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**

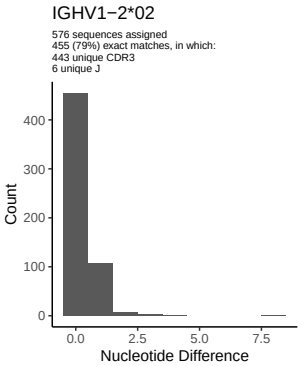
4 Haplotype plots **10**

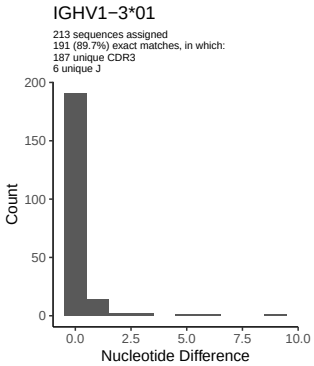
5 Configuration settings **11**

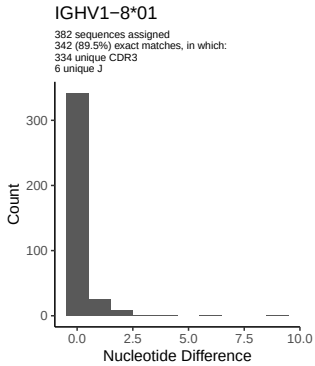
1 Novel sequence analysis

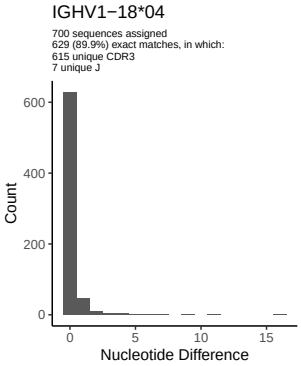
1.1 CDR3 length distribution, in assignments to novel alleles

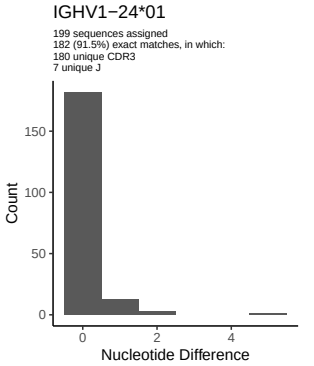
2 Variation from germline, in assignments to each allele

