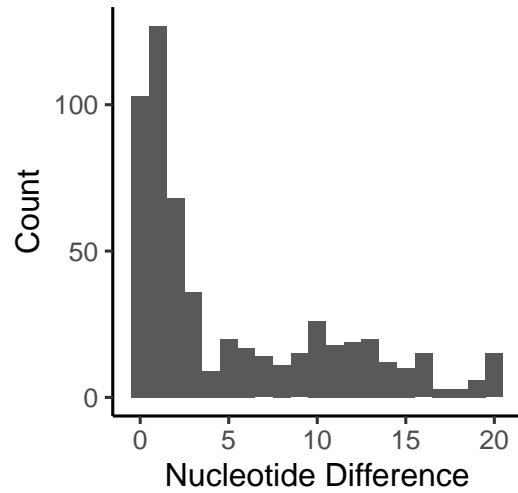


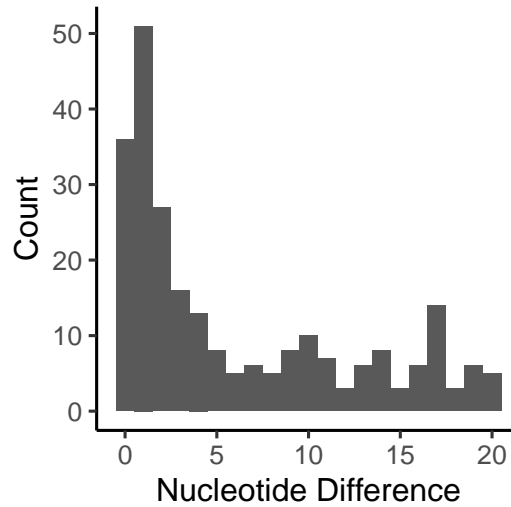
IGHV1-2*02

616 sequences assigned
103 (16.7%) exact matches, in which:
92 unique CDR3
6 unique J



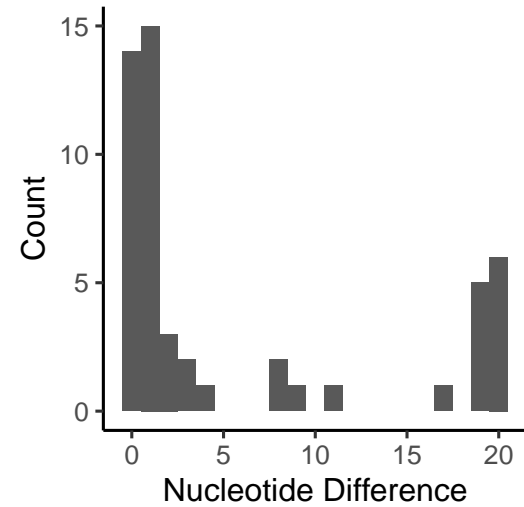
IGHV1-3*01_05

282 sequences assigned
36 (12.8%) exact matches, in which:
34 unique CDR3
4 unique J



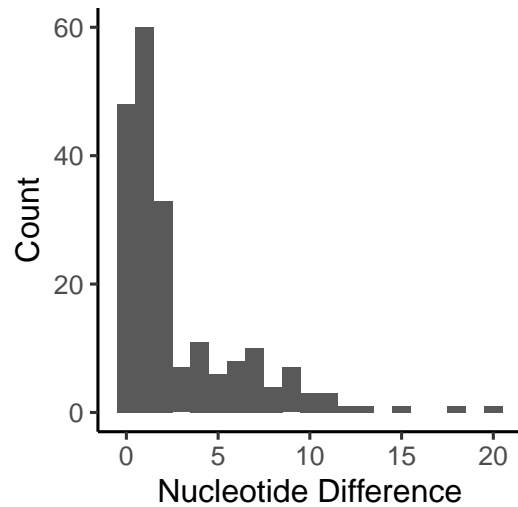
IGHV1-24*01

53 sequences assigned
14 (26.4%) exact matches, in which:
13 unique CDR3
4 unique J



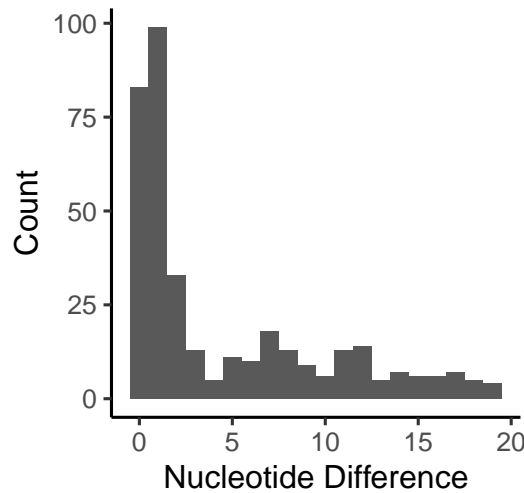
IGHV1-2*04

206 sequences assigned
48 (23.3%) exact matches, in which:
43 unique CDR3
5 unique J



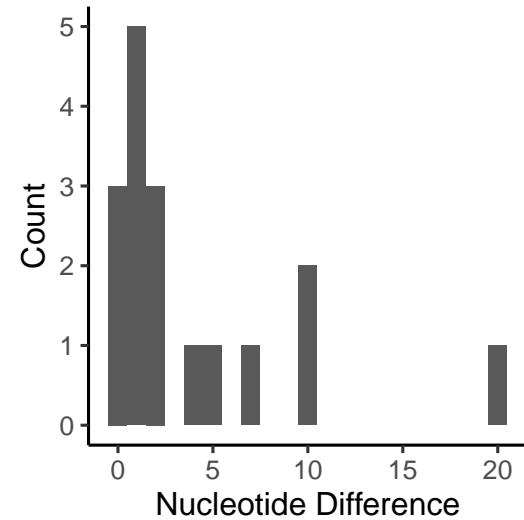
IGHV1-8*01

372 sequences assigned
83 (22.3%) exact matches, in which:
72 unique CDR3
4 unique J



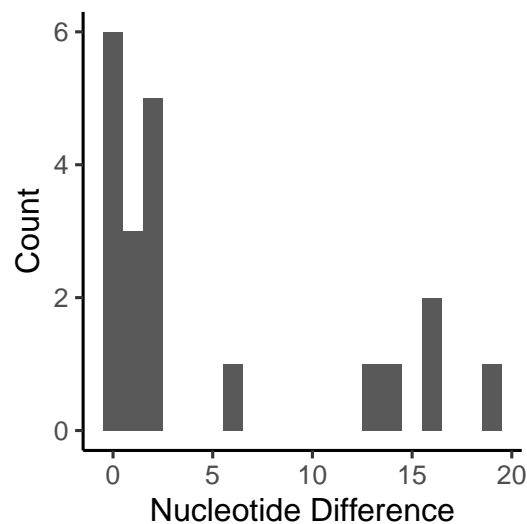
IGHV1-45*02

17 sequences assigned
3 (17.6%) exact matches, in which:
3 unique CDR3
1 unique J



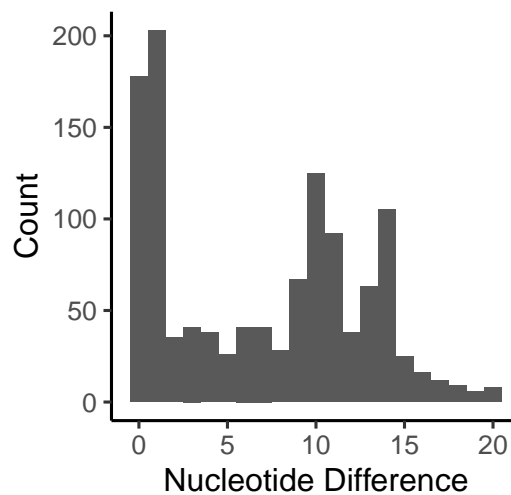
IGHV1-2*06

23 sequences assigned
6 (26.1%) exact matches, in which:
6 unique CDR3
3 unique J



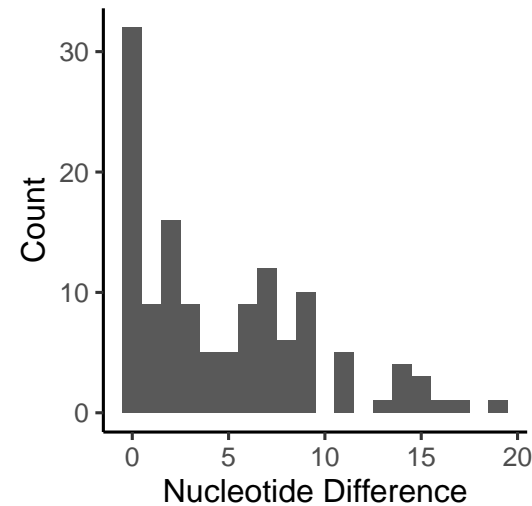
IGHV1-18*01

1209 sequences assigned
178 (14.7%) exact matches, in which:
148 unique CDR3
4 unique J



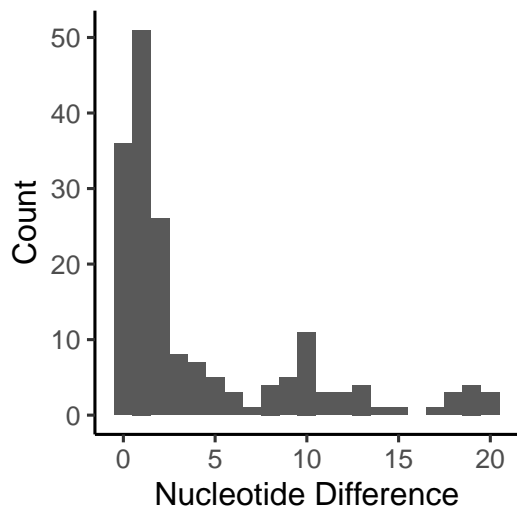
IGHV1-46*01

133 sequences assigned
32 (24.1%) exact matches, in which:
32 unique CDR3
5 unique J



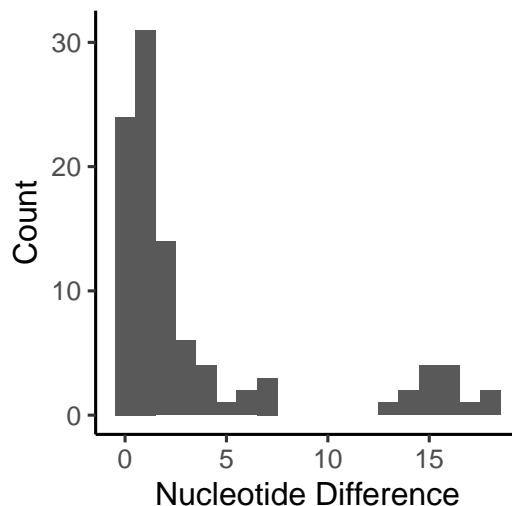
IGHV1-46*03

181 sequences assigned
36 (19.9%) exact matches, in which:
31 unique CDR3
4 unique J



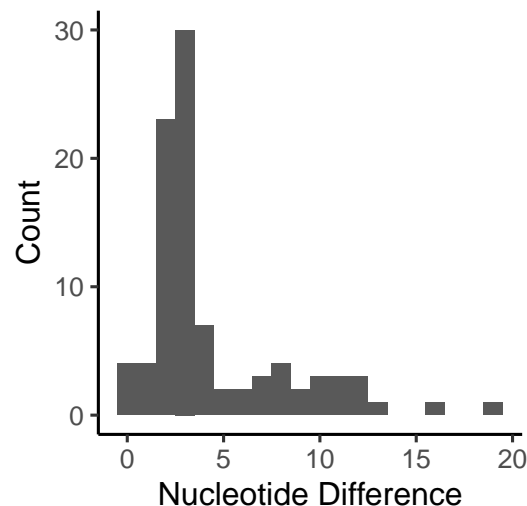
IGHV1-69*02

99 sequences assigned
24 (24.2%) exact matches, in which:
24 unique CDR3
4 unique J



