

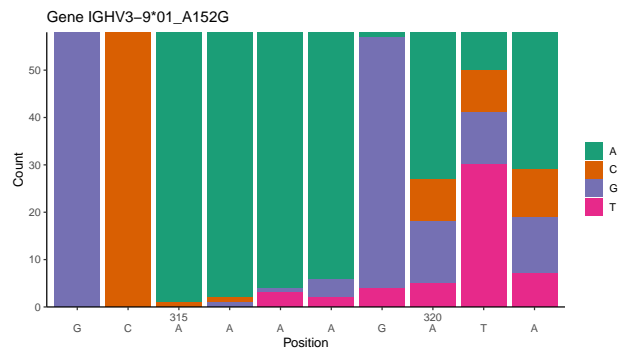
OGRDBstats Report

Contents

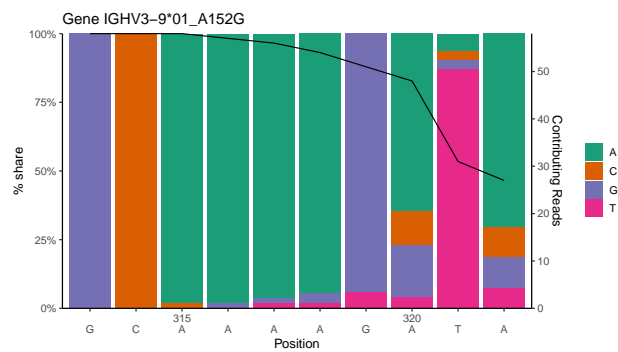
1	Novel sequence analysis	2
1.1	End-nucleotide composition	2
1.2	Per-nucleotide consensus where previous nucleotides match the consensus	2
1.3	Whole-sequence composition of each assigned read	2
1.4	Final three nucleotides: frequency of each observed triplet	2
1.5	CDR3 length distribution, in assignments to novel alleles	3
2	Variation from germline, in assignments to each allele	4
3	Allele usage in potential haplotype anchor genes	9
4	Haplotype plots	10
5	Configuration settings	11

1 Novel sequence analysis

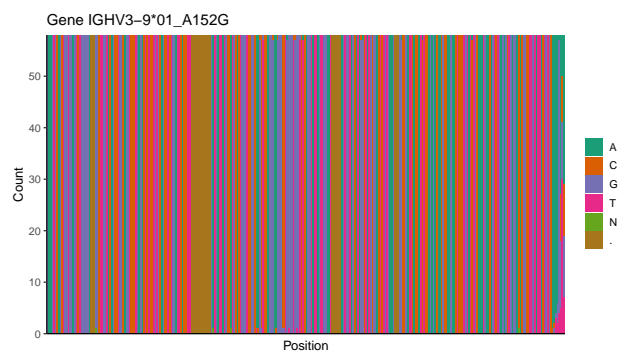
1.1 End-nucleotide composition



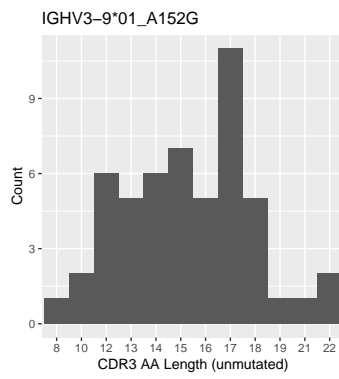
1.2 Per-nucleotide consensus where previous nucleotides match the consensus



