OGRDBstats Report

Contents

1 Novel sequence analysis **2**
1.1 CDR3 length distribution, in assignments to novel alleles 2

2 Variation from germline, in assignments to each allele **3**

3 Allele usage in potential haplotype anchor genes **8**

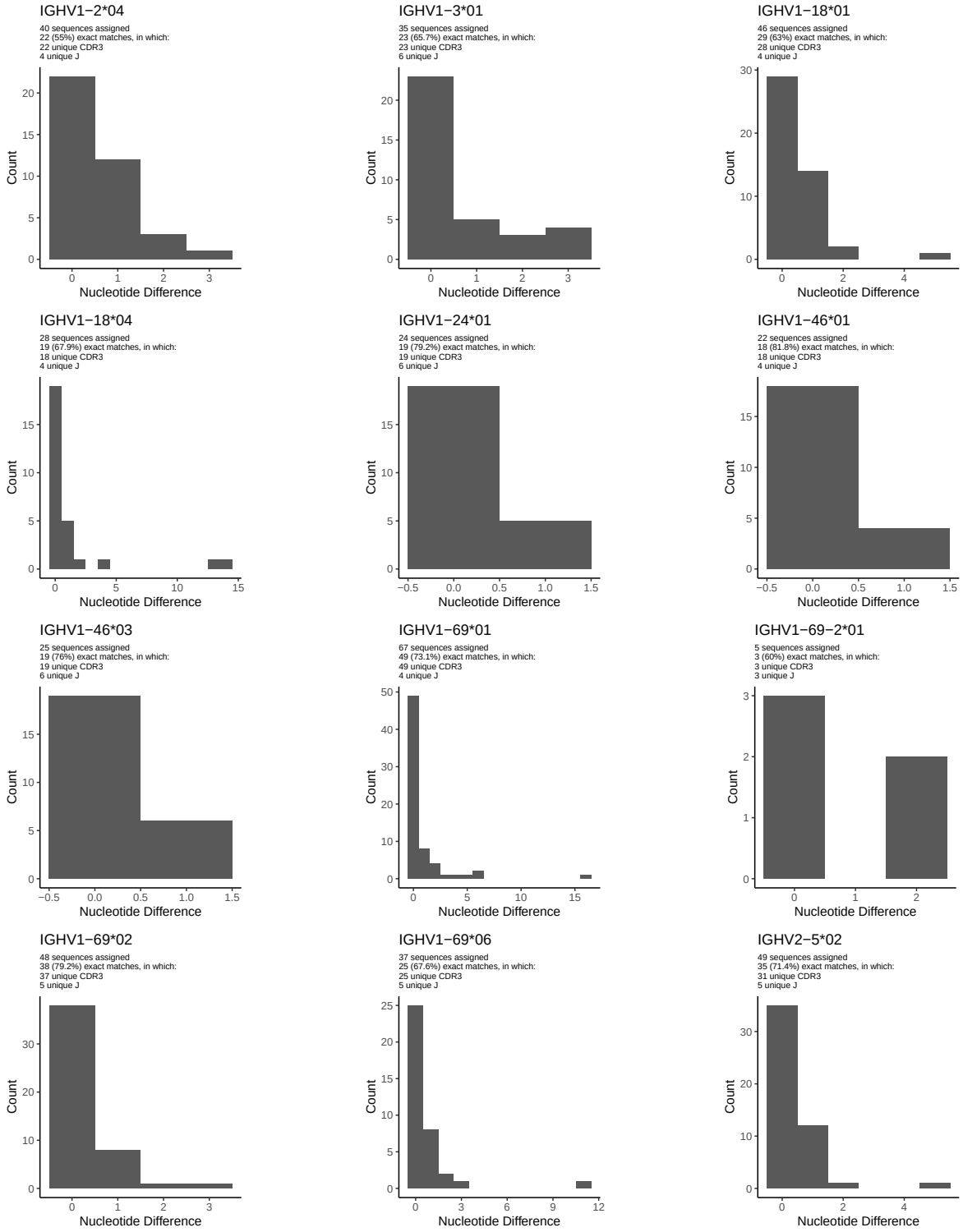
