

# OGRDBstats Report

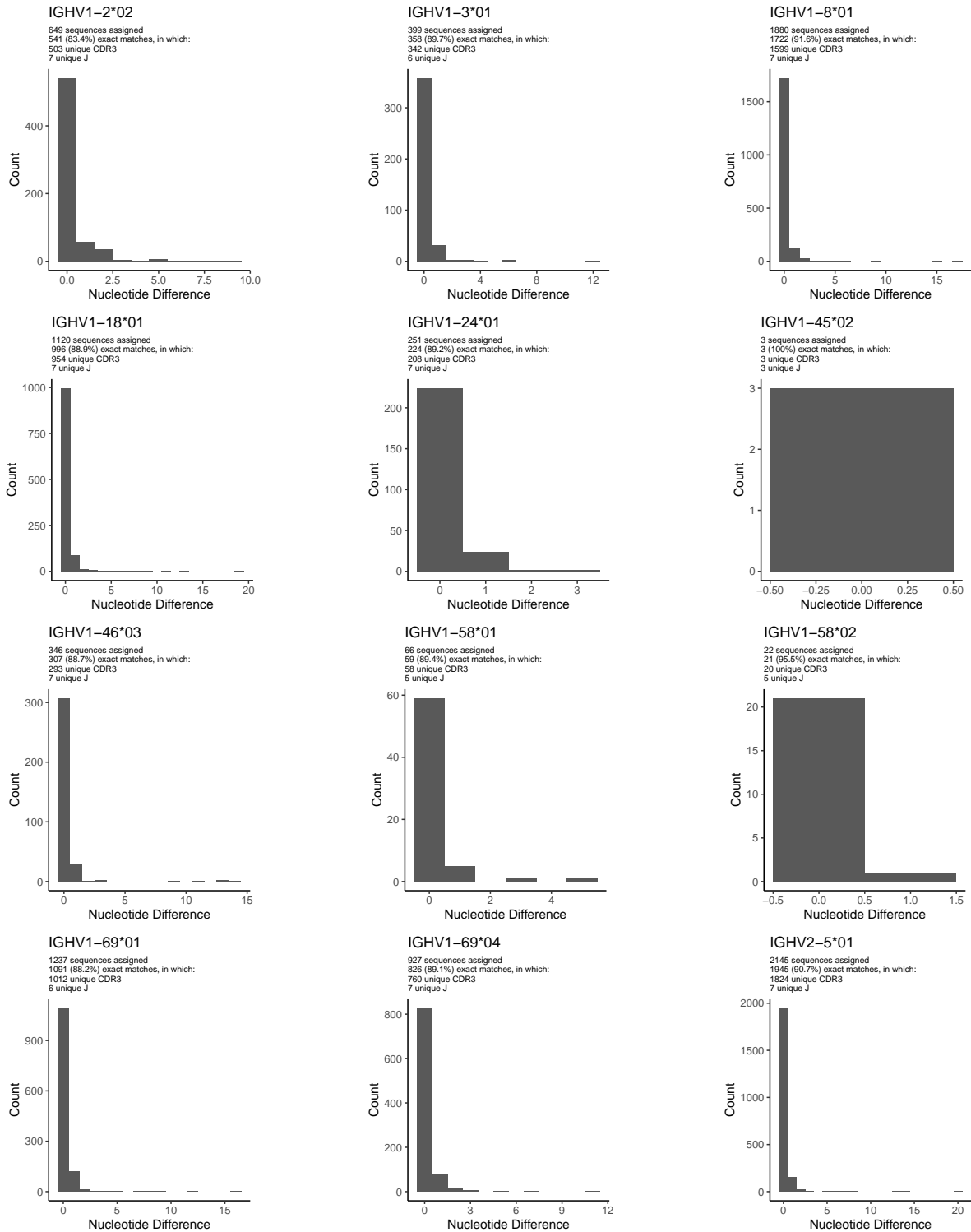
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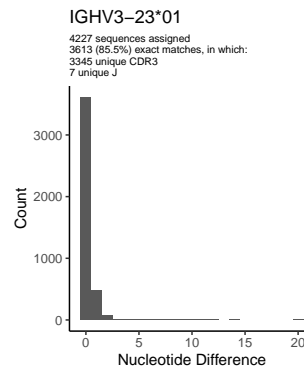
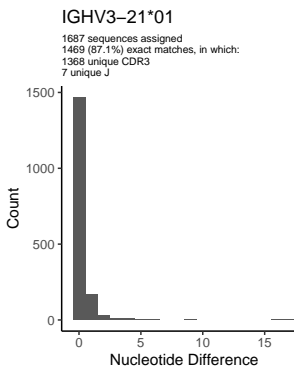
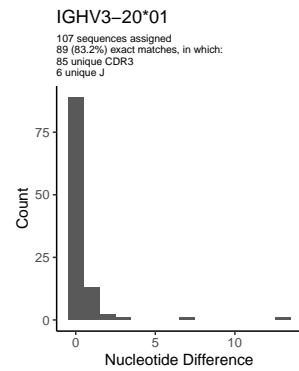
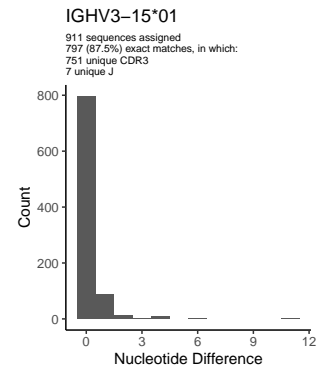
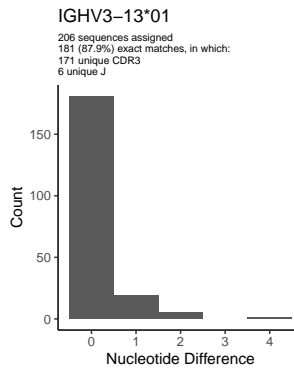
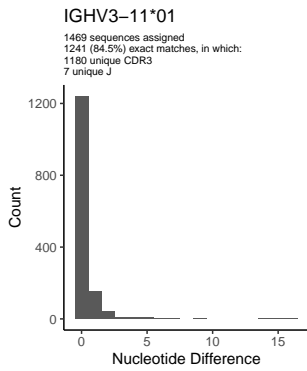
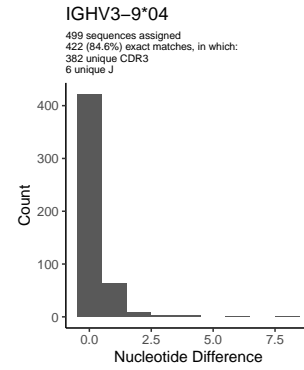
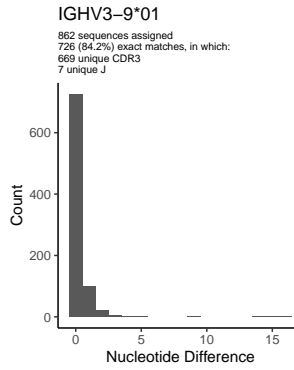
