

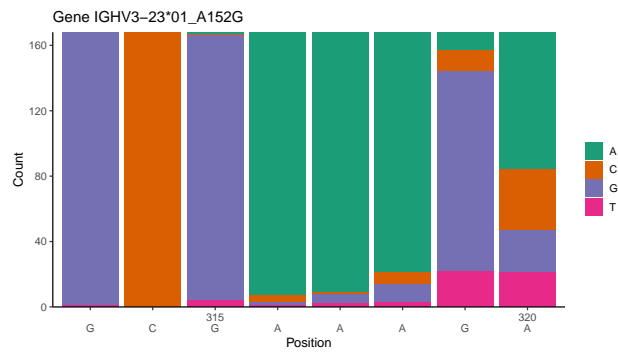
OGRDBstats Report

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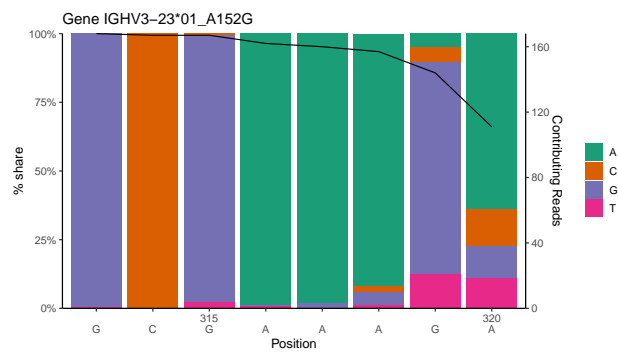
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1 Novel sequence analysis

1.1 End-nucleotide composition



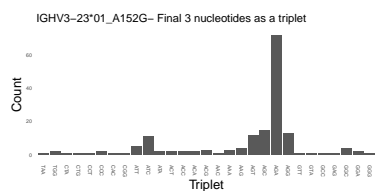
1.2 Per-nucleotide consensus where previous nucleotides match the consensus



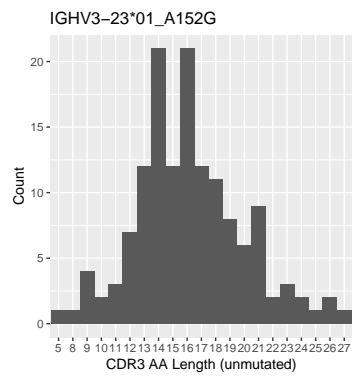
1.3 Whole-sequence composition of each assigned read



