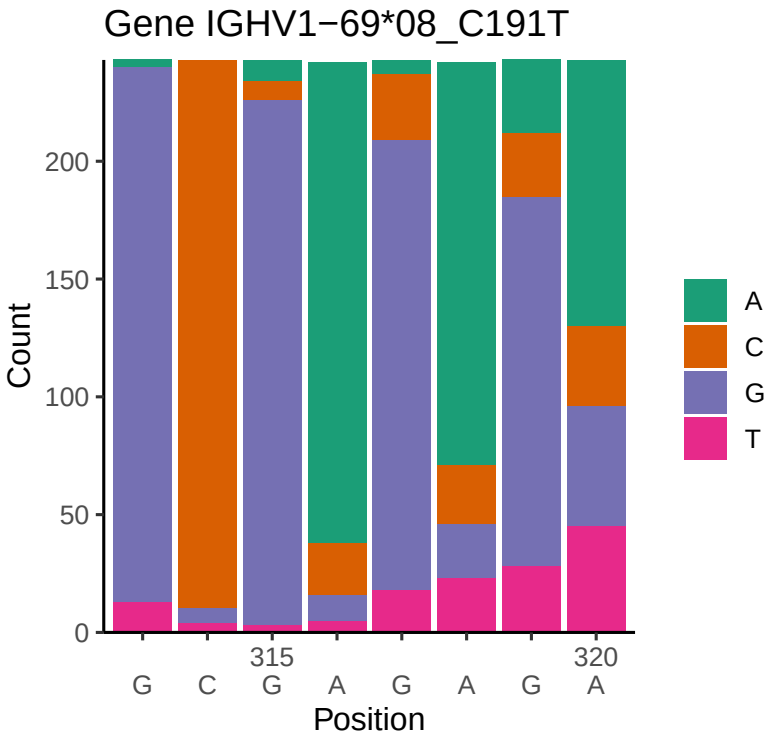
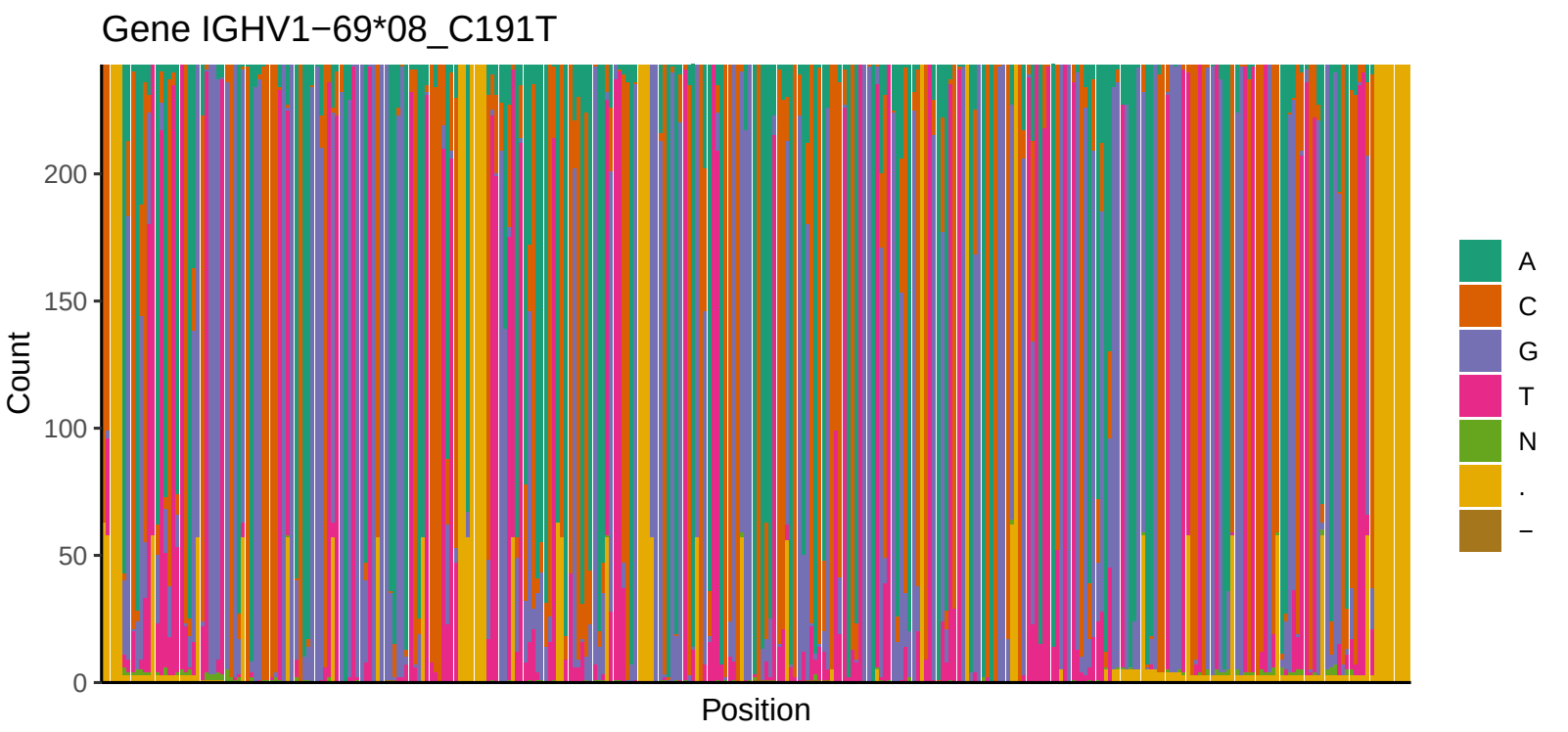
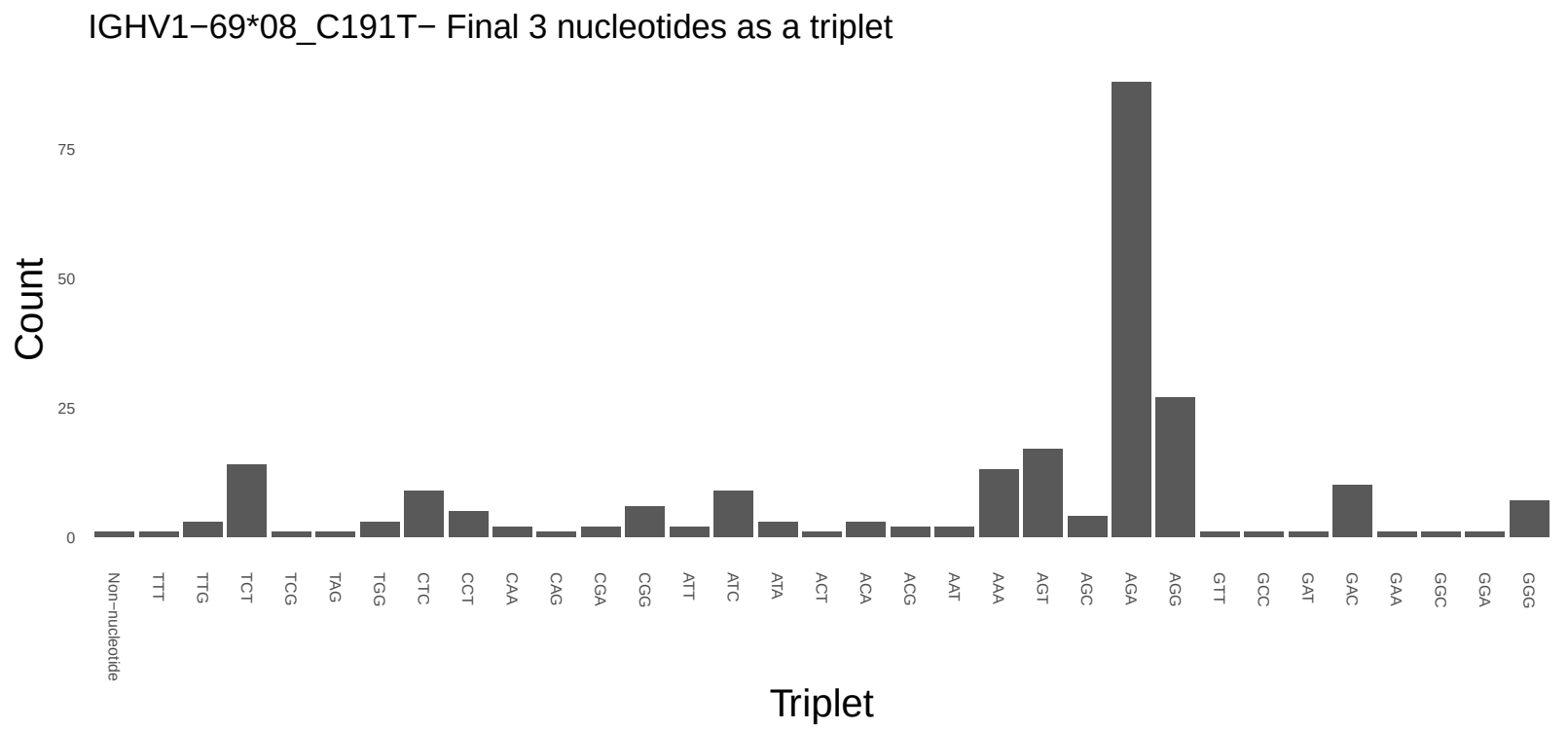
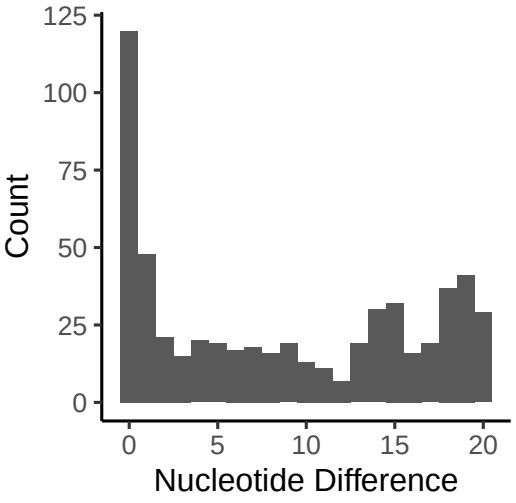