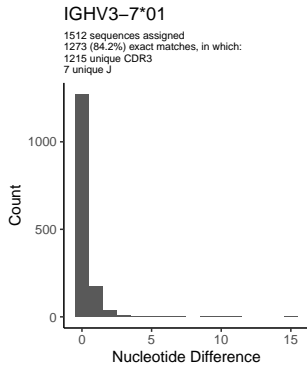
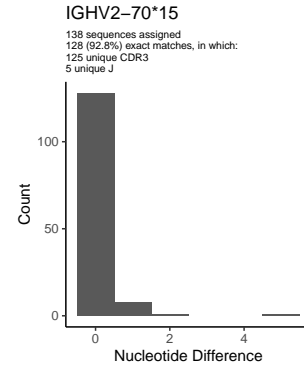
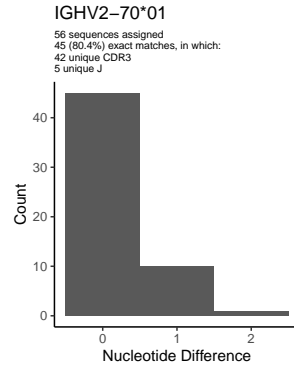
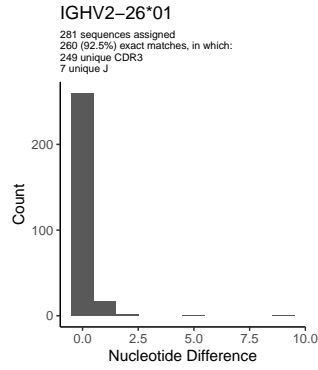
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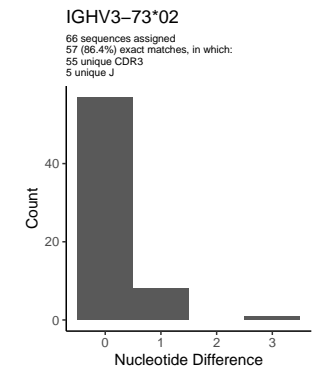
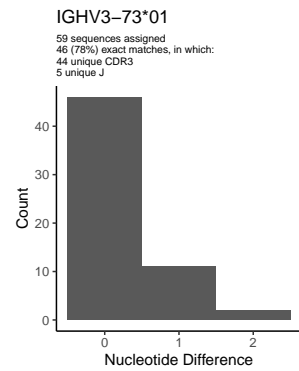
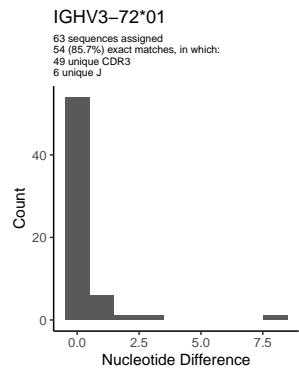
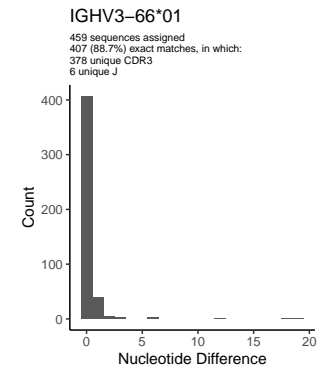
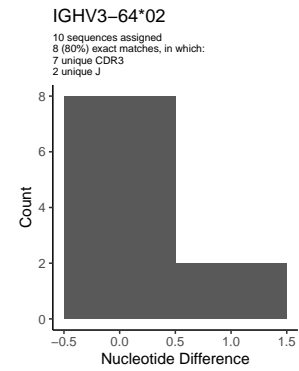
