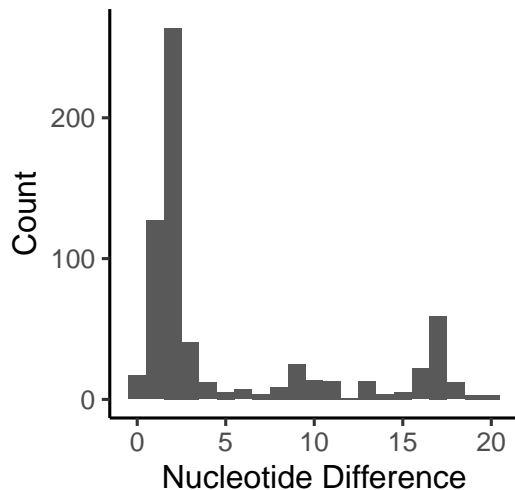


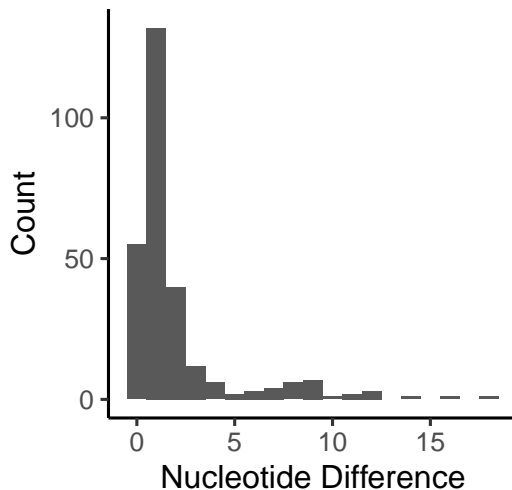
IGHV1-2*02

723 sequences assigned
17 (2.4%) exact matches, in which:
14 unique CDR3
3 unique J



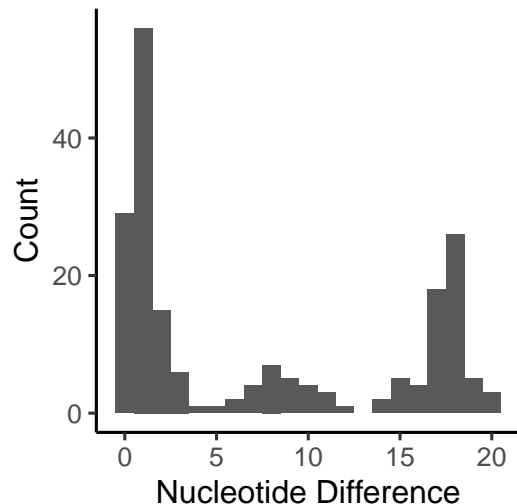
IGHV1-8*01

278 sequences assigned
55 (19.8%) exact matches, in which:
39 unique CDR3
4 unique J



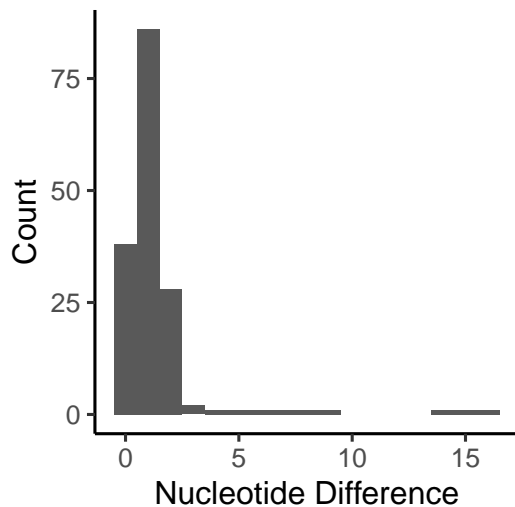
IGHV1-46*01

228 sequences assigned
29 (12.7%) exact matches, in which:
29 unique CDR3
4 unique J



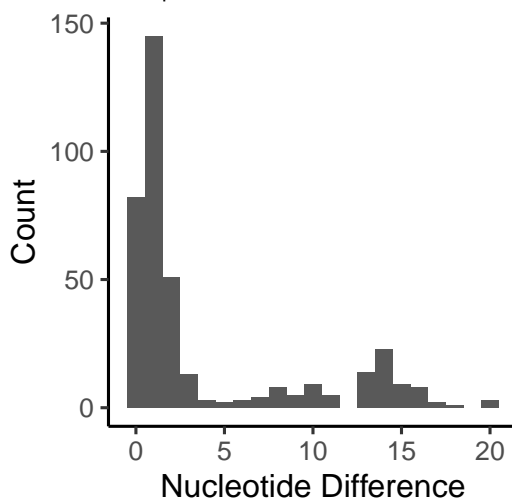
IGHV1-2*04

164 sequences assigned
38 (23.2%) exact matches, in which:
29 unique CDR3
4 unique J



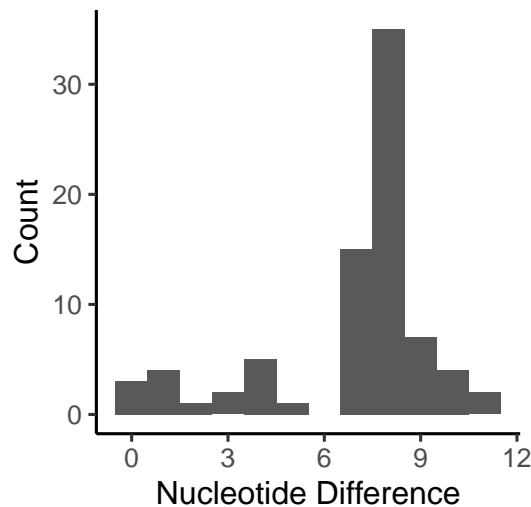
IGHV1-18*01

433 sequences assigned
82 (18.9%) exact matches, in which:
67 unique CDR3
4 unique J



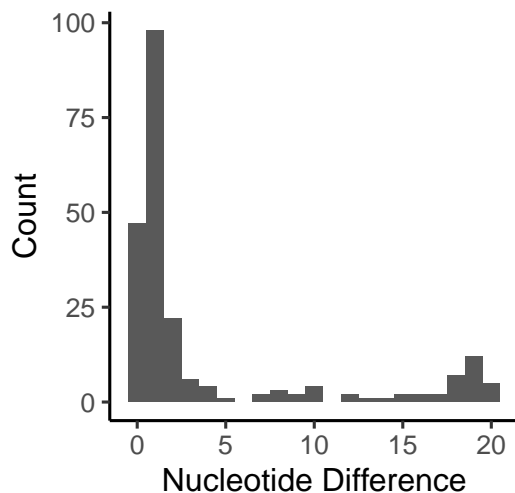
IGHV1-58*01_03

79 sequences assigned
3 (3.8%) exact matches, in which:
3 unique CDR3
2 unique J



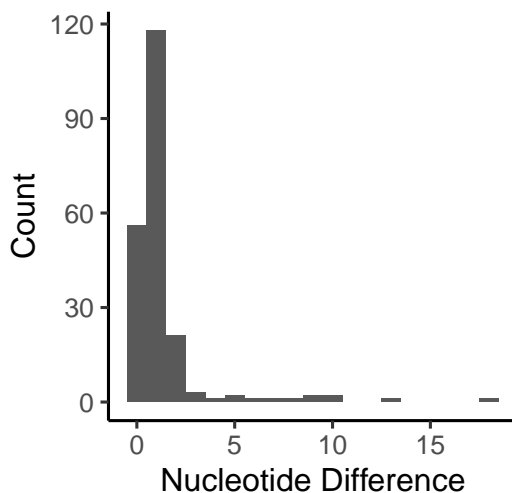
IGHV1-3*01_05

238 sequences assigned
47 (19.7%) exact matches, in which:
36 unique CDR3
4 unique J



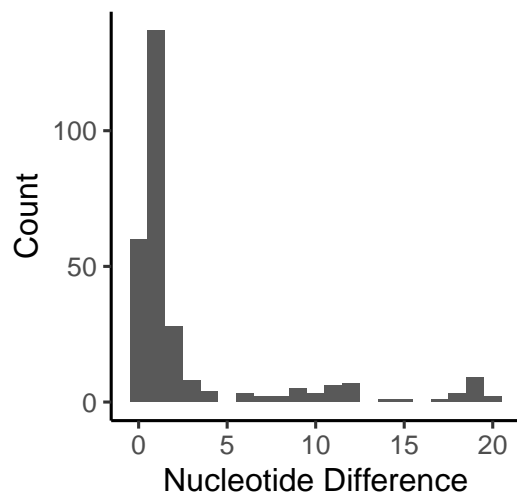
IGHV1-24*01

210 sequences assigned
56 (26.7%) exact matches, in which:
37 unique CDR3
4 unique J



