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**

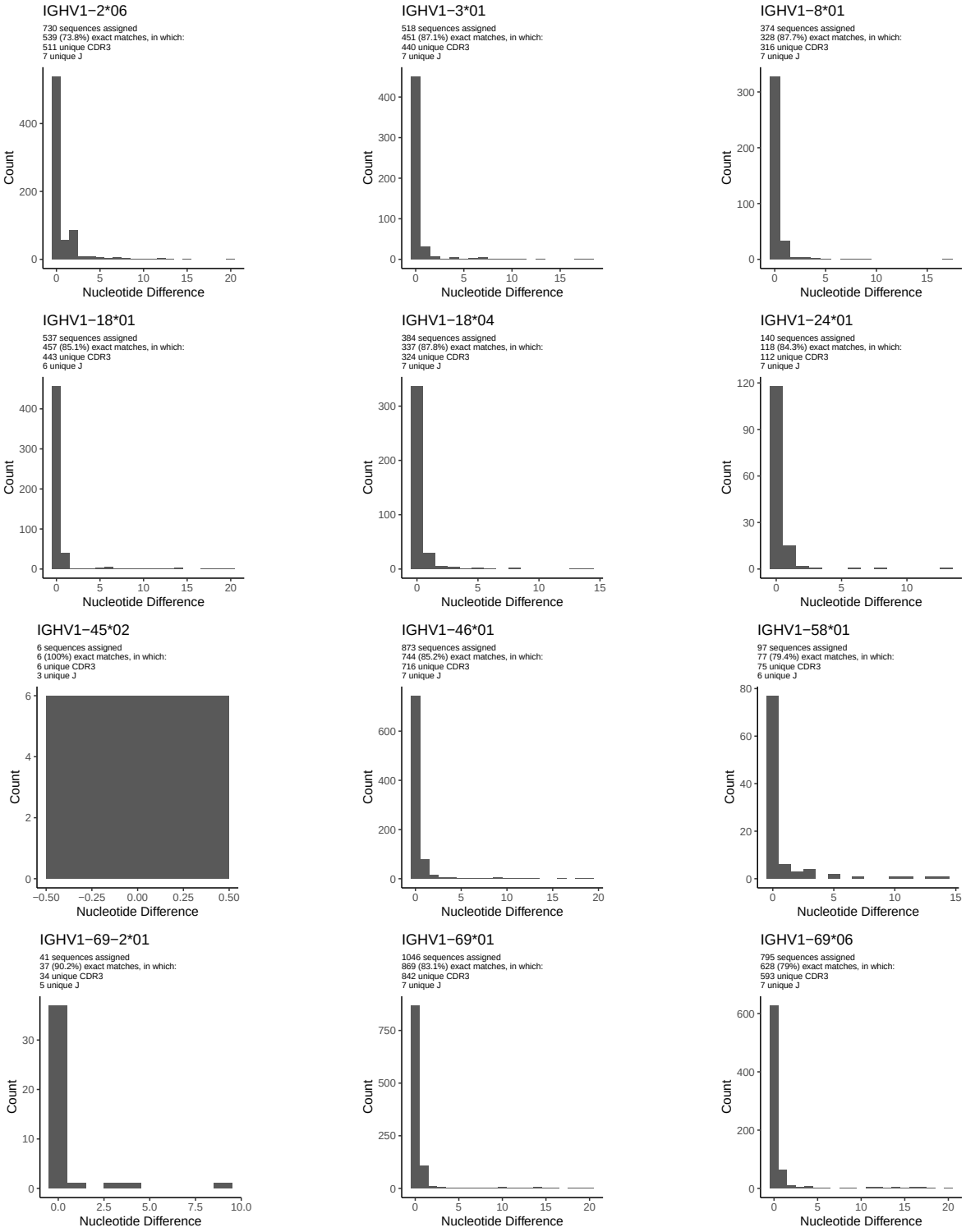
4 Haplotype plots **9**

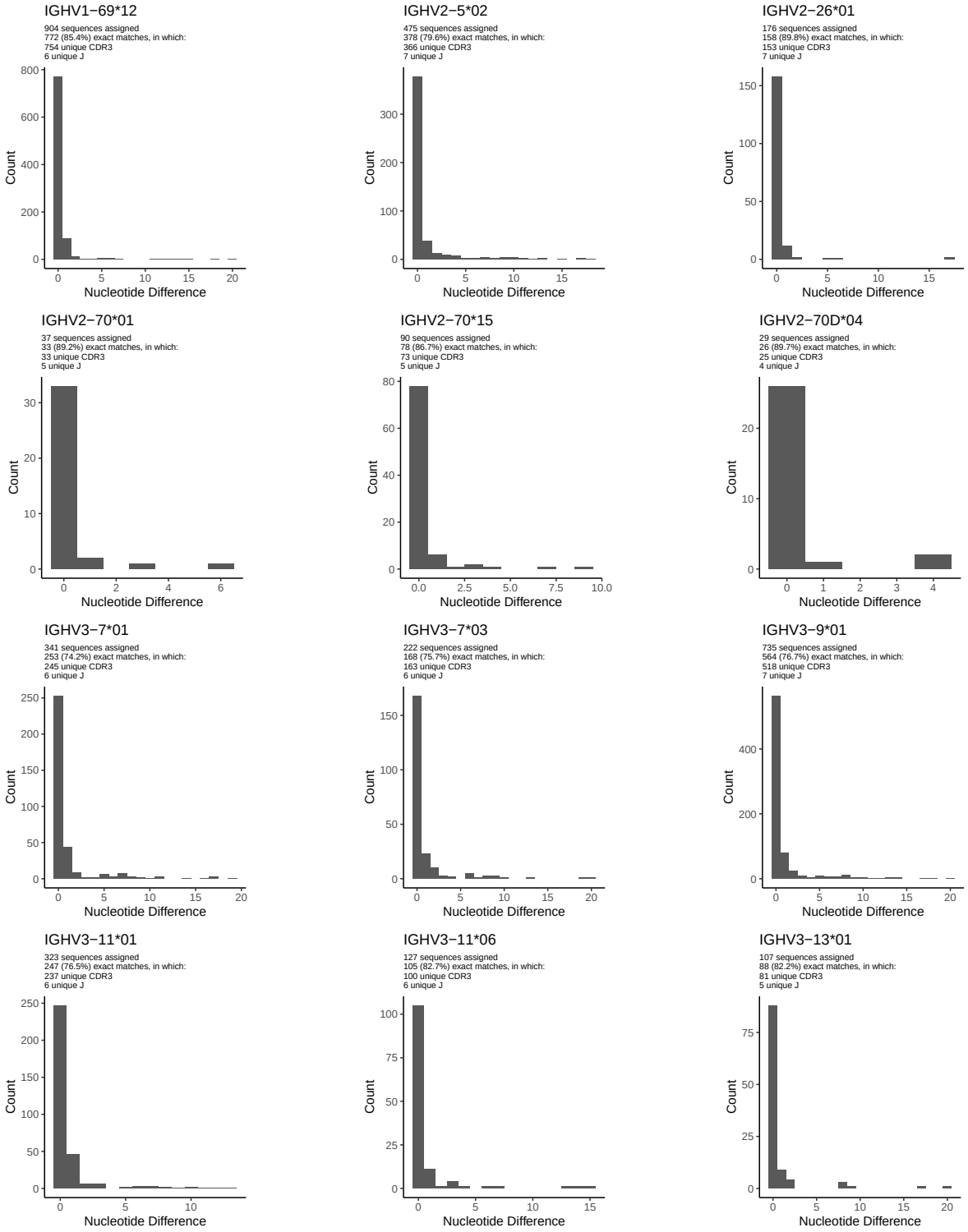
5 Configuration settings **10**

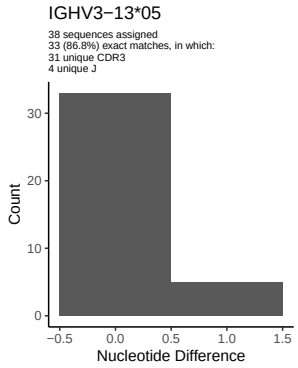
1 Novel sequence analysis

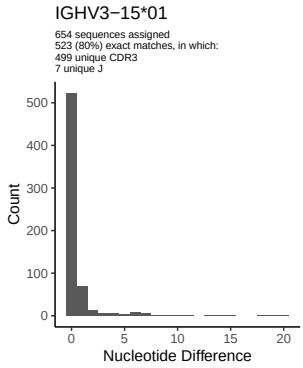
1.1 CDR3 length distribution, in assignments to novel alleles

