OGRDBstats Report

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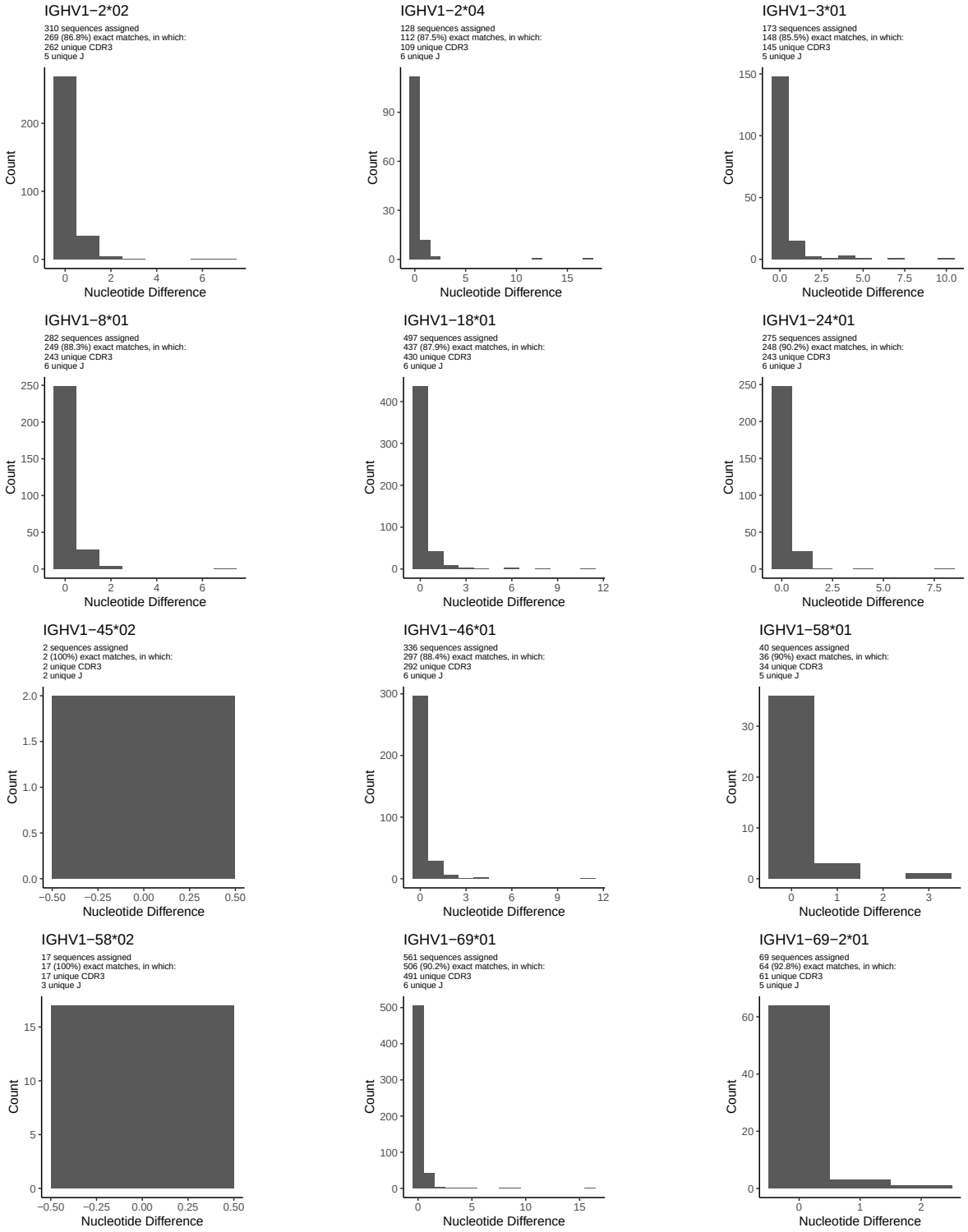
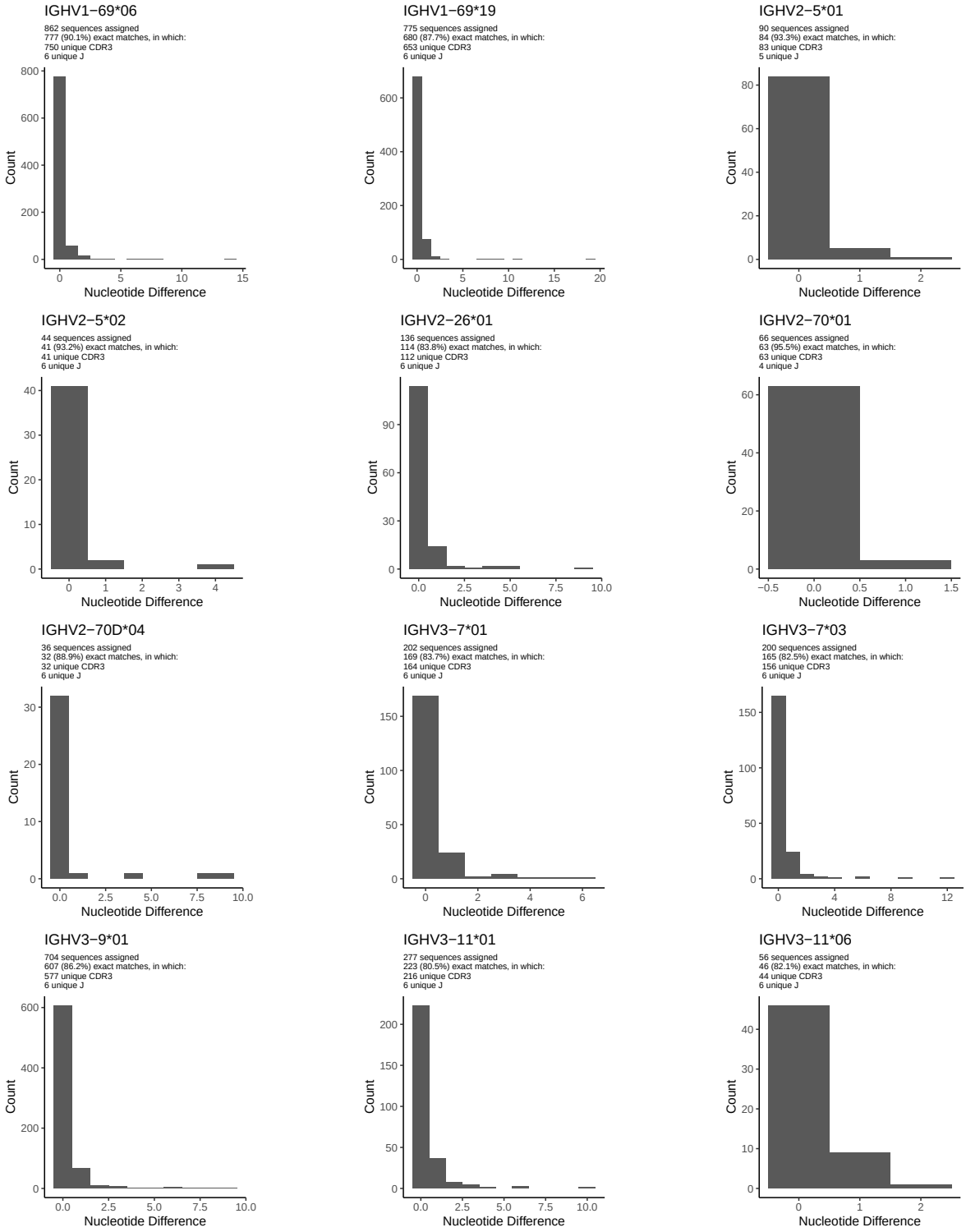
