OGRDBstats Report

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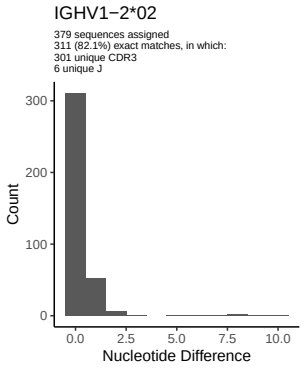
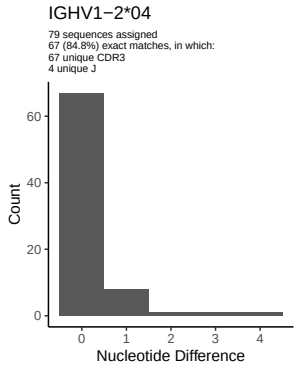
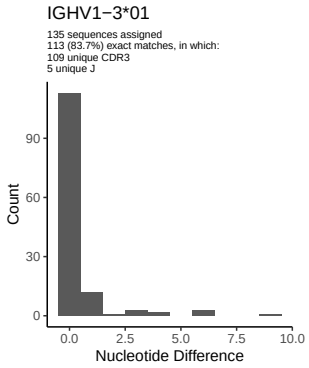
1 Novel sequence analysis

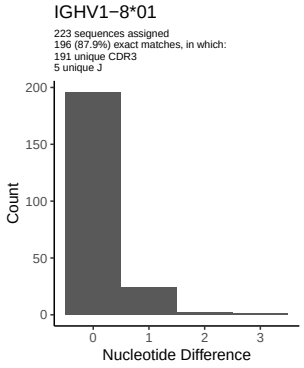
1.1 CDR3 length distribution, in assignments to novel alleles

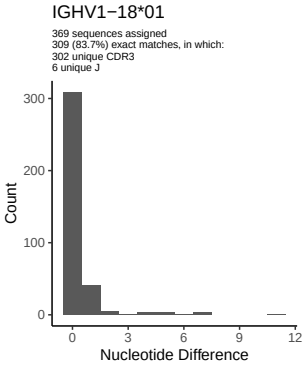
2 Variation from germline, in assignments to each allele

