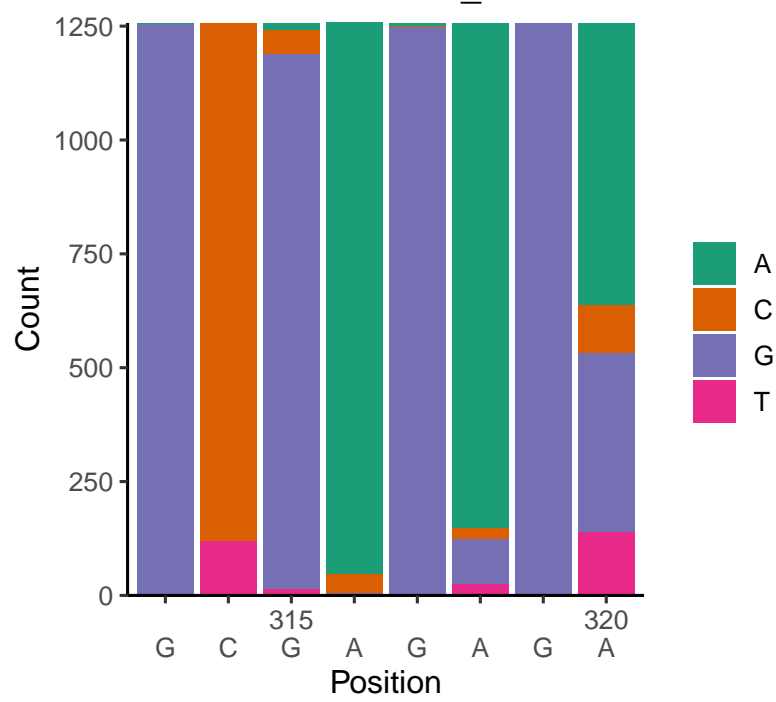
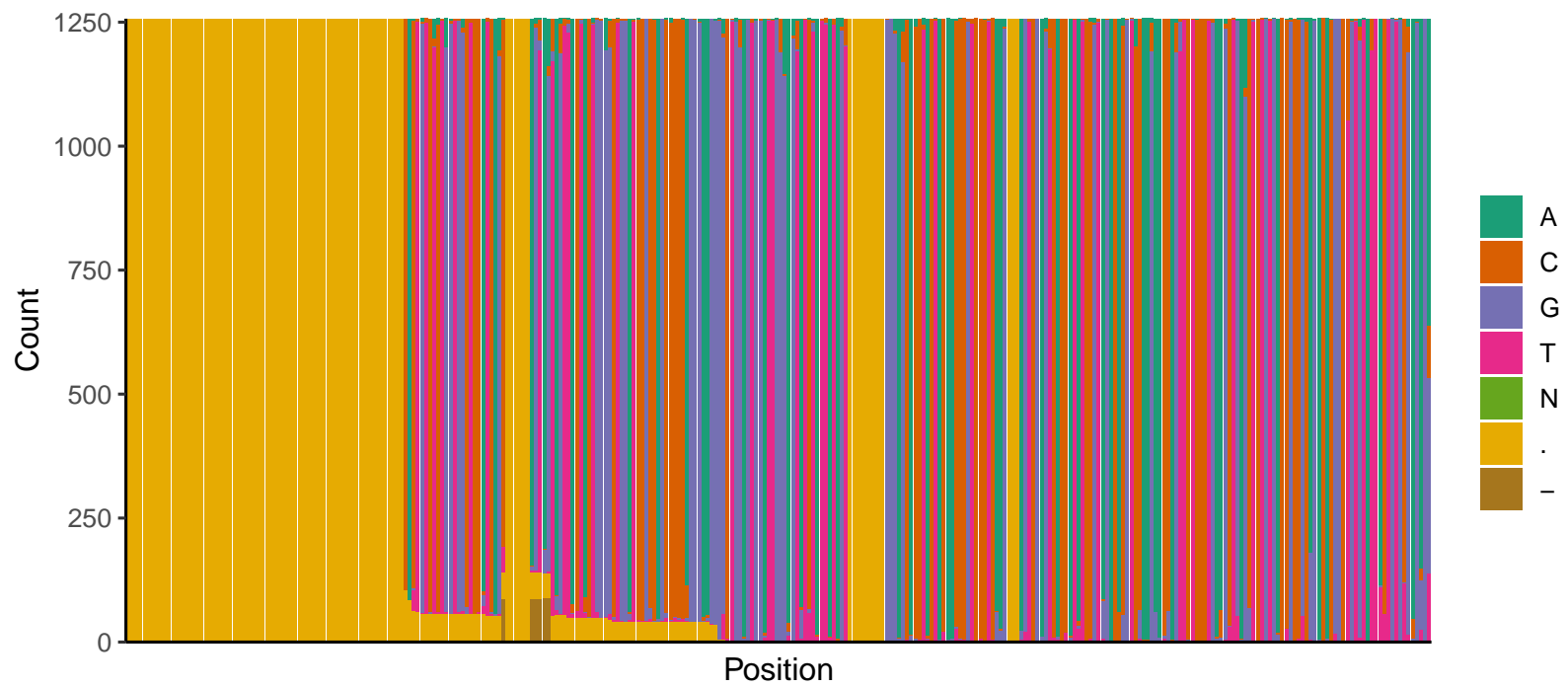


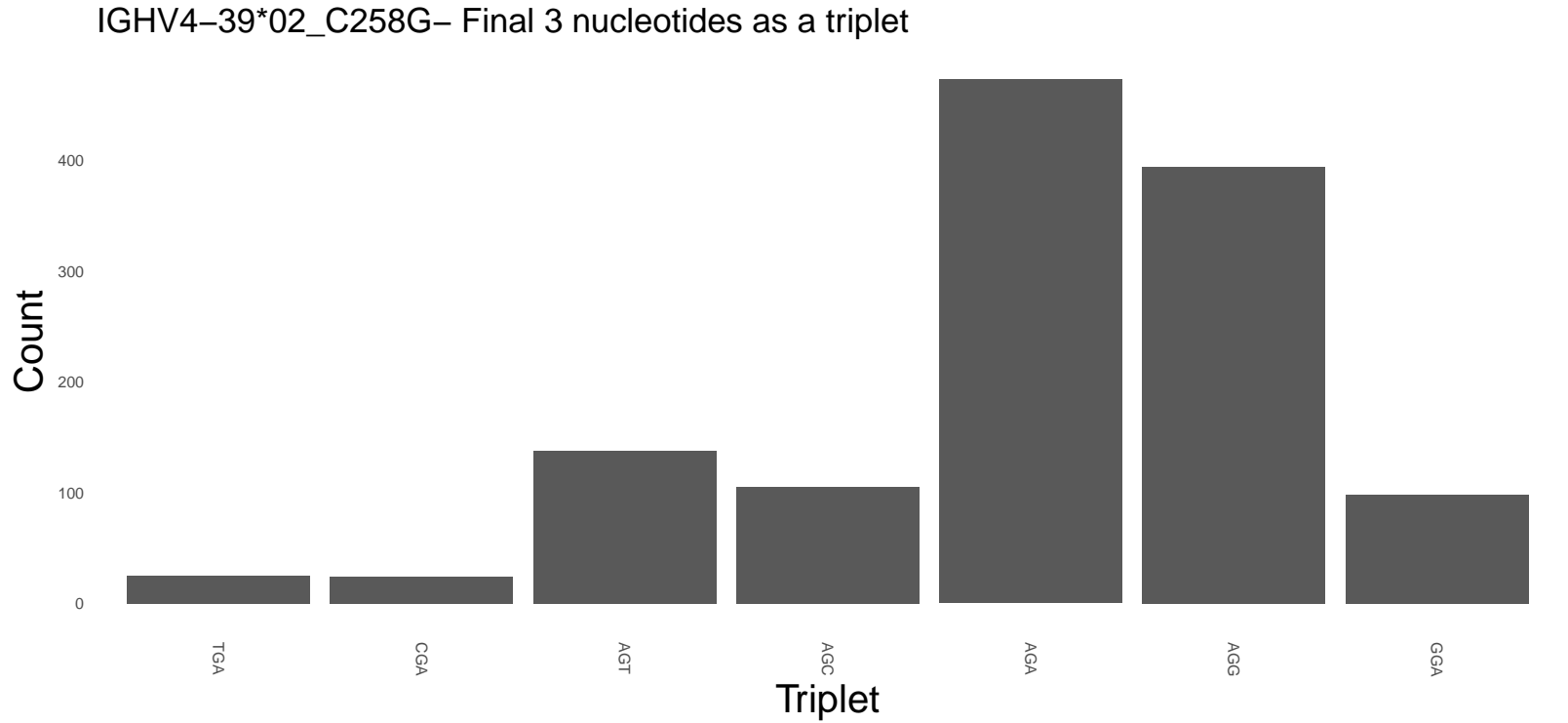
Gene IGHV4-39*02_C258G



Gene IGHV4-39*02_C258G

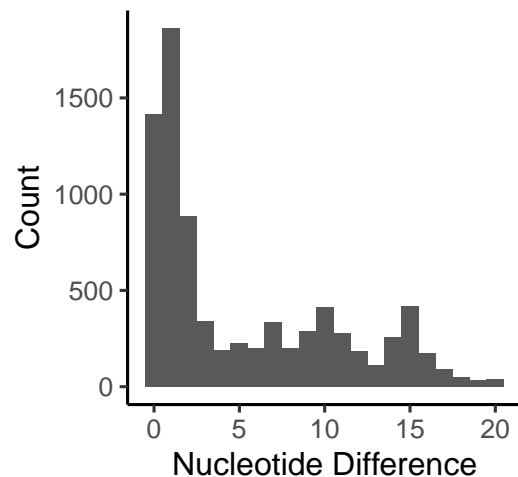


IGHV4-39*02_C258G- Final 3 nucleotides as a triplet



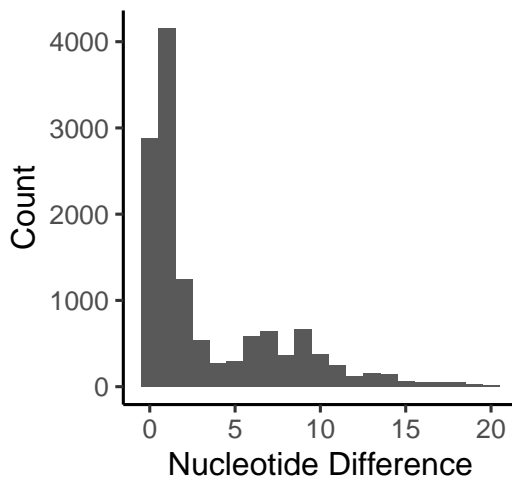
IGHV1-2*02

8674 sequences assigned
1417 (16.3%) exact matches, in which:
1138 unique CDR3
6 unique J



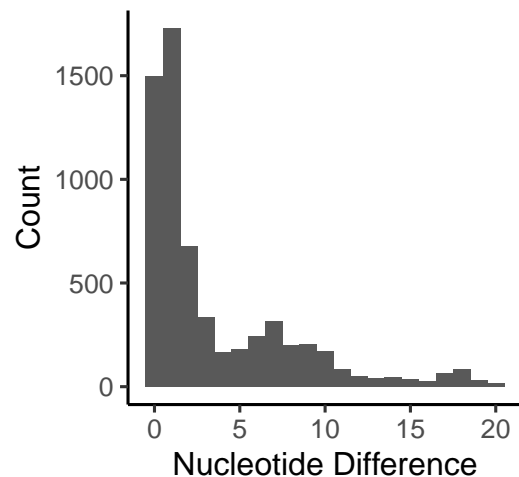
IGHV1-18*01

14920 sequences assigned
2883 (19.3%) exact matches, in which:
2204 unique CDR3
6 unique J