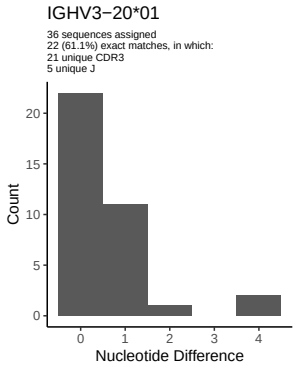
2 Variation from germline, in assignments to each allele

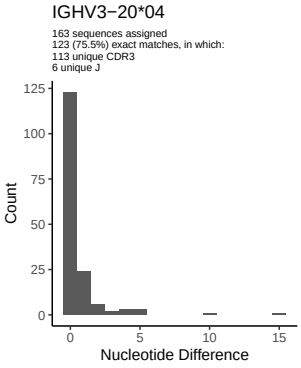


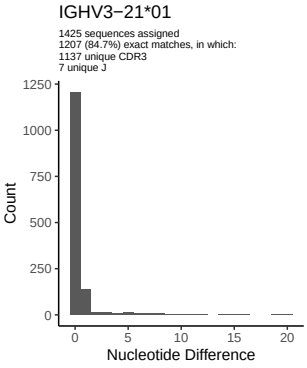

IGHV1−69*12
904 sequences assigned
772 (85.4%) exact matches, in which:
754 unique CDR3
6 unique J
IGHV2−5*02
475 sequences assigned
378 (79.6%) exact matches, in which:
366 unique CDR3
7 unique J
IGHV2−26*01
176 sequences assigned
158 (89.8%) exact matches, in which:
153 unique CDR3
7 unique J
IGHV2−70*01
37 sequences assigned
33 (89.2%) exact matches, in which:
33 unique CDR3
5 unique J
IGHV2−70*15
90 sequences assigned
78 (86.7%) exact matches, in which:
73 unique CDR3
5 unique J
IGHV2−70D*04
29 sequences assigned
26 (89.7%) exact matches, in which:
25 unique CDR3
4 unique J
IGHV3−7*01
341 sequences assigned
253 (74.2%) exact matches, in which:
245 unique CDR3
6 unique J
IGHV3−7*03
222 sequences assigned
168 (75.7%) exact matches, in which:
163 unique CDR3
6 unique J
IGHV3−9*01
735 sequences assigned
564 (76.7%) exact matches, in which:
518 unique CDR3
7 unique J
IGHV3−11*01
323 sequences assigned
247 (76.5%) exact matches, in which:
237 unique CDR3
6 unique J
IGHV3−11*06
127 sequences assigned
105 (82.7%) exact matches, in which:
100 unique CDR3
6 unique J
IGHV3−13*01
107 sequences assigned
88 (82.2%) exact matches, in which:
81 unique CDR3
5 unique J
Count
Nucleotide Difference

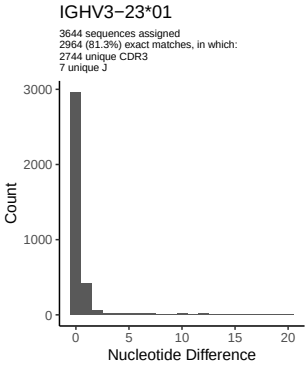

IGHV3−13*05
38 sequences assigned
33 (86.8%) exact matches, in which:
31 unique CDR3
4 unique J
Count
Nucleotide Difference

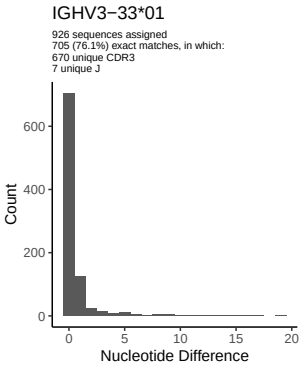

IGHV3−15*01
654 sequences assigned
523 (80%) exact matches, in which:
499 unique CDR3
7 unique J
Count
Nucleotide Difference

