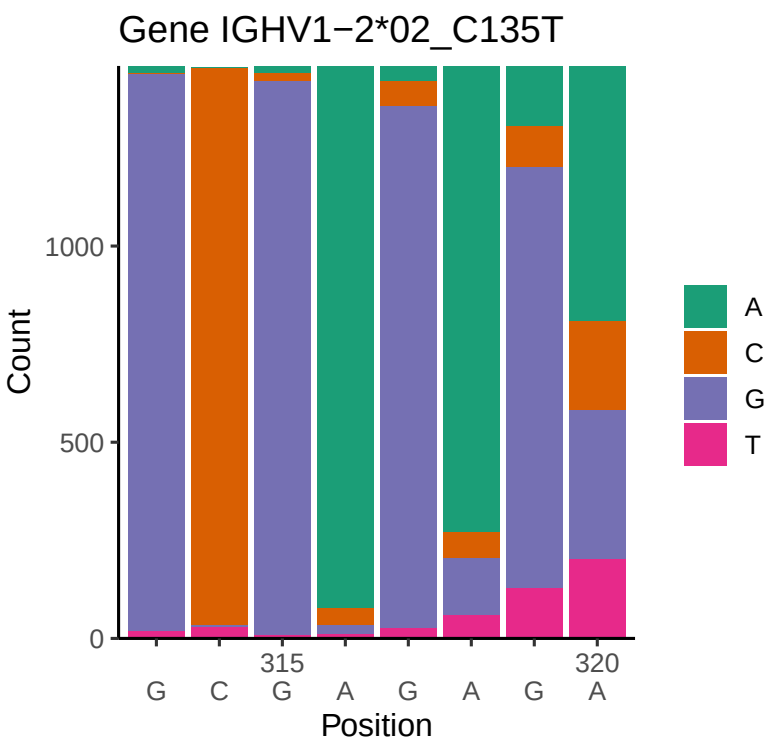
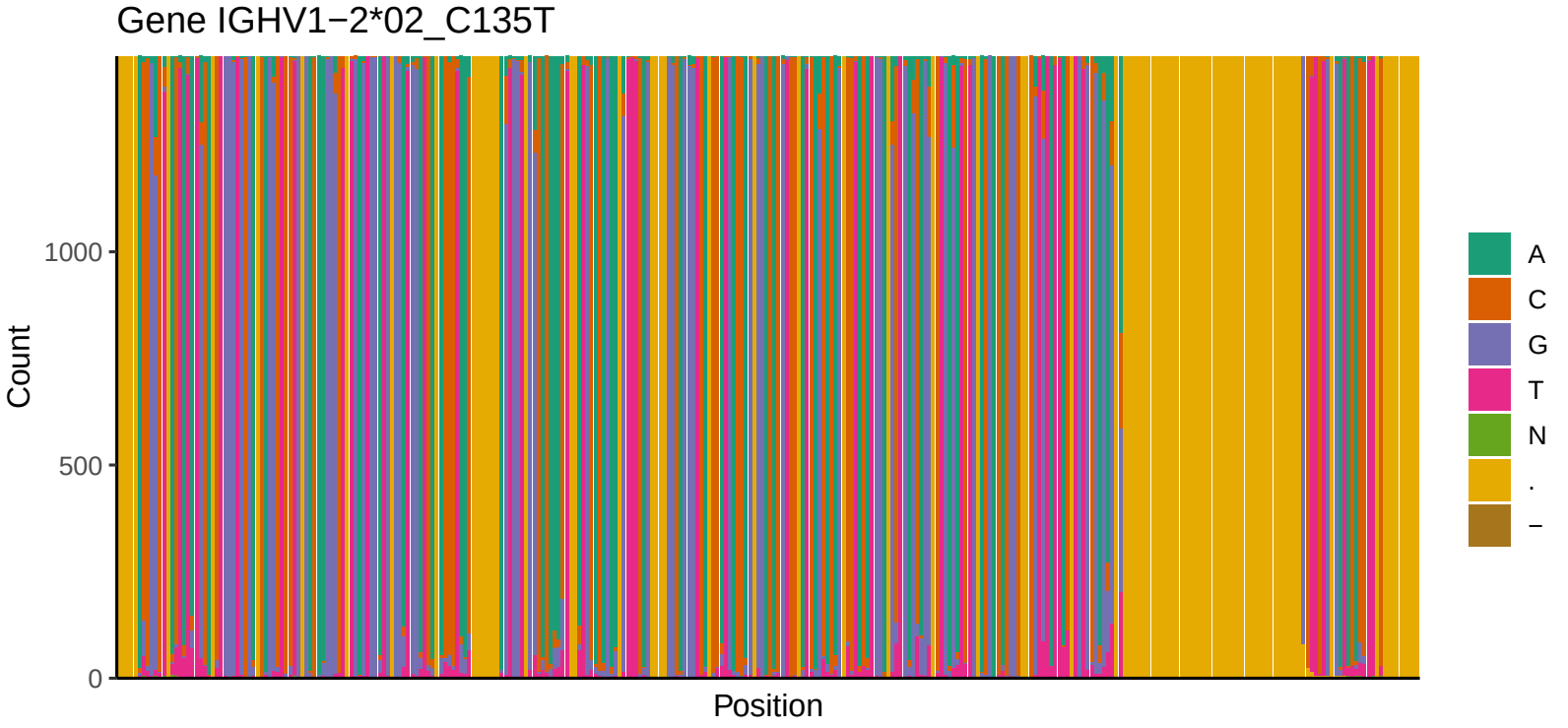
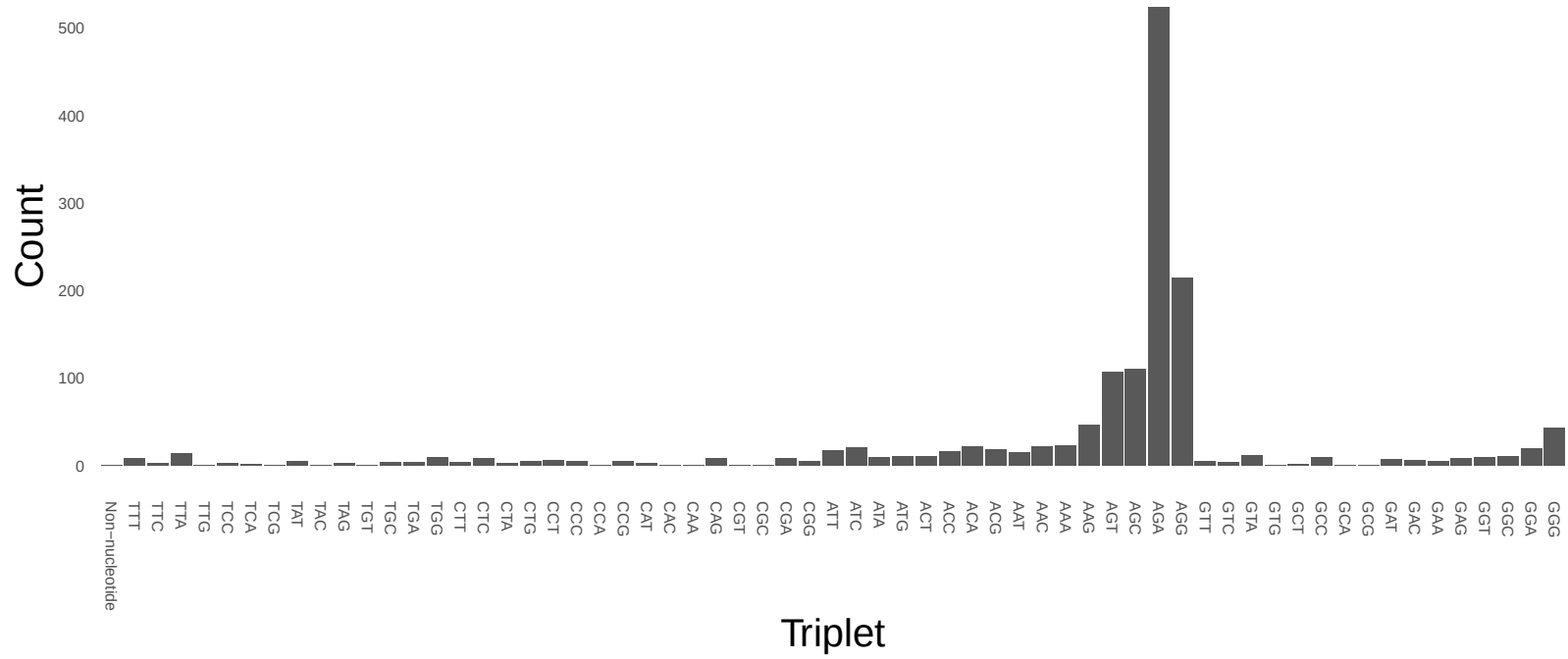