Gene IGHV1−69*08_C191T
Count
0
50
100
150
200
G
C
315
G
A
G
A
G
320
A
Position
A
C
G
T


Gene IGHV1−69*08_C191T
Count
0
50
100
150
200
Position
A
C
G
T
N
.
–


IGHV1−69*08_C191T− Final 3 nucleotides as a triplet
Count
75
50
25
0
Non−nucleotide
TTT
TTG
TCT
TCG
TAG
TGG
CTC
CCT
CAA
CAG
CGA
CGG
ATT
ATC
ATA
ACT
ACA
ACG
AAT
AAA
AGT
AGC
AGA
AGG
GTT
GCC
GAT
GAC
GAA
GGC
GGA
GGG
Triplet

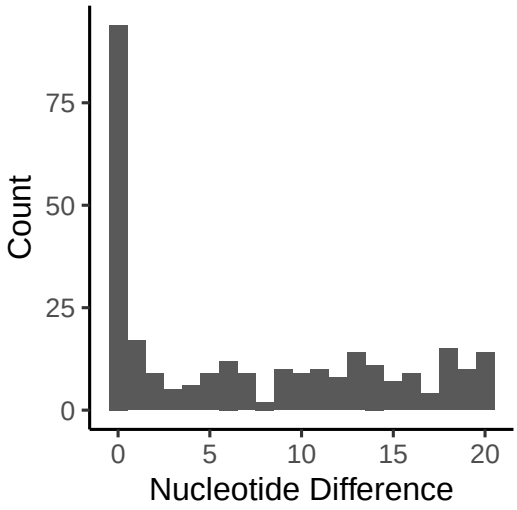
IGHV1−2*02

1010 sequences assigned
120 (11.9%) exact matches, in which:
116 unique CDR3
7 unique J



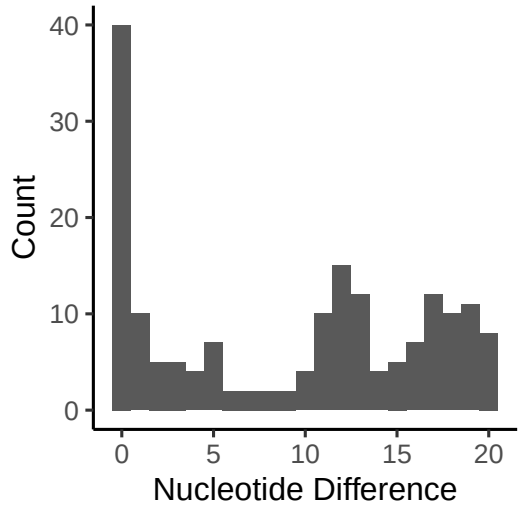
IGHV1−18*01

621 sequences assigned
94 (15.1%) exact matches, in which:
94 unique CDR3
6 unique J



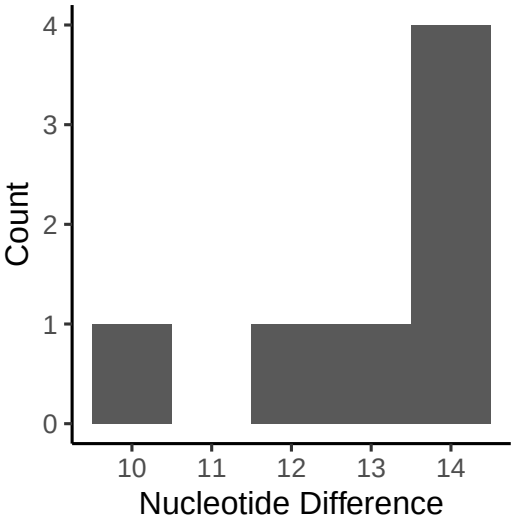
IGHV1−46*03

376 sequences assigned
40 (10.6%) exact matches, in which:
38 unique CDR3
6 unique J



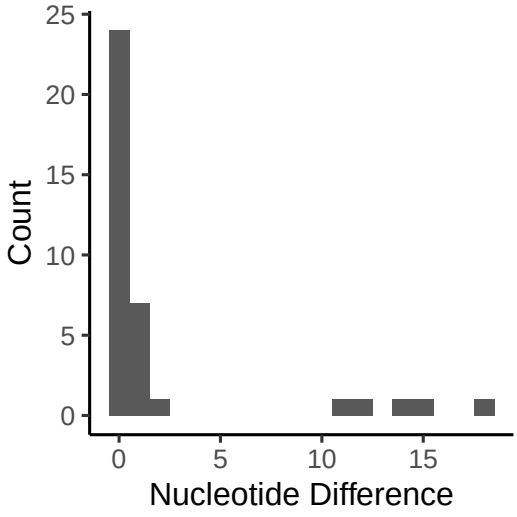
IGHV1−3*02

10 sequences assigned
No exact matches.



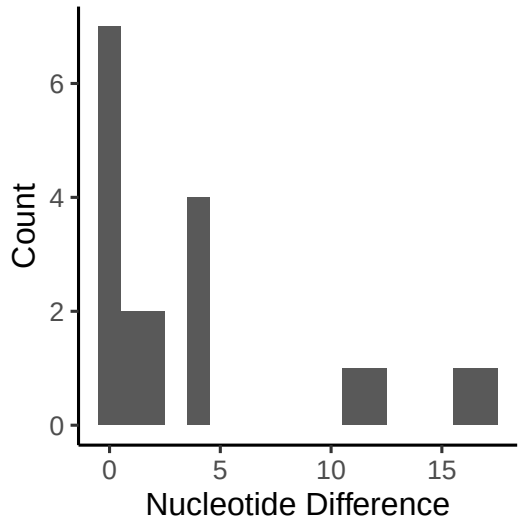
IGHV1−24*01

67 sequences assigned
24 (35.8%) exact matches, in which:
24 unique CDR3
5 unique J



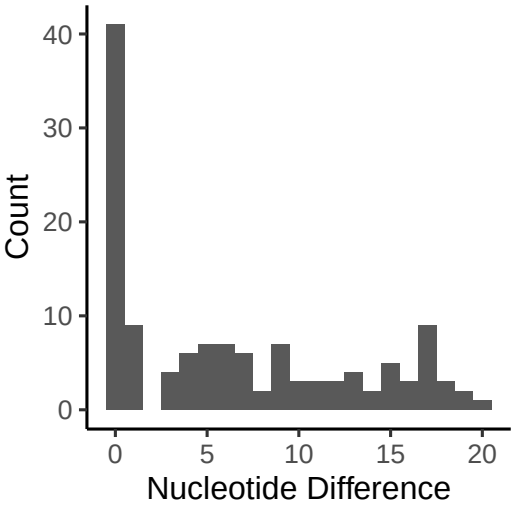
IGHV1−58*02

36 sequences assigned
7 (19.4%) exact matches, in which:
7 unique CDR3
2 unique J



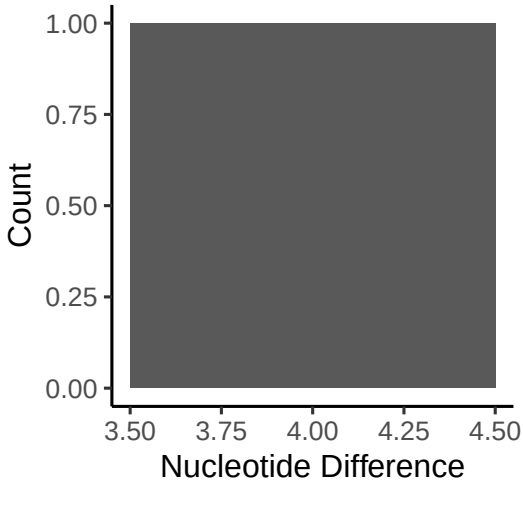
IGHV1−8*01

217 sequences assigned
41 (18.9%) exact matches, in which:
40 unique CDR3
7 unique J



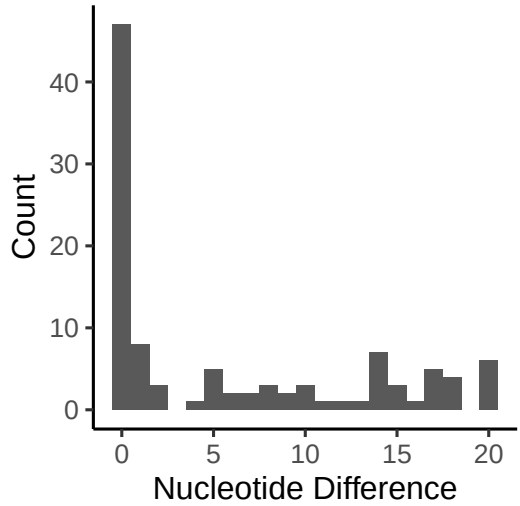
IGHV1−45*02

17 sequences assigned
No exact matches.