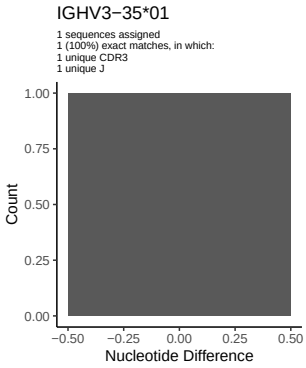

IGHV3−20*01
36 sequences assigned
22 (61.1%) exact matches, in which:
21 unique CDR3
5 unique J
Count
Nucleotide Difference

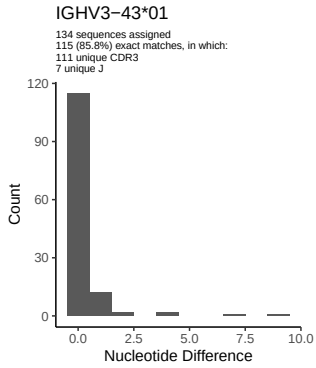

IGHV3−20*04
163 sequences assigned
123 (75.5%) exact matches, in which:
113 unique CDR3
6 unique J
Count
Nucleotide Difference

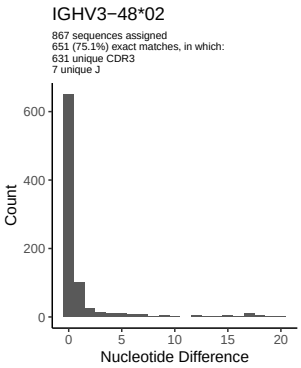

IGHV3−21*01
1425 sequences assigned
1207 (84.7%) exact matches, in which:
1137 unique CDR3
7 unique J
Count
Nucleotide Difference

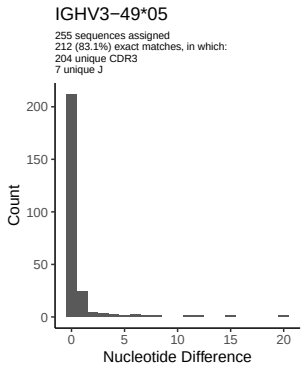

IGHV3−23*01
3644 sequences assigned
2964 (81.3%) exact matches, in which:
2744 unique CDR3
7 unique J
Count
Nucleotide Difference

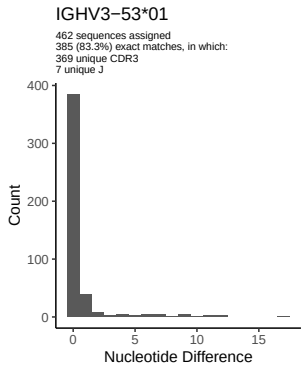

IGHV3−33*01
926 sequences assigned
705 (76.1%) exact matches, in which:
670 unique CDR3
7 unique J
Count
Nucleotide Difference

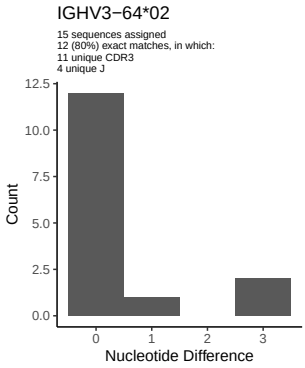

IGHV3−35*01
1 sequences assigned
1 (100%) exact matches, in which:
1 unique CDR3
1 unique J
Count
Nucleotide Difference

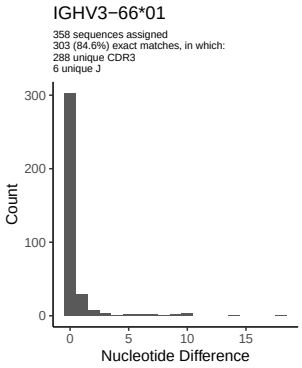

IGHV3−43*01
134 sequences assigned
115 (85.8%) exact matches, in which:
111 unique CDR3
7 unique J
Count
Nucleotide Difference

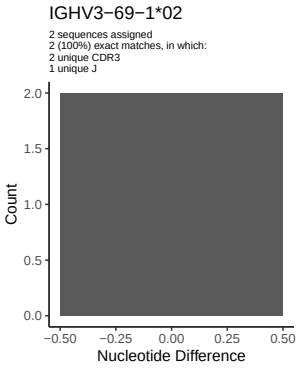

IGHV3−48*02
867 sequences assigned
651 (75.1%) exact matches, in which:
631 unique CDR3
7 unique J
Count
Nucleotide Difference