Gene IGHV1−2*02_C135T
Count
1000
500
0
315
320
G C G A G A G A
Position
A
C
G
T

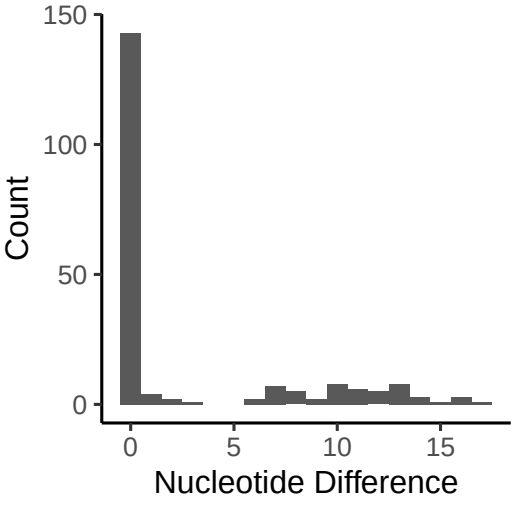

Gene IGHV1−2*02_C135T
Count
1000
500
0
Position
A
C
G
T
N
.
−

IGHV1−2*02_C135T− Final 3 nucleotides as a triplet



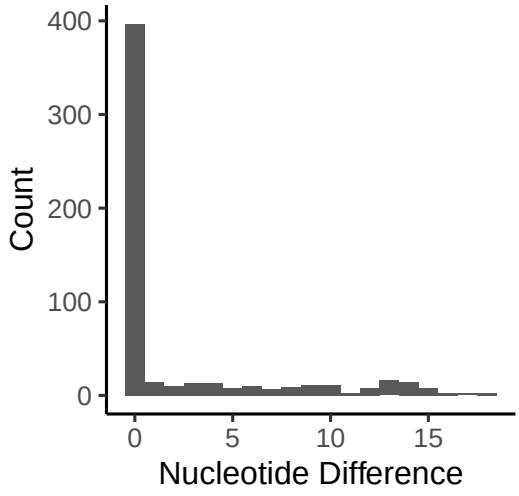
IGHV1−2*04

204 sequences assigned
143 (70.1%) exact matches, in which:
139 unique CDR3
4 unique J



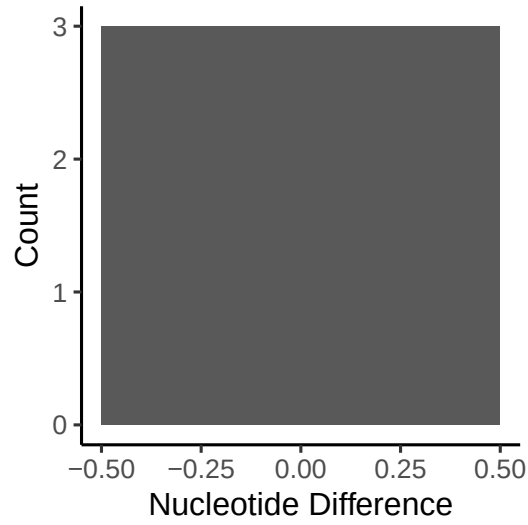
IGHV1−8*01

577 sequences assigned
397 (68.8%) exact matches, in which:
387 unique CDR3
5 unique J



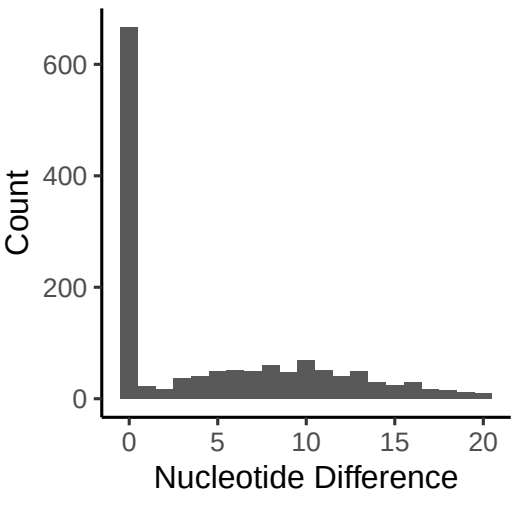
IGHV1−45*02

3 sequences assigned
3 (100%) exact matches, in which:
3 unique CDR3
2 unique J



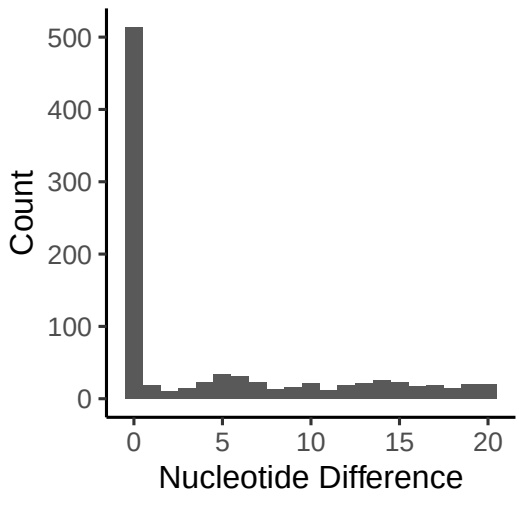
IGHV1−2*02_C135T

1459 sequences assigned
667 (45.7%) exact matches, in which:
654 unique CDR3
6 unique J



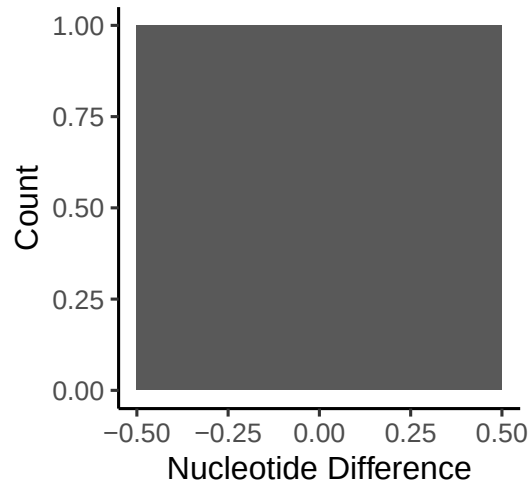
IGHV1−18*01

1115 sequences assigned
514 (46.1%) exact matches, in which:
499 unique CDR3
6 unique J



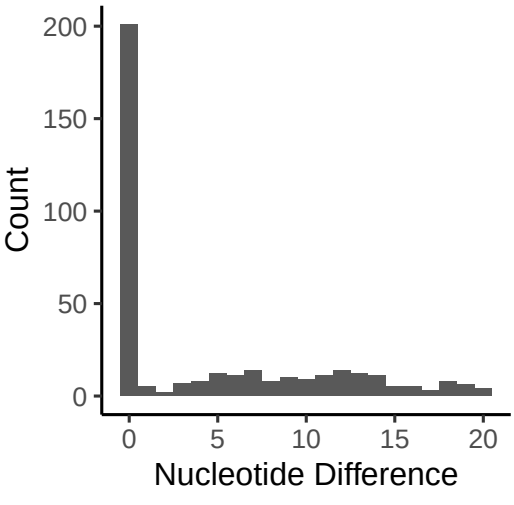
IGHV1−45*03

1 sequences assigned
1 (100%) exact matches, in which:
1 unique CDR3
1 unique J



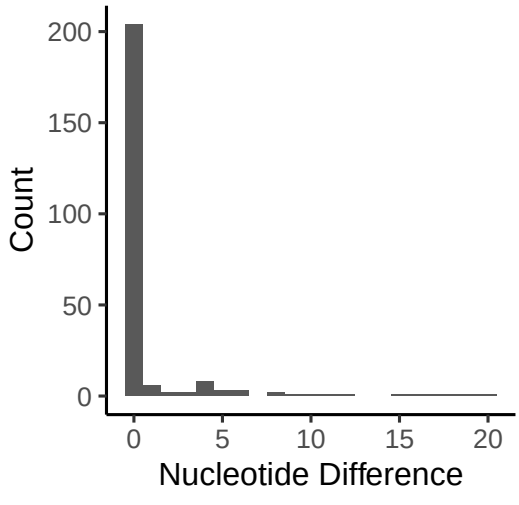
IGHV1−3*01_05

420 sequences assigned
201 (47.9%) exact matches, in which:
200 unique CDR3
6 unique J



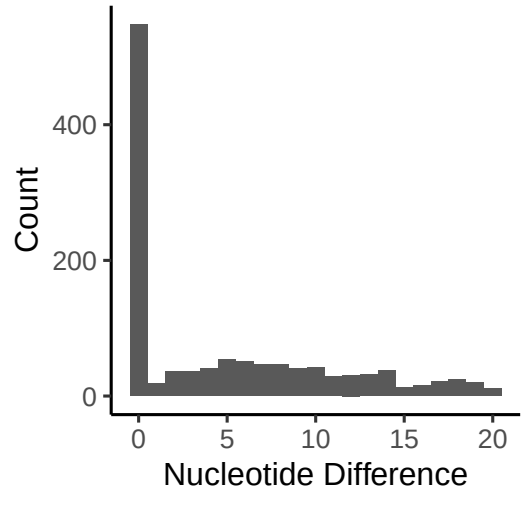
IGHV1−24*01

255 sequences assigned
204 (80%) exact matches, in which:
197 unique CDR3
6 unique J