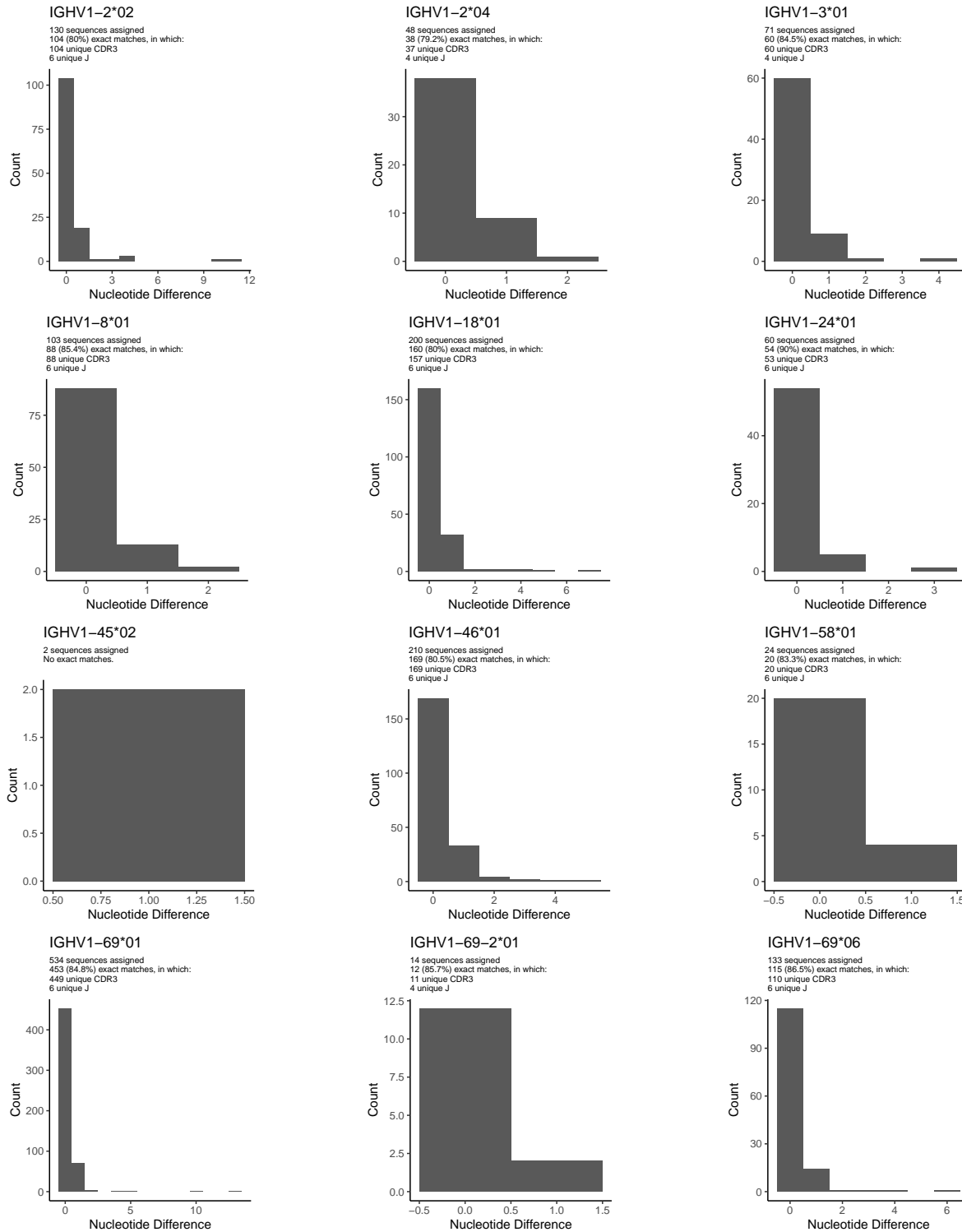
1.4 Final three nucleotides: frequency of each observed triplet

