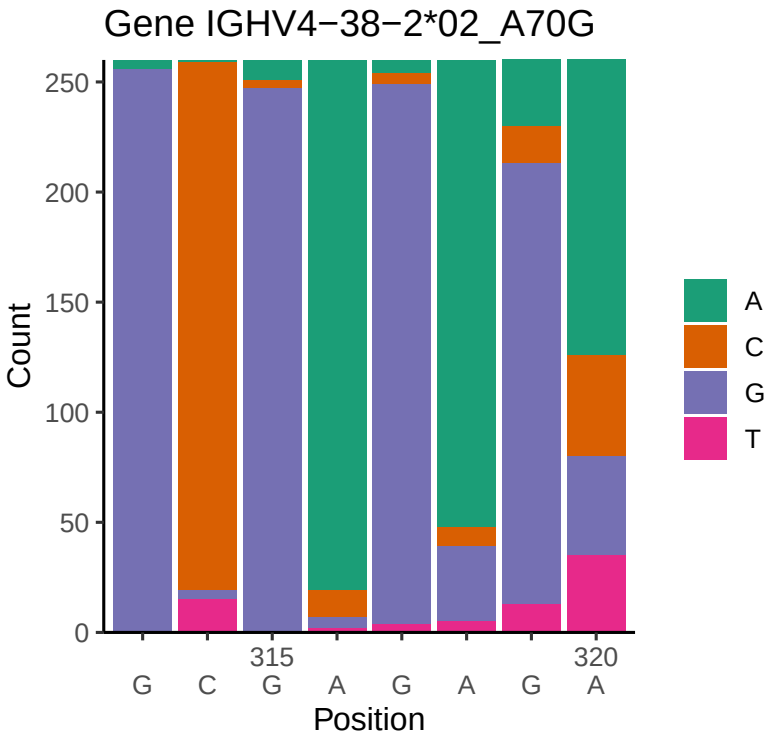
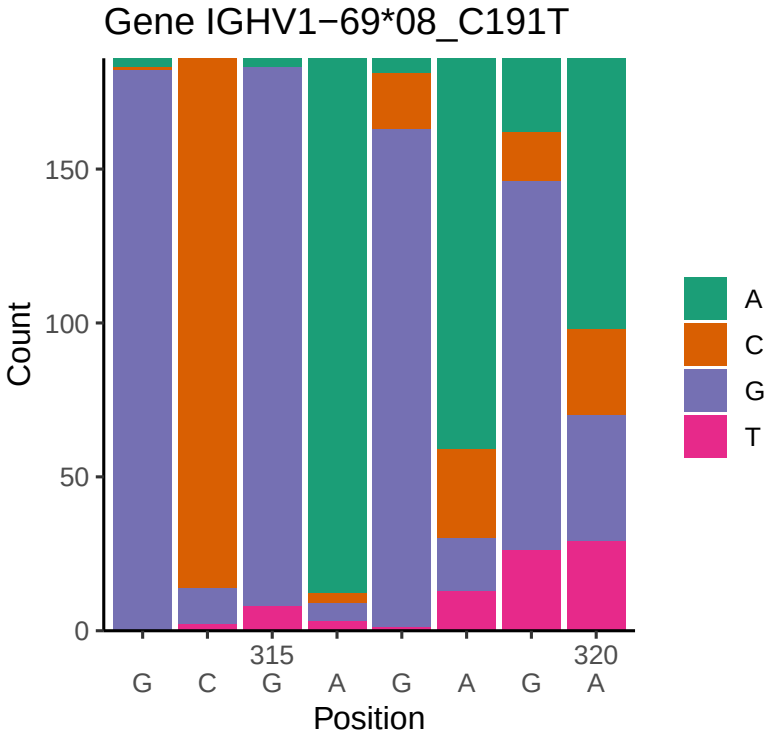
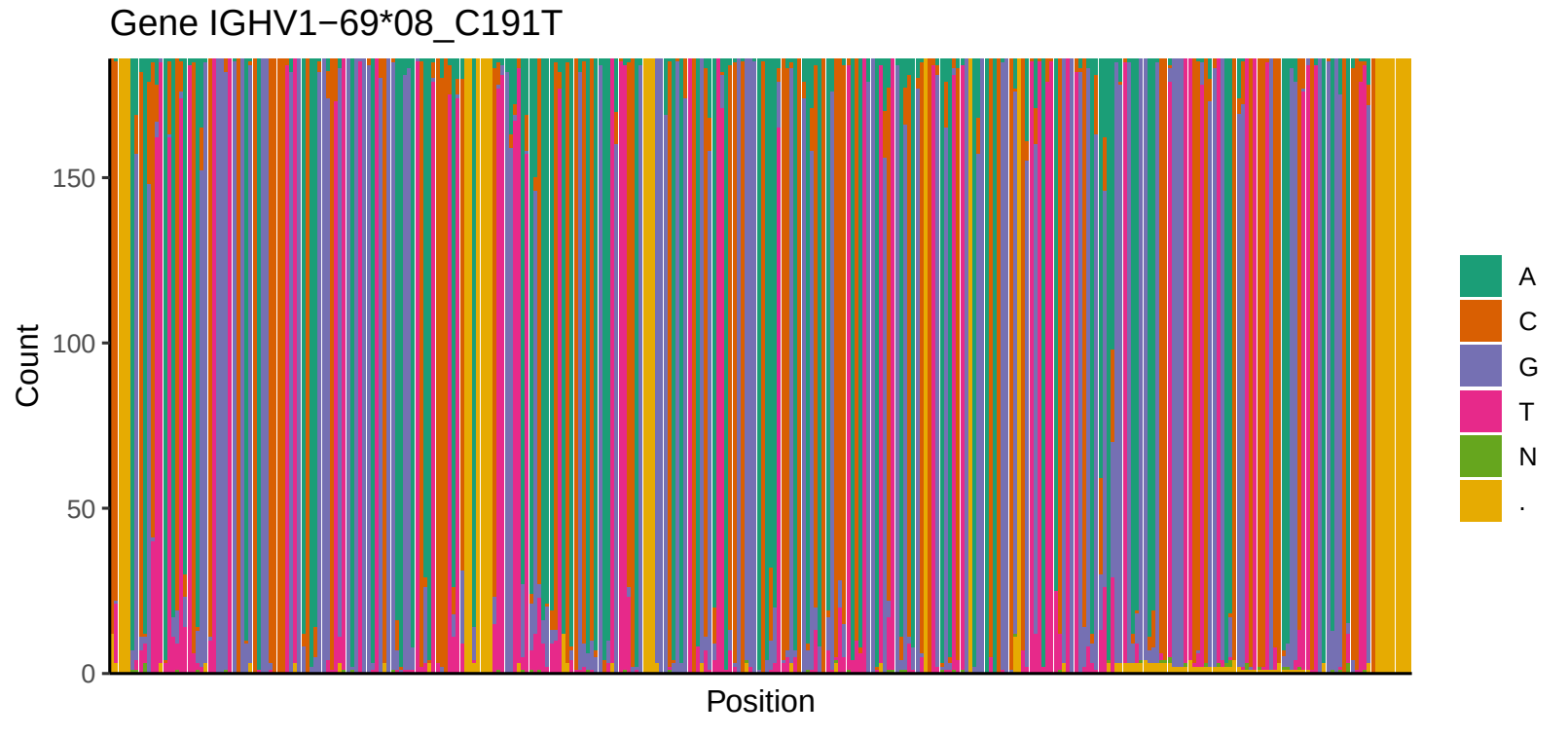
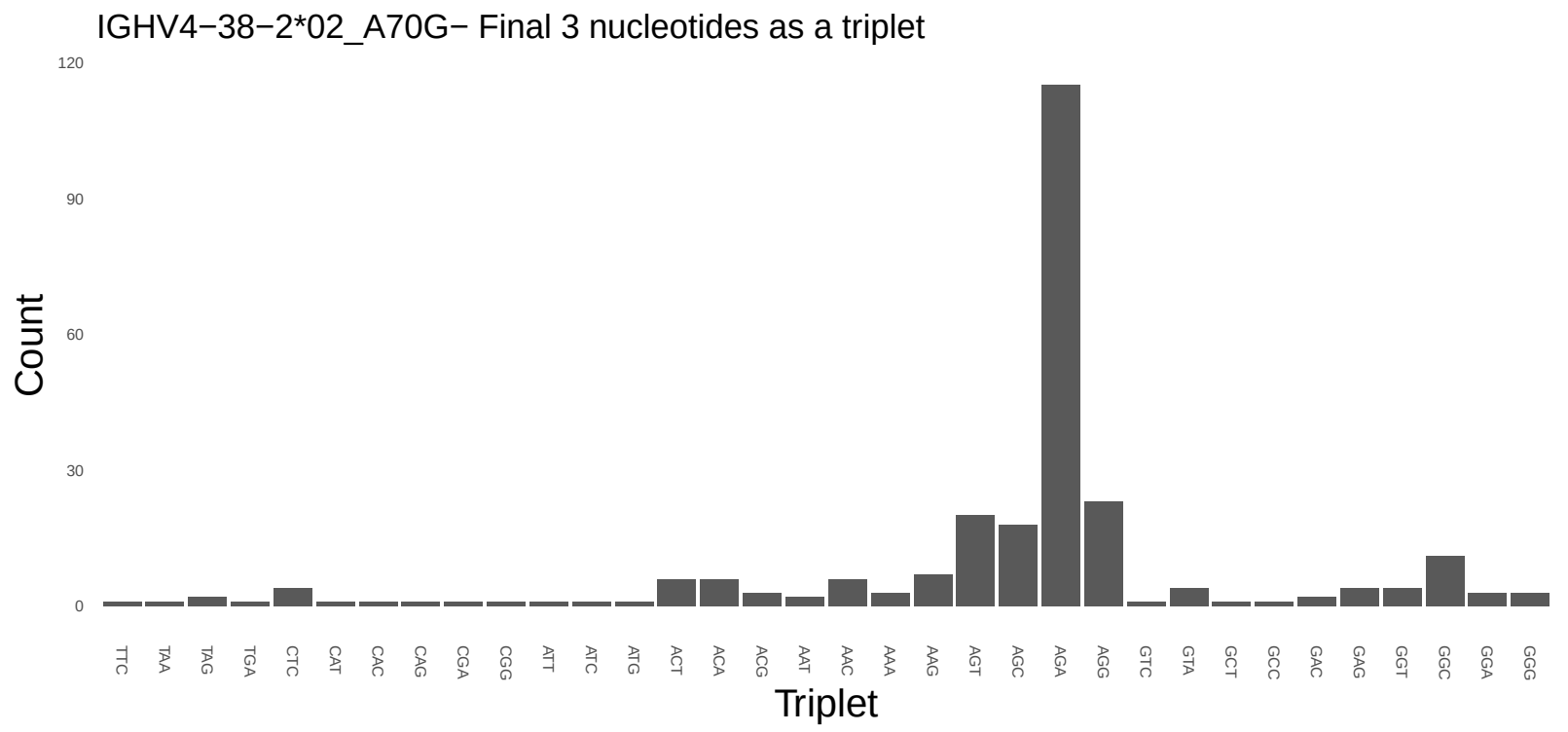
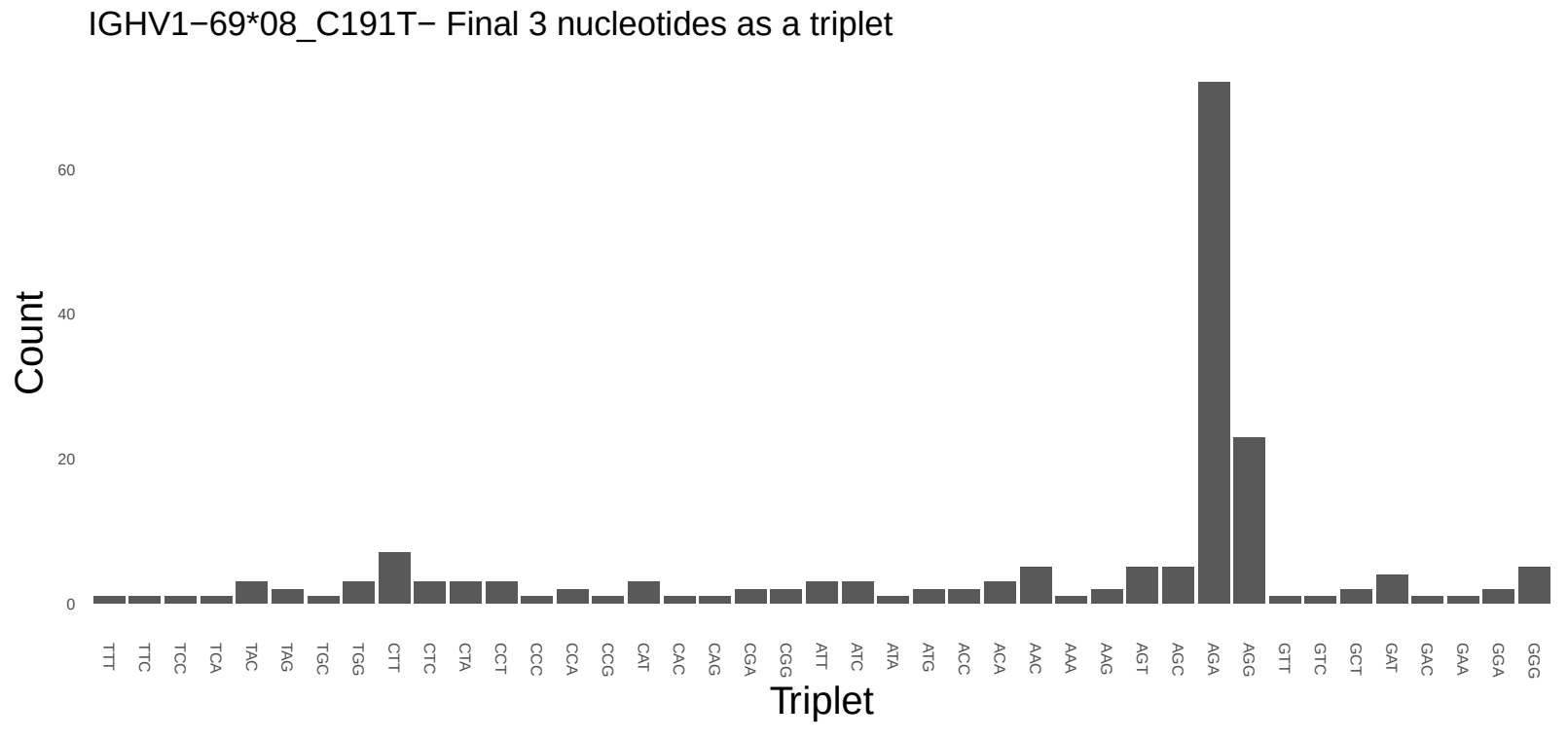

