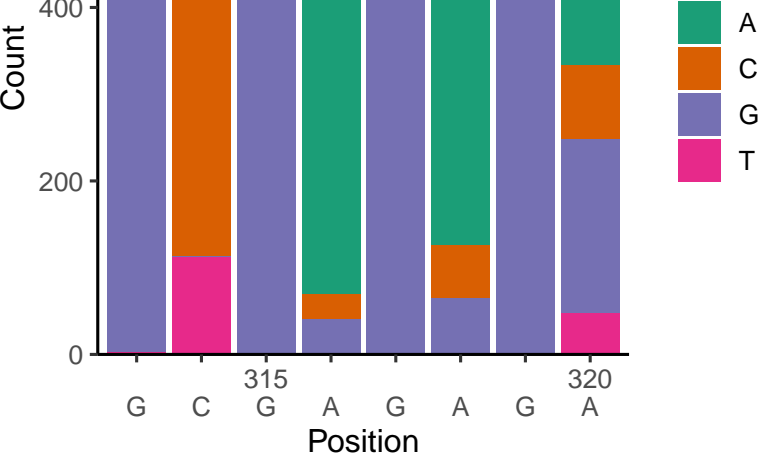


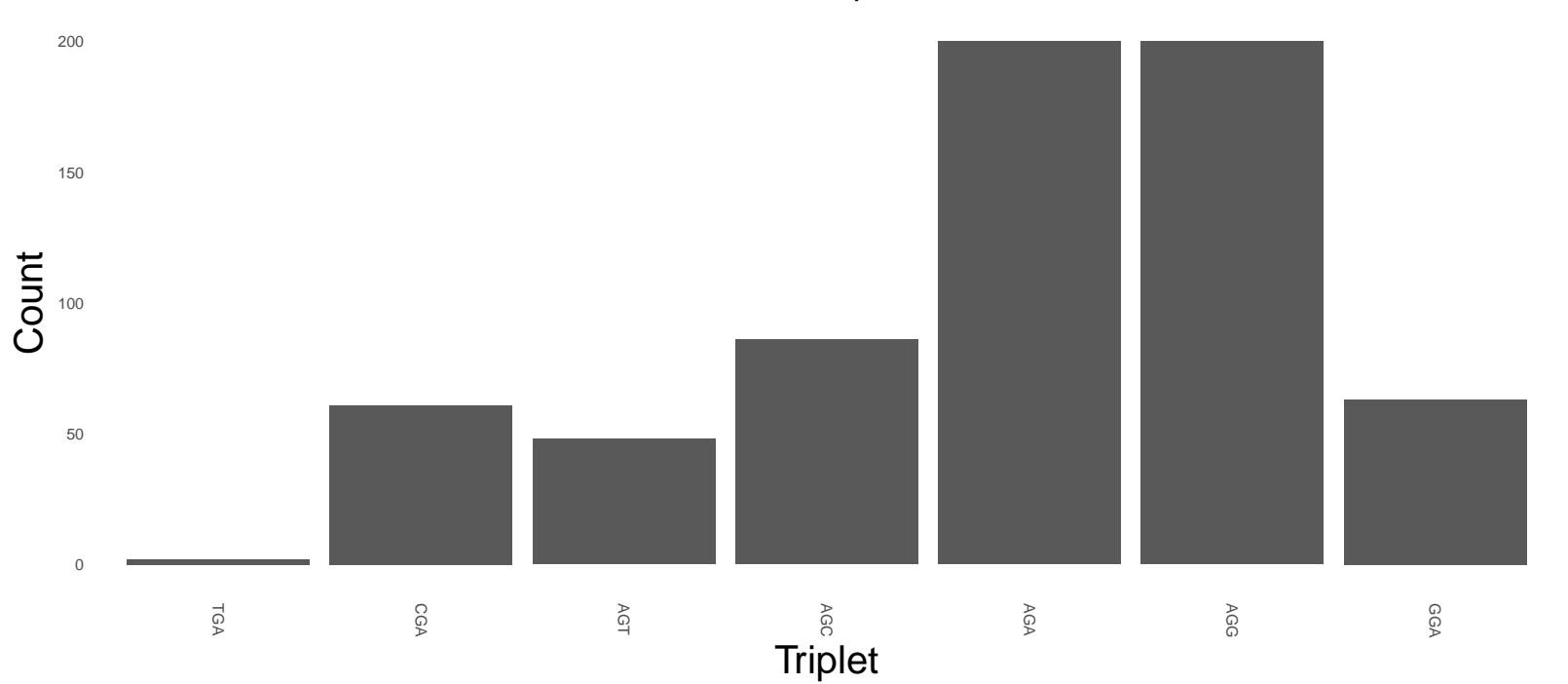
Gene IGHV4-39*02_C258G



Gene IGHV4-39*02_C258G

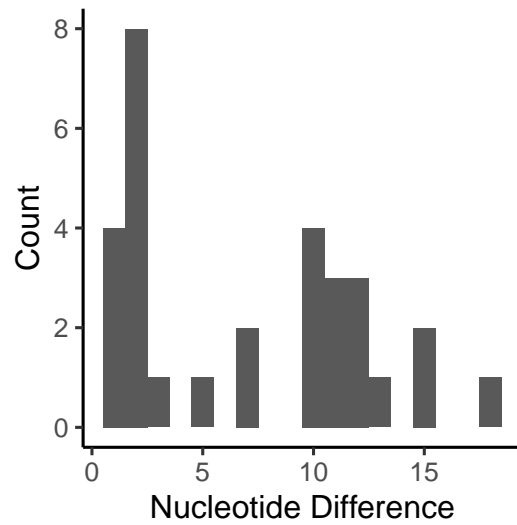


IGHV4-39*02_C258G- Final 3 nucleotides as a triplet



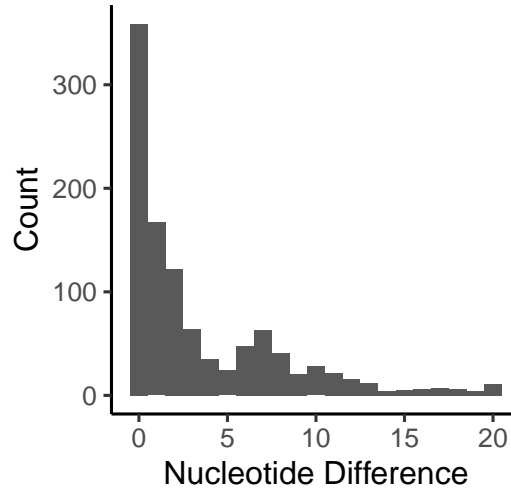
IGHV1-2*02

34 sequences assigned
No exact matches.



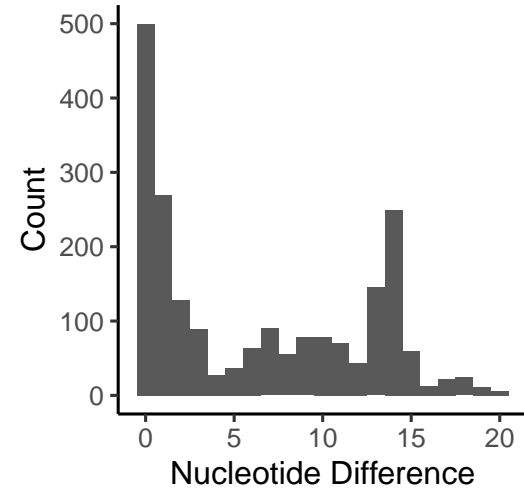
IGHV1-3*01_05

1353 sequences assigned
359 (26.5%) exact matches, in which:
338 unique CDR3
7 unique J



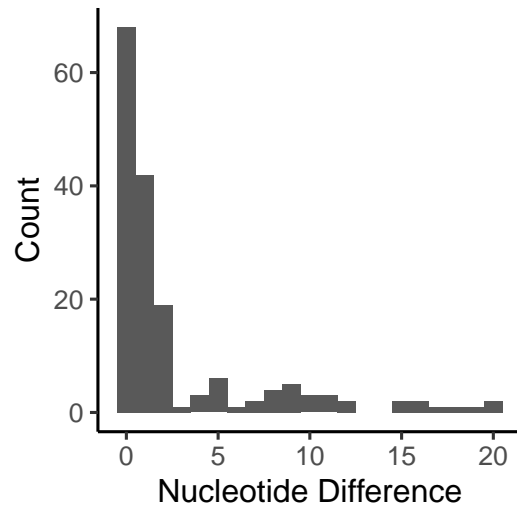
IGHV1-18*01

2265 sequences assigned
500 (22.1%) exact matches, in which:
478 unique CDR3
7 unique J



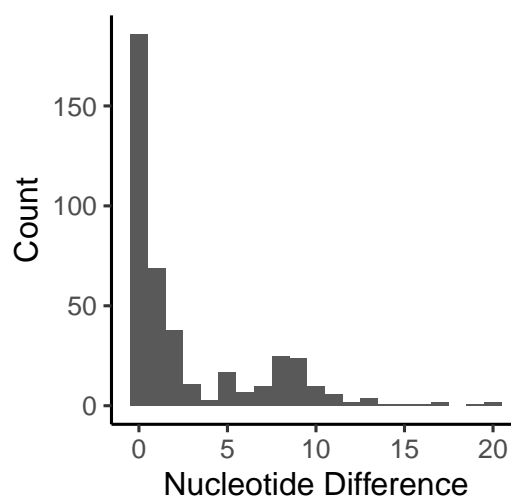
IGHV1-2*04

221 sequences assigned
68 (30.8%) exact matches, in which:
64 unique CDR3
5 unique J



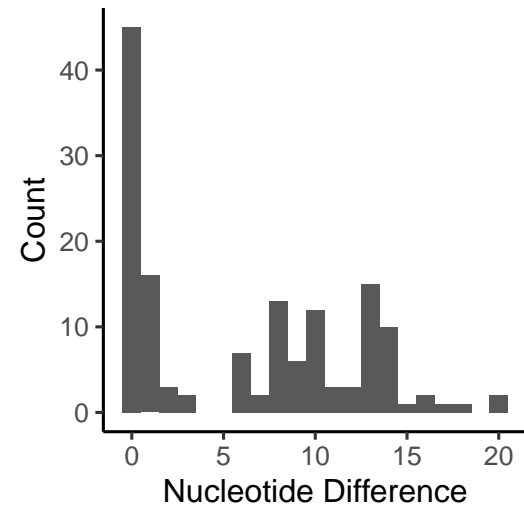
IGHV1-8*01

458 sequences assigned
186 (40.6%) exact matches, in which:
181 unique CDR3
7 unique J



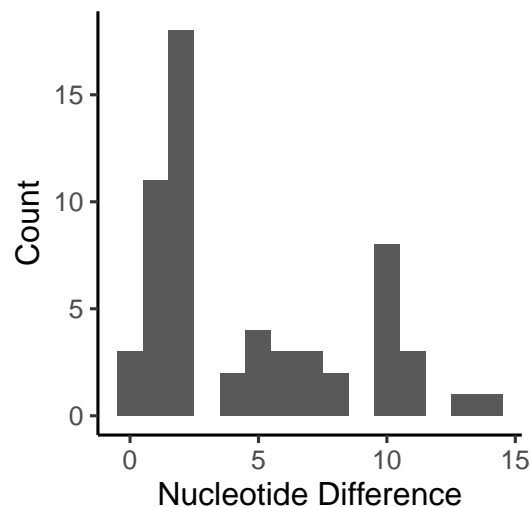
IGHV1-24*01

165 sequences assigned
45 (27.3%) exact matches, in which:
45 unique CDR3
4 unique J