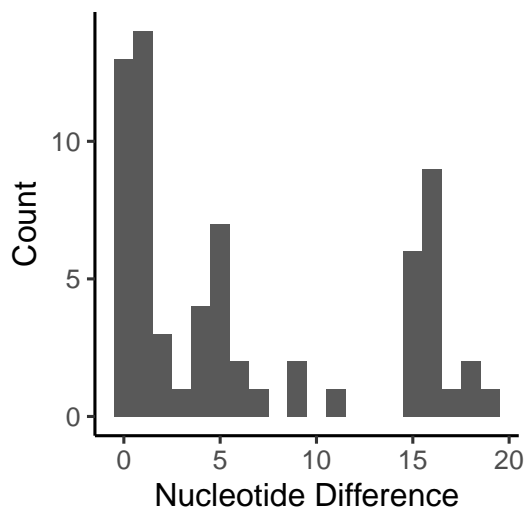
IGHV1-69*06_14

96 sequences assigned
4 (4.2%) exact matches, in which:
4 unique CDR3
2 unique J



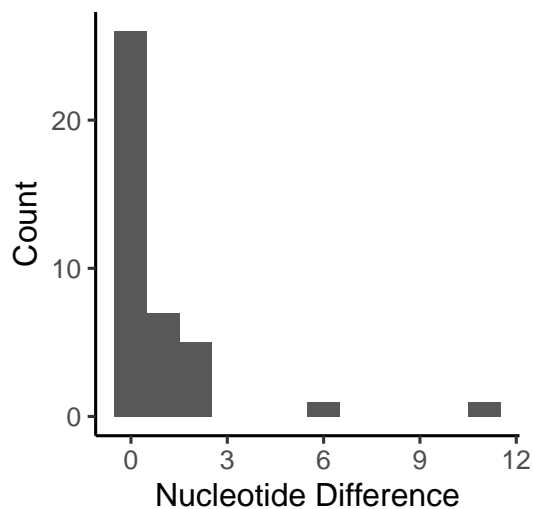
IGHV1-58*02

69 sequences assigned
13 (18.8%) exact matches, in which:
9 unique CDR3
3 unique J



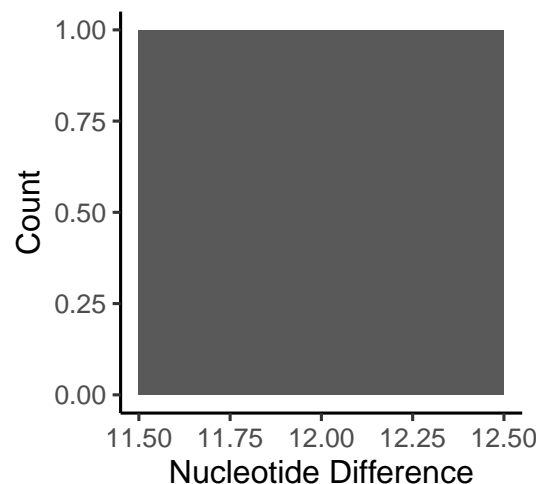
IGHV1-69*01_12_13

40 sequences assigned
26 (65%) exact matches, in which:
26 unique CDR3
4 unique J



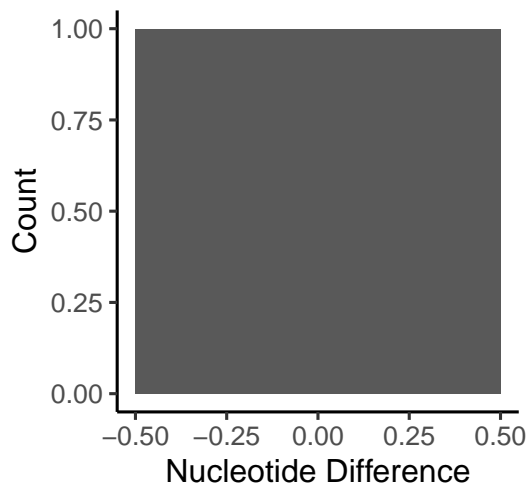
IGHV1-NL1*01

1 sequences assigned
No exact matches.



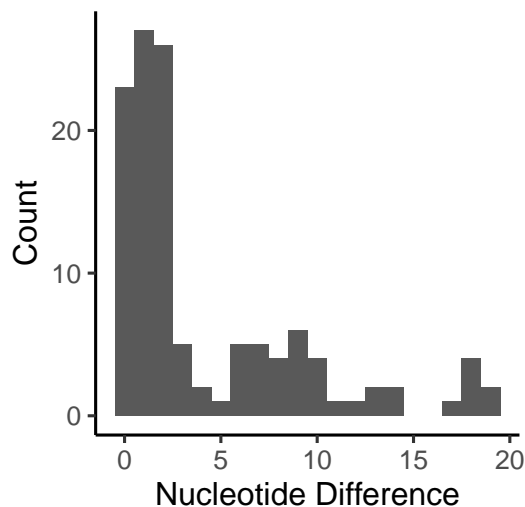
IGHV1-69-2*01

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



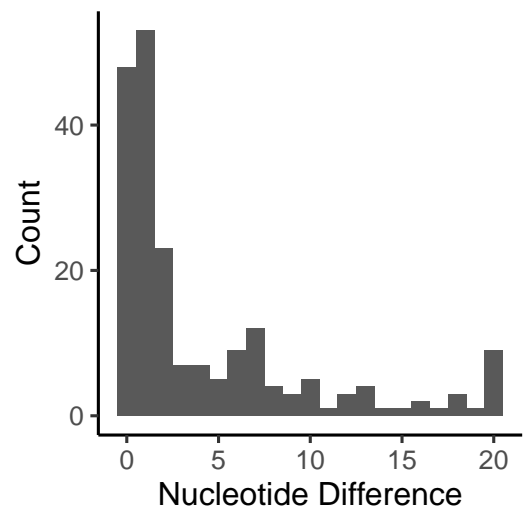
IGHV1-69*04_09

121 sequences assigned
23 (19%) exact matches, in which:
18 unique CDR3
4 unique J



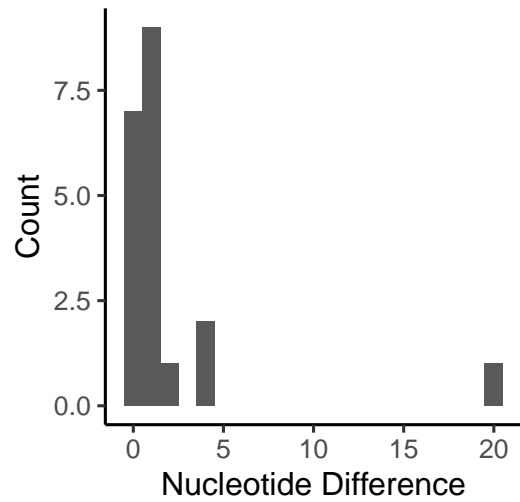
IGHV2-5*02

226 sequences assigned
48 (21.2%) exact matches, in which:
40 unique CDR3
4 unique J



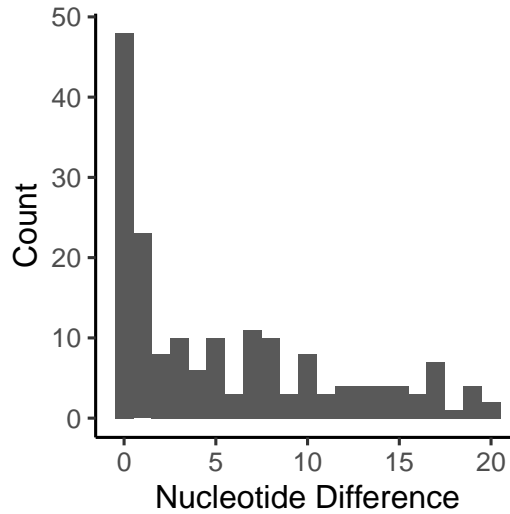
IGHV2-26*01

20 sequences assigned
7 (35%) exact matches, in which:
6 unique CDR3
3 unique J



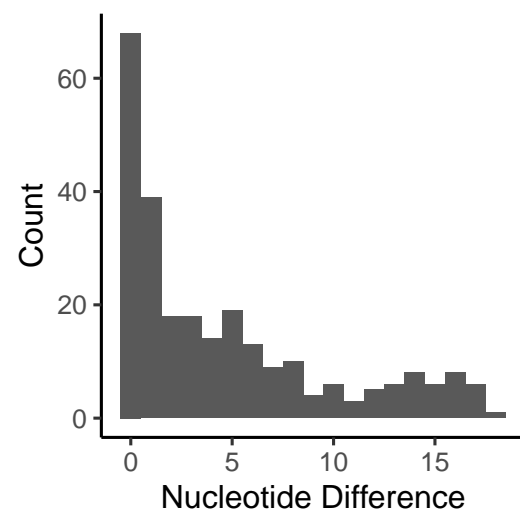
IGHV3-7*01

214 sequences assigned
48 (22.4%) exact matches, in which:
40 unique CDR3
4 unique J



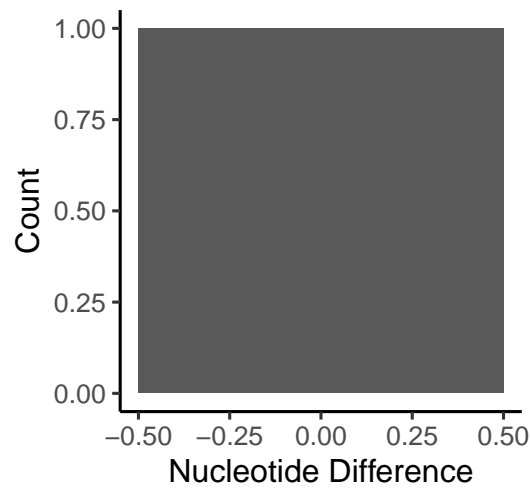
IGHV3-9*01

277 sequences assigned
68 (24.5%) exact matches, in which:
48 unique CDR3
5 unique J



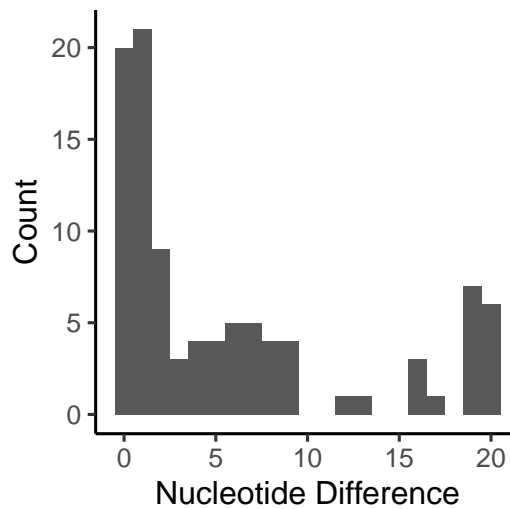
IGHV2-70*01

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



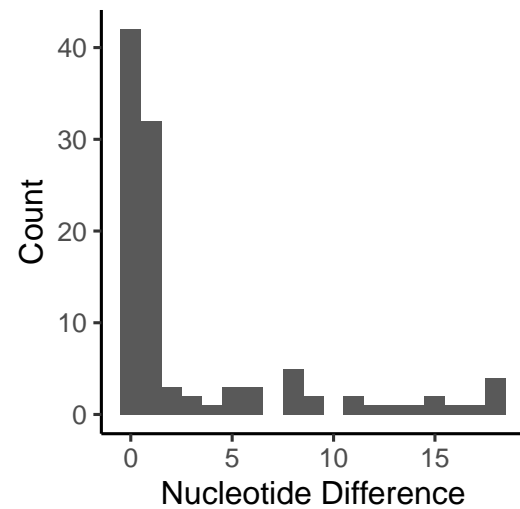
IGHV3-7*03

145 sequences assigned
20 (13.8%) exact matches, in which:
16 unique CDR3
3 unique J



