OGRDBstats Report

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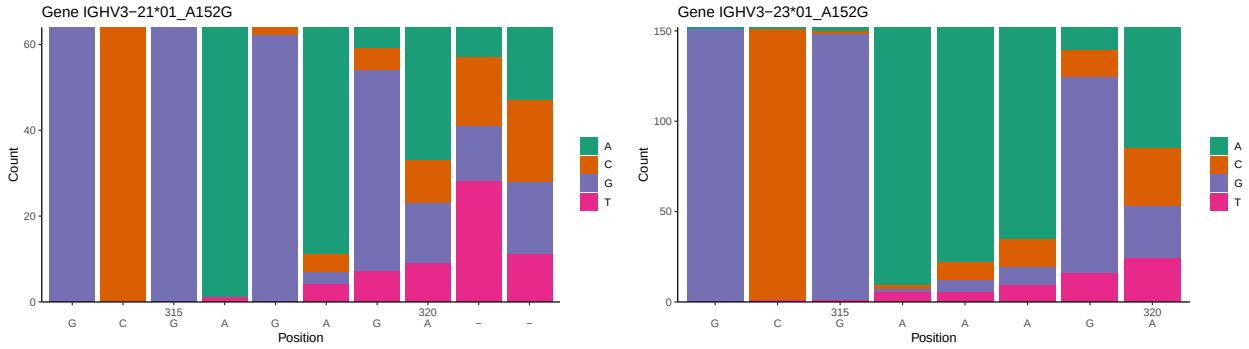
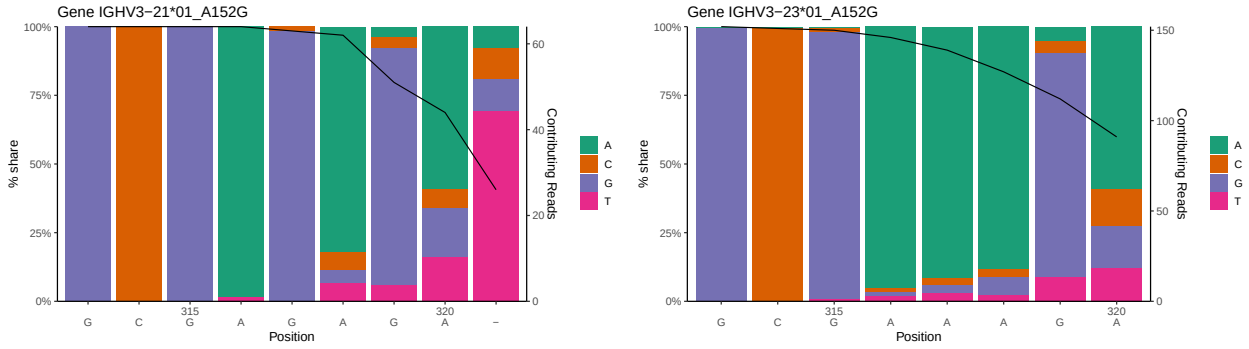
1 Novel sequence analysis

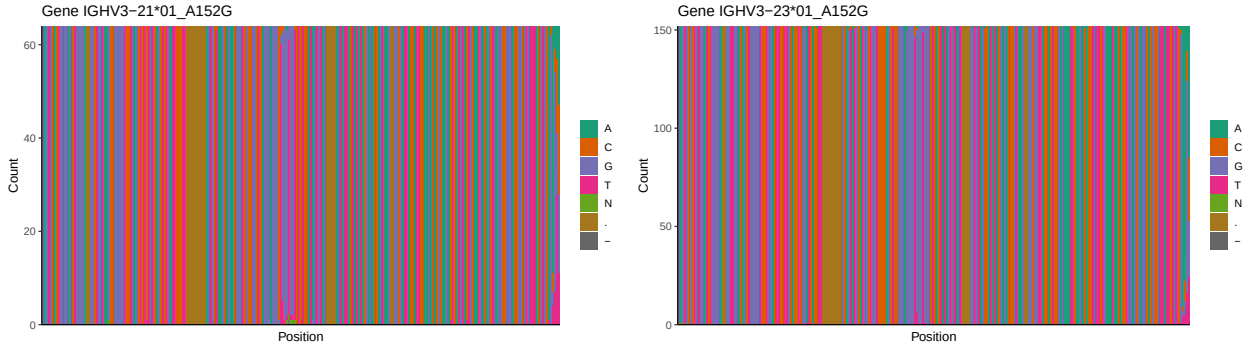
1.1 End-nucleotide composition



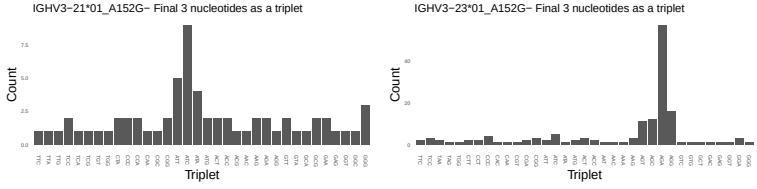
1.2 Per-nucleotide consensus where previous nucleotides match the consensus



