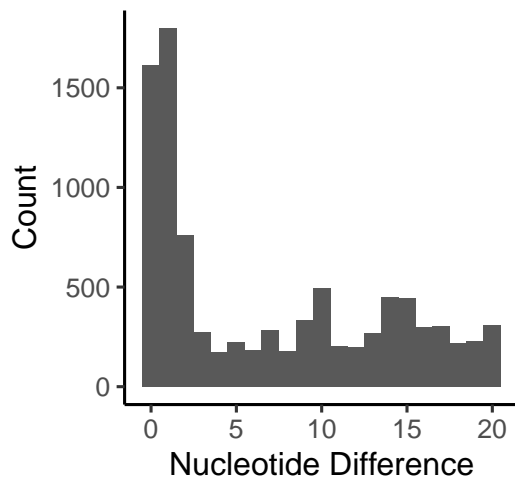


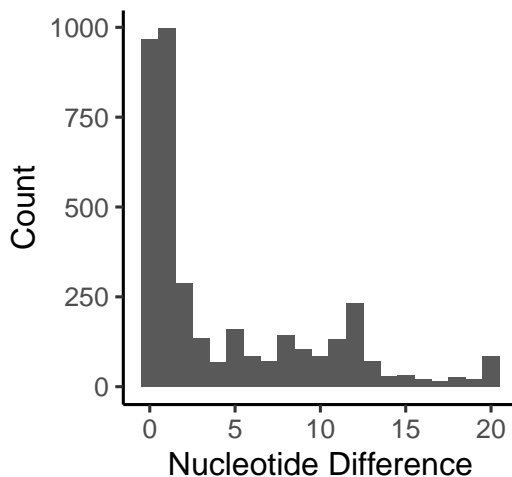
IGHV1-2*02

11994 sequences assigned
1613 (13.4%) exact matches, in which:
1338 unique CDR3
6 unique J



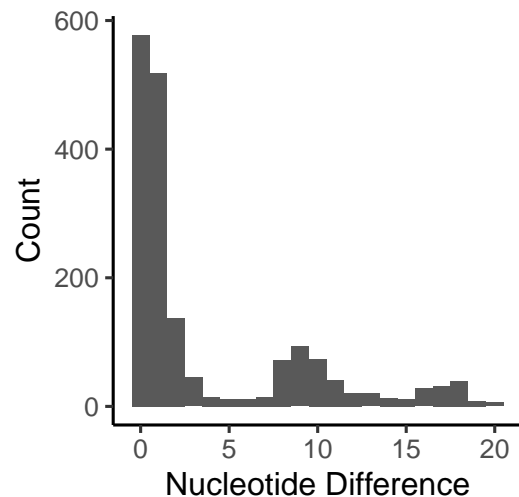
IGHV1-8*01

4250 sequences assigned
968 (22.8%) exact matches, in which:
802 unique CDR3
6 unique J



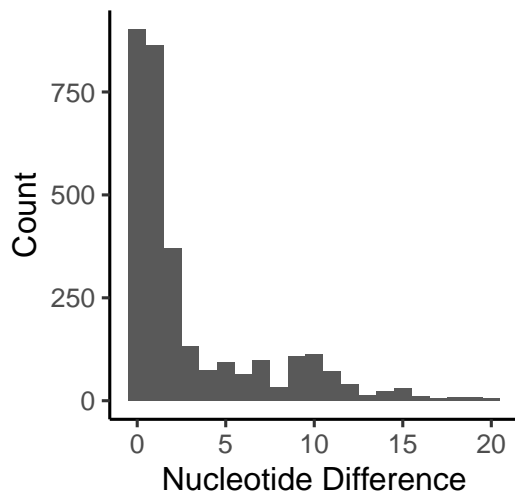
IGHV1-24*01

1963 sequences assigned
578 (29.4%) exact matches, in which:
484 unique CDR3
6 unique J



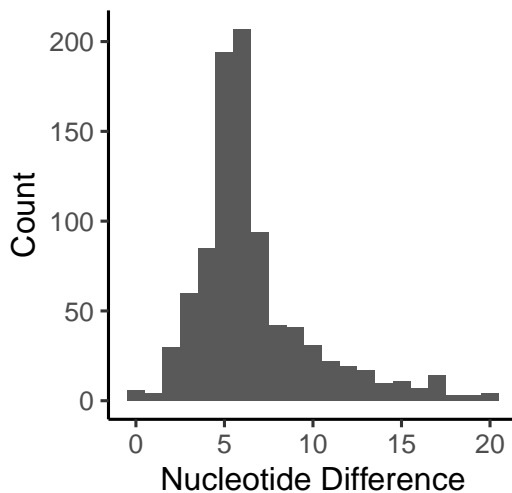
IGHV1-2*04

3113 sequences assigned
903 (29%) exact matches, in which:
762 unique CDR3
6 unique J



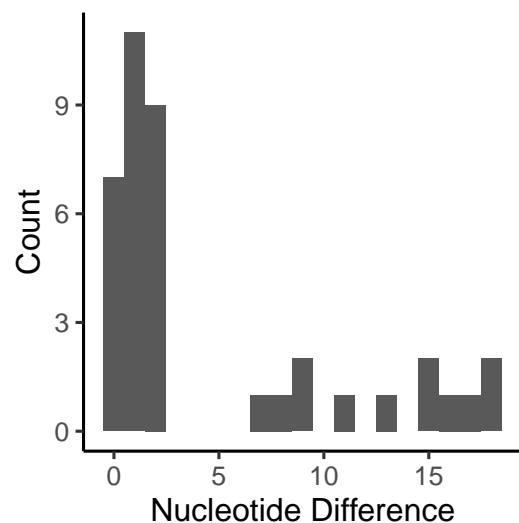
IGHV1-8*02

1004 sequences assigned
6 (0.6%) exact matches, in which:
6 unique CDR3
2 unique J



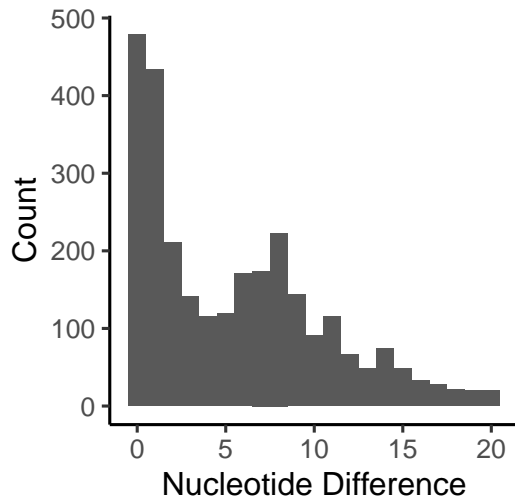
IGHV1-45*02

43 sequences assigned
7 (16.3%) exact matches, in which:
6 unique CDR3
2 unique J



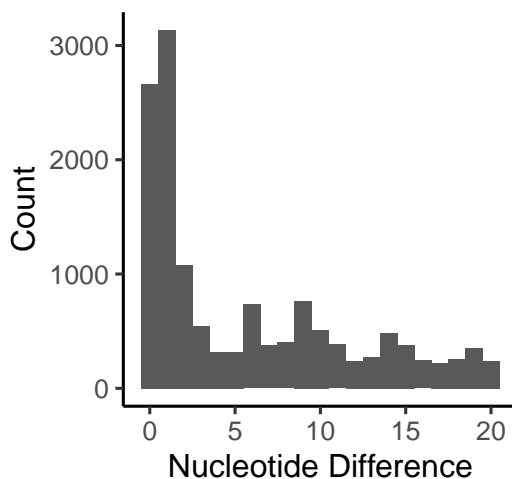
IGHV1-3*01_05

3563 sequences assigned
479 (13.4%) exact matches, in which:
398 unique CDR3
6 unique J



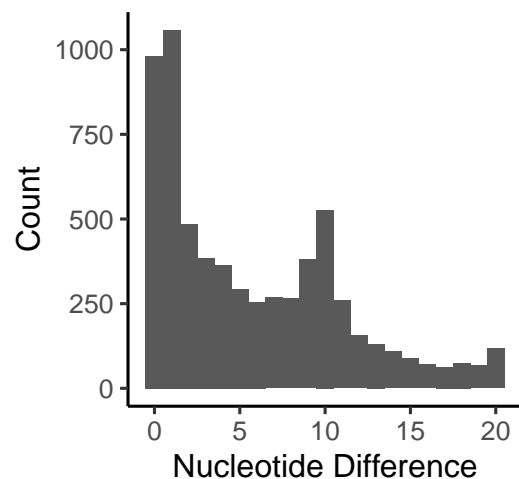
IGHV1-18*01

17642 sequences assigned
2664 (15.1%) exact matches, in which:
2142 unique CDR3
6 unique J



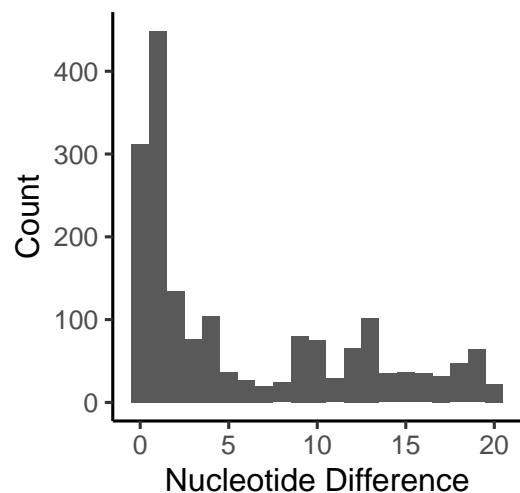
IGHV1-46*01

7020 sequences assigned
982 (14%) exact matches, in which:
836 unique CDR3
6 unique J



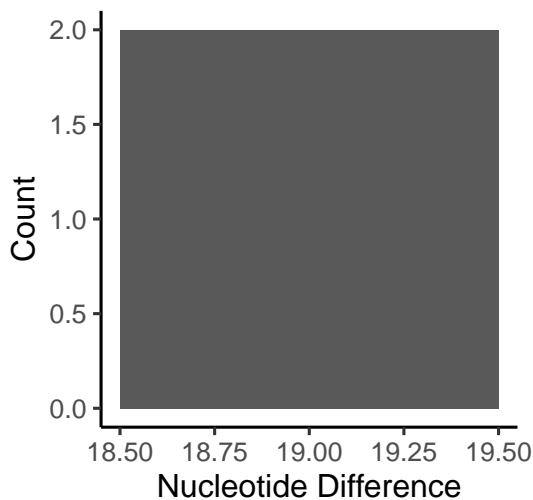
IGHV1-46*03

2592 sequences assigned
312 (12%) exact matches, in which:
234 unique CDR3
6 unique J



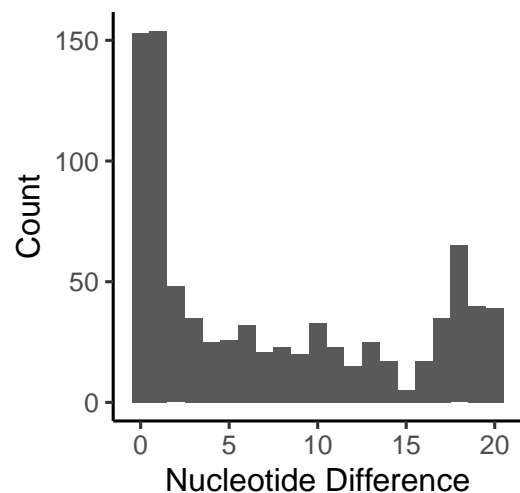
IGHV1-69-2*01

2 sequences assigned
No exact matches.