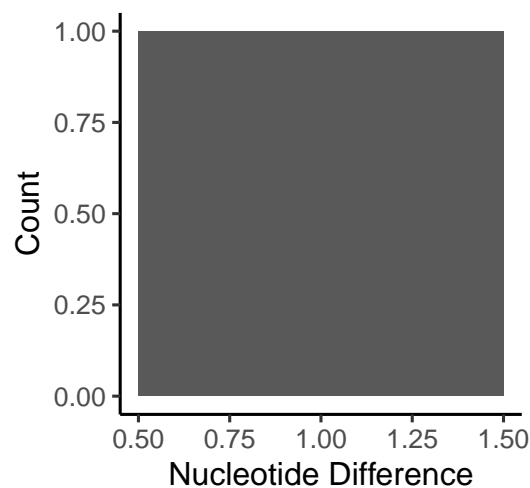
IGHV3-11*01

106 sequences assigned
42 (39.6%) exact matches, in which:
26 unique CDR3
4 unique J



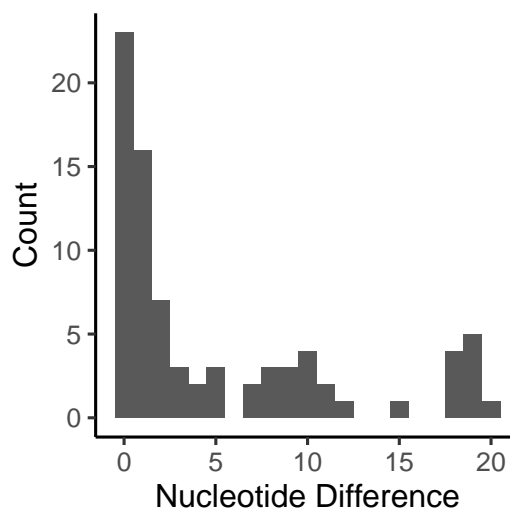
IGHV2-70*12

1 sequences assigned
No exact matches.



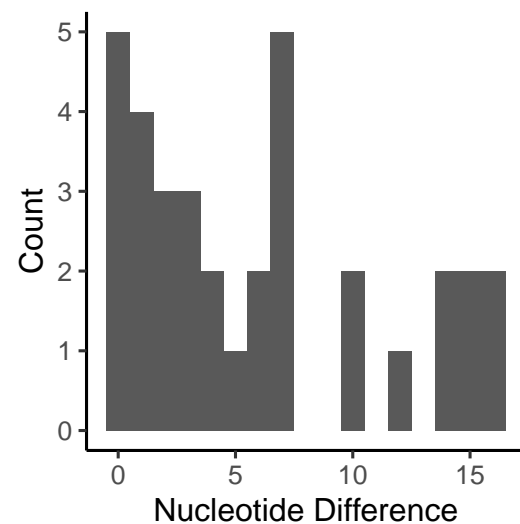
IGHV3-7*04

89 sequences assigned
23 (25.8%) exact matches, in which:
15 unique CDR3
4 unique J



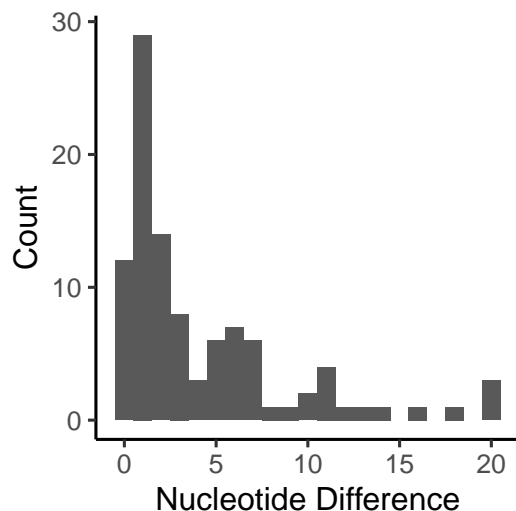
IGHV3-11*04

34 sequences assigned
5 (14.7%) exact matches, in which:
5 unique CDR3
2 unique J



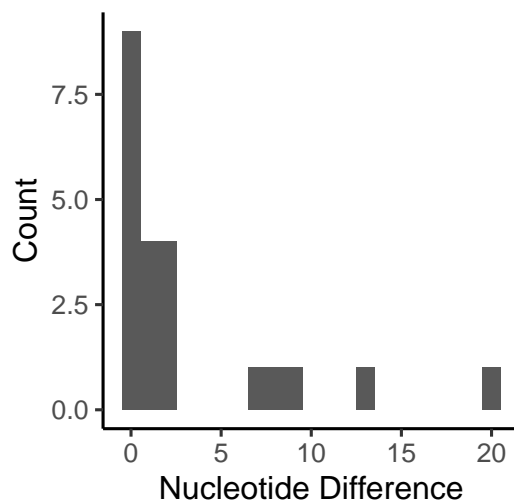
IGHV3-11*06

102 sequences assigned
12 (11.8%) exact matches, in which:
11 unique CDR3
3 unique J



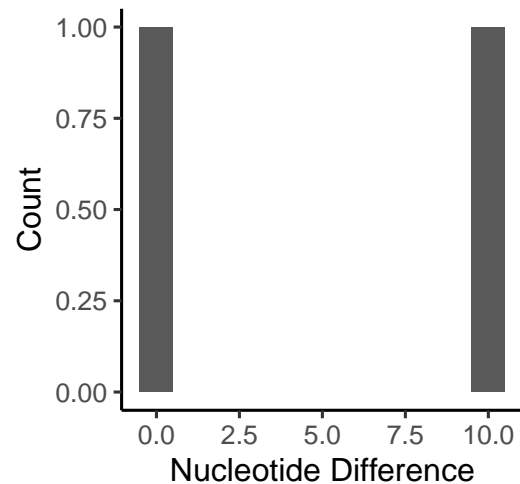
IGHV3-13*04

23 sequences assigned
9 (39.1%) exact matches, in which:
7 unique CDR3
4 unique J



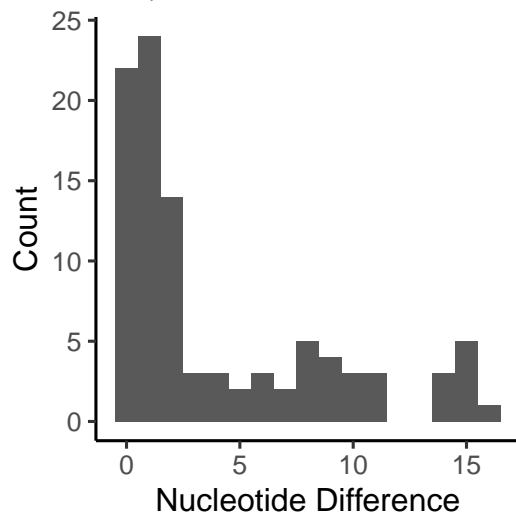
IGHV3-19*01

2 sequences assigned
1 (50%) exact matches, in which:
1 unique CDR3
1 unique J



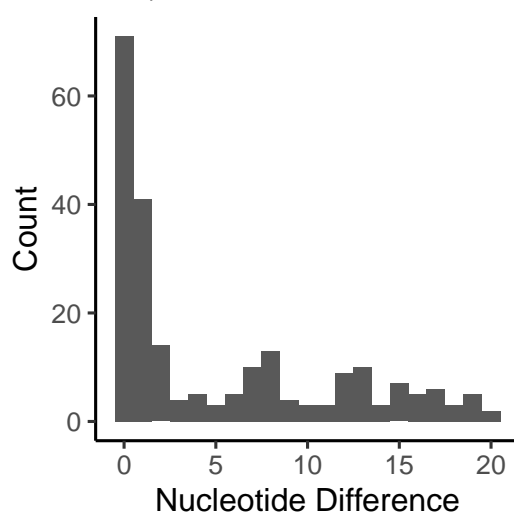
IGHV3-11*03_05

100 sequences assigned
22 (22%) exact matches, in which:
15 unique CDR3
4 unique J



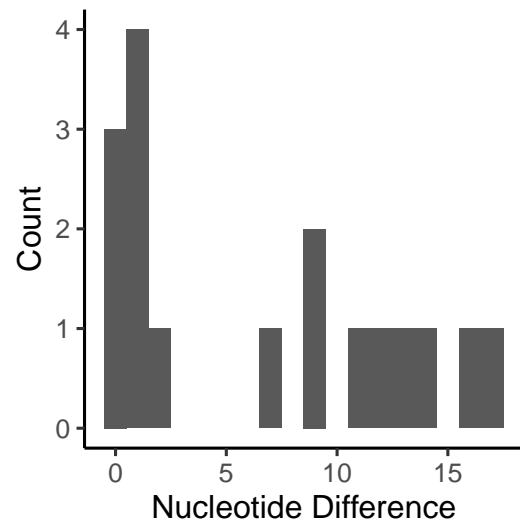
IGHV3-15*07

252 sequences assigned
71 (28.2%) exact matches, in which:
49 unique CDR3
5 unique J



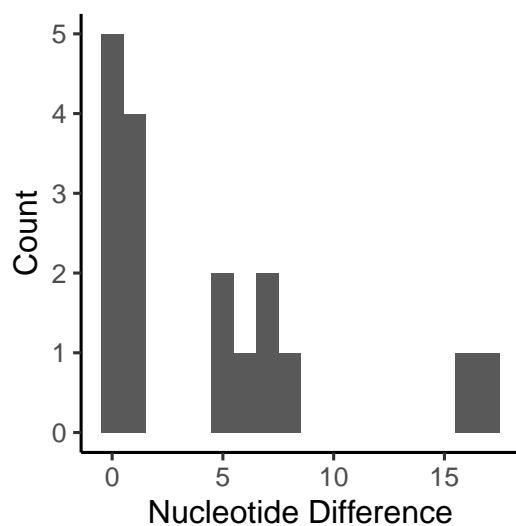
IGHV3-20*03_04

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



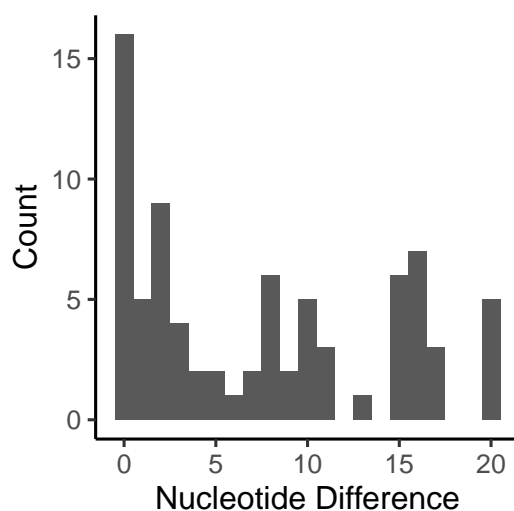
IGHV3-13*01

17 sequences assigned
5 (29.4%) exact matches, in which:
4 unique CDR3
2 unique J



