

OGRDBstats Report

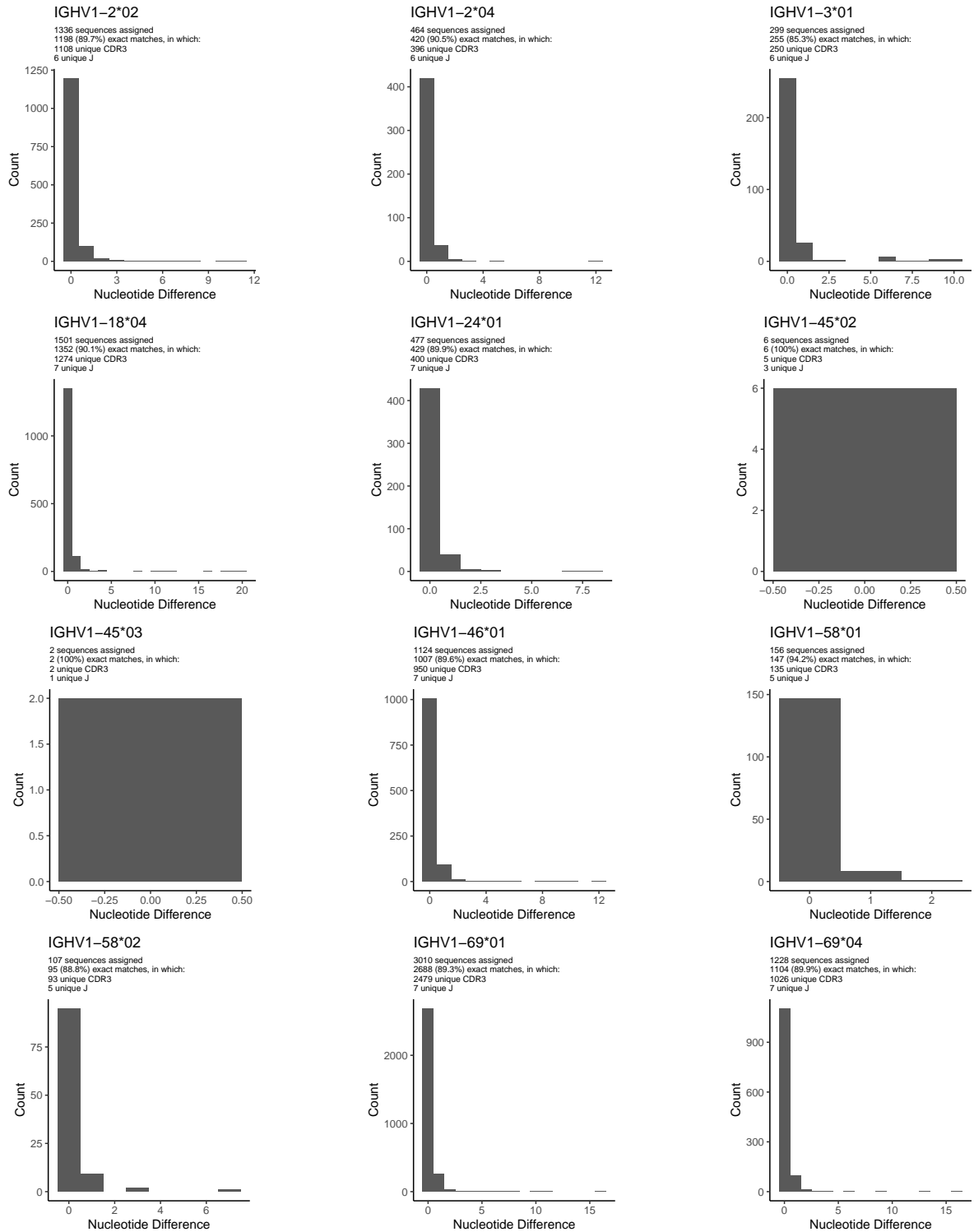
Contents

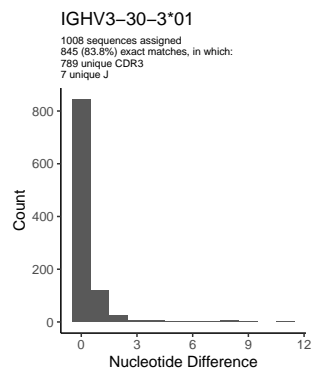
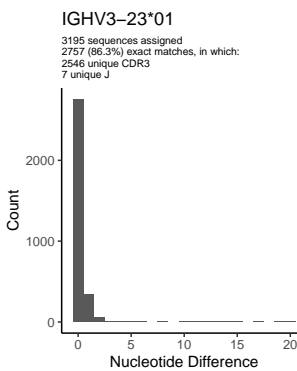
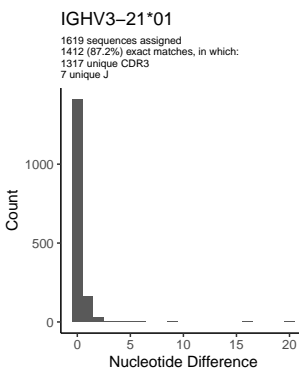
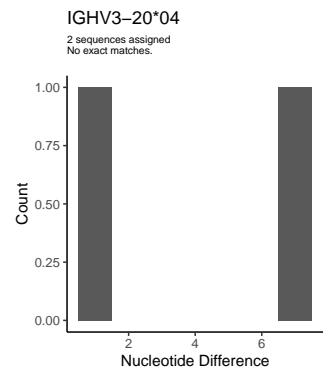
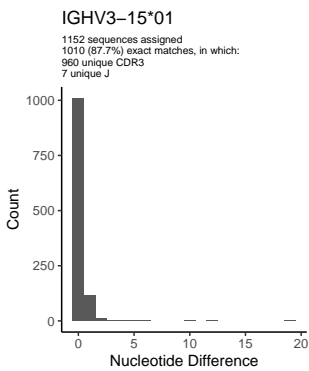
