OGRDBstats Report

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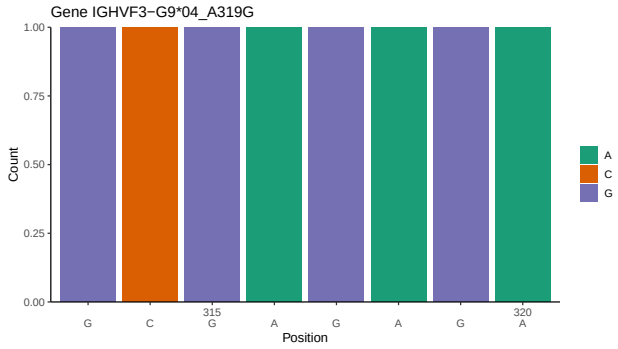
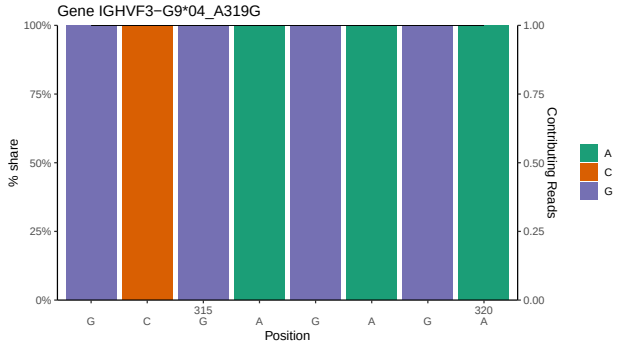
1 Novel sequence analysis

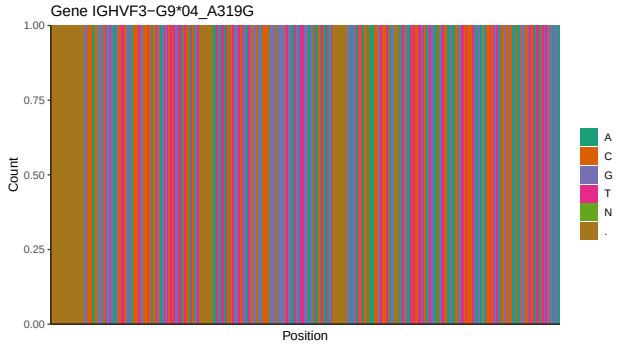
1.1 End-nucleotide composition



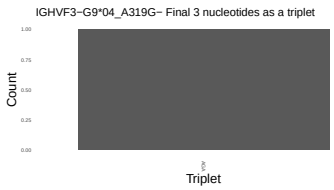
1.2 Per-nucleotide consensus where previous nucleotides match the consensus



1.3 Whole-sequence composition of each assigned read

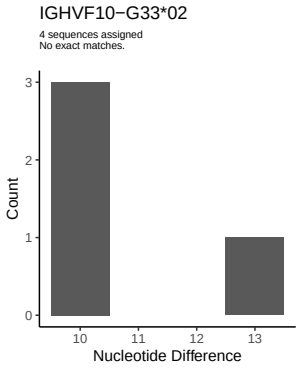


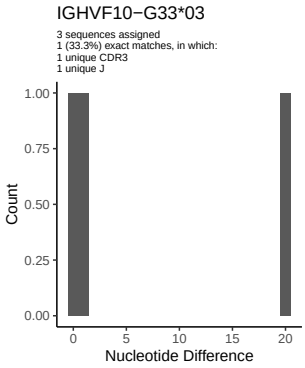
1.4 Final three nucleotides: frequency of each observed triplet

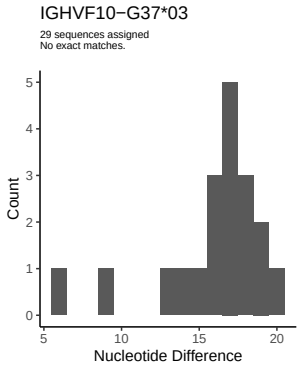


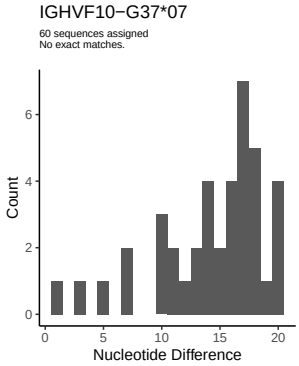
1.5 CDR3 length distribution, in assignments to novel alleles

