OGRDBstats Report

Contents

1 Novel sequence analysis **2**
1.1 CDR3 length distribution, in assignments to novel alleles 2

2 Variation from germline, in assignments to each allele **3**

3 Allele usage in potential haplotype anchor genes **9**

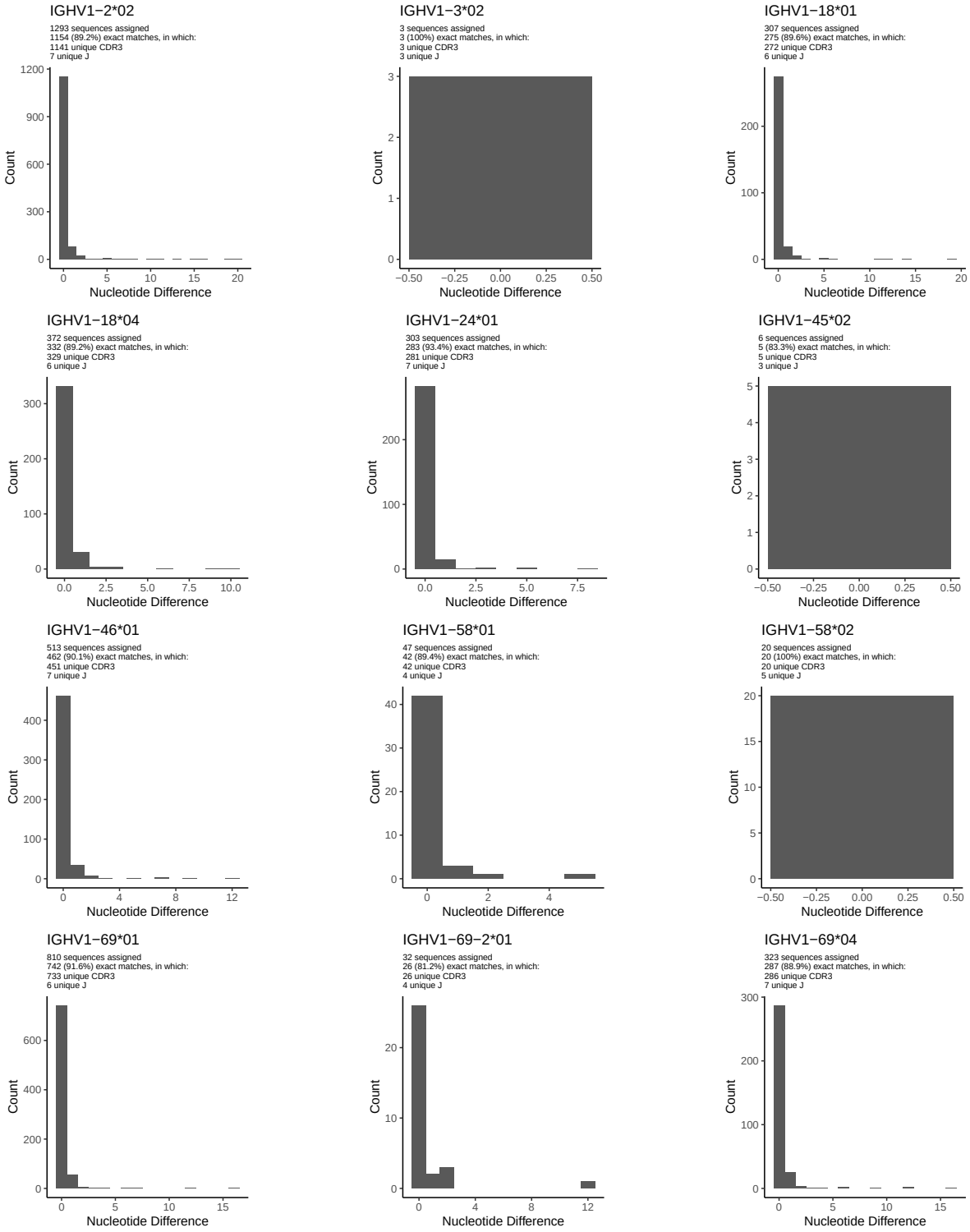