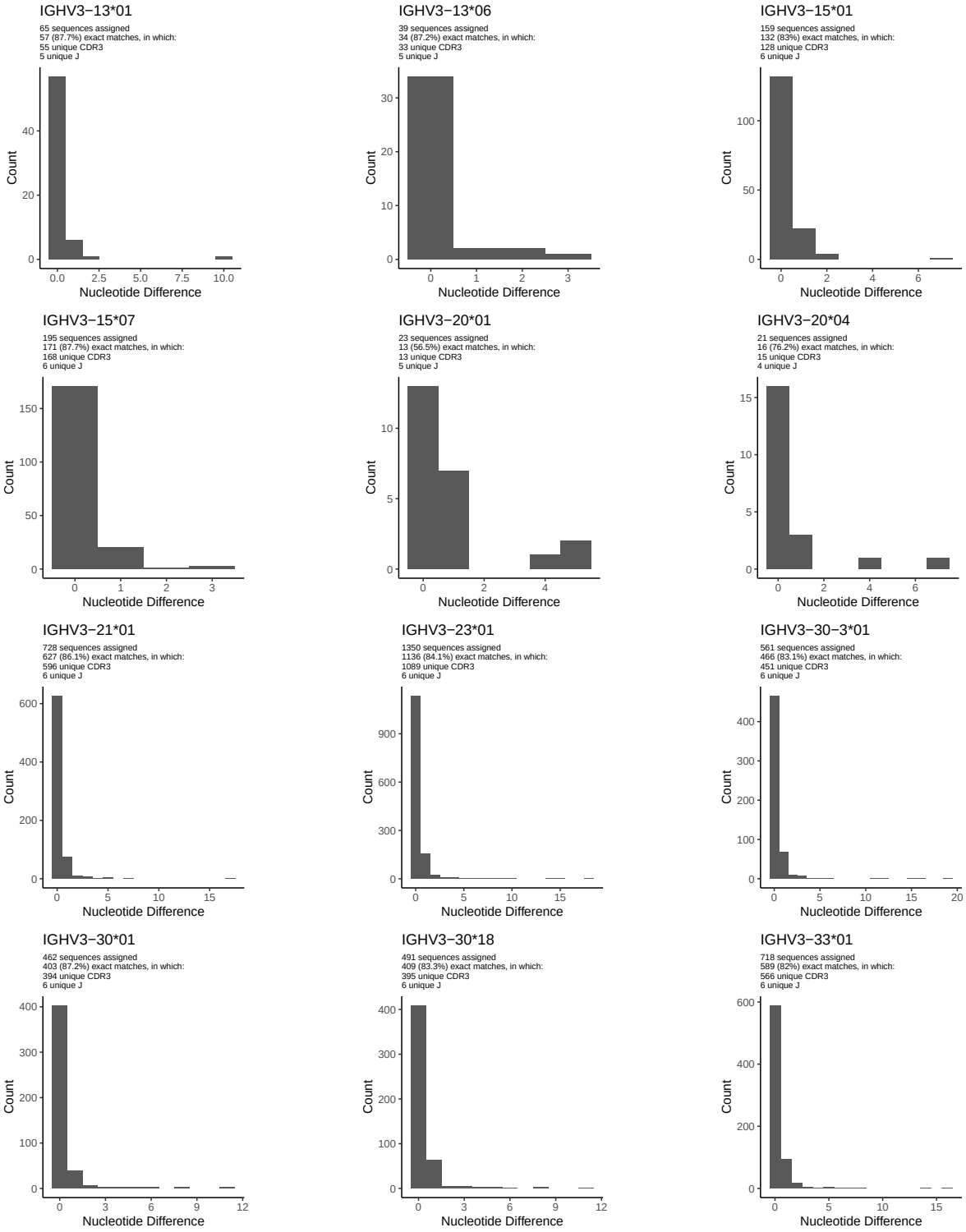
1 Novel sequence analysis