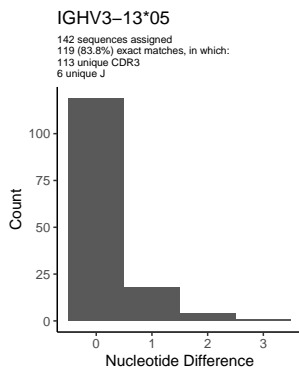
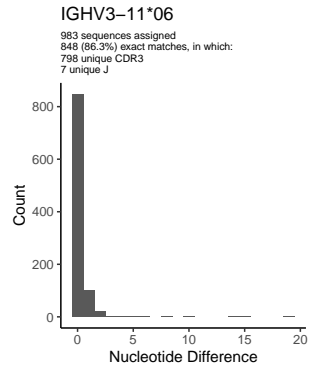
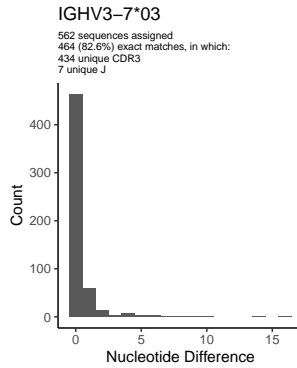
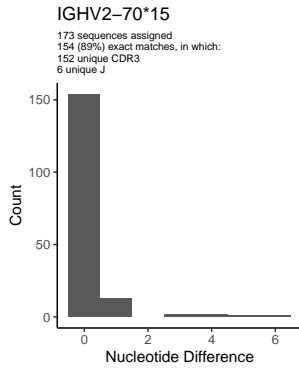
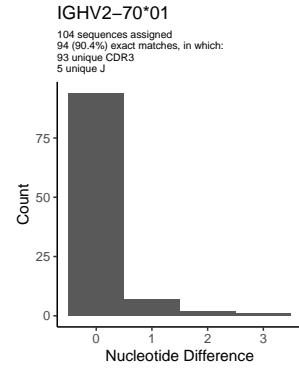
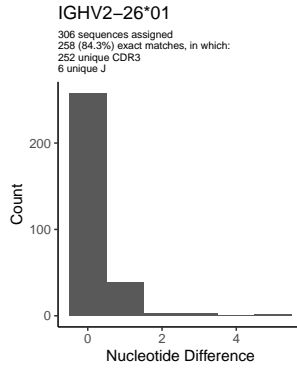
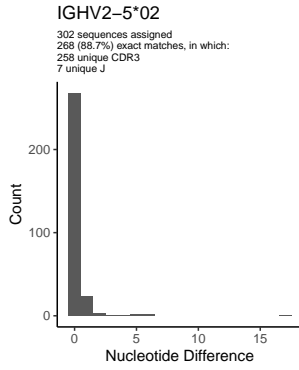
1	Novel sequence analysis	2
1.1	CDR3 length distribution, in assignments to novel alleles	2
2	Variation from germline, in assignments to each allele	3
3	Allele usage in potential haplotype anchor genes	9
4	Haplotype plots	10
5	Configuration settings	11