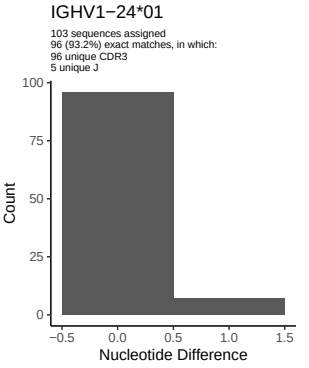


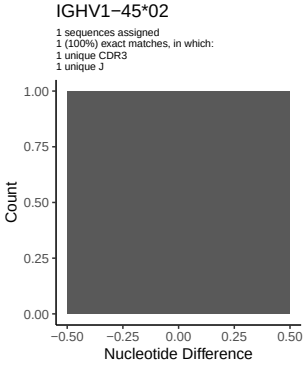


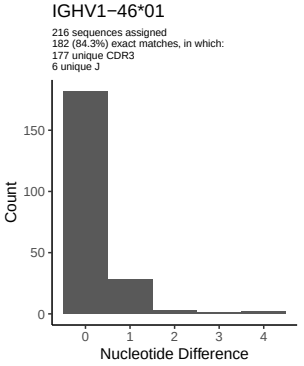


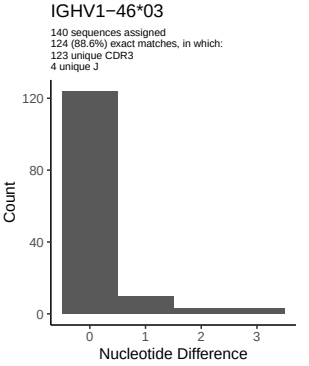


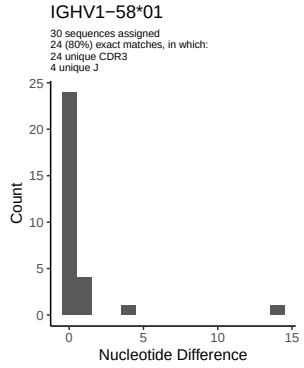


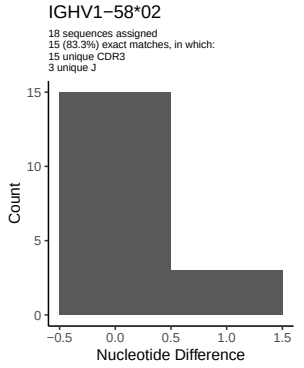


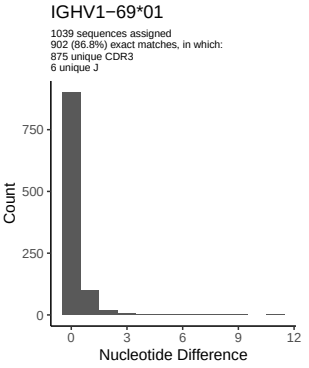


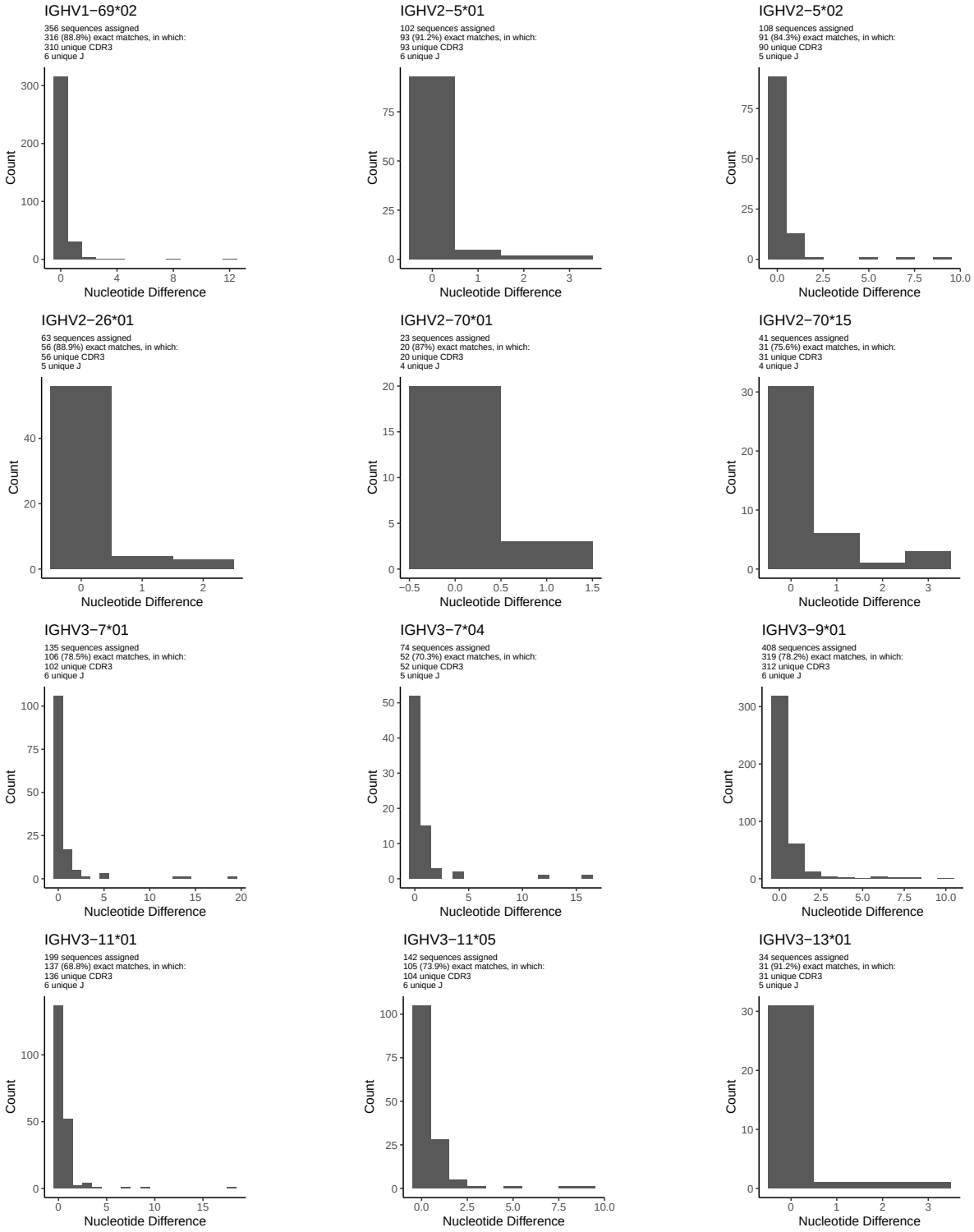