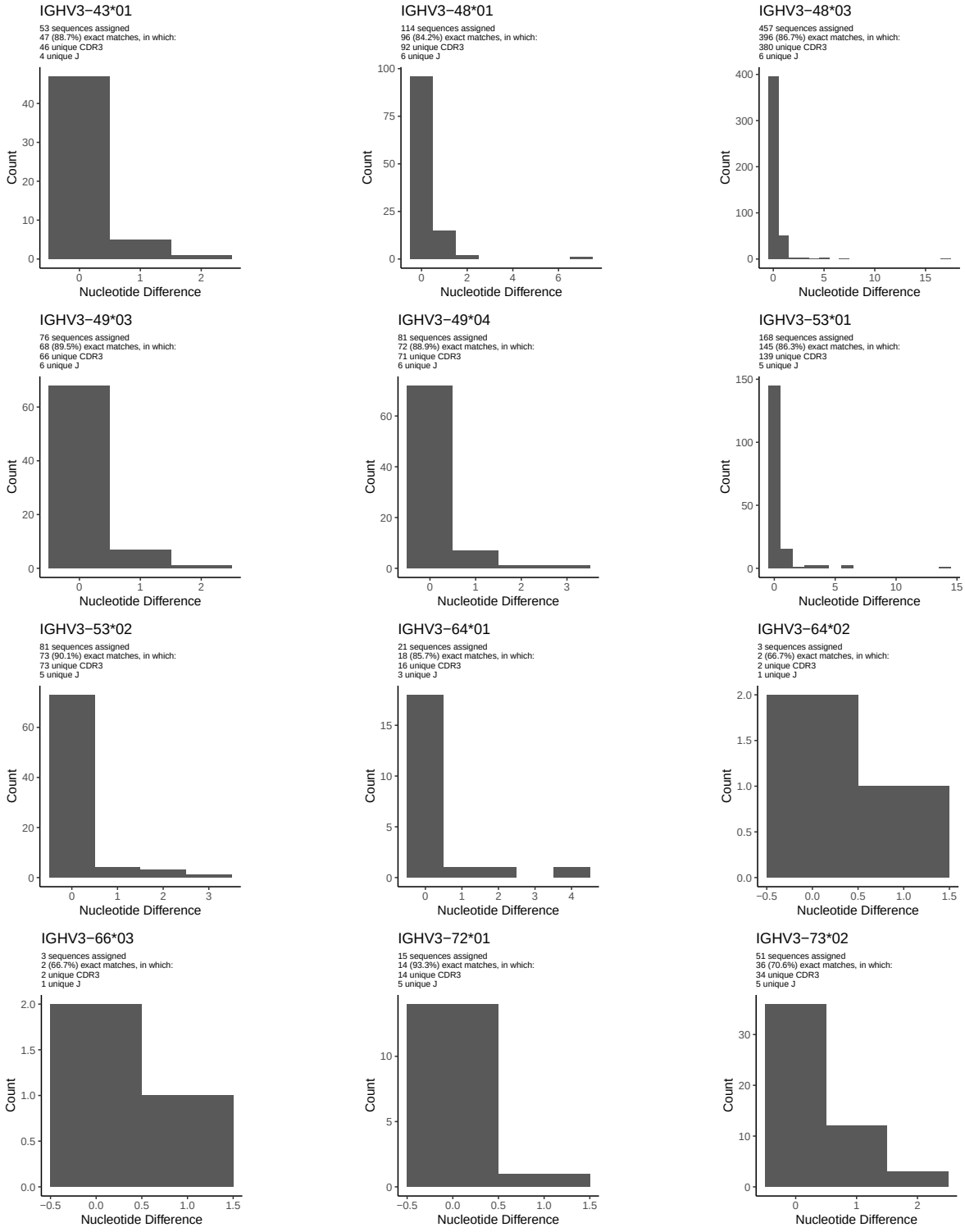
1.1 CDR3 length distribution, in assignments to novel alleles

