OGRDBstats Report

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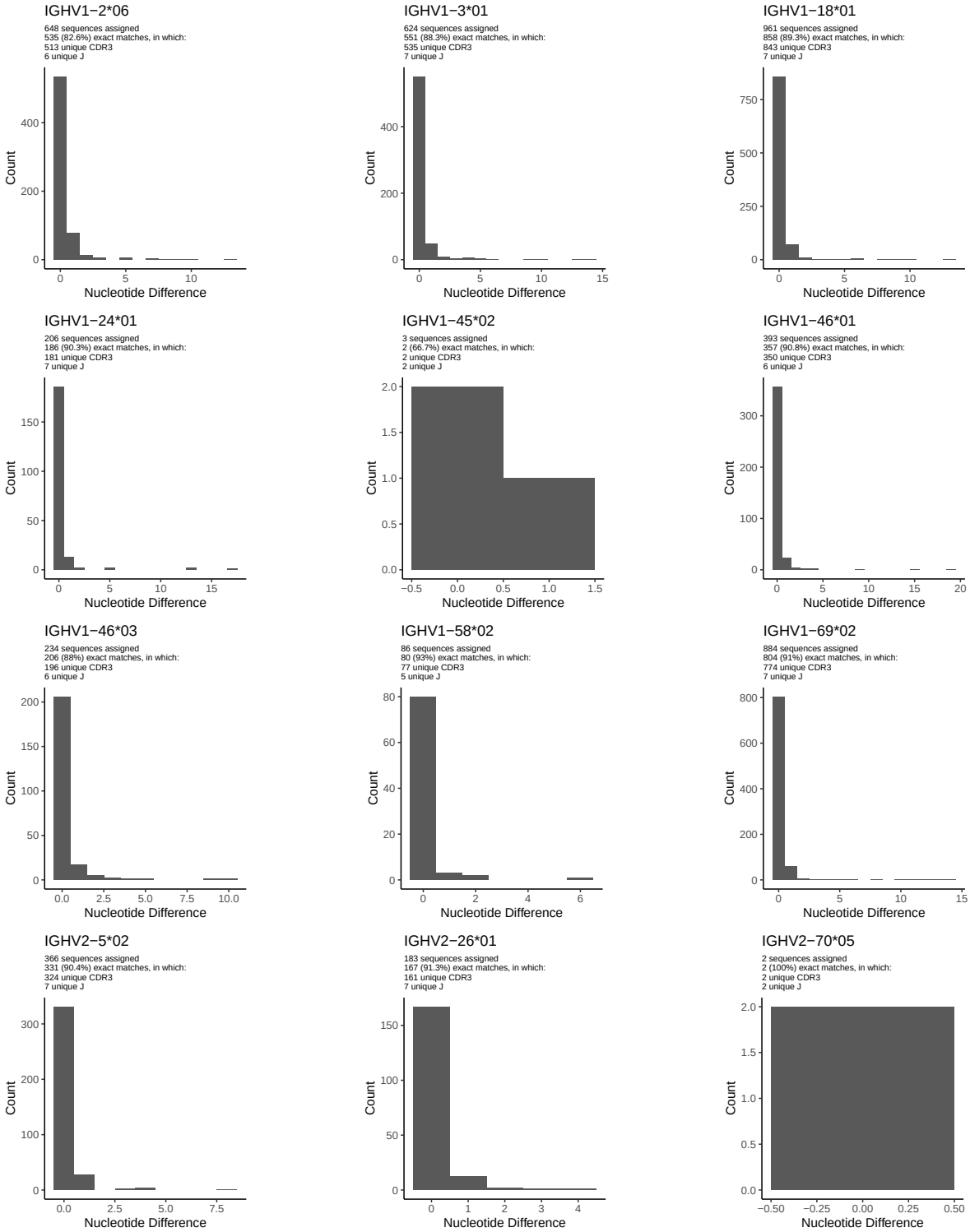
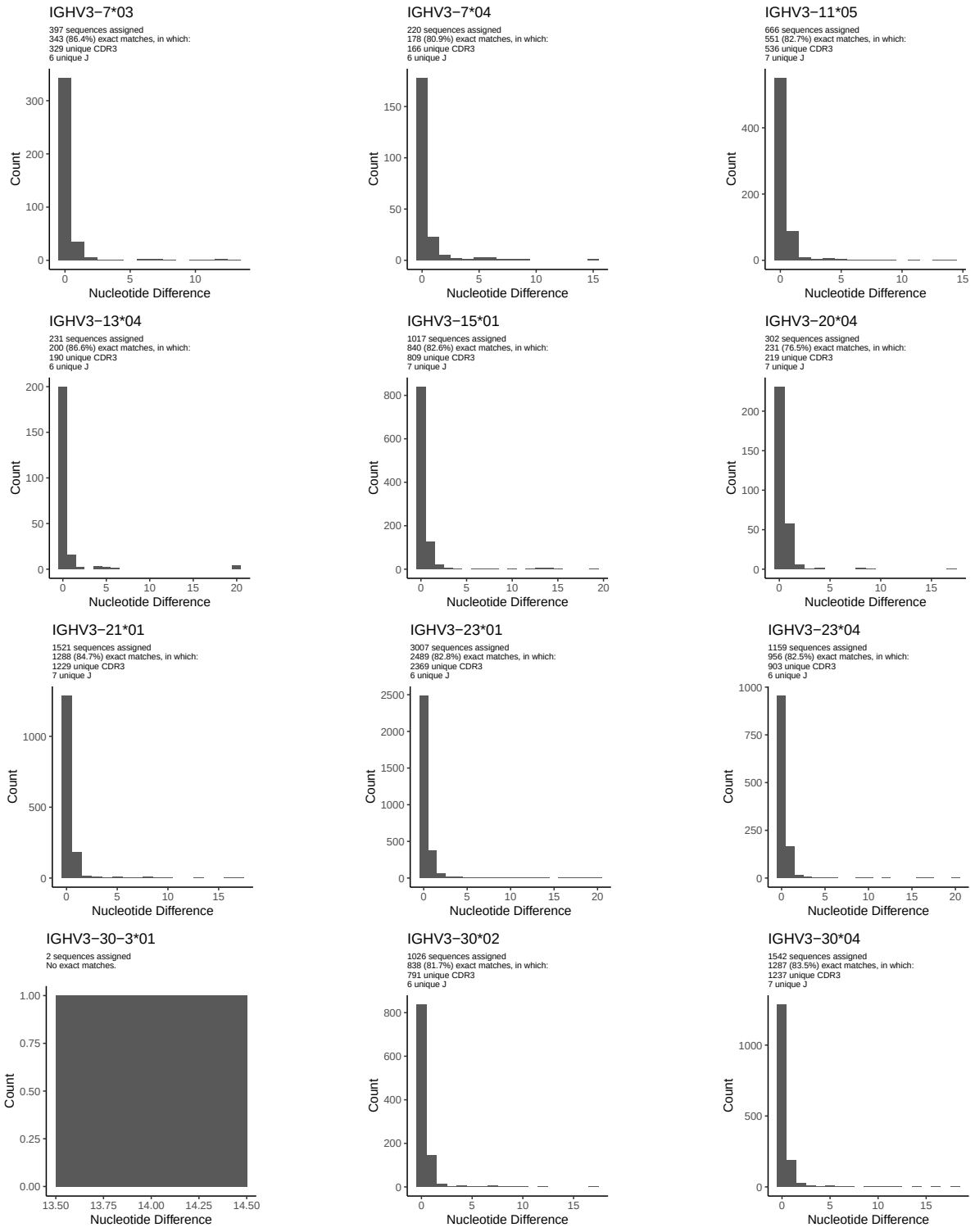
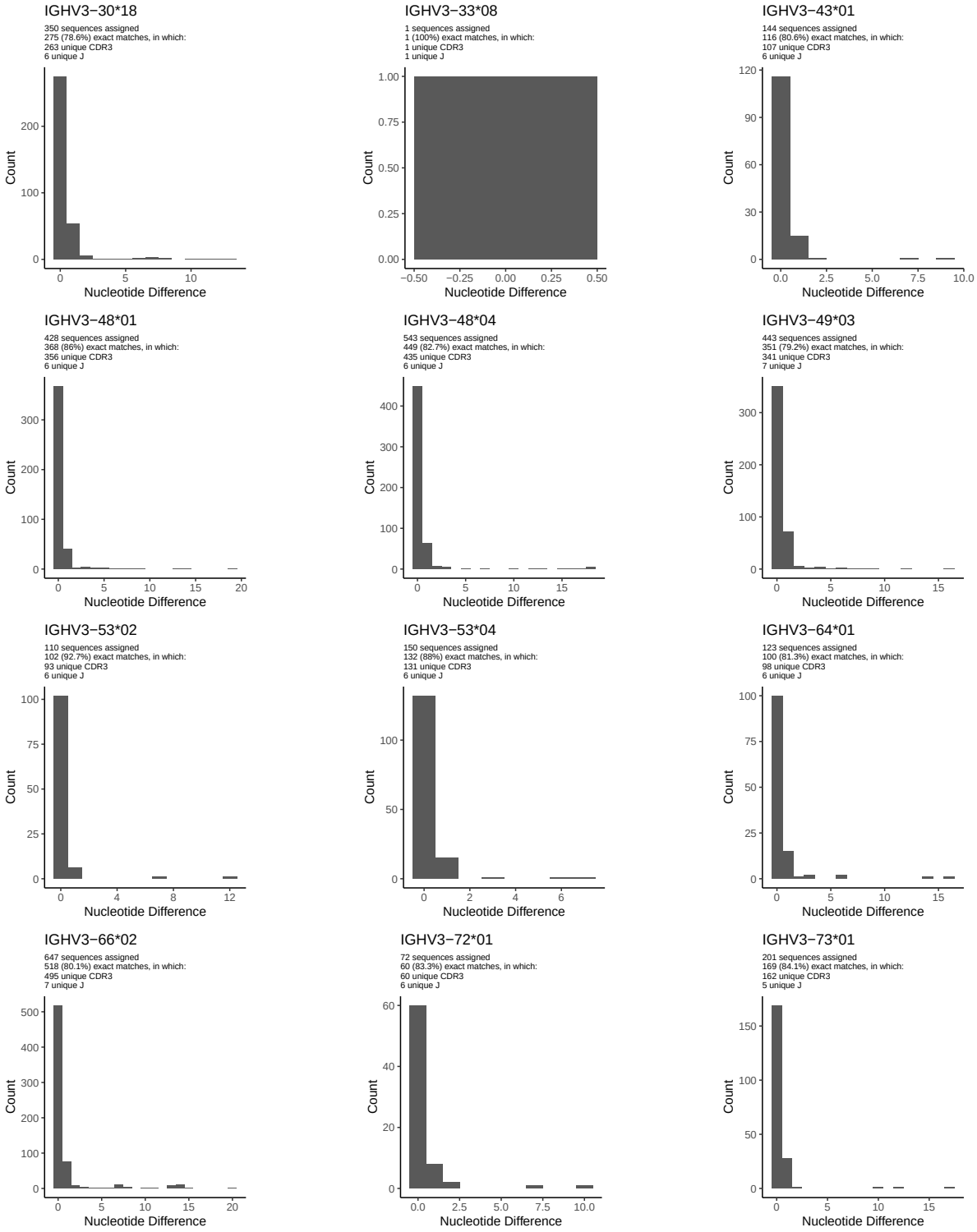
1 Novel sequence analysis

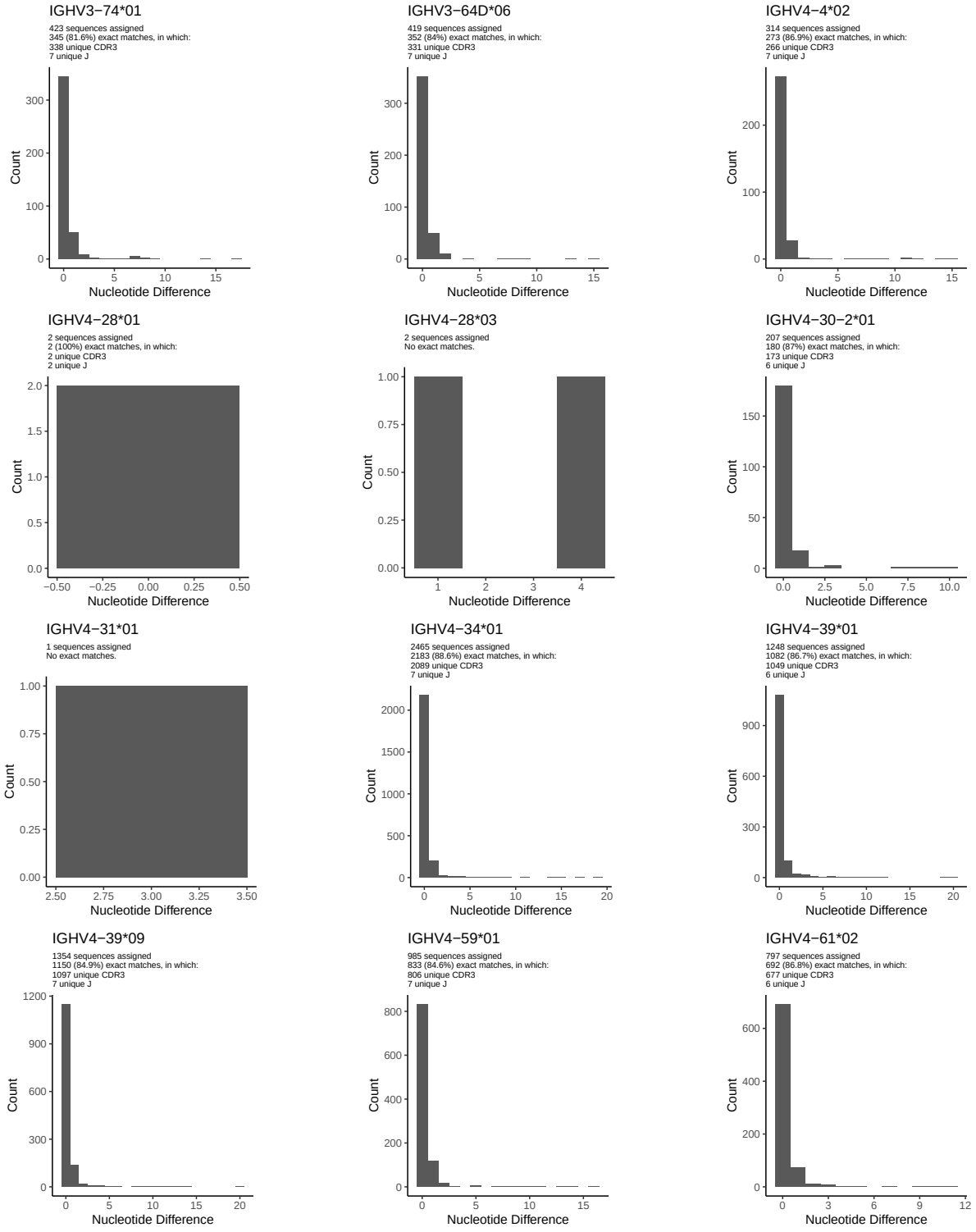
1.1 CDR3 length distribution, in assignments to novel alleles

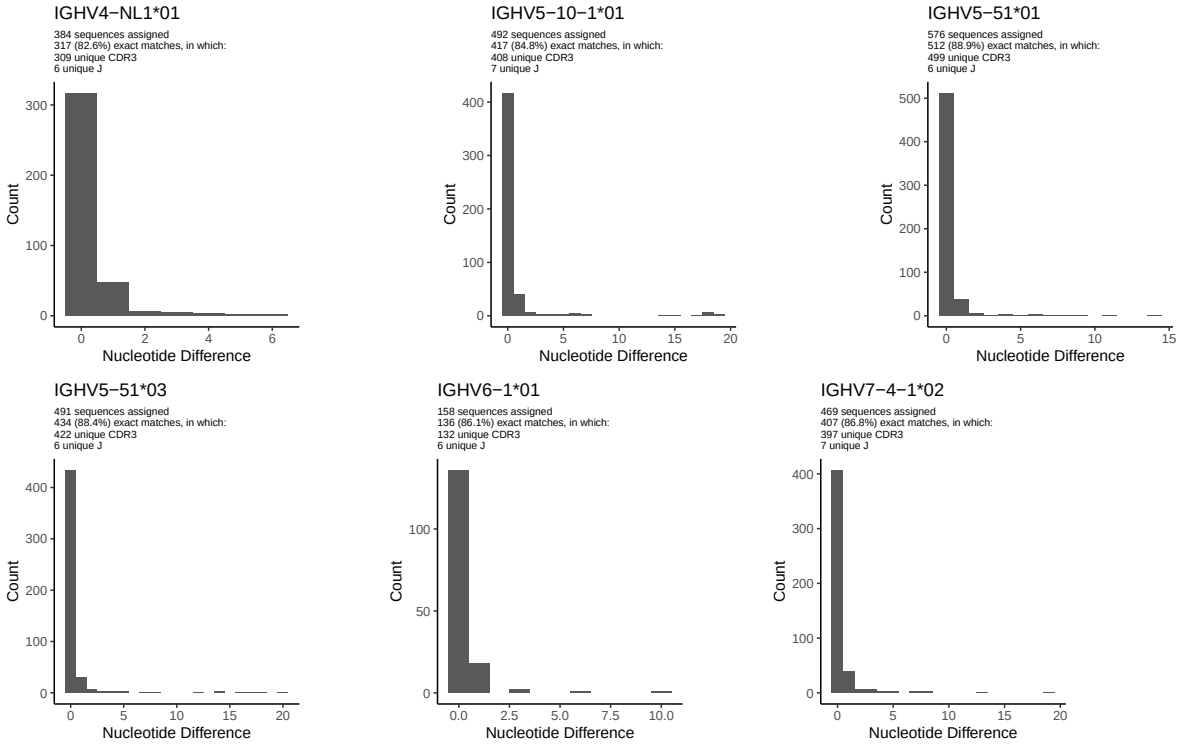
2 Variation from germline, in assignments to each allele



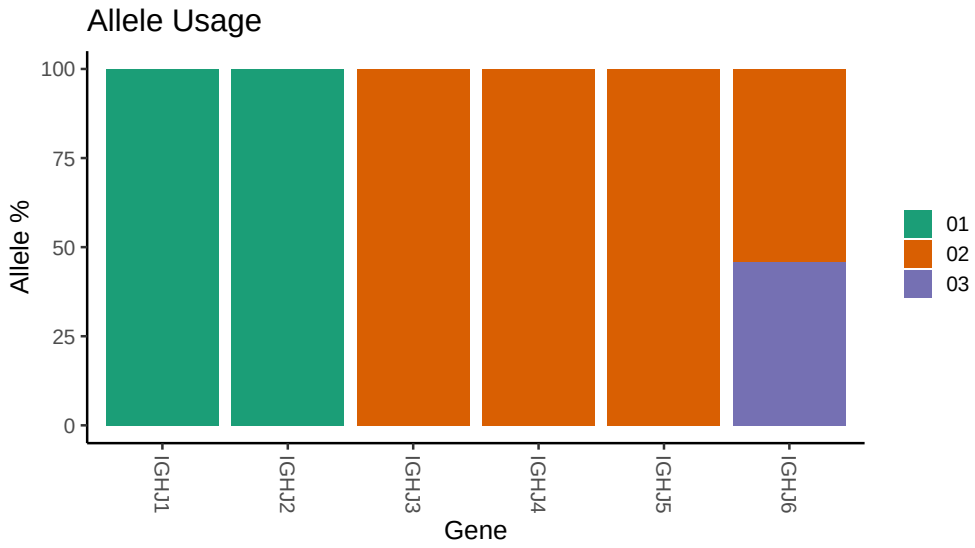

IGHV3−7*03
397 sequences assigned
343 (86.4%) exact matches, in which:
329 unique CDR3
6 unique J
IGHV3−7*04
220 sequences assigned
178 (80.9%) exact matches, in which:
166 unique CDR3
6 unique J
IGHV3−11*05
666 sequences assigned
551 (82.7%) exact matches, in which:
536 unique CDR3
7 unique J
IGHV3−13*04
231 sequences assigned
200 (86.6%) exact matches, in which:
190 unique CDR3
6 unique J
IGHV3−15*01
1017 sequences assigned
840 (82.6%) exact matches, in which:
809 unique CDR3
7 unique J
IGHV3−20*04
302 sequences assigned
231 (76.5%) exact matches, in which:
219 unique CDR3
7 unique J
IGHV3−21*01
1521 sequences assigned
1288 (84.7%) exact matches, in which:
1229 unique CDR3
7 unique J
IGHV3−23*01
3007 sequences assigned
2489 (82.8%) exact matches, in which:
2369 unique CDR3
6 unique J
IGHV3−23*04
1159 sequences assigned
956 (82.5%) exact matches, in which:
903 unique CDR3
6 unique J
IGHV3−30−3*01
2 sequences assigned
No exact matches.
IGHV3−30*02
1026 sequences assigned
838 (81.7%) exact matches, in which:
791 unique CDR3
6 unique J
IGHV3−30*04
1542 sequences assigned
1287 (83.5%) exact matches, in which:
1237 unique CDR3
7 unique J
Count
Nucleotide Difference


IGHV3−30*18
350 sequences assigned
275 (78.6%) exact matches, in which:
263 unique CDR3
6 unique J
IGHV3−33*08
1 sequences assigned
1 (100%) exact matches, in which:
1 unique CDR3
1 unique J
IGHV3−43*01
144 sequences assigned
116 (80.6%) exact matches, in which:
107 unique CDR3
6 unique J
IGHV3−48*01
428 sequences assigned
368 (86%) exact matches, in which:
356 unique CDR3
6 unique J
IGHV3−48*04
543 sequences assigned
449 (82.7%) exact matches, in which:
435 unique CDR3
6 unique J
IGHV3−49*03
443 sequences assigned
