OGRDBstats Report

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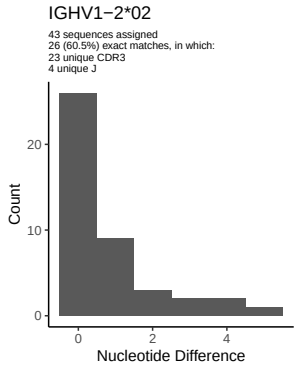
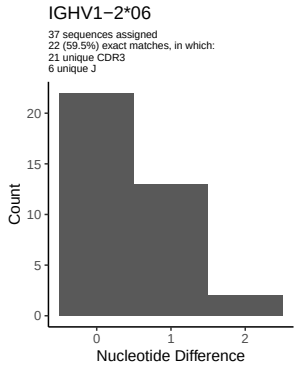
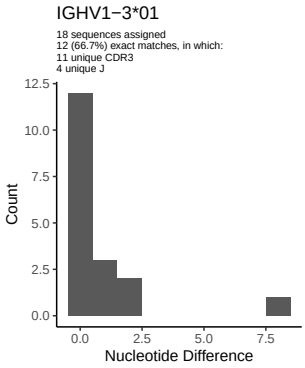
1 Novel sequence analysis

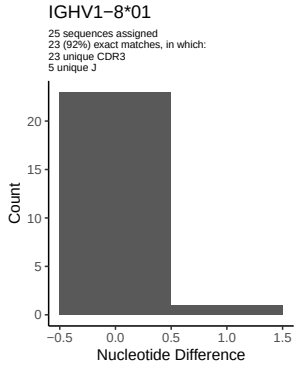
1.1 CDR3 length distribution, in assignments to novel alleles

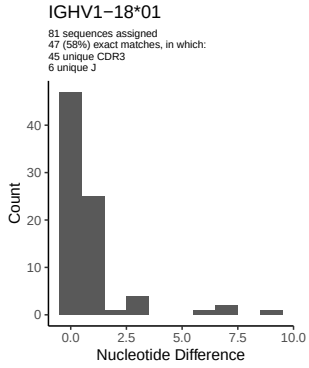
2 Variation from germline, in assignments to each allele