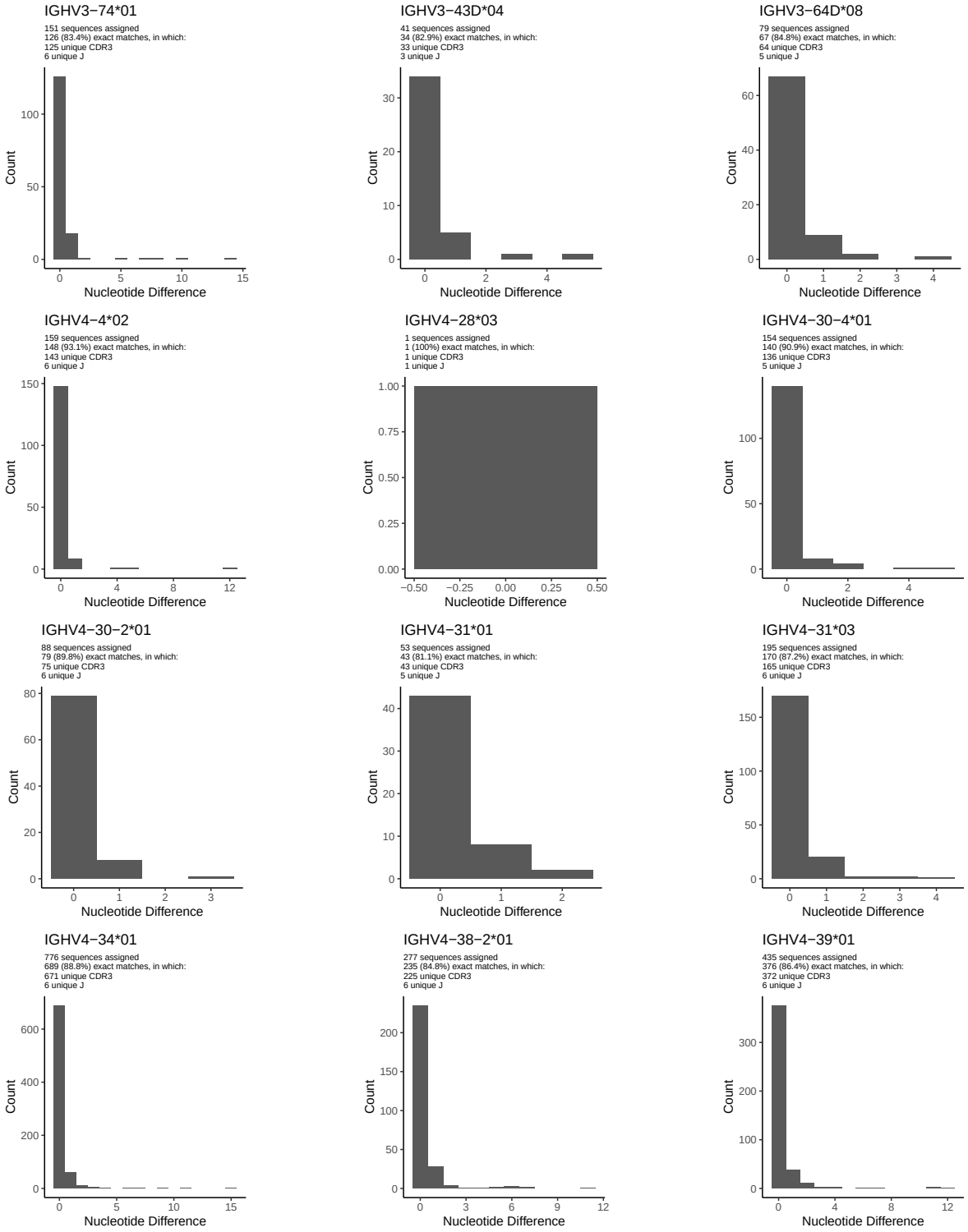
2 Variation from germline, in assignments to each allele

