

OGRDBstats Report

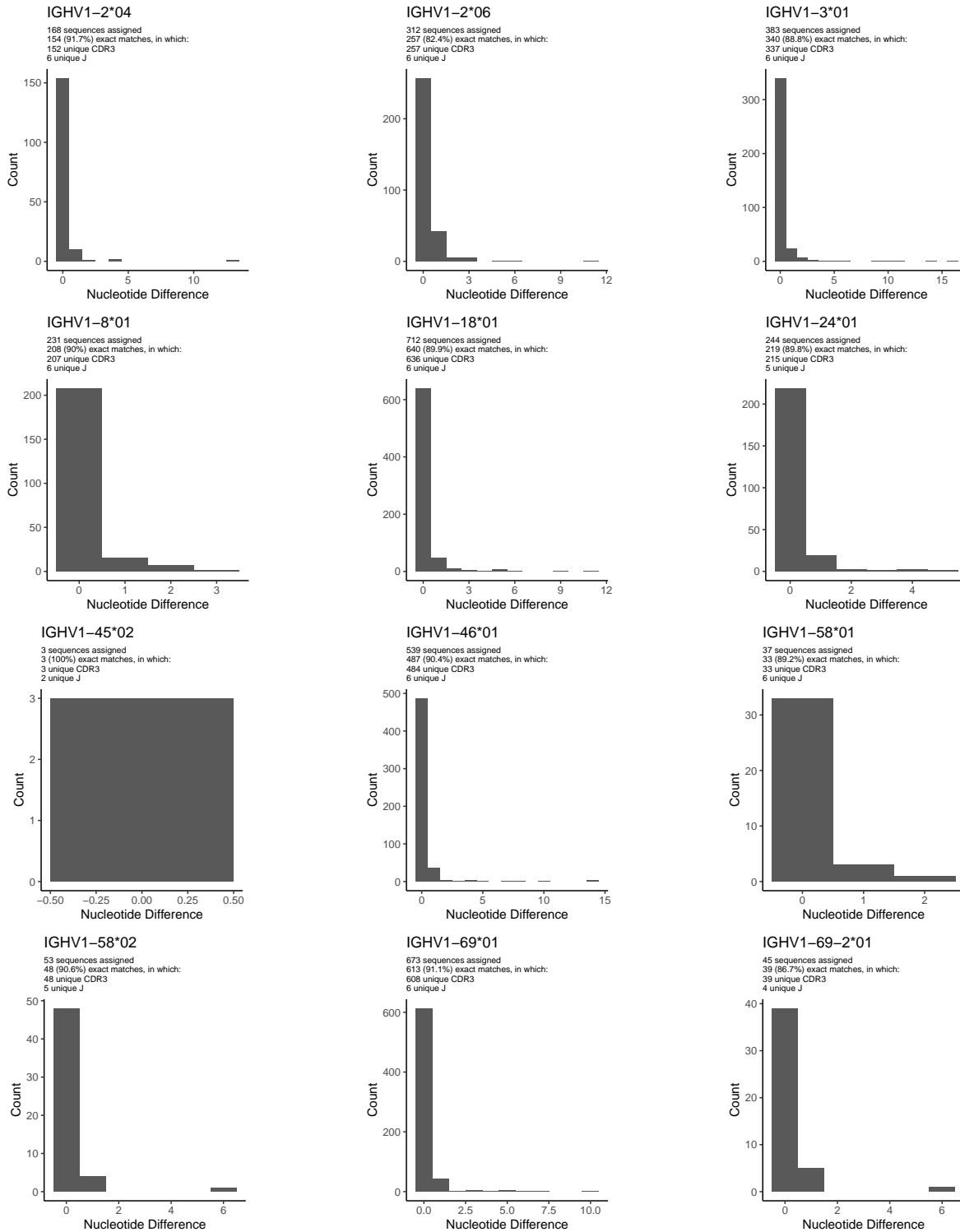
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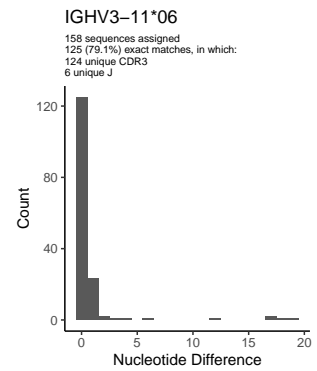
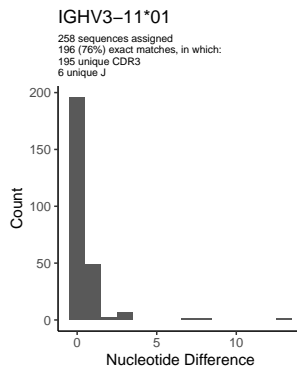
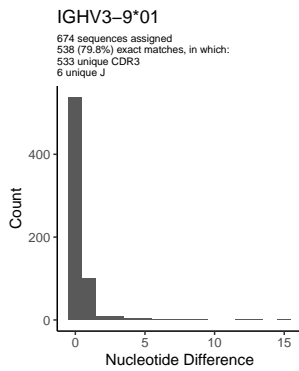
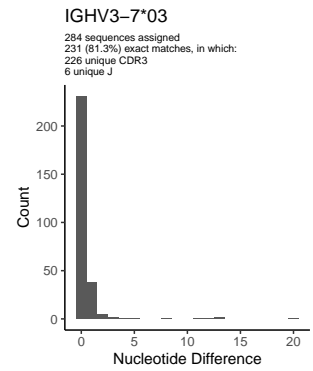
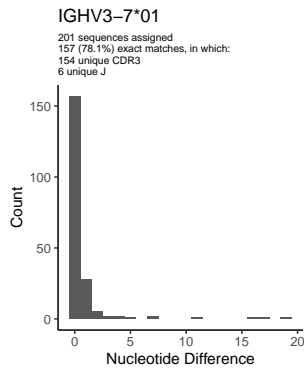
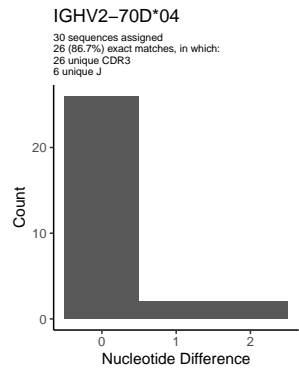
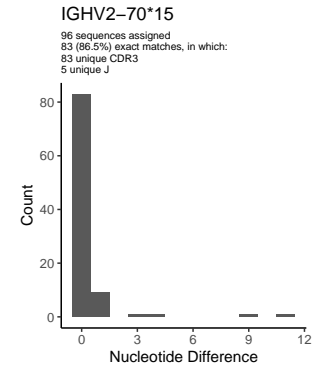