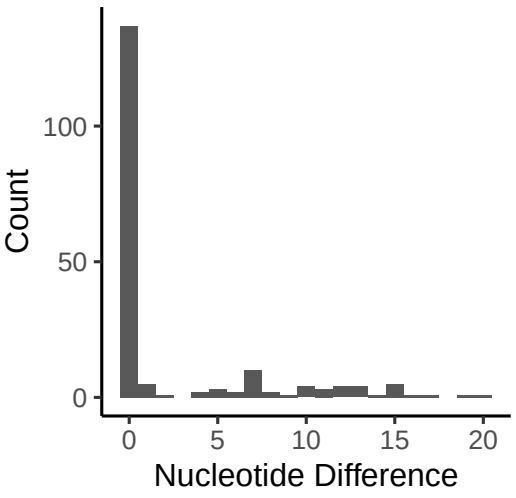
IGHV1−46*01

1283 sequences assigned
548 (42.7%) exact matches, in which:
537 unique CDR3
6 unique J



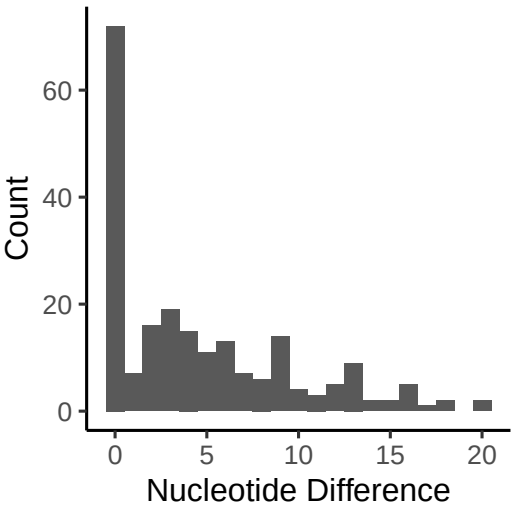
IGHV1−58*01_03

192 sequences assigned
137 (71.4%) exact matches, in which:
134 unique CDR3
6 unique J



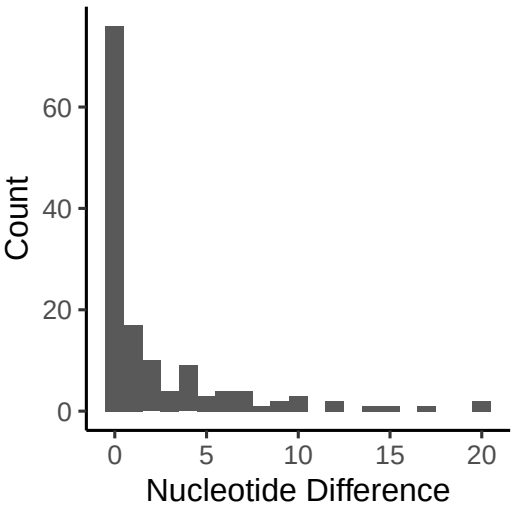
IGHV2−5*02

232 sequences assigned
72 (31%) exact matches, in which:
71 unique CDR3
6 unique J



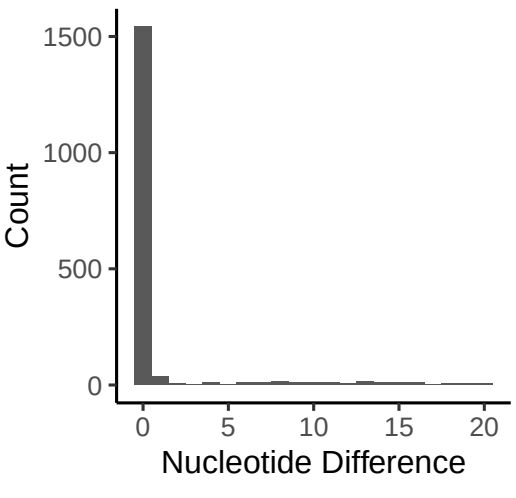
IGHV2−70*11_15

146 sequences assigned
76 (52.1%) exact matches, in which:
74 unique CDR3
5 unique J



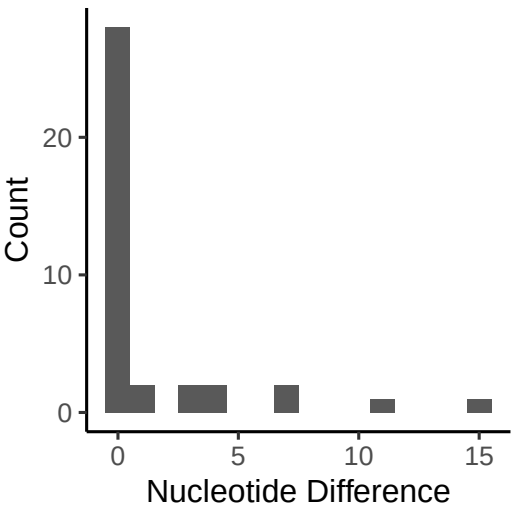
IGHV1−69*04_09

1813 sequences assigned
1542 (85.1%) exact matches, in which:
1512 unique CDR3
6 unique J



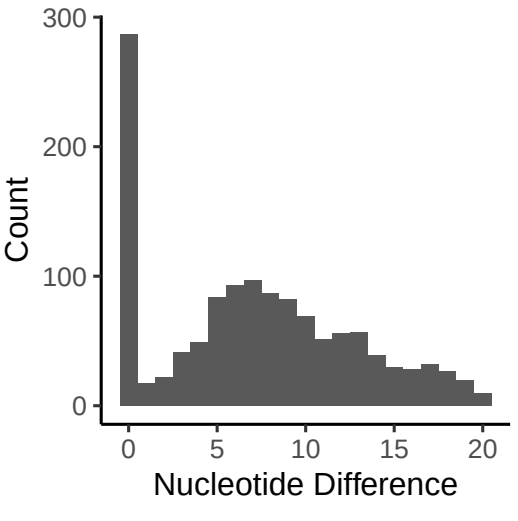
IGHV2−26*01

41 sequences assigned
28 (68.3%) exact matches, in which:
28 unique CDR3
5 unique J



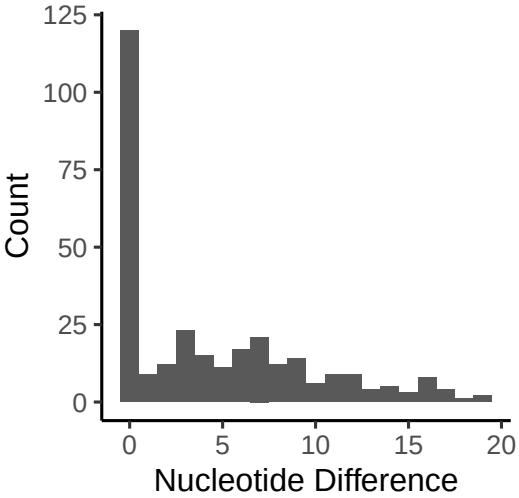
IGHV3−7*01

1372 sequences assigned
287 (20.9%) exact matches, in which:
264 unique CDR3
6 unique J



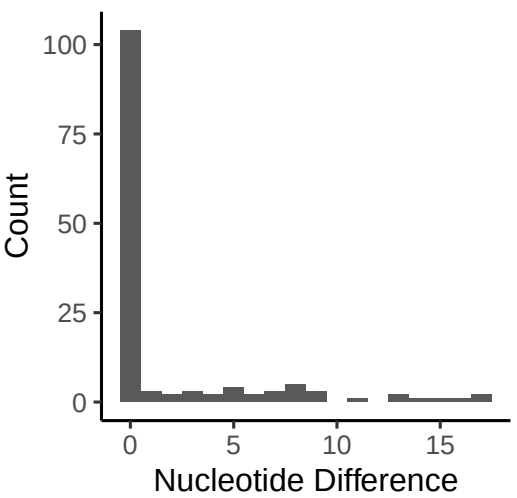
IGHV2−5*01

317 sequences assigned
120 (37.9%) exact matches, in which:
119 unique CDR3
5 unique J



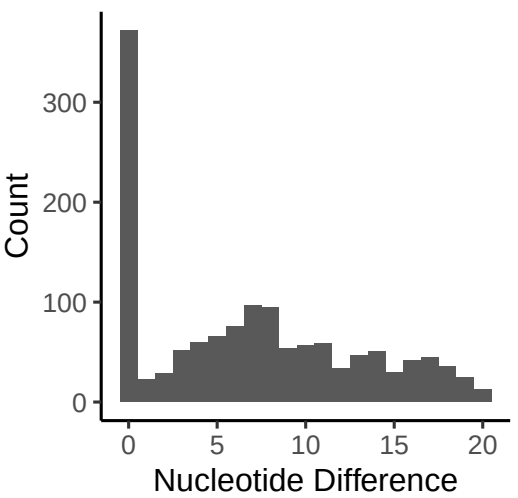
IGHV2−70*01

144 sequences assigned
104 (72.2%) exact matches, in which:
103 unique CDR3
6 unique J



