

OGRDBstats Report

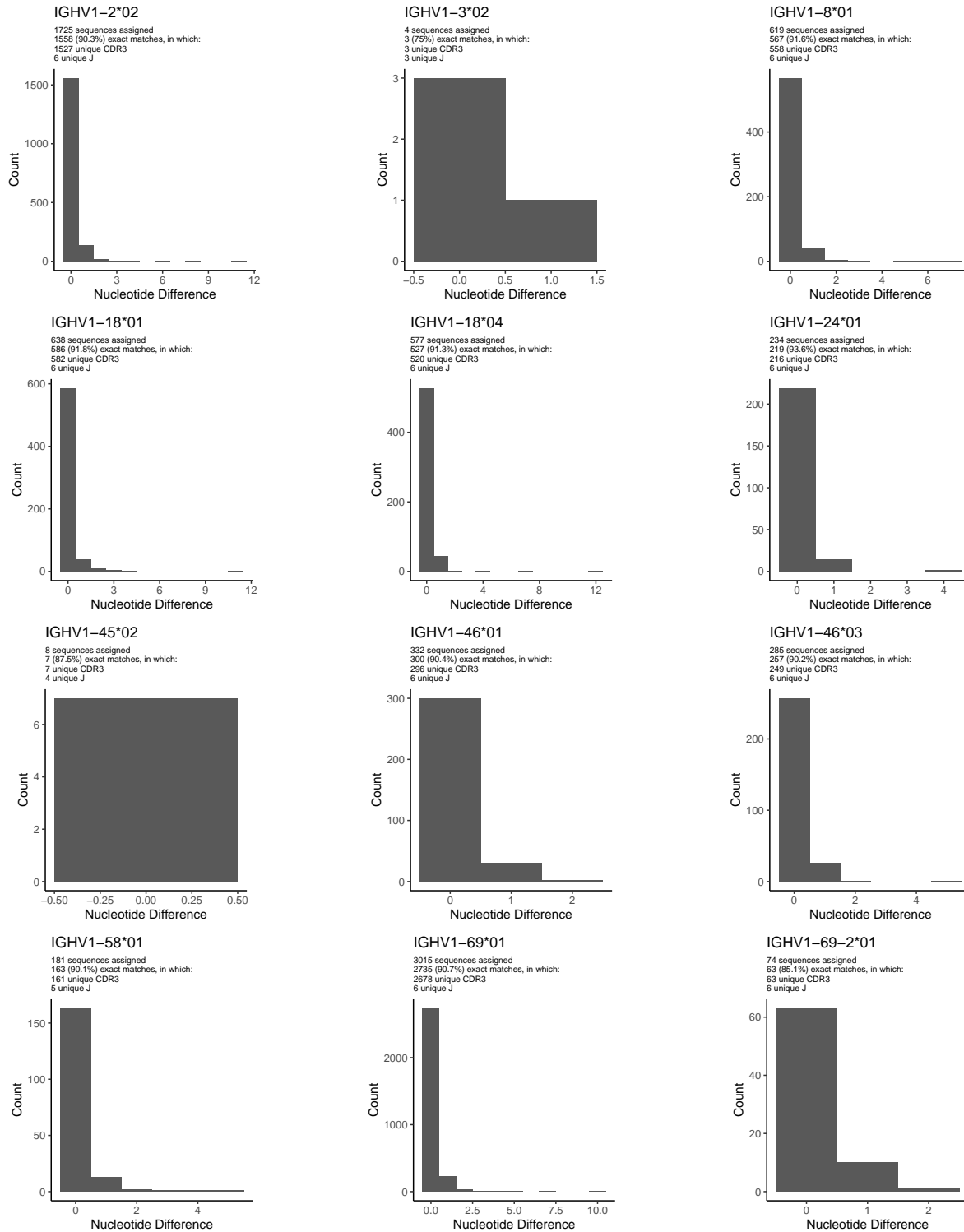
Contents

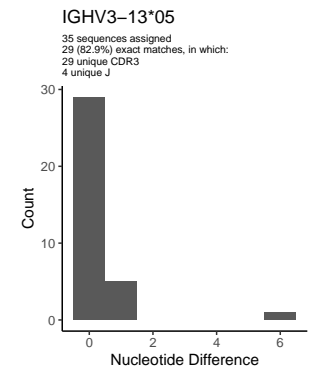
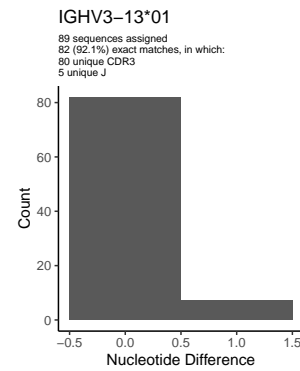
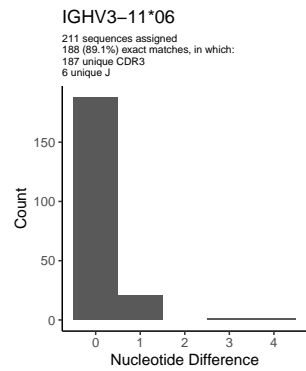
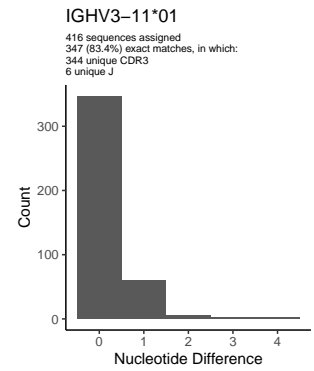
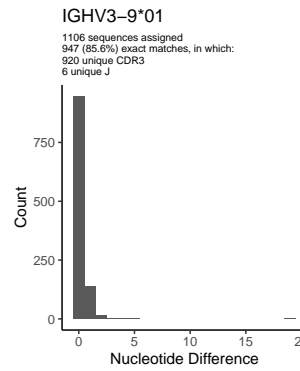
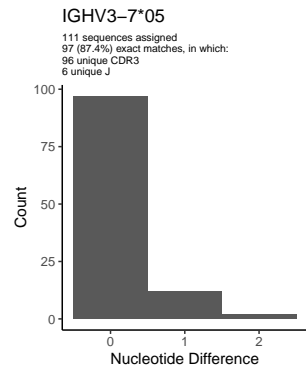
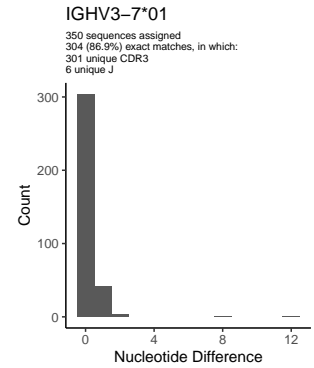
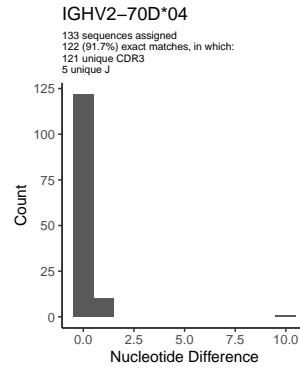
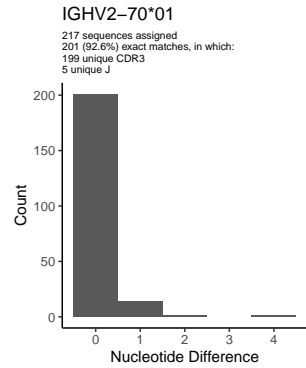