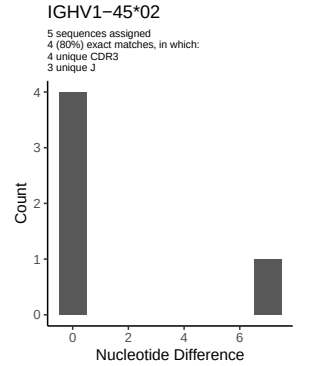


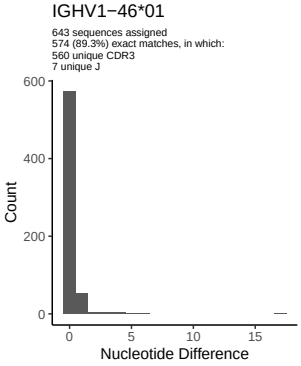


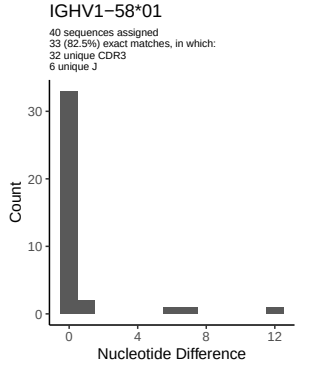


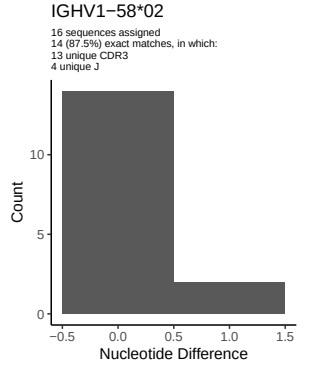


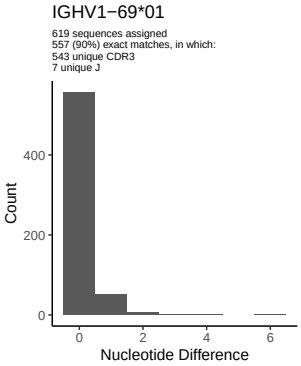


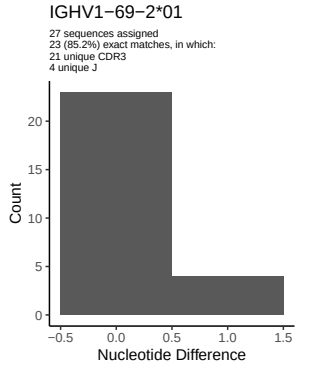


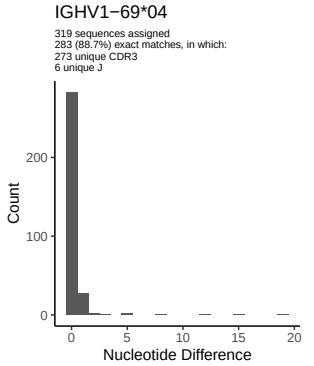


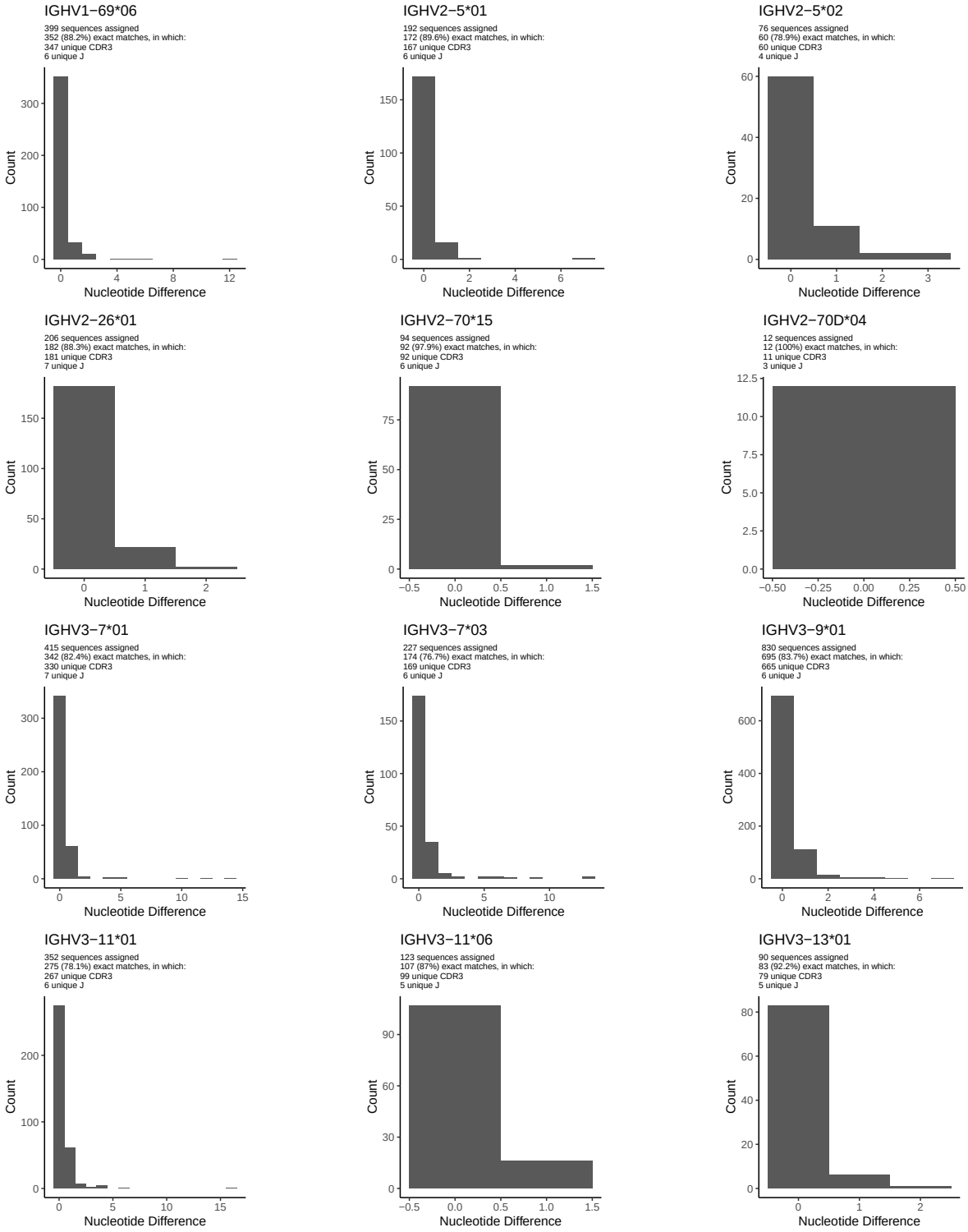


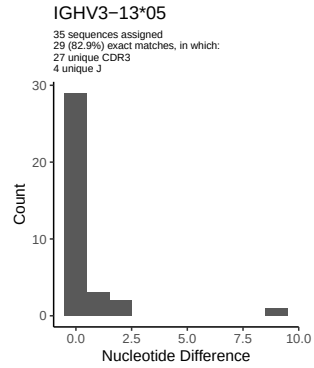


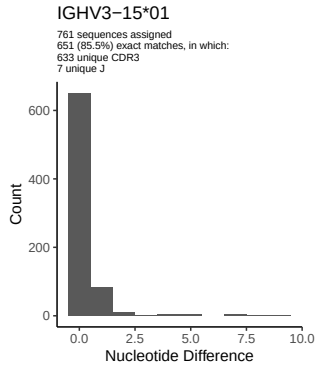


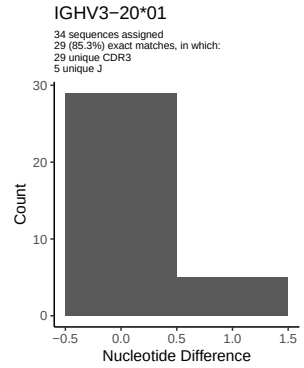


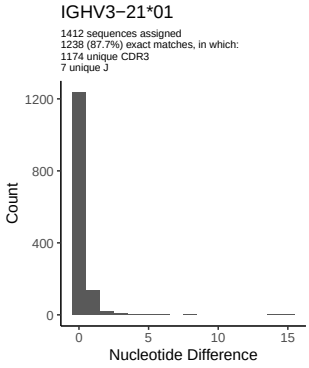


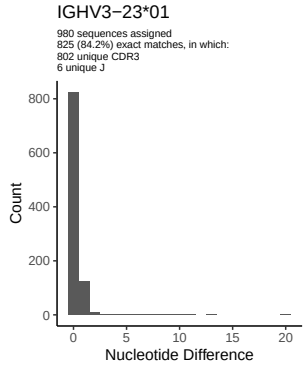

IGHV1−69*06
399 sequences assigned
352 (88.2%) exact matches, in which:
347 unique CDR3
6 unique J
IGHV2−5*01
192 sequences assigned
172 (89.6%) exact matches, in which:
167 unique CDR3
6 unique J
IGHV2−5*02
76 sequences assigned
60 (78.9%) exact matches, in which:
60 unique CDR3
4 unique J
IGHV2−26*01
206 sequences assigned
182 (88.3%) exact matches, in which:
181 unique CDR3
7 unique J
IGHV2−70*15