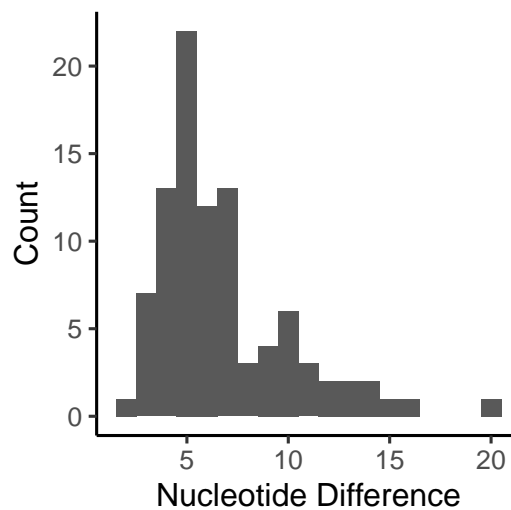
IGHV1-2*06

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



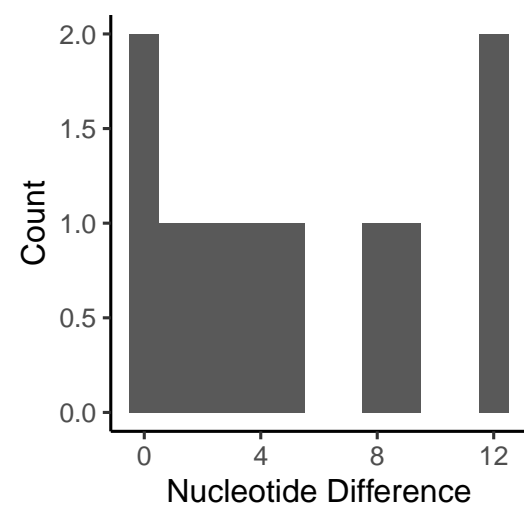
IGHV1-8*02

95 sequences assigned
No exact matches.



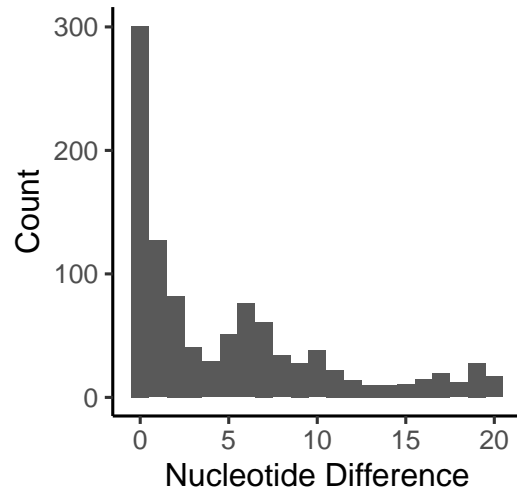
IGHV1-45*02

11 sequences assigned
2 (18.2%) exact matches, in which:
2 unique CDR3
2 unique J



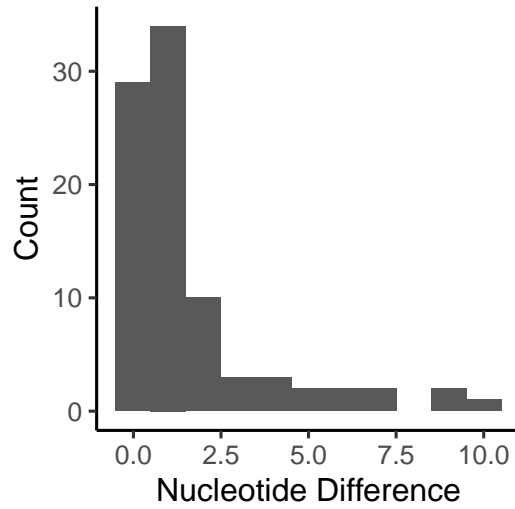
IGHV1-46*01

1251 sequences assigned
301 (24.1%) exact matches, in which:
285 unique CDR3
7 unique J



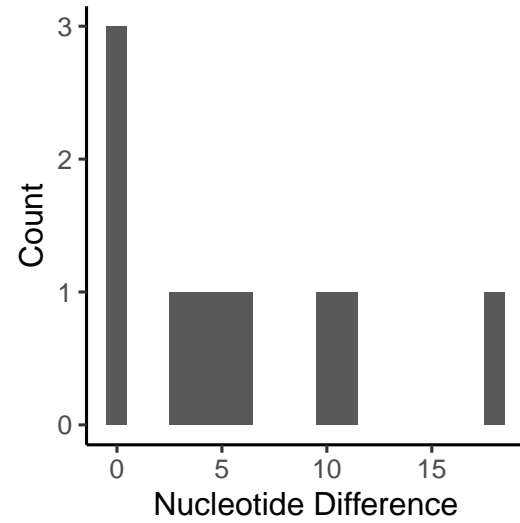
IGHV1-58*01_03

94 sequences assigned
29 (30.9%) exact matches, in which:
28 unique CDR3
5 unique J



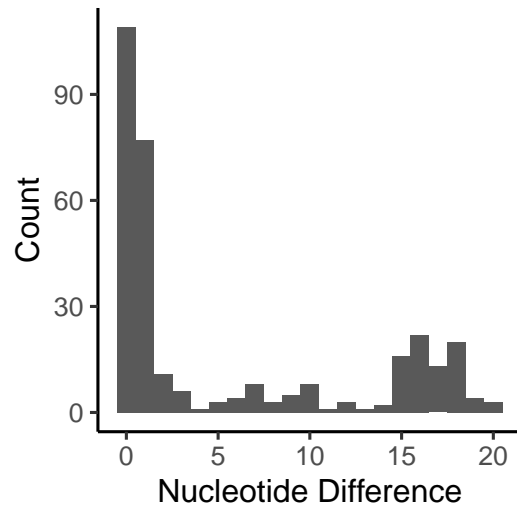
IGHV1-69D*01

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



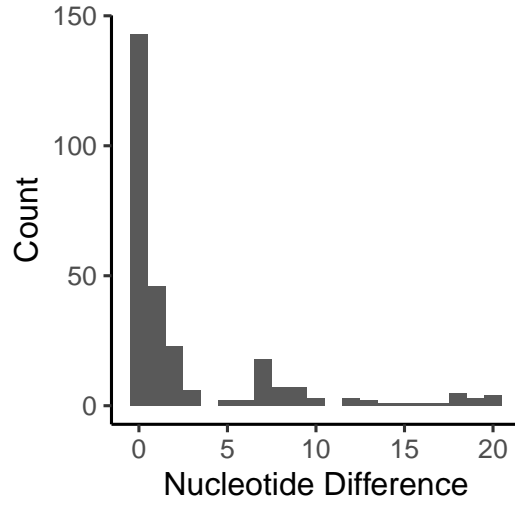
IGHV1-46*03

353 sequences assigned
109 (30.9%) exact matches, in which:
101 unique CDR3
7 unique J



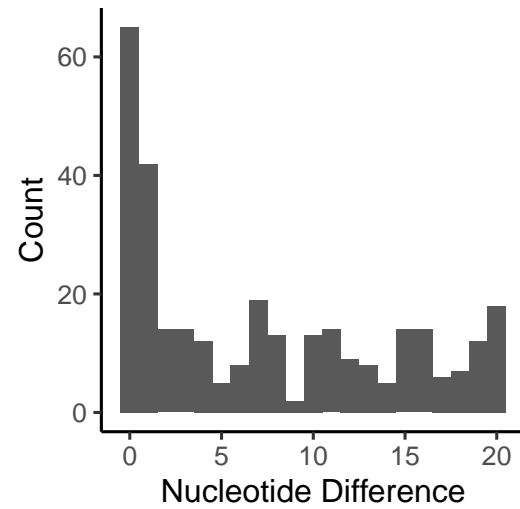
IGHV1-69*02

331 sequences assigned
143 (43.2%) exact matches, in which:
141 unique CDR3
7 unique J



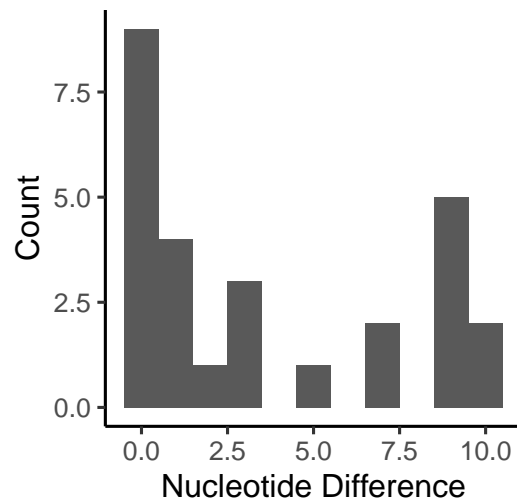
IGHV2-5*02

421 sequences assigned
65 (15.4%) exact matches, in which:
60 unique CDR3
6 unique J



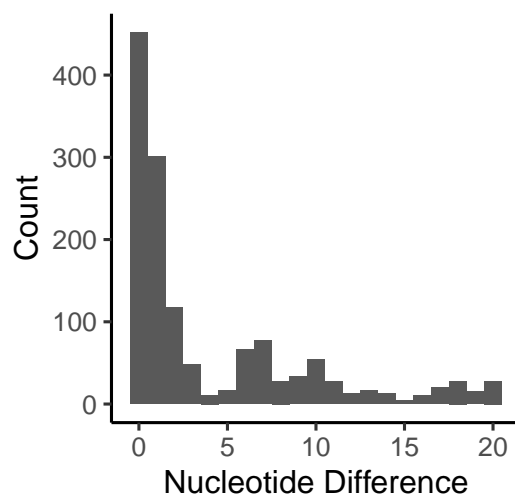
IGHV1-58*02

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



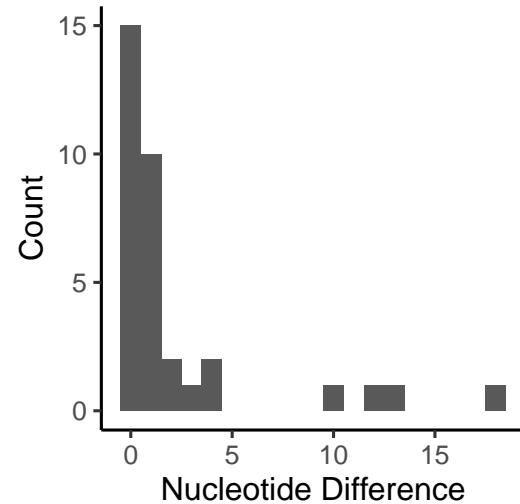
IGHV1-69*04_09

1499 sequences assigned
452 (30.2%) exact matches, in which:
437 unique CDR3
7 unique J



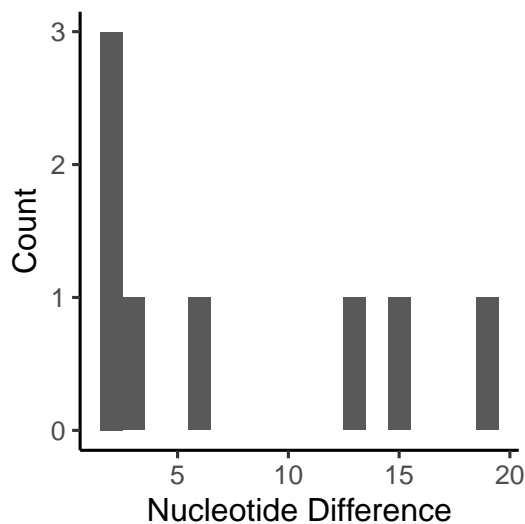
IGHV2-26*01

35 sequences assigned
15 (42.9%) exact matches, in which:
12 unique CDR3
4 unique J



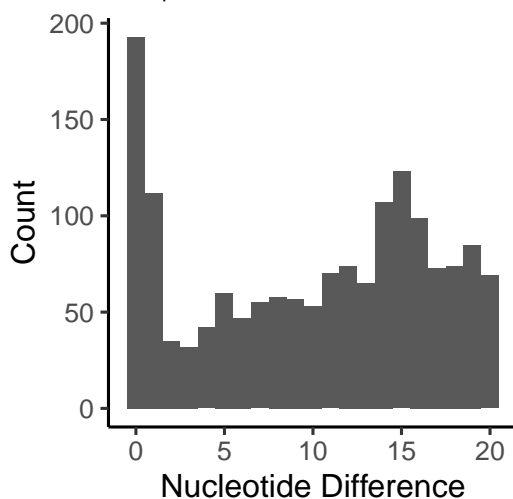
IGHV2-70*12

14 sequences assigned
No exact matches.



