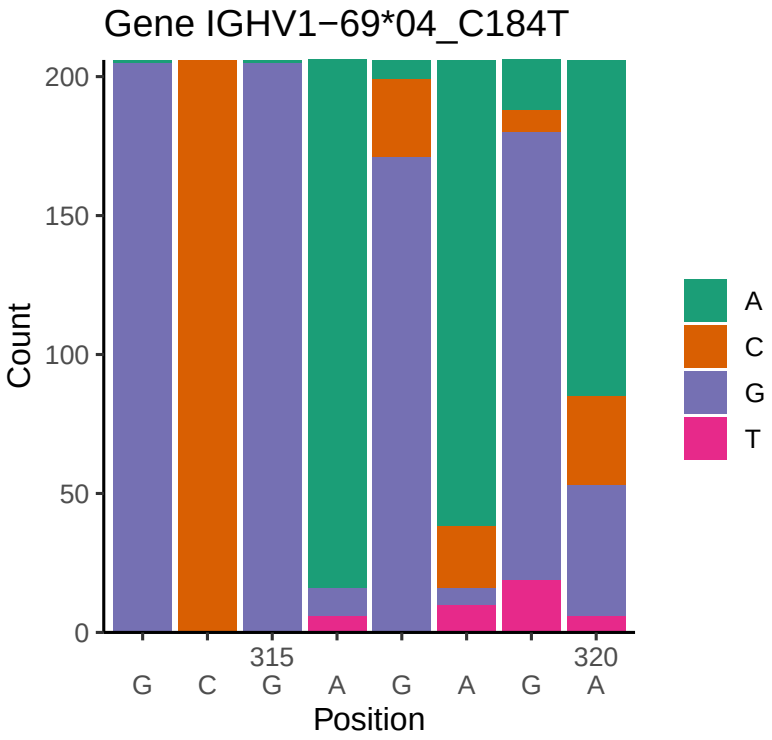
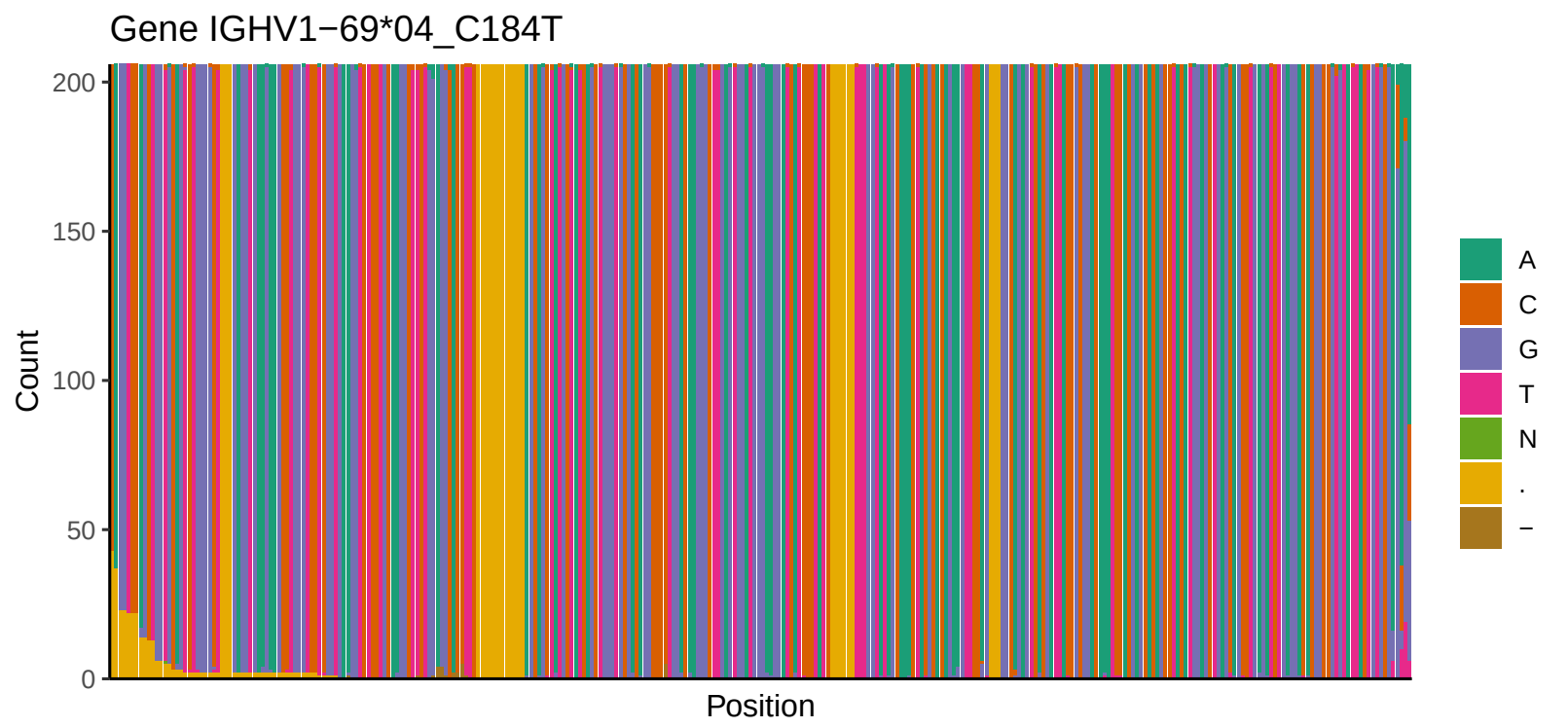
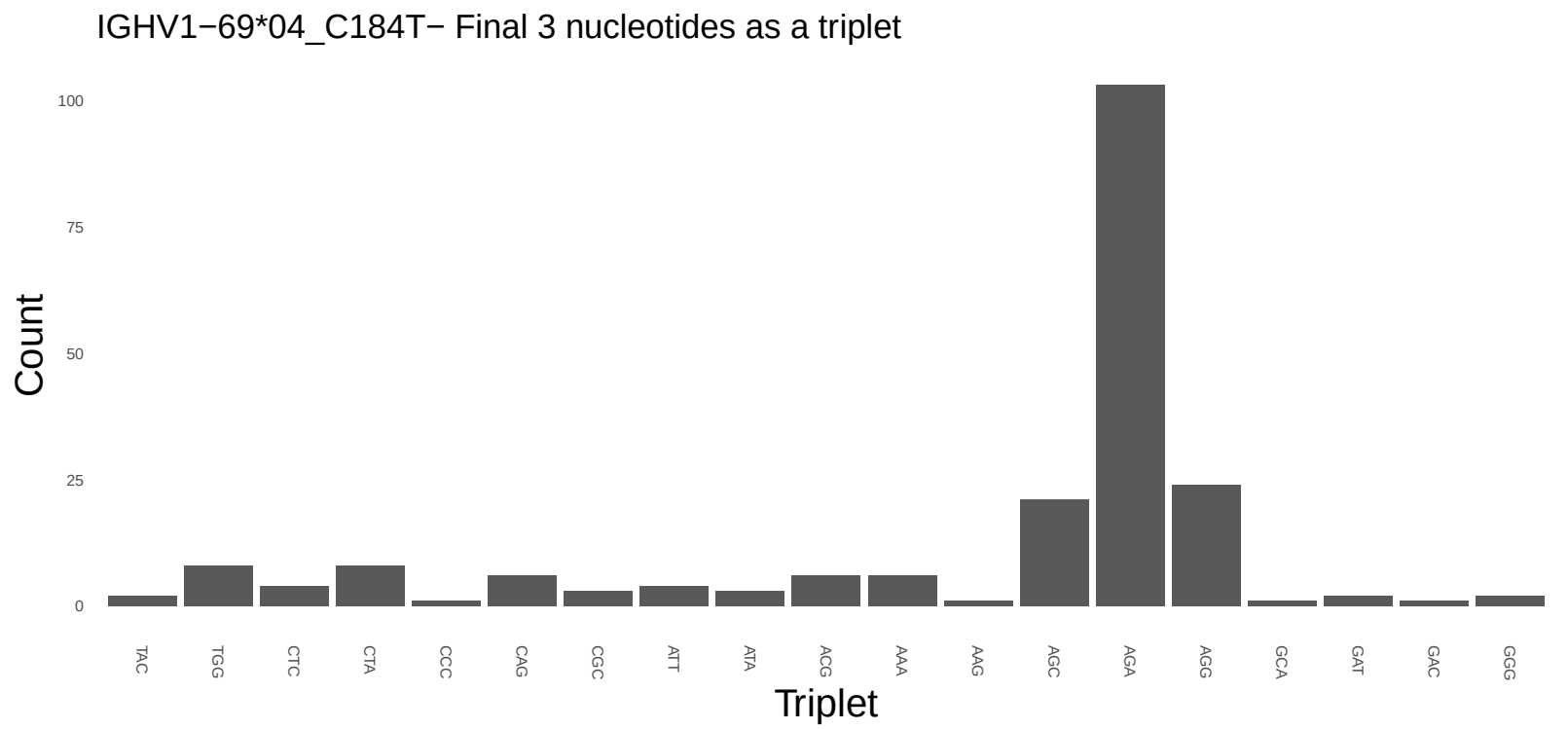
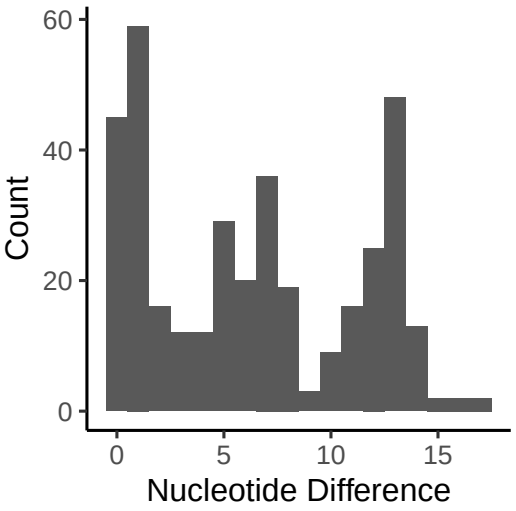

