OGRDBstats Report

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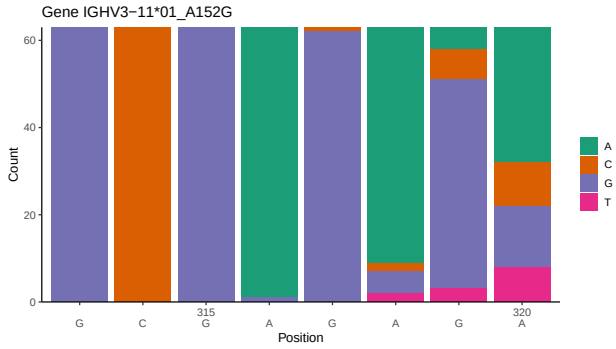
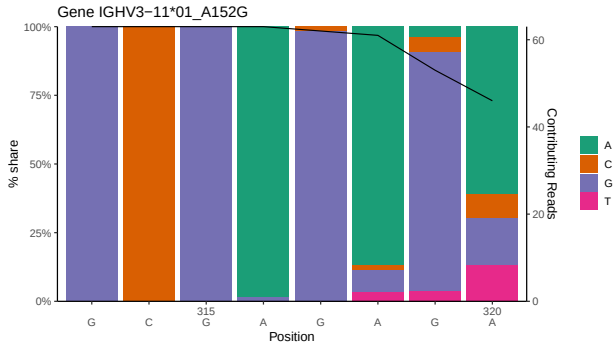
1 Novel sequence analysis

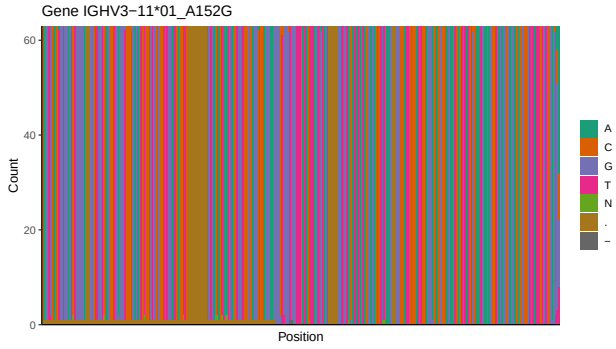
1.1 End-nucleotide composition



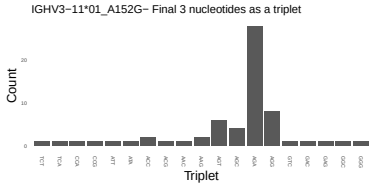
1.2 Per-nucleotide consensus where previous nucleotides match the consensus



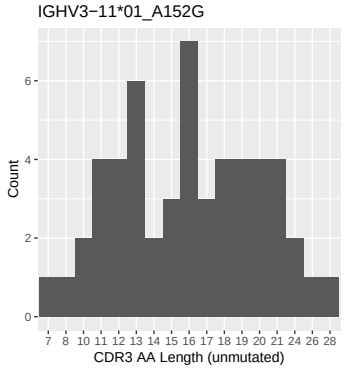
1.3 Whole-sequence composition of each assigned read



