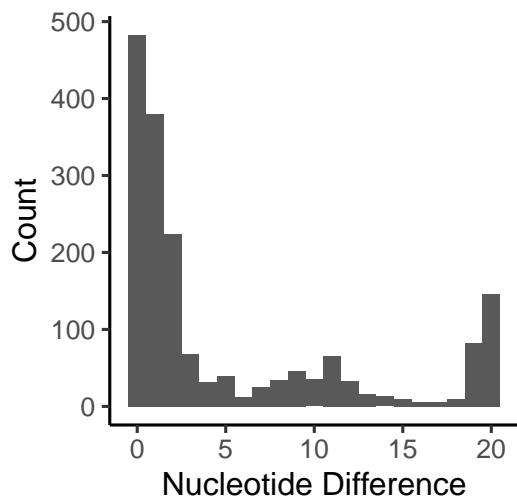


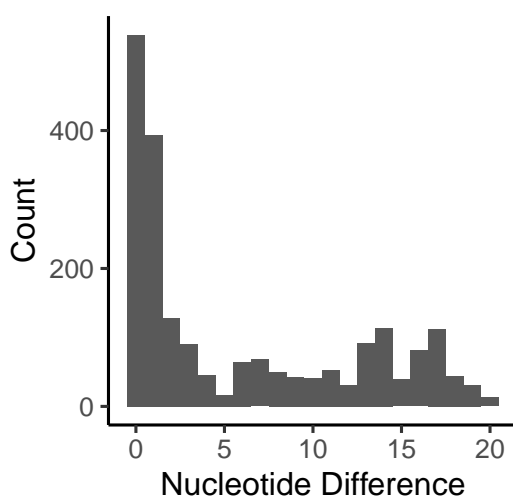
IGHV1-2*04

1872 sequences assigned
483 (25.8%) exact matches, in which:
448 unique CDR3
5 unique J



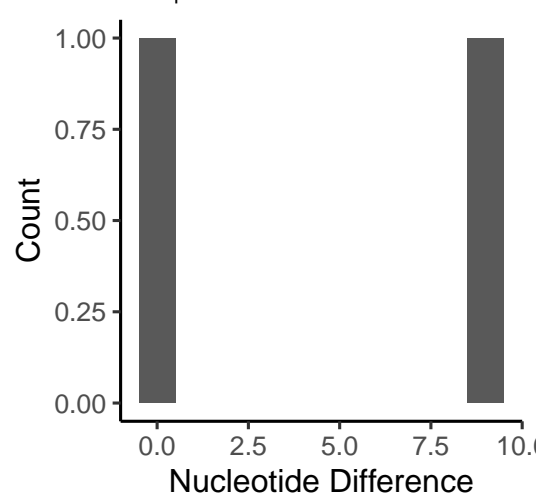
IGHV1-18*01

2146 sequences assigned
539 (25.1%) exact matches, in which:
503 unique CDR3
6 unique J



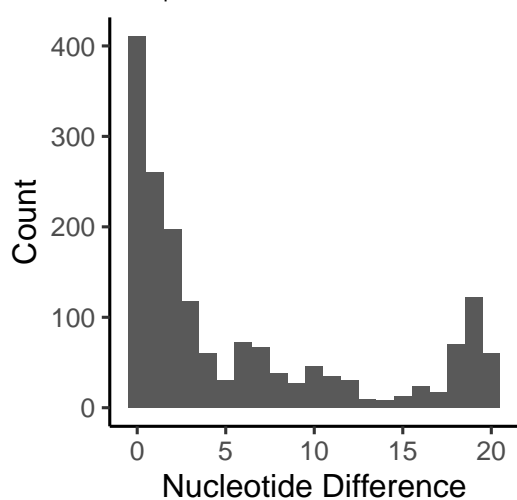
IGHV1-45*02

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



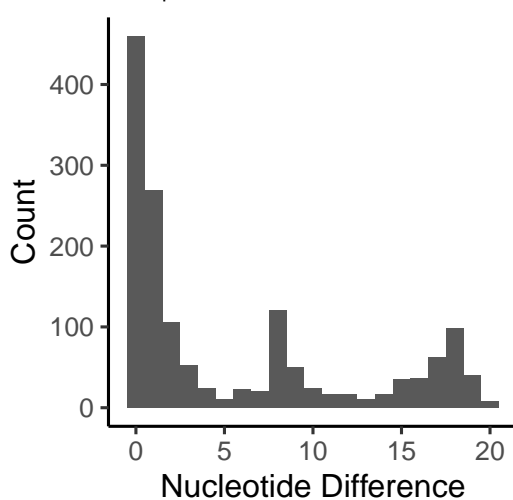
IGHV1-3*01_05

1955 sequences assigned
411 (21%) exact matches, in which:
381 unique CDR3
6 unique J



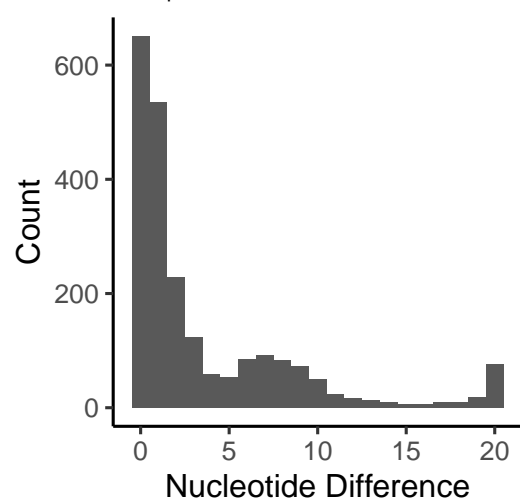
IGHV1-18*04

1783 sequences assigned
460 (25.8%) exact matches, in which:
434 unique CDR3
6 unique J



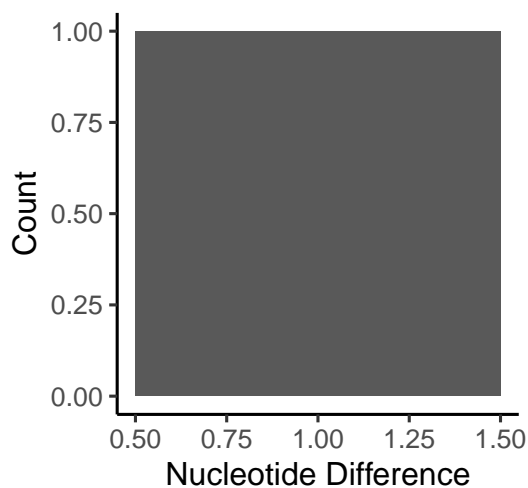
IGHV1-46*01

2953 sequences assigned
651 (22%) exact matches, in which:
600 unique CDR3
6 unique J



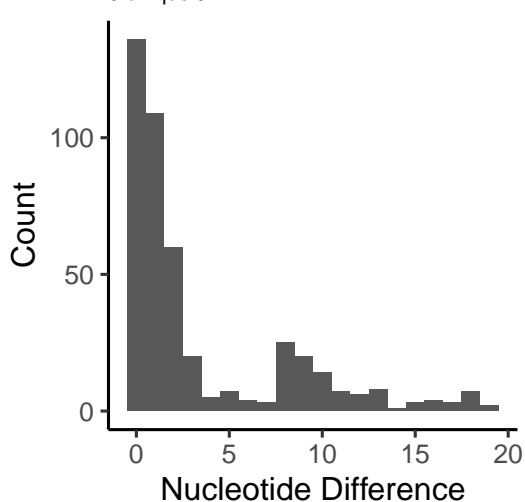
IGHV1-8*01

1 sequences assigned
No exact matches.



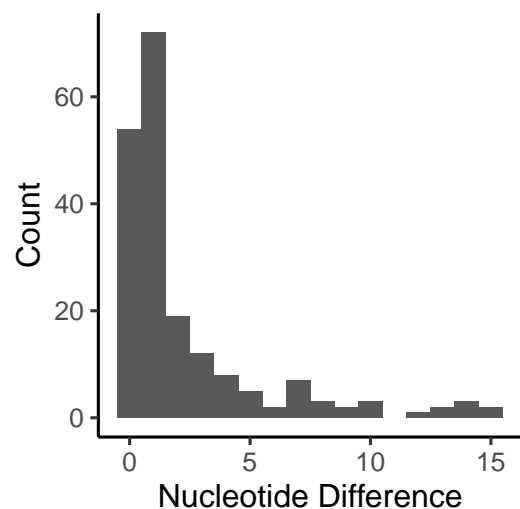
IGHV1-24*01

662 sequences assigned
136 (20.5%) exact matches, in which:
126 unique CDR3
5 unique J



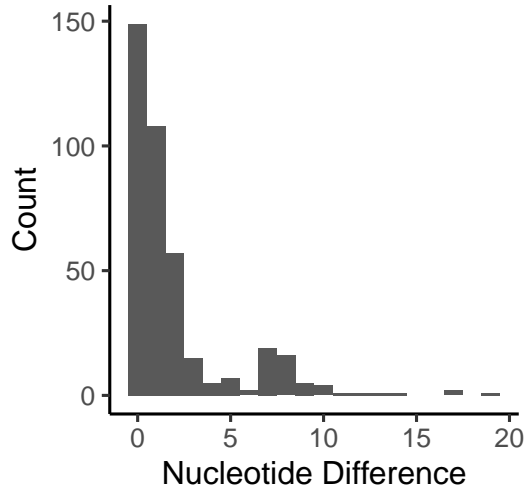
IGHV1-58*02

199 sequences assigned
54 (27.1%) exact matches, in which:
51 unique CDR3
4 unique J



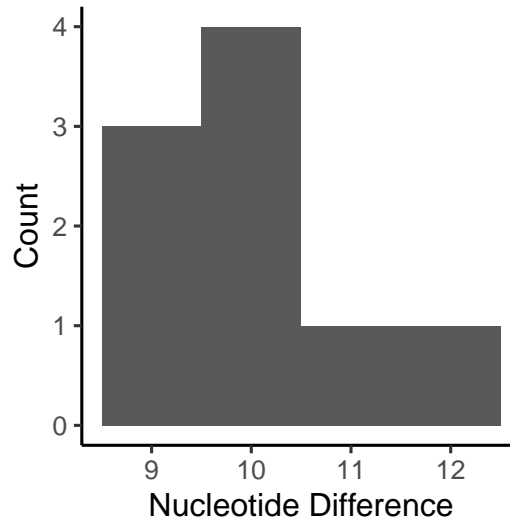
IGHV1-69*02

418 sequences assigned
149 (35.6%) exact matches, in which:
142 unique CDR3
6 unique J



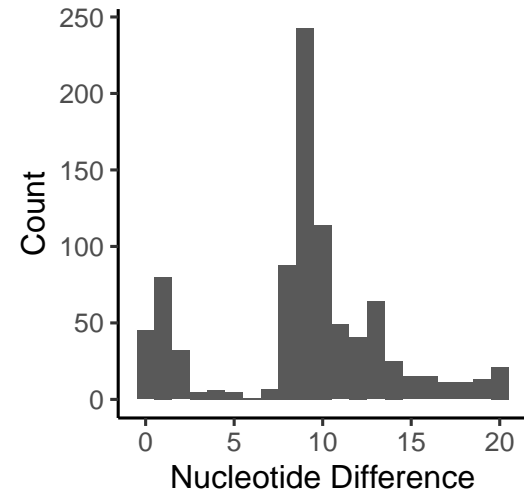
IGHV1-NL1*01

9 sequences assigned
No exact matches.



