OGRDBstats Report

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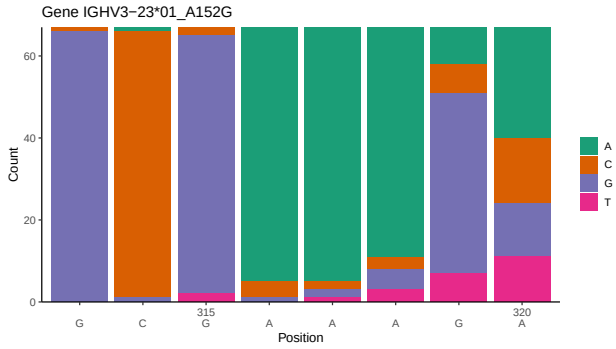
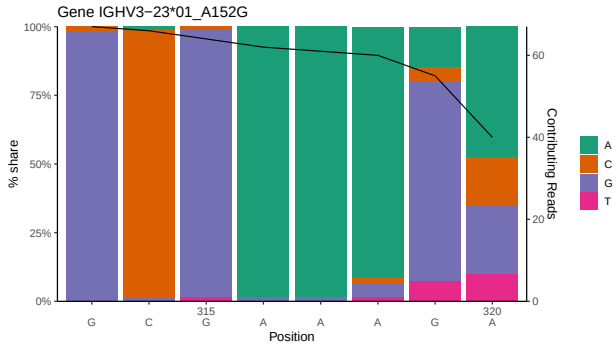
1 Novel sequence analysis

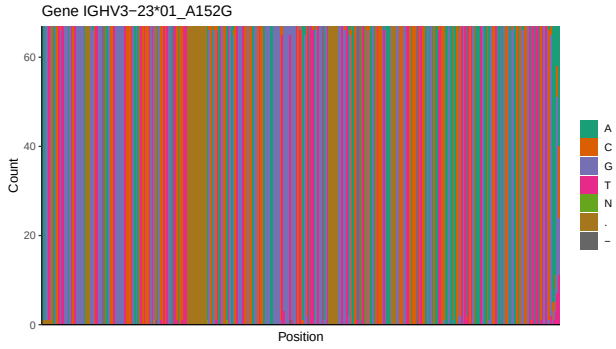
1.1 End-nucleotide composition



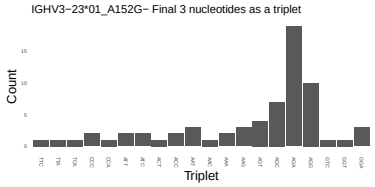
1.2 Per-nucleotide consensus where previous nucleotides match the consensus



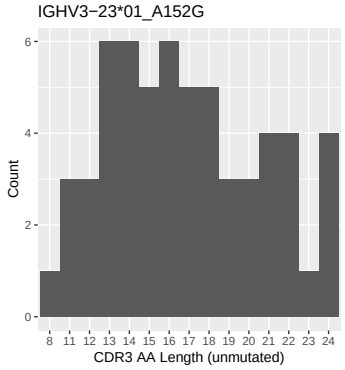
1.3 Whole-sequence composition of each assigned read



