OGRDBstats Report

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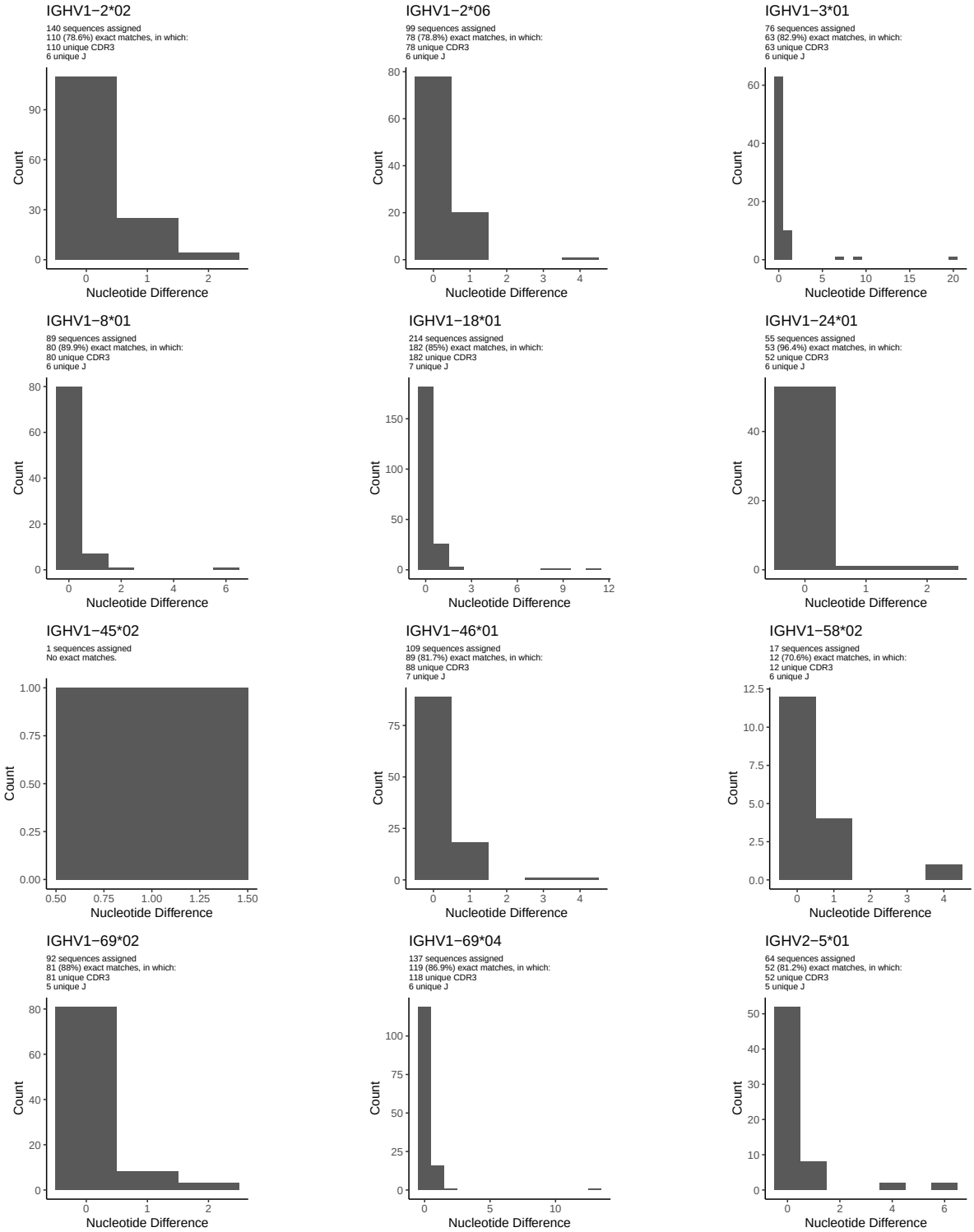
