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 **8**

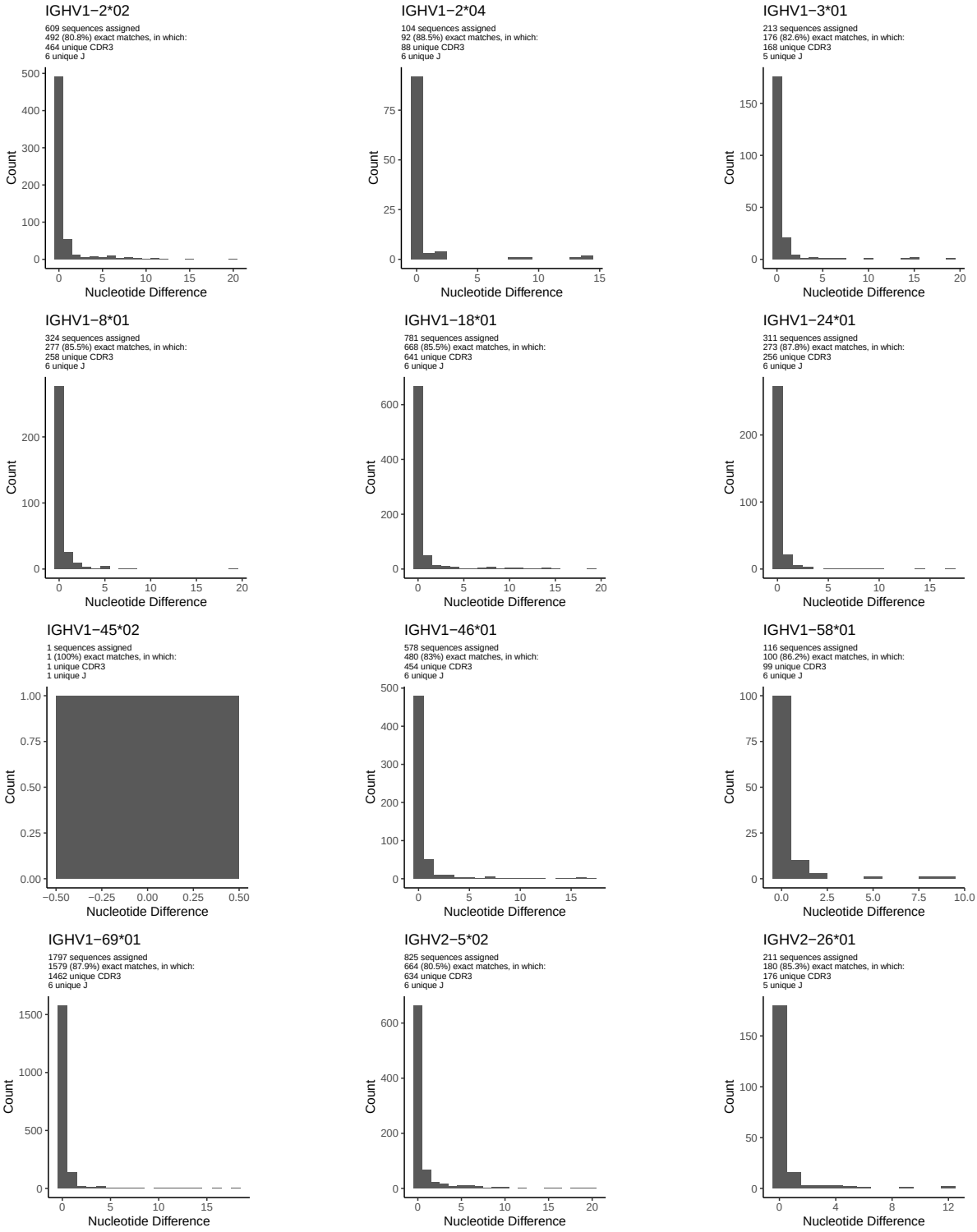
4 Haplotype plots **9**

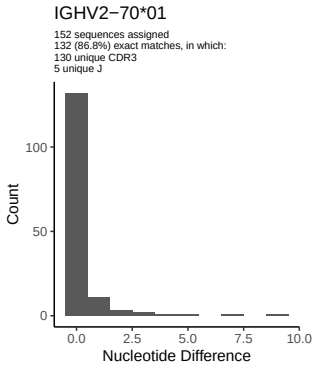
5 Configuration settings **10**

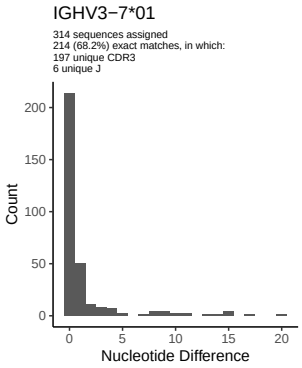
1 Novel sequence analysis

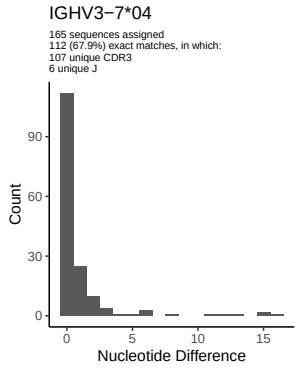
1.1 CDR3 length distribution, in assignments to novel alleles

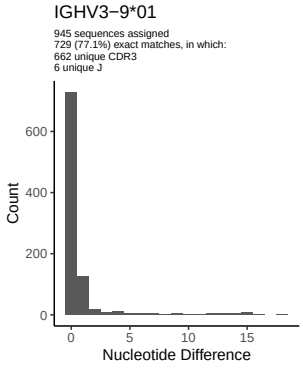
2 Variation from germline, in assignments to each allele

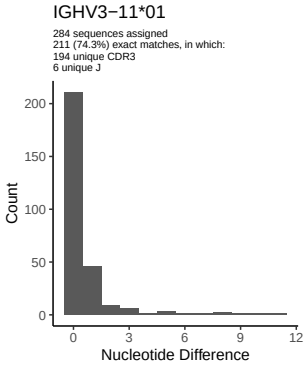


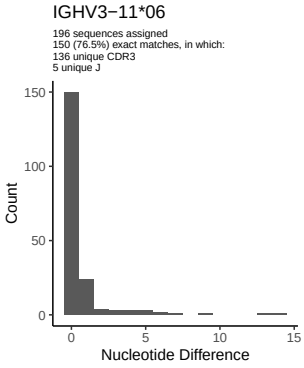

IGHV2−70*01
152 sequences assigned
132 (86.8%) exact matches, in which:
130 unique CDR3
5 unique J
Count
Nucleotide Difference