Gene IGHV1−69*04_C184T
Count
200
150
100
50
0
G
C
315
G
A
G
A
G
320
A
Position
A
C
G
T


Gene IGHV1−69*04_C184T
Count
200
150
100
50
0
Position
A
C
G
T
N
.
–


IGHV1−69*04_C184T− Final 3 nucleotides as a triplet
Count
100
75
50
25
0
TAC
TGG
CTC
CTA
CCC
CAG
CGC
ATT
ATA
ACG
AAA
AAG
AGC
AGA
AGG
GCA
GAT
GAC
GGG
Triplet

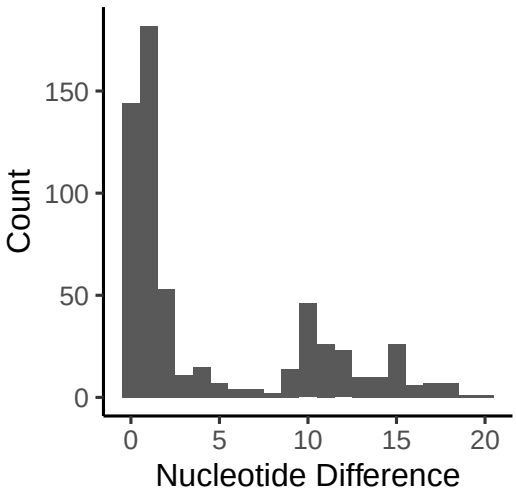
IGHV1−2*02

404 sequences assigned
45 (11.1%) exact matches, in which:
34 unique CDR3
4 unique J



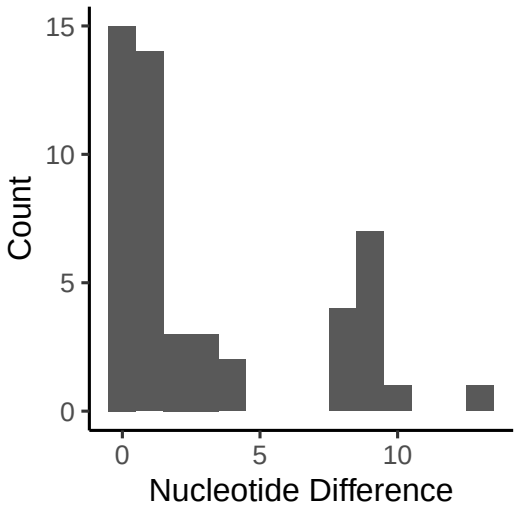
IGHV1−18*01

601 sequences assigned
144 (24%) exact matches, in which:
92 unique CDR3
7 unique J



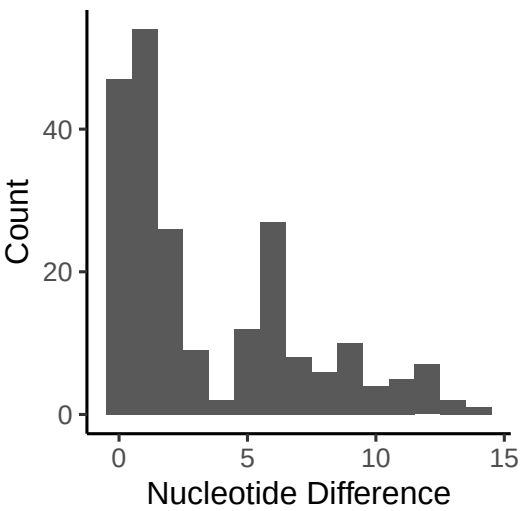
IGHV1−46*03

50 sequences assigned
15 (30%) exact matches, in which:
10 unique CDR3
2 unique J



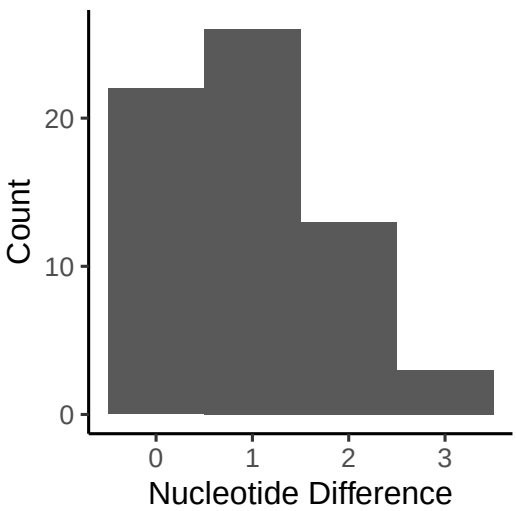
IGHV1−3*01

220 sequences assigned
47 (21.4%) exact matches, in which:
29 unique CDR3
4 unique J



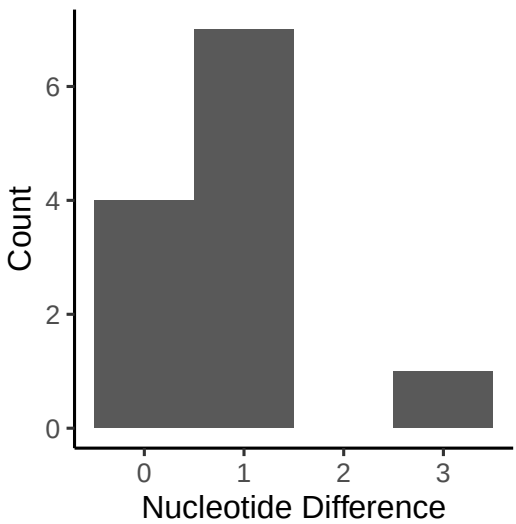
IGHV1−24*01

64 sequences assigned
22 (34.4%) exact matches, in which:
20 unique CDR3
5 unique J



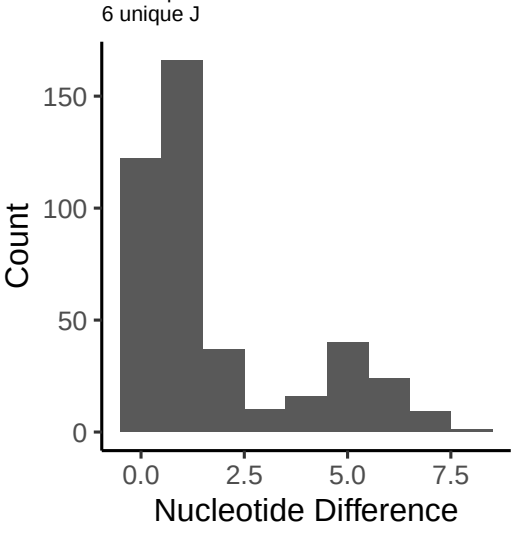
IGHV1−58*01

12 sequences assigned
4 (33.3%) exact matches, in which:
3 unique CDR3
2 unique J