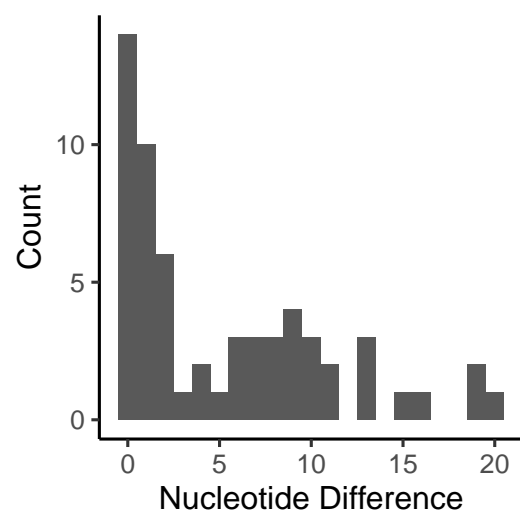
IGHV3-15*01_02

100 sequences assigned
16 (16%) exact matches, in which:
14 unique CDR3
3 unique J



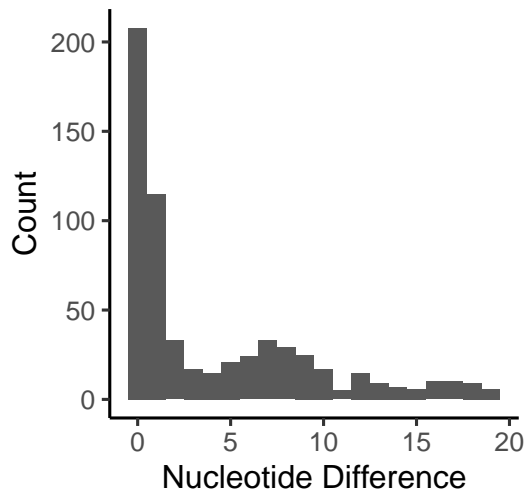
IGHV3-21*04

68 sequences assigned
14 (20.6%) exact matches, in which:
14 unique CDR3
3 unique J



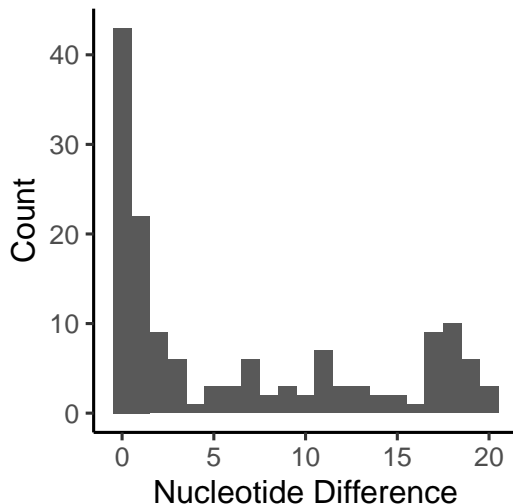
IGHV3-21*01_02

680 sequences assigned
208 (30.6%) exact matches, in which:
149 unique CDR3
6 unique J



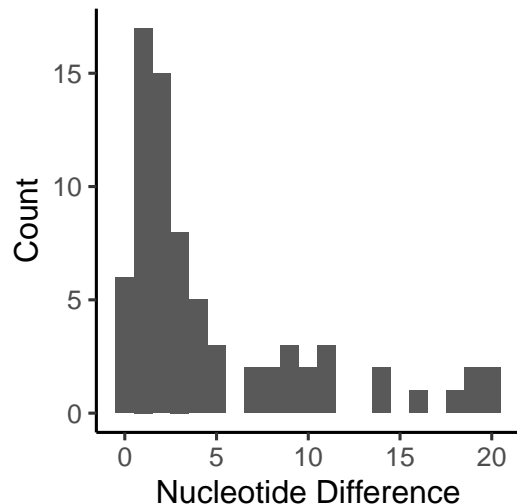
IGHV3-30*03

206 sequences assigned
43 (20.9%) exact matches, in which:
42 unique CDR3
5 unique J



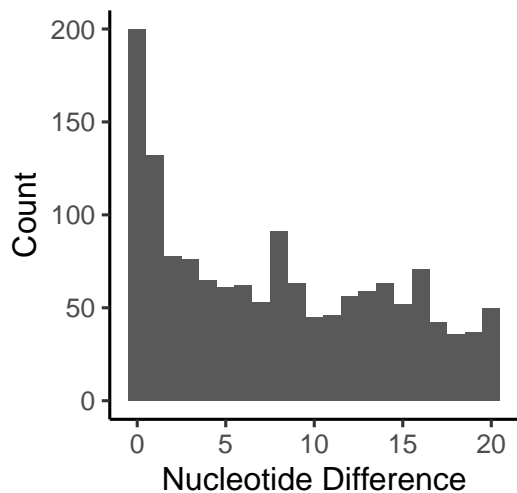
IGHV3-33*06

74 sequences assigned
6 (8.1%) exact matches, in which:
6 unique CDR3
3 unique J



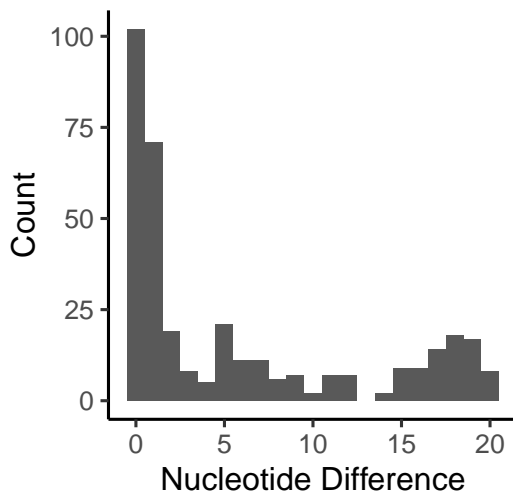
IGHV3-23*01_04

1634 sequences assigned
200 (12.2%) exact matches, in which:
132 unique CDR3
5 unique J



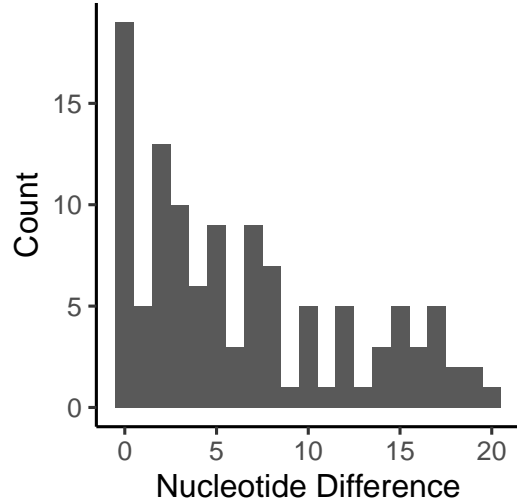
IGHV3-33*01

374 sequences assigned
102 (27.3%) exact matches, in which:
71 unique CDR3
6 unique J



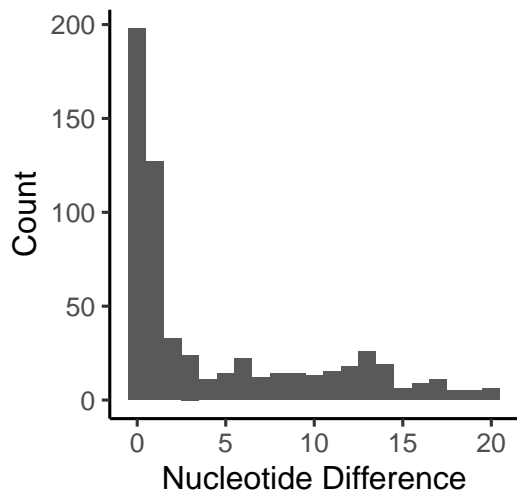
IGHV3-33*08

123 sequences assigned
19 (15.4%) exact matches, in which:
17 unique CDR3
4 unique J



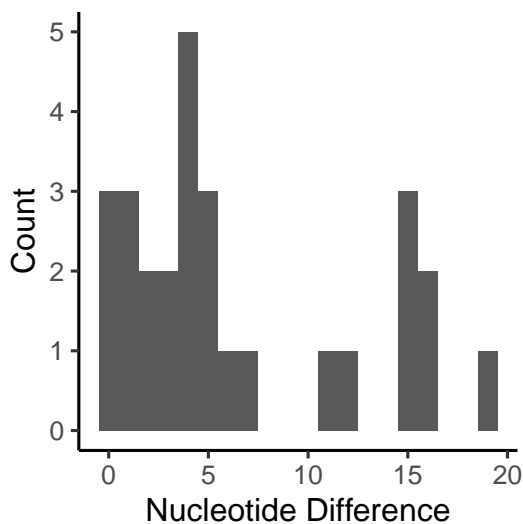
IGHV3-30-3*01

654 sequences assigned
198 (30.3%) exact matches, in which:
135 unique CDR3
5 unique J



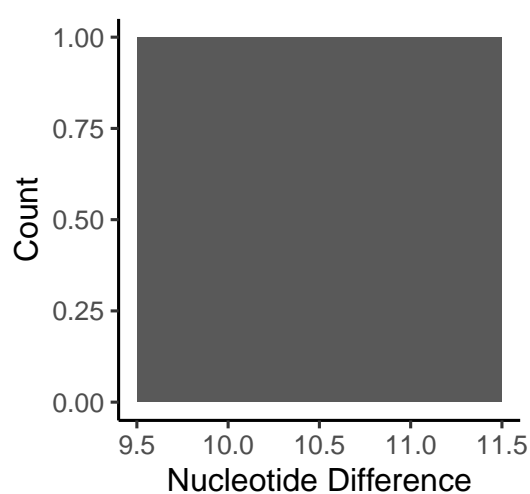
IGHV3-33*05

28 sequences assigned
3 (10.7%) exact matches, in which:
3 unique CDR3
3 unique J



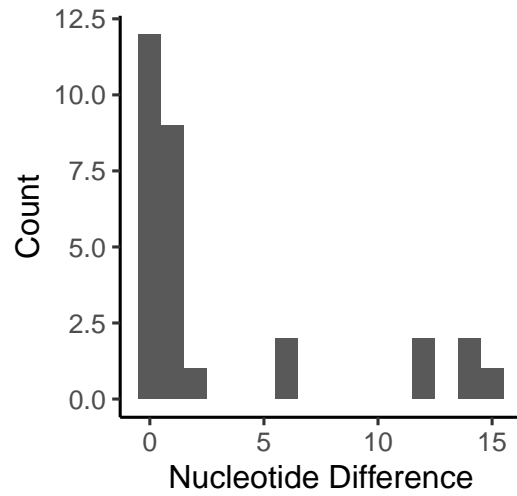
IGHV3-35*01

2 sequences assigned
No exact matches.