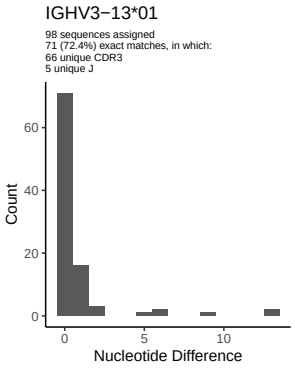

IGHV3−7*01
314 sequences assigned
214 (68.2%) exact matches, in which:
197 unique CDR3
6 unique J
Count
Nucleotide Difference

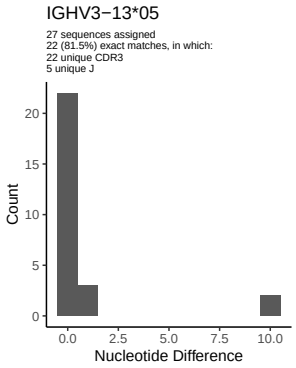

IGHV3−7*04
165 sequences assigned
112 (67.9%) exact matches, in which:
107 unique CDR3
6 unique J
Count
Nucleotide Difference

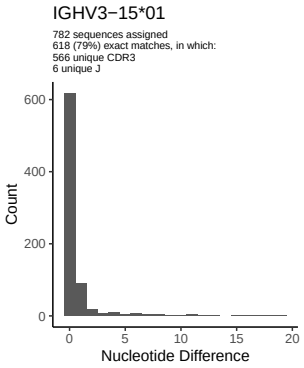

IGHV3−9*01
945 sequences assigned
729 (77.1%) exact matches, in which:
662 unique CDR3
6 unique J
Count
Nucleotide Difference

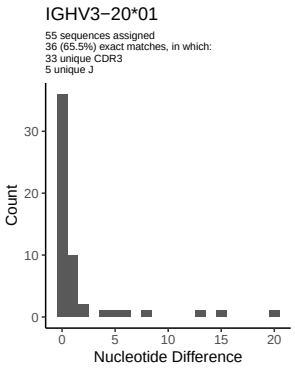

IGHV3−11*01
284 sequences assigned
211 (74.3%) exact matches, in which:
194 unique CDR3
6 unique J
Count
Nucleotide Difference