4 Haplotype plots **10**

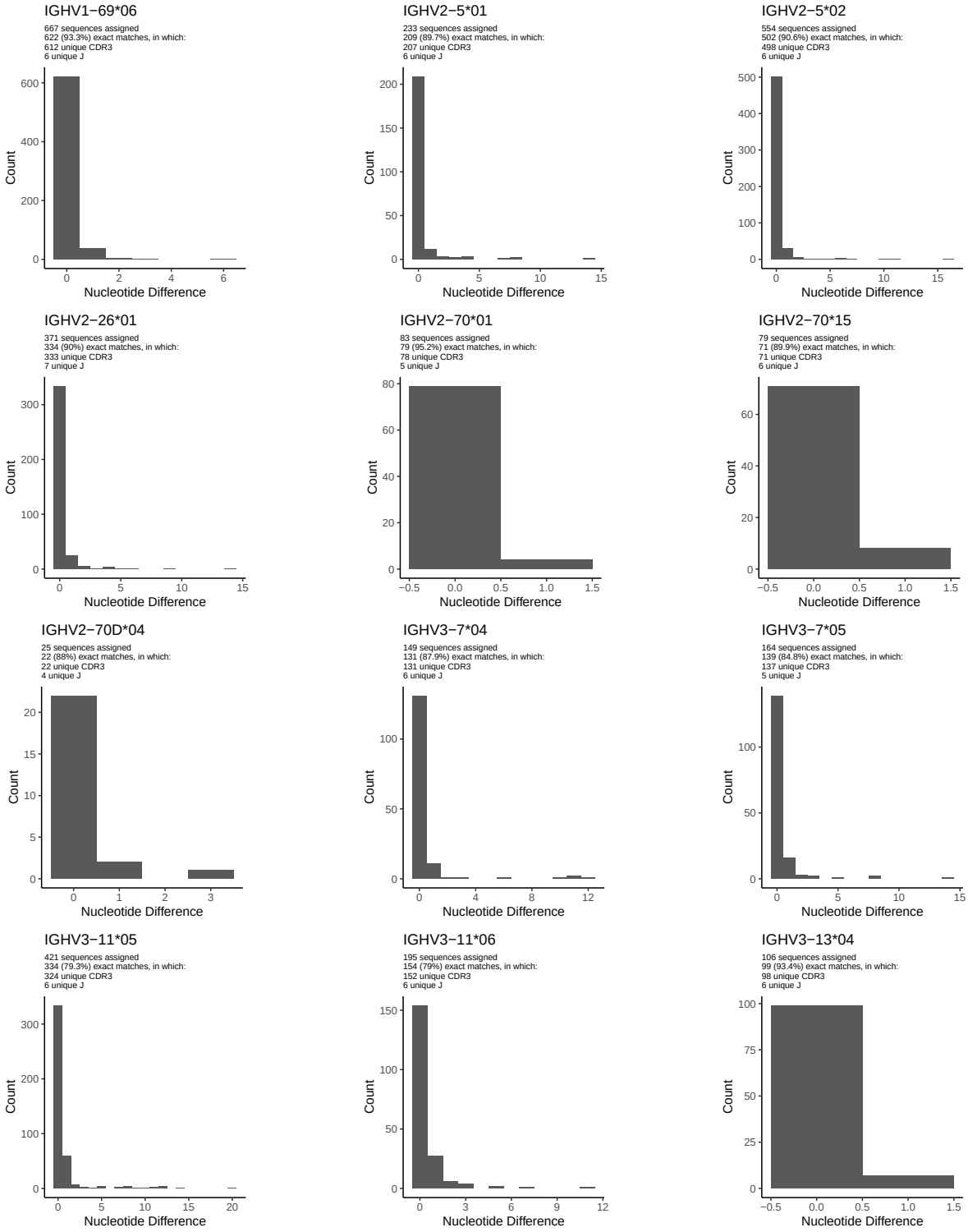
5 Configuration settings **11**

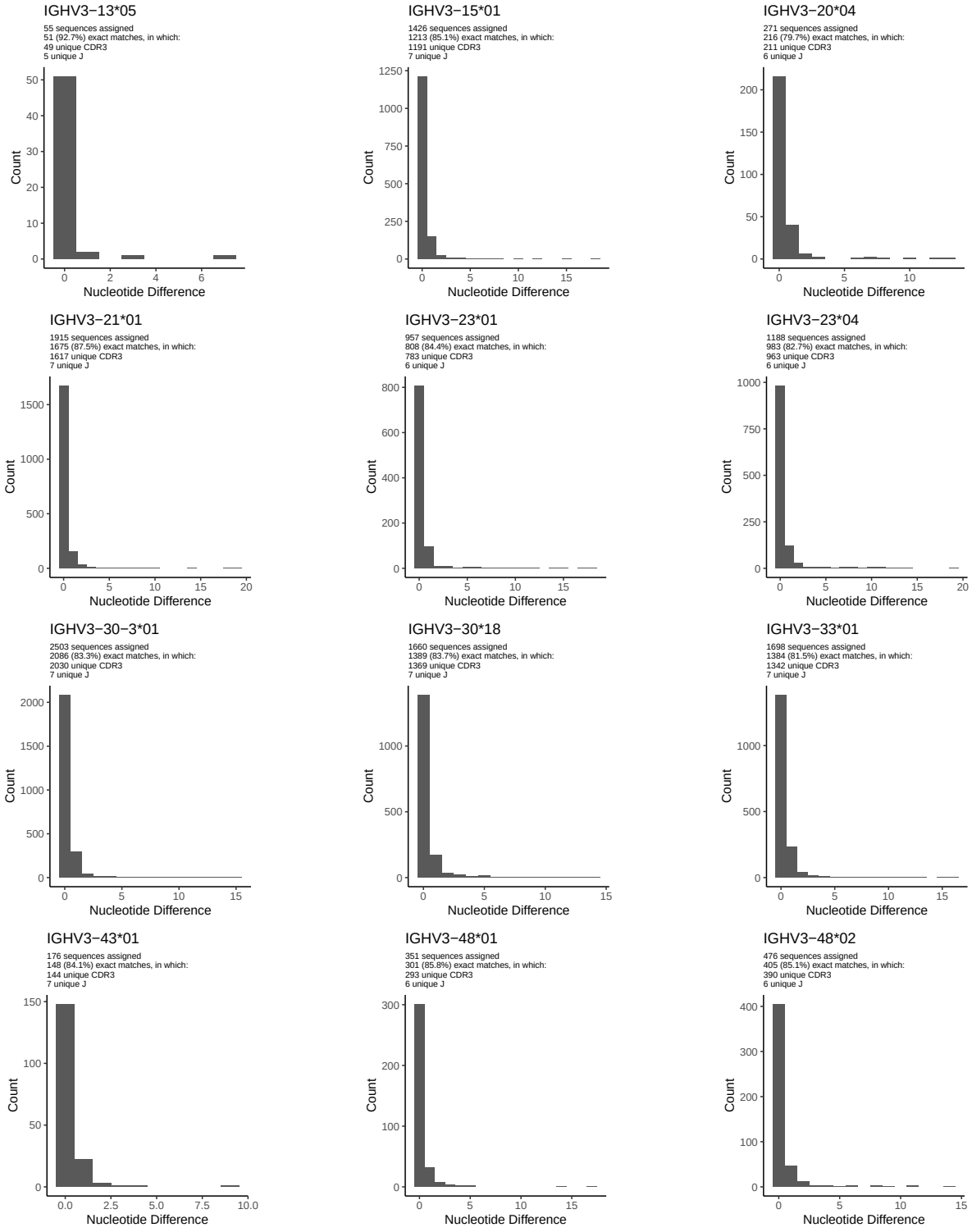