94 sequences assigned
92 (97.9%) exact matches, in which:
92 unique CDR3
6 unique J
IGHV2−70D*04
12 sequences assigned
12 (100%) exact matches, in which:
11 unique CDR3
3 unique J
IGHV3−7*01
415 sequences assigned
342 (82.4%) exact matches, in which:
330 unique CDR3
7 unique J
IGHV3−7*03
227 sequences assigned
174 (76.7%) exact matches, in which:
169 unique CDR3
6 unique J
IGHV3−9*01
830 sequences assigned
695 (83.7%) exact matches, in which:
665 unique CDR3
6 unique J
IGHV3−11*01
352 sequences assigned
275 (78.1%) exact matches, in which:
267 unique CDR3
6 unique J
IGHV3−11*06
123 sequences assigned
107 (87%) exact matches, in which:
99 unique CDR3
5 unique J
IGHV3−13*01
90 sequences assigned
83 (92.2%) exact matches, in which:
79 unique CDR3
5 unique J
Count
Nucleotide Difference

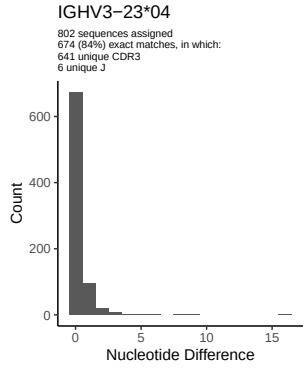

IGHV3−13*05
35 sequences assigned
29 (82.9%) exact matches, in which:
27 unique CDR3
4 unique J
Count
Nucleotide Difference