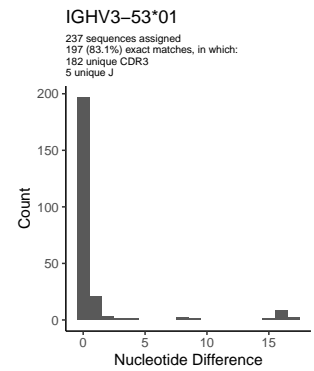
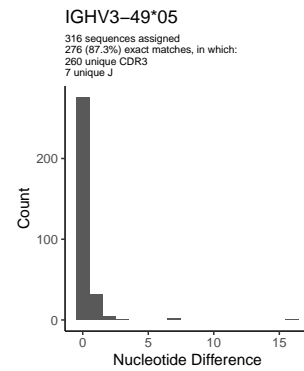
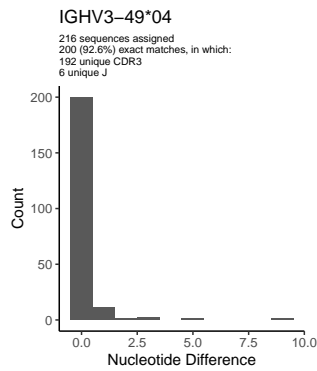
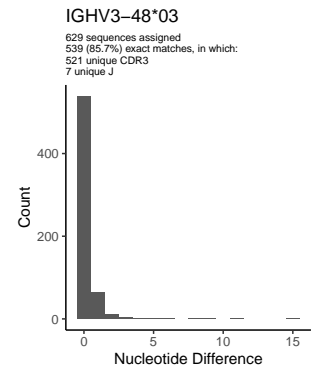
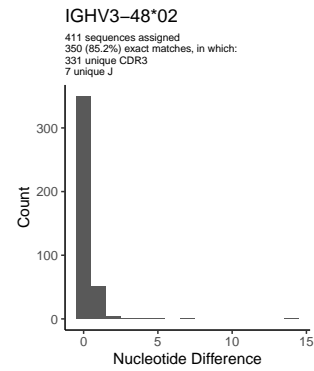
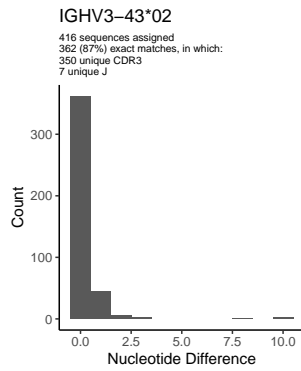
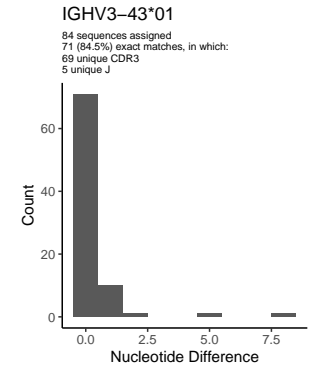
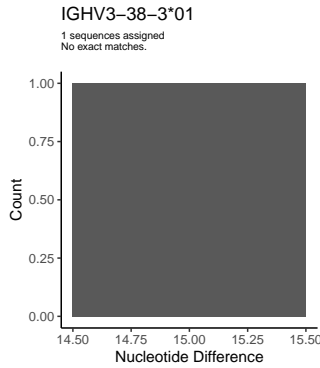
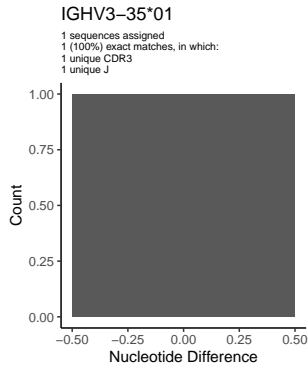
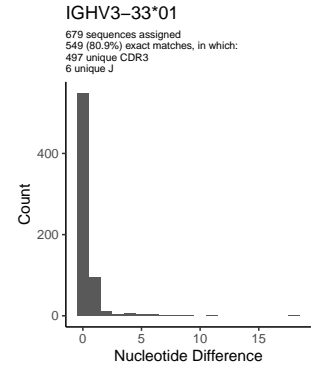
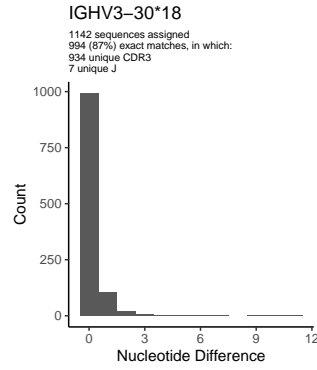
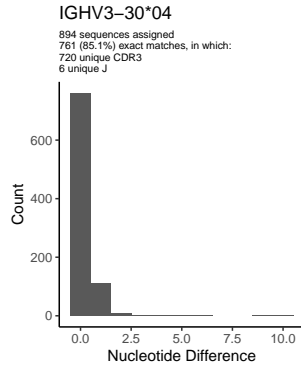
1 Novel sequence analysis