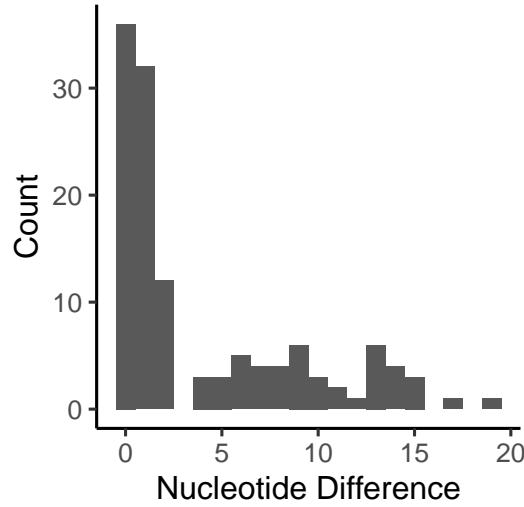
IGHV3-43*01

29 sequences assigned
12 (41.4%) exact matches, in which:
7 unique CDR3
2 unique J



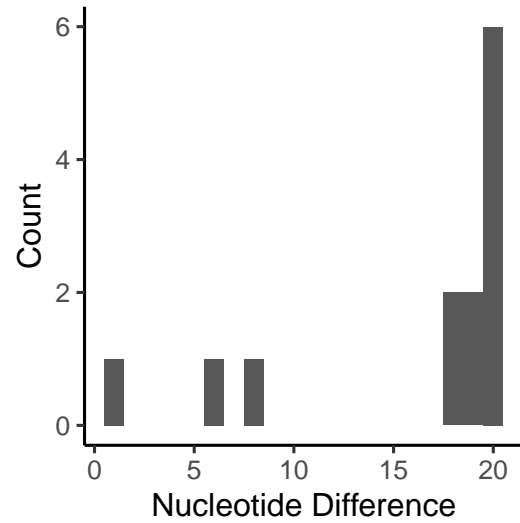
IGHV3-49*03_05

149 sequences assigned
36 (24.2%) exact matches, in which:
20 unique CDR3
3 unique J



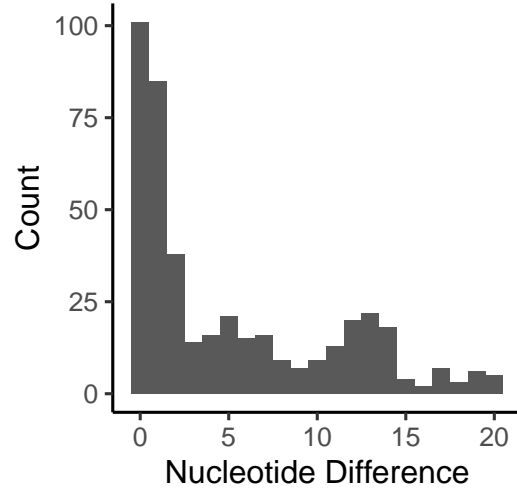
IGHV3-53*05

21 sequences assigned
No exact matches.



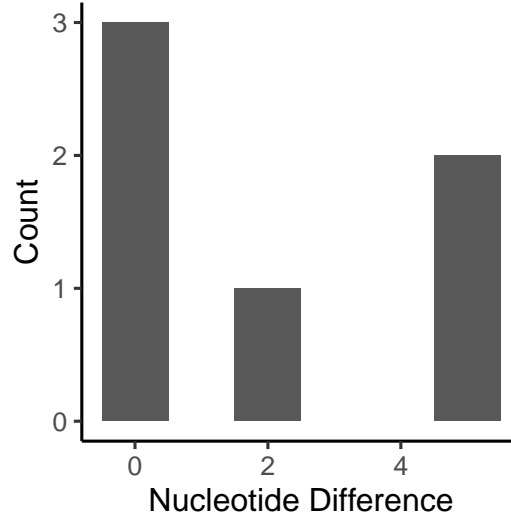
IGHV3-48*01

441 sequences assigned
101 (22.9%) exact matches, in which:
70 unique CDR3
6 unique J



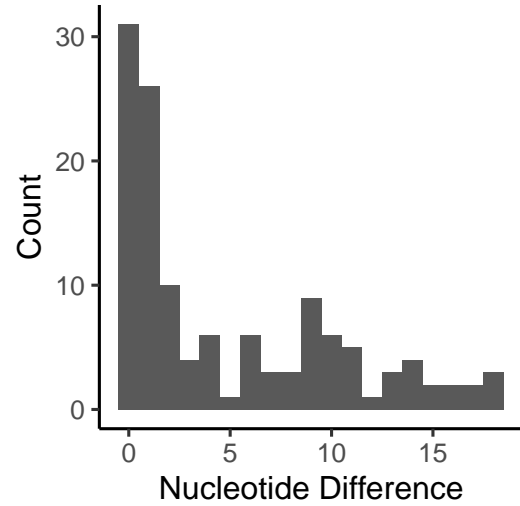
IGHV3-52*02

6 sequences assigned
3 (50%) exact matches, in which:
2 unique CDR3
2 unique J



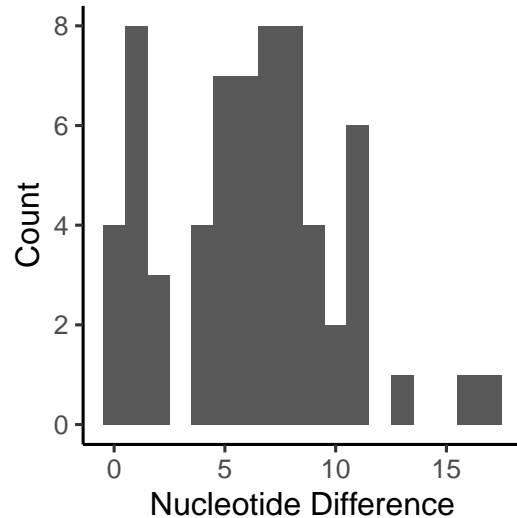
IGHV3-53*01_02

131 sequences assigned
31 (23.7%) exact matches, in which:
22 unique CDR3
4 unique J



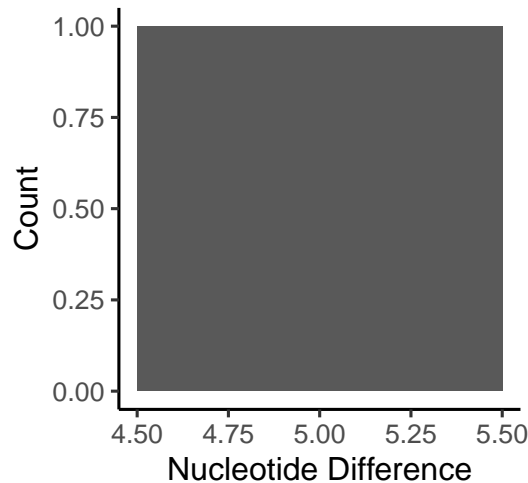
IGHV3-48*04

68 sequences assigned
4 (5.9%) exact matches, in which:
4 unique CDR3
2 unique J



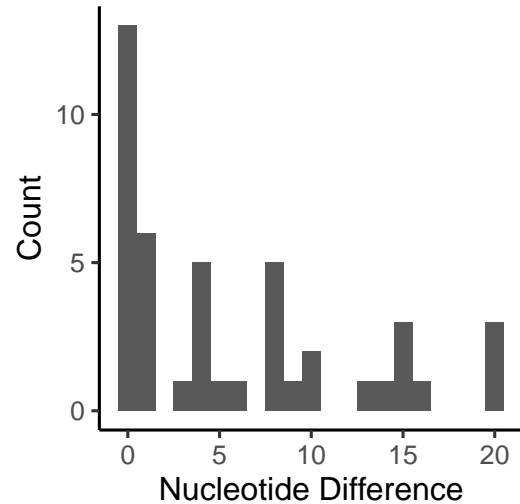
IGHV3-52*01_03

1 sequences assigned
No exact matches.



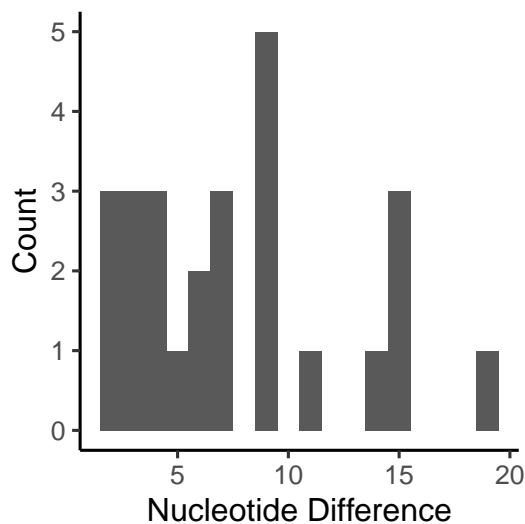
IGHV3-64*01

60 sequences assigned
13 (21.7%) exact matches, in which:
10 unique CDR3
3 unique J



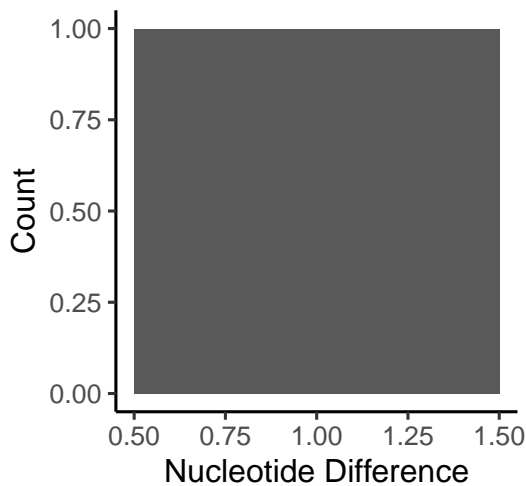
IGHV3-64*04

28 sequences assigned
No exact matches.



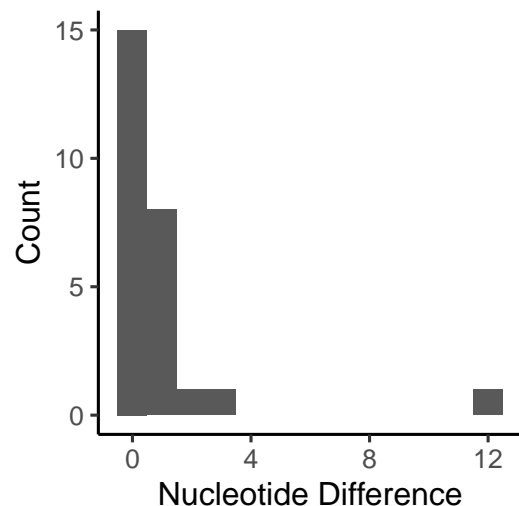
IGHV3-66*03

1 sequences assigned
No exact matches.



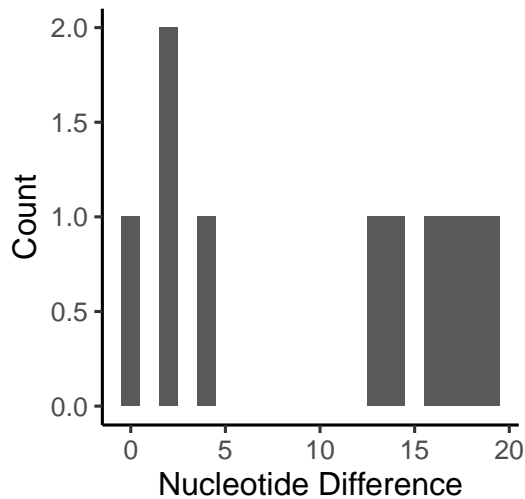
IGHV3-73*01_02

28 sequences assigned
15 (53.6%) exact matches, in which:
11 unique CDR3
3 unique J



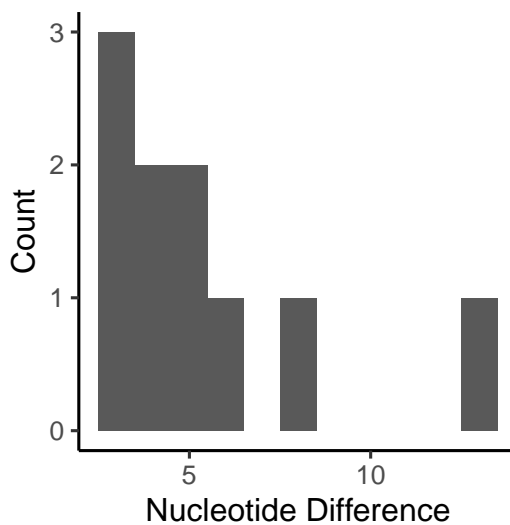
IGHV3-66*01

10 sequences assigned
1 (10%) exact matches, in which:
1 unique CDR3
1 unique J



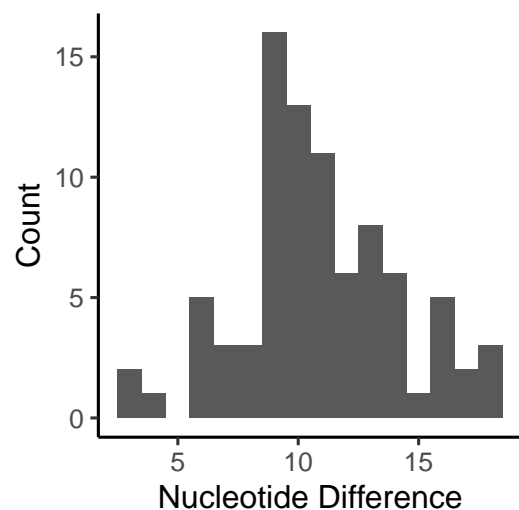
IGHV3-69-1*01

10 sequences assigned
No exact matches.



