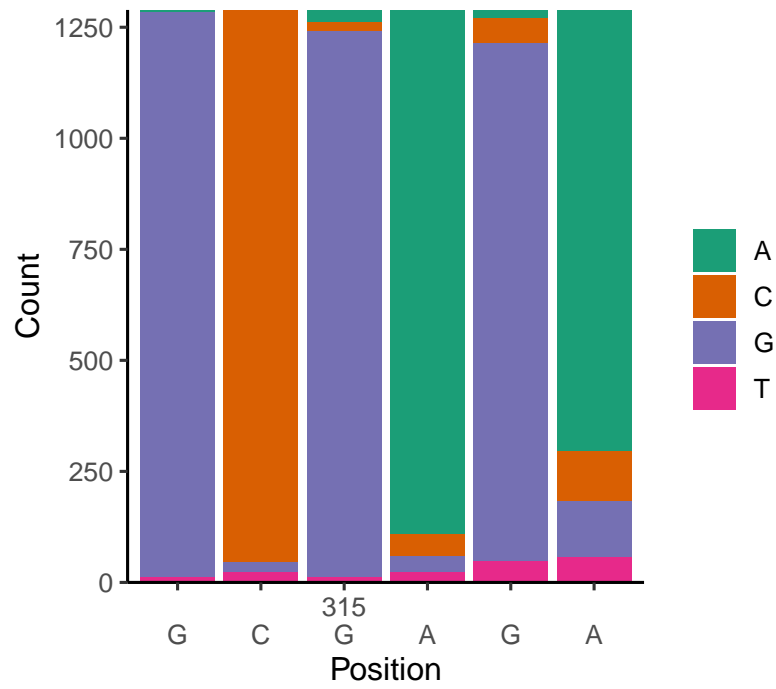


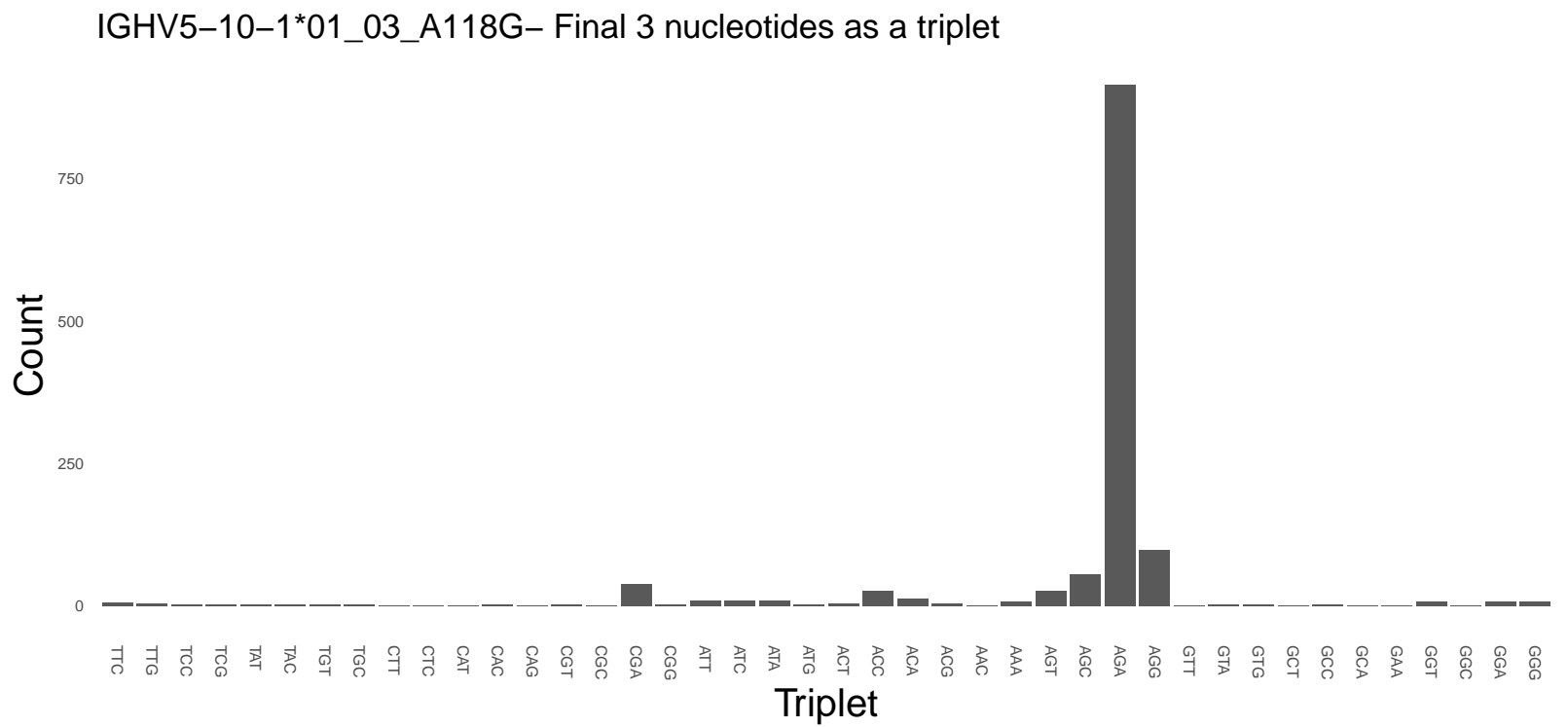
Gene IGHV5-10-1*01_03_A118G



Gene IGHV5-10-1*01_03_A118G

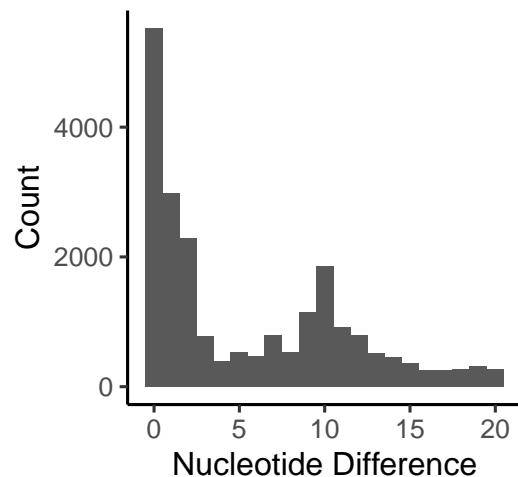


IGHV5-10-1*01_03_A118G- Final 3 nucleotides as a triplet



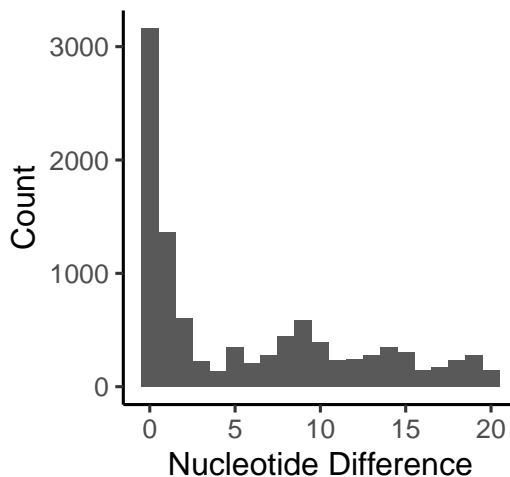
IGHV1-2*02

26092 sequences assigned
5522 (21.2%) exact matches, in which:
5143 unique CDR3
6 unique J



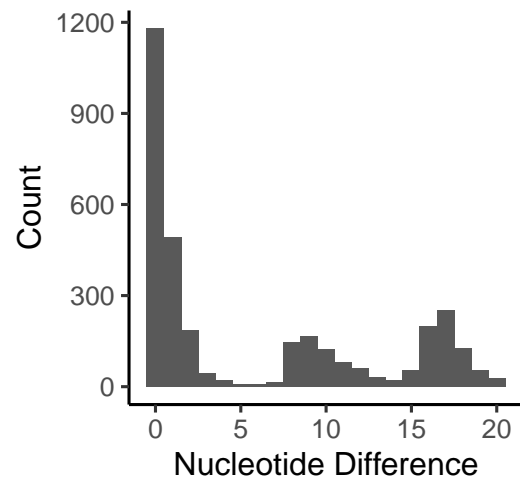
IGHV1-8*01

11662 sequences assigned
3161 (27.1%) exact matches, in which:
3028 unique CDR3
6 unique J



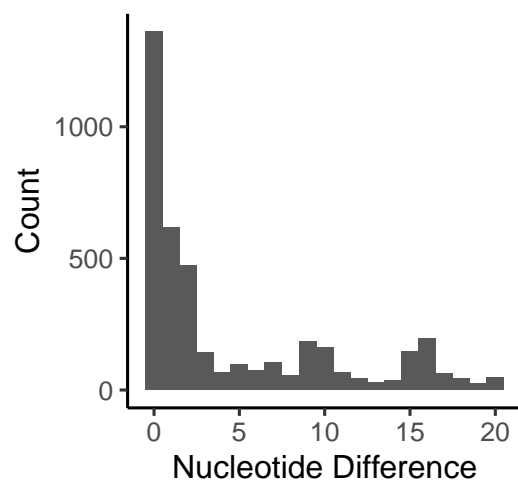
IGHV1-24*01

3572 sequences assigned
1180 (33%) exact matches, in which:
1132 unique CDR3
6 unique J



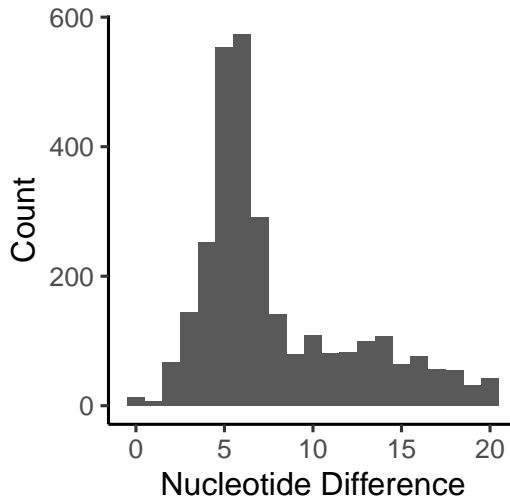
IGHV1-2*04

4468 sequences assigned
1361 (30.5%) exact matches, in which:
1301 unique CDR3
6 unique J



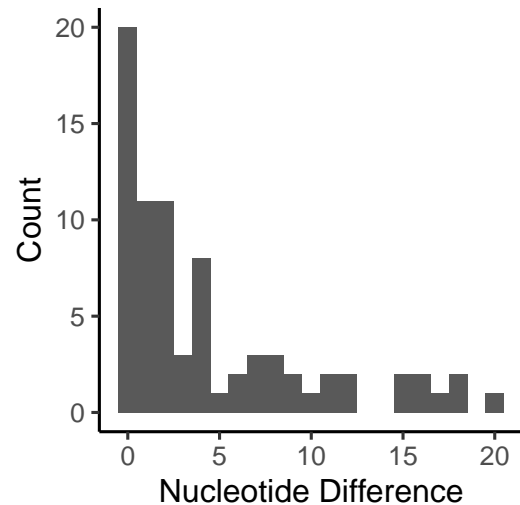
IGHV1-8*02

3387 sequences assigned
13 (0.4%) exact matches, in which:
13 unique CDR3
4 unique J



