

OGRDBstats Report

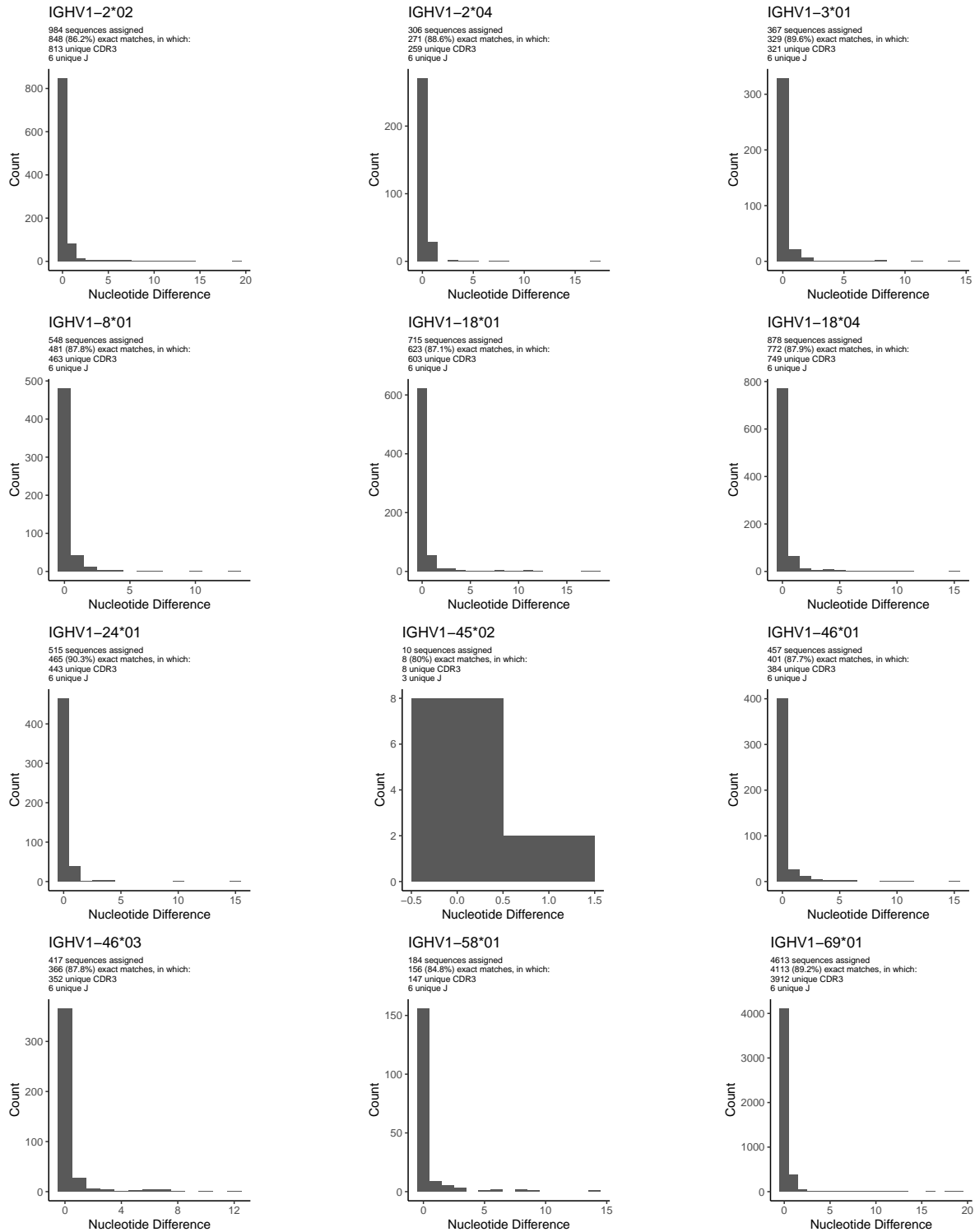
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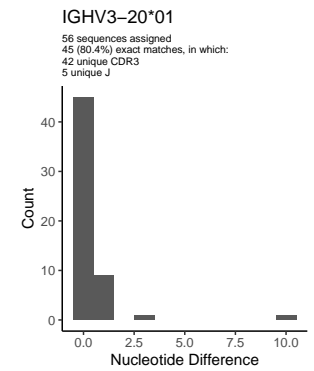
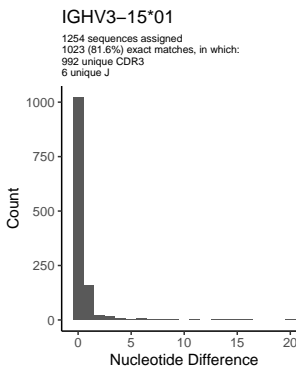
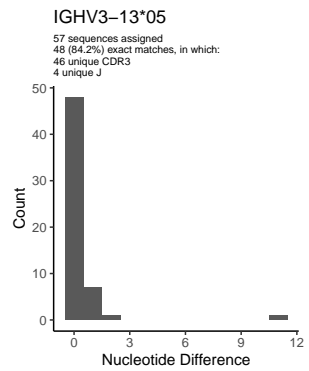
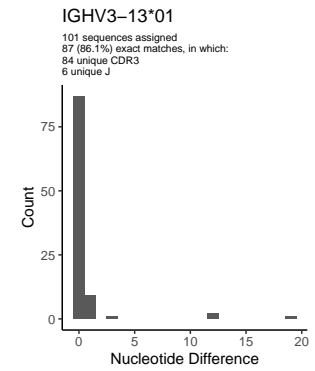
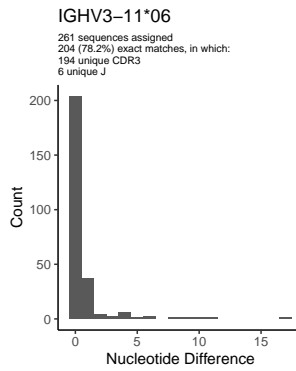
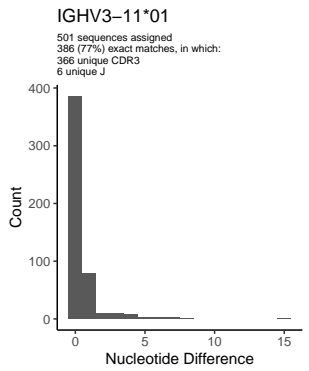
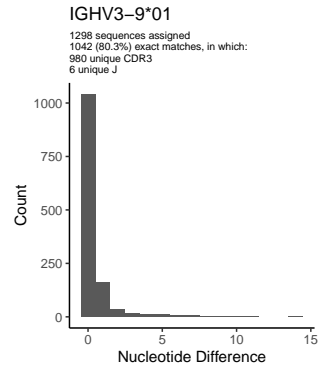
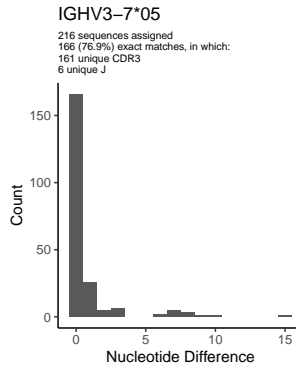
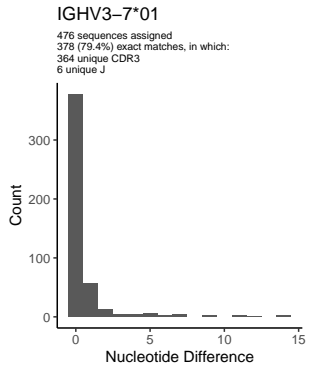