Gene IGHV4−38−2*02_A70G
Count
250
200
150
100
50
0
315
320
G C G A G A G A
Position
A
C
G
T


Gene IGHV1−69*08_C191T
Count
150
100
50
0
315
320
G C G A G A G A
Position
A
C
G
T

Gene IGHV4−38−2*02_A70G
Count
250
200
150
100
50
0
Position
A
C
G
T
N
.

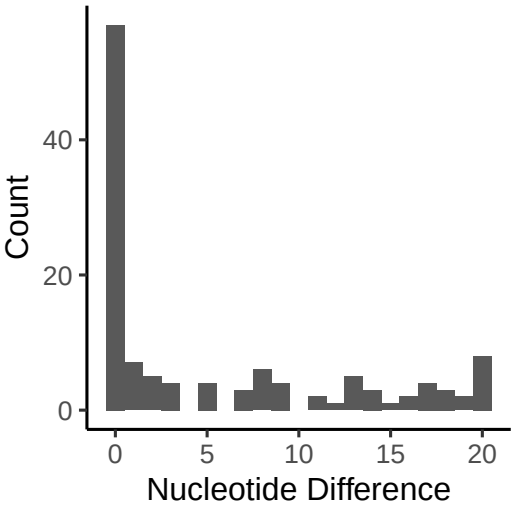

Gene IGHV1−69*08_C191T
Count
150
100
50
0
Position
A
C
G
T
N
.


IGHV4−38−2*02_A70G− Final 3 nucleotides as a triplet
Count
120
90
60
30
0
TTC TAA TAG TGA CTC CAT CAC CAG CGA CGG ATT ATC ATG ACT ACA ACG AAT AAC AAA AAG AGT AGC AGA AGG GTC GTA GCT GCC GAC GAG GGT GGC GGA GGG
Triplet


IGHV1−69*08_C191T− Final 3 nucleotides as a triplet
Count
60
40
20
0
TTT TTC TCC TCA TAC TAG TGC TGG CTT CTC CTA CCT CCC CCA CCG CAT CAC CAG CGA CGG ATT ATC ATA ATG ACC ACA AAC AAA AAG AGT AGC AGA AGG GTT GTC GCT GAT GAC GAA GGA GGG
Triplet

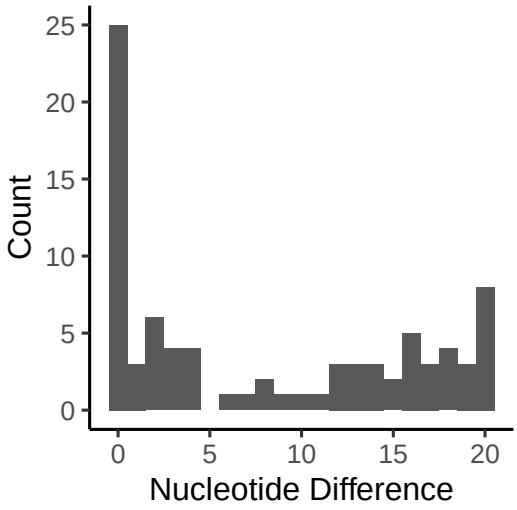
IGHV1−2*04

135 sequences assigned
57 (42.2%) exact matches, in which:
57 unique CDR3
7 unique J



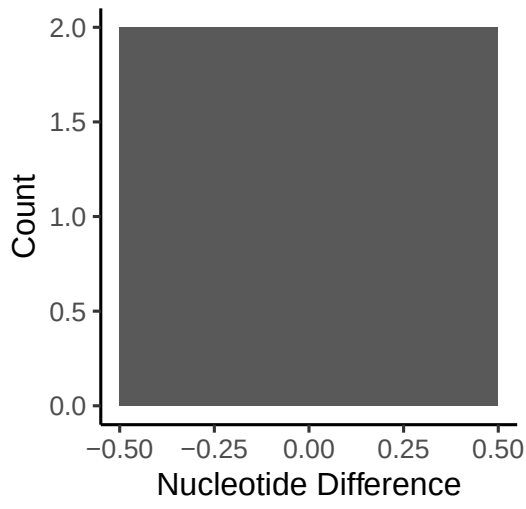
IGHV1−18*04

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



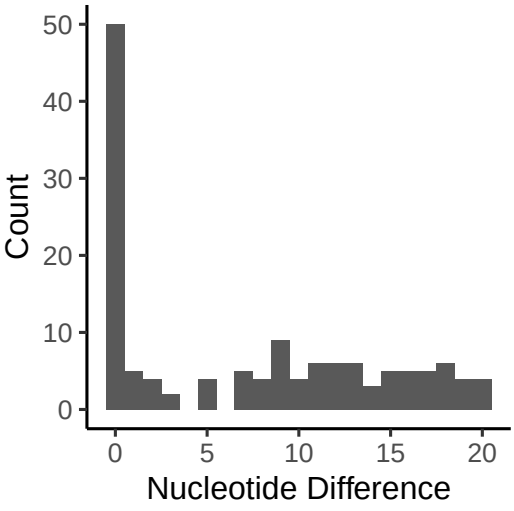
IGHV1−58*01

3 sequences assigned
2 (66.7%) exact matches, in which:
2 unique CDR3
1 unique J



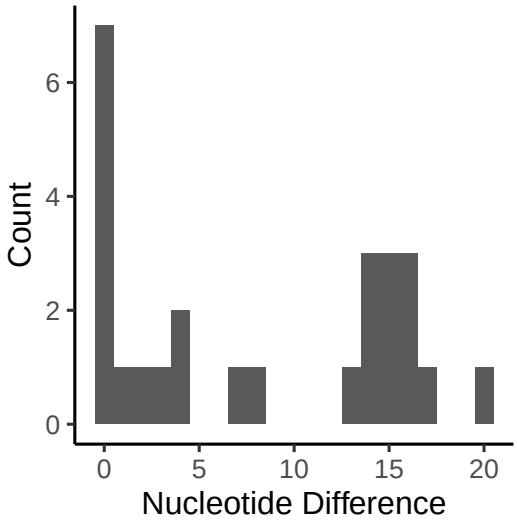
IGHV1−3*01

174 sequences assigned
50 (28.7%) exact matches, in which:
50 unique CDR3
6 unique J