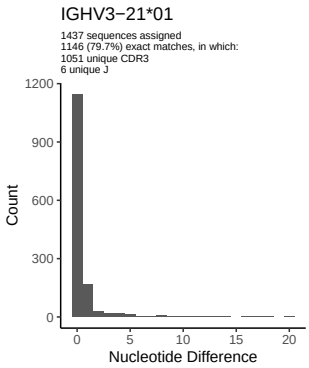

IGHV3−11*06
196 sequences assigned
150 (76.5%) exact matches, in which:
136 unique CDR3
5 unique J
Count
Nucleotide Difference

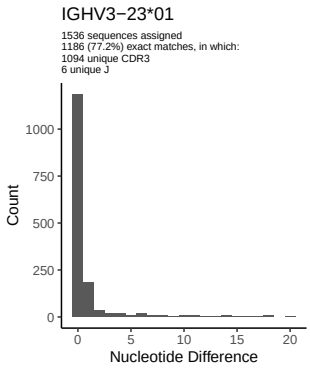

IGHV3−13*01
98 sequences assigned
71 (72.4%) exact matches, in which:
66 unique CDR3
5 unique J
Count
Nucleotide Difference

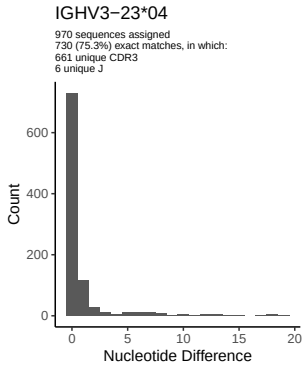

IGHV3−13*05
27 sequences assigned
22 (81.5%) exact matches, in which:
22 unique CDR3
5 unique J
Count
Nucleotide Difference

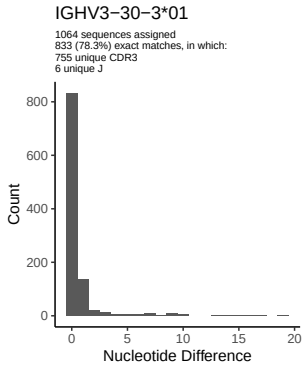

IGHV3−15*01
782 sequences assigned
618 (79%) exact matches, in which:
566 unique CDR3
6 unique J
Count
Nucleotide Difference

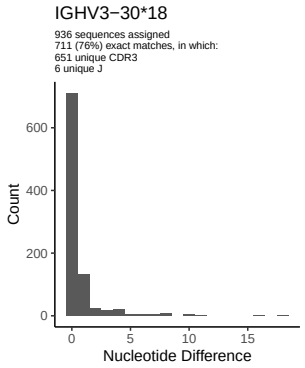

IGHV3−20*01
55 sequences assigned
36 (65.5%) exact matches, in which:
33 unique CDR3
5 unique J
Count
Nucleotide Difference

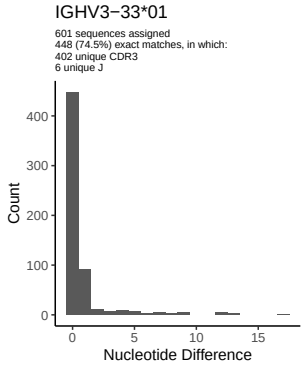

IGHV3−21*01
1437 sequences assigned
1146 (79.7%) exact matches, in which:
1051 unique CDR3
6 unique J
Count
Nucleotide Difference

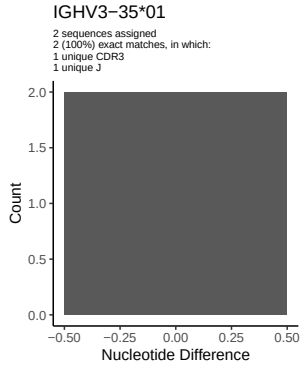

IGHV3−23*01
1536 sequences assigned
1186 (77.2%) exact matches, in which:
1094 unique CDR3
6 unique J
Count
Nucleotide Difference

