OGRDBstats Report

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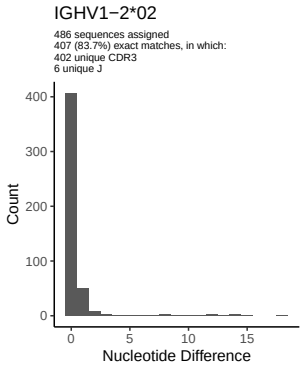
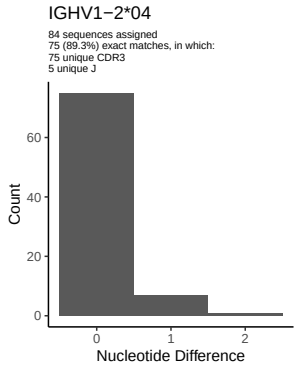
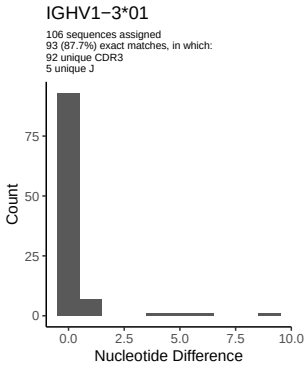
1 Novel sequence analysis

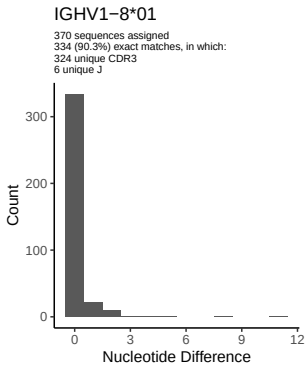
1.1 CDR3 length distribution, in assignments to novel alleles

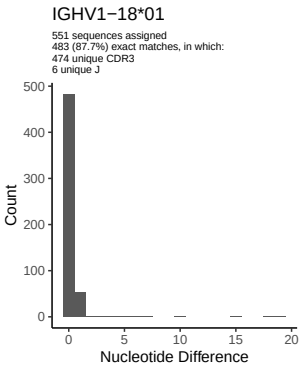
2 Variation from germline, in assignments to each allele