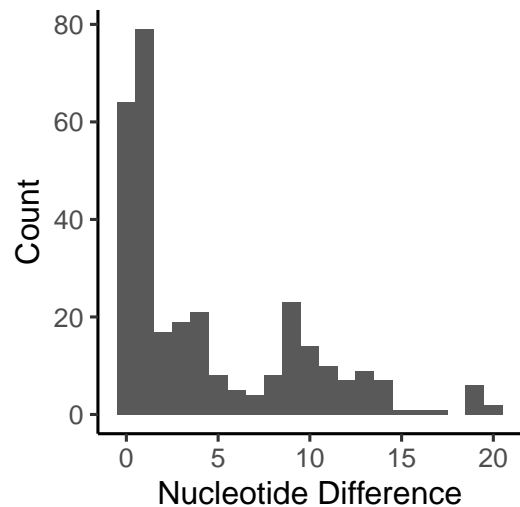
IGHV2-5*01

921 sequences assigned
153 (16.6%) exact matches, in which:
128 unique CDR3
6 unique J



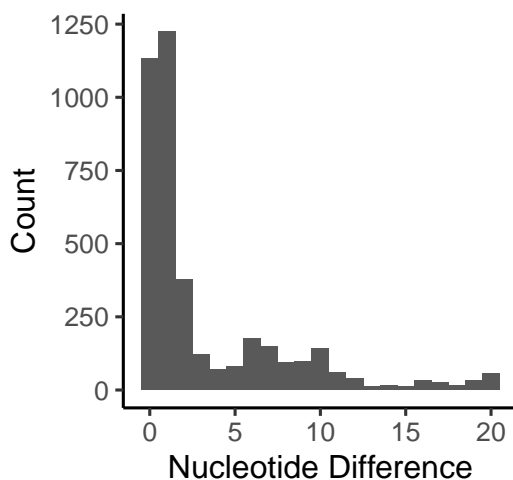
IGHV1-58*02

326 sequences assigned
64 (19.6%) exact matches, in which:
58 unique CDR3
4 unique J



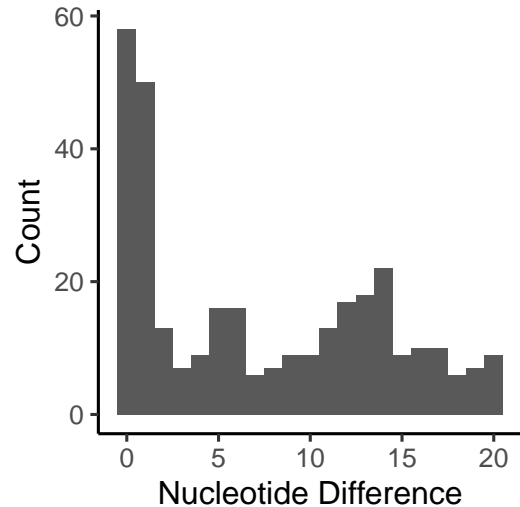
IGHV1-69*04_09

4238 sequences assigned
1132 (26.7%) exact matches, in which:
975 unique CDR3
6 unique J



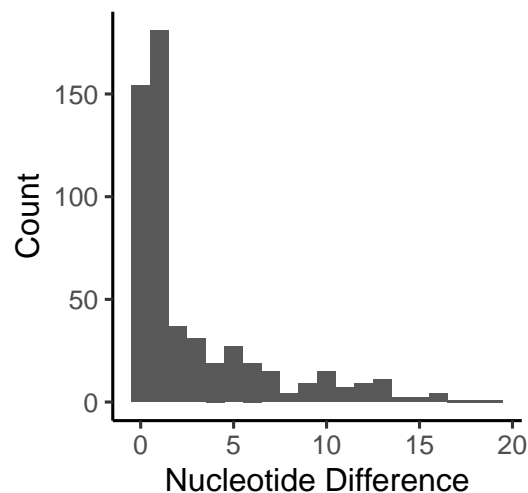
IGHV2-5*02

547 sequences assigned
58 (10.6%) exact matches, in which:
51 unique CDR3
6 unique J



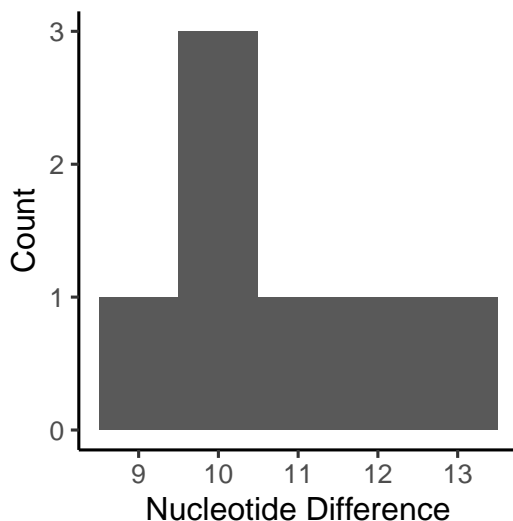
IGHV1-58*01_03

598 sequences assigned
154 (25.8%) exact matches, in which:
131 unique CDR3
5 unique J



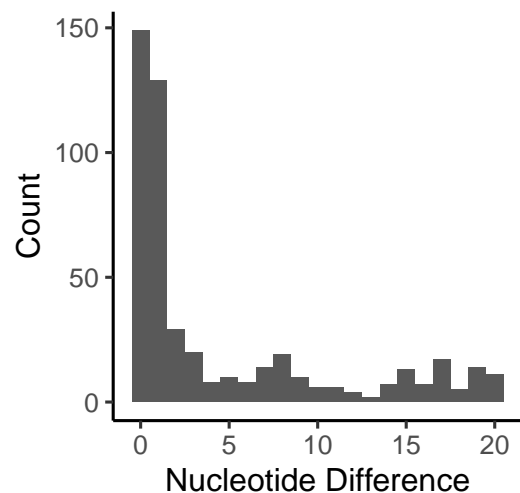
IGHV1-NL1*01

7 sequences assigned
No exact matches.



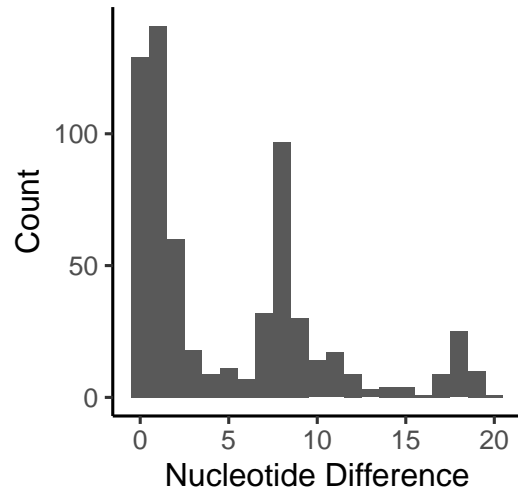
IGHV2-26*01

499 sequences assigned
149 (29.9%) exact matches, in which:
124 unique CDR3
6 unique J



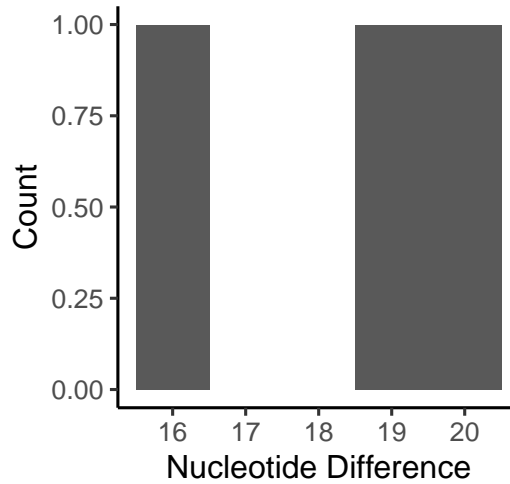
IGHV2-70*01

673 sequences assigned
129 (19.2%) exact matches, in which:
104 unique CDR3
5 unique J



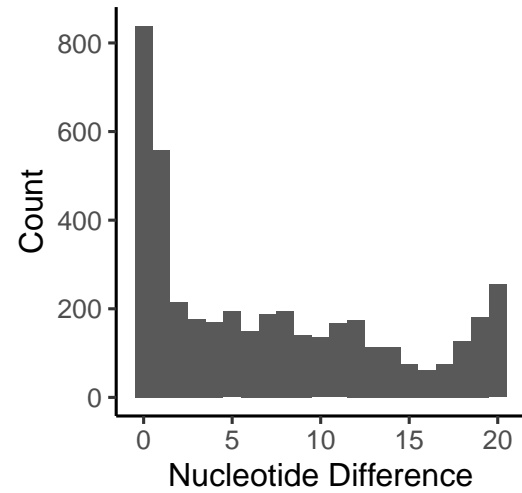
IGHV2-70D*04

5 sequences assigned
No exact matches.