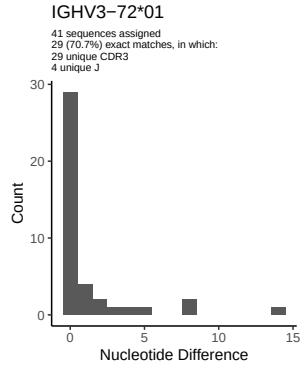

IGHV3−49*05
255 sequences assigned
212 (83.1%) exact matches, in which:
204 unique CDR3
7 unique J
Count
Nucleotide Difference

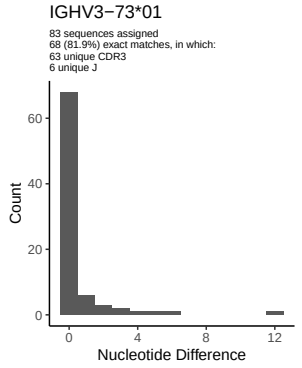

IGHV3−53*01
462 sequences assigned
385 (83.3%) exact matches, in which:
369 unique CDR3
7 unique J
Count
Nucleotide Difference

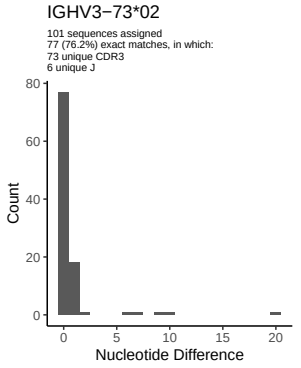

IGHV3−64*02
15 sequences assigned
12 (80%) exact matches, in which:
11 unique CDR3
4 unique J
Count
Nucleotide Difference

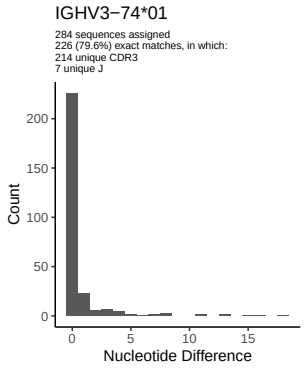

IGHV3−66*01
358 sequences assigned
303 (84.6%) exact matches, in which:
288 unique CDR3
6 unique J
Count
Nucleotide Difference

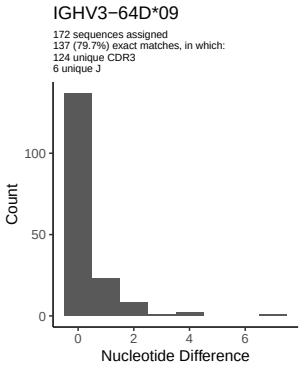

IGHV3−69−1*02
2 sequences assigned
2 (100%) exact matches, in which:
2 unique CDR3
1 unique J
Count
Nucleotide Difference

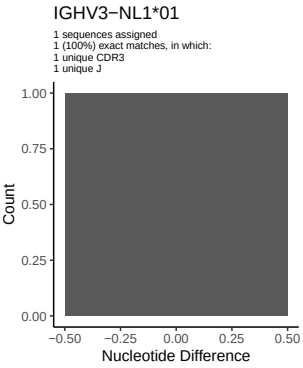

IGHV3−72*01
41 sequences assigned
29 (70.7%) exact matches, in which:
29 unique CDR3
4 unique J
Count
Nucleotide Difference

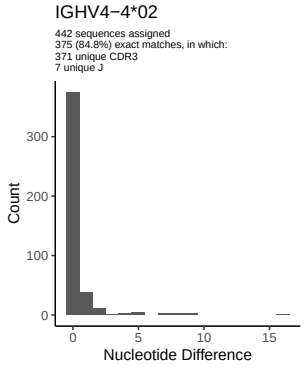

IGHV3−73*01
83 sequences assigned
68 (81.9%) exact matches, in which:
63 unique CDR3
6 unique J
Count
Nucleotide Difference

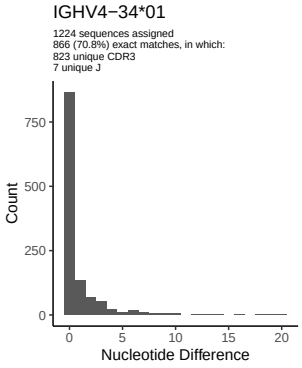

IGHV3−73*02
101 sequences assigned
77 (76.2%) exact matches, in which:
73 unique CDR3
6 unique J
Count
Nucleotide Difference

