OGRDBstats Report

Contents

1 Novel sequence analysis **2**
- 1.1 End-nucleotide composition . . . 2
- 1.2 Per-nucleotide consensus where previous nucleotides match the consensus . . . 2
- 1.3 Whole-sequence composition of each assigned read . . . 3
- 1.4 Final three nucleotides: frequency of each observed triplet . . . 3
- 1.5 CDR3 length distribution, in assignments to novel alleles . . . 4

2 Variation from germline, in assignments to each allele **5**

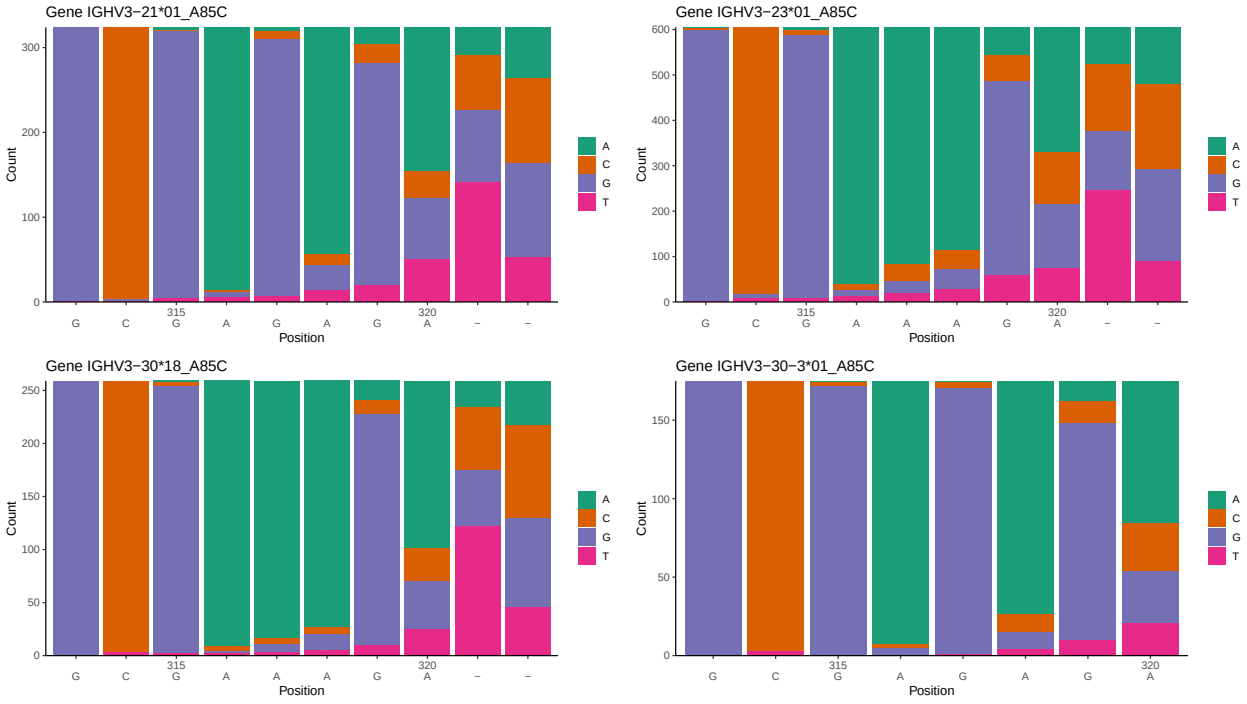
3 Allele usage in potential haplotype anchor genes **11**

