

OGRDBstats Report

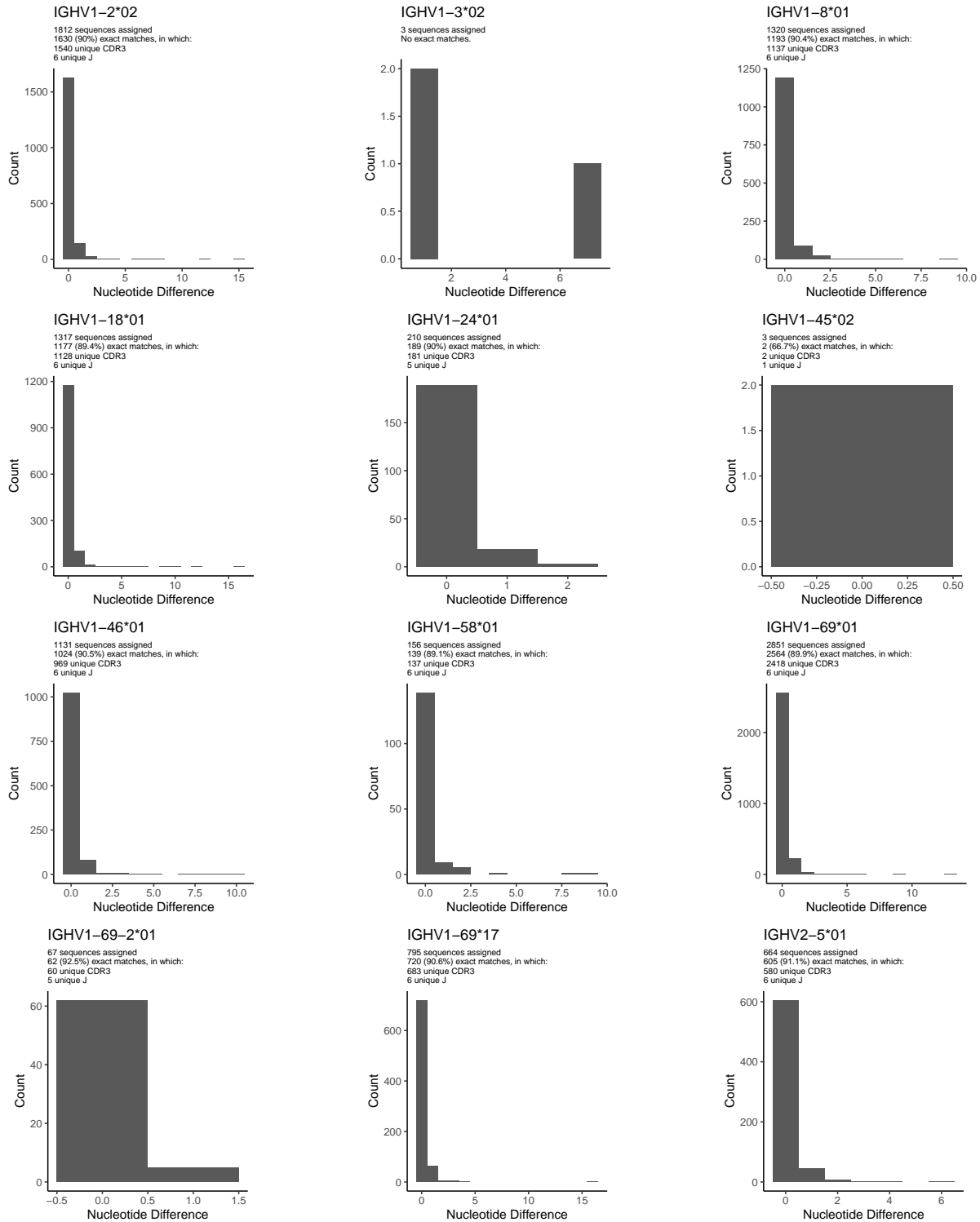
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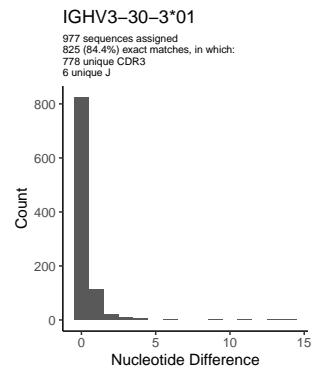
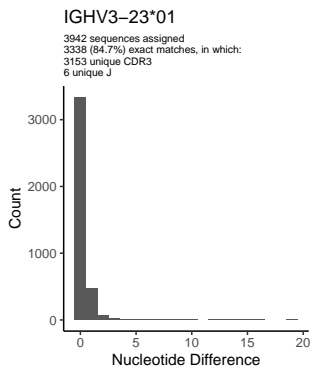
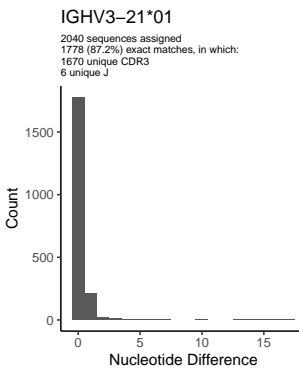
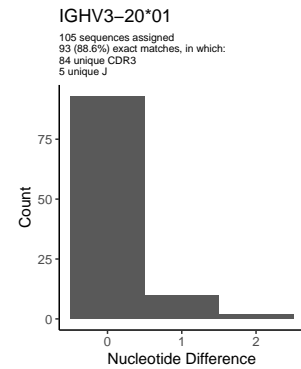
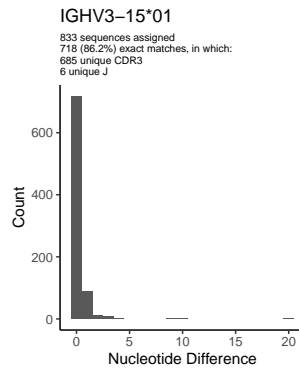
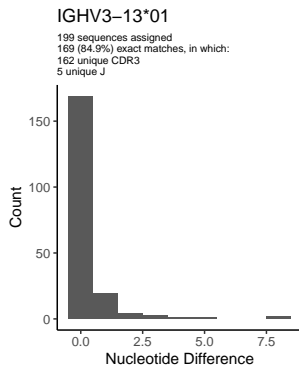
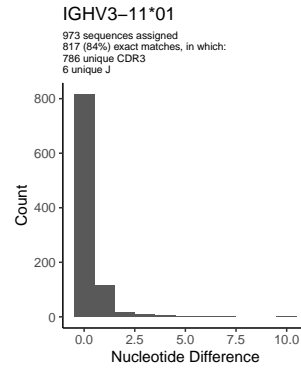
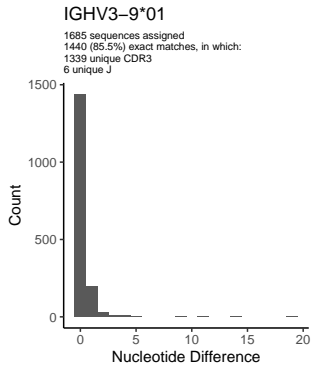
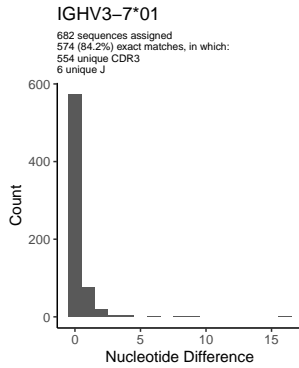