1 Novel sequence analysis

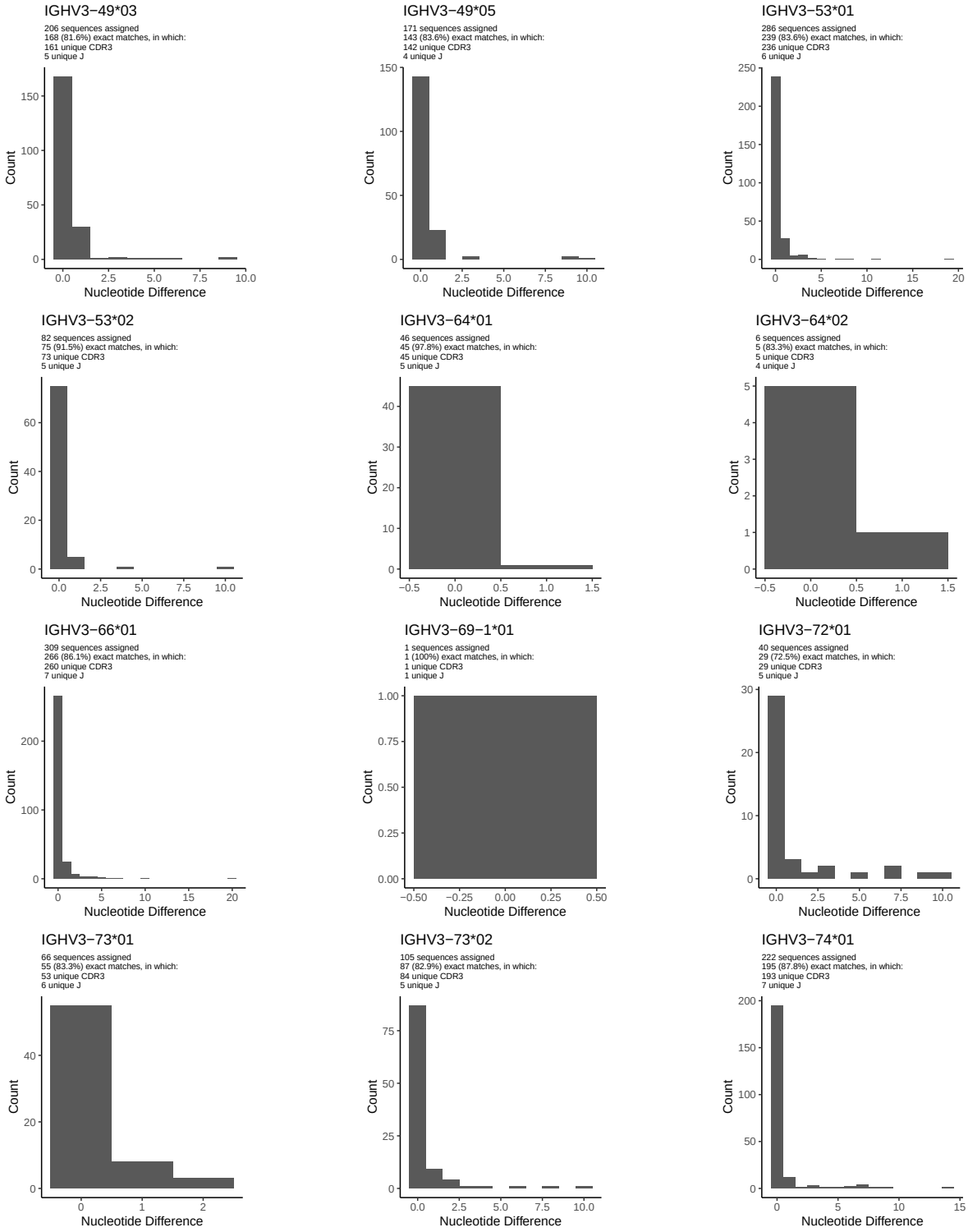
1.1 CDR3 length distribution, in assignments to novel alleles