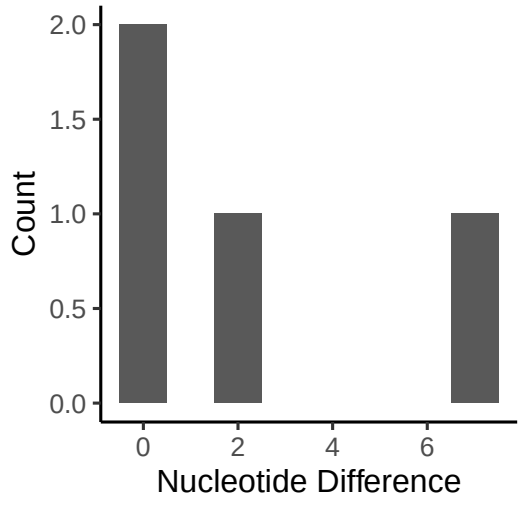
IGHV1−24*01

29 sequences assigned
7 (24.1%) exact matches, in which:
7 unique CDR3
2 unique J



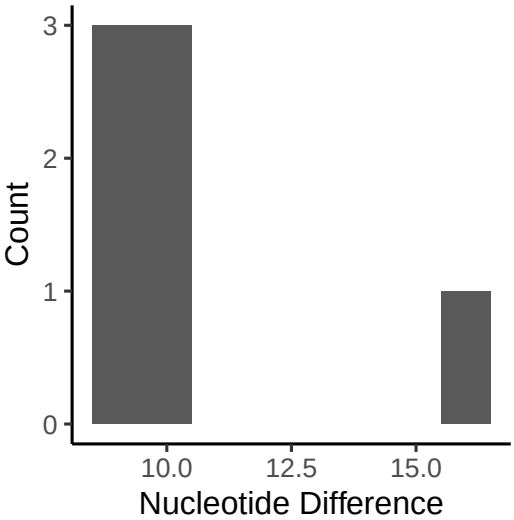
IGHV1−58*02

5 sequences assigned
2 (40%) exact matches, in which:
2 unique CDR3
2 unique J



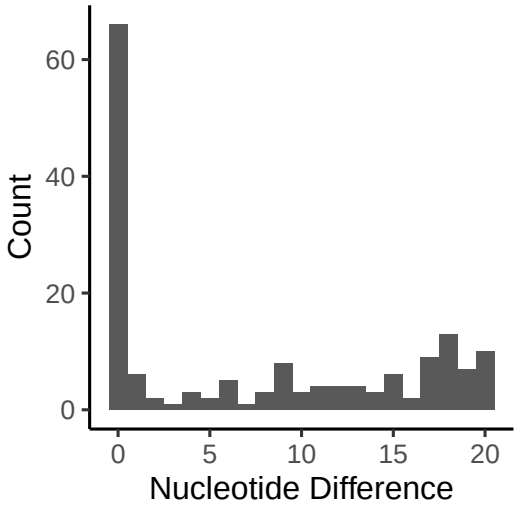
IGHV1−18*01

27 sequences assigned
No exact matches.



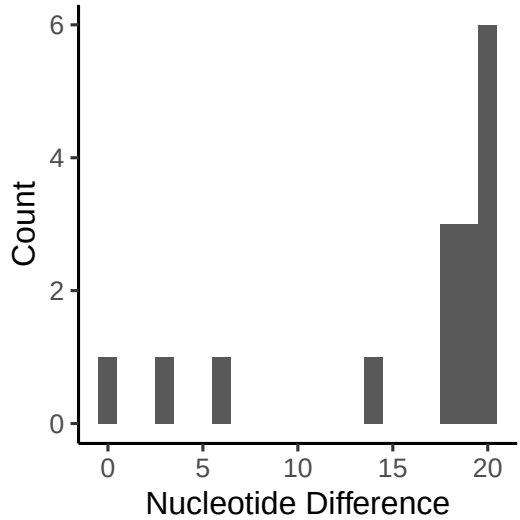
IGHV1−46*01

206 sequences assigned
66 (32%) exact matches, in which:
66 unique CDR3
6 unique J



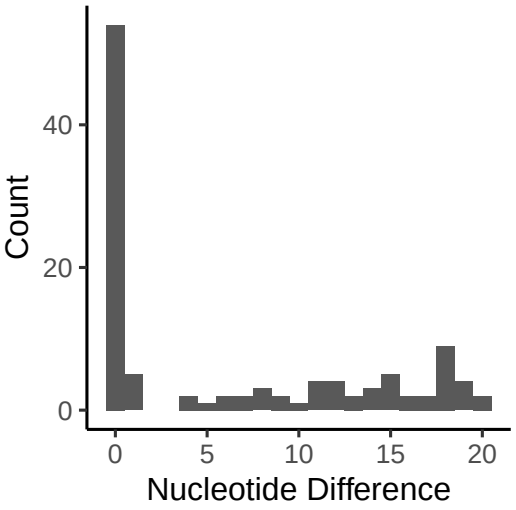
IGHV1−69−2*01

21 sequences assigned
1 (4.8%) exact matches, in which:
1 unique CDR3
1 unique J



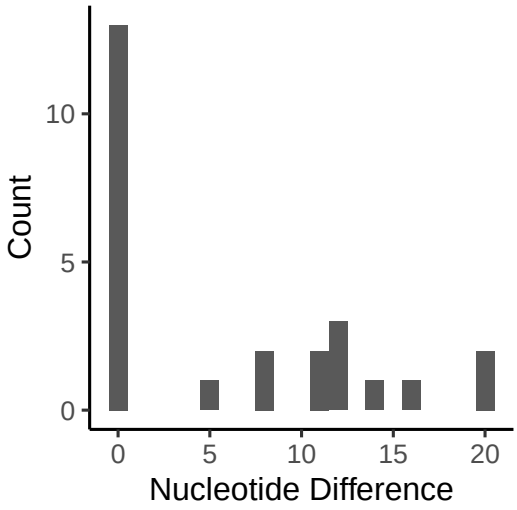
IGHV1−69*06

148 sequences assigned
54 (36.5%) exact matches, in which:
54 unique CDR3
5 unique J



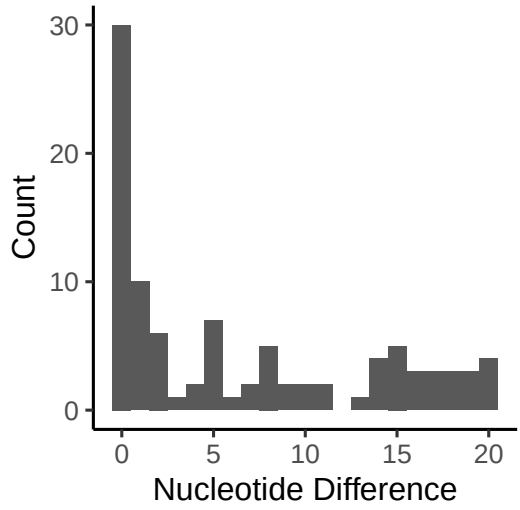
IGHV2−26*01

27 sequences assigned
13 (48.1%) exact matches, in which:
12 unique CDR3
5 unique J



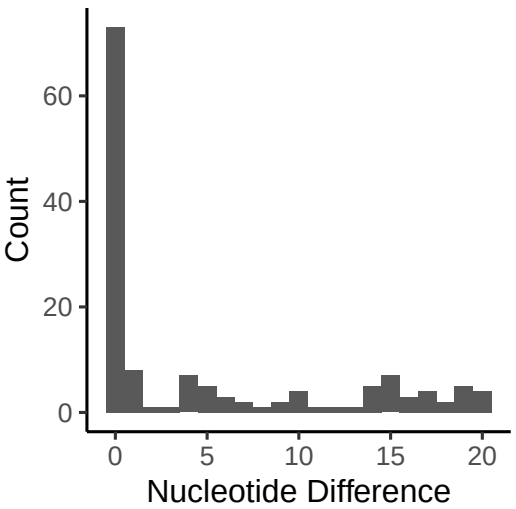
IGHV3−11*06

112 sequences assigned
30 (26.8%) exact matches, in which:
29 unique CDR3
5 unique J



