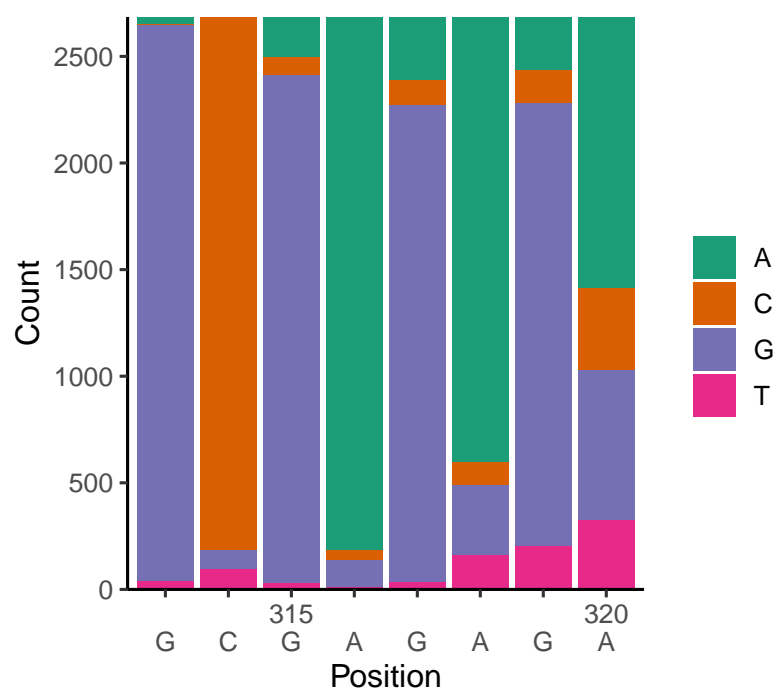
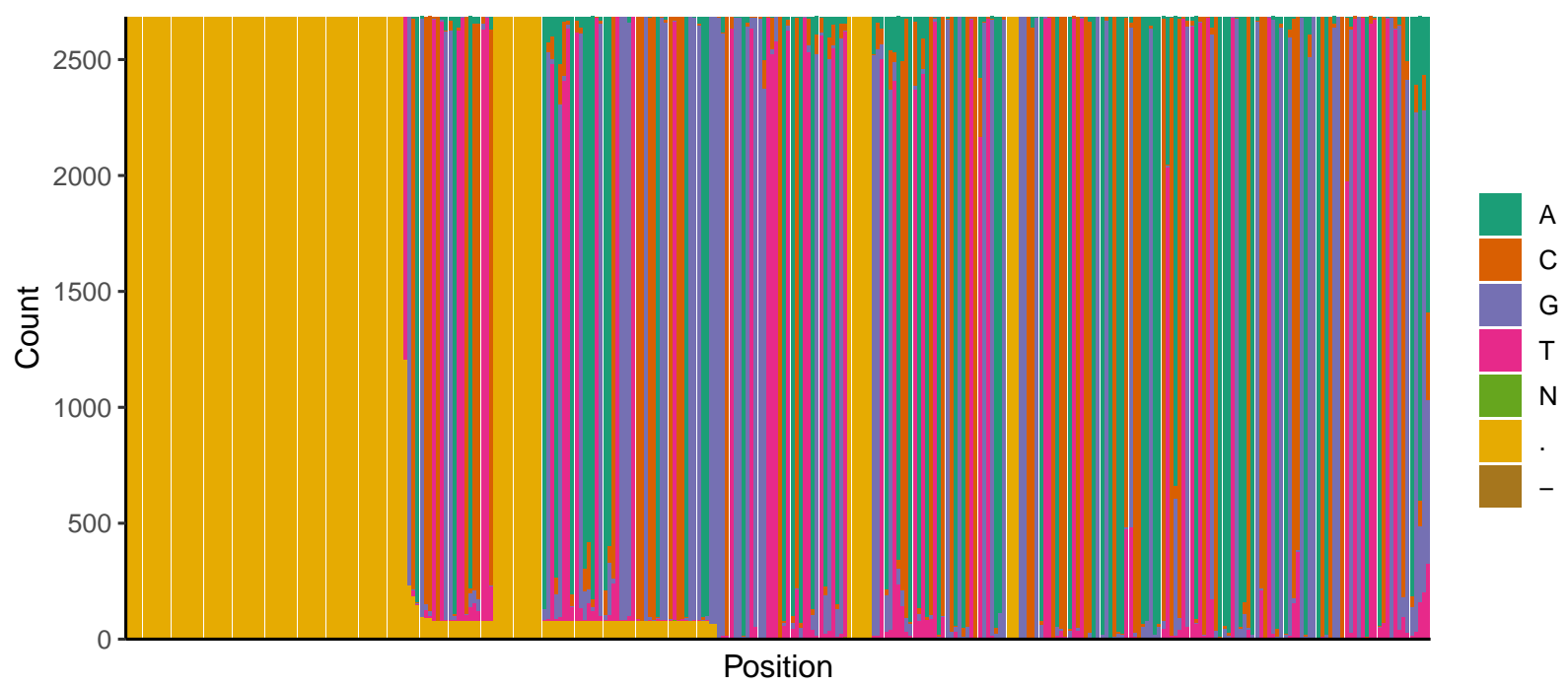


