

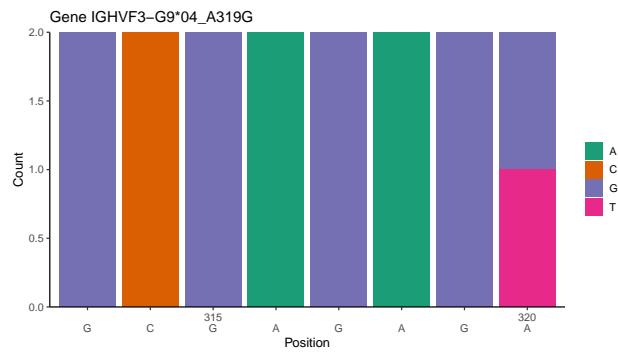
# OGRDBstats Report

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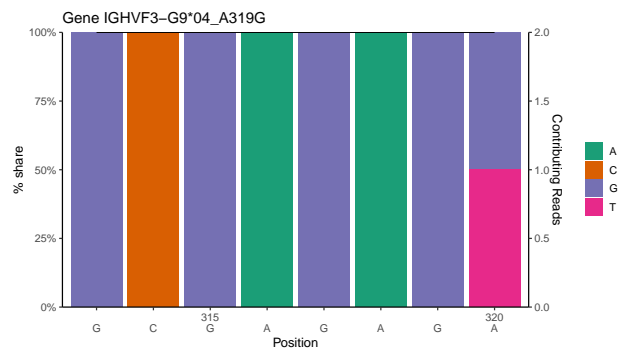
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# 1 Novel sequence analysis

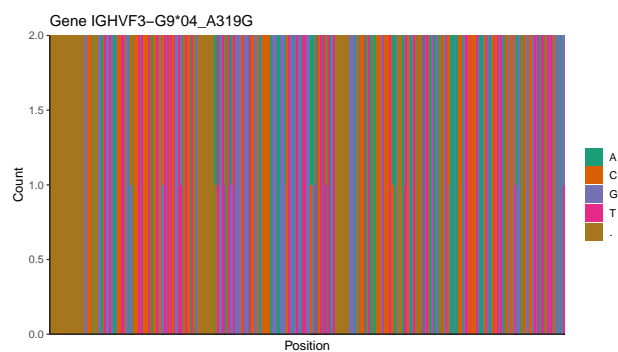
## 1.1 End-nucleotide composition



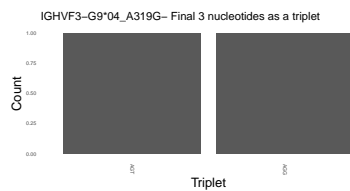
## 1.2 Per-nucleotide consensus where previous nucleotides match the consensus