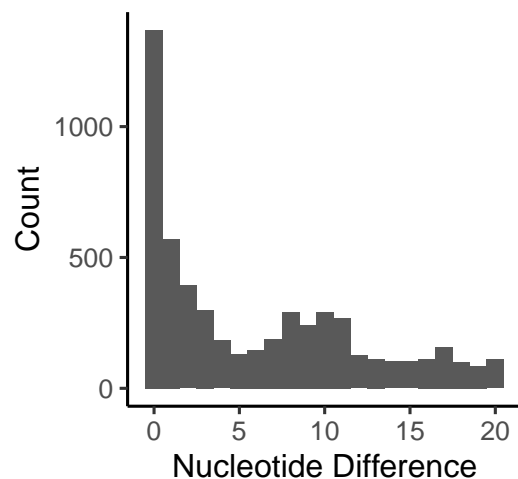
IGHV1-45*02

80 sequences assigned
20 (25%) exact matches, in which:
19 unique CDR3
4 unique J



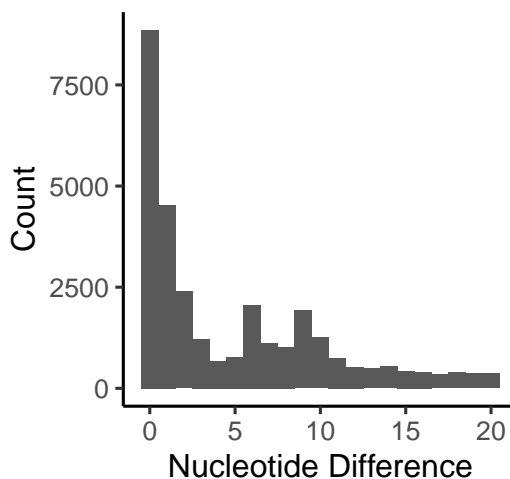
IGHV1-3*01_05

7197 sequences assigned
1369 (19%) exact matches, in which:
1293 unique CDR3
6 unique J



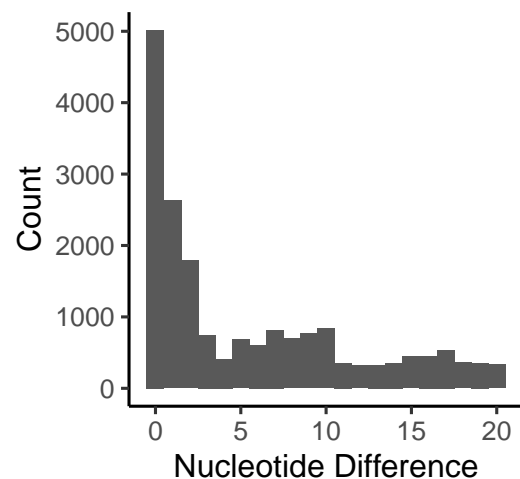
IGHV1-18*01

38401 sequences assigned
8857 (23.1%) exact matches, in which:
8257 unique CDR3
6 unique J



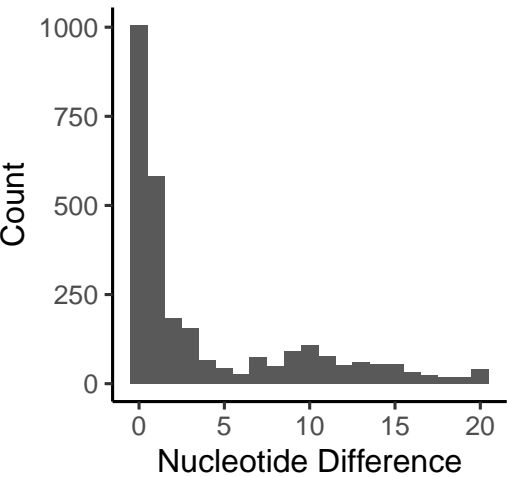
IGHV1-46*01

25881 sequences assigned
5017 (19.4%) exact matches, in which:
4743 unique CDR3
6 unique J



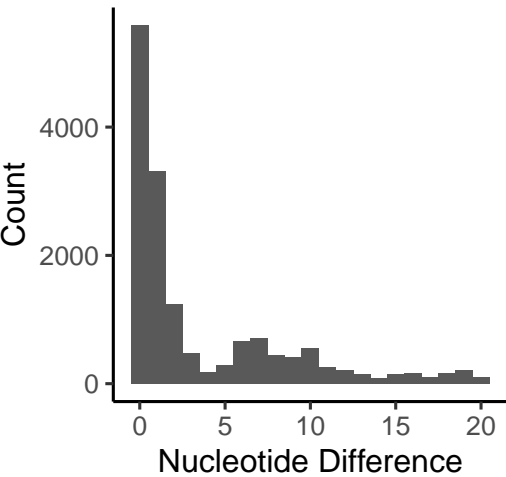
IGHV1-58*01_03

3410 sequences assigned
1005 (29.5%) exact matches, in which:
947 unique CDR3
6 unique J



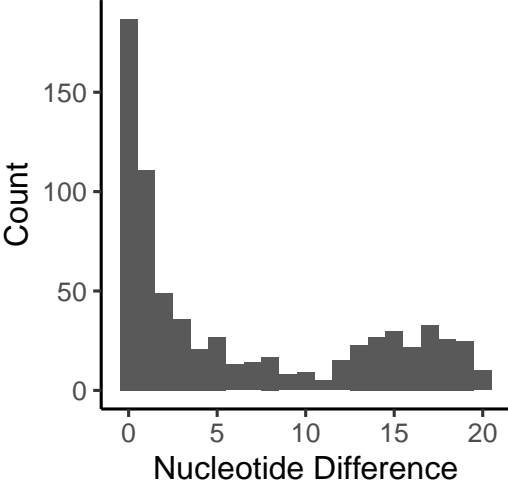
IGHV1-69*04_09

16201 sequences assigned
5585 (34.5%) exact matches, in which:
5334 unique CDR3
6 unique J



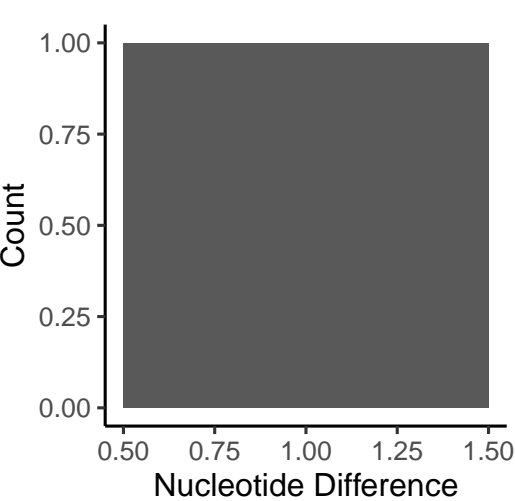
IGHV2-5*02

976 sequences assigned
187 (19.2%) exact matches, in which:
179 unique CDR3
6 unique J



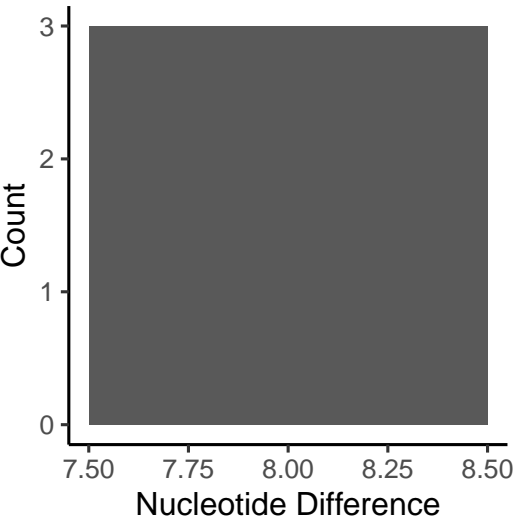
IGHV1-68*01

1 sequences assigned
No exact matches.



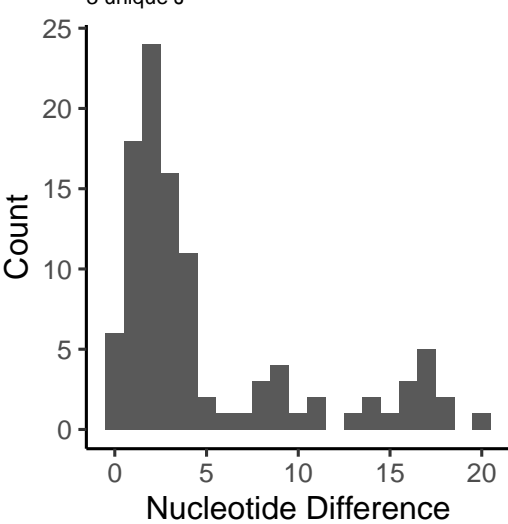
IGHV1-NL1*01

3 sequences assigned
No exact matches.



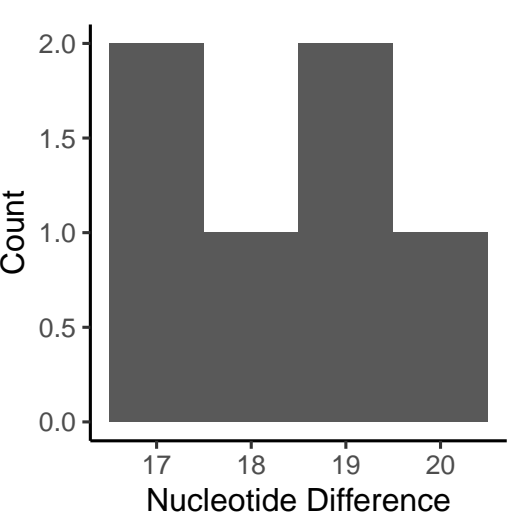
IGHV2-5*08

132 sequences assigned
6 (4.5%) exact matches, in which:
6 unique CDR3
3 unique J



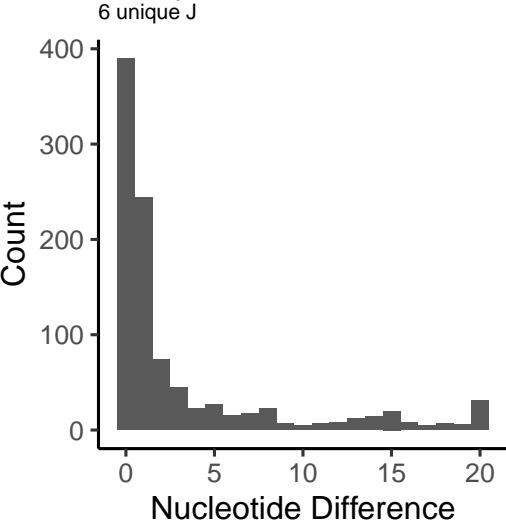
IGHV1-69-2*01

8 sequences assigned
No exact matches.