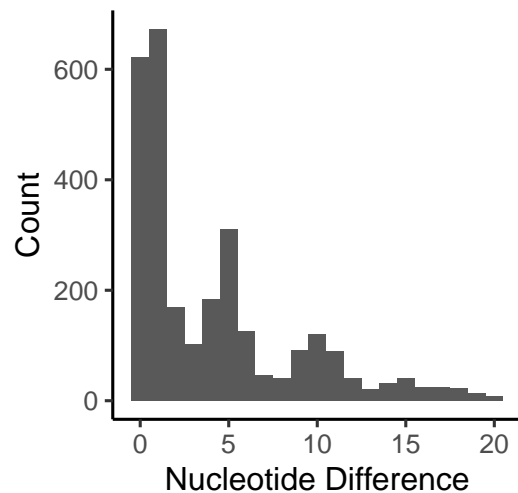
IGHV1-46*01

9090 sequences assigned
1498 (16.5%) exact matches, in which:
1247 unique CDR3
6 unique J



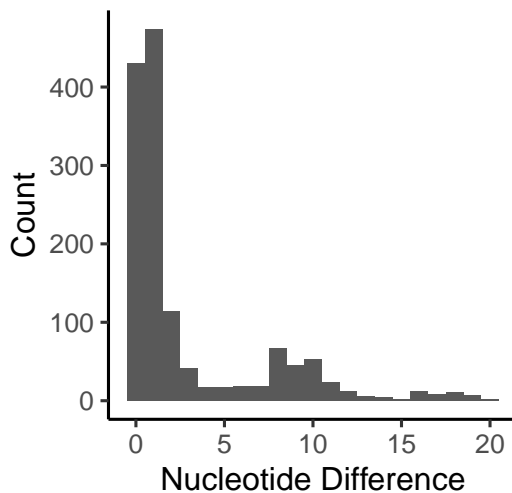
IGHV1-3*01_05

2852 sequences assigned
621 (21.8%) exact matches, in which:
502 unique CDR3
6 unique J



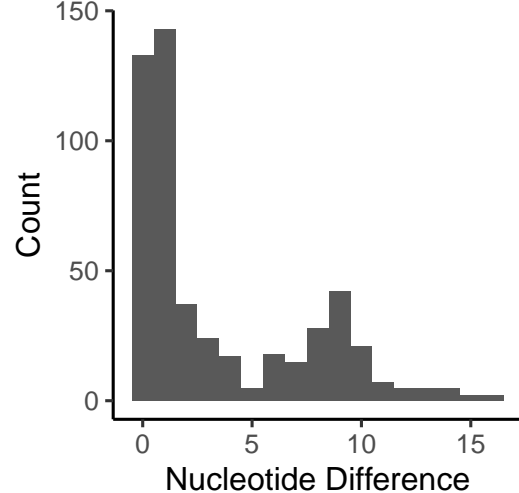
IGHV1-24*01

1426 sequences assigned
430 (30.2%) exact matches, in which:
356 unique CDR3
6 unique J



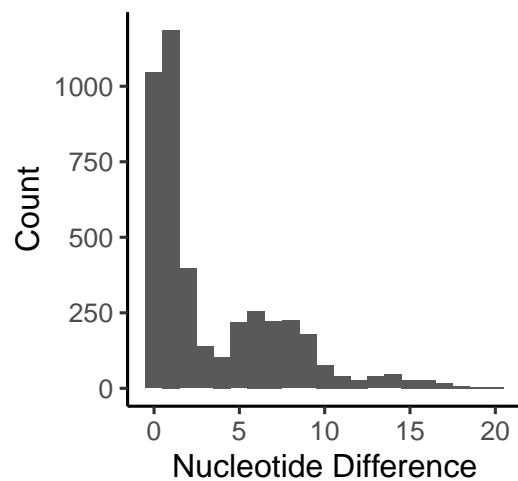
IGHV1-58*02

514 sequences assigned
133 (25.9%) exact matches, in which:
106 unique CDR3
5 unique J



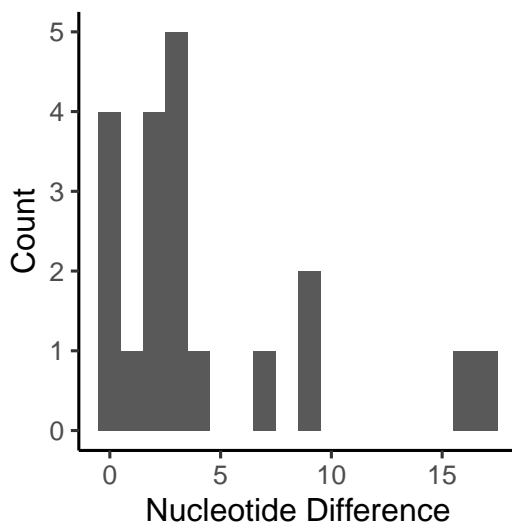
IGHV1-8*01

4404 sequences assigned
1045 (23.7%) exact matches, in which:
871 unique CDR3
6 unique J



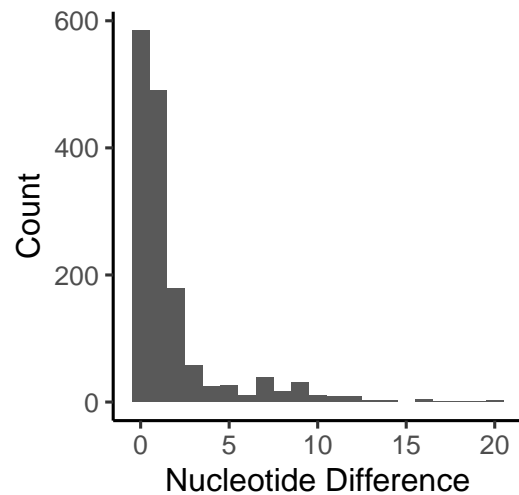
IGHV1-45*03

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



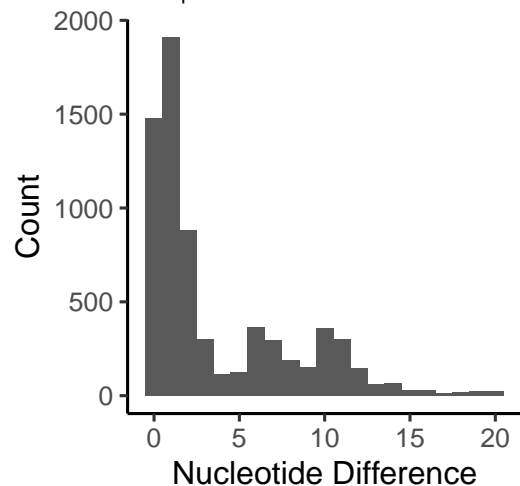
IGHV1-69*02

1604 sequences assigned
585 (36.5%) exact matches, in which:
518 unique CDR3
6 unique J



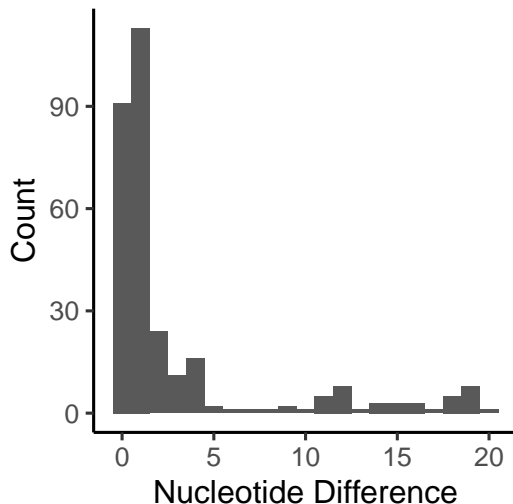
IGHV1-69*04_09

6978 sequences assigned
1481 (21.2%) exact matches, in which:
1246 unique CDR3
6 unique J



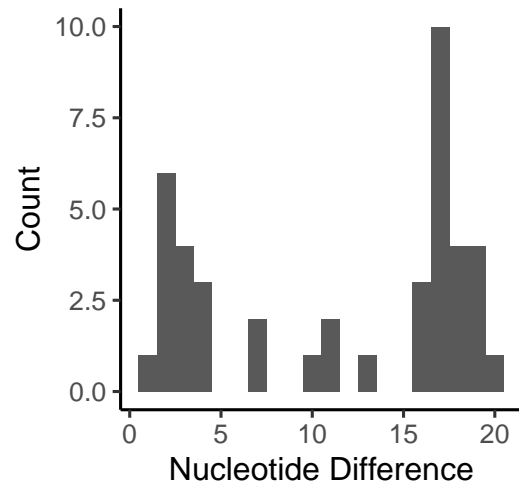
IGHV2-5*01

312 sequences assigned
91 (29.2%) exact matches, in which:
72 unique CDR3
6 unique J



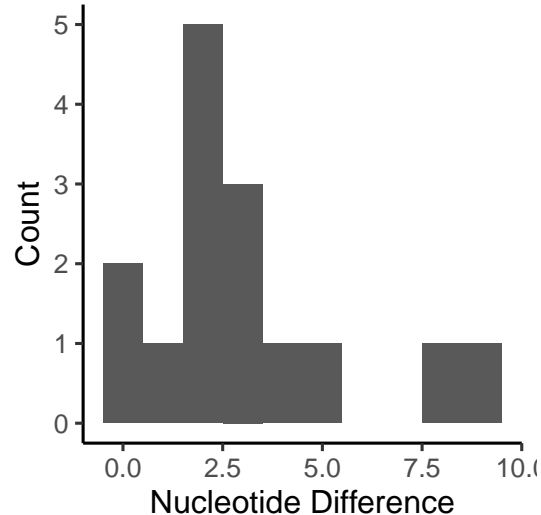
IGHV2-70*12

782 sequences assigned
No exact matches.