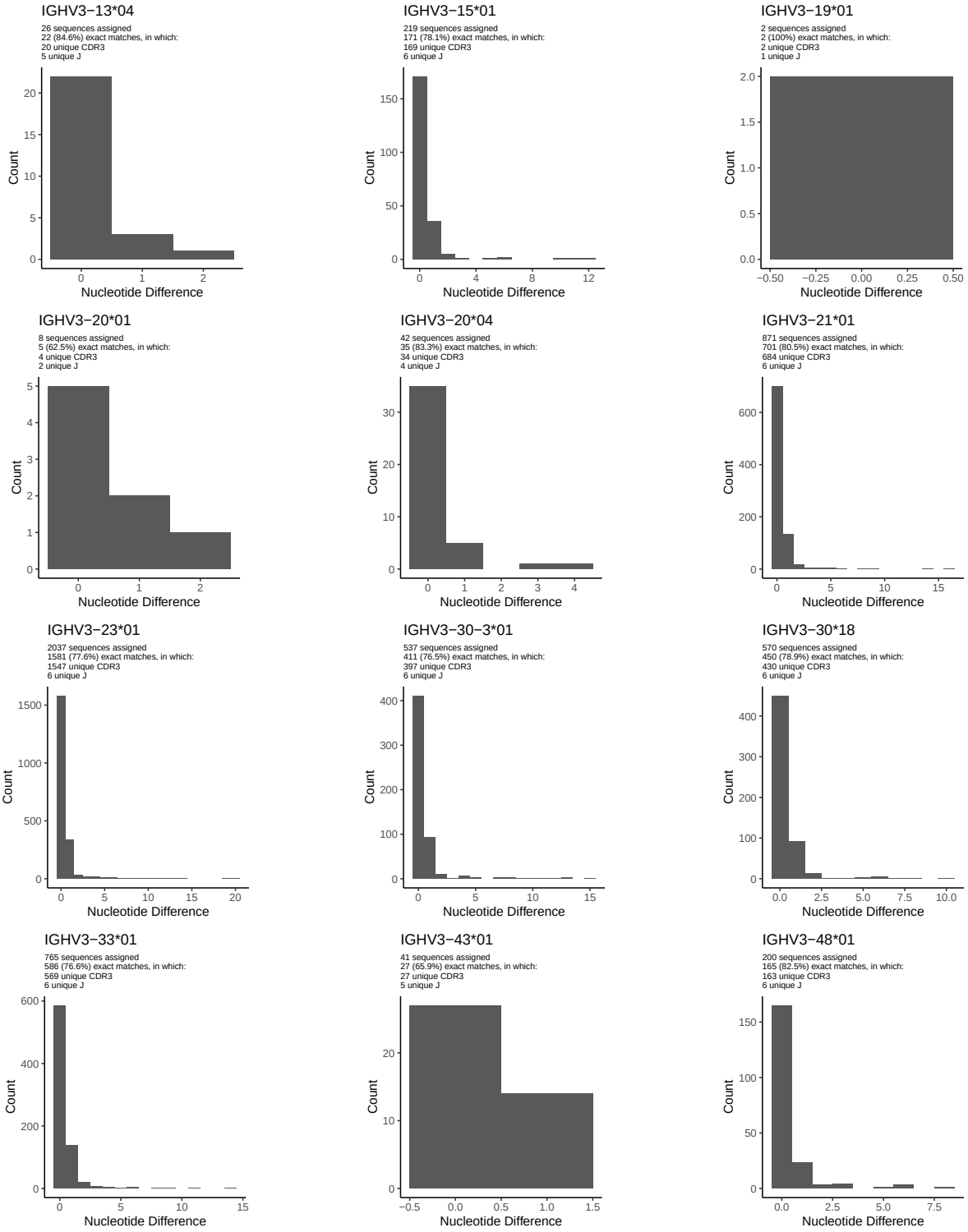


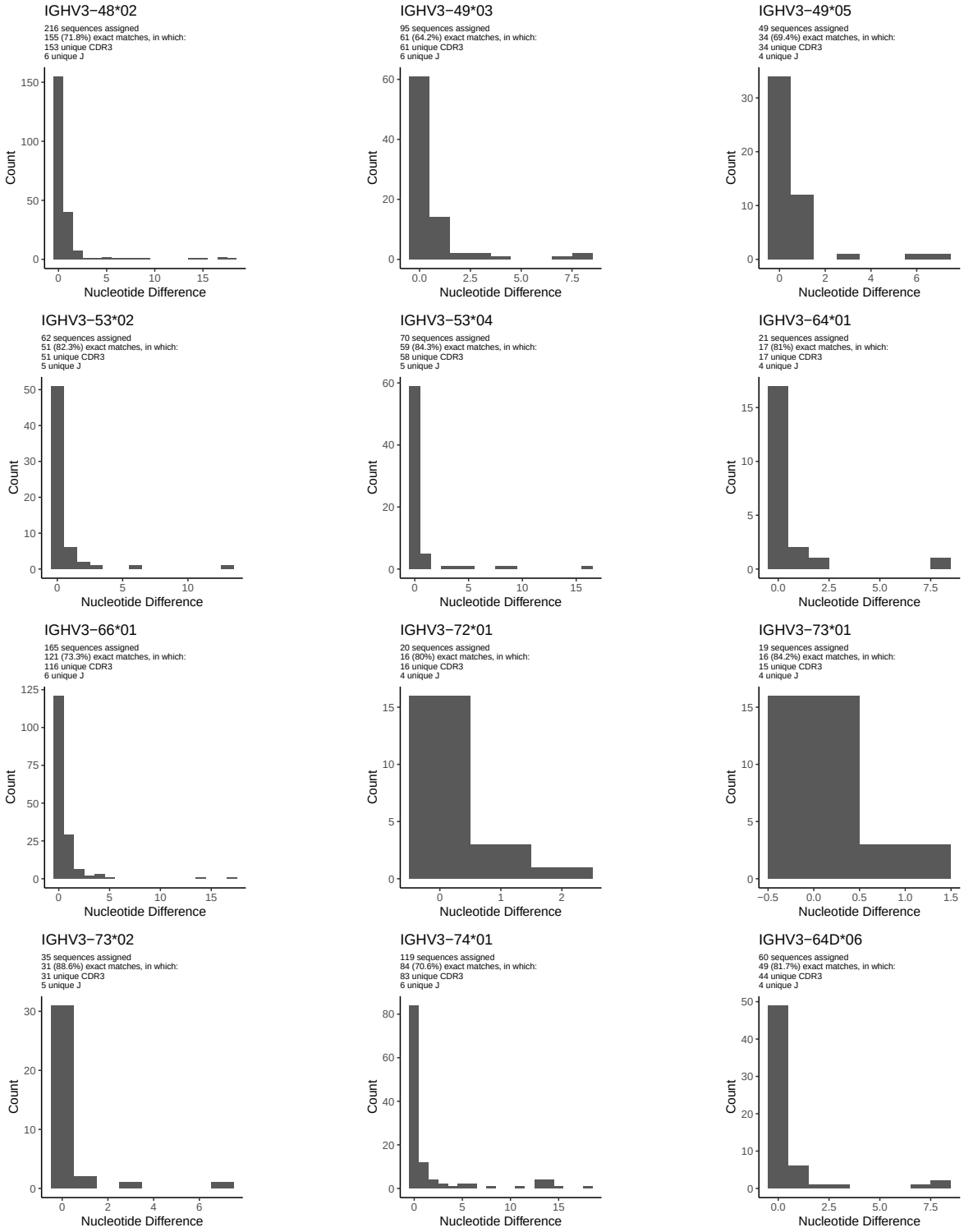


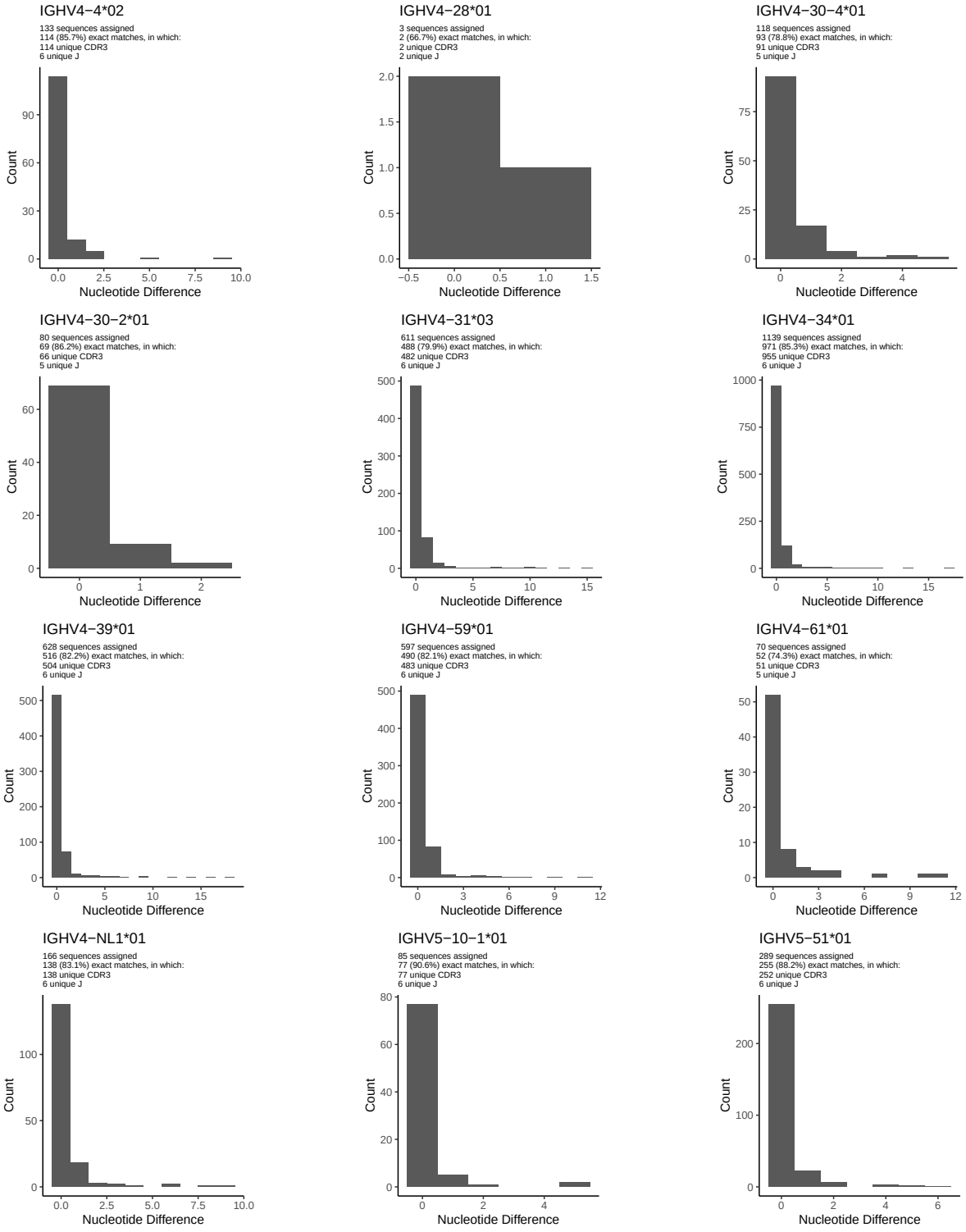


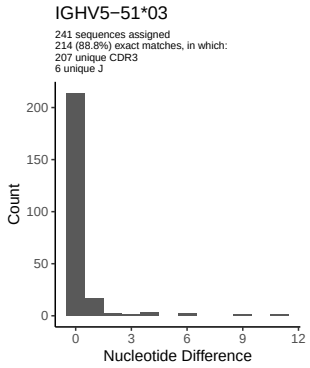


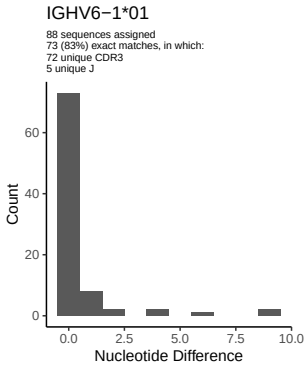

IGHV1−69*02
356 sequences assigned
316 (88.8%) exact matches, in which:
310 unique CDR3
6 unique J
IGHV2−5*01
102 sequences assigned