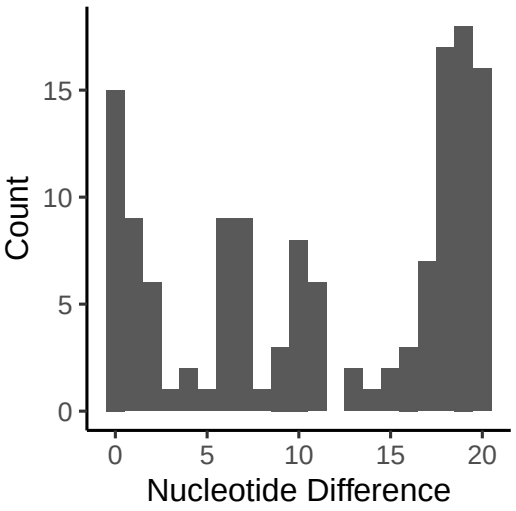
IGHV1−69*08_C191T

243 sequences assigned
47 (19.3%) exact matches, in which:
46 unique CDR3
6 unique J



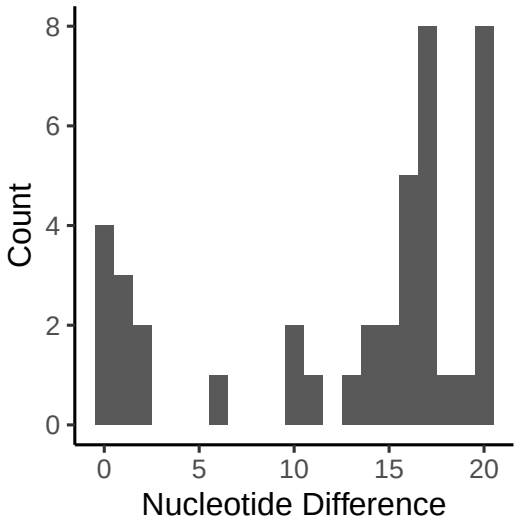
IGHV2−5*01

231 sequences assigned
15 (6.5%) exact matches, in which:
15 unique CDR3
4 unique J



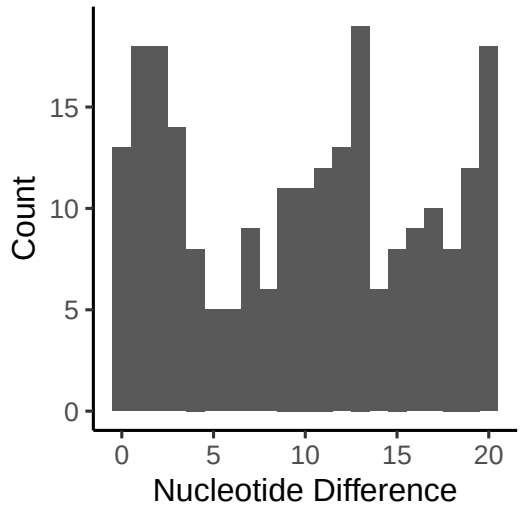
IGHV2−70*01

70 sequences assigned
4 (5.7%) exact matches, in which:
4 unique CDR3
3 unique J



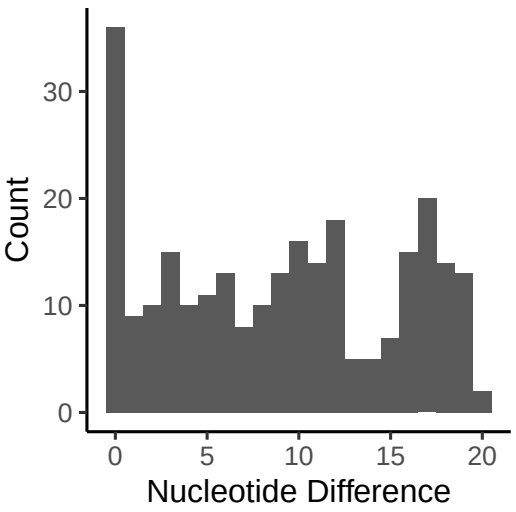
IGHV3−7*01

527 sequences assigned
13 (2.5%) exact matches, in which:
11 unique CDR3
4 unique J



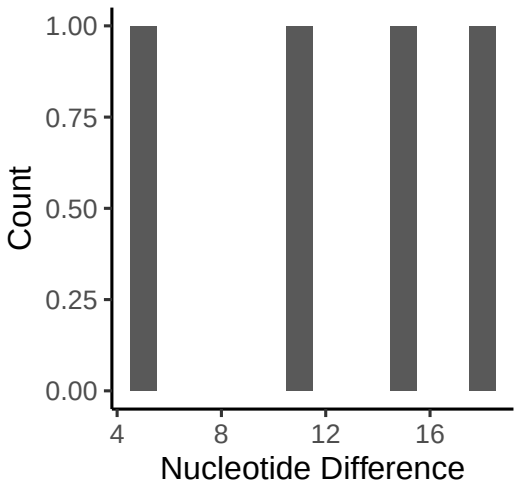
IGHV2−5*02

507 sequences assigned
36 (7.1%) exact matches, in which:
36 unique CDR3
5 unique J



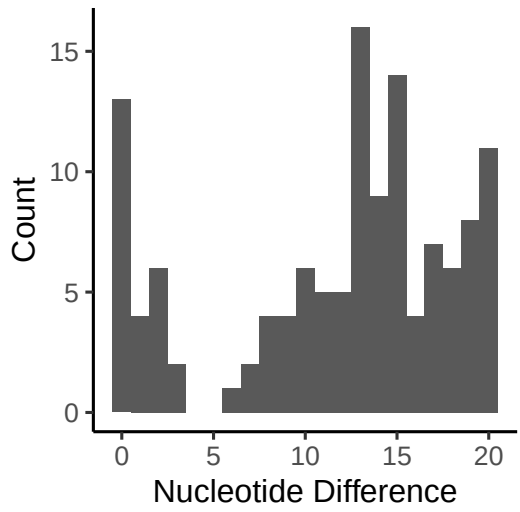
IGHV2−70*20

4 sequences assigned
No exact matches.



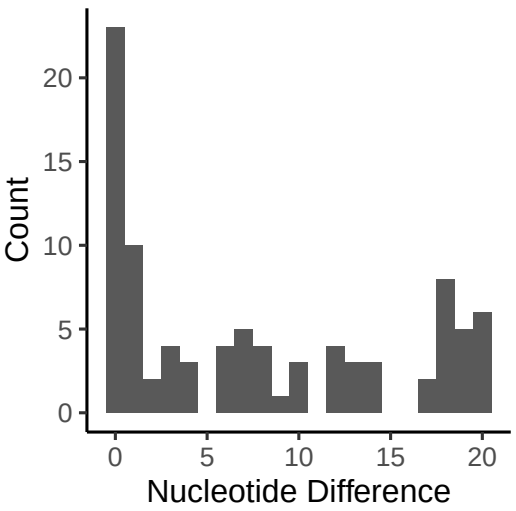
IGHV3−7*04

221 sequences assigned
13 (5.9%) exact matches, in which:
11 unique CDR3
3 unique J



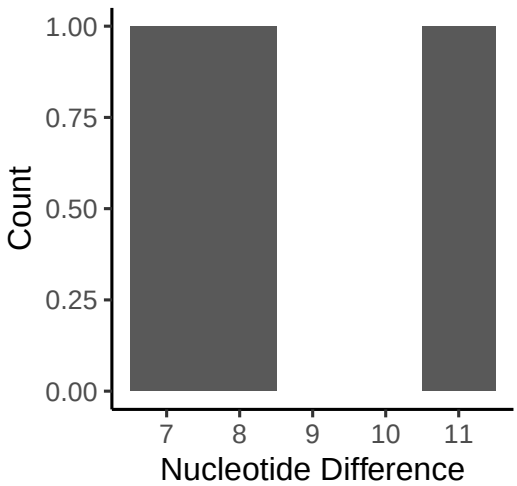
IGHV2−26*01

138 sequences assigned
23 (16.7%) exact matches, in which:
23 unique CDR3
6 unique J



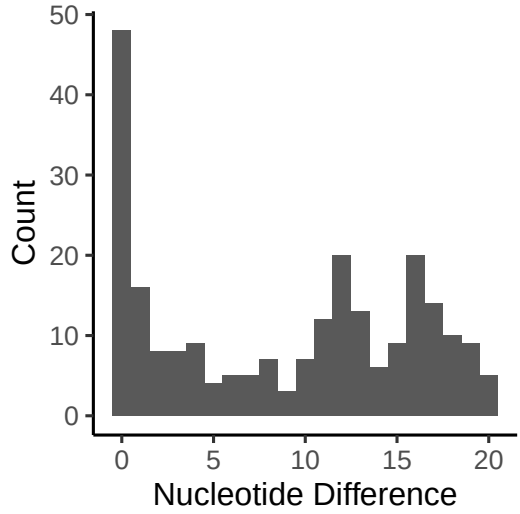
IGHV2−70D*04

3 sequences assigned
No exact matches.