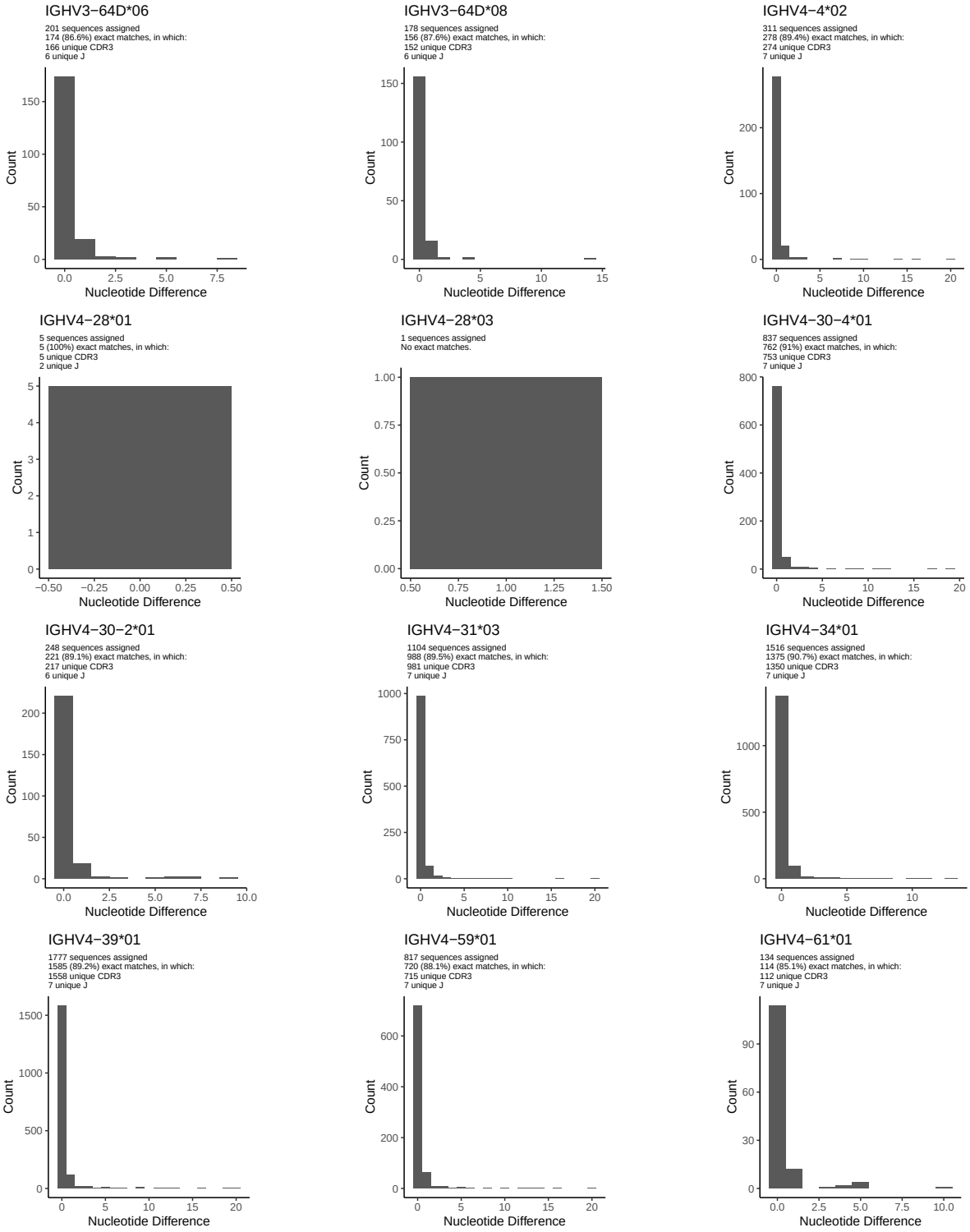
2 Variation from germline, in assignments to each allele

