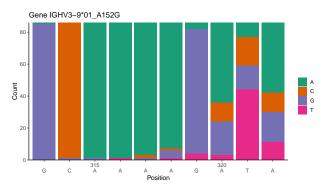
OGRDBstats Report

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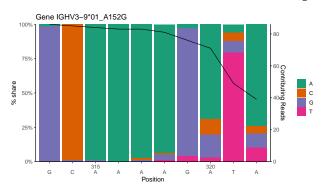
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1 Novel sequence analysis

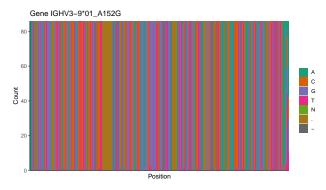
1.1 End-nucleotide composition



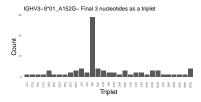
1.2 Per-nucleotide consensus where previous nucleotides match the consensus



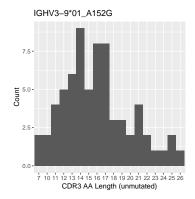
1.3 Whole-sequence composition of each assigned read



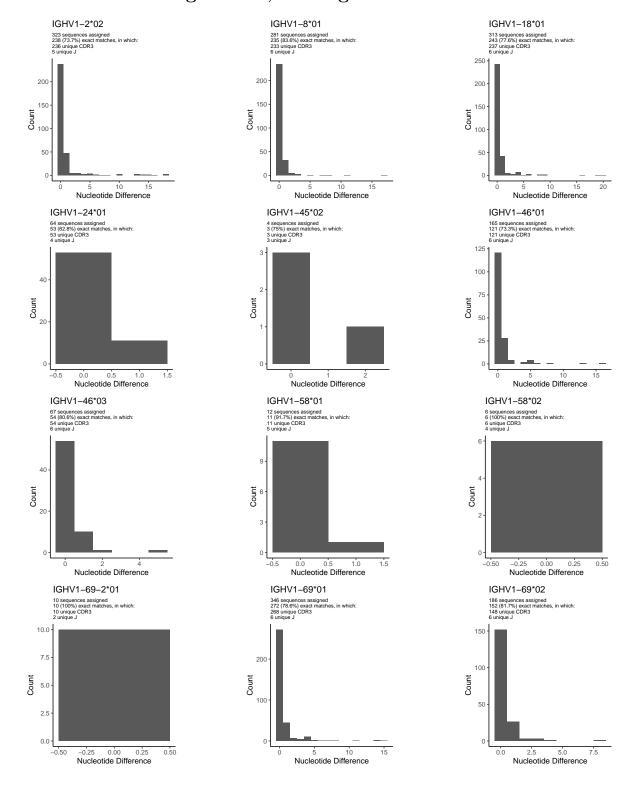
1.4 Final three nucleotides: frequency of each observed triplet

