OGRDBstats Report

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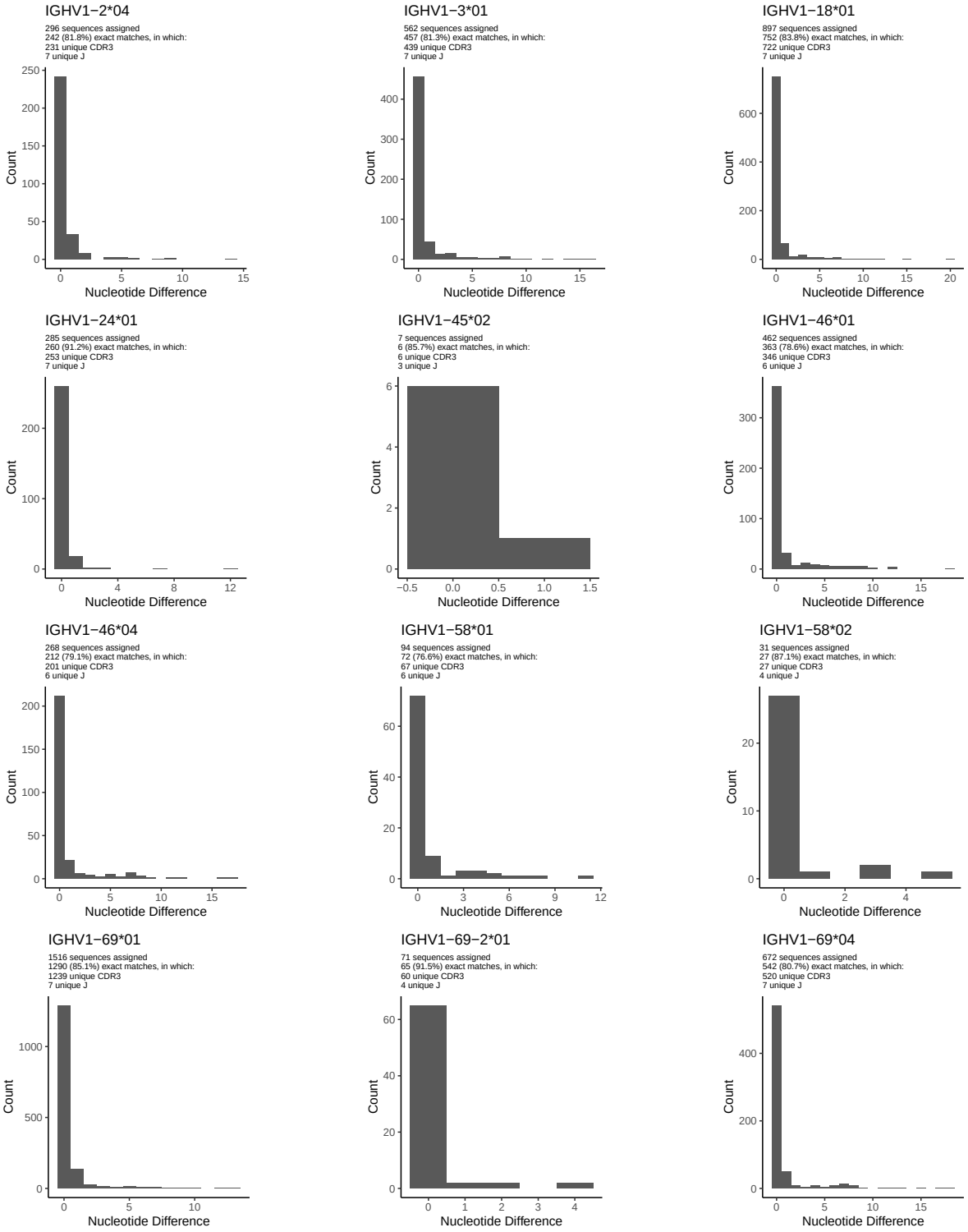
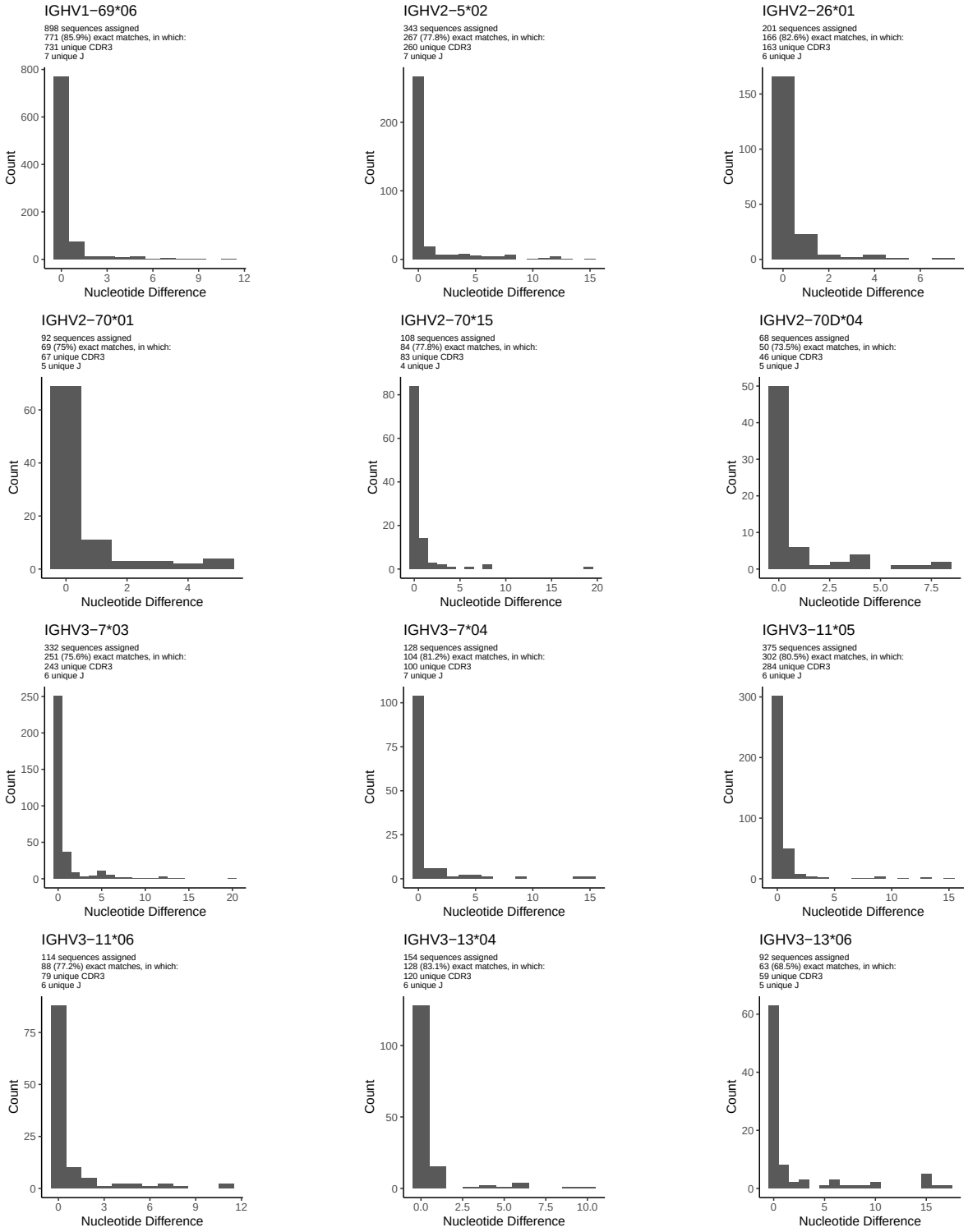