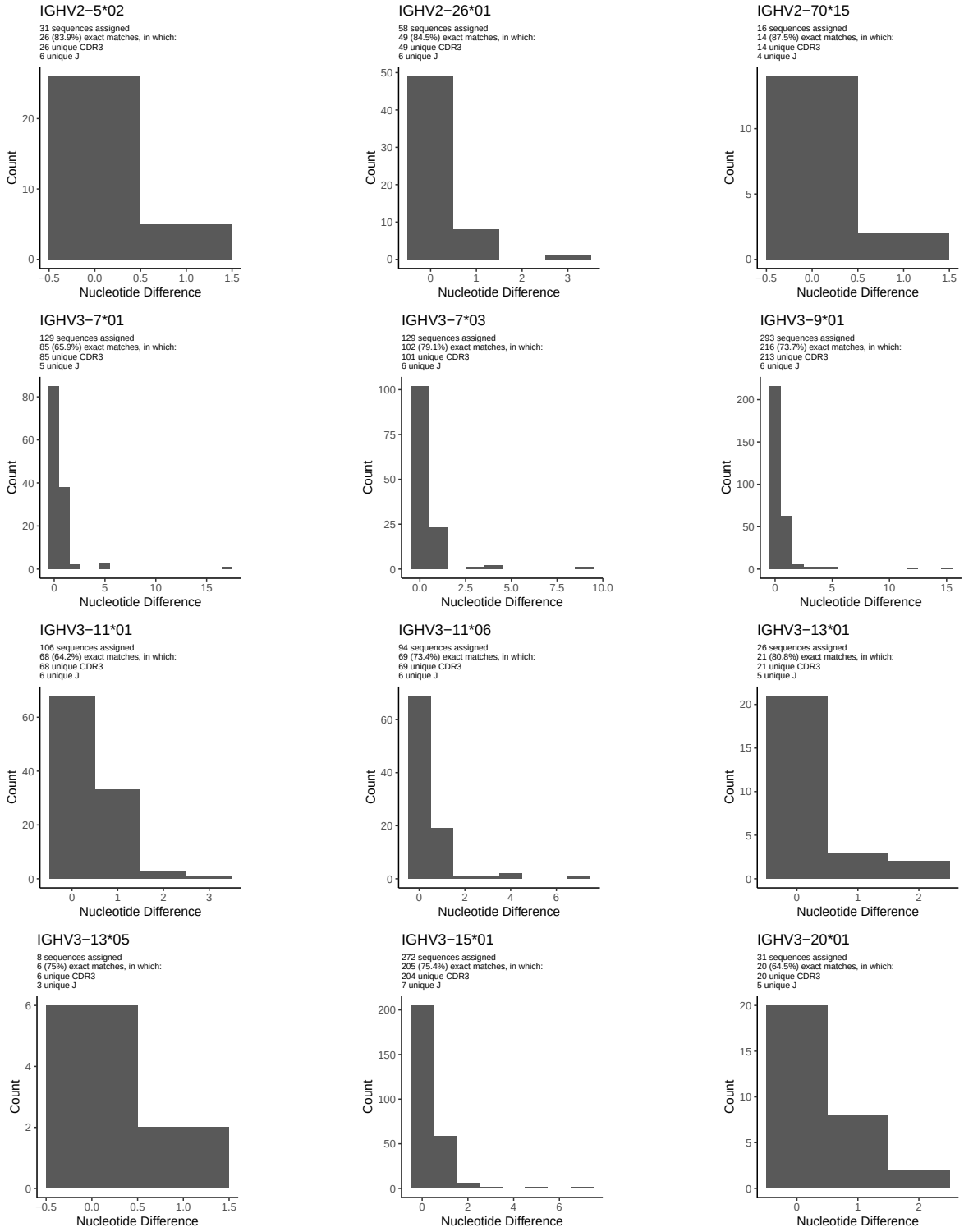
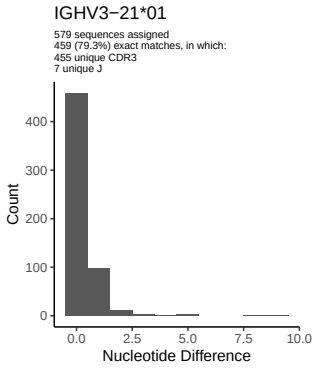
1 Novel sequence analysis