4 Haplotype plots **9**

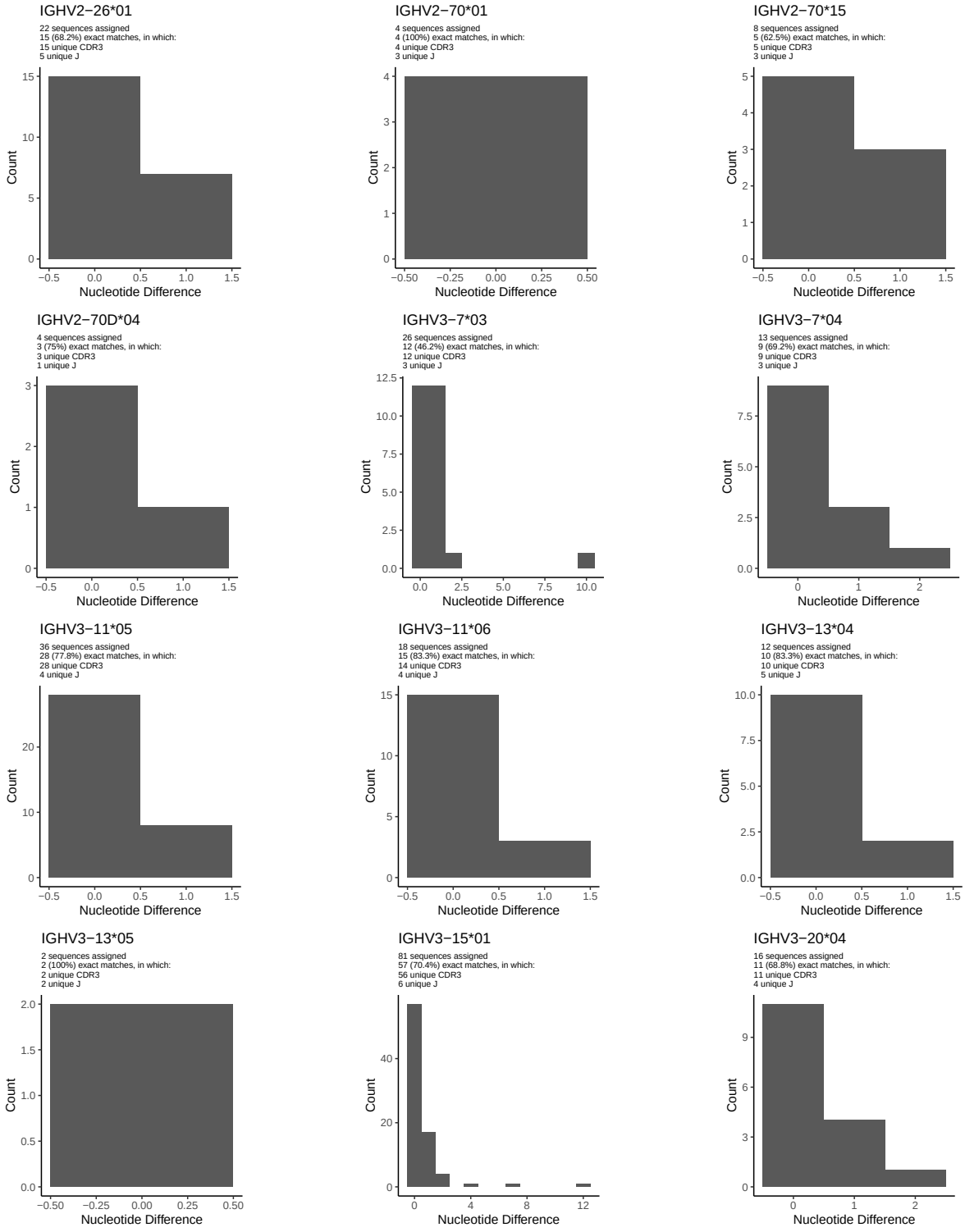
5 Configuration settings **10**

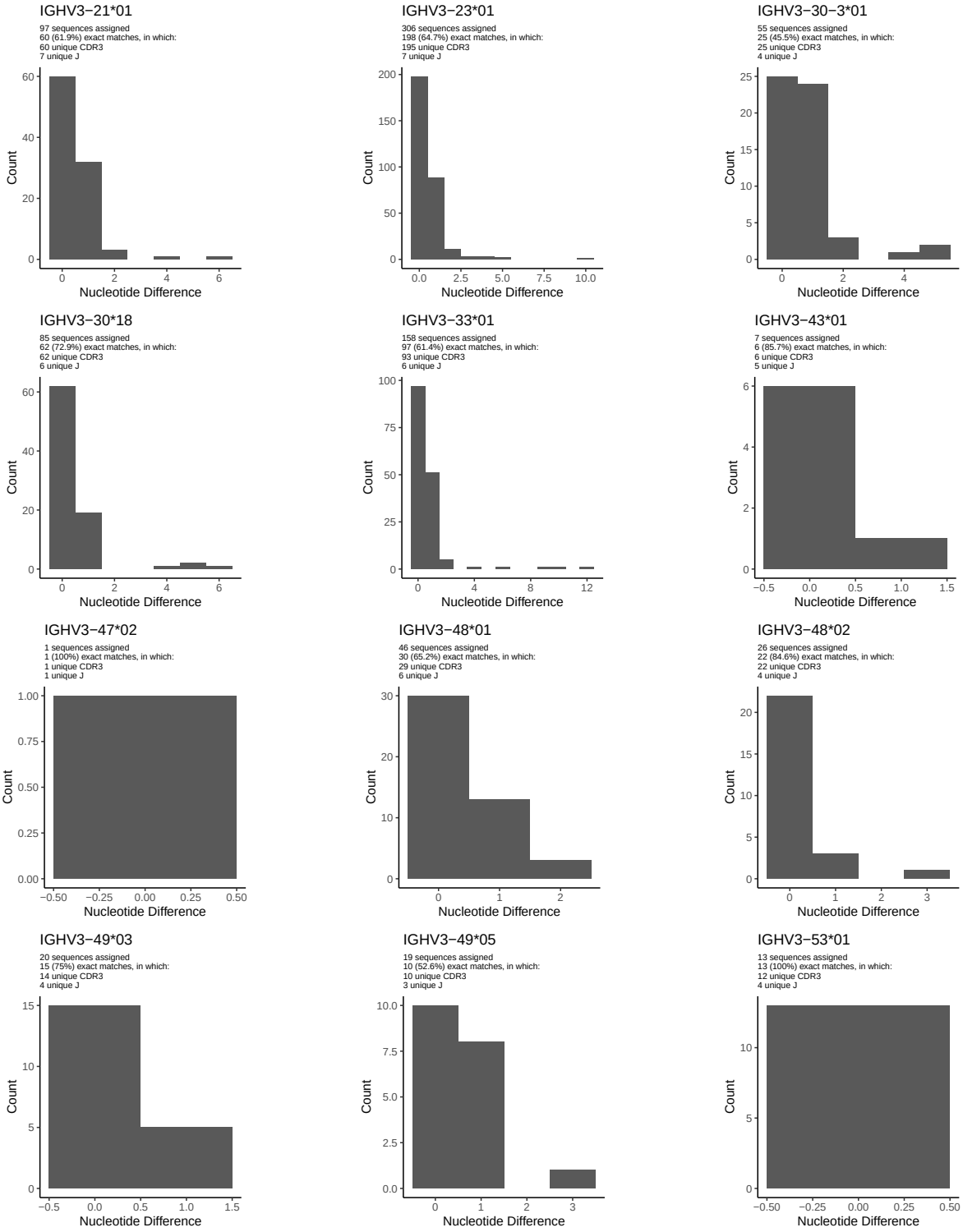