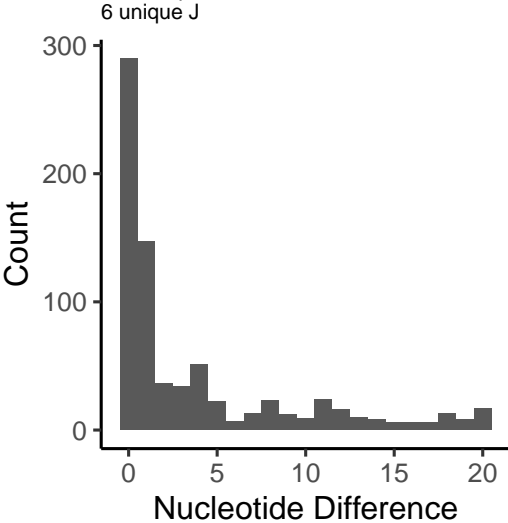
IGHV2-5*01

1142 sequences assigned
390 (34.2%) exact matches, in which:
366 unique CDR3
6 unique J



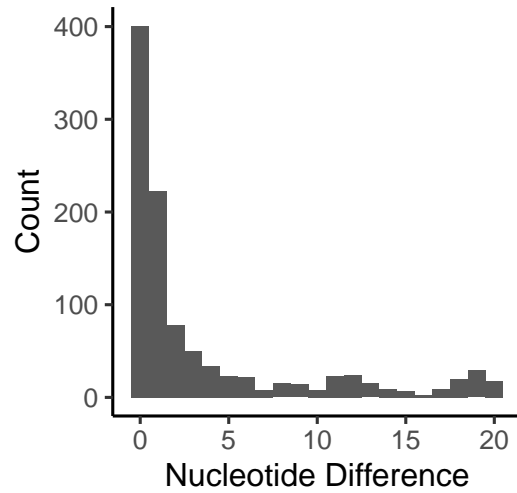
IGHV2-26*01

932 sequences assigned
290 (31.1%) exact matches, in which:
270 unique CDR3
6 unique J



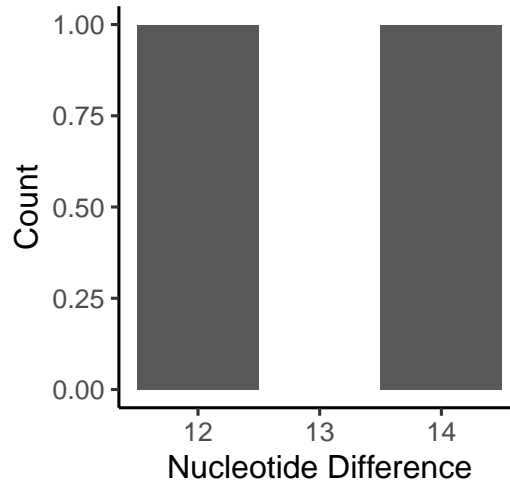
IGHV2-70*01

1259 sequences assigned
401 (31.9%) exact matches, in which:
376 unique CDR3
6 unique J



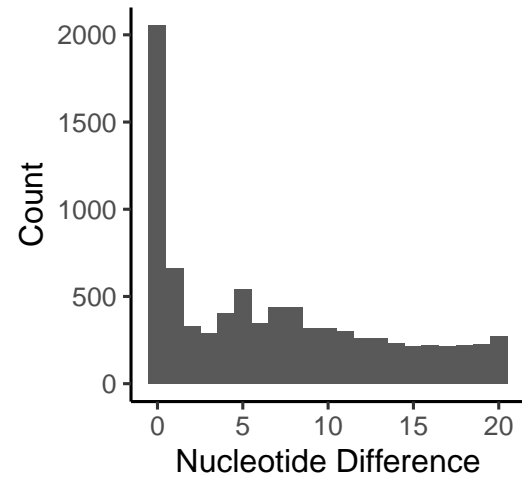
IGHV2-70D*14

3 sequences assigned
No exact matches.



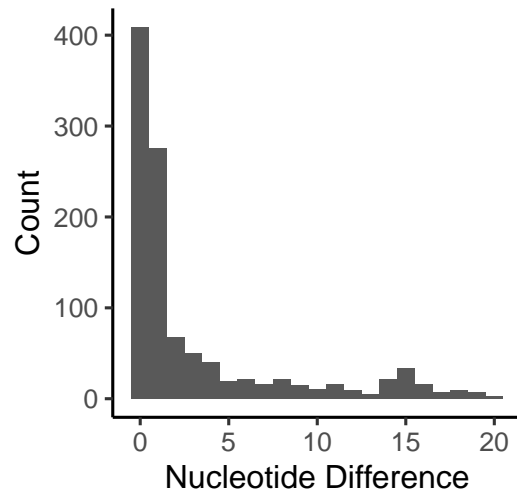
IGHV3-9*01

10929 sequences assigned
2054 (18.8%) exact matches, in which:
1615 unique CDR3
6 unique J



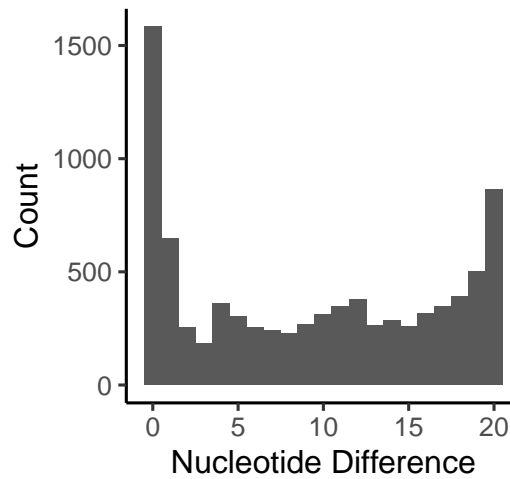
IGHV2-70*11_15

1160 sequences assigned
409 (35.3%) exact matches, in which:
380 unique CDR3
6 unique J



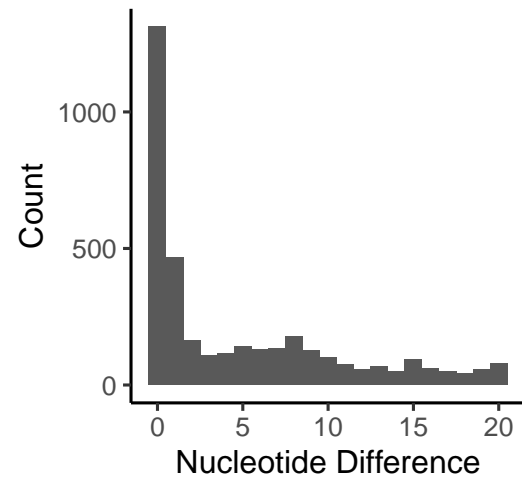
IGHV3-7*01

14916 sequences assigned
1583 (10.6%) exact matches, in which:
1362 unique CDR3
6 unique J



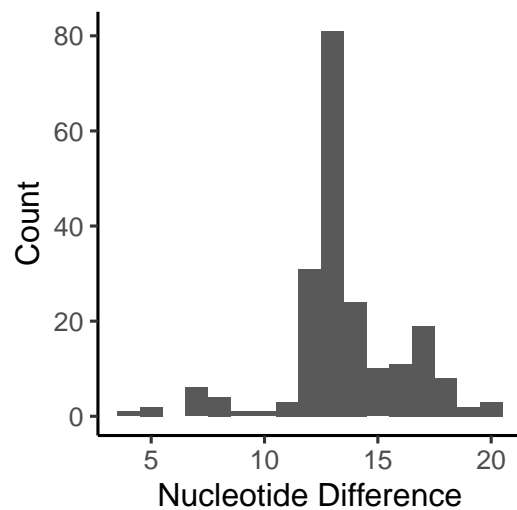
IGHV3-11*01

7412 sequences assigned
1312 (17.7%) exact matches, in which:
1113 unique CDR3
6 unique J



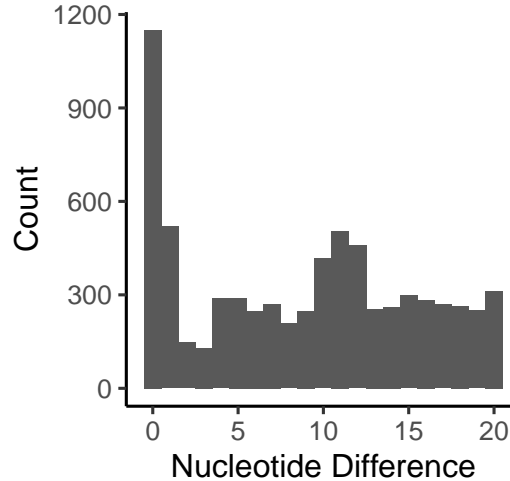
IGHV2-70D*04

223 sequences assigned
No exact matches.



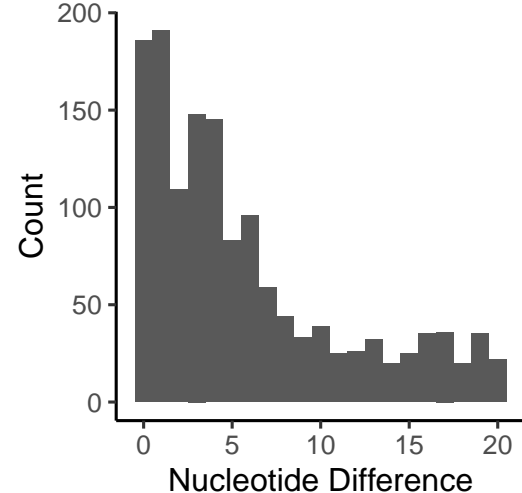
IGHV3-7*03

10925 sequences assigned
1150 (10.5%) exact matches, in which:
975 unique CDR3
6 unique J



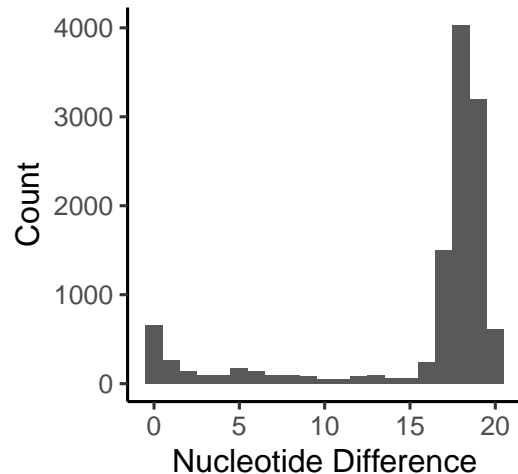
IGHV3-11*04

1878 sequences assigned
186 (9.9%) exact matches, in which:
181 unique CDR3
6 unique J



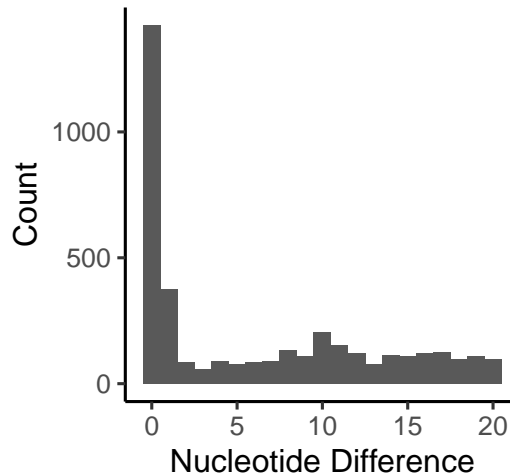
IGHV3-11*06

13479 sequences assigned
658 (4.9%) exact matches, in which:
573 unique CDR3
6 unique J



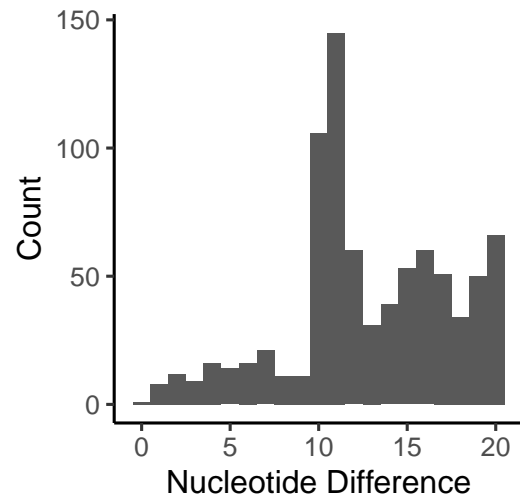
IGHV3-15*01_02

6638 sequences assigned
1423 (21.4%) exact matches, in which:
1182 unique CDR3
6 unique J