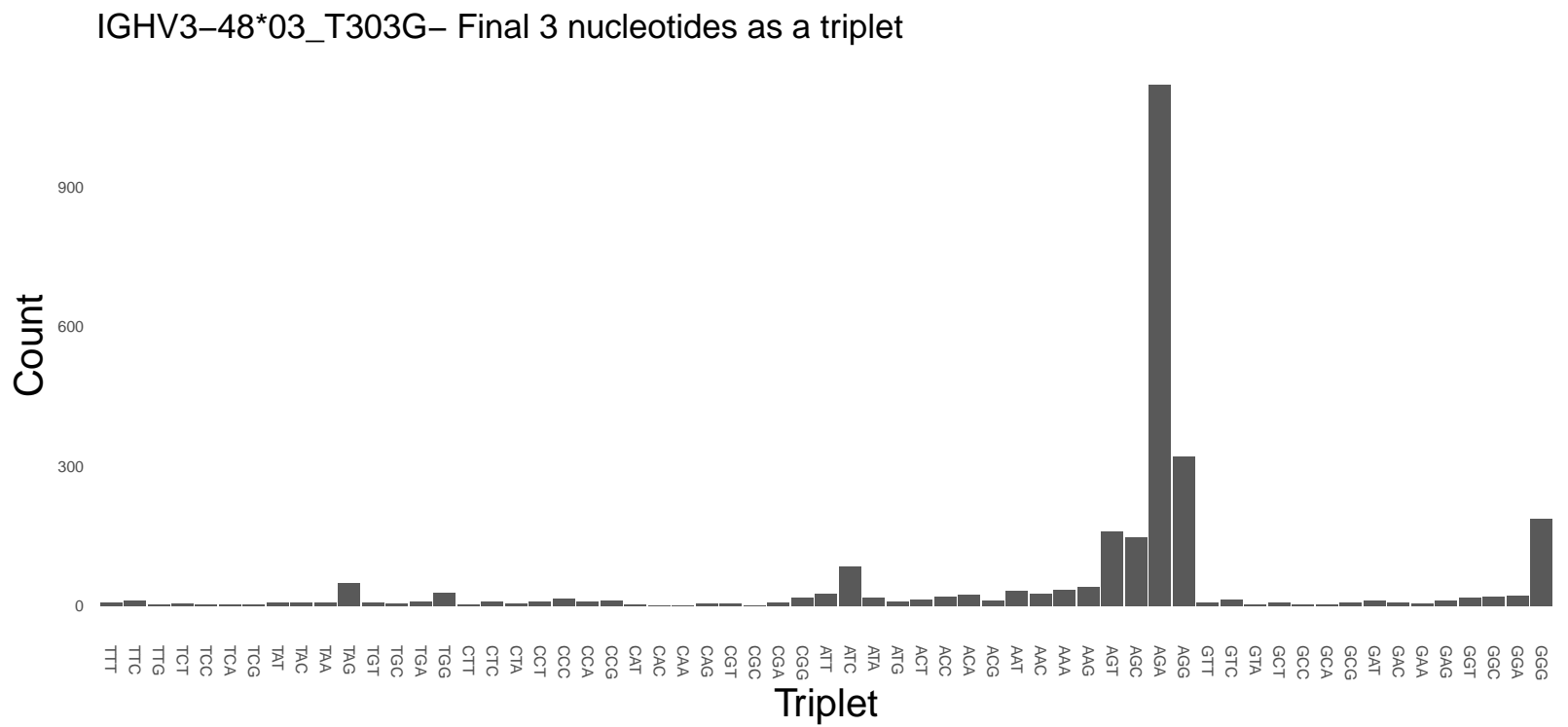
Gene IGHV3-48*03_T303G



Gene IGHV3-48*03_T303G

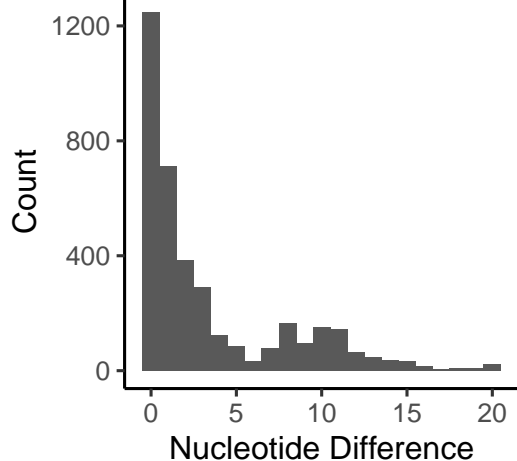


IGHV3-48*03_T303G- Final 3 nucleotides as a triplet



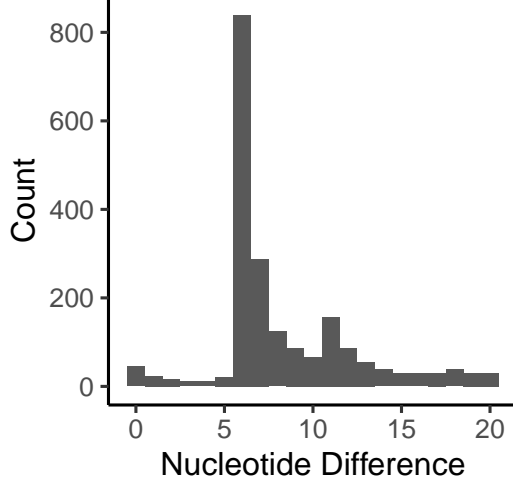
IGHV1-2*04

4905 sequences assigned
1247 (25.4%) exact matches, in which:
1147 unique CDR3
6 unique J



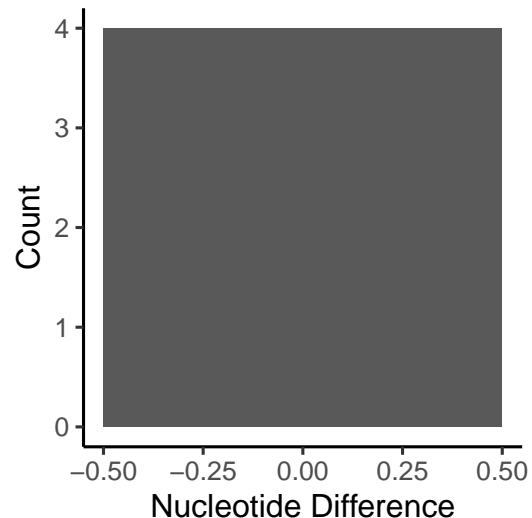
IGHV1-18*01

2552 sequences assigned
45 (1.8%) exact matches, in which:
45 unique CDR3
5 unique J



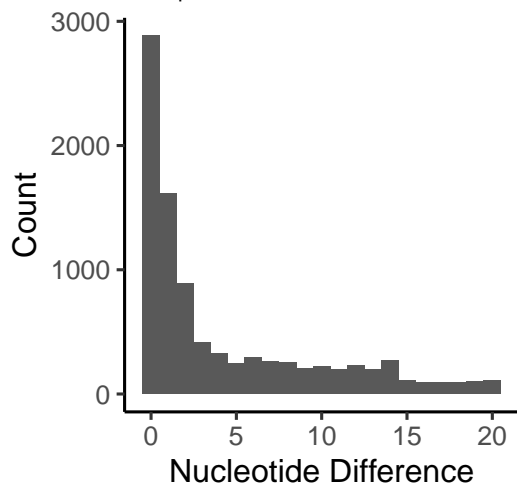
IGHV1-45*02

4 sequences assigned
4 (100%) exact matches, in which:
4 unique CDR3
3 unique J



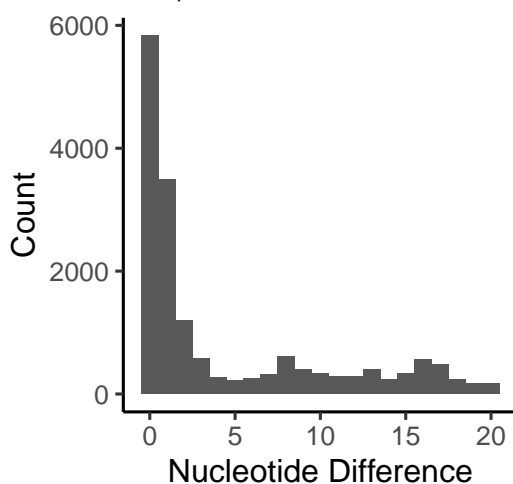
IGHV1-3*01_05

9492 sequences assigned
2884 (30.4%) exact matches, in which:
2612 unique CDR3
6 unique J



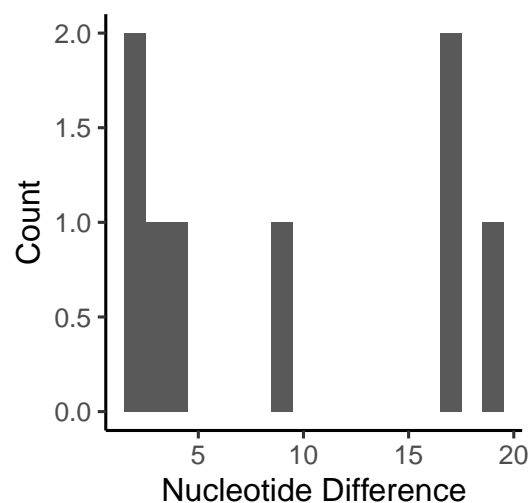
IGHV1-18*04

18176 sequences assigned
5831 (32.1%) exact matches, in which:
5288 unique CDR3
6 unique J



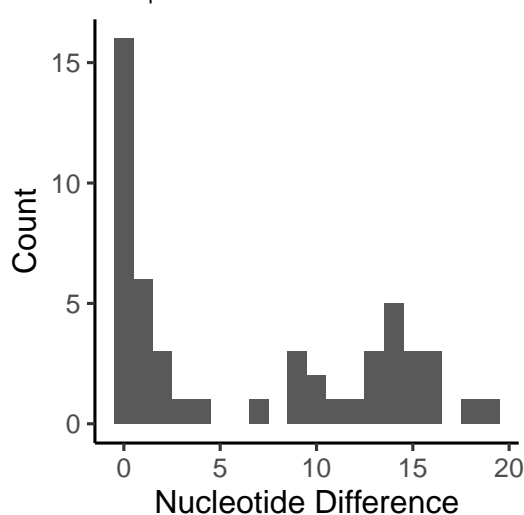
IGHV1-45*03

8 sequences assigned
No exact matches.