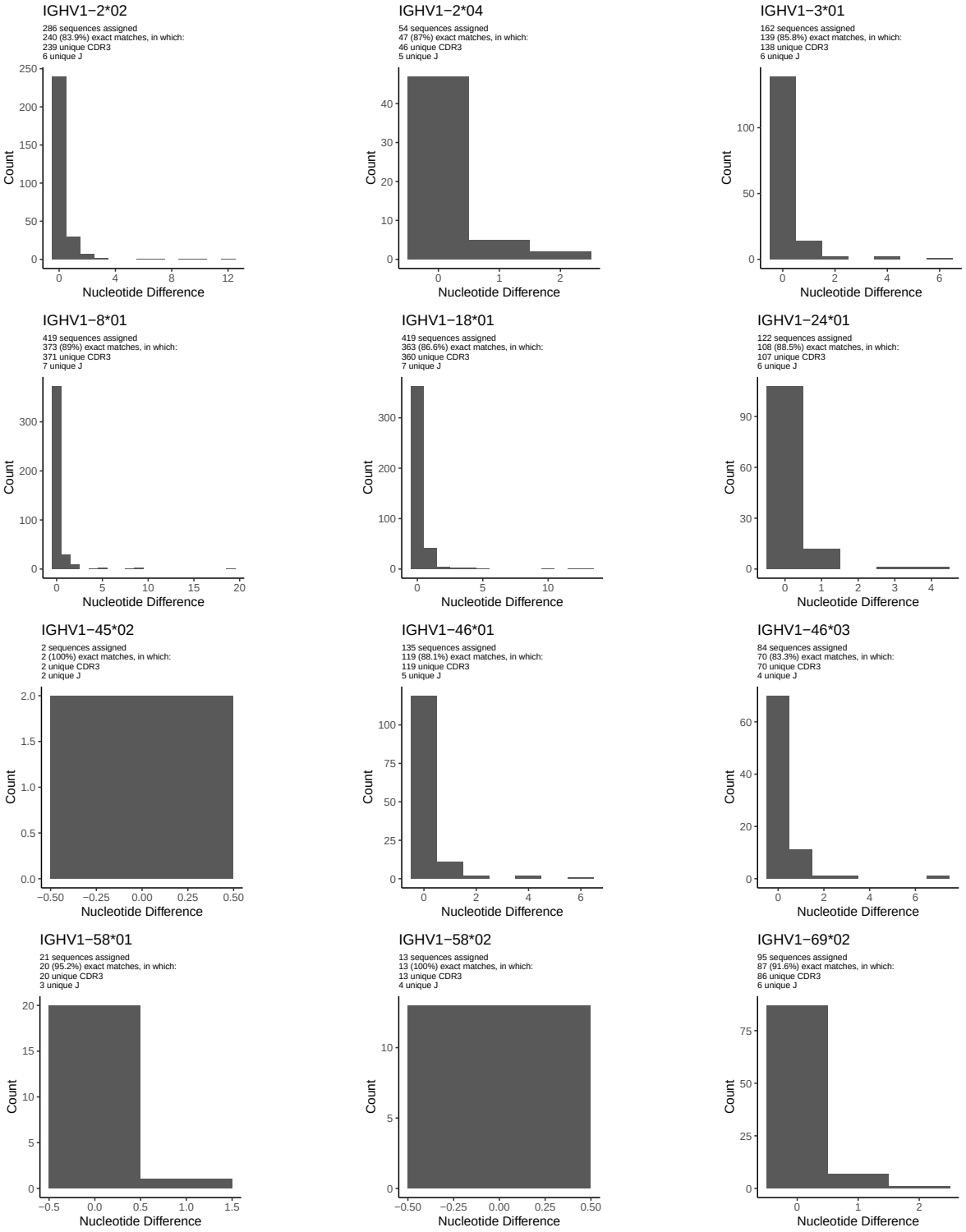
1.4 Final three nucleotides: frequency of each observed triplet

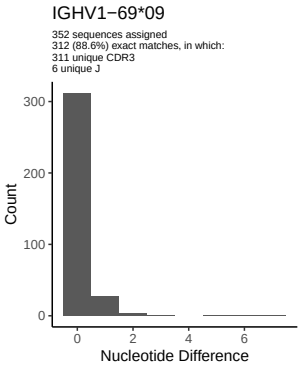


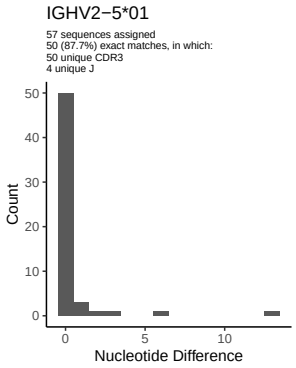
1.5 CDR3 length distribution, in assignments to novel alleles

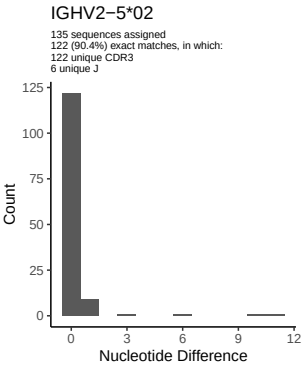


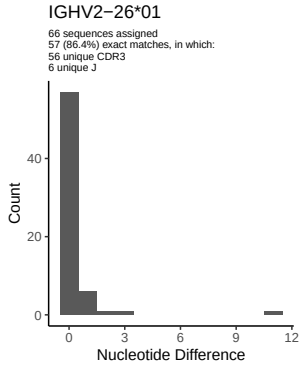
2 Variation from germline, in assignments to each allele