1 Novel sequence analysis

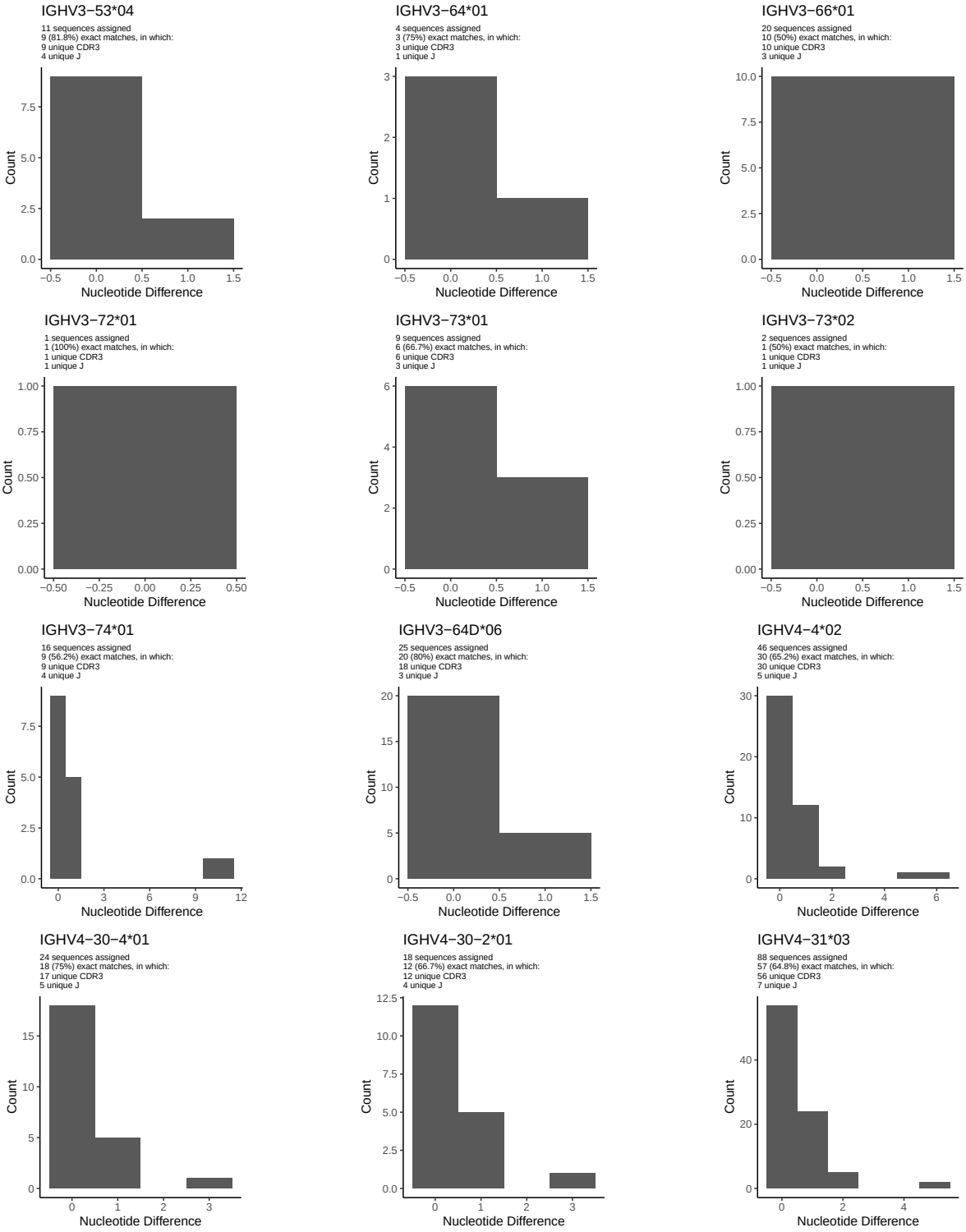
1.1 CDR3 length distribution, in assignments to novel alleles