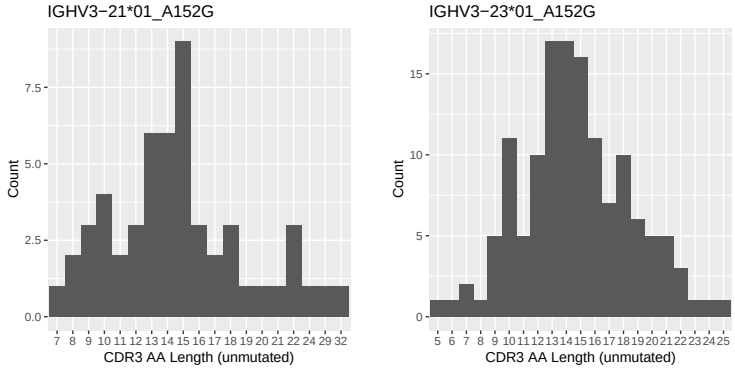
1.3 Whole-sequence composition of each assigned read



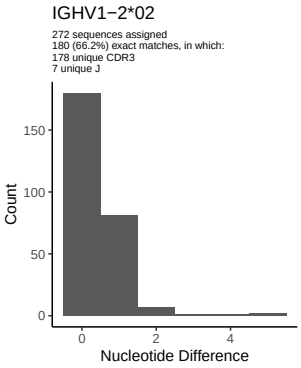
1.4 Final three nucleotides: frequency of each observed triplet

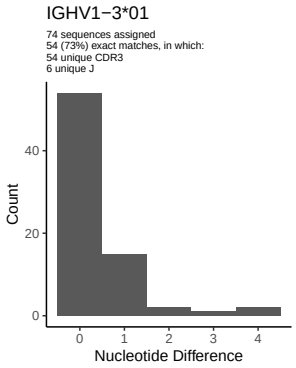


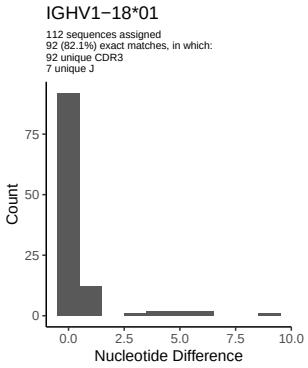
1.5 CDR3 length distribution, in assignments to novel alleles

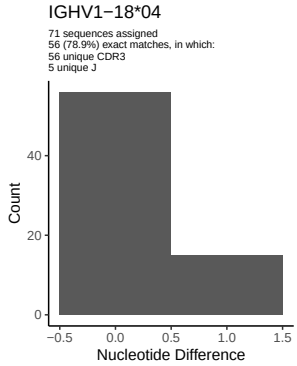


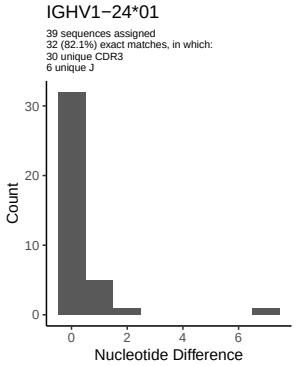
2 Variation from germline, in assignments to each allele