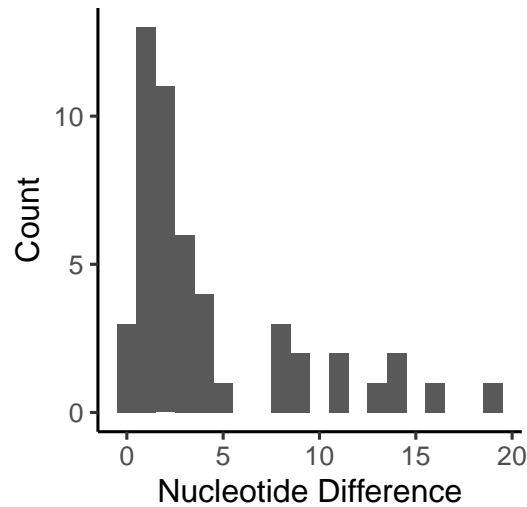
IGHV3-9*01

5584 sequences assigned
839 (15%) exact matches, in which:
493 unique CDR3
6 unique J



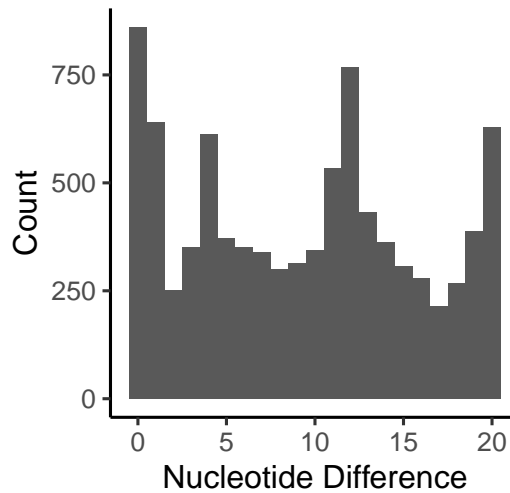
IGHV2-70*12

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



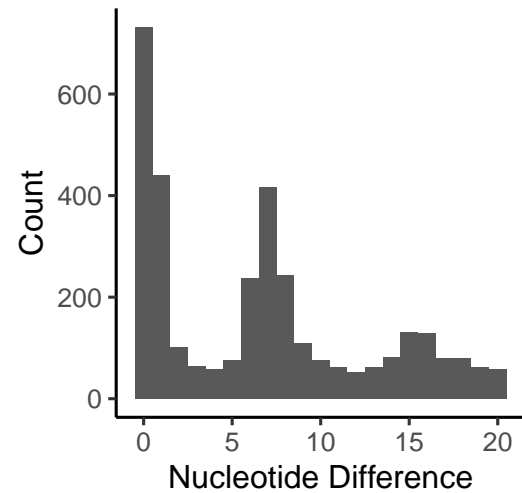
IGHV3-7*01

11598 sequences assigned
861 (7.4%) exact matches, in which:
612 unique CDR3
6 unique J



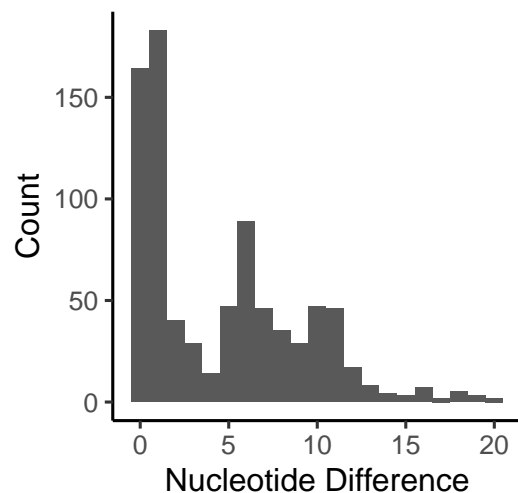
IGHV3-11*01

4089 sequences assigned
732 (17.9%) exact matches, in which:
489 unique CDR3
6 unique J



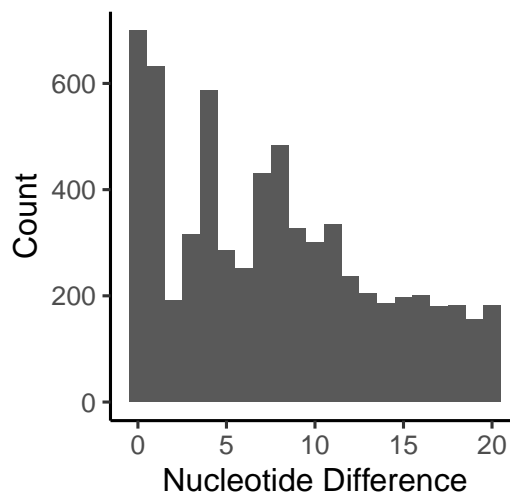
IGHV2-70*11_15

860 sequences assigned
164 (19.1%) exact matches, in which:
132 unique CDR3
6 unique J



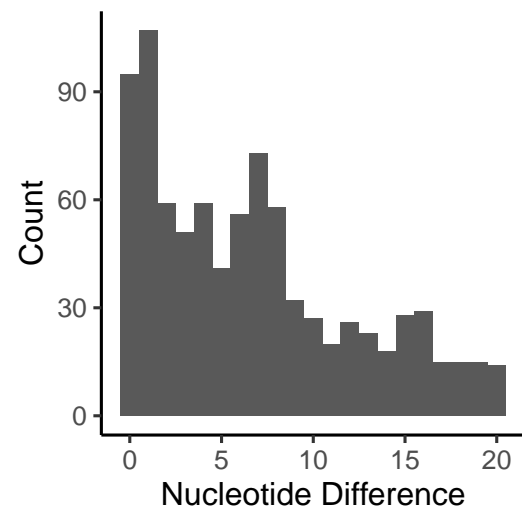
IGHV3-7*03

8129 sequences assigned
700 (8.6%) exact matches, in which:
469 unique CDR3
6 unique J



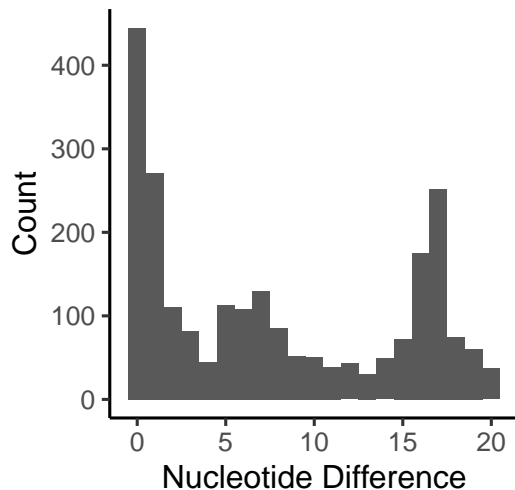
IGHV3-11*04

954 sequences assigned
95 (10%) exact matches, in which:
92 unique CDR3
6 unique J



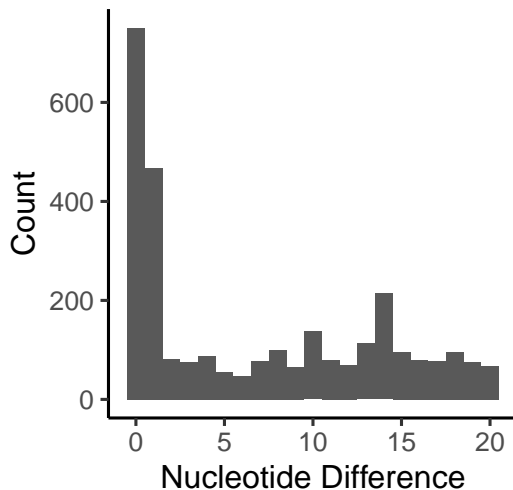
IGHV3-11*06

2887 sequences assigned
445 (15.4%) exact matches, in which:
314 unique CDR3
6 unique J



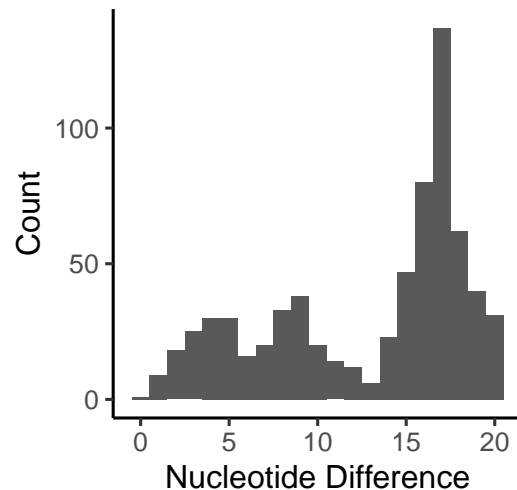
IGHV3-15*01_02

3342 sequences assigned
751 (22.5%) exact matches, in which:
466 unique CDR3
6 unique J



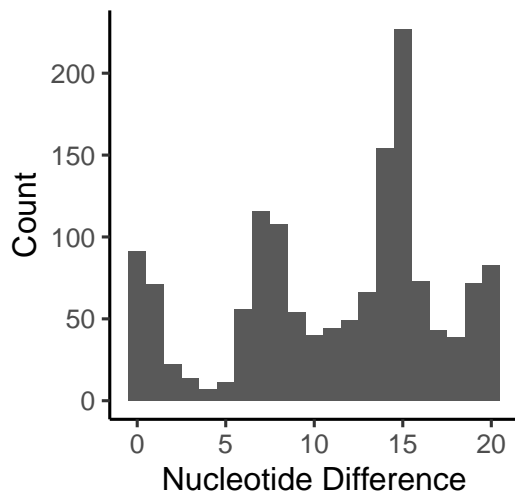
IGHV3-20*03_04

797 sequences assigned
1 (0.1%) exact matches, in which:
1 unique CDR3
1 unique J



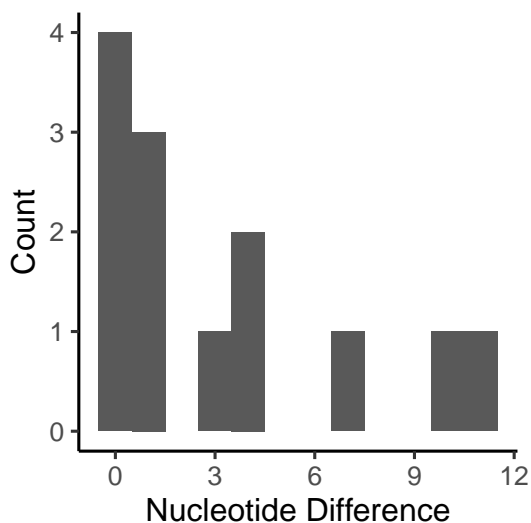
IGHV3-13*01

1843 sequences assigned
91 (4.9%) exact matches, in which:
58 unique CDR3
5 unique J



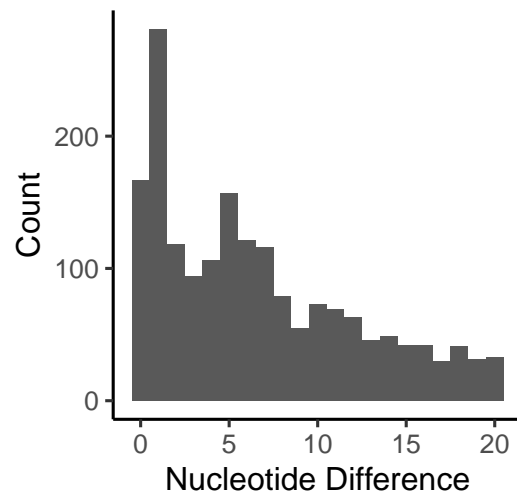
IGHV3-19*01

13 sequences assigned
4 (30.8%) exact matches, in which:
4 unique CDR3
2 unique J