## 1.3 Whole-sequence composition of each assigned read

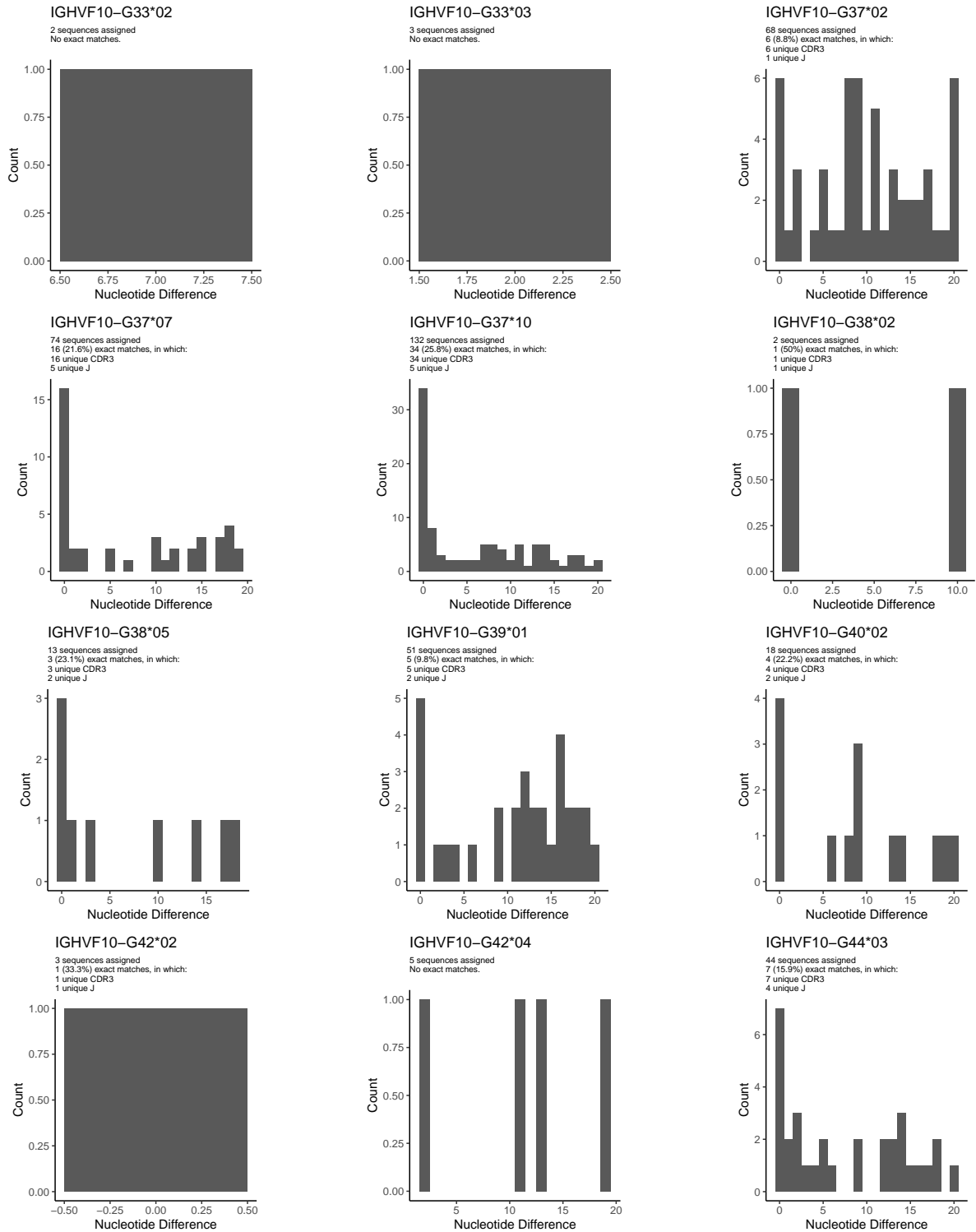


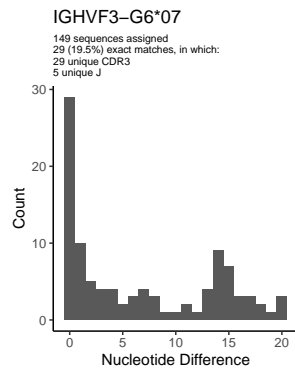
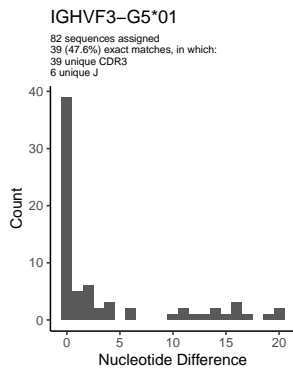
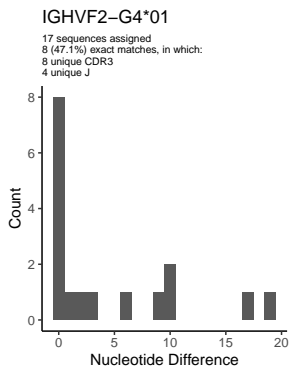
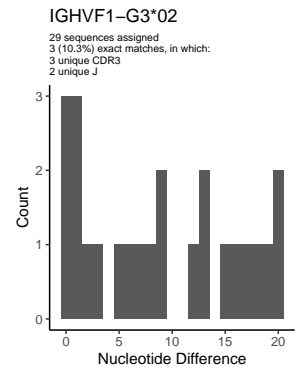
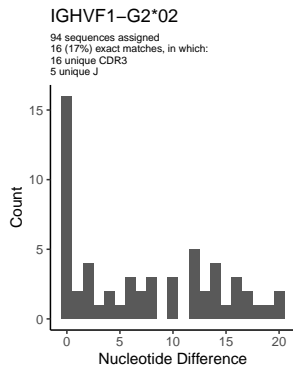
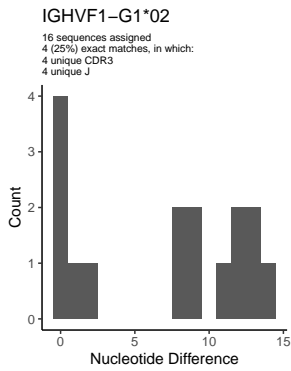