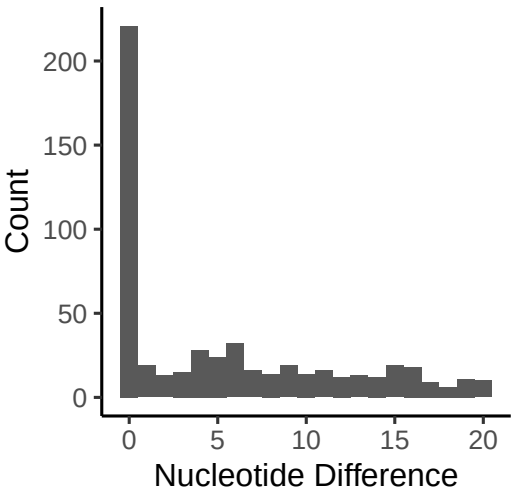
IGHV3−7*03

1468 sequences assigned
372 (25.3%) exact matches, in which:
332 unique CDR3
6 unique J



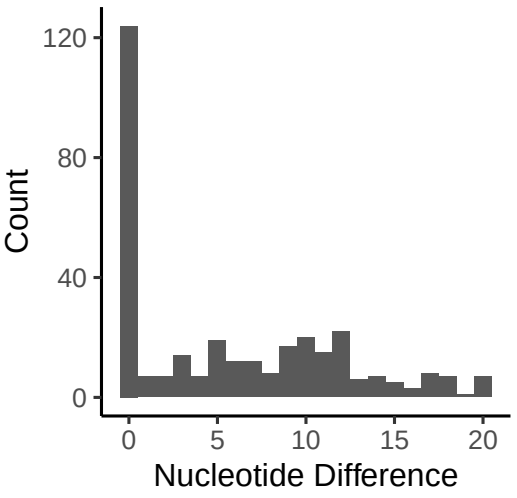
IGHV3−9*01

582 sequences assigned
221 (38%) exact matches, in which:
213 unique CDR3
6 unique J



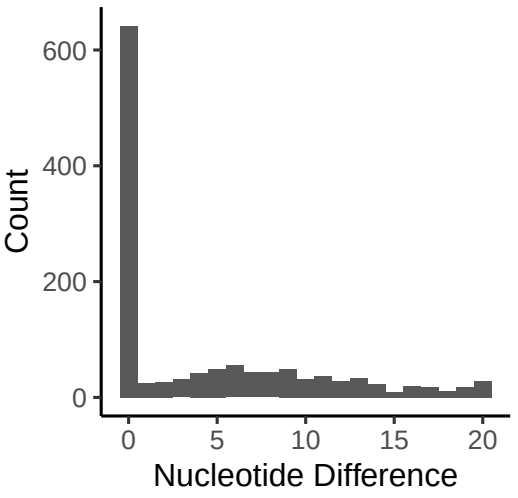
IGHV3−15*01_02

351 sequences assigned
124 (35.3%) exact matches, in which:
118 unique CDR3
6 unique J



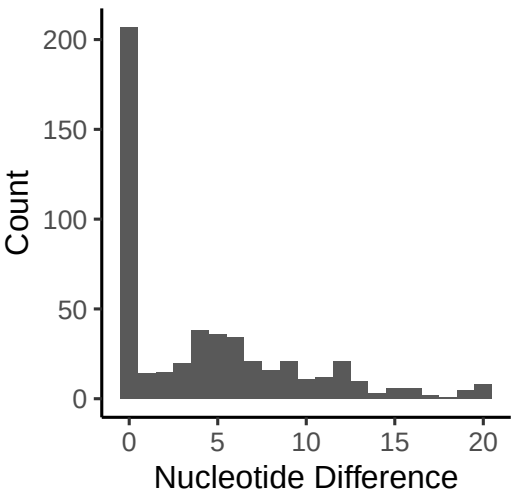
IGHV3−21*01_02

1349 sequences assigned
642 (47.6%) exact matches, in which:
586 unique CDR3
6 unique J



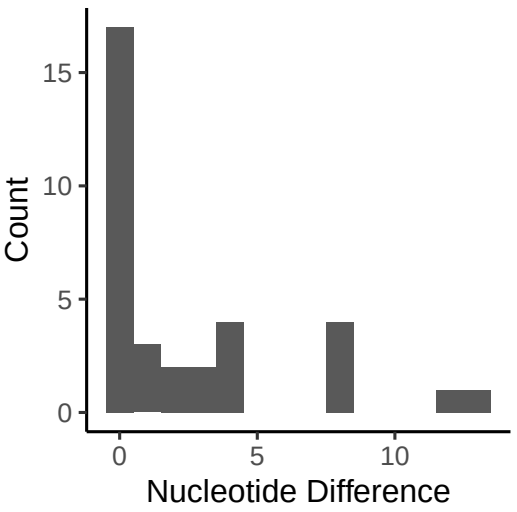
IGHV3−11*01

558 sequences assigned
207 (37.1%) exact matches, in which:
196 unique CDR3
5 unique J



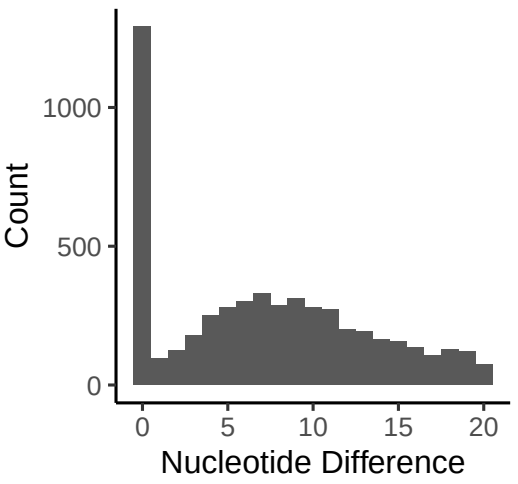
IGHV3−20*01_02

34 sequences assigned
17 (50%) exact matches, in which:
17 unique CDR3
5 unique J



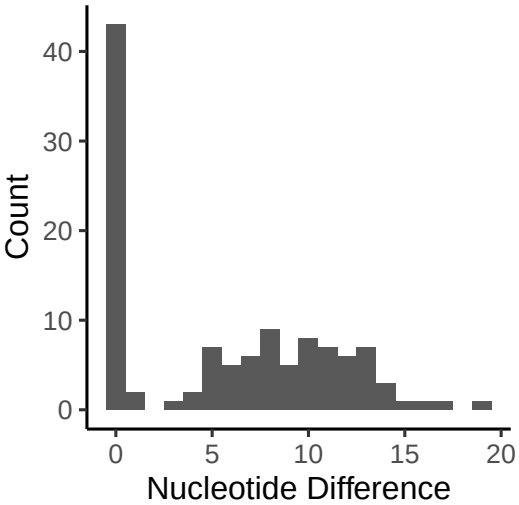
IGHV3−23*01_04

5701 sequences assigned
1291 (22.6%) exact matches, in which:
1184 unique CDR3
6 unique J



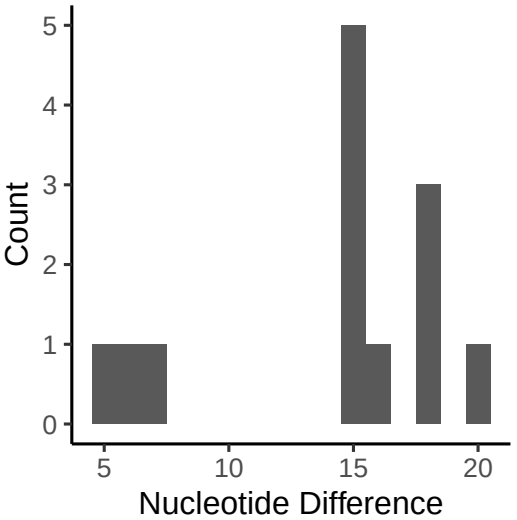
IGHV3−13*01

135 sequences assigned
43 (31.9%) exact matches, in which:
38 unique CDR3
5 unique J



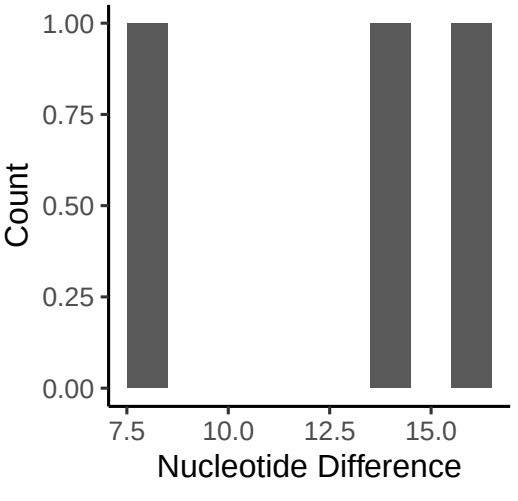
IGHV3−20*03_04

17 sequences assigned
No exact matches.



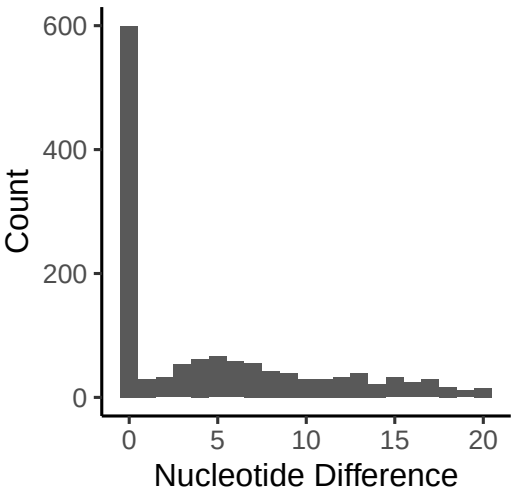
IGHV3−30−3*03

5 sequences assigned
No exact matches.