93 (91.2%) exact matches, in which:
93 unique CDR3
6 unique J
IGHV2−5*02
108 sequences assigned
91 (84.3%) exact matches, in which:
90 unique CDR3
5 unique J
IGHV2−26*01
63 sequences assigned
56 (88.9%) exact matches, in which:
56 unique CDR3
5 unique J
IGHV2−70*01
23 sequences assigned
20 (87%) exact matches, in which:
20 unique CDR3
4 unique J
IGHV2−70*15
41 sequences assigned
31 (75.6%) exact matches, in which:
31 unique CDR3
4 unique J
IGHV3−7*01
135 sequences assigned
106 (78.5%) exact matches, in which:
102 unique CDR3
6 unique J
IGHV3−7*04
74 sequences assigned
52 (70.3%) exact matches, in which:
52 unique CDR3
5 unique J
IGHV3−9*01
408 sequences assigned
319 (78.2%) exact matches, in which:
312 unique CDR3
6 unique J
IGHV3−11*01
199 sequences assigned
137 (68.8%) exact matches, in which:
136 unique CDR3
6 unique J
IGHV3−11*05
142 sequences assigned
105 (73.9%) exact matches, in which:
104 unique CDR3
6 unique J
IGHV3−13*01
34 sequences assigned
31 (91.2%) exact matches, in which:
31 unique CDR3
5 unique J
Count
Nucleotide Difference