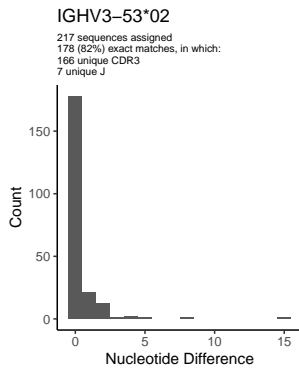
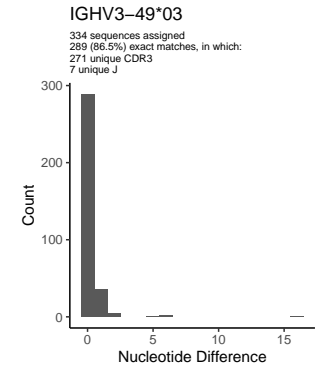
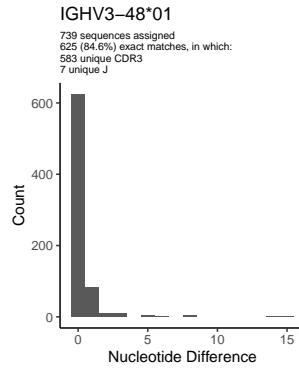
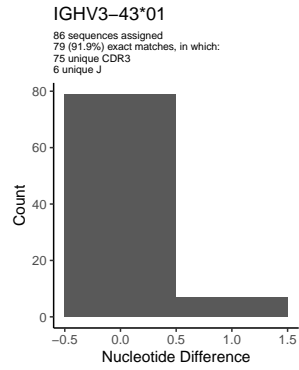
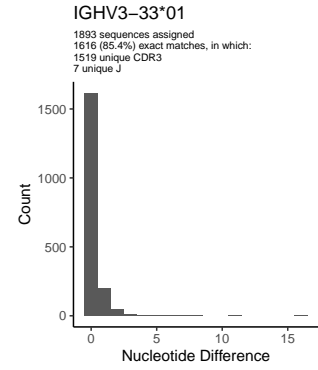
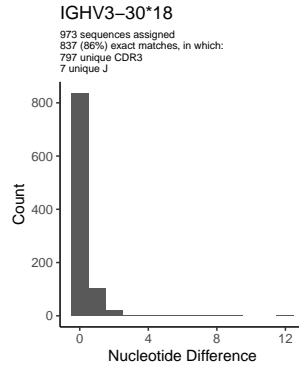
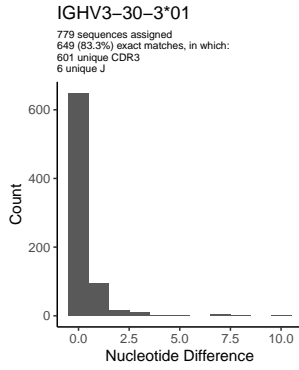
# 1 Novel sequence analysis

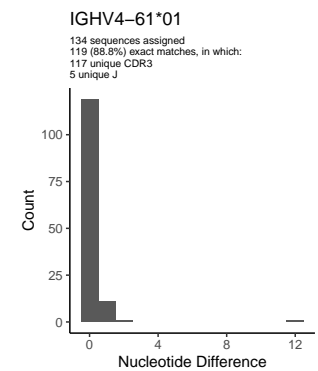
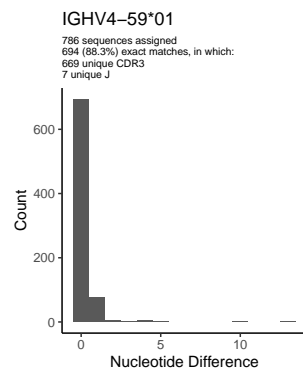