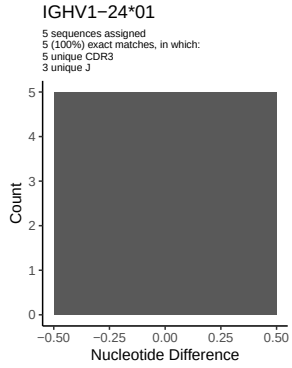


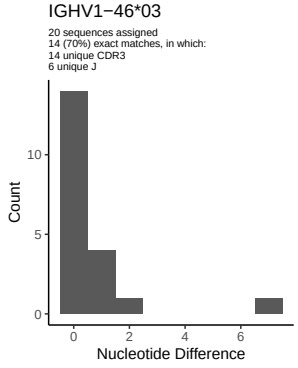


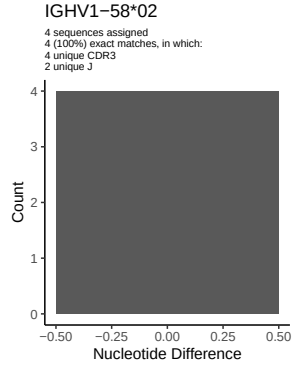


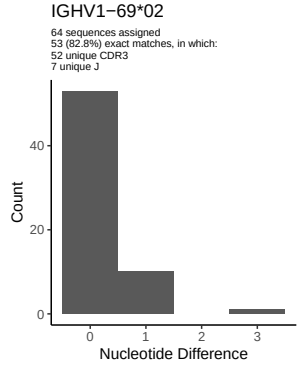


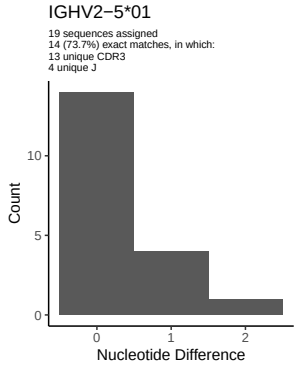


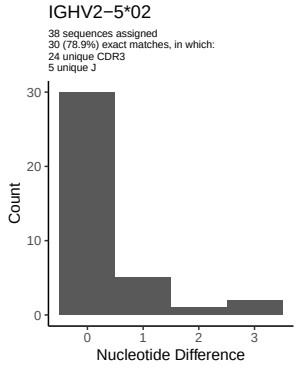


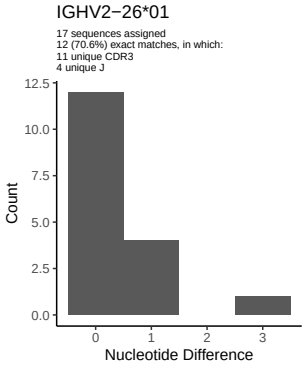


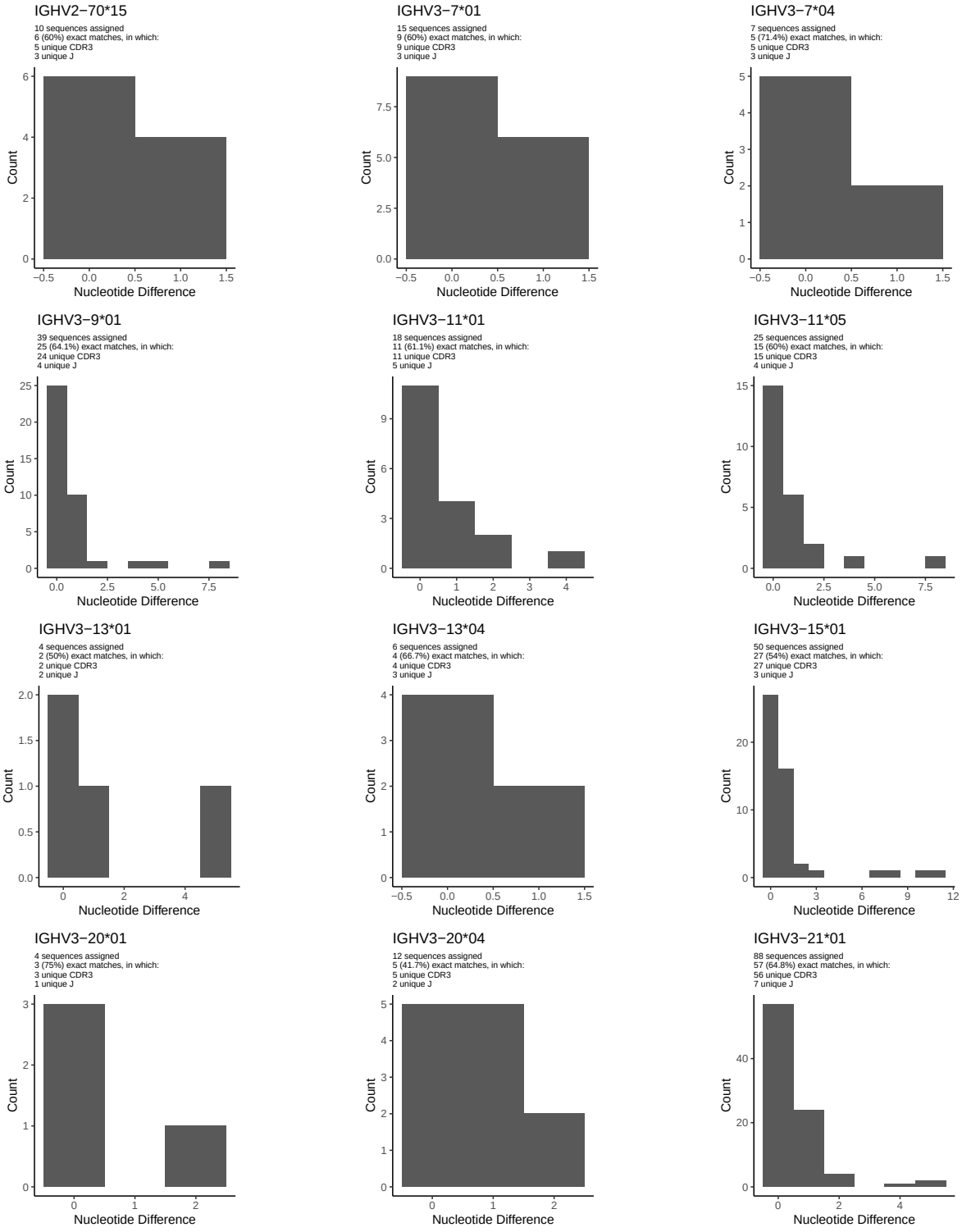


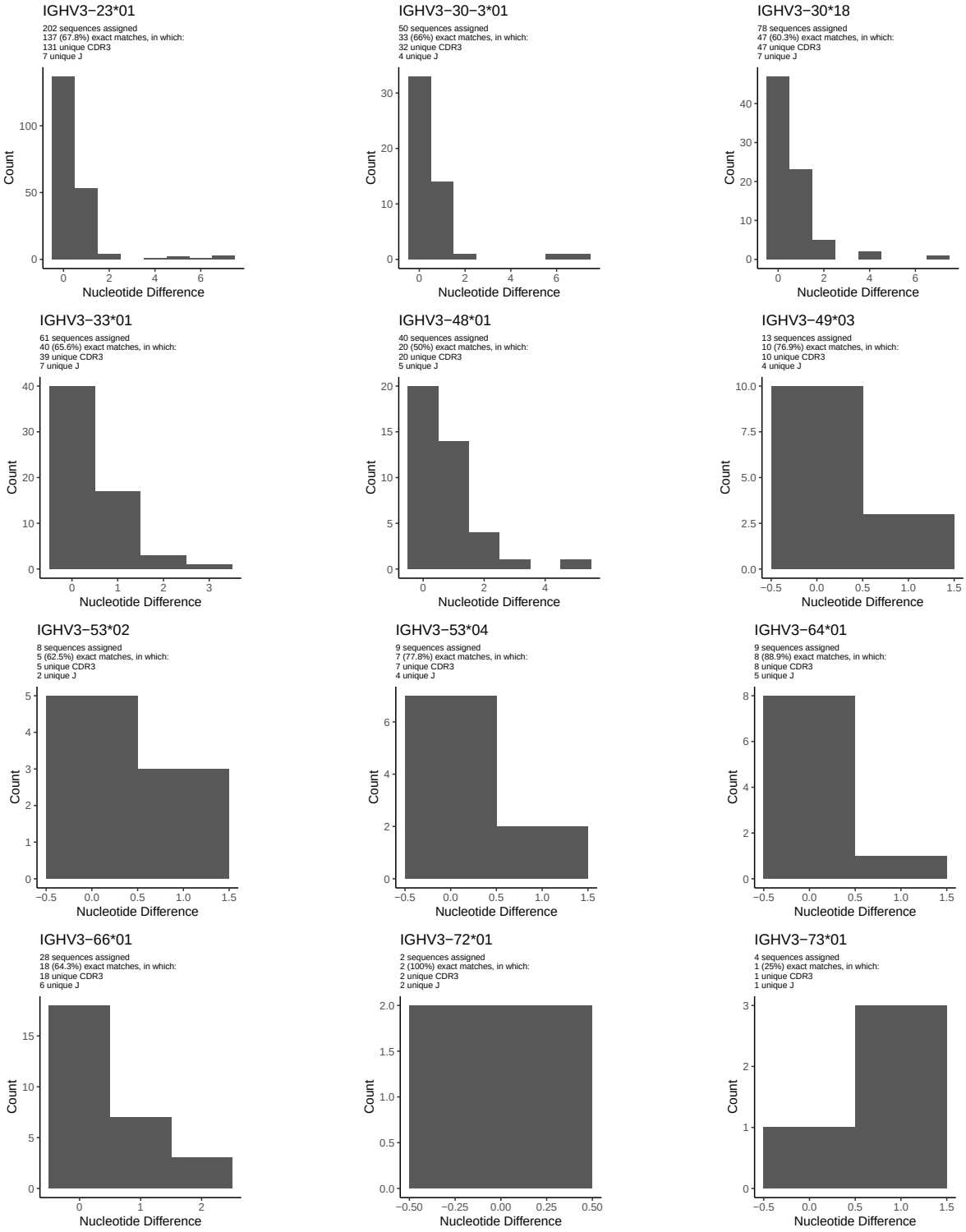


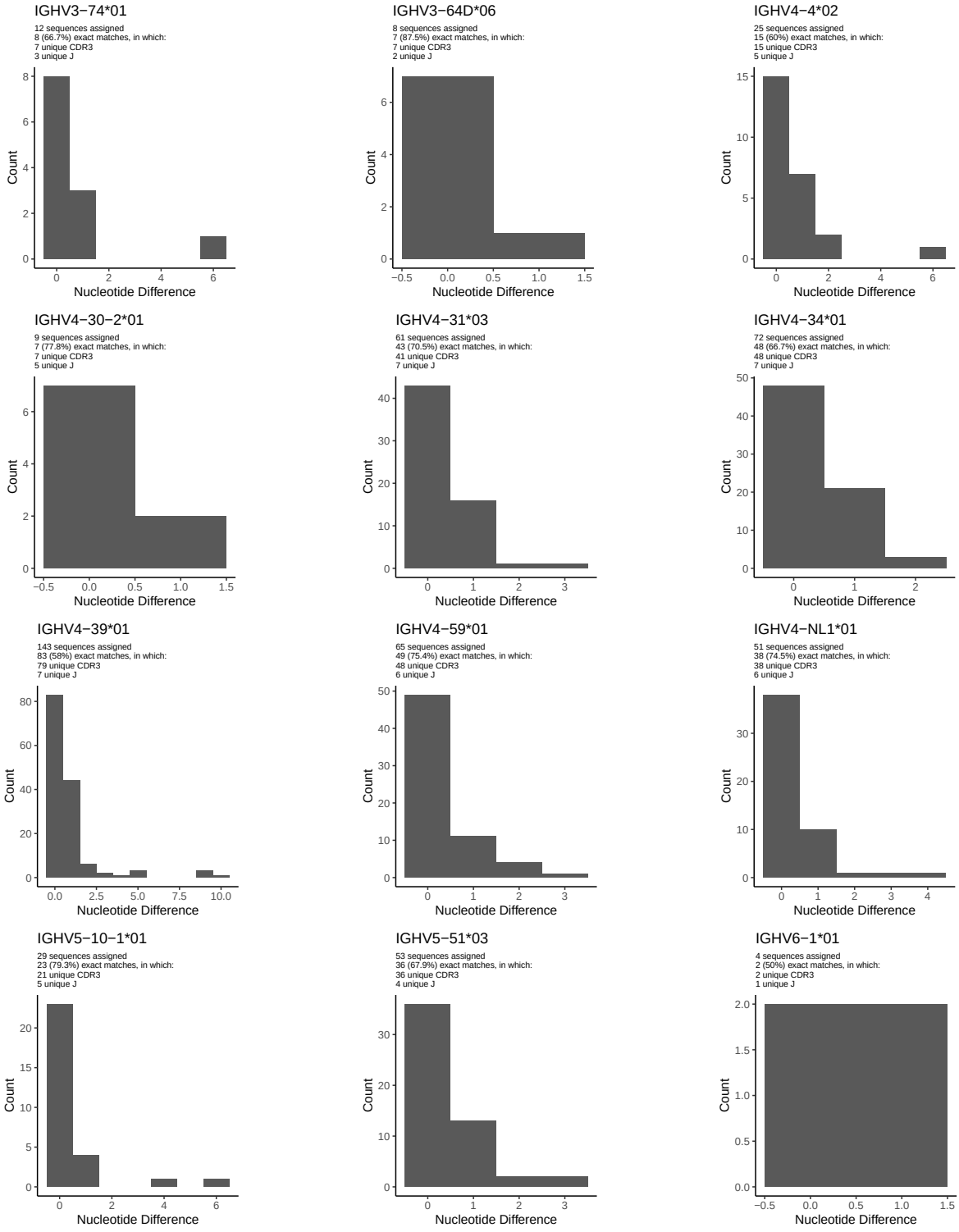