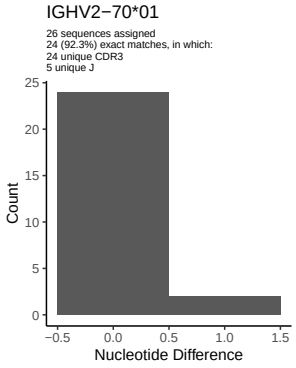


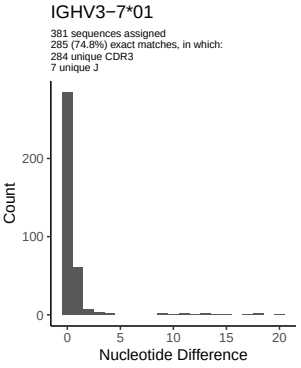

IGHV1−69*09
352 sequences assigned
312 (88.6%) exact matches, in which:
311 unique CDR3
6 unique J
Count
Nucleotide Difference

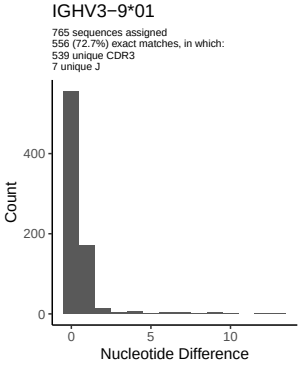

IGHV2−5*01
57 sequences assigned
50 (87.7%) exact matches, in which:
50 unique CDR3
4 unique J
Count
Nucleotide Difference

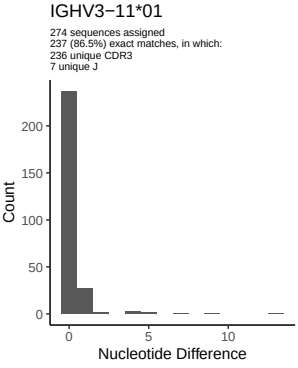

IGHV2−5*02
135 sequences assigned
122 (90.4%) exact matches, in which:
122 unique CDR3
6 unique J
Count
Nucleotide Difference

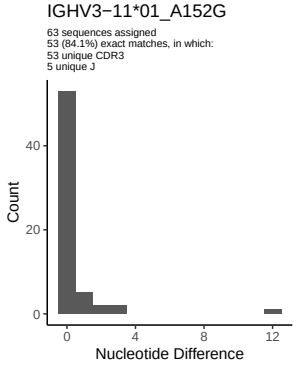

IGHV2−26*01
66 sequences assigned
57 (86.4%) exact matches, in which:
56 unique CDR3
6 unique J
Count
Nucleotide Difference

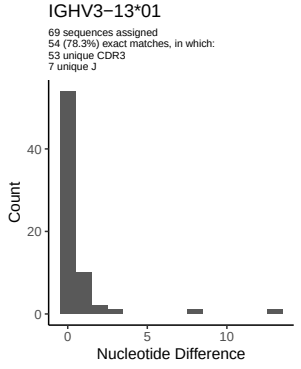

IGHV2−70*01
26 sequences assigned
24 (92.3%) exact matches, in which:
24 unique CDR3
5 unique J
Count
Nucleotide Difference

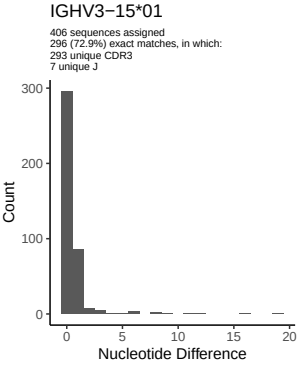

IGHV3−7*01
381 sequences assigned
285 (74.8%) exact matches, in which:
284 unique CDR3
7 unique J
Count
Nucleotide Difference