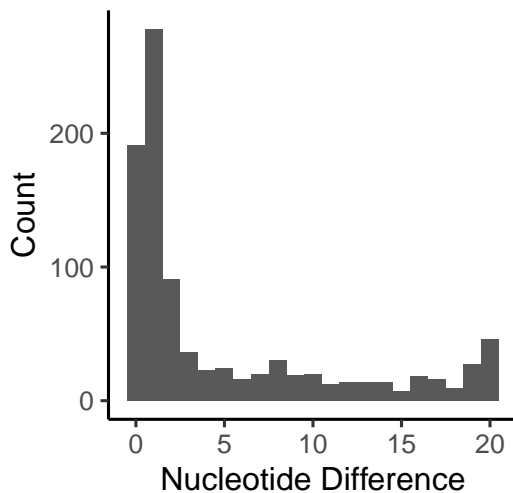
IGHV1-69D*01

16 sequences assigned
2 (12.5%) exact matches, in which:
2 unique CDR3
2 unique J



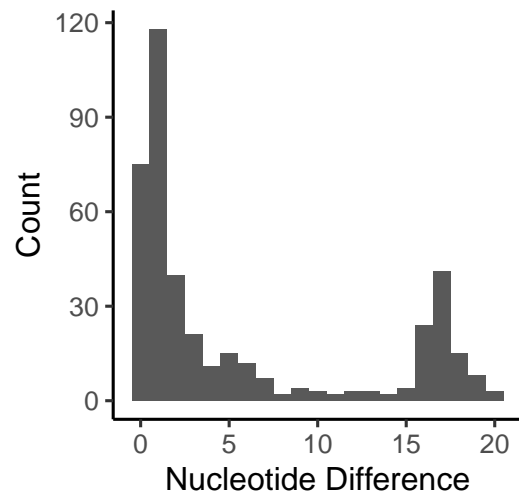
IGHV2-5*02

1188 sequences assigned
191 (16.1%) exact matches, in which:
145 unique CDR3
6 unique J



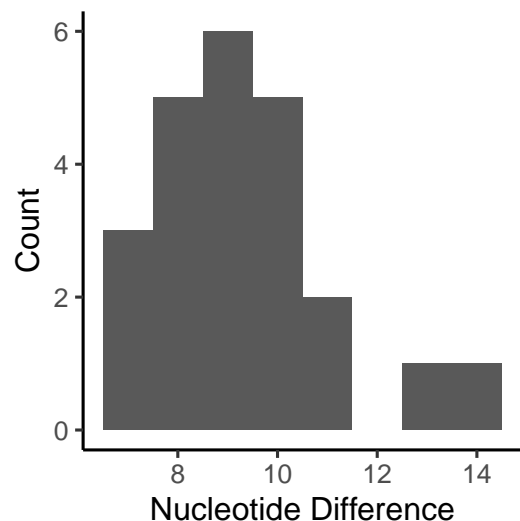
IGHV2-70*11_15

457 sequences assigned
75 (16.4%) exact matches, in which:
53 unique CDR3
4 unique J



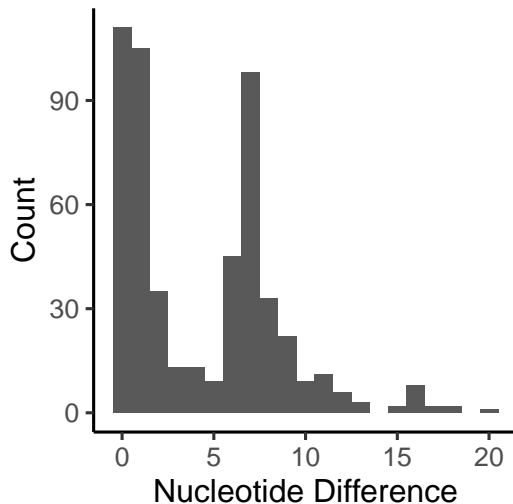
IGHV1-NL1*01

23 sequences assigned
No exact matches.



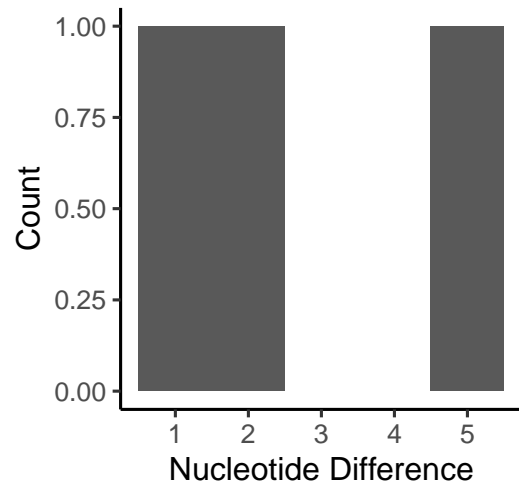
IGHV2-26*01

530 sequences assigned
111 (20.9%) exact matches, in which:
95 unique CDR3
5 unique J



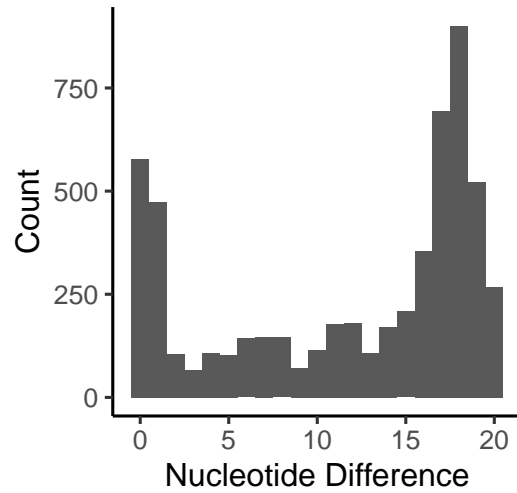
IGHV2-70D*04

3 sequences assigned
No exact matches.



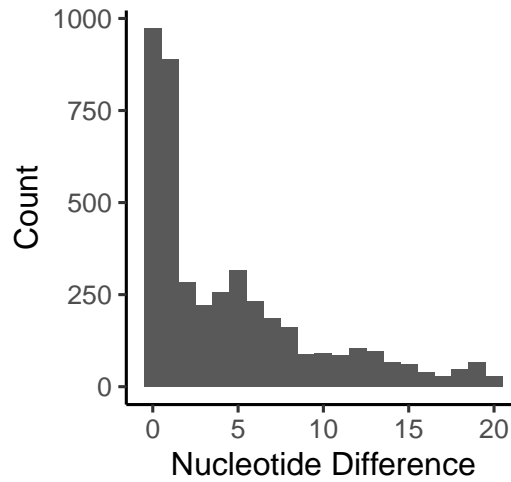
IGHV3-7*01

8492 sequences assigned
577 (6.8%) exact matches, in which:
410 unique CDR3
6 unique J



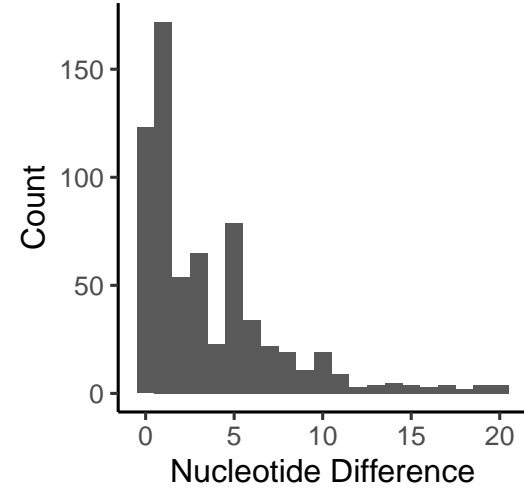
IGHV3-9*01

4657 sequences assigned
973 (20.9%) exact matches, in which:
578 unique CDR3
6 unique J



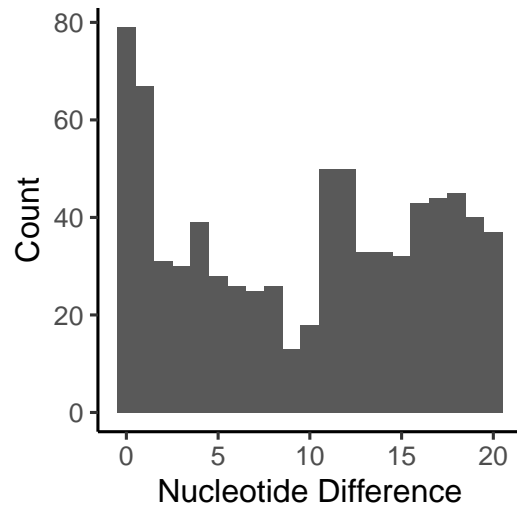
IGHV3-11*06

722 sequences assigned
123 (17%) exact matches, in which:
117 unique CDR3
4 unique J



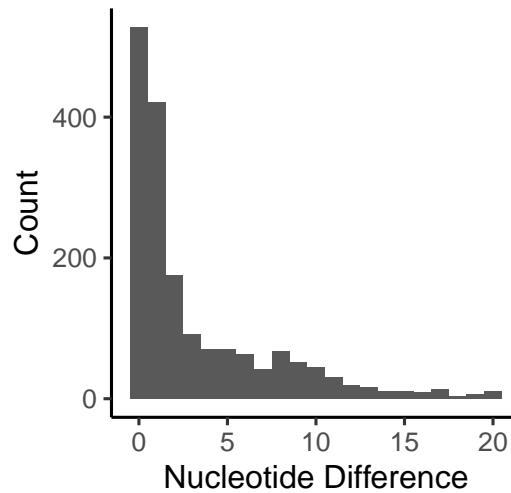
IGHV3-7*03

1147 sequences assigned
79 (6.9%) exact matches, in which:
67 unique CDR3
6 unique J



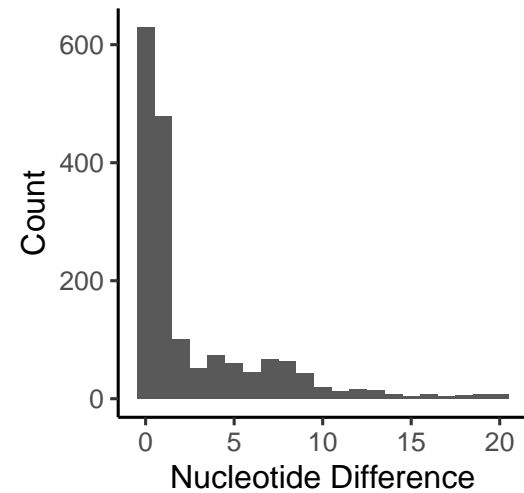
IGHV3-11*01

2629 sequences assigned
528 (20.1%) exact matches, in which:
370 unique CDR3
6 unique J



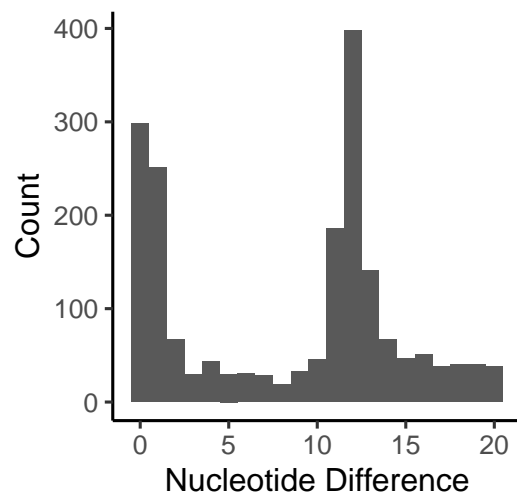
IGHV3-11*03_05

1853 sequences assigned
630 (34%) exact matches, in which:
421 unique CDR3
6 unique J



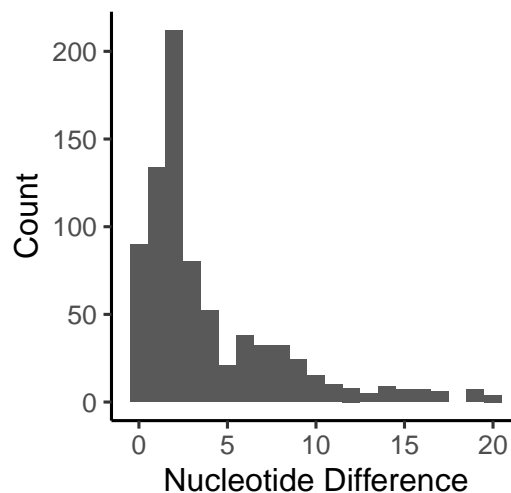
IGHV3-7*05

2114 sequences assigned
298 (14.1%) exact matches, in which:
205 unique CDR3
6 unique J



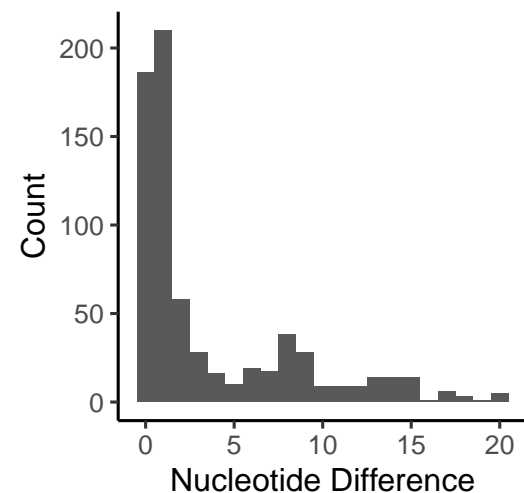
IGHV3-11*04

865 sequences assigned
90 (10.4%) exact matches, in which:
87 unique CDR3
5 unique J