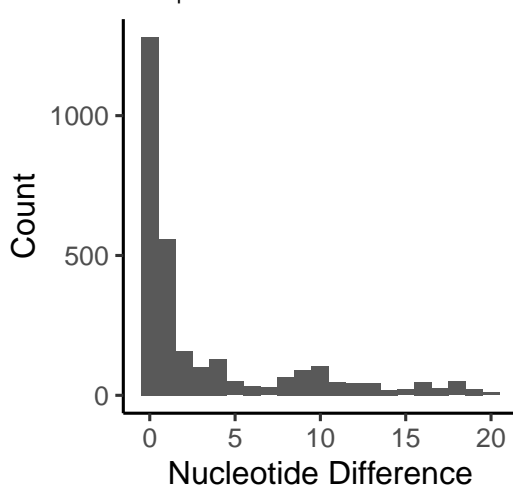
IGHV1-8*01

59 sequences assigned
16 (27.1%) exact matches, in which:
16 unique CDR3
3 unique J



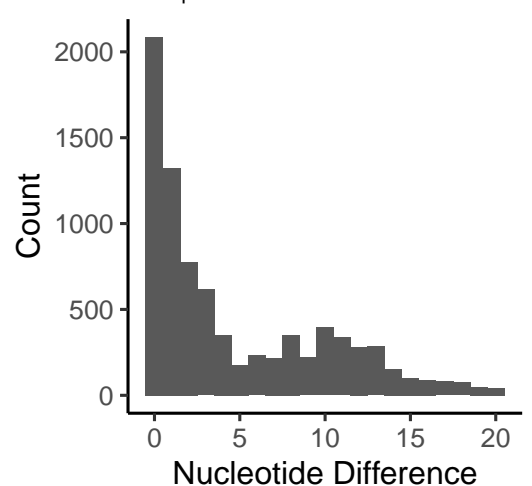
IGHV1-24*01

3006 sequences assigned
1281 (42.6%) exact matches, in which:
1201 unique CDR3
6 unique J



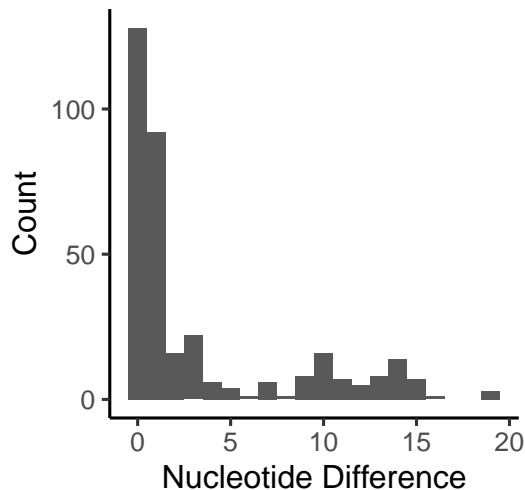
IGHV1-46*01

8777 sequences assigned
2086 (23.8%) exact matches, in which:
1926 unique CDR3
6 unique J



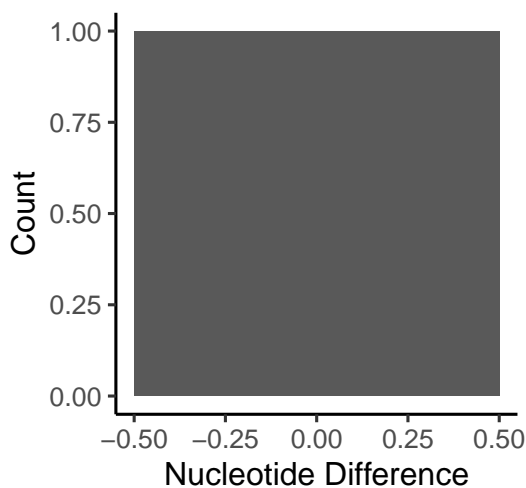
IGHV1–58*02

351 sequences assigned
128 (36.5%) exact matches, in which:
118 unique CDR3
6 unique J



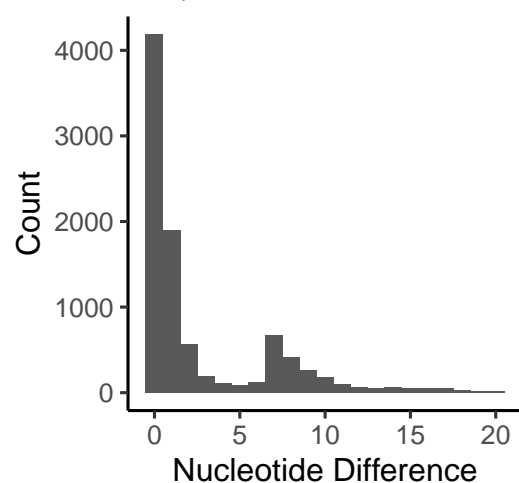
IGHV1–68*02

1 sequences assigned
1 (100%) exact matches, in which:
1 unique CDR3
1 unique J



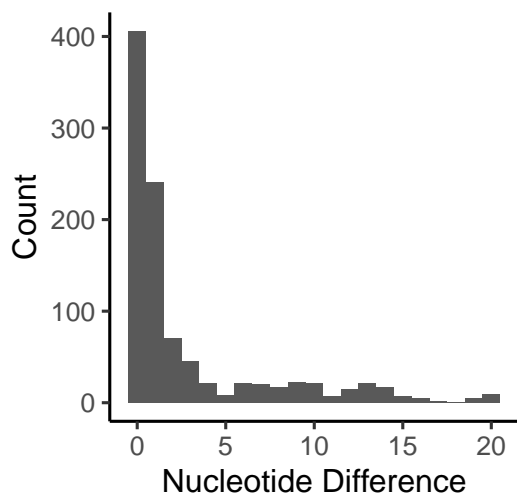
IGHV1–69*06_14

9767 sequences assigned
4186 (42.9%) exact matches, in which:
3973 unique CDR3
6 unique J



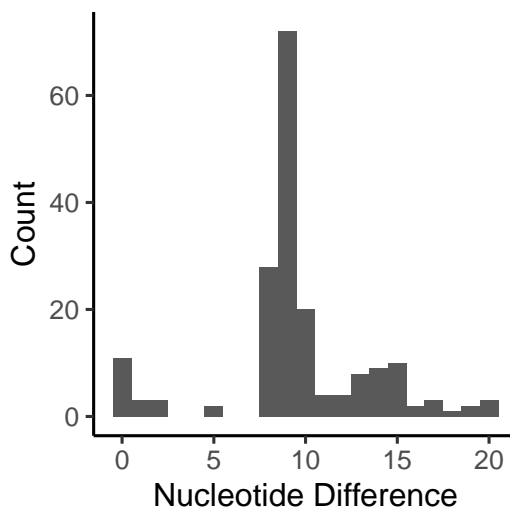
IGHV1–58*01_03

1031 sequences assigned
406 (39.4%) exact matches, in which:
380 unique CDR3
6 unique J



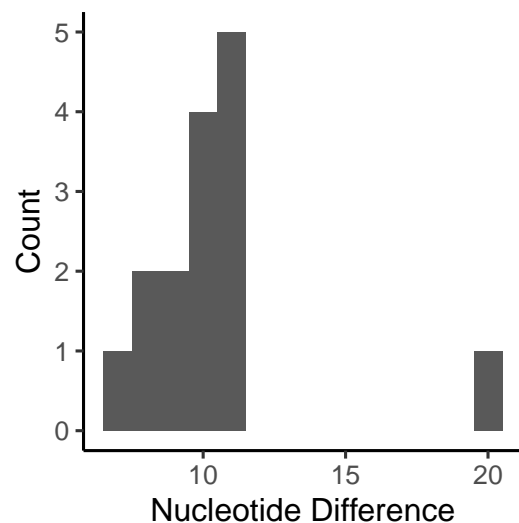
IGHV1–69–2*01

195 sequences assigned
11 (5.6%) exact matches, in which:
9 unique CDR3
4 unique J



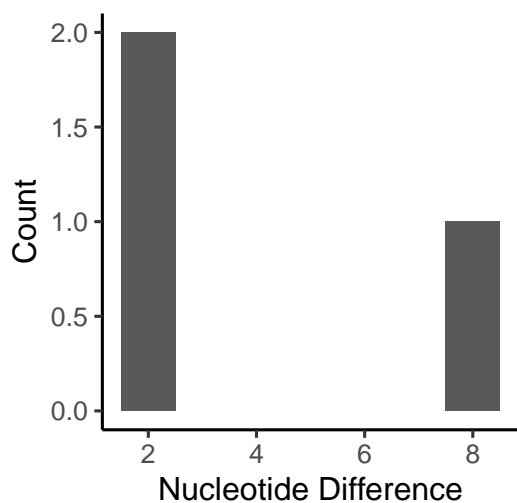
IGHV1–NL1*01

15 sequences assigned
No exact matches.