2 Variation from germline, in assignments to each allele



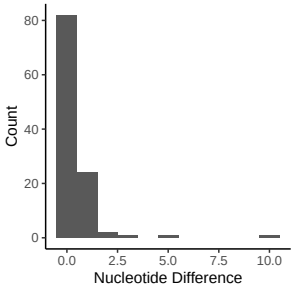

IGHV2−26*01
22 sequences assigned
15 (68.2%) exact matches, in which:
15 unique CDR3
5 unique J
IGHV2−70*01
4 sequences assigned
4 (100%) exact matches, in which:
4 unique CDR3
3 unique J
IGHV2−70*15
8 sequences assigned
5 (62.5%) exact matches, in which:
5 unique CDR3
3 unique J
IGHV2−70D*04
4 sequences assigned
3 (75%) exact matches, in which:
3 unique CDR3
1 unique J
IGHV3−7*03
26 sequences assigned
12 (46.2%) exact matches, in which:
12 unique CDR3
3 unique J
IGHV3−7*04
13 sequences assigned
9 (69.2%) exact matches, in which:
9 unique CDR3
3 unique J
IGHV3−11*05
36 sequences assigned
28 (77.8%) exact matches, in which:
28 unique CDR3
4 unique J
IGHV3−11*06
18 sequences assigned
15 (83.3%) exact matches, in which:
14 unique CDR3
4 unique J
IGHV3−13*04
12 sequences assigned
10 (83.3%) exact matches, in which:
10 unique CDR3
5 unique J
IGHV3−13*05
2 sequences assigned
2 (100%) exact matches, in which:
2 unique CDR3
2 unique J
IGHV3−15*01
81 sequences assigned
57 (70.4%) exact matches, in which:
56 unique CDR3
6 unique J
IGHV3−20*04
16 sequences assigned
11 (68.8%) exact matches, in which:
11 unique CDR3
4 unique J
Count
Nucleotide Difference


IGHV3−21*01
97 sequences assigned
60 (61.9%) exact matches, in which:
60 unique CDR3
7 unique J
IGHV3−23*01
306 sequences assigned
198 (64.7%) exact matches, in which:
195 unique CDR3
7 unique J
IGHV3−30−3*01
55 sequences assigned
25 (45.5%) exact matches, in which:
25 unique CDR3
4 unique J
IGHV3−30*18
85 sequences assigned
62 (72.9%) exact matches, in which:
62 unique CDR3
6 unique J
IGHV3−33*01
158 sequences assigned
97 (61.4%) exact matches, in which:
93 unique CDR3
6 unique J
IGHV3−43*01
7 sequences assigned
6 (85.7%) exact matches, in which:
6 unique CDR3
5 unique J
IGHV3−47*02
1 sequences assigned
1 (100%) exact matches, in which:
1 unique CDR3
1 unique J
IGHV3−48*01
46 sequences assigned
30 (65.2%) exact matches, in which:
29 unique CDR3
6 unique J
IGHV3−48*02
26 sequences assigned
22 (84.6%) exact matches, in which:
22 unique CDR3
4 unique J
IGHV3−49*03
20 sequences assigned
15 (75%) exact matches, in which:
14 unique CDR3
4 unique J
IGHV3−49*05
19 sequences assigned
10 (52.6%) exact matches, in which:
10 unique CDR3
3 unique J
IGHV3−53*01
13 sequences assigned
13 (100%) exact matches, in which:
12 unique CDR3
4 unique J
Count
Nucleotide Difference


IGHV3−53*04
11 sequences assigned
9 (81.8%) exact matches, in which:
9 unique CDR3
4 unique J
IGHV3−64*01
4 sequences assigned
3 (75%) exact matches, in which:
3 unique CDR3
1 unique J
IGHV3−66*01
20 sequences assigned
10 (50%) exact matches, in which:
10 unique CDR3
3 unique J
IGHV3−72*01
1 sequences assigned
1 (100%) exact matches, in which:
1 unique CDR3
1 unique J
IGHV3−73*01
9 sequences assigned
6 (66.7%) exact matches, in which:
6 unique CDR3
3 unique J
IGHV3−73*02
2 sequences assigned
1 (50%) exact matches, in which:
1 unique CDR3
1 unique J
IGHV3−74*01
16 sequences assigned
9 (56.2%) exact matches, in which:
9 unique CDR3
4 unique J
IGHV3−64D*06
25 sequences assigned
20 (80%) exact matches, in which:
18 unique CDR3
3 unique J
IGHV4−4*02
46 sequences assigned
30 (65.2%) exact matches, in which:
30 unique CDR3
5 unique J
IGHV4−30−4*01
24 sequences assigned
18 (75%) exact matches, in which:
17 unique CDR3
5 unique J
IGHV4−30−2*01
18 sequences assigned
12 (66.7%) exact matches, in which:
12 unique CDR3
4 unique J
IGHV4−31*03
88 sequences assigned
57 (64.8%) exact matches, in which:
56 unique CDR3
7 unique J
Count
Nucleotide Difference