4 Haplotype plots **12**

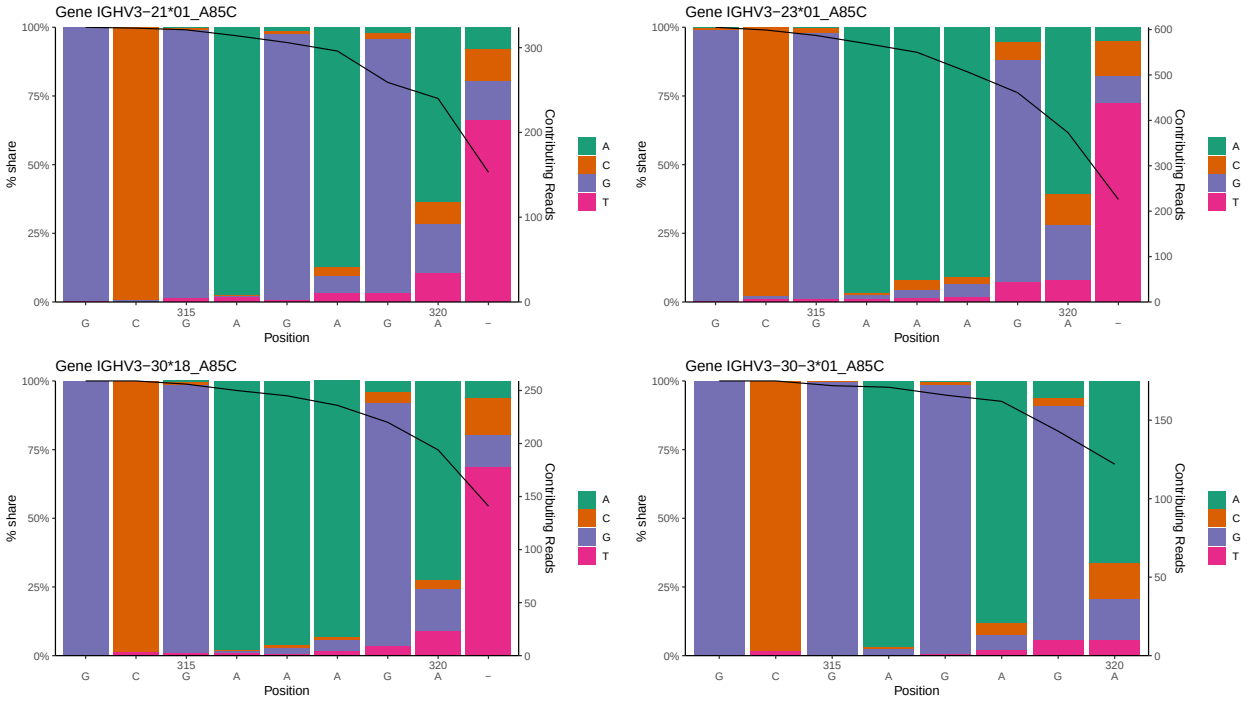
5 Configuration settings **13**

1 Novel sequence analysis

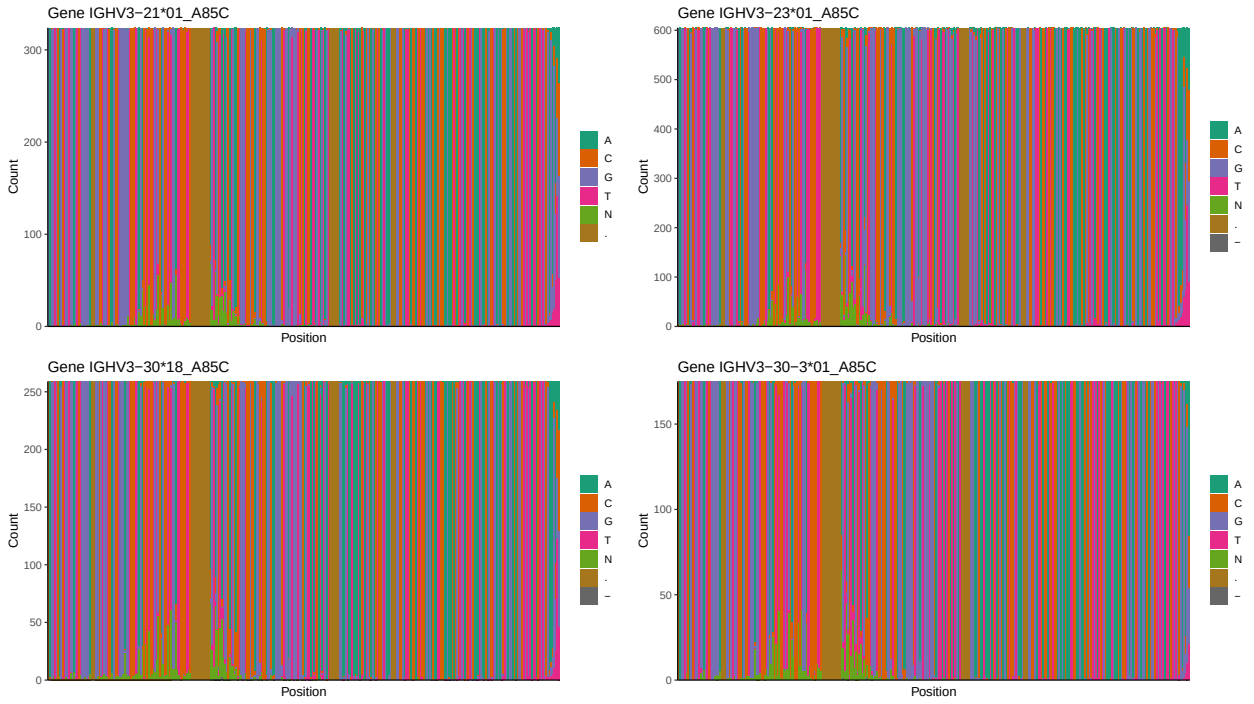
1.1 End-nucleotide composition



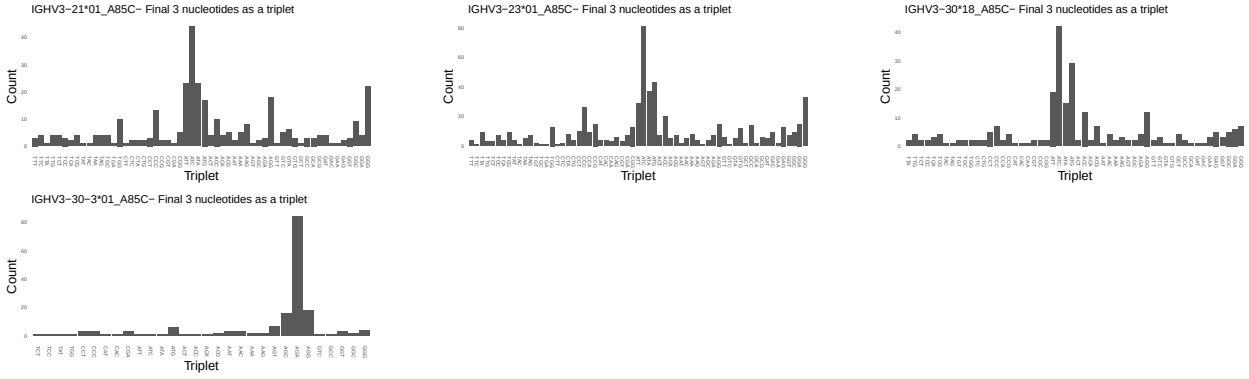
1.2 Per-nucleotide consensus where previous nucleotides match the consensus



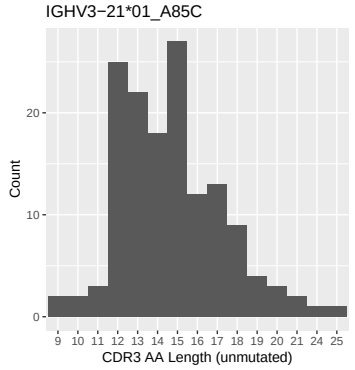
1.3 Whole-sequence composition of each assigned read