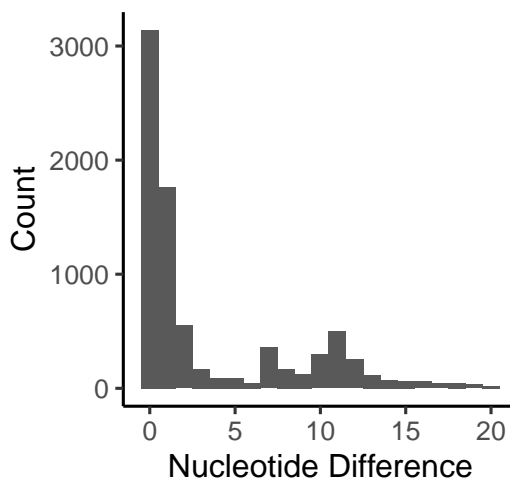
IGHV1–68*01

3 sequences assigned
No exact matches.



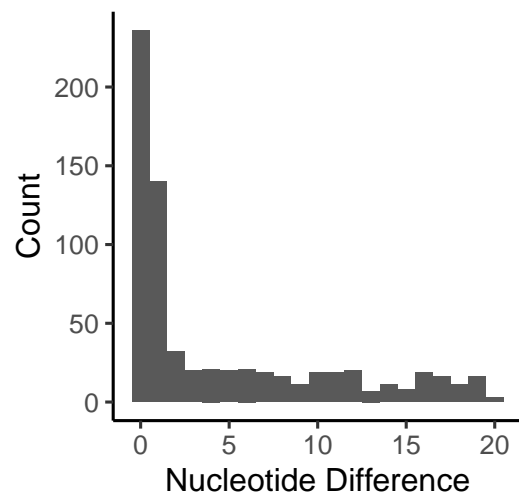
IGHV1–69*04_09

8134 sequences assigned
3140 (38.6%) exact matches, in which:
2972 unique CDR3
6 unique J



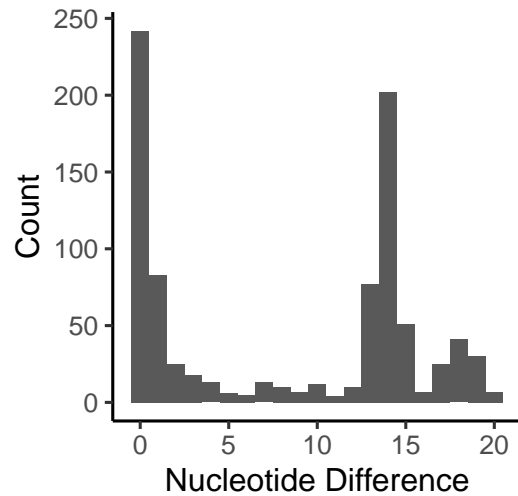
IGHV2–5*02

803 sequences assigned
236 (29.4%) exact matches, in which:
223 unique CDR3
6 unique J



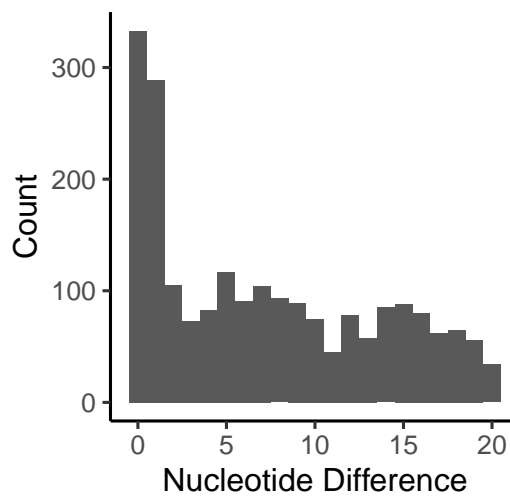
IGHV2-26*01

899 sequences assigned
242 (26.9%) exact matches, in which:
226 unique CDR3
5 unique J



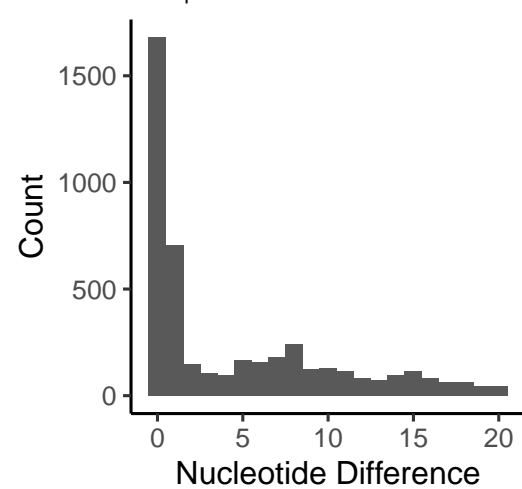
IGHV3-7*01

2337 sequences assigned
333 (14.2%) exact matches, in which:
328 unique CDR3
6 unique J



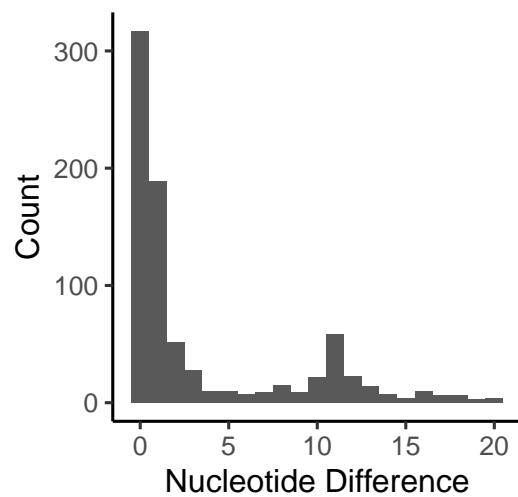
IGHV3-11*06

4740 sequences assigned
1680 (35.4%) exact matches, in which:
1267 unique CDR3
6 unique J



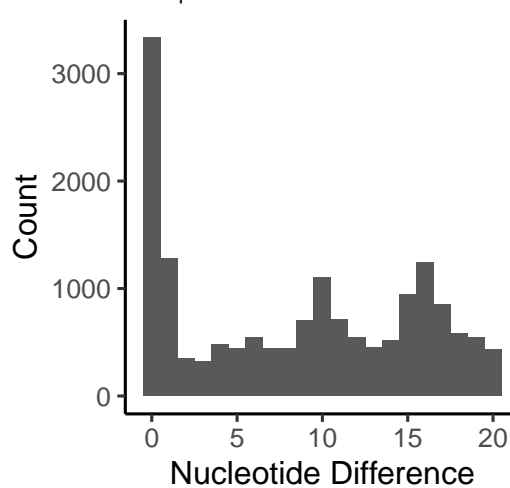
IGHV2-70*01

811 sequences assigned
317 (39.1%) exact matches, in which:
294 unique CDR3
6 unique J



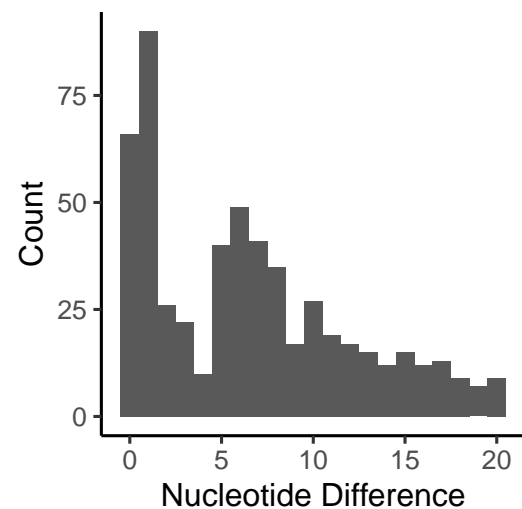
IGHV3-7*03

21704 sequences assigned
3334 (15.4%) exact matches, in which:
2405 unique CDR3
6 unique J