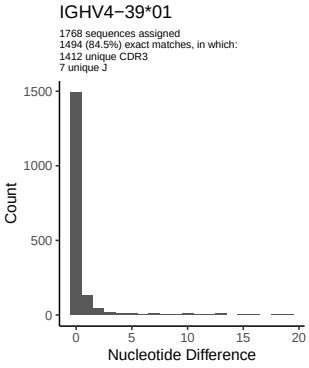

IGHV3−74*01
284 sequences assigned
226 (79.6%) exact matches, in which:
214 unique CDR3
7 unique J
Count
Nucleotide Difference

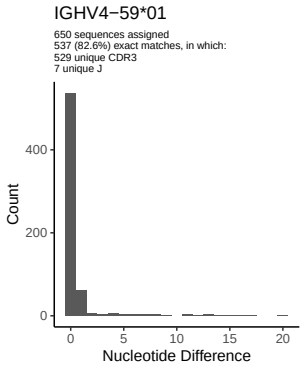

IGHV3−64D*09
172 sequences assigned
137 (79.7%) exact matches, in which:
124 unique CDR3
6 unique J
Count
Nucleotide Difference

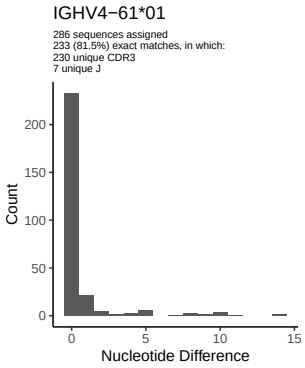

IGHV3−NL1*01
1 sequences assigned
1 (100%) exact matches, in which:
1 unique CDR3
1 unique J
Count
Nucleotide Difference

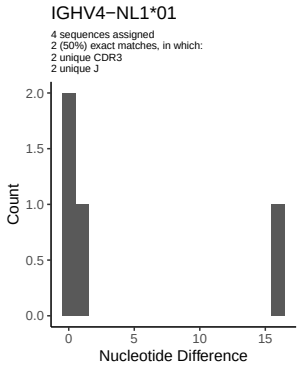

IGHV4−4*02
442 sequences assigned
375 (84.8%) exact matches, in which:
371 unique CDR3
7 unique J
Count
Nucleotide Difference

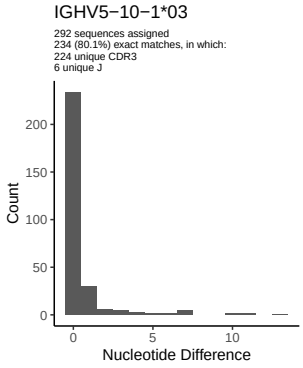

IGHV4−34*01
1224 sequences assigned
866 (70.8%) exact matches, in which:
823 unique CDR3
7 unique J
Count
Nucleotide Difference

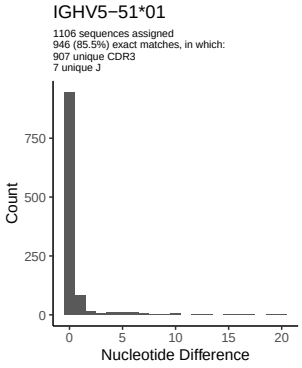

IGHV4−39*01
1768 sequences assigned
1494 (84.5%) exact matches, in which:
1412 unique CDR3
7 unique J
Count
Nucleotide Difference

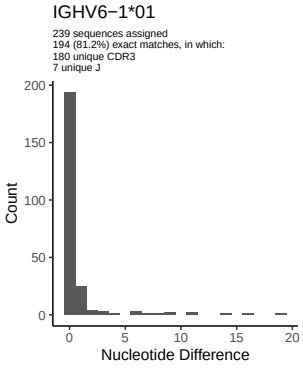

IGHV4−59*01
650 sequences assigned
537 (82.6%) exact matches, in which:
529 unique CDR3
7 unique J
Count
Nucleotide Difference