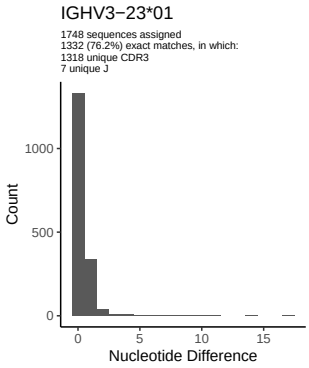
1.1 CDR3 length distribution, in assignments to novel alleles

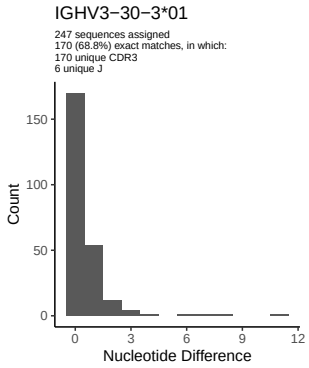
2 Variation from germline, in assignments to each allele

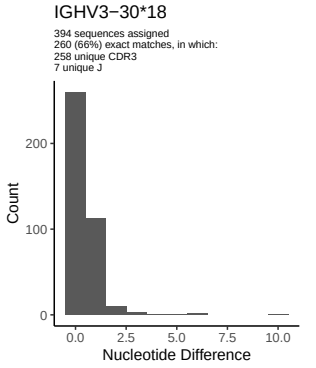


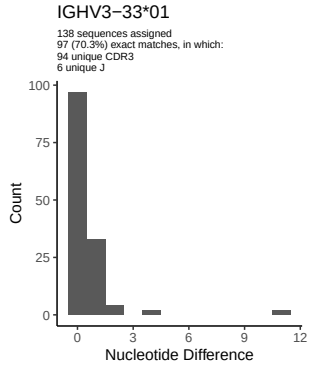

IGHV2−5*02
31 sequences assigned
26 (83.9%) exact matches, in which:
26 unique CDR3
6 unique J
IGHV2−26*01
58 sequences assigned
49 (84.5%) exact matches, in which:
49 unique CDR3
6 unique J
IGHV2−70*15
16 sequences assigned
14 (87.5%) exact matches, in which:
14 unique CDR3
4 unique J
IGHV3−7*01
129 sequences assigned
85 (65.9%) exact matches, in which:
85 unique CDR3
5 unique J
IGHV3−7*03
129 sequences assigned
102 (79.1%) exact matches, in which:
101 unique CDR3
6 unique J
IGHV3−9*01
293 sequences assigned
216 (73.7%) exact matches, in which:
213 unique CDR3
6 unique J
IGHV3−11*01
106 sequences assigned
68 (64.2%) exact matches, in which:
68 unique CDR3
6 unique J
IGHV3−11*06
94 sequences assigned
69 (73.4%) exact matches, in which:
69 unique CDR3
6 unique J
IGHV3−13*01
26 sequences assigned
21 (80.8%) exact matches, in which:
21 unique CDR3
5 unique J
IGHV3−13*05
8 sequences assigned
6 (75%) exact matches, in which:
6 unique CDR3
3 unique J
IGHV3−15*01
272 sequences assigned
205 (75.4%) exact matches, in which:
204 unique CDR3
7 unique J
IGHV3−20*01
31 sequences assigned
20 (64.5%) exact matches, in which:
20 unique CDR3
5 unique J
Count
Nucleotide Difference

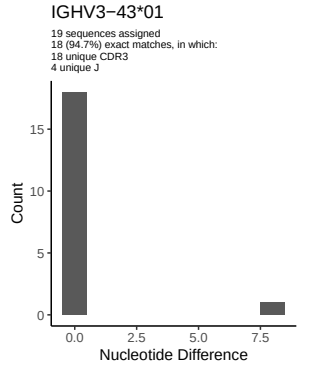

IGHV3−21*01
579 sequences assigned
459 (79.3%) exact matches, in which:
455 unique CDR3
7 unique J
Count
Nucleotide Difference

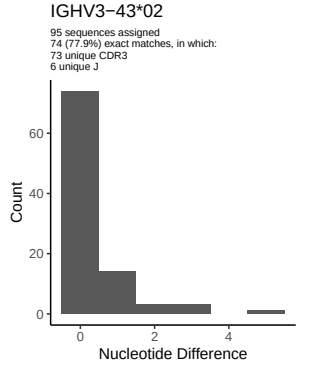

IGHV3−23*01
1748 sequences assigned
1332 (76.2%) exact matches, in which:
1318 unique CDR3
7 unique J
Count
Nucleotide Difference

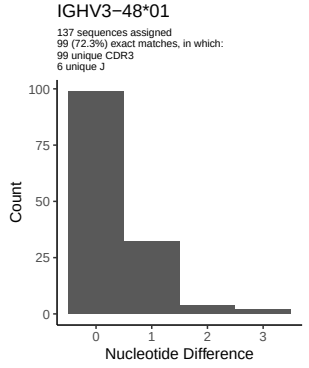

IGHV3−30−3*01
247 sequences assigned
170 (68.8%) exact matches, in which:
170 unique CDR3
6 unique J
Count
Nucleotide Difference