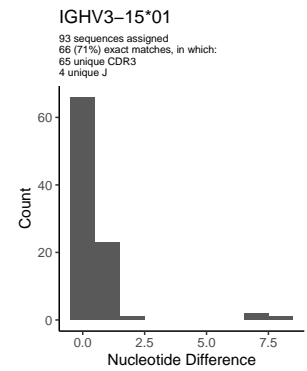
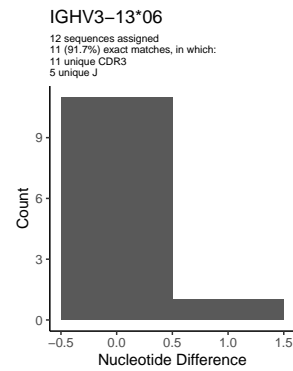
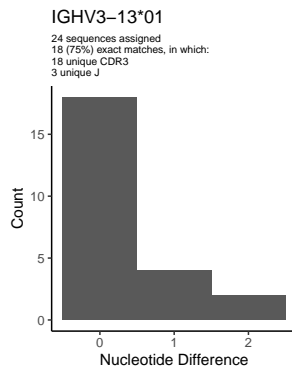
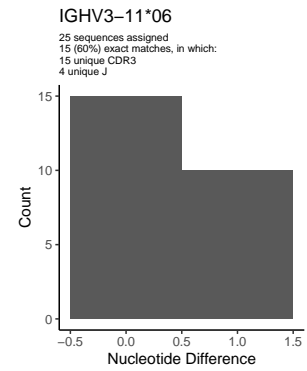
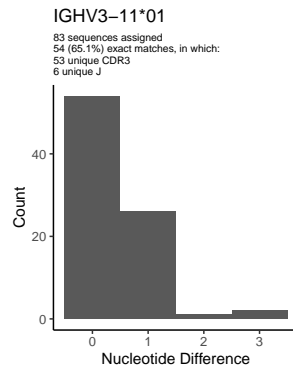
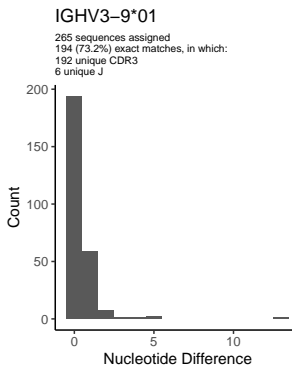
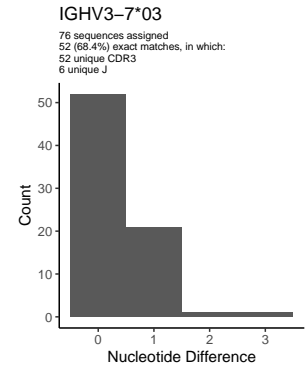
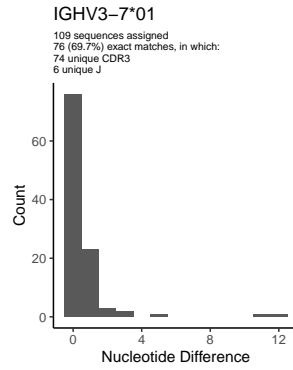
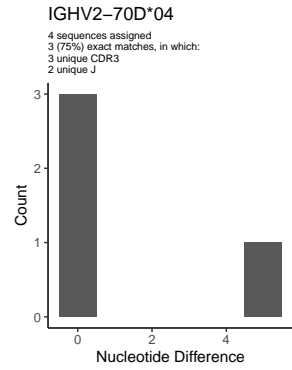
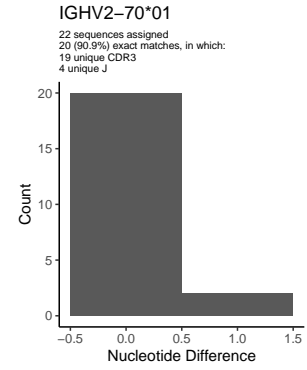
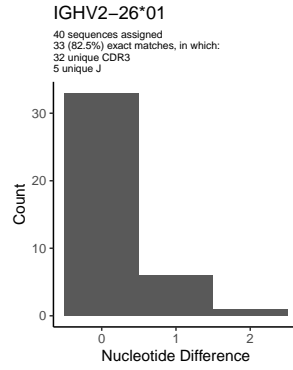
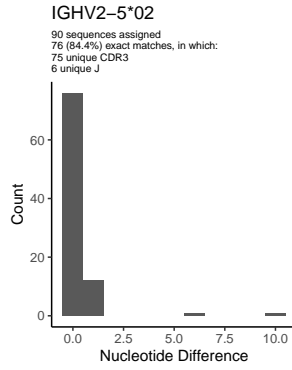


