

OGRDBstats Report

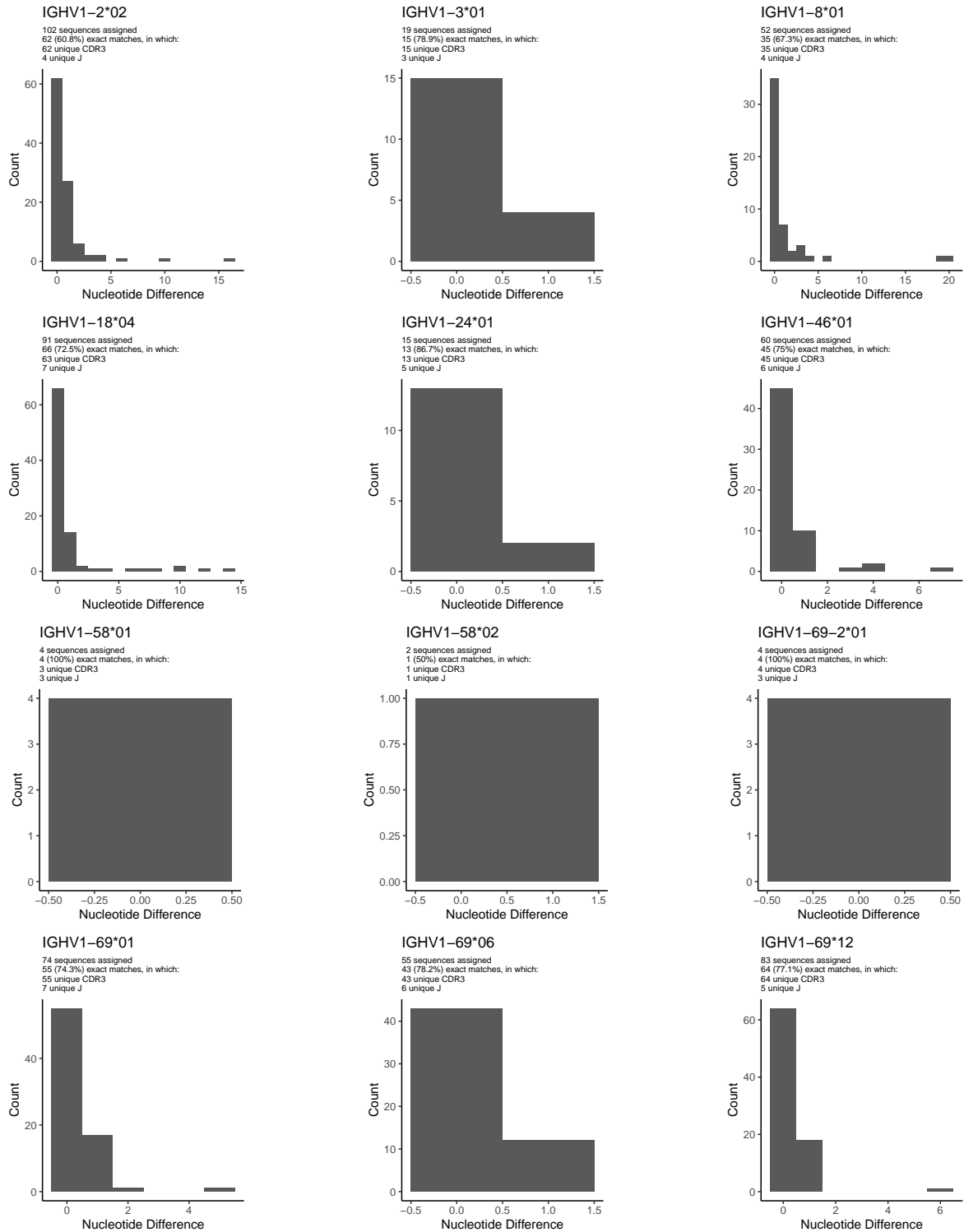
Contents

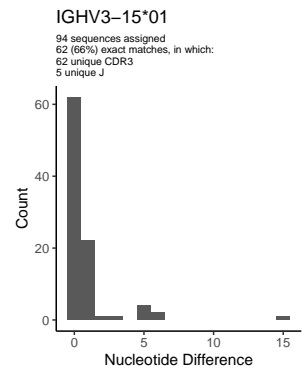
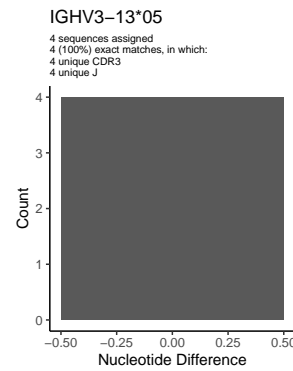
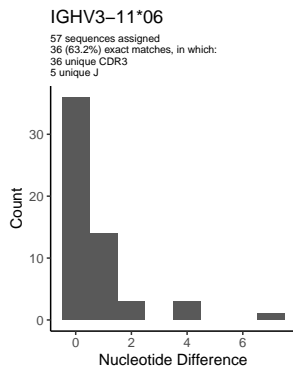
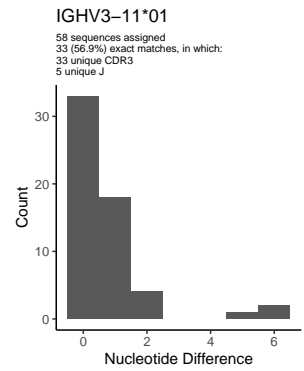
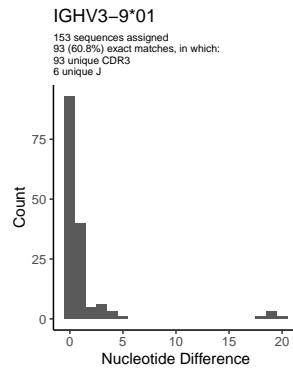
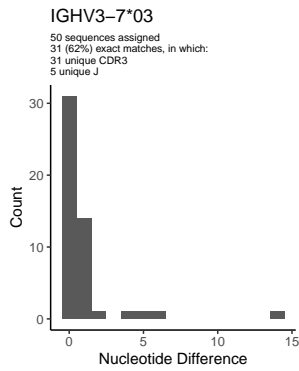
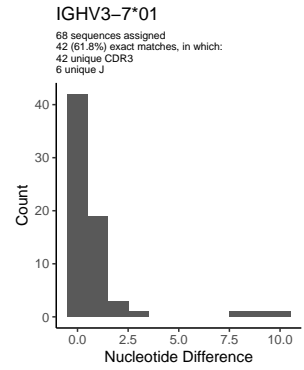
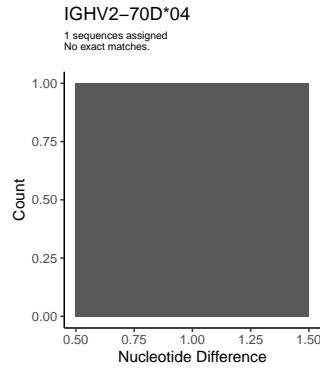
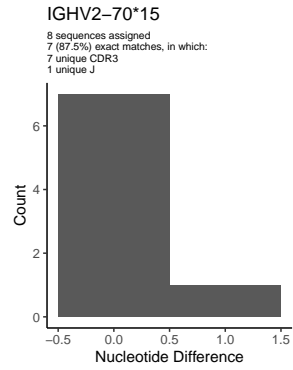