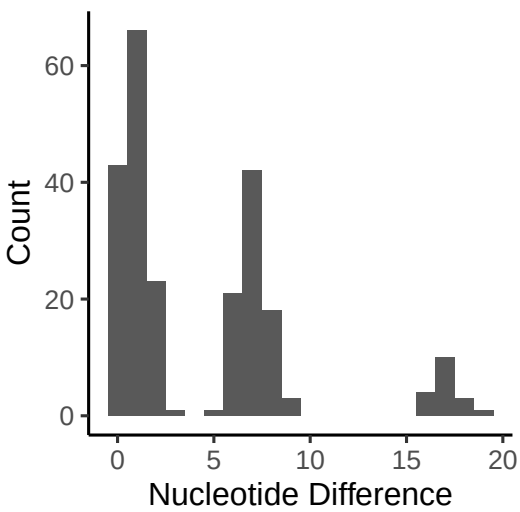
IGHV1−8*01

425 sequences assigned
122 (28.7%) exact matches, in which:
85 unique CDR3
6 unique J



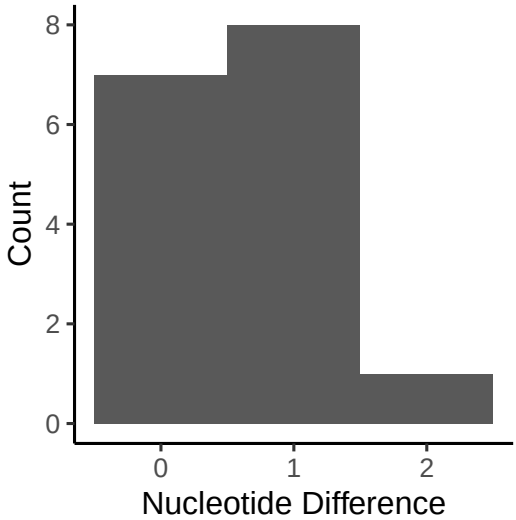
IGHV1−46*01

236 sequences assigned
43 (18.2%) exact matches, in which:
25 unique CDR3
5 unique J



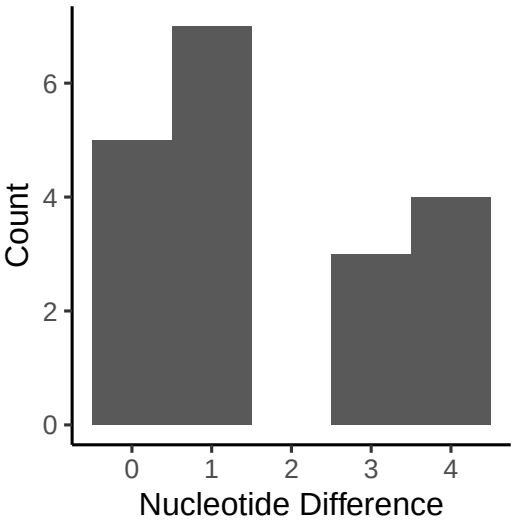
IGHV1−58*02

16 sequences assigned
7 (43.8%) exact matches, in which:
4 unique CDR3
3 unique J



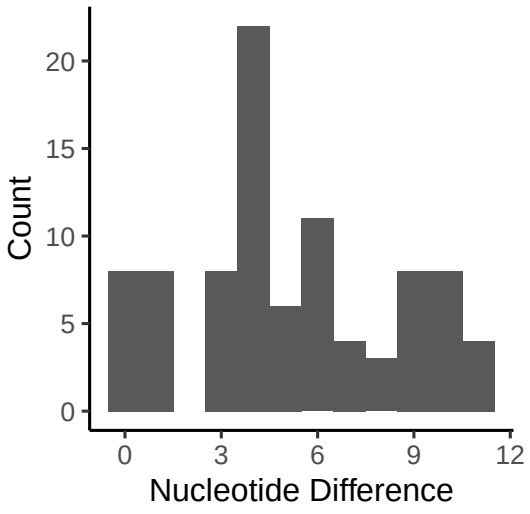
IGHV1−69−2*01

19 sequences assigned
5 (26.3%) exact matches, in which:
5 unique CDR3
1 unique J



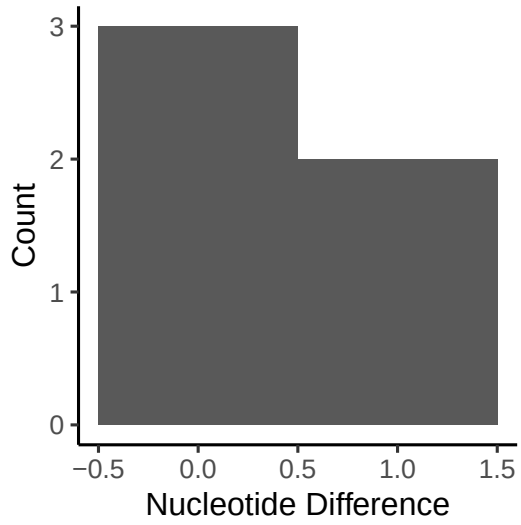
IGHV2−5*01

90 sequences assigned
8 (8.9%) exact matches, in which:
6 unique CDR3
4 unique J



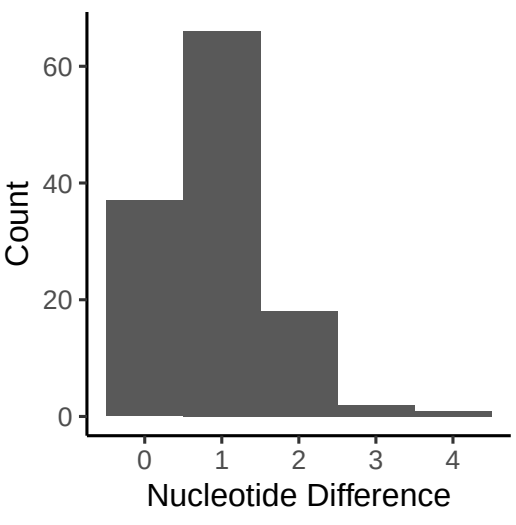
IGHV2−70*01

5 sequences assigned
3 (60%) exact matches, in which:
2 unique CDR3
2 unique J



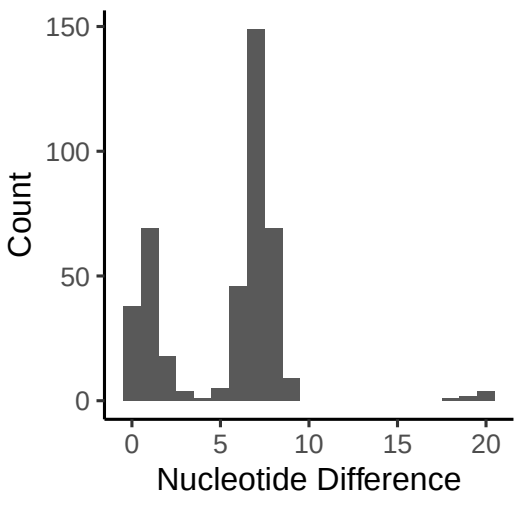
IGHV1−69*02

124 sequences assigned
37 (29.8%) exact matches, in which:
30 unique CDR3
4 unique J



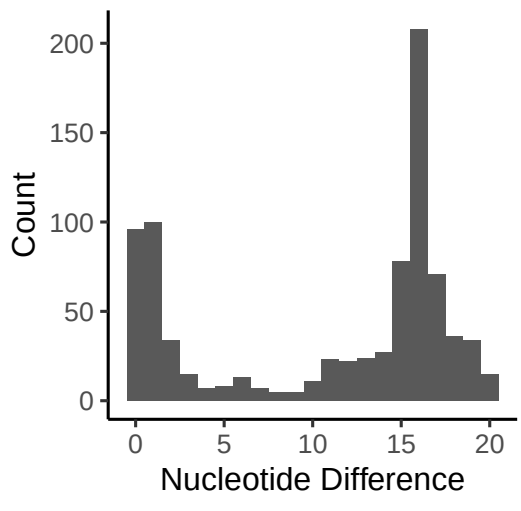
IGHV2−5*02

423 sequences assigned
38 (9%) exact matches, in which:
22 unique CDR3
3 unique J