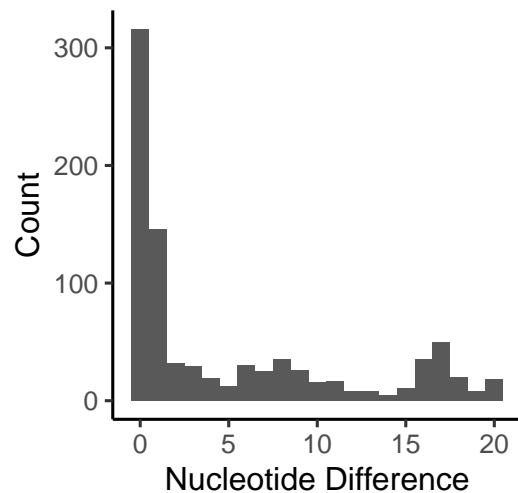
IGHV3-20*03_04

1319 sequences assigned
1 (0.1%) exact matches, in which:
1 unique CDR3
1 unique J



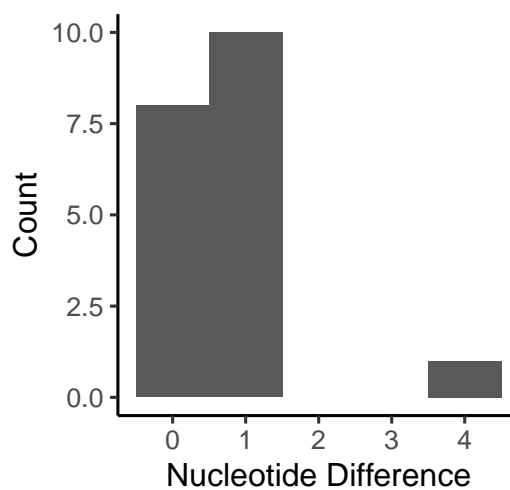
IGHV3-13*01

1209 sequences assigned
316 (26.1%) exact matches, in which:
254 unique CDR3
6 unique J



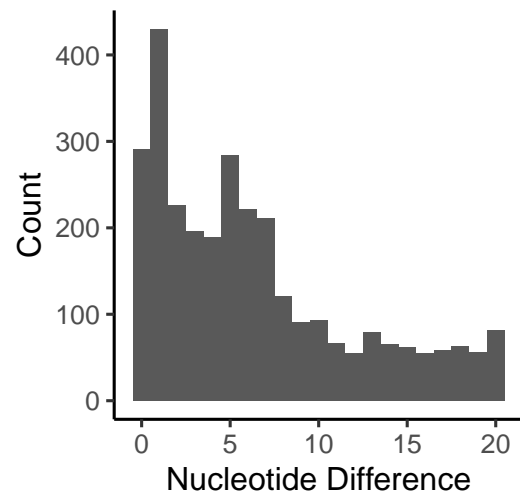
IGHV3-19*01

19 sequences assigned
8 (42.1%) exact matches, in which:
6 unique CDR3
1 unique J



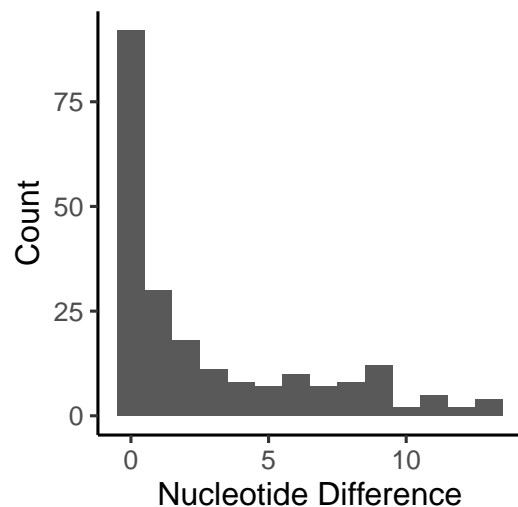
IGHV3-21*04

4124 sequences assigned
291 (7.1%) exact matches, in which:
288 unique CDR3
6 unique J



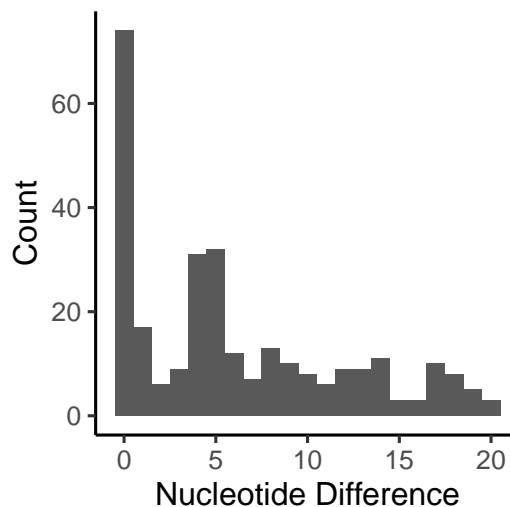
IGHV3-13*05

222 sequences assigned
92 (41.4%) exact matches, in which:
76 unique CDR3
6 unique J



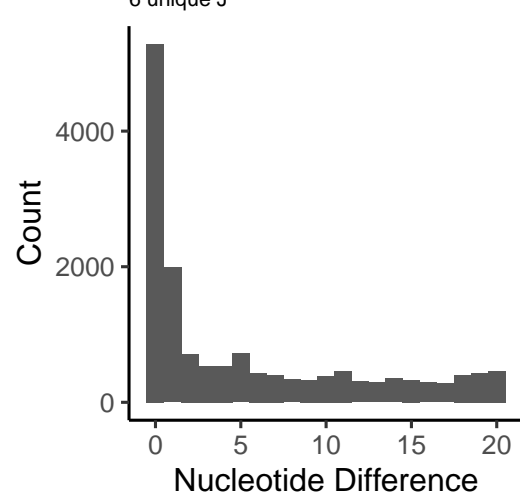
IGHV3-20*01_02

583 sequences assigned
74 (12.7%) exact matches, in which:
56 unique CDR3
6 unique J



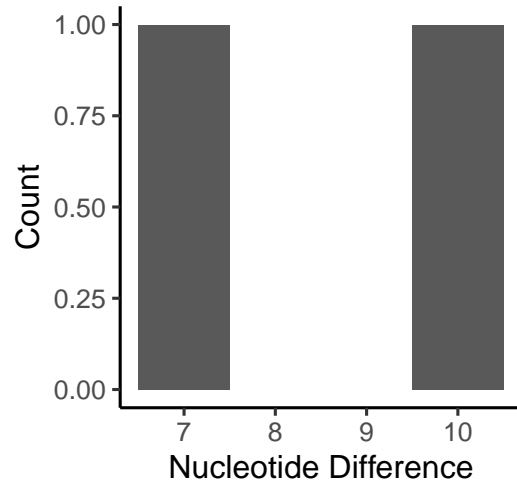
IGHV3-21*01_02

21224 sequences assigned
5284 (24.9%) exact matches, in which:
4285 unique CDR3
6 unique J



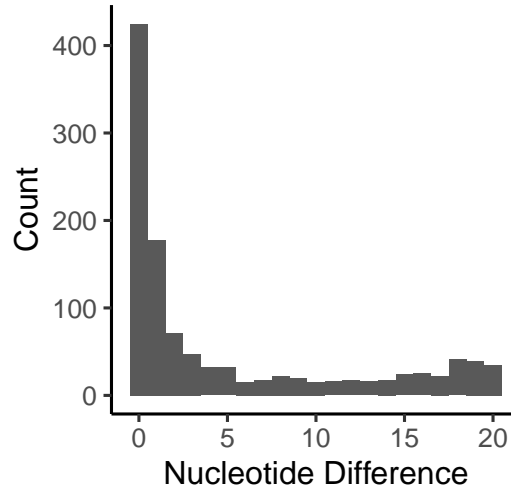
IGHV3-22*01_02

2 sequences assigned
No exact matches.



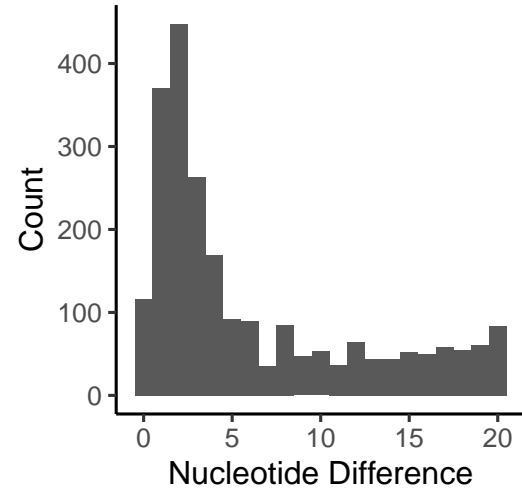
IGHV3-30*03

2032 sequences assigned
425 (20.9%) exact matches, in which:
408 unique CDR3
6 unique J



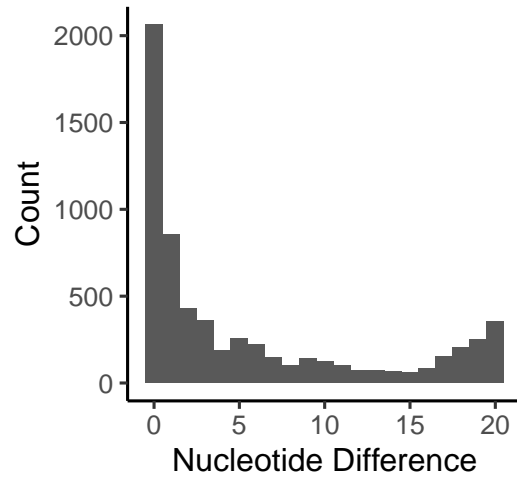
IGHV3-33*06

2929 sequences assigned
116 (4%) exact matches, in which:
116 unique CDR3
6 unique J



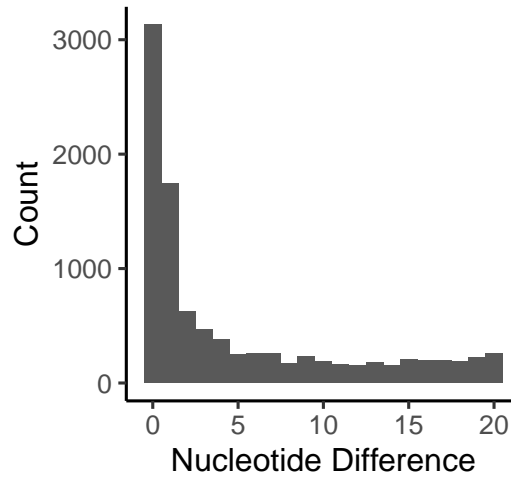
IGHV3-30-3*01

8571 sequences assigned
2063 (24.1%) exact matches, in which:
1740 unique CDR3
6 unique J



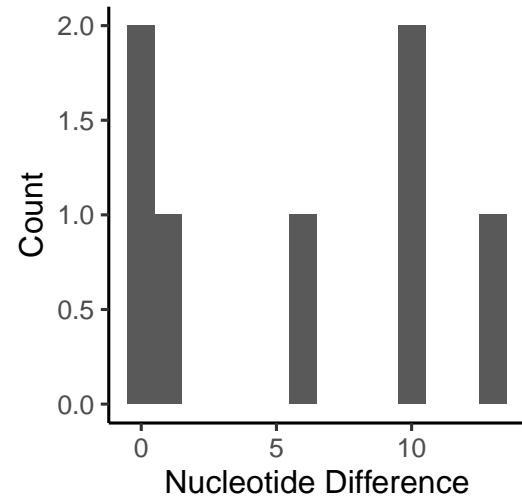
IGHV3-33*01

12688 sequences assigned
3131 (24.7%) exact matches, in which:
2661 unique CDR3
6 unique J



