OGRDBstats Report

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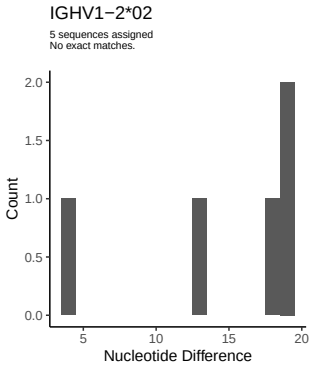
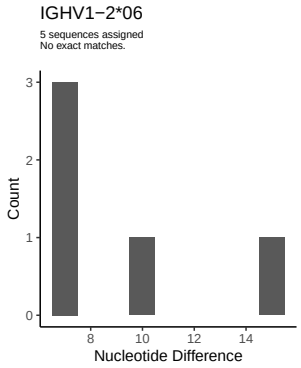
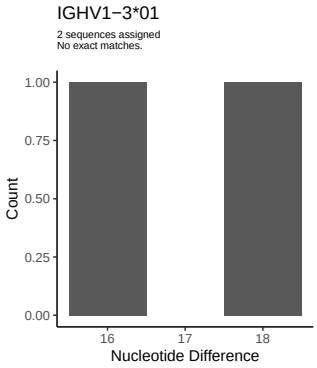
1 Novel sequence analysis

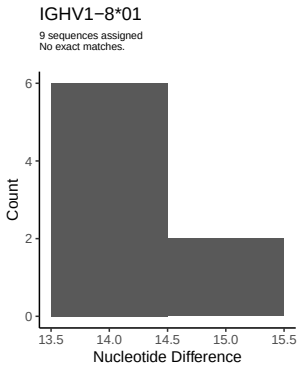
1.1 CDR3 length distribution, in assignments to novel alleles

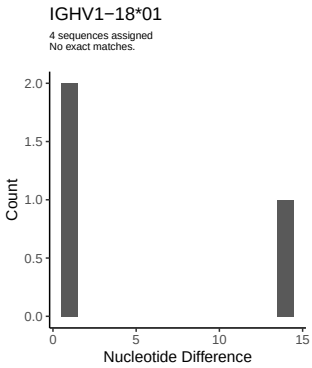
2 Variation from germline, in assignments to each allele