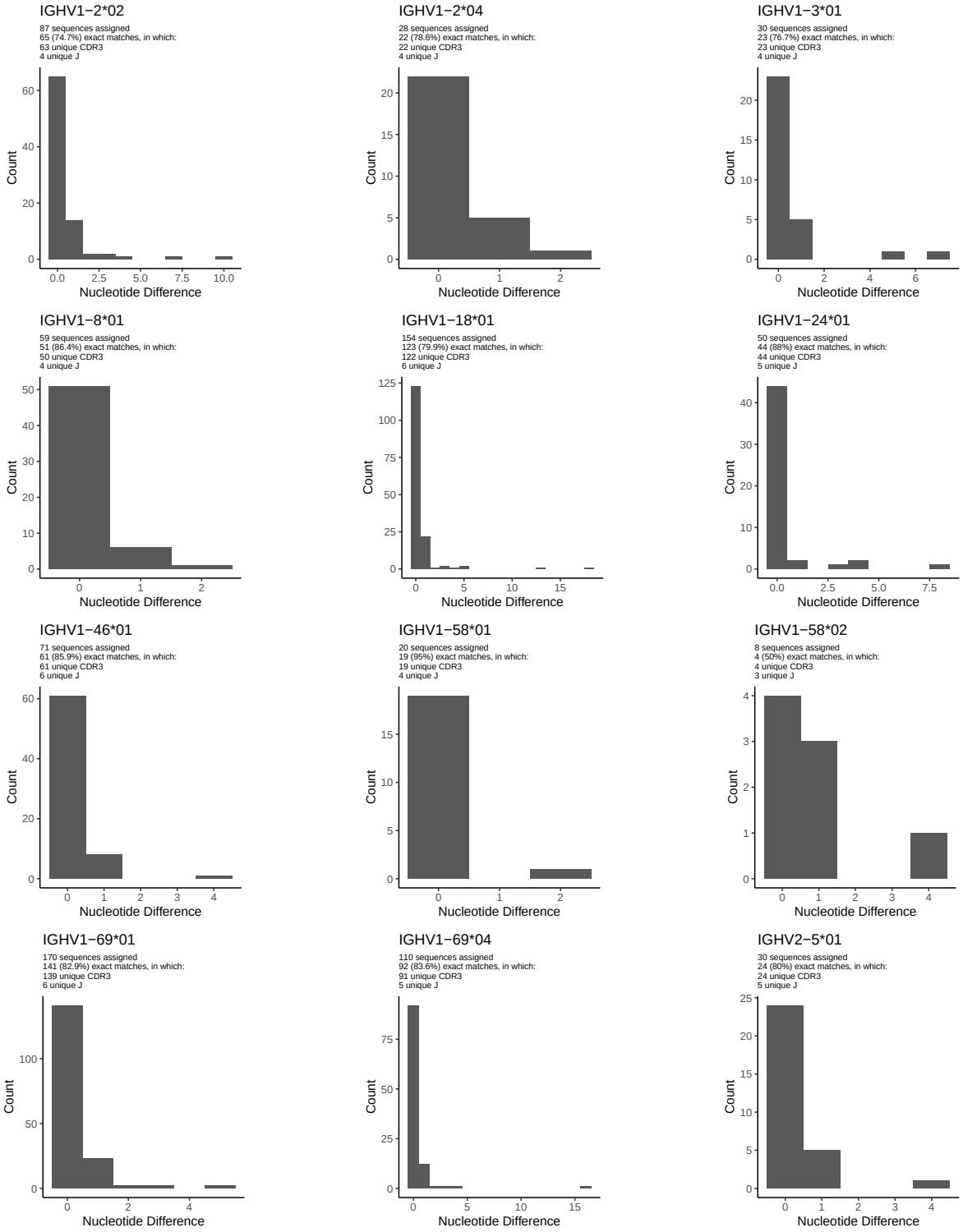
1.4 Final three nucleotides: frequency of each observed triplet