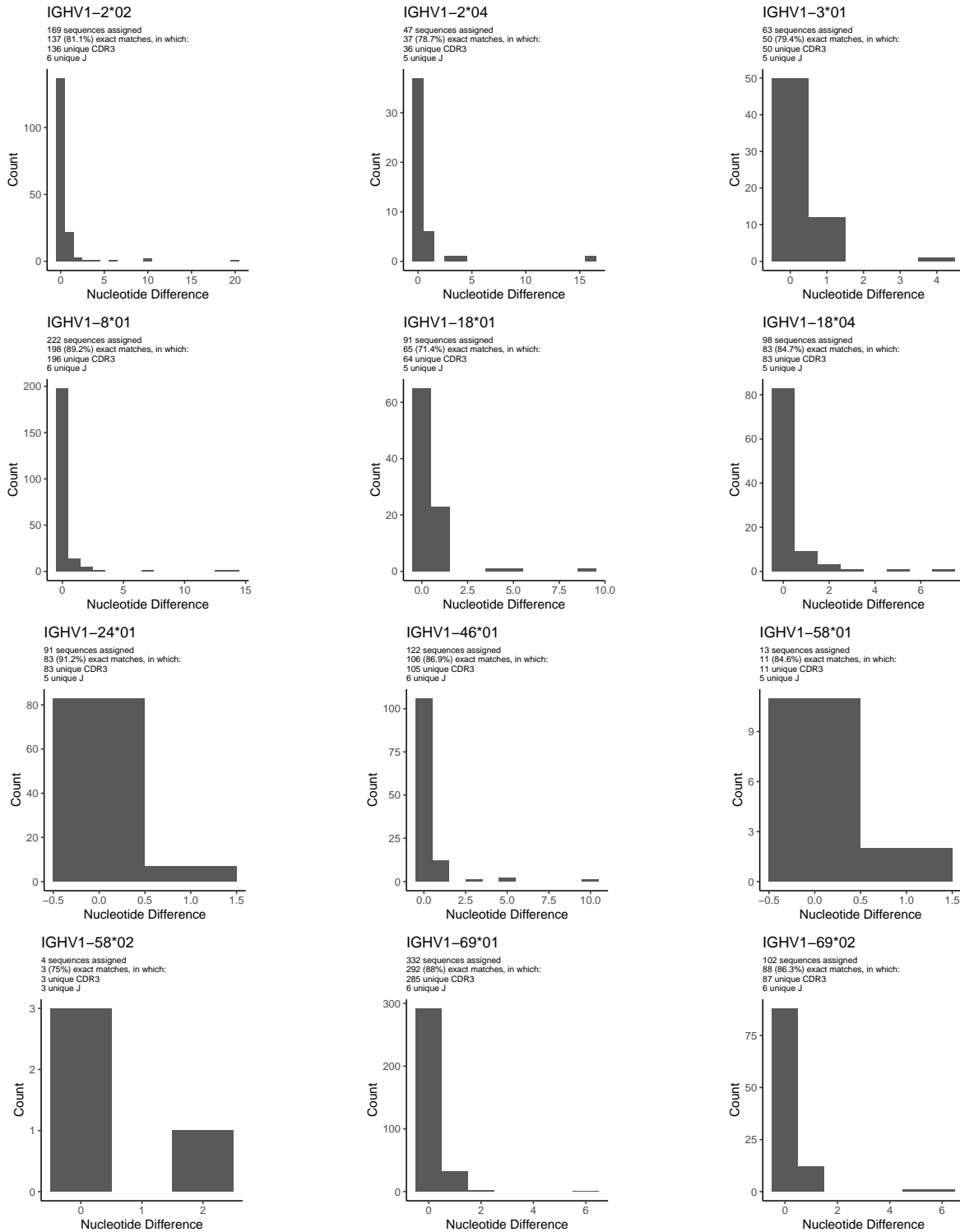
1.3 Whole-sequence composition of each assigned read