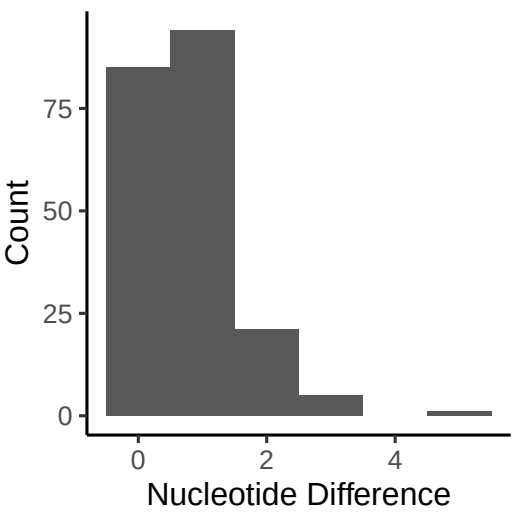
IGHV3−7*01

888 sequences assigned
96 (10.8%) exact matches, in which:
70 unique CDR3
7 unique J



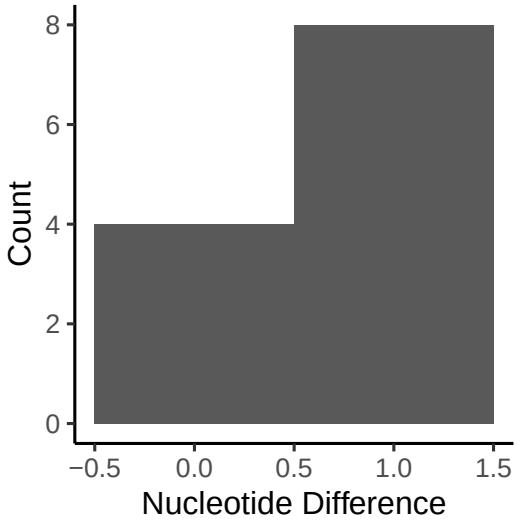
IGHV1−69*04_C184T

206 sequences assigned
85 (41.3%) exact matches, in which:
68 unique CDR3
6 unique J



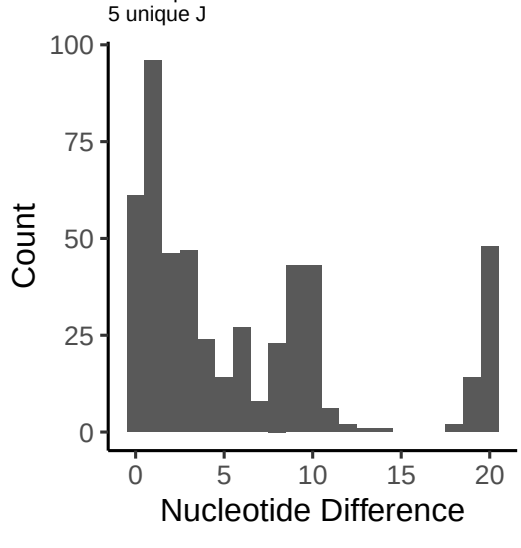
IGHV2−26*01

12 sequences assigned
4 (33.3%) exact matches, in which:
3 unique CDR3
1 unique J



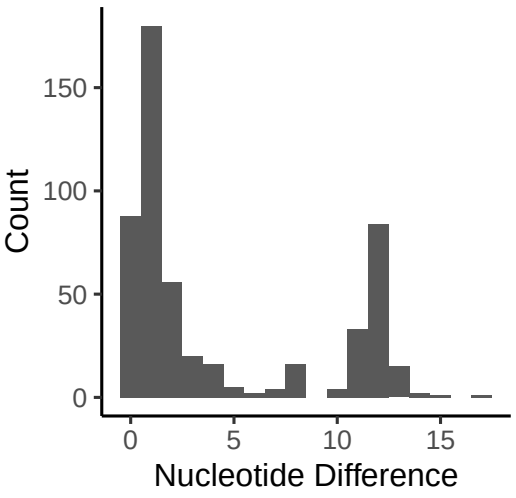
IGHV3−9*01

726 sequences assigned
61 (8.4%) exact matches, in which:
48 unique CDR3
5 unique J



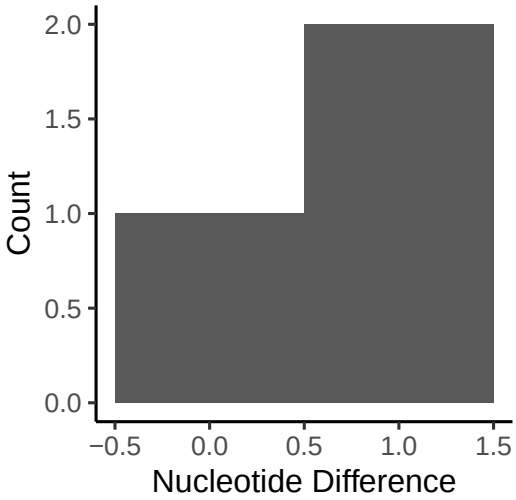
IGHV3−11*01

527 sequences assigned
88 (16.7%) exact matches, in which:
57 unique CDR3
5 unique J



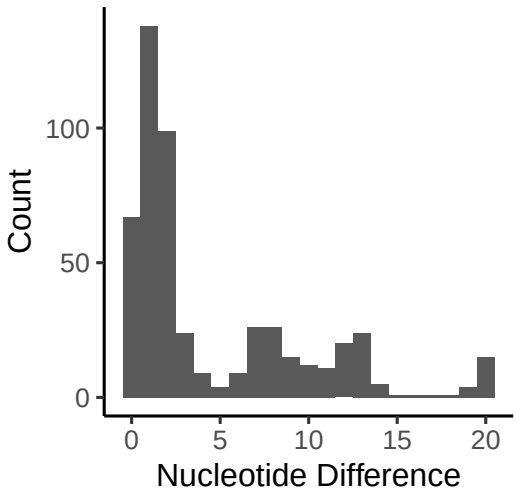
IGHV3−20*01

3 sequences assigned
1 (33.3%) exact matches, in which:
1 unique CDR3
1 unique J



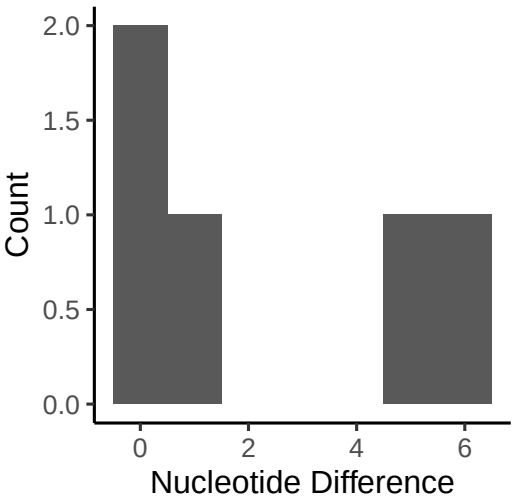
IGHV3−33*01

546 sequences assigned
67 (12.3%) exact matches, in which:
44 unique CDR3
4 unique J



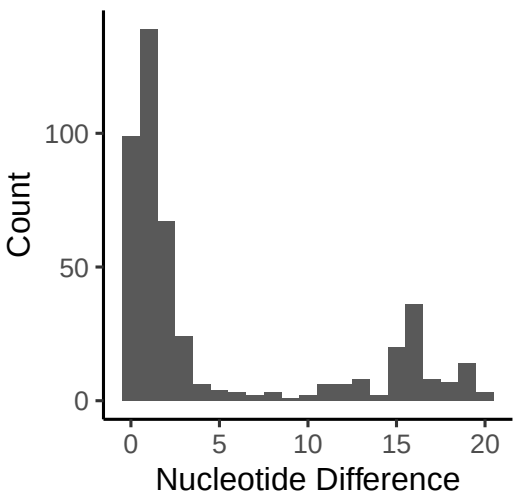
IGHV3−13*01

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



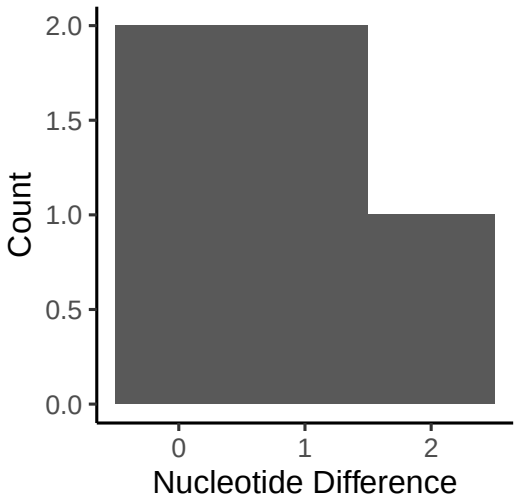
IGHV3−21*01

462 sequences assigned
99 (21.4%) exact matches, in which:
57 unique CDR3
6 unique J