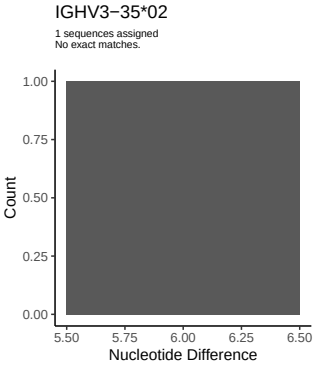

IGHV3−23*04
970 sequences assigned
730 (75.3%) exact matches, in which:
661 unique CDR3
6 unique J
Count
Nucleotide Difference

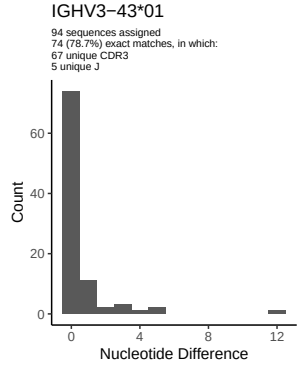

IGHV3−30−3*01
1064 sequences assigned
833 (78.3%) exact matches, in which:
755 unique CDR3
6 unique J
Count
Nucleotide Difference

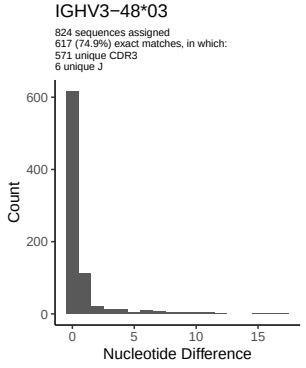

IGHV3−30*18
936 sequences assigned
711 (76%) exact matches, in which:
651 unique CDR3
6 unique J
Count
Nucleotide Difference

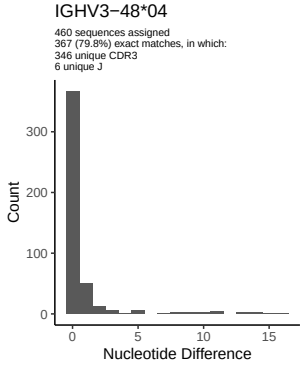

IGHV3−33*01
601 sequences assigned
448 (74.5%) exact matches, in which:
402 unique CDR3
6 unique J
Count
Nucleotide Difference

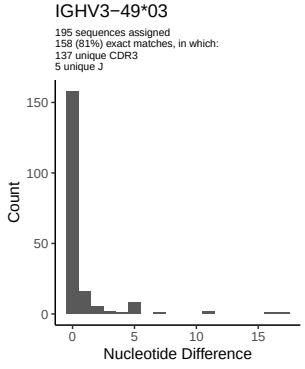

IGHV3−35*01
2 sequences assigned
2 (100%) exact matches, in which:
1 unique CDR3
1 unique J
Count
Nucleotide Difference

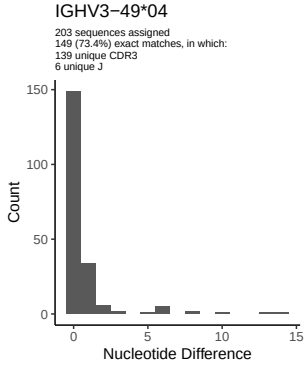

IGHV3−35*02
1 sequences assigned
No exact matches.
Count
Nucleotide Difference

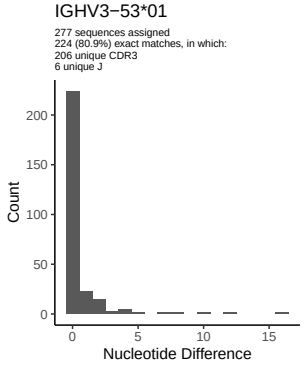

IGHV3−43*01
94 sequences assigned
74 (78.7%) exact matches, in which:
67 unique CDR3
5 unique J
Count
Nucleotide Difference