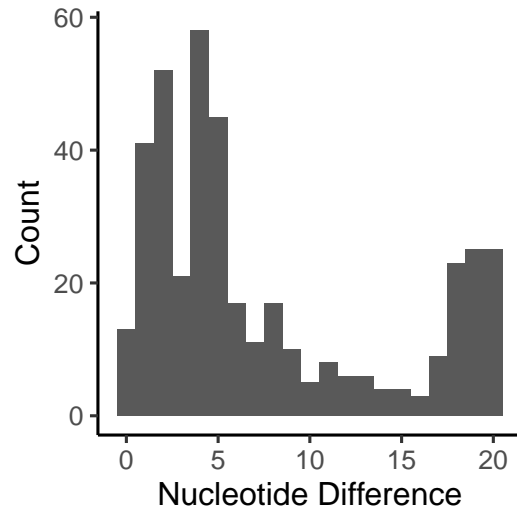
IGHV3-35*01

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



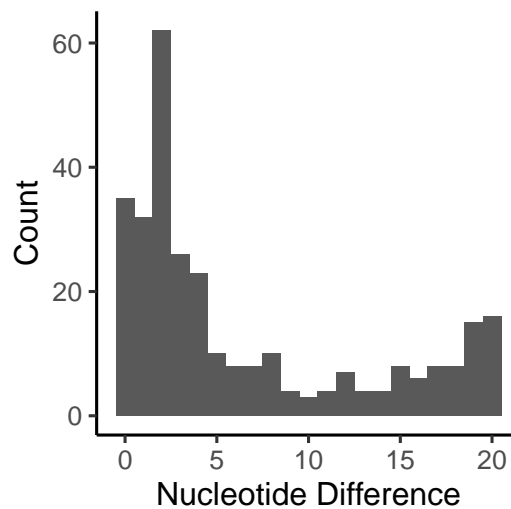
IGHV3-30-3*02

528 sequences assigned
13 (2.5%) exact matches, in which:
13 unique CDR3
5 unique J



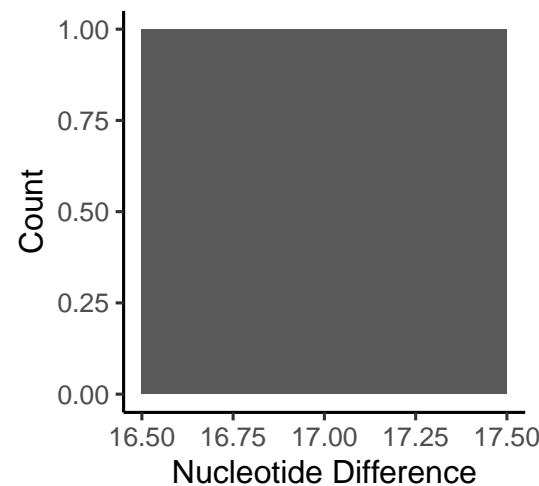
IGHV3-33*05

653 sequences assigned
35 (5.4%) exact matches, in which:
35 unique CDR3
4 unique J



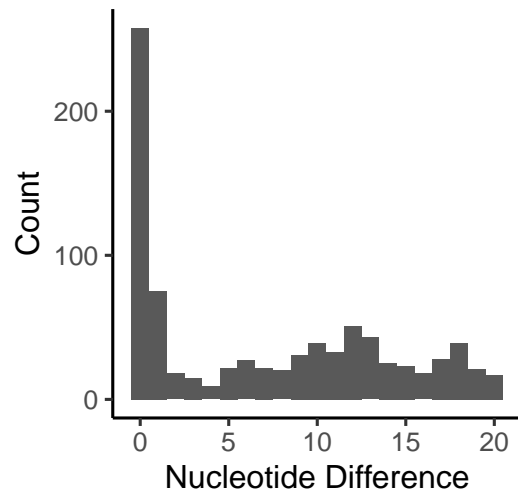
IGHV3-38-3*01

1 sequences assigned
No exact matches.



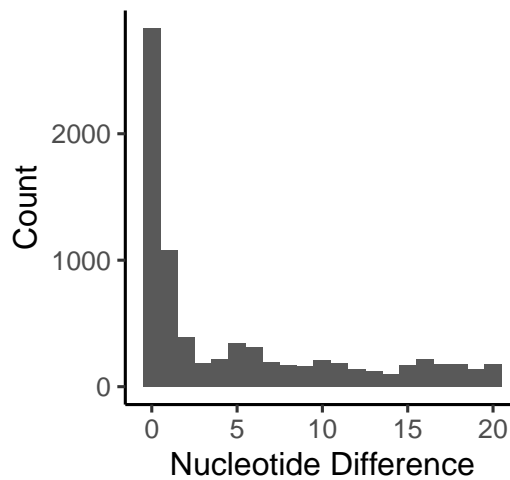
IGHV3-43*01

1253 sequences assigned
258 (20.6%) exact matches, in which:
215 unique CDR3
6 unique J



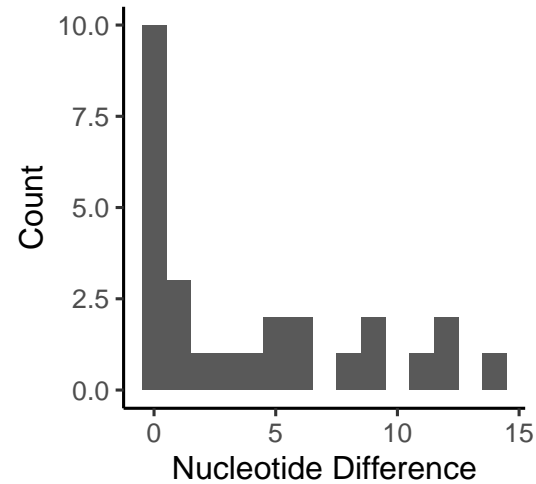
IGHV3-48*02

12108 sequences assigned
2833 (23.4%) exact matches, in which:
2294 unique CDR3
6 unique J



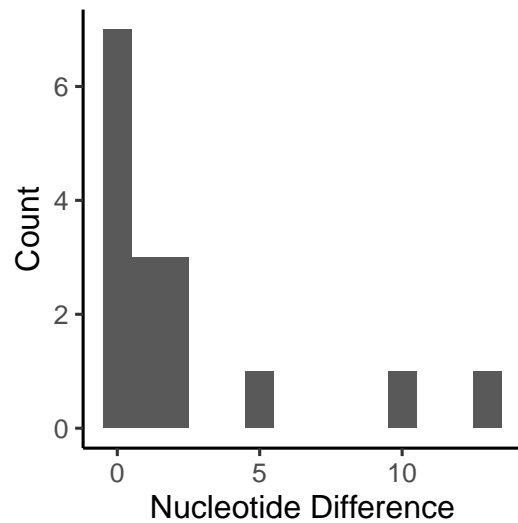
IGHV3-52*01_03

27 sequences assigned
10 (37%) exact matches, in which:
9 unique CDR3
3 unique J



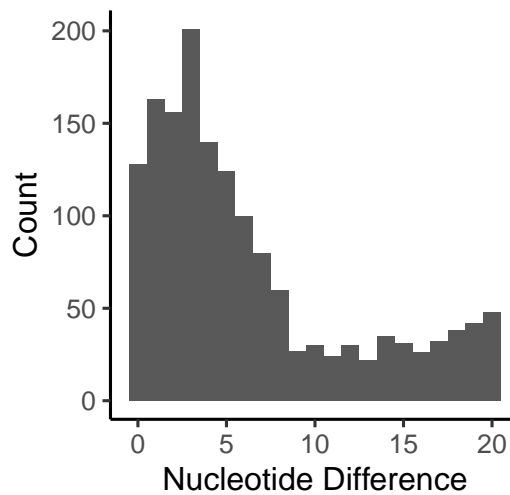
IGHV3-47*02

16 sequences assigned
7 (43.8%) exact matches, in which:
3 unique CDR3
2 unique J



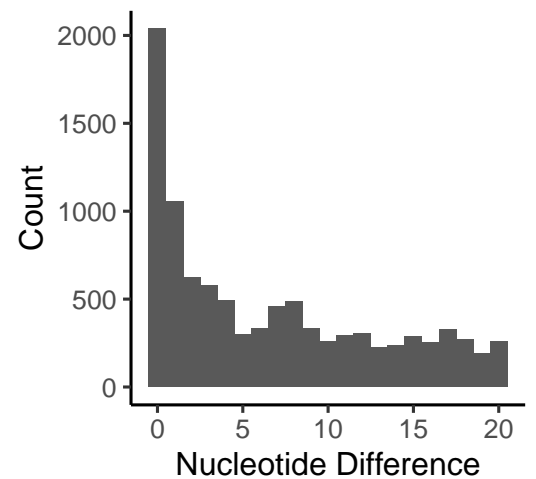
IGHV3-48*04

2689 sequences assigned
128 (4.8%) exact matches, in which:
128 unique CDR3
5 unique J



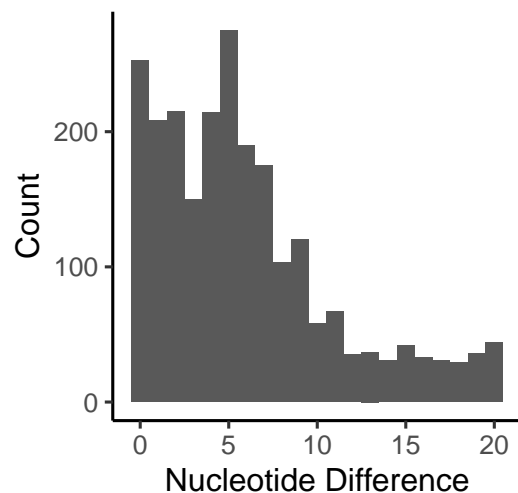
IGHV3-53*01_02

15581 sequences assigned
2038 (13.1%) exact matches, in which:
1727 unique CDR3
6 unique J



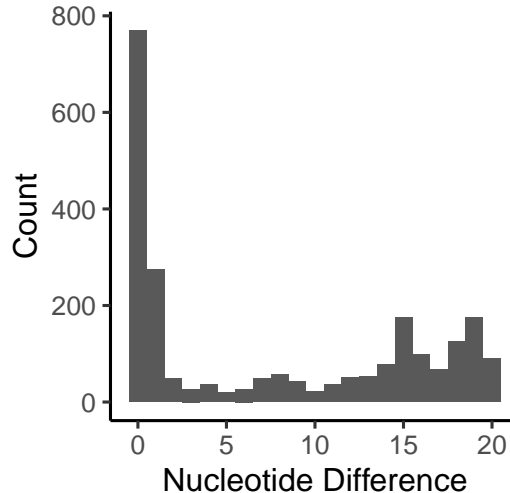
IGHV3-48*01

2896 sequences assigned
253 (8.7%) exact matches, in which:
251 unique CDR3
5 unique J



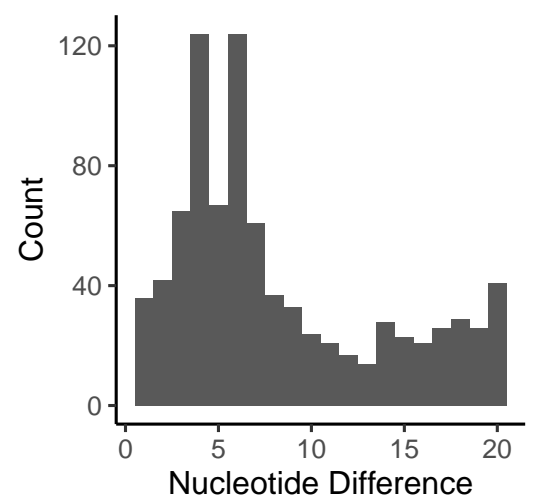
IGHV3-49*03_05

3390 sequences assigned
770 (22.7%) exact matches, in which:
664 unique CDR3
6 unique J



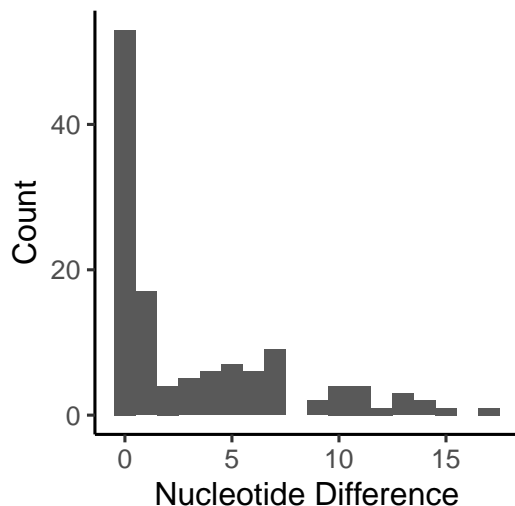
IGHV3-64*04

1057 sequences assigned
No exact matches.