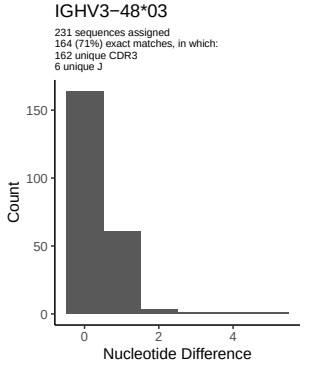

IGHV3−30*18
394 sequences assigned
260 (66%) exact matches, in which:
258 unique CDR3
7 unique J
Count
Nucleotide Difference

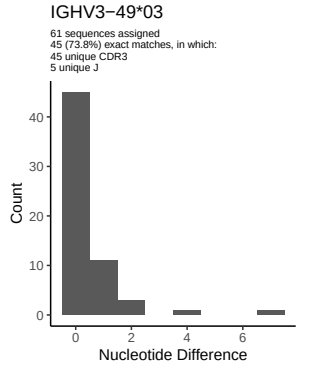

IGHV3−33*01
138 sequences assigned
97 (70.3%) exact matches, in which:
94 unique CDR3
6 unique J
Count
Nucleotide Difference

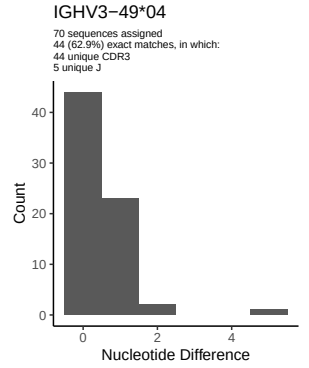

IGHV3−43*01
19 sequences assigned
18 (94.7%) exact matches, in which:
18 unique CDR3
4 unique J
Count
Nucleotide Difference

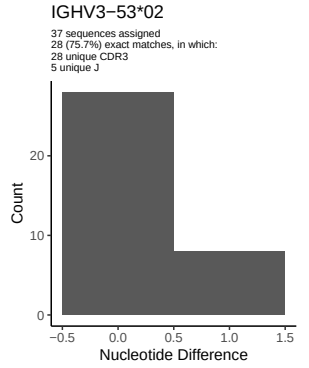

IGHV3−43*02
95 sequences assigned
74 (77.9%) exact matches, in which:
73 unique CDR3
6 unique J
Count
Nucleotide Difference