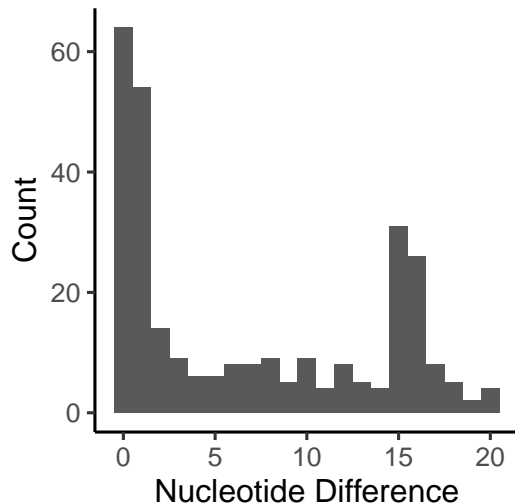
IGHV3-21*04

2126 sequences assigned
167 (7.9%) exact matches, in which:
155 unique CDR3
6 unique J



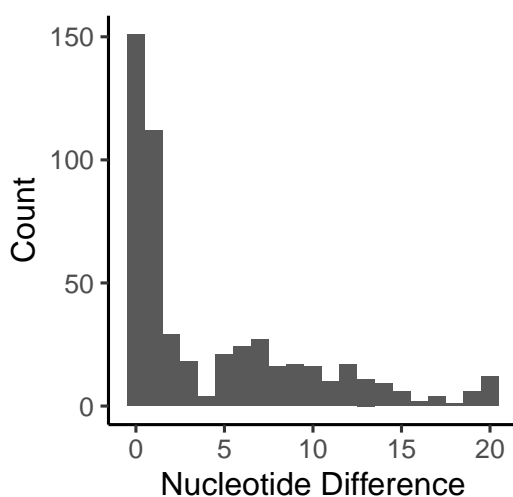
IGHV3-13*05

303 sequences assigned
64 (21.1%) exact matches, in which:
42 unique CDR3
5 unique J



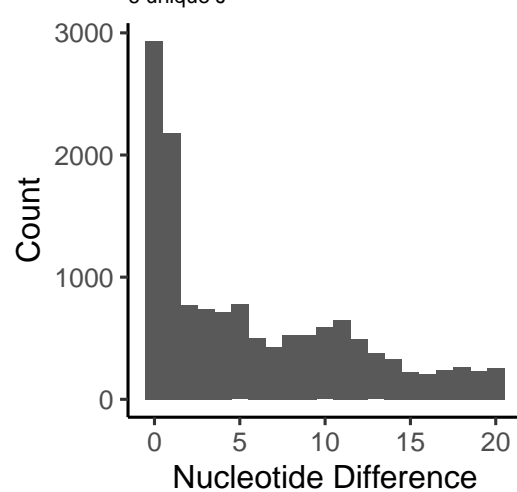
IGHV3-20*01_02

528 sequences assigned
151 (28.6%) exact matches, in which:
87 unique CDR3
5 unique J



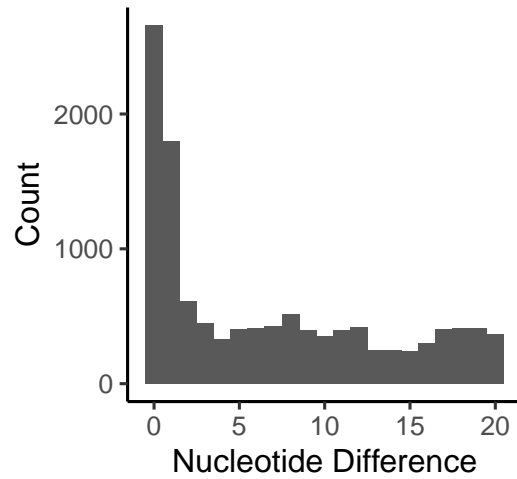
IGHV3-21*01_02

17660 sequences assigned
2933 (16.6%) exact matches, in which:
1833 unique CDR3
6 unique J



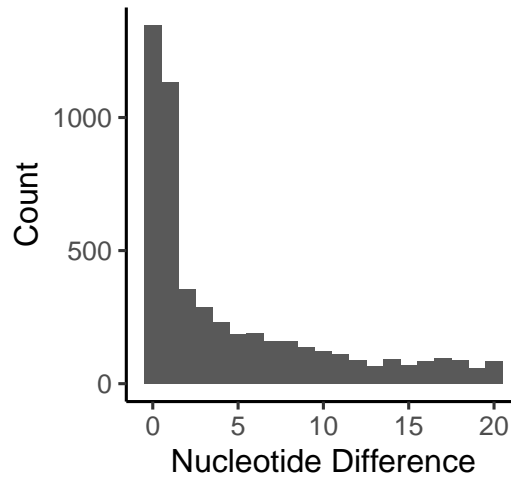
IGHV3-30-3*01

14801 sequences assigned
2657 (18%) exact matches, in which:
1695 unique CDR3
6 unique J



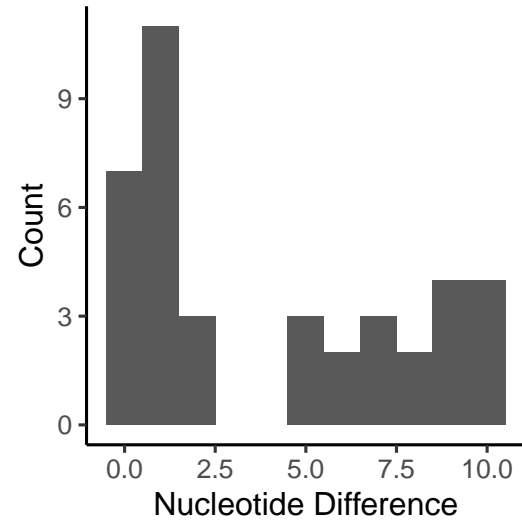
IGHV3-33*01

5929 sequences assigned
1346 (22.7%) exact matches, in which:
889 unique CDR3
6 unique J



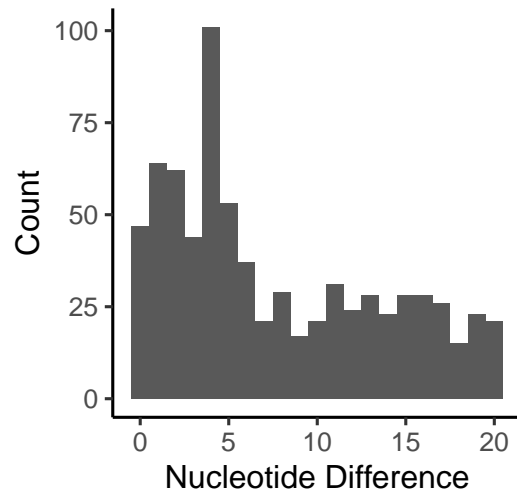
IGHV3-35*01

39 sequences assigned
7 (17.9%) exact matches, in which:
4 unique CDR3
2 unique J



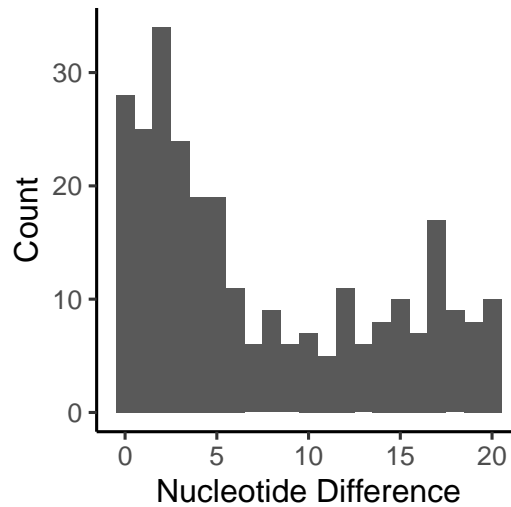
IGHV3-30-3*02

901 sequences assigned
47 (5.2%) exact matches, in which:
47 unique CDR3
5 unique J



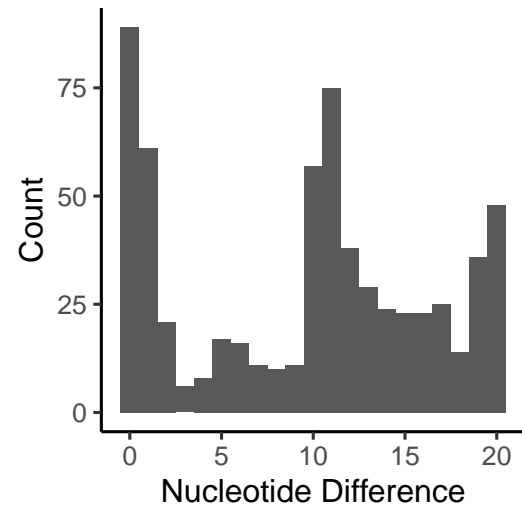
IGHV3-33*05

368 sequences assigned
28 (7.6%) exact matches, in which:
26 unique CDR3
5 unique J



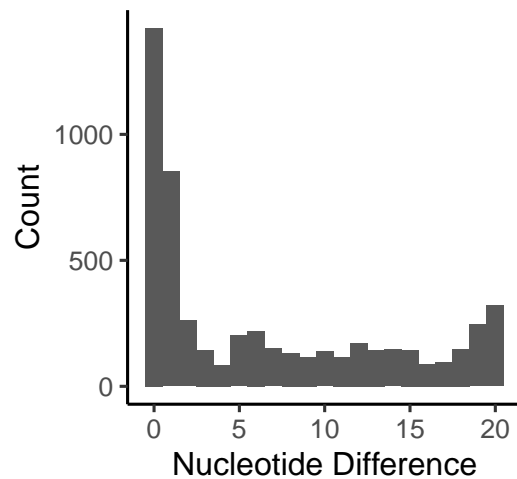
IGHV3-43*01

1002 sequences assigned
89 (8.9%) exact matches, in which:
52 unique CDR3
6 unique J



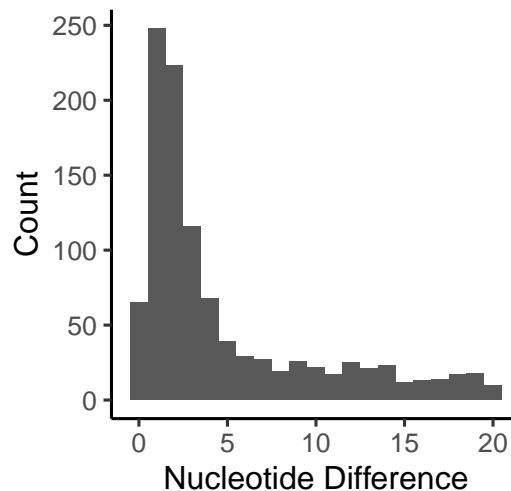
IGHV3-30*03

7106 sequences assigned
1422 (20%) exact matches, in which:
1006 unique CDR3
6 unique J