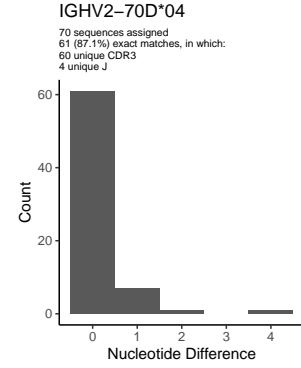
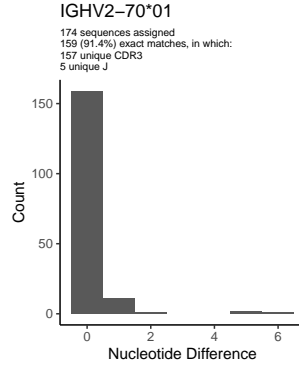
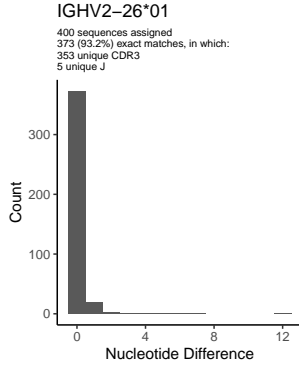
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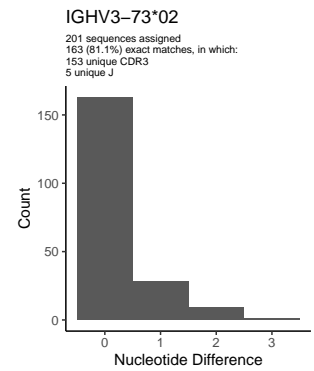
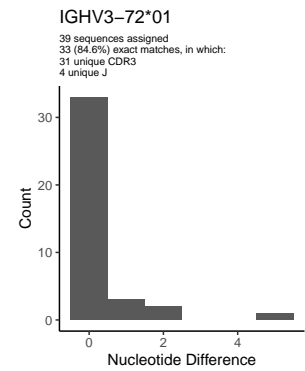
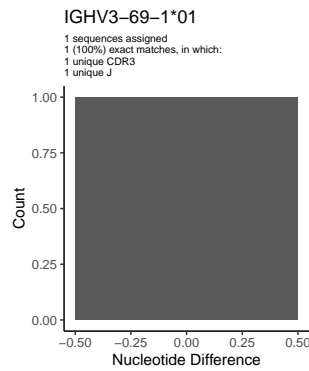
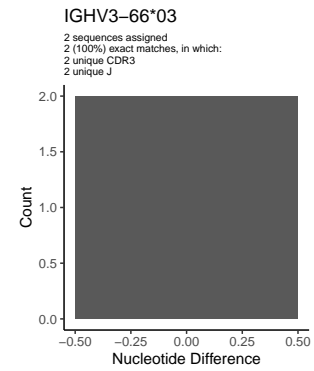
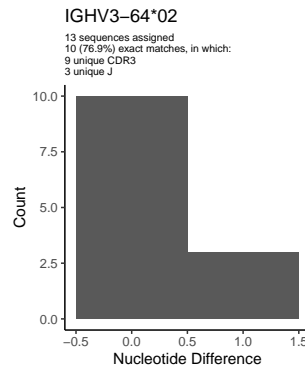
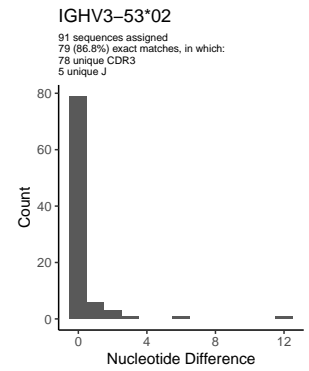
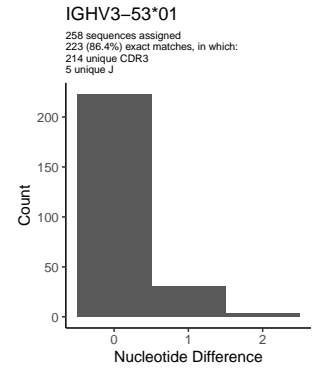