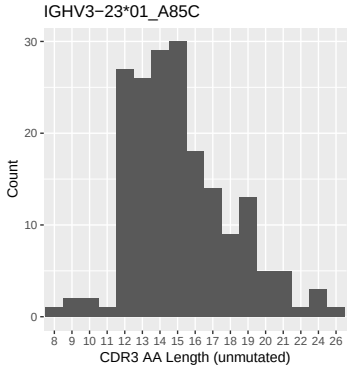


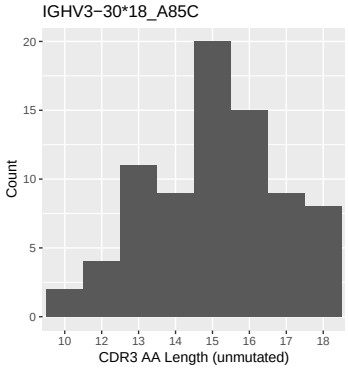
1.4 Final three nucleotides: frequency of each observed triplet

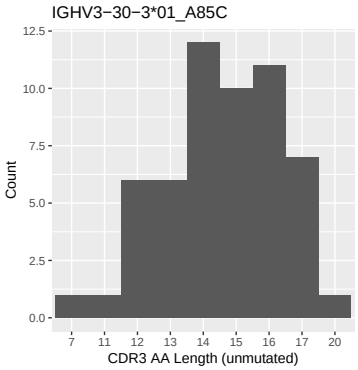


1.5 CDR3 length distribution, in assignments to novel alleles

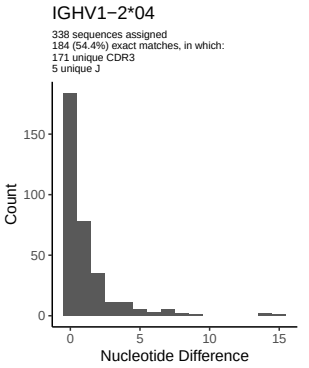


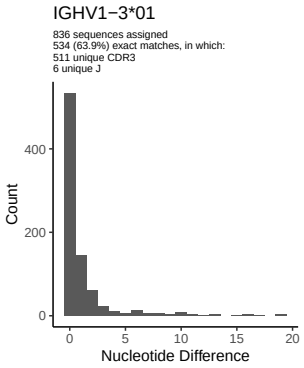


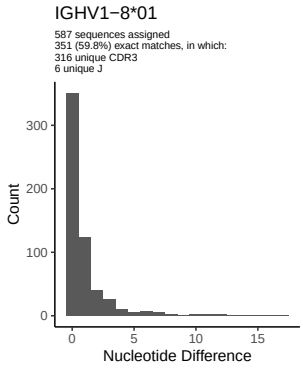


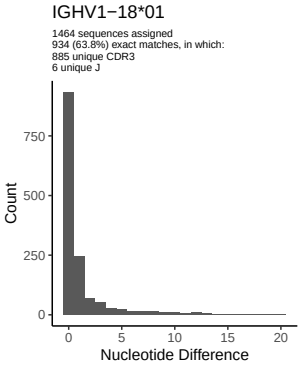


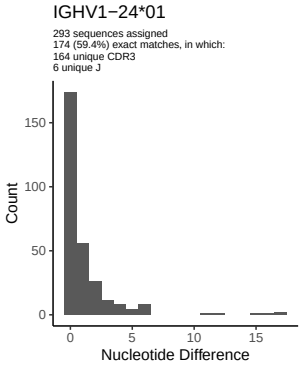
2 Variation from germline, in assignments to each allele