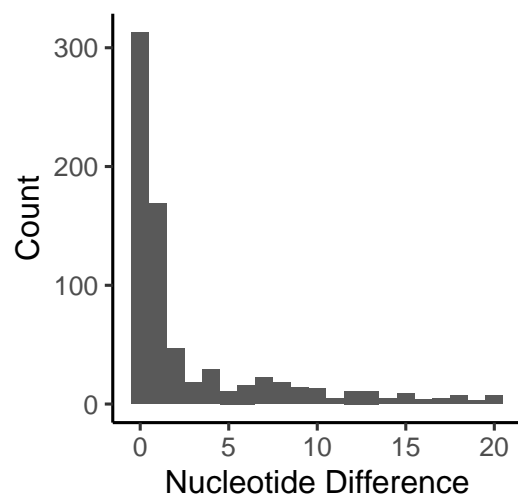
IGHV3-11*03_05

603 sequences assigned
66 (10.9%) exact matches, in which:
66 unique CDR3
5 unique J



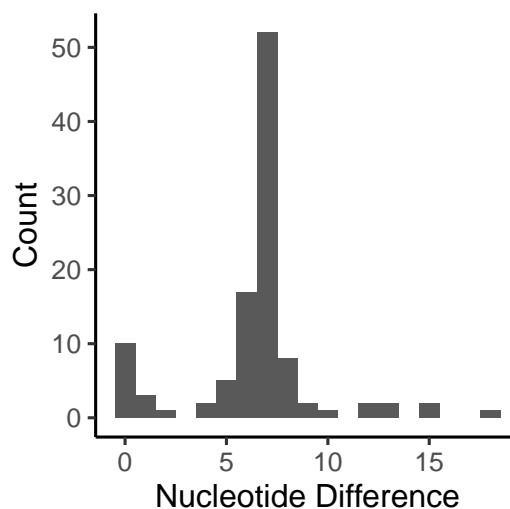
IGHV2-70*11_15

836 sequences assigned
313 (37.4%) exact matches, in which:
290 unique CDR3
6 unique J



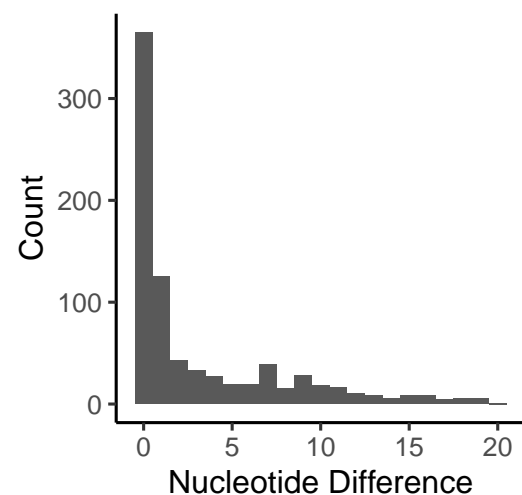
IGHV3-9*01

130 sequences assigned
10 (7.7%) exact matches, in which:
7 unique CDR3
4 unique J



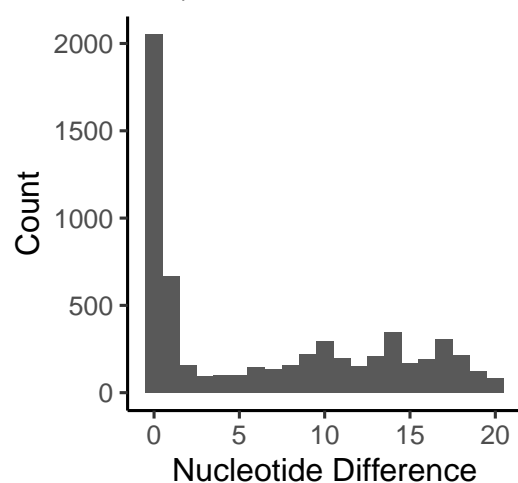
IGHV3-13*05

884 sequences assigned
365 (41.3%) exact matches, in which:
268 unique CDR3
5 unique J



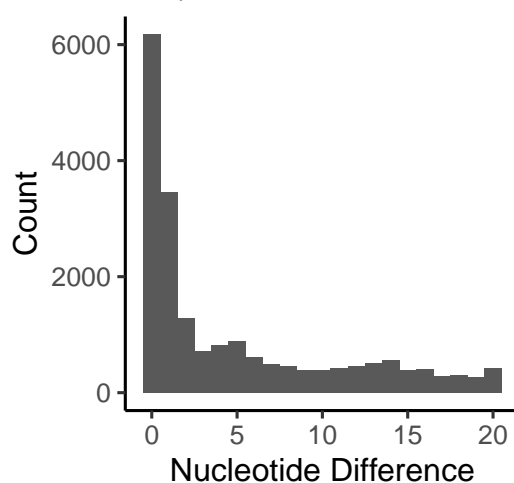
IGHV3-15*01_02

7185 sequences assigned
2052 (28.6%) exact matches, in which:
1571 unique CDR3
6 unique J



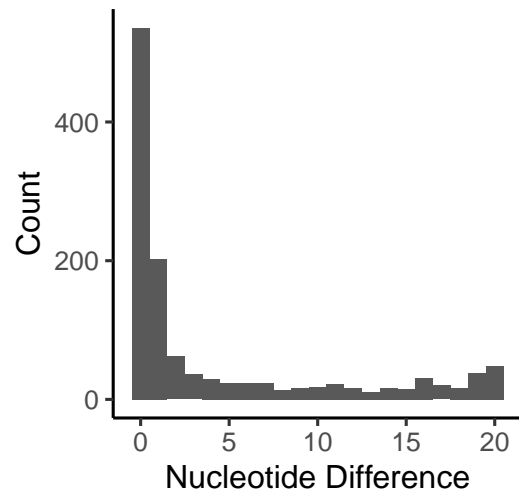
IGHV3-21*01_02

26237 sequences assigned
6176 (23.5%) exact matches, in which:
4412 unique CDR3
6 unique J



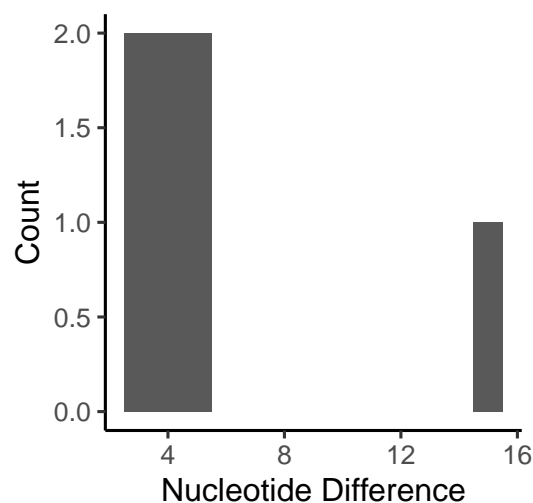
IGHV3-30*03

1307 sequences assigned
536 (41%) exact matches, in which:
507 unique CDR3
6 unique J



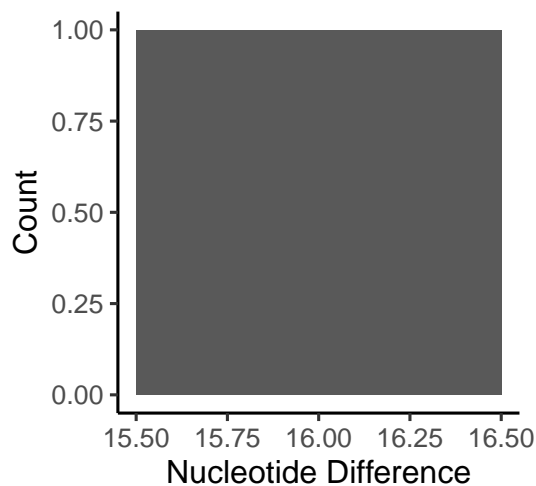
IGHV3-19*01

7 sequences assigned
No exact matches.



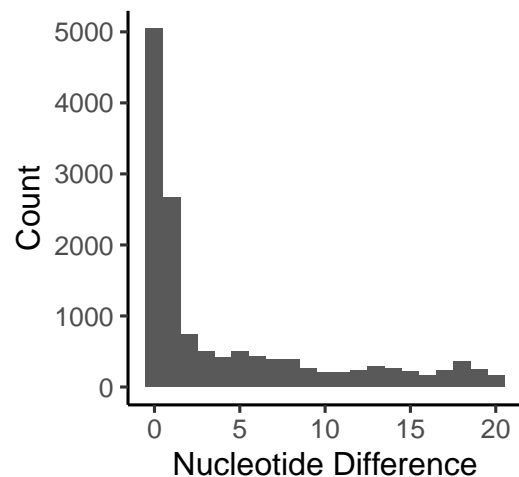
IGHV3-22*01_02

1 sequences assigned
No exact matches.