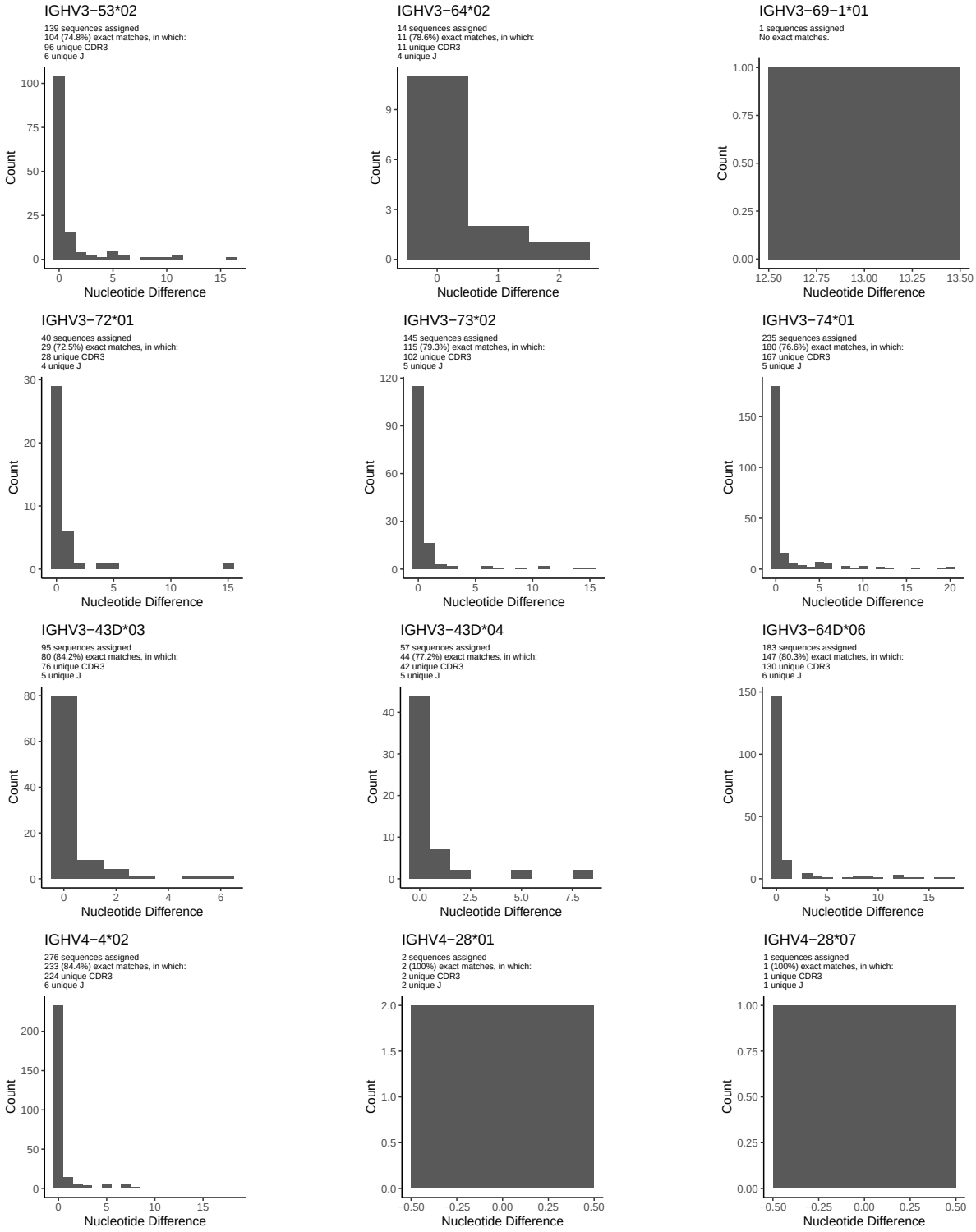

IGHV3−48*03
824 sequences assigned
617 (74.9%) exact matches, in which:
571 unique CDR3
6 unique J
Count
Nucleotide Difference