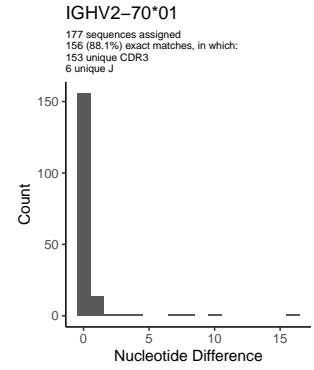
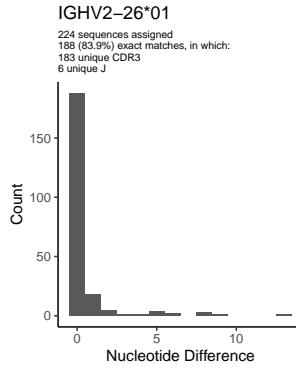
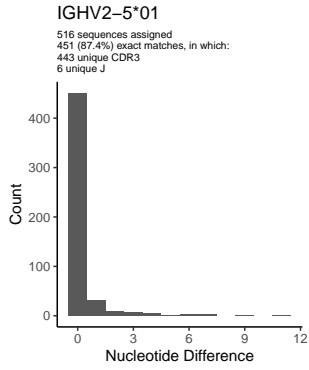
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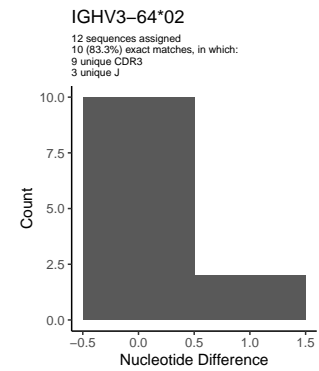
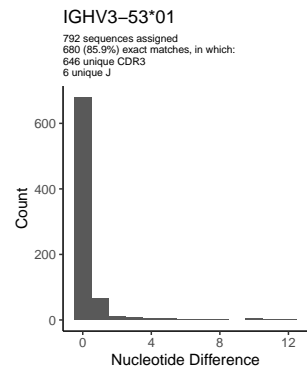
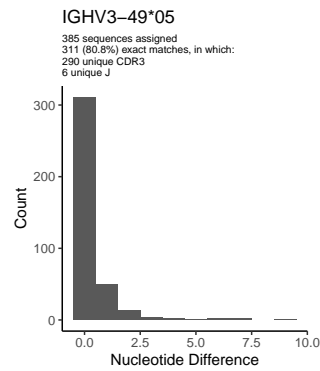
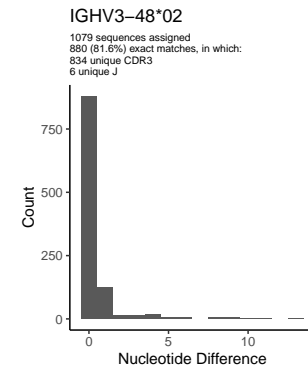
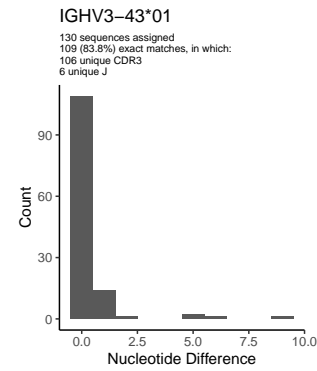
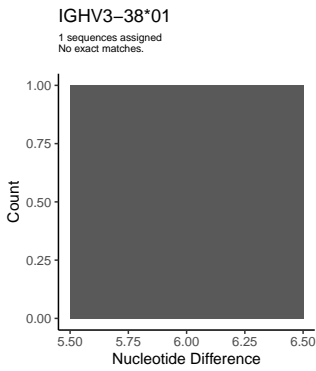
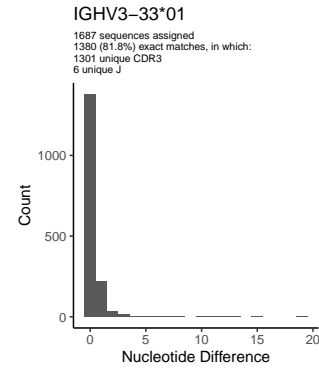