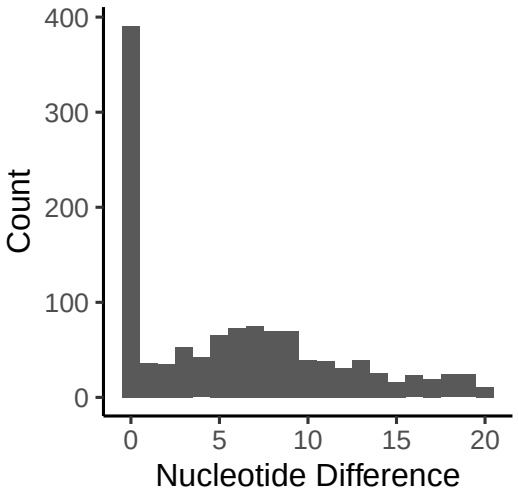
IGHV3−33*01

1422 sequences assigned
600 (42.2%) exact matches, in which:
566 unique CDR3
6 unique J



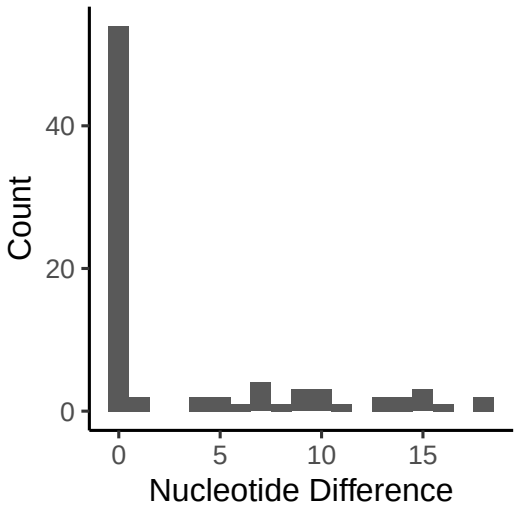
IGHV3−48*02

1273 sequences assigned
391 (30.7%) exact matches, in which:
352 unique CDR3
6 unique J



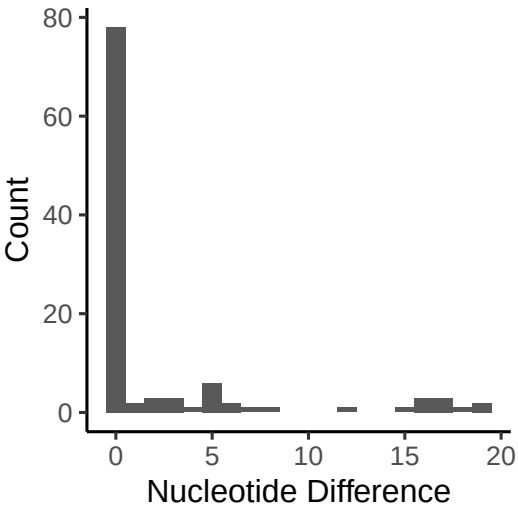
IGHV3−49*03_05

89 sequences assigned
54 (60.7%) exact matches, in which:
52 unique CDR3
5 unique J



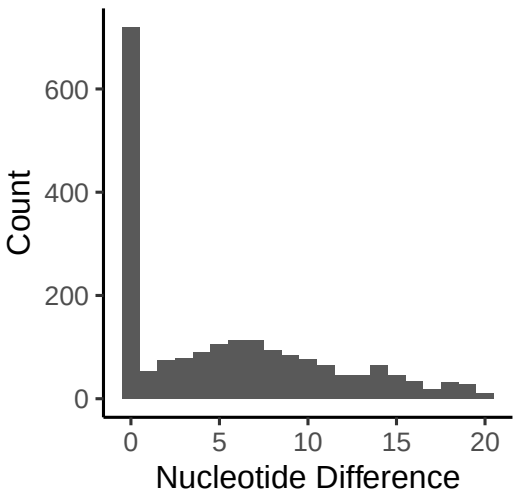
IGHV3−43*01

119 sequences assigned
78 (65.5%) exact matches, in which:
72 unique CDR3
6 unique J



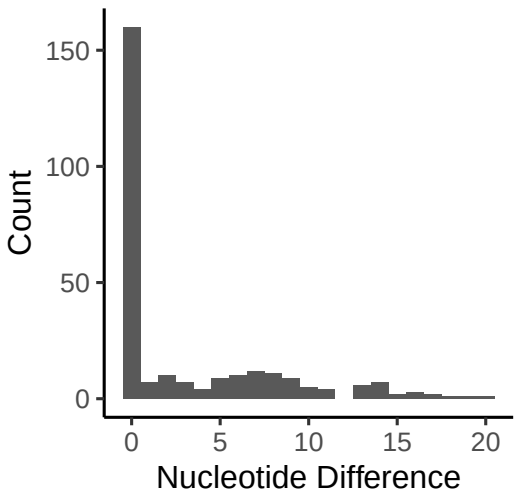
IGHV3−48*03

2111 sequences assigned
720 (34.1%) exact matches, in which:
673 unique CDR3
6 unique J



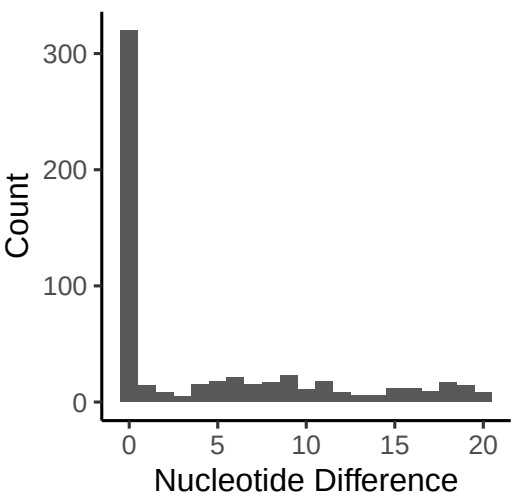
IGHV3−53*04

278 sequences assigned
160 (57.6%) exact matches, in which:
152 unique CDR3
6 unique J



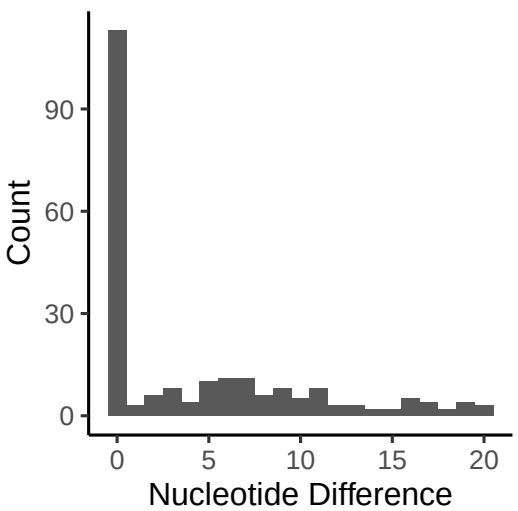
IGHV3−43*02

758 sequences assigned
320 (42.2%) exact matches, in which:
304 unique CDR3
6 unique J



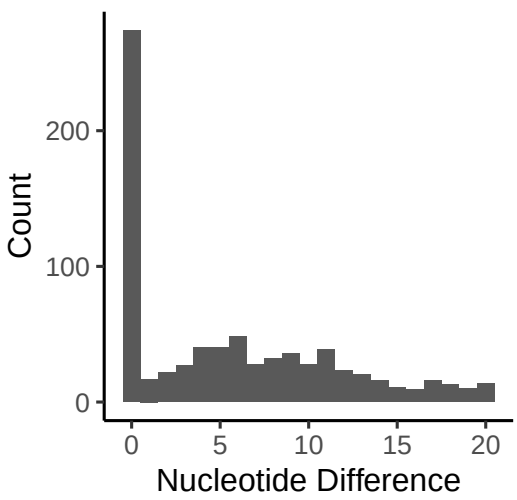
IGHV3−49*04

239 sequences assigned
113 (47.3%) exact matches, in which:
109 unique CDR3
6 unique J



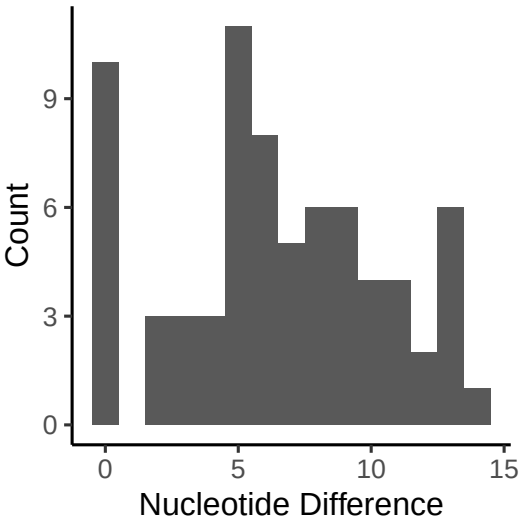
IGHV3−53*01_02

935 sequences assigned
274 (29.3%) exact matches, in which:
253 unique CDR3
6 unique J