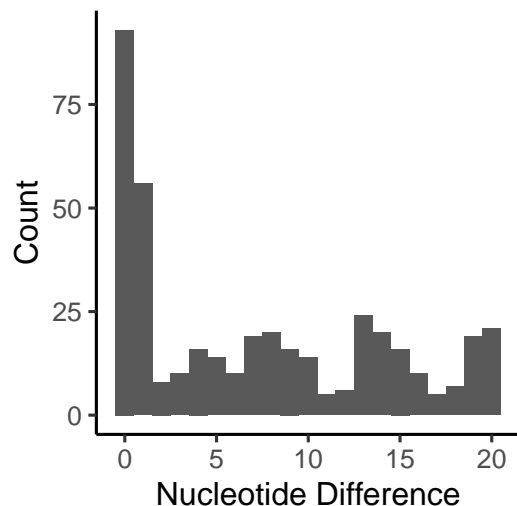
IGHV3-7*01

2072 sequences assigned
193 (9.3%) exact matches, in which:
175 unique CDR3
7 unique J



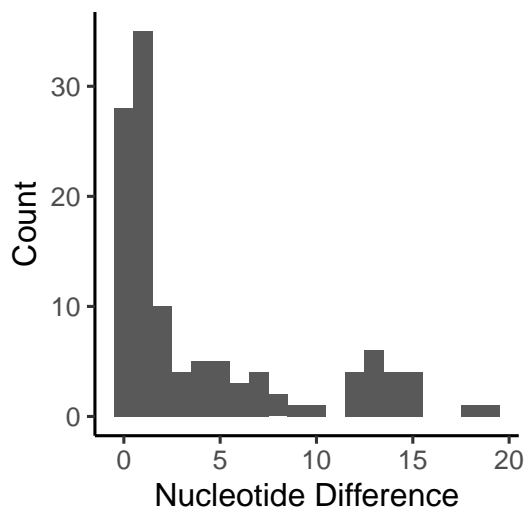
IGHV3-11*01

550 sequences assigned
93 (16.9%) exact matches, in which:
81 unique CDR3
5 unique J



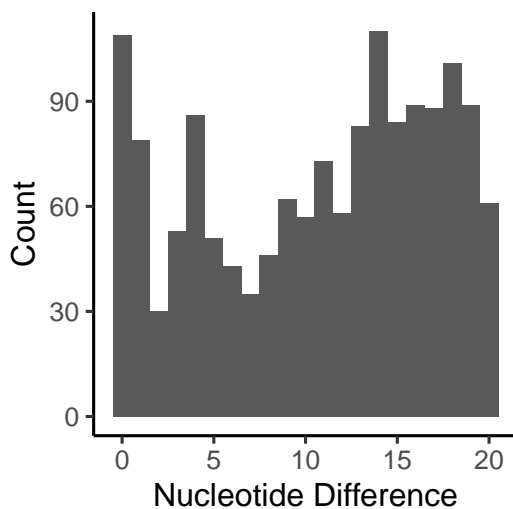
IGHV2-70*11_15

121 sequences assigned
28 (23.1%) exact matches, in which:
23 unique CDR3
4 unique J



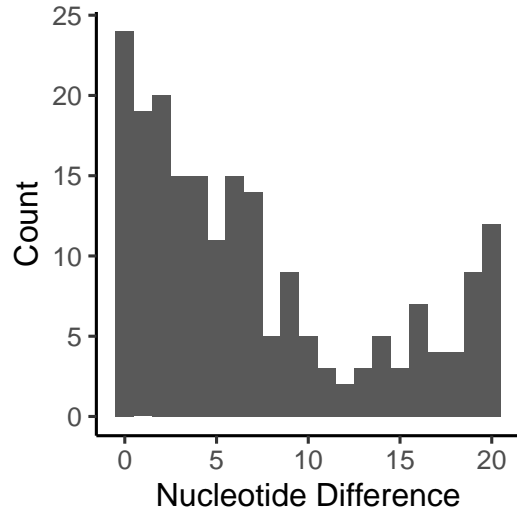
IGHV3-7*03

2220 sequences assigned
109 (4.9%) exact matches, in which:
89 unique CDR3
7 unique J



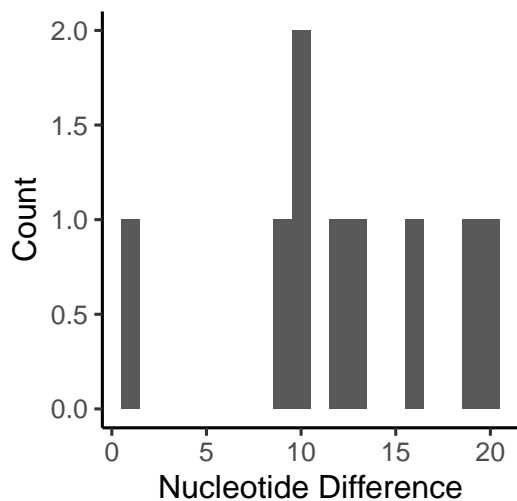
IGHV3-11*04

238 sequences assigned
24 (10.1%) exact matches, in which:
24 unique CDR3
5 unique J



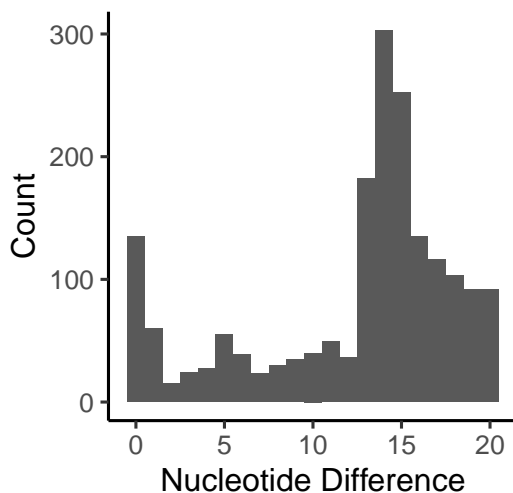
IGHV2-70D*04

10 sequences assigned
No exact matches.



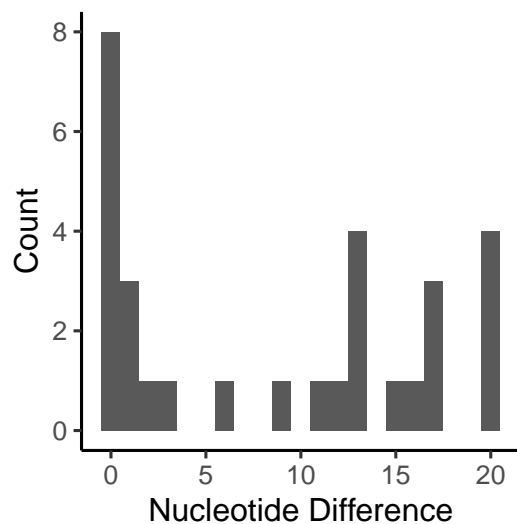
IGHV3-9*01

2378 sequences assigned
135 (5.7%) exact matches, in which:
108 unique CDR3
7 unique J



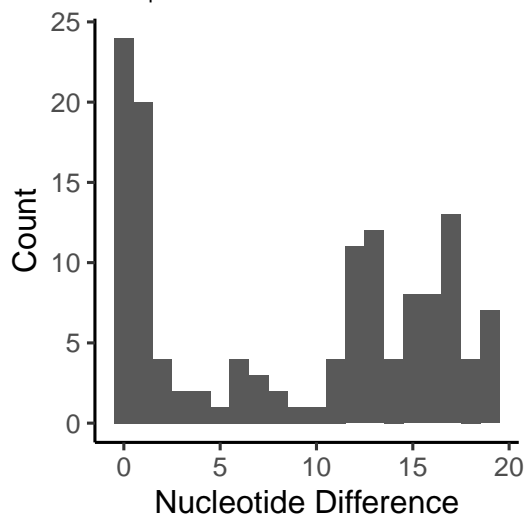
IGHV3-11*06

43 sequences assigned
8 (18.6%) exact matches, in which:
5 unique CDR3
2 unique J



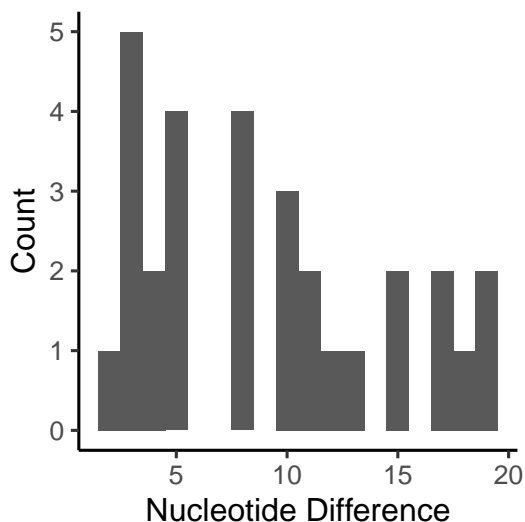
IGHV3-13*01

207 sequences assigned
24 (11.6%) exact matches, in which:
21 unique CDR3
5 unique J



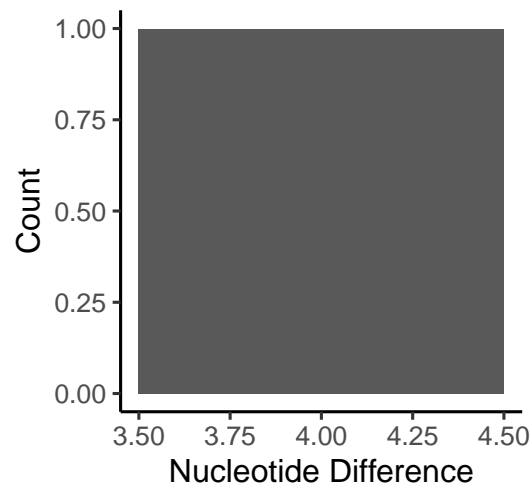
IGHV3-20*03_04

45 sequences assigned
No exact matches.