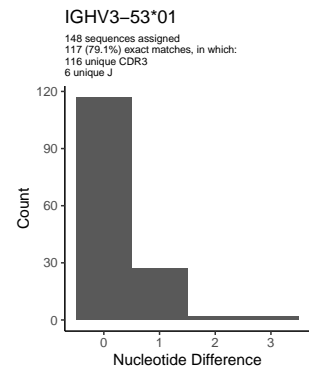
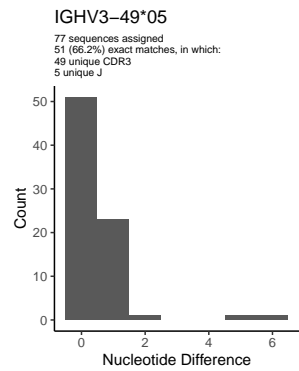
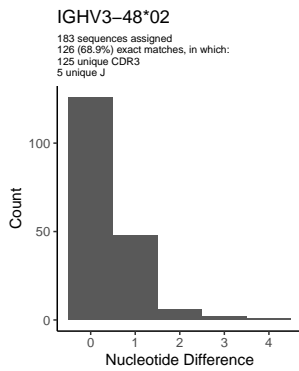
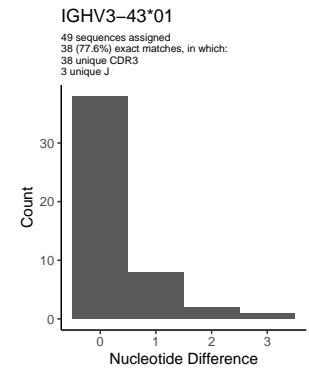
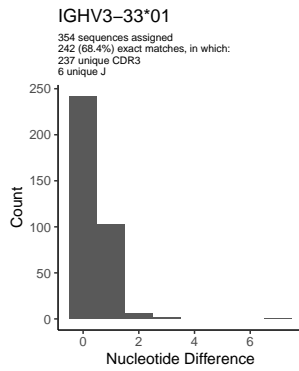
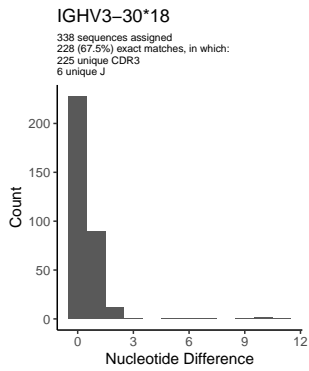
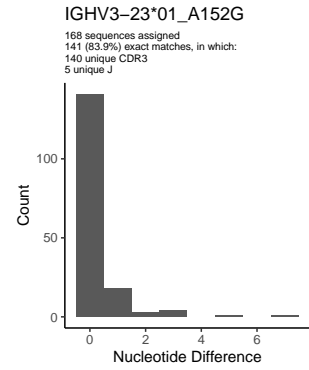
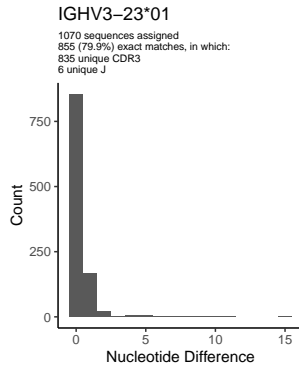
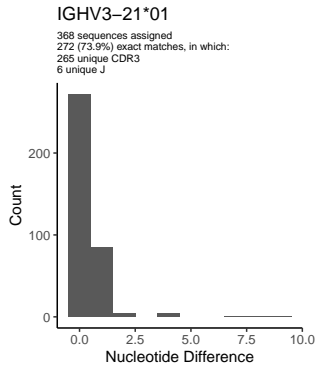
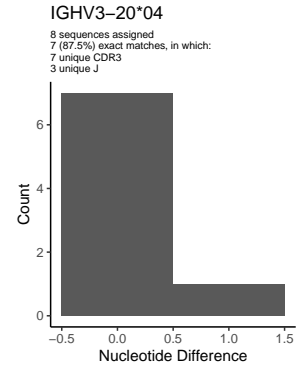
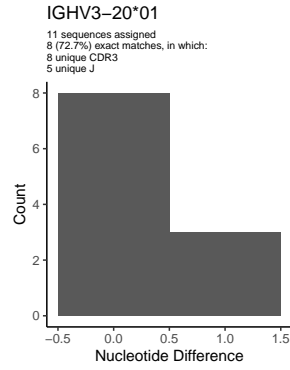
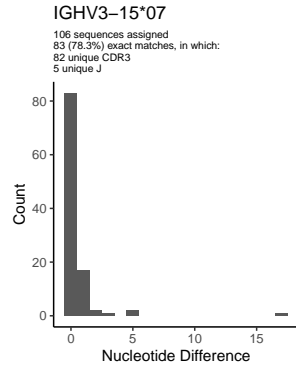
1.5 CDR3 length distribution, in assignments to novel alleles

