

OGRDBstats Report

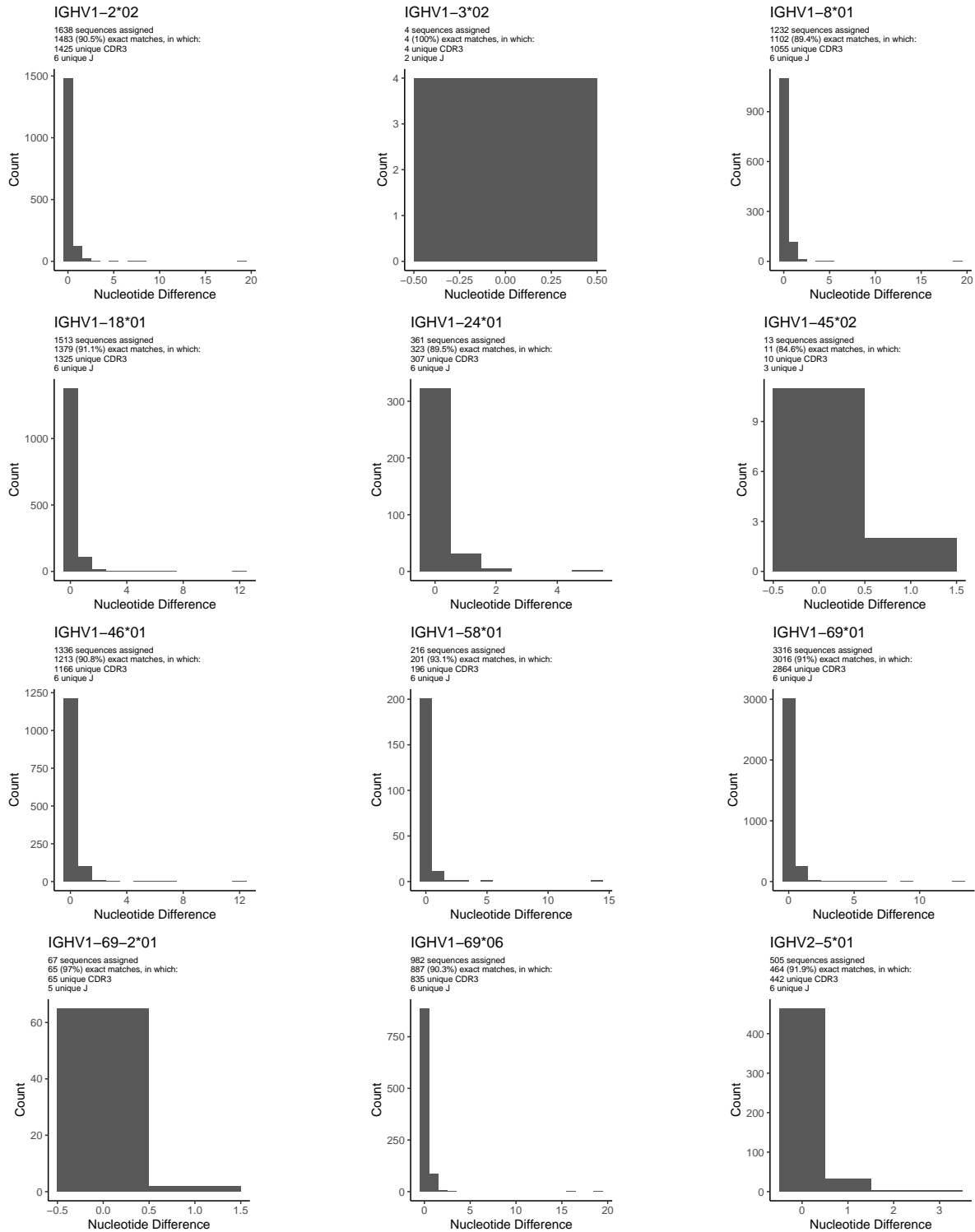
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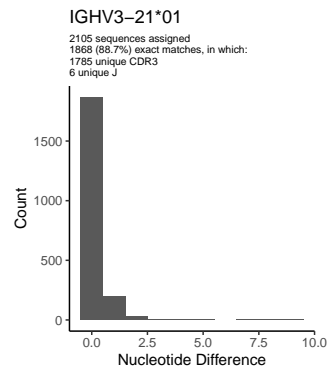
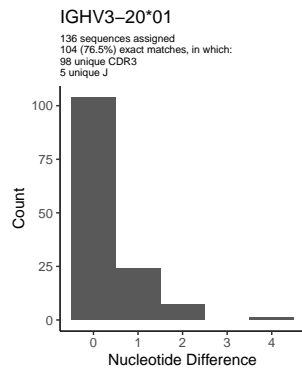
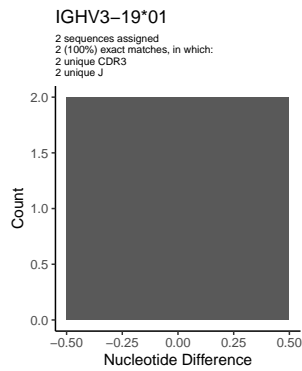
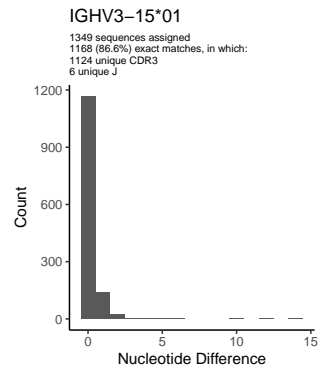
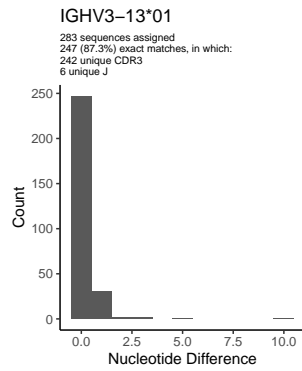
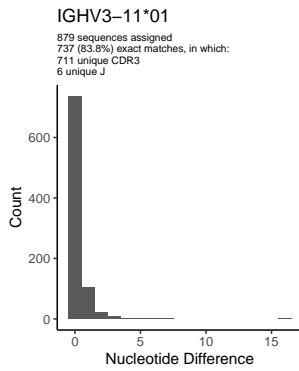
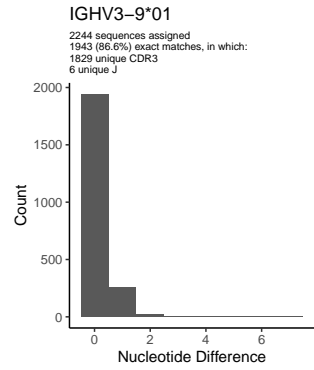
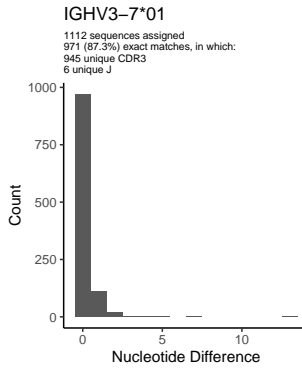
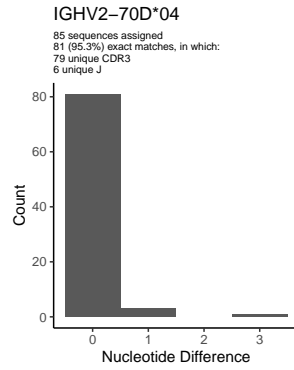
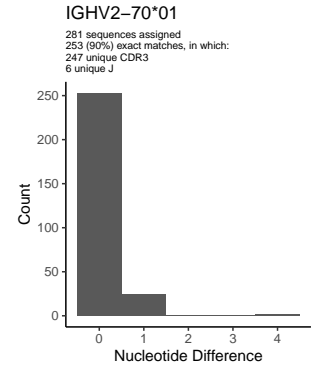