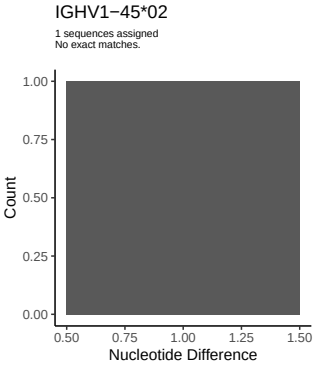


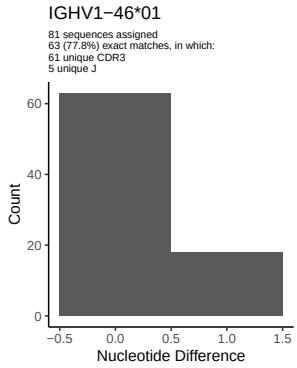


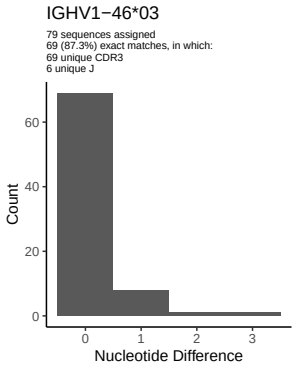


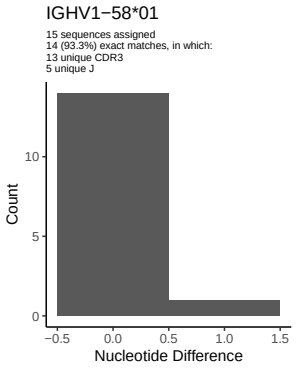


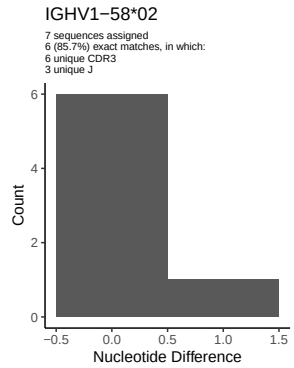


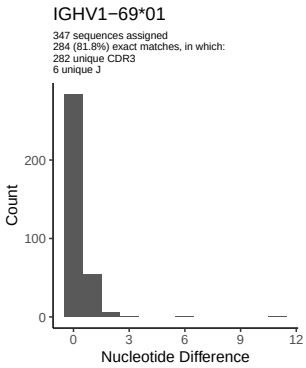


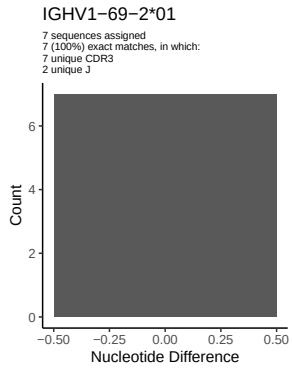


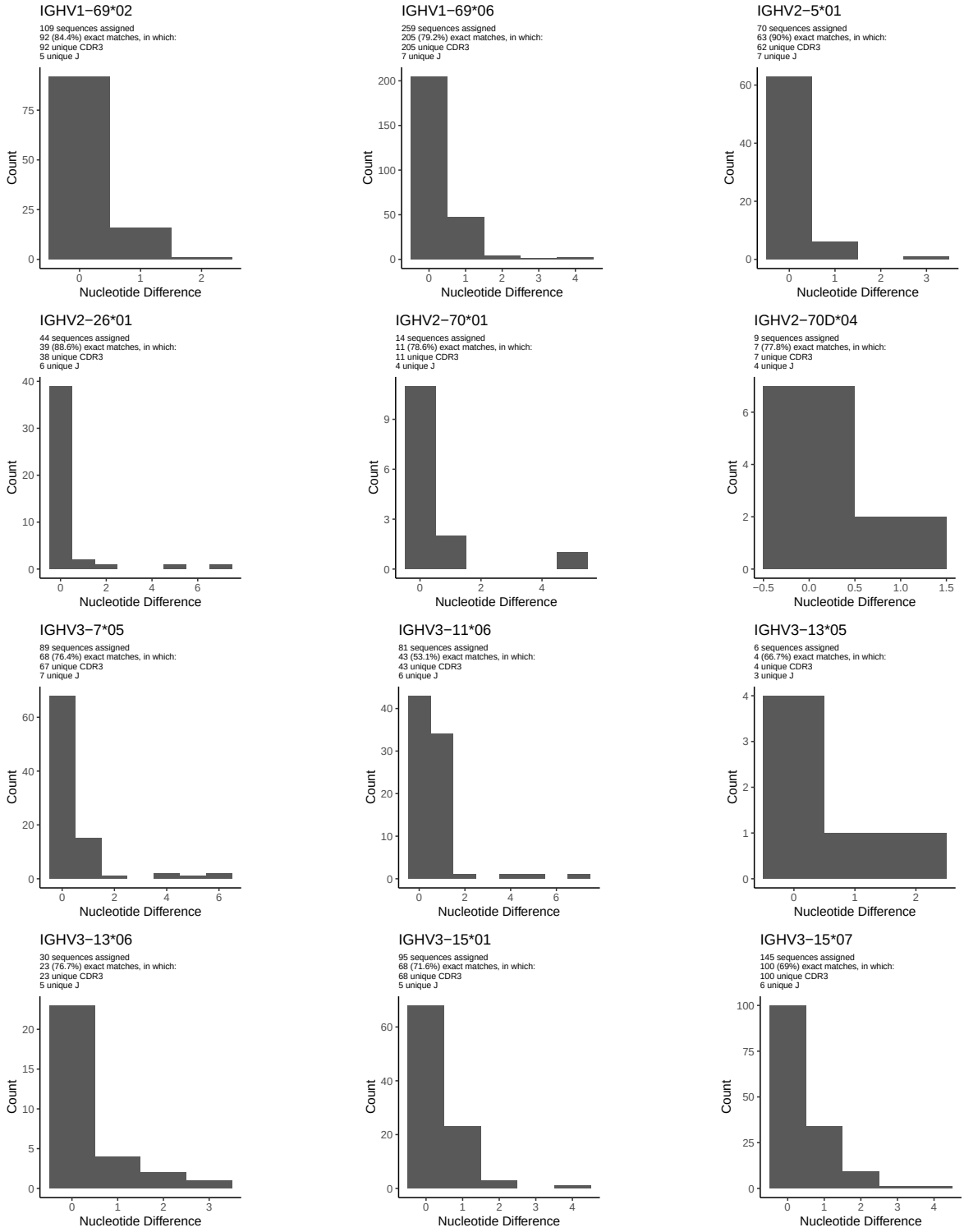


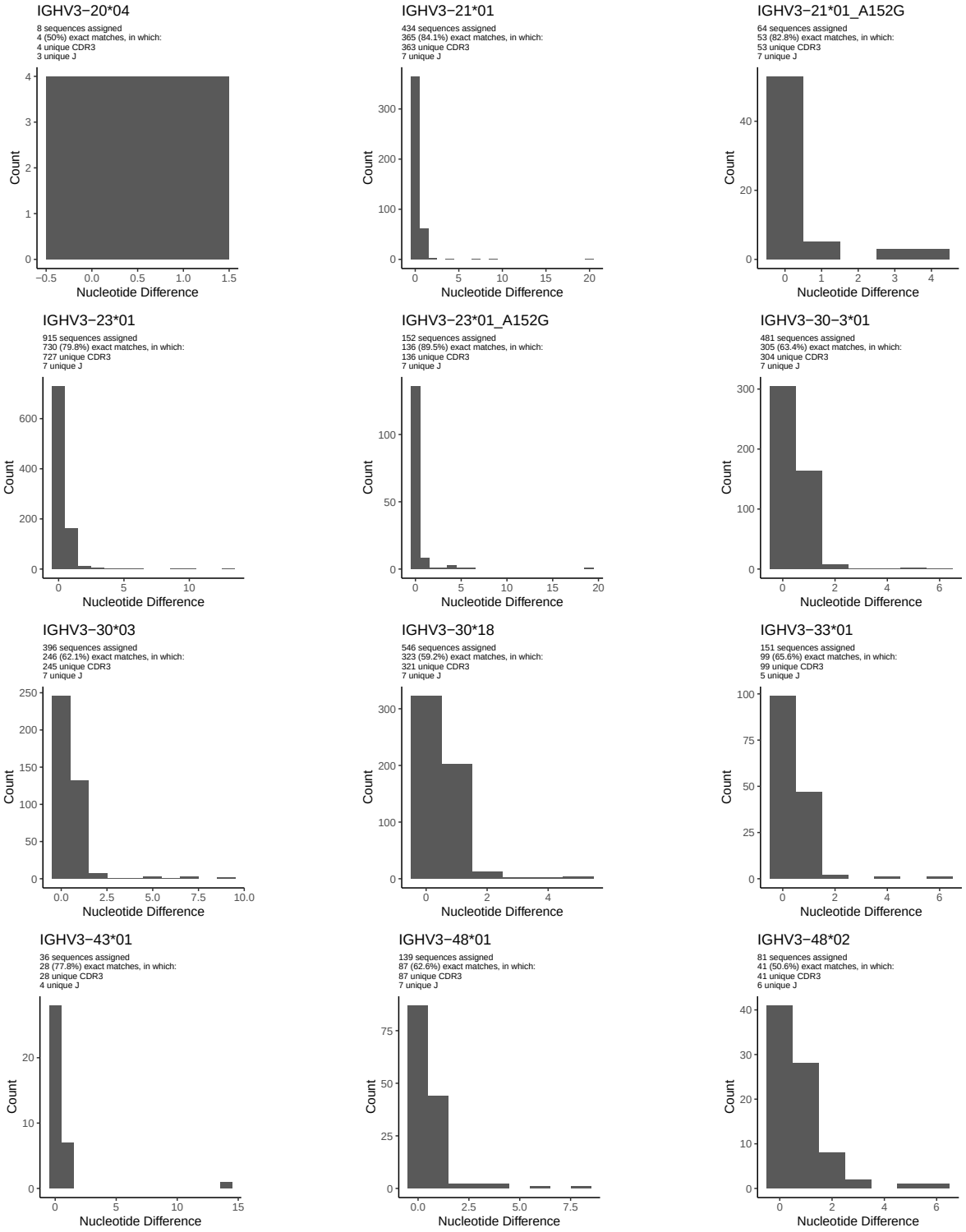


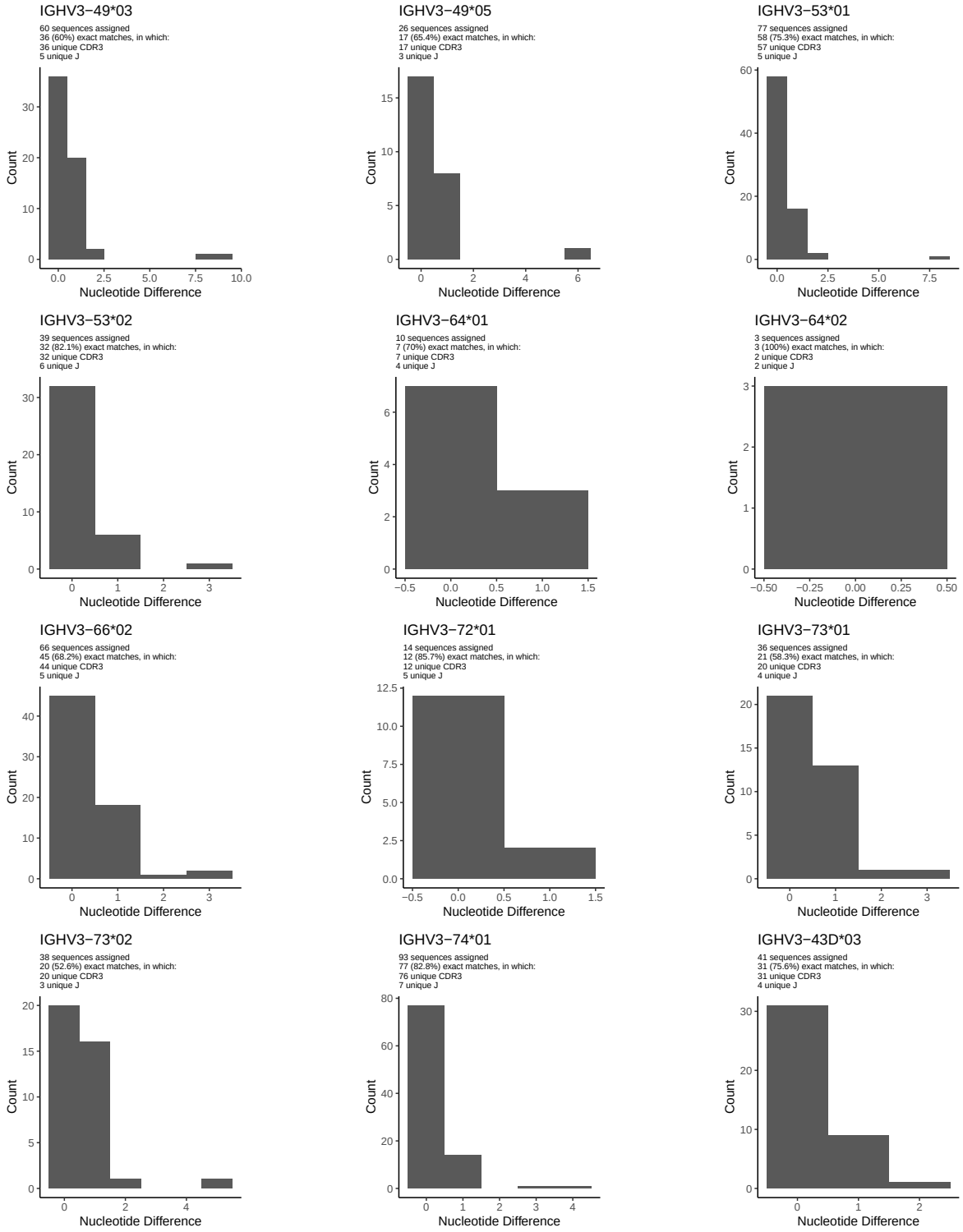


