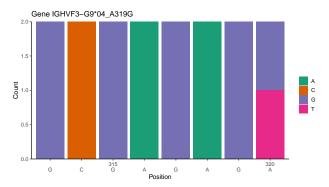
OGRDBstats Report

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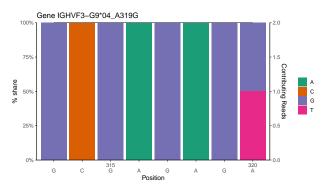
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1 Novel sequence analysis

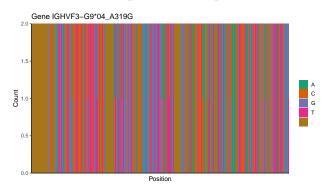
1.1 End-nucleotide composition



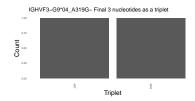
1.2 Per-nucleotide consensus where previous nucleotides match the consensus



1.3 Whole-sequence composition of each assigned read

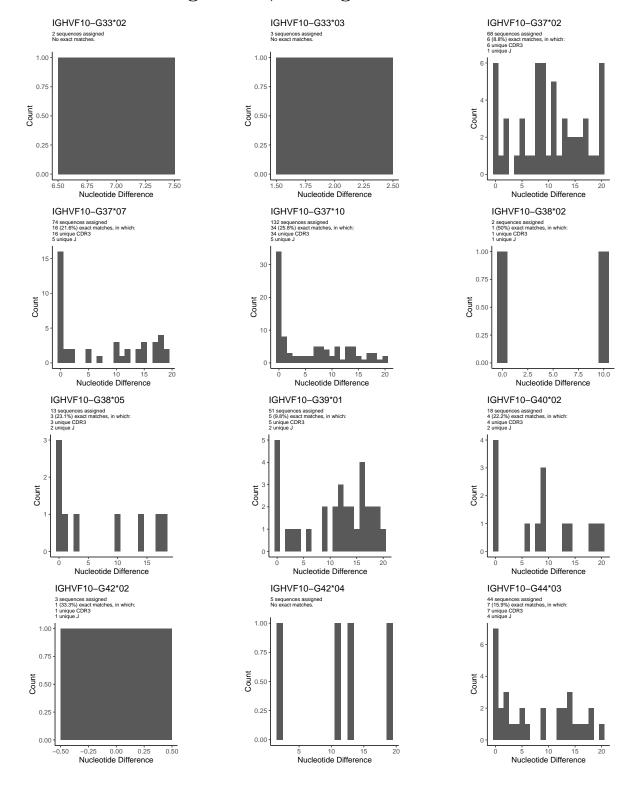


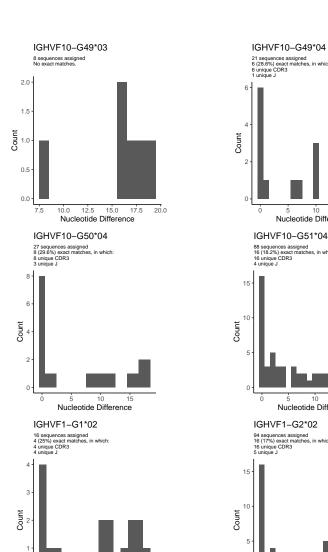
1.4 Final three nucleotides: frequency of each observed triplet

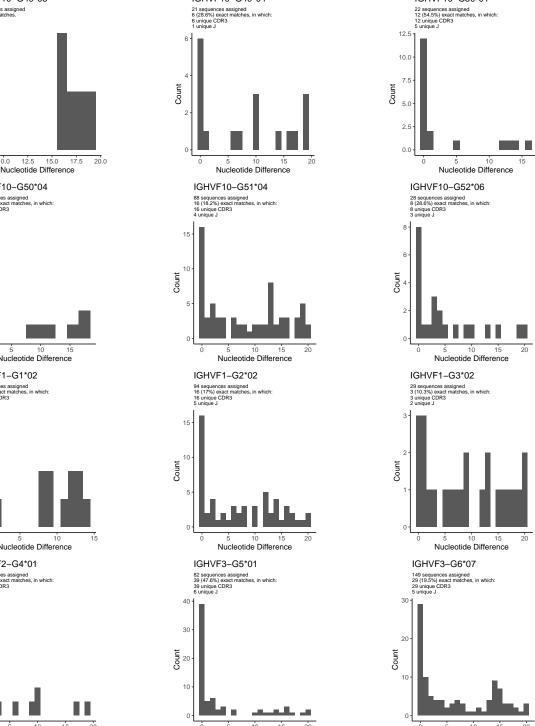


1.5 CDR3 length distribution, in assignments to novel alleles

2 Variation from germline, in assignments to each allele

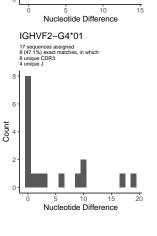


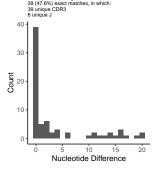


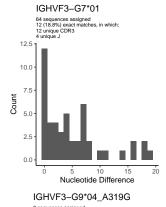


IGHVF10-G50*01

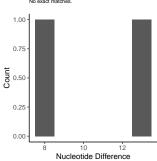
Nucleotide Difference





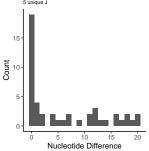


2 sequences assigned No exact matches.