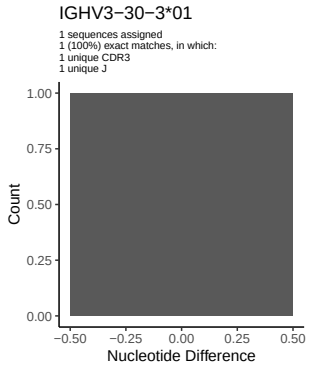

IGHV3−15*01
761 sequences assigned
651 (85.5%) exact matches, in which:
633 unique CDR3
7 unique J
Count
Nucleotide Difference

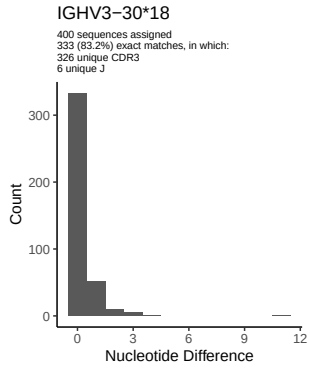

IGHV3−20*01
34 sequences assigned
29 (85.3%) exact matches, in which:
29 unique CDR3
5 unique J
Count
Nucleotide Difference

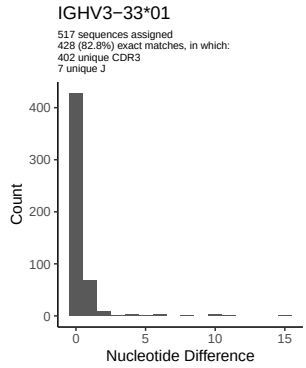

IGHV3−21*01
1412 sequences assigned
1238 (87.7%) exact matches, in which:
1174 unique CDR3
7 unique J
Count
Nucleotide Difference

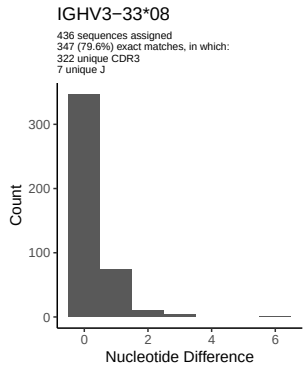

IGHV3−23*01
980 sequences assigned
825 (84.2%) exact matches, in which:
802 unique CDR3
6 unique J
Count
Nucleotide Difference

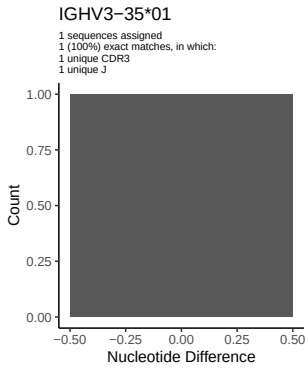

IGHV3−23*04
802 sequences assigned
674 (84%) exact matches, in which:
641 unique CDR3
6 unique J
Count
Nucleotide Difference

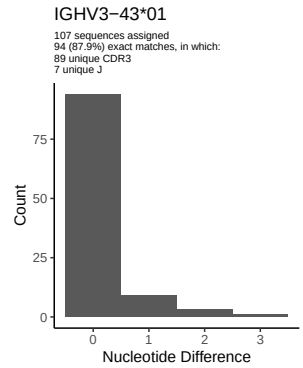

IGHV3−30−3*01
1 sequences assigned
1 (100%) exact matches, in which:
1 unique CDR3
1 unique J
Count
Nucleotide Difference