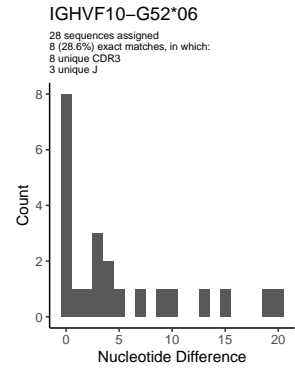
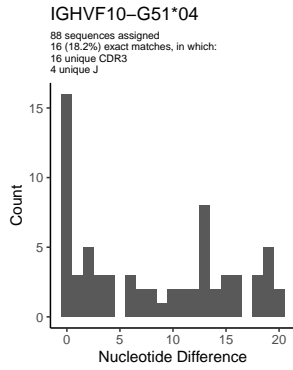
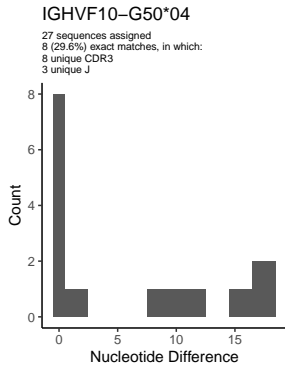
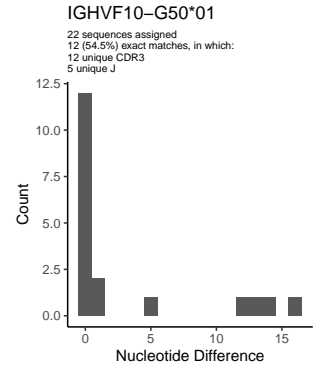
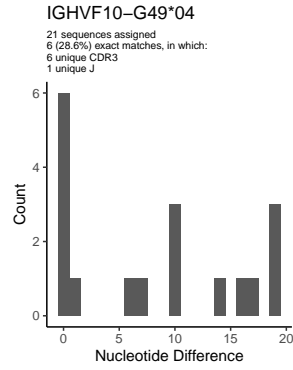
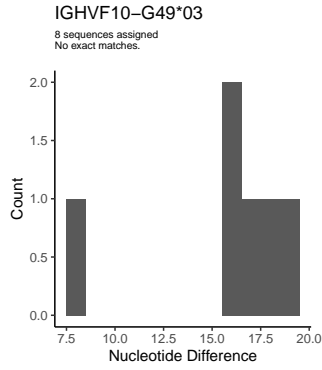
## 1.4 Final three nucleotides: frequency of each observed triplet