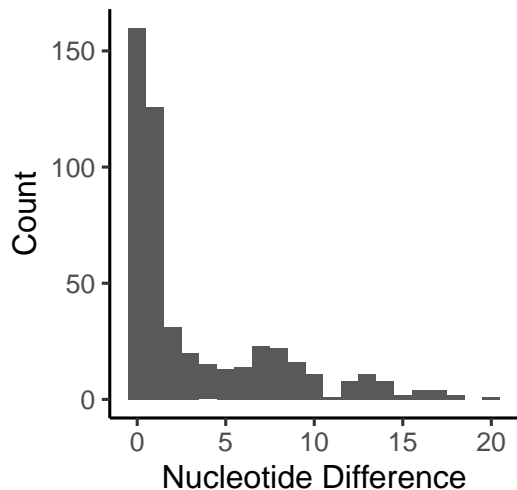
IGHV3-13*01

1112 sequences assigned
186 (16.7%) exact matches, in which:
123 unique CDR3
6 unique J



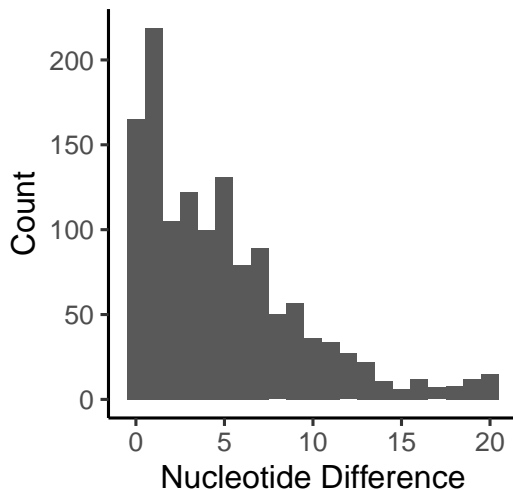
IGHV3-13*04

508 sequences assigned
160 (31.5%) exact matches, in which:
109 unique CDR3
6 unique J



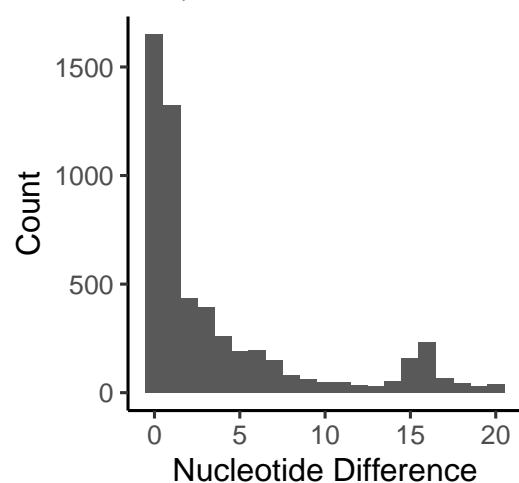
IGHV3-21*04

1411 sequences assigned
165 (11.7%) exact matches, in which:
143 unique CDR3
6 unique J



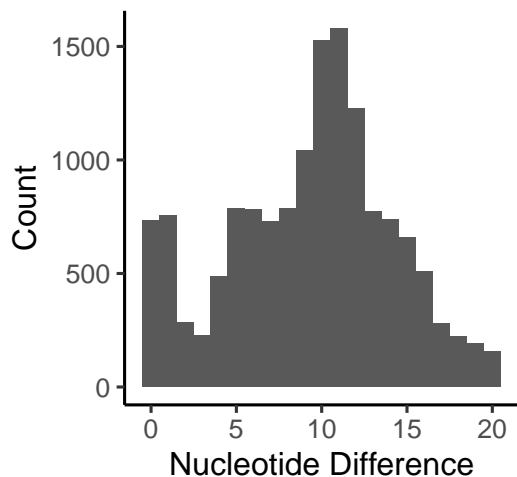
IGHV3-30-3*01

5782 sequences assigned
1650 (28.5%) exact matches, in which:
1138 unique CDR3
6 unique J



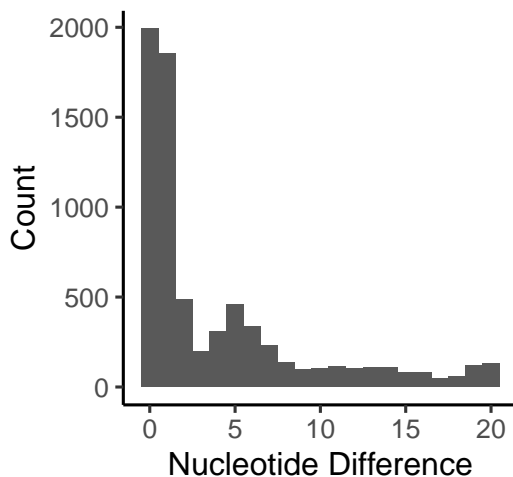
IGHV3-15*01_02

15456 sequences assigned
735 (4.8%) exact matches, in which:
420 unique CDR3
6 unique J



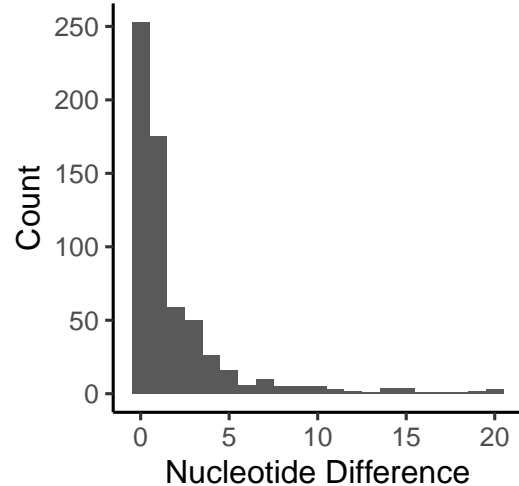
IGHV3-21*01_02

8793 sequences assigned
1992 (22.7%) exact matches, in which:
1251 unique CDR3
6 unique J



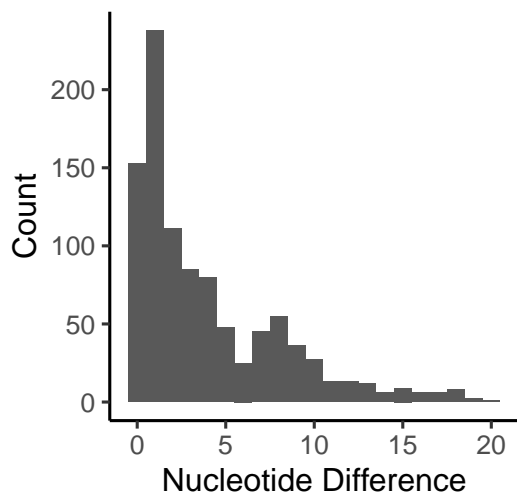
IGHV3-30*03

743 sequences assigned
253 (34.1%) exact matches, in which:
235 unique CDR3
6 unique J



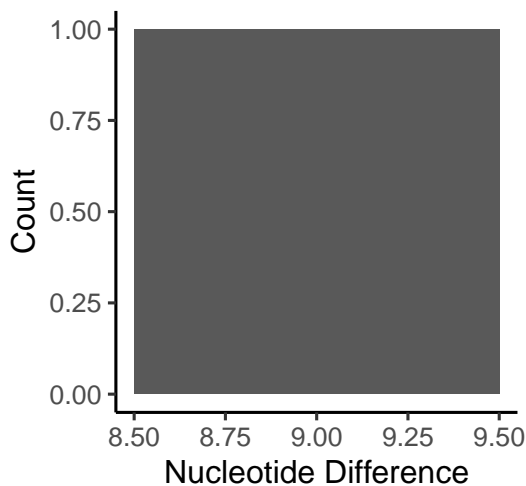
IGHV3-20*03_04

1253 sequences assigned
153 (12.2%) exact matches, in which:
87 unique CDR3
5 unique J



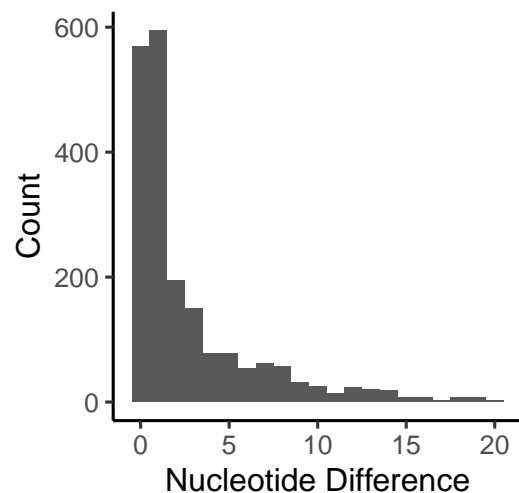
IGHV3-22*01_02

1 sequences assigned
No exact matches.



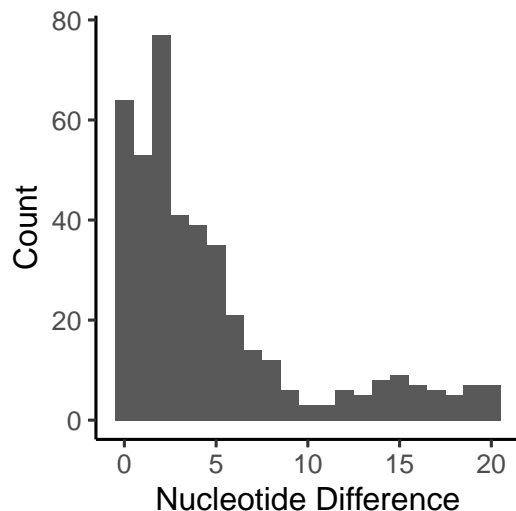
IGHV3-33*01

2559 sequences assigned
569 (22.2%) exact matches, in which:
386 unique CDR3
6 unique J



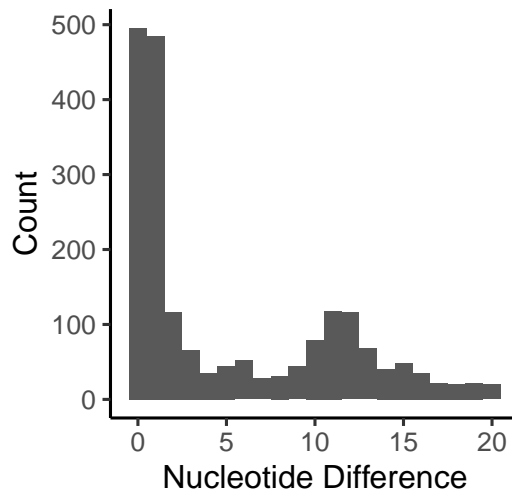
IGHV3-33*05

462 sequences assigned
64 (13.9%) exact matches, in which:
61 unique CDR3
5 unique J



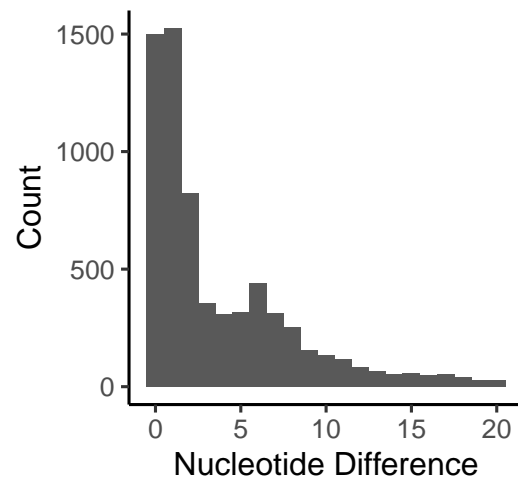
IGHV3-43*02

2232 sequences assigned
496 (22.2%) exact matches, in which:
284 unique CDR3
6 unique J



