OGRDBstats Report

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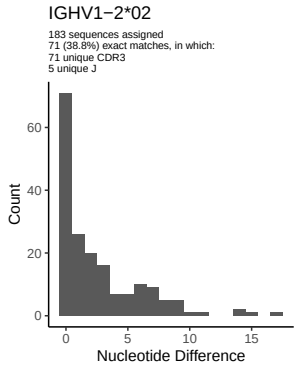
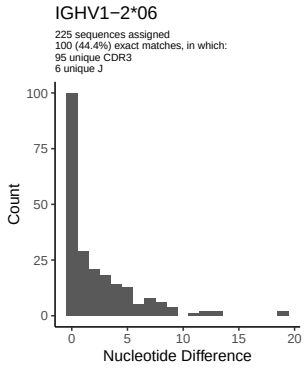
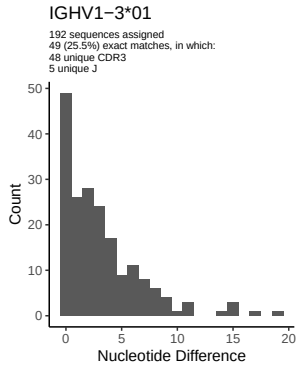
1 Novel sequence analysis

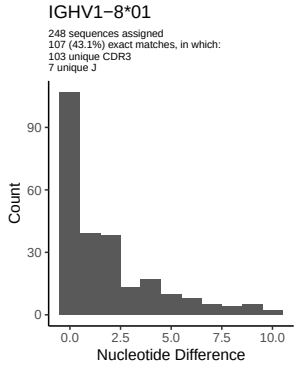
1.1 CDR3 length distribution, in assignments to novel alleles

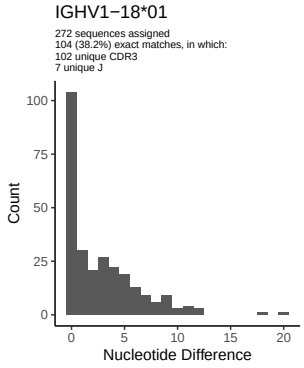
2 Variation from germline, in assignments to each allele