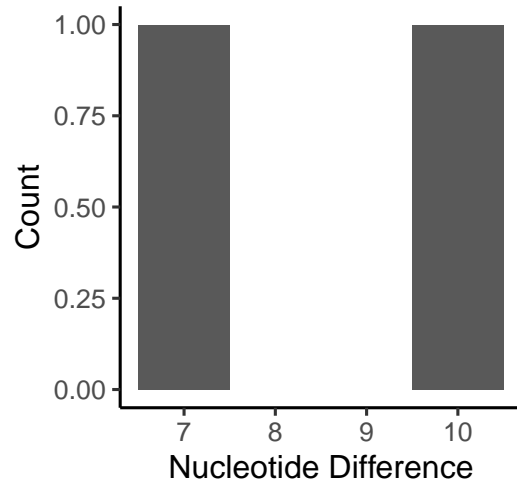
IGHV1-69*04_09

291 sequences assigned
60 (20.6%) exact matches, in which:
44 unique CDR3
4 unique J



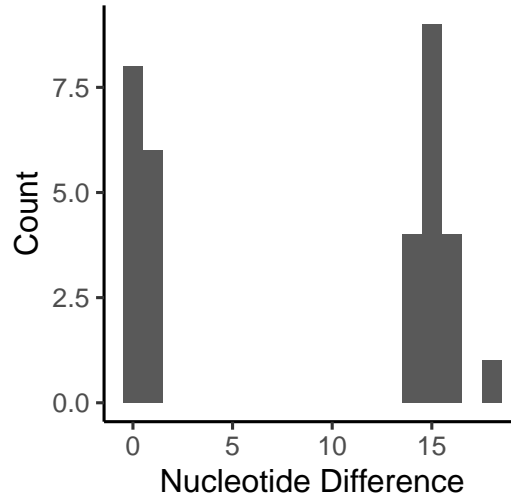
IGHV1–NL1*01

2 sequences assigned
No exact matches.



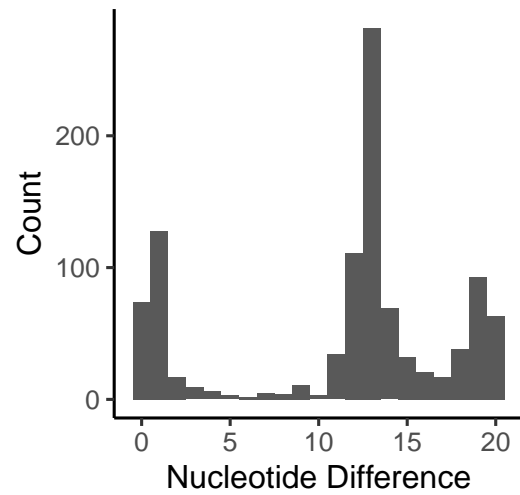
IGHV2–26*01

33 sequences assigned
8 (24.2%) exact matches, in which:
7 unique CDR3
3 unique J



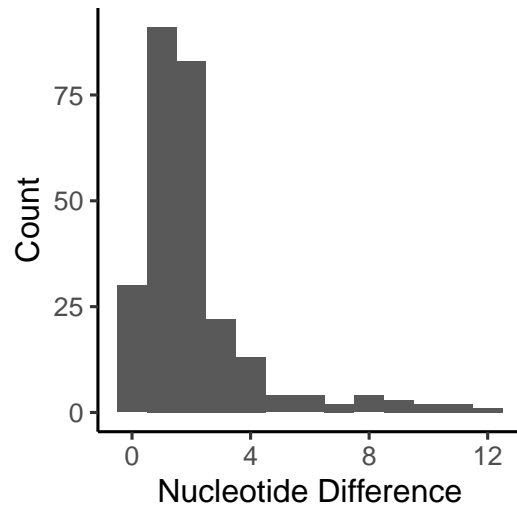
IGHV3–7*01

1070 sequences assigned
74 (6.9%) exact matches, in which:
44 unique CDR3
4 unique J



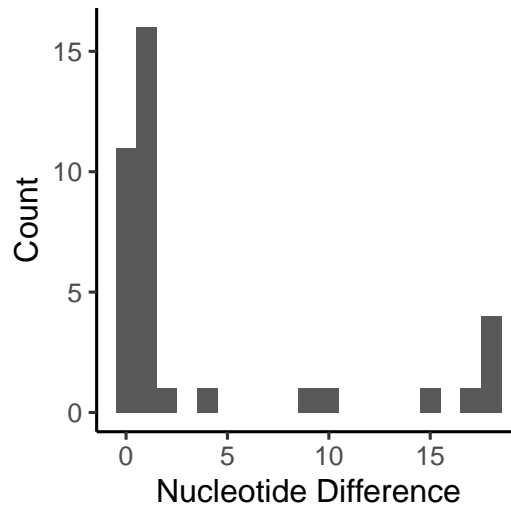
IGHV2–5*01

266 sequences assigned
30 (11.3%) exact matches, in which:
21 unique CDR3
3 unique J



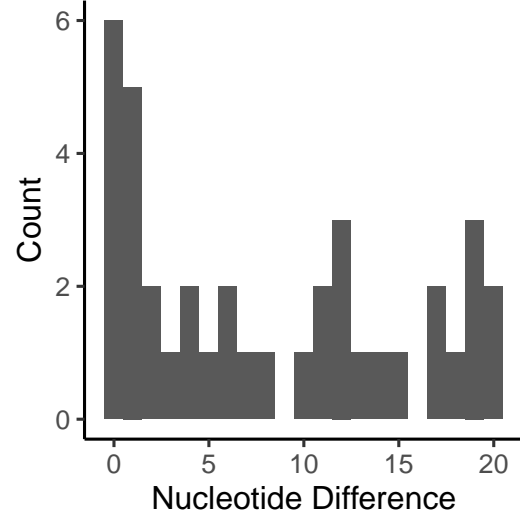
IGHV2–70*01

47 sequences assigned
11 (23.4%) exact matches, in which:
8 unique CDR3
3 unique J



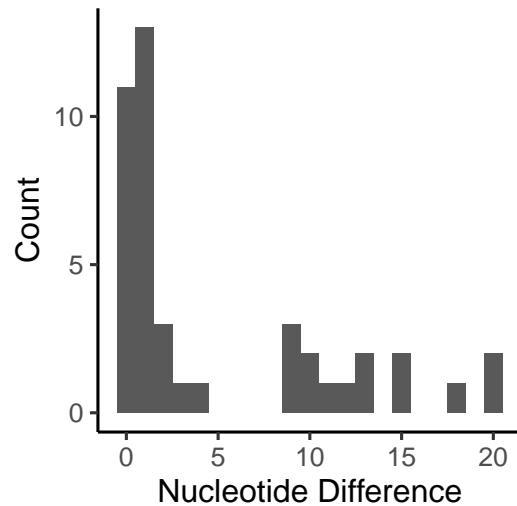
IGHV3–7*03

216 sequences assigned
6 (2.8%) exact matches, in which:
4 unique CDR3
2 unique J



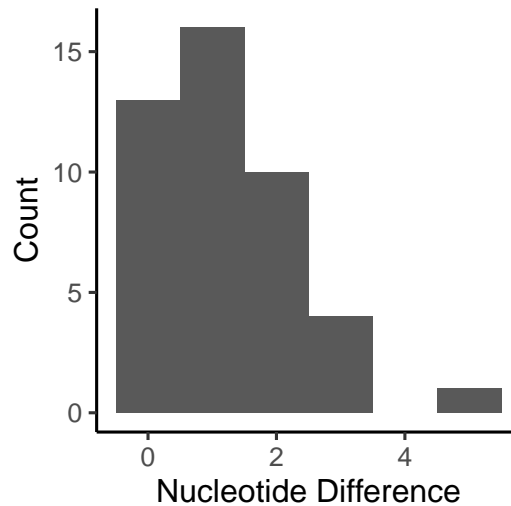
IGHV2–5*02

44 sequences assigned
11 (25%) exact matches, in which:
11 unique CDR3
4 unique J



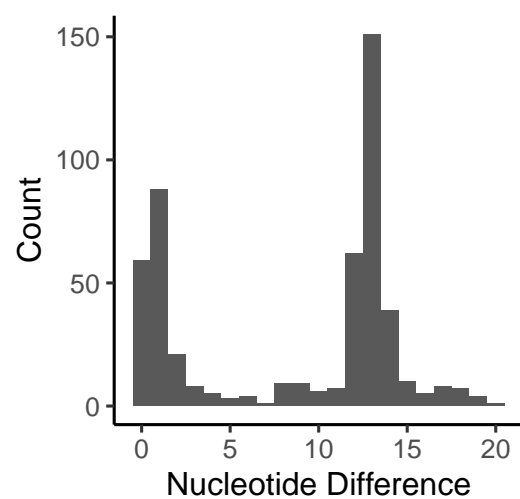
IGHV2–70*11_15

44 sequences assigned
13 (29.5%) exact matches, in which:
11 unique CDR3
3 unique J