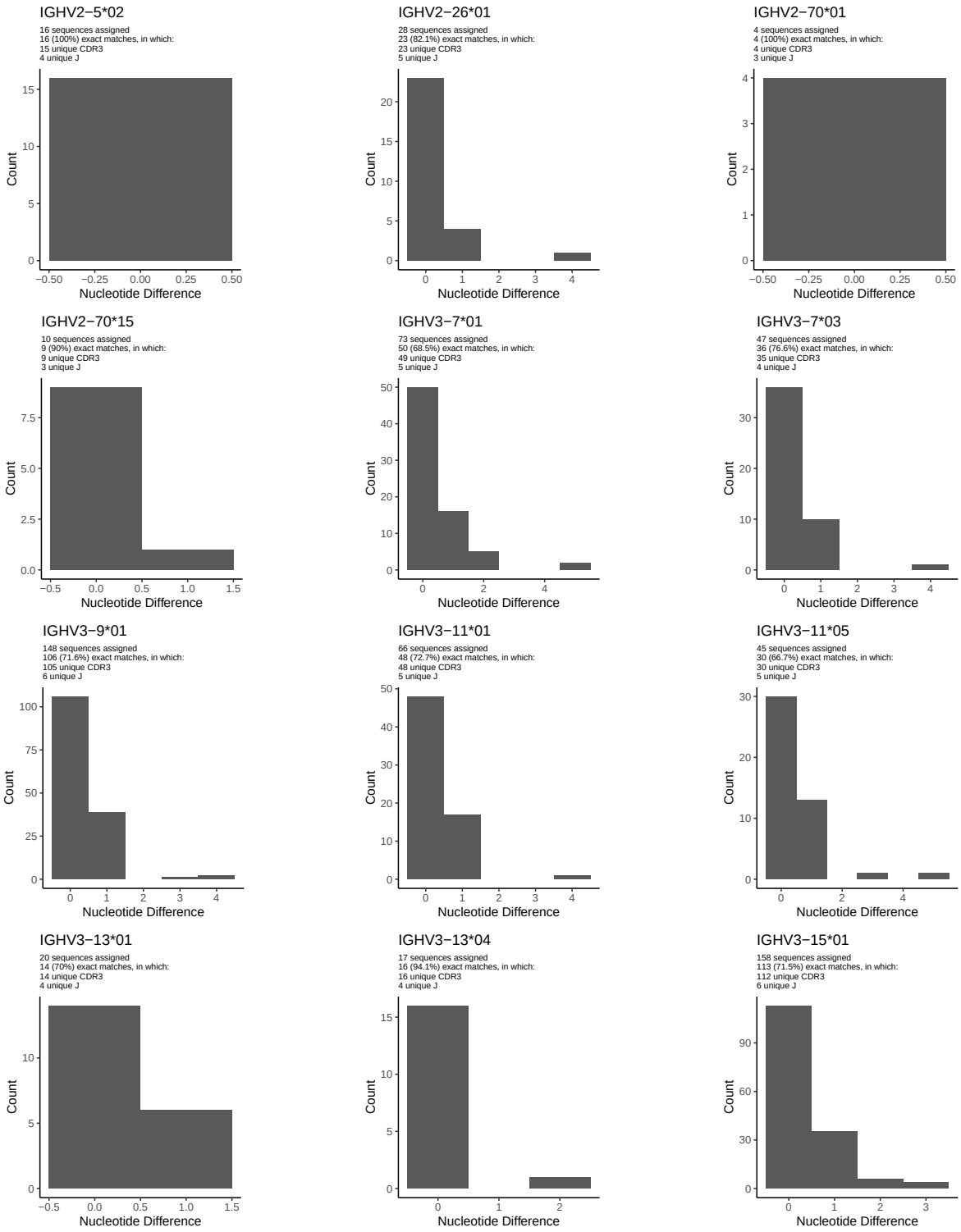


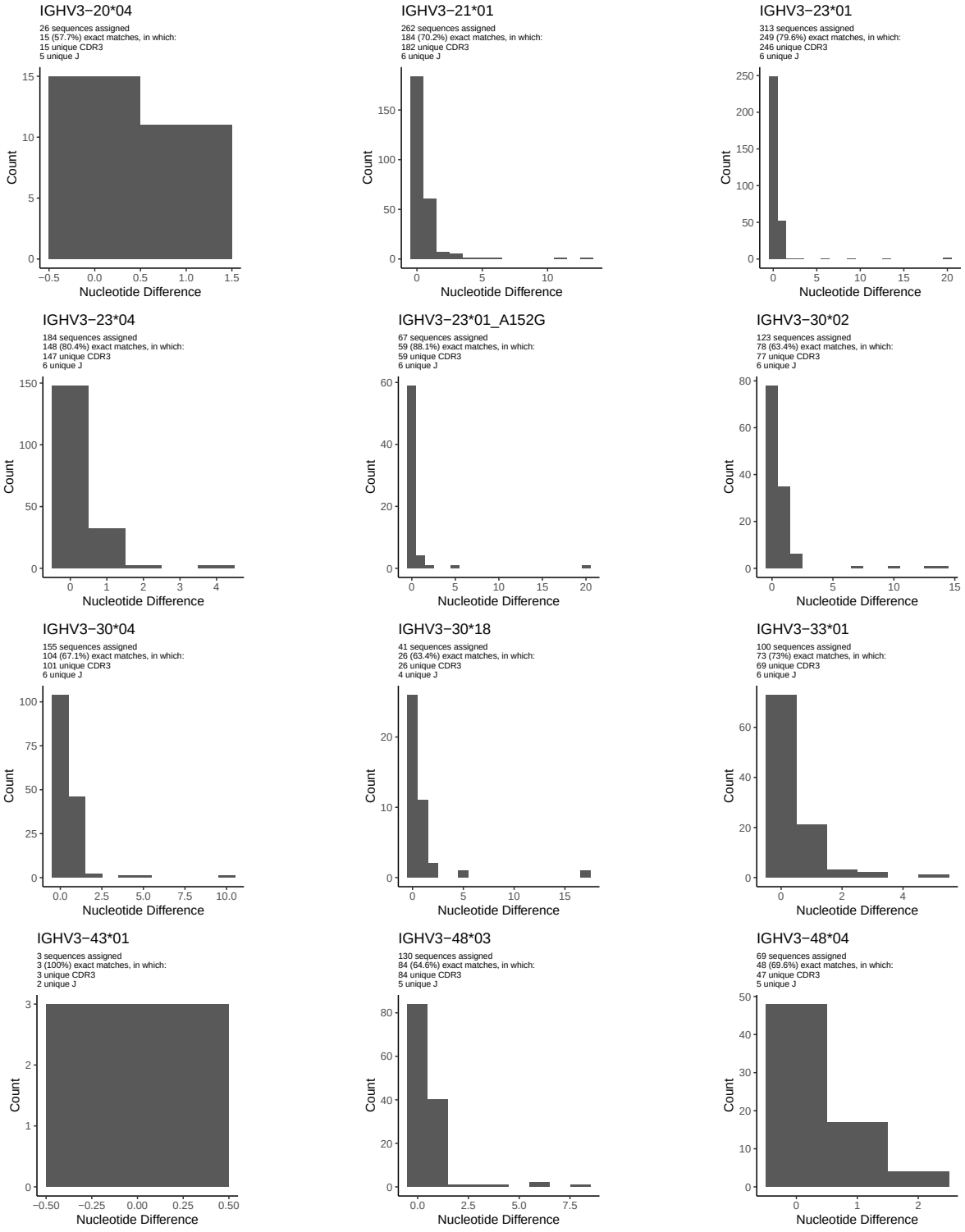
1.5 CDR3 length distribution, in assignments to novel alleles