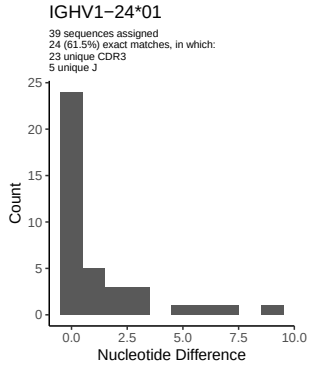


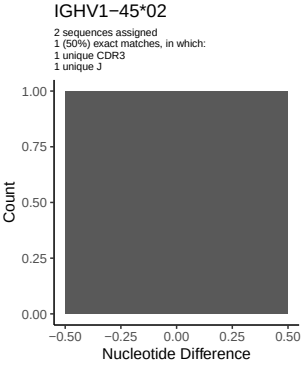


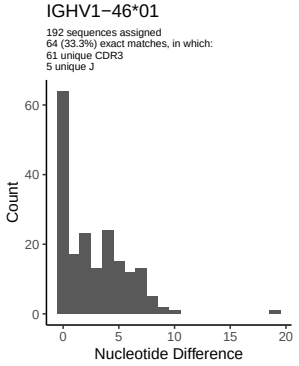


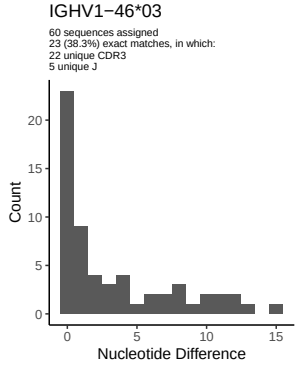


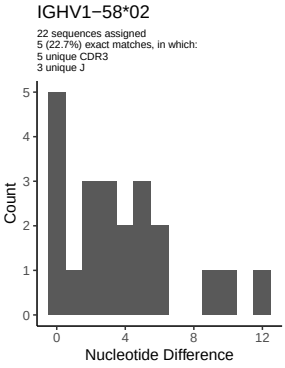


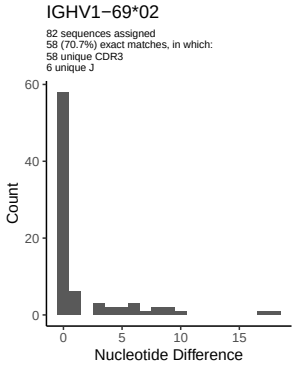


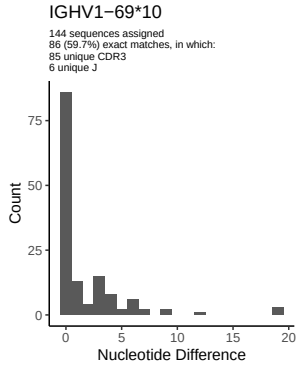


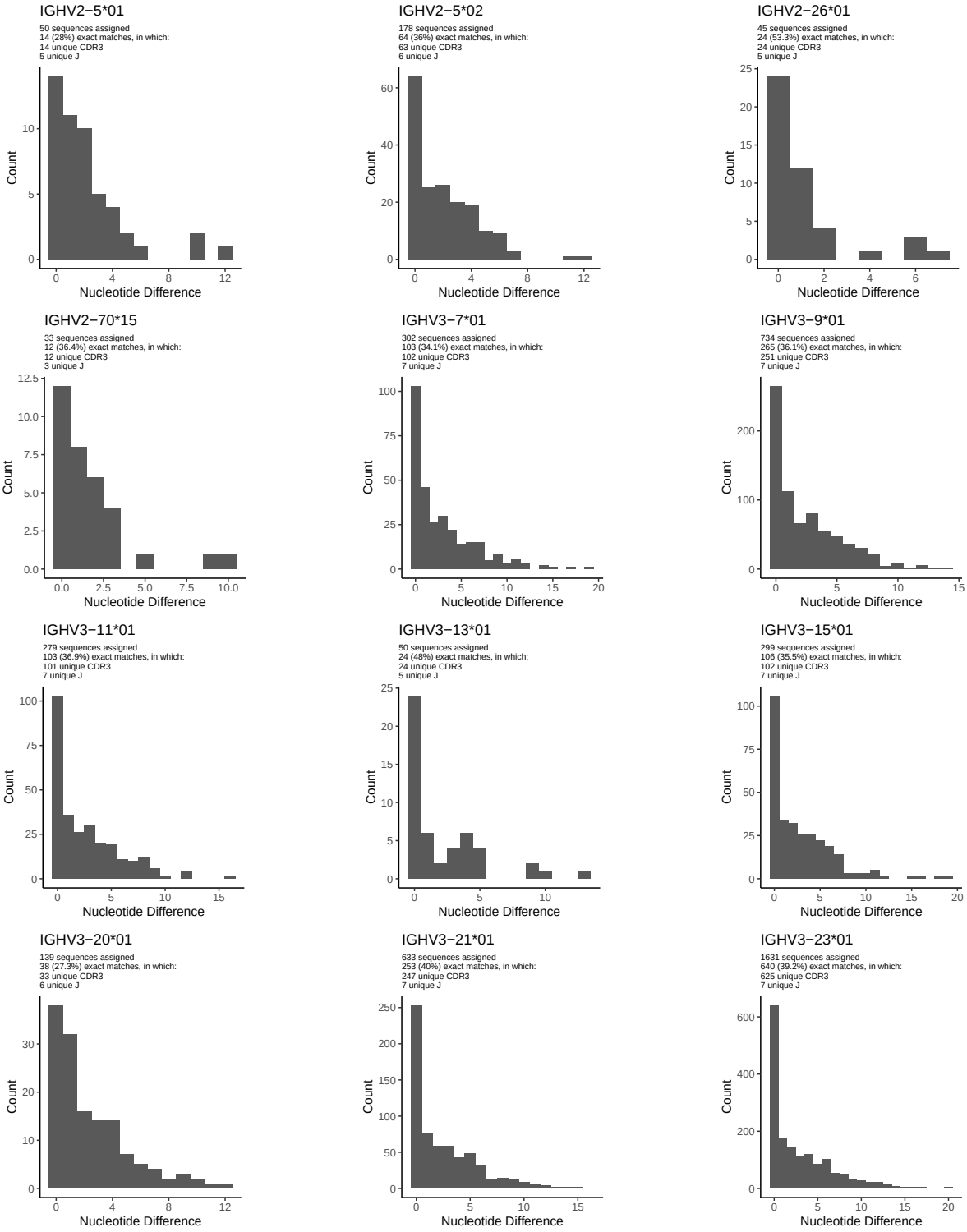


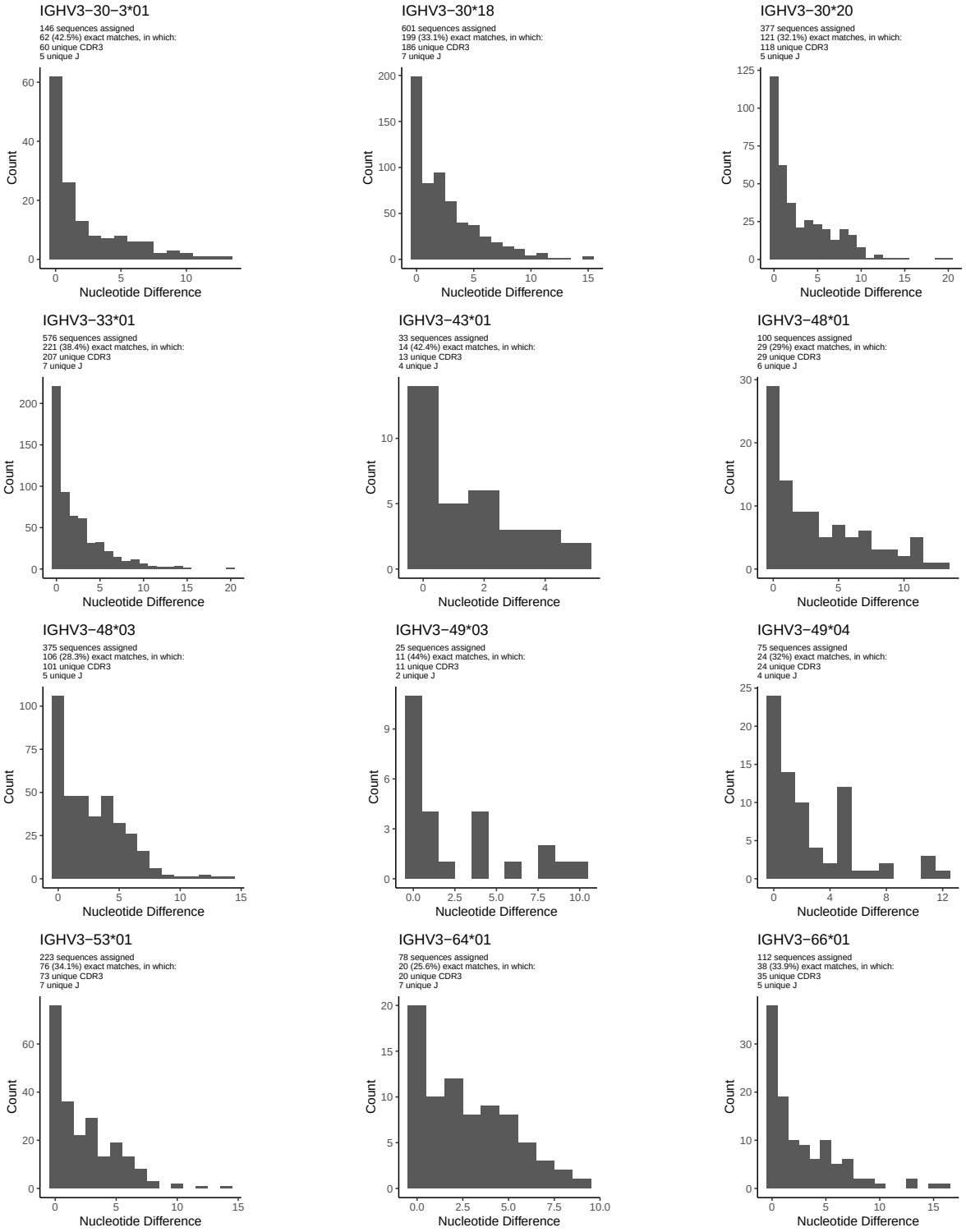


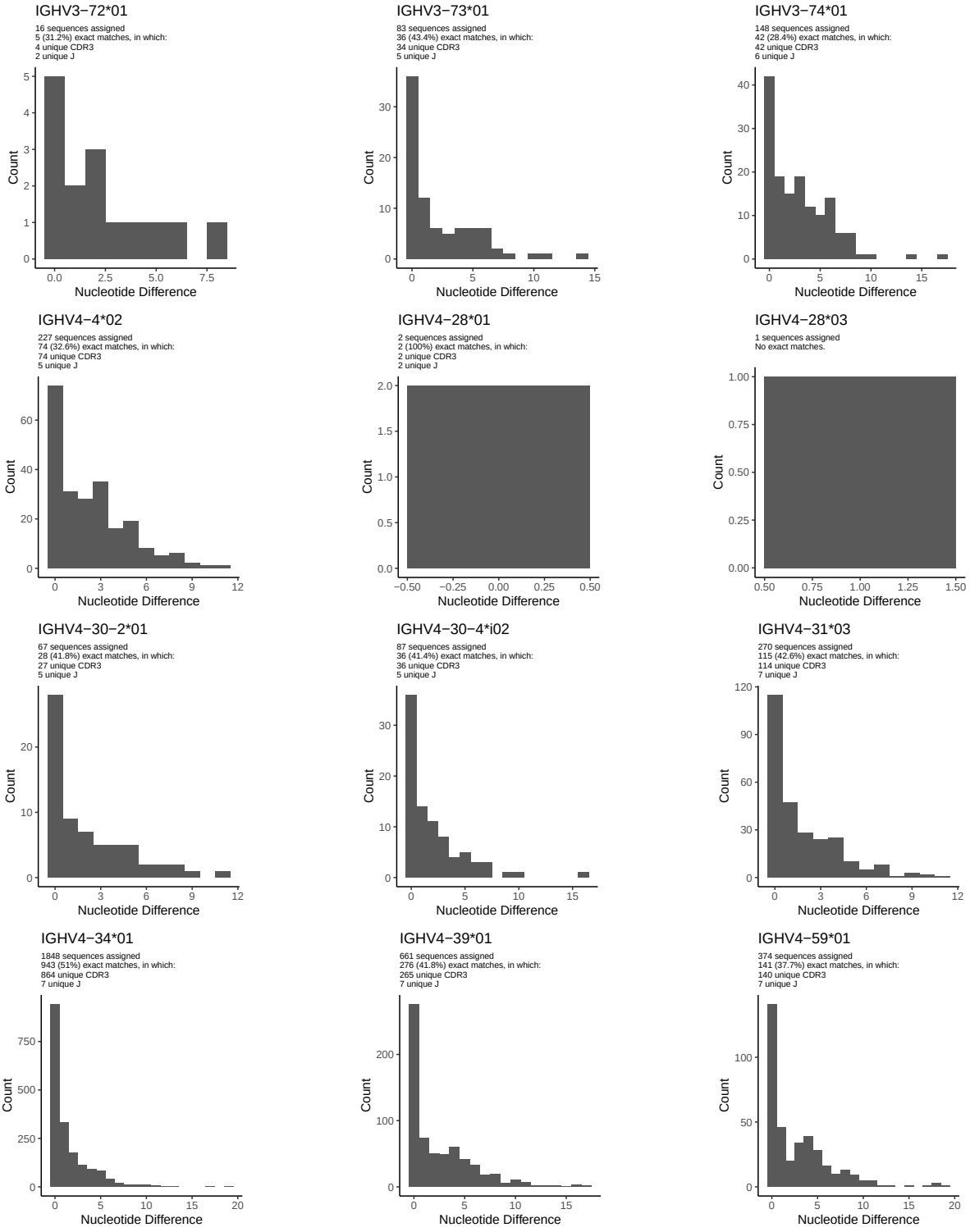


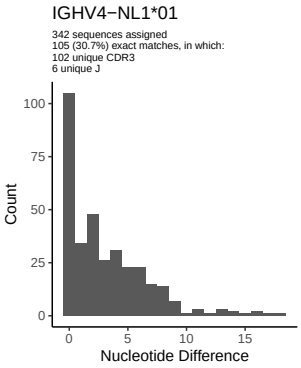


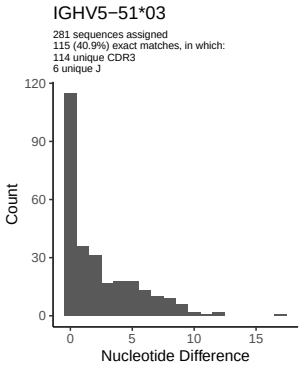


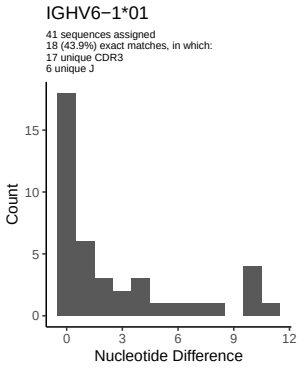

IGHV2−5*01
50 sequences assigned
14 (28%) exact matches, in which:
14 unique CDR3
5 unique J
IGHV2−5*02
178 sequences assigned
64 (36%) exact matches, in which:
63 unique CDR3
6 unique J
IGHV2−26*01
45 sequences assigned
24 (53.3%) exact matches, in which:
24 unique CDR3
5 unique J
IGHV2−70*15
33 sequences assigned
12 (36.4%) exact matches, in which:
12 unique CDR3
3 unique J
IGHV3−7*01
302 sequences assigned
103 (34.1%) exact matches, in which:
102 unique CDR3
7 unique J