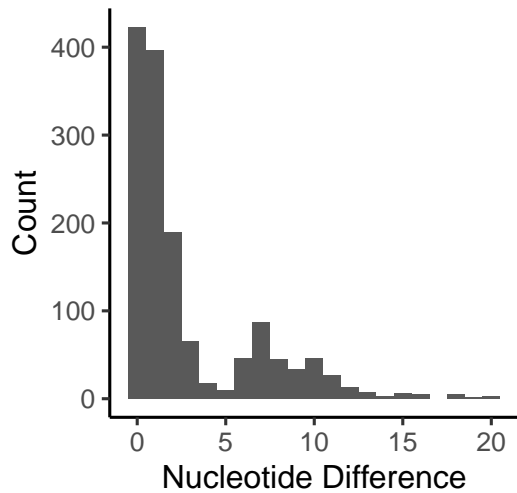
IGHV2-70*11_15

961 sequences assigned
45 (4.7%) exact matches, in which:
40 unique CDR3
4 unique J



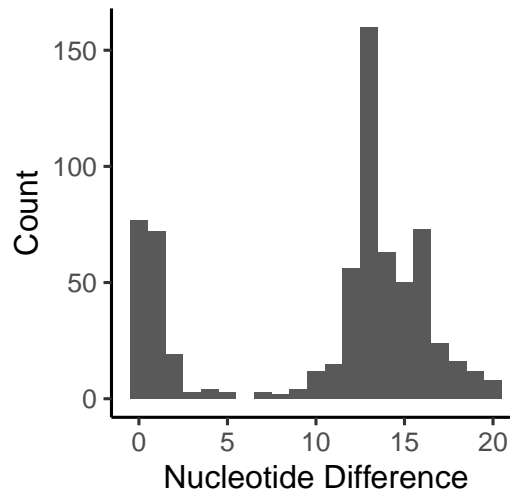
IGHV1-69*04_09

1458 sequences assigned
423 (29%) exact matches, in which:
392 unique CDR3
6 unique J



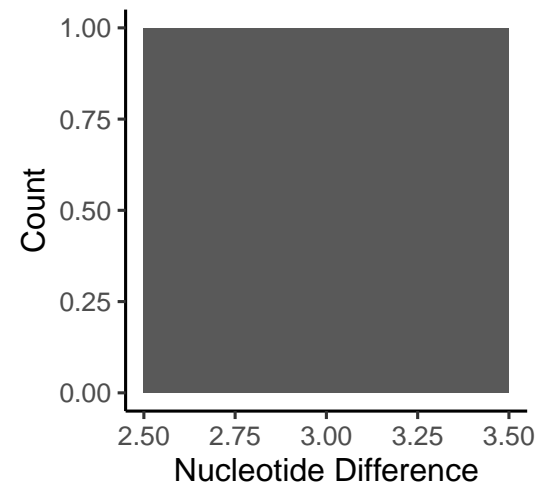
IGHV2-5*02

740 sequences assigned
77 (10.4%) exact matches, in which:
72 unique CDR3
5 unique J



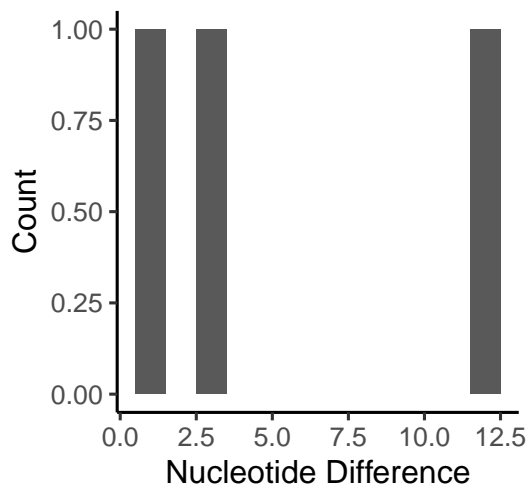
IGHV2-70D*04

1 sequences assigned
No exact matches.



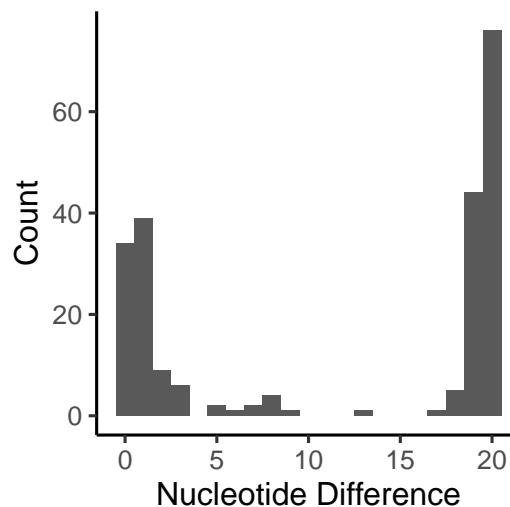
IGHV1-69D*01

4 sequences assigned
No exact matches.



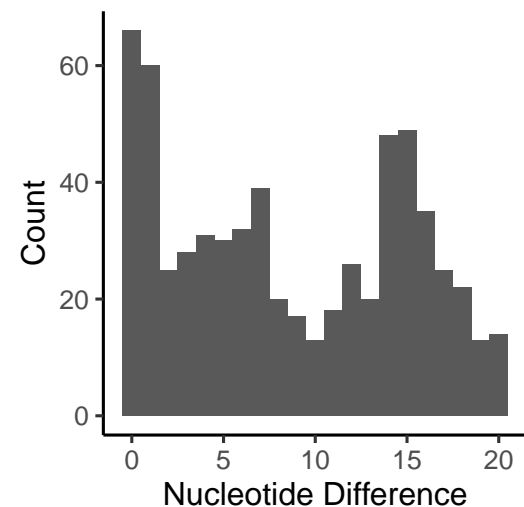
IGHV2-26*01

298 sequences assigned
34 (11.4%) exact matches, in which:
31 unique CDR3
3 unique J



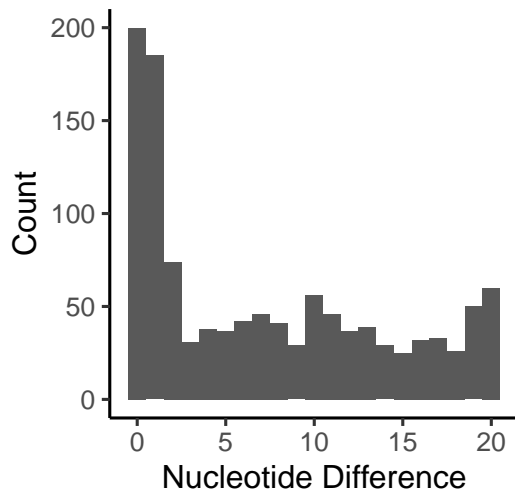
IGHV3-7*01

761 sequences assigned
66 (8.7%) exact matches, in which:
59 unique CDR3
4 unique J



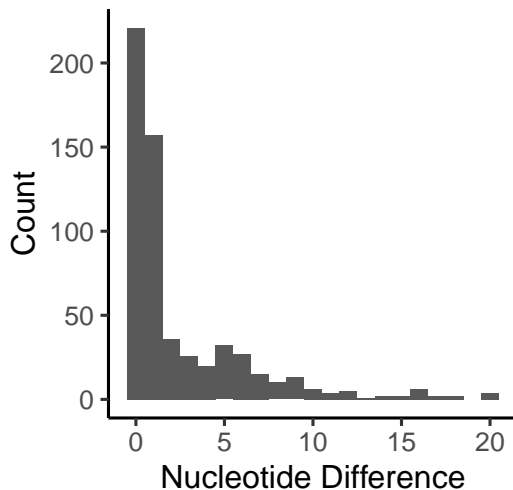
IGHV3-7*03

2811 sequences assigned
200 (7.1%) exact matches, in which:
137 unique CDR3
5 unique J



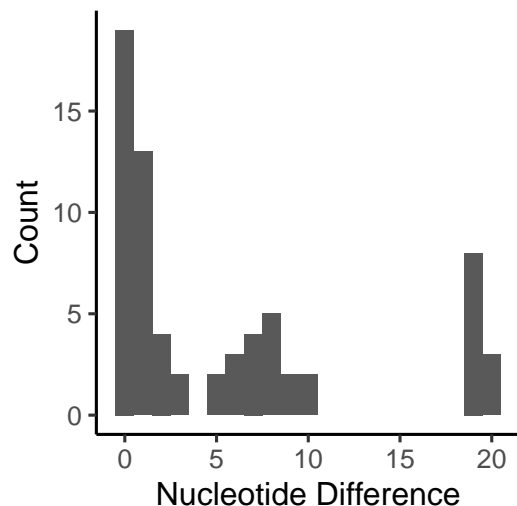
IGHV3-11*06

615 sequences assigned
221 (35.9%) exact matches, in which:
187 unique CDR3
5 unique J



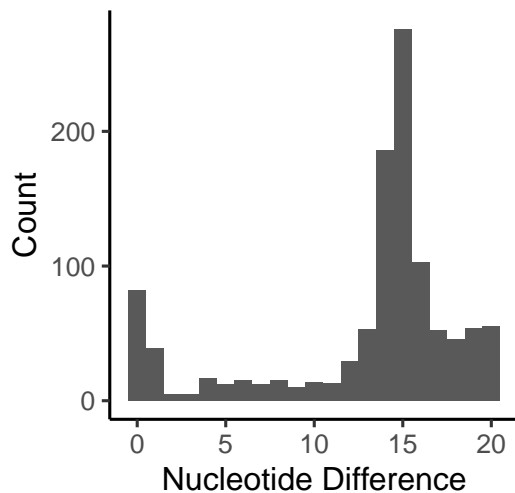
IGHV3-13*05

442 sequences assigned
19 (4.3%) exact matches, in which:
17 unique CDR3
2 unique J