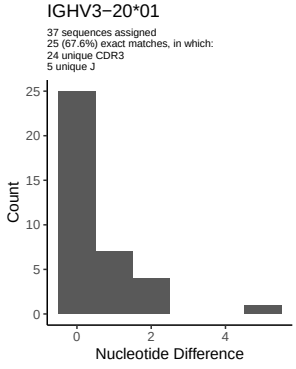

IGHV3−9*01
765 sequences assigned
556 (72.7%) exact matches, in which:
539 unique CDR3
7 unique J
Count
Nucleotide Difference

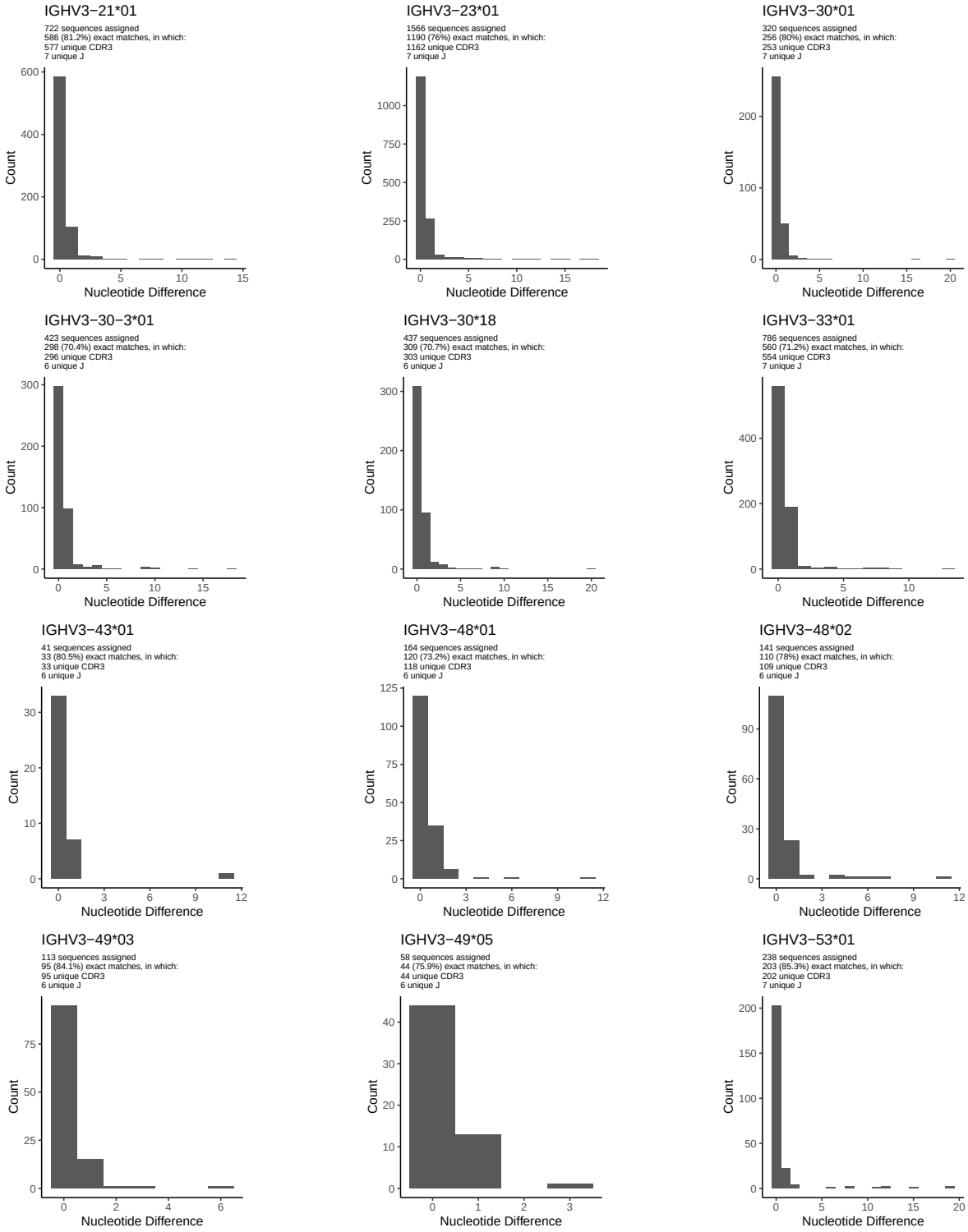

IGHV3−11*01
274 sequences assigned
237 (86.5%) exact matches, in which:
236 unique CDR3
7 unique J
Count
Nucleotide Difference