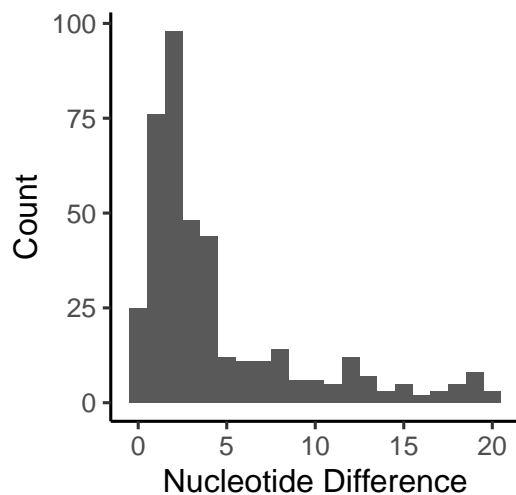
IGHV3-48*03

7675 sequences assigned
1501 (19.6%) exact matches, in which:
895 unique CDR3
6 unique J



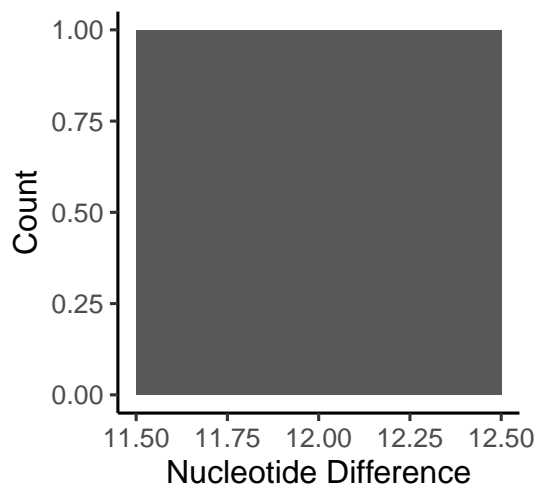
IGHV3-33*06

460 sequences assigned
25 (5.4%) exact matches, in which:
24 unique CDR3
4 unique J



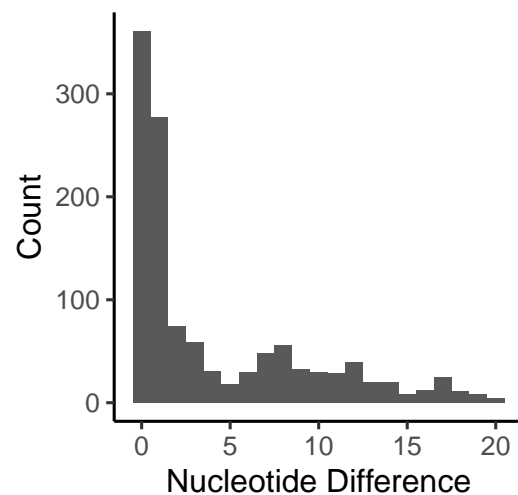
IGHV3-47*01

1 sequences assigned
No exact matches.



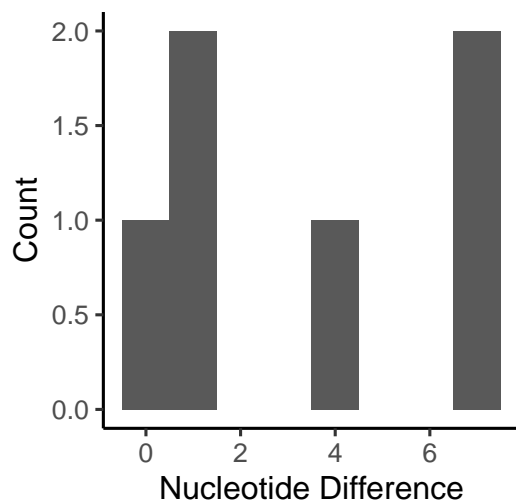
IGHV3-49*04

2047 sequences assigned
361 (17.6%) exact matches, in which:
223 unique CDR3
6 unique J



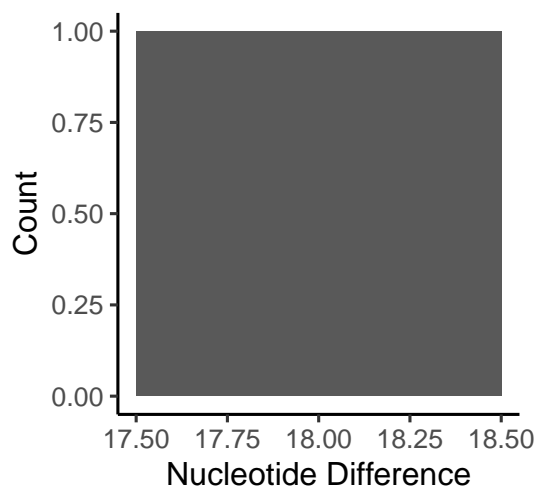
IGHV3-35*01

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



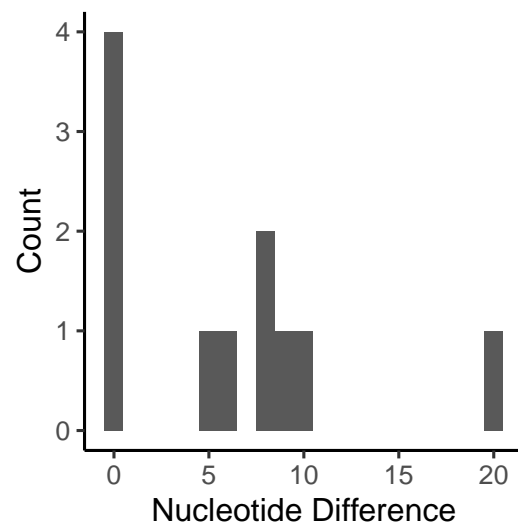
IGHV3-47*02

1 sequences assigned
No exact matches.



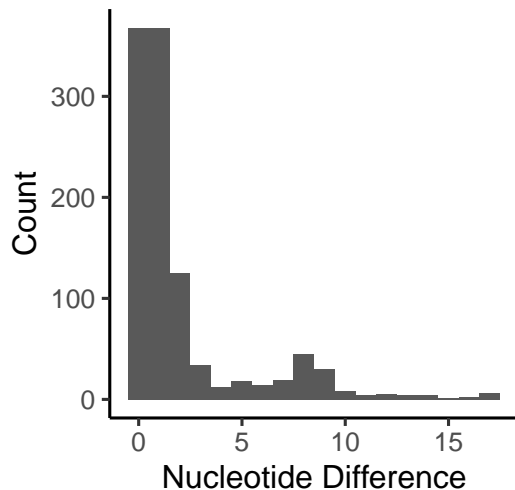
IGHV3-52*01_03

11 sequences assigned
4 (36.4%) exact matches, in which:
4 unique CDR3
4 unique J



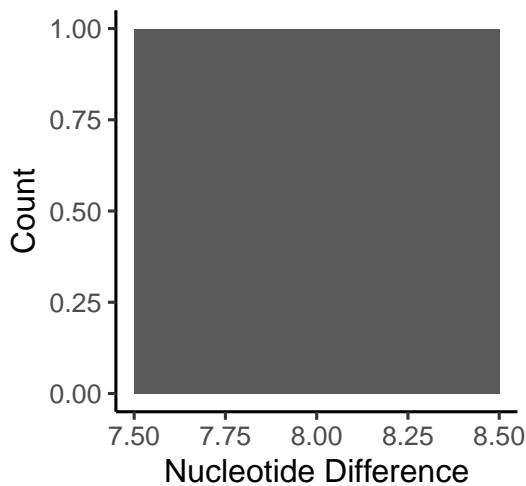
IGHV3-53*04

1125 sequences assigned
368 (32.7%) exact matches, in which:
246 unique CDR3
5 unique J



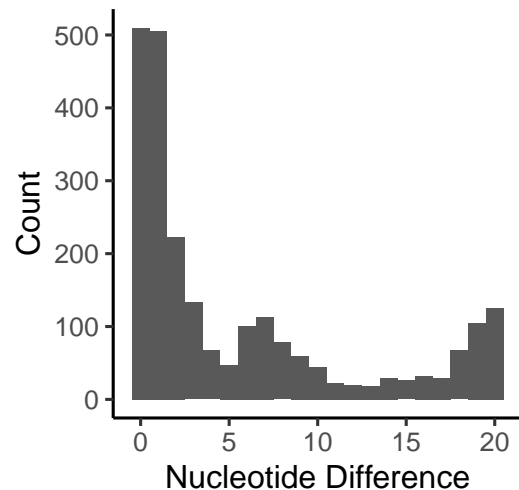
IGHV3-62*04

1 sequences assigned
No exact matches.



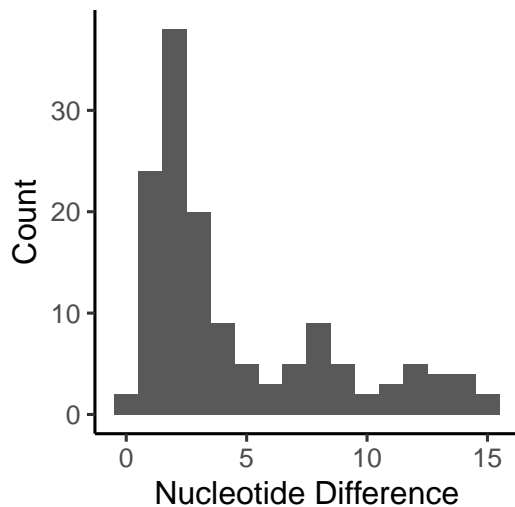
IGHV3-66*01

5853 sequences assigned
510 (8.7%) exact matches, in which:
372 unique CDR3
5 unique J



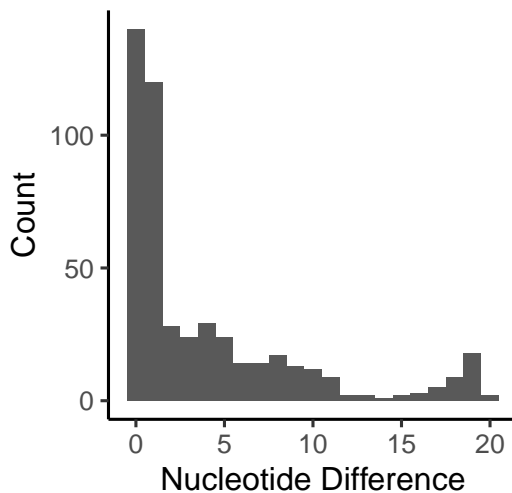
IGHV3-53*05

282 sequences assigned
2 (0.7%) exact matches, in which:
2 unique CDR3
1 unique J



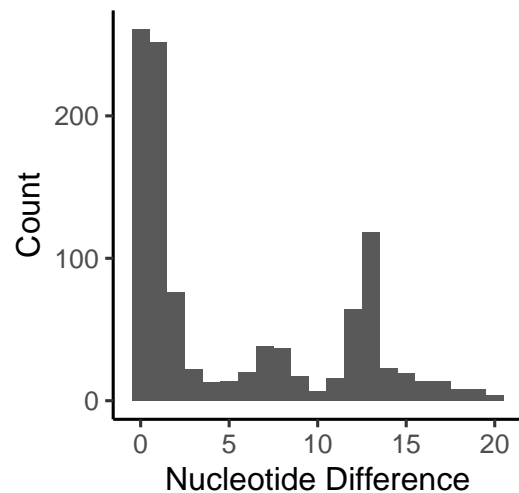
IGHV3-64*01

508 sequences assigned
140 (27.6%) exact matches, in which:
87 unique CDR3
5 unique J