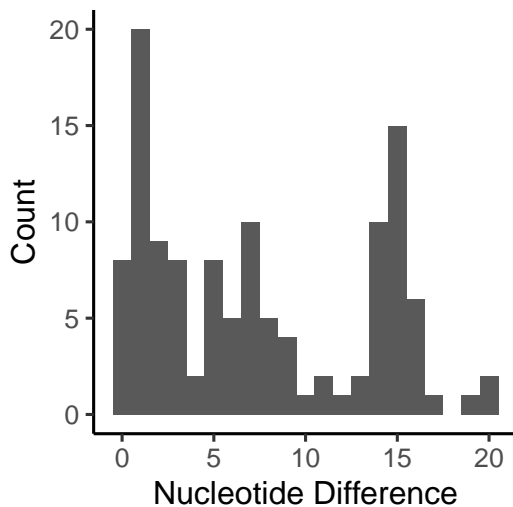
IGHV3-7*04

1397 sequences assigned
82 (5.9%) exact matches, in which:
64 unique CDR3
6 unique J



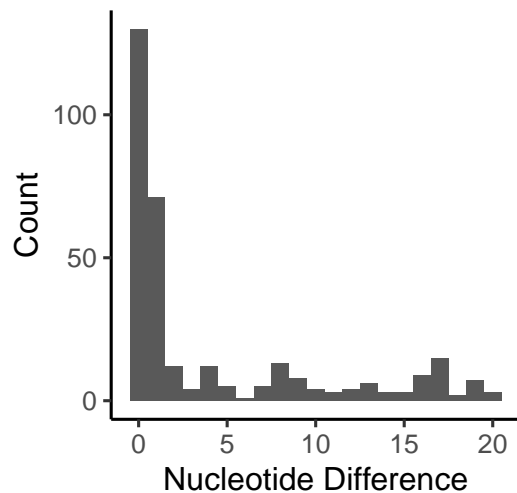
IGHV3-11*03_05

124 sequences assigned
8 (6.5%) exact matches, in which:
8 unique CDR3
3 unique J



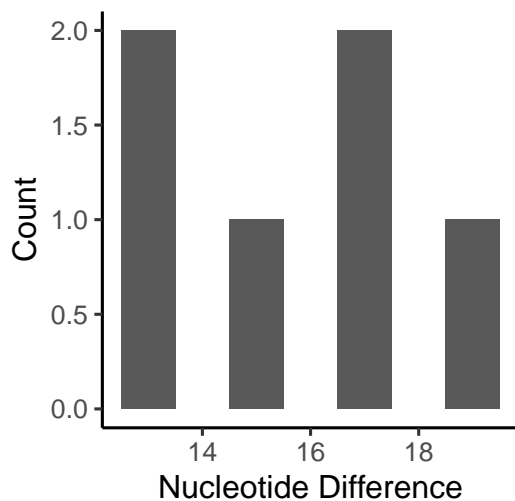
IGHV3-15*07

409 sequences assigned
130 (31.8%) exact matches, in which:
94 unique CDR3
5 unique J



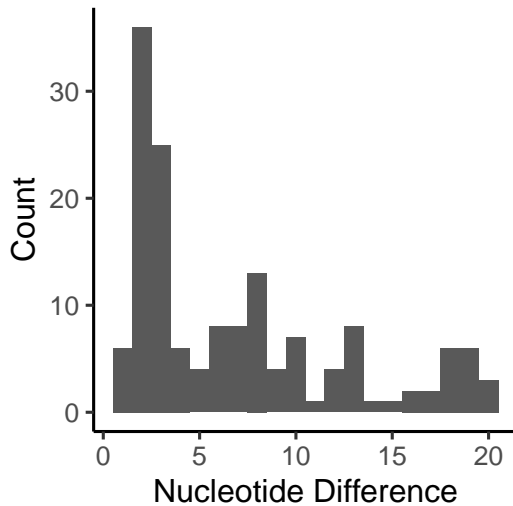
IGHV3-9*01

19 sequences assigned
No exact matches.



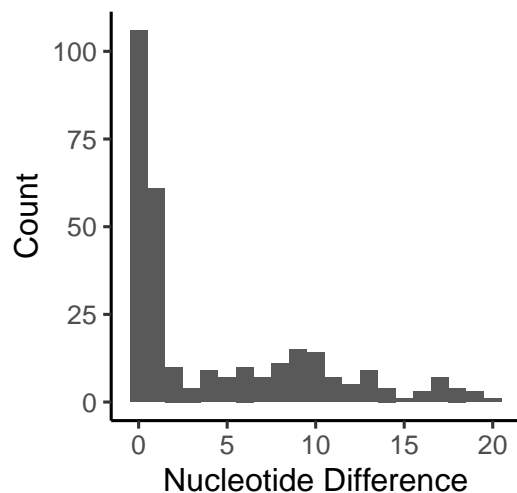
IGHV3-13*01

157 sequences assigned
No exact matches.



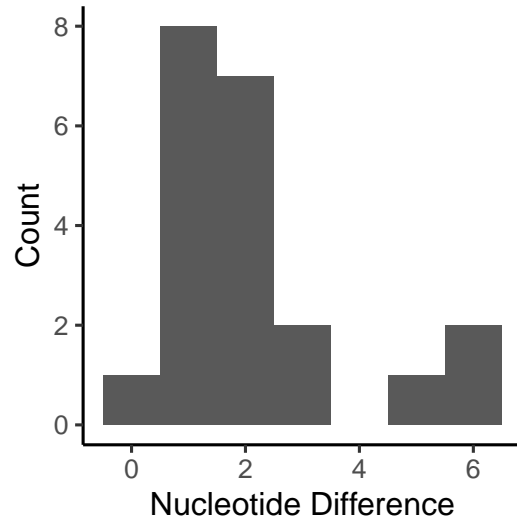
IGHV3-15*01_02

355 sequences assigned
106 (29.9%) exact matches, in which:
74 unique CDR3
6 unique J



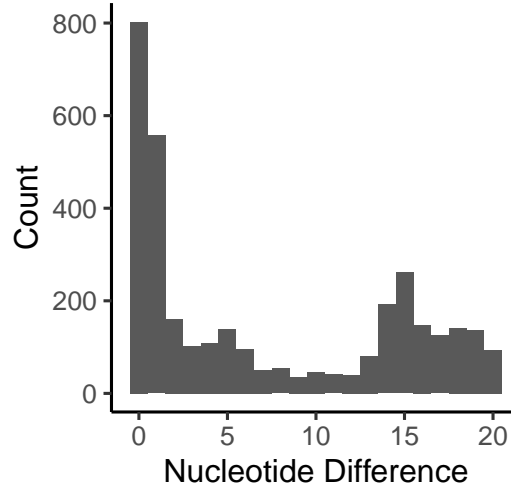
IGHV3-19*01

21 sequences assigned
1 (4.8%) exact matches, in which:
1 unique CDR3
1 unique J



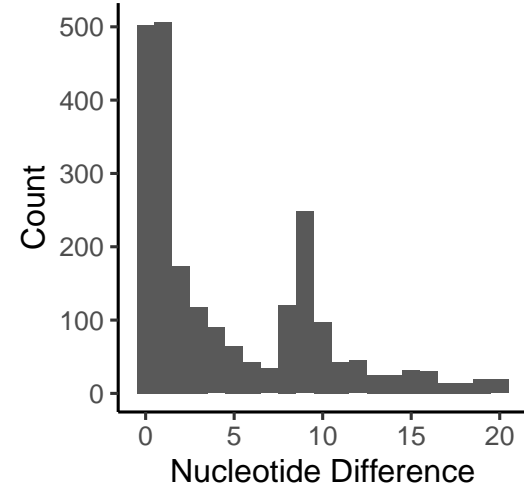
IGHV3-21*01_02

3722 sequences assigned
803 (21.6%) exact matches, in which:
662 unique CDR3
6 unique J



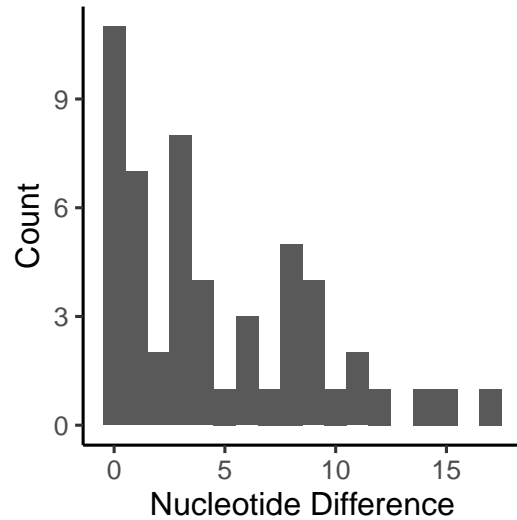
IGHV3-33*01

3750 sequences assigned
502 (13.4%) exact matches, in which:
393 unique CDR3
6 unique J



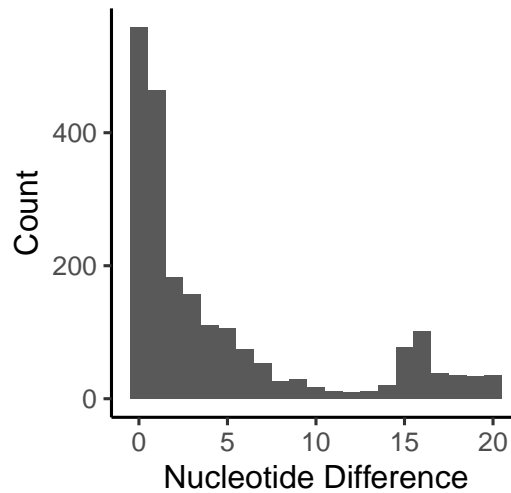
IGHV3-20*03_04

55 sequences assigned
11 (20%) exact matches, in which:
9 unique CDR3
4 unique J



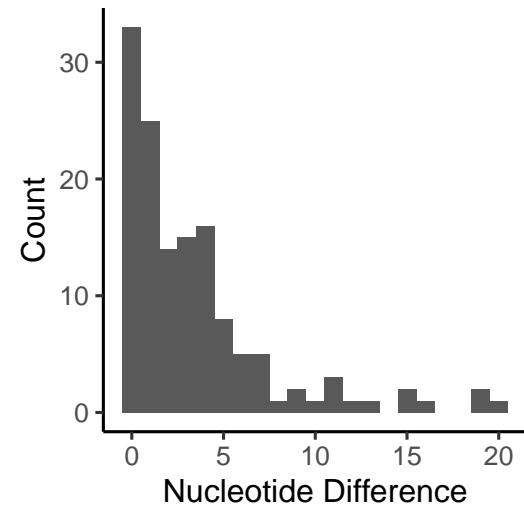
IGHV3-30-3*01

2419 sequences assigned
559 (23.1%) exact matches, in which:
442 unique CDR3
6 unique J