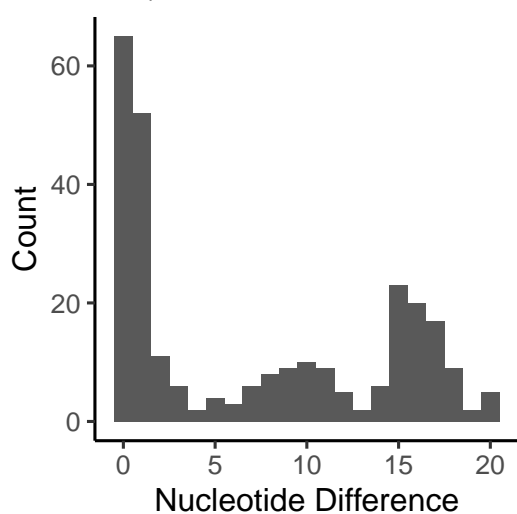
IGHV3-30-3*01

6 sequences assigned
No exact matches.



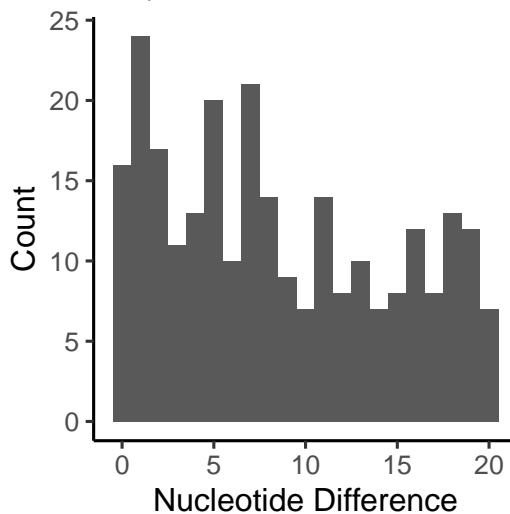
IGHV3-15*01_02

434 sequences assigned
65 (15%) exact matches, in which:
45 unique CDR3
6 unique J



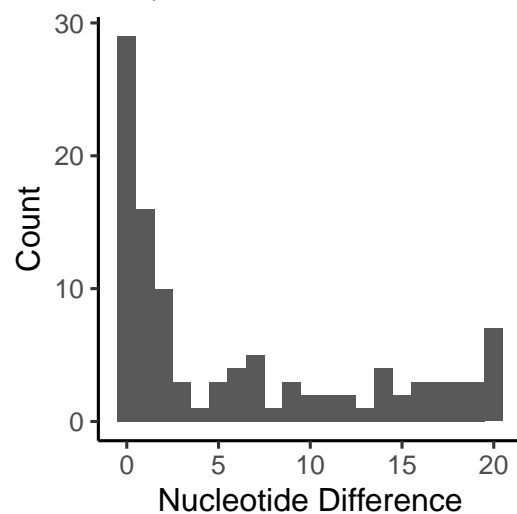
IGHV3-21*04

323 sequences assigned
16 (5%) exact matches, in which:
16 unique CDR3
4 unique J



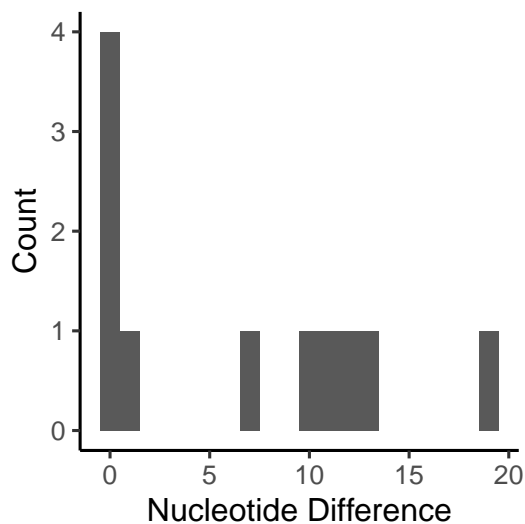
IGHV3-30*03

155 sequences assigned
29 (18.7%) exact matches, in which:
29 unique CDR3
6 unique J



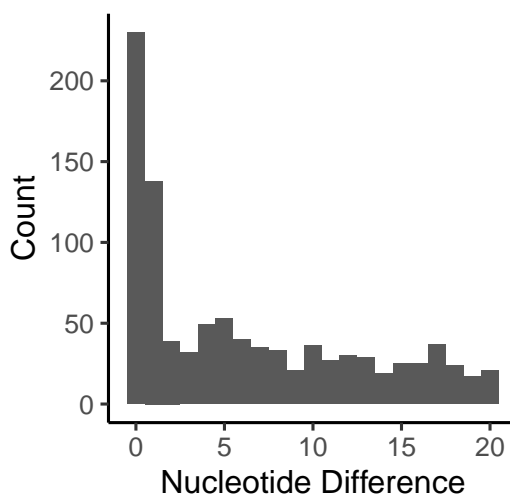
IGHV3-20*01_02

14 sequences assigned
4 (28.6%) exact matches, in which:
4 unique CDR3
3 unique J



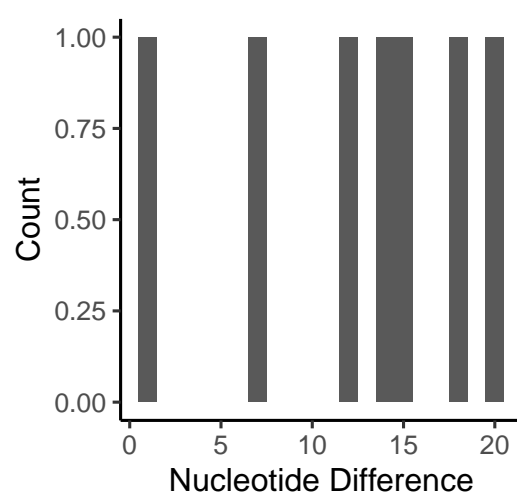
IGHV3-21*01_02

1114 sequences assigned
230 (20.6%) exact matches, in which:
187 unique CDR3
7 unique J



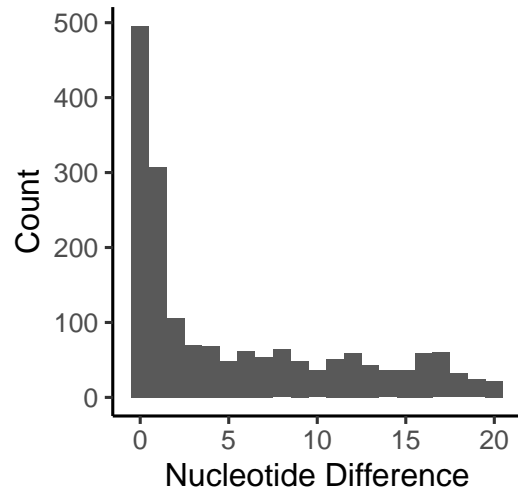
IGHV3-30-3*03

14 sequences assigned
No exact matches.



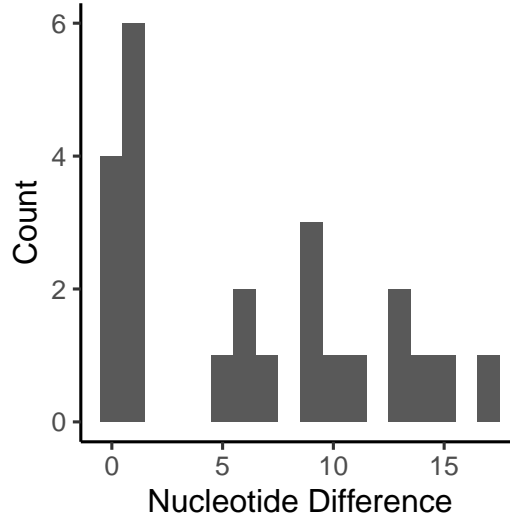
IGHV3–33*01

2121 sequences assigned
496 (23.4%) exact matches, in which:
413 unique CDR3
7 unique J



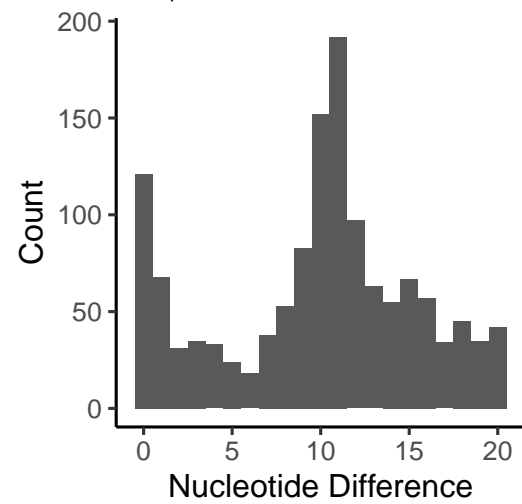
IGHV3–43*01

77 sequences assigned
4 (5.2%) exact matches, in which:
3 unique CDR3
2 unique J



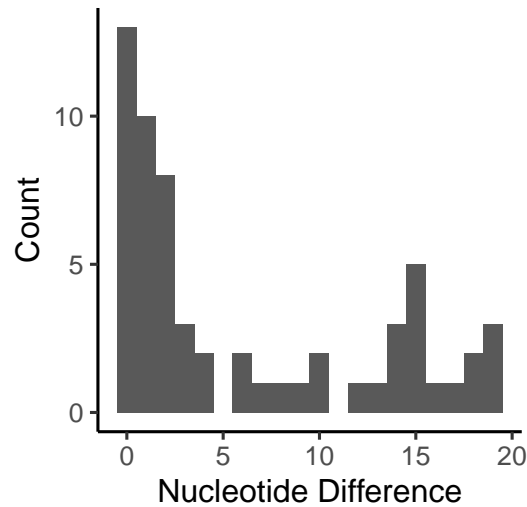
IGHV3–48*02

1637 sequences assigned
121 (7.4%) exact matches, in which:
108 unique CDR3
7 unique J



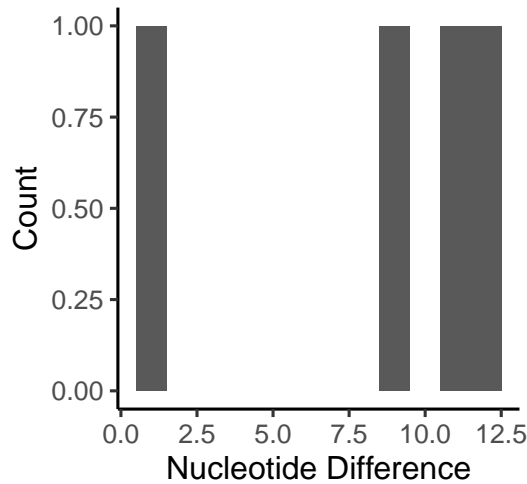
IGHV3–33*05

103 sequences assigned
13 (12.6%) exact matches, in which:
13 unique CDR3
4 unique J



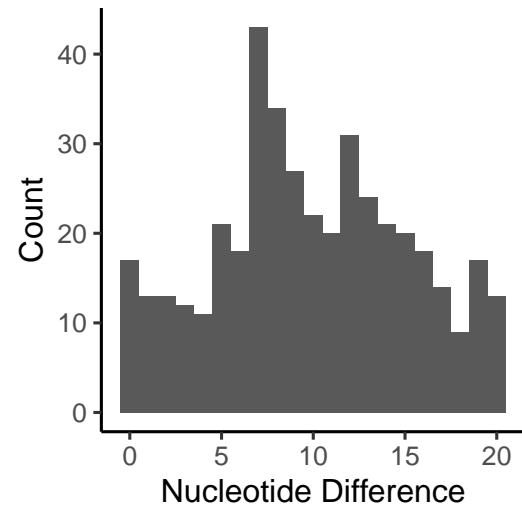
IGHV3–47*02

4 sequences assigned
No exact matches.