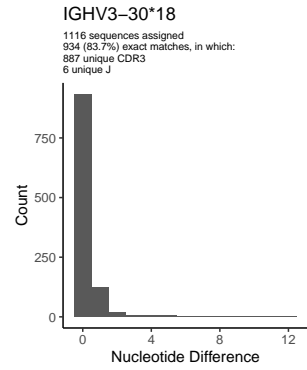
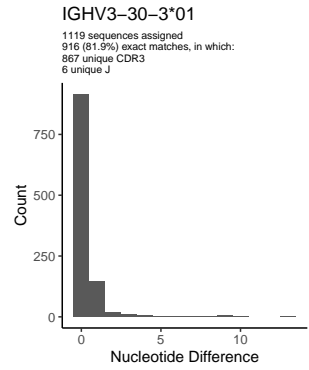
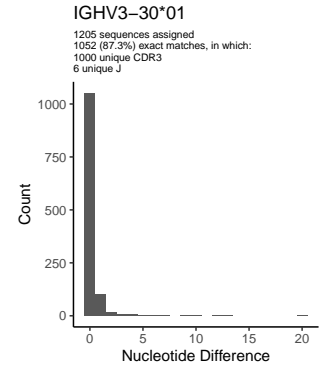
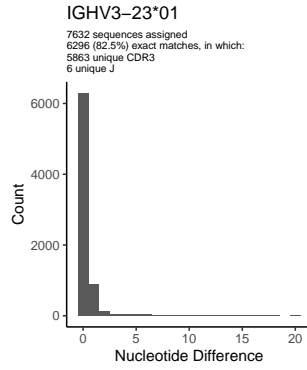
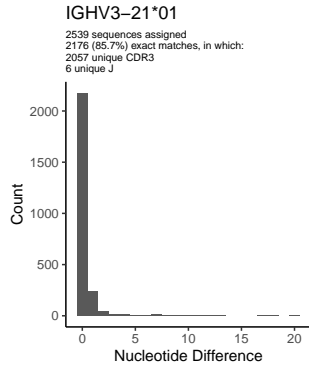
1 Novel sequence analysis

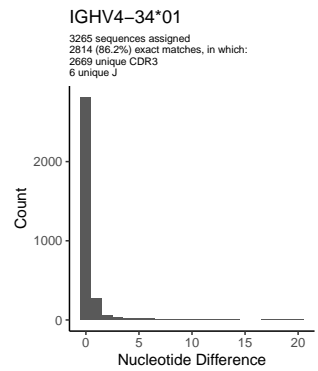
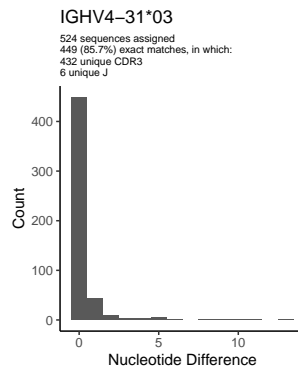
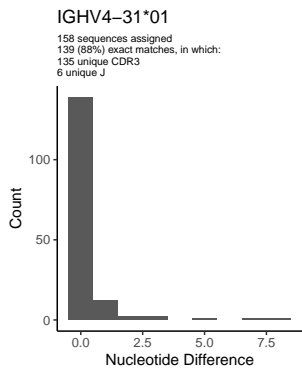
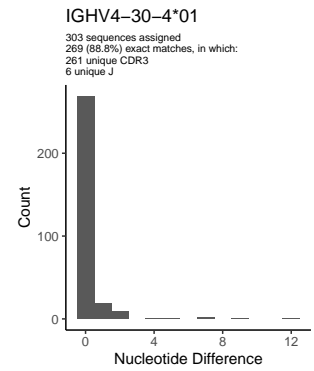
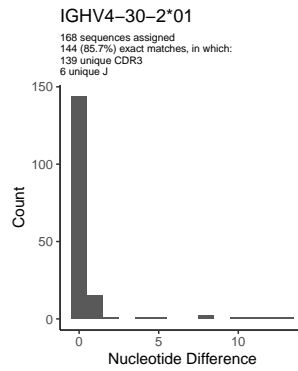