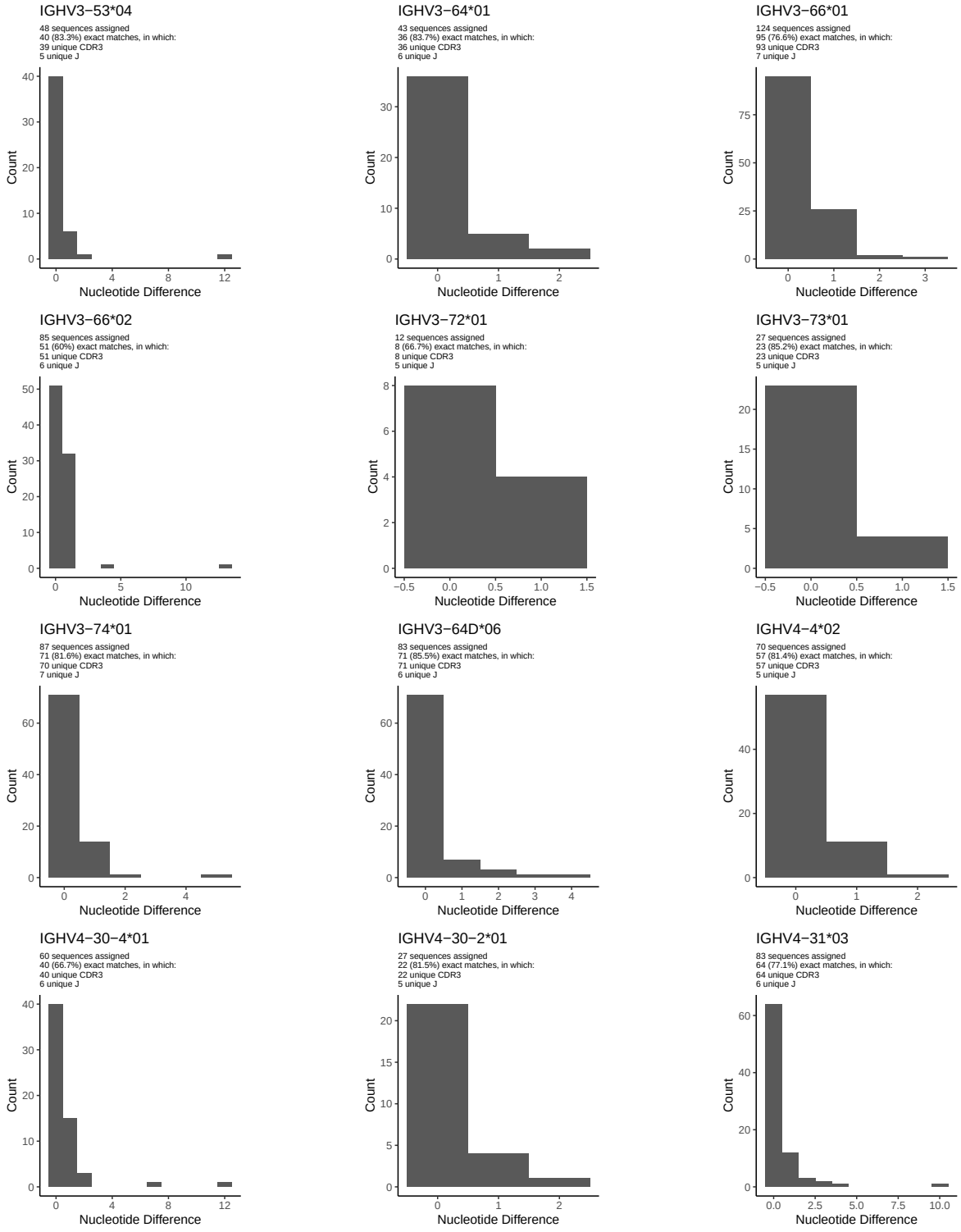

IGHV3−48*01
137 sequences assigned
99 (72.3%) exact matches, in which:
99 unique CDR3
6 unique J
Count
Nucleotide Difference