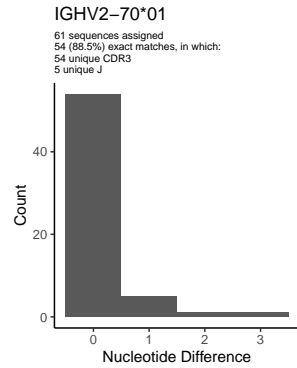
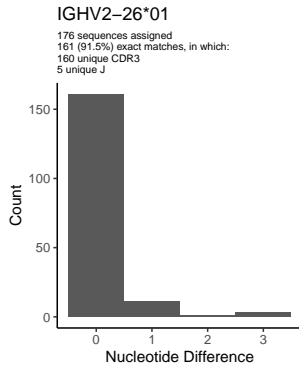
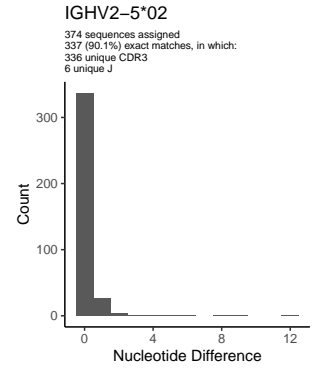
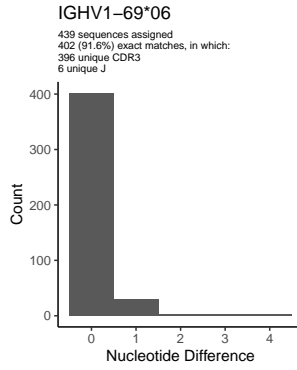
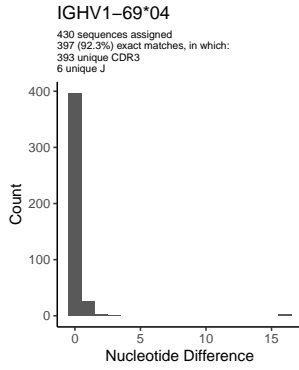
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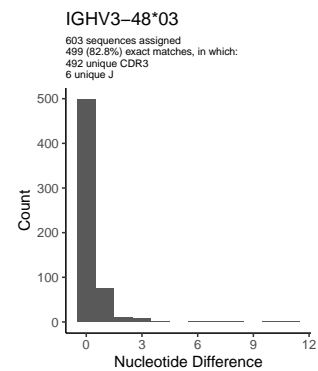
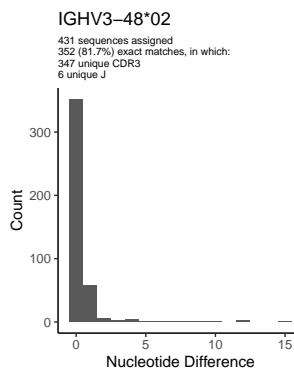
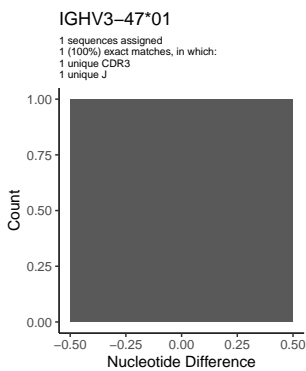