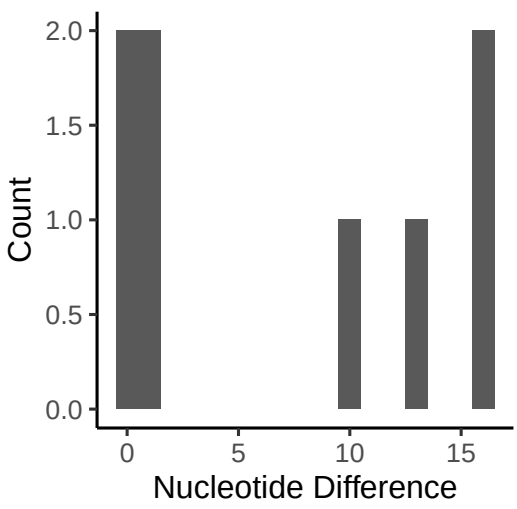
IGHV1−69*08_C191T

186 sequences assigned
73 (39.2%) exact matches, in which:
73 unique CDR3
6 unique J



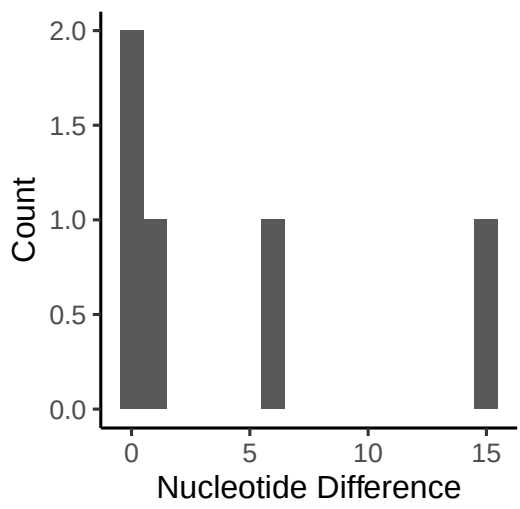
IGHV2−70*01

9 sequences assigned
2 (22.2%) exact matches, in which:
2 unique CDR3
1 unique J



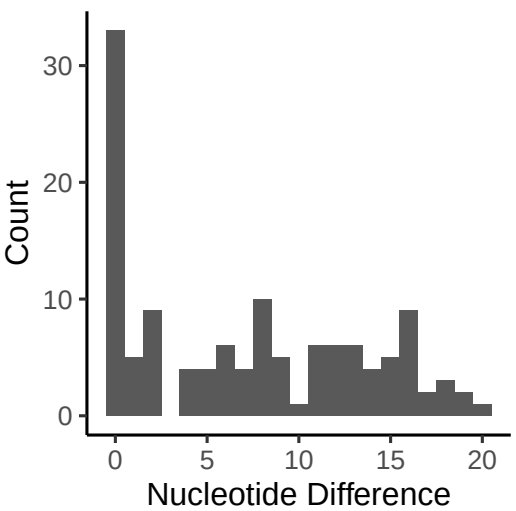
IGHV3−13*05

5 sequences assigned
2 (40%) exact matches, in which:
2 unique CDR3
2 unique J



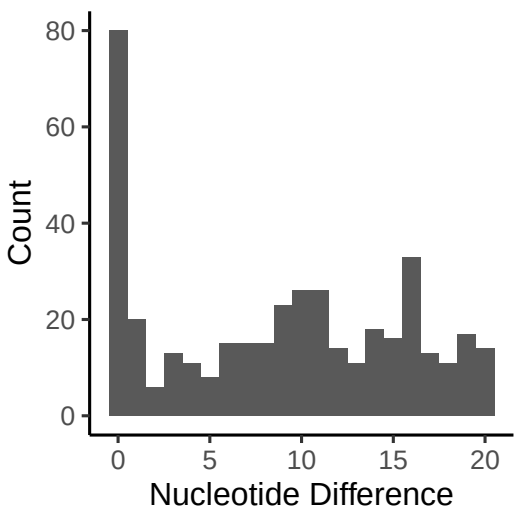
IGHV2−5*02

137 sequences assigned
33 (24.1%) exact matches, in which:
33 unique CDR3
3 unique J



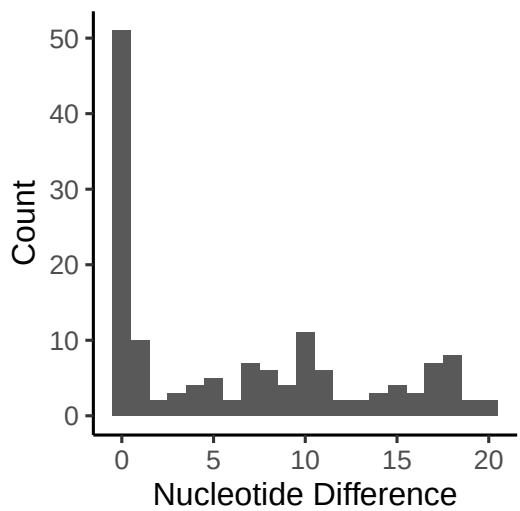
IGHV3−7*03

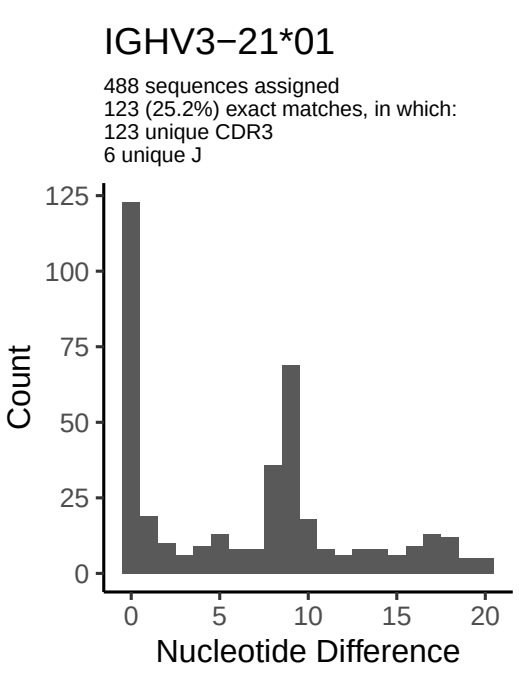
448 sequences assigned
80 (17.9%) exact matches, in which:
80 unique CDR3
7 unique J

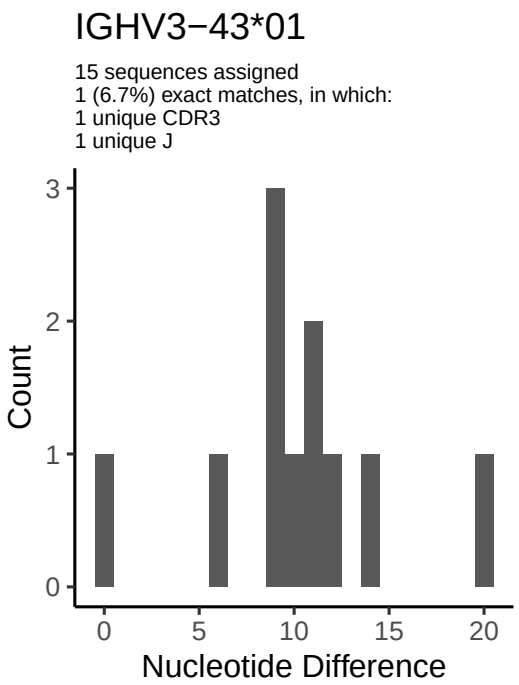


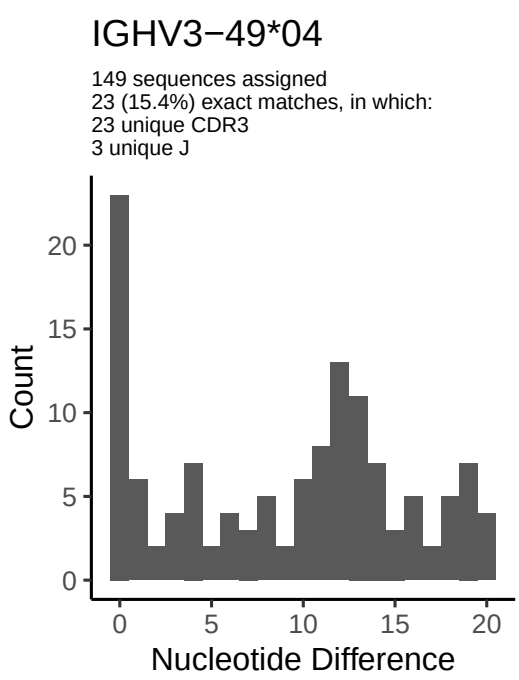
IGHV3−15*01

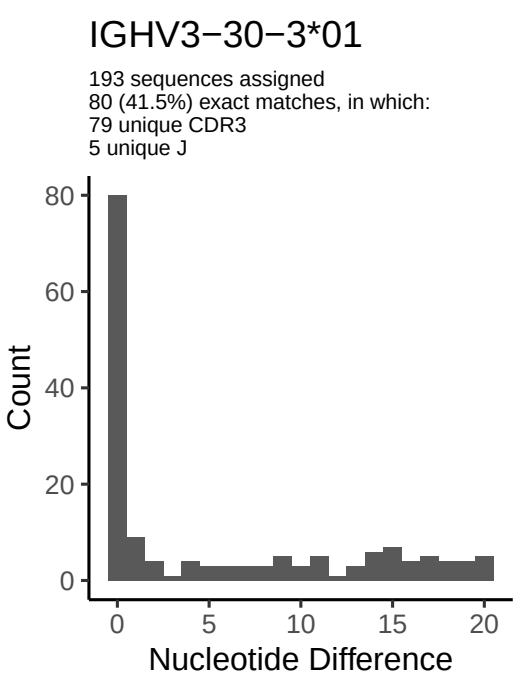
161 sequences assigned
51 (31.7%) exact matches, in which:
51 unique CDR3
6 unique J