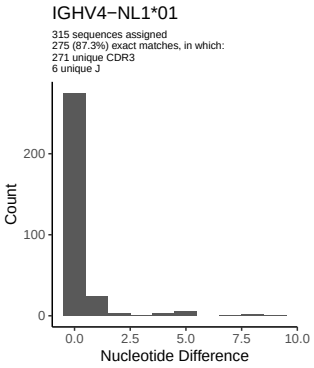


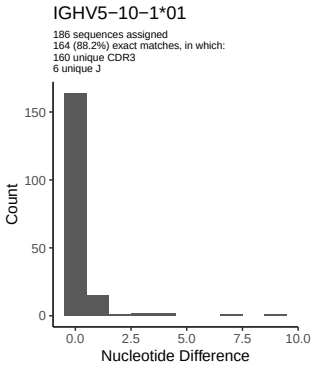

IGHV1−69*06
667 sequences assigned
622 (93.3%) exact matches, in which:
612 unique CDR3
6 unique J
IGHV2−5*01
233 sequences assigned
209 (89.7%) exact matches, in which:
207 unique CDR3
6 unique J
IGHV2−5*02
554 sequences assigned
502 (90.6%) exact matches, in which:
498 unique CDR3
6 unique J
IGHV2−26*01
371 sequences assigned
334 (90%) exact matches, in which:
333 unique CDR3
7 unique J
IGHV2−70*01
83 sequences assigned
79 (95.2%) exact matches, in which:
78 unique CDR3
5 unique J
IGHV2−70*15
79 sequences assigned
71 (89.9%) exact matches, in which:
71 unique CDR3
6 unique J
IGHV2−70D*04
25 sequences assigned
22 (88%) exact matches, in which:
22 unique CDR3
4 unique J
IGHV3−7*04
149 sequences assigned
131 (87.9%) exact matches, in which:
131 unique CDR3
6 unique J
IGHV3−7*05
164 sequences assigned
139 (84.8%) exact matches, in which:
137 unique CDR3
5 unique J
IGHV3−11*05
421 sequences assigned
334 (79.3%) exact matches, in which:
324 unique CDR3
6 unique J
IGHV3−11*06
195 sequences assigned
154 (79%) exact matches, in which:
152 unique CDR3
6 unique J
IGHV3−13*04
106 sequences assigned
99 (93.4%) exact matches, in which:
98 unique CDR3
6 unique J
Count
Nucleotide Difference

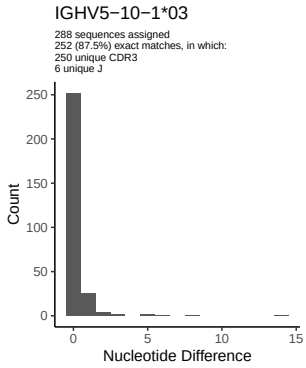

IGHV3−13*05
55 sequences assigned
51 (92.7%) exact matches, in which:
49 unique CDR3
5 unique J
IGHV3−15*01
1426 sequences assigned
1213 (85.1%) exact matches, in which:
1191 unique CDR3
7 unique J
IGHV3−20*04
271 sequences assigned
216 (79.7%) exact matches, in which:
211 unique CDR3
6 unique J
IGHV3−21*01
1915 sequences assigned
1675 (87.5%) exact matches, in which:
1617 unique CDR3
7 unique J
IGHV3−23*01
957 sequences assigned
808 (84.4%) exact matches, in which:
783 unique CDR3
6 unique J
IGHV3−23*04
1188 sequences assigned
983 (82.7%) exact matches, in which:
963 unique CDR3
6 unique J
IGHV3−30−3*01
2503 sequences assigned
2086 (83.3%) exact matches, in which:
2030 unique CDR3
7 unique J
IGHV3−30*18
1660 sequences assigned
1389 (83.7%) exact matches, in which:
1369 unique CDR3
7 unique J
IGHV3−33*01
1698 sequences assigned
1384 (81.5%) exact matches, in which:
1342 unique CDR3
7 unique J
IGHV3−43*01
176 sequences assigned
148 (84.1%) exact matches, in which:
144 unique CDR3
7 unique J
IGHV3−48*01
351 sequences assigned
301 (85.8%) exact matches, in which:
293 unique CDR3
6 unique J
IGHV3−48*02
476 sequences assigned
405 (85.1%) exact matches, in which:
390 unique CDR3
6 unique J
Count
Nucleotide Difference