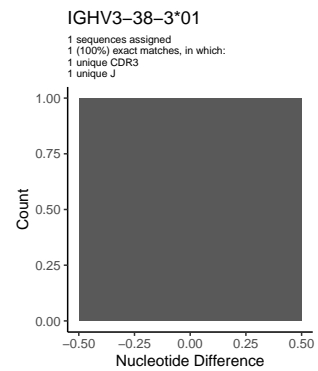
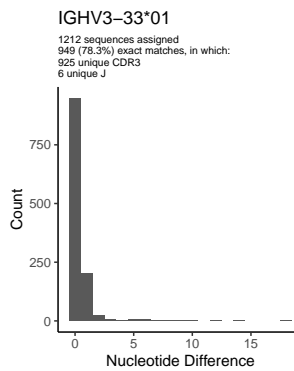
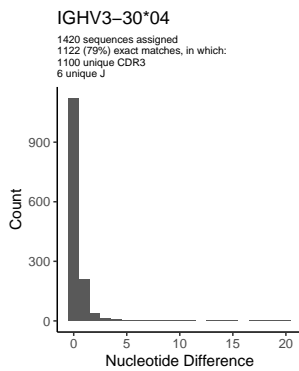
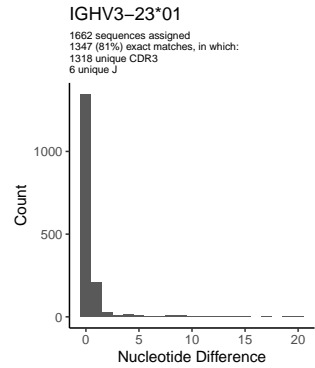
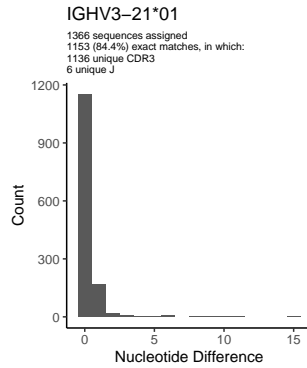
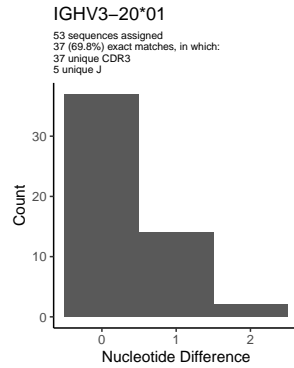
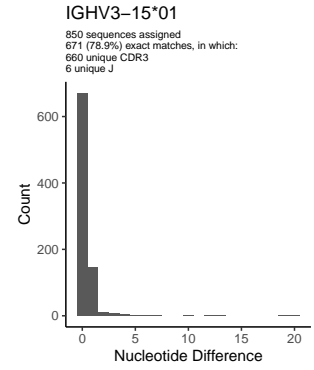
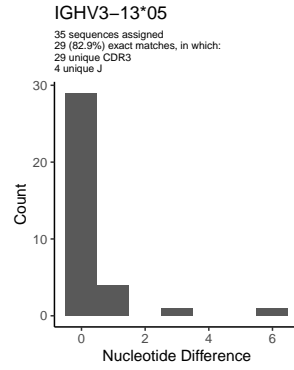
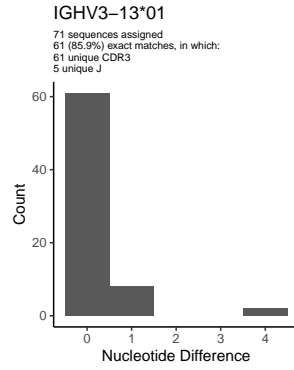
1 Novel sequence analysis