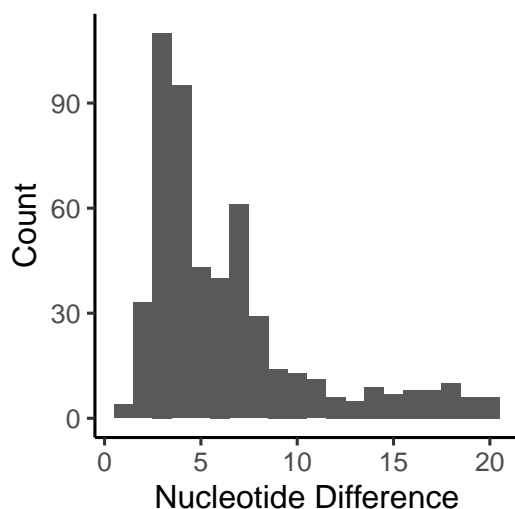
IGHV3-66*02

1202 sequences assigned
261 (21.7%) exact matches, in which:
183 unique CDR3
5 unique J



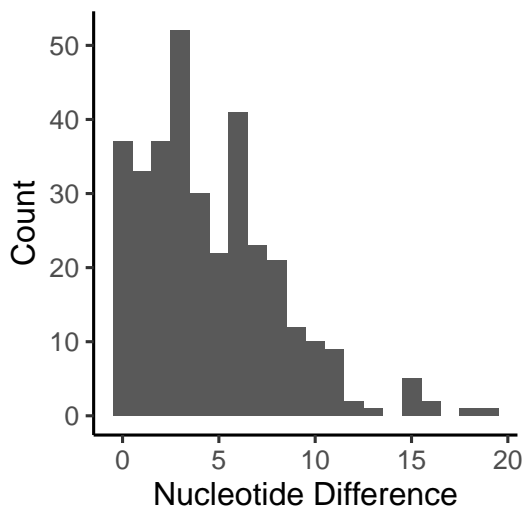
IGHV3-53*01_02

635 sequences assigned
No exact matches.



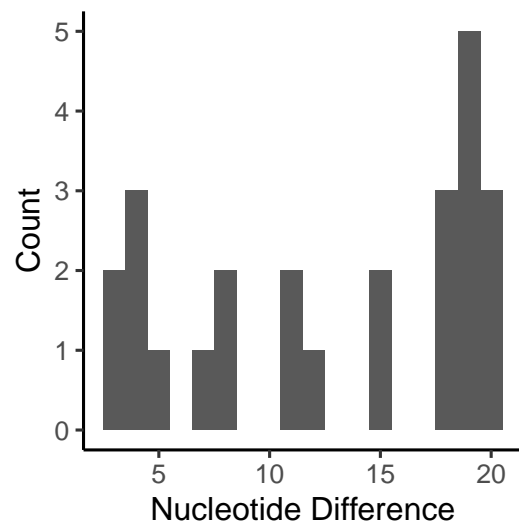
IGHV3-64*04

363 sequences assigned
37 (10.2%) exact matches, in which:
36 unique CDR3
4 unique J



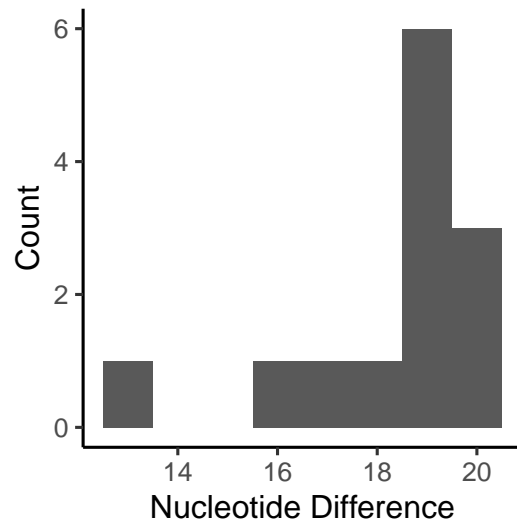
IGHV3-69-1*01

45 sequences assigned
No exact matches.



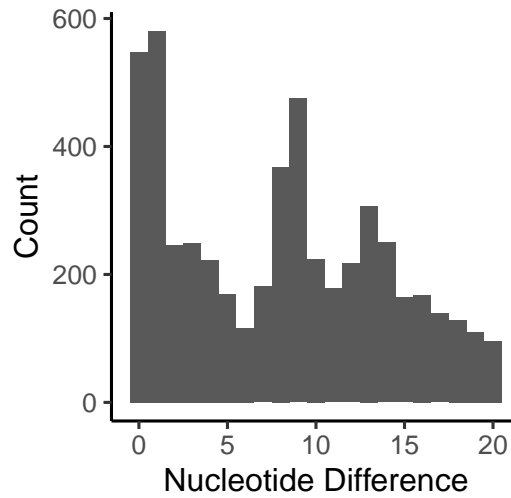
IGHV3-69-1*02

26 sequences assigned
No exact matches.



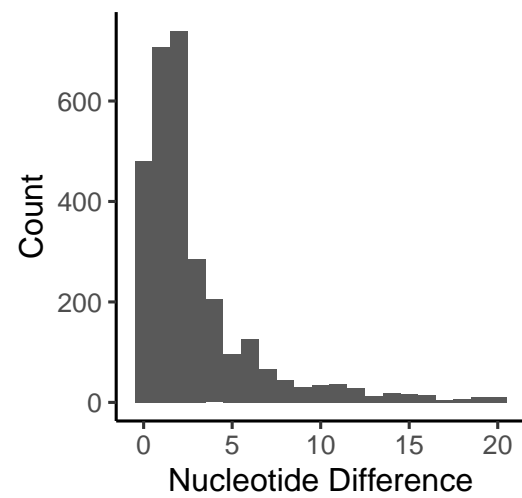
IGHV3-74*01_02

8176 sequences assigned
548 (6.7%) exact matches, in which:
370 unique CDR3
6 unique J



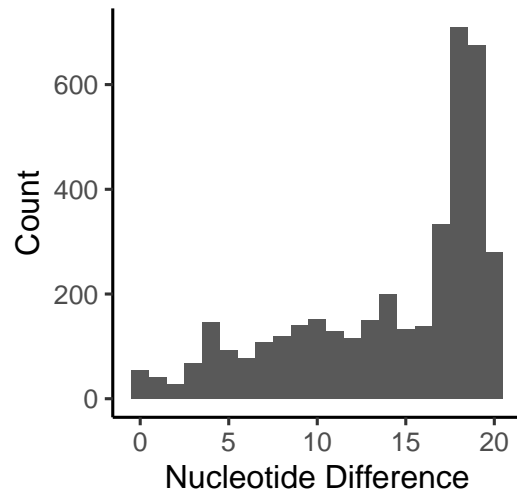
IGHV4-4*07

3120 sequences assigned
481 (15.4%) exact matches, in which:
404 unique CDR3
6 unique J



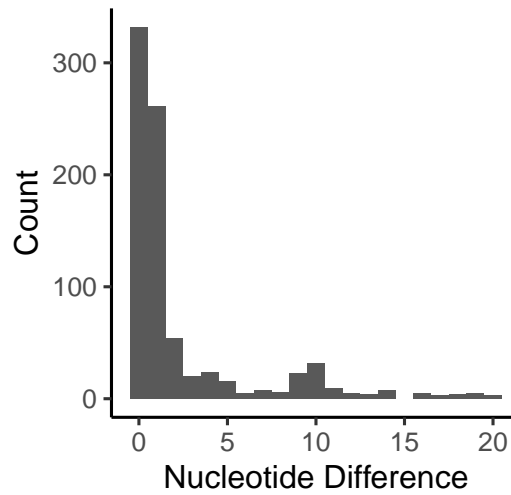
IGHV3-72*01

5382 sequences assigned
54 (1%) exact matches, in which:
34 unique CDR3
5 unique J



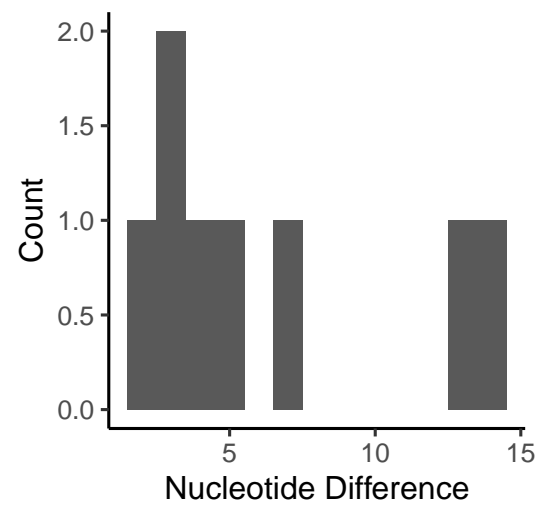
IGHV3-64D*09

940 sequences assigned
332 (35.3%) exact matches, in which:
199 unique CDR3
5 unique J



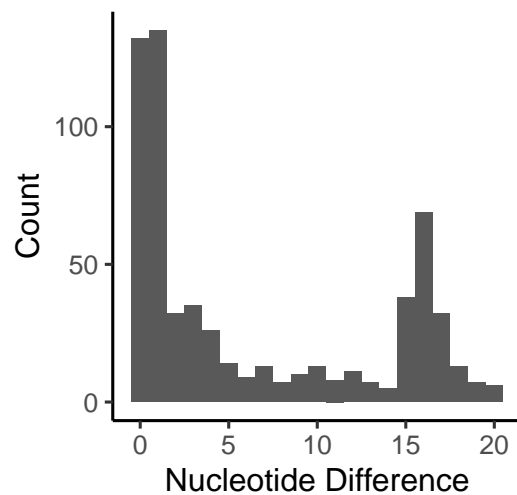
IGHV4-28*03

10 sequences assigned
No exact matches.