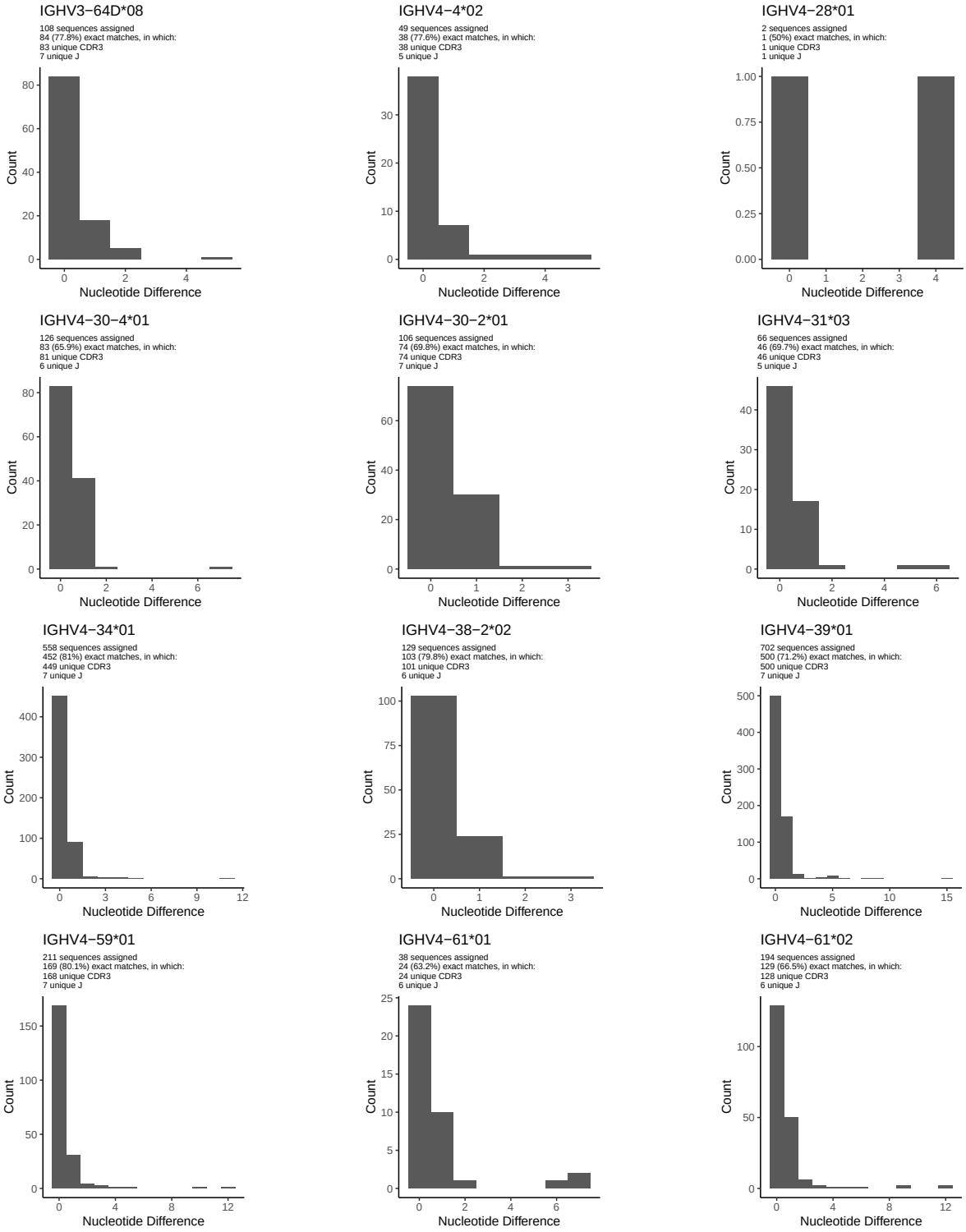


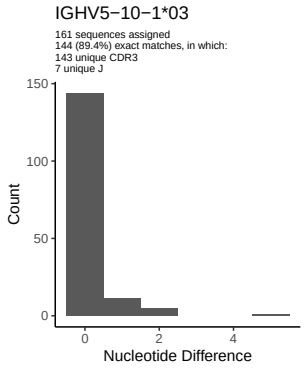


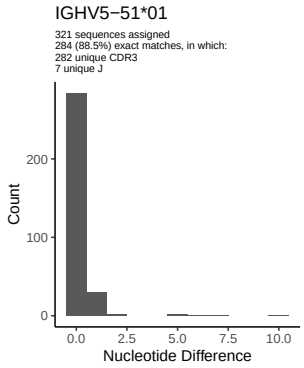

IGHV1−69*02
109 sequences assigned
92 (84.4%) exact matches, in which:
92 unique CDR3
5 unique J
IGHV1−69*06
259 sequences assigned
205 (79.2%) exact matches, in which:
205 unique CDR3
7 unique J
IGHV2−5*01
70 sequences assigned
63 (90%) exact matches, in which:
62 unique CDR3
7 unique J
IGHV2−26*01
44 sequences assigned
39 (88.6%) exact matches, in which:
38 unique CDR3
6 unique J
IGHV2−70*01
14 sequences assigned
11 (78.6%) exact matches, in which:
11 unique CDR3
4 unique J
IGHV2−70D*04
9 sequences assigned
7 (77.8%) exact matches, in which:
7 unique CDR3
4 unique J
IGHV3−7*05
89 sequences assigned
68 (76.4%) exact matches, in which:
67 unique CDR3
7 unique J
IGHV3−11*06
81 sequences assigned
43 (53.1%) exact matches, in which:
43 unique CDR3
6 unique J
IGHV3−13*05
6 sequences assigned
4 (66.7%) exact matches, in which:
4 unique CDR3
3 unique J
IGHV3−13*06
30 sequences assigned
23 (76.7%) exact matches, in which:
23 unique CDR3
5 unique J
IGHV3−15*01
95 sequences assigned
68 (71.6%) exact matches, in which:
68 unique CDR3
5 unique J
IGHV3−15*07
145 sequences assigned
100 (69%) exact matches, in which:
100 unique CDR3
6 unique J
Count
Nucleotide Difference