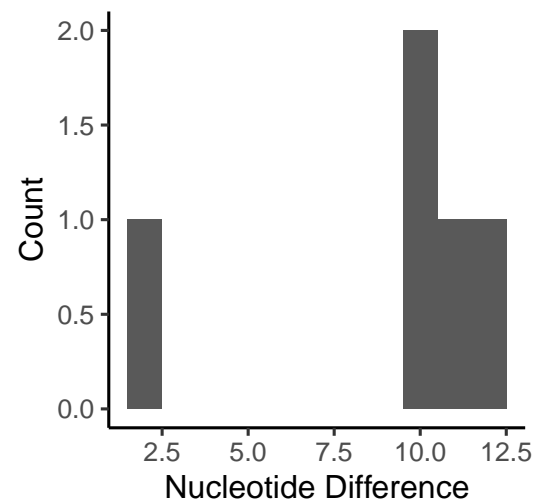
IGHV3-33*06

1139 sequences assigned
65 (5.7%) exact matches, in which:
62 unique CDR3
6 unique J



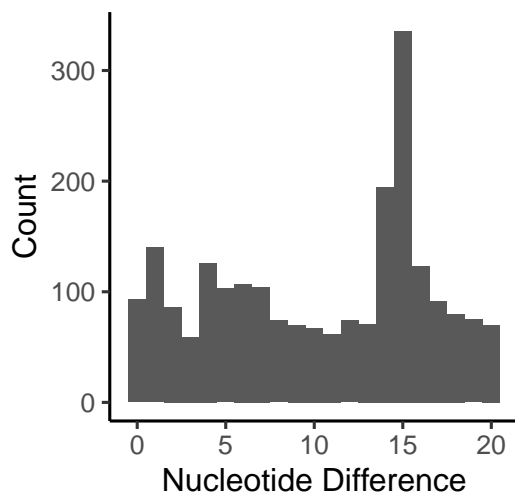
IGHV3-47*02

5 sequences assigned
No exact matches.



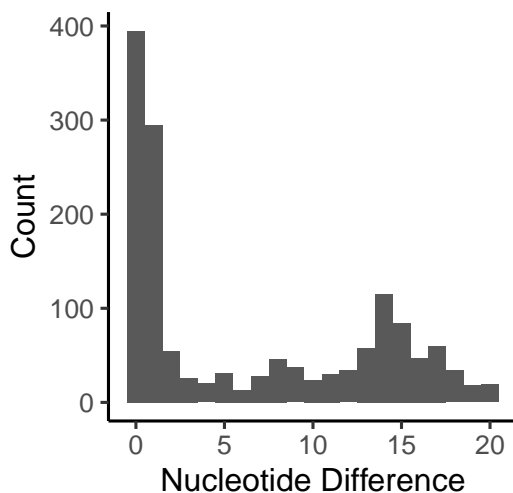
IGHV3-48*01

2411 sequences assigned
93 (3.9%) exact matches, in which:
89 unique CDR3
6 unique J



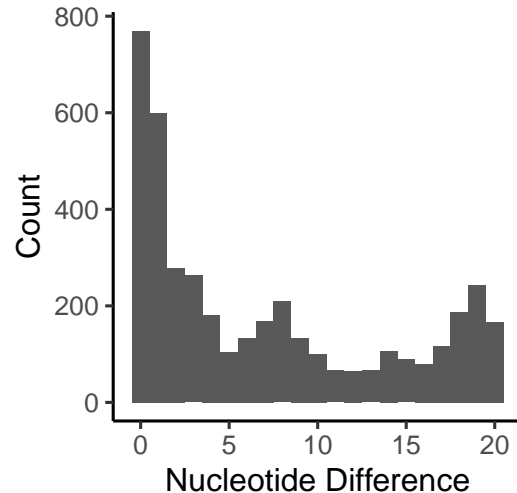
IGHV3-49*03_05

1538 sequences assigned
395 (25.7%) exact matches, in which:
231 unique CDR3
6 unique J



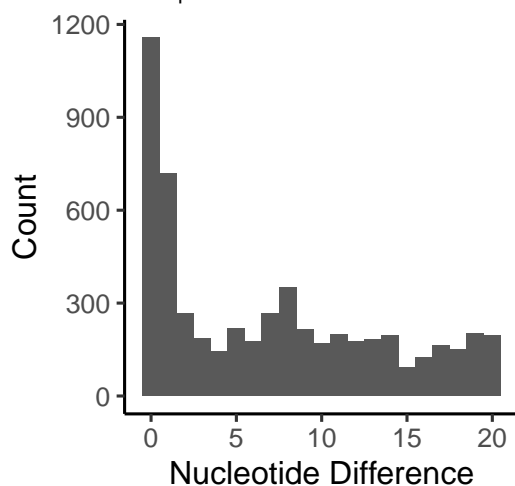
IGHV3-53*01_02

5664 sequences assigned
770 (13.6%) exact matches, in which:
469 unique CDR3
6 unique J



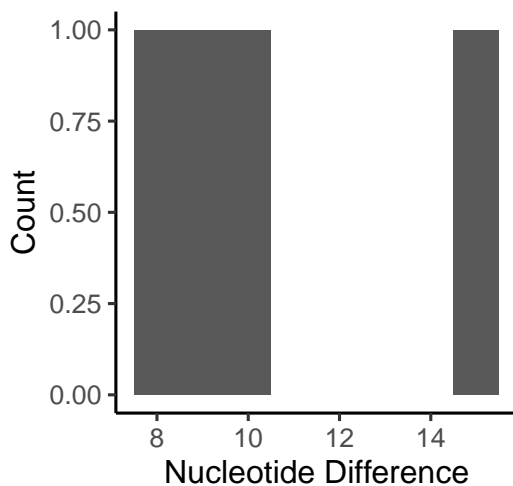
IGHV3-48*02

6206 sequences assigned
1157 (18.6%) exact matches, in which:
702 unique CDR3
6 unique J



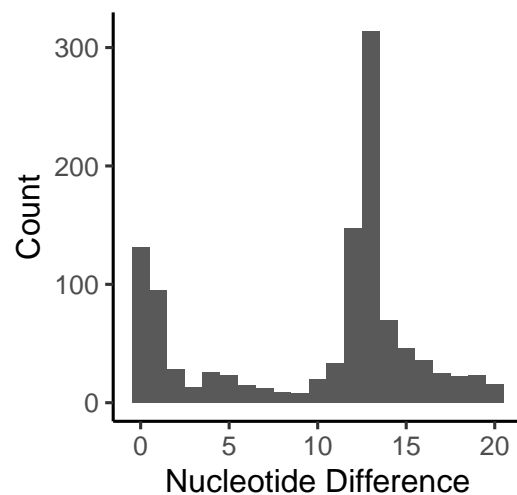
IGHV3-52*01_03

4 sequences assigned
No exact matches.



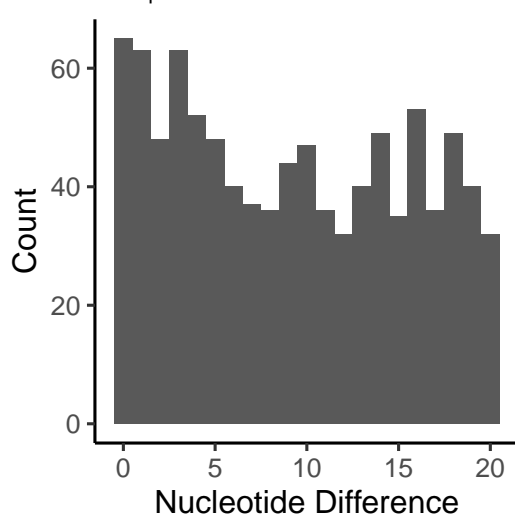
IGHV3-64*01

1185 sequences assigned
131 (11.1%) exact matches, in which:
80 unique CDR3
5 unique J



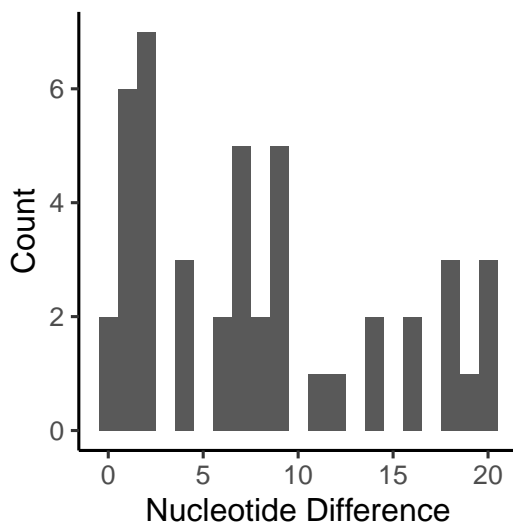
IGHV3-48*04

1382 sequences assigned
65 (4.7%) exact matches, in which:
63 unique CDR3
6 unique J



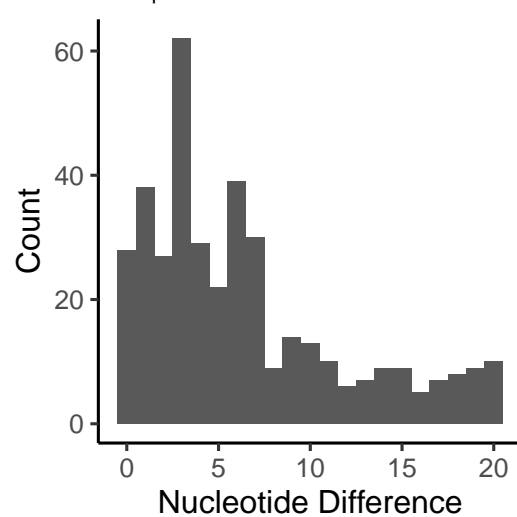
IGHV3-53*05

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



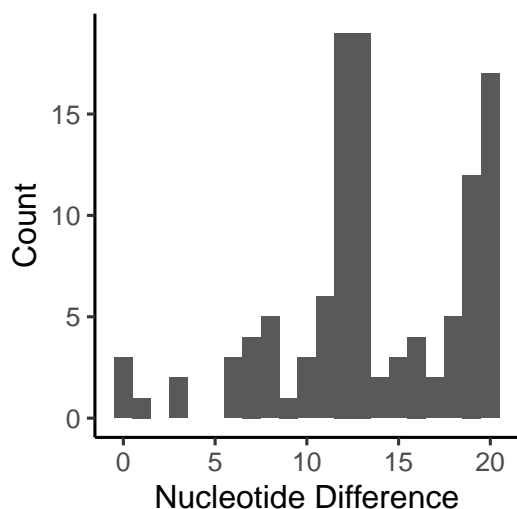
IGHV3-64*04

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



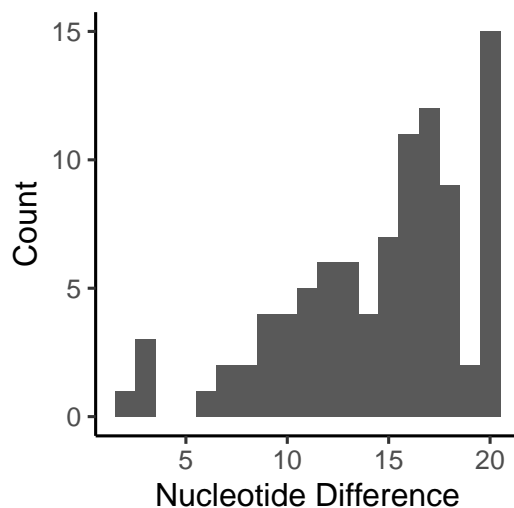
IGHV3-64*02_07

669 sequences assigned
3 (0.4%) exact matches, in which:
2 unique CDR3
1 unique J