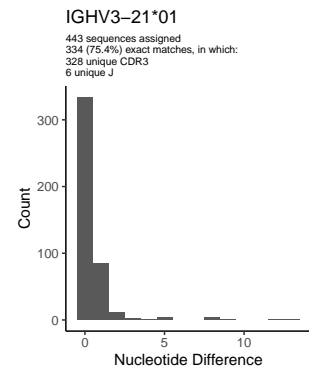
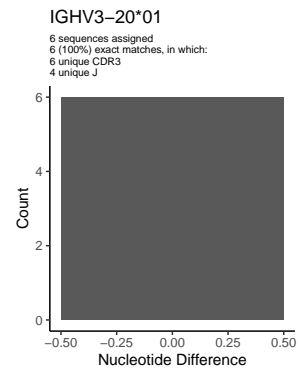
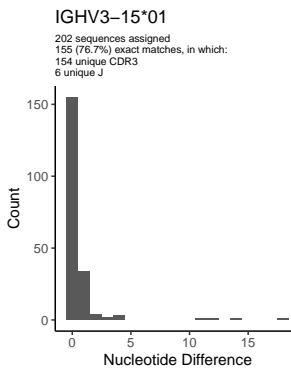
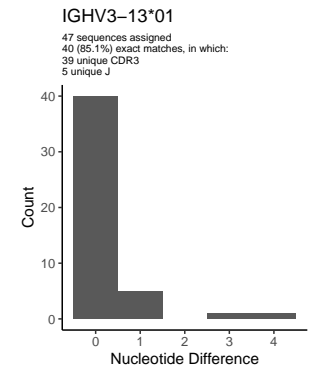
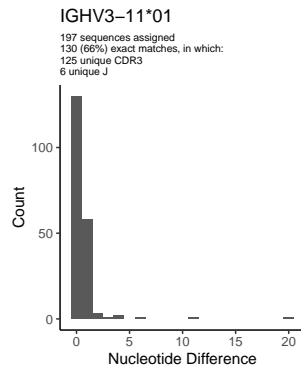
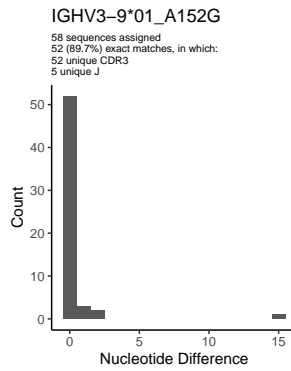
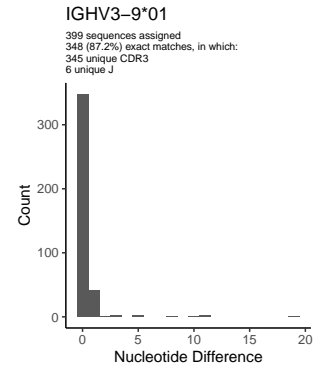
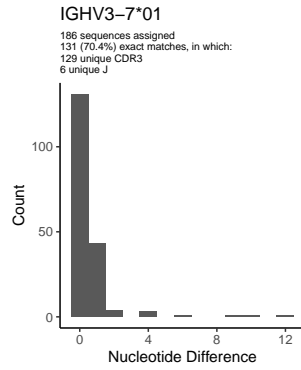
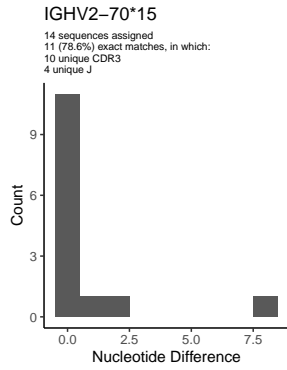
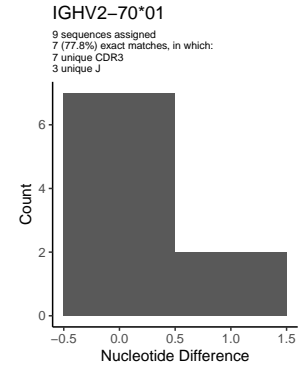
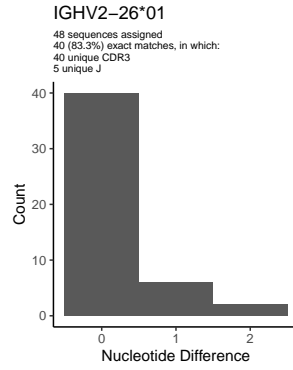
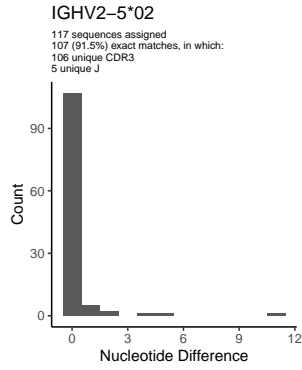