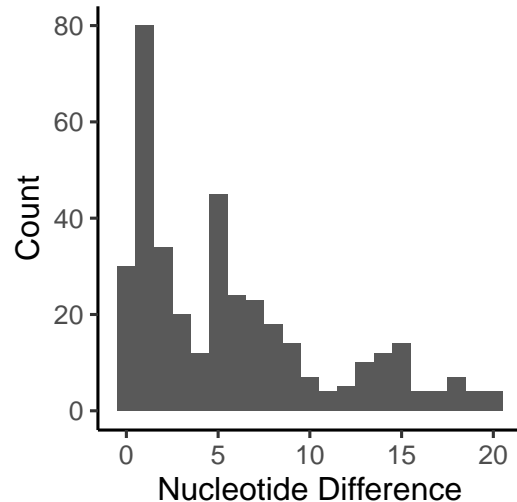
IGHV3-33*05

139 sequences assigned
33 (23.7%) exact matches, in which:
30 unique CDR3
4 unique J



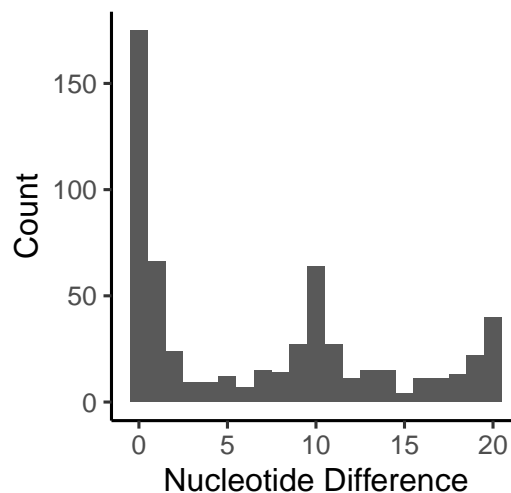
IGHV3-21*04

467 sequences assigned
30 (6.4%) exact matches, in which:
27 unique CDR3
4 unique J



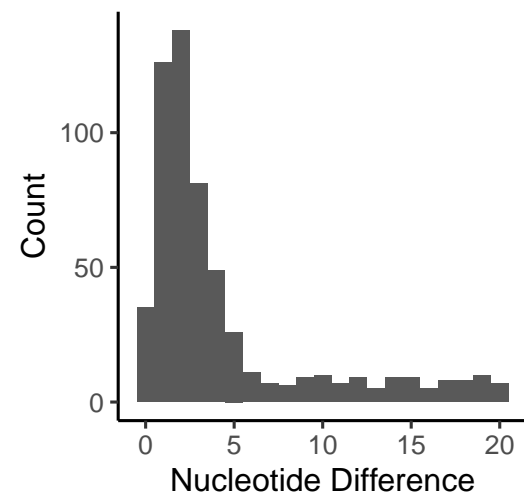
IGHV3-30*03

650 sequences assigned
175 (26.9%) exact matches, in which:
164 unique CDR3
6 unique J



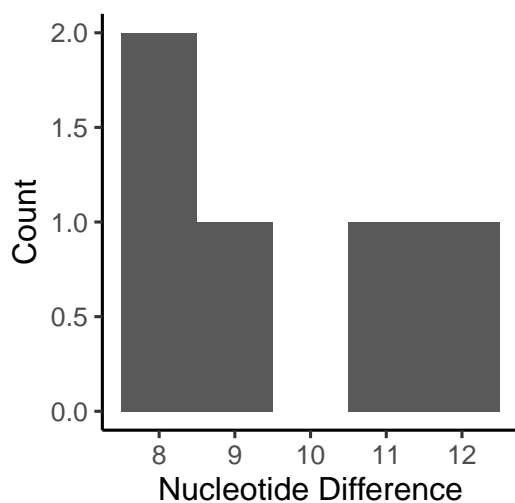
IGHV3-33*06

679 sequences assigned
35 (5.2%) exact matches, in which:
34 unique CDR3
3 unique J



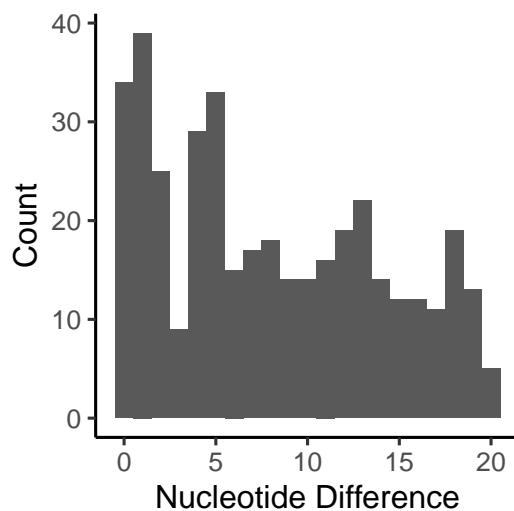
IGHV3-35*01

5 sequences assigned
No exact matches.



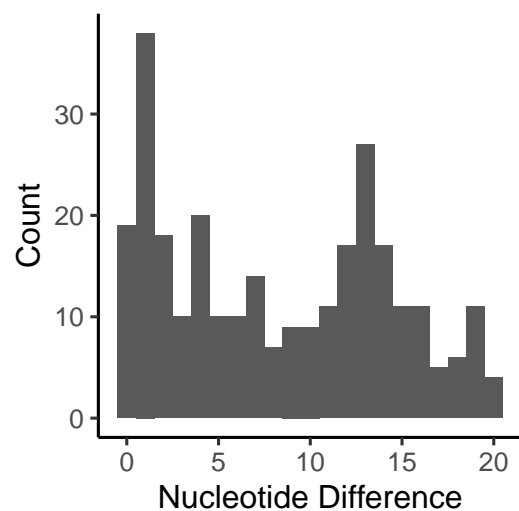
IGHV3-48*01

440 sequences assigned
34 (7.7%) exact matches, in which:
33 unique CDR3
4 unique J



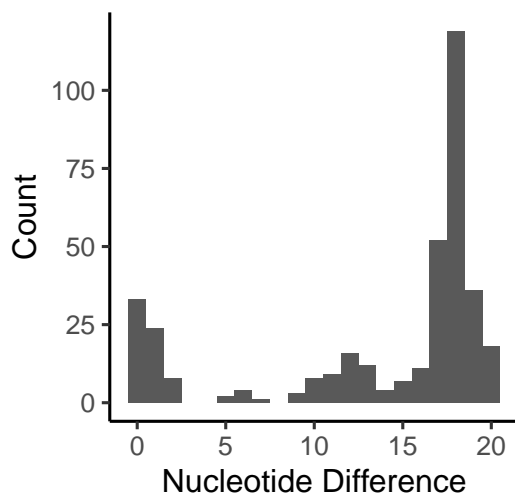
IGHV3-48*04

314 sequences assigned
19 (6.1%) exact matches, in which:
19 unique CDR3
4 unique J



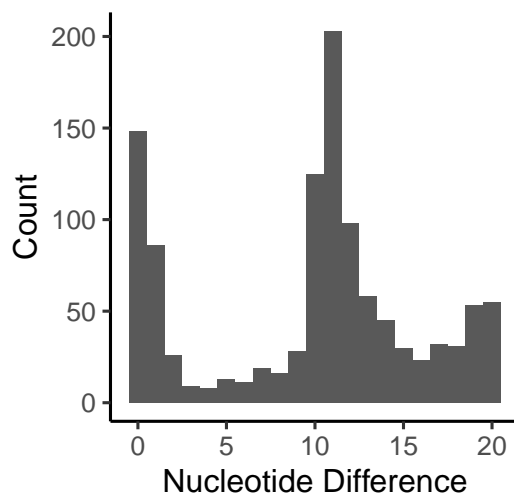
IGHV3-43*02

464 sequences assigned
33 (7.1%) exact matches, in which:
27 unique CDR3
5 unique J



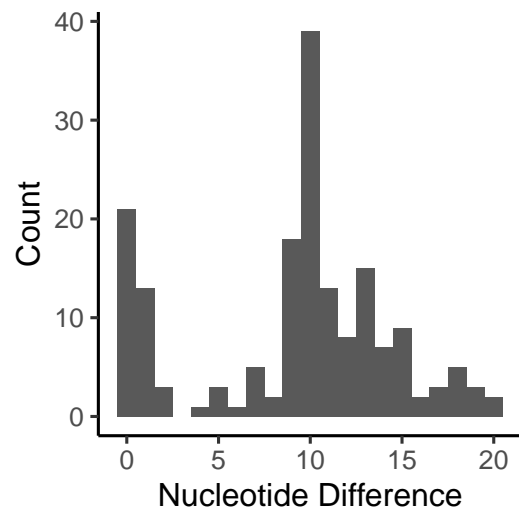
IGHV3-48*02

1588 sequences assigned
148 (9.3%) exact matches, in which:
114 unique CDR3
5 unique J



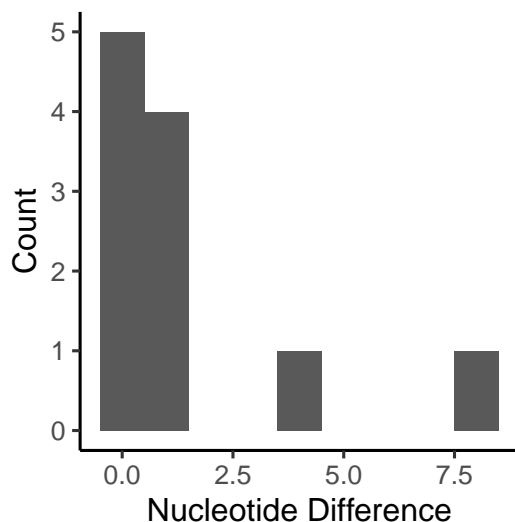
IGHV3-49*04

201 sequences assigned
21 (10.4%) exact matches, in which:
18 unique CDR3
4 unique J



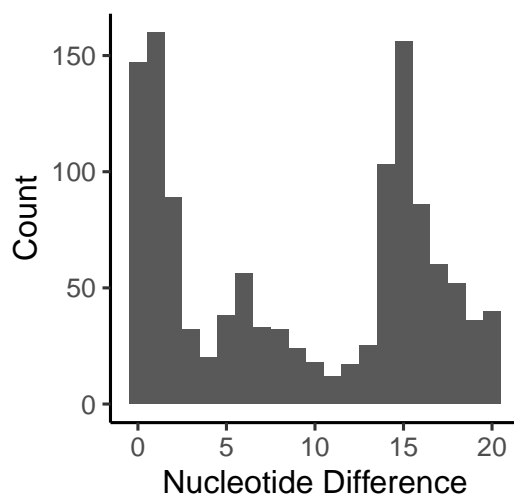
IGHV3-47*02

11 sequences assigned
5 (45.5%) exact matches, in which:
3 unique CDR3
1 unique J