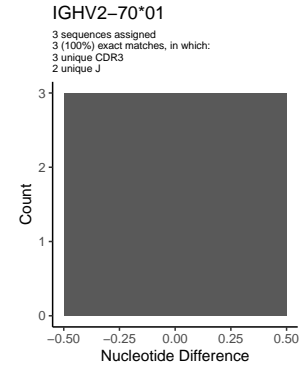
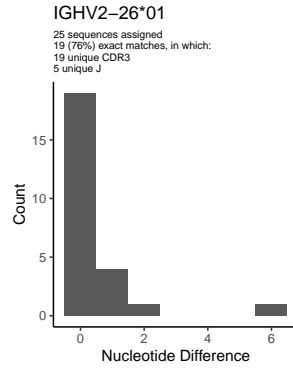
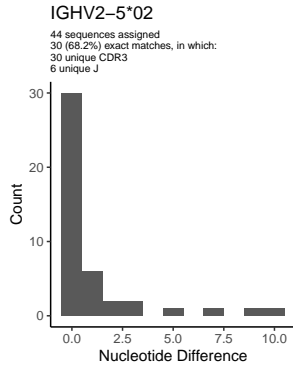
1	Novel sequence analysis	2
1.1	CDR3 length distribution, in assignments to novel alleles	2
2	Variation from germline, in assignments to each allele	3
3	Allele usage in potential haplotype anchor genes	9
4	Haplotype plots	10
5	Configuration settings	11

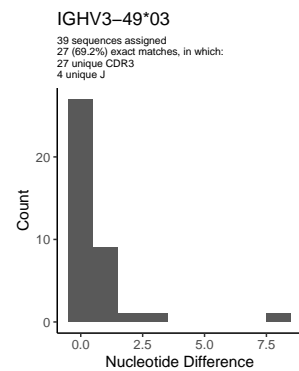
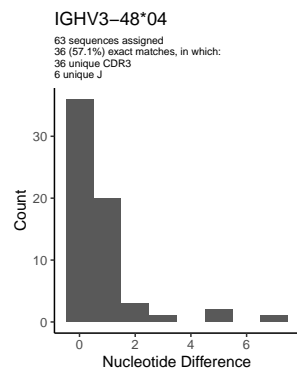