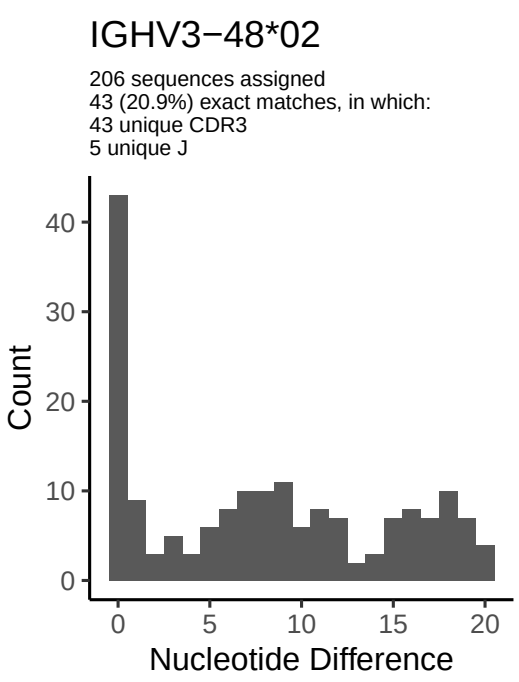


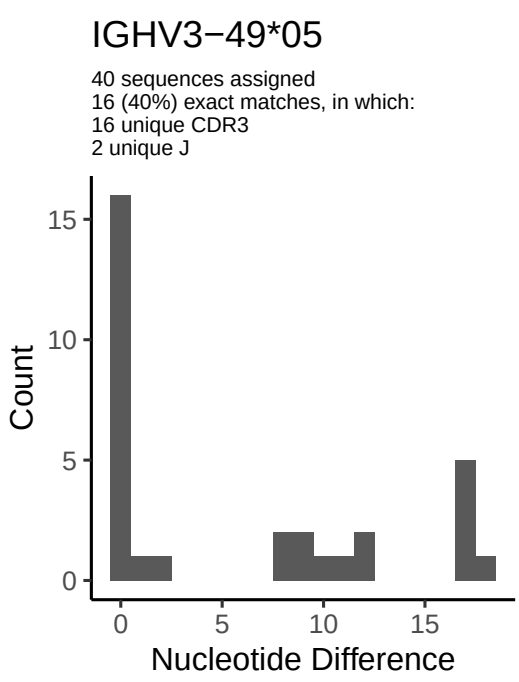

IGHV3−21*01
488 sequences assigned
123 (25.2%) exact matches, in which:
123 unique CDR3
6 unique J
Count
Nucleotide Difference

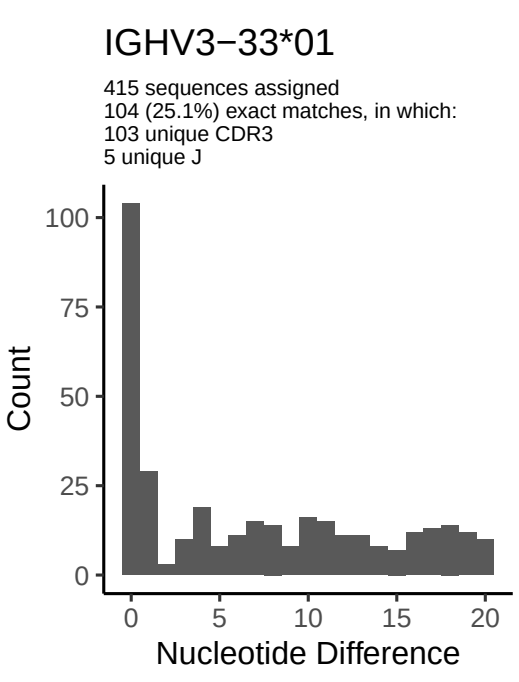

IGHV3−43*01
15 sequences assigned
1 (6.7%) exact matches, in which:
1 unique CDR3
1 unique J
Count
Nucleotide Difference

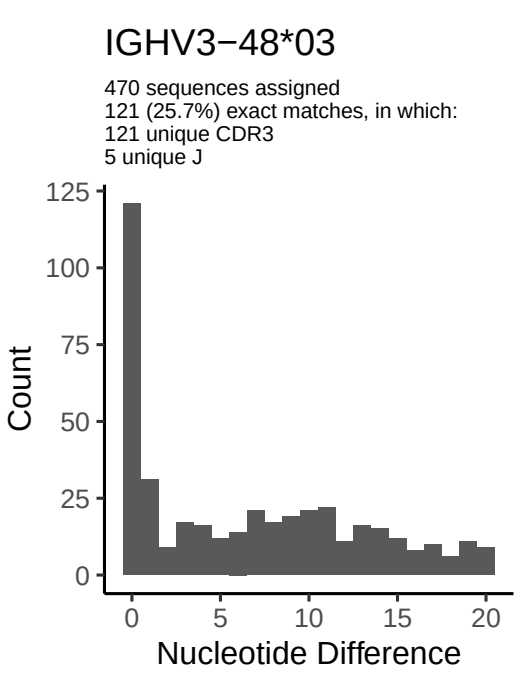

IGHV3−49*04
149 sequences assigned
23 (15.4%) exact matches, in which:
23 unique CDR3
3 unique J
Count
Nucleotide Difference

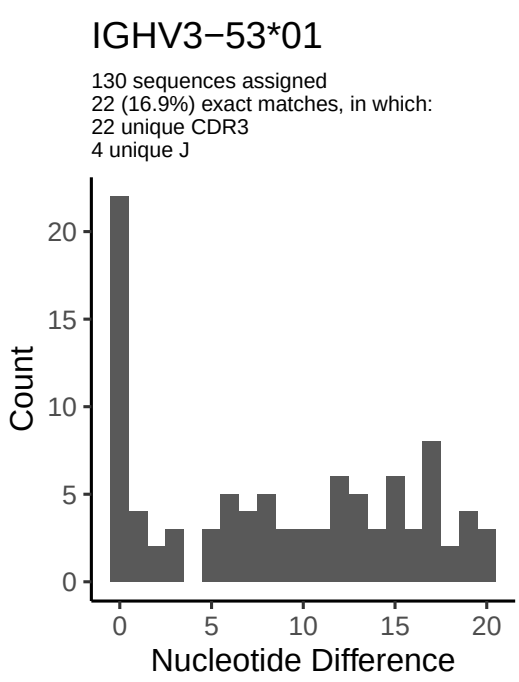

IGHV3−30−3*01
193 sequences assigned
80 (41.5%) exact matches, in which:
79 unique CDR3
5 unique J
Count
Nucleotide Difference


IGHV3−48*02
206 sequences assigned
43 (20.9%) exact matches, in which:
43 unique CDR3
5 unique J
Count
Nucleotide Difference


IGHV3−49*05
40 sequences assigned
16 (40%) exact matches, in which:
16 unique CDR3
2 unique J
Count
Nucleotide Difference

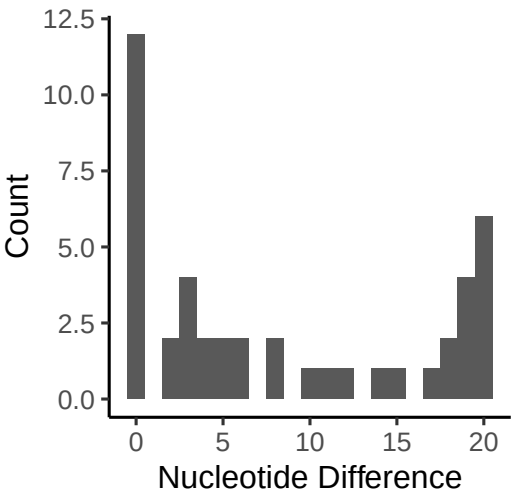

IGHV3−33*01
415 sequences assigned
104 (25.1%) exact matches, in which:
103 unique CDR3
5 unique J
Count
Nucleotide Difference


IGHV3−48*03
470 sequences assigned
121 (25.7%) exact matches, in which:
121 unique CDR3
5 unique J
Count
Nucleotide Difference


IGHV3−53*01
130 sequences assigned
22 (16.9%) exact matches, in which:
22 unique CDR3
4 unique J
Count
Nucleotide Difference

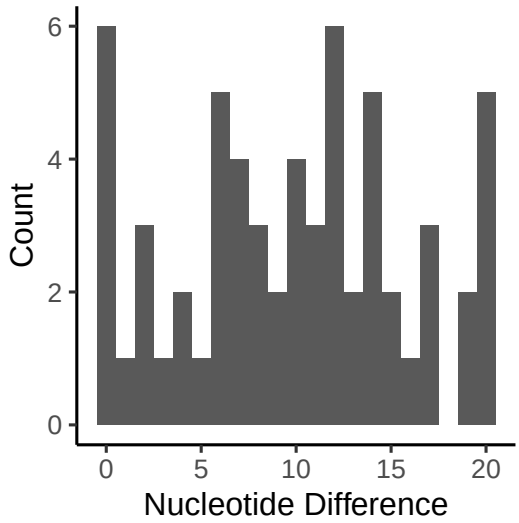
IGHV3−53*02

52 sequences assigned
12 (23.1%) exact matches, in which:
12 unique CDR3
3 unique J



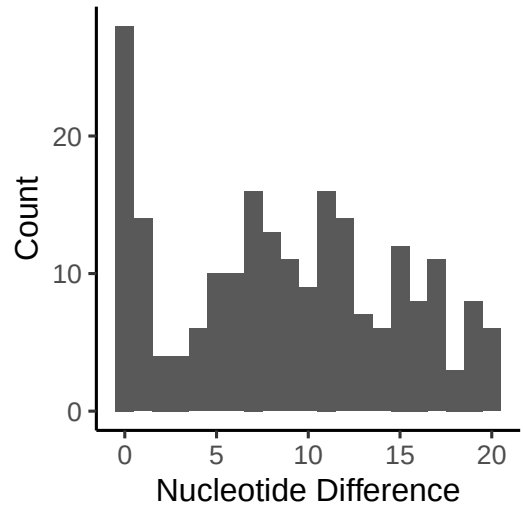
IGHV3−72*01

80 sequences assigned
6 (7.5%) exact matches, in which:
6 unique CDR3
4 unique J



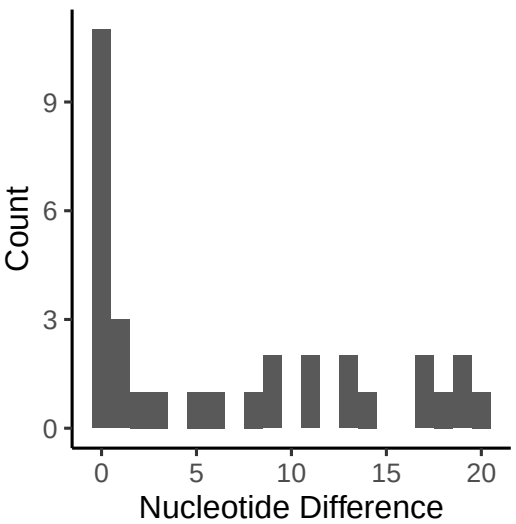
IGHV3−74*01

271 sequences assigned
28 (10.3%) exact matches, in which:
28 unique CDR3
4 unique J