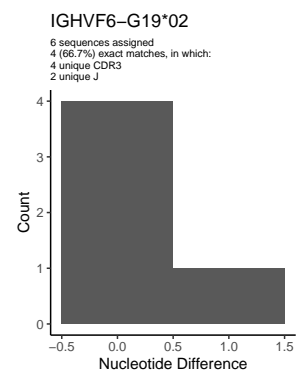
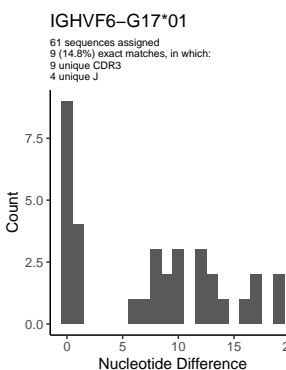
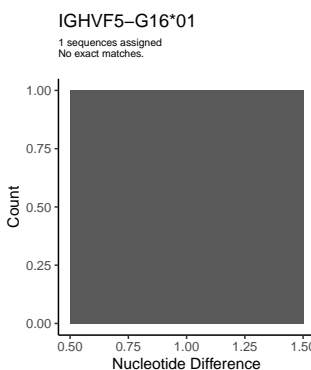
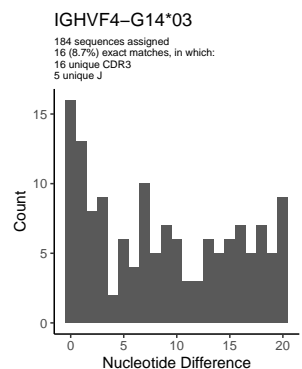
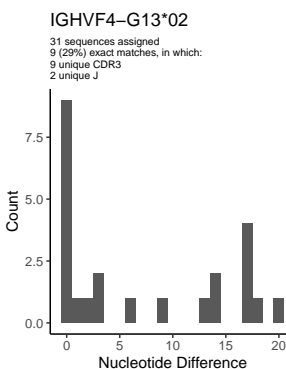
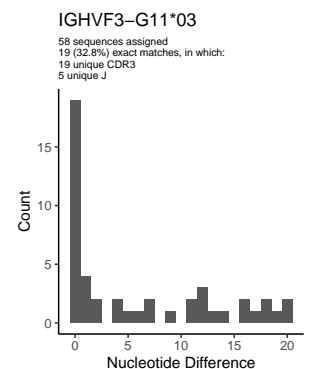
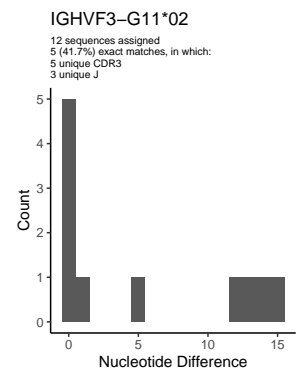
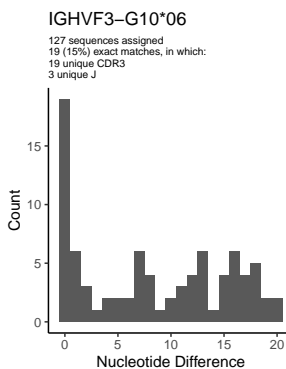
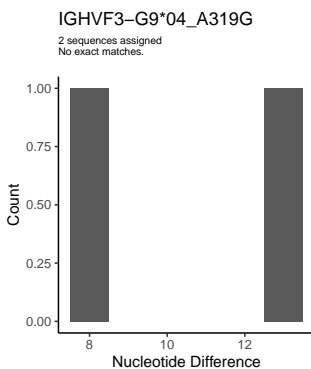
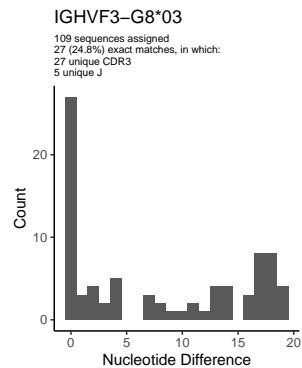
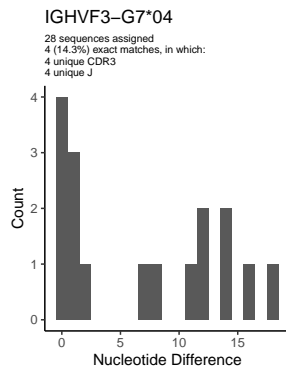
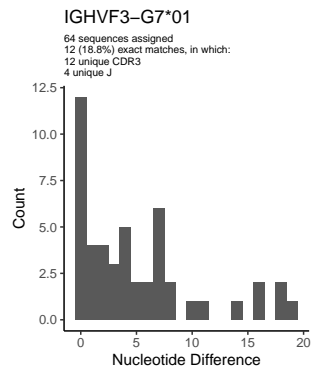