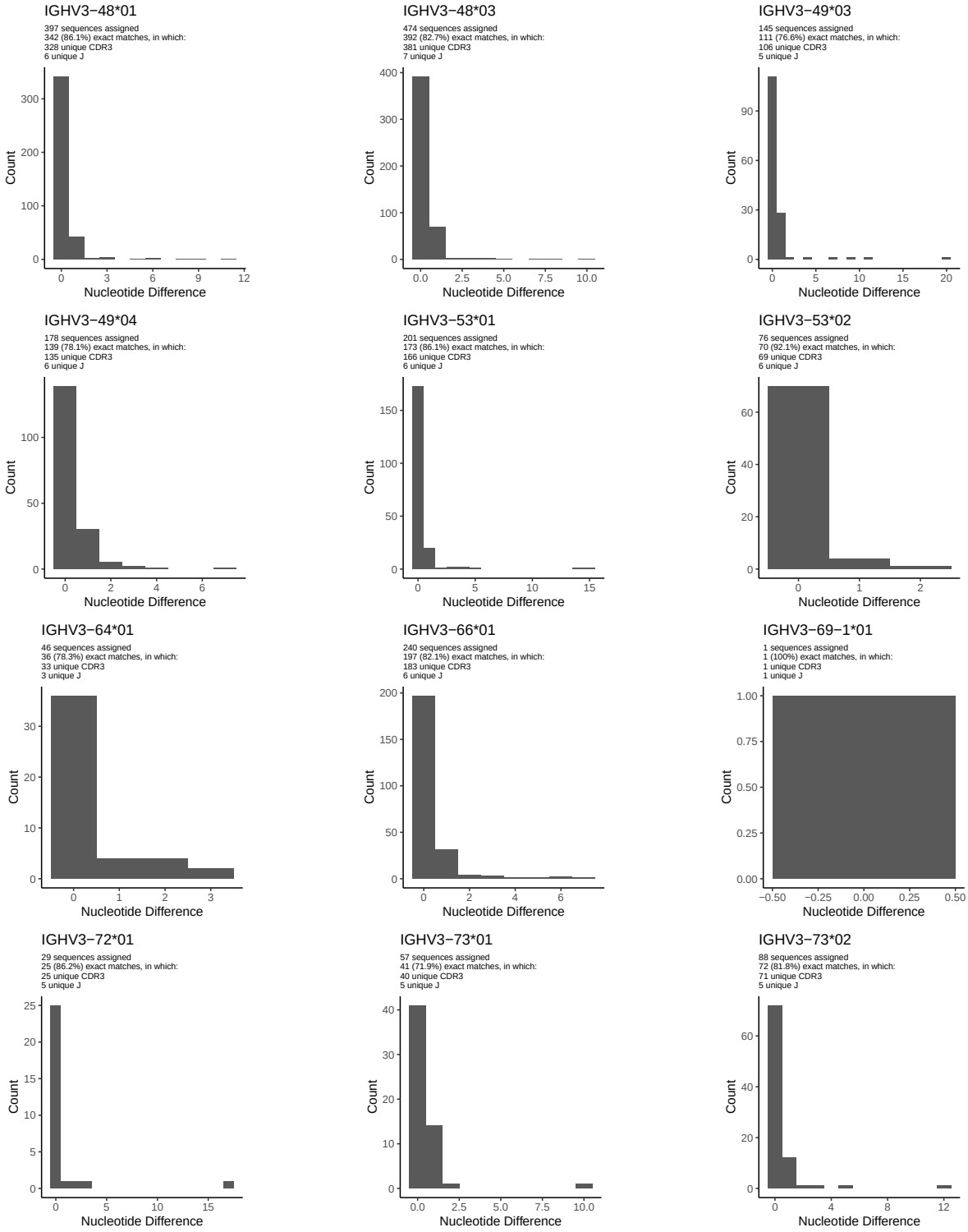

IGHV3−30*18
400 sequences assigned
333 (83.2%) exact matches, in which:
326 unique CDR3
6 unique J
Count
Nucleotide Difference

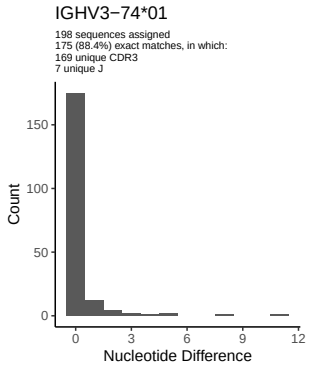

IGHV3−33*01
517 sequences assigned
428 (82.8%) exact matches, in which:
402 unique CDR3
7 unique J
Count
Nucleotide Difference

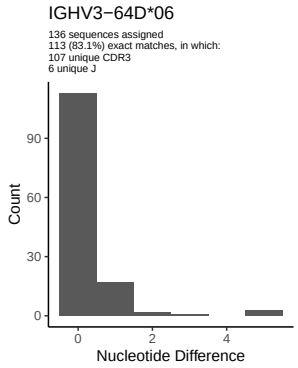

IGHV3−33*08
436 sequences assigned
347 (79.6%) exact matches, in which:
322 unique CDR3
7 unique J
Count
Nucleotide Difference