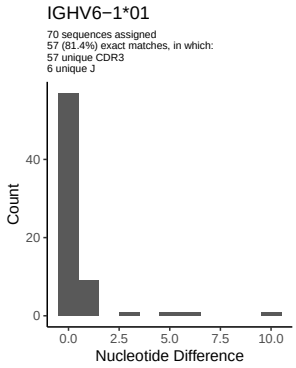

IGHV3−20*04
8 sequences assigned
4 (50%) exact matches, in which:
4 unique CDR3
3 unique J
IGHV3−21*01
434 sequences assigned
365 (84.1%) exact matches, in which:
363 unique CDR3
7 unique J
IGHV3−21*01_A152G
64 sequences assigned
53 (82.8%) exact matches, in which:
53 unique CDR3
7 unique J
IGHV3−23*01
915 sequences assigned
730 (79.8%) exact matches, in which:
727 unique CDR3
7 unique J
IGHV3−23*01_A152G
152 sequences assigned
136 (89.5%) exact matches, in which:
136 unique CDR3
7 unique J
IGHV3−30−3*01
481 sequences assigned
305 (63.4%) exact matches, in which:
304 unique CDR3
7 unique J
IGHV3−30*03
396 sequences assigned
246 (62.1%) exact matches, in which:
245 unique CDR3
7 unique J
IGHV3−30*18
546 sequences assigned
323 (59.2%) exact matches, in which:
321 unique CDR3
7 unique J
IGHV3−33*01
151 sequences assigned
99 (65.6%) exact matches, in which:
99 unique CDR3
5 unique J
IGHV3−43*01
36 sequences assigned
28 (77.8%) exact matches, in which:
28 unique CDR3
4 unique J
IGHV3−48*01
139 sequences assigned
87 (62.6%) exact matches, in which:
87 unique CDR3
7 unique J
IGHV3−48*02
81 sequences assigned
41 (50.6%) exact matches, in which:
41 unique CDR3
6 unique J
Count
Nucleotide Difference

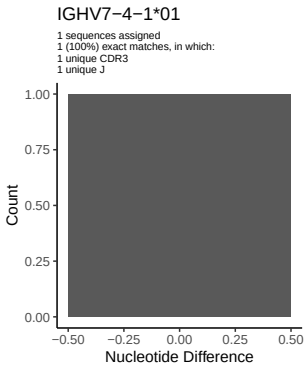

IGHV3−49*03
60 sequences assigned
36 (60%) exact matches, in which:
36 unique CDR3
5 unique J
IGHV3−49*05
26 sequences assigned
17 (65.4%) exact matches, in which:
17 unique CDR3
3 unique J
IGHV3−53*01
77 sequences assigned
58 (75.3%) exact matches, in which:
57 unique CDR3
5 unique J
IGHV3−53*02
39 sequences assigned
32 (82.1%) exact matches, in which:
32 unique CDR3
6 unique J
IGHV3−64*01
10 sequences assigned
7 (70%) exact matches, in which:
7 unique CDR3
4 unique J
IGHV3−64*02
3 sequences assigned
3 (100%) exact matches, in which:
2 unique CDR3
2 unique J
IGHV3−66*02
66 sequences assigned
45 (68.2%) exact matches, in which:
44 unique CDR3
5 unique J
IGHV3−72*01
14 sequences assigned
12 (85.7%) exact matches, in which:
12 unique CDR3
5 unique J
IGHV3−73*01
36 sequences assigned
21 (58.3%) exact matches, in which:
20 unique CDR3
4 unique J
IGHV3−73*02
38 sequences assigned
20 (52.6%) exact matches, in which:
20 unique CDR3
3 unique J
IGHV3−74*01
93 sequences assigned
77 (82.8%) exact matches, in which:
76 unique CDR3
7 unique J
IGHV3−43D*03
41 sequences assigned
31 (75.6%) exact matches, in which:
31 unique CDR3
4 unique J
Count
Nucleotide Difference