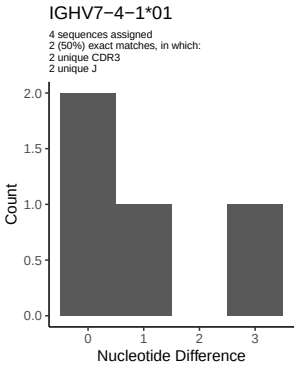

IGHV3−13*04
26 sequences assigned
22 (84.6%) exact matches, in which:
20 unique CDR3
5 unique J
IGHV3−15*01
219 sequences assigned
171 (78.1%) exact matches, in which:
169 unique CDR3
6 unique J
IGHV3−19*01
2 sequences assigned
2 (100%) exact matches, in which:
2 unique CDR3
1 unique J
IGHV3−20*01
8 sequences assigned
5 (62.5%) exact matches, in which:
4 unique CDR3
2 unique J
IGHV3−20*04
42 sequences assigned
35 (83.3%) exact matches, in which:
34 unique CDR3
4 unique J
IGHV3−21*01
871 sequences assigned
701 (80.5%) exact matches, in which:
684 unique CDR3
6 unique J
IGHV3−23*01
2037 sequences assigned
1581 (77.6%) exact matches, in which:
1547 unique CDR3
6 unique J
IGHV3−30−3*01
537 sequences assigned
411 (76.5%) exact matches, in which:
397 unique CDR3
6 unique J
IGHV3−30*18
570 sequences assigned
450 (78.9%) exact matches, in which:
430 unique CDR3
6 unique J
IGHV3−33*01
765 sequences assigned
586 (76.6%) exact matches, in which:
569 unique CDR3
6 unique J
IGHV3−43*01
41 sequences assigned
27 (65.9%) exact matches, in which:
27 unique CDR3
5 unique J
IGHV3−48*01
200 sequences assigned
165 (82.5%) exact matches, in which:
163 unique CDR3
6 unique J
Count
Nucleotide Difference

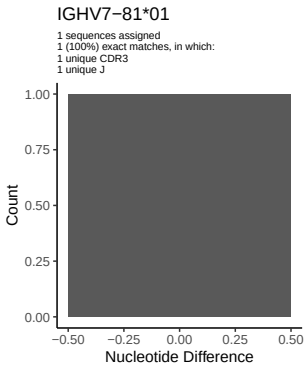

IGHV3−48*02
216 sequences assigned
155 (71.8%) exact matches, in which:
153 unique CDR3
6 unique J
IGHV3−49*03
95 sequences assigned
61 (64.2%) exact matches, in which:
61 unique CDR3
6 unique J
IGHV3−49*05
49 sequences assigned
34 (69.4%) exact matches, in which:
34 unique CDR3
4 unique J
IGHV3−53*02
62 sequences assigned
51 (82.3%) exact matches, in which:
51 unique CDR3
5 unique J
IGHV3−53*04
70 sequences assigned
59 (84.3%) exact matches, in which:
58 unique CDR3
5 unique J
IGHV3−64*01
21 sequences assigned
17 (81%) exact matches, in which:
17 unique CDR3
4 unique J
IGHV3−66*01
165 sequences assigned
121 (73.3%) exact matches, in which:
116 unique CDR3
6 unique J
IGHV3−72*01
20 sequences assigned
16 (80%) exact matches, in which:
16 unique CDR3
4 unique J
IGHV3−73*01
19 sequences assigned
16 (84.2%) exact matches, in which:
15 unique CDR3
4 unique J
IGHV3−73*02
35 sequences assigned
31 (88.6%) exact matches, in which:
31 unique CDR3
5 unique J
IGHV3−74*01
119 sequences assigned
84 (70.6%) exact matches, in which:
83 unique CDR3
6 unique J
IGHV3−64D*06
60 sequences assigned
49 (81.7%) exact matches, in which:
44 unique CDR3
4 unique J
Count
Nucleotide Difference