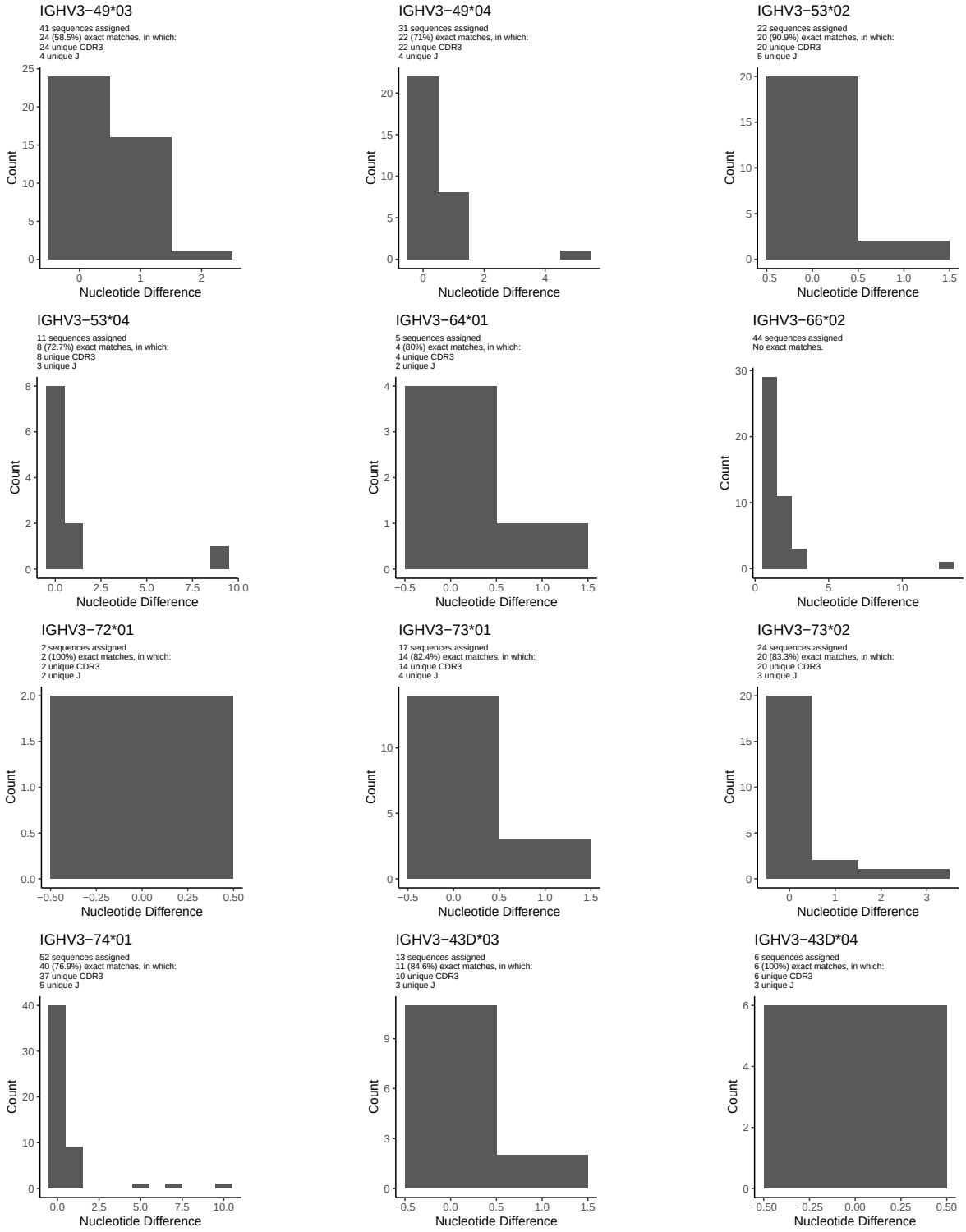


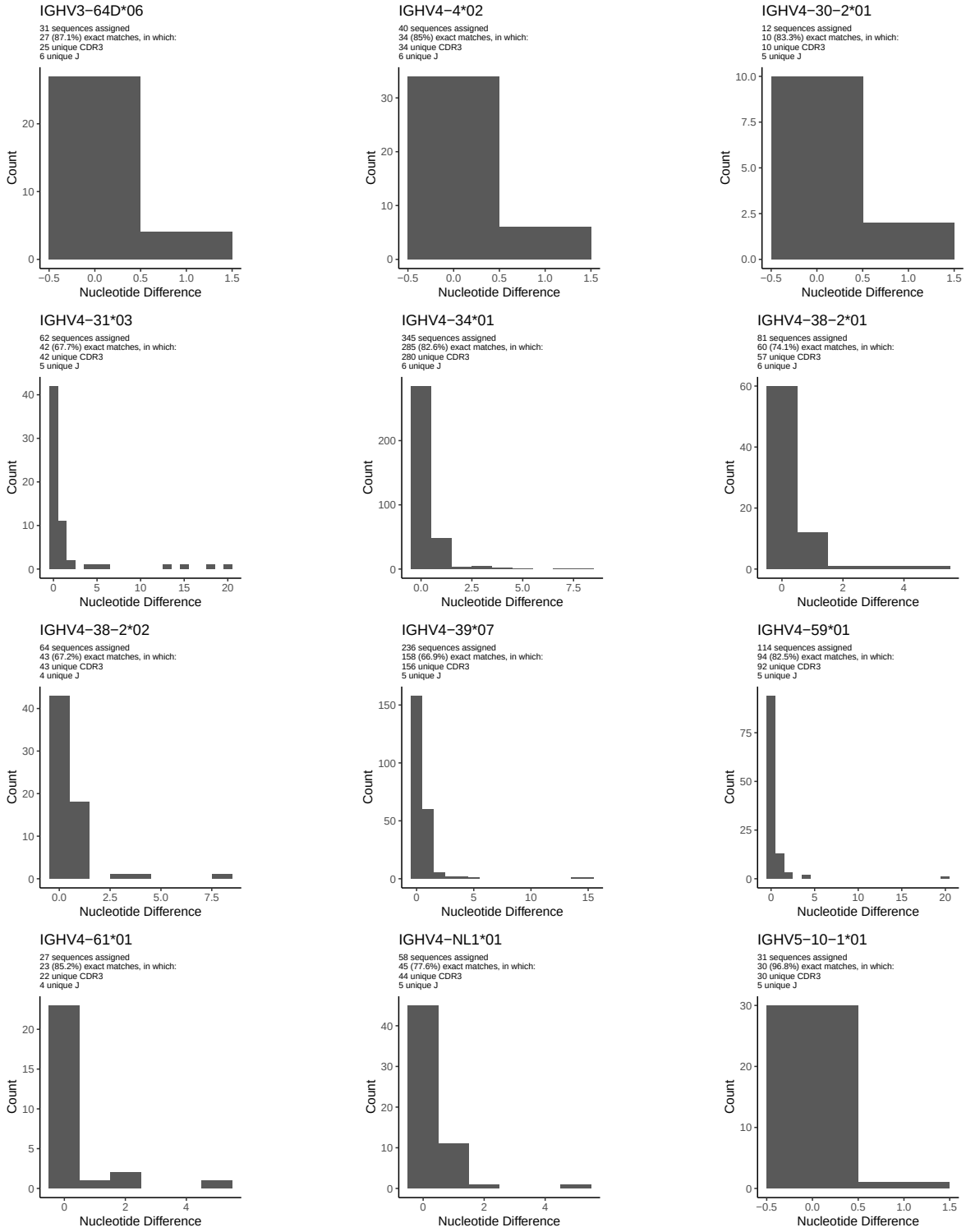
2 Variation from germline, in assignments to each allele