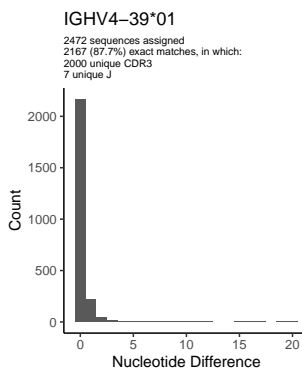
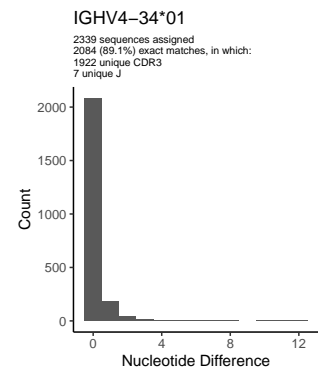
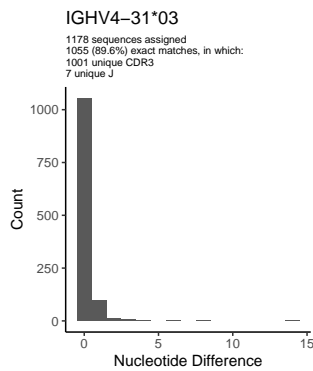
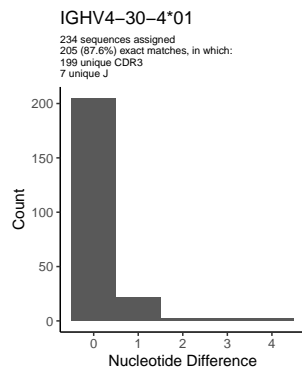
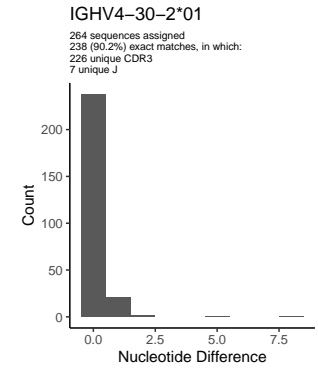
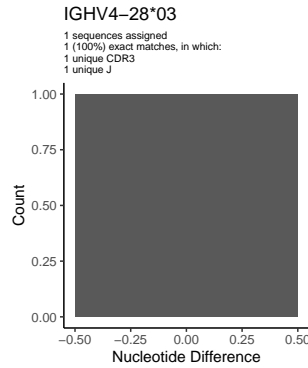
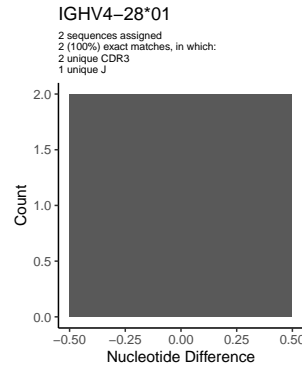
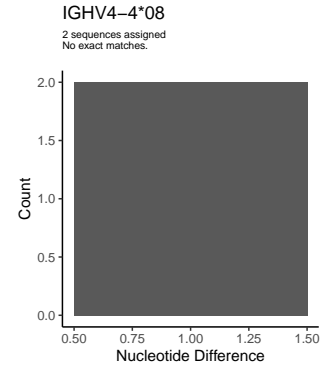
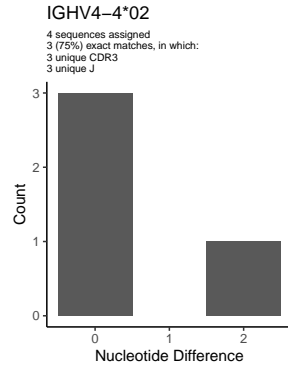
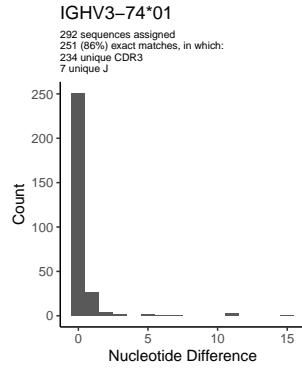