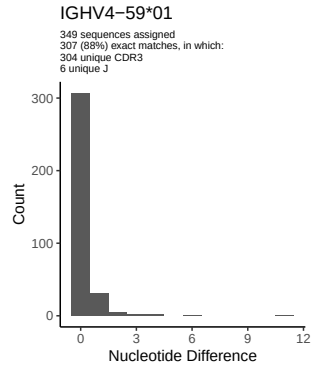


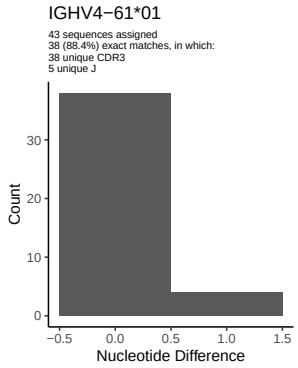

IGHV1−69*06
862 sequences assigned
777 (90.1%) exact matches, in which:
750 unique CDR3
6 unique J
IGHV1−69*19
775 sequences assigned
680 (87.7%) exact matches, in which:
653 unique CDR3
6 unique J
IGHV2−5*01
90 sequences assigned
84 (93.3%) exact matches, in which:
83 unique CDR3
5 unique J
IGHV2−5*02
44 sequences assigned
41 (93.2%) exact matches, in which:
41 unique CDR3
6 unique J
IGHV2−26*01
136 sequences assigned
114 (83.8%) exact matches, in which:
112 unique CDR3
6 unique J
IGHV2−70*01
66 sequences assigned
63 (95.5%) exact matches, in which:
63 unique CDR3
4 unique J
IGHV2−70D*04
36 sequences assigned
32 (88.9%) exact matches, in which:
32 unique CDR3
6 unique J
IGHV3−7*01
202 sequences assigned
169 (83.7%) exact matches, in which:
164 unique CDR3
6 unique J
IGHV3−7*03
200 sequences assigned
165 (82.5%) exact matches, in which:
156 unique CDR3
6 unique J
IGHV3−9*01
704 sequences assigned
607 (86.2%) exact matches, in which:
577 unique CDR3
6 unique J
IGHV3−11*01
277 sequences assigned
223 (80.5%) exact matches, in which:
216 unique CDR3
6 unique J
IGHV3−11*06
56 sequences assigned
46 (82.1%) exact matches, in which:
44 unique CDR3
6 unique J
Count
Nucleotide Difference

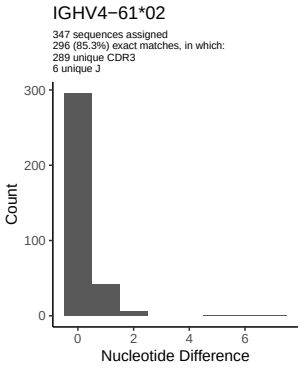

IGHV3−13*01
65 sequences assigned
57 (87.7%) exact matches, in which:
55 unique CDR3
5 unique J
IGHV3−13*06
39 sequences assigned
34 (87.2%) exact matches, in which:
33 unique CDR3
5 unique J
IGHV3−15*01
159 sequences assigned
132 (83%) exact matches, in which:
128 unique CDR3
6 unique J
IGHV3−15*07
195 sequences assigned
171 (87.7%) exact matches, in which:
168 unique CDR3
6 unique J
IGHV3−20*01
23 sequences assigned
13 (56.5%) exact matches, in which:
13 unique CDR3
5 unique J
IGHV3−20*04
21 sequences assigned
16 (76.2%) exact matches, in which:
15 unique CDR3
4 unique J
IGHV3−21*01
728 sequences assigned
627 (86.1%) exact matches, in which:
596 unique CDR3
6 unique J
IGHV3−23*01
1350 sequences assigned
1136 (84.1%) exact matches, in which:
1089 unique CDR3
6 unique J
IGHV3−30−3*01
561 sequences assigned
466 (83.1%) exact matches, in which:
451 unique CDR3
6 unique J
IGHV3−30*01
462 sequences assigned
403 (87.2%) exact matches, in which:
394 unique CDR3
6 unique J
IGHV3−30*18
491 sequences assigned
409 (83.3%) exact matches, in which:
395 unique CDR3
6 unique J
IGHV3−33*01
718 sequences assigned
589 (82%) exact matches, in which:
566 unique CDR3
6 unique J
Count
Nucleotide Difference