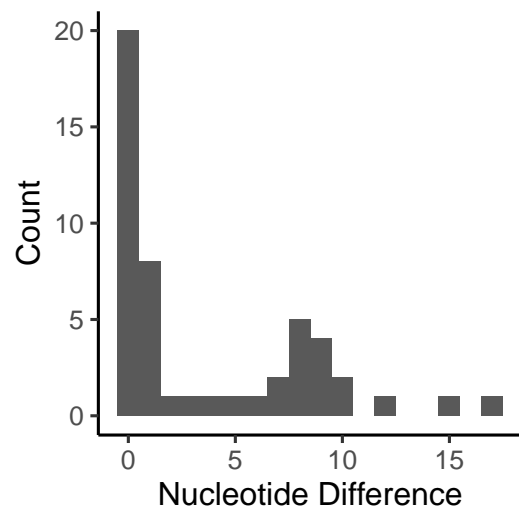
IGHV3-48*03

2125 sequences assigned
147 (6.9%) exact matches, in which:
111 unique CDR3
5 unique J



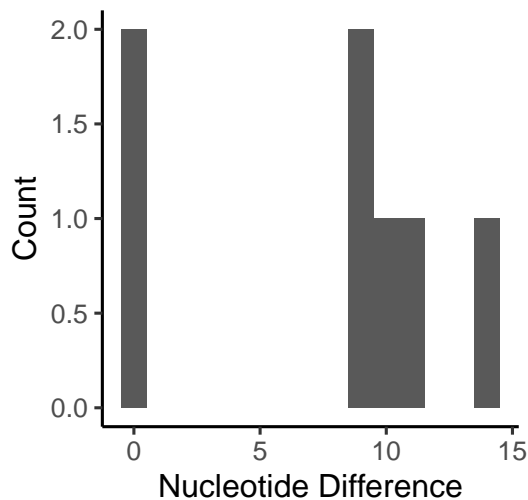
IGHV3-49*03_05

50 sequences assigned
20 (40%) exact matches, in which:
13 unique CDR3
3 unique J



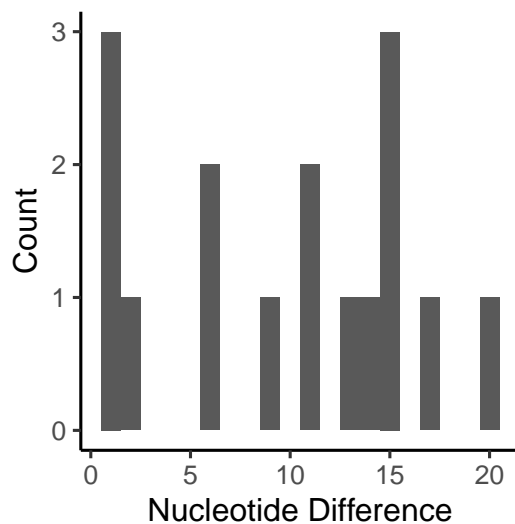
IGHV3-52*02

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



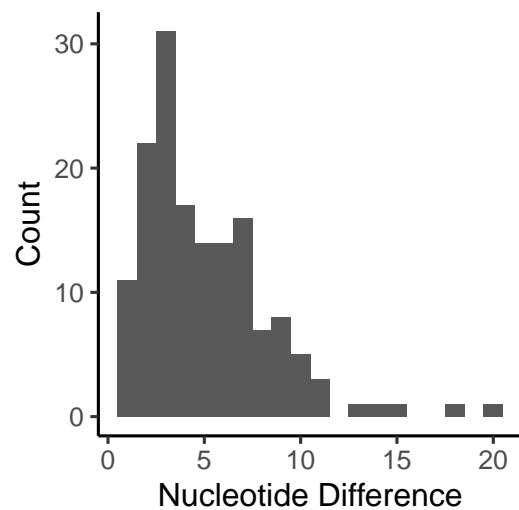
IGHV3-53*05

34 sequences assigned
No exact matches.



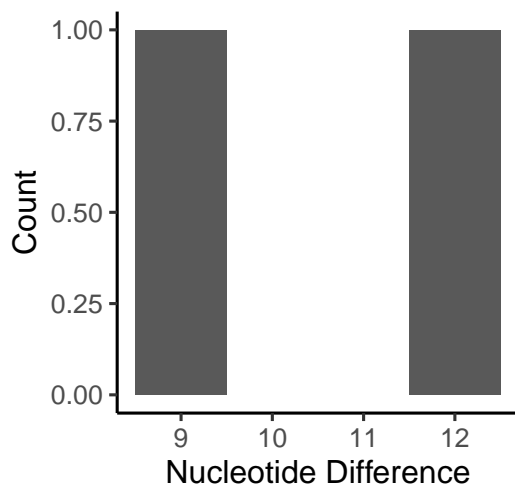
IGHV3-64*04

254 sequences assigned
No exact matches.



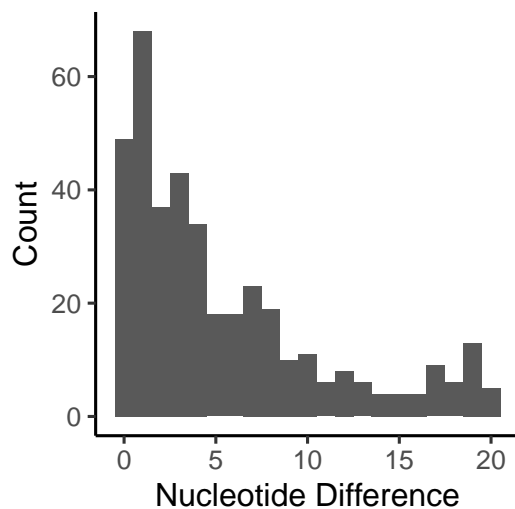
IGHV3-52*01_03

2 sequences assigned
No exact matches.



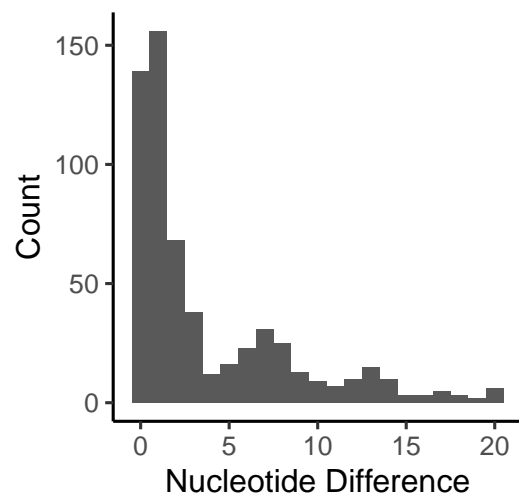
IGHV3-53*01_02

466 sequences assigned
49 (10.5%) exact matches, in which:
42 unique CDR3
4 unique J



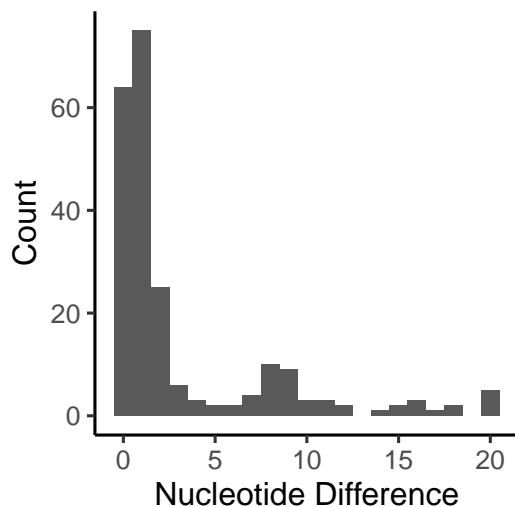
IGHV3-66*01

675 sequences assigned
139 (20.6%) exact matches, in which:
113 unique CDR3
5 unique J



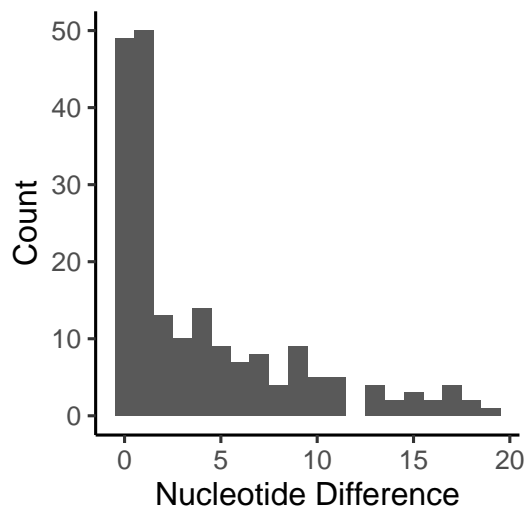
IGHV3-53*04

398 sequences assigned
64 (16.1%) exact matches, in which:
46 unique CDR3
4 unique J



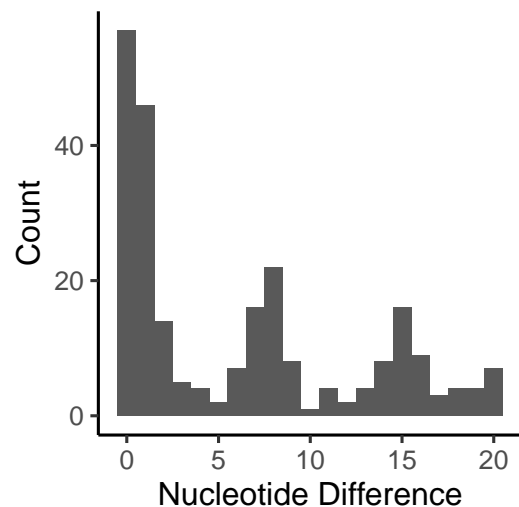
IGHV3-64*01

246 sequences assigned
49 (19.9%) exact matches, in which:
39 unique CDR3
4 unique J



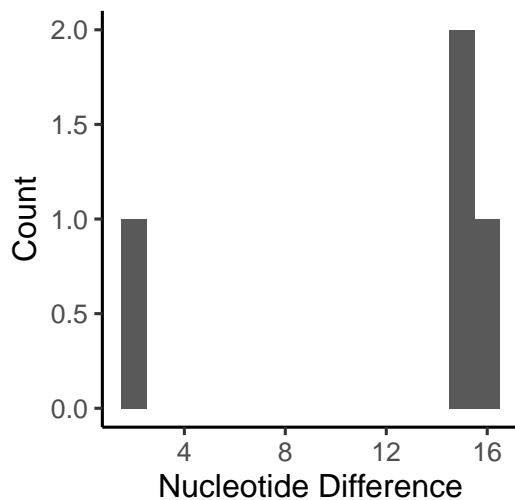
IGHV3-66*02

300 sequences assigned
57 (19%) exact matches, in which:
48 unique CDR3
6 unique J



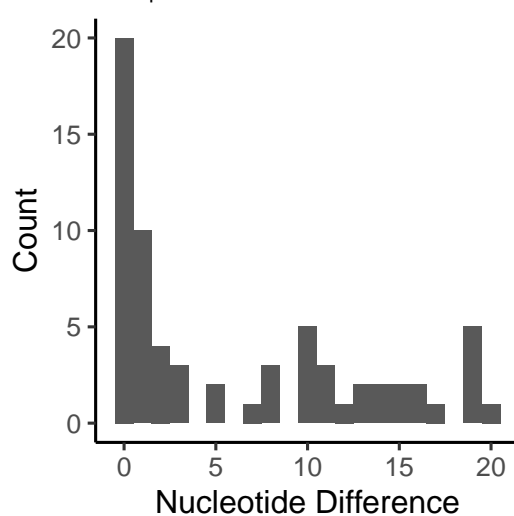
IGHV3-66*03

7 sequences assigned
No exact matches.