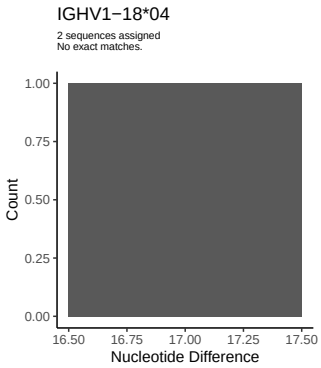


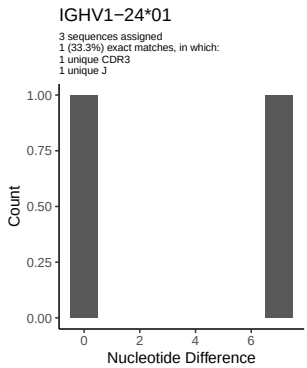


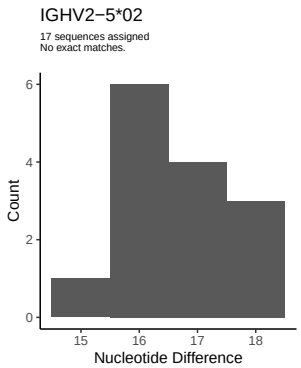


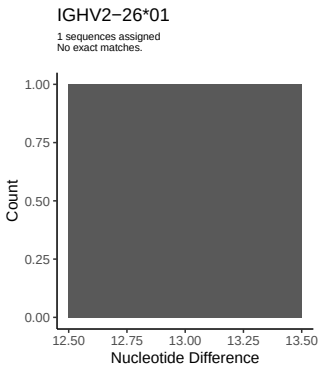


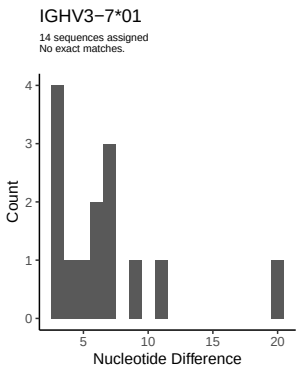


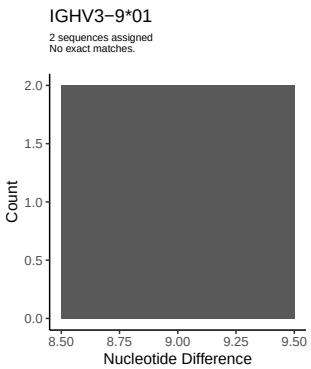


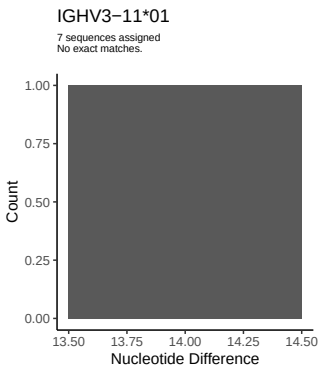


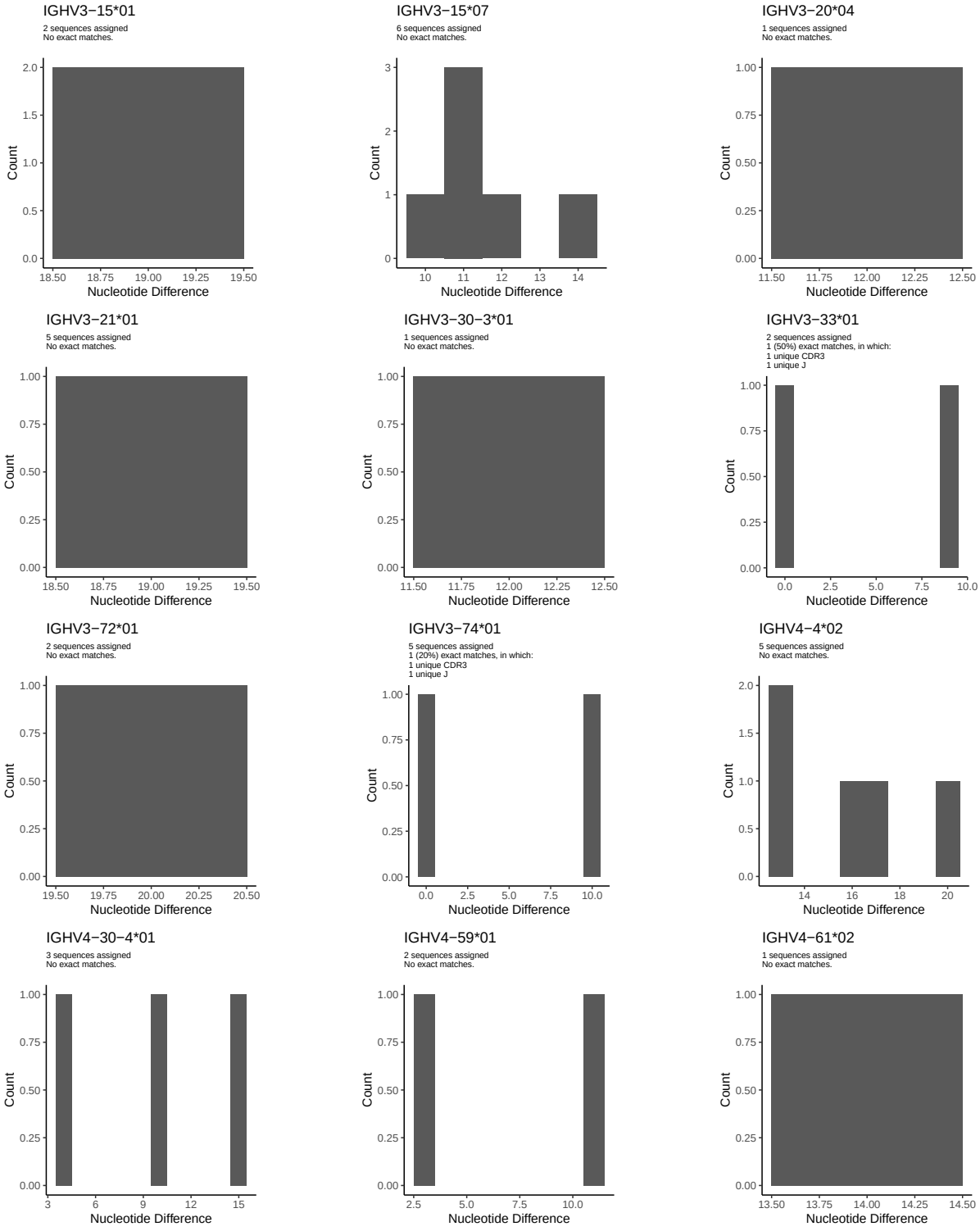


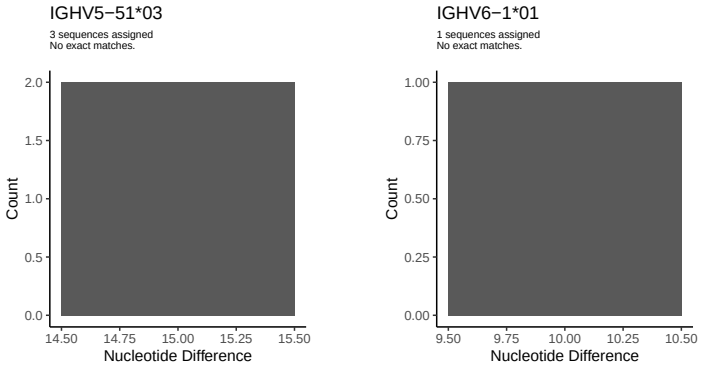




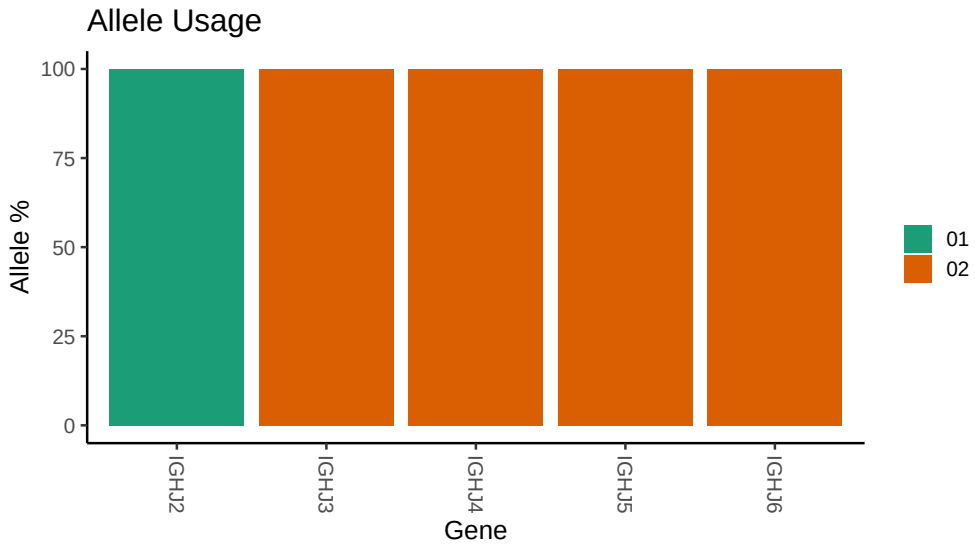





IGHV3−15*01
2 sequences assigned
No exact matches.
IGHV3−15*07
6 sequences assigned
No exact matches.
IGHV3−20*04
1 sequences assigned
No exact matches.
IGHV3−21*01
5 sequences assigned
No exact matches.
IGHV3−30−3*01
1 sequences assigned
No exact matches.
IGHV3−33*01
2 sequences assigned
1 (50%) exact matches, in which:
1 unique CDR3
1 unique J
IGHV3−72*01
2 sequences assigned
No exact matches.
IGHV3−74*01
5 sequences assigned
1 (20%) exact matches, in which:
1 unique CDR3
1 unique J
IGHV4−4*02
5 sequences assigned
No exact matches.
IGHV4−30−4*01
3 sequences assigned
No exact matches.
IGHV4−59*01
2 sequences assigned
No exact matches.
IGHV4−61*02
1 sequences assigned
No exact matches.
Count
Nucleotide Difference


IGHV5−51*03
3 sequences assigned
No exact matches.
Count
2.0
1.5
1.0
0.5
0.0
14.50
14.75
15.00
15.25
15.50
Nucleotide Difference
IGHV6−1*01
1 sequences assigned
No exact matches.
Count
1.00
0.75
0.50
0.25
0.00
9.50
9.75
10.00
10.25
10.50
Nucleotide Difference

3 Allele usage in potential haplotype anchor genes



4 Haplotype plots

5 Configuration settings

```
## Repertoire file: /work/jenkins/PRJNA248475/M4/M4_lesion/M4_lesion/M4_lesion/fc/24eebb10682e52bf34cb3
##
## Germline reference file: /work/jenkins/PRJNA248475/M4/M4_lesion/M4_lesion/M4_lesion/b8/33d6d26d1a43a
##
## Novel allele file:
##
## Species: Homosapiens
##
## Chain: IGHV
##
## Segment: V
##
## Warning   no inferred sequences found.
```