351 (79.2%) exact matches, in which:
341 unique CDR3
7 unique J
IGHV3−53*02
110 sequences assigned
102 (92.7%) exact matches, in which:
93 unique CDR3
6 unique J
IGHV3−53*04
150 sequences assigned
132 (88%) exact matches, in which:
131 unique CDR3
6 unique J
IGHV3−64*01
123 sequences assigned
100 (81.3%) exact matches, in which:
98 unique CDR3
6 unique J
IGHV3−66*02
647 sequences assigned
518 (80.1%) exact matches, in which:
495 unique CDR3
7 unique J
IGHV3−72*01
72 sequences assigned
60 (83.3%) exact matches, in which:
60 unique CDR3
6 unique J
IGHV3−73*01
201 sequences assigned
169 (84.1%) exact matches, in which:
162 unique CDR3
5 unique J
Count
Nucleotide Difference

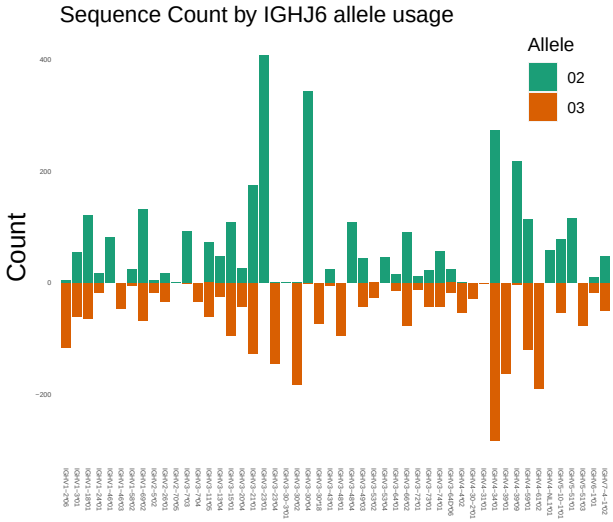

IGHV3−74*01