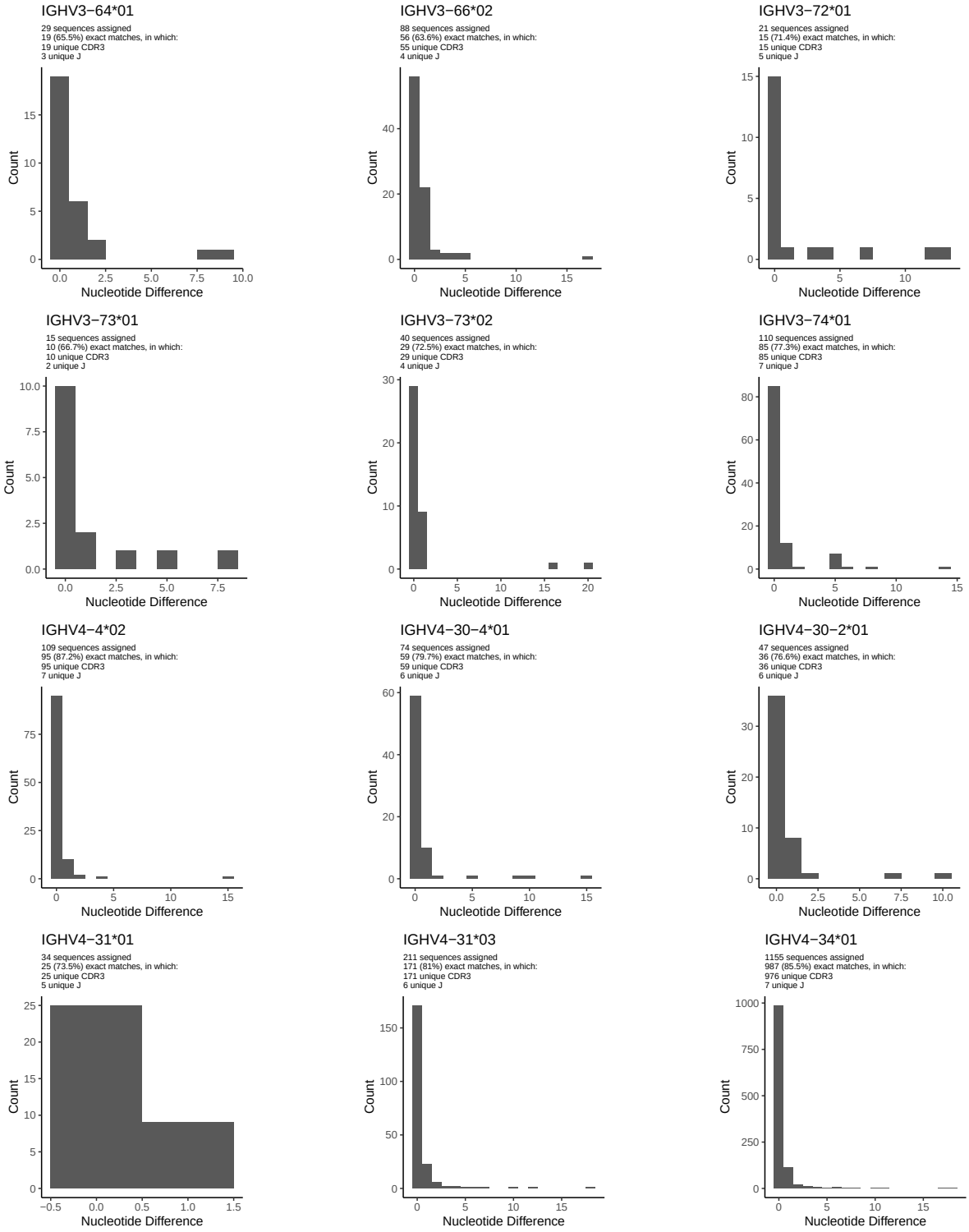

IGHV3−11*01_A152G
63 sequences assigned
53 (84.1%) exact matches, in which:
53 unique CDR3
5 unique J
Count
Nucleotide Difference