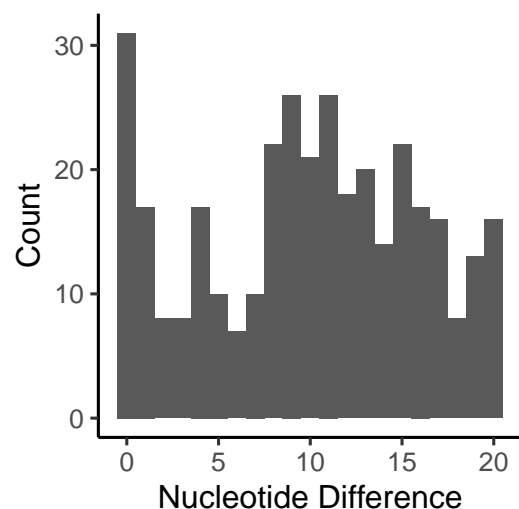
IGHV3-69-1*01

244 sequences assigned
No exact matches.



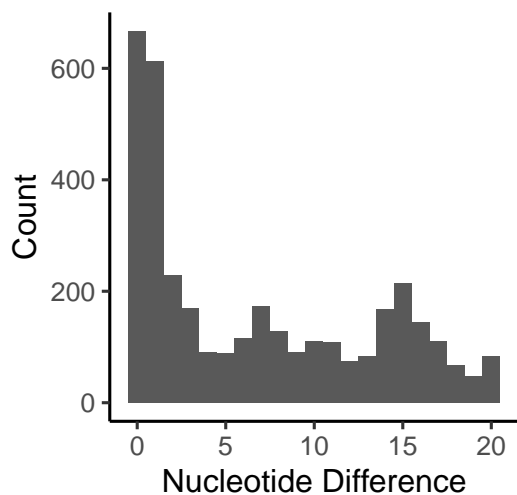
IGHV3-72*01

475 sequences assigned
31 (6.5%) exact matches, in which:
20 unique CDR3
4 unique J



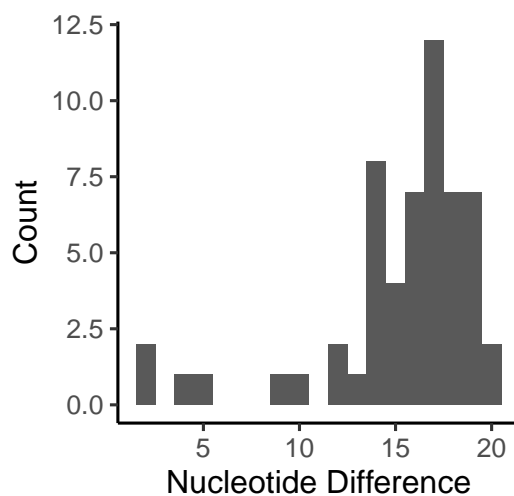
IGHV3-66*01

4491 sequences assigned
667 (14.9%) exact matches, in which:
444 unique CDR3
6 unique J



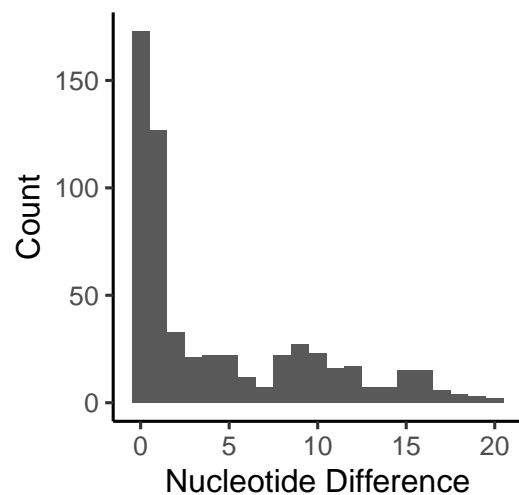
IGHV3-69-1*02

70 sequences assigned
No exact matches.



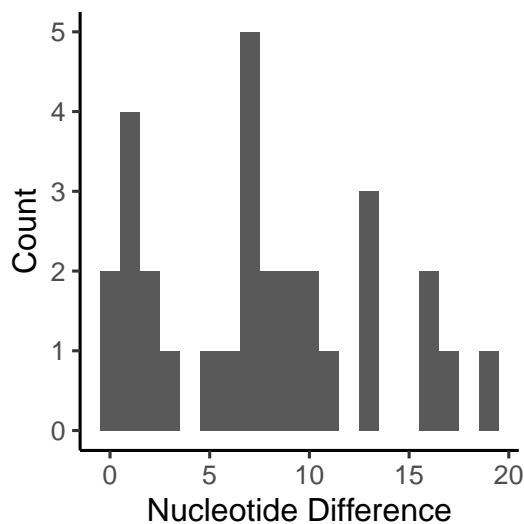
IGHV3-73*01_02

600 sequences assigned
173 (28.8%) exact matches, in which:
106 unique CDR3
5 unique J



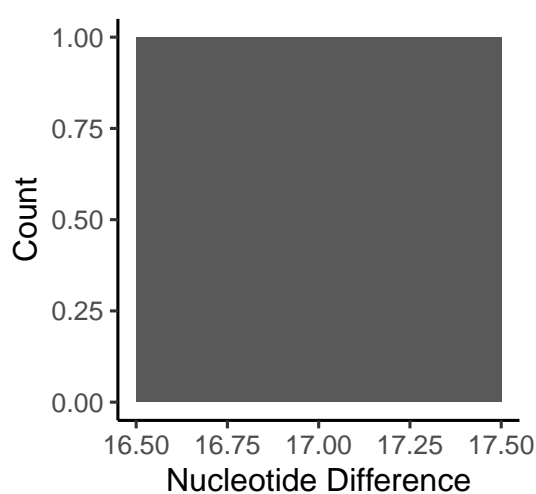
IGHV3-66*03

35 sequences assigned
2 (5.7%) exact matches, in which:
2 unique CDR3
1 unique J



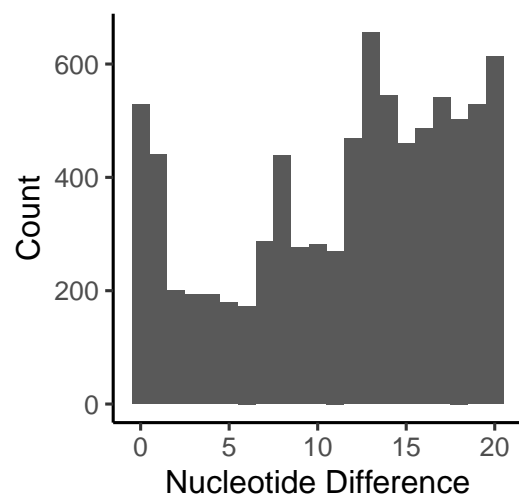
IGHV3-71*01_04

2 sequences assigned
No exact matches.



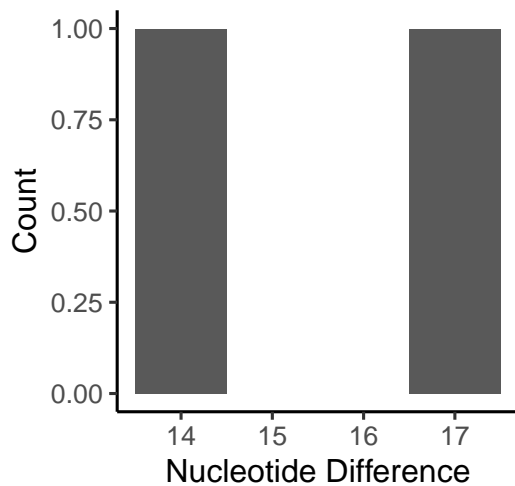
IGHV3-74*01_02

12247 sequences assigned
529 (4.3%) exact matches, in which:
353 unique CDR3
6 unique J



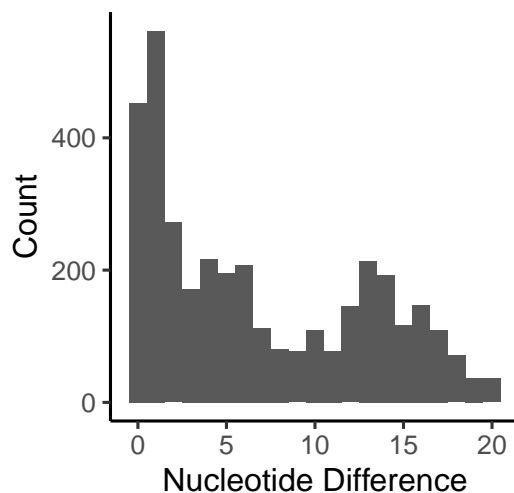
IGHV3-43D*04

3 sequences assigned
No exact matches.