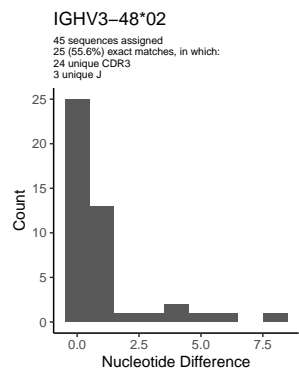
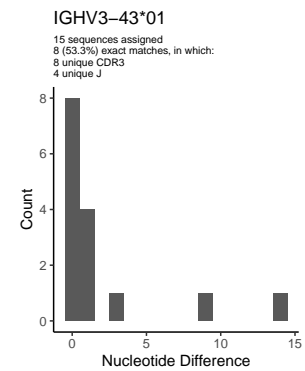
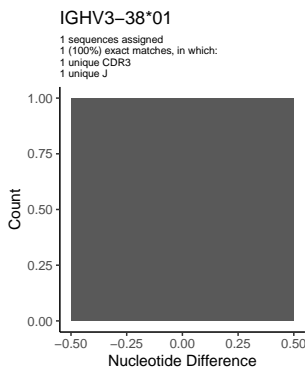
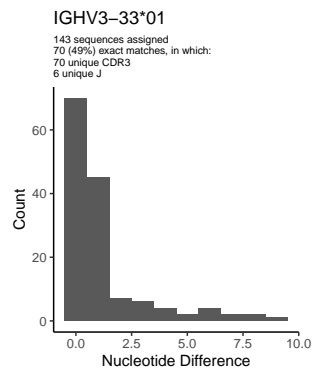
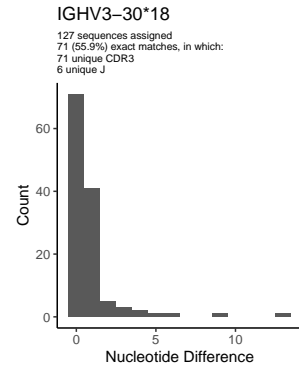
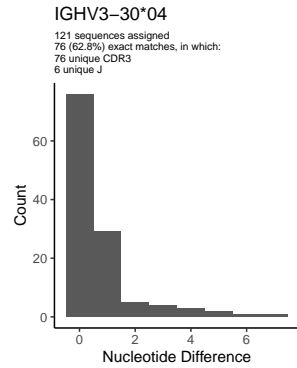
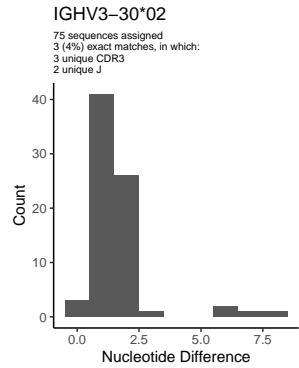
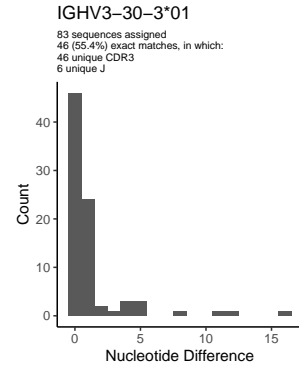
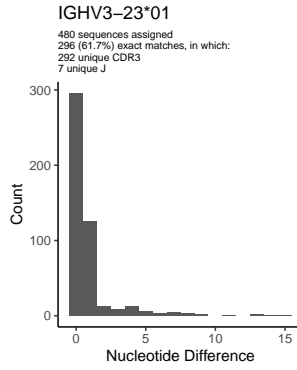
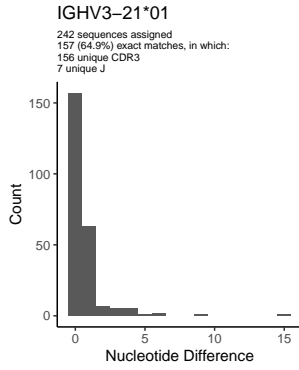
1 Novel sequence analysis