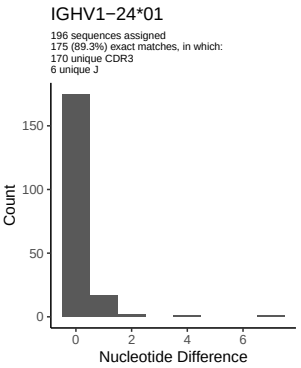


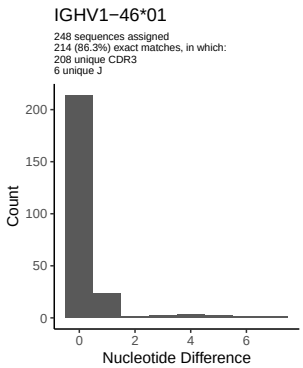


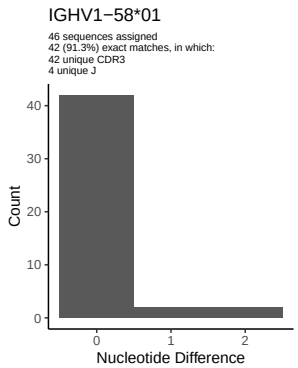


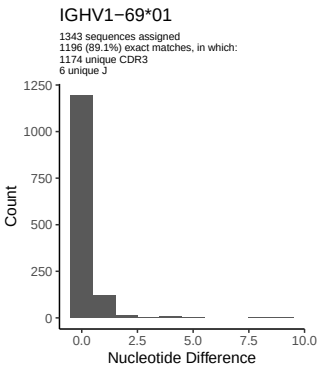


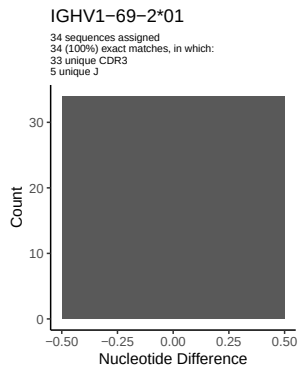


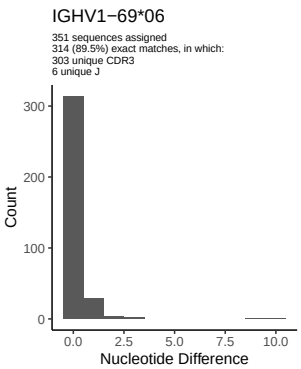


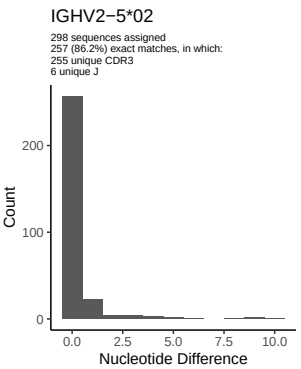


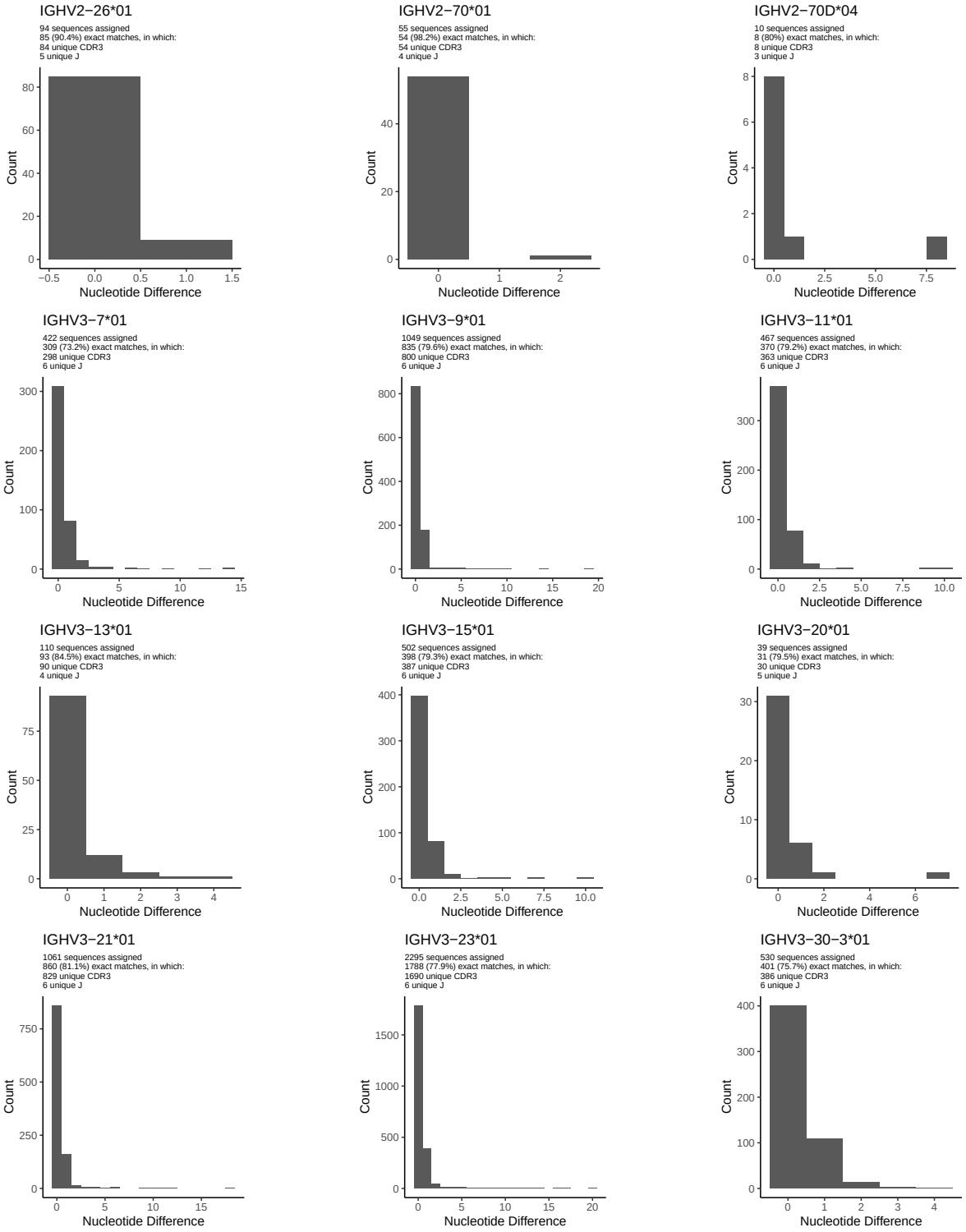


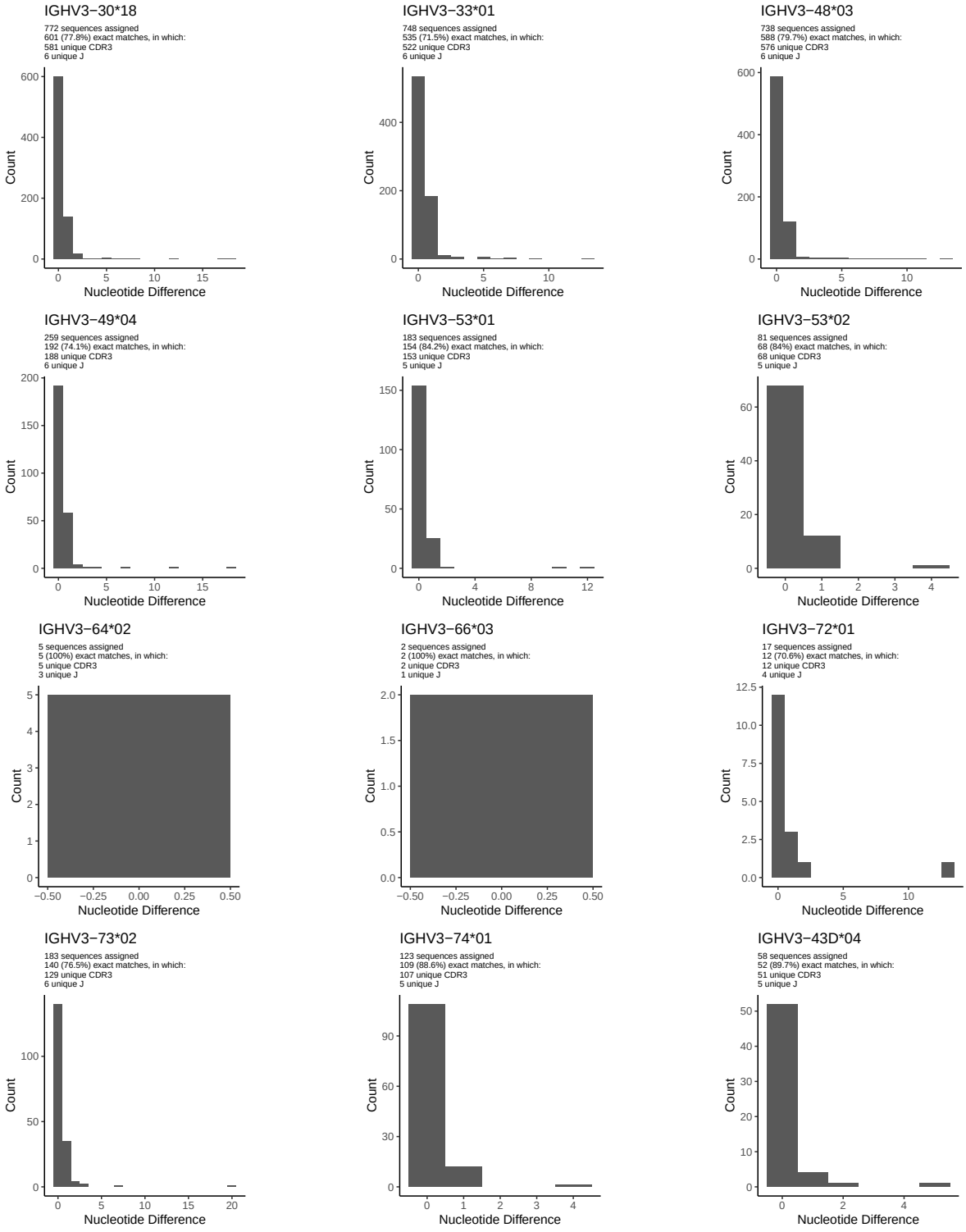


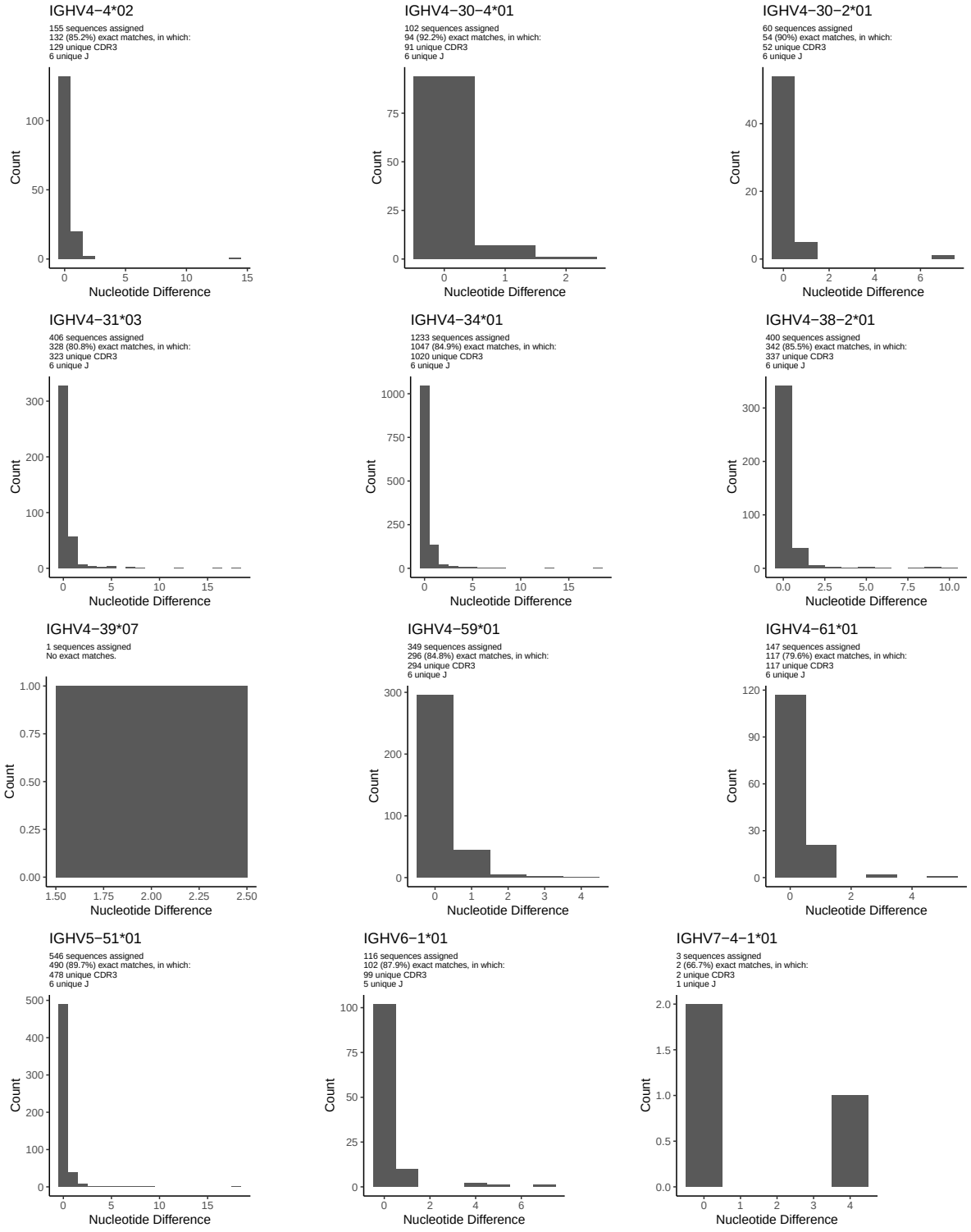