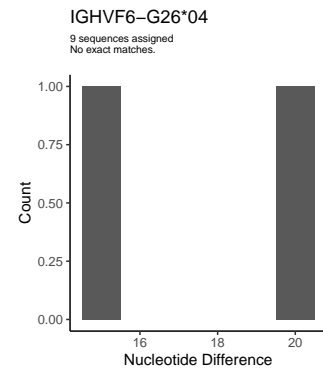
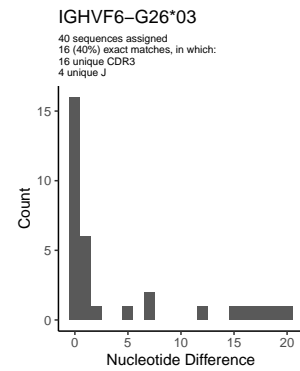
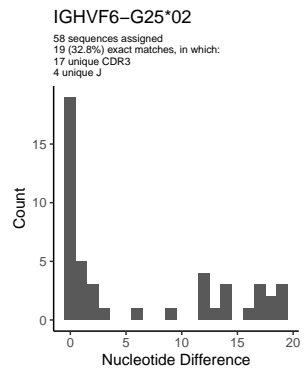
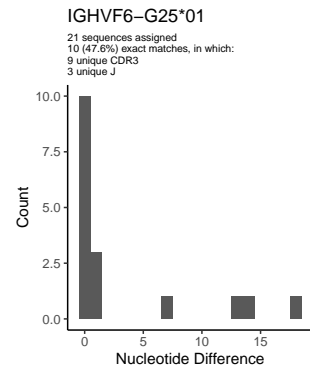
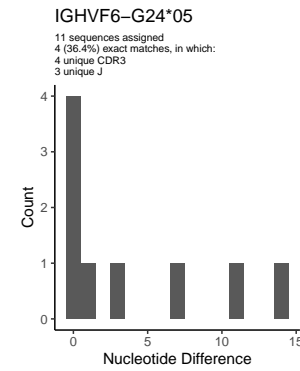
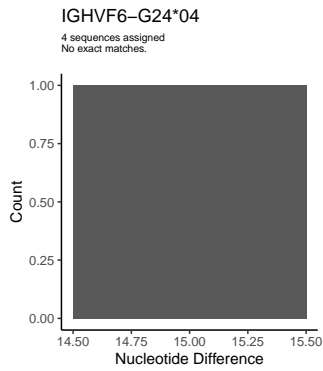
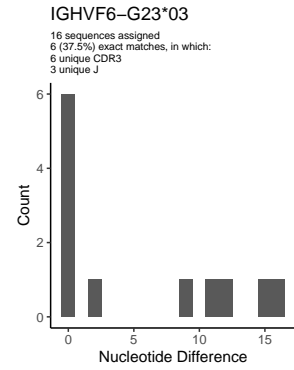
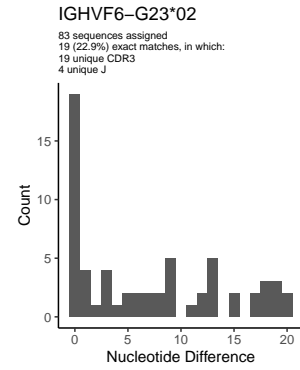
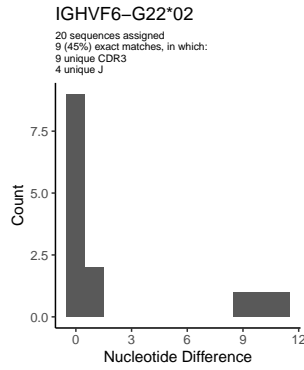
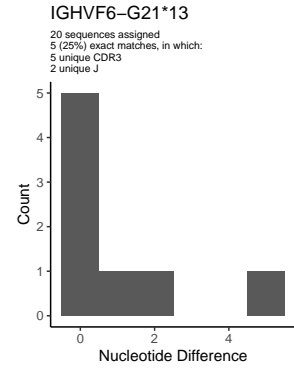
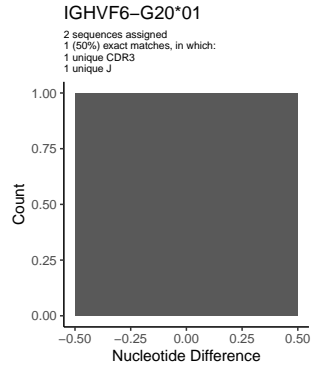
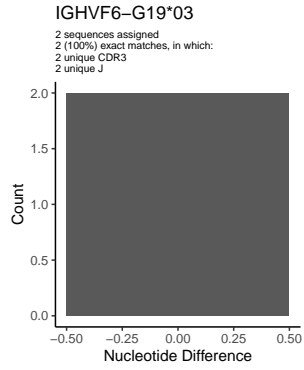
## 1.5 CDR3 length distribution, in assignments to novel alleles