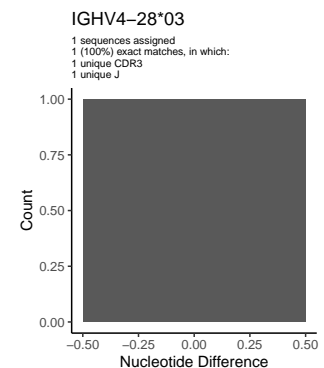
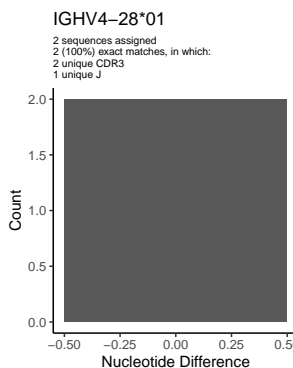
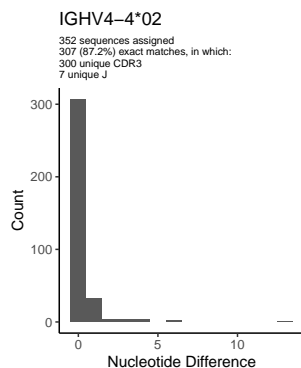
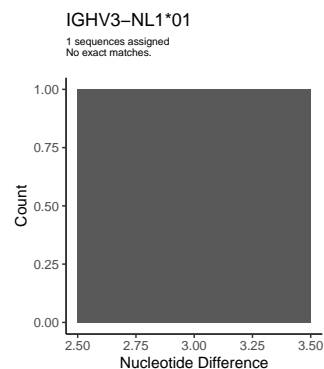
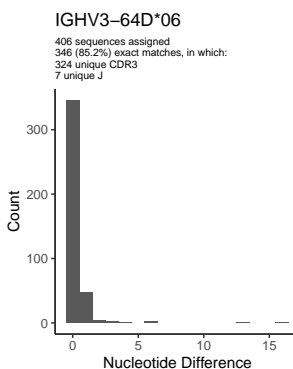
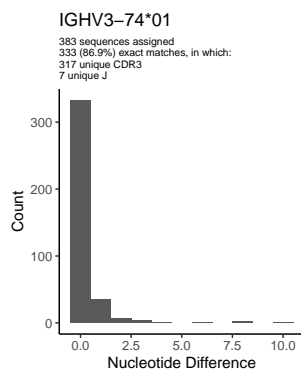
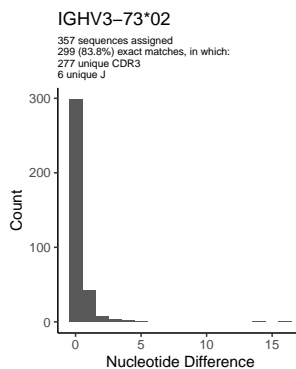
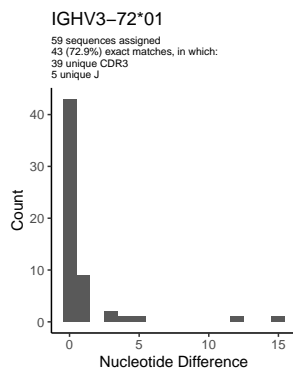
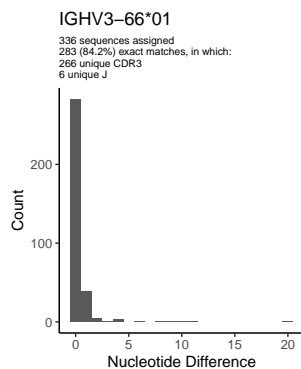
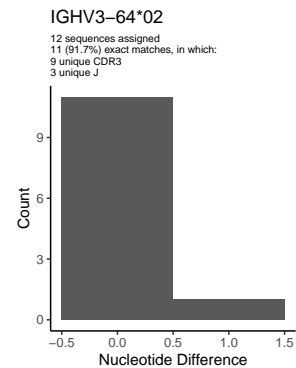
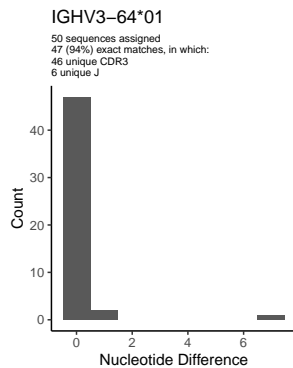
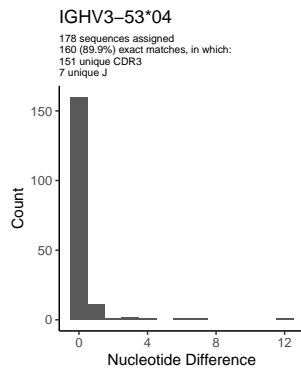
1.1 CDR3 length distribution, in assignments to novel alleles