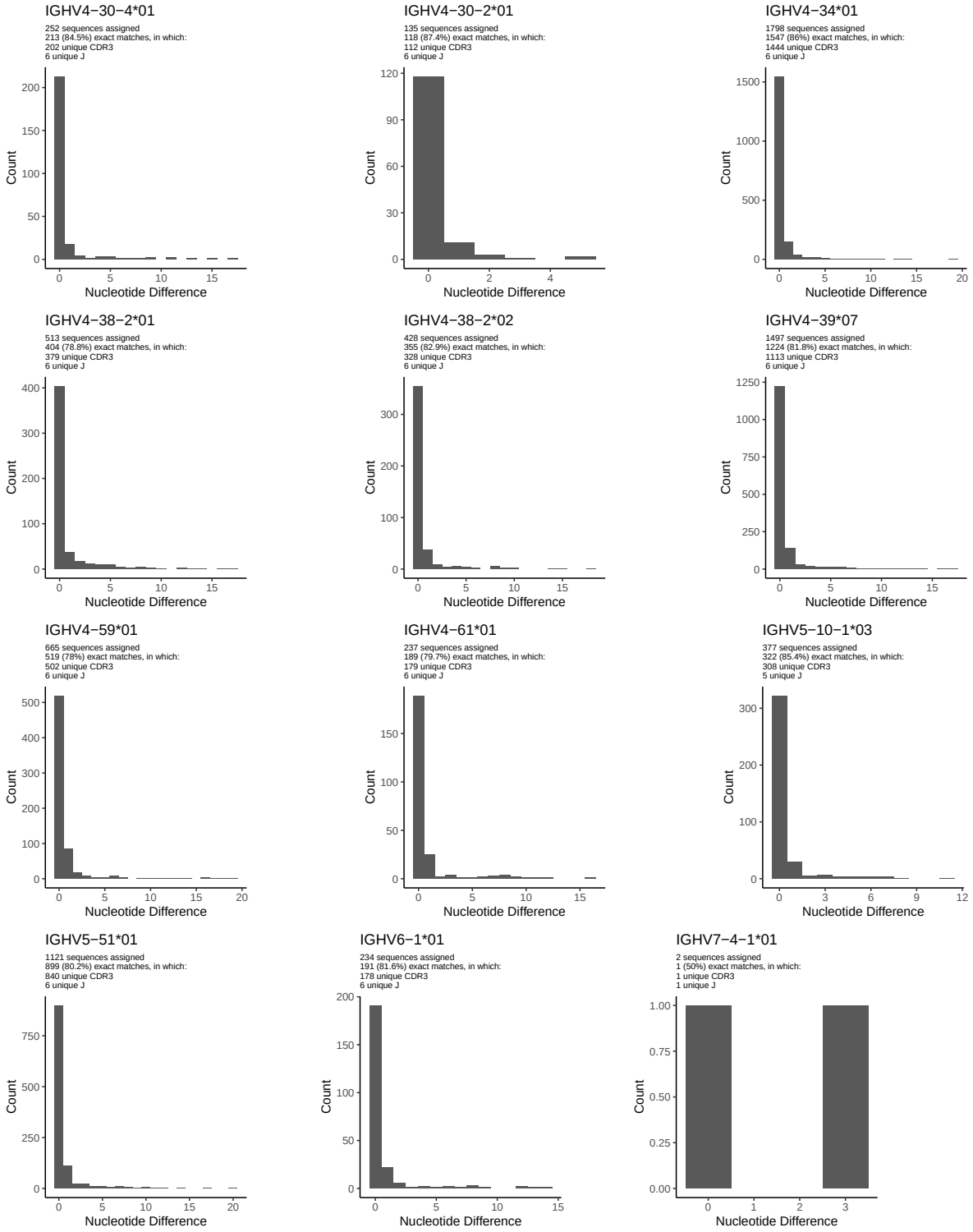

IGHV3−48*04
460 sequences assigned
367 (79.8%) exact matches, in which:
346 unique CDR3
6 unique J
Count
Nucleotide Difference


IGHV3−49*03
195 sequences assigned
158 (81%) exact matches, in which:
137 unique CDR3
5 unique J
Count
Nucleotide Difference