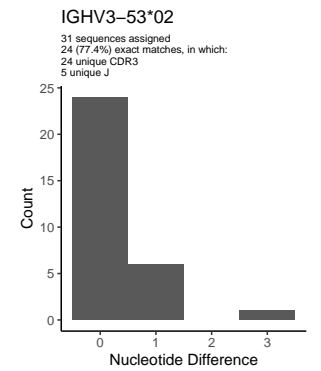
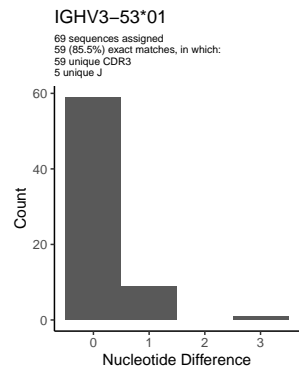
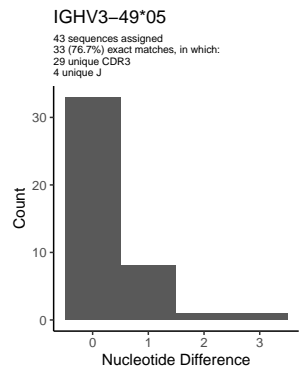
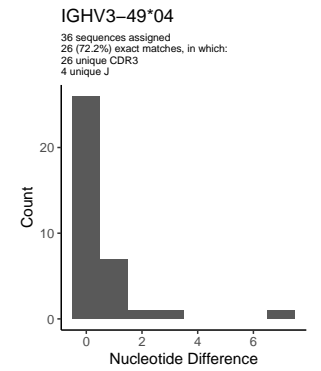
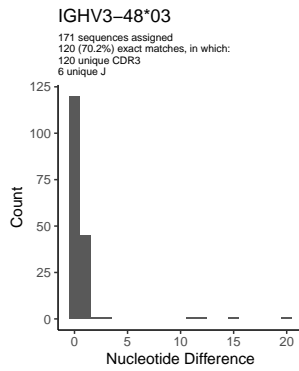
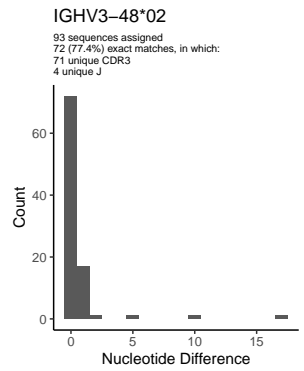
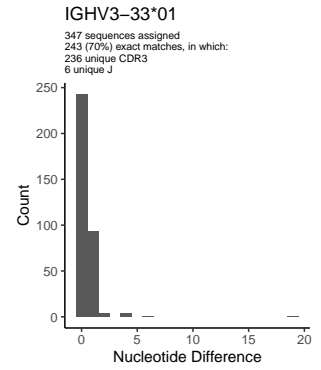
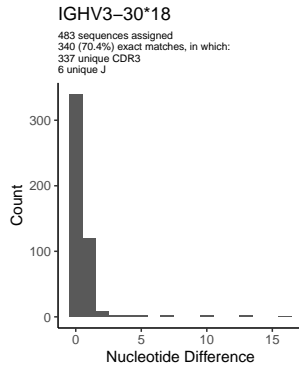
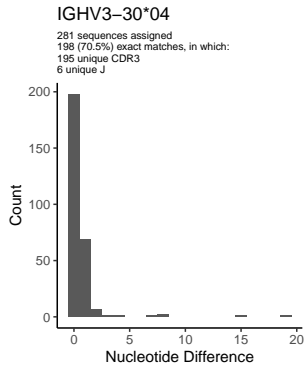
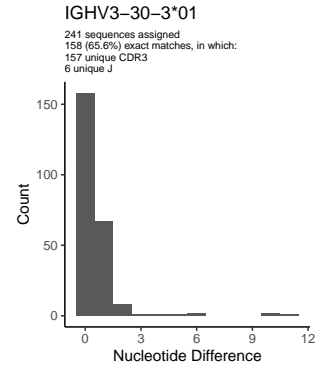
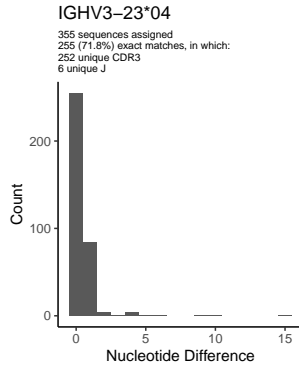
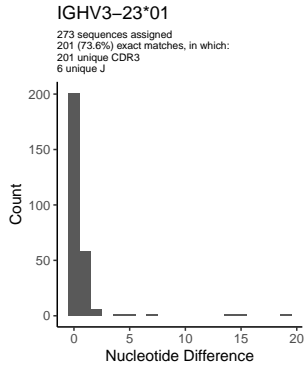
1.5 CDR3 length distribution, in assignments to novel alleles