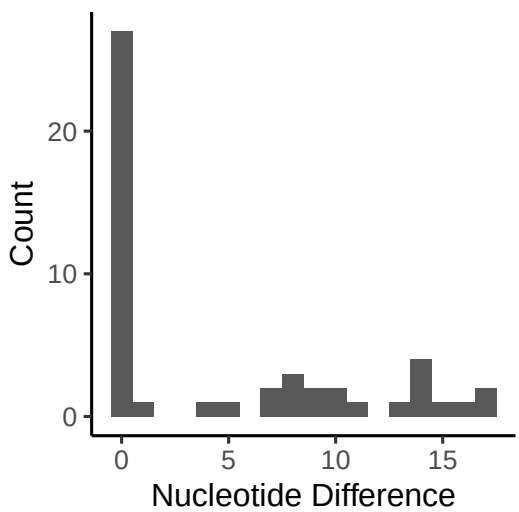
IGHV3−64*01

45 sequences assigned
11 (24.4%) exact matches, in which:
10 unique CDR3
5 unique J



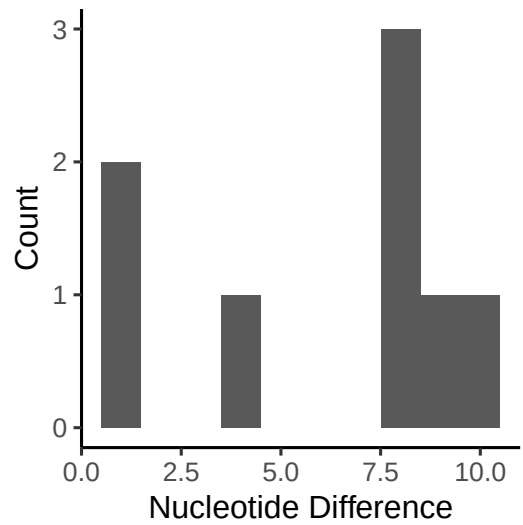
IGHV3−73*01

52 sequences assigned
27 (51.9%) exact matches, in which:
27 unique CDR3
4 unique J



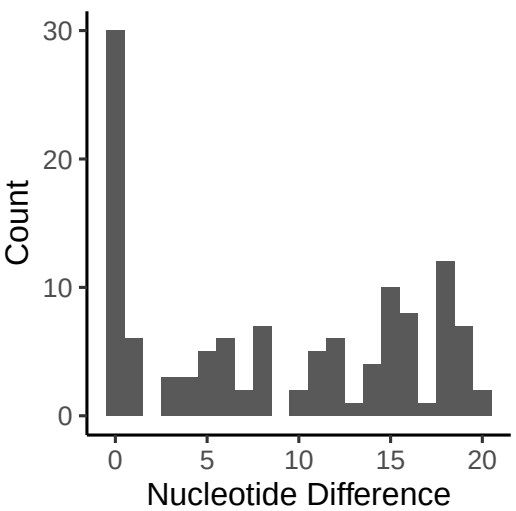
IGHV3−43D*04

14 sequences assigned
No exact matches.



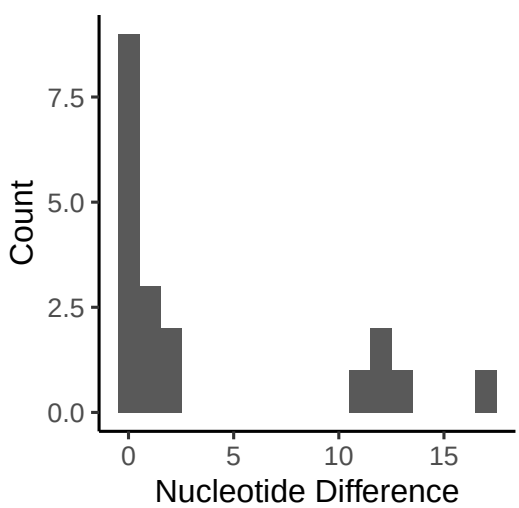
IGHV3−66*02

140 sequences assigned
30 (21.4%) exact matches, in which:
30 unique CDR3
5 unique J



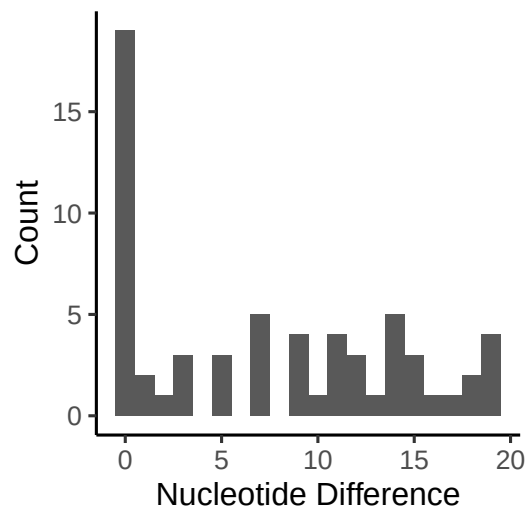
IGHV3−73*02

25 sequences assigned
9 (36%) exact matches, in which:
9 unique CDR3
4 unique J



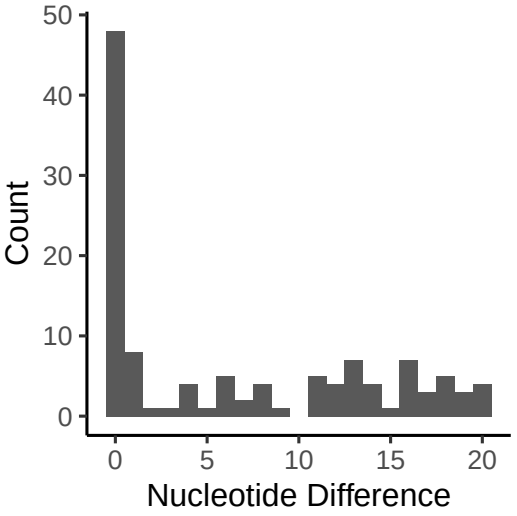
IGHV3−64D*09

83 sequences assigned
19 (22.9%) exact matches, in which:
19 unique CDR3
4 unique J



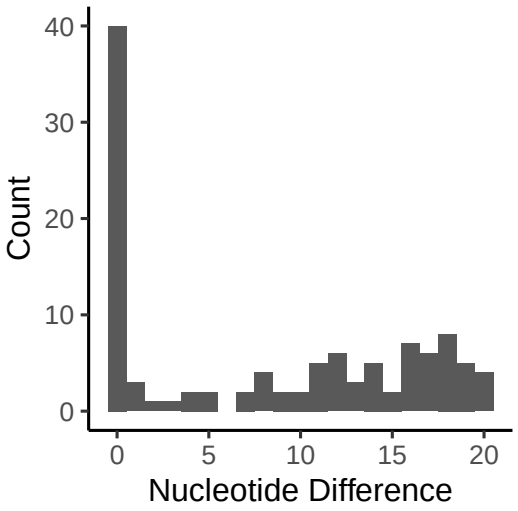
IGHV4−4*02

139 sequences assigned
48 (34.5%) exact matches, in which:
48 unique CDR3
5 unique J



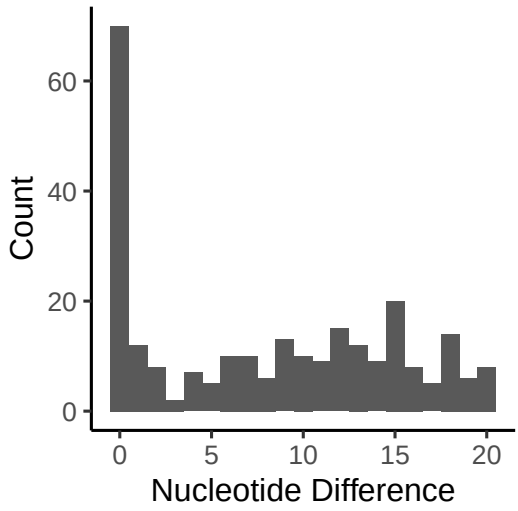
IGHV4−31*03

141 sequences assigned
40 (28.4%) exact matches, in which:
40 unique CDR3
6 unique J



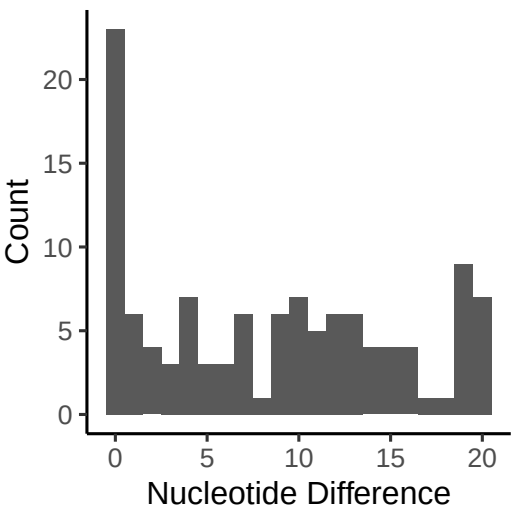
IGHV4−39*07

416 sequences assigned
70 (16.8%) exact matches, in which:
70 unique CDR3
5 unique J