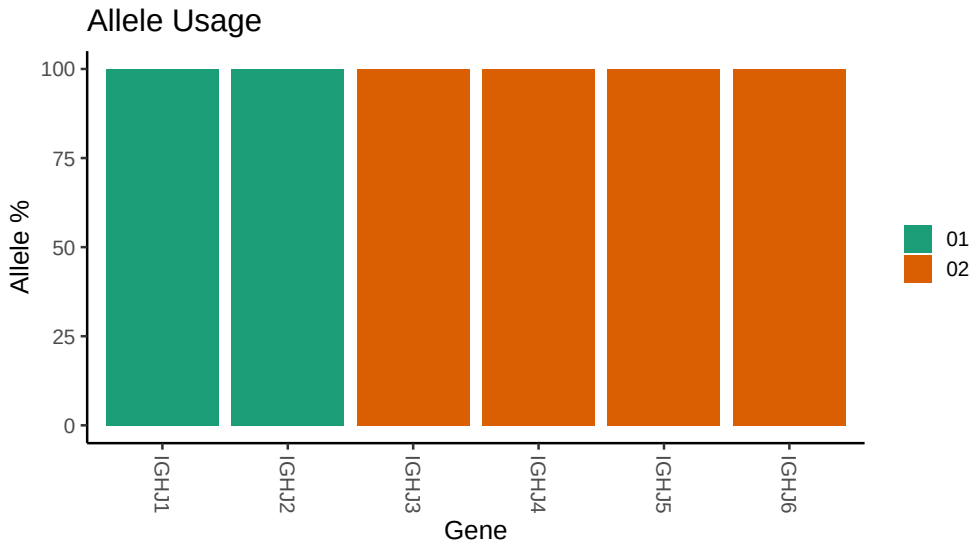



IGHV2−26*01
94 sequences assigned
85 (90.4%) exact matches, in which:
84 unique CDR3
5 unique J
IGHV2−70*01
55 sequences assigned
54 (98.2%) exact matches, in which:
54 unique CDR3
4 unique J
IGHV2−70D*04
10 sequences assigned
8 (80%) exact matches, in which:
8 unique CDR3
3 unique J
IGHV3−7*01
422 sequences assigned
309 (73.2%) exact matches, in which:
298 unique CDR3
6 unique J
IGHV3−9*01
1049 sequences assigned
835 (79.6%) exact matches, in which:
800 unique CDR3
6 unique J
IGHV3−11*01
467 sequences assigned
370 (79.2%) exact matches, in which:
363 unique CDR3
6 unique J
IGHV3−13*01
110 sequences assigned
93 (84.5%) exact matches, in which:
90 unique CDR3
4 unique J
IGHV3−15*01
502 sequences assigned
398 (79.3%) exact matches, in which:
387 unique CDR3
6 unique J
IGHV3−20*01
39 sequences assigned
31 (79.5%) exact matches, in which:
30 unique CDR3
5 unique J
IGHV3−21*01
1061 sequences assigned
860 (81.1%) exact matches, in which:
829 unique CDR3
6 unique J
IGHV3−23*01
2295 sequences assigned
1788 (77.9%) exact matches, in which:
1690 unique CDR3
6 unique J
IGHV3−30−3*01
530 sequences assigned
401 (75.7%) exact matches, in which:
386 unique CDR3
6 unique J
Count
Nucleotide Difference