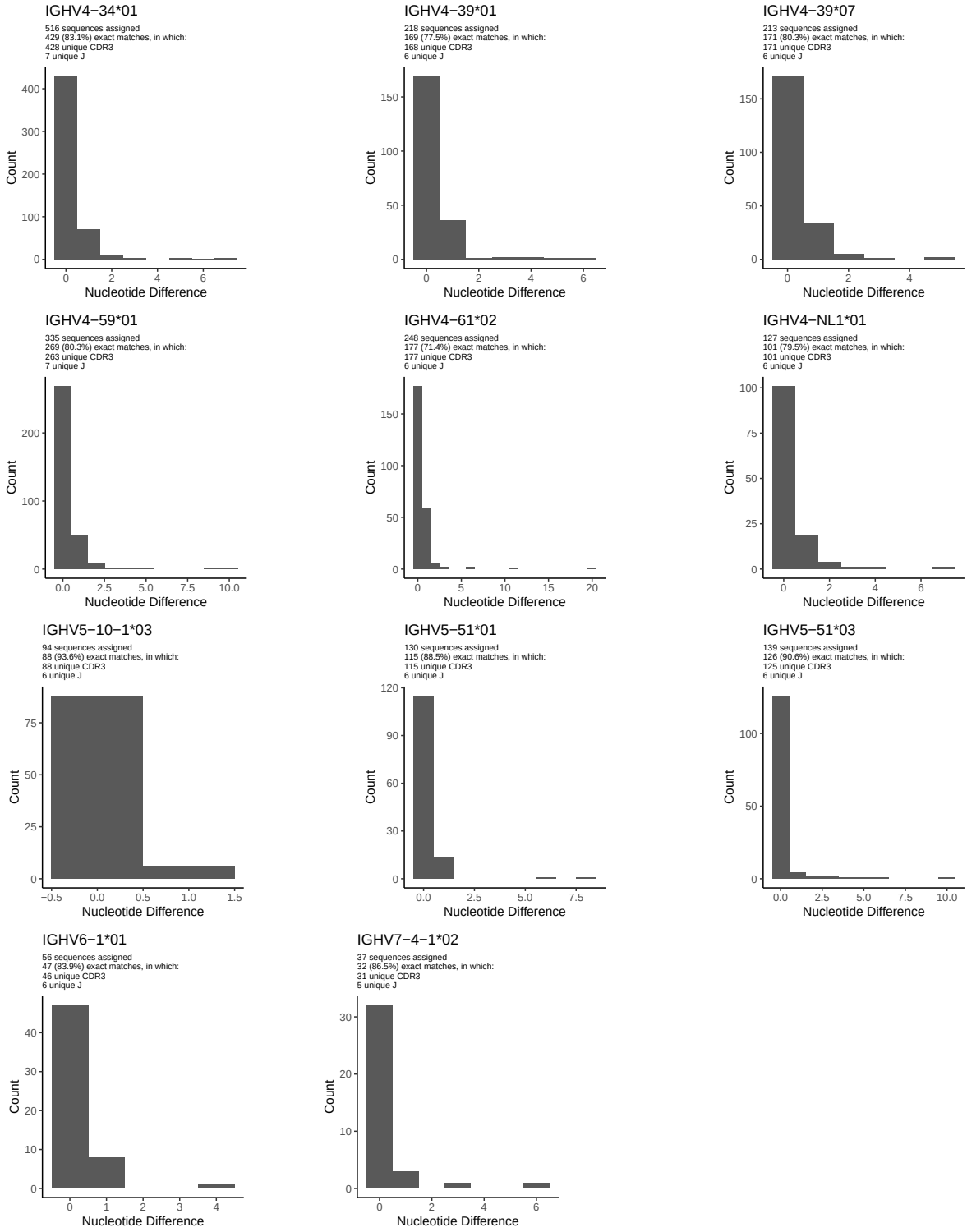

IGHV3−48*03
231 sequences assigned
164 (71%) exact matches, in which:
162 unique CDR3
6 unique J
Count
Nucleotide Difference


IGHV3−49*03
61 sequences assigned
45 (73.8%) exact matches, in which:
45 unique CDR3
5 unique J
Count
Nucleotide Difference

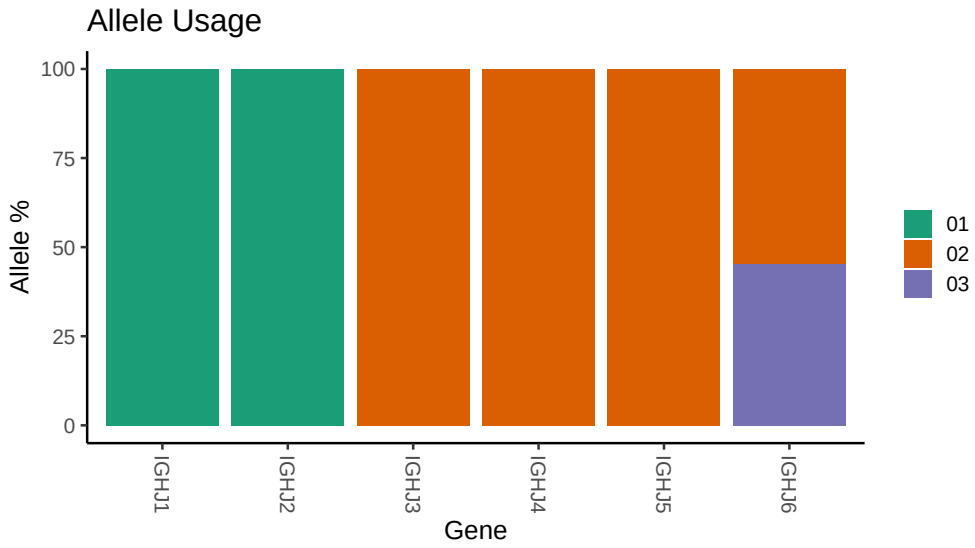

IGHV3−49*04
70 sequences assigned
44 (62.9%) exact matches, in which:
44 unique CDR3
5 unique J
Count
Nucleotide Difference


IGHV3−53*02
37 sequences assigned
28 (75.7%) exact matches, in which:
28 unique CDR3
5 unique J
Count
Nucleotide Difference