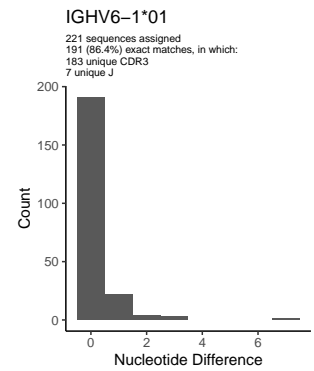
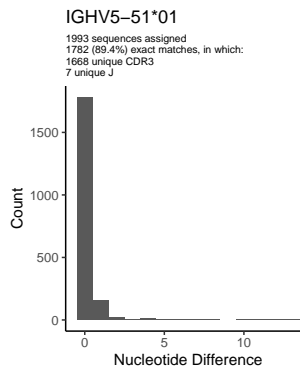
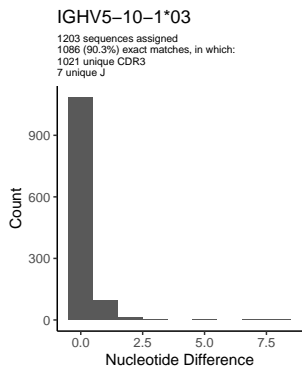
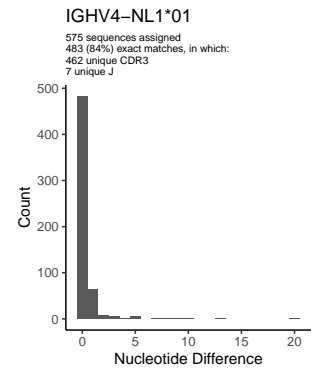
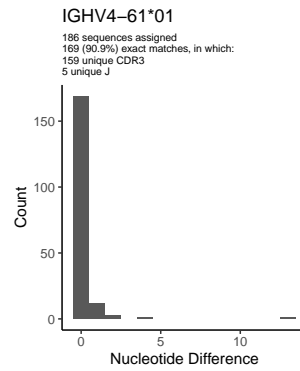
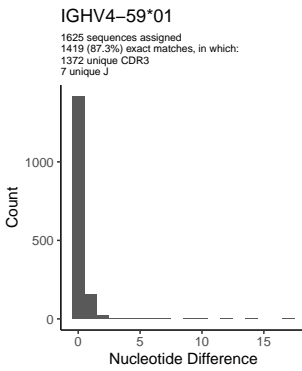
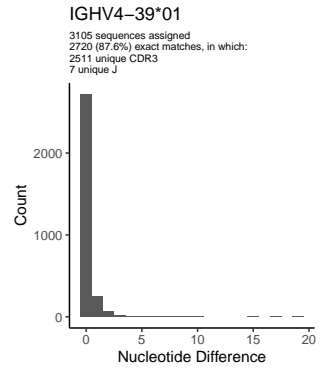
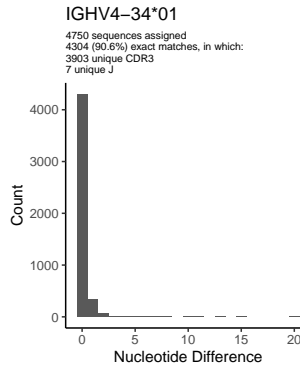
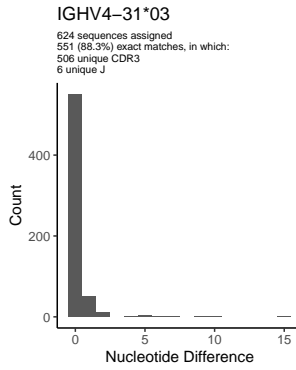
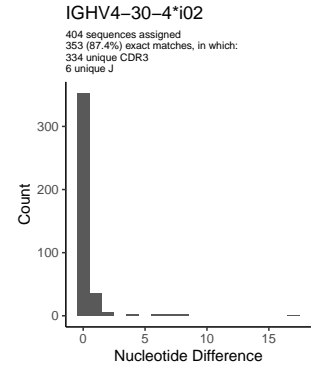
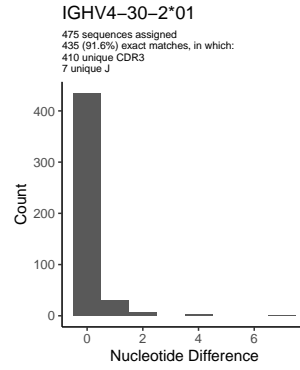
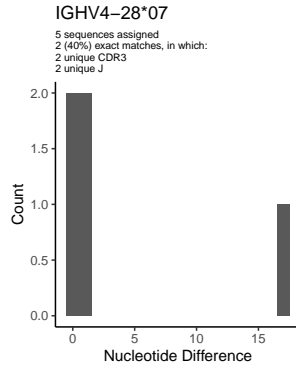
2 Variation from germline, in assignments to each allele