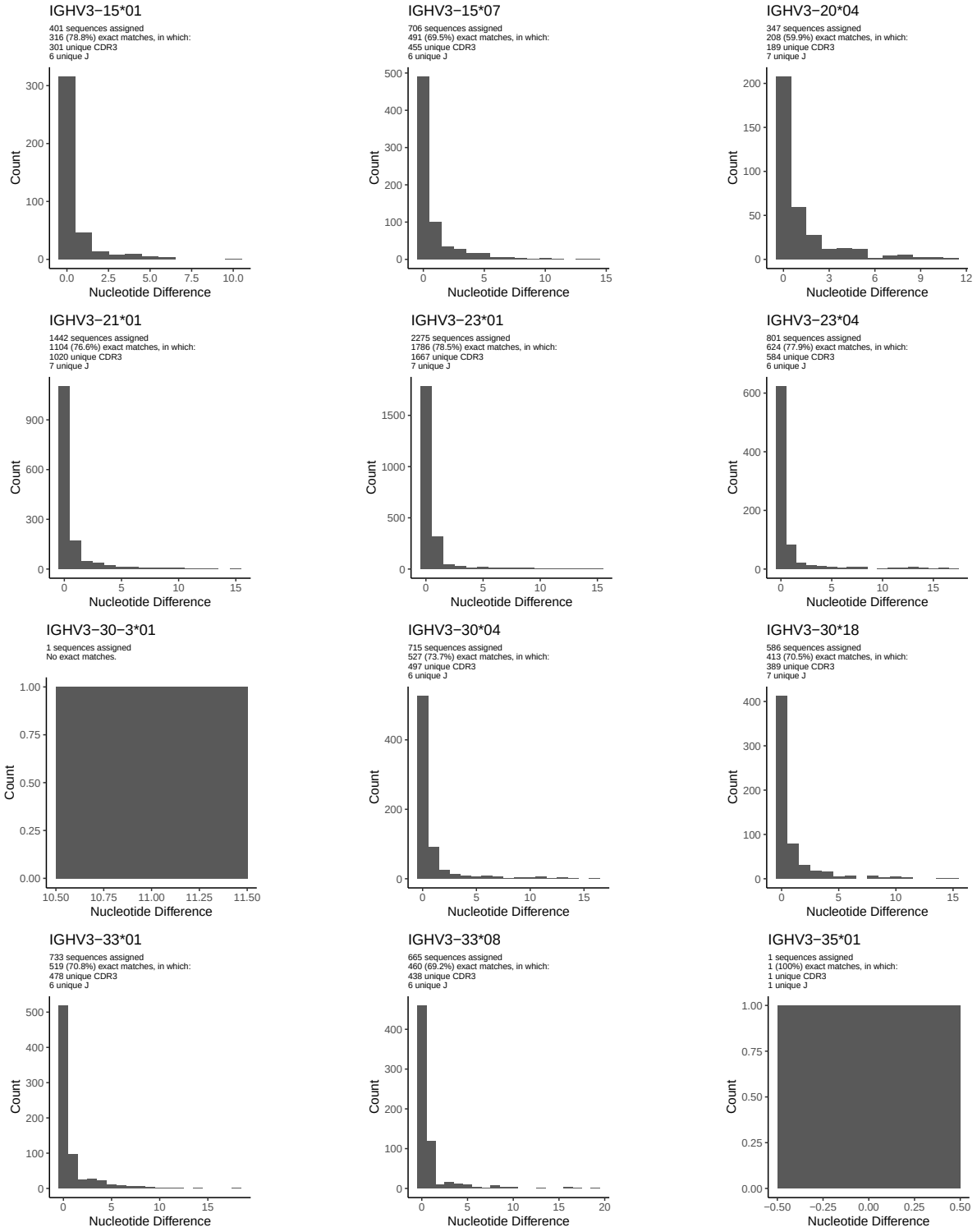
1 Novel sequence analysis