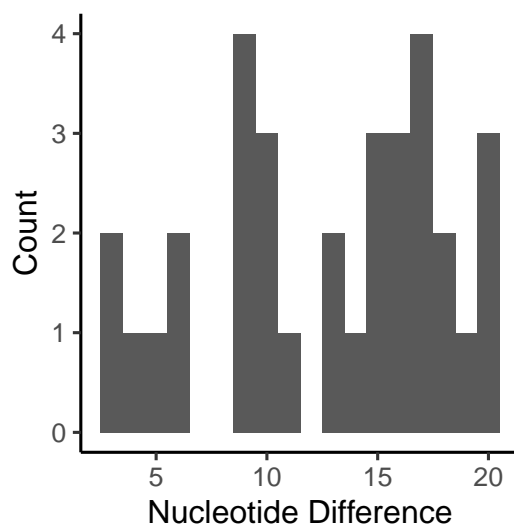
IGHV3-64*02_07

136 sequences assigned
53 (39%) exact matches, in which:
42 unique CDR3
5 unique J



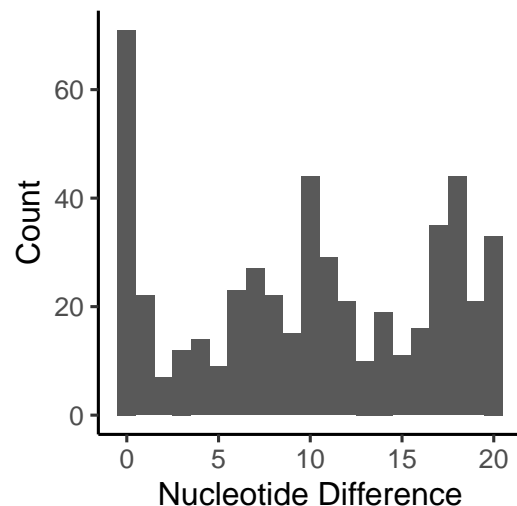
IGHV3-69-1*01

175 sequences assigned
No exact matches.



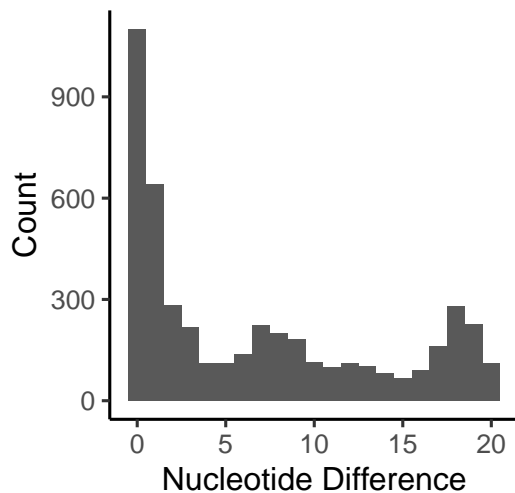
IGHV3-72*01

1254 sequences assigned
71 (5.7%) exact matches, in which:
63 unique CDR3
5 unique J



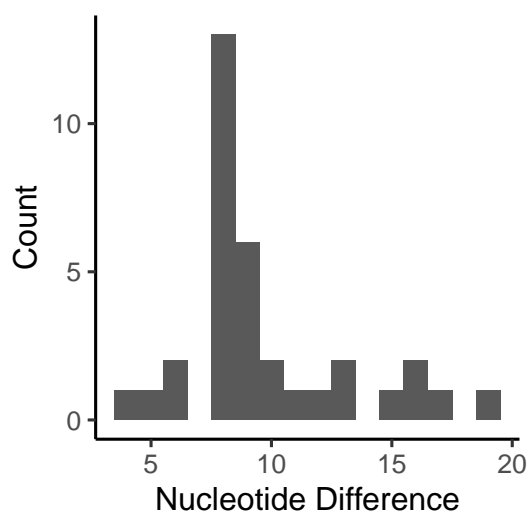
IGHV3-66*01

7273 sequences assigned
1101 (15.1%) exact matches, in which:
926 unique CDR3
6 unique J



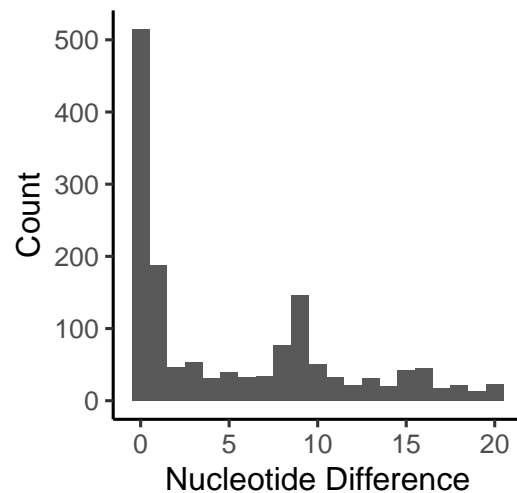
IGHV3-69-1*02

711 sequences assigned
No exact matches.



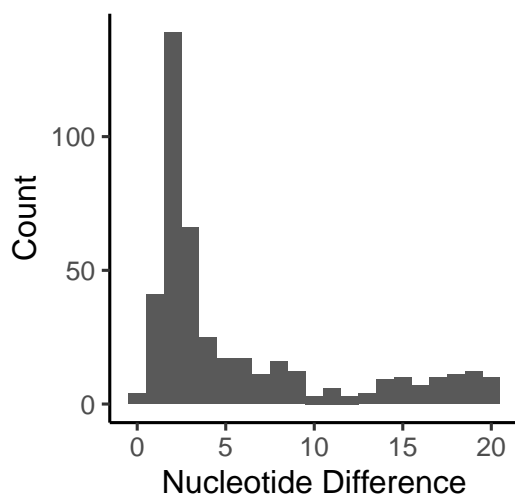
IGHV3-73*01_02

1693 sequences assigned
515 (30.4%) exact matches, in which:
426 unique CDR3
6 unique J



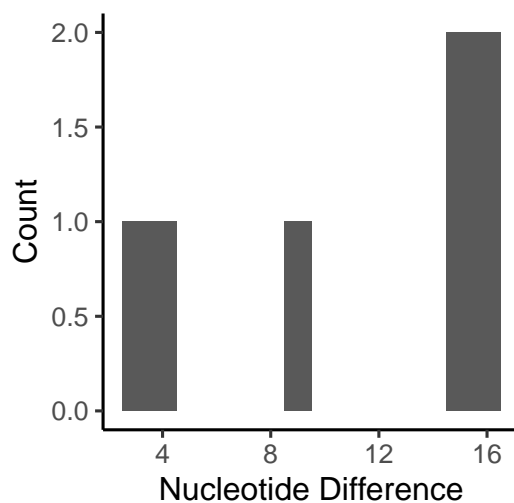
IGHV3-66*03

576 sequences assigned
4 (0.7%) exact matches, in which:
4 unique CDR3
3 unique J



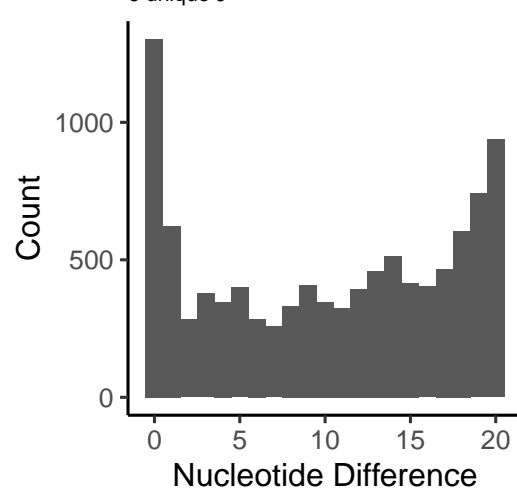
IGHV3-71*01_04

19 sequences assigned
No exact matches.



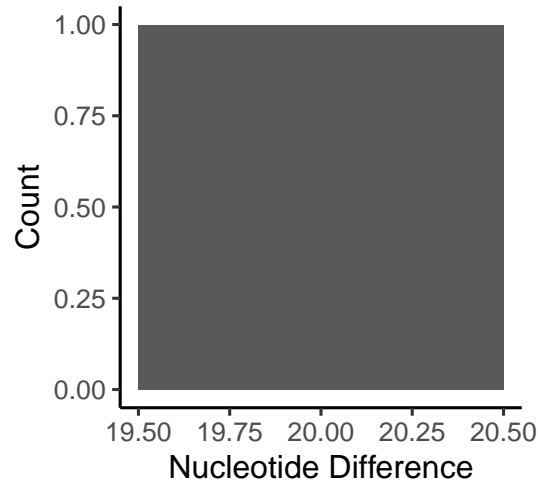
IGHV3-74*01_02

17795 sequences assigned
1303 (7.3%) exact matches, in which:
1053 unique CDR3
6 unique J



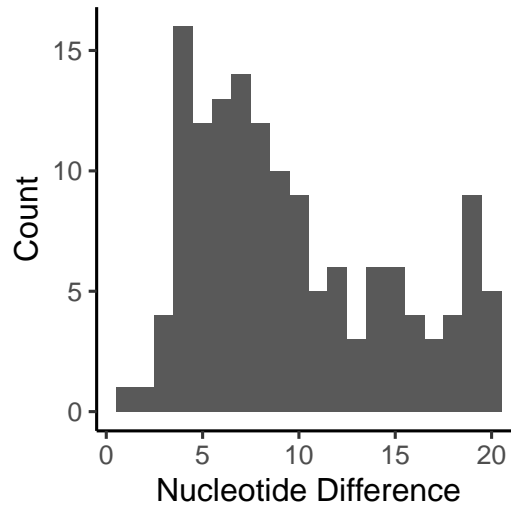
IGHV3-43D*03

3 sequences assigned
No exact matches.



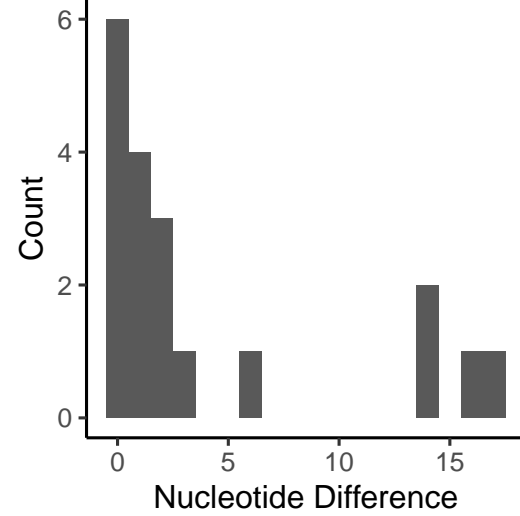
IGHV3-NL1*01

260 sequences assigned
No exact matches.