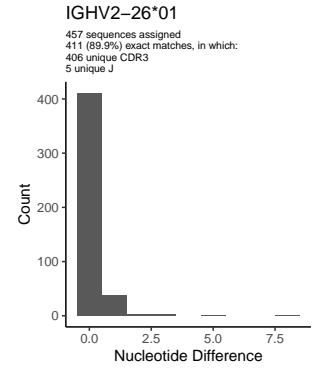
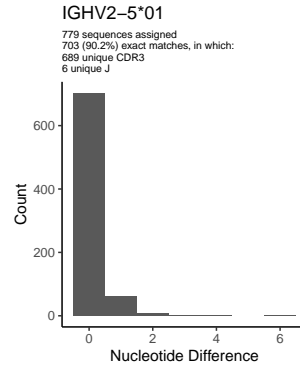
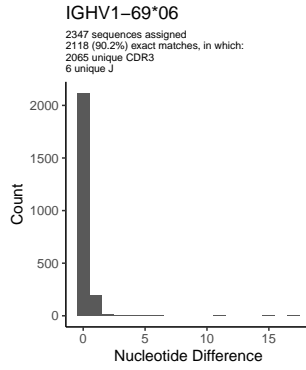
1	Novel sequence analysis	2
1.1	CDR3 length distribution, in assignments to novel alleles	2
2	Variation from germline, in assignments to each allele	3
3	Allele usage in potential haplotype anchor genes	9
4	Haplotype plots	10
5	Configuration settings	11

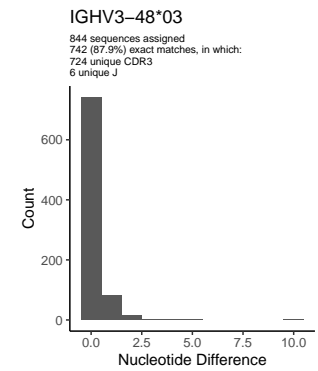