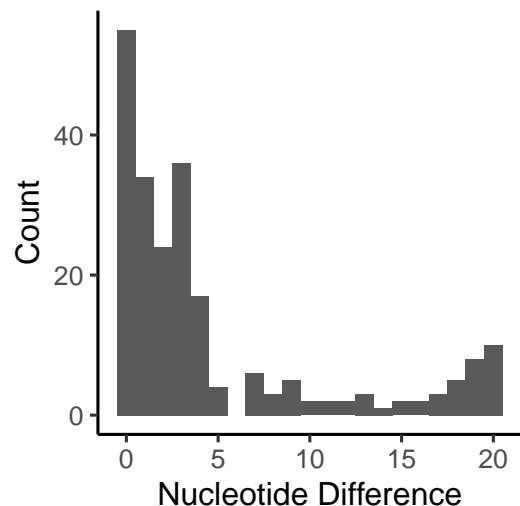
IGHV3–7*04

516 sequences assigned
59 (11.4%) exact matches, in which:
33 unique CDR3
5 unique J



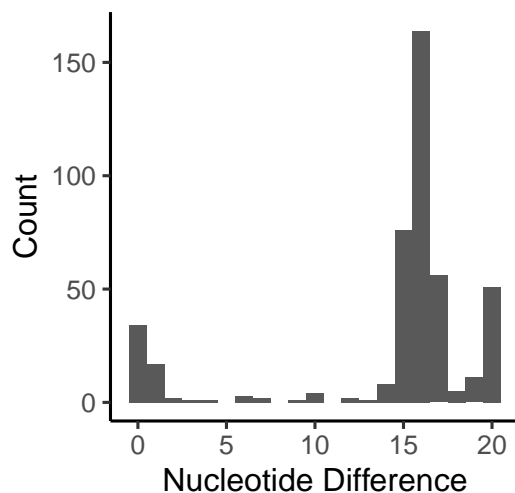
IGHV3-9*01

338 sequences assigned
55 (16.3%) exact matches, in which:
33 unique CDR3
4 unique J



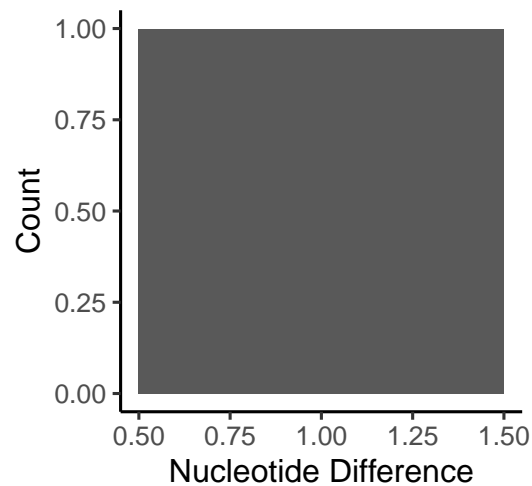
IGHV3-11*03_05

631 sequences assigned
34 (5.4%) exact matches, in which:
22 unique CDR3
5 unique J



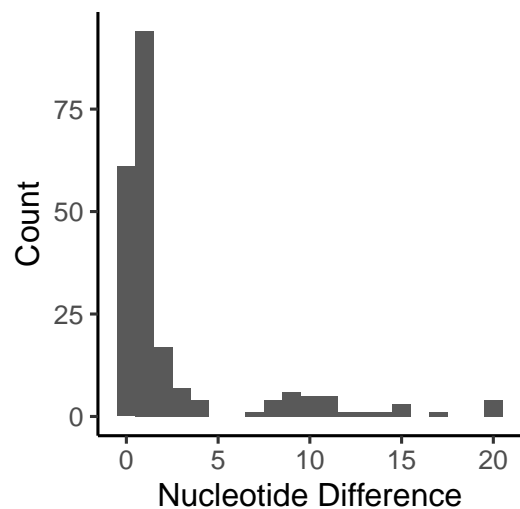
IGHV3-13*05

1 sequences assigned
No exact matches.



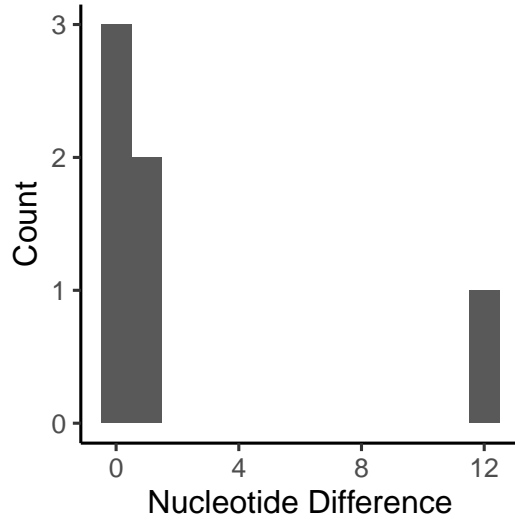
IGHV3-11*01

428 sequences assigned
61 (14.3%) exact matches, in which:
38 unique CDR3
3 unique J



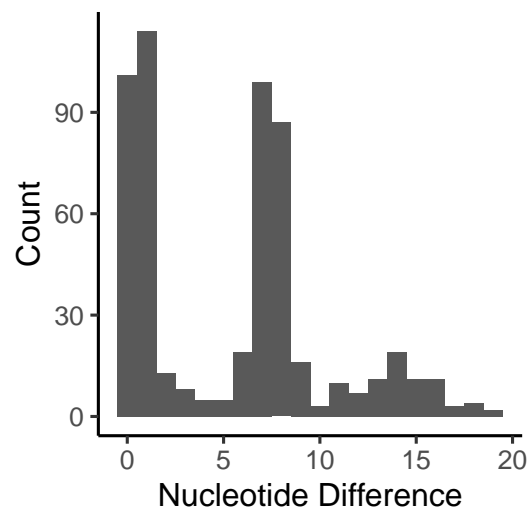
IGHV3-13*01

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



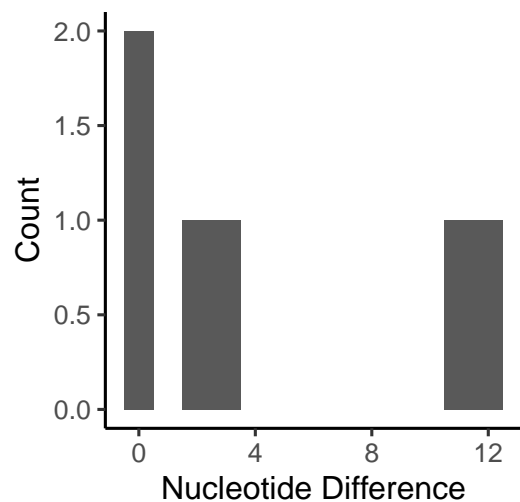
IGHV3-15*01_02

775 sequences assigned
101 (13%) exact matches, in which:
57 unique CDR3
5 unique J



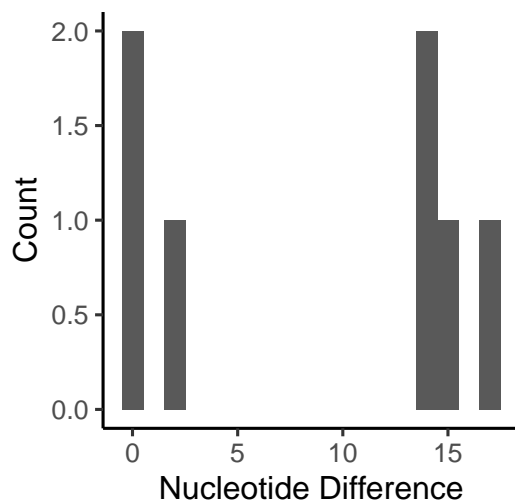
IGHV3-11*04

9 sequences assigned
2 (22.2%) exact matches, in which:
2 unique CDR3
1 unique J



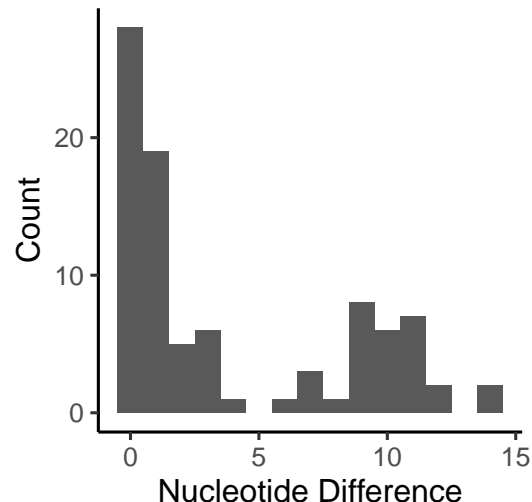
IGHV3-13*04

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



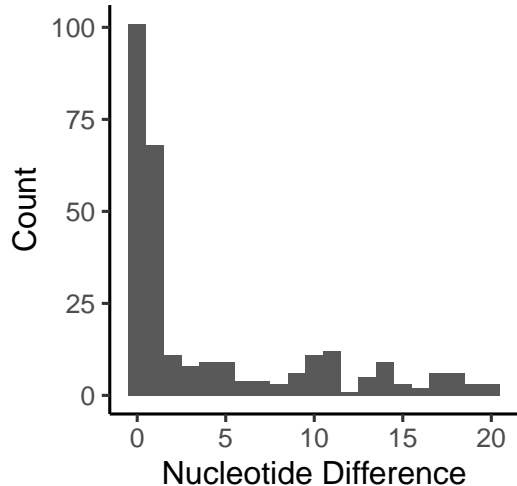
IGHV3-20*03_04

92 sequences assigned
28 (30.4%) exact matches, in which:
16 unique CDR3
3 unique J