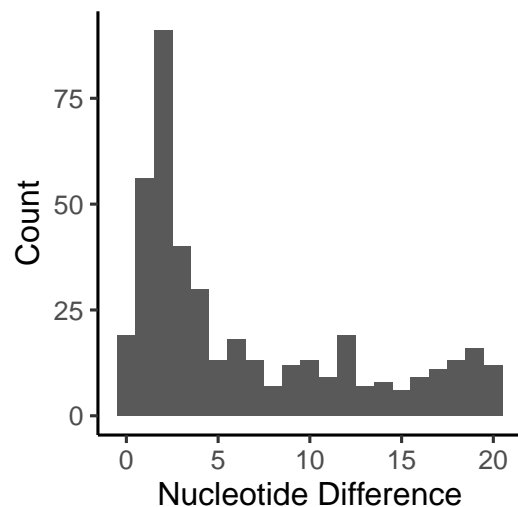
IGHV3–48*04

552 sequences assigned
17 (3.1%) exact matches, in which:
17 unique CDR3
5 unique J



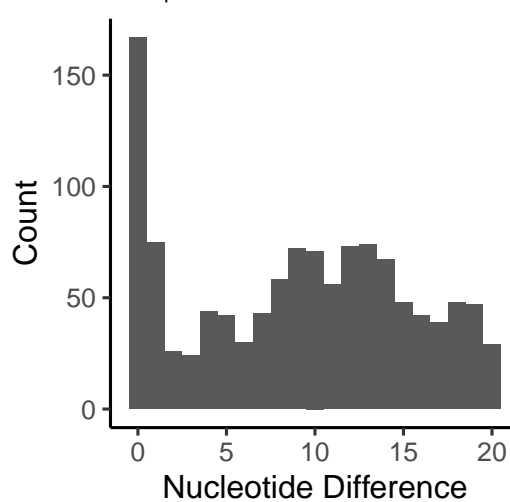
IGHV3–33*06

498 sequences assigned
19 (3.8%) exact matches, in which:
19 unique CDR3
5 unique J



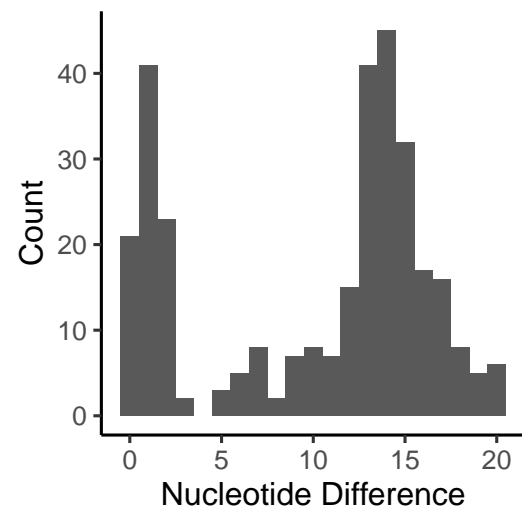
IGHV3–48*01

1400 sequences assigned
167 (11.9%) exact matches, in which:
150 unique CDR3
7 unique J



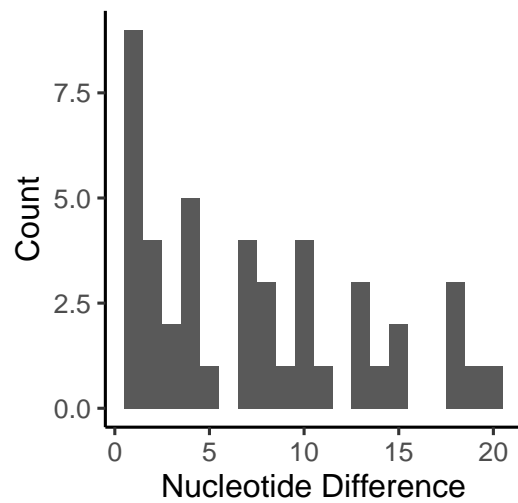
IGHV3–49*03_05

454 sequences assigned
21 (4.6%) exact matches, in which:
19 unique CDR3
3 unique J



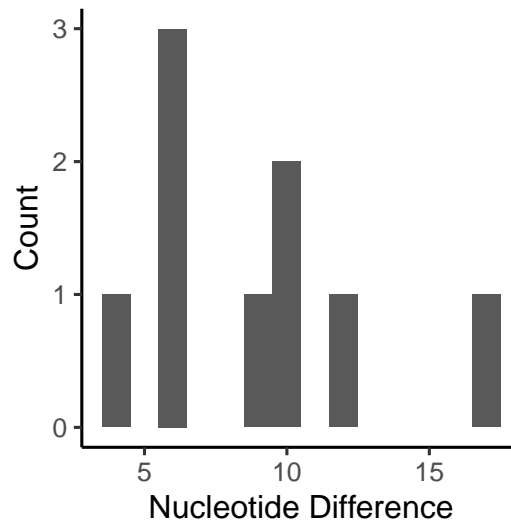
IGHV3-53*05

55 sequences assigned
No exact matches.



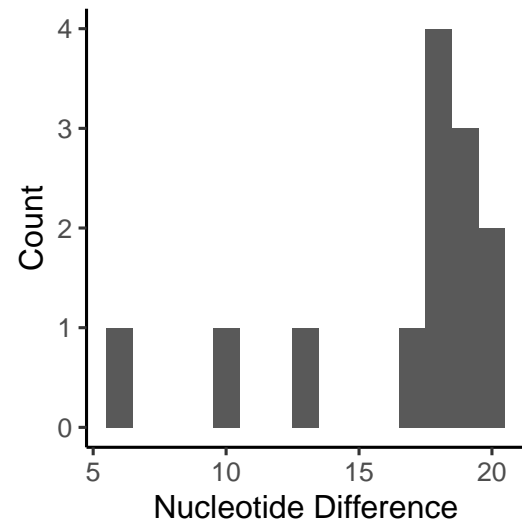
IGHV3-64*04

15 sequences assigned
No exact matches.



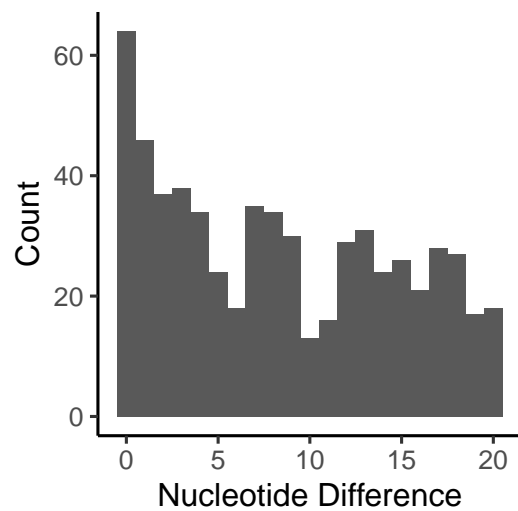
IGHV3-69-1*01

26 sequences assigned
No exact matches.



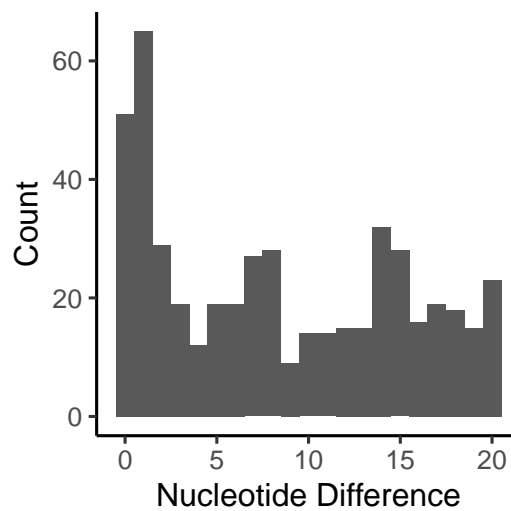
IGHV3-53*01_02

817 sequences assigned
64 (7.8%) exact matches, in which:
57 unique CDR3
7 unique J



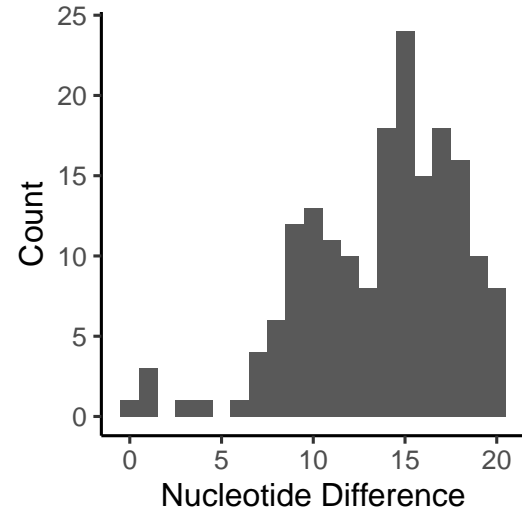
IGHV3-66*01

667 sequences assigned
51 (7.6%) exact matches, in which:
45 unique CDR3
7 unique J



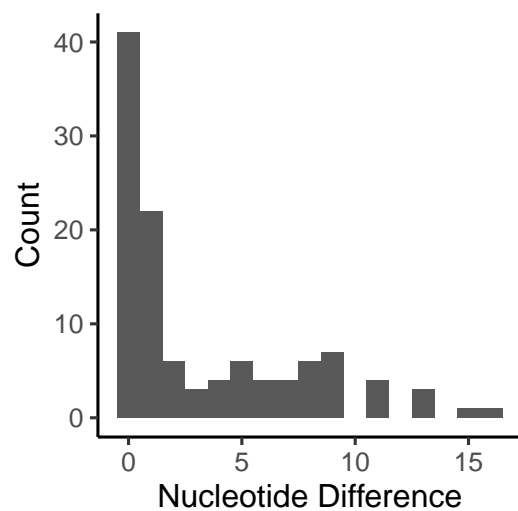
IGHV3-72*01

450 sequences assigned
1 (0.2%) exact matches, in which:
1 unique CDR3
1 unique J



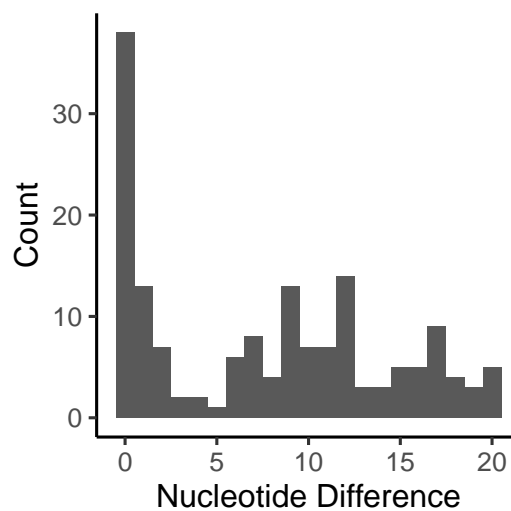
IGHV3-64*01

191 sequences assigned
41 (21.5%) exact matches, in which:
33 unique CDR3
4 unique J