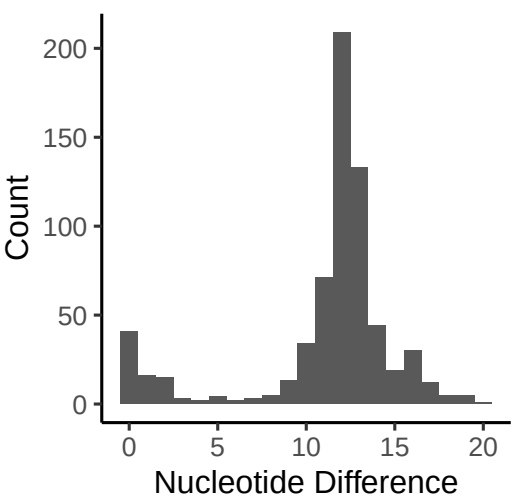
IGHV3−43*01

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



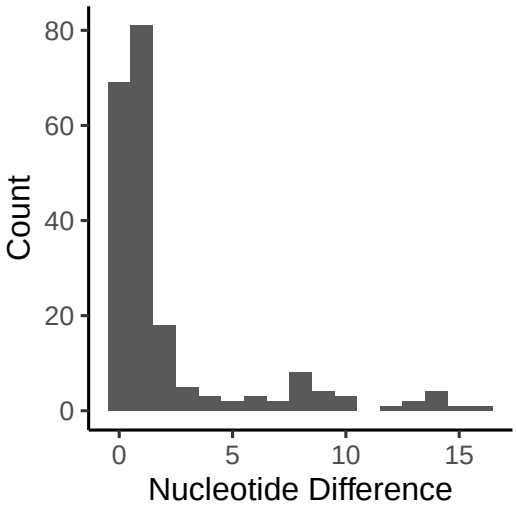
IGHV3−15*01

667 sequences assigned
41 (6.1%) exact matches, in which:
36 unique CDR3
5 unique J



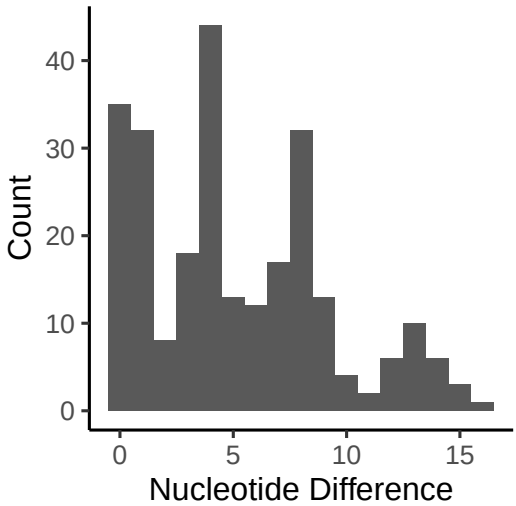
IGHV3−30−3*01

207 sequences assigned
69 (33.3%) exact matches, in which:
39 unique CDR3
6 unique J



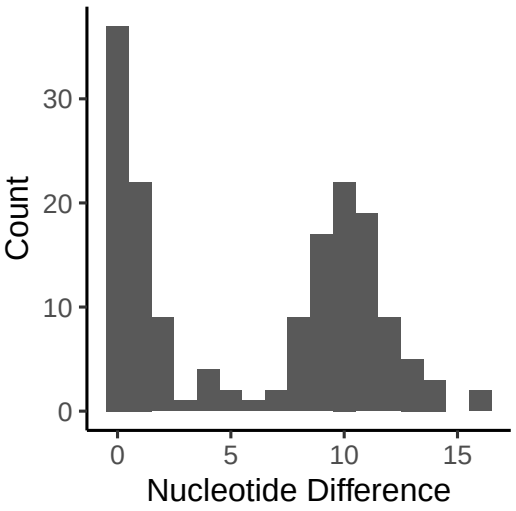
IGHV3−48*01

256 sequences assigned
35 (13.7%) exact matches, in which:
22 unique CDR3
4 unique J



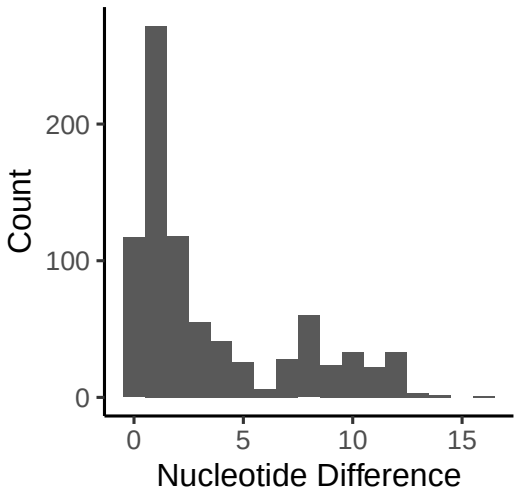
IGHV3−48*02

164 sequences assigned
37 (22.6%) exact matches, in which:
24 unique CDR3
6 unique J



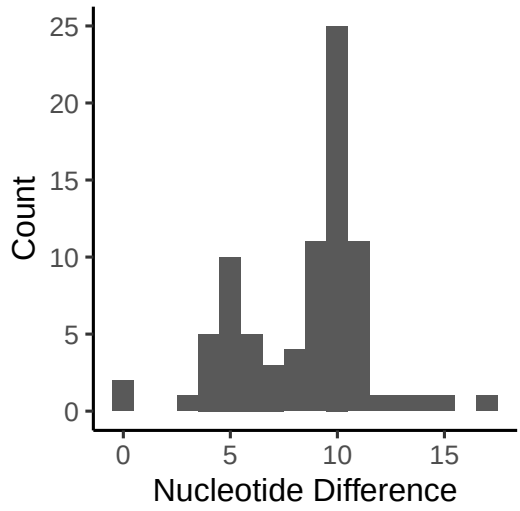
IGHV3−53*01

844 sequences assigned
117 (13.9%) exact matches, in which:
81 unique CDR3
6 unique J



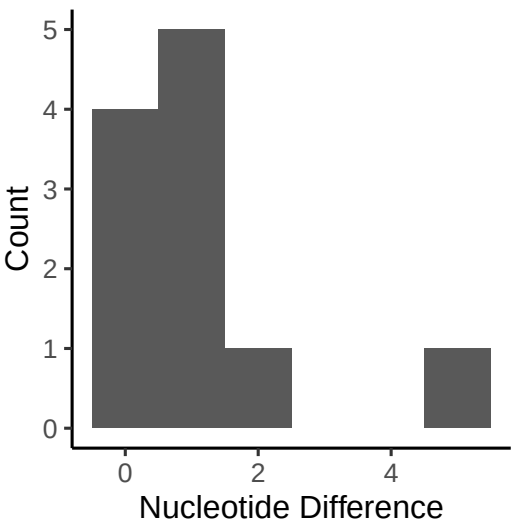
IGHV3−72*01

82 sequences assigned
2 (2.4%) exact matches, in which:
1 unique CDR3
1 unique J



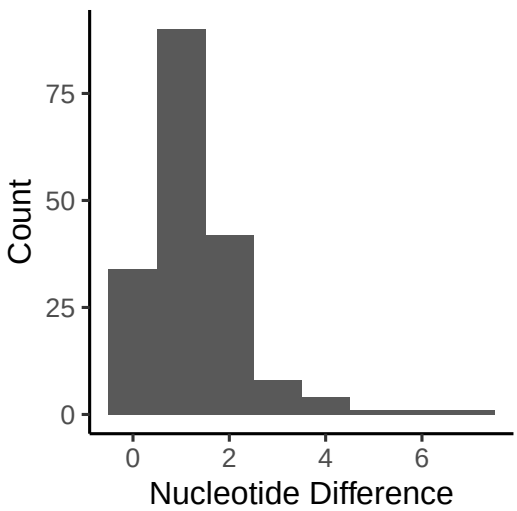
IGHV3−49*03

11 sequences assigned
4 (36.4%) exact matches, in which:
4 unique CDR3
3 unique J