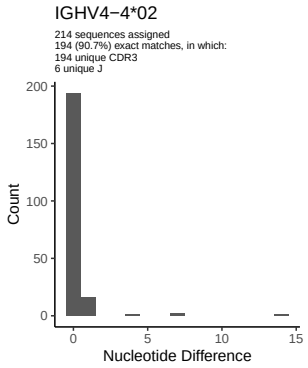

IGHV3−35*01
1 sequences assigned
1 (100%) exact matches, in which:
1 unique CDR3
1 unique J
Count
Nucleotide Difference

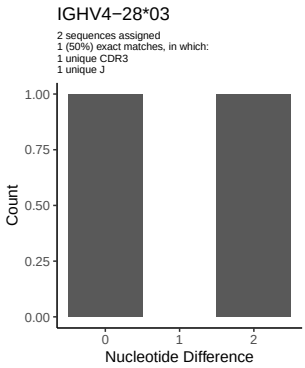

IGHV3−43*01
107 sequences assigned
94 (87.9%) exact matches, in which:
89 unique CDR3
7 unique J
Count
Nucleotide Difference

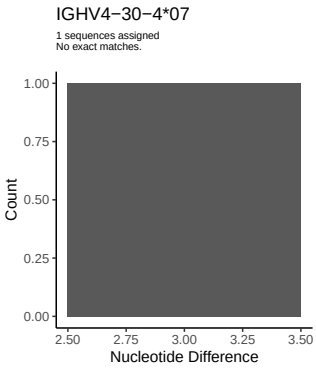

IGHV3−48*01
397 sequences assigned
342 (86.1%) exact matches, in which:
328 unique CDR3
6 unique J
Count
Nucleotide Difference
IGHV3−48*03
474 sequences assigned
392 (82.7%) exact matches, in which:
381 unique CDR3
7 unique J
Count
Nucleotide Difference
IGHV3−49*03
145 sequences assigned
111 (76.6%) exact matches, in which:
106 unique CDR3
5 unique J
Count
Nucleotide Difference
IGHV3−49*04
178 sequences assigned
139 (78.1%) exact matches, in which:
135 unique CDR3
6 unique J
Count
Nucleotide Difference
IGHV3−53*01
201 sequences assigned
173 (86.1%) exact matches, in which:
166 unique CDR3
6 unique J
Count
Nucleotide Difference
IGHV3−53*02
76 sequences assigned
70 (92.1%) exact matches, in which:
69 unique CDR3
6 unique J
Count
Nucleotide Difference
IGHV3−64*01
46 sequences assigned
36 (78.3%) exact matches, in which:
33 unique CDR3
3 unique J
Count
Nucleotide Difference
IGHV3−66*01
240 sequences assigned
197 (82.1%) exact matches, in which:
183 unique CDR3
6 unique J
Count
Nucleotide Difference
IGHV3−69−1*01
1 sequences assigned
1 (100%) exact matches, in which:
1 unique CDR3
1 unique J
Count
Nucleotide Difference
IGHV3−72*01
29 sequences assigned
25 (86.2%) exact matches, in which:
25 unique CDR3
5 unique J
Count
Nucleotide Difference
IGHV3−73*01
57 sequences assigned
41 (71.9%) exact matches, in which:
40 unique CDR3
5 unique J
Count
Nucleotide Difference
IGHV3−73*02
88 sequences assigned
72 (81.8%) exact matches, in which:
71 unique CDR3
5 unique J
Count
Nucleotide Difference

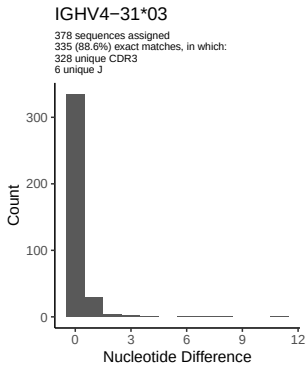

IGHV3−74*01
198 sequences assigned
175 (88.4%) exact matches, in which:
169 unique CDR3
7 unique J
Count
Nucleotide Difference

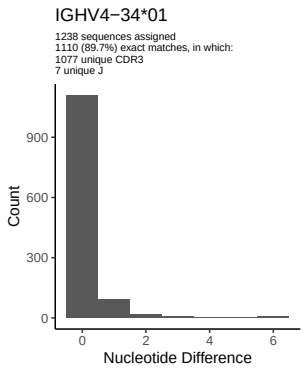

IGHV3−64D*06
136 sequences assigned
113 (83.1%) exact matches, in which:
107 unique CDR3
6 unique J
Count
Nucleotide Difference