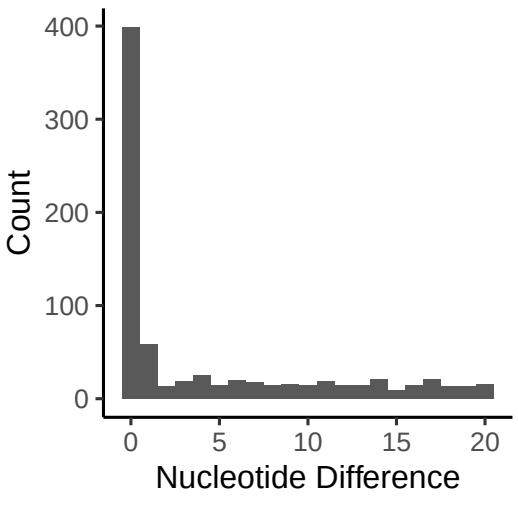
IGHV4−30−4*01

147 sequences assigned
23 (15.6%) exact matches, in which:
22 unique CDR3
6 unique J



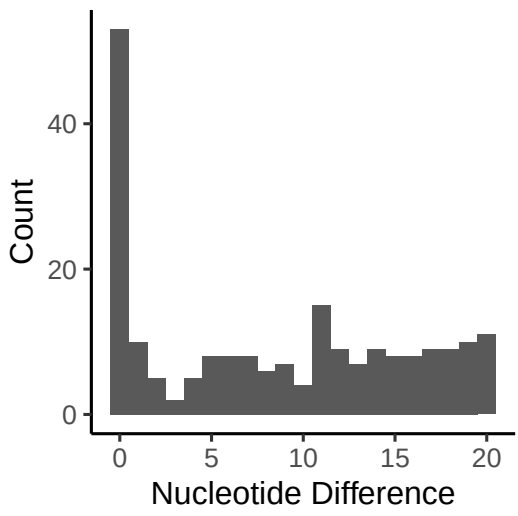
IGHV4−34*01

855 sequences assigned
399 (46.7%) exact matches, in which:
397 unique CDR3
7 unique J



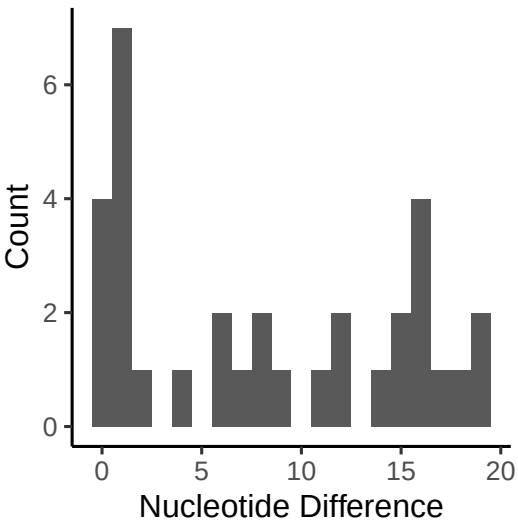
IGHV4−59*01

297 sequences assigned
53 (17.8%) exact matches, in which:
52 unique CDR3
7 unique J



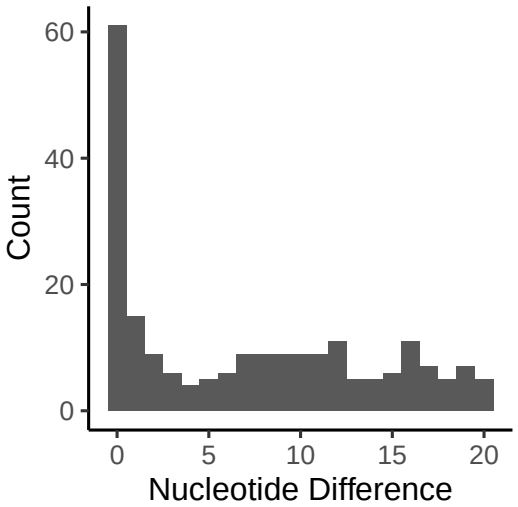
IGHV4−30−2*01

51 sequences assigned
4 (7.8%) exact matches, in which:
4 unique CDR3
2 unique J



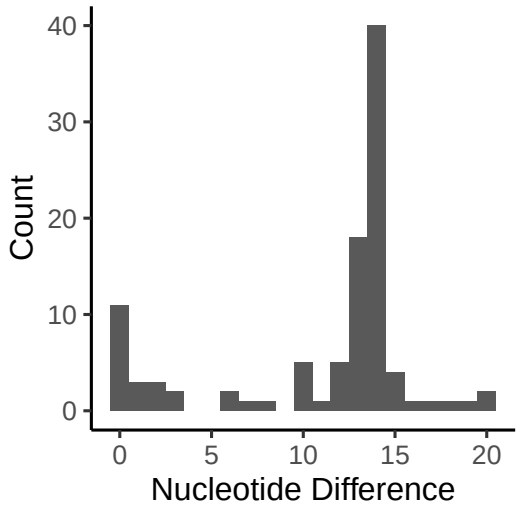
IGHV4−38−2*02_A70G

260 sequences assigned
61 (23.5%) exact matches, in which:
61 unique CDR3
6 unique J



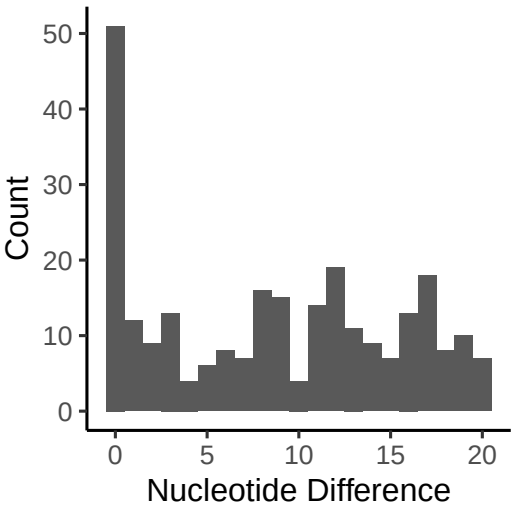
IGHV4−61*01

119 sequences assigned
11 (9.2%) exact matches, in which:
11 unique CDR3
5 unique J



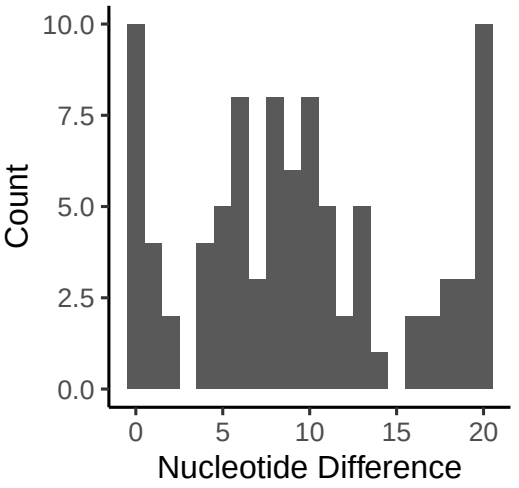
IGHV4−61*02

313 sequences assigned
51 (16.3%) exact matches, in which:
51 unique CDR3
6 unique J



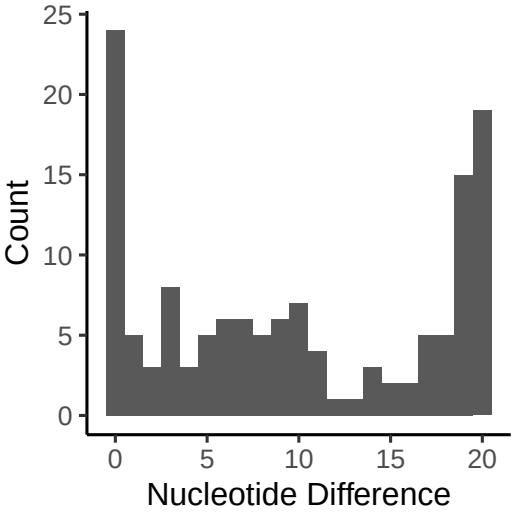
IGHV6−1*01

132 sequences assigned
10 (7.6%) exact matches, in which:
10 unique CDR3
2 unique J



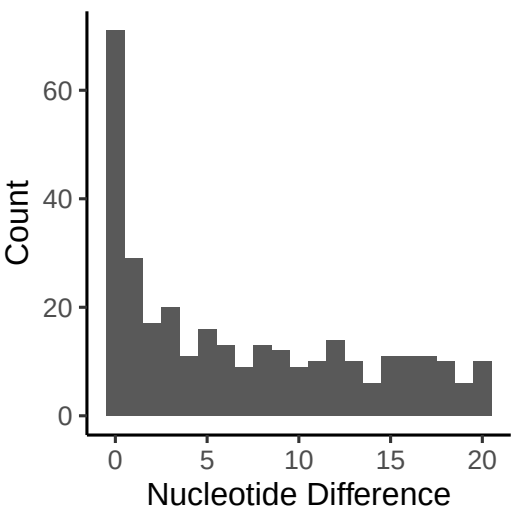
IGHV5−10−1*03

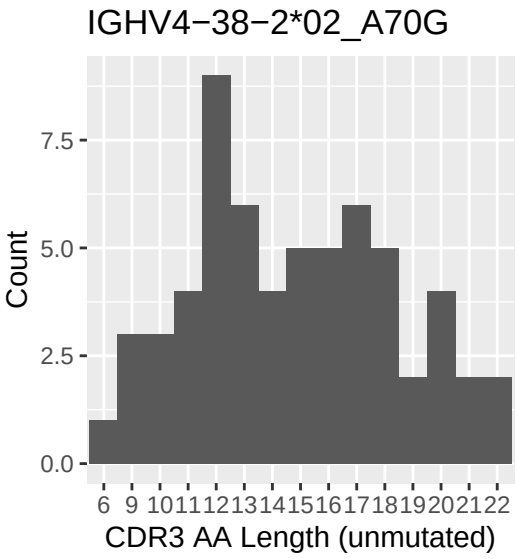
149 sequences assigned
24 (16.1%) exact matches, in which:
24 unique CDR3
6 unique J