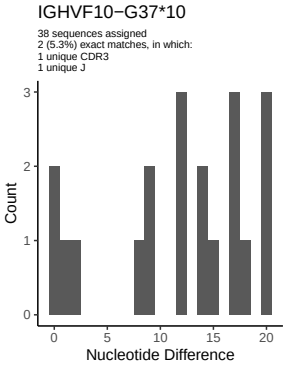
2 Variation from germline, in assignments to each allele

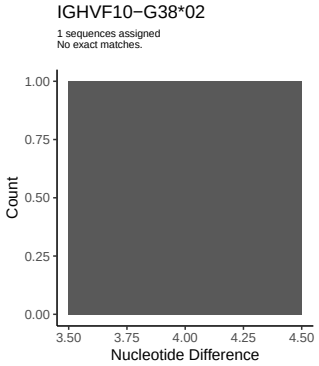


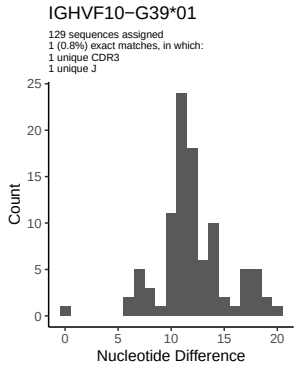


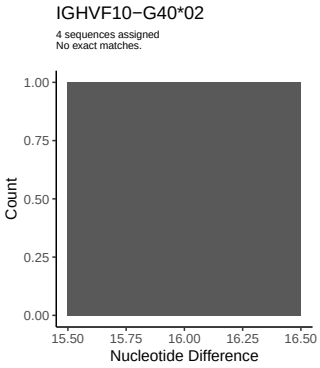


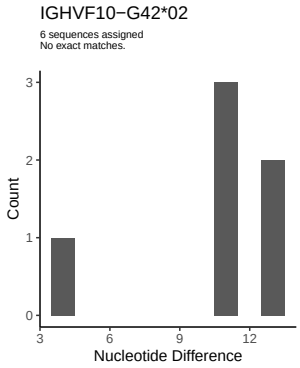


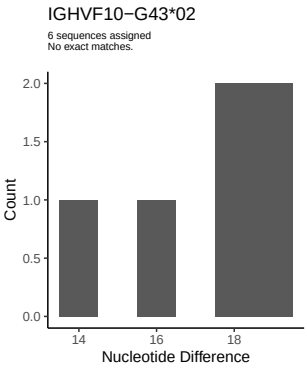


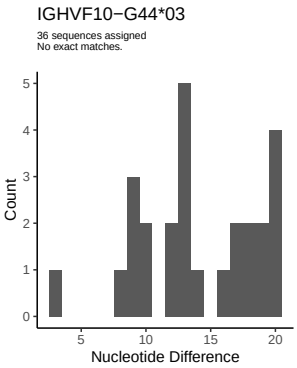