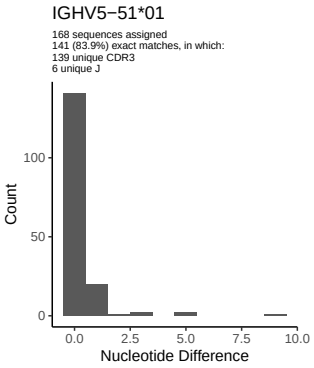


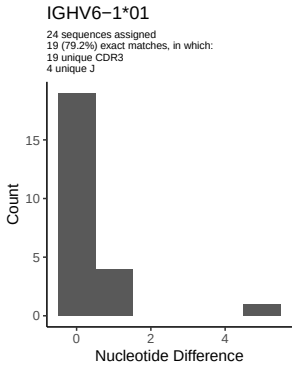

IGHV2−5*02
16 sequences assigned
16 (100%) exact matches, in which:
15 unique CDR3
4 unique J
IGHV2−26*01
28 sequences assigned
23 (82.1%) exact matches, in which:
23 unique CDR3
5 unique J
IGHV2−70*01
4 sequences assigned
4 (100%) exact matches, in which:
4 unique CDR3
3 unique J
IGHV2−70*15
10 sequences assigned
9 (90%) exact matches, in which:
9 unique CDR3
3 unique J
IGHV3−7*01
73 sequences assigned
50 (68.5%) exact matches, in which:
49 unique CDR3
5 unique J
IGHV3−7*03
47 sequences assigned
36 (76.6%) exact matches, in which:
35 unique CDR3
4 unique J
IGHV3−9*01
148 sequences assigned
106 (71.6%) exact matches, in which:
105 unique CDR3
6 unique J
IGHV3−11*01
66 sequences assigned
48 (72.7%) exact matches, in which:
48 unique CDR3
5 unique J
IGHV3−11*05
45 sequences assigned
30 (66.7%) exact matches, in which:
30 unique CDR3
5 unique J
IGHV3−13*01
20 sequences assigned
14 (70%) exact matches, in which:
14 unique CDR3
4 unique J
IGHV3−13*04
17 sequences assigned
16 (94.1%) exact matches, in which:
16 unique CDR3
4 unique J
IGHV3−15*01
158 sequences assigned
113 (71.5%) exact matches, in which:
112 unique CDR3
6 unique J
Count
Nucleotide Difference