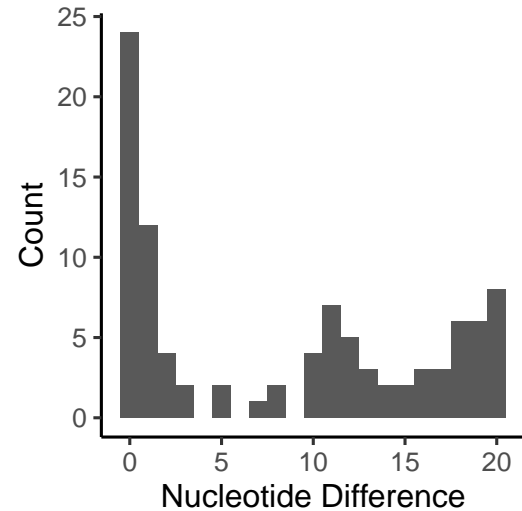
IGHV3-66*02

202 sequences assigned
38 (18.8%) exact matches, in which:
36 unique CDR3
5 unique J



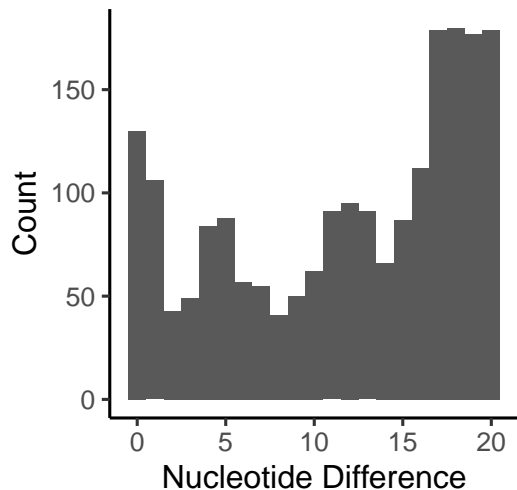
IGHV3-73*01_02

245 sequences assigned
24 (9.8%) exact matches, in which:
19 unique CDR3
5 unique J



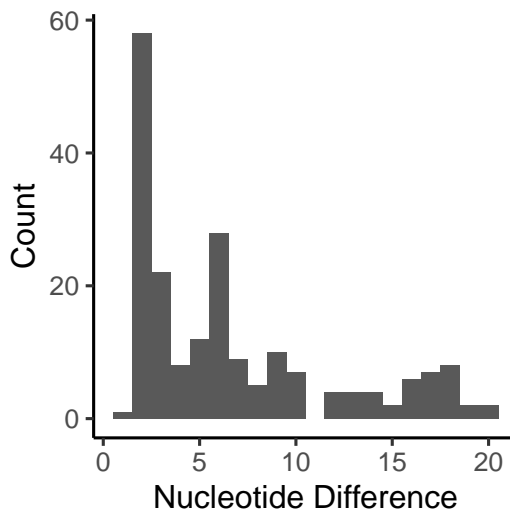
IGHV3-74*01_02

3847 sequences assigned
130 (3.4%) exact matches, in which:
108 unique CDR3
7 unique J



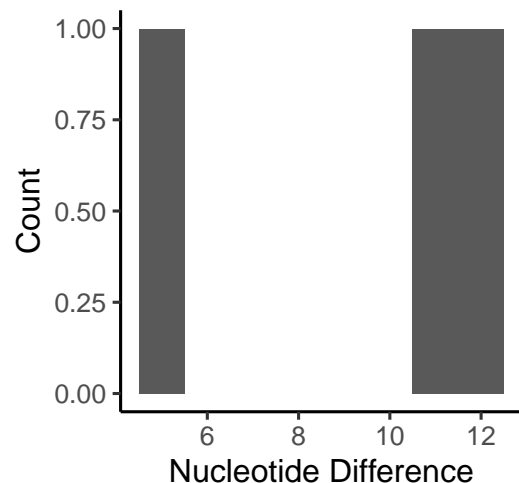
IGHV4-4*07

238 sequences assigned
No exact matches.



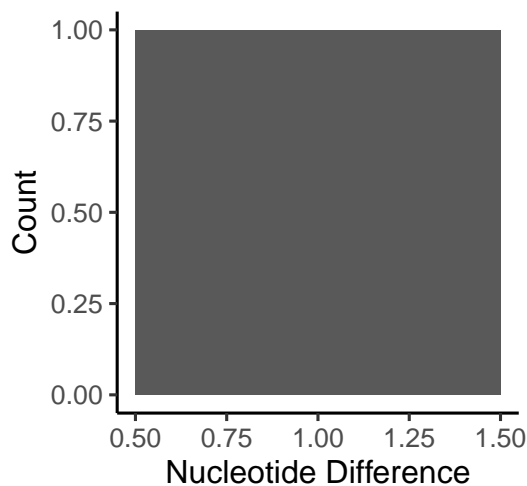
IGHV4-30-2*01

7 sequences assigned
No exact matches.



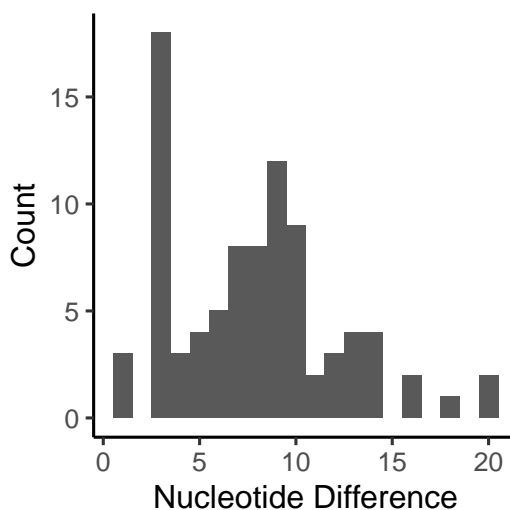
IGHV3-64D*06

198 sequences assigned
No exact matches.



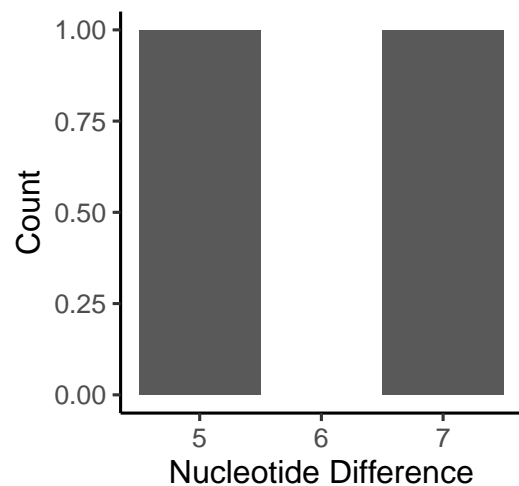
IGHV4-4*08

111 sequences assigned
No exact matches.



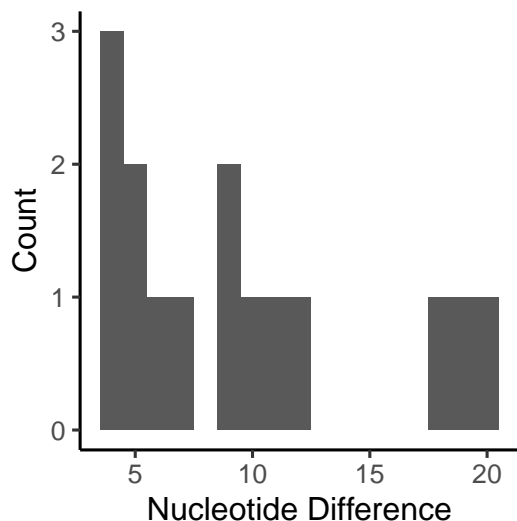
IGHV4-30-4*01

6 sequences assigned
No exact matches.



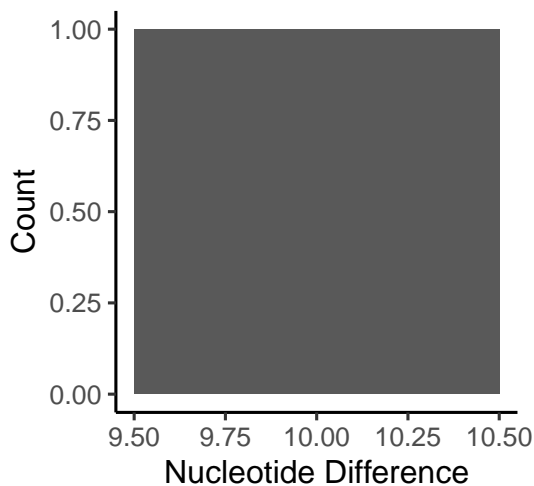
IGHV3-NL1*01

29 sequences assigned
No exact matches.



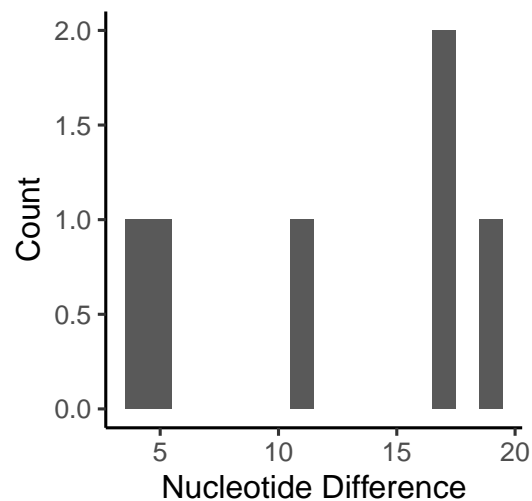
IGHV4-28*03

2 sequences assigned
No exact matches.



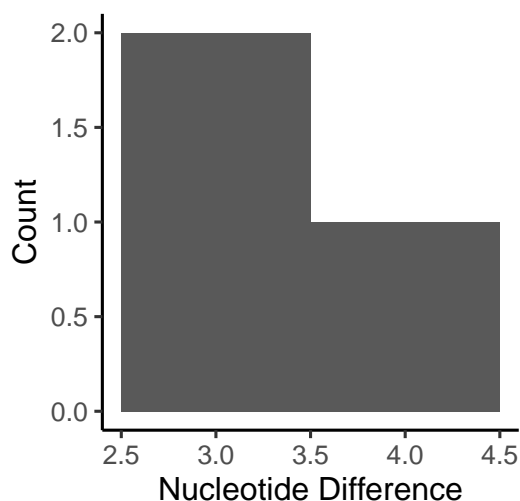
IGHV4-30-2*03

9 sequences assigned
No exact matches.



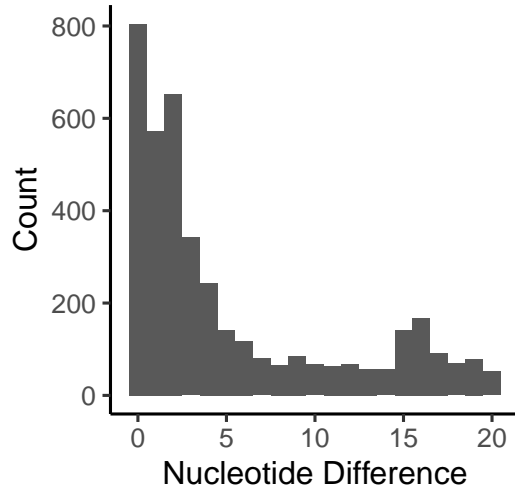
IGHV4-30-2*04

4 sequences assigned
No exact matches.