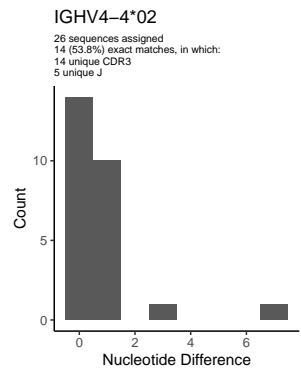
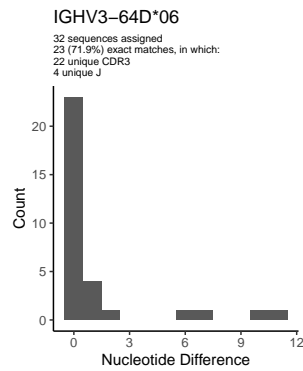
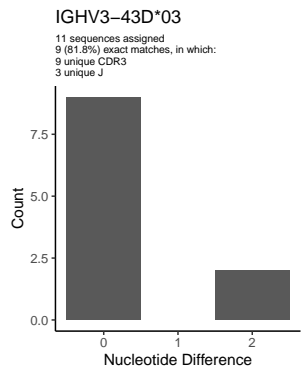
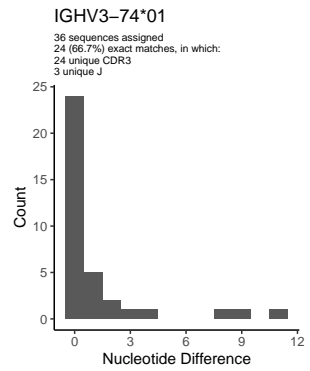
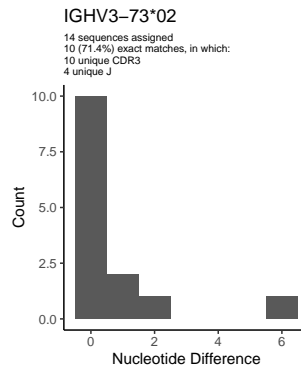
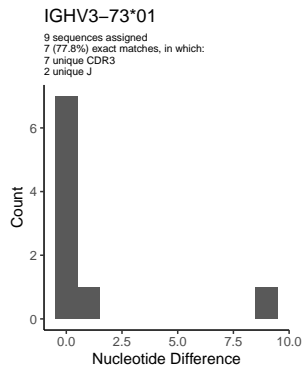
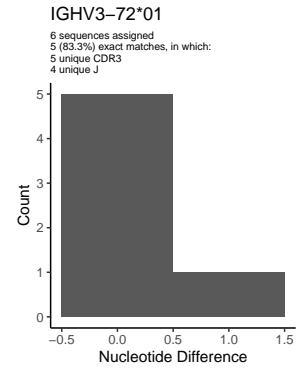
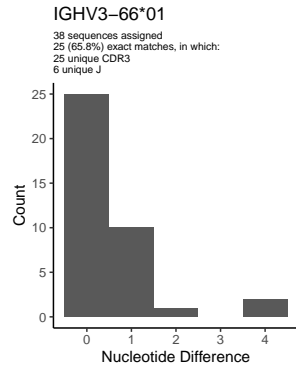
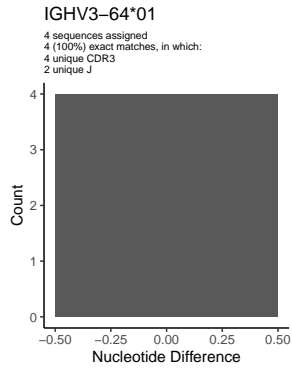
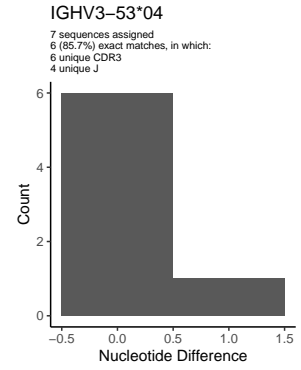
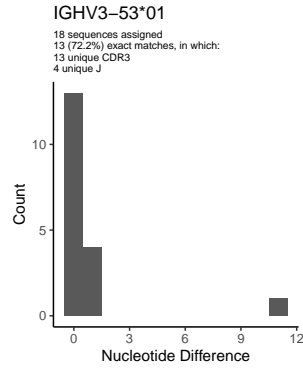