423 sequences assigned
345 (81.6%) exact matches, in which:
338 unique CDR3
7 unique J
IGHV3−64D*06
419 sequences assigned
352 (84%) exact matches, in which:
331 unique CDR3
7 unique J
IGHV4−4*02
314 sequences assigned
273 (86.9%) exact matches, in which:
266 unique CDR3
7 unique J
IGHV4−28*01
2 sequences assigned
2 (100%) exact matches, in which:
2 unique CDR3
2 unique J
IGHV4−28*03
2 sequences assigned
No exact matches.
IGHV4−30−2*01
207 sequences assigned
180 (87%) exact matches, in which:
173 unique CDR3
6 unique J
IGHV4−31*01
1 sequences assigned
No exact matches.
IGHV4−34*01
2465 sequences assigned
2183 (88.6%) exact matches, in which:
2089 unique CDR3
7 unique J
IGHV4−39*01
1248 sequences assigned
1082 (86.7%) exact matches, in which:
1049 unique CDR3
6 unique J
IGHV4−39*09
1354 sequences assigned
1150 (84.9%) exact matches, in which:
1097 unique CDR3
7 unique J
IGHV4−59*01
985 sequences assigned
833 (84.6%) exact matches, in which:
806 unique CDR3
7 unique J
IGHV4−61*02
797 sequences assigned
692 (86.8%) exact matches, in which:
677 unique CDR3
6 unique J
Count
Nucleotide Difference


IGHV4−NL1*01
384 sequences assigned
317 (82.6%) exact matches, in which:
309 unique CDR3
6 unique J
Count
Nucleotide Difference
IGHV5−10−1*01
492 sequences assigned
417 (84.8%) exact matches, in which:
408 unique CDR3
7 unique J
Count
Nucleotide Difference
IGHV5−51*01
576 sequences assigned
512 (88.9%) exact matches, in which:
499 unique CDR3
6 unique J
Count
Nucleotide Difference
IGHV5−51*03
491 sequences assigned
434 (88.4%) exact matches, in which:
422 unique CDR3
6 unique J
Count
Nucleotide Difference
IGHV6−1*01
158 sequences assigned
136 (86.1%) exact matches, in which:
132 unique CDR3
6 unique J
Count
Nucleotide Difference
IGHV7−4−1*02
469 sequences assigned
407 (86.8%) exact matches, in which:
397 unique CDR3
7 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/S29/S29/29/29/c9/25f9b0692bd57b8902035f1a9cabbe/29_Fi
##
## Germline reference file: /misc/work/jenkins/PRJEB26509/S29/S29/29/29/51/677735b8c96415f130c622a36607
##
## Novel allele file:
##
## Species: Homosapiens
##
## Chain: IGHV
##
## Segment: V
##
## Warning   no inferred sequences found.
```