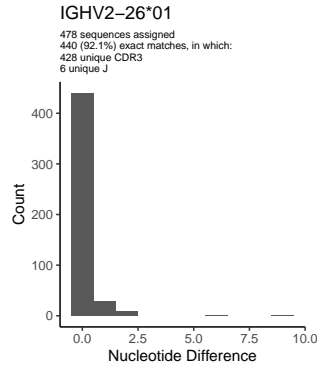
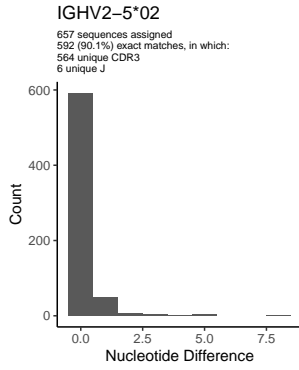
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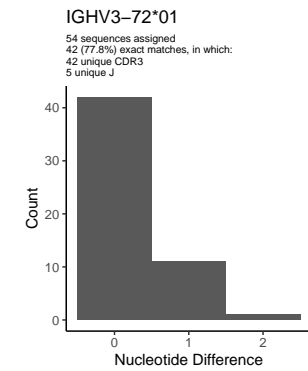
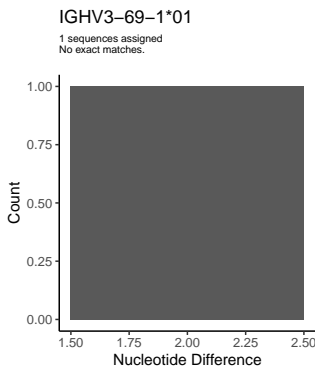
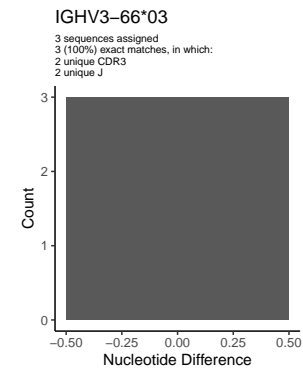
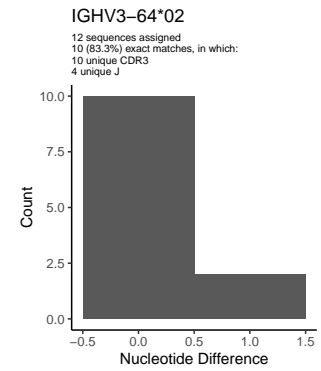
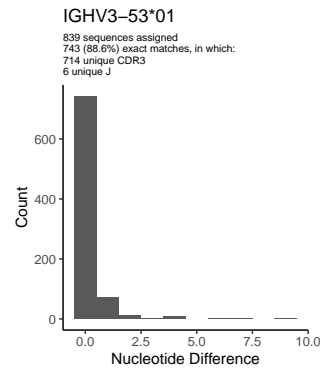
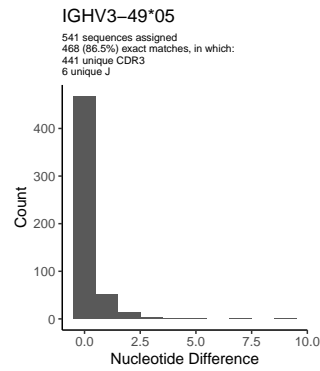
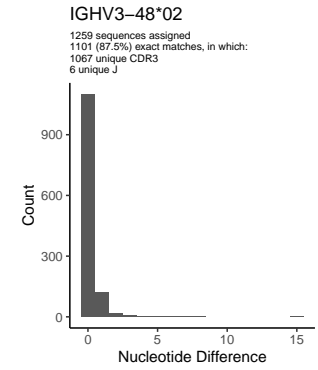
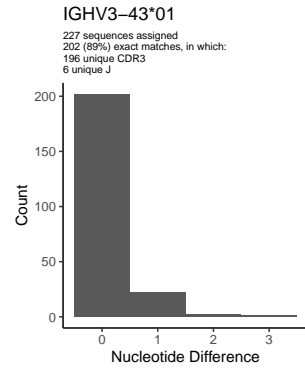
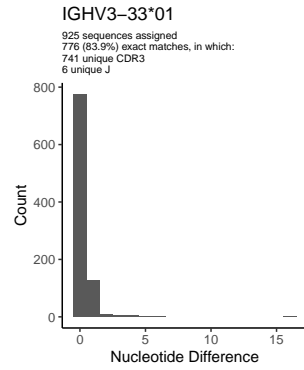