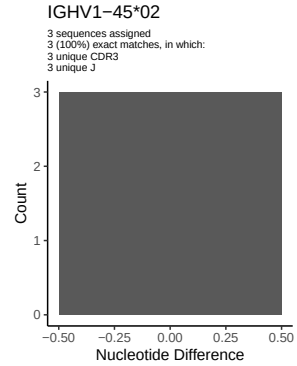


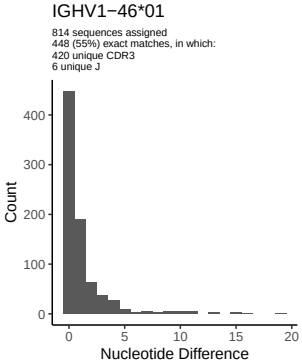


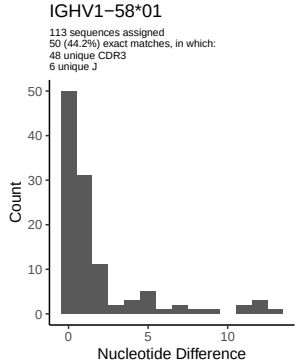


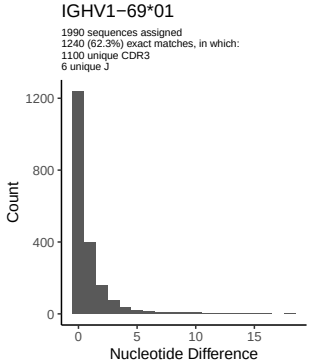


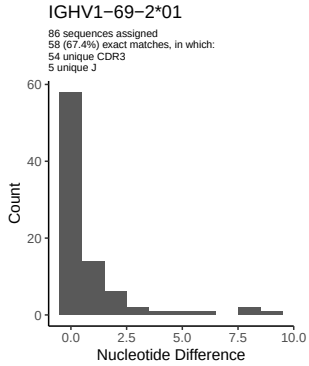


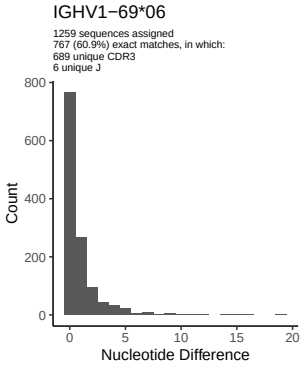


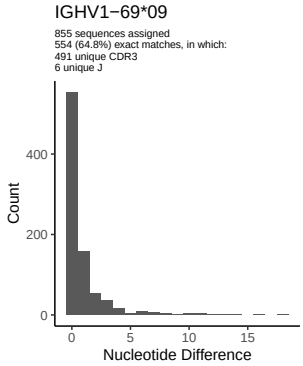


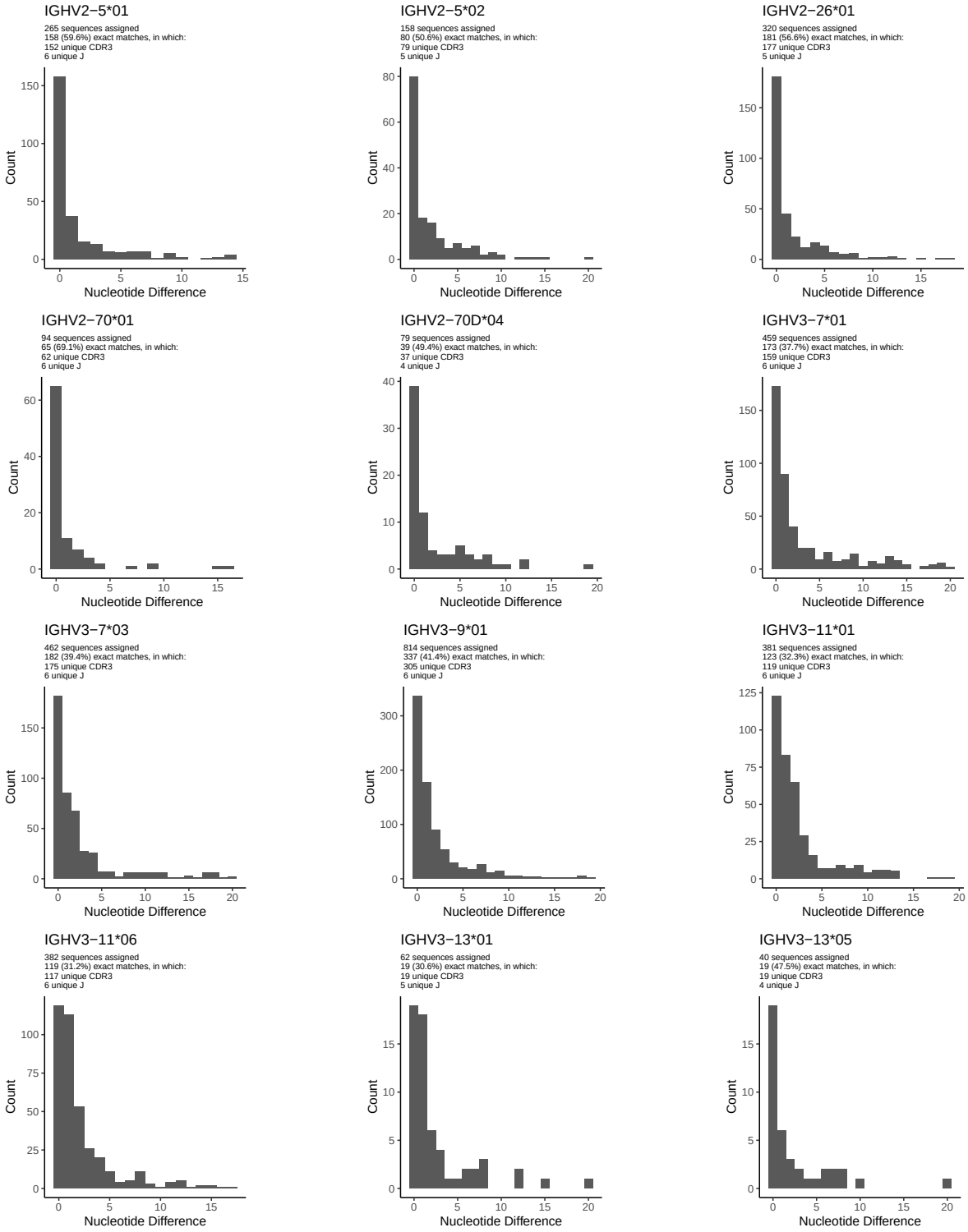


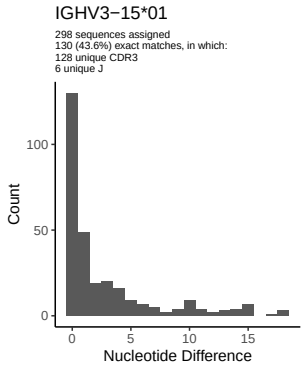


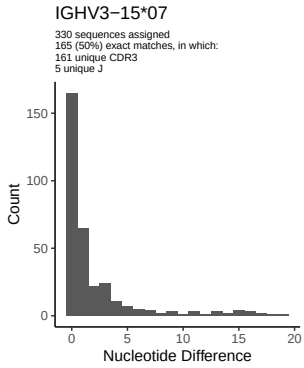


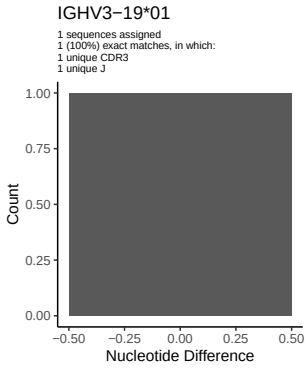


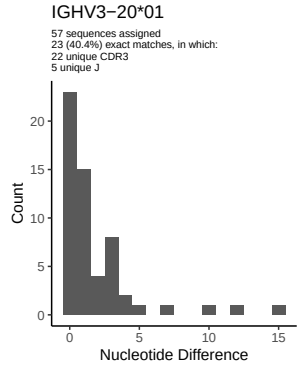


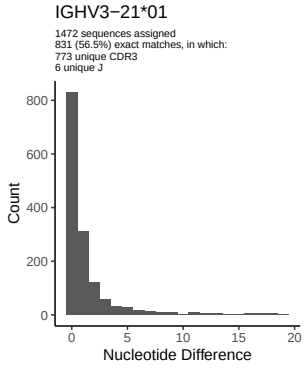

IGHV2−5*01
265 sequences assigned
158 (59.6%) exact matches, in which:
152 unique CDR3
6 unique J
IGHV2−5*02
158 sequences assigned
80 (50.6%) exact matches, in which:
79 unique CDR3
5 unique J
IGHV2−26*01
320 sequences assigned
181 (56.6%) exact matches, in which:
177 unique CDR3
5 unique J
IGHV2−70*01
94 sequences assigned
65 (69.1%) exact matches, in which:
62 unique CDR3
6 unique J
IGHV2−70D*04
79 sequences assigned
39 (49.4%) exact matches, in which:
37 unique CDR3
4 unique J
IGHV3−7*01
459 sequences assigned
173 (37.7%) exact matches, in which:
159 unique CDR3
6 unique J
IGHV3−7*03
462 sequences assigned
182 (39.4%) exact matches, in which:
175 unique CDR3
6 unique J
IGHV3−9*01
814 sequences assigned
337 (41.4%) exact matches, in which:
305 unique CDR3
6 unique J
IGHV3−11*01
381 sequences assigned