IGHV3−9*01
734 sequences assigned
265 (36.1%) exact matches, in which:
251 unique CDR3
7 unique J
IGHV3−11*01
279 sequences assigned
103 (36.9%) exact matches, in which:
101 unique CDR3
7 unique J
IGHV3−13*01
50 sequences assigned
24 (48%) exact matches, in which:
24 unique CDR3
5 unique J
IGHV3−15*01
299 sequences assigned
106 (35.5%) exact matches, in which:
102 unique CDR3
7 unique J
IGHV3−20*01
139 sequences assigned
38 (27.3%) exact matches, in which:
33 unique CDR3
6 unique J
IGHV3−21*01
633 sequences assigned
253 (40%) exact matches, in which:
247 unique CDR3
7 unique J
IGHV3−23*01
1631 sequences assigned
640 (39.2%) exact matches, in which:
625 unique CDR3
7 unique J
Count
Nucleotide Difference

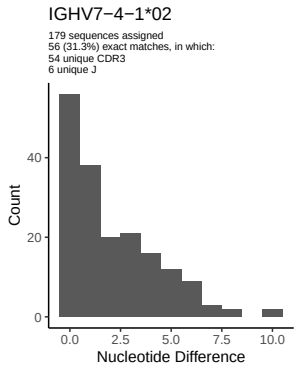

IGHV3−30−3*01
146 sequences assigned
62 (42.5%) exact matches, in which:
60 unique CDR3
5 unique J
IGHV3−30*18
601 sequences assigned
199 (33.1%) exact matches, in which:
186 unique CDR3
7 unique J
IGHV3−30*20
377 sequences assigned
121 (32.1%) exact matches, in which:
118 unique CDR3
5 unique J
IGHV3−33*01
576 sequences assigned
221 (38.4%) exact matches, in which:
207 unique CDR3
7 unique J
IGHV3−43*01
33 sequences assigned
14 (42.4%) exact matches, in which:
13 unique CDR3
4 unique J
IGHV3−48*01
100 sequences assigned
29 (29%) exact matches, in which:
29 unique CDR3
6 unique J
IGHV3−48*03
375 sequences assigned
106 (28.3%) exact matches, in which:
101 unique CDR3
5 unique J
IGHV3−49*03
25 sequences assigned
11 (44%) exact matches, in which:
11 unique CDR3
2 unique J
IGHV3−49*04
75 sequences assigned
24 (32%) exact matches, in which:
24 unique CDR3
4 unique J
IGHV3−53*01
223 sequences assigned
76 (34.1%) exact matches, in which:
73 unique CDR3
7 unique J
IGHV3−64*01
78 sequences assigned
20 (25.6%) exact matches, in which:
20 unique CDR3
7 unique J
IGHV3−66*01
112 sequences assigned
38 (33.9%) exact matches, in which:
35 unique CDR3
5 unique J
Count
Nucleotide Difference


IGHV3−72*01
16 sequences assigned
5 (31.2%) exact matches, in which:
4 unique CDR3
2 unique J
IGHV3−73*01