IGHV3−30*18
772 sequences assigned
601 (77.8%) exact matches, in which:
581 unique CDR3
6 unique J
IGHV3−33*01
748 sequences assigned
535 (71.5%) exact matches, in which:
522 unique CDR3
6 unique J
IGHV3−48*03
738 sequences assigned
588 (79.7%) exact matches, in which:
576 unique CDR3
6 unique J
IGHV3−49*04
259 sequences assigned
192 (74.1%) exact matches, in which:
188 unique CDR3
6 unique J
IGHV3−53*01
183 sequences assigned
154 (84.2%) exact matches, in which:
153 unique CDR3
5 unique J
IGHV3−53*02
81 sequences assigned
68 (84%) exact matches, in which:
68 unique CDR3
5 unique J
IGHV3−64*02
5 sequences assigned
5 (100%) exact matches, in which:
5 unique CDR3
3 unique J
IGHV3−66*03
2 sequences assigned
2 (100%) exact matches, in which:
2 unique CDR3
1 unique J
IGHV3−72*01
17 sequences assigned
12 (70.6%) exact matches, in which:
12 unique CDR3
4 unique J
IGHV3−73*02
183 sequences assigned
140 (76.5%) exact matches, in which:
129 unique CDR3
6 unique J
IGHV3−74*01
123 sequences assigned
109 (88.6%) exact matches, in which:
107 unique CDR3
5 unique J
IGHV3−43D*04
58 sequences assigned
52 (89.7%) exact matches, in which:
51 unique CDR3
5 unique J
Count
Nucleotide Difference


IGHV4−4*02
155 sequences assigned
132 (85.2%) exact matches, in which:
129 unique CDR3
6 unique J
IGHV4−30−4*01
102 sequences assigned
94 (92.2%) exact matches, in which:
91 unique CDR3
6 unique J
IGHV4−30−2*01
60 sequences assigned
54 (90%) exact matches, in which:
52 unique CDR3
6 unique J
IGHV4−31*03
406 sequences assigned
328 (80.8%) exact matches, in which:
323 unique CDR3
6 unique J
IGHV4−34*01
1233 sequences assigned
1047 (84.9%) exact matches, in which:
1020 unique CDR3
6 unique J
IGHV4−38−2*01
400 sequences assigned
342 (85.5%) exact matches, in which:
337 unique CDR3
6 unique J
IGHV4−39*07
1 sequences assigned
No exact matches.
IGHV4−59*01
349 sequences assigned
296 (84.8%) exact matches, in which:
294 unique CDR3
6 unique J
IGHV4−61*01
147 sequences assigned
117 (79.6%) exact matches, in which:
117 unique CDR3
6 unique J
IGHV5−51*01
546 sequences assigned
490 (89.7%) exact matches, in which:
478 unique CDR3
6 unique J
IGHV6−1*01
116 sequences assigned
102 (87.9%) exact matches, in which:
99 unique CDR3
5 unique J
IGHV7−4−1*01
3 sequences assigned
2 (66.7%) exact matches, in which:
2 unique CDR3
1 unique J
Count
Nucleotide Difference

3 Allele usage in potential haplotype anchor genes



4 Haplotype plots

5 Configuration settings

```
## Repertoire file: /work/jenkins/PRJEB26509/S16/S16/16/16/fa/a3a0fd68e378b7252fc0183536eea1/16_Finale_
##
## Germline reference file: /work/jenkins/PRJEB26509/S16/S16/16/16/f4/fa1dabe039ec26959adef193dadaf9/re
##
## Novel allele file:
##
## Species: Homosapiens
##
## Chain: IGHV
##
## Segment: V
##
## Warning   no inferred sequences found.
```