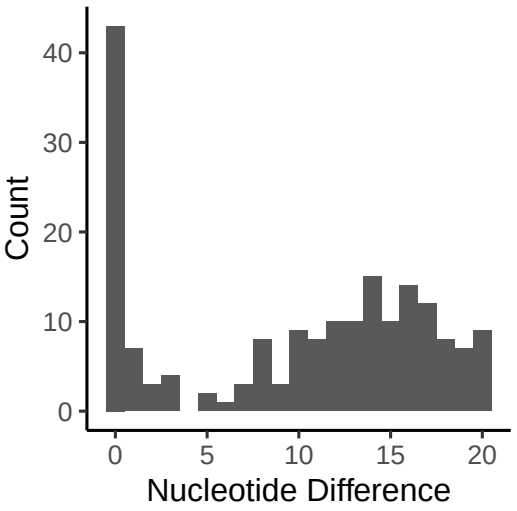
IGHV3−9*01

644 sequences assigned
48 (7.5%) exact matches, in which:
47 unique CDR3
5 unique J



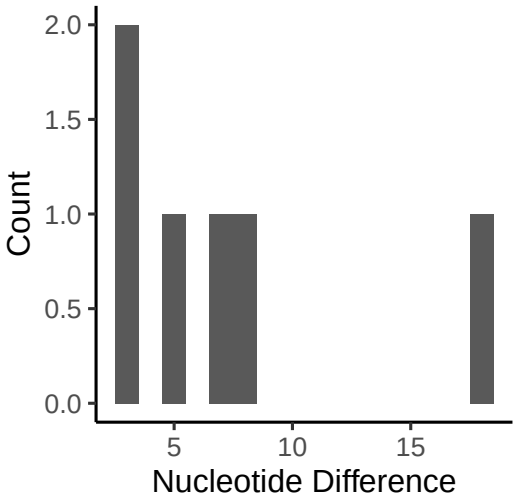
IGHV3−11*01

500 sequences assigned
43 (8.6%) exact matches, in which:
41 unique CDR3
5 unique J



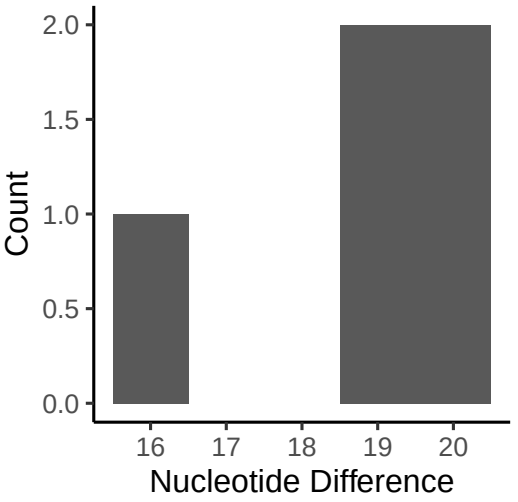
IGHV3−13*05

7 sequences assigned
No exact matches.



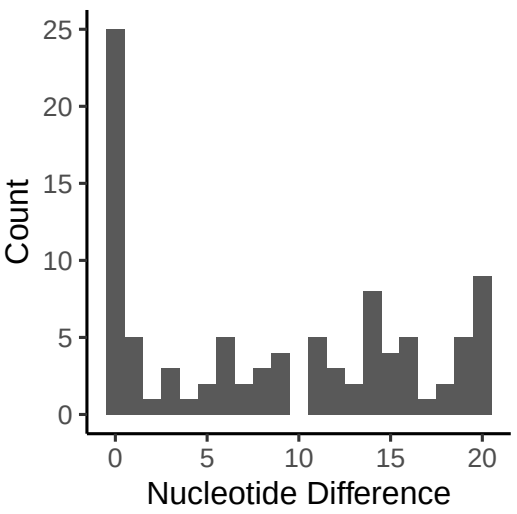
IGHV3−20*04

90 sequences assigned
No exact matches.



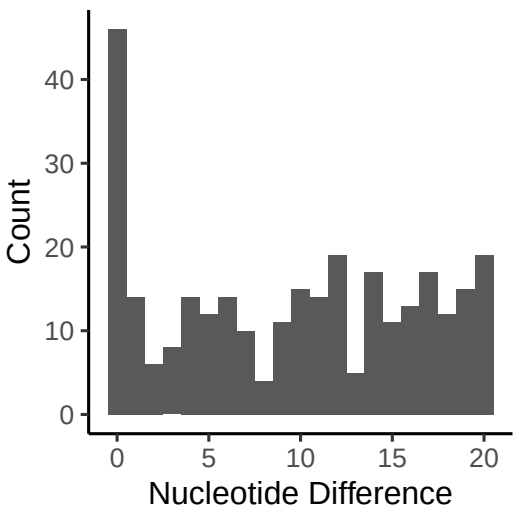
IGHV3−11*06

199 sequences assigned
25 (12.6%) exact matches, in which:
24 unique CDR3
4 unique J



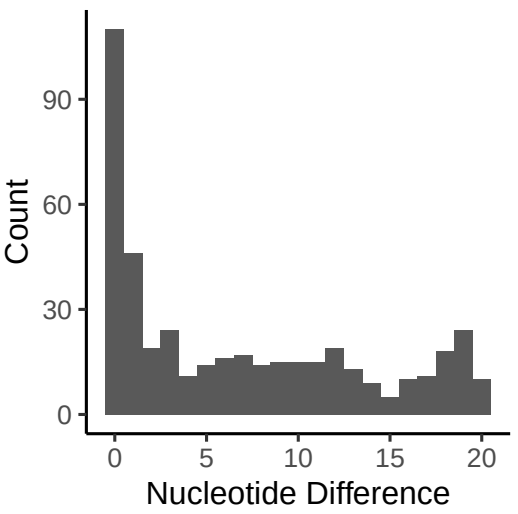
IGHV3−15*01

650 sequences assigned
46 (7.1%) exact matches, in which:
46 unique CDR3
6 unique J



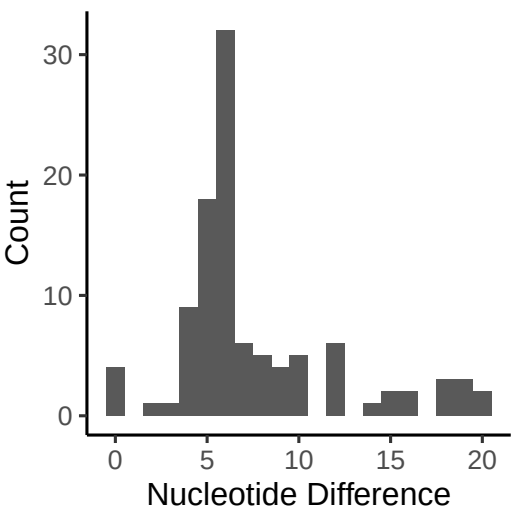
IGHV3−21*01

856 sequences assigned
110 (12.9%) exact matches, in which:
107 unique CDR3
5 unique J



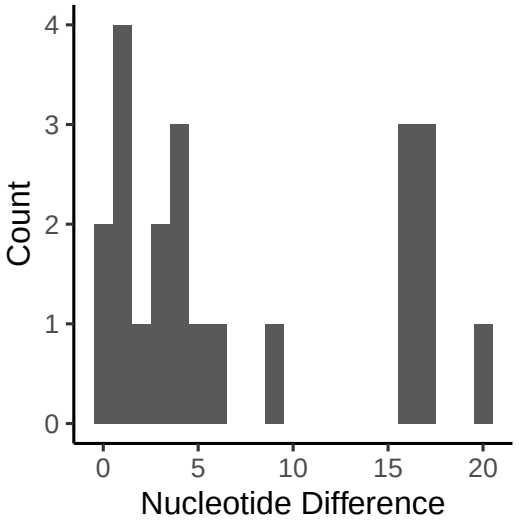
IGHV3−13*01

121 sequences assigned
4 (3.3%) exact matches, in which:
4 unique CDR3
3 unique J



