OGRDBstats Report

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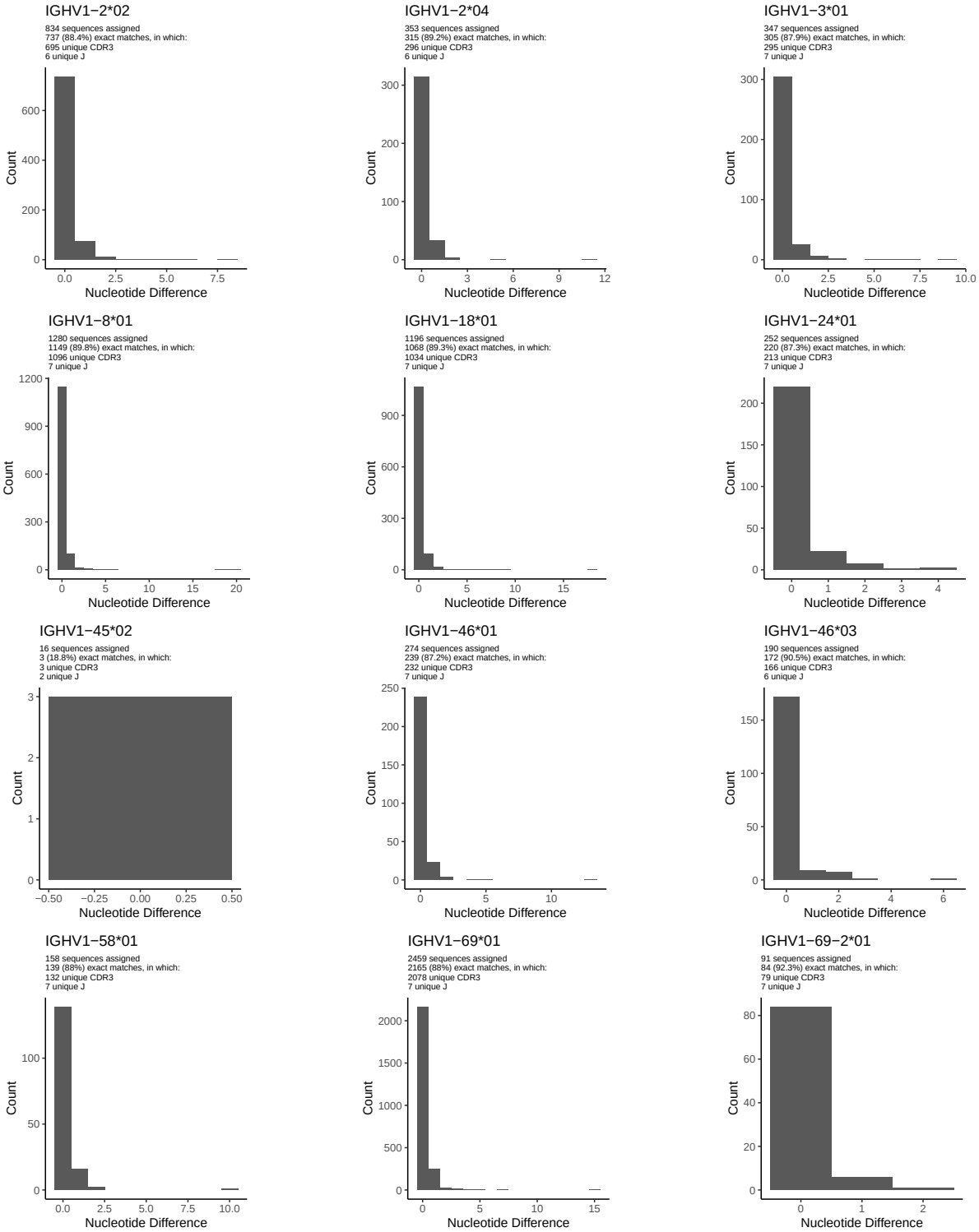
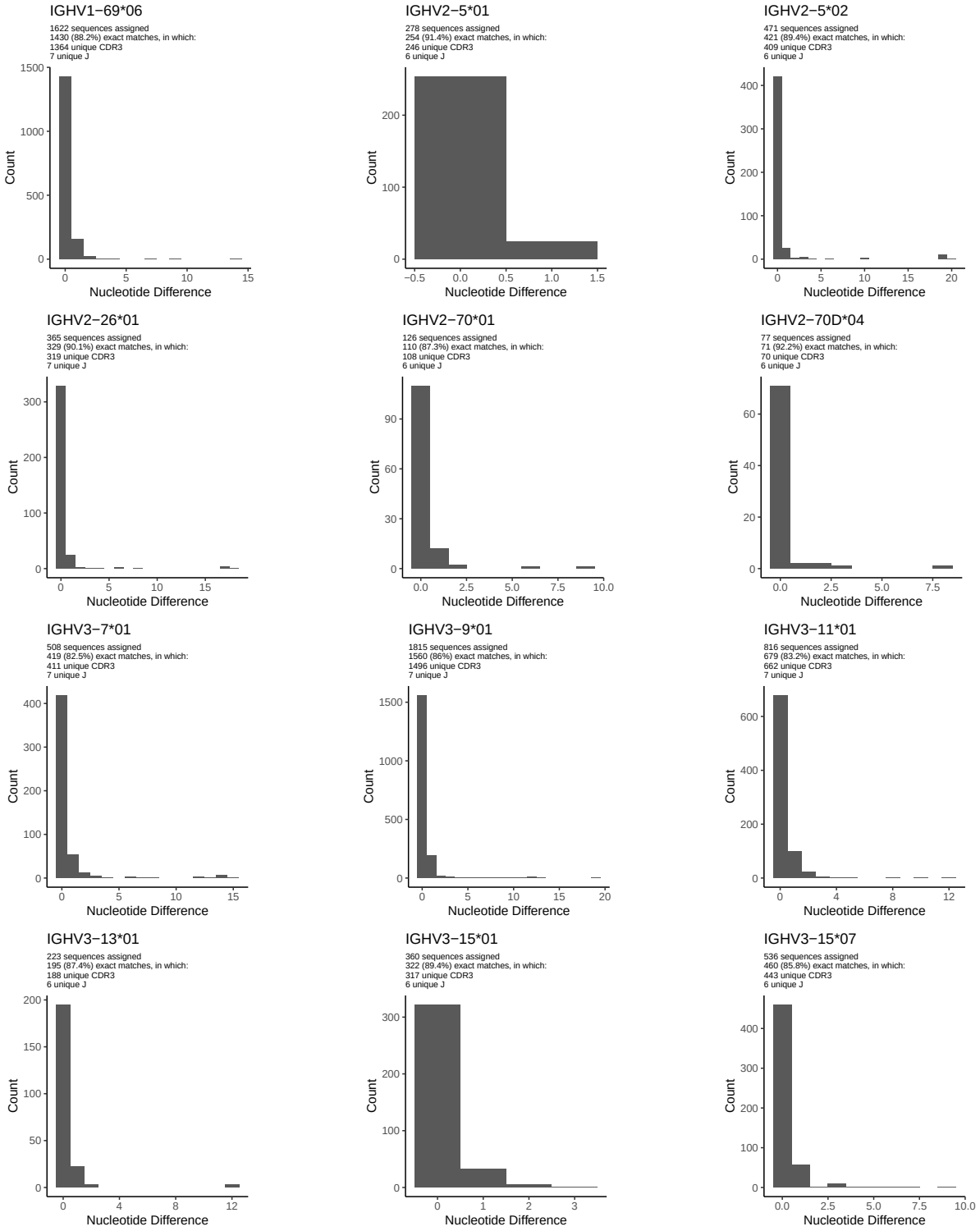
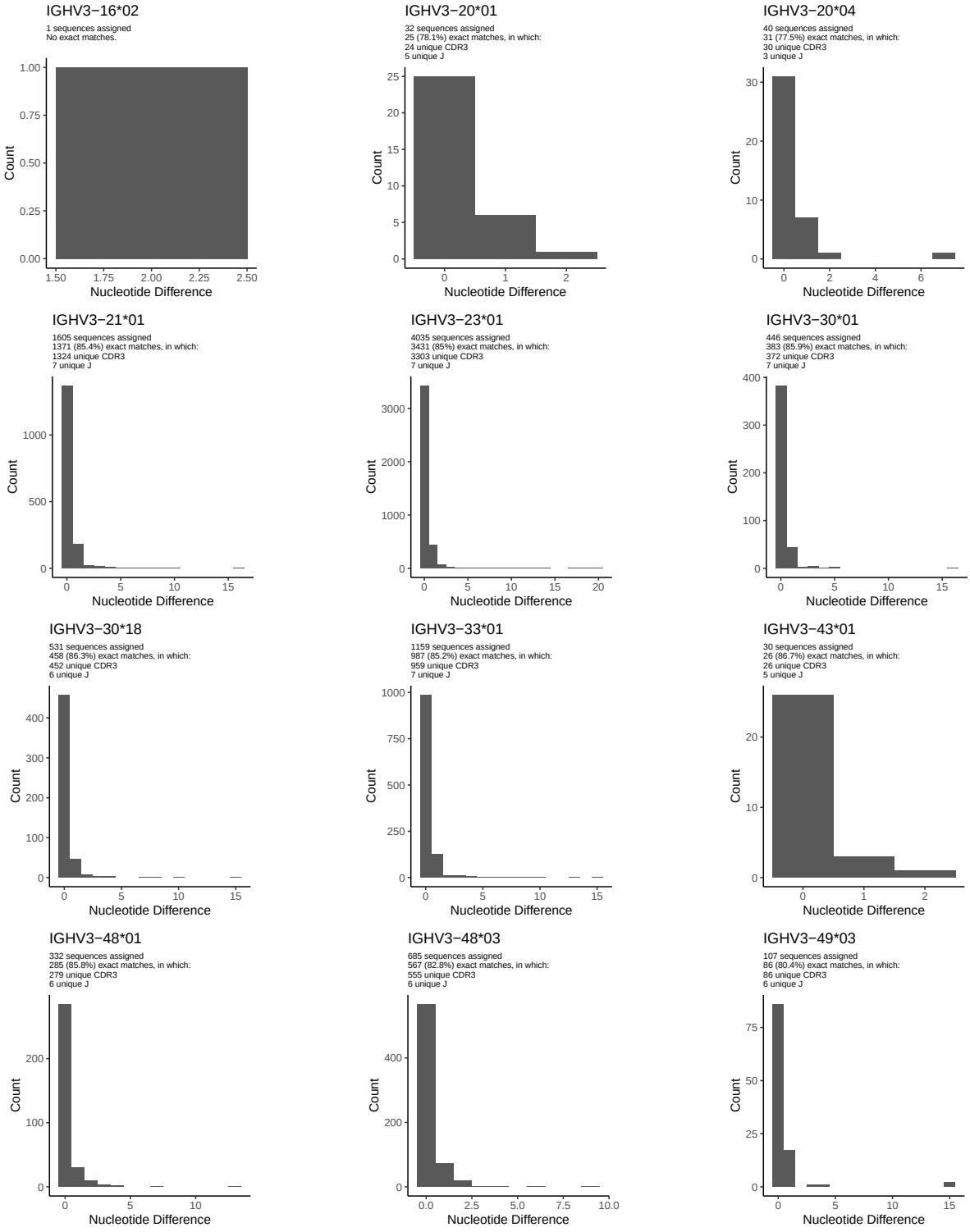
1 Novel sequence analysis

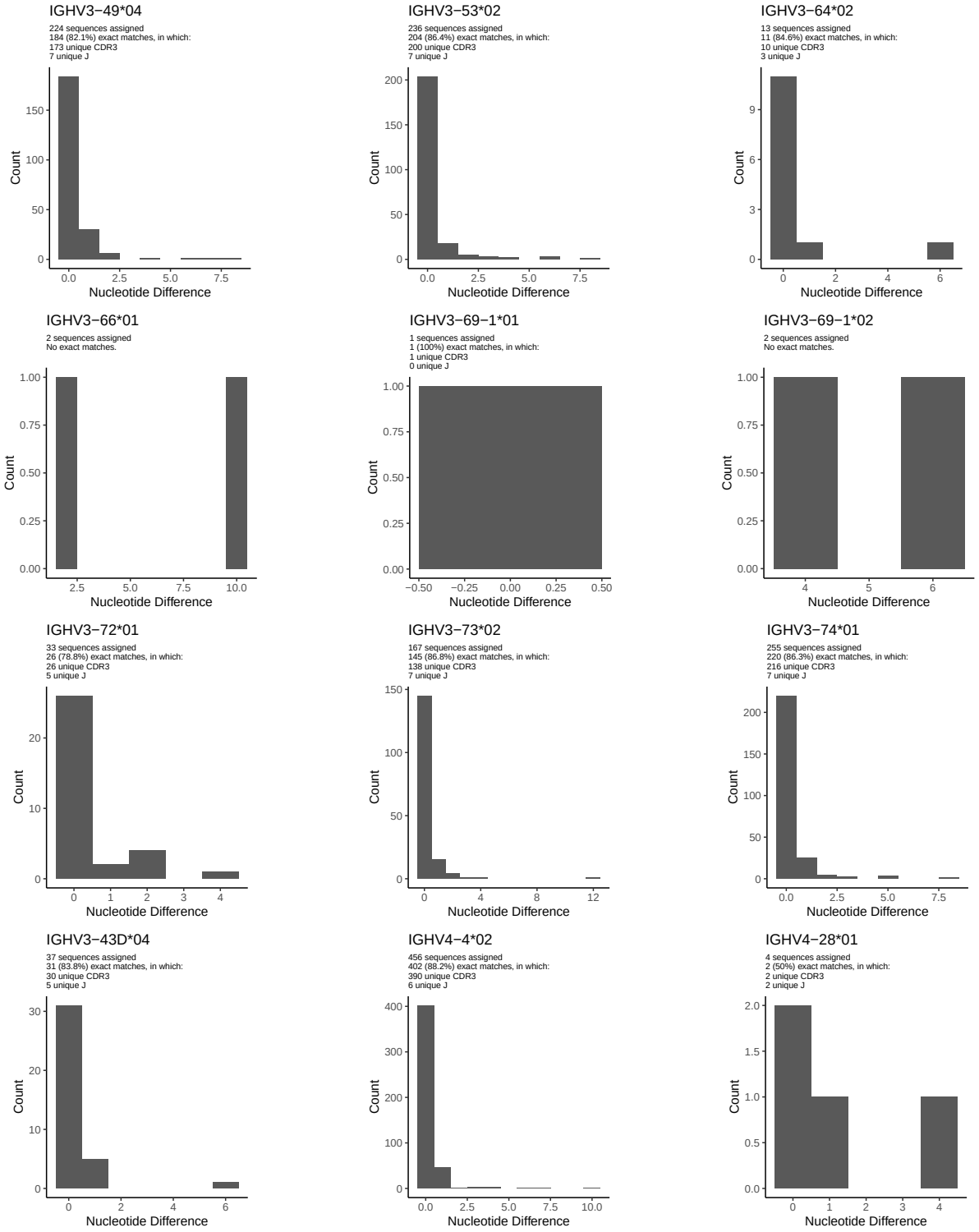
1.1 CDR3 length distribution, in assignments to novel alleles

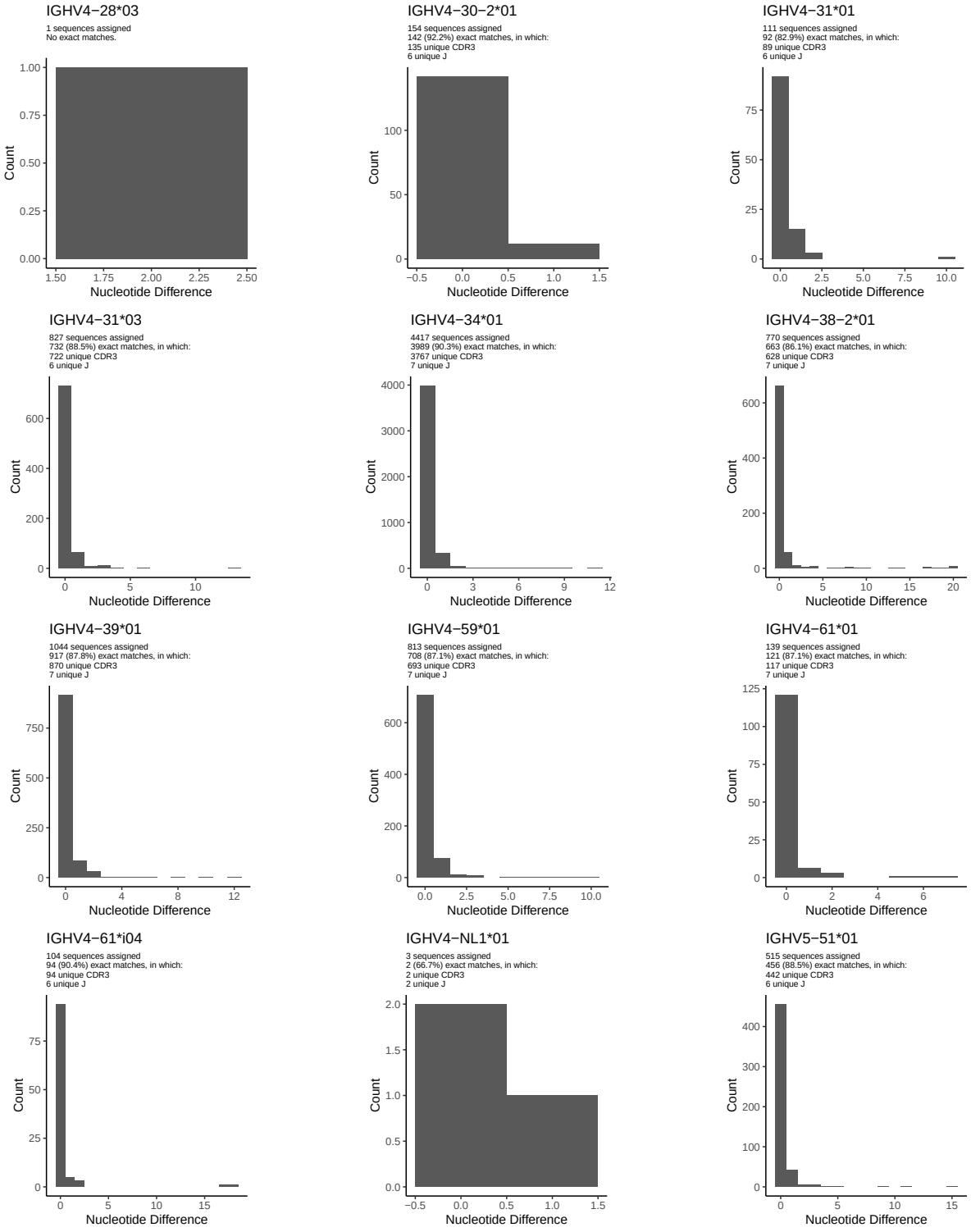
2 Variation from germline, in assignments to each allele

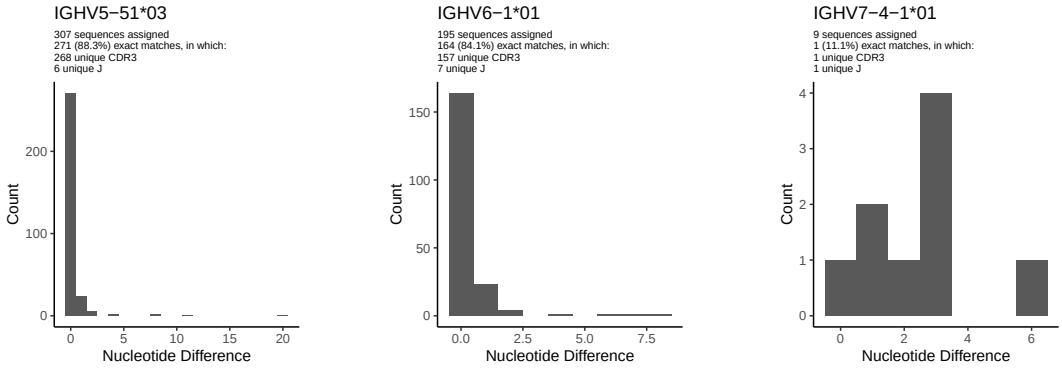



IGHV1−69*06
1622 sequences assigned
1430 (88.2%) exact matches, in which:
1364 unique CDR3
7 unique J
IGHV2−5*01
278 sequences assigned
254 (91.4%) exact matches, in which:
246 unique CDR3
6 unique J
IGHV2−5*02
471 sequences assigned
421 (89.4%) exact matches, in which:
409 unique CDR3
6 unique J
IGHV2−26*01
365 sequences assigned
329 (90.1%) exact matches, in which:
319 unique CDR3
7 unique J
IGHV2−70*01
126 sequences assigned
110 (87.3%) exact matches, in which:
108 unique CDR3
6 unique J
IGHV2−70D*04
77 sequences assigned
71 (92.2%) exact matches, in which:
70 unique CDR3
6 unique J
IGHV3−7*01
508 sequences assigned
419 (82.5%) exact matches, in which:
411 unique CDR3
7 unique J
IGHV3−9*01
1815 sequences assigned
1560 (86%) exact matches, in which:
1496 unique CDR3
7 unique J
IGHV3−11*01
816 sequences assigned
679 (83.2%) exact matches, in which:
662 unique CDR3
7 unique J
IGHV3−13*01
223 sequences assigned
195 (87.4%) exact matches, in which:
188 unique CDR3
6 unique J
IGHV3−15*01
360 sequences assigned
322 (89.4%) exact matches, in which:
317 unique CDR3
6 unique J
IGHV3−15*07
536 sequences assigned
460 (85.8%) exact matches, in which:
443 unique CDR3
6 unique J
Count
Nucleotide Difference

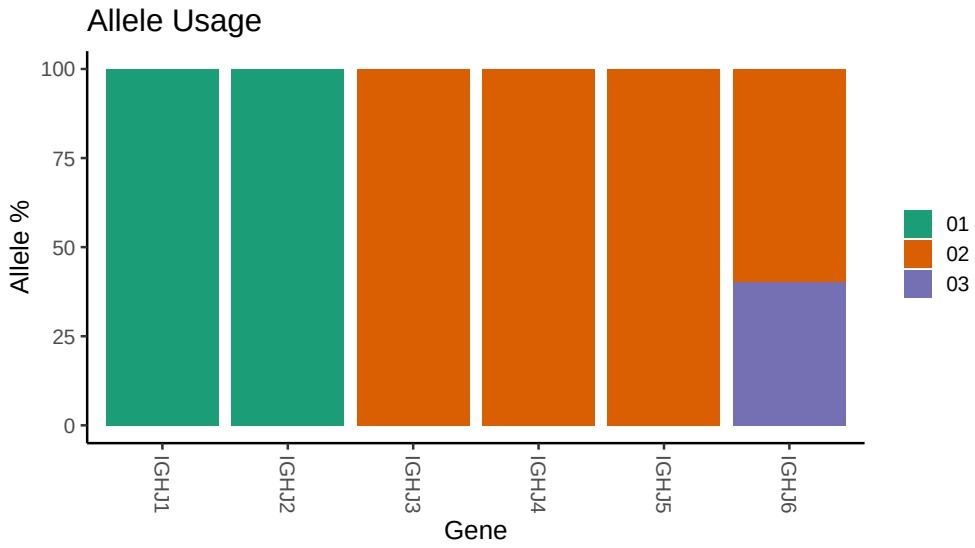

IGHV3−16*02
1 sequences assigned
No exact matches.
IGHV3−20*01
32 sequences assigned
25 (78.1%) exact matches, in which:
24 unique CDR3
5 unique J
IGHV3−20*04
40 sequences assigned
31 (77.5%) exact matches, in which:
30 unique CDR3
3 unique J
IGHV3−21*01
1605 sequences assigned
1371 (85.4%) exact matches, in which:
1324 unique CDR3
7 unique J
IGHV3−23*01
4035 sequences assigned
3431 (85%) exact matches, in which:
3303 unique CDR3