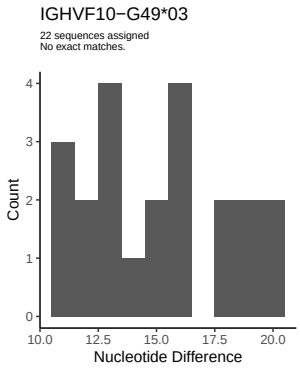


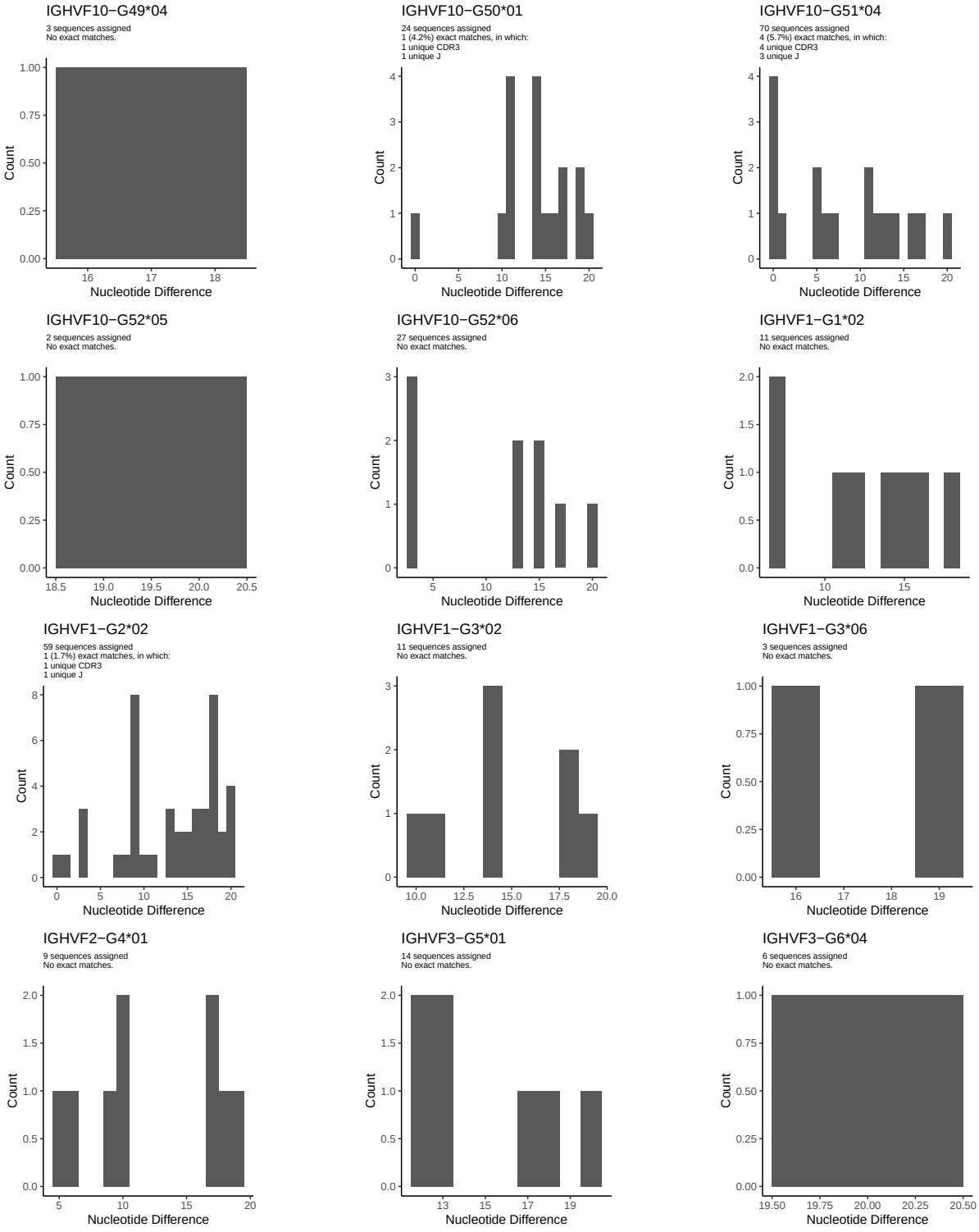


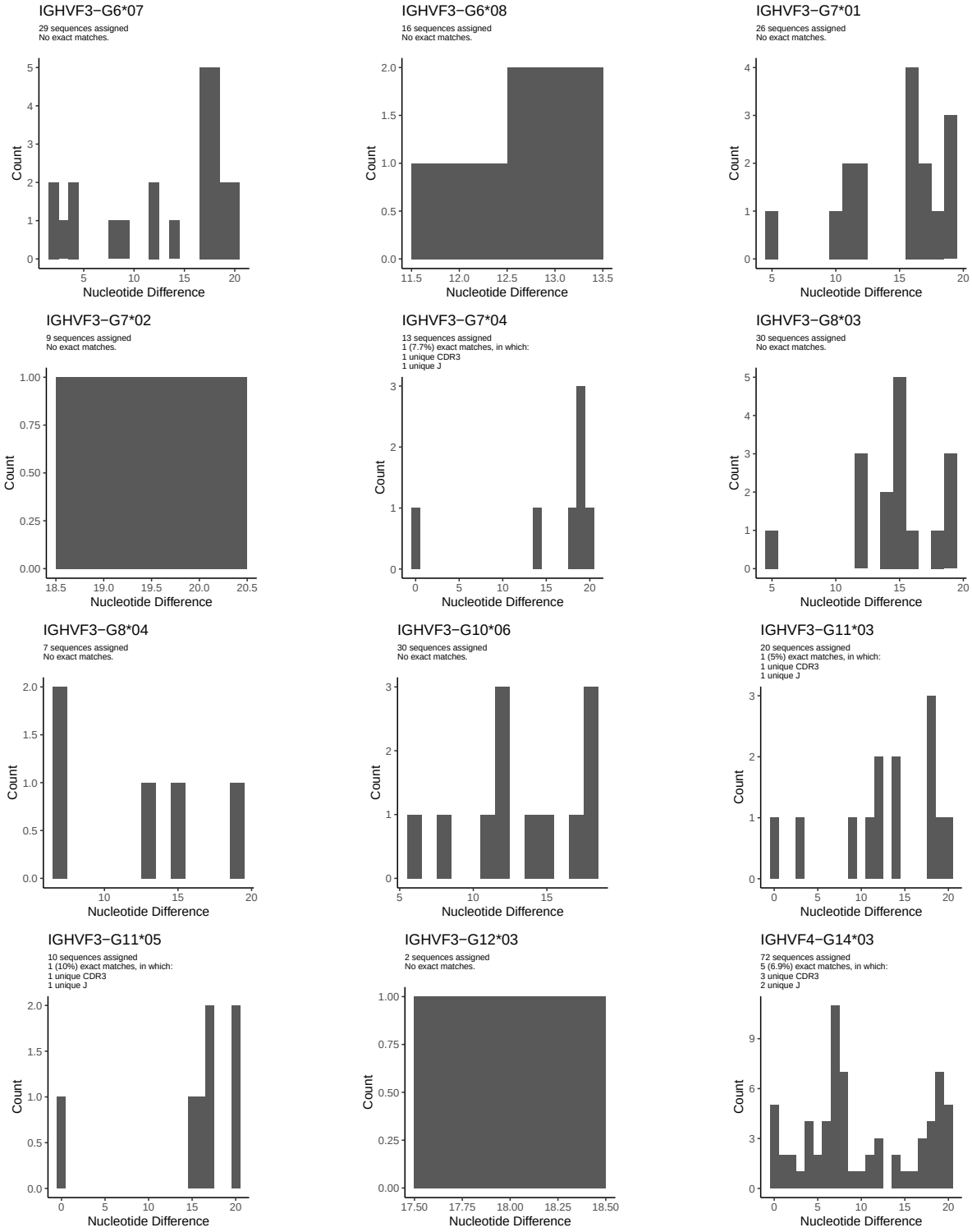


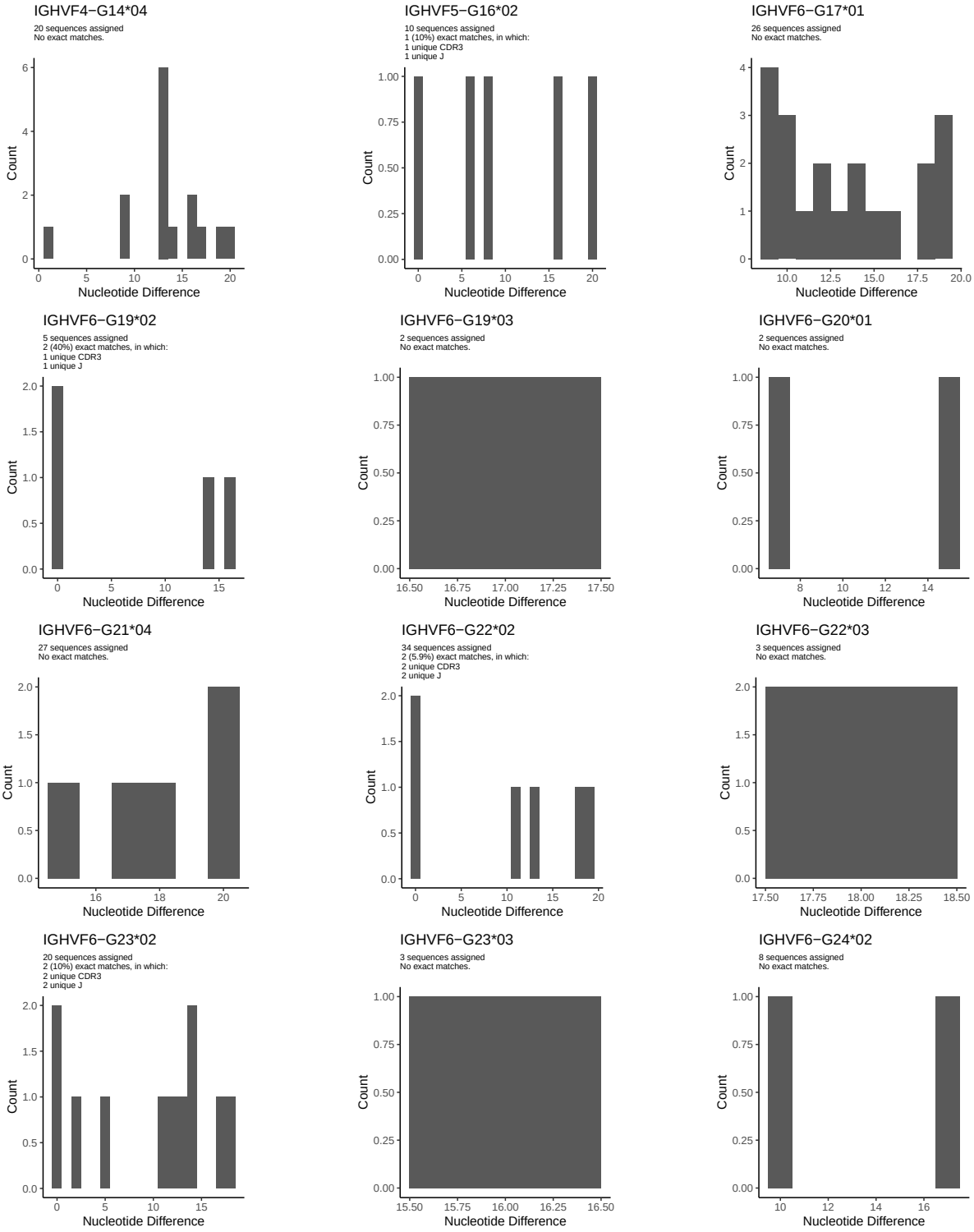


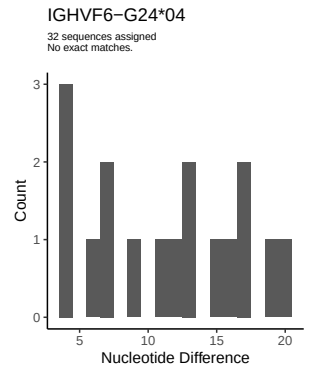


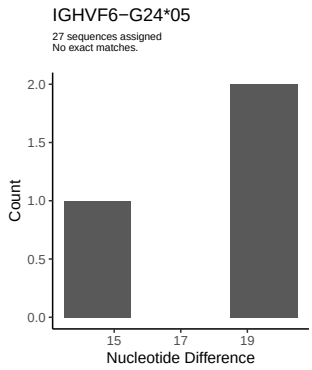


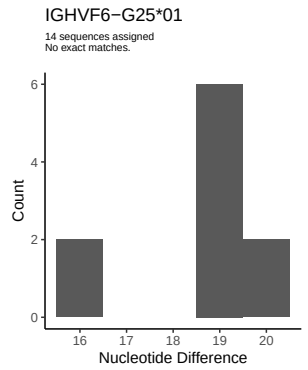

IGHVF10−G49*04
3 sequences assigned
No exact matches.
IGHVF10−G50*01
24 sequences assigned
1 (4.2%) exact matches, in which:
1 unique CDR3
1 unique J
IGHVF10−G51*04
70 sequences assigned
4 (5.7%) exact matches, in which:
4 unique CDR3
3 unique J
IGHVF10−G52*05
2 sequences assigned
No exact matches.
IGHVF10−G52*06
27 sequences assigned
No exact matches.
IGHVF1−G1*02
11 sequences assigned
No exact matches.
IGHVF1−G2*02
59 sequences assigned
1 (1.7%) exact matches, in which:
1 unique CDR3
1 unique J
IGHVF1−G3*02
11 sequences assigned
No exact matches.
IGHVF1−G3*06
3 sequences assigned
No exact matches.
IGHVF2−G4*01
9 sequences assigned
No exact matches.
IGHVF3−G5*01
14 sequences assigned
No exact matches.
IGHVF3−G6*04
6 sequences assigned
No exact matches.
Count
Nucleotide Difference