## 1.1 CDR3 length distribution, in assignments to novel alleles

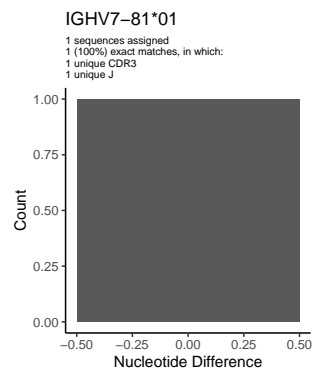
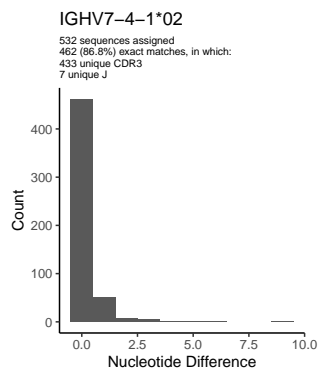
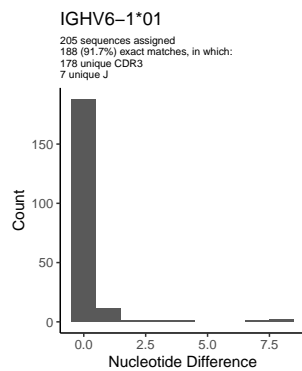
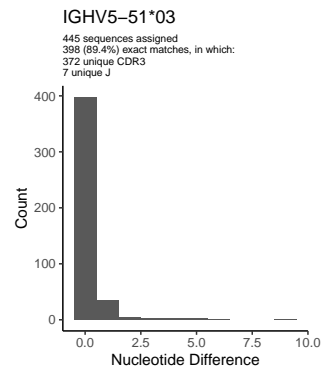
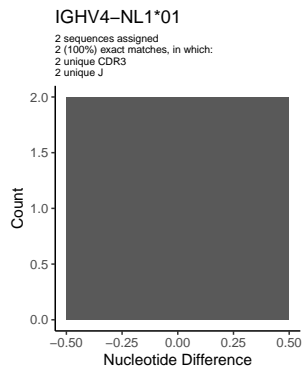
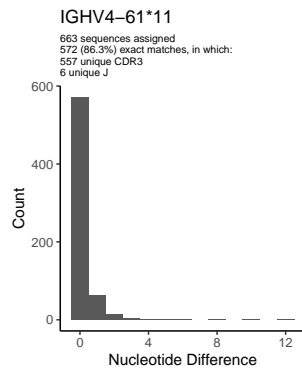
## 2 Variation from germline, in assignments to each allele



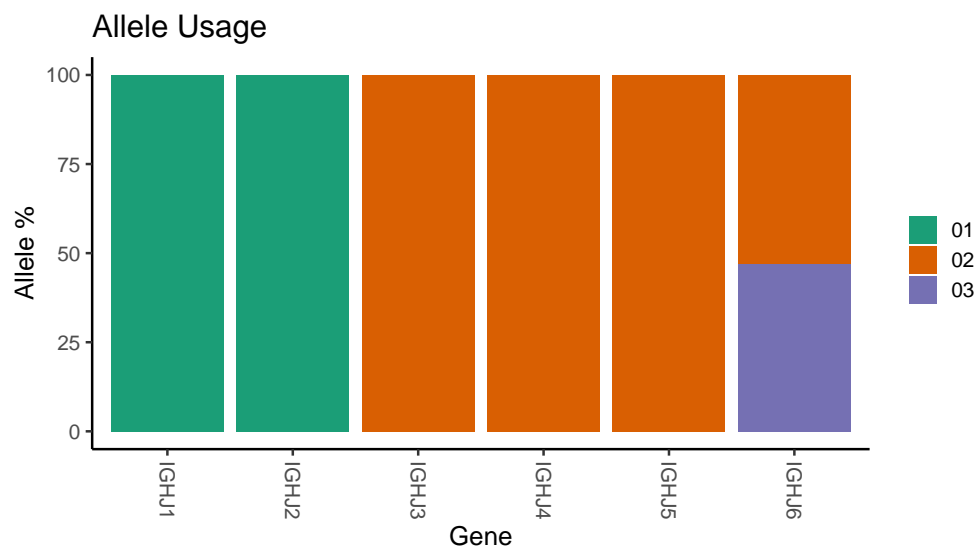






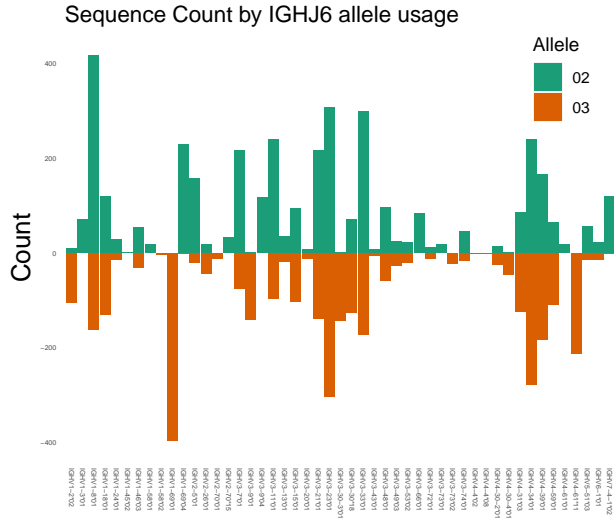


### 3 Allele usage in potential haplotype anchor genes





# 4 Haplotype plots



## 5 Configuration settings

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##
## Germline reference file: /misc/work/jenkins/PRJEB26509/S82/S82/86/86/b0/d644dbf7d5a7ff57a69be31bc84a
##
## Novel allele file:
##
## Species: Homosapiens
##
## Chain: IGHV
##
## Segment: V
##
## Warning    no inferred sequences found.
```