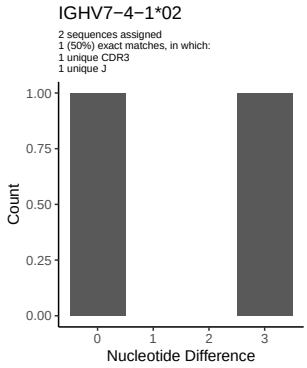

IGHV3−20*04
26 sequences assigned
15 (57.7%) exact matches, in which:
15 unique CDR3
5 unique J
IGHV3−21*01
262 sequences assigned
184 (70.2%) exact matches, in which:
182 unique CDR3
6 unique J
IGHV3−23*01
313 sequences assigned
249 (79.6%) exact matches, in which:
246 unique CDR3
6 unique J
IGHV3−23*04
184 sequences assigned
148 (80.4%) exact matches, in which:
147 unique CDR3
6 unique J
IGHV3−23*01_A152G
67 sequences assigned
59 (88.1%) exact matches, in which:
59 unique CDR3
6 unique J
IGHV3−30*02
123 sequences assigned
78 (63.4%) exact matches, in which:
77 unique CDR3
6 unique J
IGHV3−30*04
155 sequences assigned
104 (67.1%) exact matches, in which:
101 unique CDR3
6 unique J
IGHV3−30*18
41 sequences assigned
26 (63.4%) exact matches, in which:
26 unique CDR3
4 unique J
IGHV3−33*01
100 sequences assigned
73 (73%) exact matches, in which:
69 unique CDR3
6 unique J
IGHV3−43*01
3 sequences assigned
3 (100%) exact matches, in which:
3 unique CDR3
2 unique J
IGHV3−48*03
130 sequences assigned
84 (64.6%) exact matches, in which:
84 unique CDR3
5 unique J
IGHV3−48*04
69 sequences assigned
48 (69.6%) exact matches, in which:
47 unique CDR3
5 unique J
Count
Nucleotide Difference


IGHV3−49*03
41 sequences assigned
24 (58.5%) exact matches, in which:
24 unique CDR3
4 unique J
IGHV3−49*04
31 sequences assigned
22 (71%) exact matches, in which:
22 unique CDR3
4 unique J
IGHV3−53*02
22 sequences assigned
20 (90.9%) exact matches, in which:
20 unique CDR3
5 unique J
IGHV3−53*04
11 sequences assigned
8 (72.7%) exact matches, in which:
8 unique CDR3
3 unique J
IGHV3−64*01
5 sequences assigned
4 (80%) exact matches, in which:
4 unique CDR3
2 unique J
IGHV3−66*02
44 sequences assigned
No exact matches.
IGHV3−72*01
2 sequences assigned
2 (100%) exact matches, in which:
2 unique CDR3
2 unique J
IGHV3−73*01
17 sequences assigned
14 (82.4%) exact matches, in which:
14 unique CDR3
4 unique J
IGHV3−73*02
24 sequences assigned
20 (83.3%) exact matches, in which:
20 unique CDR3
3 unique J
IGHV3−74*01
52 sequences assigned
40 (76.9%) exact matches, in which:
37 unique CDR3
5 unique J
IGHV3−43D*03
13 sequences assigned
11 (84.6%) exact matches, in which:
10 unique CDR3
3 unique J
IGHV3−43D*04
6 sequences assigned
6 (100%) exact matches, in which:
6 unique CDR3
3 unique J
Count
Nucleotide Difference