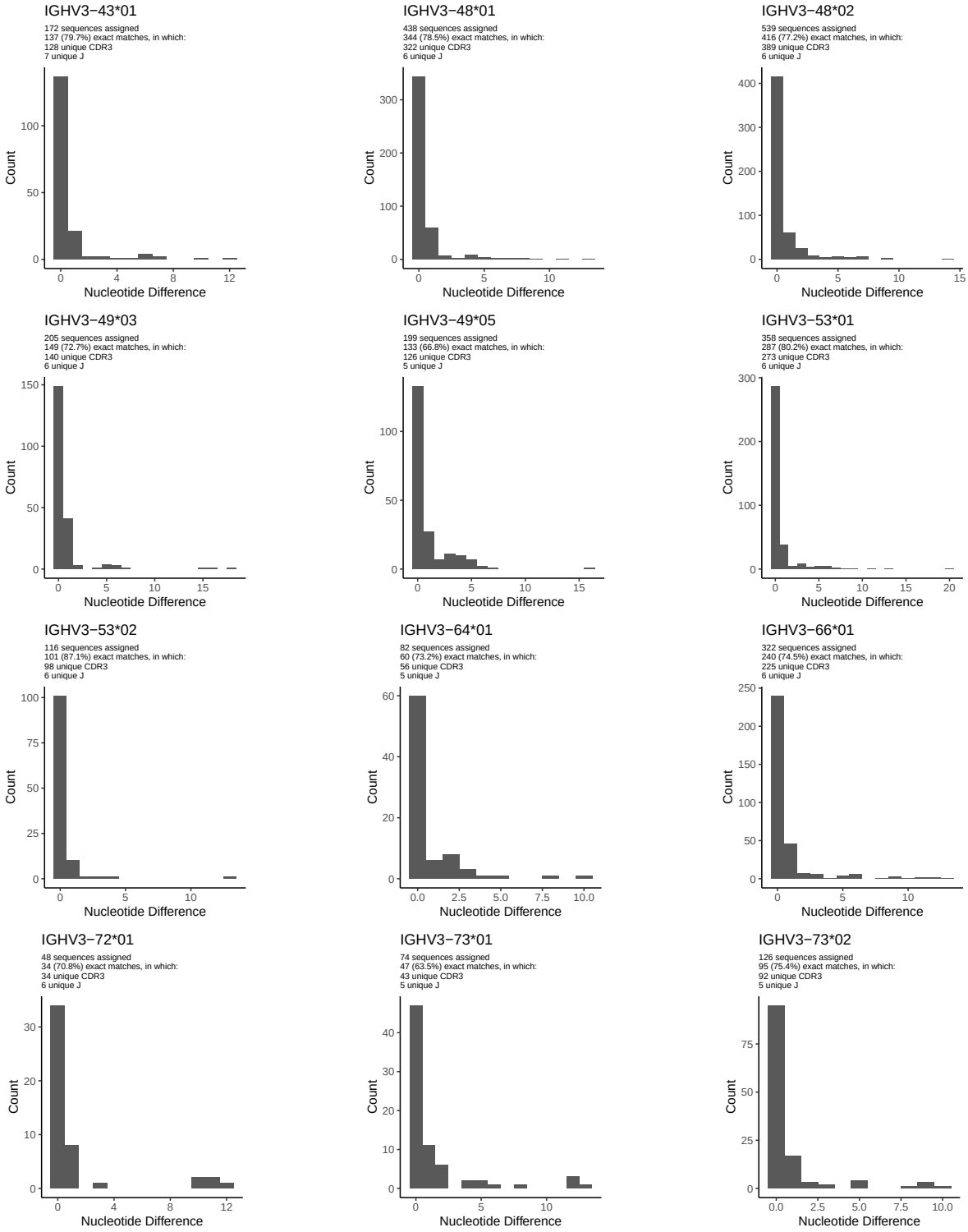
1.1 CDR3 length distribution, in assignments to novel alleles