IGHV3−64D*08
108 sequences assigned
84 (77.8%) exact matches, in which:
83 unique CDR3
7 unique J
IGHV4−4*02
49 sequences assigned
38 (77.6%) exact matches, in which:
38 unique CDR3
5 unique J
IGHV4−28*01
2 sequences assigned
1 (50%) exact matches, in which:
1 unique CDR3
1 unique J
IGHV4−30−4*01
126 sequences assigned
83 (65.9%) exact matches, in which:
81 unique CDR3
6 unique J
IGHV4−30−2*01
106 sequences assigned
74 (69.8%) exact matches, in which:
74 unique CDR3
7 unique J
IGHV4−31*03
66 sequences assigned
46 (69.7%) exact matches, in which:
46 unique CDR3
5 unique J
IGHV4−34*01
558 sequences assigned
452 (81%) exact matches, in which:
449 unique CDR3
7 unique J
IGHV4−38−2*02
129 sequences assigned
103 (79.8%) exact matches, in which:
101 unique CDR3
6 unique J
IGHV4−39*01
702 sequences assigned
500 (71.2%) exact matches, in which:
500 unique CDR3
7 unique J
IGHV4−59*01
211 sequences assigned
169 (80.1%) exact matches, in which:
168 unique CDR3
7 unique J
IGHV4−61*01
38 sequences assigned
24 (63.2%) exact matches, in which:
24 unique CDR3
6 unique J
IGHV4−61*02
194 sequences assigned
129 (66.5%) exact matches, in which:
128 unique CDR3
6 unique J
Count
Nucleotide Difference

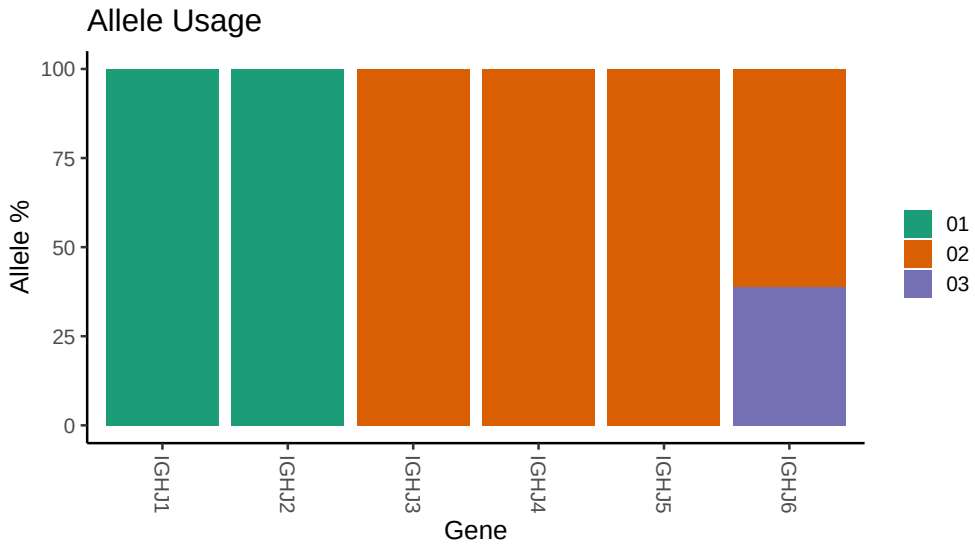

IGHV5−10−1*03
161 sequences assigned
144 (89.4%) exact matches, in which:
143 unique CDR3
7 unique J
Count
Nucleotide Difference


IGHV5−51*01
321 sequences assigned
284 (88.5%) exact matches, in which:
282 unique CDR3
7 unique J
Count
Nucleotide Difference

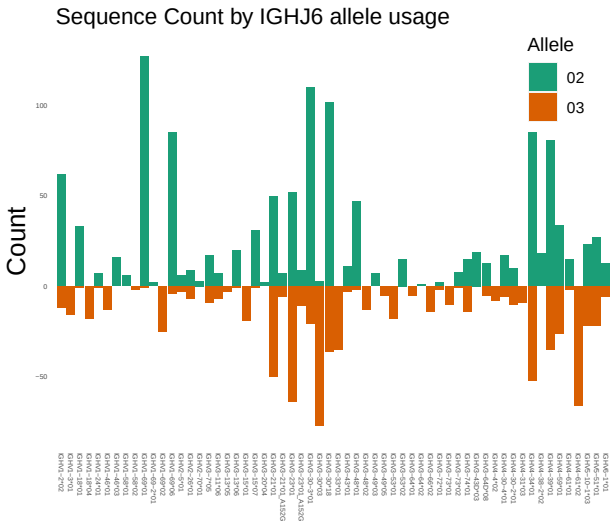

IGHV6−1*01
70 sequences assigned
57 (81.4%) exact matches, in which:
57 unique CDR3
6 unique J
Count
Nucleotide Difference


IGHV7−4−1*01
1 sequences assigned
1 (100%) 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/S65/S65/69/69/8f/0105e28d6bff92a844a3d66208889a/69_Fi
##
## Germline reference file: /misc/work/jenkins/PRJEB26509/S65/S65/69/69/8f/0105e28d6bff92a844a3d6620888
##
## Novel allele file: /misc/work/jenkins/PRJEB26509/S65/S65/69/69/8f/0105e28d6bff92a844a3d66208889a/nov
##
## Species: Homosapiens
##
## Chain: IGHV
##
## Segment: V
##
## warning: non codon aligned gaps were found in novel sequence IGHV3 21 01_A152G
```