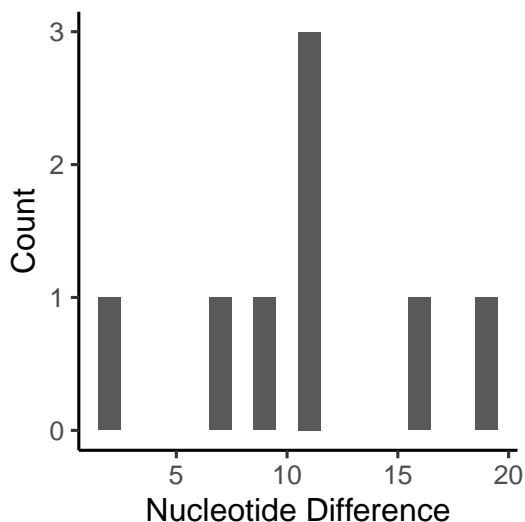
IGHV3-21*01_02

299 sequences assigned
101 (33.8%) exact matches, in which:
62 unique CDR3
5 unique J



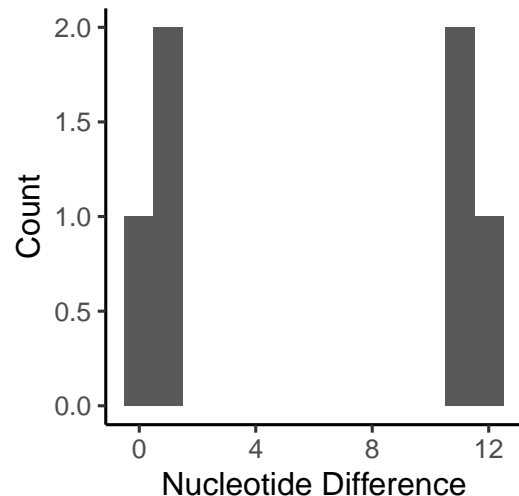
IGHV3-30-3*03

9 sequences assigned
No exact matches.



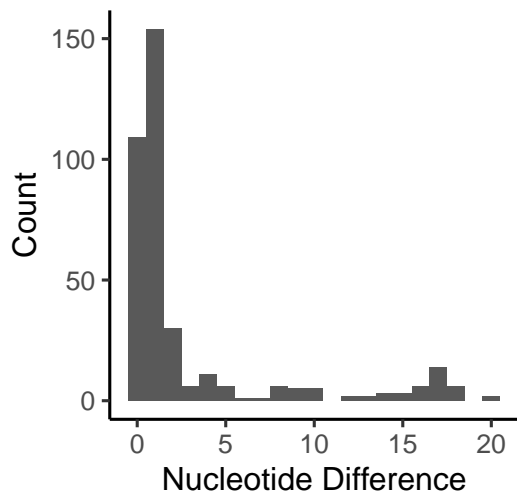
IGHV3-43*01

6 sequences assigned
1 (16.7%) exact matches, in which:
1 unique CDR3
1 unique J



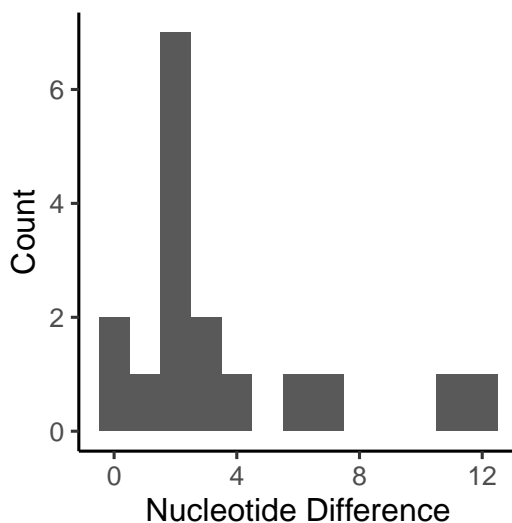
IGHV3-30*01

383 sequences assigned
109 (28.5%) exact matches, in which:
57 unique CDR3
4 unique J



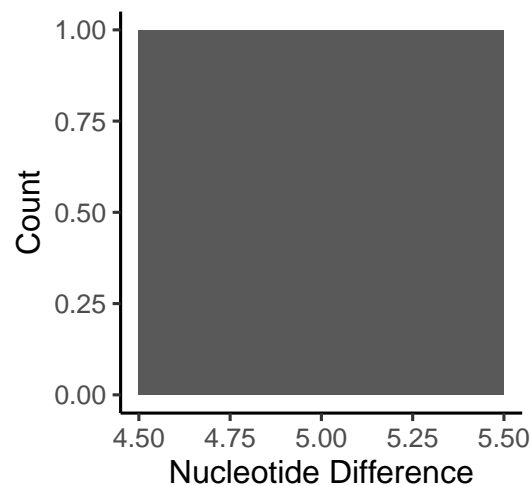
IGHV3-30*07

17 sequences assigned
2 (11.8%) exact matches, in which:
2 unique CDR3
1 unique J



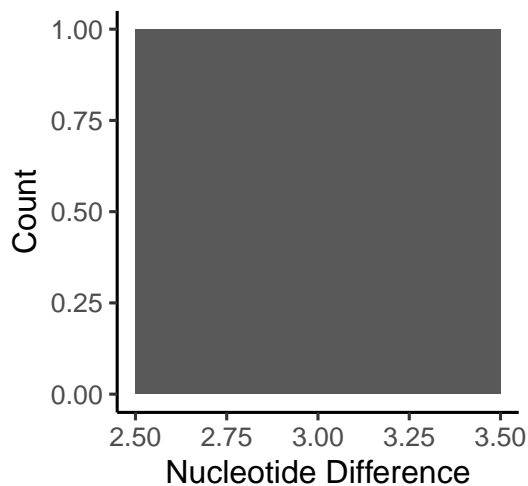
IGHV3-43*02

1 sequences assigned
No exact matches.



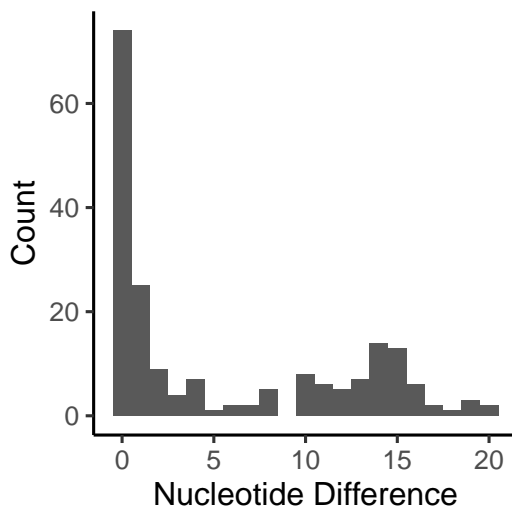
IGHV3-30-3*01

3 sequences assigned
No exact matches.