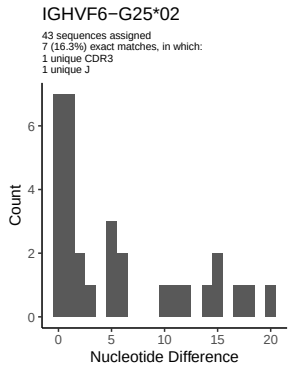

IGHVF3−G6*07
29 sequences assigned
No exact matches.
IGHVF3−G6*08
16 sequences assigned
No exact matches.
IGHVF3−G7*01
26 sequences assigned
No exact matches.
IGHVF3−G7*02
9 sequences assigned
No exact matches.
IGHVF3−G7*04
13 sequences assigned
1 (7.7%) exact matches, in which:
1 unique CDR3
1 unique J
IGHVF3−G8*03
30 sequences assigned
No exact matches.
IGHVF3−G8*04
7 sequences assigned
No exact matches.
IGHVF3−G10*06
30 sequences assigned
No exact matches.
IGHVF3−G11*03
20 sequences assigned
1 (5%) exact matches, in which:
1 unique CDR3
1 unique J
IGHVF3−G11*05
10 sequences assigned
1 (10%) exact matches, in which:
1 unique CDR3
1 unique J
IGHVF3−G12*03
2 sequences assigned
No exact matches.
IGHVF4−G14*03
72 sequences assigned
5 (6.9%) exact matches, in which:
3 unique CDR3
2 unique J
Count
Nucleotide Difference

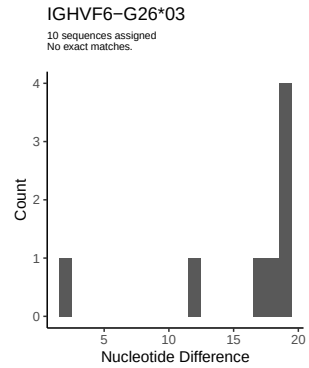

IGHVF4−G14*04
20 sequences assigned
No exact matches.
IGHVF5−G16*02
10 sequences assigned
1 (10%) exact matches, in which:
1 unique CDR3
1 unique J
IGHVF6−G17*01
26 sequences assigned
No exact matches.
IGHVF6−G19*02
5 sequences assigned
2 (40%) exact matches, in which:
1 unique CDR3
1 unique J
IGHVF6−G19*03
2 sequences assigned
No exact matches.
IGHVF6−G20*01
2 sequences assigned
No exact matches.
IGHVF6−G21*04
27 sequences assigned
No exact matches.
IGHVF6−G22*02
34 sequences assigned
2 (5.9%) exact matches, in which:
2 unique CDR3
2 unique J
IGHVF6−G22*03
3 sequences assigned
No exact matches.
IGHVF6−G23*02
20 sequences assigned
2 (10%) exact matches, in which:
2 unique CDR3
2 unique J
IGHVF6−G23*03
3 sequences assigned
No exact matches.
IGHVF6−G24*02
8 sequences assigned
No exact matches.
Count
Nucleotide Difference

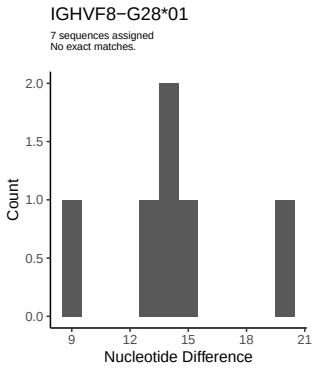

IGHVF6−G24*04
32 sequences assigned
No exact matches.
Count
Nucleotide Difference

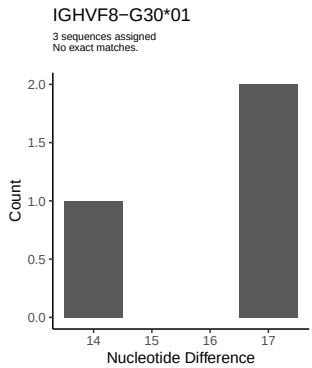

IGHVF6−G24*05
27 sequences assigned
No exact matches.
Count
Nucleotide Difference

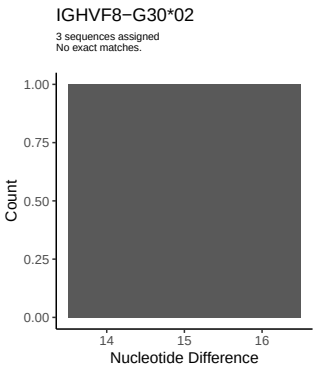

IGHVF6−G25*01
14 sequences assigned
No exact matches.
Count
Nucleotide Difference