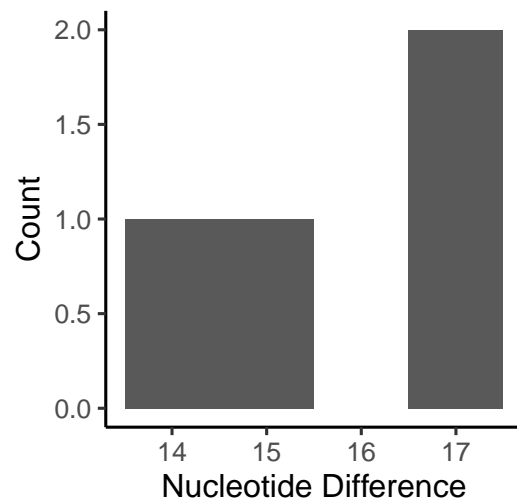
IGHV3-72*01

913 sequences assigned
20 (2.2%) exact matches, in which:
15 unique CDR3
4 unique J



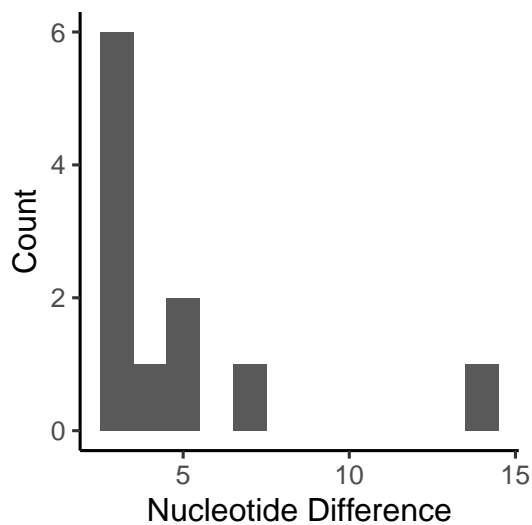
IGHV3-43D*04

4 sequences assigned
No exact matches.



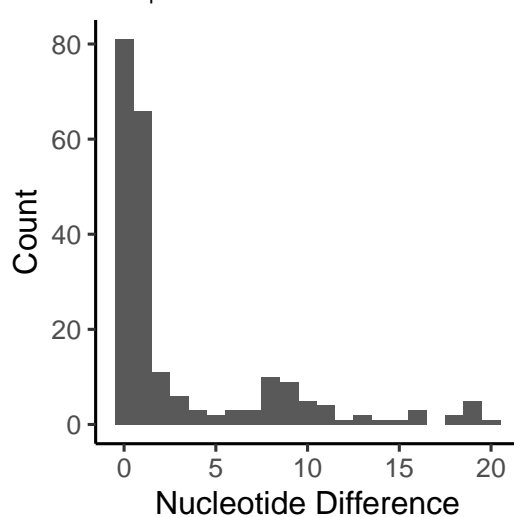
IGHV3-69-1*01

14 sequences assigned
No exact matches.



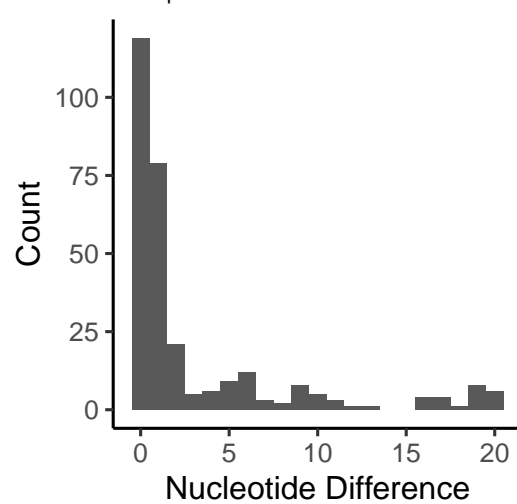
IGHV3-73*01_02

304 sequences assigned
81 (26.6%) exact matches, in which:
58 unique CDR3
4 unique J



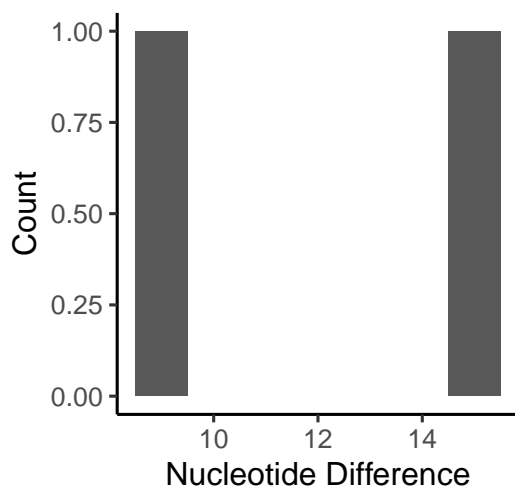
IGHV3-64D*06

1525 sequences assigned
119 (7.8%) exact matches, in which:
97 unique CDR3
5 unique J



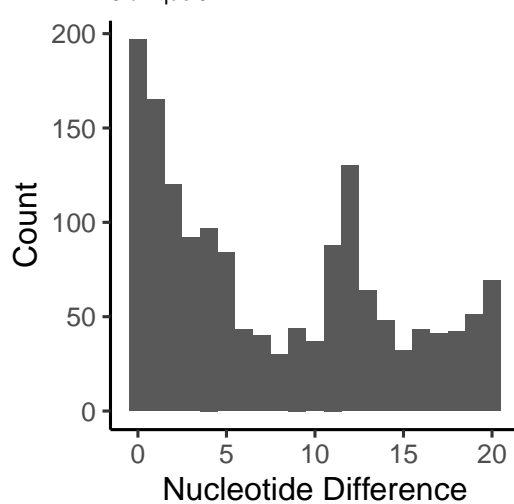
IGHV3-69-1*02

35 sequences assigned
No exact matches.



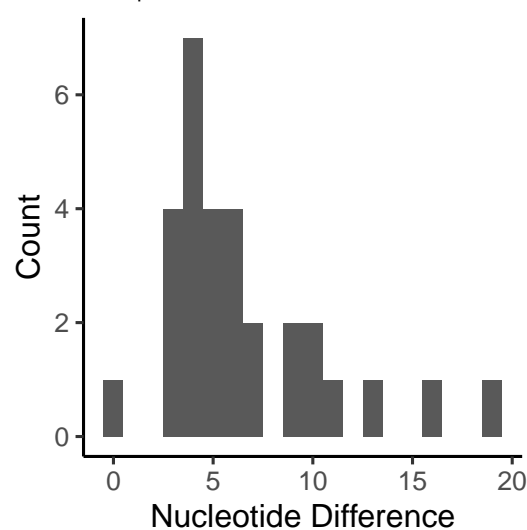
IGHV3-74*01_02

3362 sequences assigned
197 (5.9%) exact matches, in which:
167 unique CDR3
5 unique J



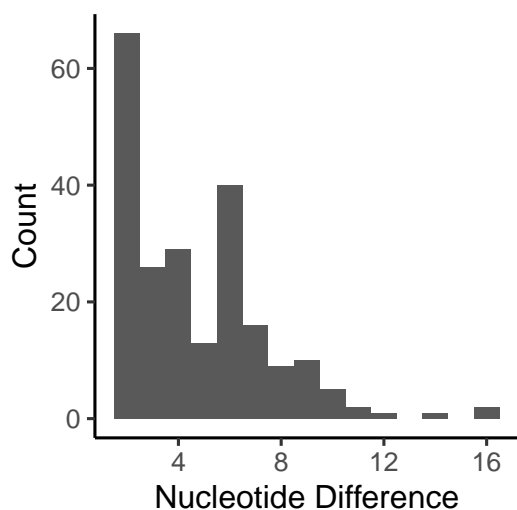
IGHV3-NL1*01

48 sequences assigned
1 (2.1%) exact matches, in which:
1 unique CDR3
1 unique J



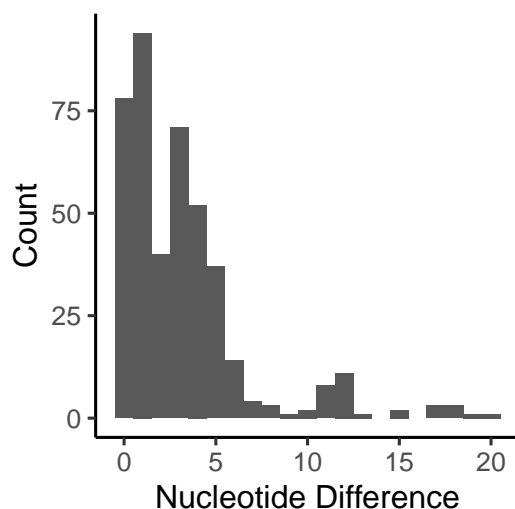
IGHV4-4*07

244 sequences assigned
No exact matches.