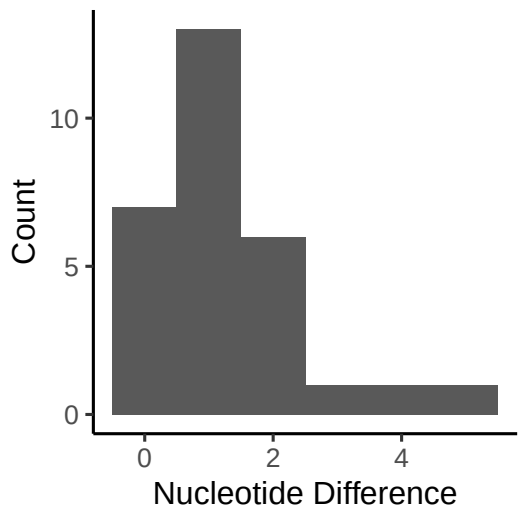
IGHV3−64*01

181 sequences assigned
34 (18.8%) exact matches, in which:
19 unique CDR3
2 unique J



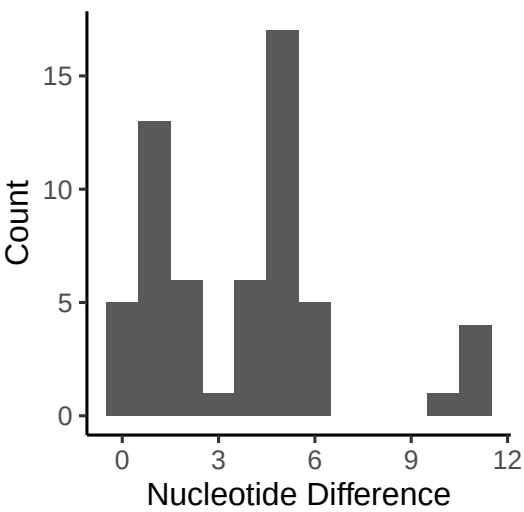
IGHV3−73*01

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



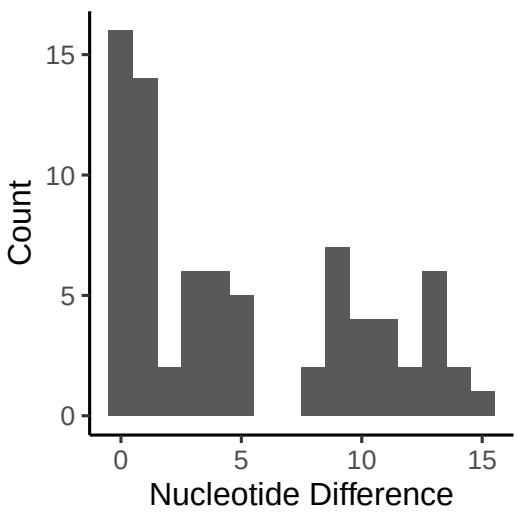
IGHV3−49*05

58 sequences assigned
5 (8.6%) exact matches, in which:
3 unique CDR3
2 unique J



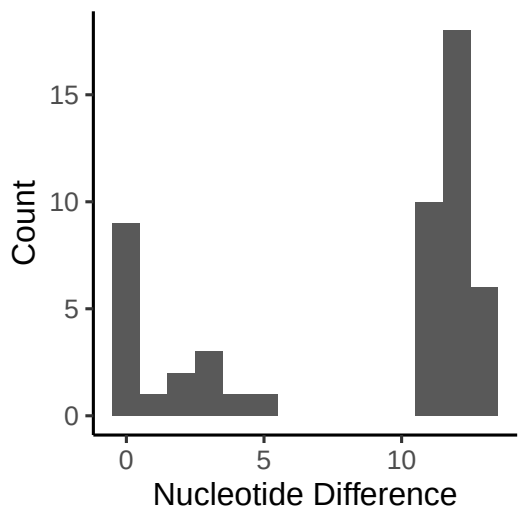
IGHV3−66*02

77 sequences assigned
16 (20.8%) exact matches, in which:
13 unique CDR3
5 unique J



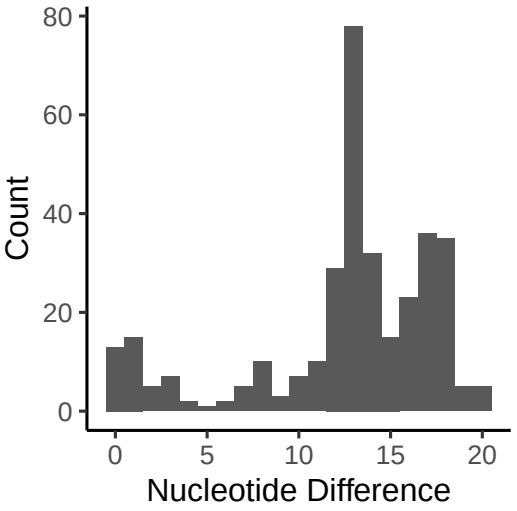
IGHV3−73*02

51 sequences assigned
9 (17.6%) exact matches, in which:
7 unique CDR3
2 unique J



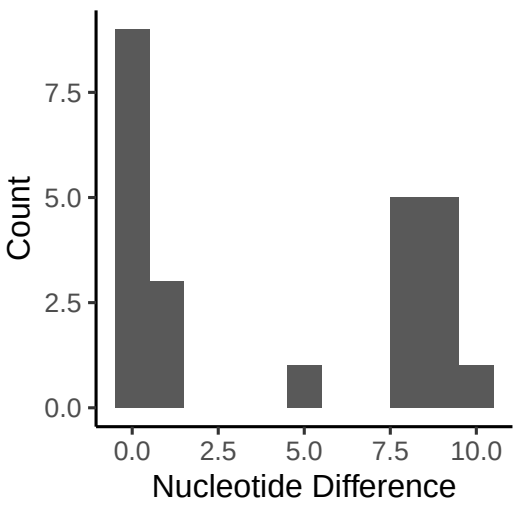
IGHV3−74*01

341 sequences assigned
13 (3.8%) exact matches, in which:
11 unique CDR3
4 unique J



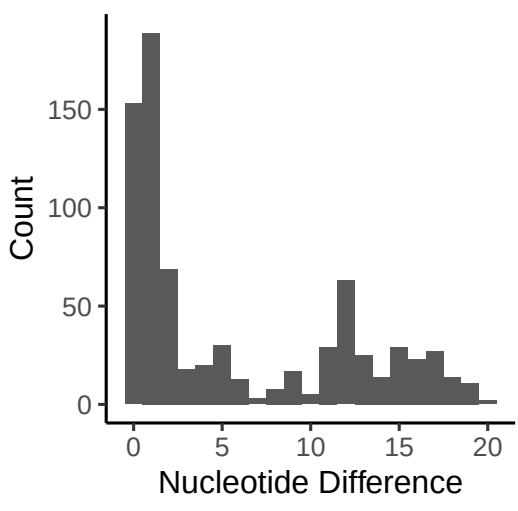
IGHV4−30−2*01

24 sequences assigned
9 (37.5%) exact matches, in which:
6 unique CDR3
3 unique J



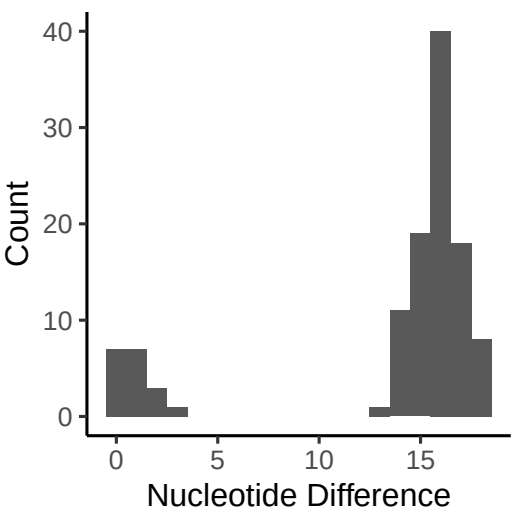
IGHV4−39*01

778 sequences assigned
153 (19.7%) exact matches, in which:
112 unique CDR3
7 unique J