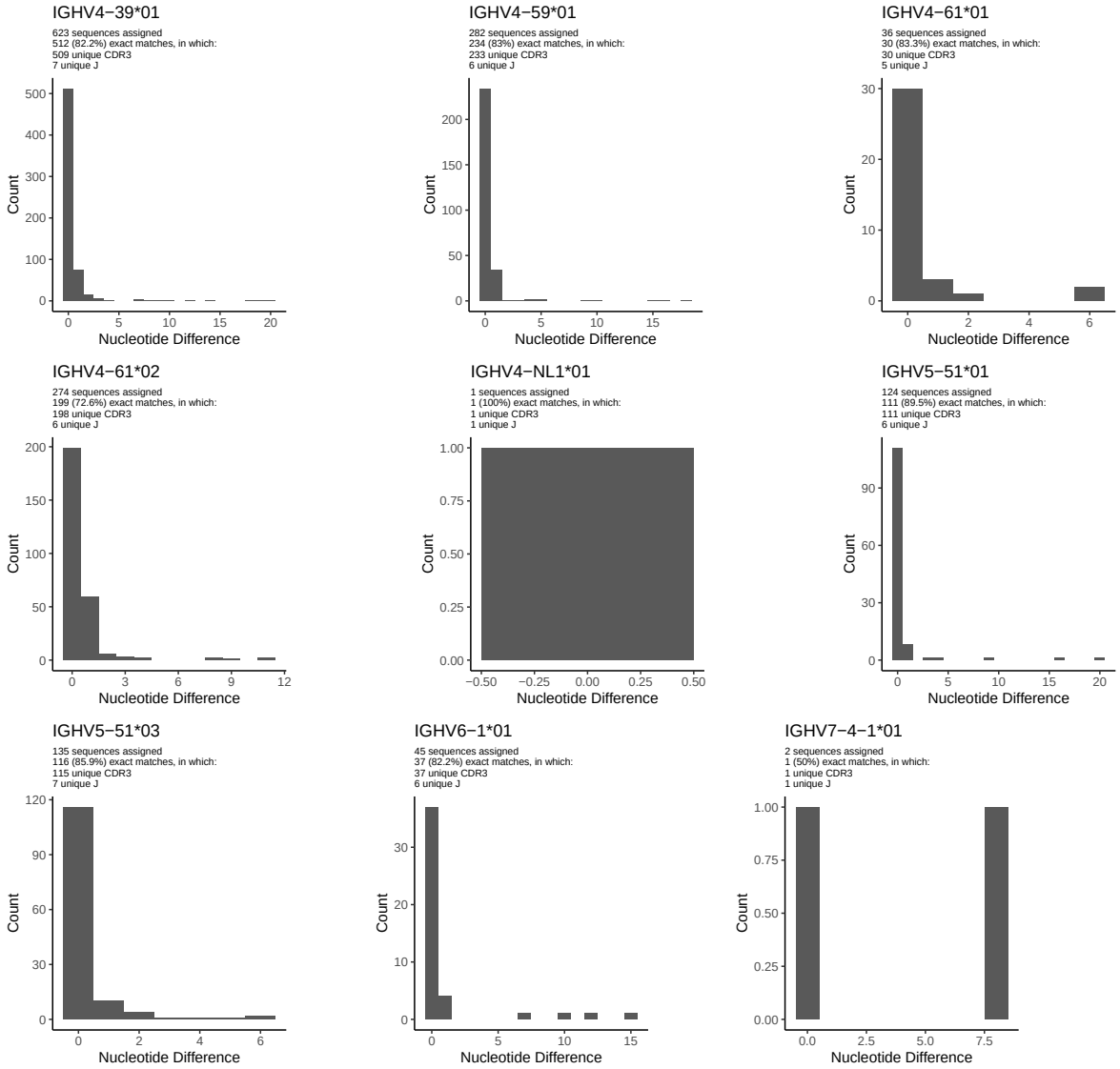

IGHV3−13*01
69 sequences assigned
54 (78.3%) exact matches, in which:
53 unique CDR3
7 unique J
Count
Nucleotide Difference