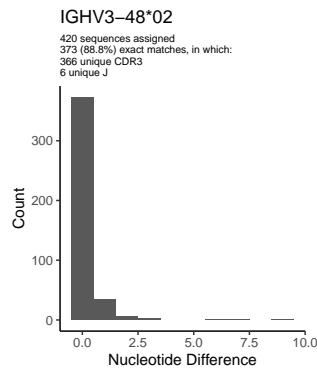
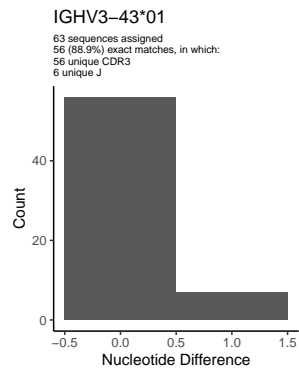
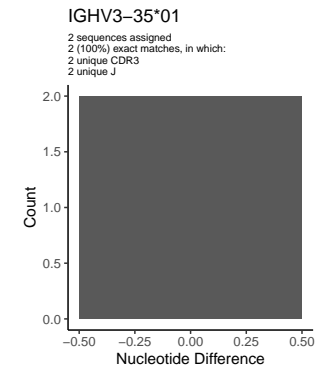
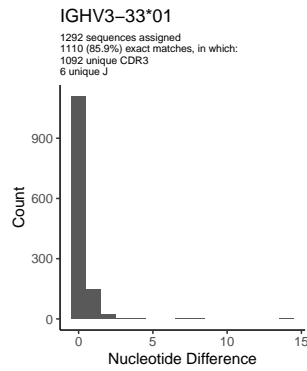
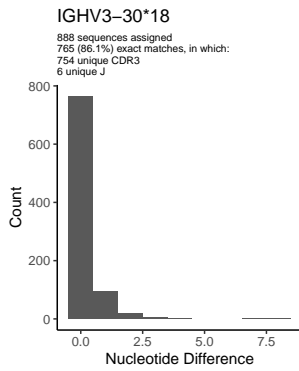
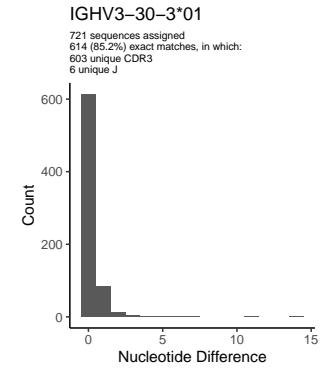
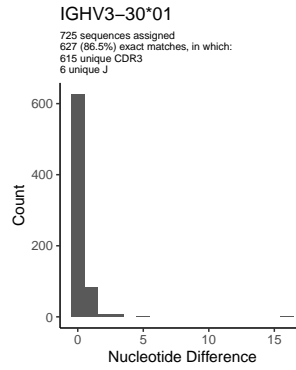
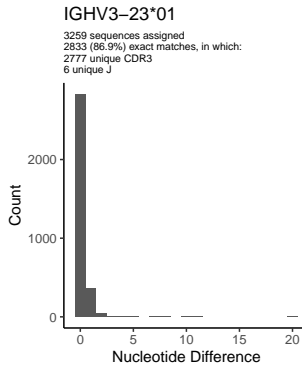
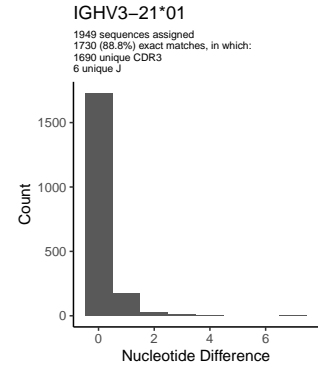
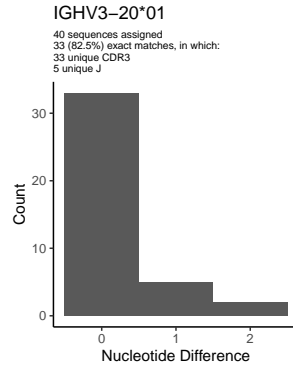
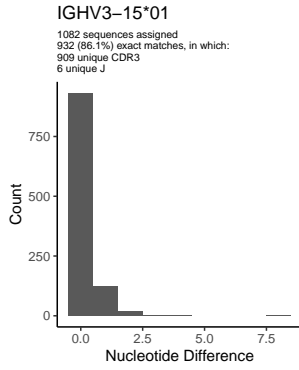