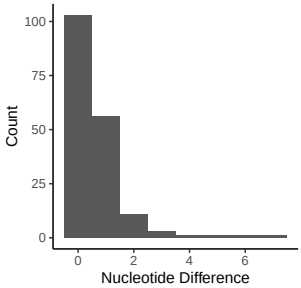
IGHV4−34*01

112 sequences assigned
82 (73.2%) exact matches, in which:
78 unique CDR3
6 unique J



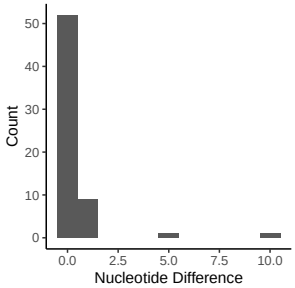
IGHV4−39*01

177 sequences assigned
103 (58.2%) exact matches, in which:
102 unique CDR3
7 unique J



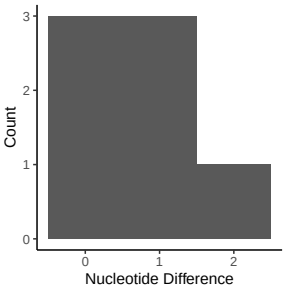
IGHV4−59*01

63 sequences assigned
52 (82.5%) exact matches, in which:
50 unique CDR3
6 unique J



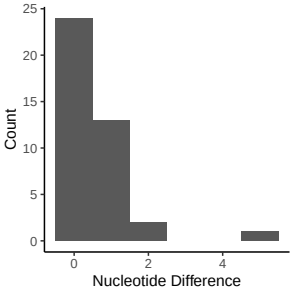
IGHV4−61*01

7 sequences assigned
3 (42.9%) exact matches, in which:
3 unique CDR3
3 unique J



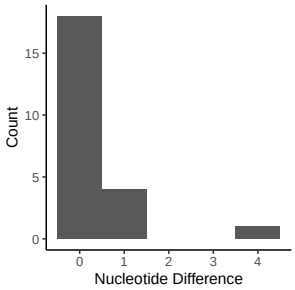
IGHV4−NL1*01

40 sequences assigned
24 (60%) exact matches, in which:
23 unique CDR3
5 unique J



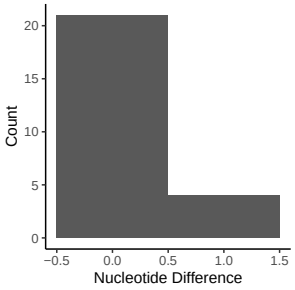
IGHV5−10−1*01

23 sequences assigned
18 (78.3%) exact matches, in which:
18 unique CDR3
4 unique J



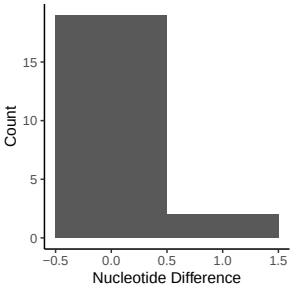
IGHV5−10−1*03

25 sequences assigned
21 (84%) exact matches, in which:
21 unique CDR3
6 unique J



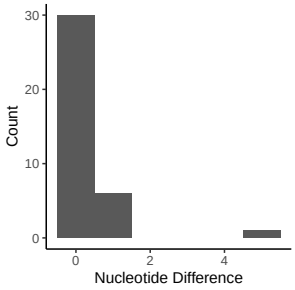
IGHV5−51*01

21 sequences assigned
19 (90.5%) exact matches, in which:
18 unique CDR3
4 unique J



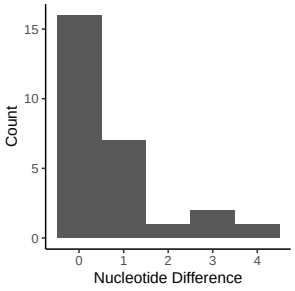
IGHV5−51*03

37 sequences assigned
30 (81.1%) exact matches, in which:
29 unique CDR3
5 unique J