123 (32.3%) exact matches, in which:
119 unique CDR3
6 unique J
IGHV3−11*06
382 sequences assigned
119 (31.2%) exact matches, in which:
117 unique CDR3
6 unique J
IGHV3−13*01
62 sequences assigned
19 (30.6%) exact matches, in which:
19 unique CDR3
5 unique J
IGHV3−13*05
40 sequences assigned
19 (47.5%) exact matches, in which:
19 unique CDR3
4 unique J
Count
Nucleotide Difference

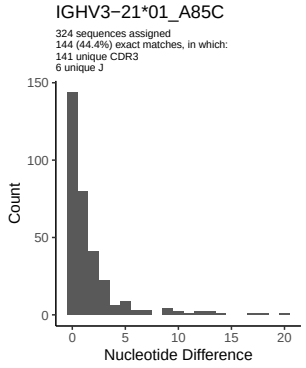

IGHV3−15*01
298 sequences assigned
130 (43.6%) exact matches, in which:
128 unique CDR3
6 unique J
Count
Nucleotide Difference

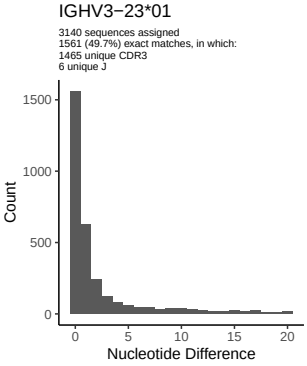

IGHV3−15*07
330 sequences assigned
165 (50%) exact matches, in which:
161 unique CDR3
5 unique J
Count
Nucleotide Difference

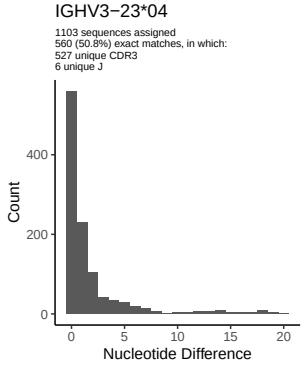

IGHV3−19*01
1 sequences assigned
1 (100%) exact matches, in which:
1 unique CDR3
1 unique J
Count
Nucleotide Difference

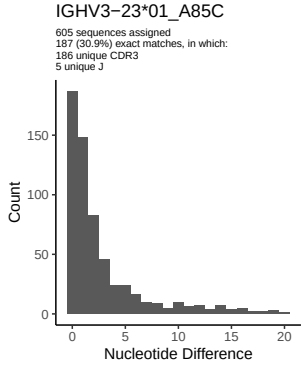

IGHV3−20*01
57 sequences assigned
23 (40.4%) exact matches, in which:
22 unique CDR3
5 unique J
Count
Nucleotide Difference

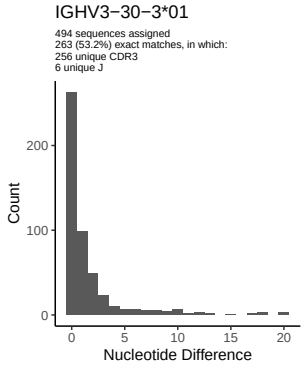

IGHV3−21*01
1472 sequences assigned
831 (56.5%) exact matches, in which:
773 unique CDR3
6 unique J
Count
Nucleotide Difference

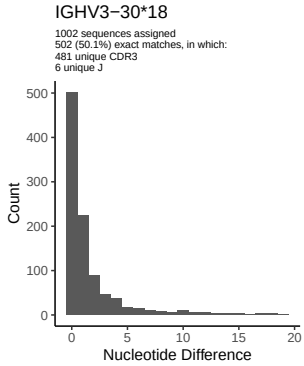

IGHV3−21*01_A85C
324 sequences assigned
144 (44.4%) exact matches, in which:
141 unique CDR3
6 unique J
Count
Nucleotide Difference