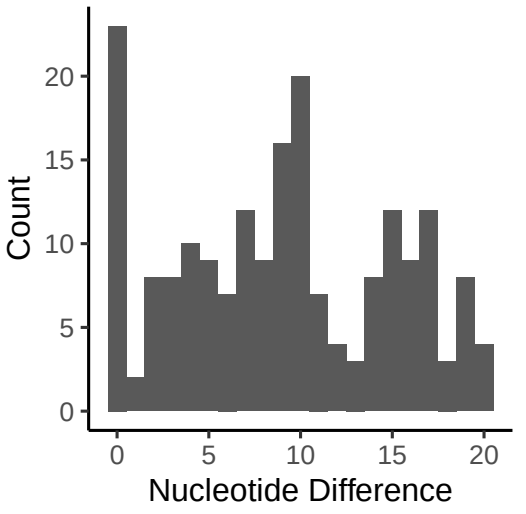
IGHV3−64*02_07

73 sequences assigned
10 (13.7%) exact matches, in which:
9 unique CDR3
4 unique J



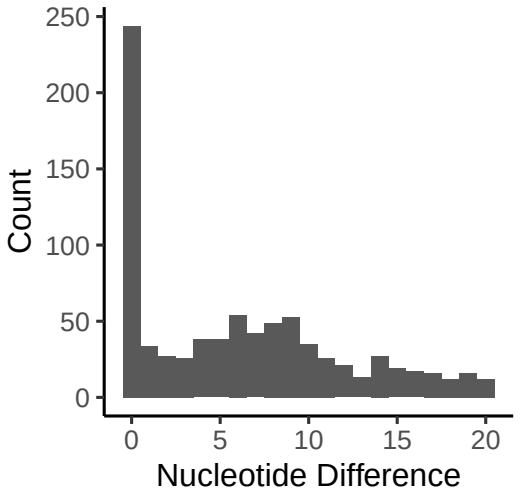
IGHV3−72*01

226 sequences assigned
23 (10.2%) exact matches, in which:
22 unique CDR3
4 unique J



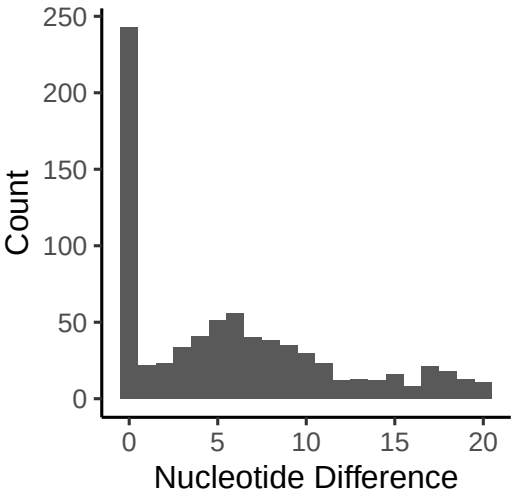
IGHV3−74*01_02

913 sequences assigned
244 (26.7%) exact matches, in which:
229 unique CDR3
6 unique J



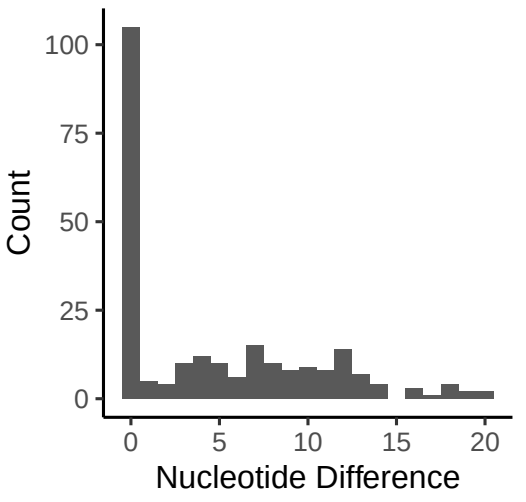
IGHV3−66*01

815 sequences assigned
243 (29.8%) exact matches, in which:
225 unique CDR3
6 unique J



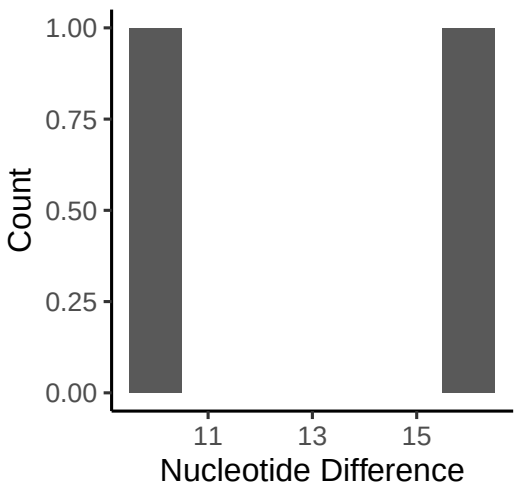
IGHV3−73*01_02

255 sequences assigned
105 (41.2%) exact matches, in which:
100 unique CDR3
6 unique J



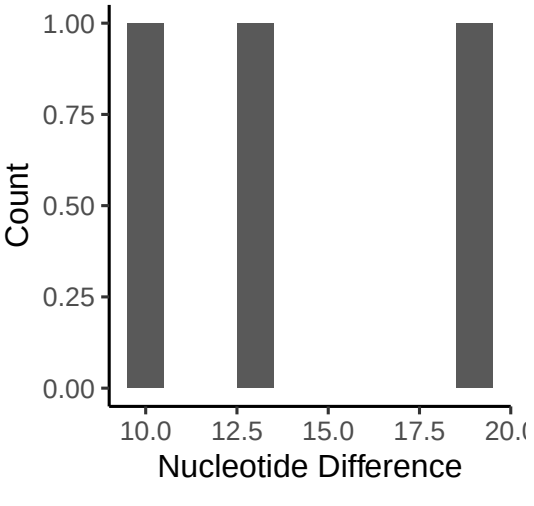
IGHV3−64D*06

2 sequences assigned
No exact matches.



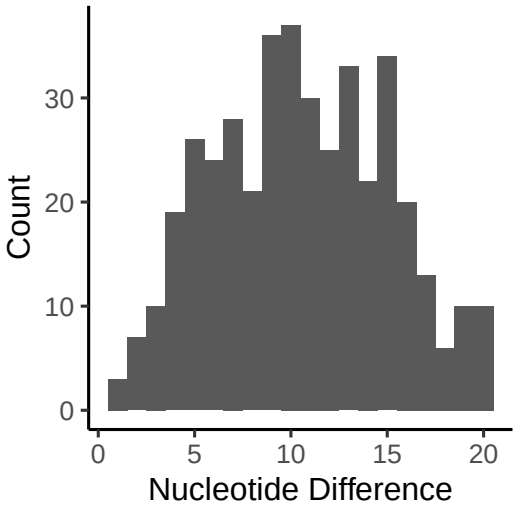
IGHV3−69−1*01

3 sequences assigned
No exact matches.



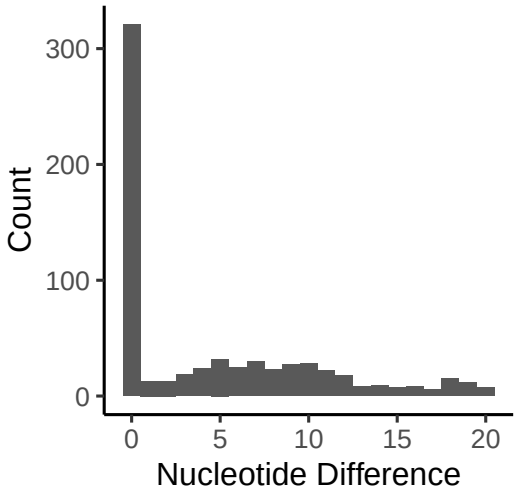
IGHV3−74*03

479 sequences assigned
No exact matches.