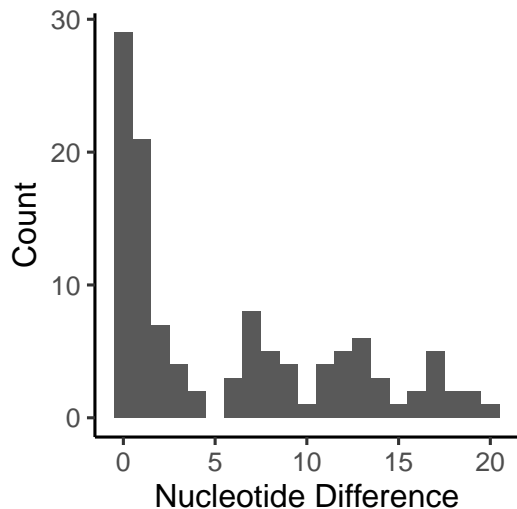
IGHV3-74*03

105 sequences assigned
No exact matches.



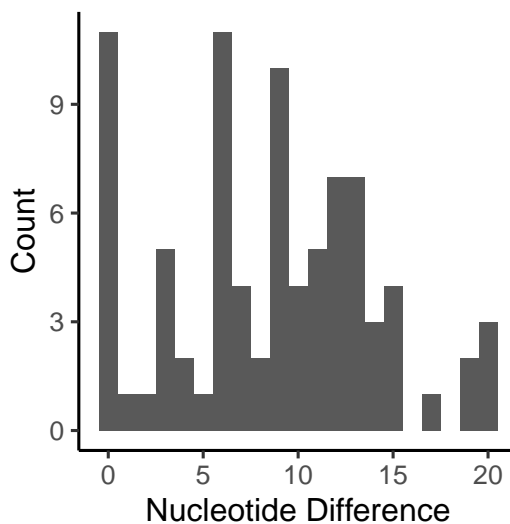
IGHV3-66*02

125 sequences assigned
29 (23.2%) exact matches, in which:
18 unique CDR3
4 unique J



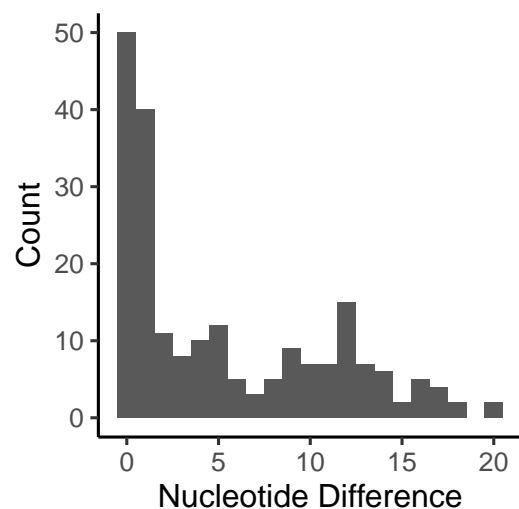
IGHV3-72*01

84 sequences assigned
11 (13.1%) exact matches, in which:
8 unique CDR3
3 unique J



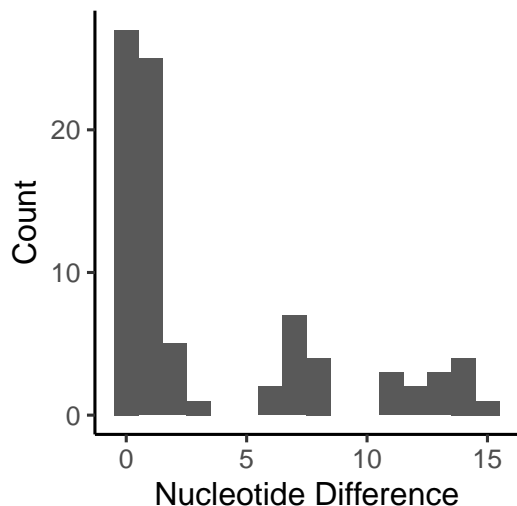
IGHV3-74*01_02

221 sequences assigned
50 (22.6%) exact matches, in which:
34 unique CDR3
4 unique J



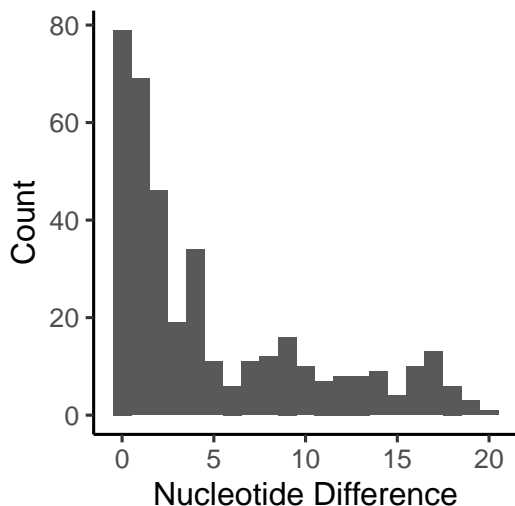
IGHV3-64D*06

89 sequences assigned
27 (30.3%) exact matches, in which:
12 unique CDR3
2 unique J



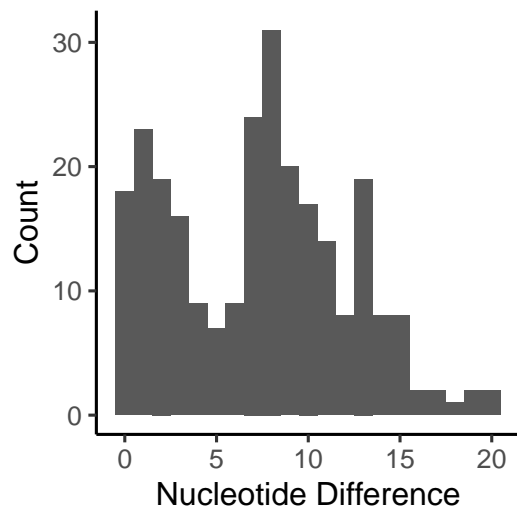
IGHV4-4*02_03

399 sequences assigned
79 (19.8%) exact matches, in which:
59 unique CDR3
4 unique J



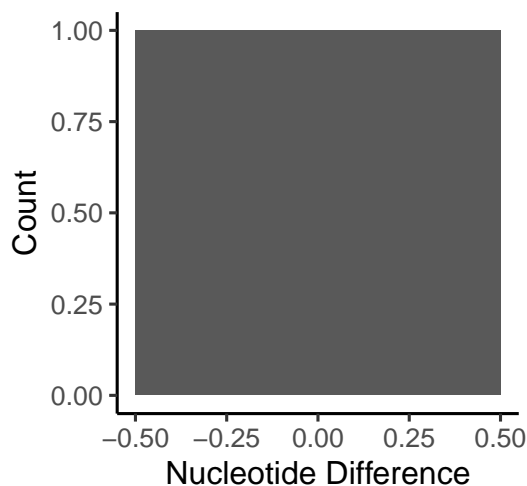
IGHV4-30-4*01

276 sequences assigned
18 (6.5%) exact matches, in which:
15 unique CDR3
3 unique J



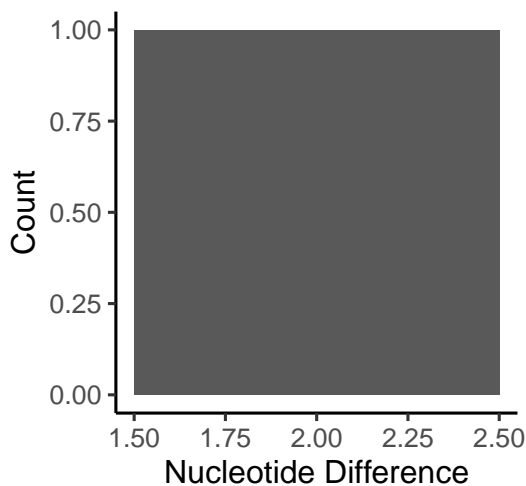
IGHV3-64D*09

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



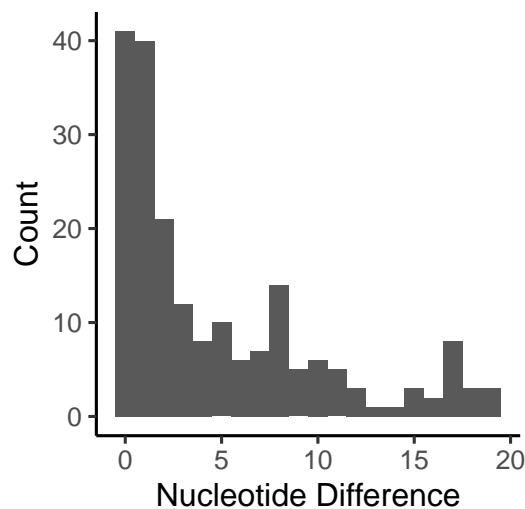
IGHV4-28*03

2 sequences assigned
No exact matches.



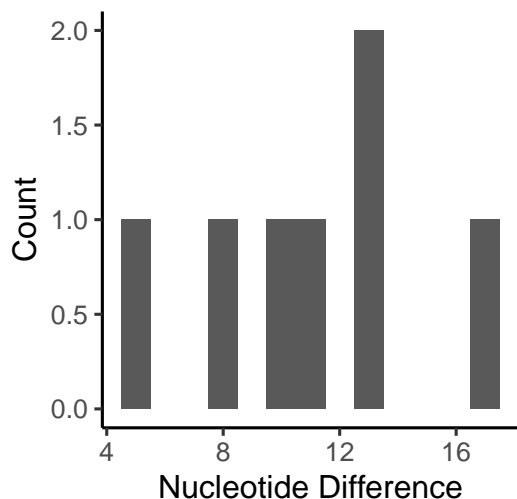
IGHV4-30-2*01

199 sequences assigned
41 (20.6%) exact matches, in which:
29 unique CDR3
5 unique J



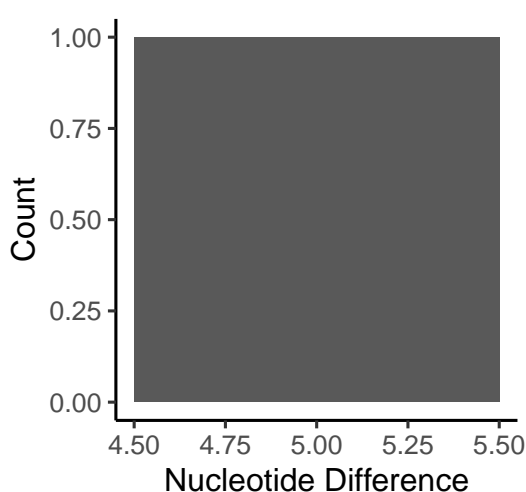
IGHV3-NL1*01

7 sequences assigned
No exact matches.