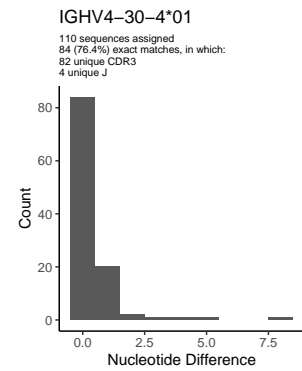
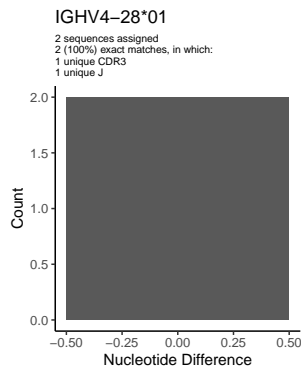
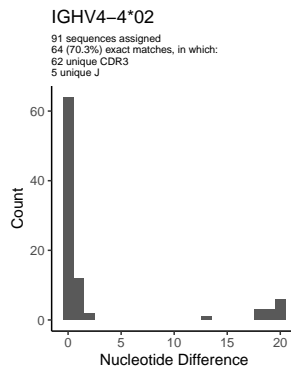
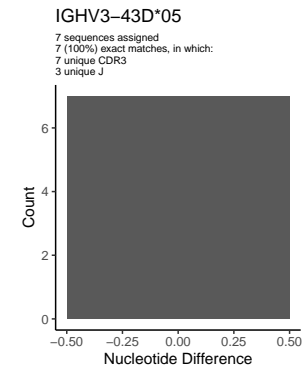
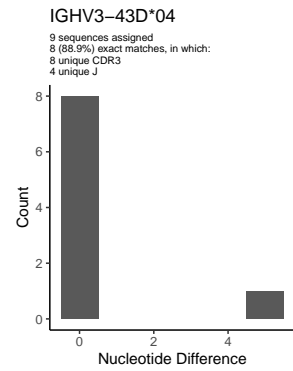
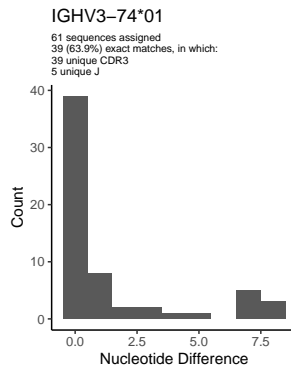
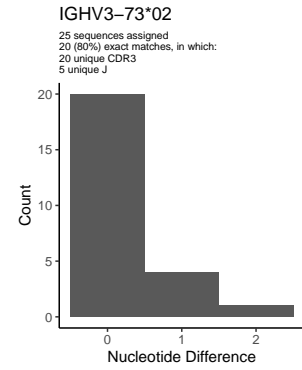
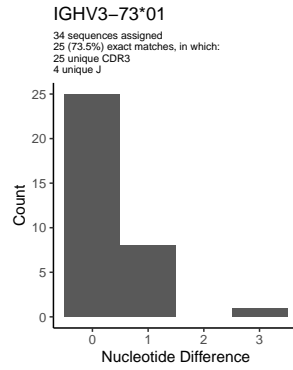
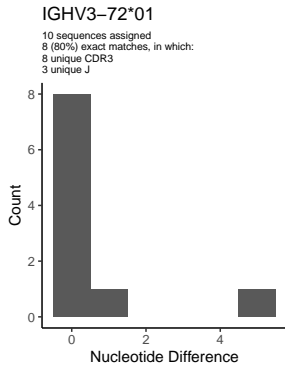
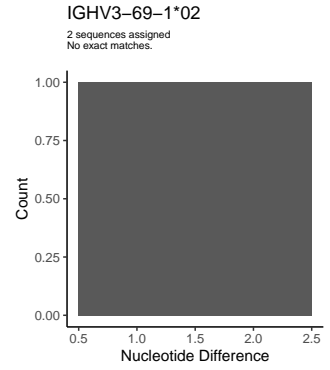
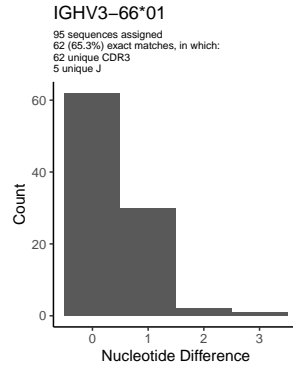
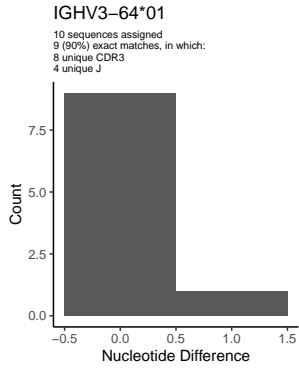