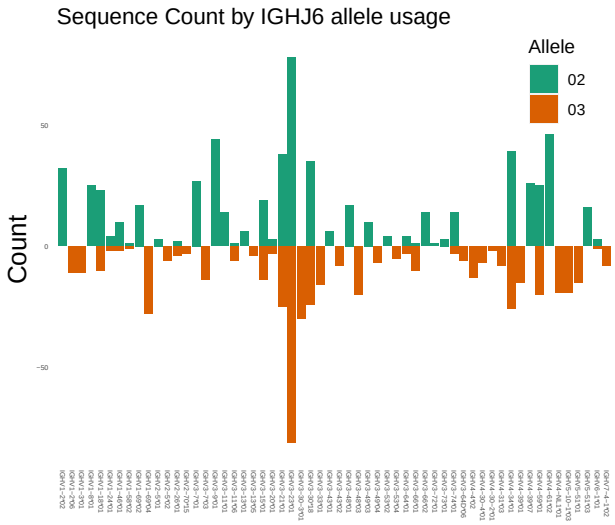

IGHV3−53*04
48 sequences assigned
40 (83.3%) exact matches, in which:
39 unique CDR3
5 unique J
IGHV3−64*01
43 sequences assigned
36 (83.7%) exact matches, in which:
36 unique CDR3
6 unique J
IGHV3−66*01
124 sequences assigned
95 (76.6%) exact matches, in which:
93 unique CDR3
7 unique J
IGHV3−66*02
85 sequences assigned
51 (60%) exact matches, in which:
51 unique CDR3
6 unique J
IGHV3−72*01
12 sequences assigned
8 (66.7%) exact matches, in which:
8 unique CDR3
5 unique J
IGHV3−73*01
27 sequences assigned
23 (85.2%) exact matches, in which:
23 unique CDR3
5 unique J
IGHV3−74*01
87 sequences assigned
71 (81.6%) exact matches, in which:
70 unique CDR3
7 unique J
IGHV3−64D*06
83 sequences assigned
71 (85.5%) exact matches, in which:
71 unique CDR3
6 unique J
IGHV4−4*02
70 sequences assigned
57 (81.4%) exact matches, in which:
57 unique CDR3
5 unique J
IGHV4−30−4*01
60 sequences assigned
40 (66.7%) exact matches, in which:
40 unique CDR3
6 unique J
IGHV4−30−2*01
27 sequences assigned
22 (81.5%) exact matches, in which:
22 unique CDR3
5 unique J
IGHV4−31*03
83 sequences assigned
64 (77.1%) exact matches, in which:
64 unique CDR3
6 unique J
Count
Nucleotide Difference


IGHV4−34*01
516 sequences assigned
429 (83.1%) exact matches, in which:
428 unique CDR3
7 unique J
IGHV4−39*01
218 sequences assigned
169 (77.5%) exact matches, in which:
168 unique CDR3
6 unique J
IGHV4−39*07
213 sequences assigned
171 (80.3%) exact matches, in which:
171 unique CDR3
6 unique J
IGHV4−59*01
335 sequences assigned
269 (80.3%) exact matches, in which:
263 unique CDR3
7 unique J
IGHV4−61*02
248 sequences assigned
177 (71.4%) exact matches, in which:
177 unique CDR3
6 unique J
IGHV4−NL1*01
127 sequences assigned
101 (79.5%) exact matches, in which:
101 unique CDR3
6 unique J
IGHV5−10−1*03
94 sequences assigned
88 (93.6%) exact matches, in which:
88 unique CDR3
6 unique J
IGHV5−51*01
130 sequences assigned
115 (88.5%) exact matches, in which:
115 unique CDR3
6 unique J
IGHV5−51*03
139 sequences assigned
126 (90.6%) exact matches, in which:
125 unique CDR3
6 unique J
IGHV6−1*01
56 sequences assigned
47 (83.9%) exact matches, in which:
46 unique CDR3
6 unique J
IGHV7−4−1*02
37 sequences assigned
32 (86.5%) exact matches, in which:
31 unique CDR3
5 unique J
Count
Nucleotide Difference

3 Allele usage in potential haplotype anchor genes



4 Haplotype plots



5 Configuration settings

```
## Repertoire file: /work/jenkins/PRJEB26509/S55/S55/58/58/1b/f69ed8819478d2efe8c63273ba66ef/58_Finale_
##
## Germline reference file: /work/jenkins/PRJEB26509/S55/S55/58/58/a0/cb5981e152db7433a2c7f4056b933b/re
##
## Novel allele file:
##
## Species: Homosapiens
##
## Chain: IGHV
##
## Segment: V
##
## Warning   no inferred sequences found.
```