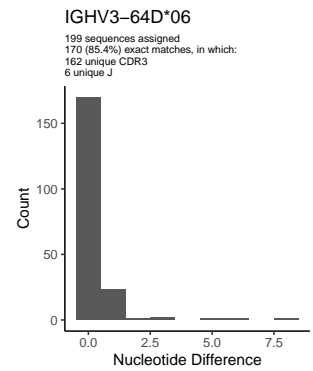
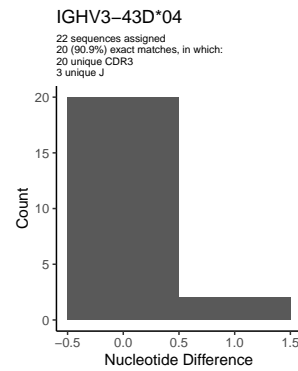
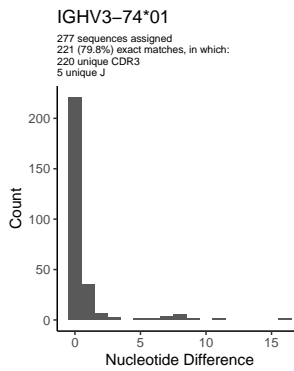
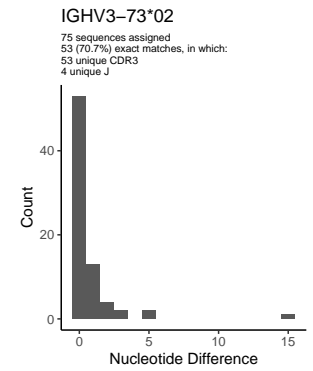
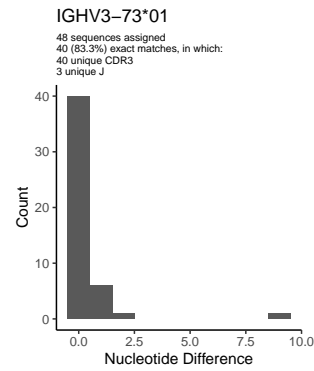
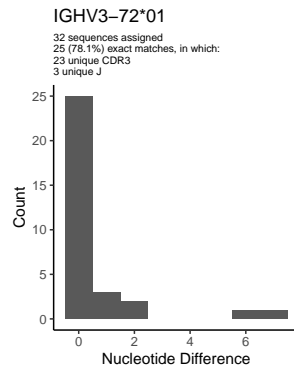
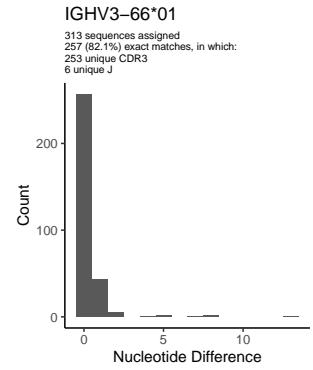
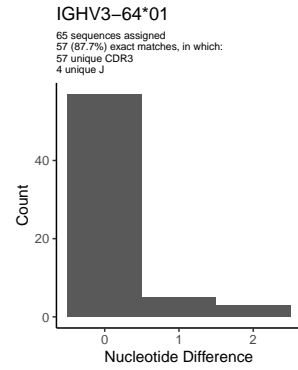
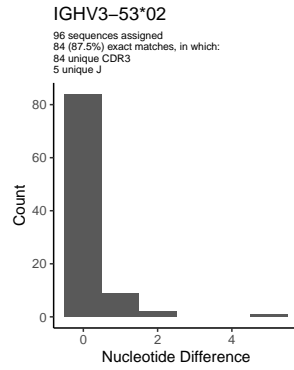
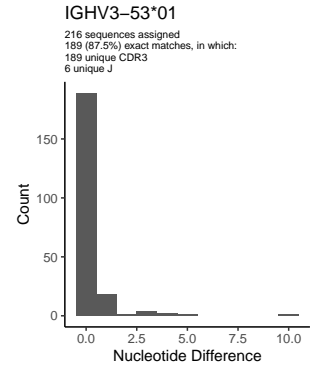
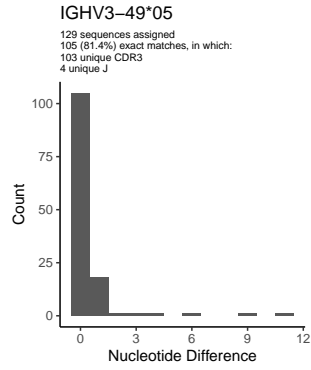
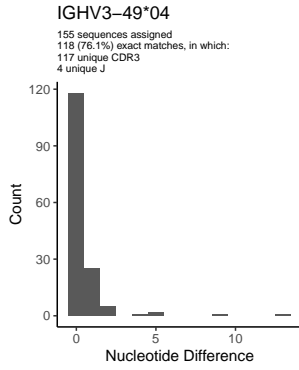
1.1 CDR3 length distribution, in assignments to novel alleles