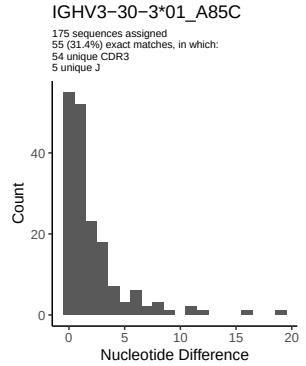

IGHV3−23*01
3140 sequences assigned
1561 (49.7%) exact matches, in which:
1465 unique CDR3
6 unique J
Count
Nucleotide Difference

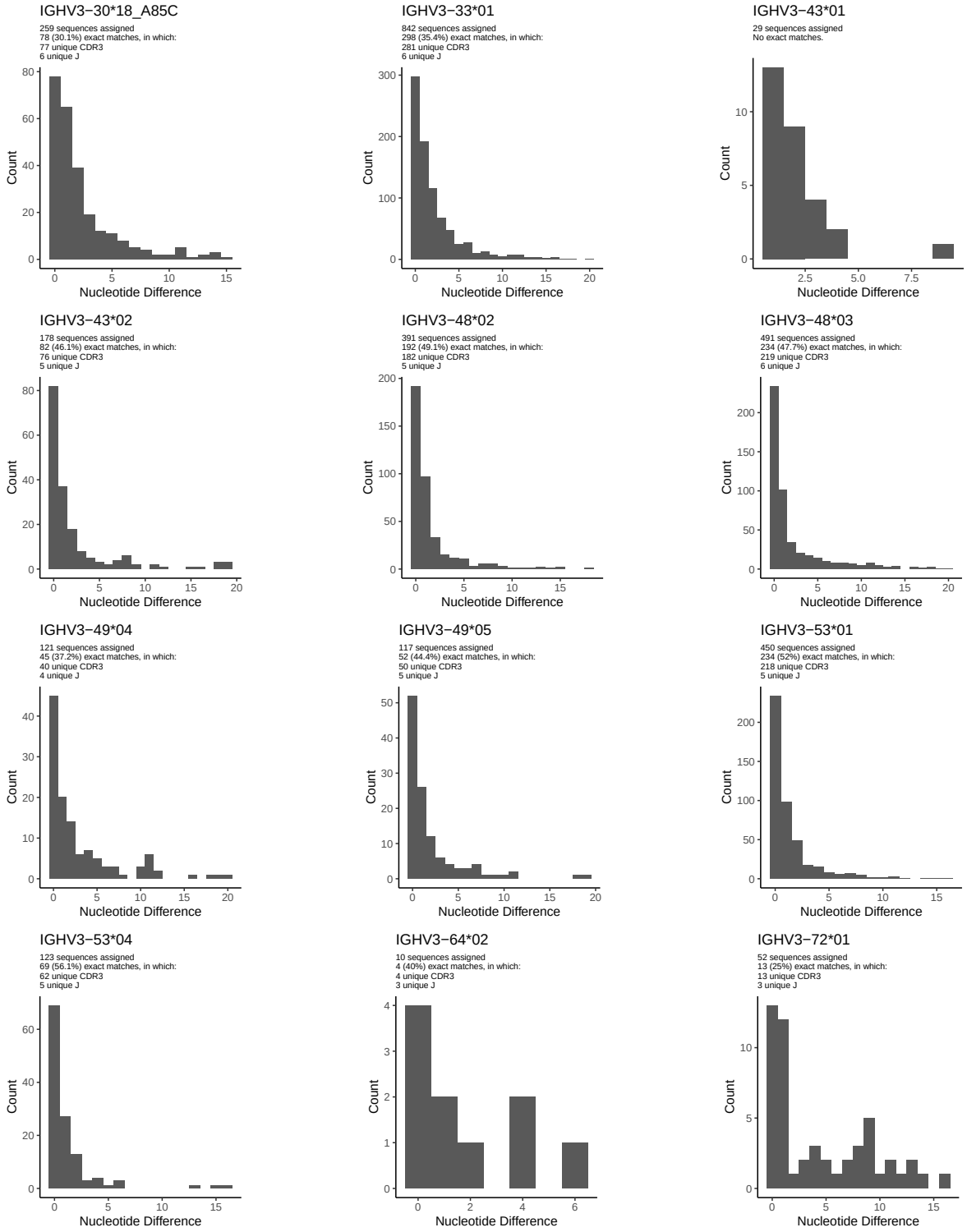

IGHV3−23*04
1103 sequences assigned
560 (50.8%) exact matches, in which:
527 unique CDR3
6 unique J
Count
Nucleotide Difference