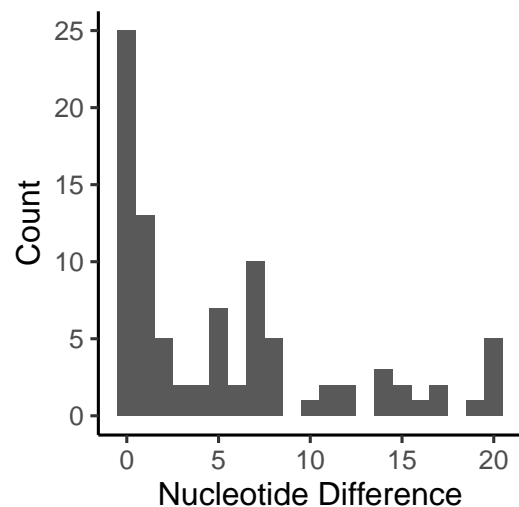
IGHV3-33*01

331 sequences assigned
74 (22.4%) exact matches, in which:
52 unique CDR3
5 unique J



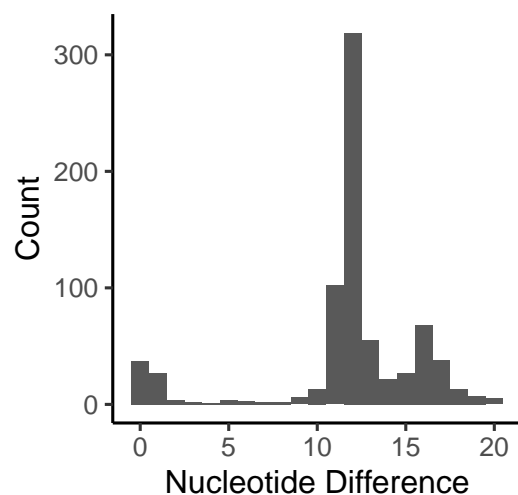
IGHV3-48*02

207 sequences assigned
25 (12.1%) exact matches, in which:
18 unique CDR3
4 unique J



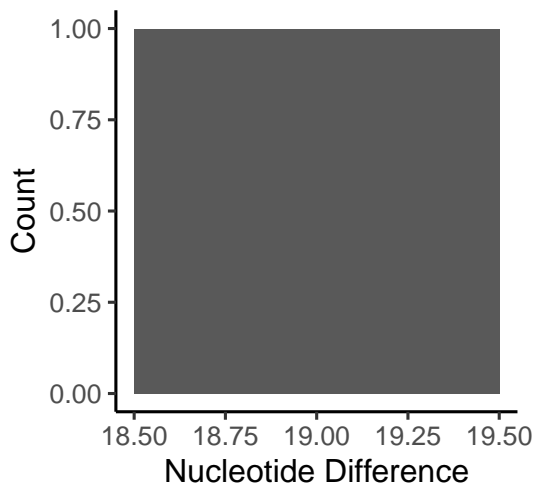
IGHV3-48*03

802 sequences assigned
37 (4.6%) exact matches, in which:
24 unique CDR3
4 unique J



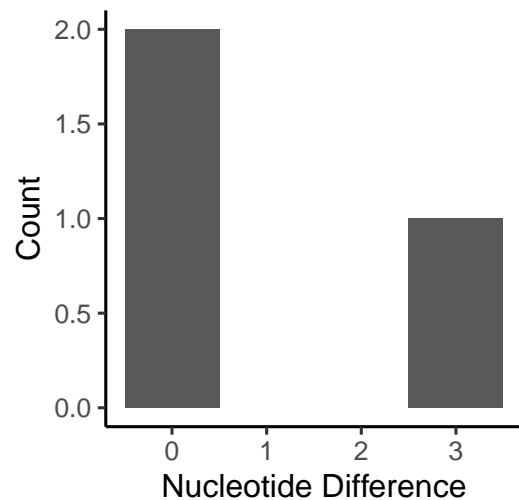
IGHV3-53*05

5 sequences assigned
No exact matches.



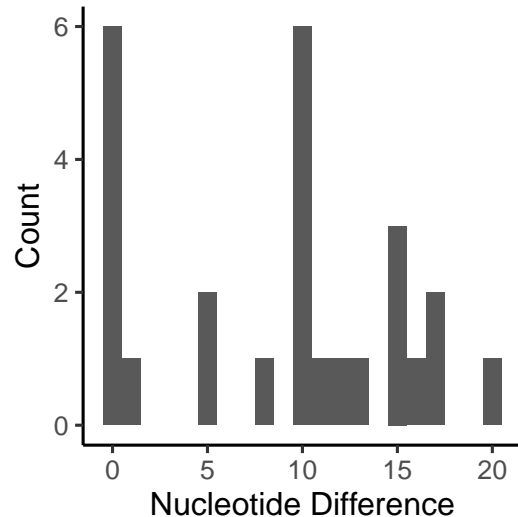
IGHV3-64*02_07

3 sequences assigned
2 (66.7%) exact matches, in which:
2 unique CDR3
2 unique J



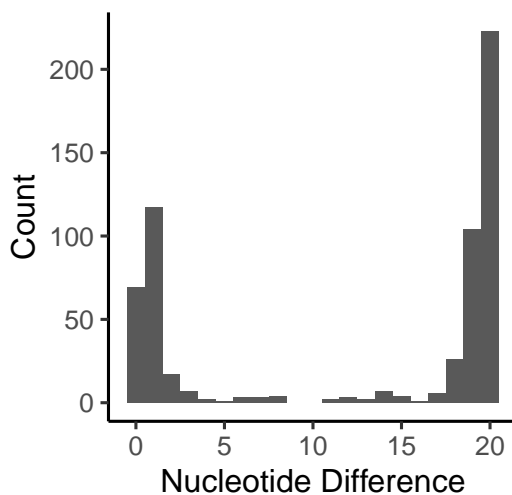
IGHV3-49*04

209 sequences assigned
6 (2.9%) exact matches, in which:
3 unique CDR3
2 unique J



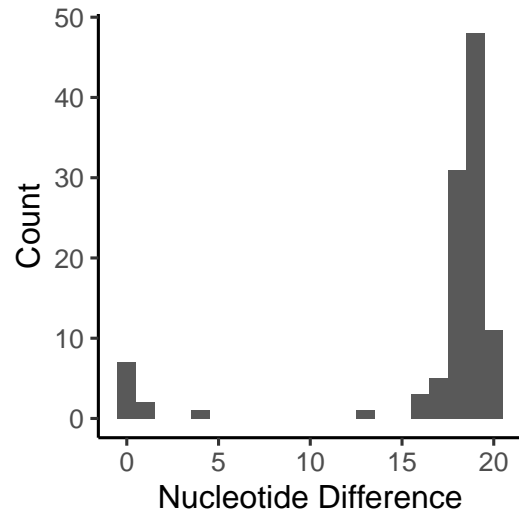
IGHV3-53*01_02

2507 sequences assigned
69 (2.8%) exact matches, in which:
38 unique CDR3
3 unique J



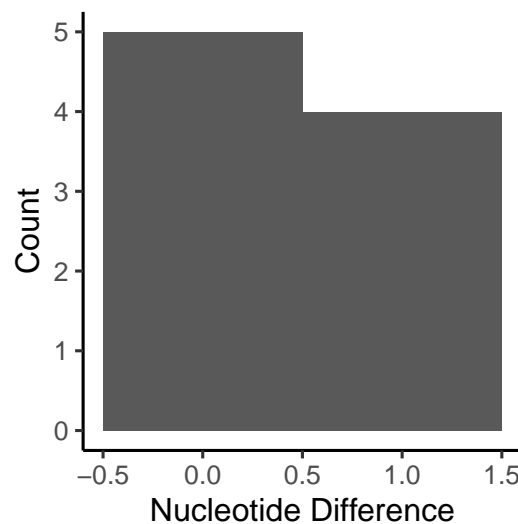
IGHV3-66*01

124 sequences assigned
7 (5.6%) exact matches, in which:
5 unique CDR3
2 unique J



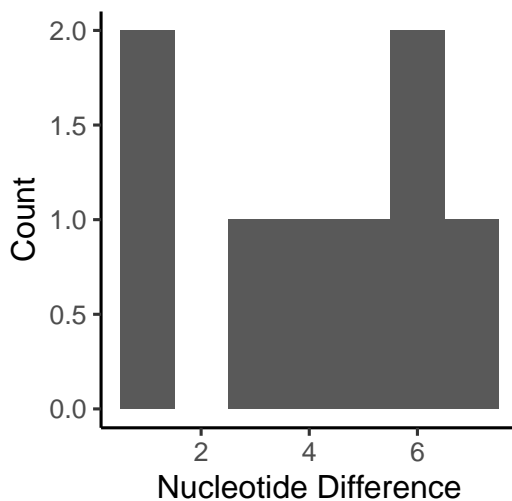
IGHV3-49*03_05

10 sequences assigned
5 (50%) exact matches, in which:
3 unique CDR3
2 unique J



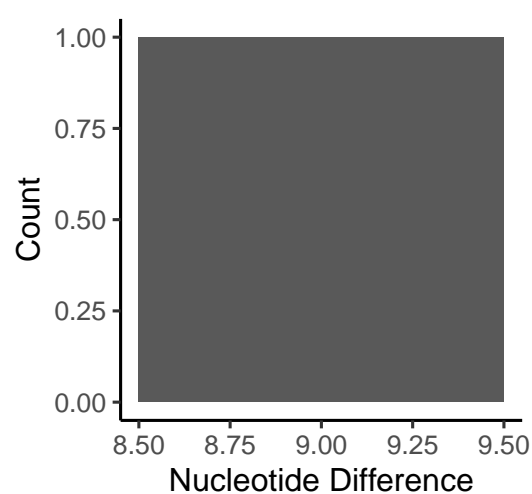
IGHV3-64*04

8 sequences assigned
No exact matches.