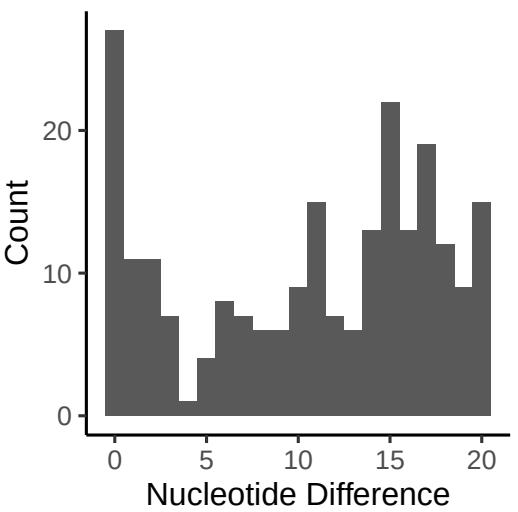
IGHV3−20*01

24 sequences assigned
2 (8.3%) exact matches, in which:
2 unique CDR3
2 unique J



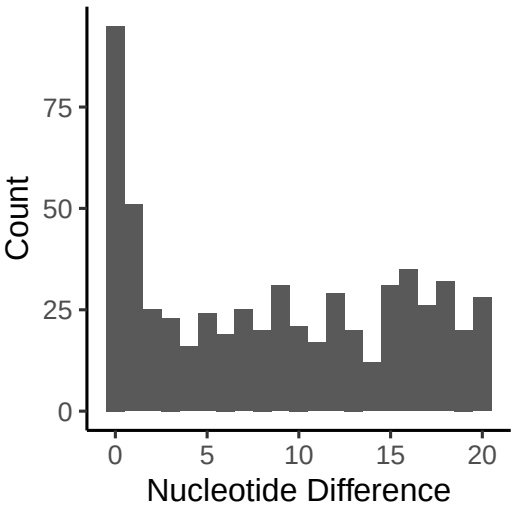
IGHV3−30−3*01

589 sequences assigned
27 (4.6%) exact matches, in which:
26 unique CDR3
5 unique J



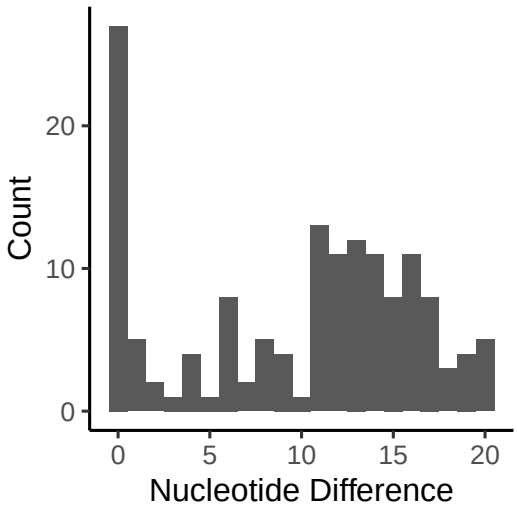
IGHV3−33*01

2087 sequences assigned
95 (4.6%) exact matches, in which:
94 unique CDR3
7 unique J



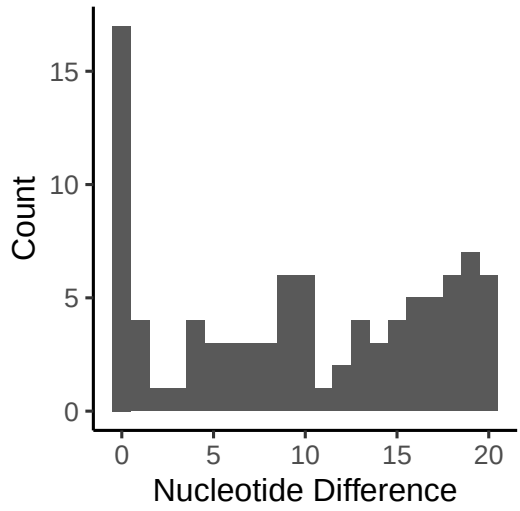
IGHV3−49*03

239 sequences assigned
27 (11.3%) exact matches, in which:
26 unique CDR3
6 unique J



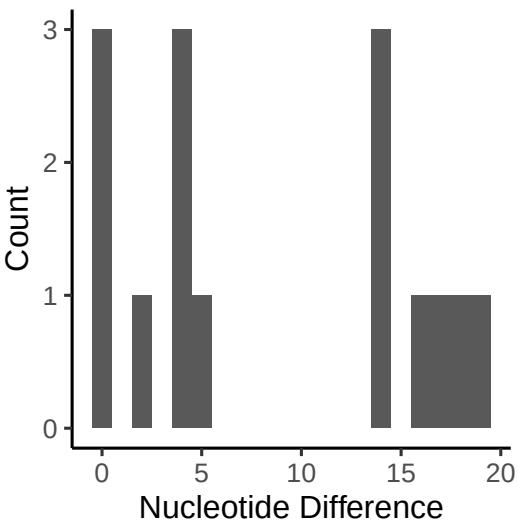
IGHV3−66*02

272 sequences assigned
17 (6.2%) exact matches, in which:
17 unique CDR3
4 unique J



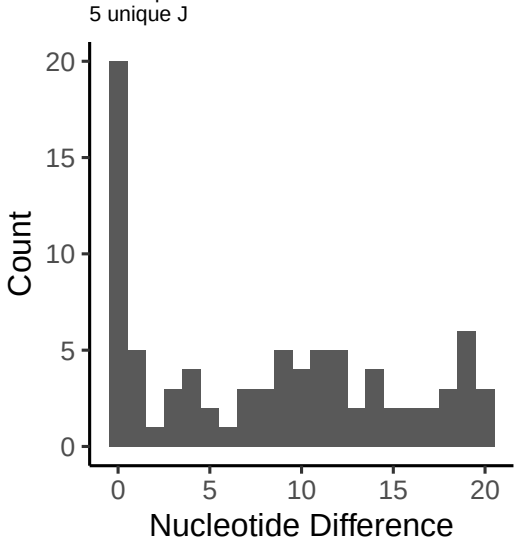
IGHV3−43*01

19 sequences assigned
3 (15.8%) exact matches, in which:
3 unique CDR3
2 unique J



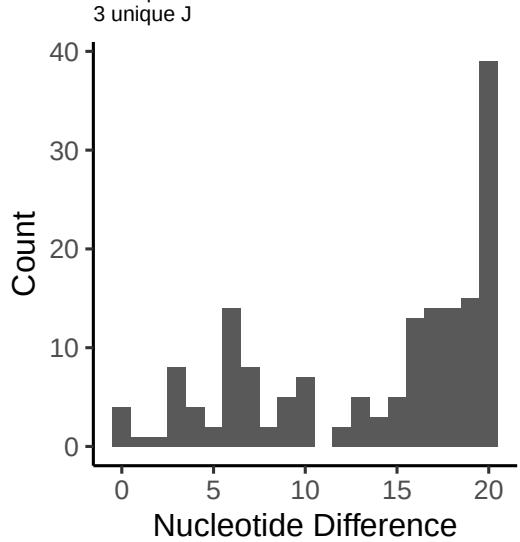
IGHV3−53*02

165 sequences assigned
20 (12.1%) exact matches, in which:
19 unique CDR3
5 unique J



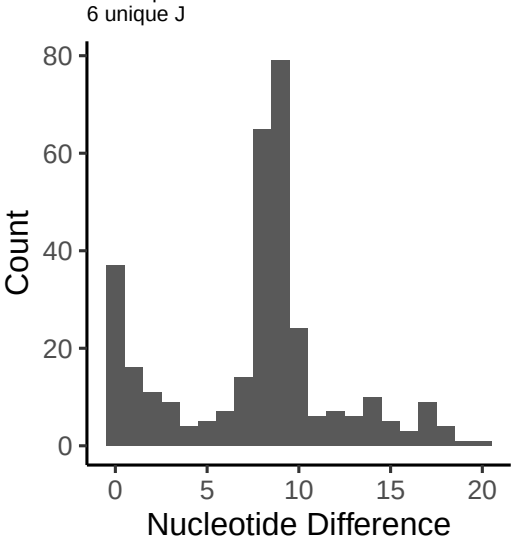
IGHV3−72*01

241 sequences assigned
4 (1.7%) exact matches, in which:
4 unique CDR3
3 unique J



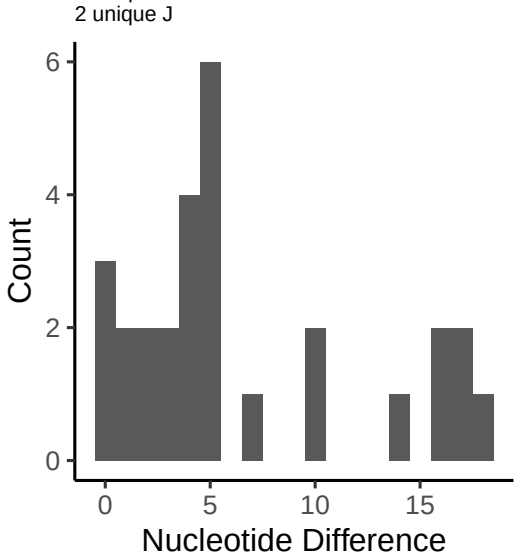
IGHV3−48*01

544 sequences assigned
37 (6.8%) exact matches, in which:
31 unique CDR3
6 unique J