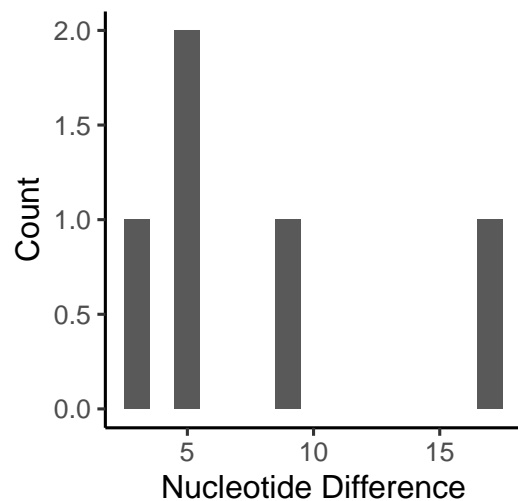
IGHV3-33*01

14820 sequences assigned
5044 (34%) exact matches, in which:
3777 unique CDR3
6 unique J



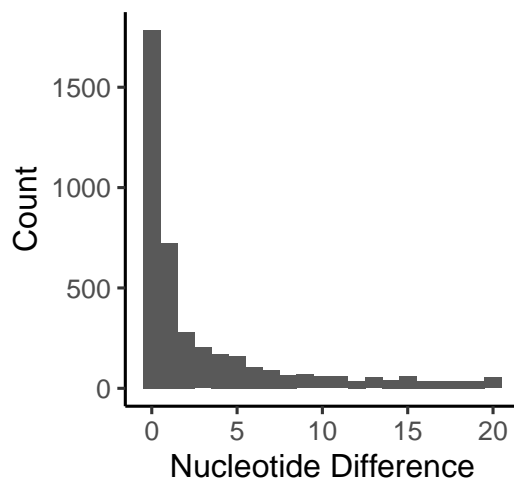
IGHV3-20*03_04

6 sequences assigned
No exact matches.



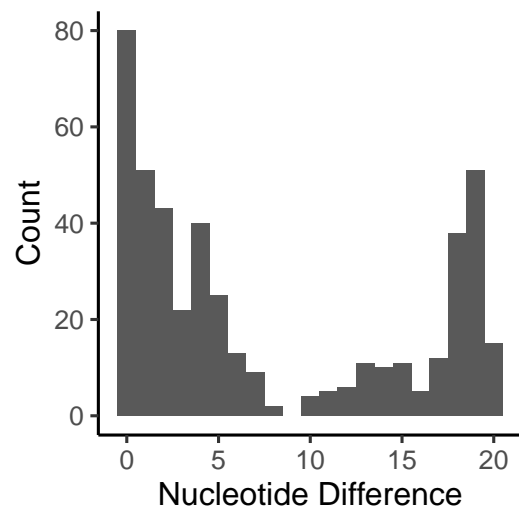
IGHV3-30-3*01

4872 sequences assigned
1785 (36.6%) exact matches, in which:
1369 unique CDR3
6 unique J



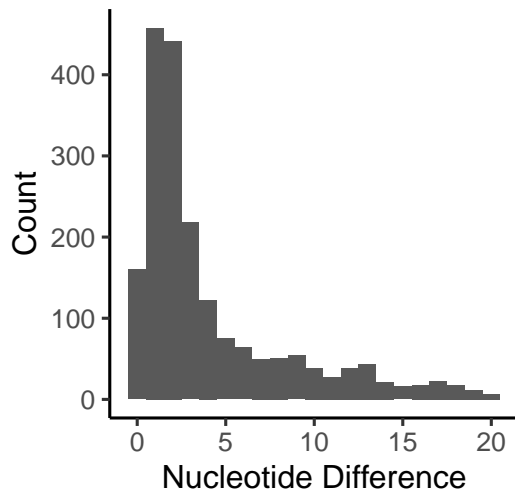
IGHV3-33*05

479 sequences assigned
80 (16.7%) exact matches, in which:
76 unique CDR3
6 unique J



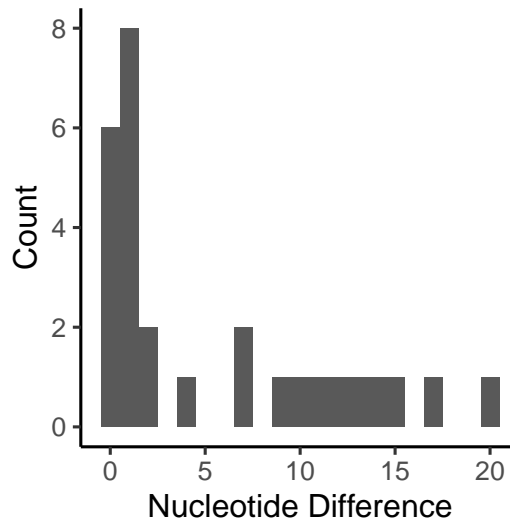
IGHV3–33*06

1999 sequences assigned
160 (8%) exact matches, in which:
159 unique CDR3
5 unique J



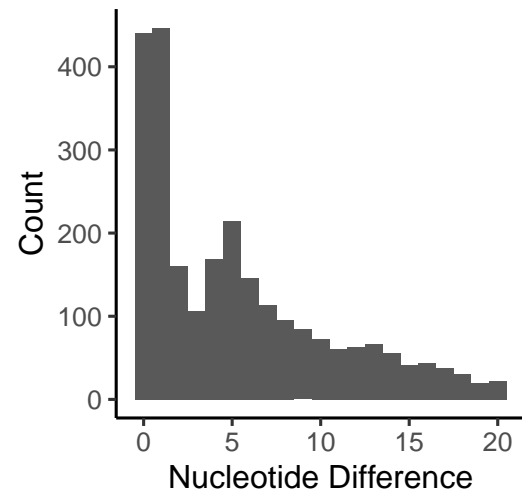
IGHV3–47*01

28 sequences assigned
6 (21.4%) exact matches, in which:
3 unique CDR3
3 unique J



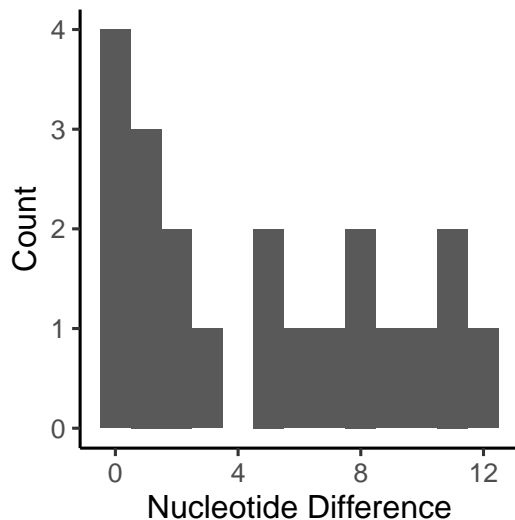
IGHV3–48*03_T303G

2685 sequences assigned
441 (16.4%) exact matches, in which:
433 unique CDR3
6 unique J



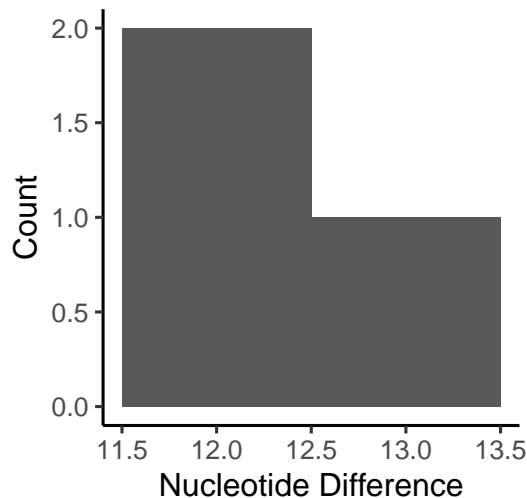
IGHV3–35*01

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



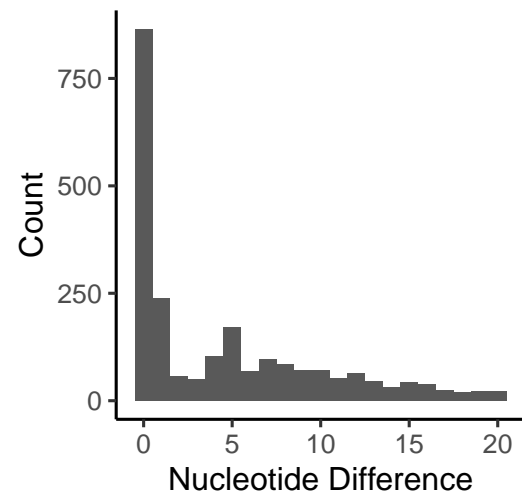
IGHV3–47*02

3 sequences assigned
No exact matches.