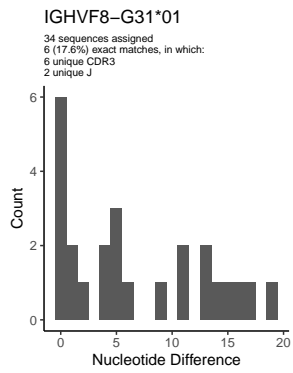
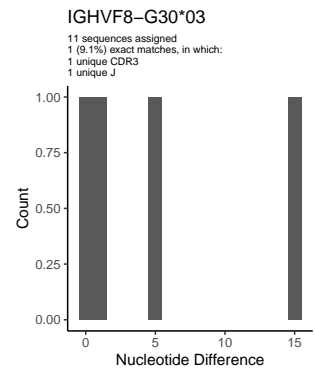
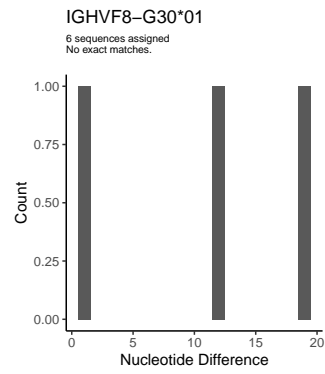
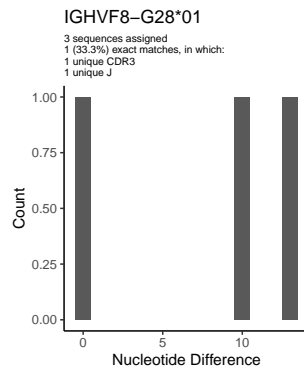
## 2 Variation from germline, in assignments to each allele











### 3 Allele usage in potential haplotype anchor genes





## 4 Haplotype plots

## 5 Configuration settings

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## Germline reference file: /misc/work/jenkins/PRJNA248475/M2/M2_cln/M2_cln/M2_cln/f1/98a0ede2f08ac21c4
##
## Novel allele file: /misc/work/jenkins/PRJNA248475/M2/M2_cln/M2_cln/M2_cln/f1/98a0ede2f08ac21c4e77f86
##
## Species: Homosapiens
##
## Chain: IGHV
##
## Segment: V
```