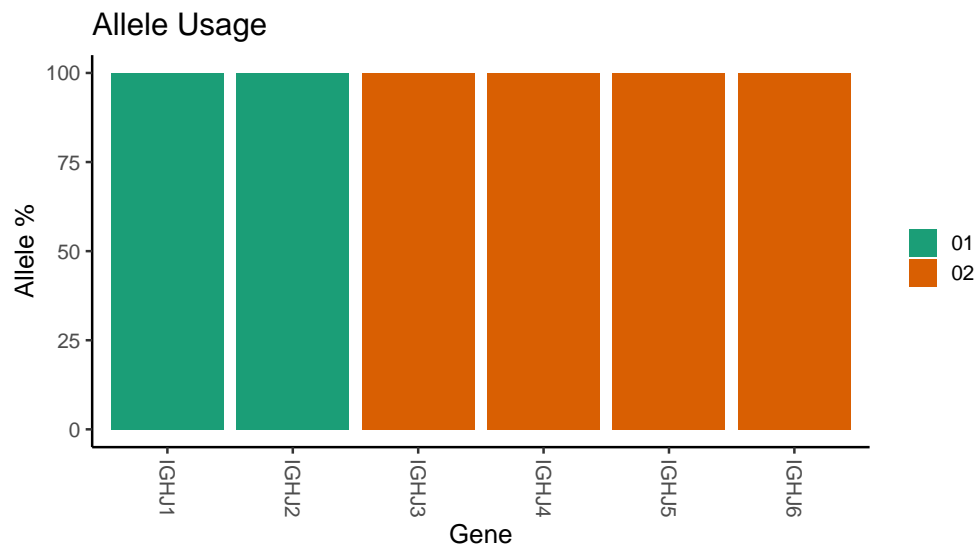








### 3 Allele usage in potential haplotype anchor genes



## 4 Haplotype plots

## 5 Configuration settings

```
## Repertoire file: /work/jenkins/PRJEB26509/S47/S47/50/50/67/a12b08e1f2a135a798d14899f4e73a/50_Finale_  
##  
## Germline reference file: /work/jenkins/PRJEB26509/S47/S47/50/50/dc/ee5a680c3d78292dbbe82260b1ebcc/re  
##  
## Novel allele file:  
##  
## Species: Homosapiens  
##  
## Chain: IGHV  
##  
## Segment: V  
##  
## Warning    no inferred sequences found.
```