7 unique J
IGHV3−30*01
446 sequences assigned
383 (85.9%) exact matches, in which:
372 unique CDR3
7 unique J
IGHV3−30*18
531 sequences assigned
458 (86.3%) exact matches, in which:
452 unique CDR3
6 unique J
IGHV3−33*01
1159 sequences assigned
987 (85.2%) exact matches, in which:
959 unique CDR3
7 unique J
IGHV3−43*01
30 sequences assigned
26 (86.7%) exact matches, in which:
26 unique CDR3
5 unique J
IGHV3−48*01
332 sequences assigned
285 (85.8%) exact matches, in which:
279 unique CDR3
6 unique J
IGHV3−48*03
685 sequences assigned
567 (82.8%) exact matches, in which:
555 unique CDR3
6 unique J
IGHV3−49*03
107 sequences assigned
86 (80.4%) exact matches, in which:
86 unique CDR3
6 unique J
Count
Nucleotide Difference


IGHV3−49*04
224 sequences assigned
184 (82.1%) exact matches, in which:
173 unique CDR3
7 unique J
IGHV3−53*02
236 sequences assigned
204 (86.4%) exact matches, in which:
200 unique CDR3
7 unique J
IGHV3−64*02
13 sequences assigned
11 (84.6%) exact matches, in which:
10 unique CDR3
3 unique J
IGHV3−66*01
2 sequences assigned
No exact matches.