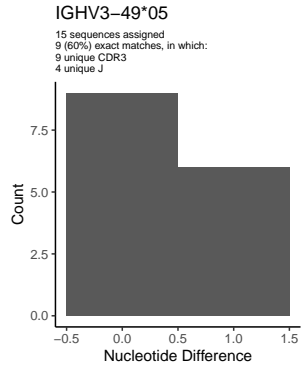
1.1 CDR3 length distribution, in assignments to novel alleles

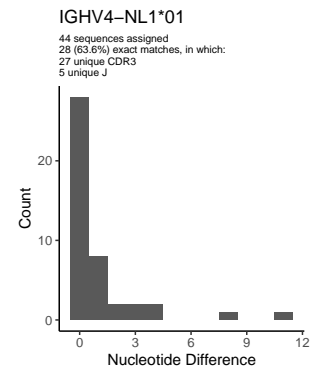
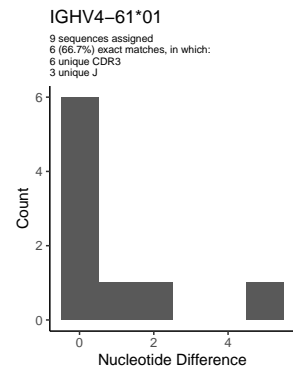
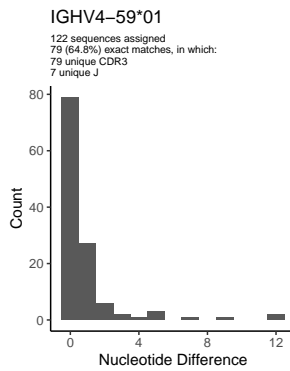
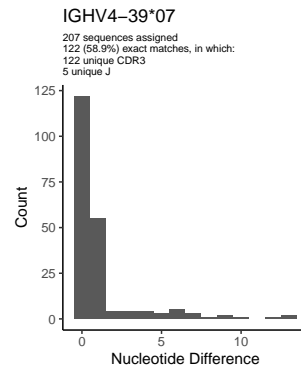
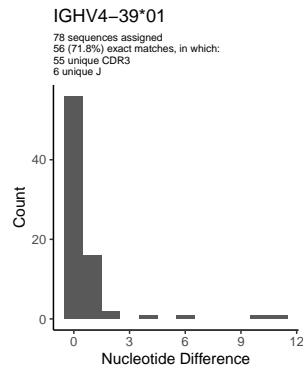
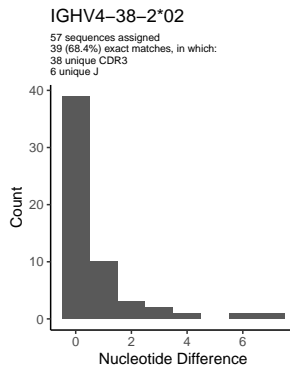
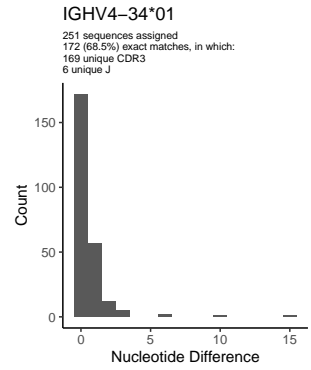
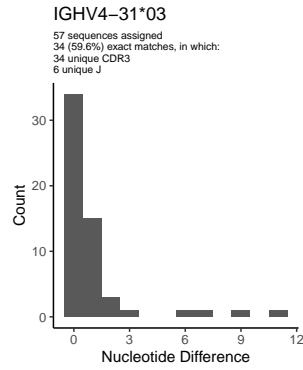