IGHV3−15*01
406 sequences assigned
296 (72.9%) exact matches, in which:
293 unique CDR3
7 unique J
Count
Nucleotide Difference

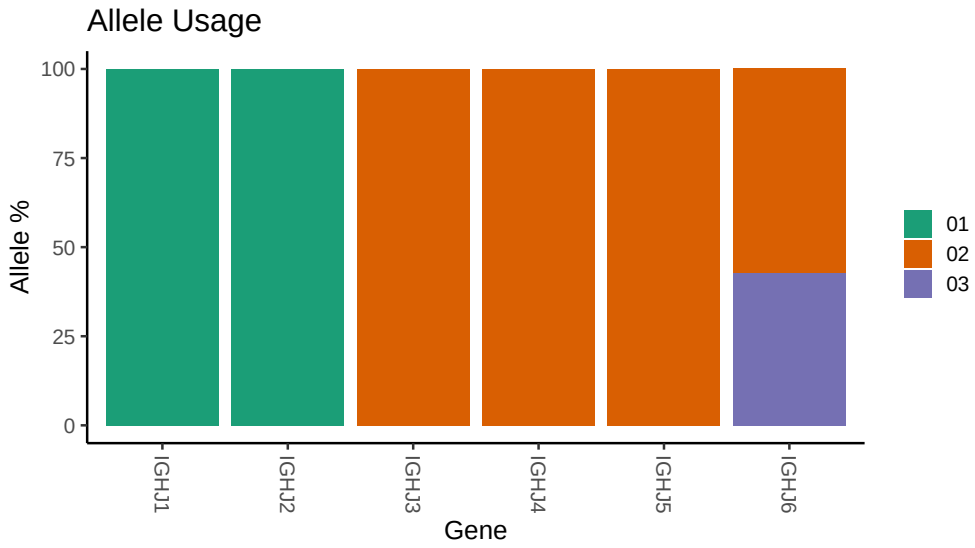

IGHV3−20*01
37 sequences assigned
25 (67.6%) exact matches, in which:
24 unique CDR3
5 unique J
Count
Nucleotide Difference


IGHV3−21*01
722 sequences assigned
586 (81.2%) exact matches, in which:
577 unique CDR3
7 unique J
IGHV3−23*01
1566 sequences assigned
1190 (76%) exact matches, in which:
1162 unique CDR3
7 unique J
IGHV3−30*01
320 sequences assigned
256 (80%) exact matches, in which:
253 unique CDR3
7 unique J
IGHV3−30−3*01
423 sequences assigned
298 (70.4%) exact matches, in which:
296 unique CDR3
6 unique J
IGHV3−30*18
437 sequences assigned
309 (70.7%) exact matches, in which:
303 unique CDR3
6 unique J
IGHV3−33*01
786 sequences assigned
560 (71.2%) exact matches, in which:
554 unique CDR3
7 unique J
IGHV3−43*01
41 sequences assigned
33 (80.5%) exact matches, in which:
33 unique CDR3
6 unique J
IGHV3−48*01
164 sequences assigned
120 (73.2%) exact matches, in which:
118 unique CDR3
6 unique J
IGHV3−48*02
141 sequences assigned
110 (78%) exact matches, in which:
109 unique CDR3
6 unique J
IGHV3−49*03
113 sequences assigned
95 (84.1%) exact matches, in which:
95 unique CDR3
6 unique J
IGHV3−49*05
58 sequences assigned
44 (75.9%) exact matches, in which:
44 unique CDR3
6 unique J
IGHV3−53*01
238 sequences assigned
203 (85.3%) exact matches, in which:
202 unique CDR3
7 unique J
Count
Nucleotide Difference