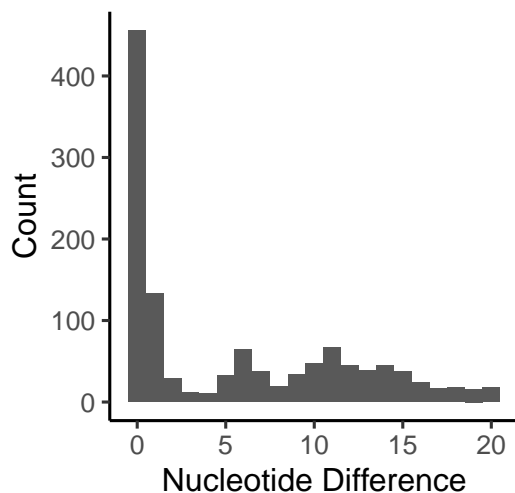
IGHV3–49*04

2409 sequences assigned
865 (35.9%) exact matches, in which:
661 unique CDR3
6 unique J



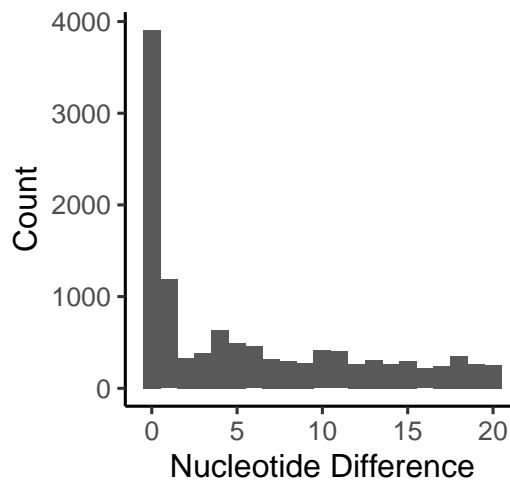
IGHV3–43*02

1302 sequences assigned
456 (35%) exact matches, in which:
335 unique CDR3
6 unique J



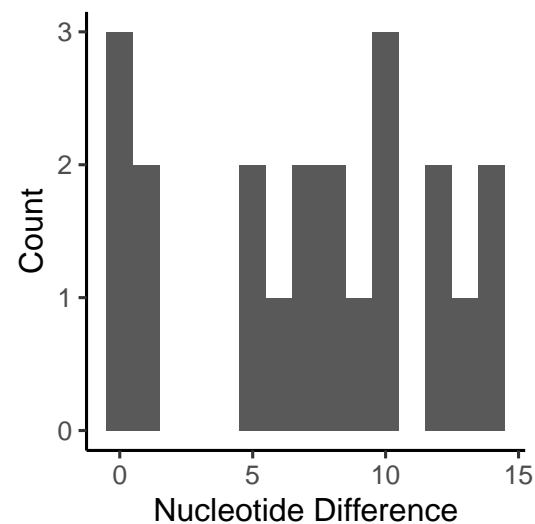
IGHV3–48*03

13494 sequences assigned
3907 (29%) exact matches, in which:
2887 unique CDR3
6 unique J



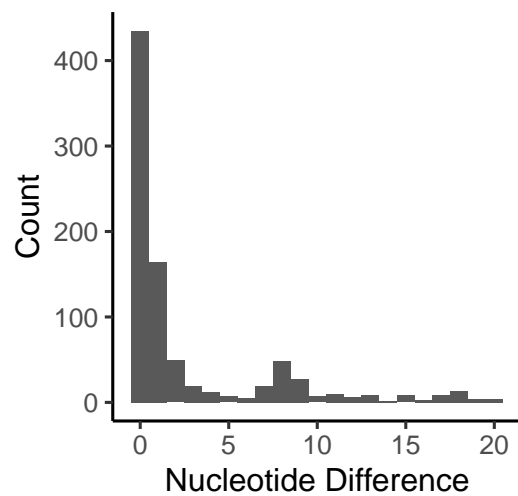
IGHV3–52*01_03

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



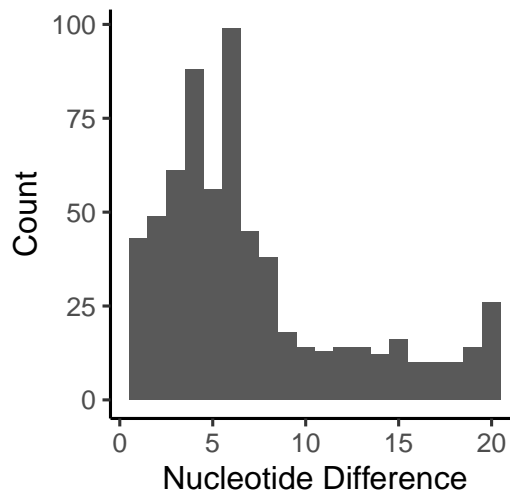
IGHV3-53*04

898 sequences assigned
435 (48.4%) exact matches, in which:
327 unique CDR3
6 unique J



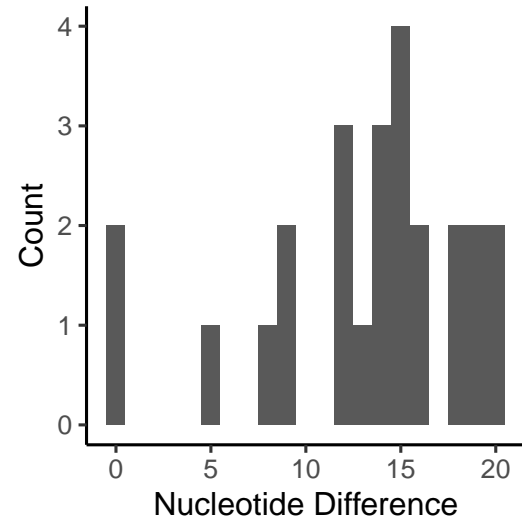
IGHV3-64*04

712 sequences assigned
No exact matches.



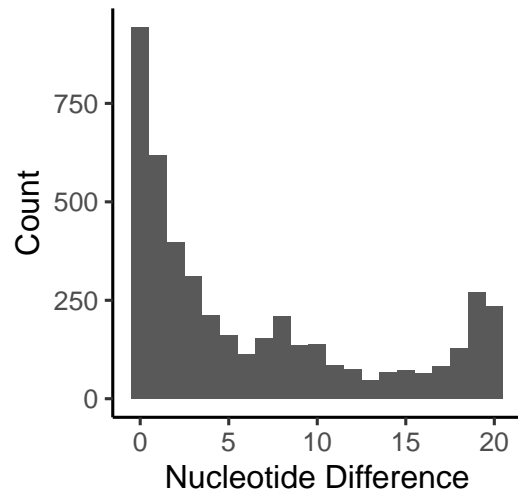
IGHV3-69-1*02

44 sequences assigned
2 (4.5%) exact matches, in which:
2 unique CDR3
2 unique J



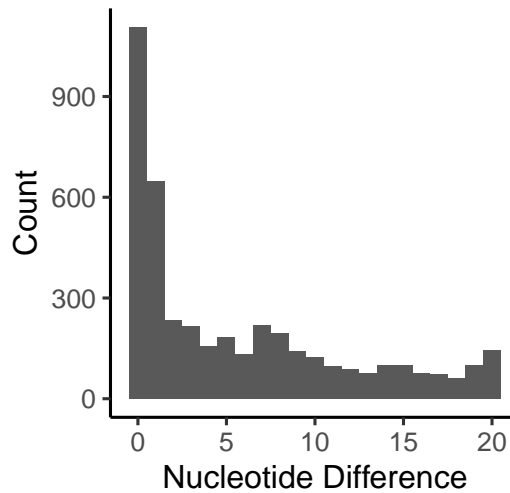
IGHV3-53*01_02

5115 sequences assigned
944 (18.5%) exact matches, in which:
691 unique CDR3
6 unique J