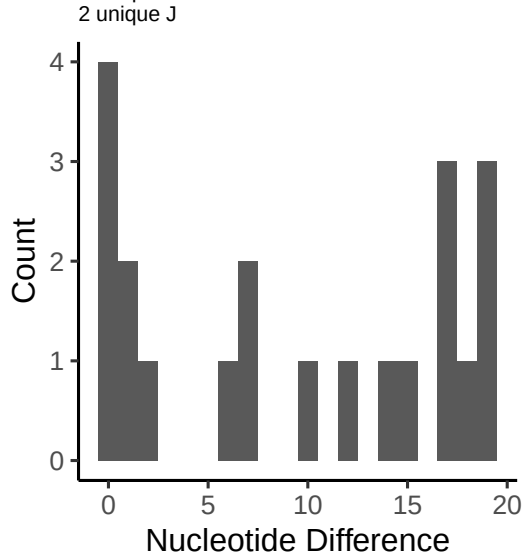
IGHV3−64*01

42 sequences assigned
3 (7.1%) exact matches, in which:
3 unique CDR3
2 unique J



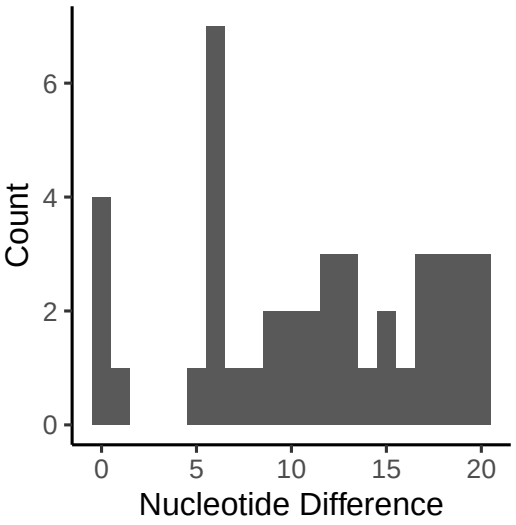
IGHV3−73*01

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



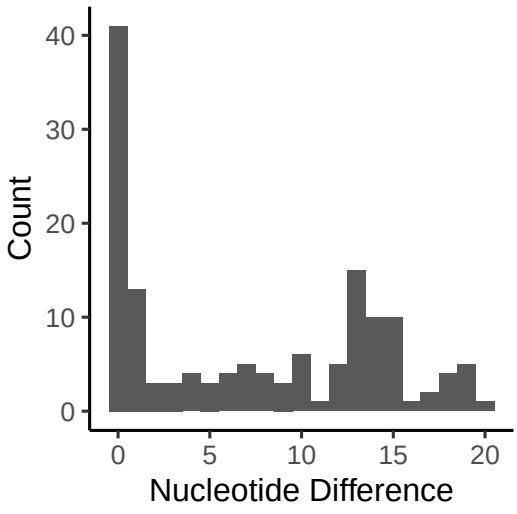
IGHV3−73*02

82 sequences assigned
4 (4.9%) exact matches, in which:
4 unique CDR3
2 unique J



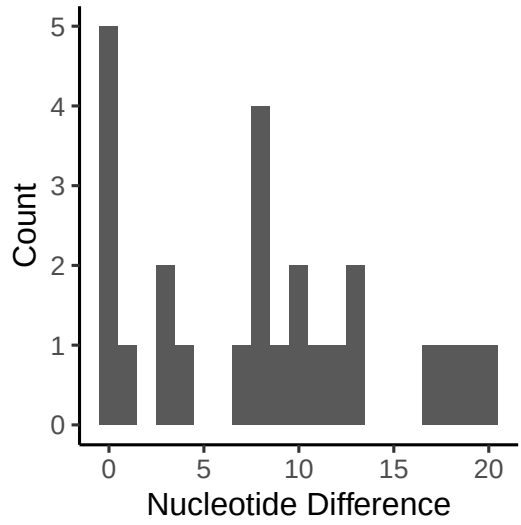
IGHV4−4*07

332 sequences assigned
41 (12.3%) exact matches, in which:
41 unique CDR3
7 unique J



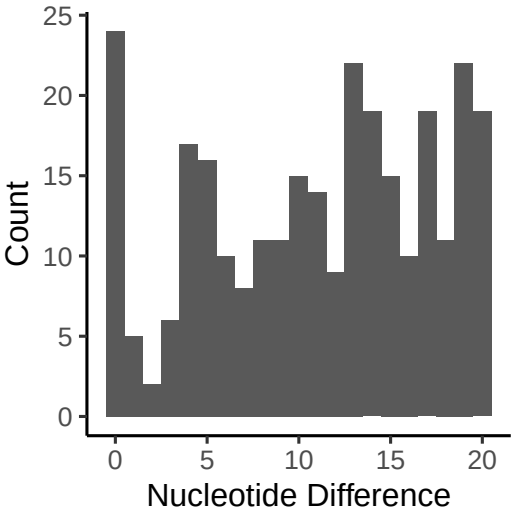
IGHV4−30−2*01

49 sequences assigned
5 (10.2%) exact matches, in which:
5 unique CDR3
4 unique J



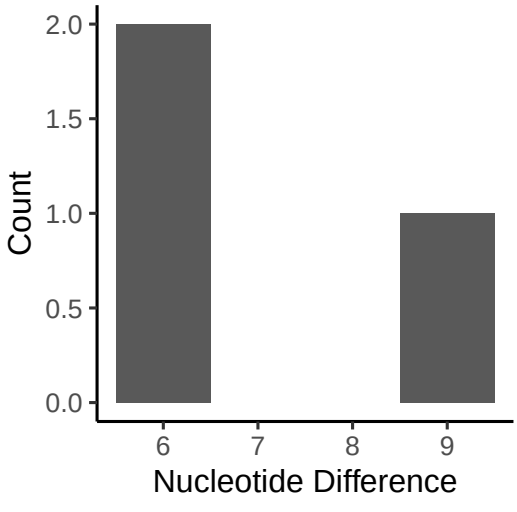
IGHV3−74*01

502 sequences assigned
24 (4.8%) exact matches, in which:
23 unique CDR3
5 unique J



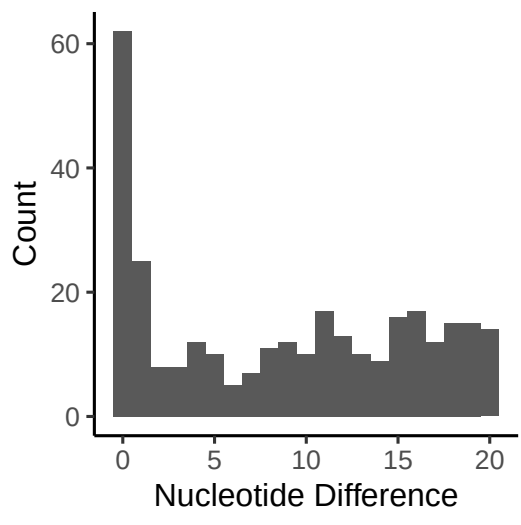
IGHV4−28*01

6 sequences assigned
No exact matches.



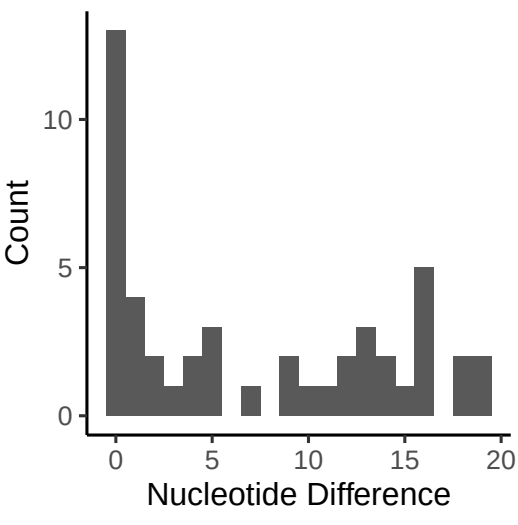
IGHV4−31*03

644 sequences assigned
62 (9.6%) exact matches, in which:
62 unique CDR3
6 unique J