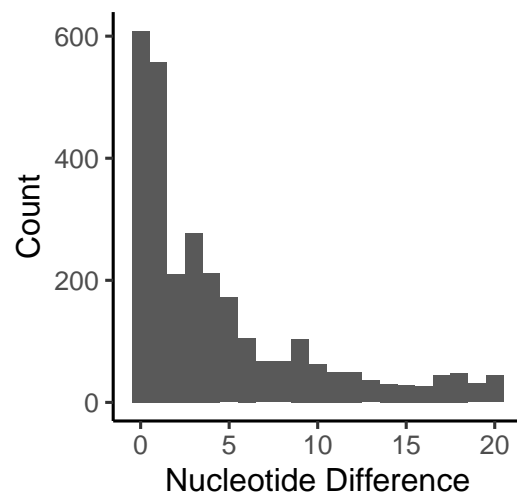
IGHV4-4*07

4608 sequences assigned
453 (9.8%) exact matches, in which:
378 unique CDR3
6 unique J



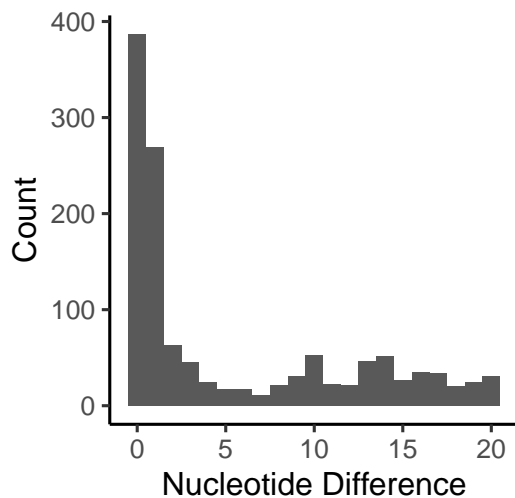
IGHV4-30-4*01

3453 sequences assigned
609 (17.6%) exact matches, in which:
508 unique CDR3
6 unique J



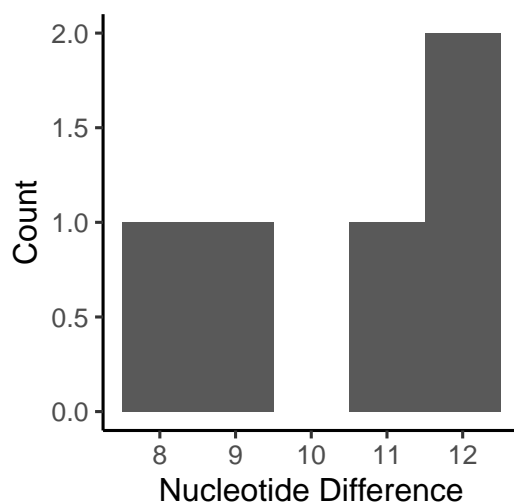
IGHV3-64D*09

2182 sequences assigned
387 (17.7%) exact matches, in which:
229 unique CDR3
6 unique J



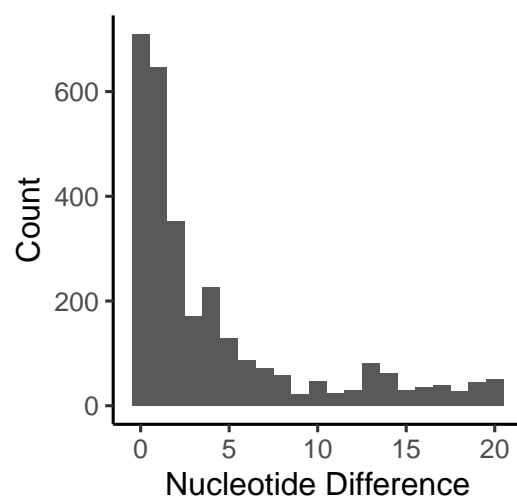
IGHV4-28*03

6 sequences assigned
No exact matches.



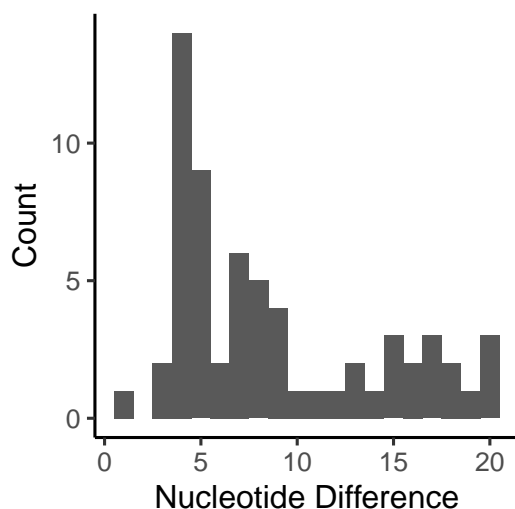
IGHV4-30-2*01

3116 sequences assigned
710 (22.8%) exact matches, in which:
551 unique CDR3
6 unique J



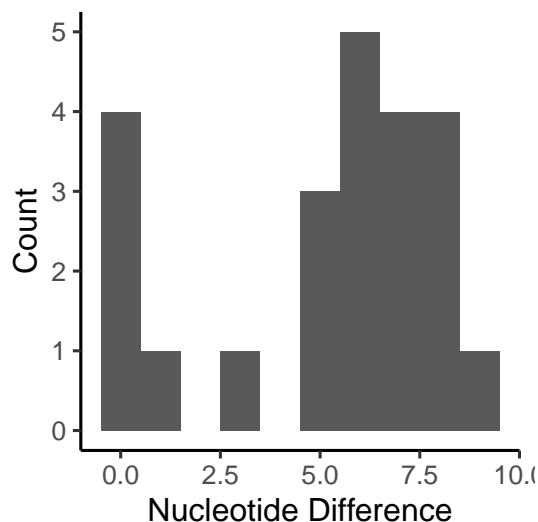
IGHV3-NL1*01

138 sequences assigned
No exact matches.



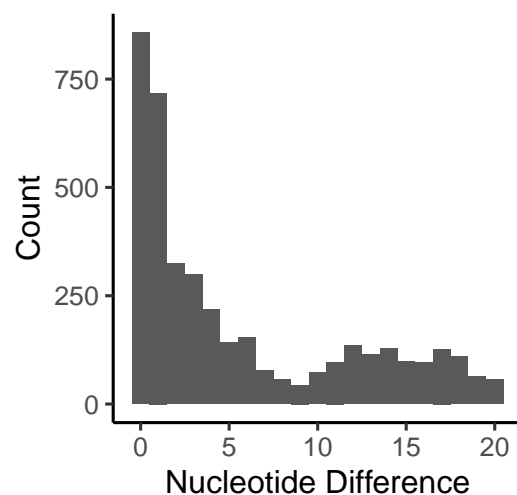
IGHV4-28*01_07

24 sequences assigned
4 (16.7%) exact matches, in which:
3 unique CDR3
1 unique J



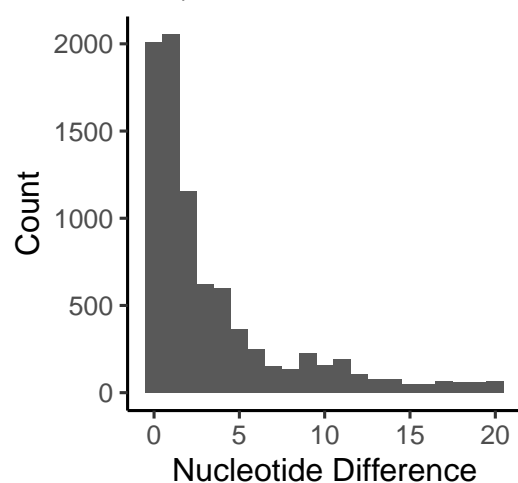
IGHV4-31*03_04

4850 sequences assigned
858 (17.7%) exact matches, in which:
723 unique CDR3
6 unique J



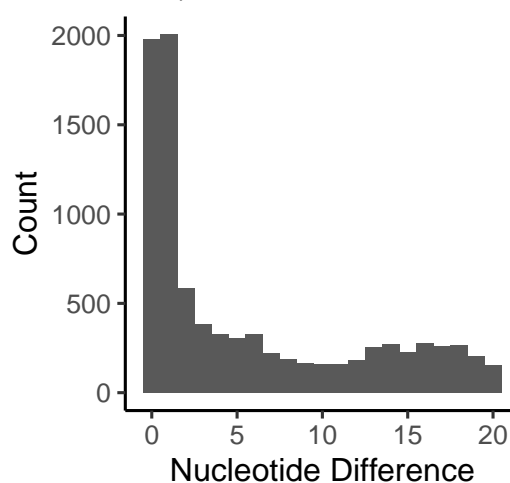
IGHV4-34*01_02

9553 sequences assigned
2007 (21%) exact matches, in which:
1601 unique CDR3
6 unique J



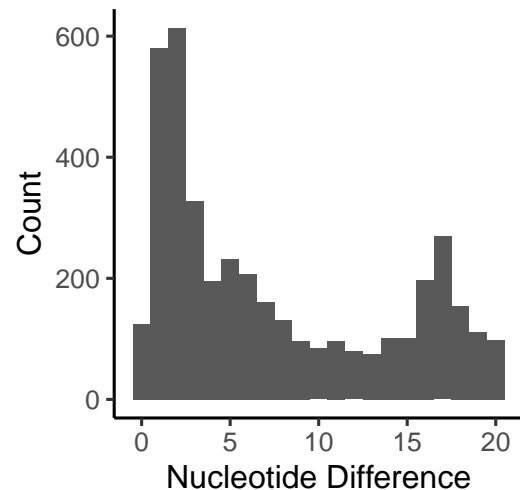
IGHV4-39*01_05

10158 sequences assigned
1978 (19.5%) exact matches, in which:
1564 unique CDR3
6 unique J



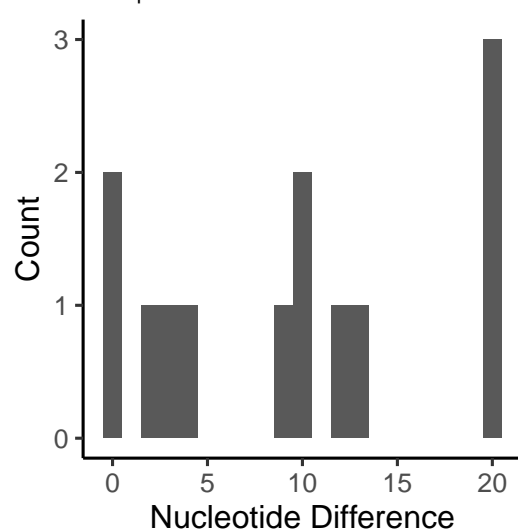
IGHV4-59*12

5210 sequences assigned
125 (2.4%) exact matches, in which:
122 unique CDR3
5 unique J



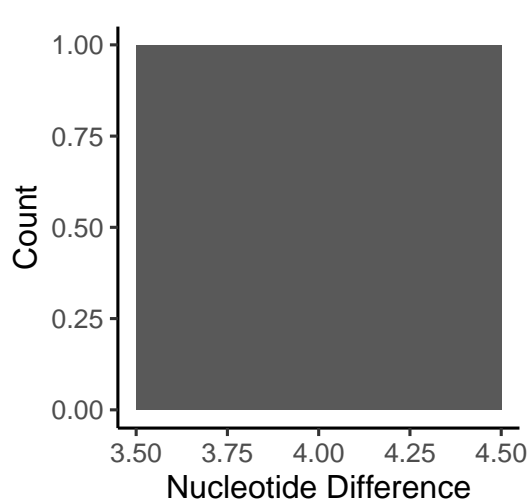
IGHV4-38-2*02

23 sequences assigned
2 (8.7%) exact matches, in which:
2 unique CDR3
2 unique J



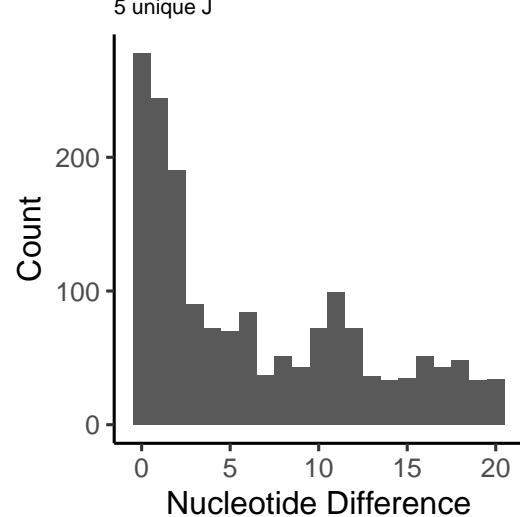
IGHV4-55*01_05

1 sequences assigned
No exact matches.