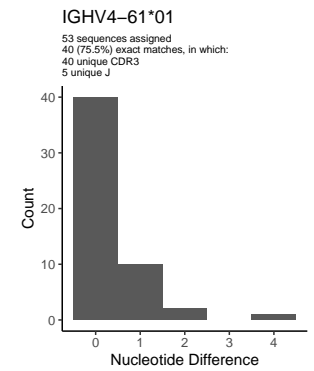
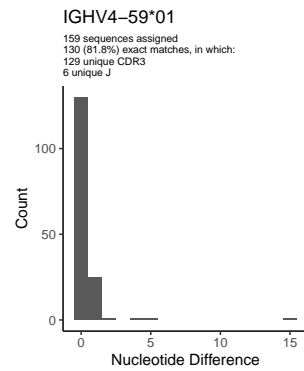
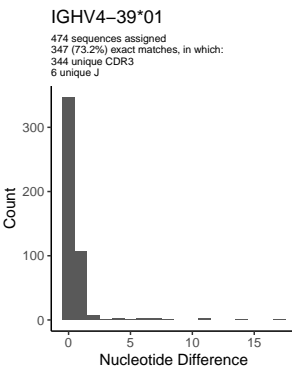
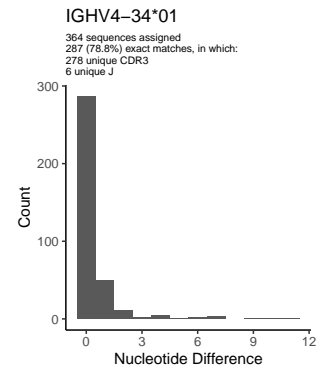
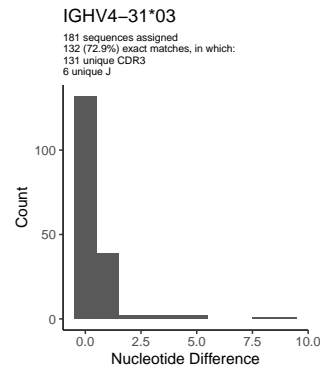
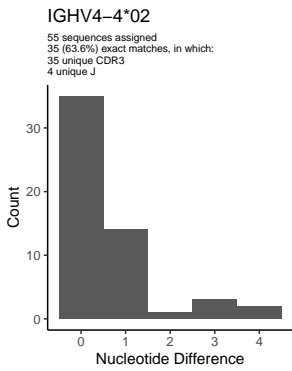
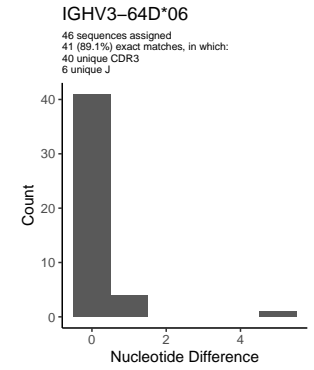
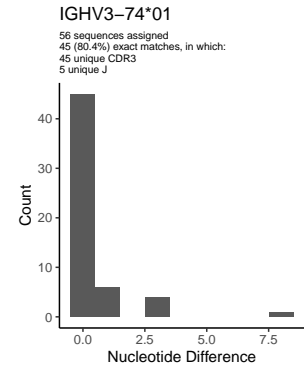
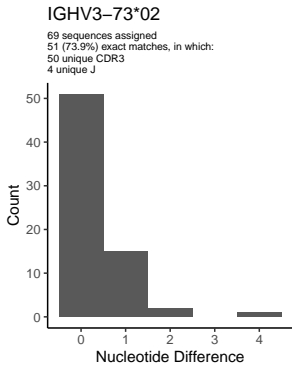
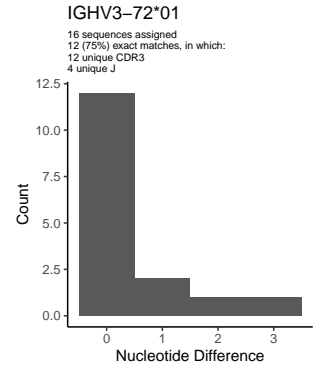
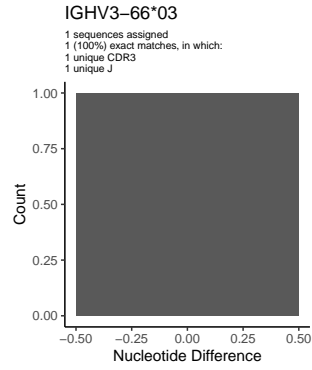
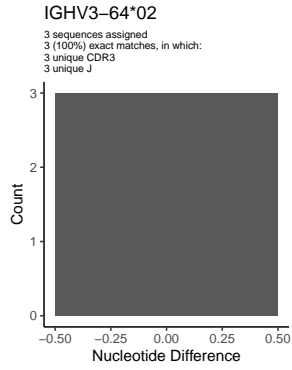