83 sequences assigned
36 (43.4%) exact matches, in which:
34 unique CDR3
5 unique J
IGHV3−74*01
148 sequences assigned
42 (28.4%) exact matches, in which:
42 unique CDR3
6 unique J
IGHV4−4*02
227 sequences assigned
74 (32.6%) exact matches, in which:
74 unique CDR3
5 unique J
IGHV4−28*01
2 sequences assigned
2 (100%) exact matches, in which:
2 unique CDR3
2 unique J
IGHV4−28*03
1 sequences assigned
No exact matches.
IGHV4−30−2*01
67 sequences assigned
28 (41.8%) exact matches, in which:
27 unique CDR3
5 unique J
IGHV4−30−4*i02
87 sequences assigned
36 (41.4%) exact matches, in which:
36 unique CDR3
5 unique J
IGHV4−31*03
270 sequences assigned
115 (42.6%) exact matches, in which:
114 unique CDR3
7 unique J
IGHV4−34*01
1848 sequences assigned
943 (51%) exact matches, in which:
864 unique CDR3
7 unique J
IGHV4−39*01
661 sequences assigned
276 (41.8%) exact matches, in which:
265 unique CDR3
7 unique J
IGHV4−59*01
374 sequences assigned
141 (37.7%) exact matches, in which:
140 unique CDR3
7 unique J
Count
Nucleotide Difference