IGHV3−69−1*01
1 sequences assigned
1 (100%) exact matches, in which:
1 unique CDR3
0 unique J
IGHV3−69−1*02
2 sequences assigned
No exact matches.
IGHV3−72*01
33 sequences assigned
26 (78.8%) exact matches, in which:
26 unique CDR3
5 unique J
IGHV3−73*02
167 sequences assigned
145 (86.8%) exact matches, in which:
138 unique CDR3
7 unique J
IGHV3−74*01
255 sequences assigned
220 (86.3%) exact matches, in which:
216 unique CDR3
7 unique J
IGHV3−43D*04
37 sequences assigned
31 (83.8%) exact matches, in which:
30 unique CDR3
5 unique J
IGHV4−4*02
456 sequences assigned
402 (88.2%) exact matches, in which:
390 unique CDR3
6 unique J
IGHV4−28*01
4 sequences assigned
2 (50%) exact matches, in which:
2 unique CDR3
2 unique J
Count
Nucleotide Difference

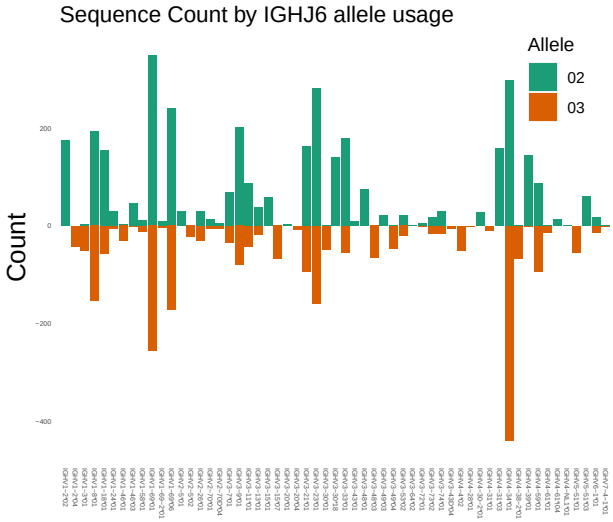

IGHV4−28*03
1 sequences assigned
No exact matches.
IGHV4−30−2*01
154 sequences assigned
142 (92.2%) exact matches, in which:
135 unique CDR3
6 unique J
IGHV4−31*01
111 sequences assigned
92 (82.9%) exact matches, in which:
89 unique CDR3
6 unique J
IGHV4−31*03
827 sequences assigned
732 (88.5%) exact matches, in which:
722 unique CDR3
6 unique J
IGHV4−34*01
4417 sequences assigned
3989 (90.3%) exact matches, in which:
3767 unique CDR3
7 unique J
IGHV4−38−2*01
770 sequences assigned
663 (86.1%) exact matches, in which:
628 unique CDR3
7 unique J
IGHV4−39*01
1044 sequences assigned
917 (87.8%) exact matches, in which:
870 unique CDR3
7 unique J
IGHV4−59*01
813 sequences assigned
708 (87.1%) exact matches, in which:
693 unique CDR3
7 unique J
IGHV4−61*01
139 sequences assigned
121 (87.1%) exact matches, in which:
117 unique CDR3
7 unique J
IGHV4−61*i04
104 sequences assigned
94 (90.4%) exact matches, in which:
94 unique CDR3
6 unique J
IGHV4−NL1*01
3 sequences assigned
2 (66.7%) exact matches, in which:
2 unique CDR3
2 unique J
IGHV5−51*01
515 sequences assigned
456 (88.5%) exact matches, in which:
442 unique CDR3
6 unique J
Count
Nucleotide Difference


IGHV5−51*03
307 sequences assigned
271 (88.3%) exact matches, in which:
268 unique CDR3
6 unique J
Count
Nucleotide Difference
IGHV6−1*01
195 sequences assigned
164 (84.1%) exact matches, in which:
157 unique CDR3
7 unique J
Count
Nucleotide Difference
IGHV7−4−1*01
9 sequences assigned
1 (11.1%) 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/S23/S23/23/23/82/9deb48735478fad8ba7a4fc0b211c2/23_Fi
##
## Germline reference file: /misc/work/jenkins/PRJEB26509/S23/S23/23/23/d7/e6a1499e16d4ab4c95053850a312
##
## Novel allele file:
##
## Species: Homosapiens
##
## Chain: IGHV
##
## Segment: V
##
## Warning   no inferred sequences found.
```