1 Novel sequence analysis

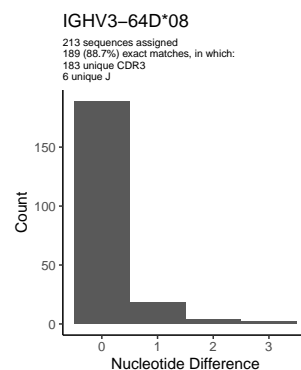
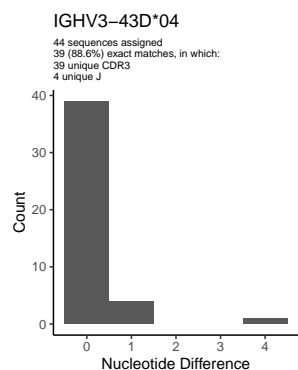
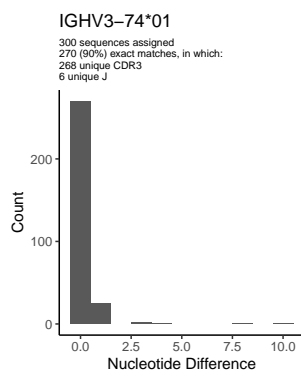
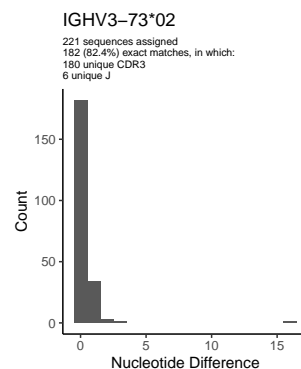
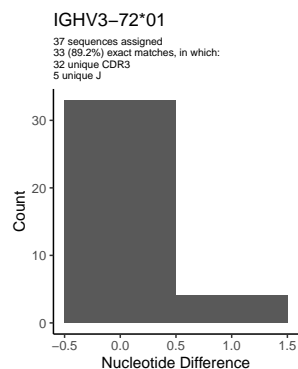
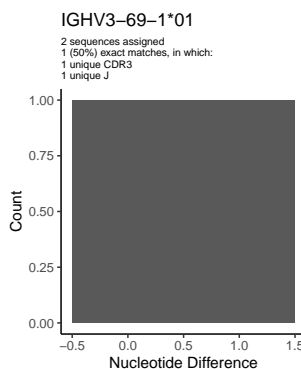
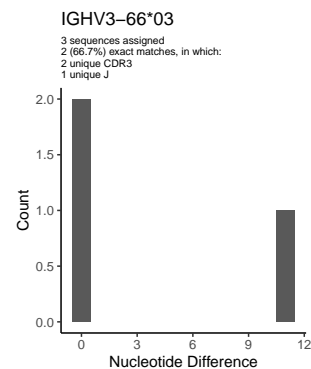
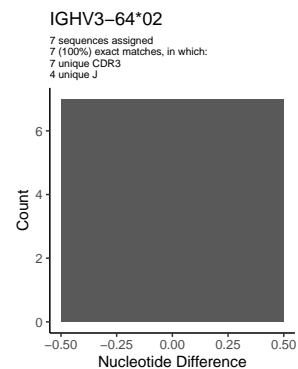
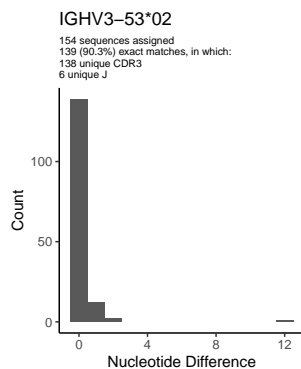
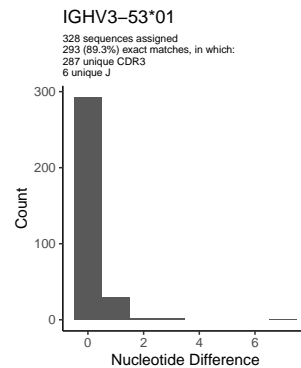