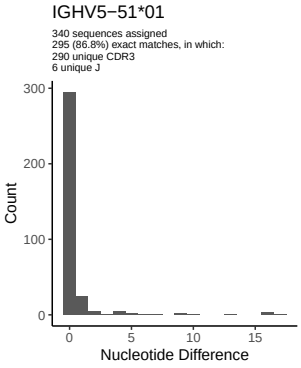

IGHV3−49*03
206 sequences assigned
168 (81.6%) exact matches, in which:
161 unique CDR3
5 unique J
IGHV3−49*05
171 sequences assigned
143 (83.6%) exact matches, in which:
142 unique CDR3
4 unique J
IGHV3−53*01
286 sequences assigned
239 (83.6%) exact matches, in which:
236 unique CDR3
6 unique J
IGHV3−53*02
82 sequences assigned
75 (91.5%) exact matches, in which:
73 unique CDR3
5 unique J
IGHV3−64*01
46 sequences assigned
45 (97.8%) exact matches, in which:
45 unique CDR3
5 unique J
IGHV3−64*02
6 sequences assigned
5 (83.3%) exact matches, in which:
5 unique CDR3
4 unique J
IGHV3−66*01
309 sequences assigned
266 (86.1%) exact matches, in which:
260 unique CDR3
7 unique J
IGHV3−69−1*01
1 sequences assigned
1 (100%) exact matches, in which:
1 unique CDR3
1 unique J
IGHV3−72*01
40 sequences assigned
29 (72.5%) exact matches, in which:
29 unique CDR3
5 unique J
IGHV3−73*01
66 sequences assigned
55 (83.3%) exact matches, in which:
53 unique CDR3
6 unique J
IGHV3−73*02
105 sequences assigned
87 (82.9%) exact matches, in which:
84 unique CDR3
5 unique J
IGHV3−74*01
222 sequences assigned
195 (87.8%) exact matches, in which:
193 unique CDR3
7 unique J
Count
Nucleotide Difference

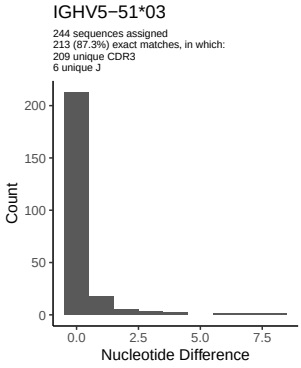

IGHV3−64D*06
201 sequences assigned
174 (86.6%) exact matches, in which:
166 unique CDR3
6 unique J
IGHV3−64D*08
178 sequences assigned
156 (87.6%) exact matches, in which:
152 unique CDR3
6 unique J
IGHV4−4*02
311 sequences assigned
278 (89.4%) exact matches, in which:
274 unique CDR3
7 unique J
IGHV4−28*01
5 sequences assigned
5 (100%) exact matches, in which:
5 unique CDR3
2 unique J
IGHV4−28*03
1 sequences assigned
No exact matches.
IGHV4−30−4*01
837 sequences assigned
762 (91%) exact matches, in which:
753 unique CDR3
7 unique J
IGHV4−30−2*01
248 sequences assigned
221 (89.1%) exact matches, in which:
217 unique CDR3
6 unique J
IGHV4−31*03
1104 sequences assigned
988 (89.5%) exact matches, in which:
981 unique CDR3
7 unique J
IGHV4−34*01
1516 sequences assigned
1375 (90.7%) exact matches, in which:
1350 unique CDR3
7 unique J
IGHV4−39*01
1777 sequences assigned
1585 (89.2%) exact matches, in which:
1558 unique CDR3
7 unique J
IGHV4−59*01
817 sequences assigned
720 (88.1%) exact matches, in which:
715 unique CDR3
7 unique J
IGHV4−61*01
134 sequences assigned
114 (85.1%) exact matches, in which:
112 unique CDR3
7 unique J
Count
Nucleotide Difference

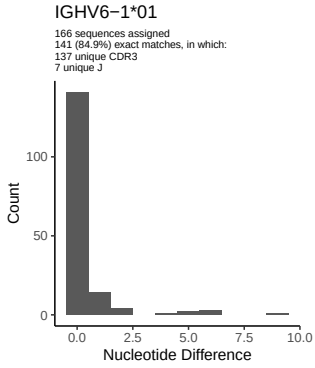

IGHV4−NL1*01
315 sequences assigned
275 (87.3%) exact matches, in which:
271 unique CDR3
6 unique J
Count
Nucleotide Difference

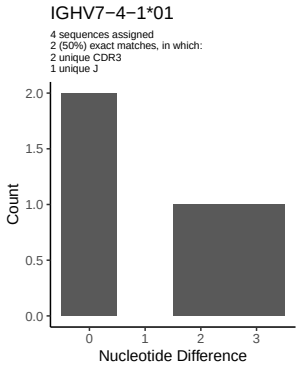

IGHV5−10−1*01
186 sequences assigned
164 (88.2%) exact matches, in which:
160 unique CDR3
6 unique J
Count
Nucleotide Difference