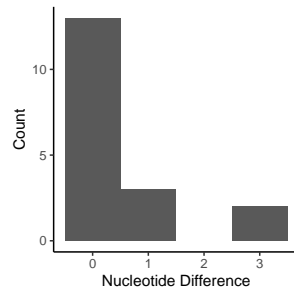




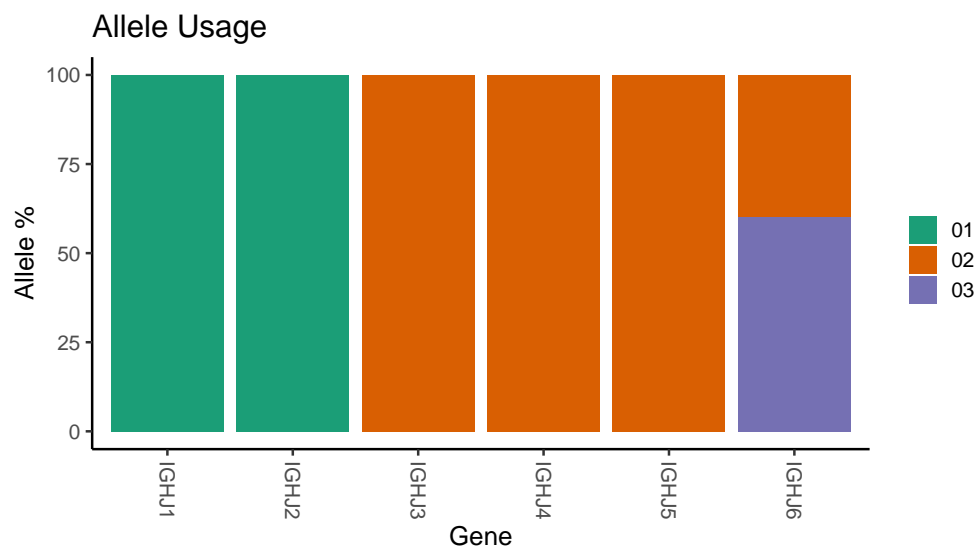


IGHV7-4-1*01

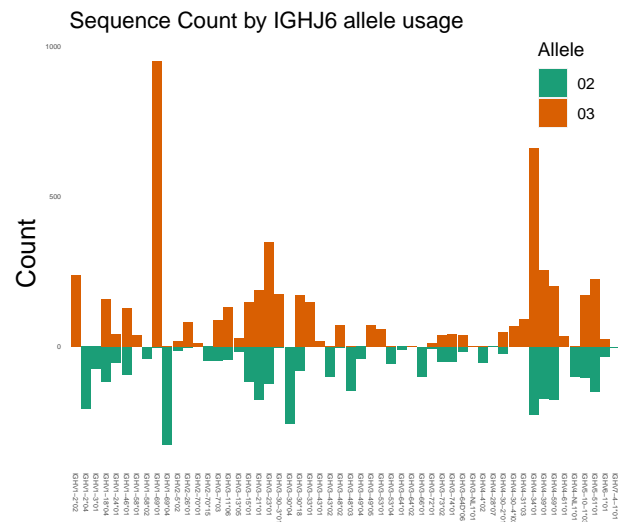
18 sequences assigned
13 (72.2%) exact matches, in which:
13 unique CDR3
4 unique J



3 Allele usage in potential haplotype anchor genes



4 Haplotype plots



5 Configuration settings

```
## Repertoire file: /misc/work/jenkins/PRJEB26509/S38/S38/41/41/86/a94c039a7116cfb0ed3f33650083f6/41_Fi
##
## Germline reference file: /misc/work/jenkins/PRJEB26509/S38/S38/41/41/70/f47c7dfbd6db24fdfaf1bed5931c
##
## Novel allele file:
##
## Species: Homosapiens
##
## Chain: IGHV
##
## Segment: V
##
## Warning    no inferred sequences found.
```