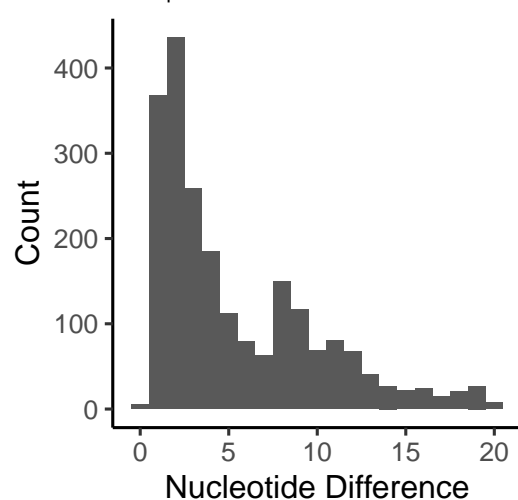
IGHV4-61*01

2021 sequences assigned
278 (13.8%) exact matches, in which:
259 unique CDR3
5 unique J



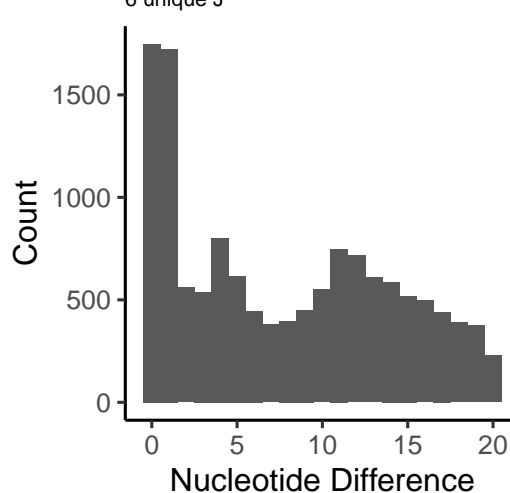
IGHV4-39*07

2247 sequences assigned
5 (0.2%) exact matches, in which:
5 unique CDR3
4 unique J



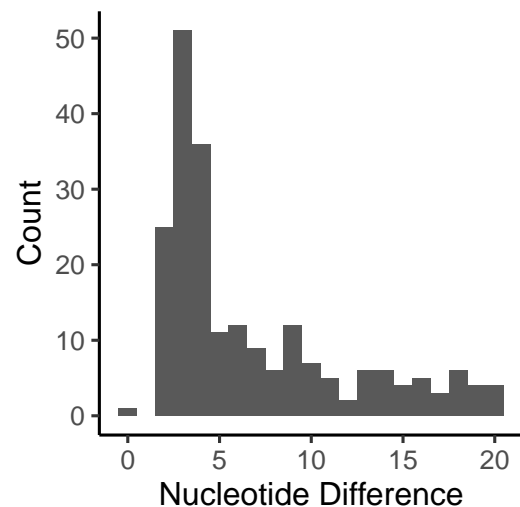
IGHV4-59*01_07

14998 sequences assigned
1748 (11.7%) exact matches, in which:
1461 unique CDR3
6 unique J



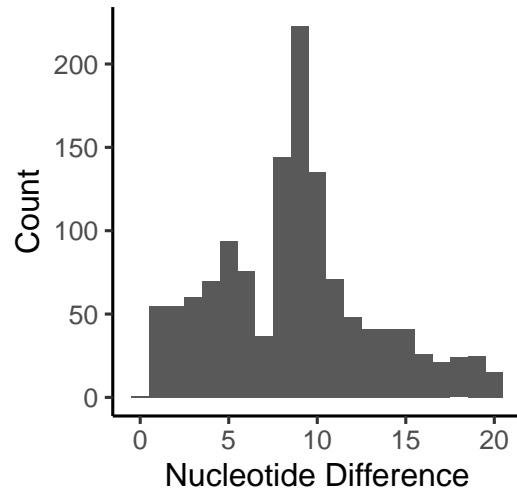
IGHV4-61*05

223 sequences assigned
1 (0.4%) exact matches, in which:
1 unique CDR3
1 unique J



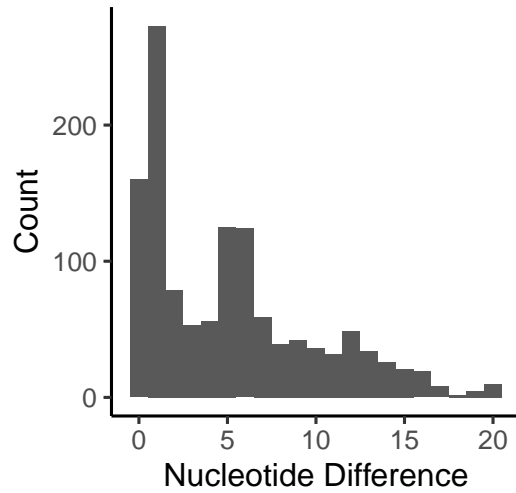
IGHV4–61*08

1463 sequences assigned
1 (0.1%) exact matches, in which:
1 unique CDR3
1 unique J



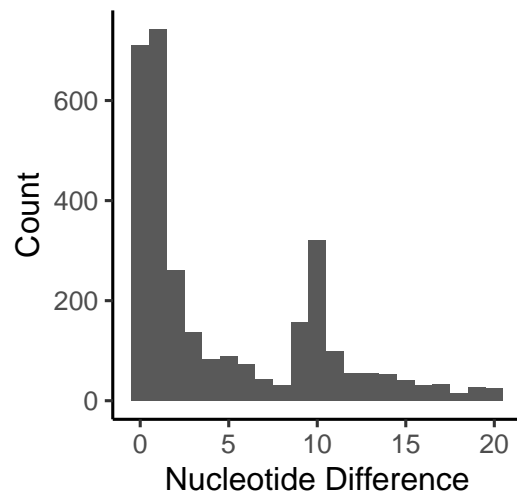
IGHV6–1*01_02

1309 sequences assigned
160 (12.2%) exact matches, in which:
142 unique CDR3
6 unique J



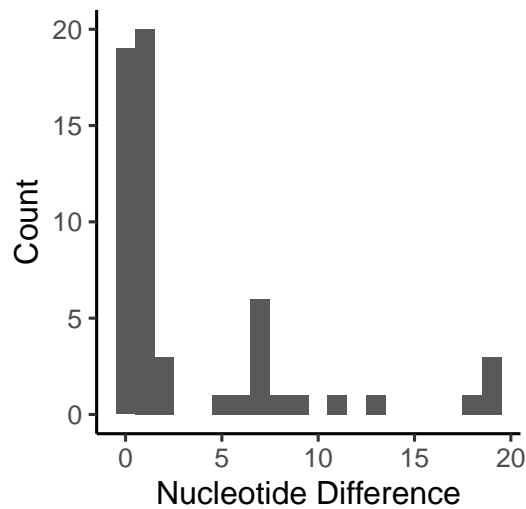
IGHV5–10–1*01_03

3169 sequences assigned
711 (22.4%) exact matches, in which:
450 unique CDR3
6 unique J



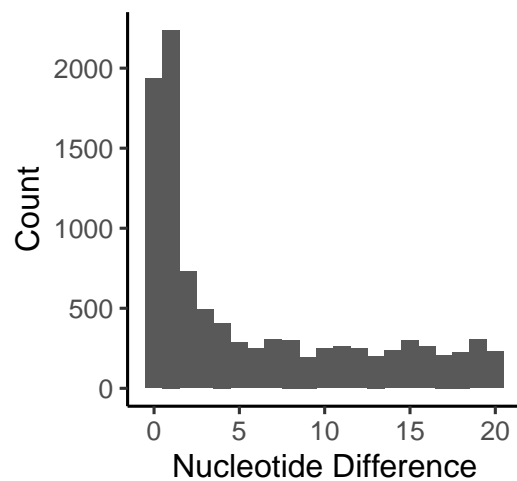
IGHV7–4–1*01

58 sequences assigned
19 (32.8%) exact matches, in which:
11 unique CDR3
4 unique J



IGHV5–51*01_03

11886 sequences assigned
1935 (16.3%) exact matches, in which:
1082 unique CDR3
6 unique J





Warning: IGHV4-31*02, IGHV4-31*03_04 have identical germline sequences.

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

Novel sequence(s) IGHV1-69*04_09_G112A 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.

Novel sequence(s) IGHV1-69*08_C191T IGHV3-30*03_T288C IGHV3-30-3*02_G75C IGHV4-59*02_G88A IGHV5-51*07_A128G are not listed in the genotype and will be ignored.

Novel sequence(s) IGHV4-59*02_G88A 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) IGHV4-4*02_03_C300T 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.

Warning – no inferred sequences found.

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

Novel sequence(s) IGHV1-69*08_C191T IGHV3-11*06_T300C IGHV3-30*03_T288C IGHV4-59*02_G88A IGHV5-51*07_A128G are not listed in the genotype and will be ignored.

Novel sequence(s) IGHV4-59*02_G88A 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.

Warning – no inferred sequences found.

Warning – no inferred sequences found.

Novel sequence(s) IGHV3-30*03_T288C IGHV3-30-3*01_T288C 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) IGHV3-48*04_A193T_C198T_A200C_C201T_T210A 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) IGHV5-51*07_A128G are not listed in the genotype and will be ignored.

Novel sequence(s) IGHV3-33*01_C288T IGHV5-51*07_A128G are not listed in the genotype and will be ignored.

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

Novel sequence(s) IGHV3-33*01_T105C_A173T_T192G_C288T are not listed in the genotype and will be ignored.

Novel sequence(s) IGHV3-30*04_T288C IGHV3-33*01_G75C IGHV4-30-2*03_T288C IGHV4-59*02_G88A are not listed in the genotype and will be ignored.

Novel sequence(s) IGHV3-11*06_T300C 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 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) IGHV5-51*07_A128G are not listed in the genotype and will be ignored.