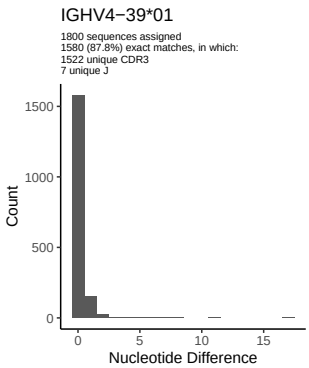

IGHV4−4*02
214 sequences assigned
194 (90.7%) exact matches, in which:
194 unique CDR3
6 unique J
Count
Nucleotide Difference

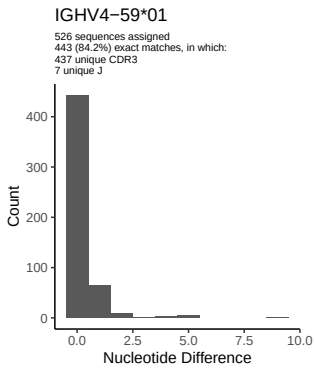

IGHV4−28*03
2 sequences assigned
1 (50%) exact matches, in which:
1 unique CDR3
1 unique J
Count
Nucleotide Difference

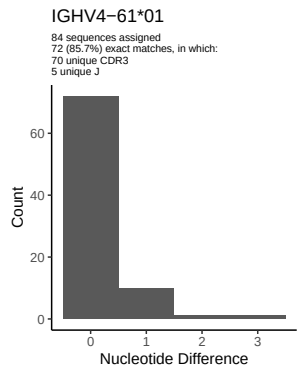

IGHV4−30−4*07
1 sequences assigned
No exact matches.
Count
Nucleotide Difference

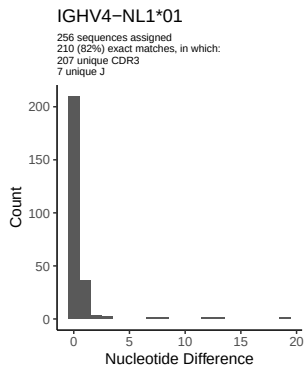

IGHV4−31*03
378 sequences assigned
335 (88.6%) exact matches, in which:
328 unique CDR3
6 unique J
Count
Nucleotide Difference

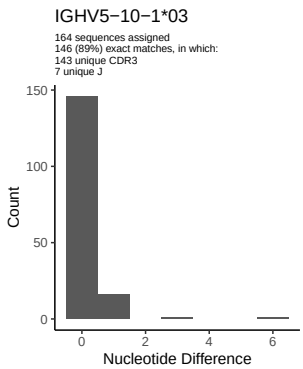

IGHV4−34*01
1238 sequences assigned
1110 (89.7%) exact matches, in which:
1077 unique CDR3
7 unique J
Count
Nucleotide Difference

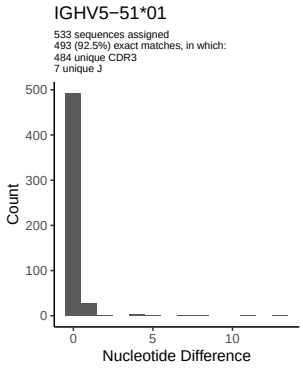

IGHV4−39*01
1800 sequences assigned
1580 (87.8%) exact matches, in which:
1522 unique CDR3
7 unique J
Count
Nucleotide Difference

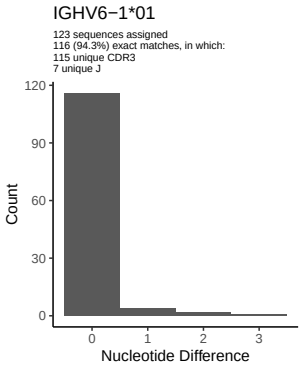

IGHV4−59*01
526 sequences assigned
443 (84.2%) exact matches, in which:
437 unique CDR3
7 unique J
Count
Nucleotide Difference

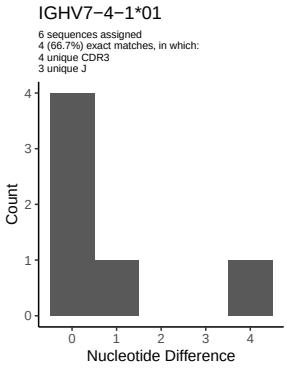

IGHV4−61*01
84 sequences assigned
72 (85.7%) exact matches, in which:
70 unique CDR3
5 unique J
Count
Nucleotide Difference