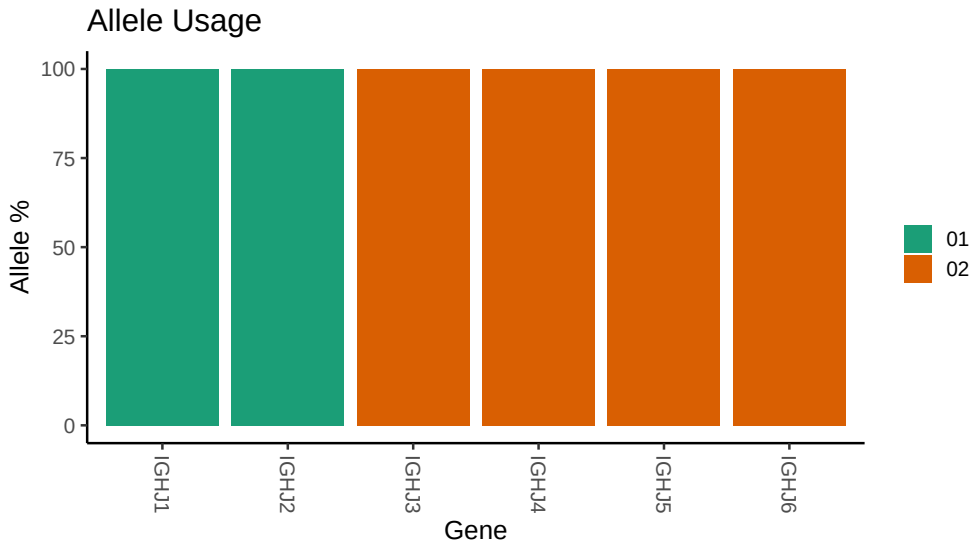

IGHV3−64D*06
31 sequences assigned
27 (87.1%) exact matches, in which:
25 unique CDR3
6 unique J
IGHV4−4*02
40 sequences assigned
34 (85%) exact matches, in which:
34 unique CDR3
6 unique J
IGHV4−30−2*01
12 sequences assigned
10 (83.3%) exact matches, in which:
10 unique CDR3
5 unique J
IGHV4−31*03
62 sequences assigned
42 (67.7%) exact matches, in which:
42 unique CDR3
5 unique J
IGHV4−34*01
345 sequences assigned
285 (82.6%) exact matches, in which:
280 unique CDR3
6 unique J
IGHV4−38−2*01
81 sequences assigned
60 (74.1%) exact matches, in which:
57 unique CDR3
6 unique J
IGHV4−38−2*02
64 sequences assigned
43 (67.2%) exact matches, in which:
43 unique CDR3
4 unique J
IGHV4−39*07
236 sequences assigned
158 (66.9%) exact matches, in which:
156 unique CDR3
5 unique J
IGHV4−59*01
114 sequences assigned
94 (82.5%) exact matches, in which:
92 unique CDR3
5 unique J
IGHV4−61*01
27 sequences assigned
23 (85.2%) exact matches, in which:
22 unique CDR3
4 unique J
IGHV4−NL1*01
58 sequences assigned
45 (77.6%) exact matches, in which:
44 unique CDR3
5 unique J
IGHV5−10−1*01
31 sequences assigned
30 (96.8%) exact matches, in which:
30 unique CDR3
5 unique J
Count
Nucleotide Difference


IGHV5−51*01
168 sequences assigned
141 (83.9%) exact matches, in which:
139 unique CDR3
6 unique J
Count
Nucleotide Difference
0
50
100
0.0
2.5
5.0
7.5
10.0


IGHV6−1*01
24 sequences assigned
19 (79.2%) exact matches, in which:
19 unique CDR3
4 unique J
Count
Nucleotide Difference
0
5
10
15
0
2
4


IGHV7−4−1*02
2 sequences assigned
1 (50%) exact matches, in which:
1 unique CDR3
1 unique J
Count
Nucleotide Difference
0.00
0.25
0.50
0.75
1.00
0
1
2
3

3 Allele usage in potential haplotype anchor genes



4 Haplotype plots

5 Configuration settings

```
## Repertoire file: /work/jenkins/PRJEB26509/S28/S28/28/28/72/1d8fddd2807b3bb29ddb2bc0be758f/28_Finale_
##
## Germline reference file: /work/jenkins/PRJEB26509/S28/S28/28/28/72/1d8fddd2807b3bb29ddb2bc0be758f/pe
##
## Novel allele file: /work/jenkins/PRJEB26509/S28/S28/28/28/72/1d8fddd2807b3bb29ddb2bc0be758f/novel_se
##
## Species: Homosapiens
##
## Chain: IGHV
##
## Segment: V
```