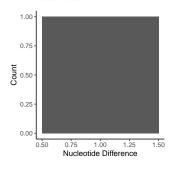
IGHVF3-G11*03

58 sequences assigned 19 (32.8%) exact matches, in which: 19 unique CDR3 5 unique J



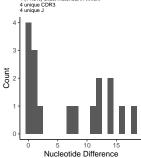
IGHVF5-G16*01

1 sequences assigned No exact matches.



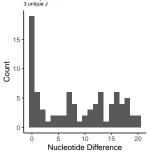
IGHVF3-G7*04

28 sequences assigned 4 (14.3%) exact matches, in which: 4 unique CDR3 4 unique J



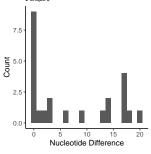
IGHVF3-G10*06

127 sequences assigned 19 (15%) exact matches, in which: 19 unique CDR3 3 unique J



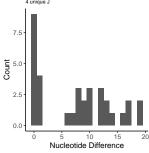
IGHVF4-G13*02

31 sequences assigned 9 (29%) exact matches, in which: 9 unique CDR3 2 unique J



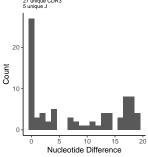
IGHVF6-G17*01

61 sequences assigned 9 (14.8%) exact matches, in which: 9 unique CDR3 4 unique J

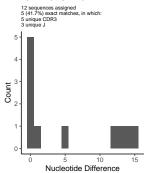


IGHVF3-G8*03

109 sequences assigned 27 (24.8%) exact matches, in which: 27 unique CDR3 5 unique J

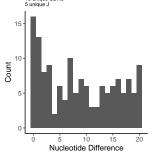


IGHVF3-G11*02



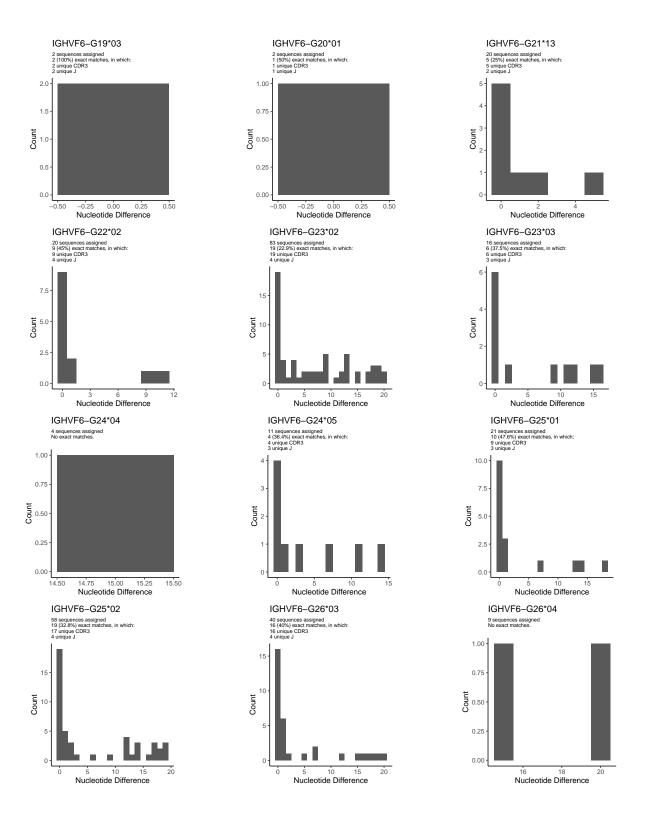
IGHVF4-G14*03

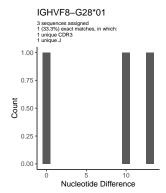
184 sequences assigned 16 (8.7%) exact matches, in which: 16 unique CDR3 5 unique J

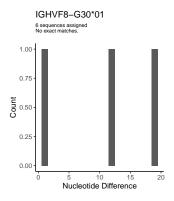


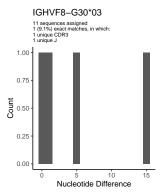
IGHVF6-G19*02

6 sequences assigned 4 (66.7%) exact matches, in which: 4 unique CDR3 2 unique J Count Nucleotide Difference

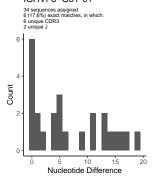












3 Allele usage in potential haplotype anchor genes



4 Haplotype plots

5 Configuration settings

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## Repertoire file: /misc/work/jenkins/PRJNA248475/M2/M2_cln/M2_cln/f1/98a0ede2f08ac21c4e77f86b5
##
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
```