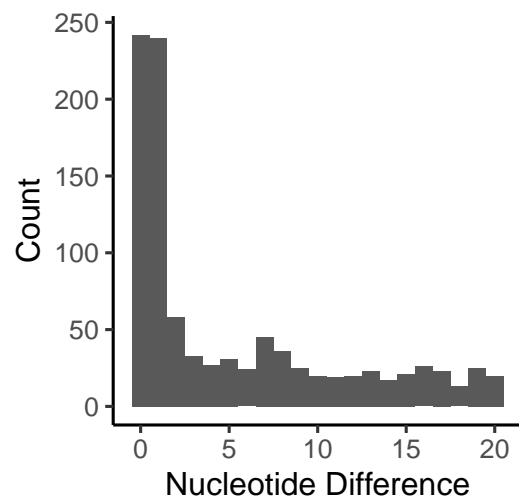
IGHV4-34*01_02

4603 sequences assigned
805 (17.5%) exact matches, in which:
734 unique CDR3
7 unique J



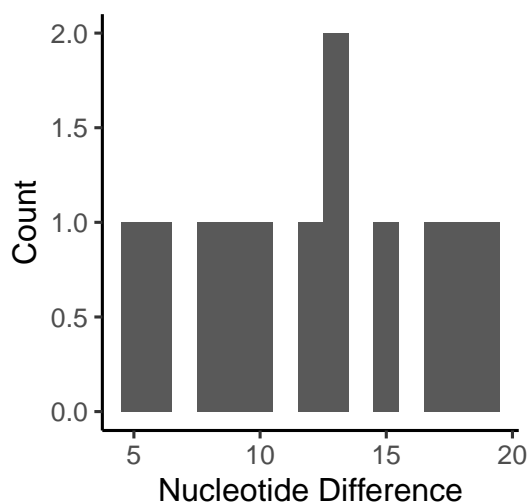
IGHV4-39*01_05

1407 sequences assigned
242 (17.2%) exact matches, in which:
212 unique CDR3
7 unique J



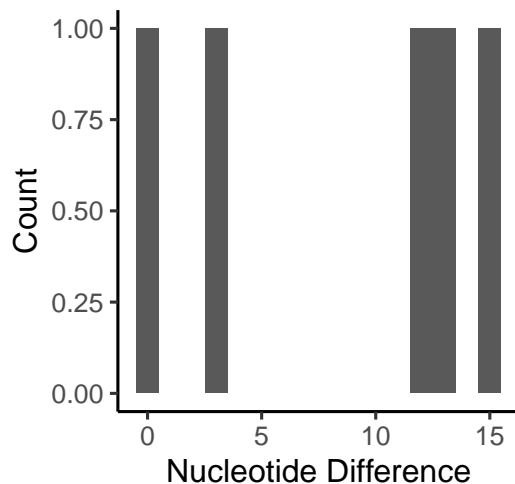
IGHV4-30-4*08

18 sequences assigned
No exact matches.



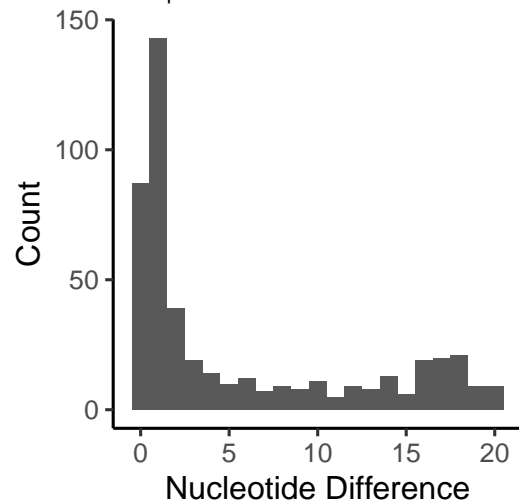
IGHV4-38-2*02

8 sequences assigned
1 (12.5%) exact matches, in which:
1 unique CDR3
1 unique J



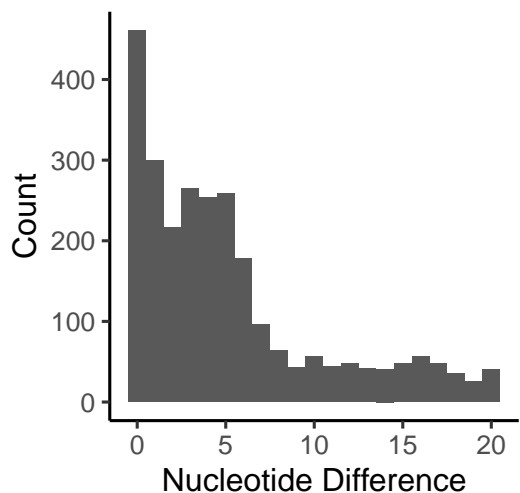
IGHV4-39*02_C258G

660 sequences assigned
87 (13.2%) exact matches, in which:
87 unique CDR3
6 unique J



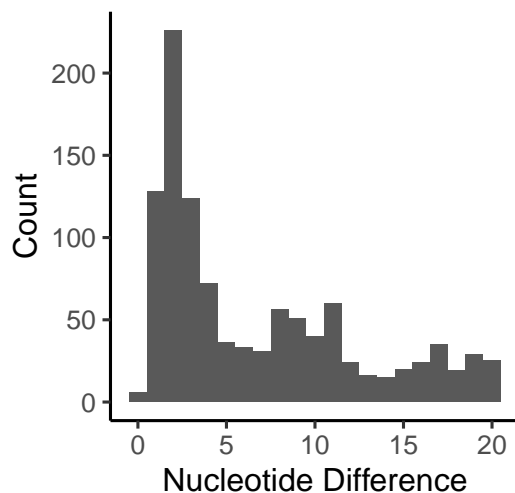
IGHV4-31*03_04

3057 sequences assigned
461 (15.1%) exact matches, in which:
442 unique CDR3
7 unique J



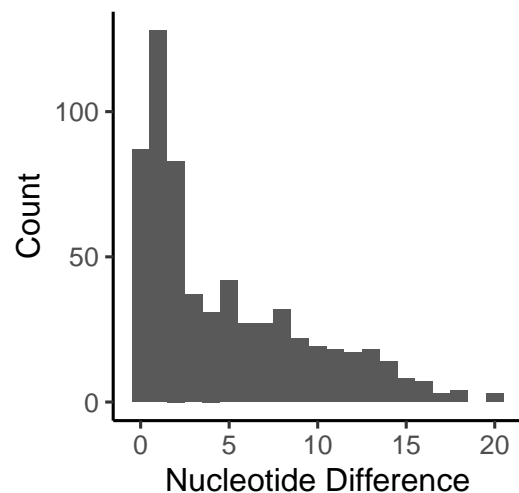
IGHV4-39*07

1219 sequences assigned
6 (0.5%) exact matches, in which:
6 unique CDR3
2 unique J



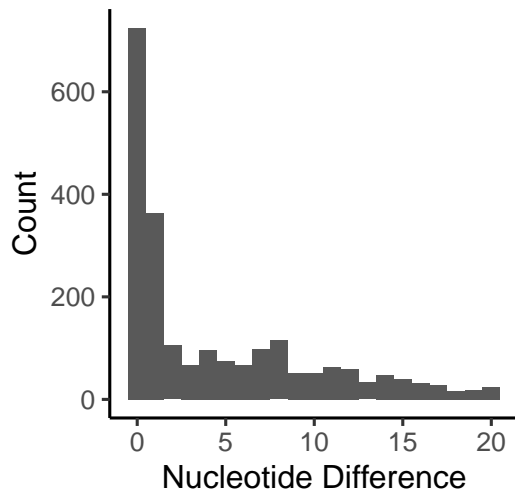
IGHV4-59*08

661 sequences assigned
87 (13.2%) exact matches, in which:
87 unique CDR3
7 unique J



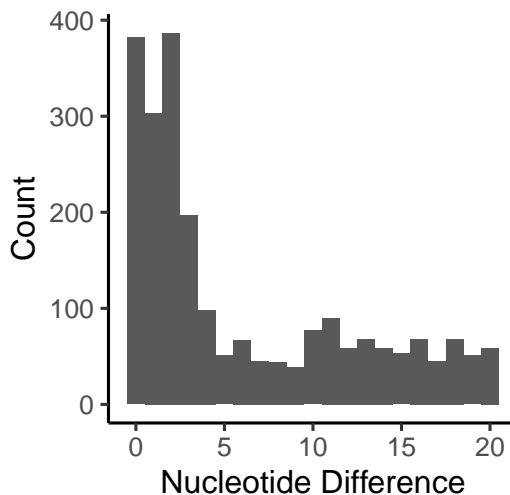
IGHV4-59*01_07

2650 sequences assigned
725 (27.4%) exact matches, in which:
690 unique CDR3
7 unique J



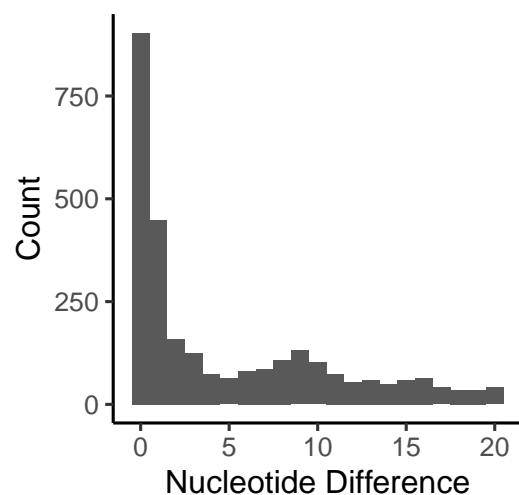
IGHV4-61*02

2856 sequences assigned
382 (13.4%) exact matches, in which:
355 unique CDR3
7 unique J



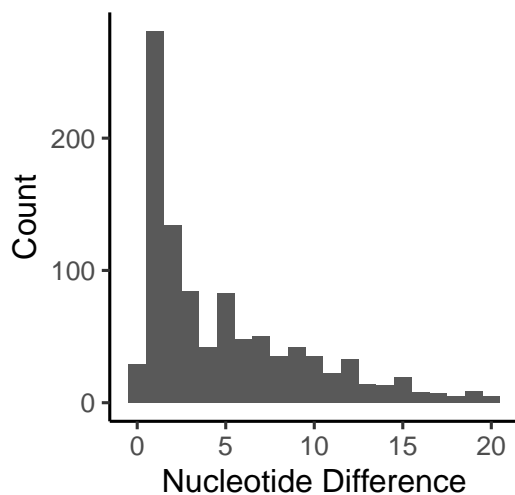
IGHV5-51*01_03

3469 sequences assigned
904 (26.1%) exact matches, in which:
725 unique CDR3
7 unique J



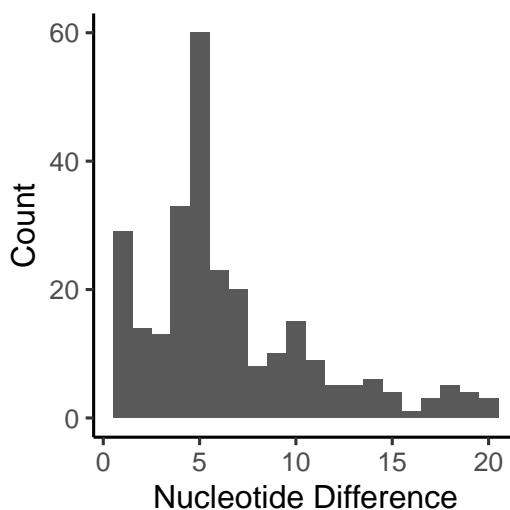
IGHV4-59*12

1078 sequences assigned
29 (2.7%) exact matches, in which:
29 unique CDR3
5 unique J



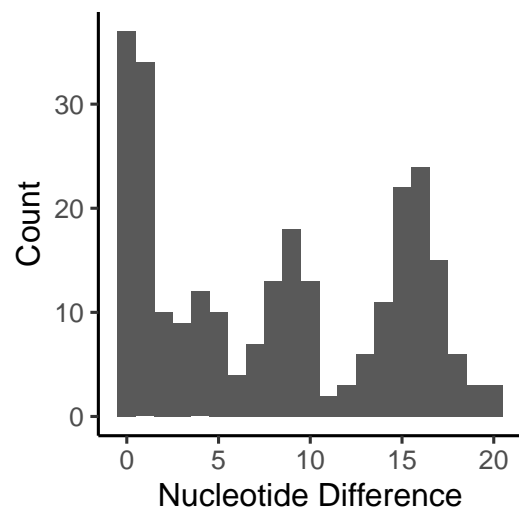
IGHV4-61*08

335 sequences assigned
No exact matches.