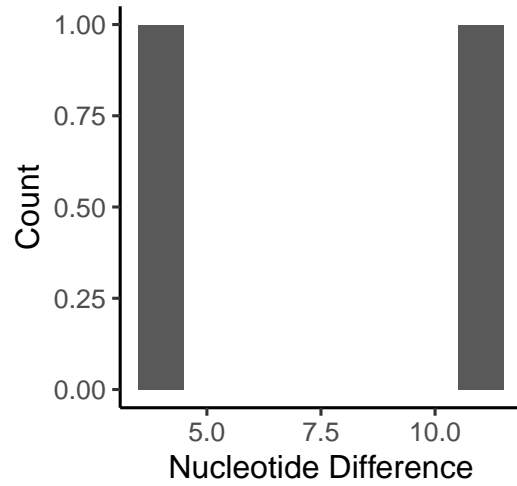
IGHV3-66*04

2 sequences assigned
No exact matches.



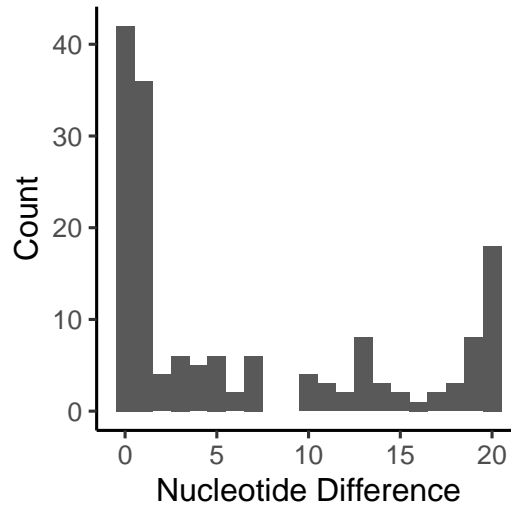
IGHV3-69-1*01

2 sequences assigned
No exact matches.



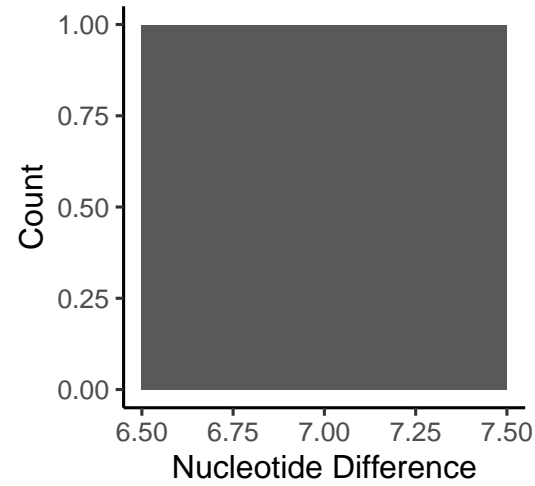
IGHV3-74*01_02

216 sequences assigned
42 (19.4%) exact matches, in which:
28 unique CDR3
6 unique J



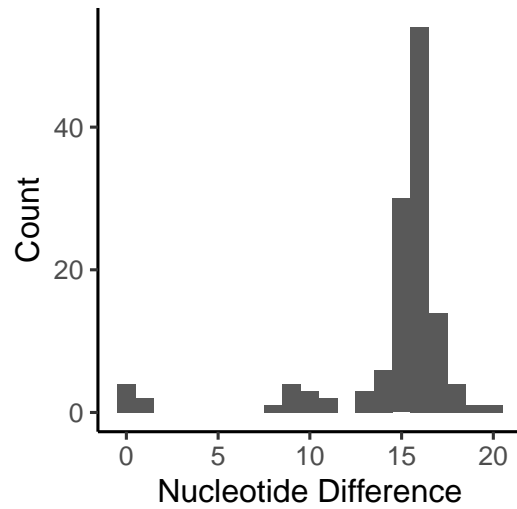
IGHV3-64D*08

1 sequences assigned
No exact matches.



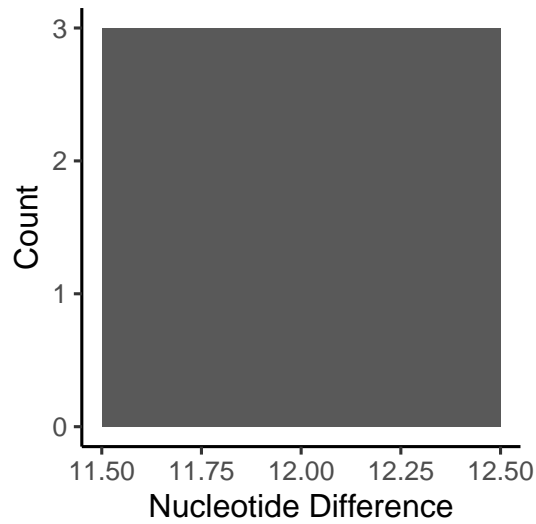
IGHV3-72*01

168 sequences assigned
4 (2.4%) exact matches, in which:
2 unique CDR3
1 unique J



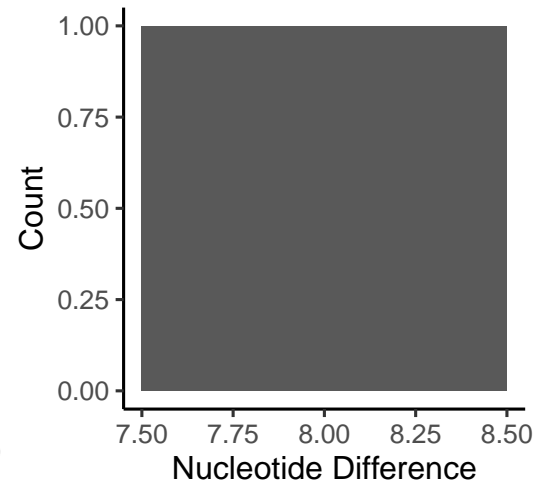
IGHV3-43D*04

3 sequences assigned
No exact matches.



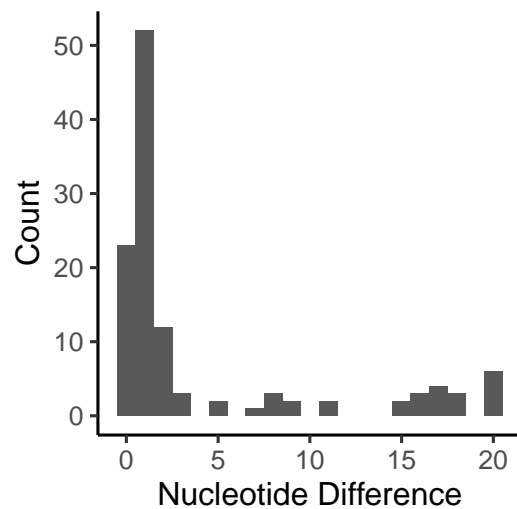
IGHV3-NL1*01

3 sequences assigned
No exact matches.



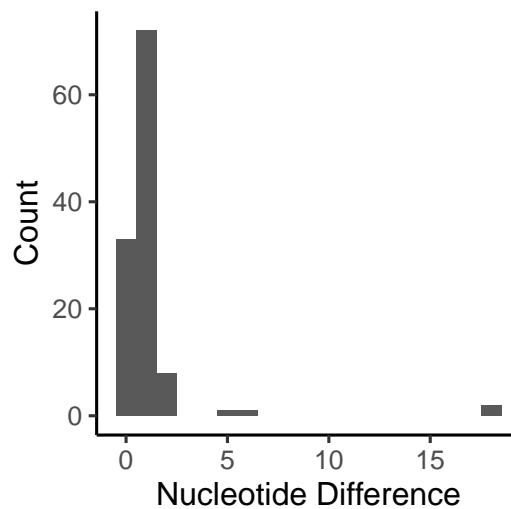
IGHV3-73*01_02

142 sequences assigned
23 (16.2%) exact matches, in which:
13 unique CDR3
2 unique J



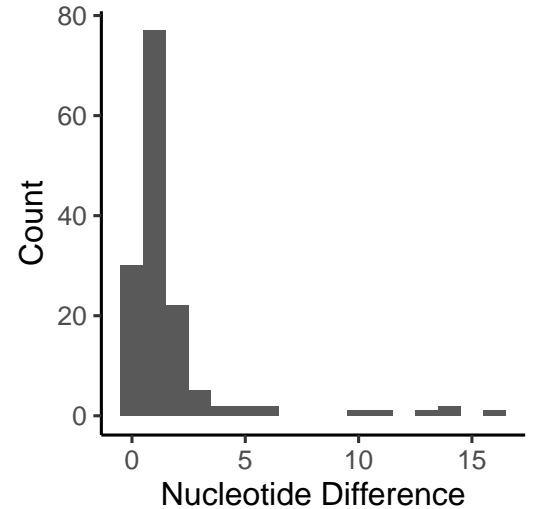
IGHV3-64D*06

120 sequences assigned
33 (27.5%) exact matches, in which:
15 unique CDR3
2 unique J