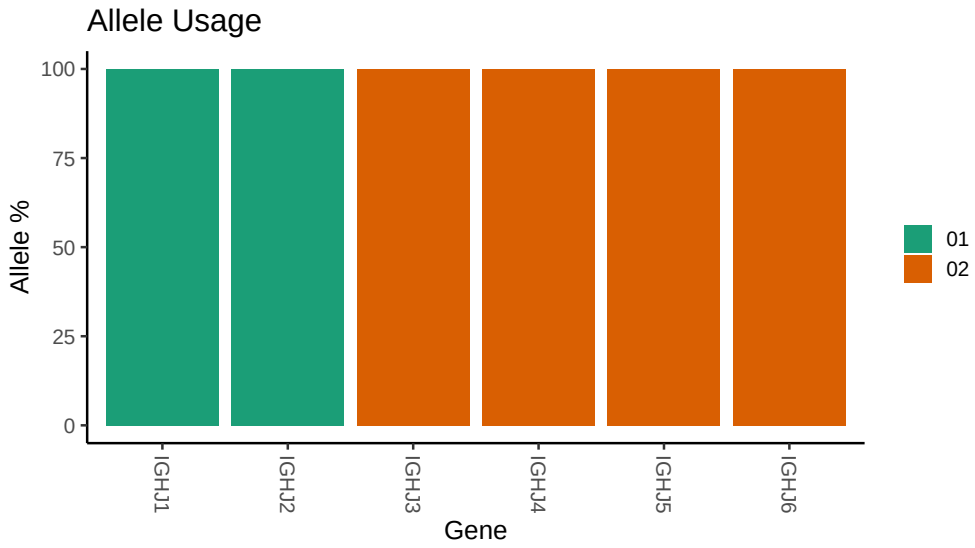

IGHV3−49*04
203 sequences assigned
149 (73.4%) exact matches, in which:
139 unique CDR3
6 unique J
Count
Nucleotide Difference


IGHV3−53*01
277 sequences assigned
224 (80.9%) exact matches, in which:
206 unique CDR3
6 unique J
Count
Nucleotide Difference


IGHV3−53*02
139 sequences assigned
104 (74.8%) exact matches, in which:
96 unique CDR3
6 unique J
IGHV3−64*02
14 sequences assigned
11 (78.6%) exact matches, in which:
11 unique CDR3
4 unique J
IGHV3−69−1*01
1 sequences assigned
No exact matches.
IGHV3−72*01
40 sequences assigned
29 (72.5%) exact matches, in which:
28 unique CDR3
4 unique J
IGHV3−73*02
145 sequences assigned
115 (79.3%) exact matches, in which:
102 unique CDR3
5 unique J
IGHV3−74*01
235 sequences assigned
180 (76.6%) exact matches, in which:
167 unique CDR3
5 unique J
IGHV3−43D*03
95 sequences assigned
80 (84.2%) exact matches, in which:
76 unique CDR3
5 unique J
IGHV3−43D*04
57 sequences assigned
44 (77.2%) exact matches, in which:
42 unique CDR3
5 unique J
IGHV3−64D*06
183 sequences assigned
147 (80.3%) exact matches, in which:
130 unique CDR3
6 unique J
IGHV4−4*02
276 sequences assigned
233 (84.4%) exact matches, in which:
224 unique CDR3
6 unique J
IGHV4−28*01
2 sequences assigned
2 (100%) exact matches, in which:
2 unique CDR3
2 unique J
IGHV4−28*07
1 sequences assigned
1 (100%) exact matches, in which:
1 unique CDR3
1 unique J
Count
Nucleotide Difference


IGHV4−30−4*01
252 sequences assigned
213 (84.5%) exact matches, in which:
202 unique CDR3
6 unique J
IGHV4−30−2*01
135 sequences assigned
118 (87.4%) exact matches, in which:
112 unique CDR3
6 unique J
IGHV4−34*01
1798 sequences assigned
1547 (86%) exact matches, in which:
1444 unique CDR3
6 unique J
IGHV4−38−2*01
513 sequences assigned
404 (78.8%) exact matches, in which:
379 unique CDR3
6 unique J
IGHV4−38−2*02
428 sequences assigned
355 (82.9%) exact matches, in which:
328 unique CDR3
6 unique J
IGHV4−39*07
1497 sequences assigned
1224 (81.8%) exact matches, in which:
1113 unique CDR3
6 unique J
IGHV4−59*01
665 sequences assigned
519 (78%) exact matches, in which:
502 unique CDR3
6 unique J
IGHV4−61*01
237 sequences assigned
189 (79.7%) exact matches, in which:
179 unique CDR3
6 unique J
IGHV5−10−1*03
377 sequences assigned
322 (85.4%) exact matches, in which:
308 unique CDR3
5 unique J
IGHV5−51*01
1121 sequences assigned
899 (80.2%) exact matches, in which:
840 unique CDR3
6 unique J
IGHV6−1*01
234 sequences assigned
191 (81.6%) exact matches, in which:
178 unique CDR3
6 unique J
IGHV7−4−1*01
2 sequences assigned
1 (50%) 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/S75/S75/79/79/ad/873feb10a10e17cbfc84714e703dcc/79_Fi
##
## Germline reference file: /misc/work/jenkins/PRJEB26509/S75/S75/79/79/34/bd76d40c799d83e8288bde79de44
##
## Novel allele file:
##
## Species: Homosapiens
##
## Chain: IGHV
##
## Segment: V
##
## Warning   no inferred sequences found.
```