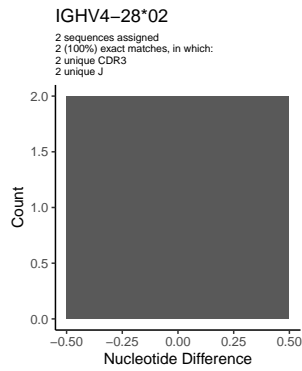
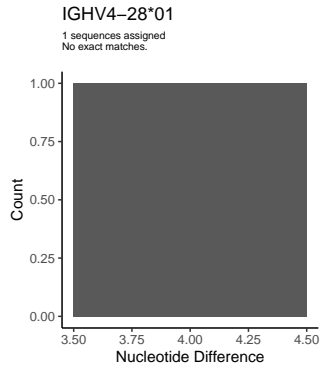
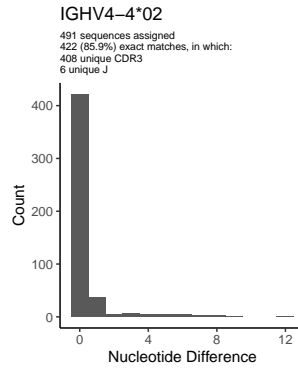
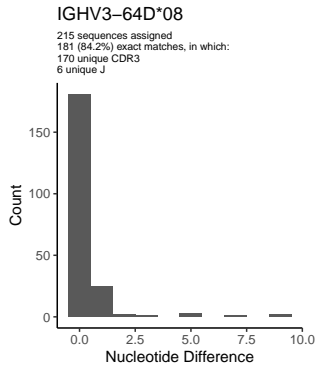
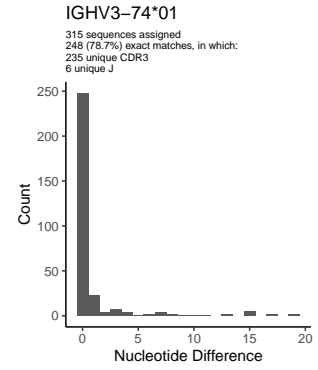
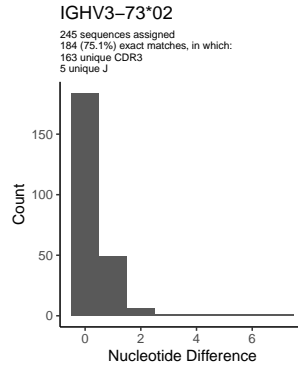
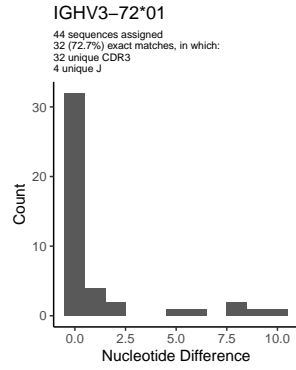
1.1 CDR3 length distribution, in assignments to novel alleles

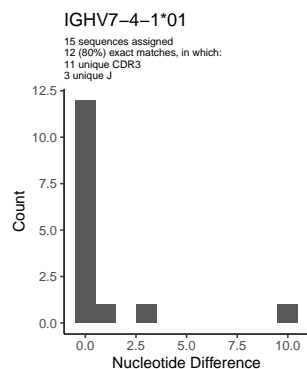
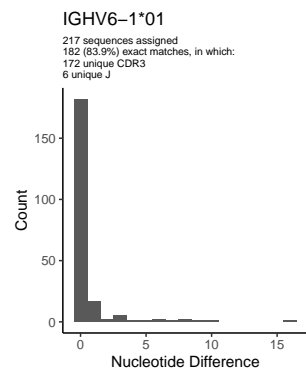
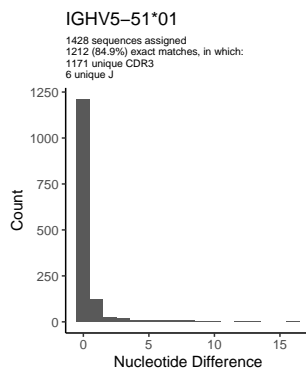