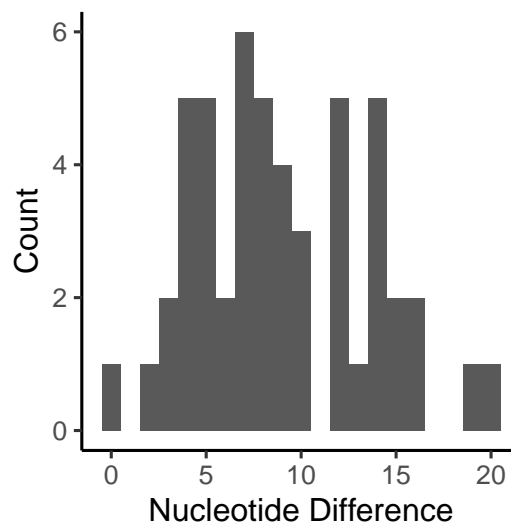
IGHV3-73*01_02

986 sequences assigned
132 (13.4%) exact matches, in which:
81 unique CDR3
5 unique J



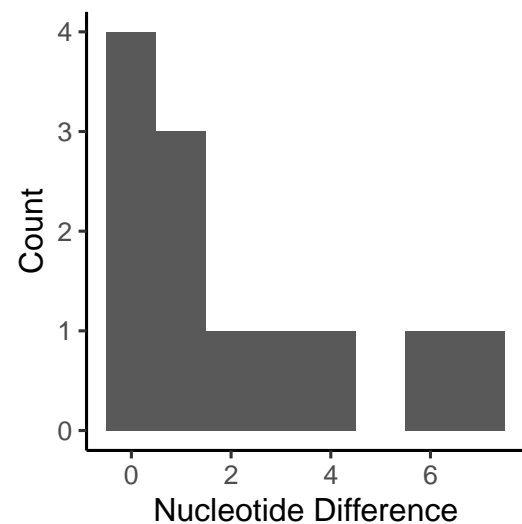
IGHV3-NL1*01

58 sequences assigned
1 (1.7%) exact matches, in which:
1 unique CDR3
1 unique J



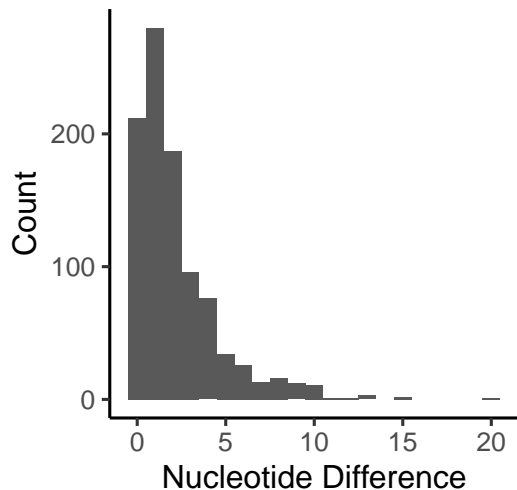
IGHV4-28*02_05

12 sequences assigned
4 (33.3%) exact matches, in which:
3 unique CDR3
3 unique J



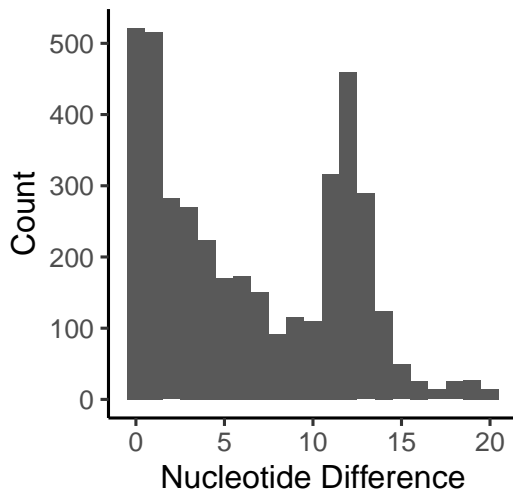
IGHV4-30-2*01

2074 sequences assigned
212 (10.2%) exact matches, in which:
150 unique CDR3
6 unique J



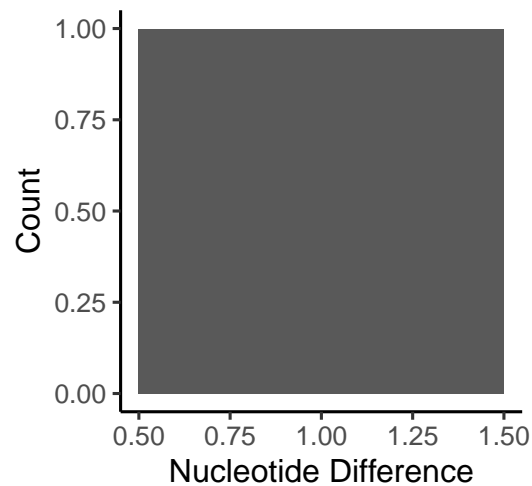
IGHV4-31*03_04

4059 sequences assigned
522 (12.9%) exact matches, in which:
412 unique CDR3
6 unique J



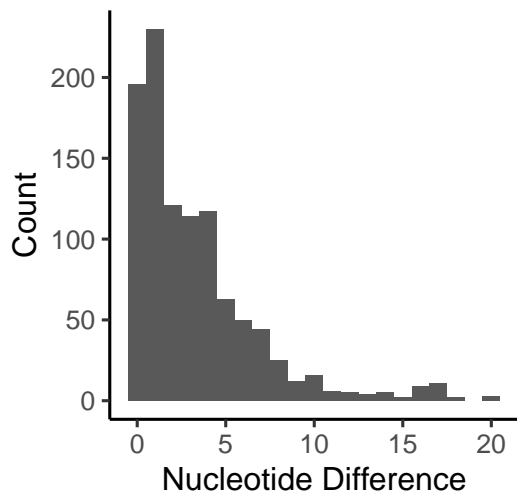
IGHV4-38-2*02

2 sequences assigned
No exact matches.



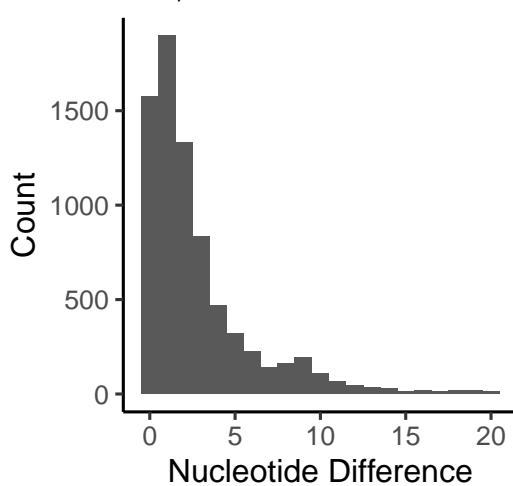
IGHV4-30-4*01

1303 sequences assigned
196 (15%) exact matches, in which:
163 unique CDR3
5 unique J



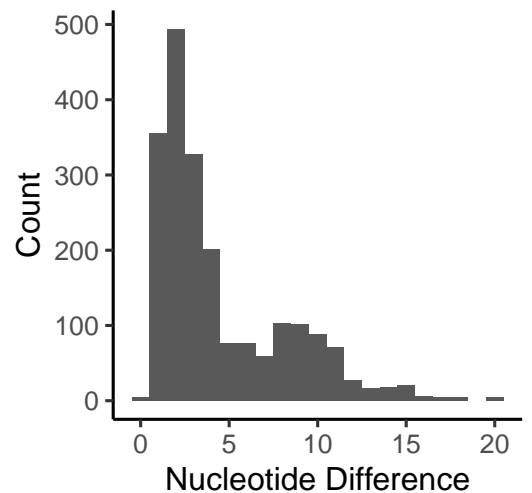
IGHV4-34*01_02

7916 sequences assigned
1575 (19.9%) exact matches, in which:
1121 unique CDR3
6 unique J



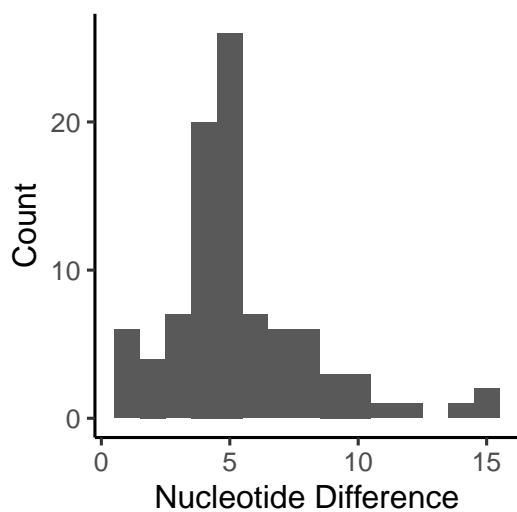
IGHV4-39*07

2105 sequences assigned
5 (0.2%) exact matches, in which:
5 unique CDR3
2 unique J



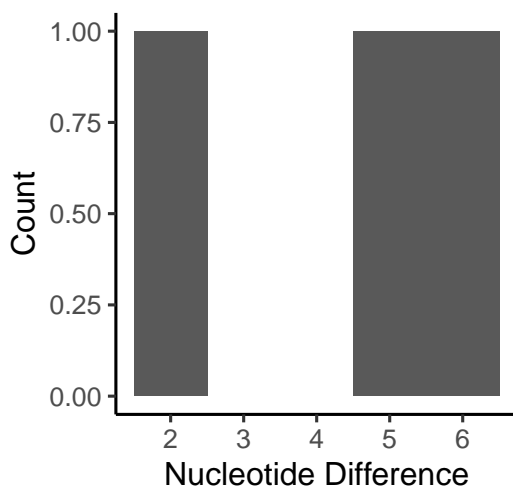
IGHV4-30-2*03

96 sequences assigned
No exact matches.



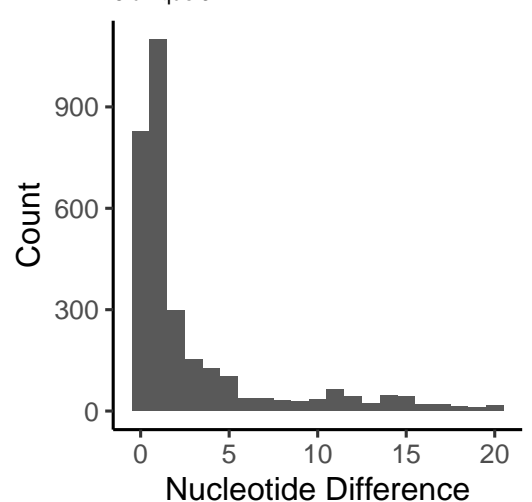
IGHV4-38-2*01

5 sequences assigned
No exact matches.



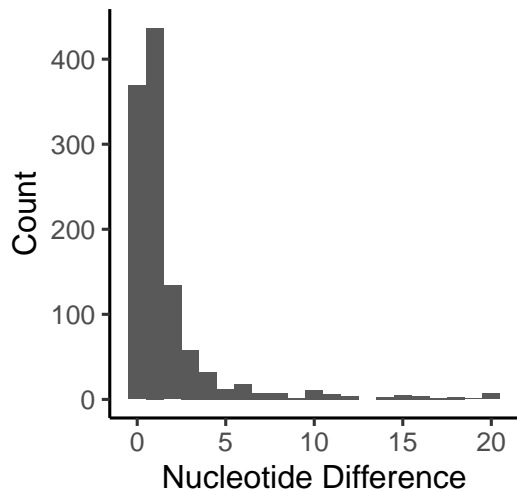
IGHV4-39*01_05

4876 sequences assigned
828 (17%) exact matches, in which:
514 unique CDR3
6 unique J



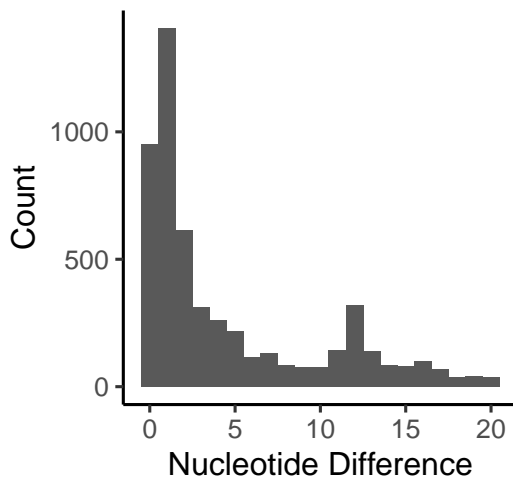
IGHV4-39*02_C258G

1257 sequences assigned
369 (29.4%) exact matches, in which:
322 unique CDR3
6 unique J