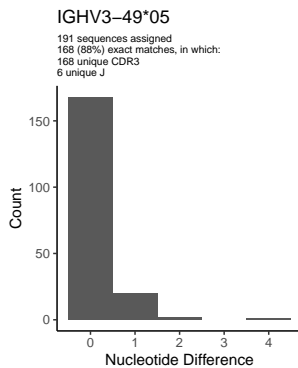
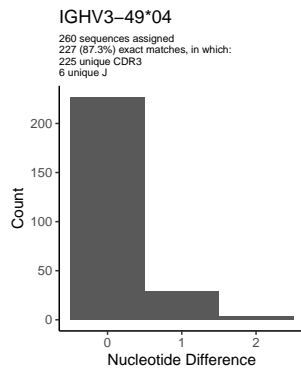
1.1 CDR3 length distribution, in assignments to novel alleles

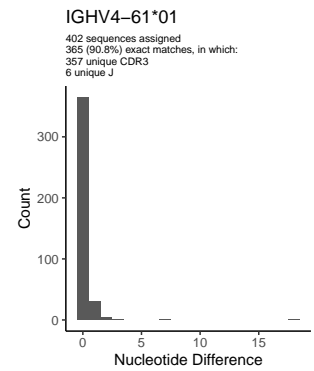
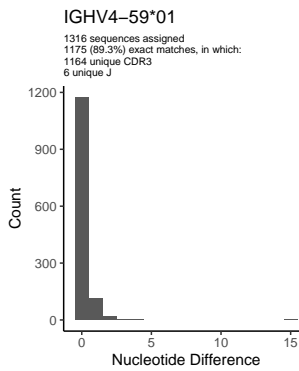
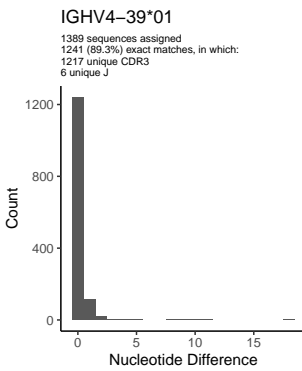
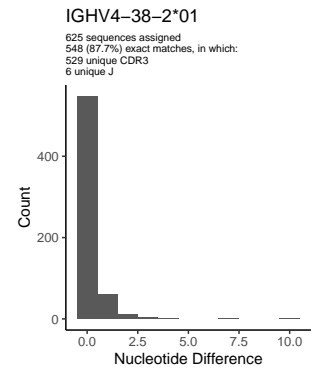
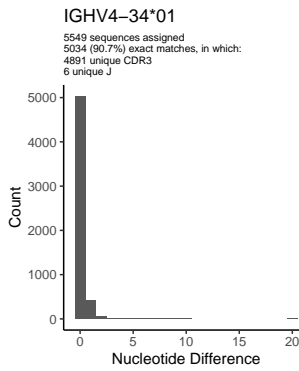
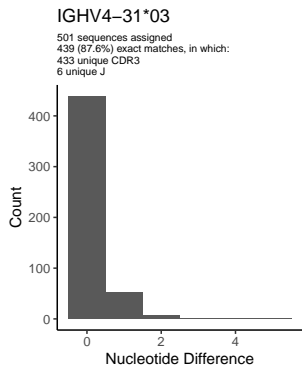
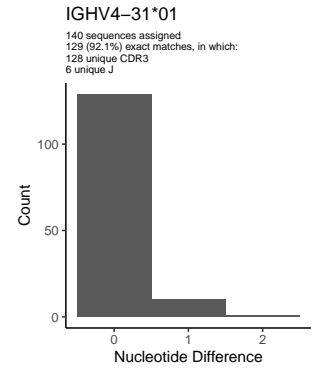