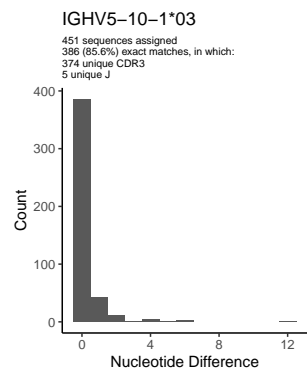
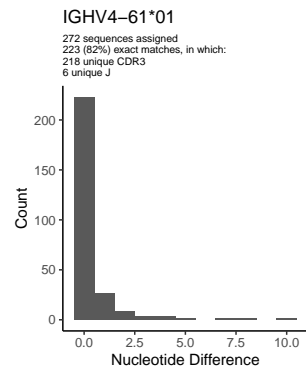
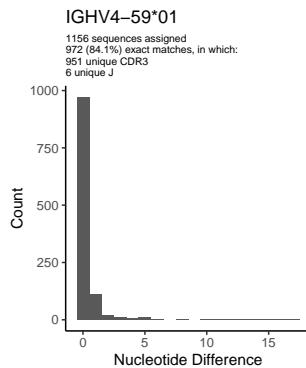
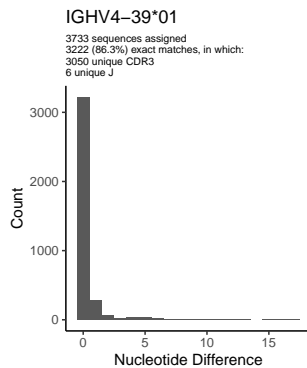
2 Variation from germline, in assignments to each allele











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/S68/S68/72/72/84/db7462b903125bf883fe8360c1d0
##
## Novel allele file:
##
## Species: Homosapiens
##
## Chain: IGHV
##
## Segment: V
##
## Warning    no inferred sequences found.
```