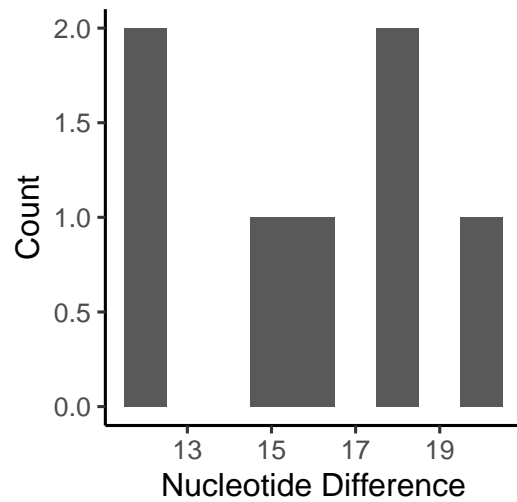
IGHV4-28*01_07

19 sequences assigned
6 (31.6%) exact matches, in which:
5 unique CDR3
3 unique J



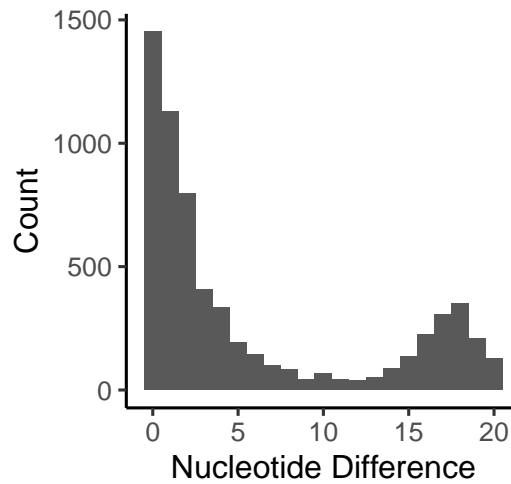
IGHV3-43D*04

31 sequences assigned
No exact matches.



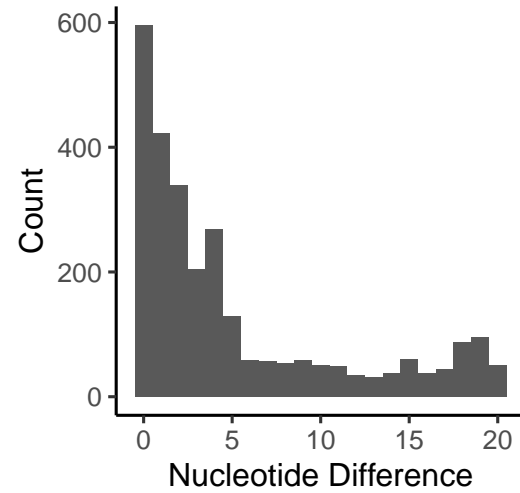
IGHV4-4*07

8684 sequences assigned
1452 (16.7%) exact matches, in which:
1346 unique CDR3
6 unique J



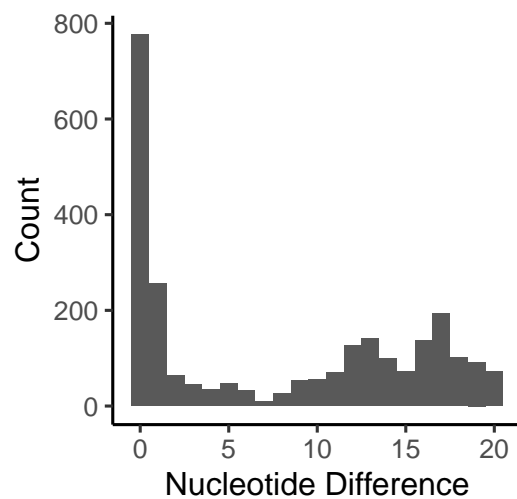
IGHV4-30-2*01

3179 sequences assigned
596 (18.7%) exact matches, in which:
519 unique CDR3
6 unique J



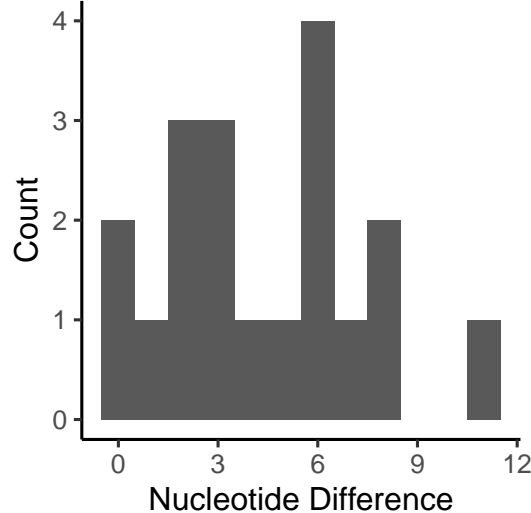
IGHV3-64D*06

3010 sequences assigned
777 (25.8%) exact matches, in which:
597 unique CDR3
6 unique J



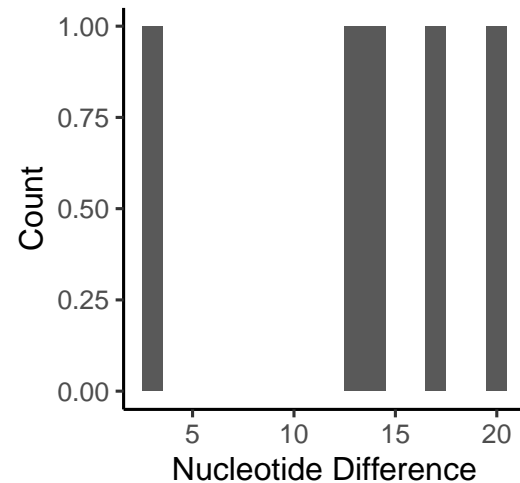
IGHV4-28*03

24 sequences assigned
2 (8.3%) exact matches, in which:
2 unique CDR3
2 unique J



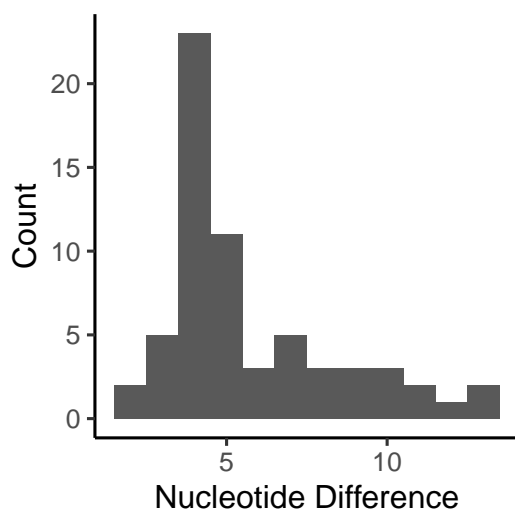
IGHV4-30-4*01

44 sequences assigned
No exact matches.



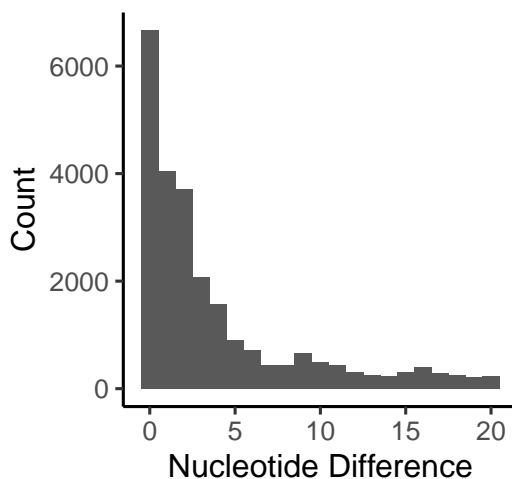
IGHV4-30-4*07

66 sequences assigned
No exact matches.



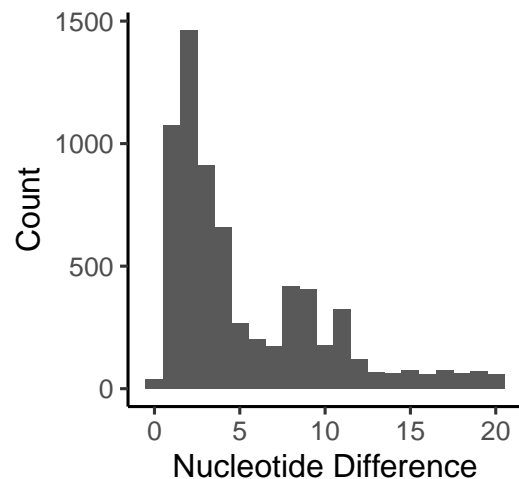
IGHV4-34*01_02

33678 sequences assigned
6663 (19.8%) exact matches, in which:
6084 unique CDR3
6 unique J



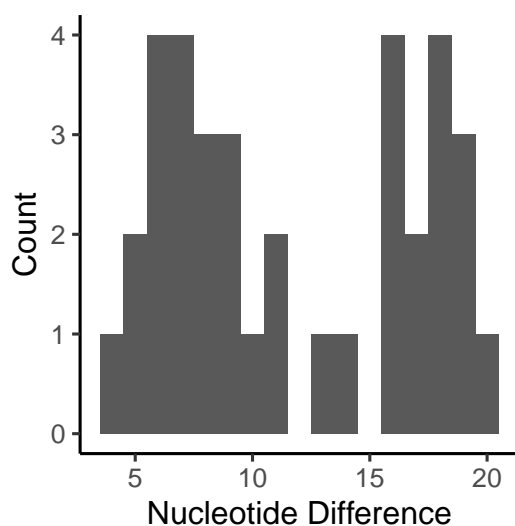
IGHV4-39*07

7935 sequences assigned
40 (0.5%) exact matches, in which:
40 unique CDR3
5 unique J



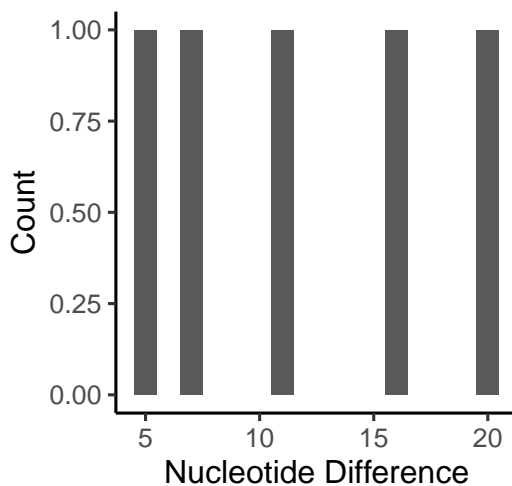
IGHV4-30-4*08

83 sequences assigned
No exact matches.



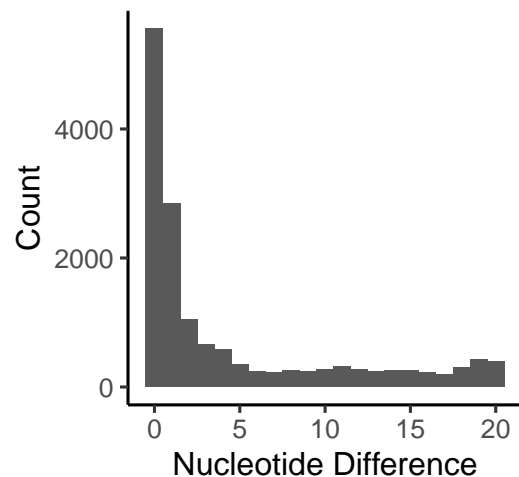
IGHV4-38-2*01

8 sequences assigned
No exact matches.