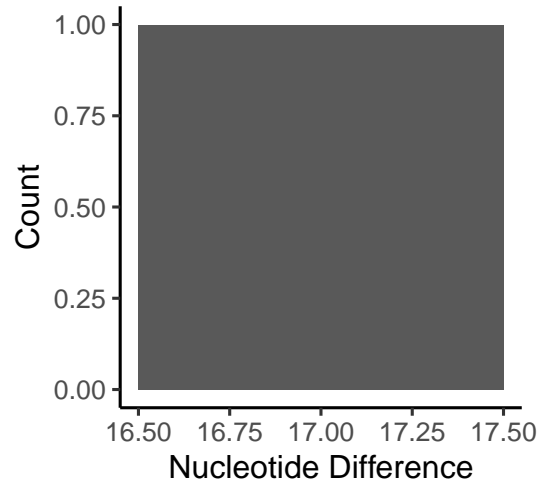
IGHV4-4*07

166 sequences assigned
30 (18.1%) exact matches, in which:
26 unique CDR3
5 unique J



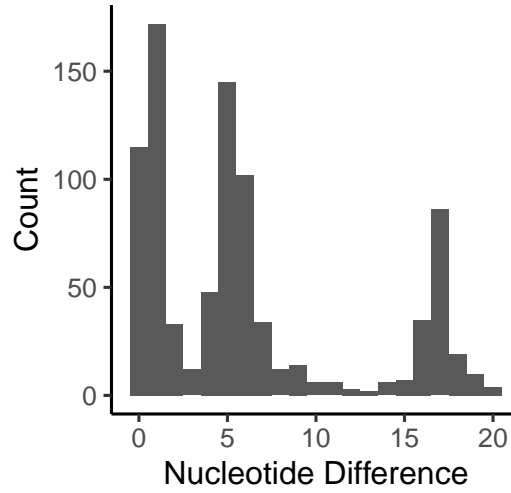
IGHV4-30-2*03

1 sequences assigned
No exact matches.



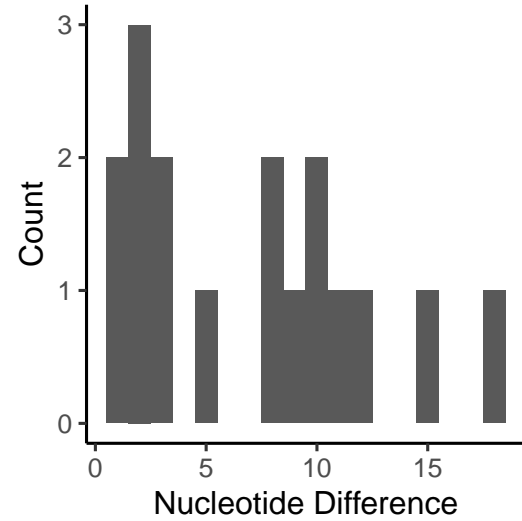
IGHV4-34*01_02

909 sequences assigned
115 (12.7%) exact matches, in which:
81 unique CDR3
6 unique J



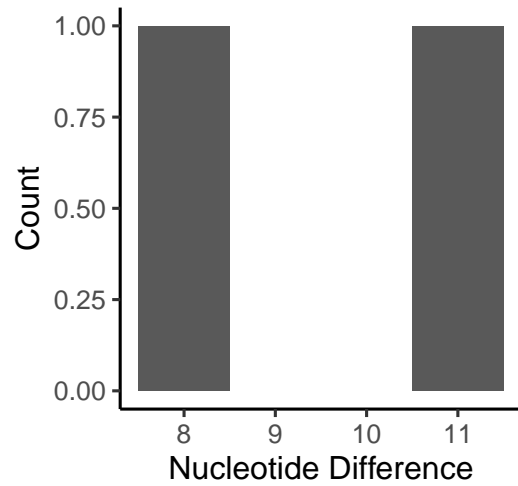
IGHV4-39*07

17 sequences assigned
No exact matches.



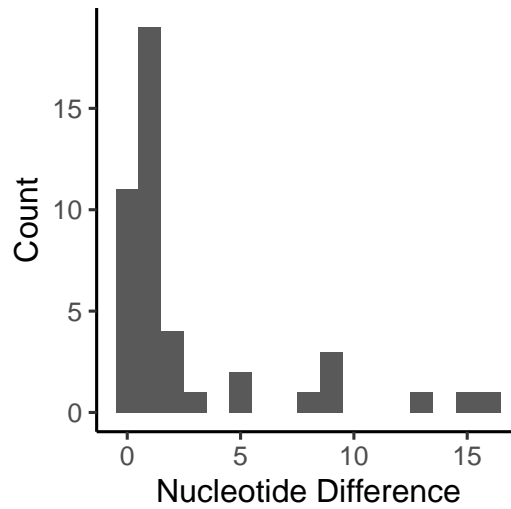
IGHV4-30-4*08

3 sequences assigned
No exact matches.



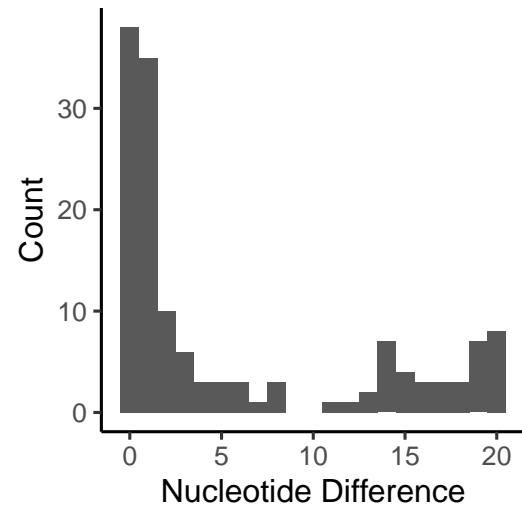
IGHV4-38-2*01

45 sequences assigned
11 (24.4%) exact matches, in which:
11 unique CDR3
3 unique J



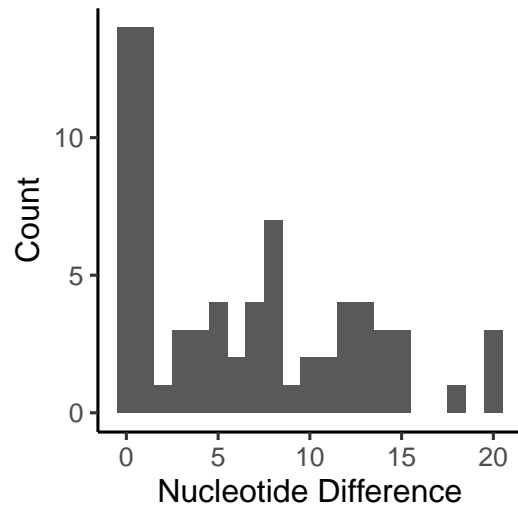
IGHV4-39*01_05

211 sequences assigned
38 (18%) exact matches, in which:
31 unique CDR3
5 unique J



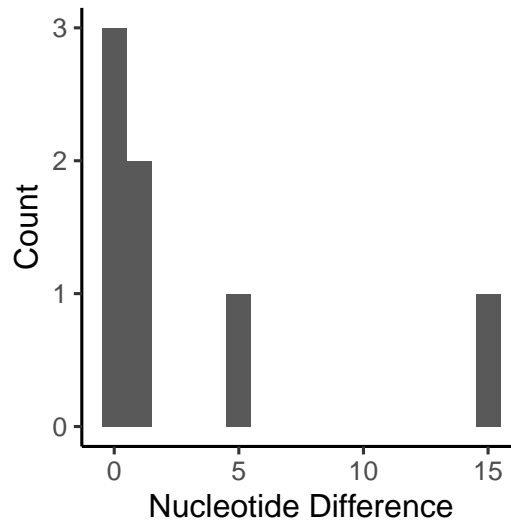
IGHV4-31*03_04

85 sequences assigned
14 (16.5%) exact matches, in which:
9 unique CDR3
3 unique J