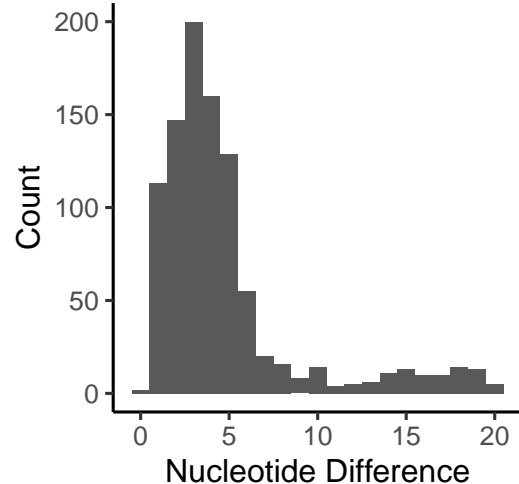
IGHV4-59*08

5810 sequences assigned
952 (16.4%) exact matches, in which:
728 unique CDR3
6 unique J



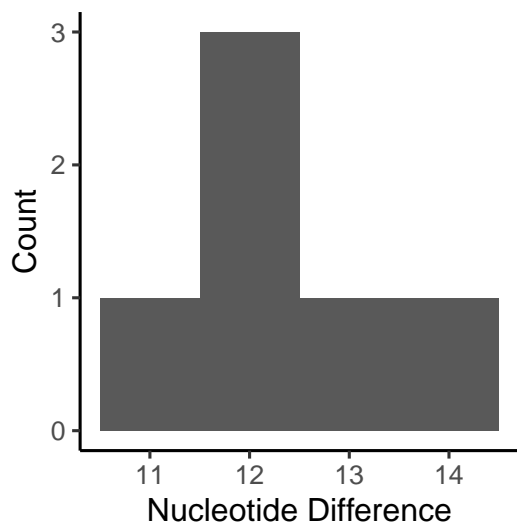
IGHV4-61*01

1005 sequences assigned
2 (0.2%) exact matches, in which:
2 unique CDR3
2 unique J



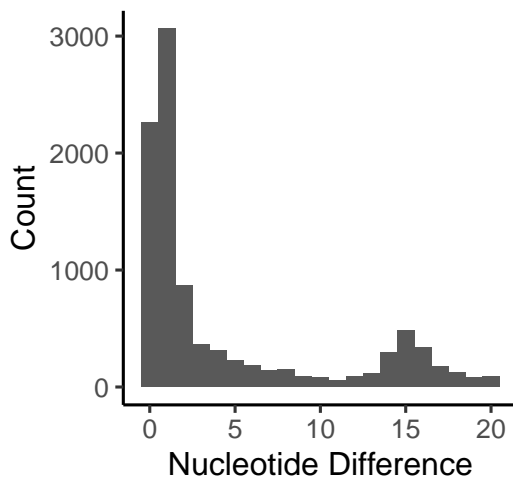
IGHV4-55*09

8 sequences assigned
No exact matches.



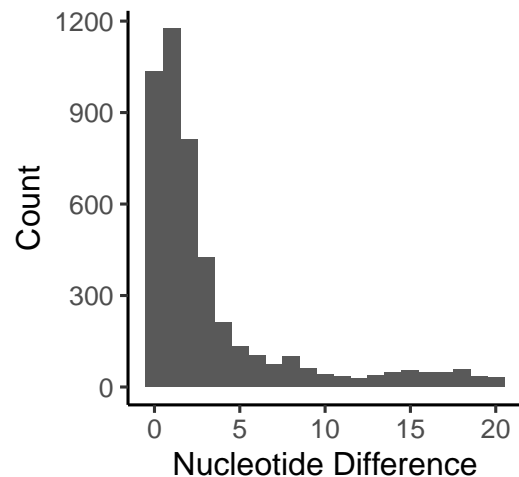
IGHV4-59*01_07

12336 sequences assigned
2260 (18.3%) exact matches, in which:
1683 unique CDR3
6 unique J



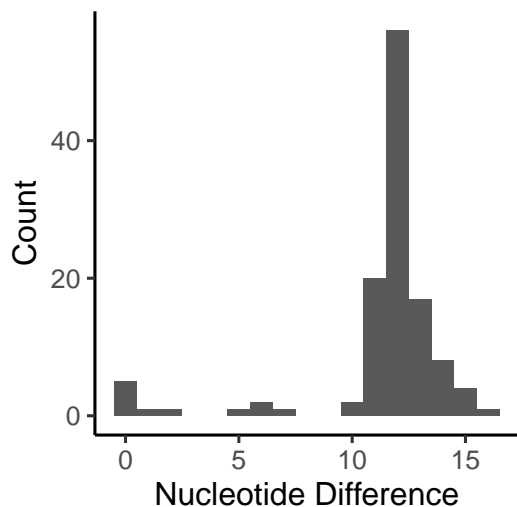
IGHV4-61*02

4774 sequences assigned
1036 (21.7%) exact matches, in which:
861 unique CDR3
6 unique J



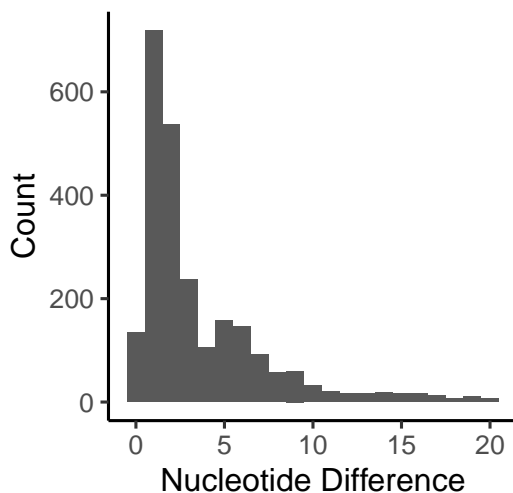
IGHV4-55*02_04_08

123 sequences assigned
5 (4.1%) exact matches, in which:
4 unique CDR3
1 unique J



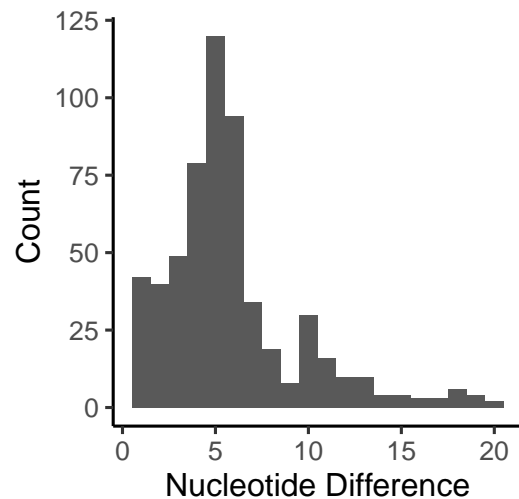
IGHV4-59*12

2527 sequences assigned
134 (5.3%) exact matches, in which:
126 unique CDR3
6 unique J



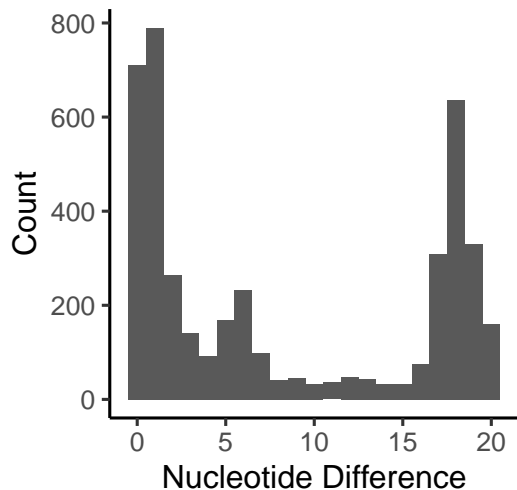
IGHV4-61*08

597 sequences assigned
No exact matches.



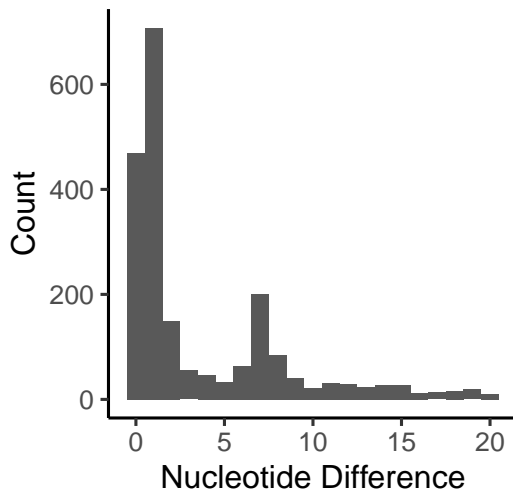
IGHV5-10-1*01_03

4801 sequences assigned
710 (14.8%) exact matches, in which:
468 unique CDR3
5 unique J



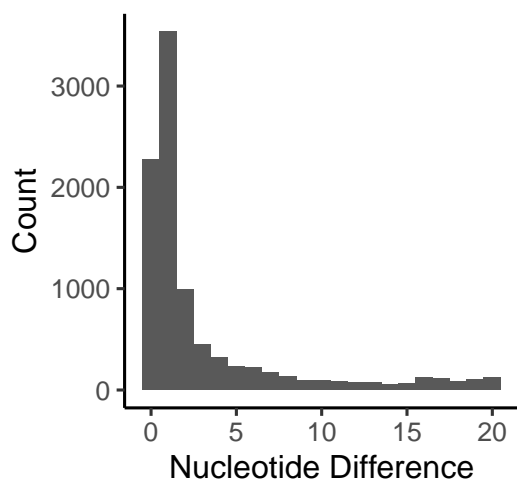
IGHV7-4-1*02

2654 sequences assigned
470 (17.7%) exact matches, in which:
360 unique CDR3
6 unique J



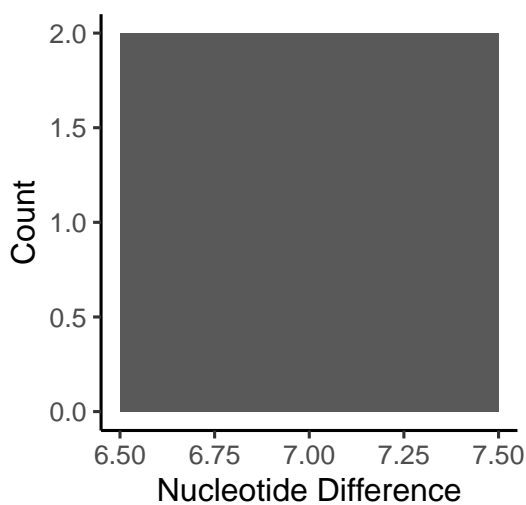
IGHV5-51*01_03

12518 sequences assigned
2274 (18.2%) exact matches, in which:
1185 unique CDR3
5 unique J



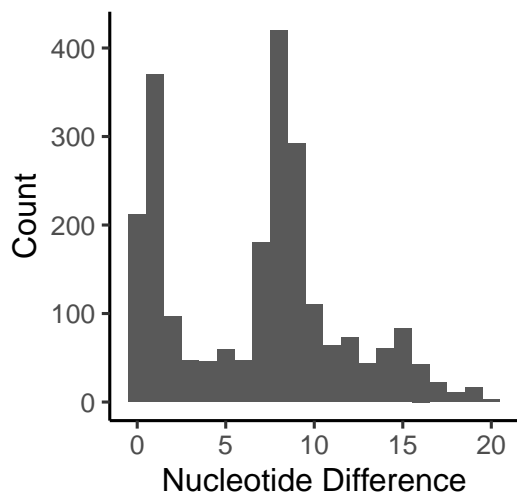
IGHV7-81*01

2 sequences assigned
No exact matches.



IGHV6-1*01_02

2491 sequences assigned
212 (8.5%) exact matches, in which:
156 unique CDR3
6 unique J





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.

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