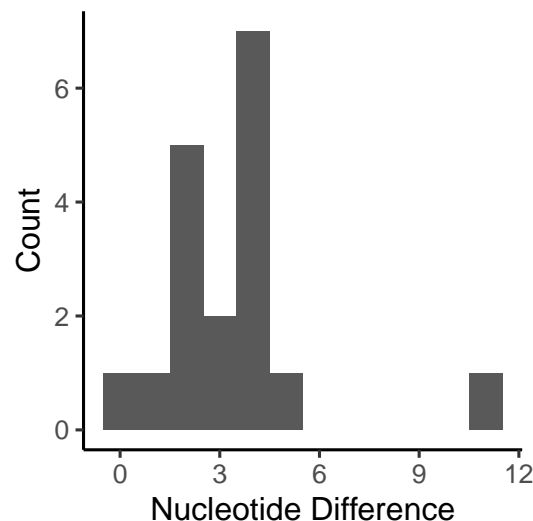
IGHV4-30-4*01

539 sequences assigned
78 (14.5%) exact matches, in which:
62 unique CDR3
5 unique J



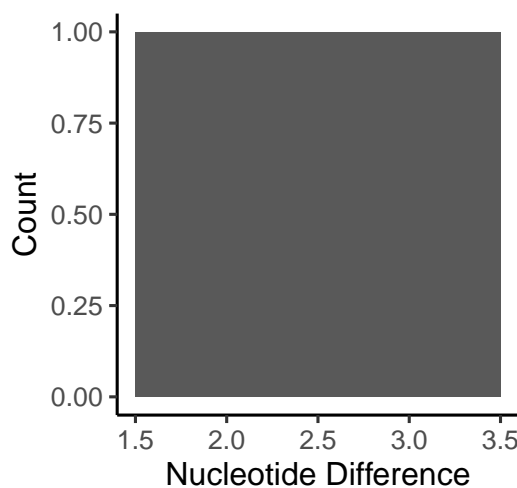
IGHV4-30-2*04

18 sequences assigned
1 (5.6%) exact matches, in which:
1 unique CDR3
1 unique J



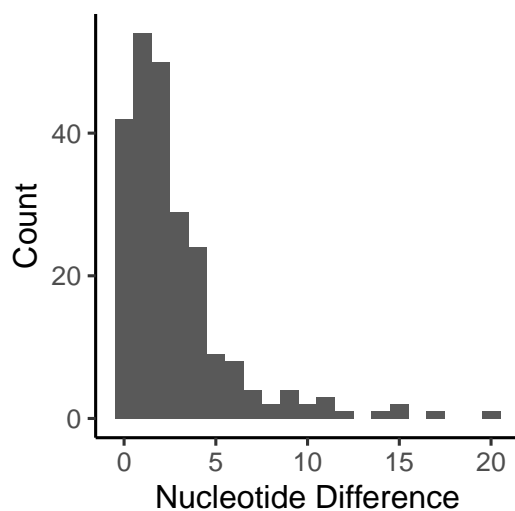
IGHV4-28*03

2 sequences assigned
No exact matches.



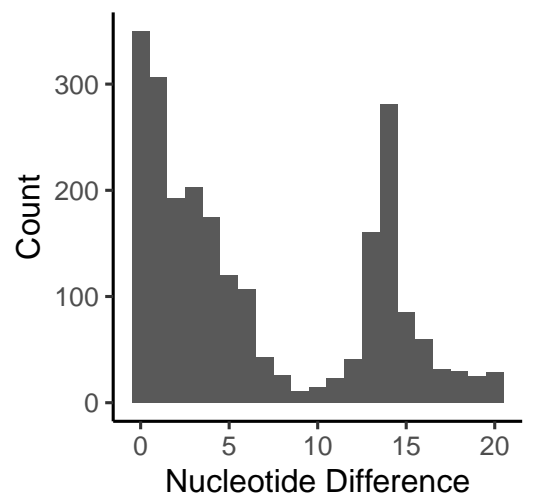
IGHV4-30-2*01

240 sequences assigned
42 (17.5%) exact matches, in which:
34 unique CDR3
4 unique J



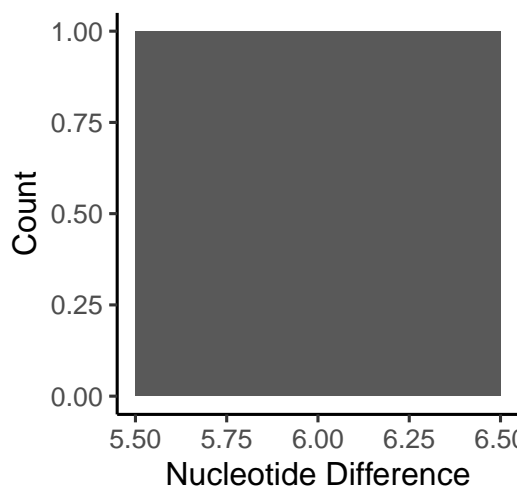
IGHV4-31*03_04

3620 sequences assigned
350 (9.7%) exact matches, in which:
303 unique CDR3
6 unique J



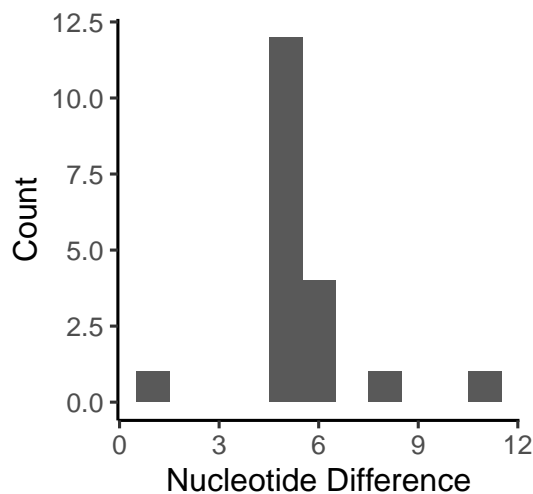
IGHV4-28*01_07

1 sequences assigned
No exact matches.



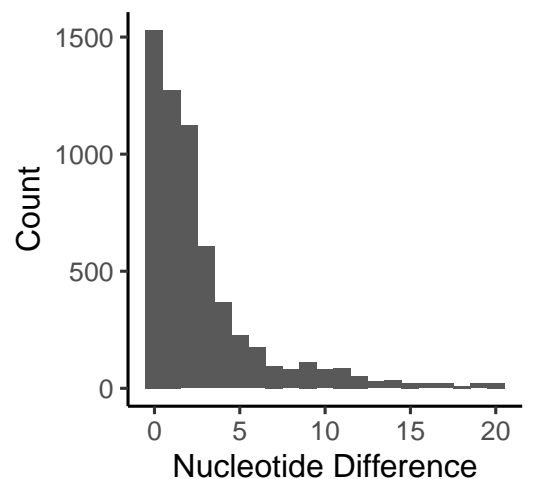
IGHV4-30-2*03

23 sequences assigned
No exact matches.



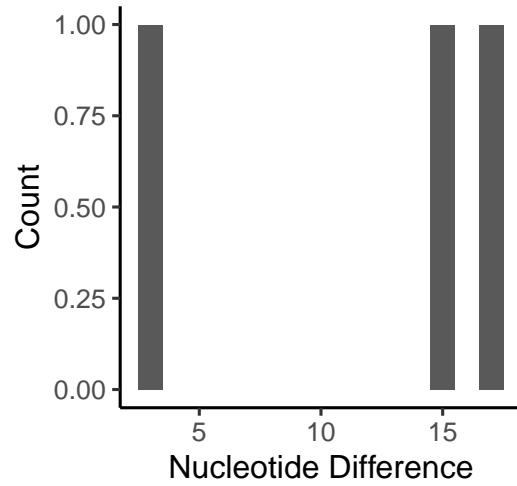
IGHV4-34*01_02

6100 sequences assigned
1530 (25.1%) exact matches, in which:
1299 unique CDR3
6 unique J



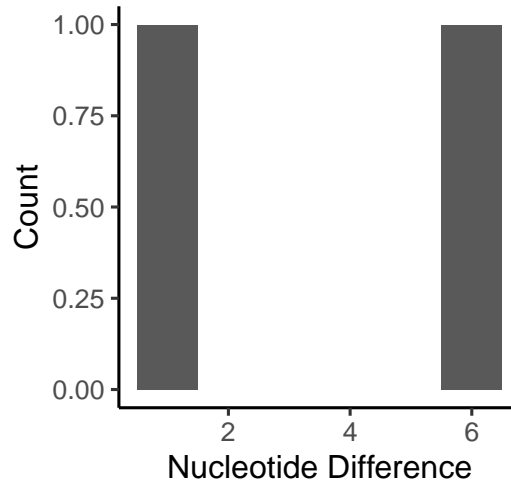
IGHV4-38-2*02

5 sequences assigned
No exact matches.



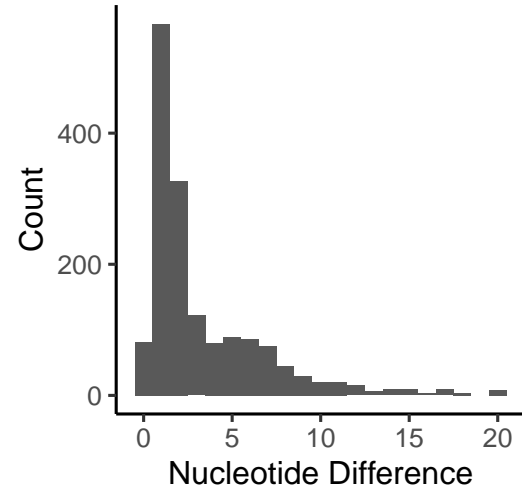
IGHV4-55*02_04_08

2 sequences assigned
No exact matches.



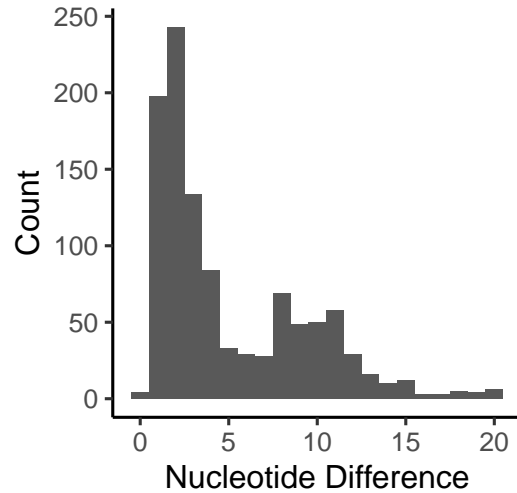
IGHV4-59*12

1861 sequences assigned
81 (4.4%) exact matches, in which:
81 unique CDR3
5 unique J



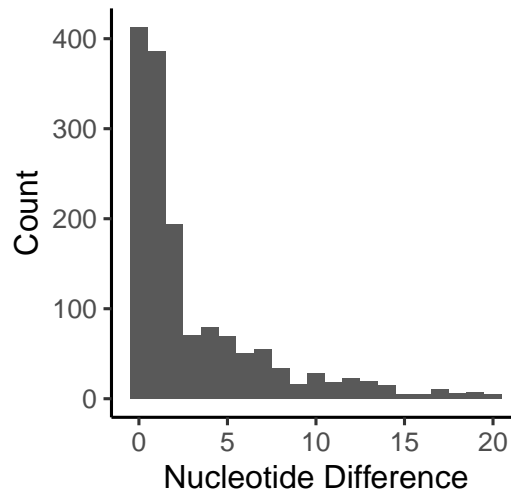
IGHV4-39*07

1103 sequences assigned
4 (0.4%) exact matches, in which:
4 unique CDR3
3 unique J