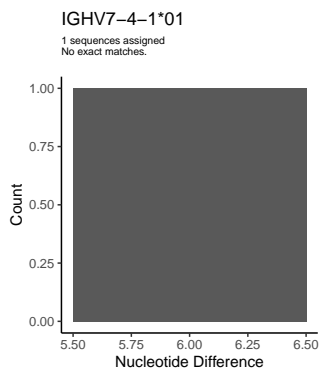
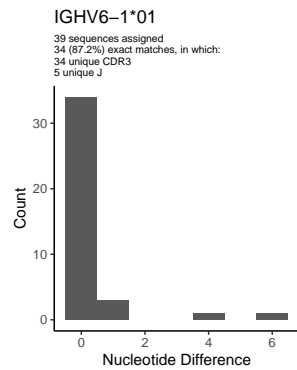
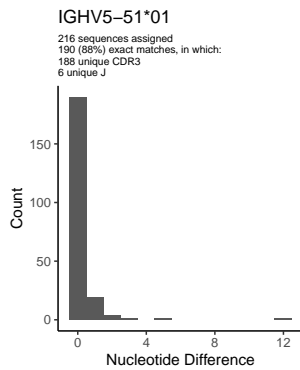
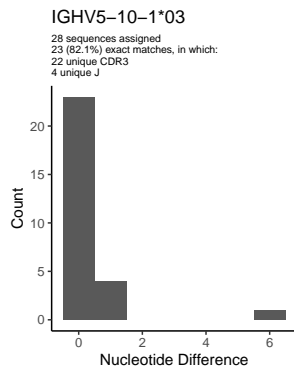
2 Variation from germline, in assignments to each allele



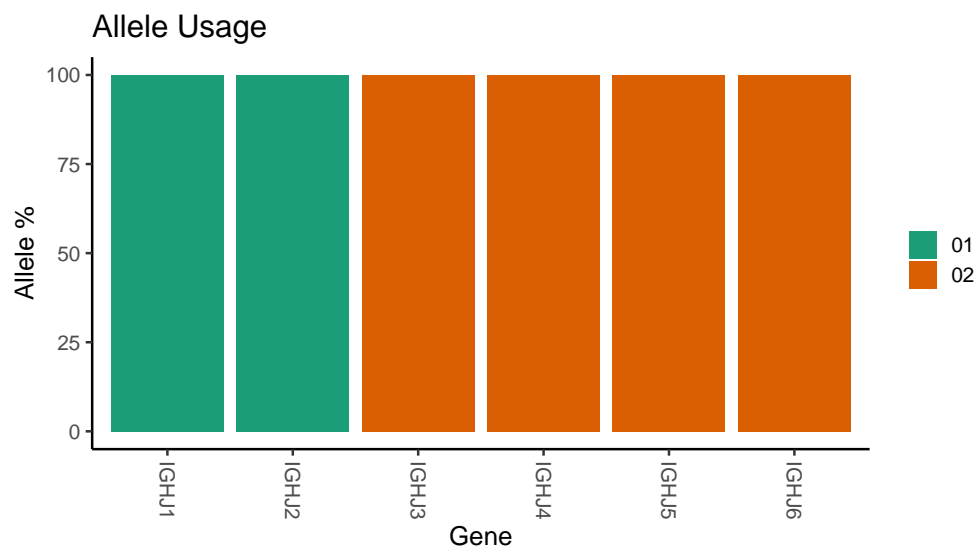








3 Allele usage in potential haplotype anchor genes



4 Haplotype plots

5 Configuration settings

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##
## Germline reference file: /misc/work/jenkins/PRJEB26509/S14/S14/14/14/2e/265accbcd0571594fd32c4573ac9
##
## Novel allele file: /misc/work/jenkins/PRJEB26509/S14/S14/14/14/2e/265accbcd0571594fd32c4573ac96b/nov
##
## Species: Homosapiens
##
## Chain: IGHV
##
## Segment: V
```