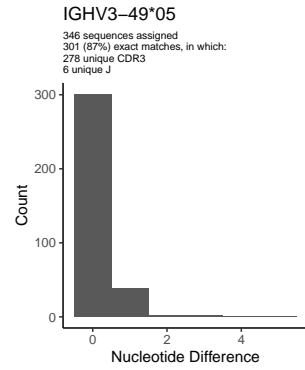
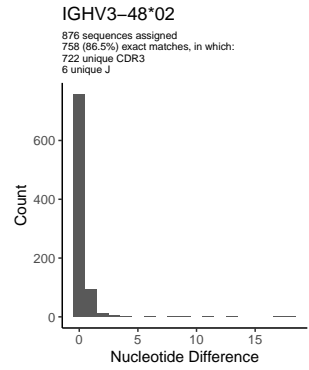
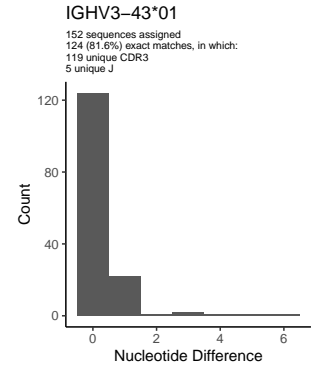
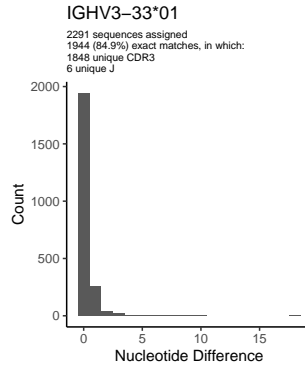
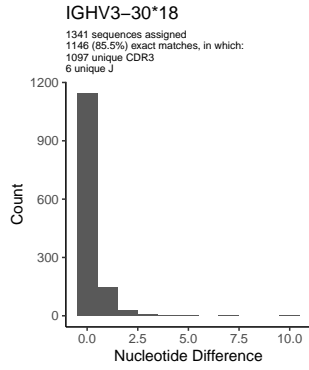
1 Novel sequence analysis

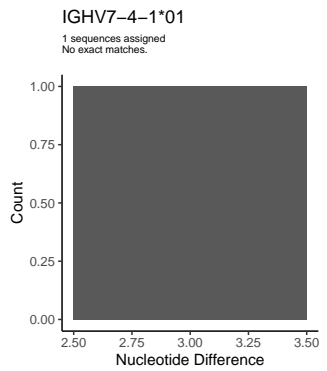
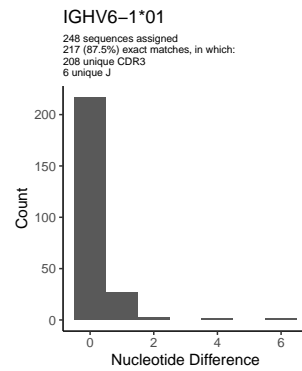
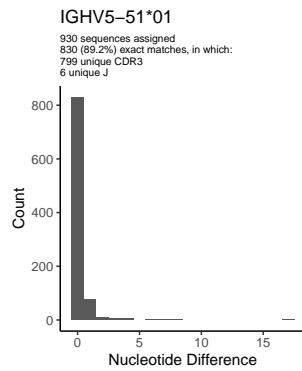
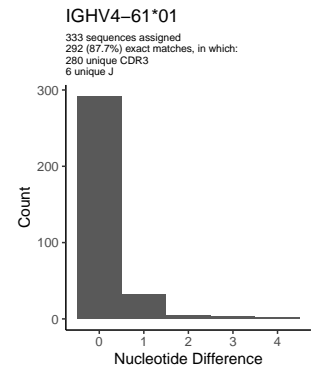
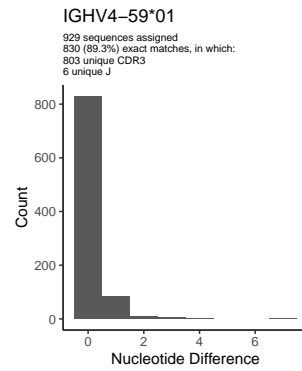
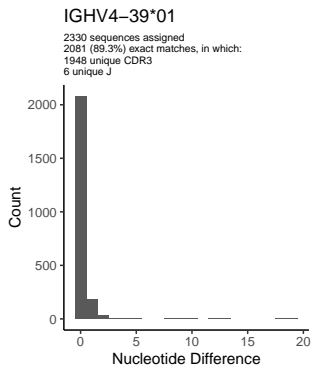