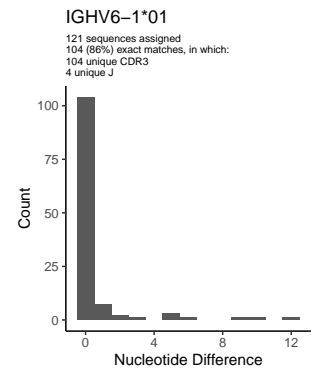
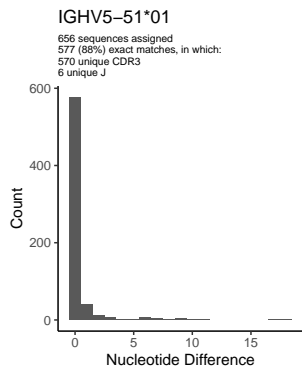
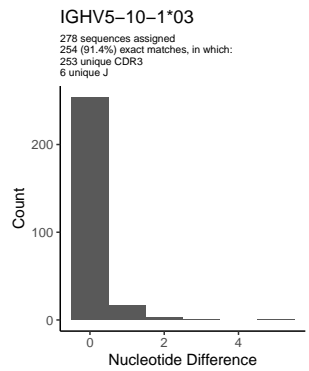
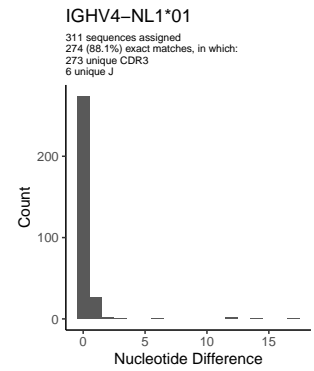
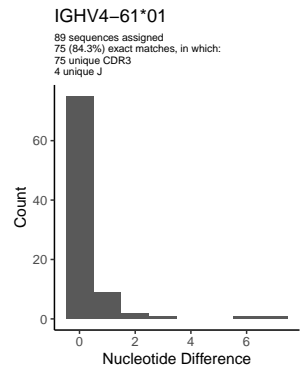
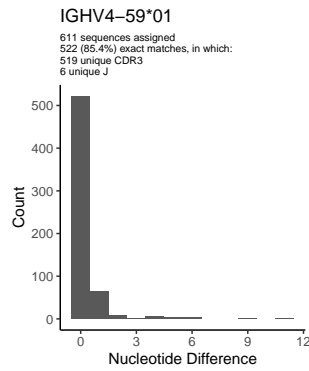
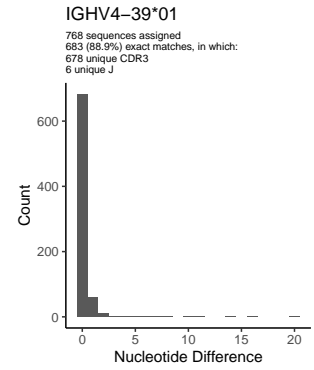
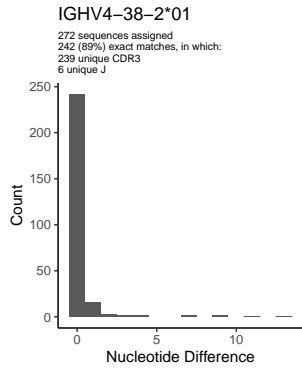
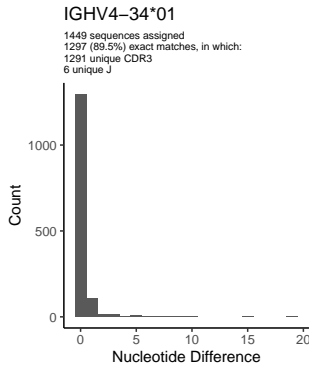
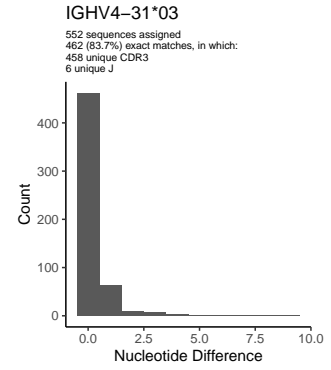
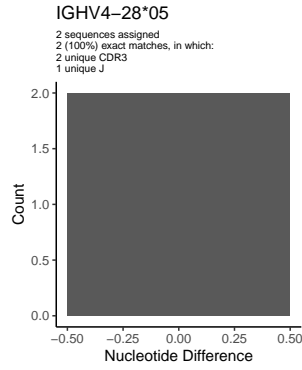
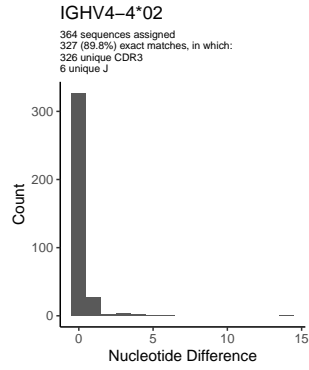
2 Variation from germline, in assignments to each allele