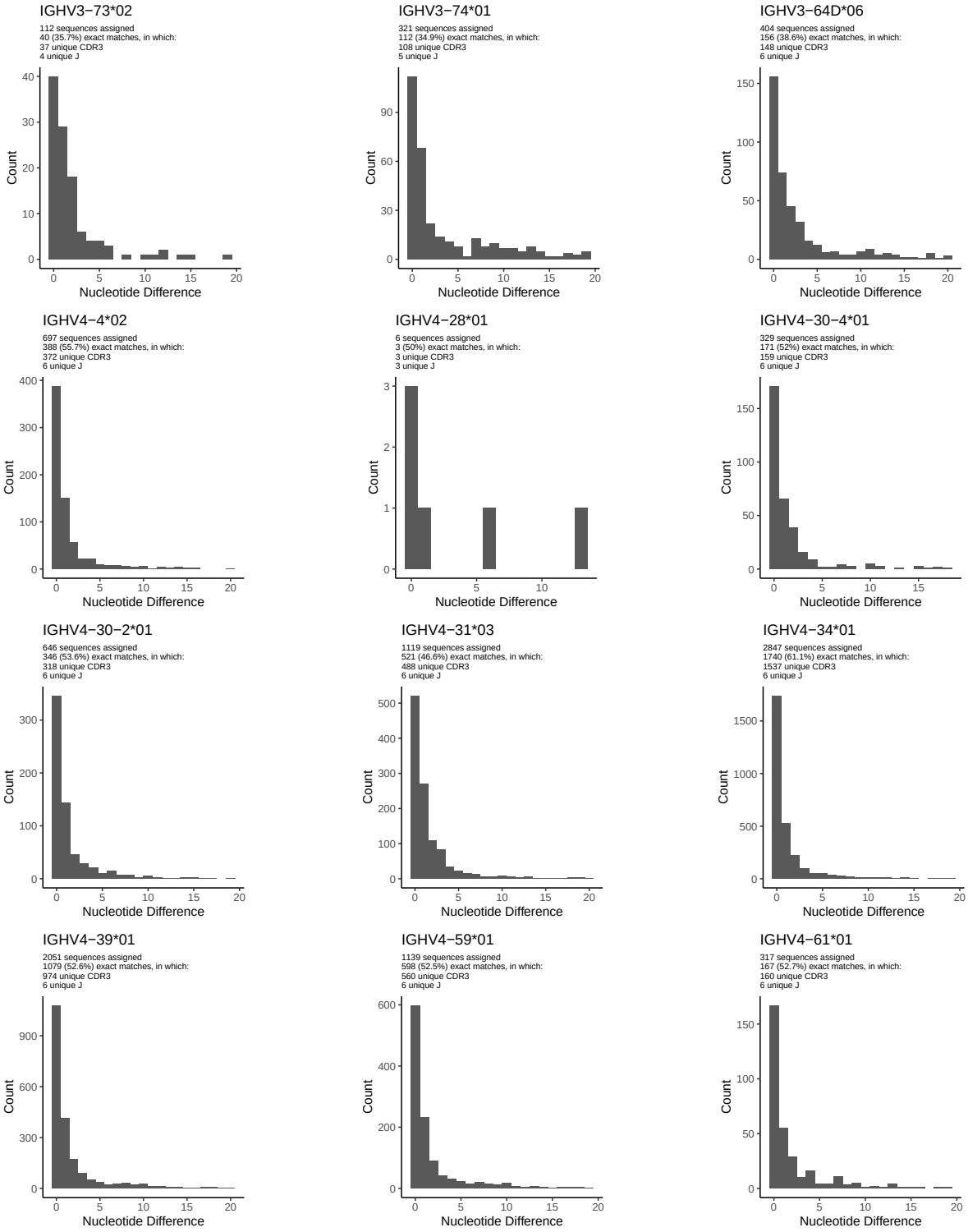

IGHV3−23*01_A85C
605 sequences assigned
187 (30.9%) exact matches, in which:
186 unique CDR3
5 unique J
Count
Nucleotide Difference

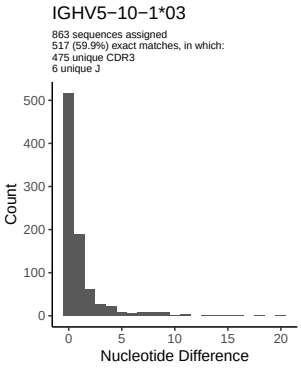

IGHV3−30−3*01
494 sequences assigned
263 (53.2%) exact matches, in which:
256 unique CDR3
6 unique J
Count
Nucleotide Difference

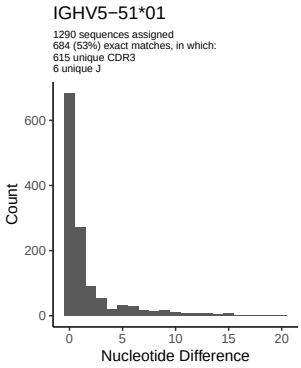

IGHV3−30*18
1002 sequences assigned
502 (50.1%) exact matches, in which:
481 unique CDR3
6 unique J
Count
Nucleotide Difference

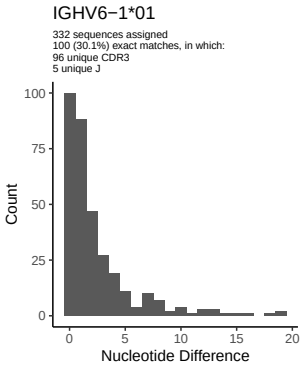

IGHV3−30−3*01_A85C
175 sequences assigned
55 (31.4%) exact matches, in which:
54 unique CDR3
5 unique J
Count
Nucleotide Difference

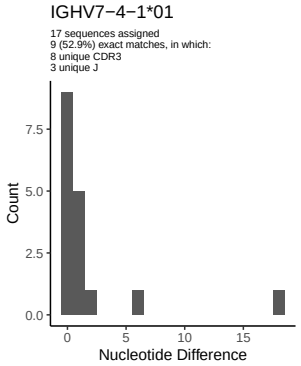

IGHV3−30*18_A85C
259 sequences assigned
78 (30.1%) exact matches, in which:
77 unique CDR3
6 unique J
IGHV3−33*01
842 sequences assigned
298 (35.4%) exact matches, in which:
281 unique CDR3
6 unique J
IGHV3−43*01
29 sequences assigned
No exact matches.
IGHV3−43*02
178 sequences assigned
82 (46.1%) exact matches, in which:
76 unique CDR3
5 unique J
IGHV3−48*02
391 sequences assigned
192 (49.1%) exact matches, in which:
182 unique CDR3
5 unique J
IGHV3−48*03
491 sequences assigned
234 (47.7%) exact matches, in which:
219 unique CDR3
6 unique J
IGHV3−49*04
121 sequences assigned
45 (37.2%) exact matches, in which:
40 unique CDR3
4 unique J
IGHV3−49*05
117 sequences assigned
52 (44.4%) exact matches, in which:
50 unique CDR3
5 unique J
IGHV3−53*01
450 sequences assigned
234 (52%) exact matches, in which:
218 unique CDR3
5 unique J
IGHV3−53*04
123 sequences assigned
69 (56.1%) exact matches, in which:
62 unique CDR3
5 unique J
IGHV3−64*02
10 sequences assigned
4 (40%) exact matches, in which:
4 unique CDR3
3 unique J
IGHV3−72*01
52 sequences assigned
13 (25%) exact matches, in which:
13 unique CDR3
3 unique J
Count
Nucleotide Difference