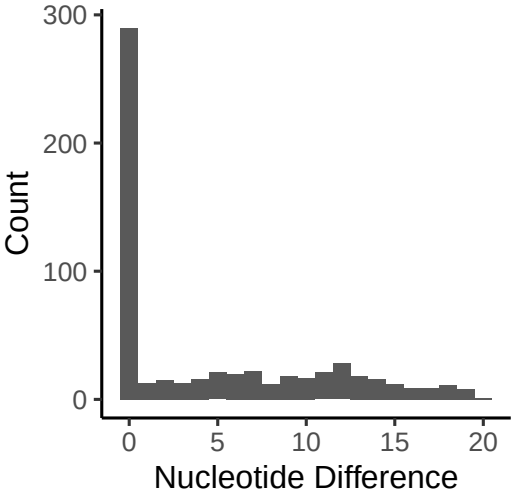
IGHV4−4*07

720 sequences assigned
321 (44.6%) exact matches, in which:
293 unique CDR3
5 unique J



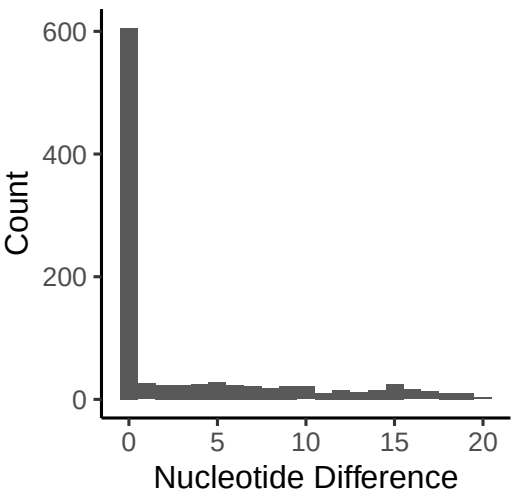
IGHV4−4*02_03

622 sequences assigned
290 (46.6%) exact matches, in which:
275 unique CDR3
6 unique J



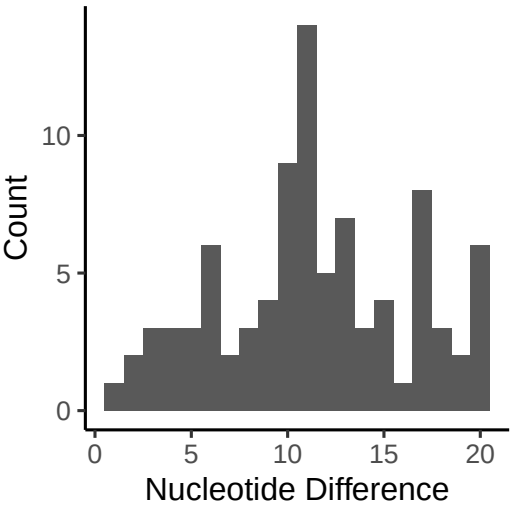
IGHV4−31*02

1054 sequences assigned
606 (57.5%) exact matches, in which:
579 unique CDR3
6 unique J



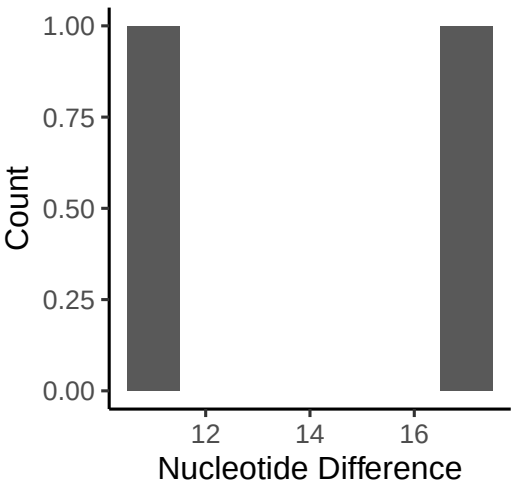
IGHV4−39*02

111 sequences assigned
No exact matches.



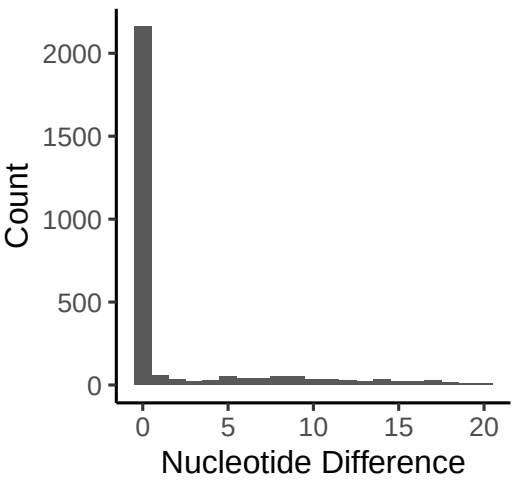
IGHV4−30−2*03

5 sequences assigned
No exact matches.



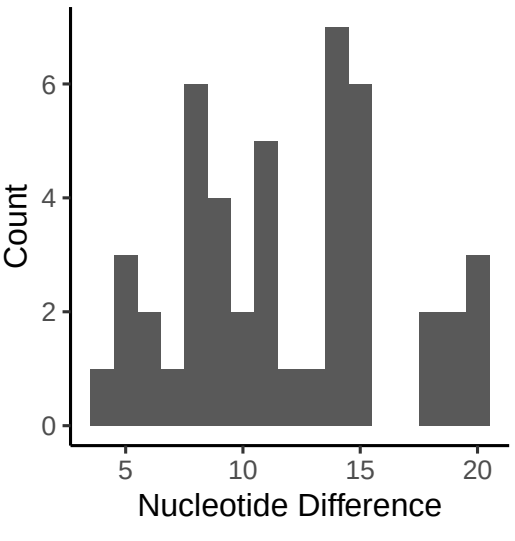
IGHV4−34*01_02

3058 sequences assigned
2160 (70.6%) exact matches, in which:
1977 unique CDR3
6 unique J



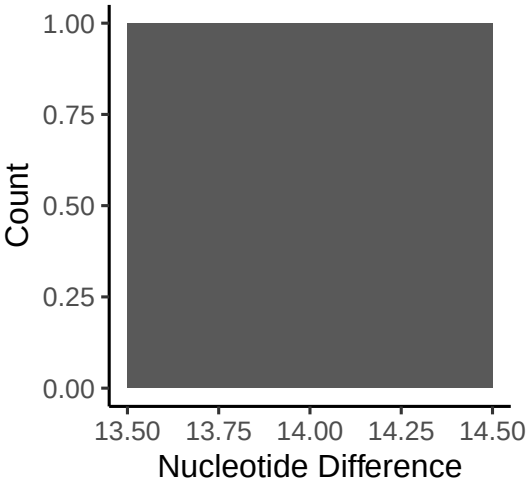
IGHV4−59*02

68 sequences assigned
No exact matches.



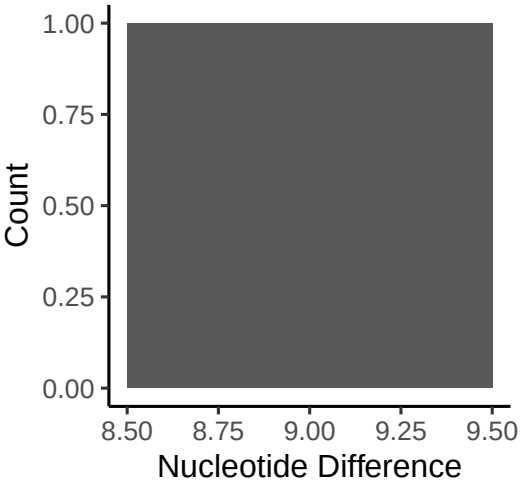
IGHV4−30−4*07

1 sequences assigned
No exact matches.



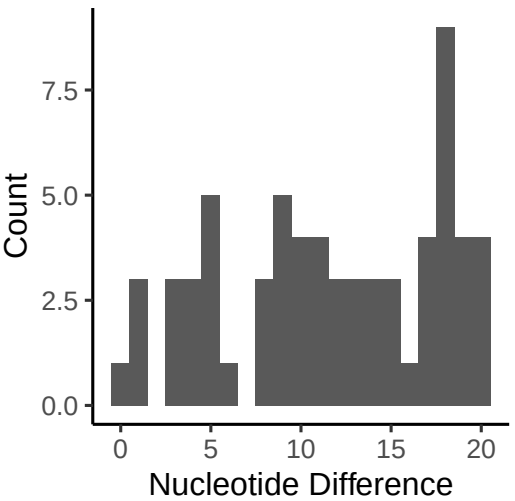
IGHV4−38−2*02

1 sequences assigned
No exact matches.



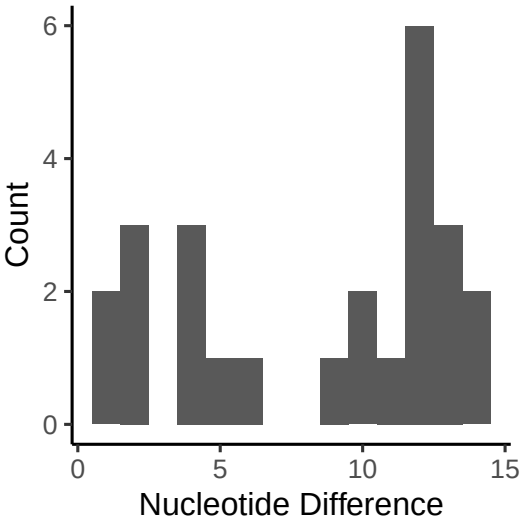
IGHV4−59*11

79 sequences assigned
1 (1.3%) exact matches, in which:
1 unique CDR3
0 unique J



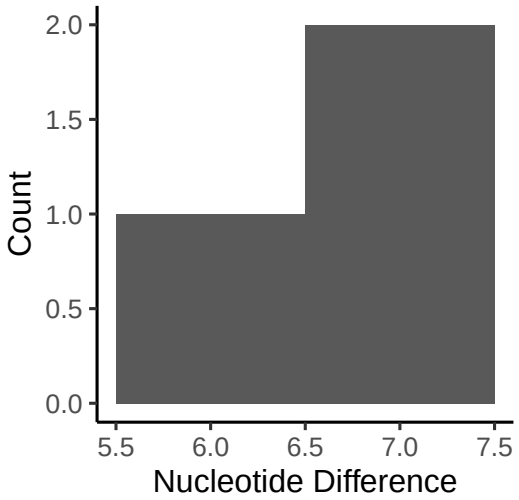
IGHV4−59*12

35 sequences assigned
No exact matches.