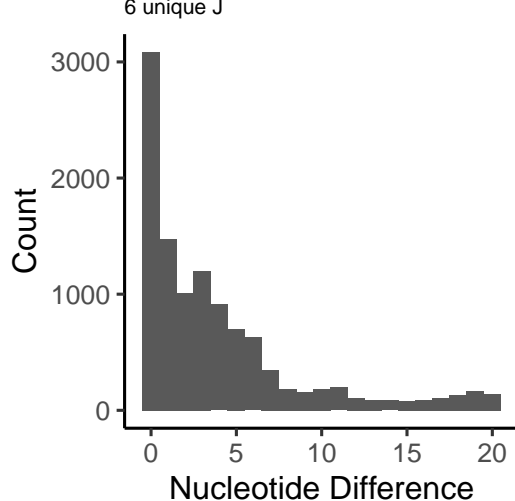
IGHV4-39*01_05

22380 sequences assigned
5554 (24.8%) exact matches, in which:
5064 unique CDR3
6 unique J



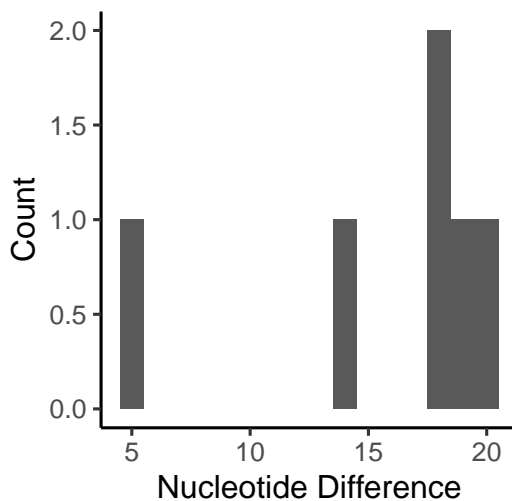
IGHV4-31*03_04

14168 sequences assigned
3085 (21.8%) exact matches, in which:
2923 unique CDR3
6 unique J



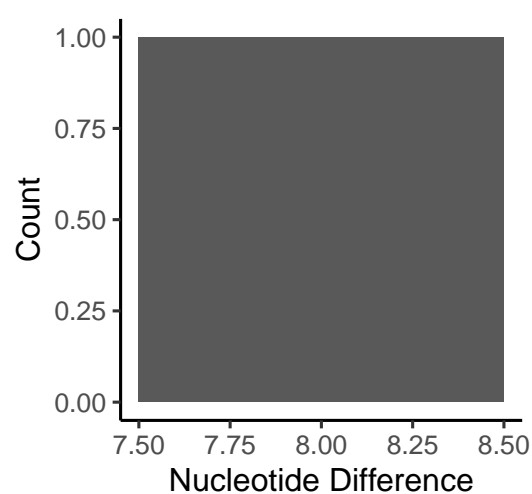
IGHV4-38-2*02

17 sequences assigned
No exact matches.



IGHV4-55*07

6 sequences assigned
No exact matches.



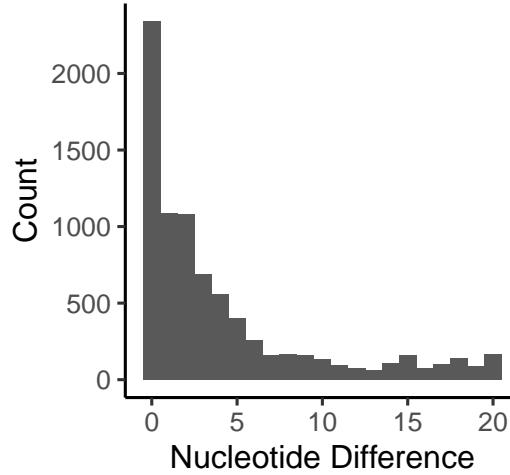
IGHV4-55*01_05

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



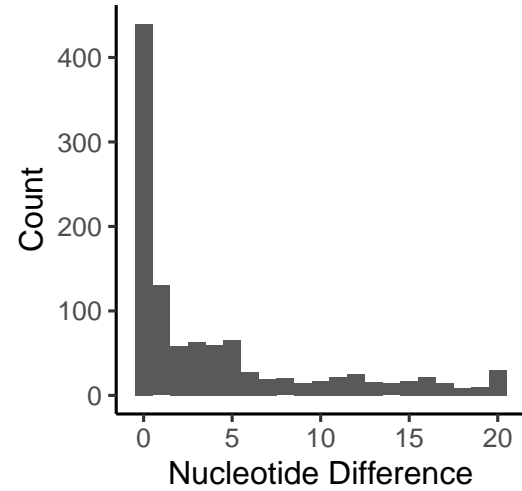
IGHV4-61*01

10466 sequences assigned
2340 (22.4%) exact matches, in which:
2264 unique CDR3
6 unique J



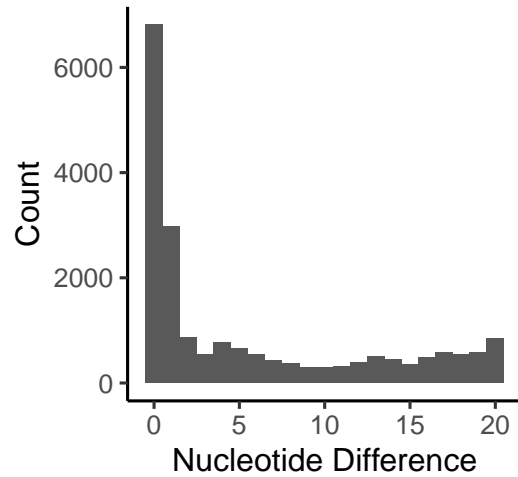
IGHV5-10-1*01_03_A11

1289 sequences assigned
440 (34.1%) exact matches, in which:
421 unique CDR3
6 unique J



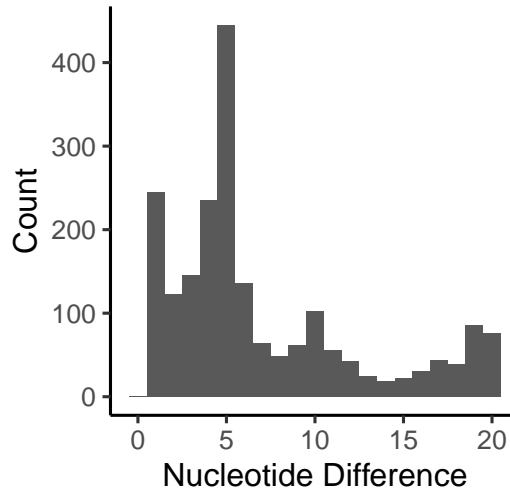
IGHV4-59*01_07

28304 sequences assigned
6812 (24.1%) exact matches, in which:
6427 unique CDR3
6 unique J



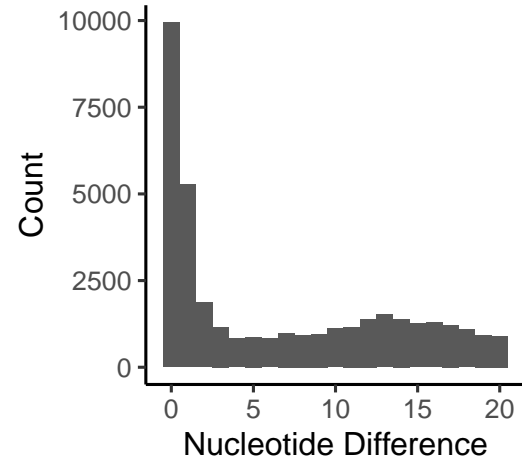
IGHV4-61*08

2712 sequences assigned
1 (0%) exact matches, in which:
1 unique CDR3
1 unique J



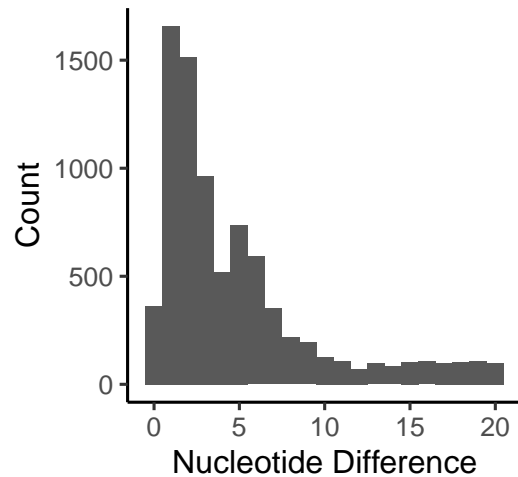
IGHV5-51*01_03

41755 sequences assigned
9945 (23.8%) exact matches, in which:
7307 unique CDR3
6 unique J



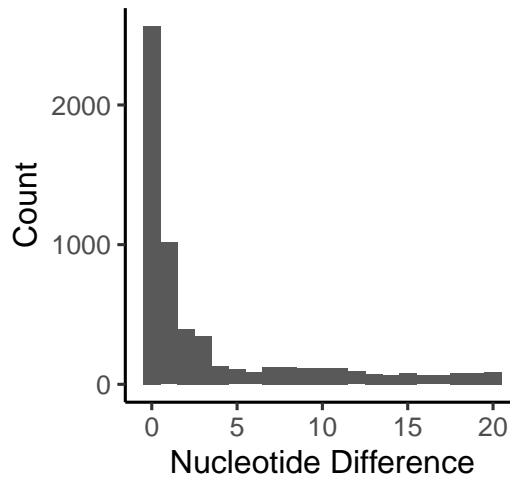
IGHV4-59*12

9465 sequences assigned
362 (3.8%) exact matches, in which:
361 unique CDR3
6 unique J



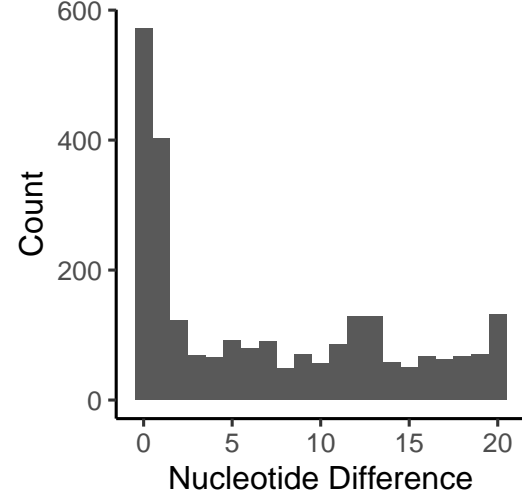
IGHV5-10-1*01_03

6623 sequences assigned
2565 (38.7%) exact matches, in which:
2161 unique CDR3
6 unique J



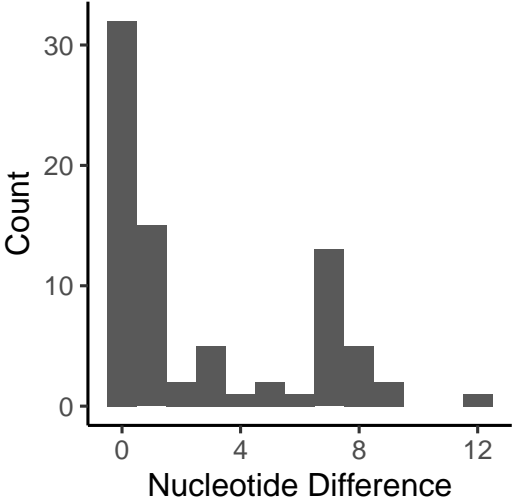
IGHV6-1*01_02

4302 sequences assigned
572 (13.3%) exact matches, in which:
545 unique CDR3
6 unique J



IGHV7-4-1*01

79 sequences assigned
32 (40.5%) exact matches, in which:
31 unique CDR3
6 unique J





Warning - no inferred sequences found.

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

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.