IGHV5−10−1*03
288 sequences assigned
252 (87.5%) exact matches, in which:
250 unique CDR3
6 unique J
Count
Nucleotide Difference

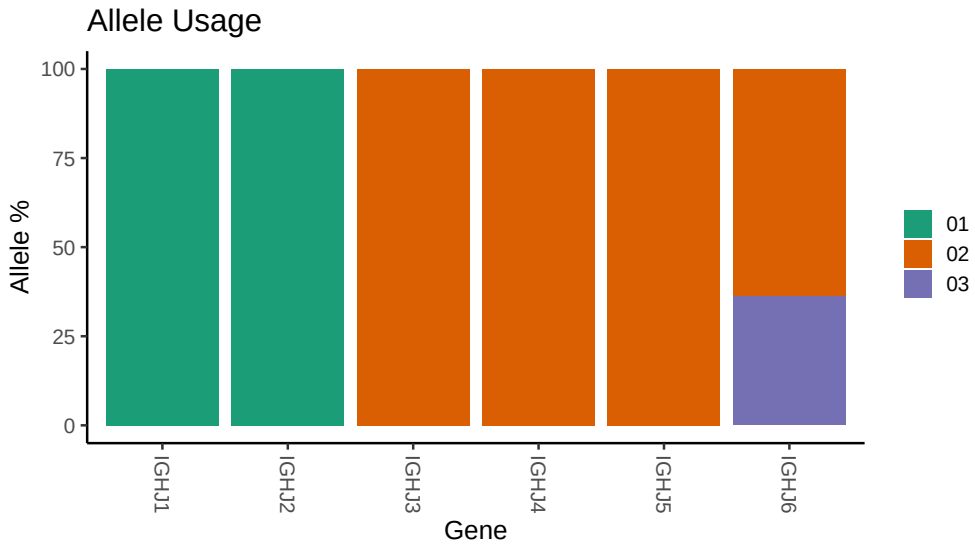

IGHV5−51*01
340 sequences assigned
295 (86.8%) exact matches, in which:
290 unique CDR3
6 unique J
Count
Nucleotide Difference


IGHV5−51*03
244 sequences assigned
213 (87.3%) exact matches, in which:
209 unique CDR3
6 unique J
Count
Nucleotide Difference

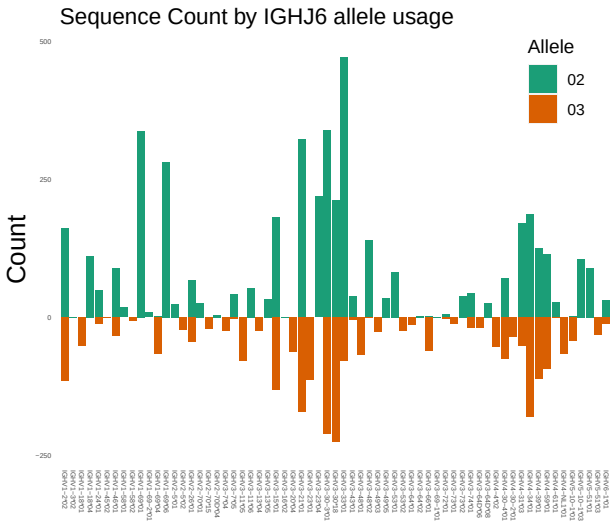

IGHV6−1*01
166 sequences assigned
141 (84.9%) exact matches, in which:
137 unique CDR3
7 unique J
Count
Nucleotide Difference


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

3 Allele usage in potential haplotype anchor genes



4 Haplotype plots



5 Configuration settings

```
## Repertoire file: /work/jenkins/PRJEB26509/S53/S53/56/56/3d/b80e8ff3cf12dd16ecb79b03e2559a/56_Finale_g
##
## Germline reference file: /work/jenkins/PRJEB26509/S53/S53/56/56/e6/c037f20b4c577786d7fa306ff96f36/ref
##
## Novel allele file:
##
## Species: Homosapiens
##
## Chain: IGHV
##
## Segment: V
##
## Warning   no inferred sequences found.
```