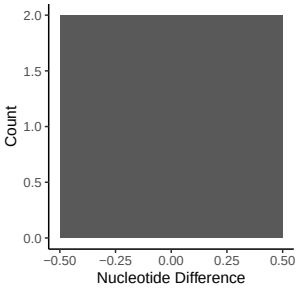
IGHV6−1*01

27 sequences assigned
16 (59.3%) exact matches, in which:
15 unique CDR3
6 unique J

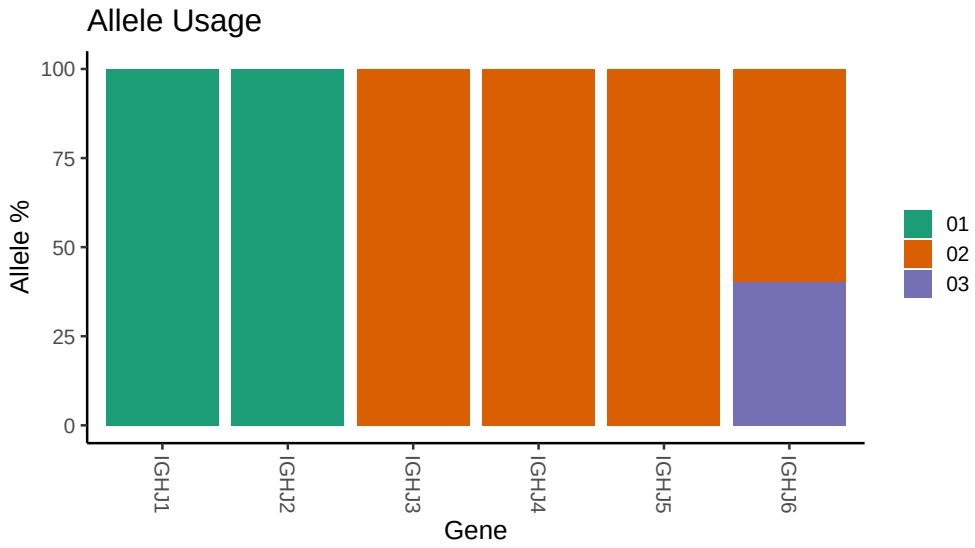


IGHV7−4−1*01

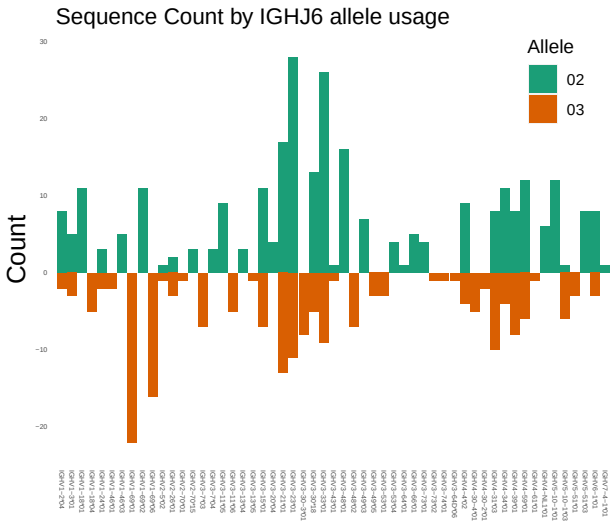
2 sequences assigned
2 (100%) exact matches, in which:
2 unique CDR3
2 unique J



3 Allele usage in potential haplotype anchor genes



4 Haplotype plots



5 Configuration settings

```
## Repertoire file: /misc/work/jenkins/PRJEB26509/S97/S97/33/33/0e/d1824e0b11116c74224e40fa61bc33/33_Fi
##
## Germline reference file: /misc/work/jenkins/PRJEB26509/S97/S97/33/33/eb/463d1d9cd5f0a1b4170c3e0c3476
##
## Novel allele file:
##
## Species: Homosapiens
##
## Chain: IGHV
##
## Segment: V
##
## Warning   no inferred sequences found.
```