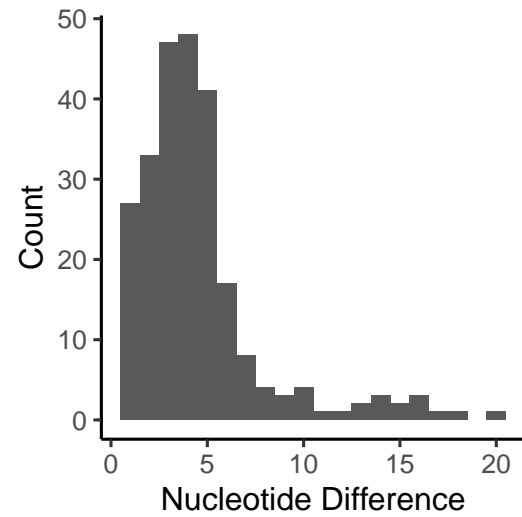
IGHV4-59*08

2047 sequences assigned
413 (20.2%) exact matches, in which:
389 unique CDR3
6 unique J



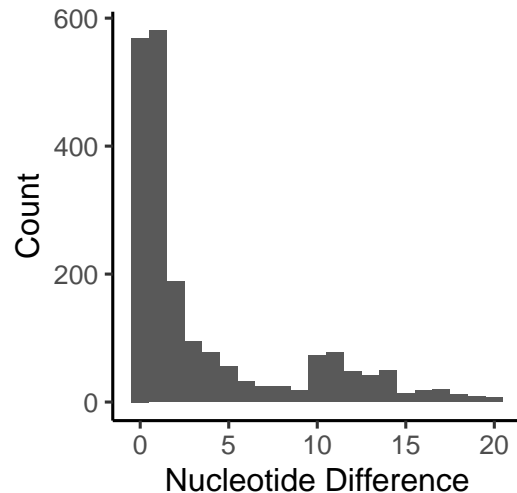
IGHV4-61*01

262 sequences assigned
No exact matches.



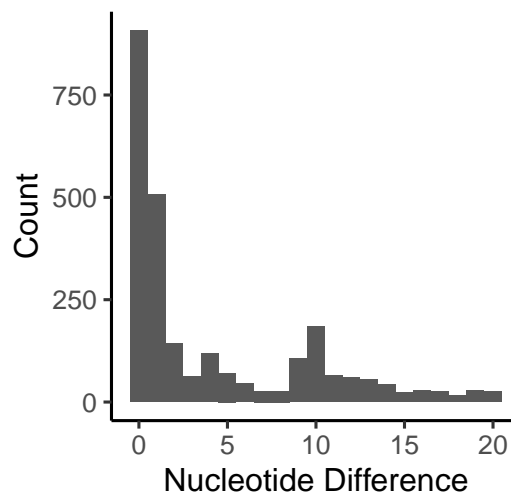
IGHV4-39*01_05

2517 sequences assigned
569 (22.6%) exact matches, in which:
468 unique CDR3
6 unique J



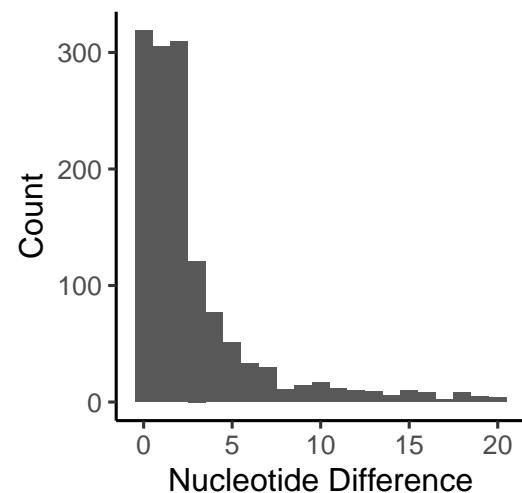
IGHV4-59*01_07

3790 sequences assigned
908 (24%) exact matches, in which:
841 unique CDR3
6 unique J



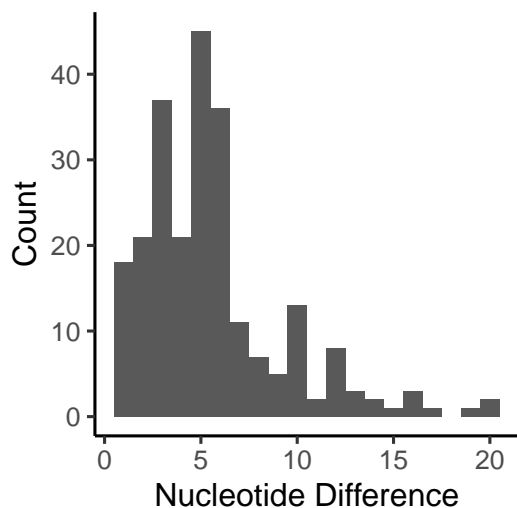
IGHV4-61*02

1735 sequences assigned
319 (18.4%) exact matches, in which:
295 unique CDR3
6 unique J



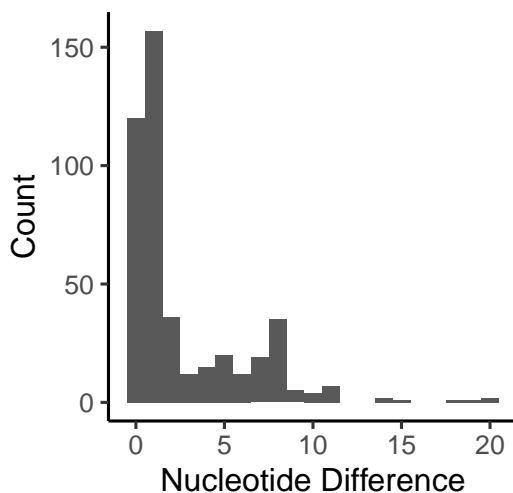
IGHV4-61*08

281 sequences assigned
No exact matches.



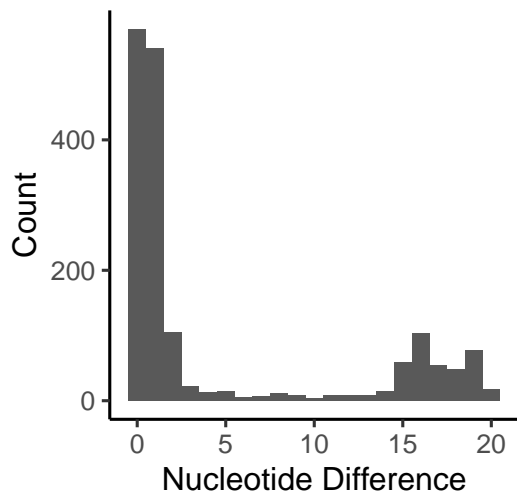
IGHV6-1*01_02

1580 sequences assigned
120 (7.6%) exact matches, in which:
108 unique CDR3
6 unique J



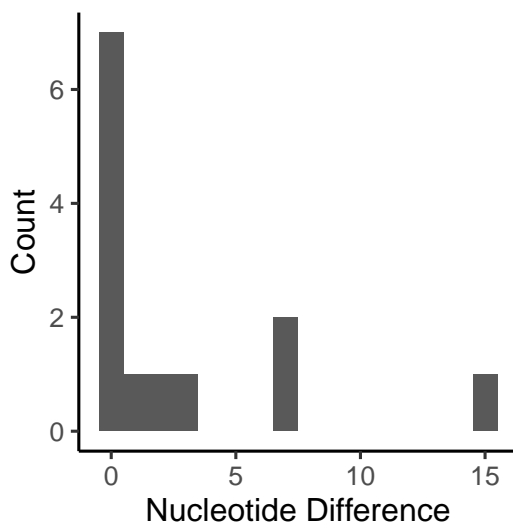
IGHV5-10-1*01_03

1799 sequences assigned
570 (31.7%) exact matches, in which:
467 unique CDR3
6 unique J



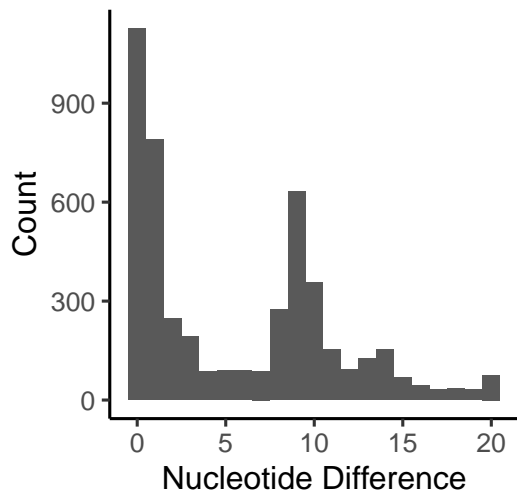
IGHV7-4-1*01

13 sequences assigned
7 (53.8%) exact matches, in which:
7 unique CDR3
2 unique J



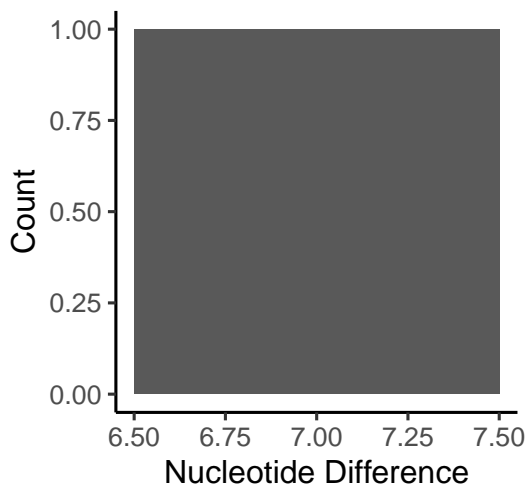
IGHV5-51*01_03

5035 sequences assigned
1127 (22.4%) exact matches, in which:
899 unique CDR3
6 unique J



IGHV7-81*01

1 sequences assigned
No exact matches.





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

Novel sequence(s) IGHV3-30-3*01_T288C IGHV4-59*02_G88A IGHV5-51*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_G75C IGHV4-59*02_G88A IGHV5-51*07_A128G are not listed in the genotype and will be ignored.

Novel sequence(s) IGHV3-33*01_G75C IGHV4-59*02_G88A IGHV5-51*07_A128G are not listed in the genotype and will be ignored.

Novel sequence(s) IGHV3-30*03_T288C IGHV4-59*02_G88A IGHV5-51*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_G112A IGHV4-59*02_G88A IGHV5-10-1*01_03_T258C IGHV5-51*07_A128G are not listed in the genotype and will be ignored.

Warning - no inferred sequences found.

Novel sequence(s) IGHV1-69*08_C191T IGHV3-48*03_T303G IGHV4-59*02_G88A IGHV5-51*07_A128G are not listed in the genotype and will be ignored.