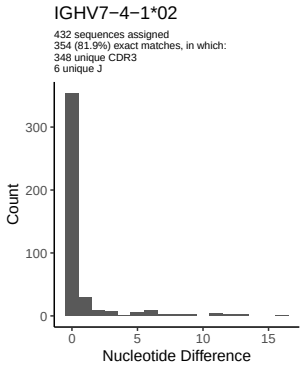

IGHV4−61*01
286 sequences assigned
233 (81.5%) exact matches, in which:
230 unique CDR3
7 unique J
Count
Nucleotide Difference


IGHV4−NL1*01
4 sequences assigned
2 (50%) exact matches, in which:
2 unique CDR3
2 unique J
Count
Nucleotide Difference

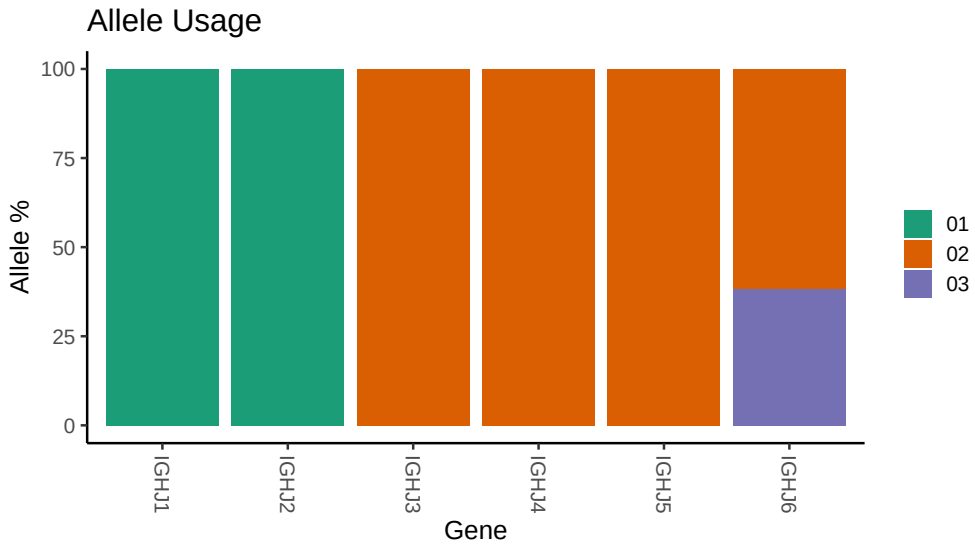

IGHV5−10−1*03
292 sequences assigned
234 (80.1%) exact matches, in which:
224 unique CDR3
6 unique J
Count
Nucleotide Difference


IGHV5−51*01
1106 sequences assigned
946 (85.5%) exact matches, in which:
907 unique CDR3
7 unique J
Count
Nucleotide Difference

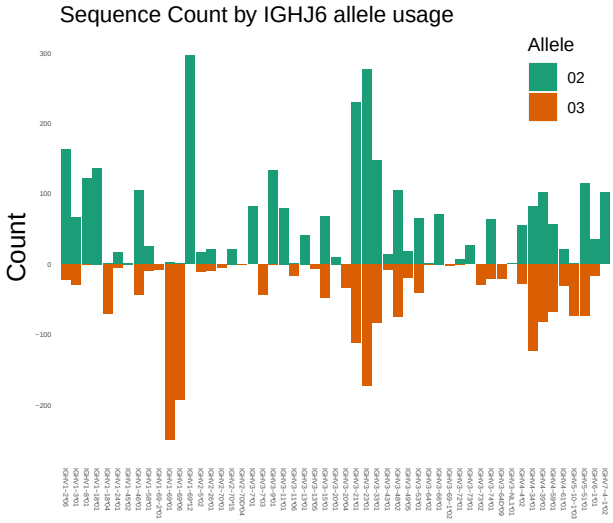

IGHV6−1*01
239 sequences assigned
194 (81.2%) exact matches, in which:
180 unique CDR3
7 unique J
Count
Nucleotide Difference


IGHV7−4−1*02
432 sequences assigned
354 (81.9%) exact matches, in which:
348 unique CDR3
6 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/S94/S94/98/98/db/9f51804af5cd3e7241587654384610/98_Fi
##
## Germline reference file: /misc/work/jenkins/PRJEB26509/S94/S94/98/98/ad/fc6e90d272d5985efc5d9448f7a6
##
## Novel allele file:
##
## Species: Homosapiens
##
## Chain: IGHV
##
## Segment: V
##
## Warning   no inferred sequences found.
```