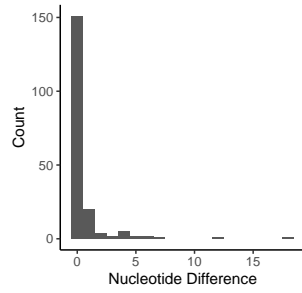




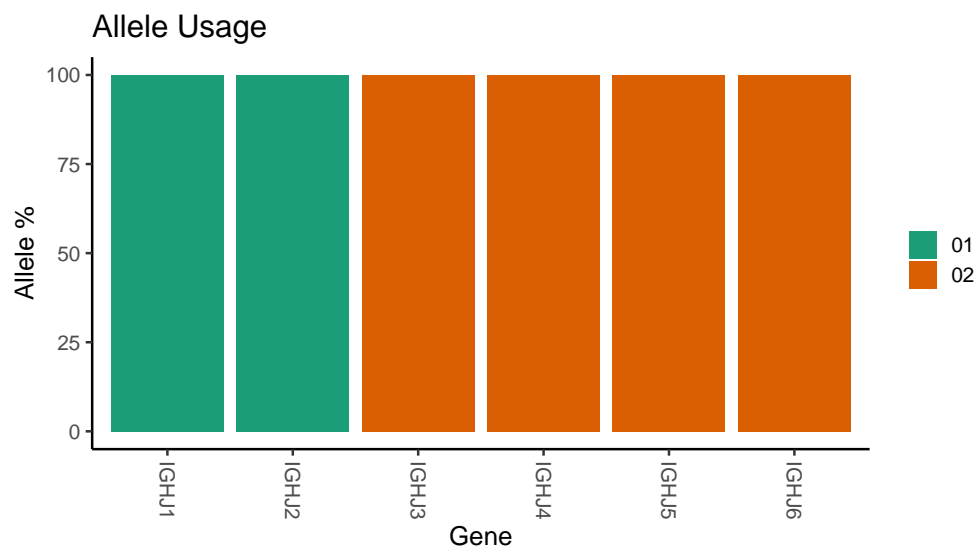


IGHV7-4-1*02

189 sequences assigned
151 (79.9%) exact matches, in which:
151 unique CDR3
6 unique J



3 Allele usage in potential haplotype anchor genes



4 Haplotype plots

5 Configuration settings

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##  
## Germline reference file: /work/jenkins/PRJEB26509/S71/S71/75/75/0f/53896f64d014401709caf873ad1ed0/re  
##  
## Novel allele file:  
##  
## Species: Homosapiens  
##  
## Chain: IGHV  
##  
## Segment: V  
##  
## Warning    no inferred sequences found.
```