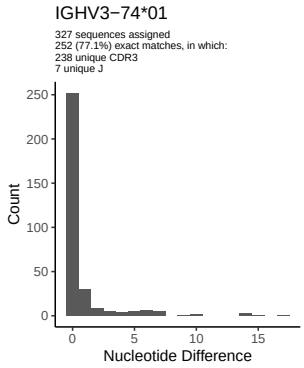
2 Variation from germline, in assignments to each allele

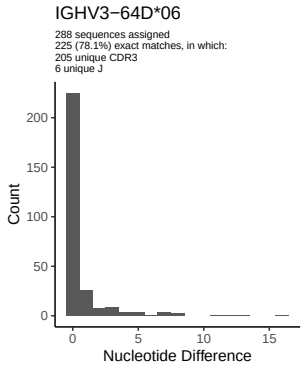


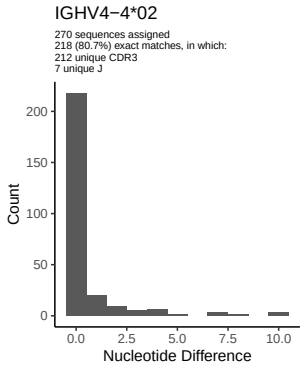

IGHV1−69*06
898 sequences assigned
771 (85.9%) exact matches, in which:
731 unique CDR3
7 unique J
IGHV2−5*02
343 sequences assigned
267 (77.8%) exact matches, in which:
260 unique CDR3
7 unique J
IGHV2−26*01
201 sequences assigned
166 (82.6%) exact matches, in which:
163 unique CDR3
6 unique J
IGHV2−70*01
92 sequences assigned
69 (75%) exact matches, in which:
67 unique CDR3
5 unique J
IGHV2−70*15
108 sequences assigned
84 (77.8%) exact matches, in which:
83 unique CDR3
4 unique J
IGHV2−70D*04
68 sequences assigned
50 (73.5%) exact matches, in which:
46 unique CDR3
5 unique J
IGHV3−7*03
332 sequences assigned
251 (75.6%) exact matches, in which:
243 unique CDR3
6 unique J
IGHV3−7*04
128 sequences assigned
104 (81.2%) exact matches, in which:
100 unique CDR3
7 unique J
IGHV3−11*05
375 sequences assigned
302 (80.5%) exact matches, in which:
284 unique CDR3
6 unique J
IGHV3−11*06
114 sequences assigned
88 (77.2%) exact matches, in which:
79 unique CDR3
6 unique J
IGHV3−13*04
154 sequences assigned
128 (83.1%) exact matches, in which:
120 unique CDR3
6 unique J
IGHV3−13*06
92 sequences assigned
63 (68.5%) exact matches, in which:
59 unique CDR3
5 unique J
Count
Nucleotide Difference

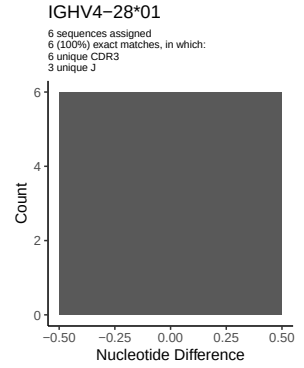

IGHV3−15*01
401 sequences assigned
316 (78.8%) exact matches, in which:
301 unique CDR3
6 unique J
IGHV3−15*07
706 sequences assigned
491 (69.5%) exact matches, in which:
455 unique CDR3
6 unique J
IGHV3−20*04
347 sequences assigned
208 (59.9%) exact matches, in which:
189 unique CDR3
7 unique J
IGHV3−21*01
1442 sequences assigned
1104 (76.6%) exact matches, in which:
1020 unique CDR3
7 unique J
IGHV3−23*01
2275 sequences assigned
1786 (78.5%) exact matches, in which:
1667 unique CDR3
7 unique J
IGHV3−23*04
801 sequences assigned
624 (77.9%) exact matches, in which:
584 unique CDR3
6 unique J
IGHV3−30−3*01
1 sequences assigned
No exact matches.
IGHV3−30*04
715 sequences assigned
527 (73.7%) exact matches, in which:
497 unique CDR3
6 unique J
IGHV3−30*18
586 sequences assigned
413 (70.5%) exact matches, in which:
389 unique CDR3
7 unique J
IGHV3−33*01
733 sequences assigned
519 (70.8%) exact matches, in which:
478 unique CDR3
6 unique J
IGHV3−33*08
665 sequences assigned
460 (69.2%) exact matches, in which:
438 unique CDR3
6 unique J
IGHV3−35*01
1 sequences assigned
1 (100%) exact matches, in which:
1 unique CDR3
1 unique J
Count
Nucleotide Difference