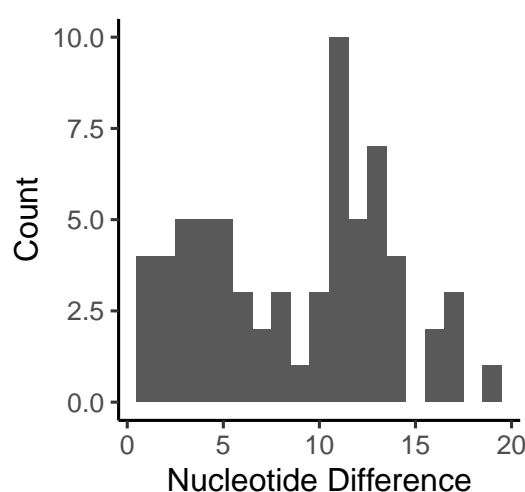
IGHV4-28*01_07

1 sequences assigned
No exact matches.



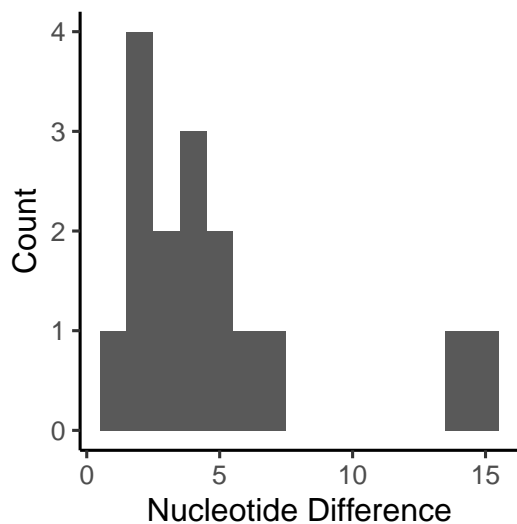
IGHV4-30-2*03

67 sequences assigned
No exact matches.



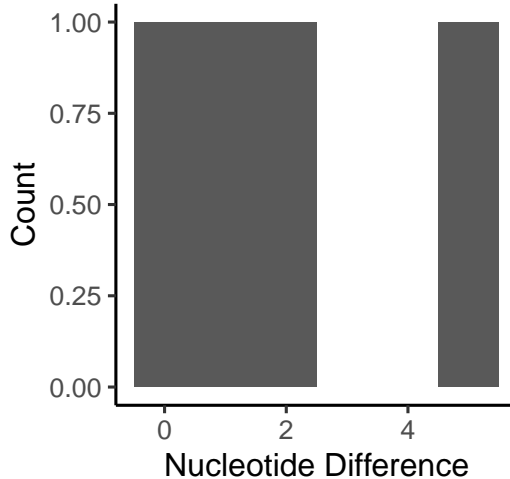
IGHV4-30-2*04

16 sequences assigned
No exact matches.



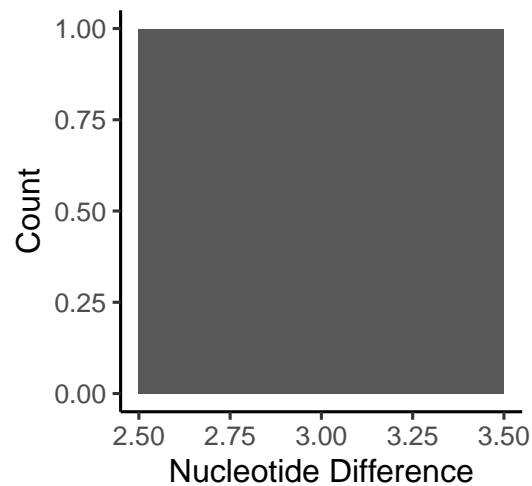
IGHV4-38-2*01

4 sequences assigned
1 (25%) exact matches, in which:
1 unique CDR3
1 unique J



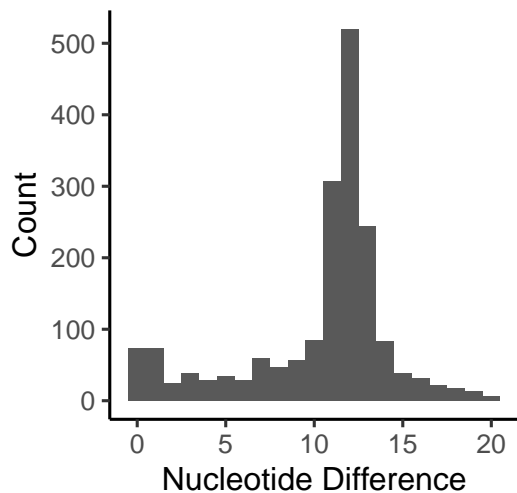
IGHV4-55*09

1 sequences assigned
No exact matches.



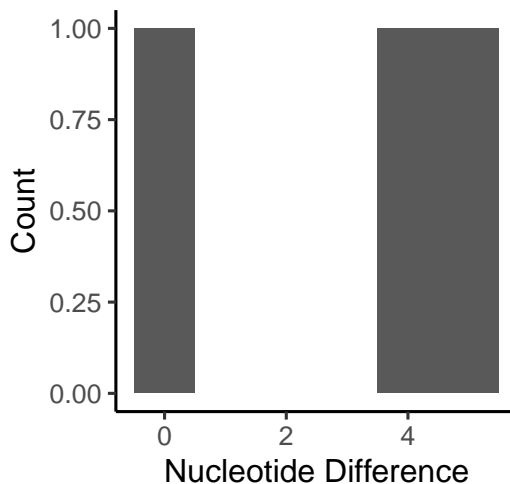
IGHV4-31*02

1864 sequences assigned
73 (3.9%) exact matches, in which:
64 unique CDR3
5 unique J



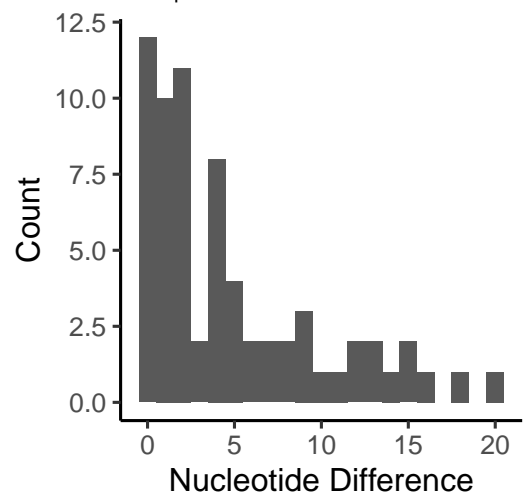
IGHV4-38-2*02

7 sequences assigned
1 (14.3%) exact matches, in which:
1 unique CDR3
1 unique J



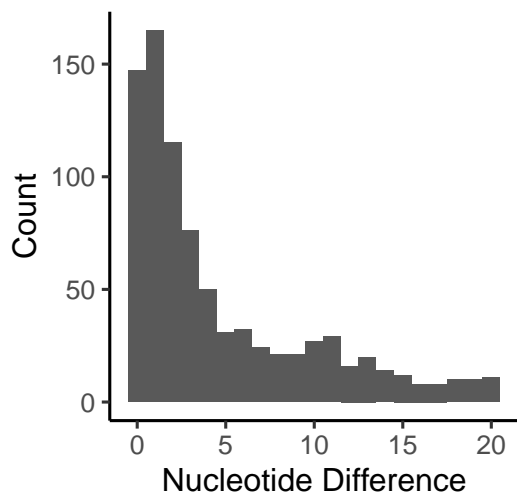
IGHV4-59*08

69 sequences assigned
12 (17.4%) exact matches, in which:
12 unique CDR3
5 unique J



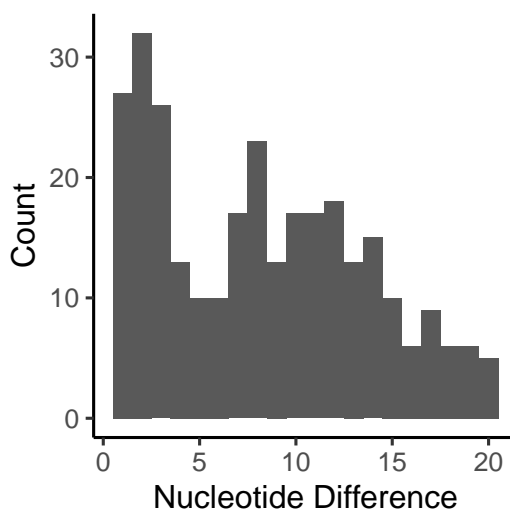
IGHV4-34*01_02

877 sequences assigned
147 (16.8%) exact matches, in which:
102 unique CDR3
4 unique J



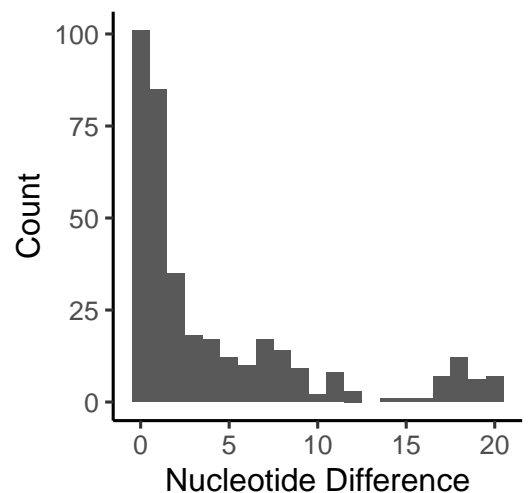
IGHV4-39*07

306 sequences assigned
No exact matches.



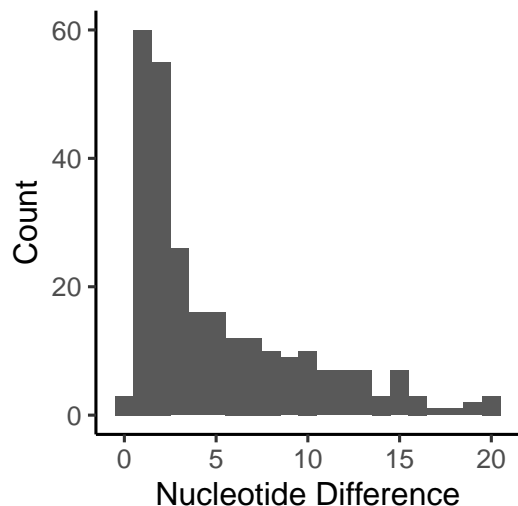
IGHV4-59*01_07

396 sequences assigned
101 (25.5%) exact matches, in which:
87 unique CDR3
5 unique J



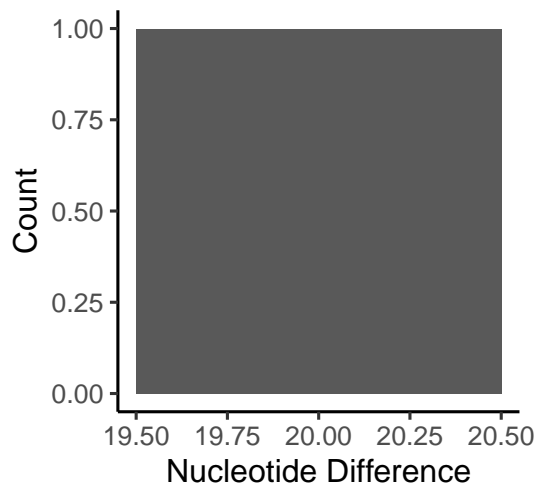
IGHV4–59*12

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



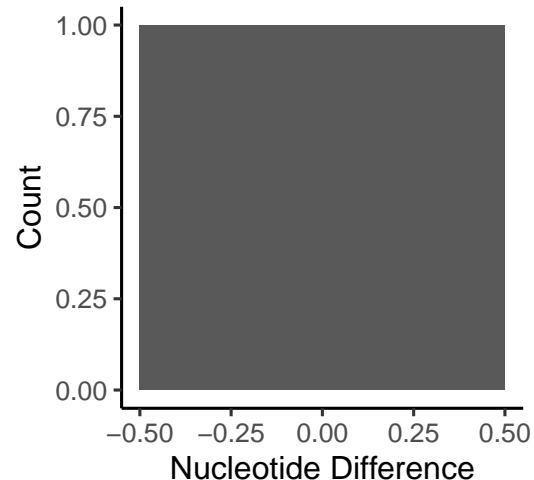
IGHV4/OR15–8*01

1 sequences assigned
No exact matches.