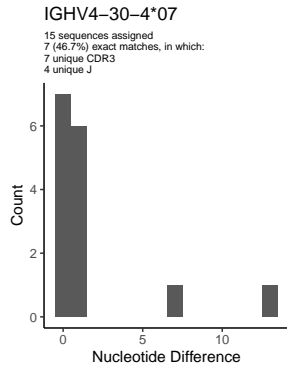
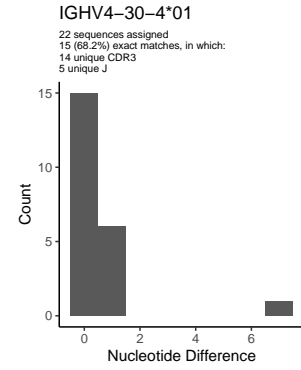
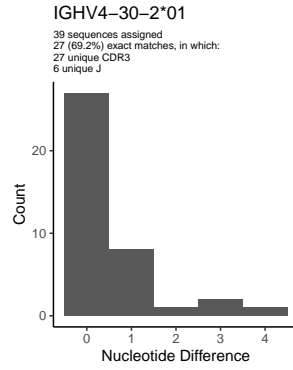
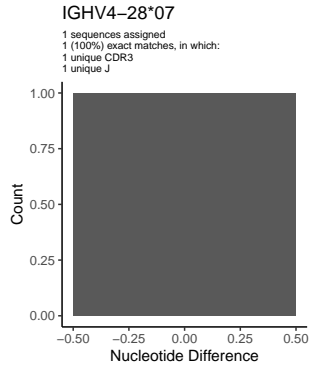
2 Variation from germline, in assignments to each allele

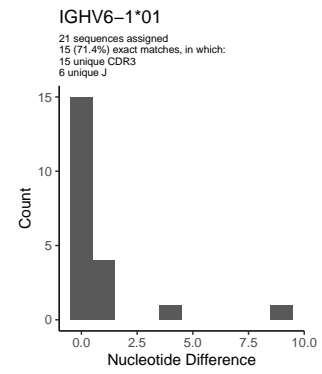
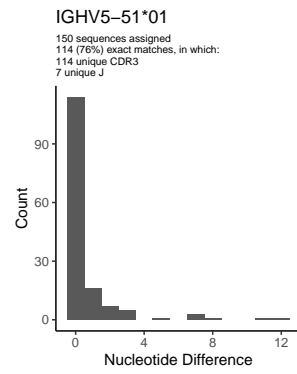
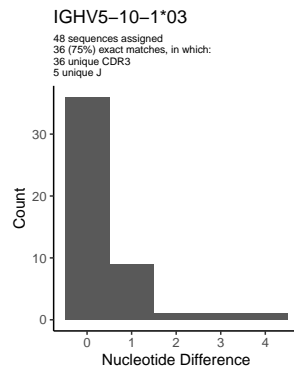




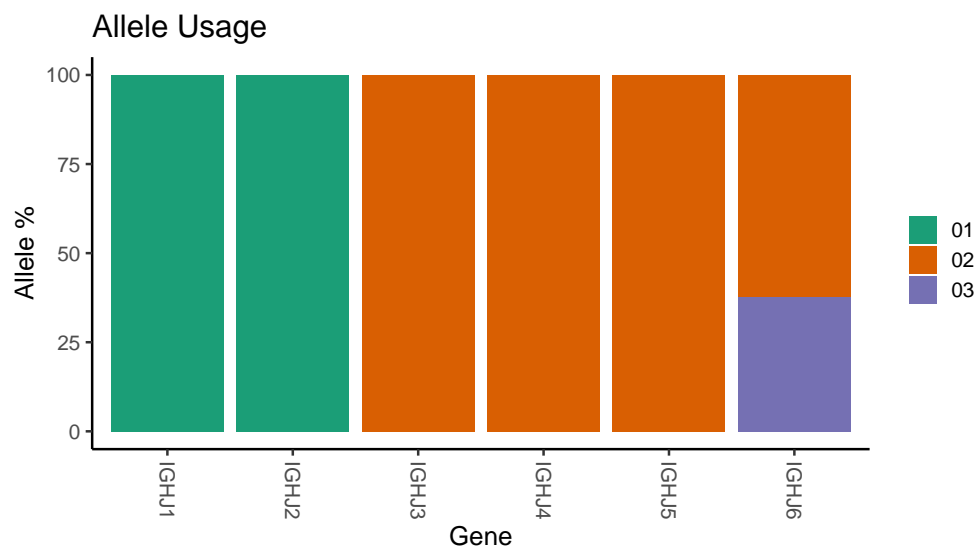




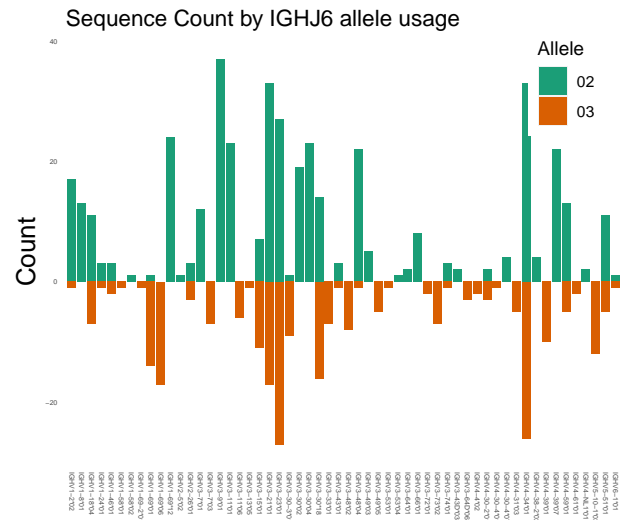




3 Allele usage in potential haplotype anchor genes



4 Haplotype plots



5 Configuration settings

```
## Repertoire file: /misc/work/jenkins/PRJEB26509/S44/S44/47/47/23/aea0770a0bb9f6a6a04f2fa3063f84/47_Fi
##
## Germline reference file: /misc/work/jenkins/PRJEB26509/S44/S44/47/47/6b/c88c03f56574f3b8cfd0ca21cea5
##
## Novel allele file:
##
## Species: Homosapiens
##
## Chain: IGHV
##
## Segment: V
##
## Warning    no inferred sequences found.
```