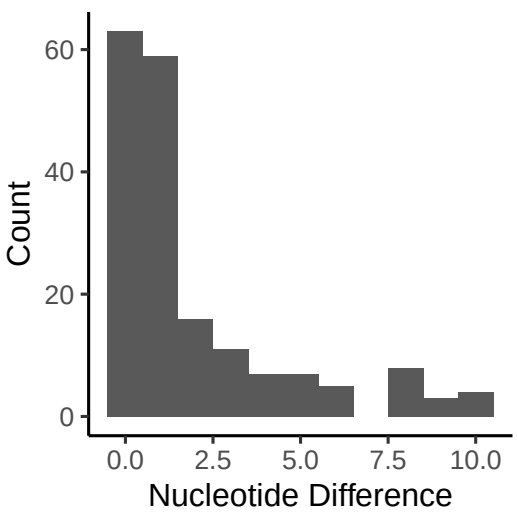
IGHV4−4*07

115 sequences assigned
7 (6.1%) exact matches, in which:
4 unique CDR3
3 unique J



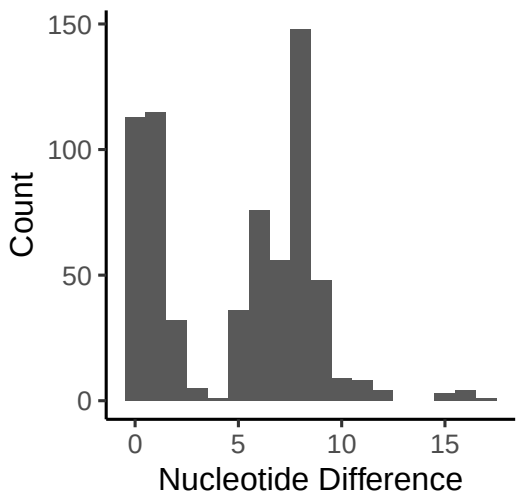
IGHV4−31*03

183 sequences assigned
63 (34.4%) exact matches, in which:
36 unique CDR3
5 unique J



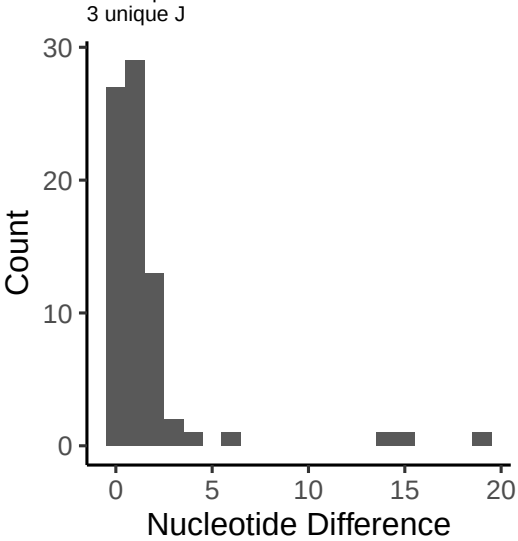
IGHV4−59*01

660 sequences assigned
113 (17.1%) exact matches, in which:
72 unique CDR3
6 unique J



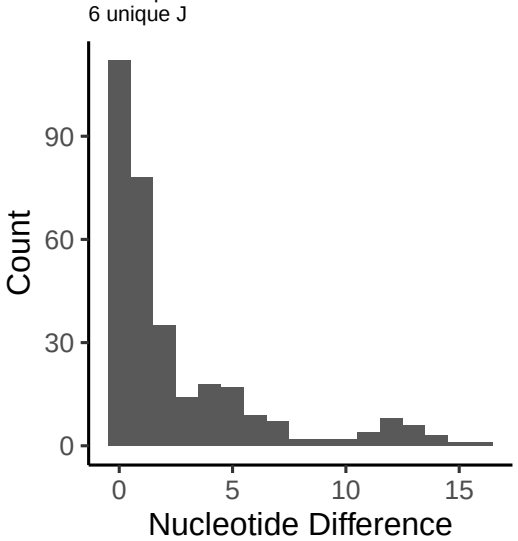
IGHV4−30−4*01

76 sequences assigned
27 (35.5%) exact matches, in which:
17 unique CDR3
3 unique J



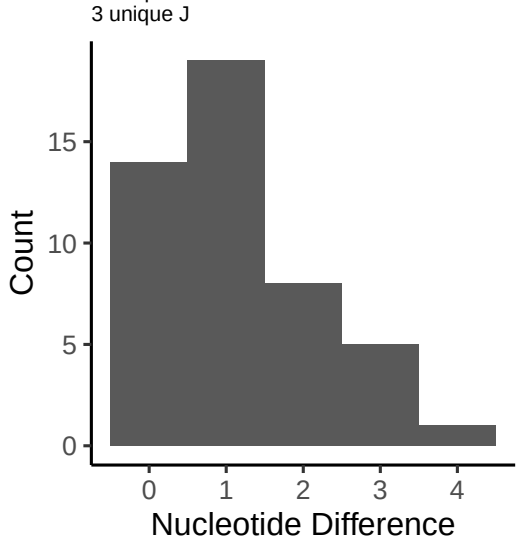
IGHV4−34*01

319 sequences assigned
112 (35.1%) exact matches, in which:
75 unique CDR3
6 unique J



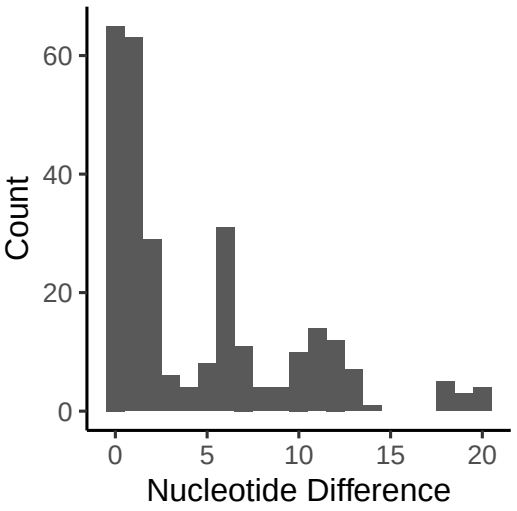
IGHV4−61*01

47 sequences assigned
14 (29.8%) exact matches, in which:
8 unique CDR3
3 unique J



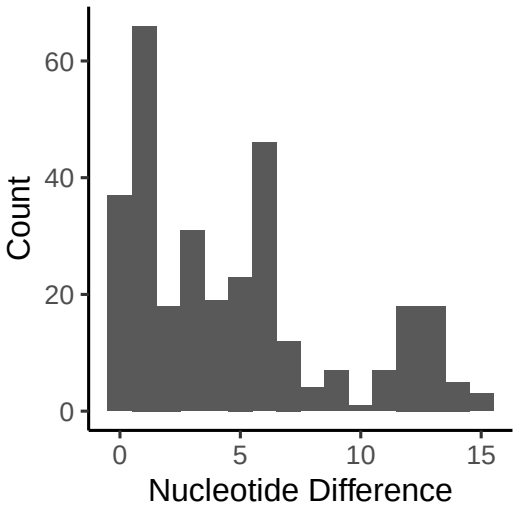
IGHV4−61*02

284 sequences assigned
65 (22.9%) exact matches, in which:
38 unique CDR3
6 unique J



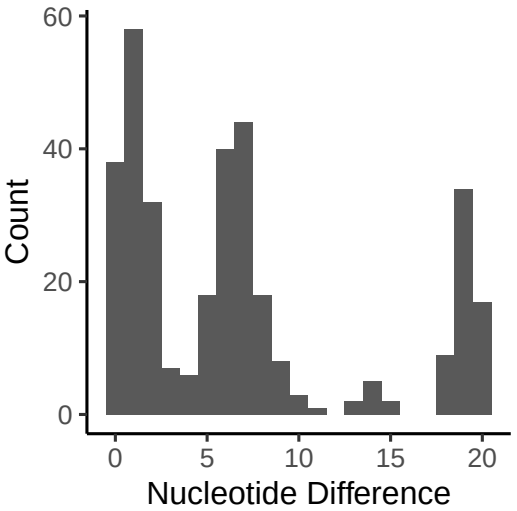
IGHV6−1*01

315 sequences assigned
37 (11.7%) exact matches, in which:
18 unique CDR3
4 unique J