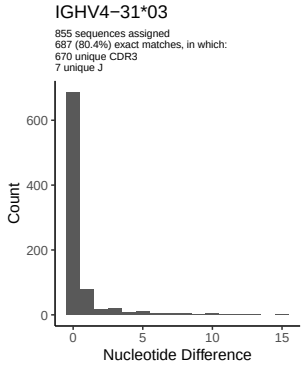

IGHV3−43*01
172 sequences assigned
137 (79.7%) exact matches, in which:
128 unique CDR3
7 unique J
IGHV3−48*01
438 sequences assigned
344 (78.5%) exact matches, in which:
322 unique CDR3
6 unique J
IGHV3−48*02
539 sequences assigned
416 (77.2%) exact matches, in which:
389 unique CDR3
6 unique J
IGHV3−49*03
205 sequences assigned
149 (72.7%) exact matches, in which:
140 unique CDR3
6 unique J
IGHV3−49*05
199 sequences assigned
133 (66.8%) exact matches, in which:
126 unique CDR3
5 unique J
IGHV3−53*01
358 sequences assigned
287 (80.2%) exact matches, in which:
273 unique CDR3
6 unique J
IGHV3−53*02
116 sequences assigned
101 (87.1%) exact matches, in which:
98 unique CDR3
6 unique J
IGHV3−64*01
82 sequences assigned
60 (73.2%) exact matches, in which:
56 unique CDR3
5 unique J
IGHV3−66*01
322 sequences assigned
240 (74.5%) exact matches, in which:
225 unique CDR3
6 unique J
IGHV3−72*01
48 sequences assigned
34 (70.8%) exact matches, in which:
34 unique CDR3
6 unique J
IGHV3−73*01
74 sequences assigned
47 (63.5%) exact matches, in which:
43 unique CDR3
5 unique J
IGHV3−73*02
126 sequences assigned
95 (75.4%) exact matches, in which:
92 unique CDR3
5 unique J
Count
Nucleotide Difference

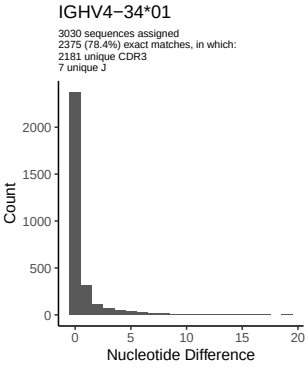

IGHV3−74*01
327 sequences assigned
252 (77.1%) exact matches, in which:
238 unique CDR3
7 unique J
Count
Nucleotide Difference

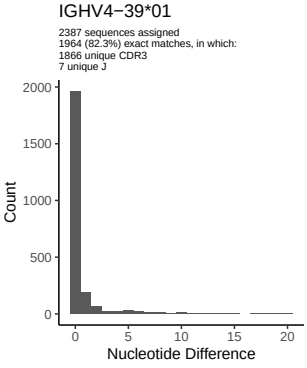

IGHV3−64D*06
288 sequences assigned
225 (78.1%) exact matches, in which:
205 unique CDR3
6 unique J
Count
Nucleotide Difference

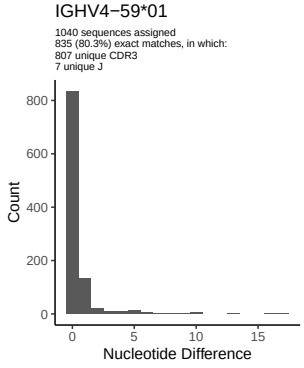

IGHV4−4*02
270 sequences assigned
218 (80.7%) exact matches, in which:
212 unique CDR3
7 unique J
Count
Nucleotide Difference