IGHV3−73*02
112 sequences assigned
40 (35.7%) exact matches, in which:
37 unique CDR3
4 unique J
IGHV3−74*01
321 sequences assigned
112 (34.9%) exact matches, in which:
108 unique CDR3
5 unique J
IGHV3−64D*06
404 sequences assigned
156 (38.6%) exact matches, in which:
148 unique CDR3
6 unique J
IGHV4−4*02
697 sequences assigned
388 (55.7%) exact matches, in which:
372 unique CDR3
6 unique J
IGHV4−28*01
6 sequences assigned
3 (50%) exact matches, in which:
3 unique CDR3
3 unique J
IGHV4−30−4*01
329 sequences assigned
171 (52%) exact matches, in which:
159 unique CDR3
6 unique J
IGHV4−30−2*01
646 sequences assigned
346 (53.6%) exact matches, in which:
318 unique CDR3
6 unique J
IGHV4−31*03
1119 sequences assigned
521 (46.6%) exact matches, in which:
488 unique CDR3
6 unique J
IGHV4−34*01
2847 sequences assigned
1740 (61.1%) exact matches, in which:
1537 unique CDR3
6 unique J
IGHV4−39*01
2051 sequences assigned
1079 (52.6%) exact matches, in which:
974 unique CDR3
6 unique J
IGHV4−59*01
1139 sequences assigned
598 (52.5%) exact matches, in which:
560 unique CDR3
6 unique J
IGHV4−61*01
317 sequences assigned
167 (52.7%) exact matches, in which:
160 unique CDR3
6 unique J
Count
Nucleotide Difference

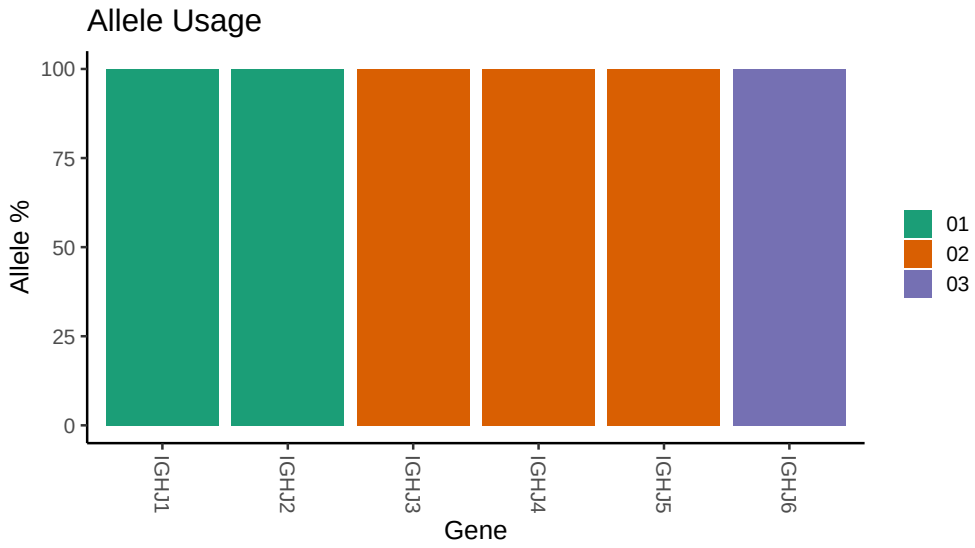

IGHV5−10−1*03
863 sequences assigned
517 (59.9%) exact matches, in which:
475 unique CDR3
6 unique J
Count
Nucleotide Difference


IGHV5−51*01
1290 sequences assigned
684 (53%) exact matches, in which:
615 unique CDR3
6 unique J
Count
Nucleotide Difference


IGHV6−1*01
332 sequences assigned
100 (30.1%) exact matches, in which:
96 unique CDR3
5 unique J
Count
Nucleotide Difference


IGHV7−4−1*01
17 sequences assigned
9 (52.9%) exact matches, in which:
8 unique CDR3
3 unique J
Count
Nucleotide Difference

3 Allele usage in potential haplotype anchor genes



4 Haplotype plots

5 Configuration settings

```
## Repertoire file: /work/jenkins/PRJEB26509/S1/S1/1/1/2e/43a2824093a896a8f24ffc6546dc86/1_Finale_genoty
##
## Germline reference file: /work/jenkins/PRJEB26509/S1/S1/1/1/2e/43a2824093a896a8f24ffc6546dc86/persona
##
## Novel allele file: /work/jenkins/PRJEB26509/S1/S1/1/1/2e/43a2824093a896a8f24ffc6546dc86/novel_sequen
##
## Species: Homosapiens
##
## Chain: IGHV
##
## Segment: V
##
## warning: non codon aligned gaps were found in novel sequence IGHV3 21 01_A85C
##
##
## warning: non codon aligned gaps were found in novel sequence IGHV3 23 01_A85C
##
##
## warning: non codon aligned gaps were found in novel sequence IGHV3 30 18_A85C
```