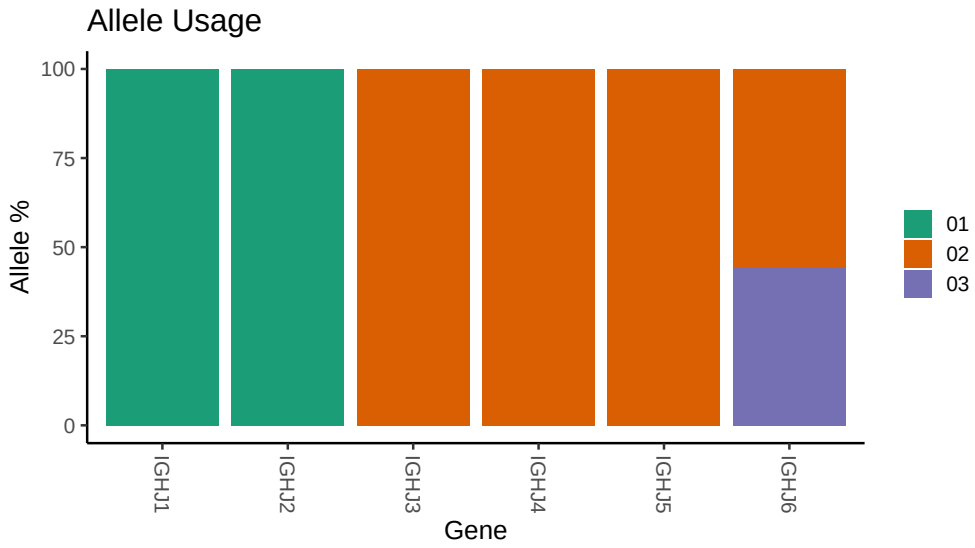

IGHV4−NL1*01
342 sequences assigned
105 (30.7%) exact matches, in which:
102 unique CDR3
6 unique J
Count
Nucleotide Difference


IGHV5−51*03
281 sequences assigned
115 (40.9%) exact matches, in which:
114 unique CDR3
6 unique J
Count
Nucleotide Difference

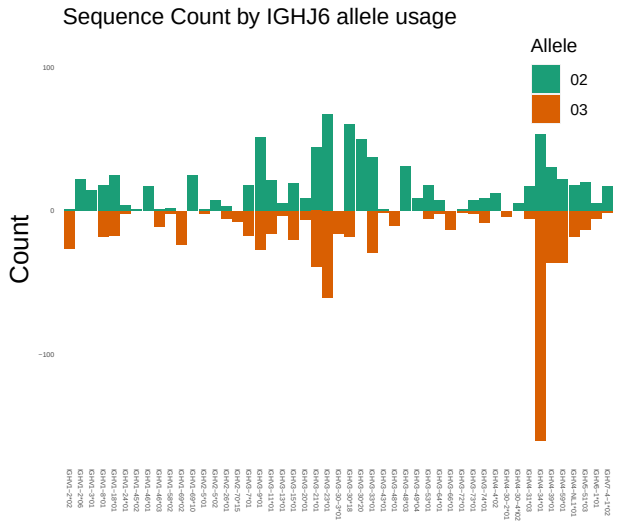

IGHV6−1*01
41 sequences assigned
18 (43.9%) exact matches, in which:
17 unique CDR3
6 unique J
Count
Nucleotide Difference


IGHV7−4−1*02
179 sequences assigned
56 (31.3%) exact matches, in which:
54 unique CDR3
6 unique J
Count
Nucleotide Difference

3 Allele usage in potential haplotype anchor genes



4 Haplotype plots



5 Configuration settings

```
## Repertoire file: /work/jenkins/PRJEB26509/S46/S46/49/49/2f/09a5f68706cd7c135f59a95901c6b0/49_Finale_
##
## Germline reference file: /work/jenkins/PRJEB26509/S46/S46/49/49/39/3c31c6a7c9e1a75369d9adb02b2a38/re
##
## Novel allele file:
##
## Species: Homosapiens
##
## Chain: IGHV
##
## Segment: V
##
## Warning   no inferred sequences found.
```