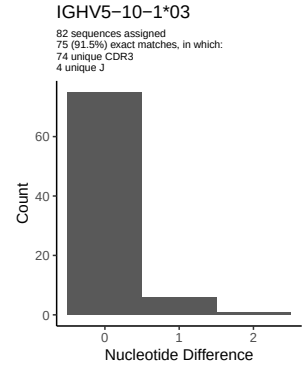

IGHV3−43*01
53 sequences assigned
47 (88.7%) exact matches, in which:
46 unique CDR3
4 unique J
IGHV3−48*01
114 sequences assigned
96 (84.2%) exact matches, in which:
92 unique CDR3
6 unique J
IGHV3−48*03
457 sequences assigned
396 (86.7%) exact matches, in which:
380 unique CDR3
6 unique J
IGHV3−49*03
76 sequences assigned
68 (89.5%) exact matches, in which:
66 unique CDR3
6 unique J
IGHV3−49*04
81 sequences assigned
72 (88.9%) exact matches, in which:
71 unique CDR3
6 unique J
IGHV3−53*01
168 sequences assigned
145 (86.3%) exact matches, in which:
139 unique CDR3
5 unique J
IGHV3−53*02
81 sequences assigned
73 (90.1%) exact matches, in which:
73 unique CDR3
5 unique J
IGHV3−64*01
21 sequences assigned
18 (85.7%) exact matches, in which:
16 unique CDR3
3 unique J
IGHV3−64*02
3 sequences assigned
2 (66.7%) exact matches, in which:
2 unique CDR3
1 unique J
IGHV3−66*03
3 sequences assigned
2 (66.7%) exact matches, in which:
2 unique CDR3
1 unique J
IGHV3−72*01
15 sequences assigned
14 (93.3%) exact matches, in which:
14 unique CDR3
5 unique J
IGHV3−73*02
51 sequences assigned
36 (70.6%) exact matches, in which:
34 unique CDR3
5 unique J
Count
Nucleotide Difference

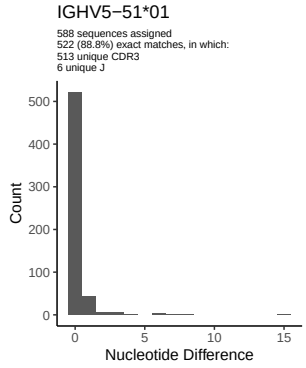

IGHV3−74*01
151 sequences assigned
126 (83.4%) exact matches, in which:
125 unique CDR3
6 unique J
Count
Nucleotide Difference
IGHV3−43D*04
41 sequences assigned
34 (82.9%) exact matches, in which:
33 unique CDR3
3 unique J
Count
Nucleotide Difference
IGHV3−64D*08
79 sequences assigned
67 (84.8%) exact matches, in which:
64 unique CDR3
5 unique J
Count
Nucleotide Difference
IGHV4−4*02
159 sequences assigned
148 (93.1%) exact matches, in which:
143 unique CDR3
6 unique J
Count
Nucleotide Difference
IGHV4−28*03
1 sequences assigned
1 (100%) exact matches, in which:
1 unique CDR3
1 unique J
Count
Nucleotide Difference
IGHV4−30−4*01
154 sequences assigned
140 (90.9%) exact matches, in which:
136 unique CDR3
5 unique J
Count
Nucleotide Difference
IGHV4−30−2*01
88 sequences assigned
79 (89.8%) exact matches, in which:
75 unique CDR3
6 unique J
Count
Nucleotide Difference
IGHV4−31*01
53 sequences assigned
43 (81.1%) exact matches, in which:
43 unique CDR3
5 unique J
Count
Nucleotide Difference
IGHV4−31*03
195 sequences assigned
170 (87.2%) exact matches, in which:
165 unique CDR3
6 unique J
Count
Nucleotide Difference
IGHV4−34*01
776 sequences assigned
689 (88.8%) exact matches, in which:
671 unique CDR3
6 unique J
Count
Nucleotide Difference
IGHV4−38−2*01
277 sequences assigned
235 (84.8%) exact matches, in which:
225 unique CDR3
6 unique J
Count
Nucleotide Difference
IGHV4−39*01
435 sequences assigned
376 (86.4%) exact matches, in which:
372 unique CDR3
6 unique J
Count
Nucleotide Difference