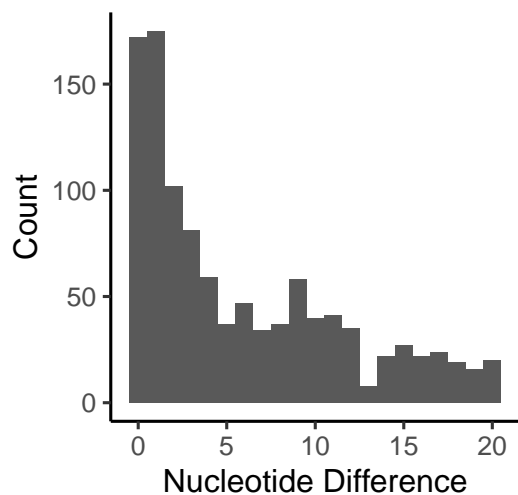
IGHV5–51*04

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



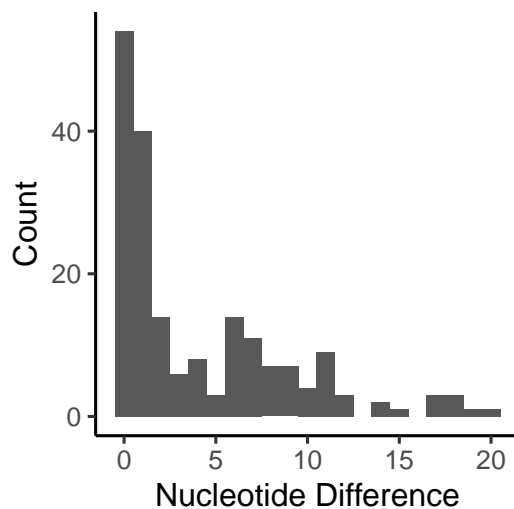
IGHV4–61*02

1128 sequences assigned
172 (15.2%) exact matches, in which:
143 unique CDR3
6 unique J



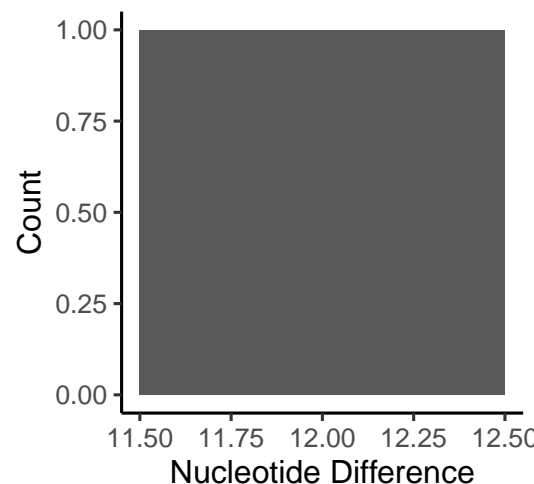
IGHV5–10–1*01_03

193 sequences assigned
54 (28%) exact matches, in which:
38 unique CDR3
4 unique J



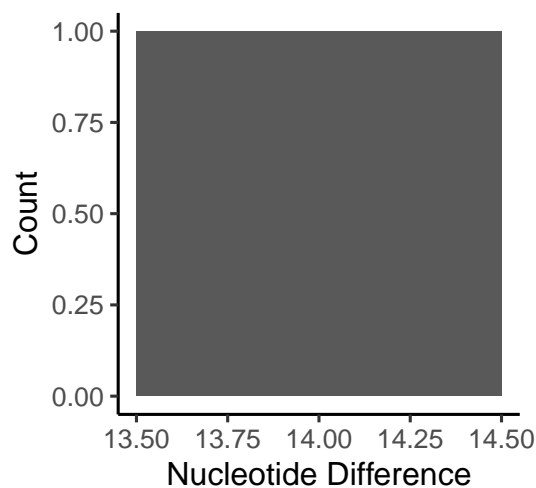
IGHV5–51*06

1 sequences assigned
No exact matches.



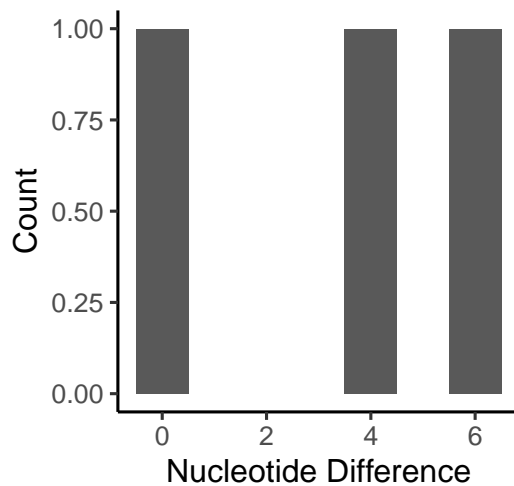
IGHV1/OR15–2*02_03

1 sequences assigned
No exact matches.



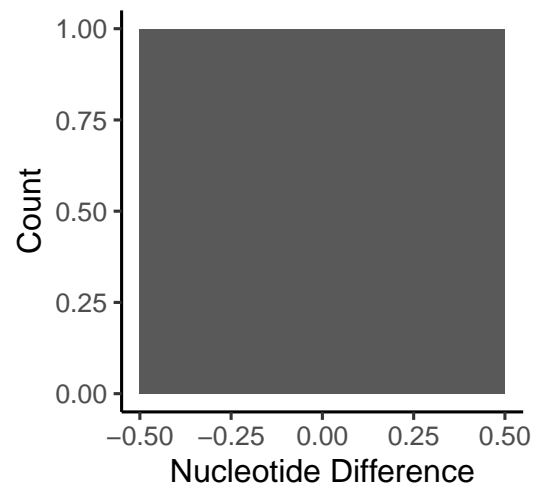
IGHV5–51*02

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



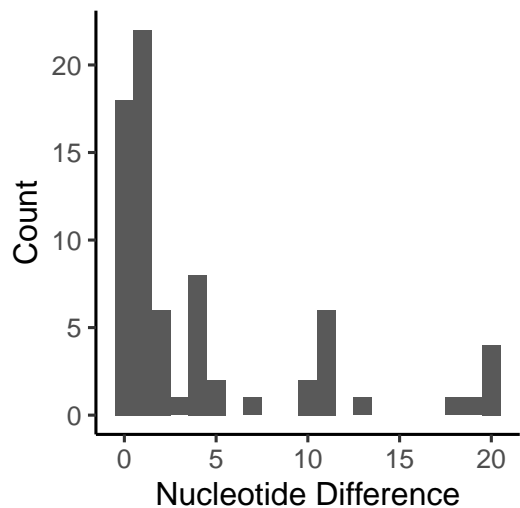
IGHV5–51*07

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



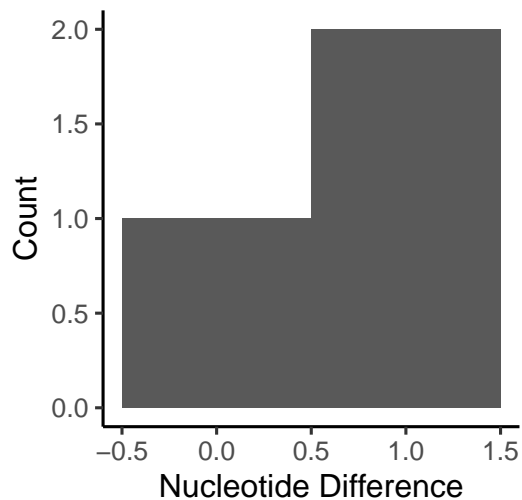
IGHV6-1*01_02

87 sequences assigned
18 (20.7%) exact matches, in which:
15 unique CDR3
3 unique J



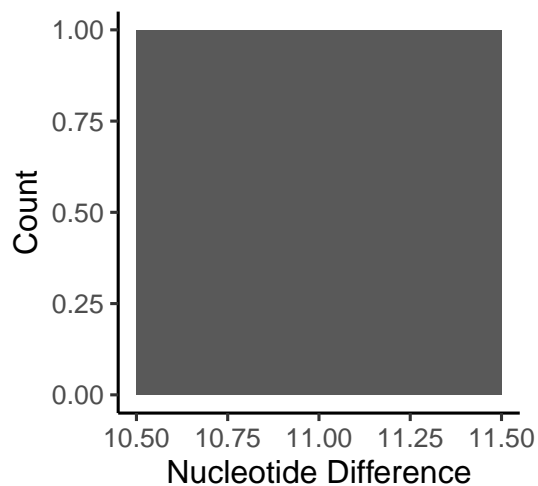
IGHV7-4-1*01

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



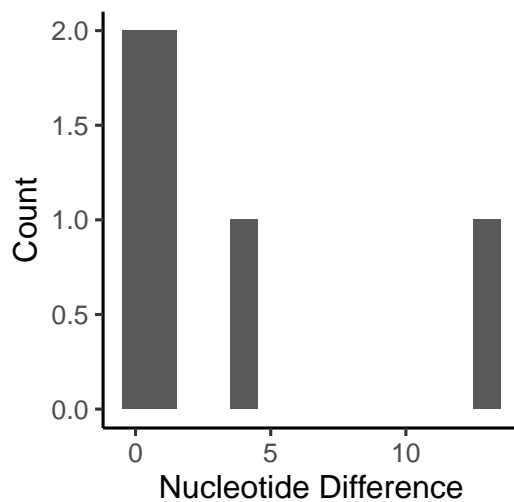
IGHV3/OR16-6*02

1 sequences assigned
No exact matches.



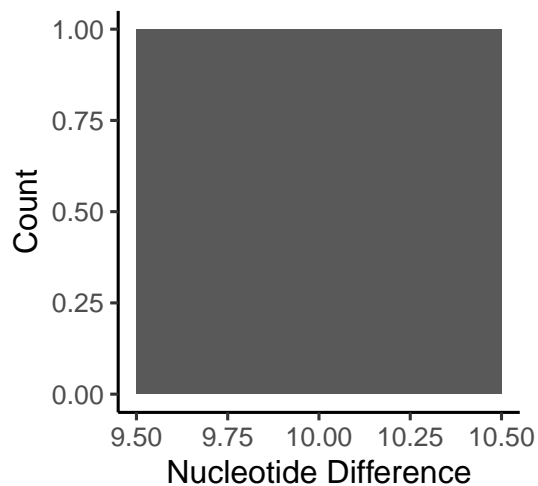
IGHV7-4-1*02

7 sequences assigned
2 (28.6%) exact matches, in which:
2 unique CDR3
2 unique J



IGHV3/OR16-10*01_03

1 sequences assigned
No exact matches.





Novel sequence(s)IGHV4-31*02_G92A_C111T_A113T_A138T_A164G_A225C_A234C_G238C_A240T_T249C_A250G are not listed in the genotype and will be ignored.