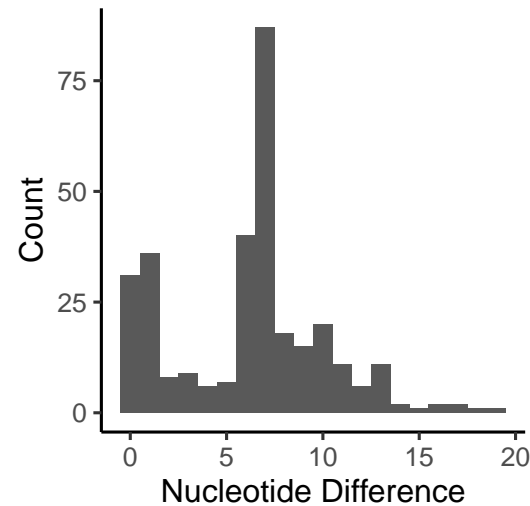
IGHV4-38-2*02

11 sequences assigned
3 (27.3%) exact matches, in which:
3 unique CDR3
2 unique J



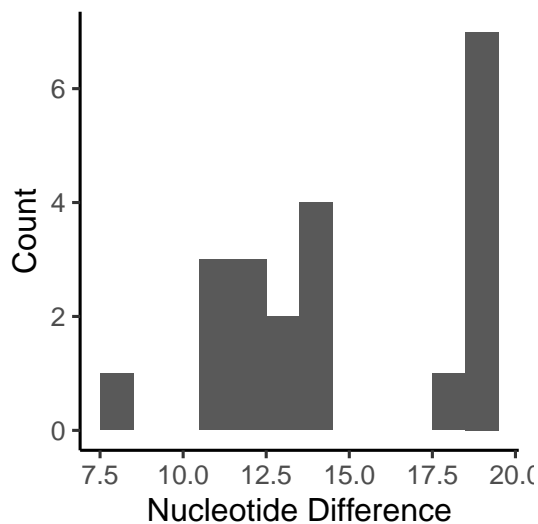
IGHV4-59*01_07

350 sequences assigned
31 (8.9%) exact matches, in which:
26 unique CDR3
5 unique J



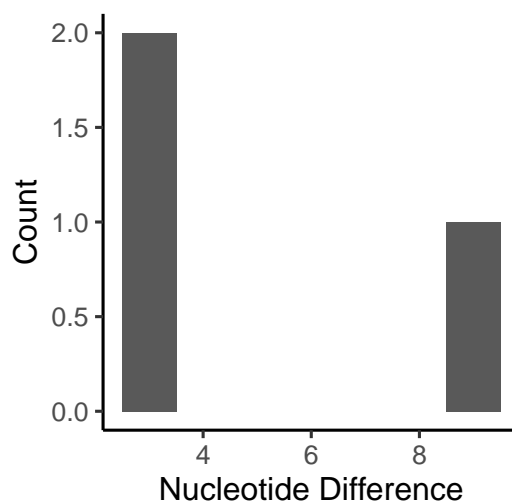
IGHV4-59*11

23 sequences assigned
No exact matches.



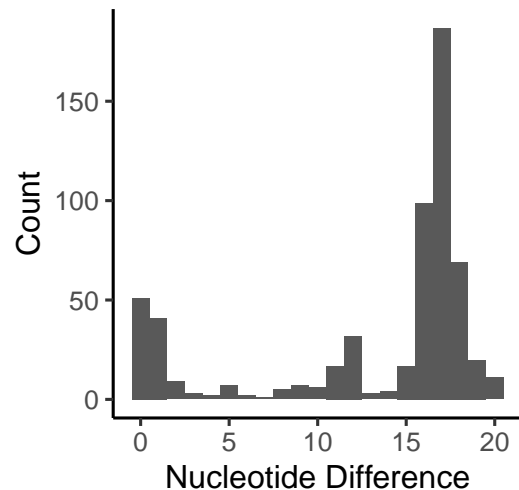
IGHV4-61*02

5 sequences assigned
No exact matches.



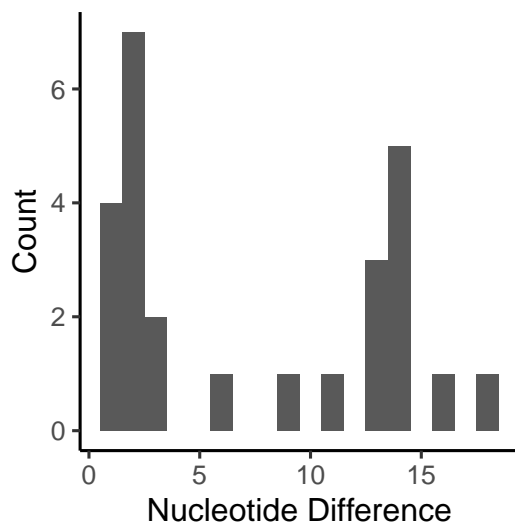
IGHV5-51*01_03

627 sequences assigned
51 (8.1%) exact matches, in which:
35 unique CDR3
5 unique J



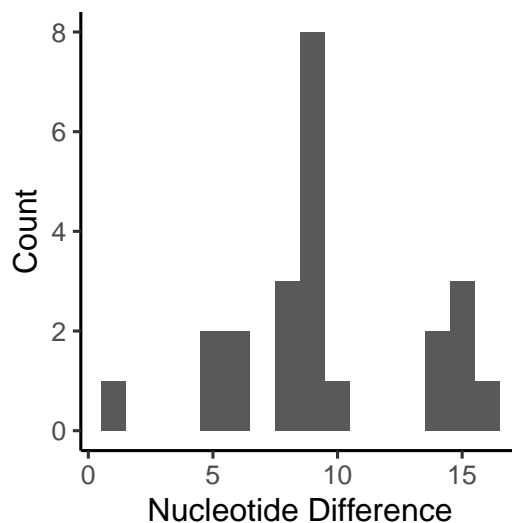
IGHV4-59*12

33 sequences assigned
No exact matches.



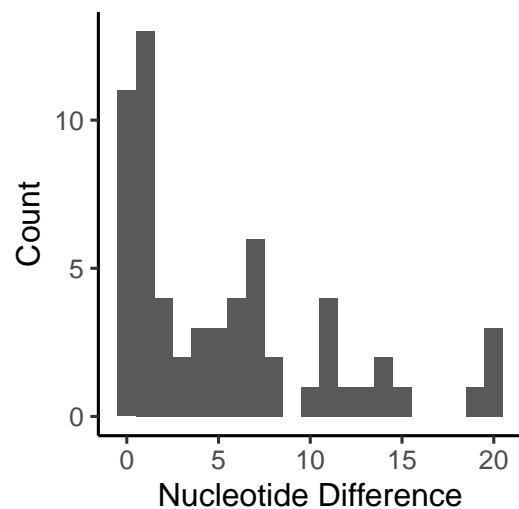
IGHV4-61*08

31 sequences assigned
No exact matches.



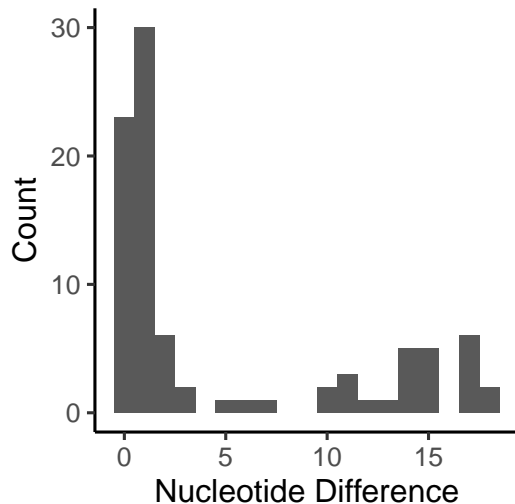
IGHV6-1*01_02

63 sequences assigned
11 (17.5%) exact matches, in which:
8 unique CDR3
5 unique J



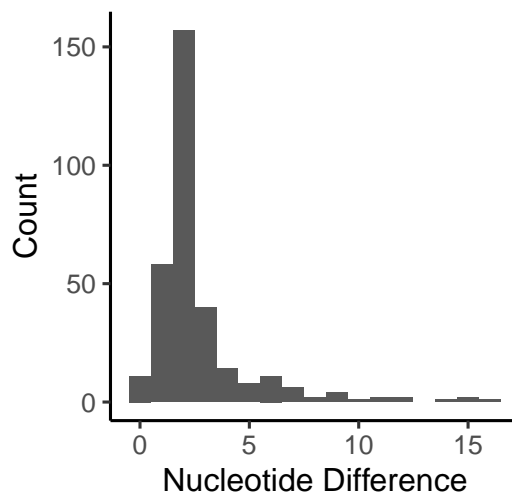
IGHV4-61*01

91 sequences assigned
23 (25.3%) exact matches, in which:
20 unique CDR3
4 unique J



IGHV5-10-1*01_03

328 sequences assigned
11 (3.4%) exact matches, in which:
8 unique CDR3
3 unique J





Novel sequence(s)IGHV1-33*01_G75CIGHV4-59*02_G88AIGHV5-51*07_A128G 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.

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

Novel sequence(s)IGHV4-59*02_G88A are not listed in the genotype and will be ignored.

Novel sequence(s)IGHV3-30*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.

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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.