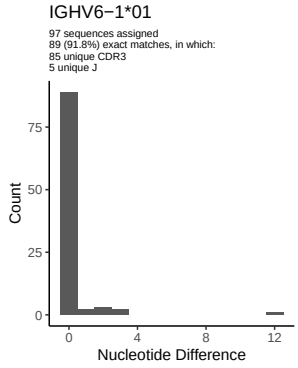

IGHV4−59*01
349 sequences assigned
307 (88%) exact matches, in which:
304 unique CDR3
6 unique J
Count
Nucleotide Difference

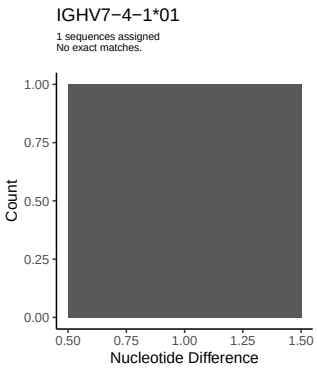

IGHV4−61*01
43 sequences assigned
38 (88.4%) exact matches, in which:
38 unique CDR3
5 unique J
Count
Nucleotide Difference


IGHV4−61*02
347 sequences assigned
296 (85.3%) exact matches, in which:
289 unique CDR3
6 unique J
Count
Nucleotide Difference

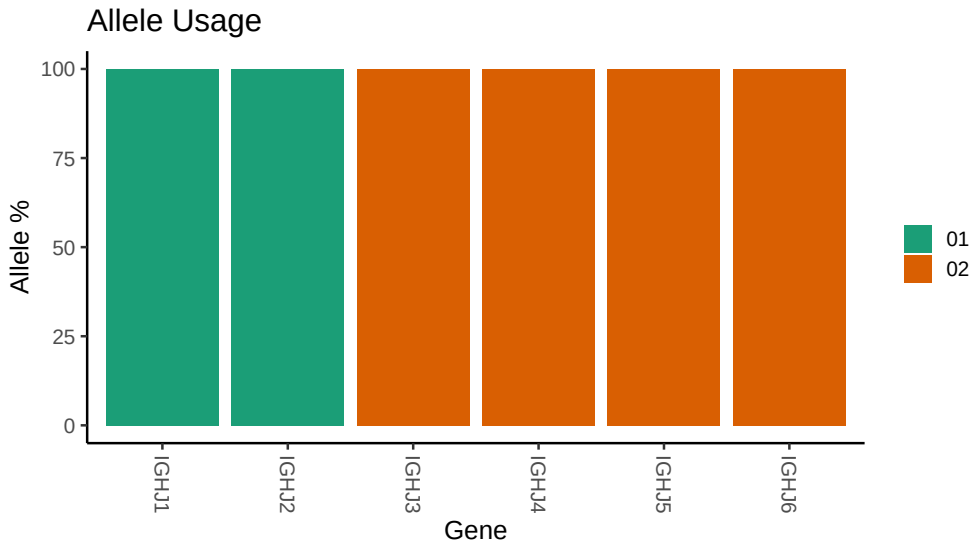

IGHV5−10−1*03
82 sequences assigned
75 (91.5%) exact matches, in which:
74 unique CDR3
4 unique J
Count
Nucleotide Difference


IGHV5−51*01
588 sequences assigned
522 (88.8%) exact matches, in which:
513 unique CDR3
6 unique J
Count
Nucleotide Difference


IGHV6−1*01
97 sequences assigned
89 (91.8%) exact matches, in which:
85 unique CDR3
5 unique J
Count
Nucleotide Difference


IGHV7−4−1*01
1 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/PRJEB26509/S35/S35/37/37/ad/65d48f40344dc4643901826d8eefb2/37_Fi
##
## Germline reference file: /misc/work/jenkins/PRJEB26509/S35/S35/37/37/a7/8db484794ec29bbbca227926ab68
##
## Novel allele file:
##
## Species: Homosapiens
##
## Chain: IGHV
##
## Segment: V
##
## Warning   no inferred sequences found.
```