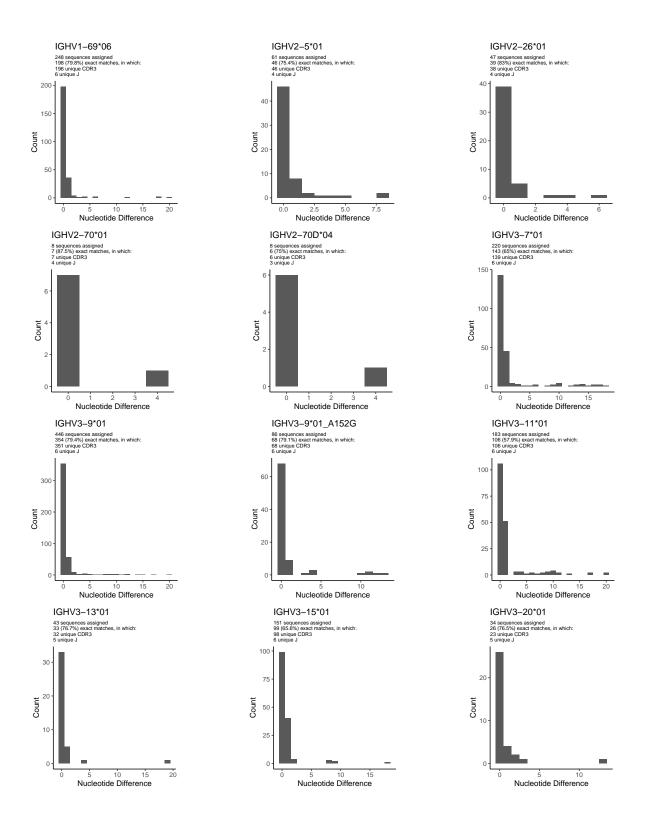


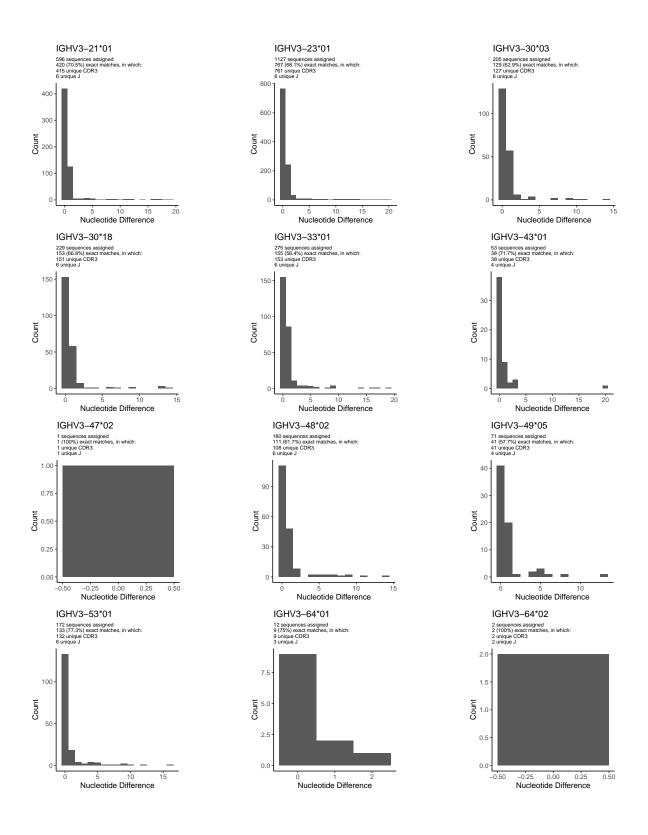
1.5 CDR3 length distribution, in assignments to novel alleles

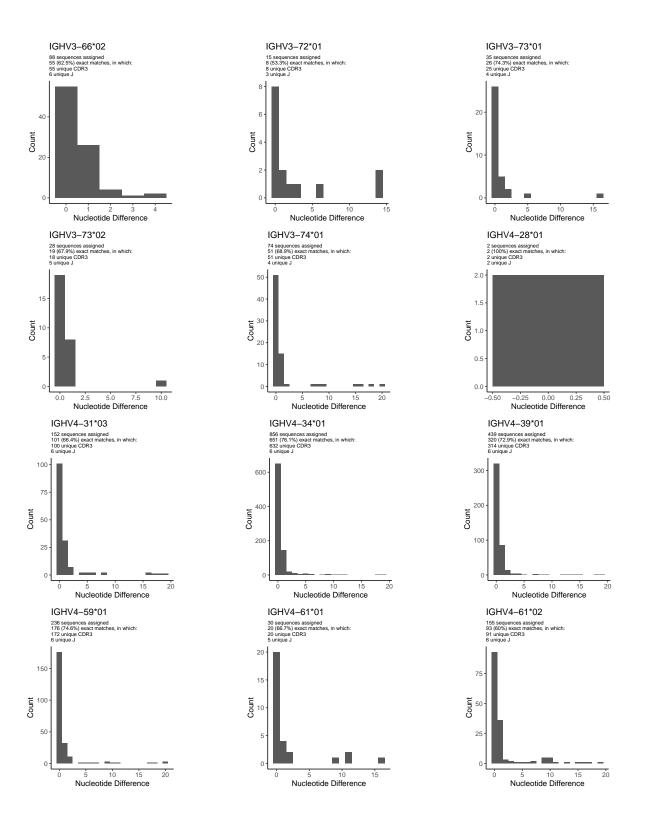


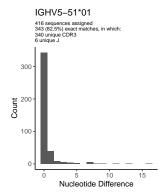
2 Variation from germline, in assignments to each allele

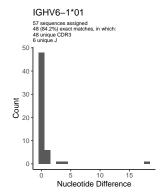












3 Allele usage in potential haplotype anchor genes



4 Haplotype plots

5 Configuration settings

```
## Repertoire file: /misc/work/jenkins/PRJEB26509/S34/S34/36/36/74/890930b1732c9912e7aaa4e58b5297/36_Fir
##
Germline reference file: /misc/work/jenkins/PRJEB26509/S34/S34/36/36/74/890930b1732c9912e7aaa4e58b52
##
Novel allele file: /misc/work/jenkins/PRJEB26509/S34/S34/36/36/74/890930b1732c9912e7aaa4e58b5297/nov
##
Species: Homosapiens
##
## Chain: IGHV
##
## Segment: V
```