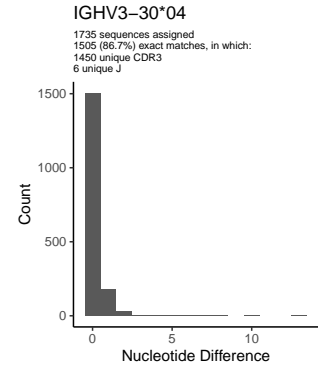
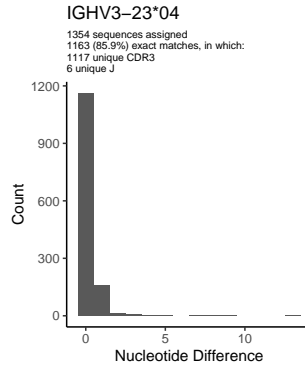
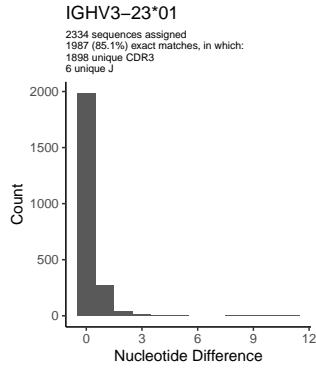
1 Novel sequence analysis

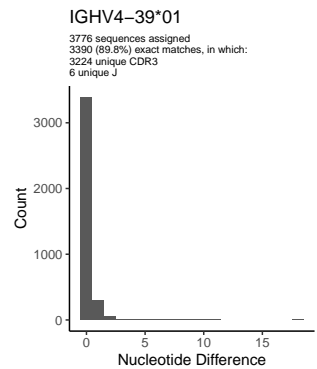
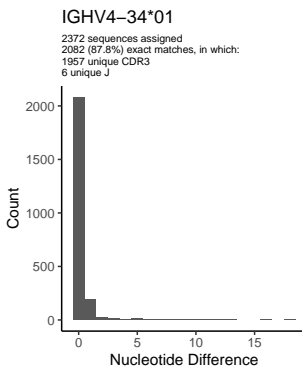
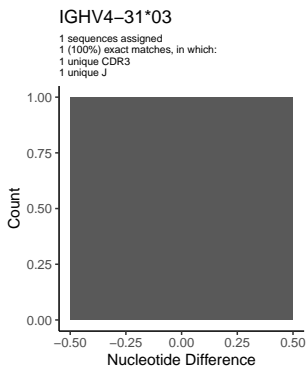
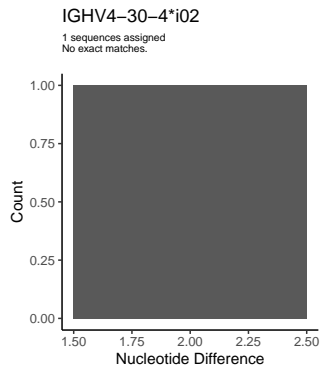
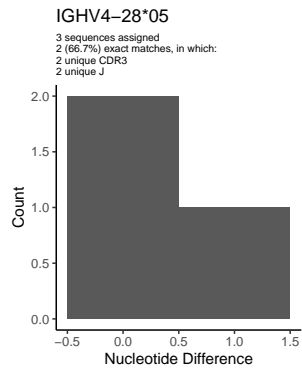
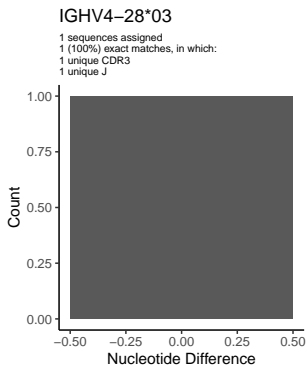
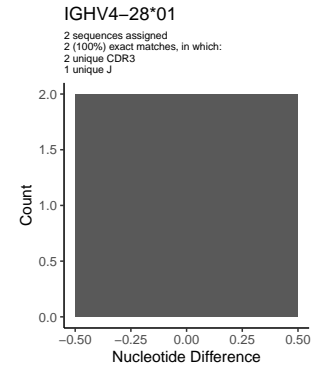
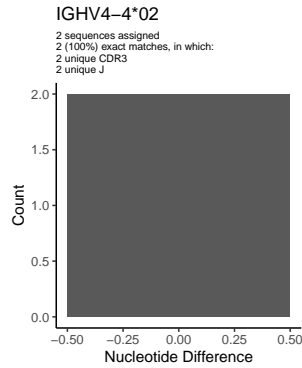
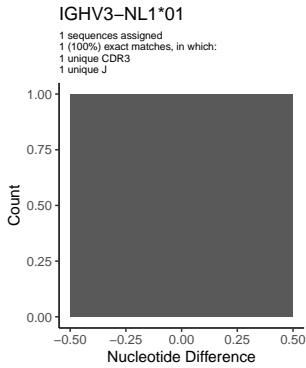