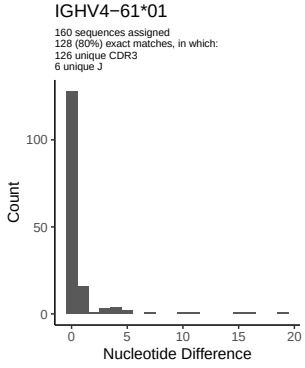

IGHV4−28*01
6 sequences assigned
6 (100%) exact matches, in which:
6 unique CDR3
3 unique J
Count
Nucleotide Difference

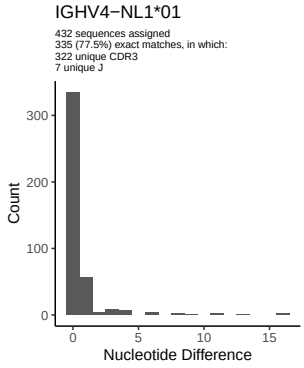

IGHV4−31*03
855 sequences assigned
687 (80.4%) exact matches, in which:
670 unique CDR3
7 unique J
Count
Nucleotide Difference

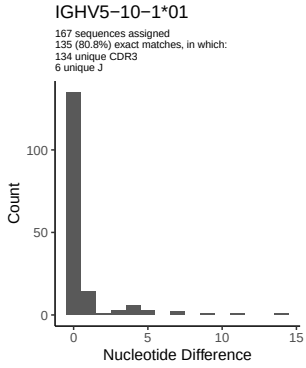

IGHV4−34*01
3030 sequences assigned
2375 (78.4%) exact matches, in which:
2181 unique CDR3
7 unique J
Count
Nucleotide Difference

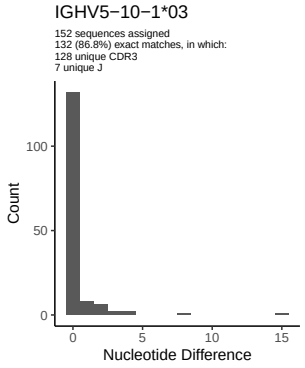

IGHV4−39*01
2387 sequences assigned
1964 (82.3%) exact matches, in which:
1866 unique CDR3
7 unique J
Count
Nucleotide Difference

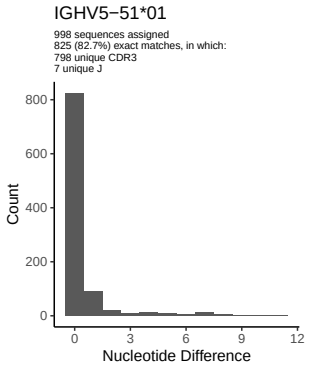

IGHV4−59*01
1040 sequences assigned
835 (80.3%) exact matches, in which:
807 unique CDR3
7 unique J
Count
Nucleotide Difference

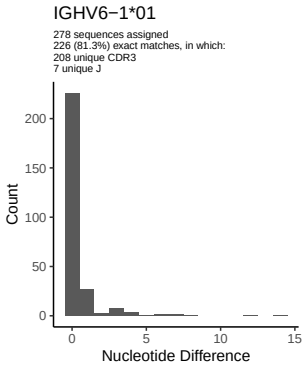

IGHV4−61*01
160 sequences assigned
128 (80%) exact matches, in which:
126 unique CDR3
6 unique J
Count
Nucleotide Difference

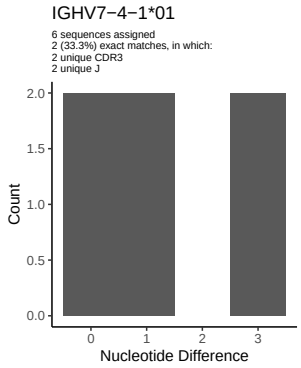

IGHV4−NL1*01
432 sequences assigned
335 (77.5%) exact matches, in which:
322 unique CDR3
7 unique J
Count
Nucleotide Difference