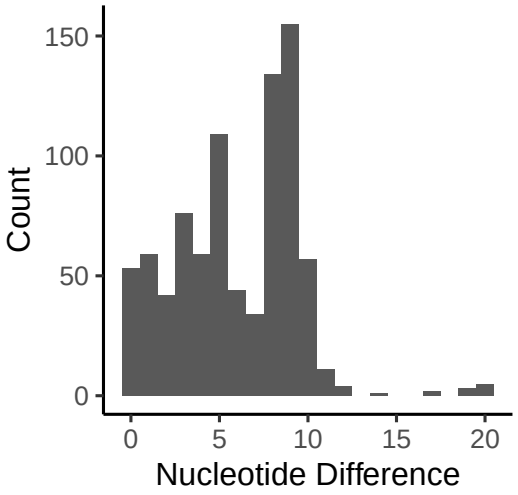
IGHV5−51*01

509 sequences assigned
38 (7.5%) exact matches, in which:
35 unique CDR3
4 unique J



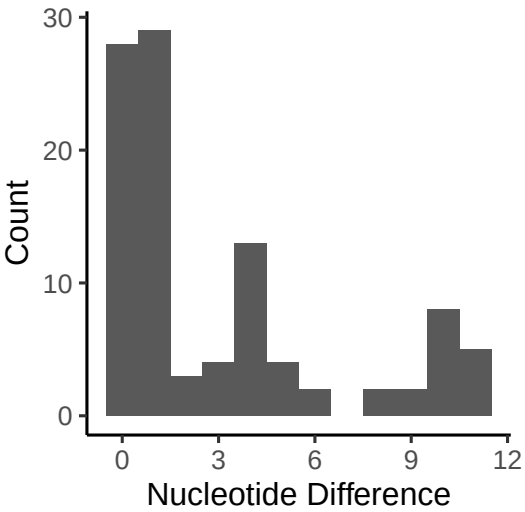
IGHV7−4−1*02

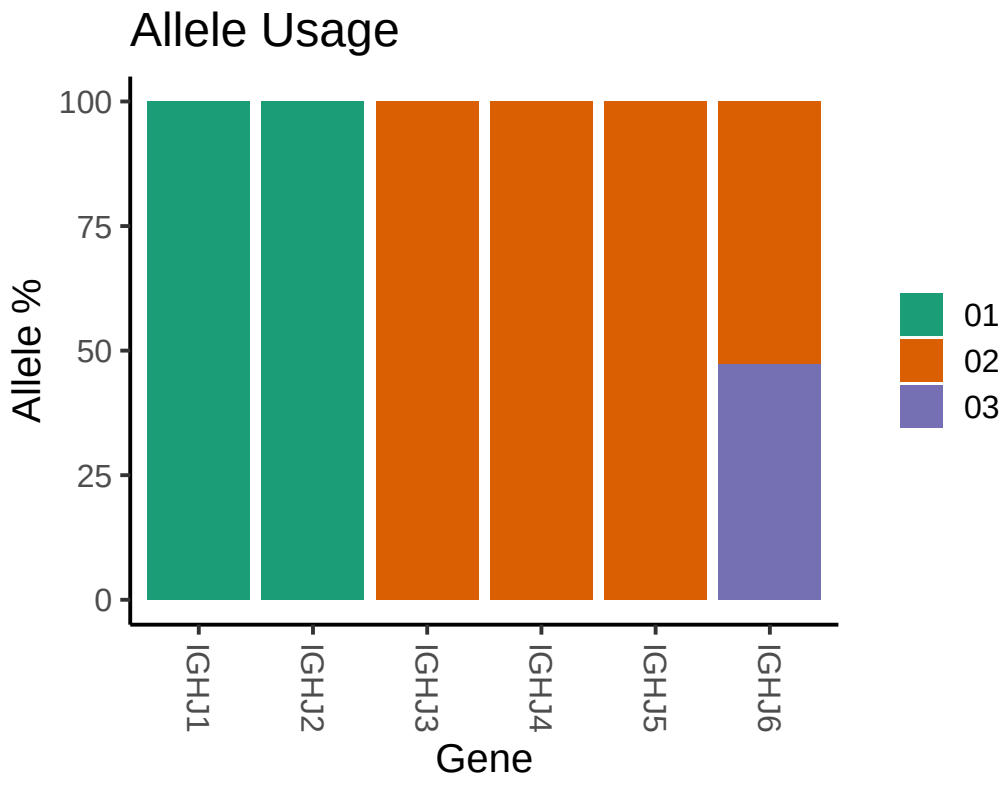
907 sequences assigned
53 (5.8%) exact matches, in which:
33 unique CDR3
6 unique J



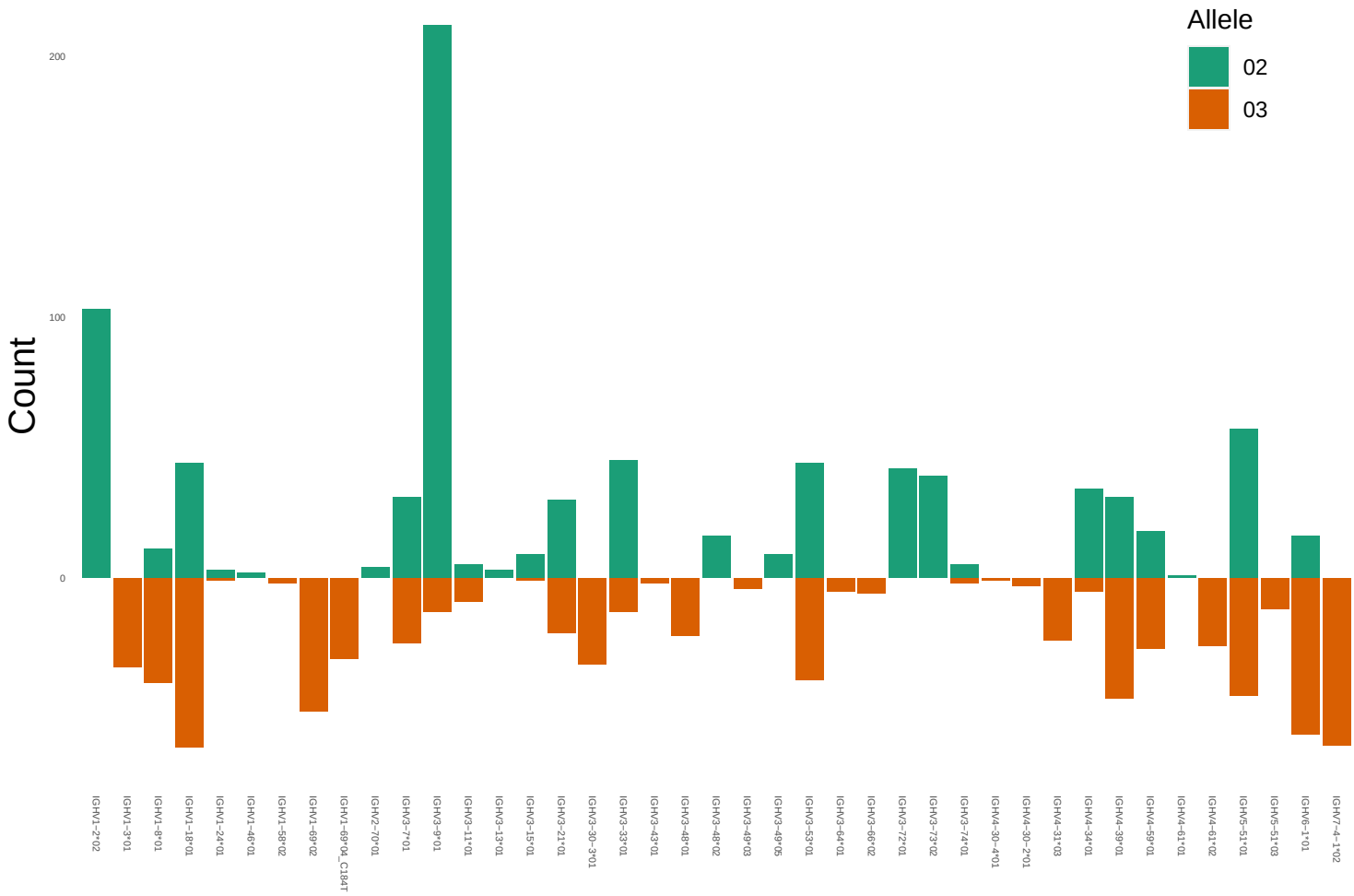
IGHV5−51*03

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




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

Sequence Count by IGHJ6 allele usage



Warning − no inferred sequences found.

Warning − no inferred sequences found.

Warning − no inferred sequences found.

Warning − no inferred sequences found.