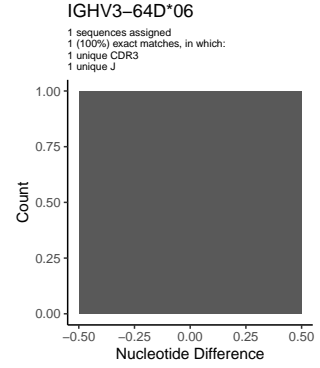
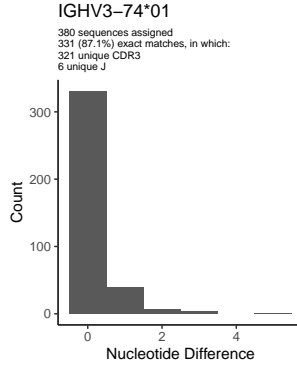
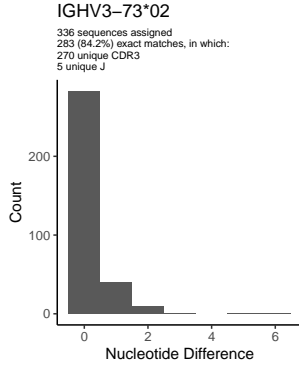
1.1 CDR3 length distribution, in assignments to novel alleles

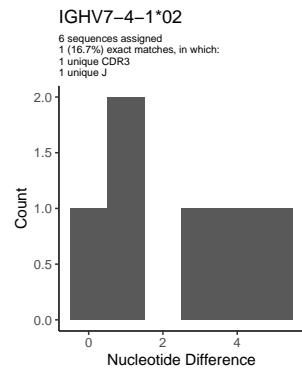
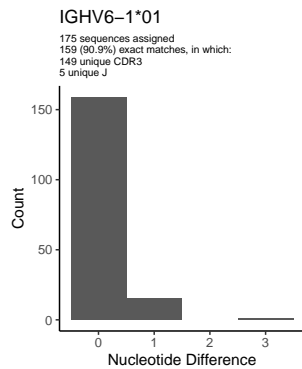
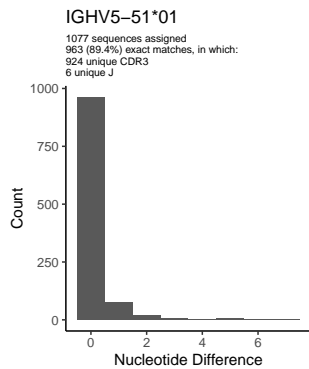
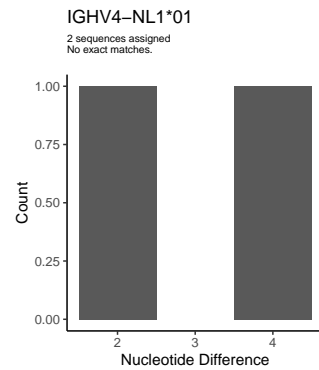
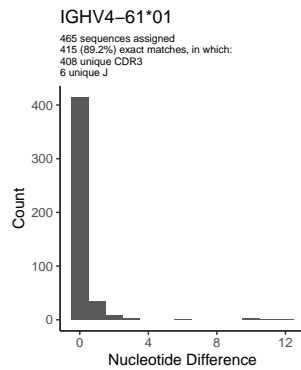
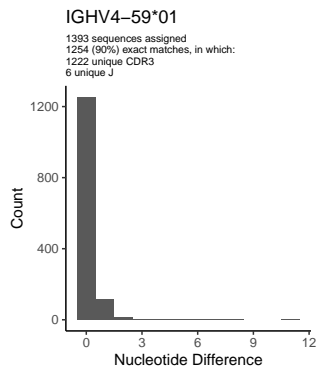
2 Variation from germline, in assignments to each allele











3 Allele usage in potential haplotype anchor genes



4 Haplotype plots

5 Configuration settings

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## Repertoire file: /misc/work/jenkins/PRJEB26509/S51/S51/54/54/38/93920276eb5b32fc8375da064435da/54_Fi
##
## Germline reference file: /misc/work/jenkins/PRJEB26509/S51/S51/54/54/fd/8dce70bae10d9f8c2f38ddd32985
##
## Novel allele file:
##
## Species: Homosapiens
##
## Chain: IGHV
##
## Segment: V
##
## Warning    no inferred sequences found.
```