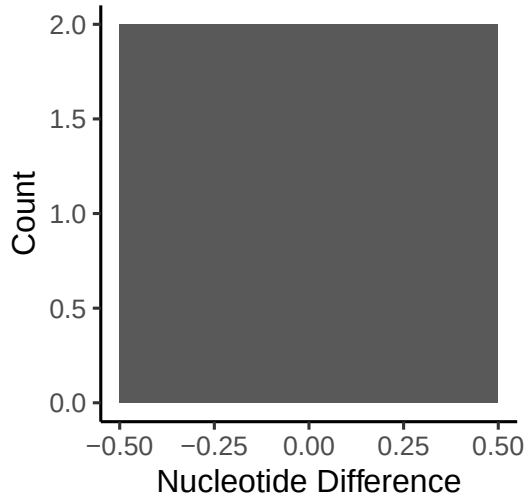
IGHV5−51*06

3 sequences assigned
No exact matches.



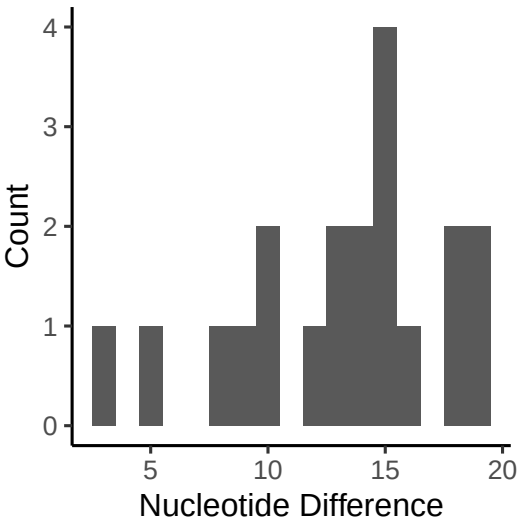
IGHV7−4−1*01

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



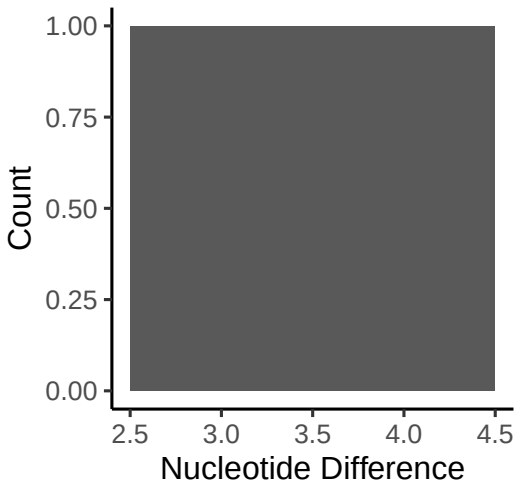
IGHV4−59*13

32 sequences assigned
No exact matches.



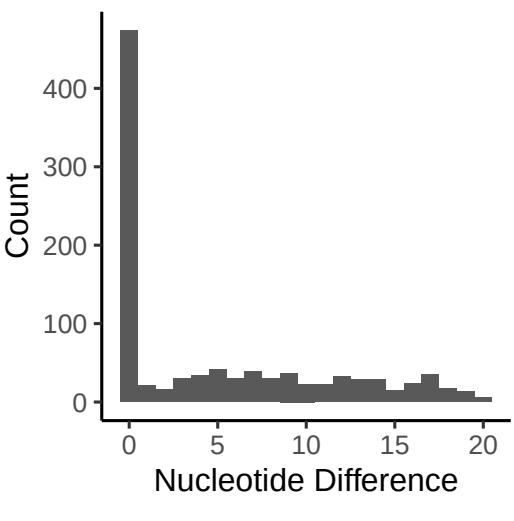
IGHV5−51*07

2 sequences assigned
No exact matches.



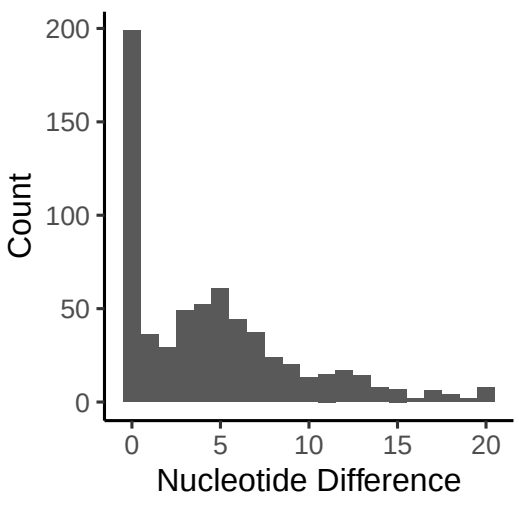
IGHV4−61*01

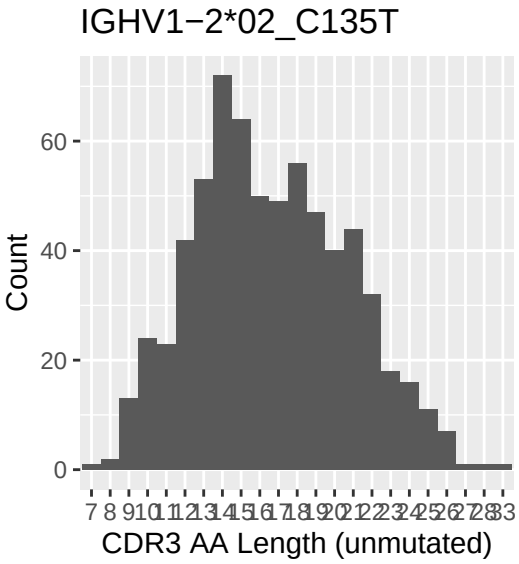
1105 sequences assigned
474 (42.9%) exact matches, in which:
444 unique CDR3
6 unique J

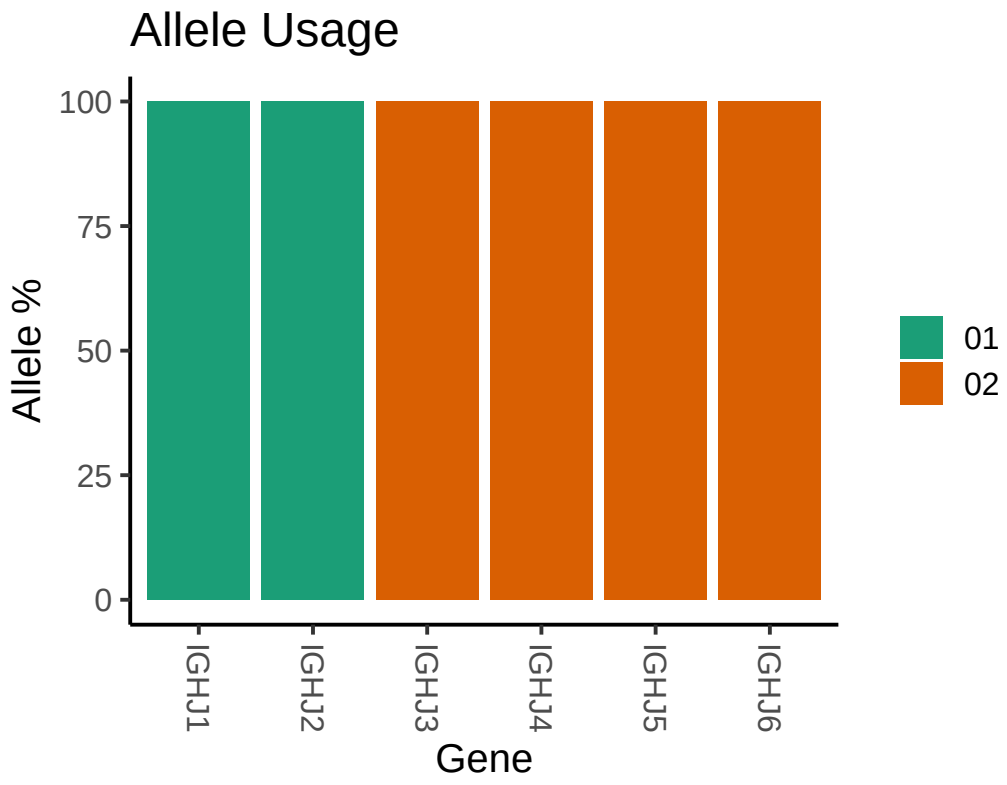


IGHV6−1*01_02

657 sequences assigned
199 (30.3%) exact matches, in which:
193 unique CDR3
6 unique J




IGHV1−2*02_C135T
Count
0
20
40
60
7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 33
CDR3 AA Length (unmutated)


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

Warning − no inferred sequences found.

Warning − no inferred sequences found.

Warning − no inferred sequences found.