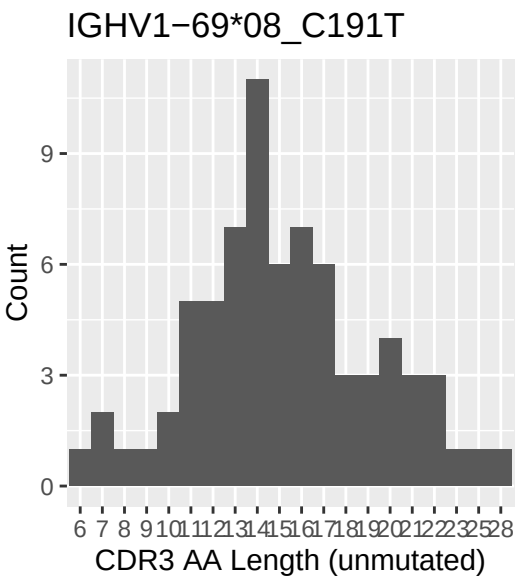


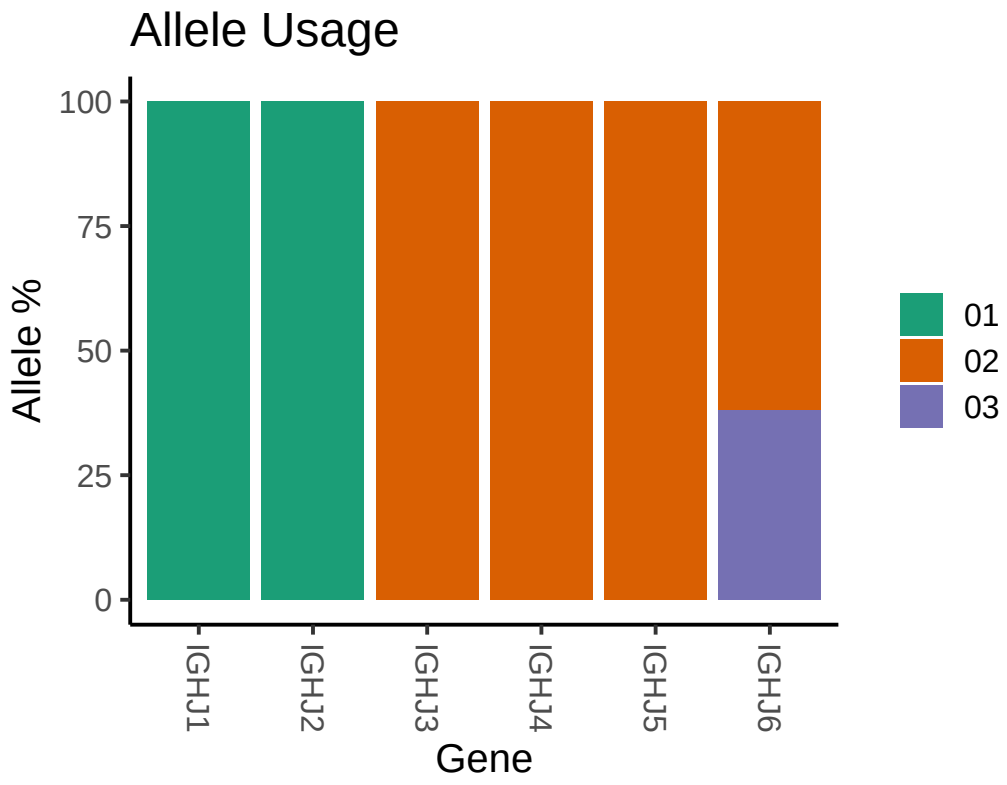
IGHV5−51*01

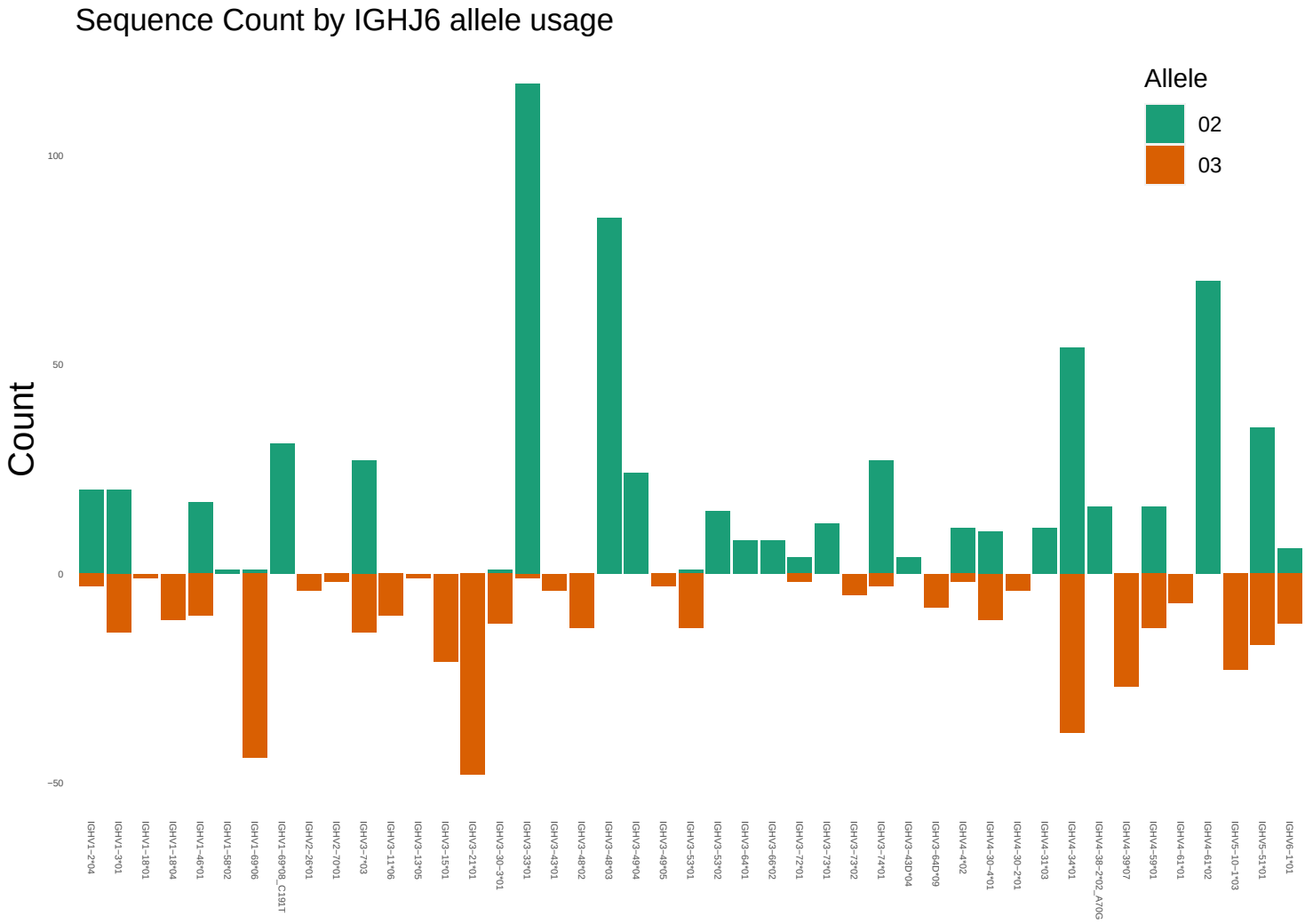
388 sequences assigned
71 (18.3%) exact matches, in which:
70 unique CDR3
6 unique J




IGHV4−38−2*02_A70G
Count
7.5
5.0
2.5
0.0
6 9 10 11 12 13 14 15 16 17 18 19 20 21 22
CDR3 AA Length (unmutated)


IGHV1−69*08_C191T
Count
9
6
3
0
6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 25 28
CDR3 AA Length (unmutated)


Allele Usage
100
75
50
25
0
Allele %
IGHJ1
IGHJ2
IGHJ3
IGHJ4
IGHJ5
IGHJ6
Gene
01
02
03


Sequence Count by IGHJ6 allele usage
Allele
02
03
Count
100
50
0
−50
IGHV1-2*04
IGHV1-3*01
IGHV1-18*01
IGHV1-18*04
IGHV1-46*01
IGHV1-58*02
IGHV1-69*06
IGHV1-69*08_C191T
IGHV2-26*01
IGHV2-70*01
IGHV3-7*03
IGHV3-11*06
IGHV3-13*05
IGHV3-15*01
IGHV3-21*01
IGHV3-30-3*01
IGHV3-33*01
IGHV3-43*01
IGHV3-48*02
IGHV3-48*03
IGHV3-49*04
IGHV3-49*05
IGHV3-53*01
IGHV3-53*02
IGHV3-64*01
IGHV3-66*02
IGHV3-72*01
IGHV3-73*01
IGHV3-73*02
IGHV3-74*01
IGHV3-43D*04
IGHV3-64D*09
IGHV4-4*02
IGHV4-30-4*01
IGHV4-30-2*01
IGHV4-31*03
IGHV4-34*01
IGHV4-38-2*02_A70G
IGHV4-39*07
IGHV4-59*01
IGHV4-61*01
IGHV4-61*02
IGHV5-10-1*03
IGHV5-51*01
IGHV6-1*01

Warning − no inferred sequences found.

Warning − no inferred sequences found.

Warning − no inferred sequences found.

Warning − no inferred sequences found.

Warning − no inferred sequences found.

Warning − no inferred sequences found.