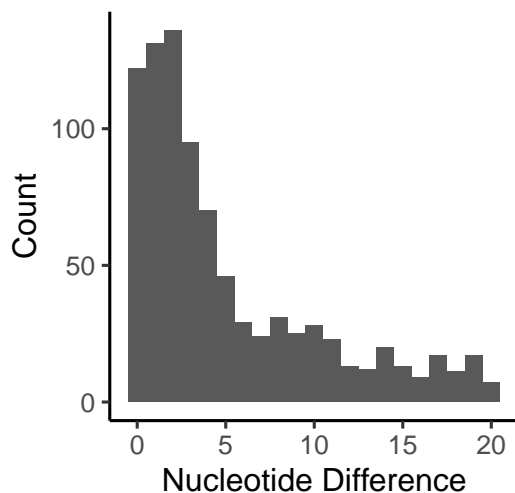
IGHV6-1*01_02

283 sequences assigned
37 (13.1%) exact matches, in which:
31 unique CDR3
6 unique J



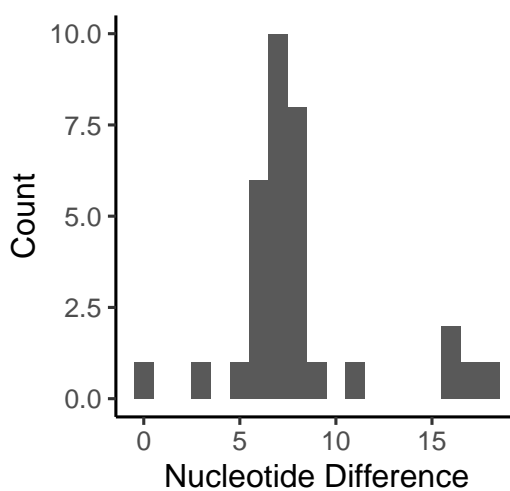
IGHV4-61*01

1015 sequences assigned
122 (12%) exact matches, in which:
116 unique CDR3
6 unique J



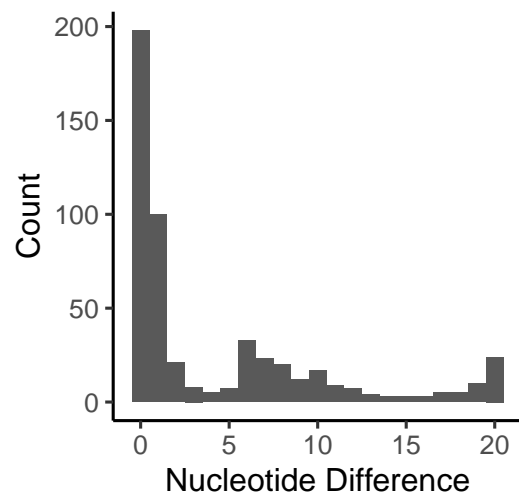
IGHV5-10-1*01_03

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

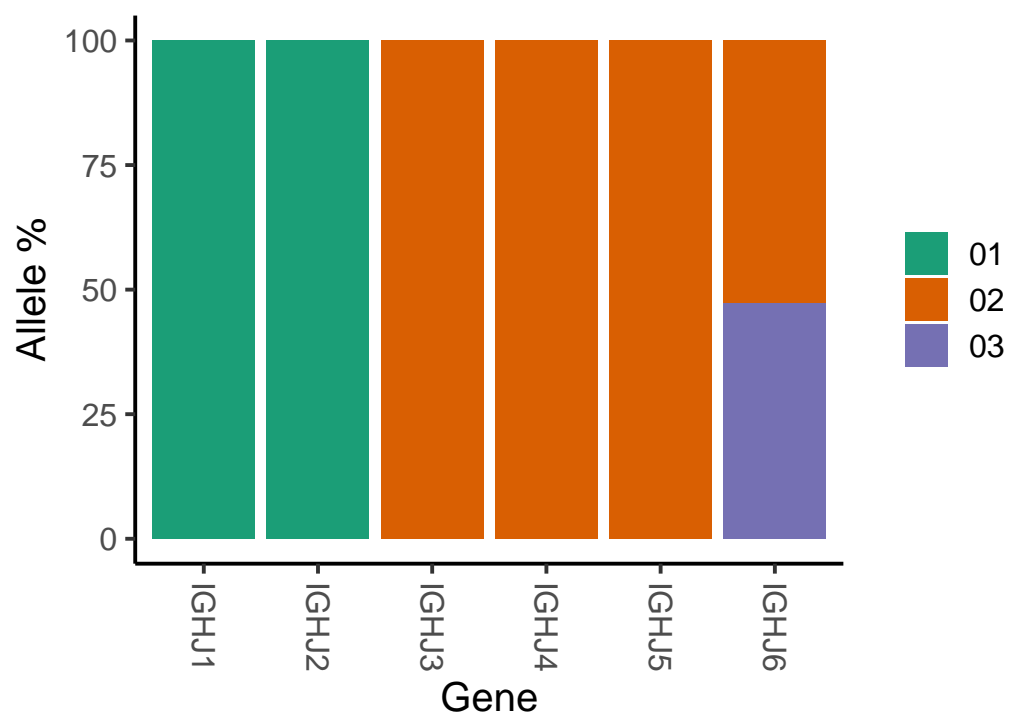


IGHV7-4-1*02

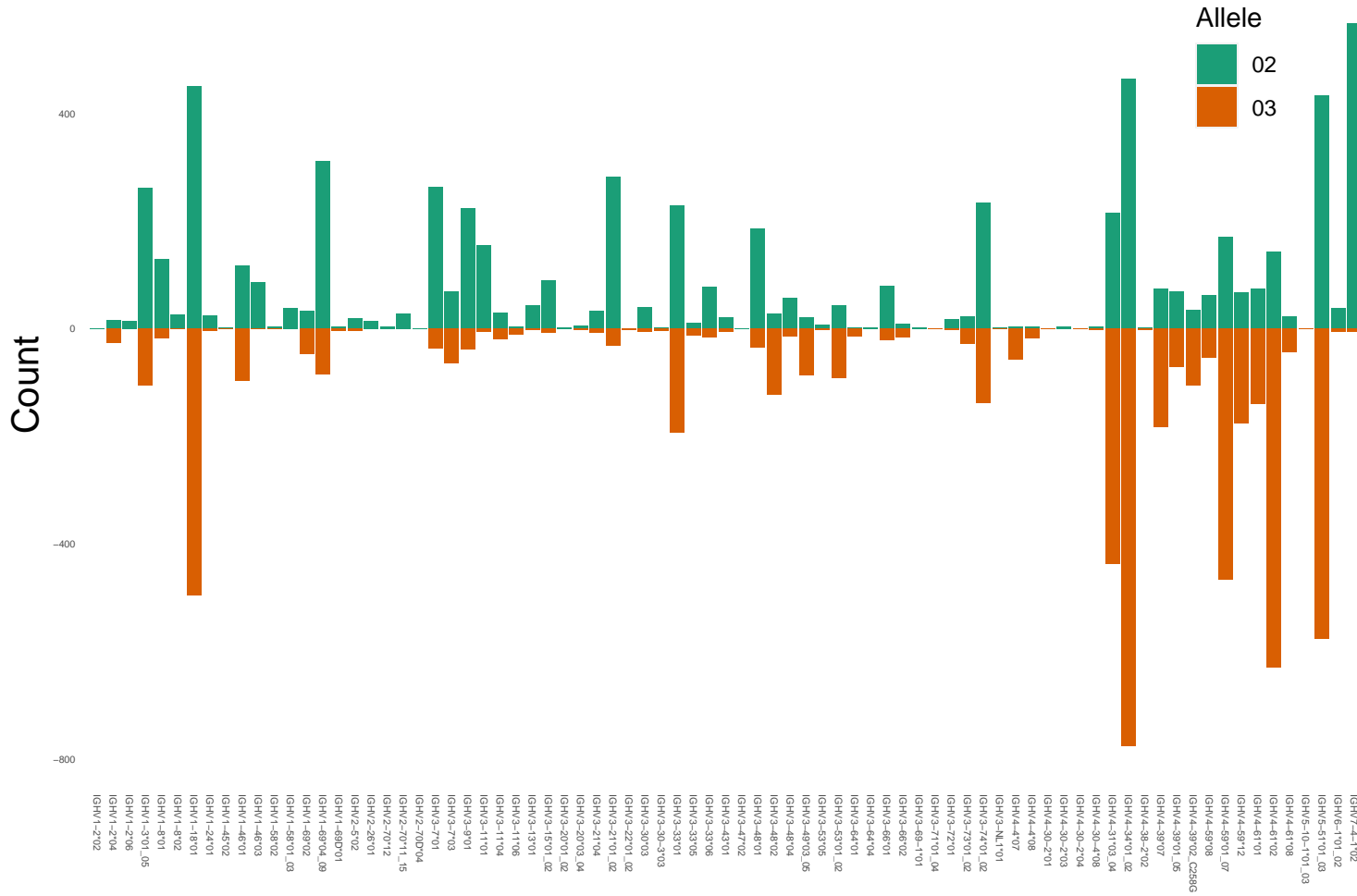
1082 sequences assigned
198 (18.3%) exact matches, in which:
183 unique CDR3
7 unique J



Allele Usage



Sequence Count byIGHJ6 allele usage



Novel sequence(s)IGHV3-51*07_T258C are not listed in the genotype and will be ignored.

Novel sequence(s)IGHV3-30-3*01_T288CIGHV4-59*02_G88AIGHV5-51*07_A128G are not listed in the genotype and will be ignored.

Novel sequence(s)IGHV3-30*03_T288C are not listed in the genotype and will be ignored.

Novel sequence(s)IGHV5-51*07_A128G are not listed in the genotype and will be ignored.

Warning – no inferred sequences found.

Warning – no inferred sequences found.

Novel sequence(s)IGHV3-33*01_G75CIGHV4-59*02_G88AIGHV5-51*07_A128G are not listed in the genotype and will be ignored.

Novel sequence(s)IGHV3-33*01_G75CIGHV4-59*02_G88AIGHV5-51*07_A128G are not listed in the genotype and will be ignored.

Novel sequence(s)IGHV3-30*03_T288CIGHV4-59*02_G88AIGHV5-51*07_A128G are not listed in the genotype and will be ignored.

Warning – no inferred sequences found.

Warning – no inferred sequences found.

Warning – no inferred sequences found.

Novel sequence(s)IGHV1-69*04_09_G112AIGHV4-59*02_G88AIGHV5-10-1*01_03_T258CIGHV5-51*07_A128G are not listed in the genotype and will be ignored.

Warning – no inferred sequences found.