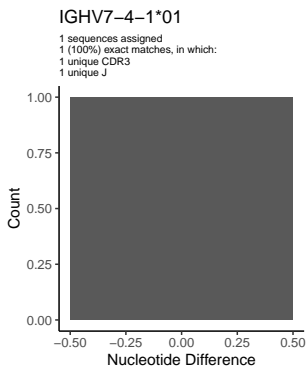
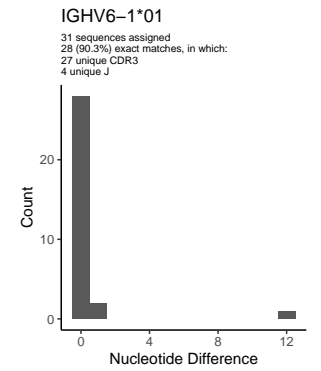
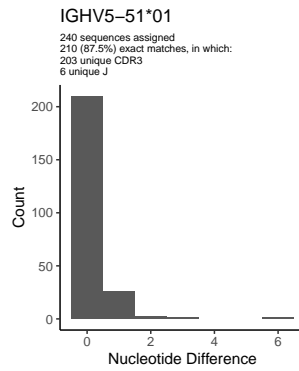
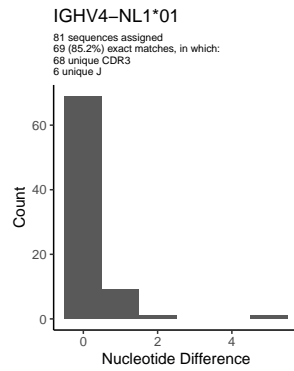
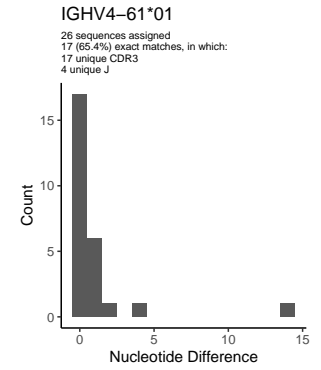
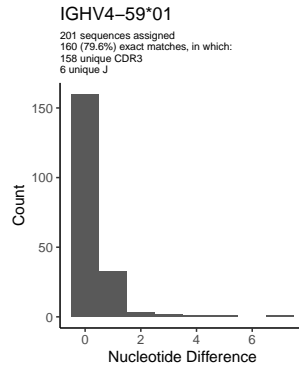
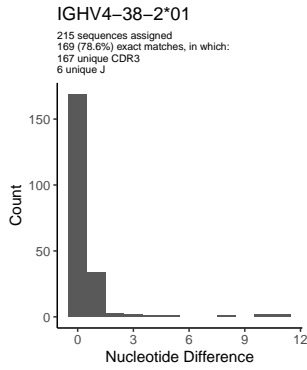
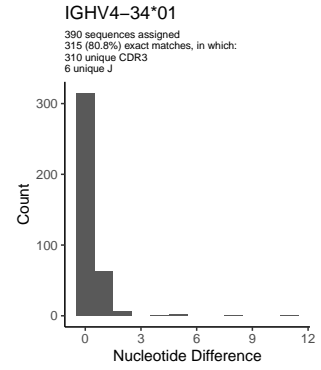
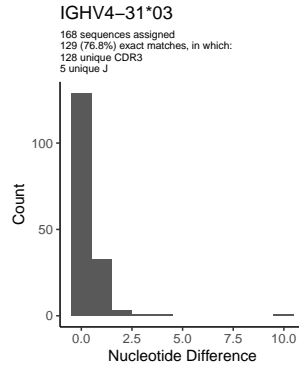
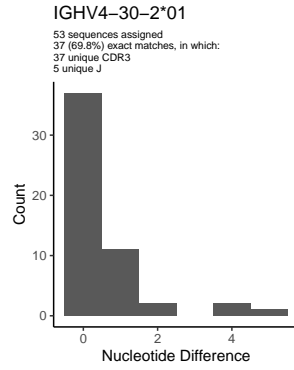
2 Variation from germline, in assignments to each allele