IGHV5−10−1*01
167 sequences assigned
135 (80.8%) exact matches, in which:
134 unique CDR3
6 unique J
Count
Nucleotide Difference

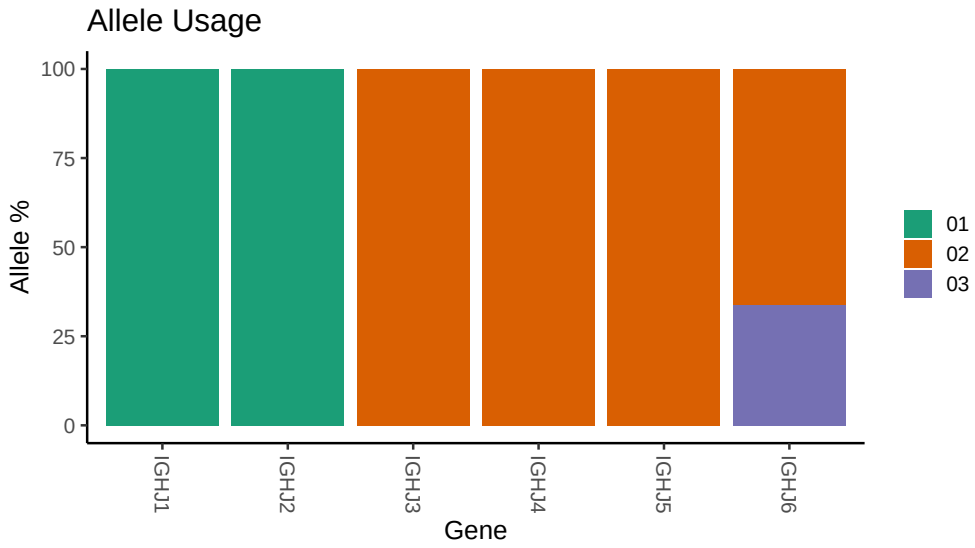

IGHV5−10−1*03
152 sequences assigned
132 (86.8%) exact matches, in which:
128 unique CDR3
7 unique J
Count
Nucleotide Difference


IGHV5−51*01
998 sequences assigned
825 (82.7%) exact matches, in which:
798 unique CDR3
7 unique J
Count
Nucleotide Difference

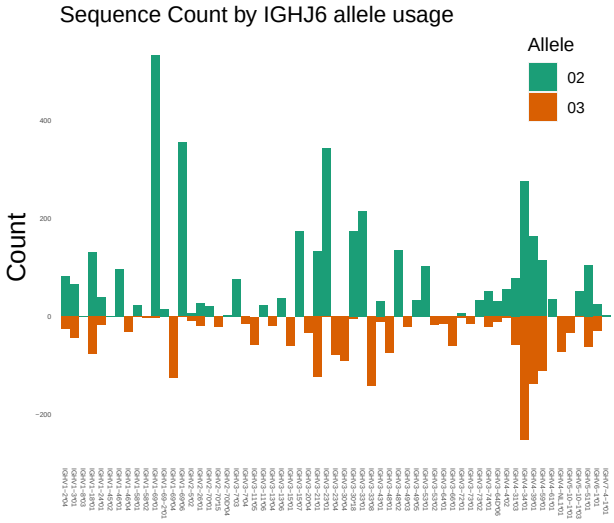

IGHV6−1*01
278 sequences assigned
226 (81.3%) exact matches, in which:
208 unique CDR3
7 unique J
Count
Nucleotide Difference


IGHV7−4−1*01
6 sequences assigned
2 (33.3%) exact matches, in which:
2 unique CDR3
2 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/S89/S89/93/93/96/eb8b7619908a576a89849a57729f09/93_Fi
##
## Germline reference file: /misc/work/jenkins/PRJEB26509/S89/S89/93/93/7c/94dfbc99bca51b958e9026bca7c1
##
## Novel allele file:
##
## Species: Homosapiens
##
## Chain: IGHV
##
## Segment: V
##
## Warning   no inferred sequences found.
```