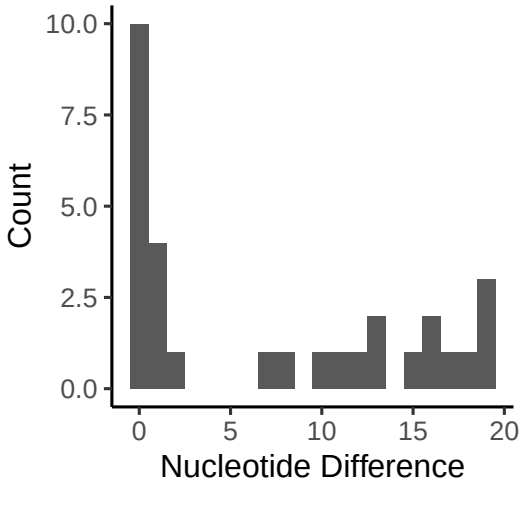
IGHV3−64D*06

177 sequences assigned
13 (7.3%) exact matches, in which:
13 unique CDR3
5 unique J



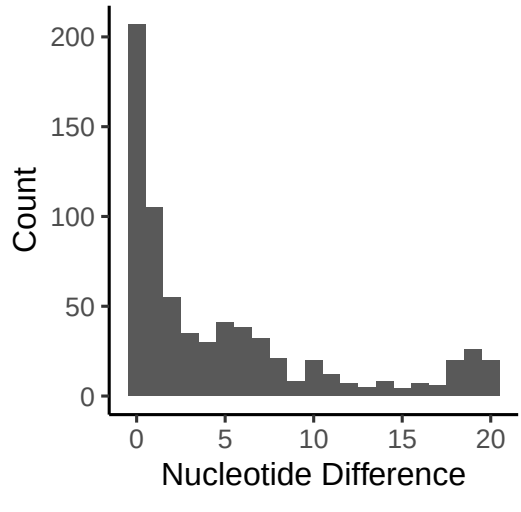
IGHV4−30−4*01

137 sequences assigned
10 (7.3%) exact matches, in which:
10 unique CDR3
4 unique J



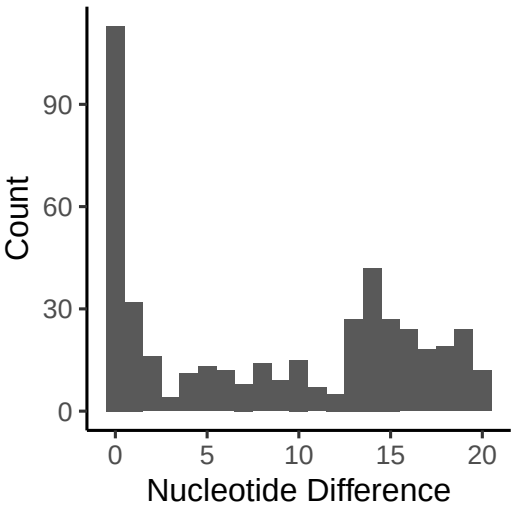
IGHV4−34*01

1292 sequences assigned
207 (16%) exact matches, in which:
193 unique CDR3
7 unique J



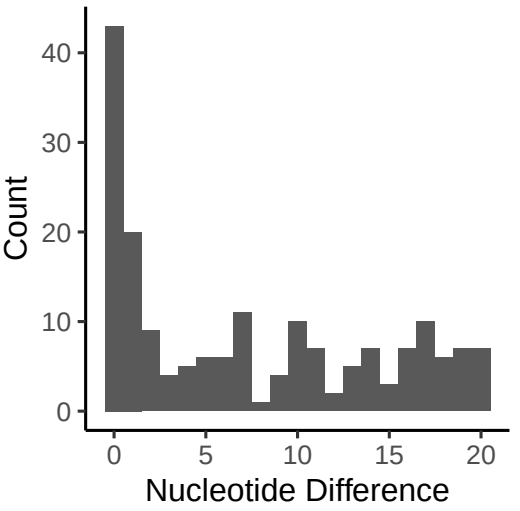
IGHV4−39*01

1163 sequences assigned
113 (9.7%) exact matches, in which:
108 unique CDR3
6 unique J



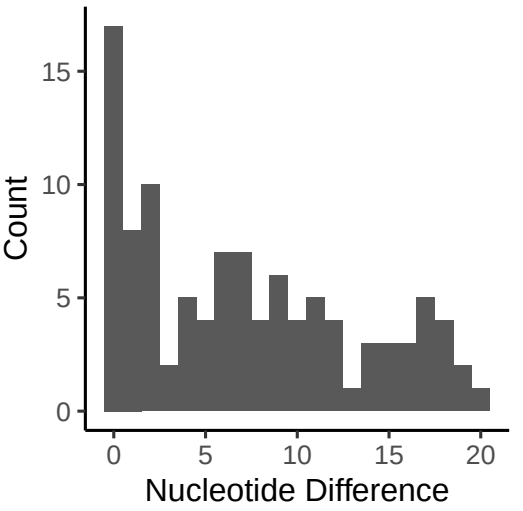
IGHV5−10−1*03

407 sequences assigned
43 (10.6%) exact matches, in which:
43 unique CDR3
4 unique J



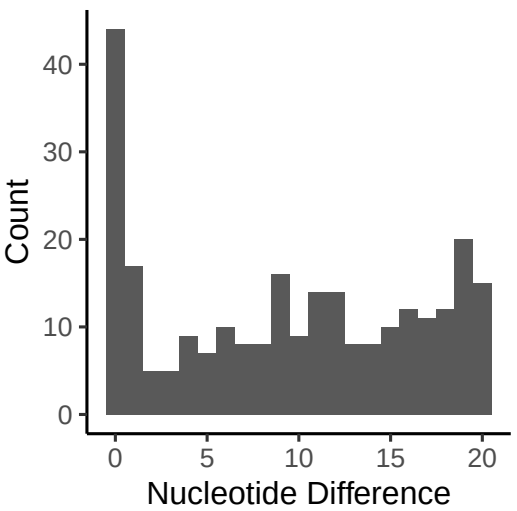
IGHV6−1*01

147 sequences assigned
17 (11.6%) exact matches, in which:
17 unique CDR3
4 unique J



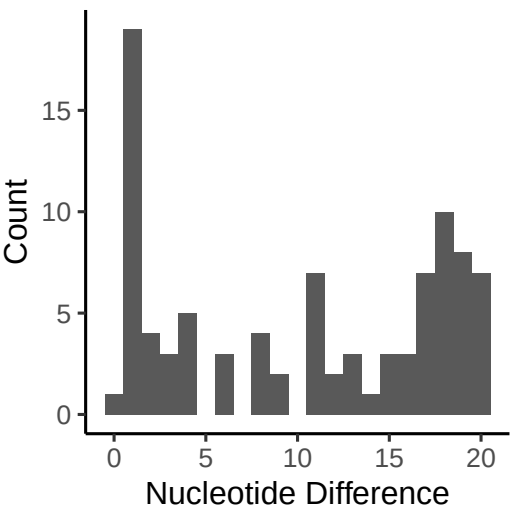
IGHV4−59*01

511 sequences assigned
44 (8.6%) exact matches, in which:
44 unique CDR3
6 unique J



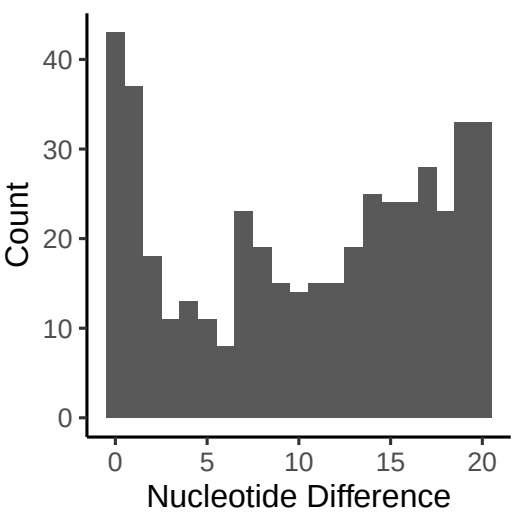
IGHV5−51*01

142 sequences assigned
1 (0.7%) exact matches, in which:
1 unique CDR3
1 unique J



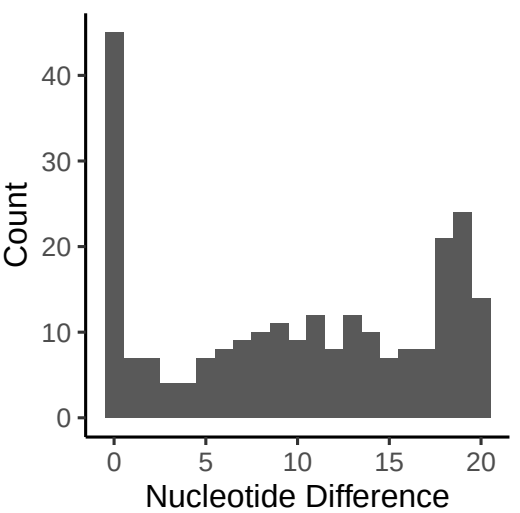
IGHV4−61*02

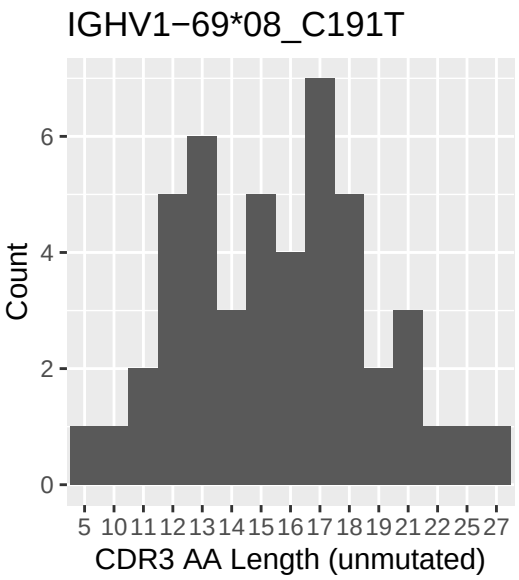
1305 sequences assigned
43 (3.3%) exact matches, in which:
42 unique CDR3
6 unique J