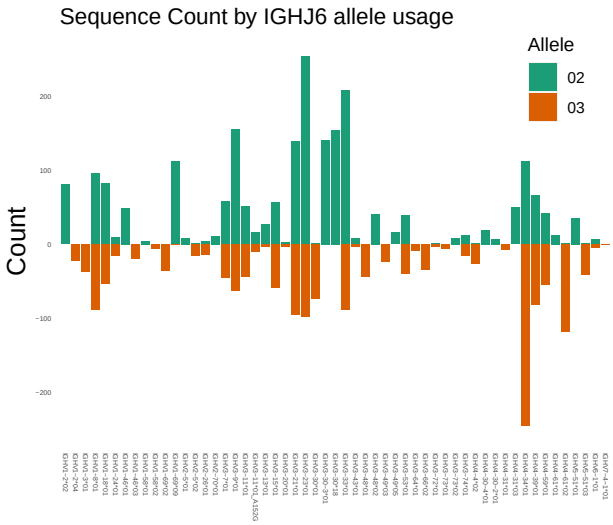

IGHV3−64*01
29 sequences assigned
19 (65.5%) exact matches, in which:
19 unique CDR3
3 unique J
IGHV3−66*02
88 sequences assigned
56 (63.6%) exact matches, in which:
55 unique CDR3
4 unique J
IGHV3−72*01
21 sequences assigned
15 (71.4%) exact matches, in which:
15 unique CDR3
5 unique J
IGHV3−73*01
15 sequences assigned
10 (66.7%) exact matches, in which:
10 unique CDR3
2 unique J
IGHV3−73*02
40 sequences assigned
29 (72.5%) exact matches, in which:
29 unique CDR3
4 unique J
IGHV3−74*01
110 sequences assigned
85 (77.3%) exact matches, in which:
85 unique CDR3
7 unique J
IGHV4−4*02
109 sequences assigned
95 (87.2%) exact matches, in which:
95 unique CDR3
7 unique J
IGHV4−30−4*01
74 sequences assigned
59 (79.7%) exact matches, in which:
59 unique CDR3
6 unique J
IGHV4−30−2*01
47 sequences assigned
36 (76.6%) exact matches, in which:
36 unique CDR3
6 unique J
IGHV4−31*01
34 sequences assigned
25 (73.5%) exact matches, in which:
25 unique CDR3
5 unique J
IGHV4−31*03
211 sequences assigned
171 (81%) exact matches, in which:
171 unique CDR3
6 unique J
IGHV4−34*01
1155 sequences assigned
987 (85.5%) exact matches, in which:
976 unique CDR3
7 unique J
Count
Nucleotide Difference


IGHV4−39*01
623 sequences assigned
512 (82.2%) exact matches, in which:
509 unique CDR3
7 unique J
IGHV4−59*01
282 sequences assigned
234 (83%) exact matches, in which:
233 unique CDR3
6 unique J
IGHV4−61*01
36 sequences assigned
30 (83.3%) exact matches, in which:
30 unique CDR3
5 unique J
IGHV4−61*02
274 sequences assigned
199 (72.6%) exact matches, in which:
198 unique CDR3
6 unique J
IGHV4−NL1*01
1 sequences assigned
1 (100%) exact matches, in which:
1 unique CDR3
1 unique J
IGHV5−51*01
124 sequences assigned
111 (89.5%) exact matches, in which:
111 unique CDR3
6 unique J
IGHV5−51*03
135 sequences assigned
116 (85.9%) exact matches, in which:
115 unique CDR3
7 unique J
IGHV6−1*01
45 sequences assigned
37 (82.2%) exact matches, in which:
37 unique CDR3
6 unique J
IGHV7−4−1*01
2 sequences assigned
1 (50%) exact matches, in which:
1 unique CDR3
1 unique J
Count
Nucleotide Difference

3 Allele usage in potential haplotype anchor genes



4 Haplotype plots



5 Configuration settings

```
## Repertoire file: /misc/work/jenkins/PRJEB26509/S100/S100/100/100/c0/b828c2861ff5c5d85487ce4b318c8f/1
##
## Germline reference file: /misc/work/jenkins/PRJEB26509/S100/S100/100/100/c0/b828c2861ff5c5d85487ce4b
##
## Novel allele file: /misc/work/jenkins/PRJEB26509/S100/S100/100/100/c0/b828c2861ff5c5d85487ce4b318c8f/
##
## Species: Homosapiens
##
## Chain: IGHV
##
## Segment: V
```