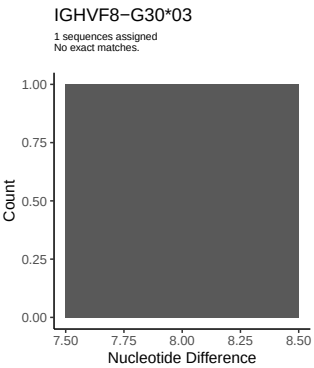

IGHVF6−G25*02
43 sequences assigned
7 (16.3%) exact matches, in which:
1 unique CDR3
1 unique J
Count
Nucleotide Difference

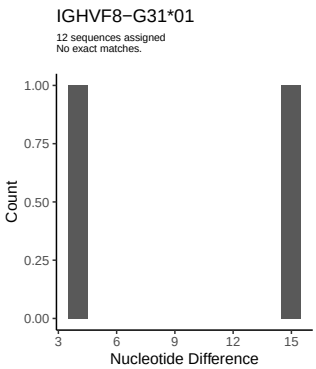

IGHVF6−G26*03
10 sequences assigned
No exact matches.
Count
Nucleotide Difference


IGHVF8−G28*01
7 sequences assigned
No exact matches.
Count
Nucleotide Difference

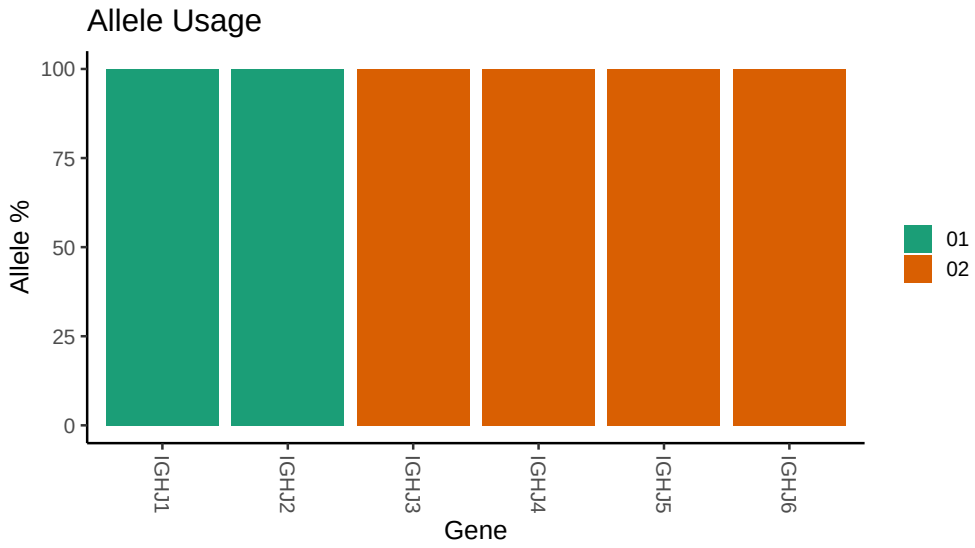

IGHVF8−G30*01
3 sequences assigned
No exact matches.
Count
Nucleotide Difference


IGHVF8−G30*02
3 sequences assigned
No exact matches.
Count
Nucleotide Difference


IGHVF8−G30*03
1 sequences assigned
No exact matches.
Count
Nucleotide Difference


IGHVF8−G31*01
12 sequences assigned
No exact matches.
Count
Nucleotide Difference

3 Allele usage in potential haplotype anchor genes



4 Haplotype plots

5 Configuration settings

```
## Repertoire file: /misc/work/jenkins/PRJNA248475/M2/M2_lesion/M2_lesion/M2_lesion/d9/b063d9b25adff8bb
##
## Germline reference file: /misc/work/jenkins/PRJNA248475/M2/M2_lesion/M2_lesion/M2_lesion/d9/b063d9b2
##
## Novel allele file: /misc/work/jenkins/PRJNA248475/M2/M2_lesion/M2_lesion/M2_lesion/d9/b063d9b25adff8
##
## Species: Homosapiens
##
## Chain: IGHV
##
## Segment: V
```