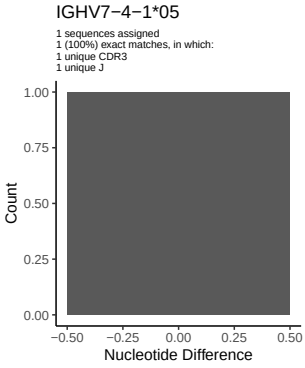

IGHV4−NL1*01
256 sequences assigned
210 (82%) exact matches, in which:
207 unique CDR3
7 unique J
Count
Nucleotide Difference


IGHV5−10−1*03
164 sequences assigned
146 (89%) exact matches, in which:
143 unique CDR3
7 unique J
Count
Nucleotide Difference

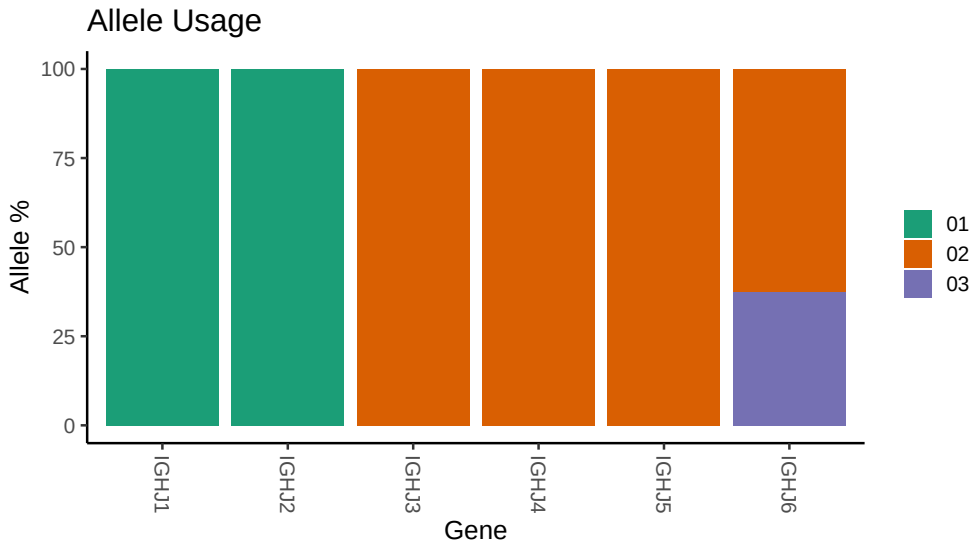

IGHV5−51*01
533 sequences assigned
493 (92.5%) exact matches, in which:
484 unique CDR3
7 unique J
Count
Nucleotide Difference


IGHV6−1*01
123 sequences assigned
116 (94.3%) exact matches, in which:
115 unique CDR3
7 unique J
Count
Nucleotide Difference

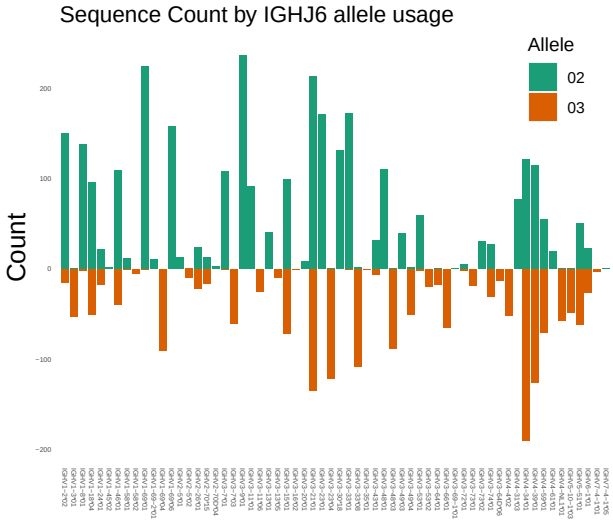

IGHV7−4−1*01
6 sequences assigned
4 (66.7%) exact matches, in which:
4 unique CDR3
3 unique J
Count
Nucleotide Difference


IGHV7−4−1*05
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/S43/S43/46/46/59/a254839dab9273024fc6b17e46e3e9/46_Fi
##
## Germline reference file: /misc/work/jenkins/PRJEB26509/S43/S43/46/46/ab/ef89e5b3151bd161a2a2072c2bc4
##
## Novel allele file:
##
## Species: Homosapiens
##
## Chain: IGHV
##
## Segment: V
##
## Warning   no inferred sequences found.
```