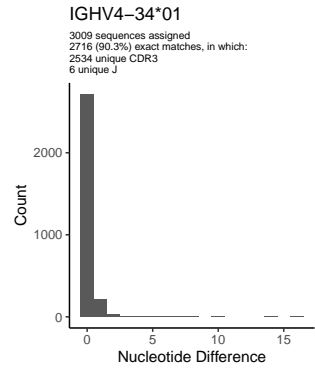
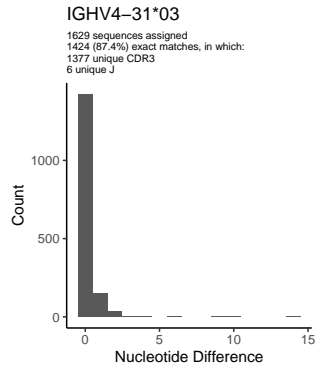
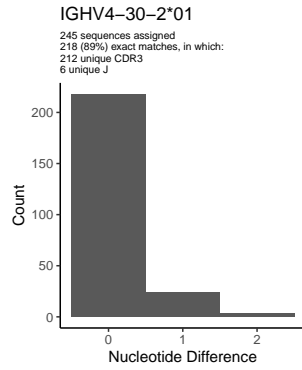
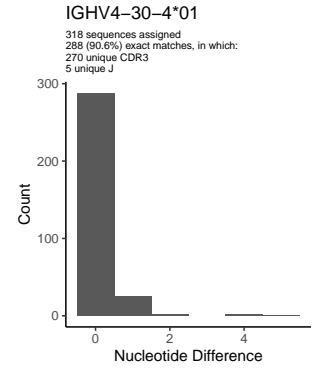
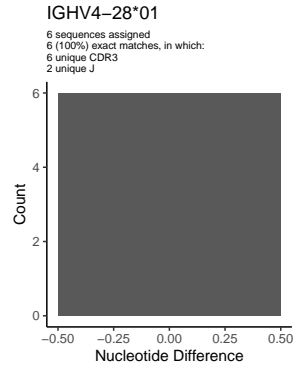
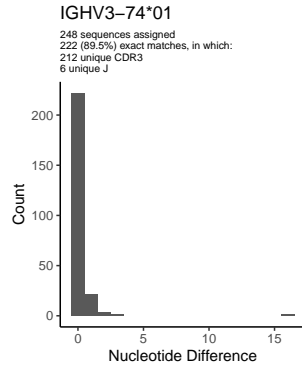
1.1 CDR3 length distribution, in assignments to novel alleles

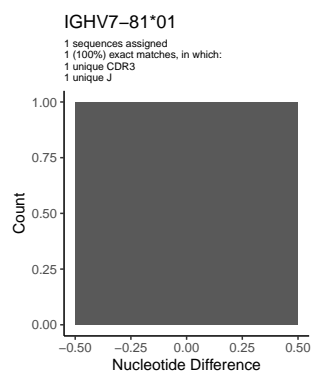
2 Variation from germline, in assignments to each allele











3 Allele usage in potential haplotype anchor genes



4 Haplotype plots

5 Configuration settings

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## Repertoire file: /misc/work/jenkins/PRJEB26509/S61/S61/65/65/93/c676e88a9fe2729ad63700da714d4a/65_Fi
##
## Germline reference file: /misc/work/jenkins/PRJEB26509/S61/S61/65/65/70/51a8eff0abb9a8b6af2e5f781286
##
## Novel allele file:
##
## Species: Homosapiens
##
## Chain: IGHV
##
## Segment: V
##
## Warning    no inferred sequences found.
```