IGHV4−4*02
133 sequences assigned
114 (85.7%) exact matches, in which:
114 unique CDR3
6 unique J
IGHV4−28*01
3 sequences assigned
2 (66.7%) exact matches, in which:
2 unique CDR3
2 unique J
IGHV4−30−4*01
118 sequences assigned
93 (78.8%) exact matches, in which:
91 unique CDR3
5 unique J
IGHV4−30−2*01
80 sequences assigned
69 (86.2%) exact matches, in which:
66 unique CDR3
5 unique J
IGHV4−31*03
611 sequences assigned
488 (79.9%) exact matches, in which:
482 unique CDR3
6 unique J
IGHV4−34*01
1139 sequences assigned
971 (85.3%) exact matches, in which:
955 unique CDR3
6 unique J
IGHV4−39*01
628 sequences assigned
516 (82.2%) exact matches, in which:
504 unique CDR3
6 unique J
IGHV4−59*01
597 sequences assigned
490 (82.1%) exact matches, in which:
483 unique CDR3
6 unique J
IGHV4−61*01
70 sequences assigned
52 (74.3%) exact matches, in which:
51 unique CDR3
5 unique J
IGHV4−NL1*01
166 sequences assigned
138 (83.1%) exact matches, in which:
138 unique CDR3
6 unique J
IGHV5−10−1*01
85 sequences assigned
77 (90.6%) exact matches, in which:
77 unique CDR3
6 unique J
IGHV5−51*01
289 sequences assigned
255 (88.2%) exact matches, in which:
252 unique CDR3
6 unique J
Count
Nucleotide Difference

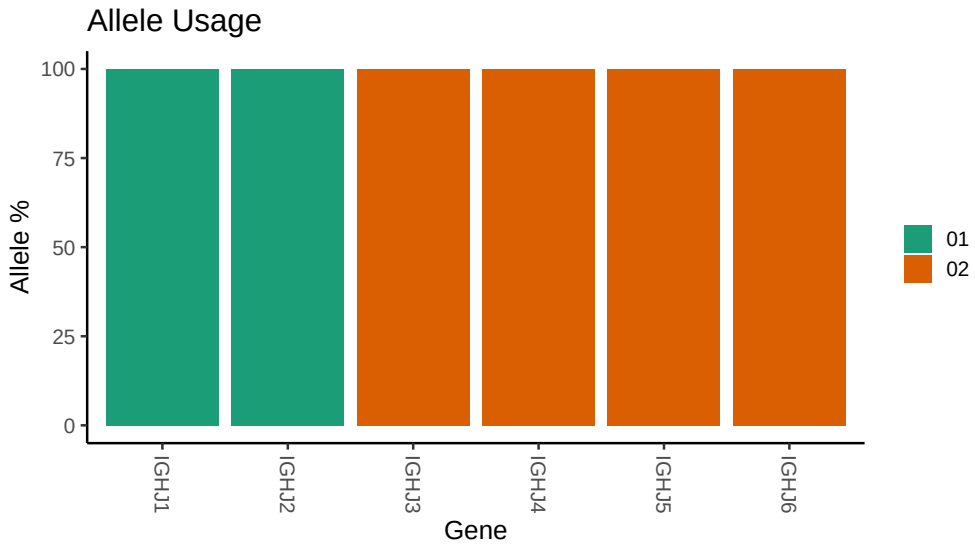

IGHV5−51*03
241 sequences assigned
214 (88.8%) exact matches, in which:
207 unique CDR3
6 unique J
Count
Nucleotide Difference


IGHV6−1*01
88 sequences assigned
73 (83%) exact matches, in which:
72 unique CDR3
5 unique J
Count
Nucleotide Difference


IGHV7−4−1*01
4 sequences assigned
2 (50%) exact matches, in which:
2 unique CDR3
2 unique J
Count
Nucleotide Difference


IGHV7−81*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/S90/S90/94/94/34/d80dc7b9824c53571c1bad62053e4a/94_Fi
##
## Germline reference file: /misc/work/jenkins/PRJEB26509/S90/S90/94/94/c0/01781048014be318a9c8b28fe676
##
## Novel allele file:
##
## Species: Homosapiens
##
## Chain: IGHV
##
## Segment: V
##
## Warning   no inferred sequences found.
```