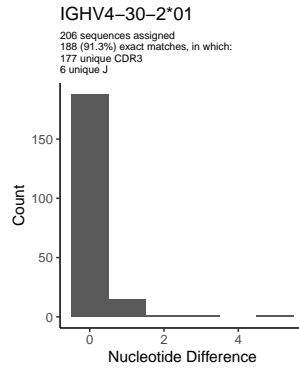
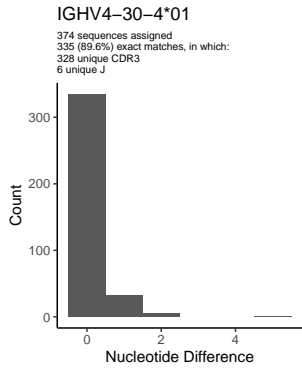
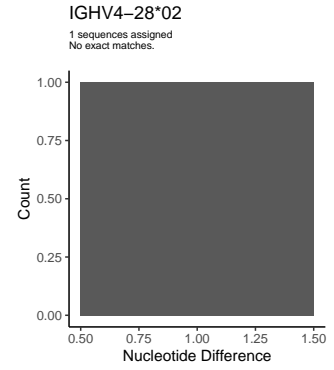
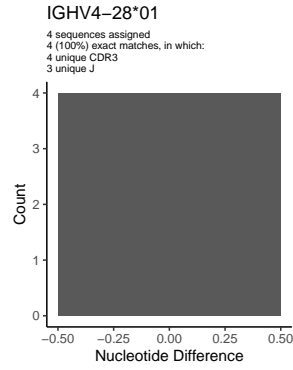
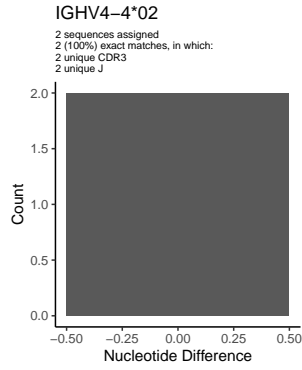
2 Variation from germline, in assignments to each allele

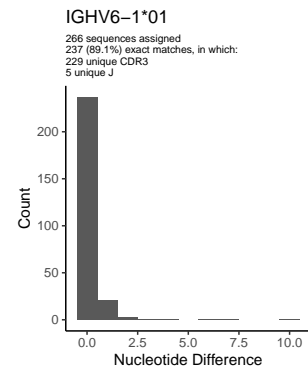
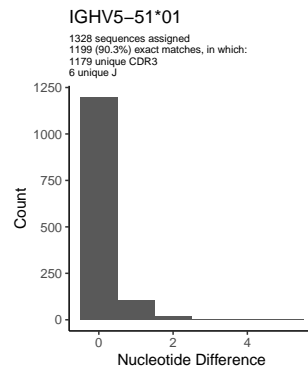
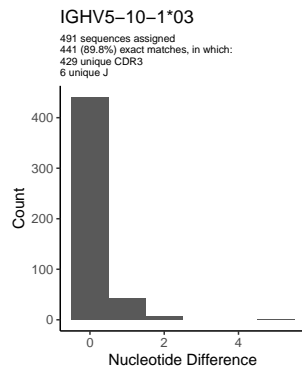




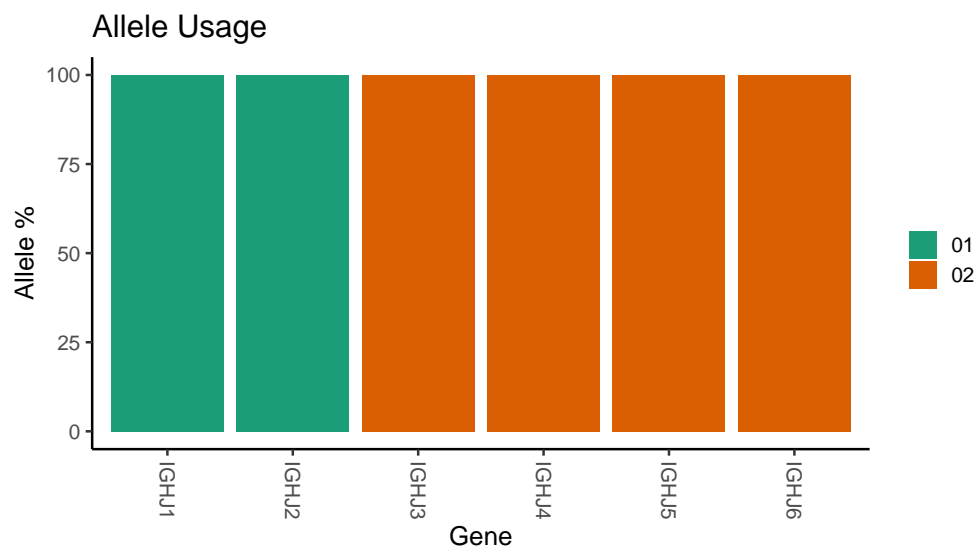








3 Allele usage in potential haplotype anchor genes



4 Haplotype plots

5 Configuration settings

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## Germline reference file: /work/jenkins/PRJEB26509/S62/S62/66/66/ab/0df2fedf85f6af2fd18a80f8b55800/re  
##  
## Novel allele file:  
##  
## Species: Homosapiens  
##  
## Chain: IGHV  
##  
## Segment: V  
##  
## Warning    no inferred sequences found.
```