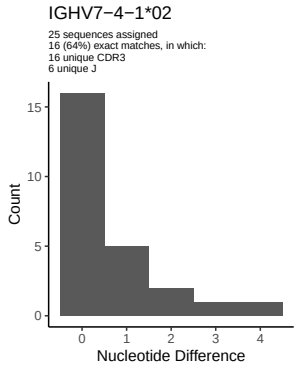




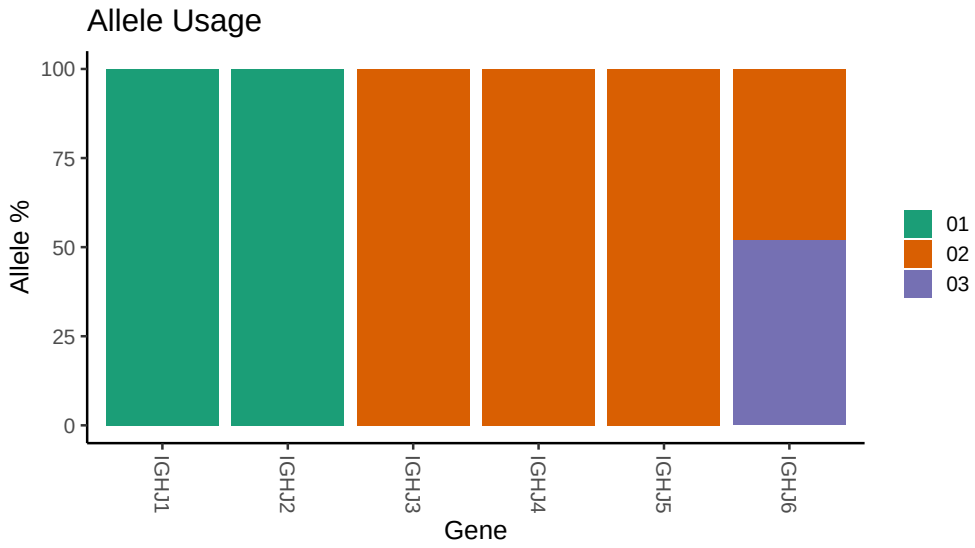

IGHV2−70*15
10 sequences assigned
6 (60%) exact matches, in which:
5 unique CDR3
3 unique J
IGHV3−7*01
15 sequences assigned
9 (60%) exact matches, in which:
9 unique CDR3
3 unique J
IGHV3−7*04
7 sequences assigned
5 (71.4%) exact matches, in which:
5 unique CDR3
3 unique J
IGHV3−9*01
39 sequences assigned
25 (64.1%) exact matches, in which:
24 unique CDR3
4 unique J
IGHV3−11*01
18 sequences assigned
11 (61.1%) exact matches, in which:
11 unique CDR3
5 unique J
IGHV3−11*05
25 sequences assigned
15 (60%) exact matches, in which:
15 unique CDR3
4 unique J
IGHV3−13*01
4 sequences assigned
2 (50%) exact matches, in which:
2 unique CDR3
2 unique J
IGHV3−13*04
6 sequences assigned
4 (66.7%) exact matches, in which:
4 unique CDR3
3 unique J
IGHV3−15*01
50 sequences assigned
27 (54%) exact matches, in which:
27 unique CDR3
3 unique J
IGHV3−20*01
4 sequences assigned
3 (75%) exact matches, in which:
3 unique CDR3
1 unique J
IGHV3−20*04
12 sequences assigned
5 (41.7%) exact matches, in which:
5 unique CDR3
2 unique J
IGHV3−21*01
88 sequences assigned
57 (64.8%) exact matches, in which:
56 unique CDR3
7 unique J
Count
Nucleotide Difference