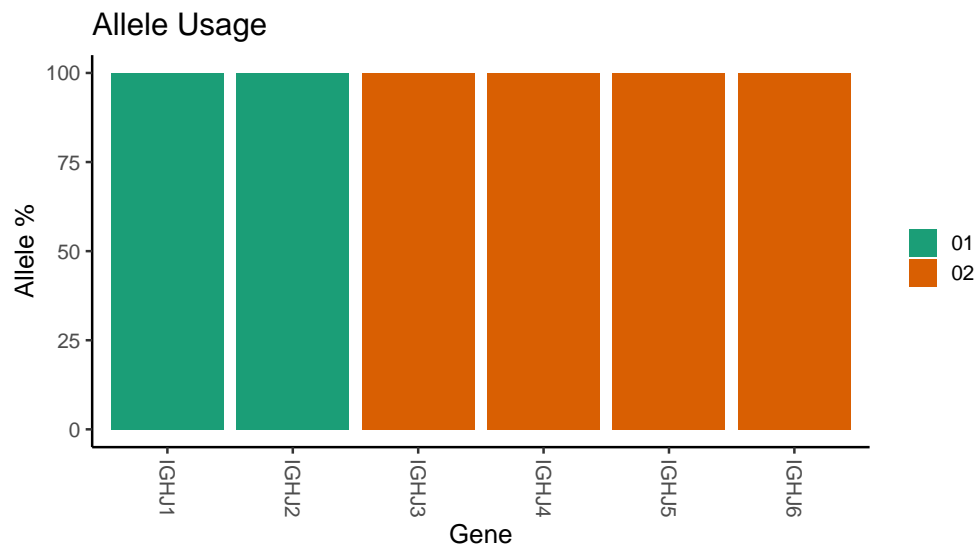








3 Allele usage in potential haplotype anchor genes



4 Haplotype plots

5 Configuration settings

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## Germline reference file: /work/jenkins/PRJEB26509/S42/S42/45/45/91/8fac70050dc9beb579b3392696c7df/pe.  
##  
## Novel allele file: /work/jenkins/PRJEB26509/S42/S42/45/45/91/8fac70050dc9beb579b3392696c7df/novel_se  
##  
## Species: Homosapiens  
##  
## Chain: IGHV  
##  
## Segment: V
```