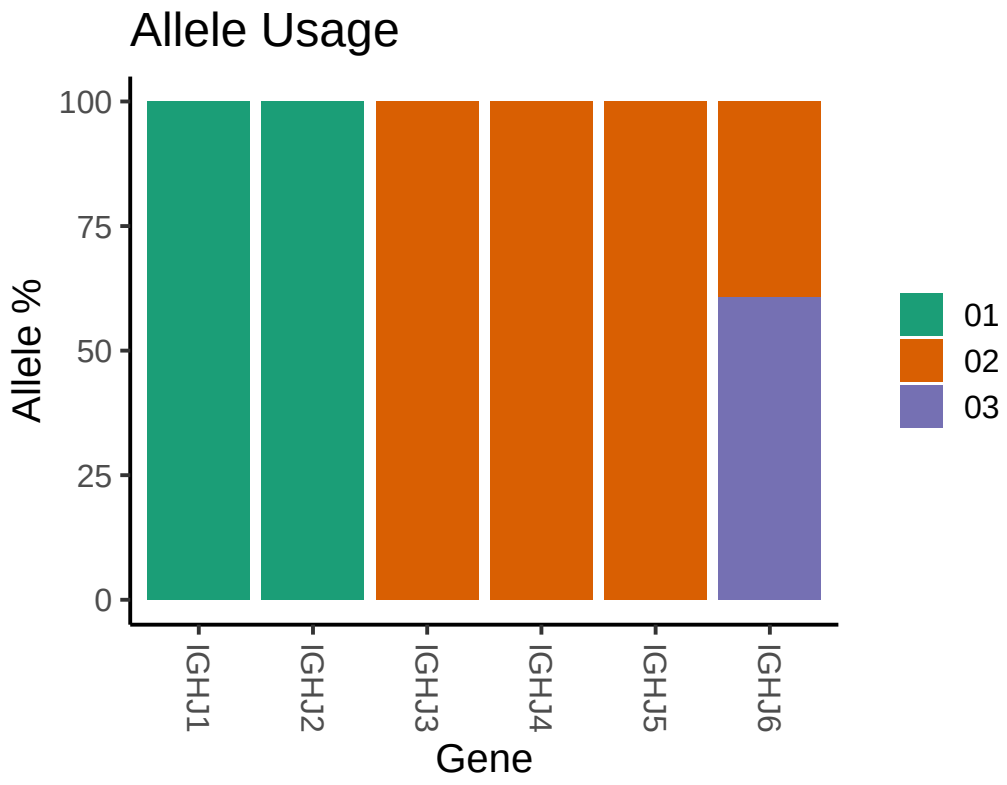


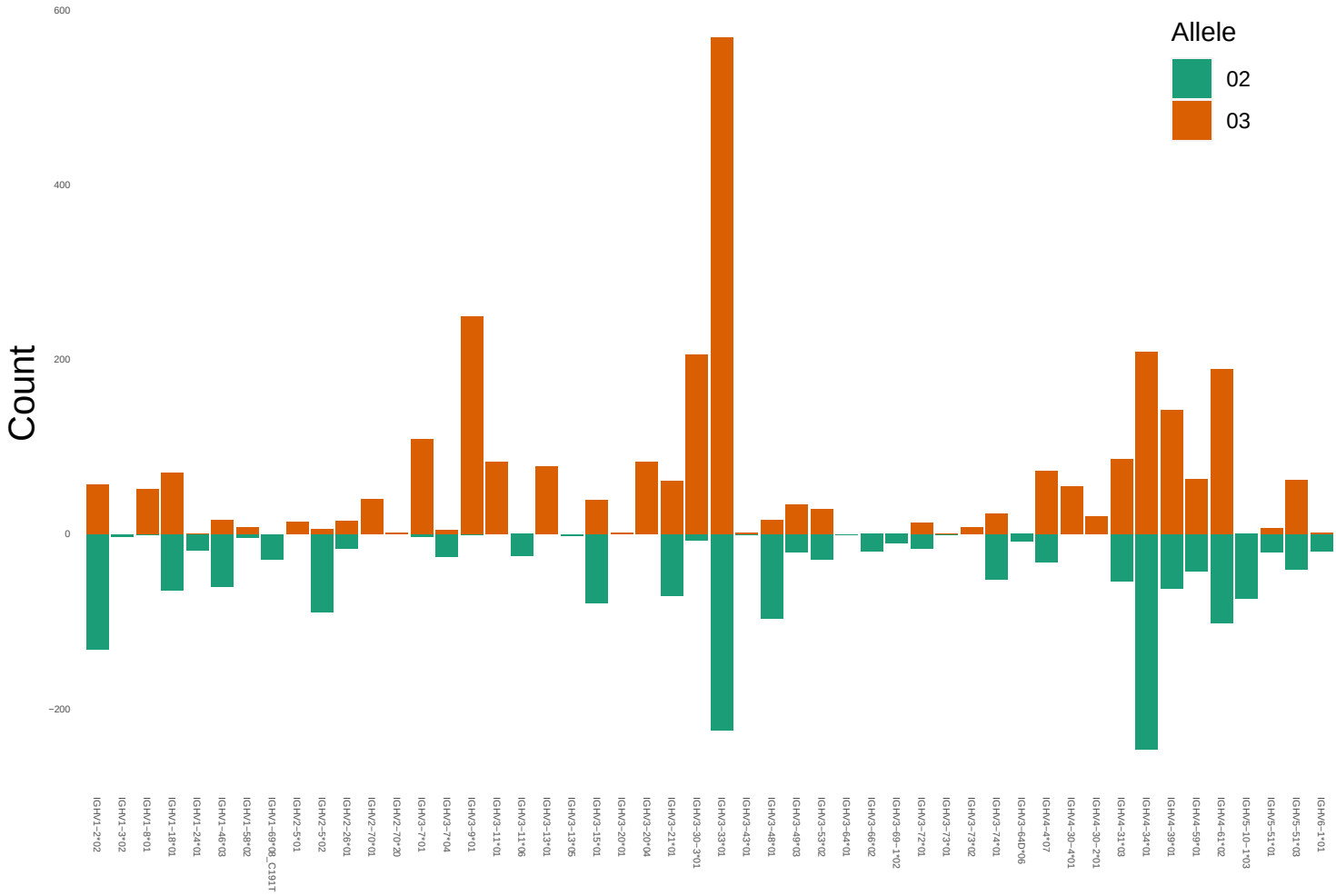
IGHV5−51*03

452 sequences assigned
45 (10%) exact matches, in which:
44 unique CDR3
7 unique J




IGHV1−69*08_C191T
Count
0
2
4
6
5 10 11 12 13 14 15 16 17 18 19 21 22 25 27
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
Count
600
400
200
0
−200
Allele
02
03
IGHV1−2*02
IGHV1−3*02
IGHV1−8*01
IGHV1−18*01
IGHV1−24*01
IGHV1−46*03
IGHV1−58*02
IGHV1−69*08_C191T
IGHV2−5*01
IGHV2−5*02
IGHV2−26*01
IGHV2−70*01
IGHV2−70*20
IGHV3−7*01
IGHV3−7*04
IGHV3−9*01
IGHV3−11*01
IGHV3−11*06
IGHV3−13*01
IGHV3−13*05
IGHV3−15*01
IGHV3−20*01
IGHV3−20*04
IGHV3−21*01
IGHV3−30−3*01
IGHV3−33*01
IGHV3−43*01
IGHV3−48*01
IGHV3−49*03
IGHV3−53*02
IGHV3−64*01
IGHV3−66*02
IGHV3−69−1*02
IGHV3−72*01
IGHV3−73*01
IGHV3−73*02
IGHV3−74*01
IGHV3−64D*06
IGHV4−4*07
IGHV4−30−4*01
IGHV4−30−2*01
IGHV4−31*03
IGHV4−34*01
IGHV4−39*01
IGHV4−59*01
IGHV4−61*02
IGHV5−10−1*03
IGHV5−51*01
IGHV5−51*03
IGHV6−1*01

Warning − no inferred sequences found.

Warning − no inferred sequences found.

Warning − no inferred sequences found.