IGHV3−23*01
202 sequences assigned
137 (67.8%) exact matches, in which:
131 unique CDR3
7 unique J
IGHV3−30−3*01
50 sequences assigned
33 (66%) exact matches, in which:
32 unique CDR3
4 unique J
IGHV3−30*18
78 sequences assigned
47 (60.3%) exact matches, in which:
47 unique CDR3
7 unique J
IGHV3−33*01
61 sequences assigned
40 (65.6%) exact matches, in which:
39 unique CDR3
7 unique J
IGHV3−48*01
40 sequences assigned
20 (50%) exact matches, in which:
20 unique CDR3
5 unique J
IGHV3−49*03
13 sequences assigned
10 (76.9%) exact matches, in which:
10 unique CDR3
4 unique J
IGHV3−53*02
8 sequences assigned
5 (62.5%) exact matches, in which:
5 unique CDR3
2 unique J
IGHV3−53*04
9 sequences assigned
7 (77.8%) exact matches, in which:
7 unique CDR3
4 unique J
IGHV3−64*01
9 sequences assigned
8 (88.9%) exact matches, in which:
8 unique CDR3
5 unique J
IGHV3−66*01
28 sequences assigned
18 (64.3%) exact matches, in which:
18 unique CDR3
6 unique J
IGHV3−72*01
2 sequences assigned
2 (100%) exact matches, in which:
2 unique CDR3
2 unique J
IGHV3−73*01
4 sequences assigned
1 (25%) exact matches, in which:
1 unique CDR3
1 unique J
Count
Nucleotide Difference

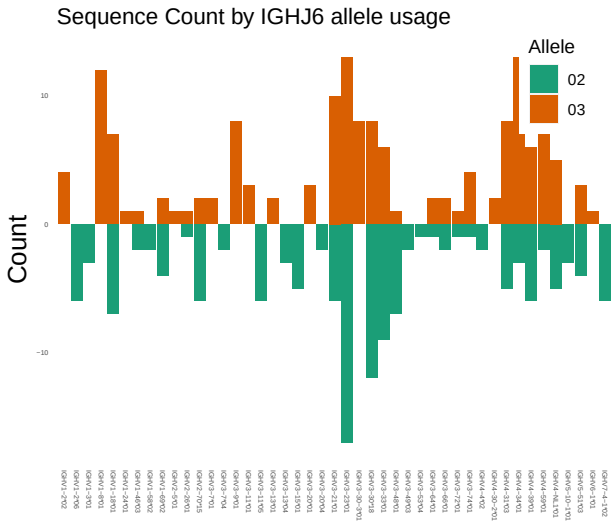

IGHV3−74*01
12 sequences assigned
8 (66.7%) exact matches, in which:
7 unique CDR3
3 unique J
IGHV3−64D*06
8 sequences assigned
7 (87.5%) exact matches, in which:
7 unique CDR3
2 unique J
IGHV4−4*02
25 sequences assigned
15 (60%) exact matches, in which:
15 unique CDR3
5 unique J
IGHV4−30−2*01
9 sequences assigned
7 (77.8%) exact matches, in which:
7 unique CDR3
5 unique J
IGHV4−31*03
61 sequences assigned
43 (70.5%) exact matches, in which:
41 unique CDR3
7 unique J
IGHV4−34*01
72 sequences assigned
48 (66.7%) exact matches, in which:
48 unique CDR3
7 unique J
IGHV4−39*01
143 sequences assigned
83 (58%) exact matches, in which:
79 unique CDR3
7 unique J
IGHV4−59*01
65 sequences assigned
49 (75.4%) exact matches, in which:
48 unique CDR3
6 unique J
IGHV4−NL1*01
51 sequences assigned
38 (74.5%) exact matches, in which:
38 unique CDR3
6 unique J
IGHV5−10−1*01
29 sequences assigned
23 (79.3%) exact matches, in which:
21 unique CDR3
5 unique J
IGHV5−51*03
53 sequences assigned
36 (67.9%) exact matches, in which:
36 unique CDR3
4 unique J
IGHV6−1*01
4 sequences assigned
2 (50%) exact matches, in which:
2 unique CDR3
1 unique J
Count
Nucleotide Difference


IGHV7−4−1*02
25 sequences assigned
16 (64%) exact matches, in which:
16 unique CDR3
6 unique J
Count
15
10
5
0
0
1
2
3
4
Nucleotide Difference

3 Allele usage in potential haplotype anchor genes



4 Haplotype plots



5 Configuration settings

```
## Repertoire file: /misc/work/jenkins/PRJEB26509/S99/S99/61/61/5d/55ebcf733adaa5c754a83660af7ac3/61_Fi
##
## Germline reference file: /misc/work/jenkins/PRJEB26509/S99/S99/61/61/3e/31a307702d3f7a014a58965499ff
##
## Novel allele file:
##
## Species: Homosapiens
##
## Chain: IGHV
##
## Segment: V
##
## Warning   no inferred sequences found.
```