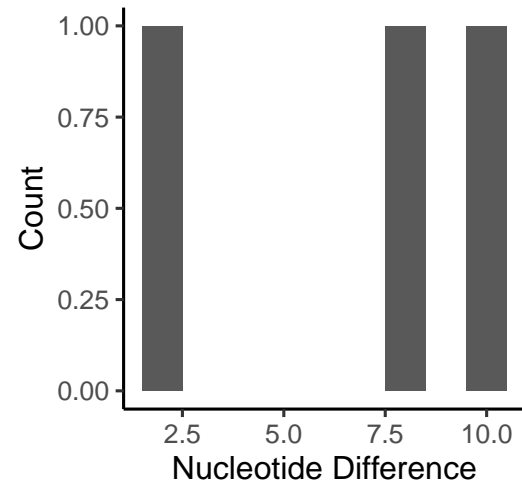
IGHV3-66*01

4593 sequences assigned
1107 (24.1%) exact matches, in which:
819 unique CDR3
6 unique J



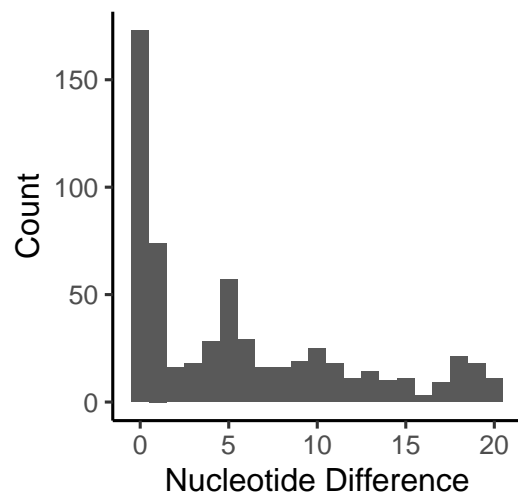
IGHV3-71*01_04

3 sequences assigned
No exact matches.



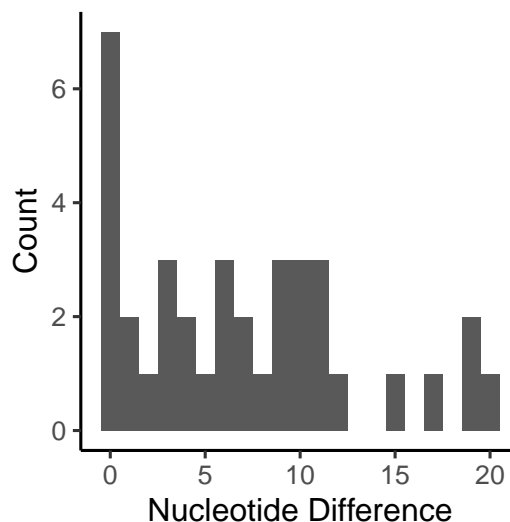
IGHV3-64*01

671 sequences assigned
173 (25.8%) exact matches, in which:
132 unique CDR3
5 unique J



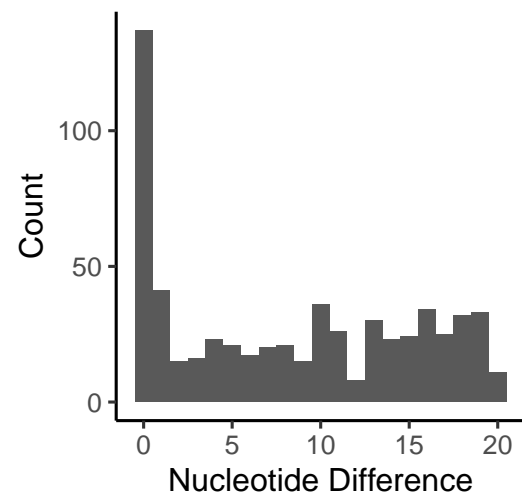
IGHV3-69-1*01

45 sequences assigned
7 (15.6%) exact matches, in which:
6 unique CDR3
2 unique J



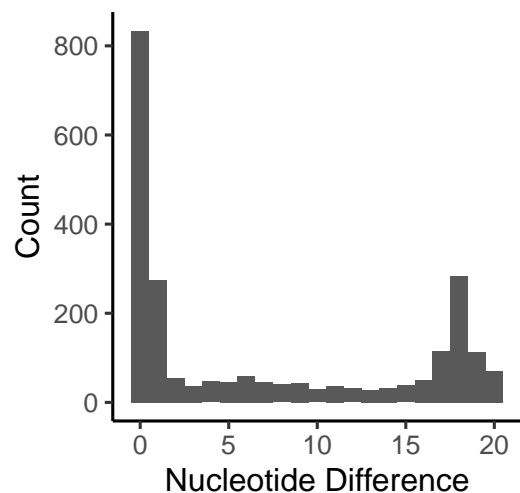
IGHV3-72*01

1490 sequences assigned
137 (9.2%) exact matches, in which:
102 unique CDR3
5 unique J



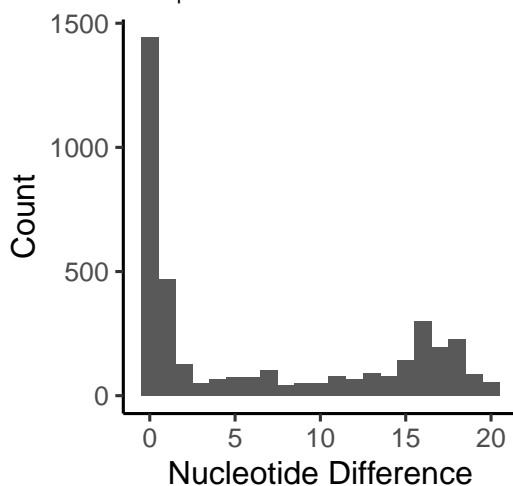
IGHV3-73*01_02

3133 sequences assigned
834 (26.6%) exact matches, in which:
609 unique CDR3
6 unique J



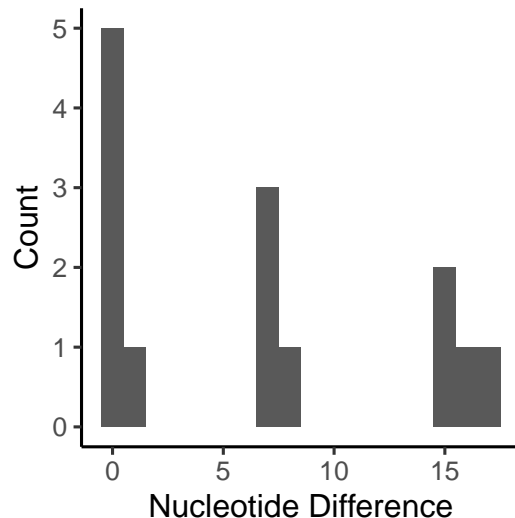
IGHV3-64D*06

5139 sequences assigned
1443 (28.1%) exact matches, in which:
979 unique CDR3
6 unique J



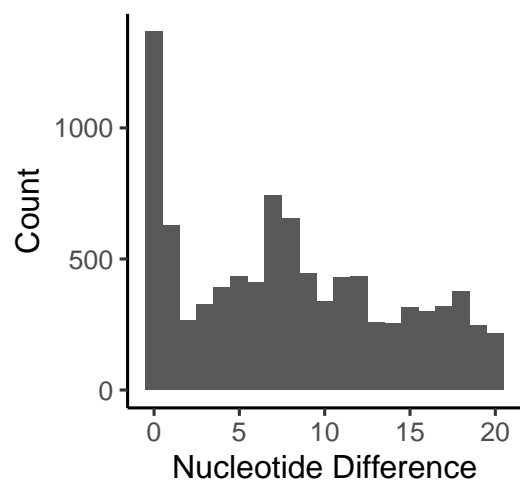
IGHV4-28*01_07

18 sequences assigned
5 (27.8%) exact matches, in which:
5 unique CDR3
3 unique J



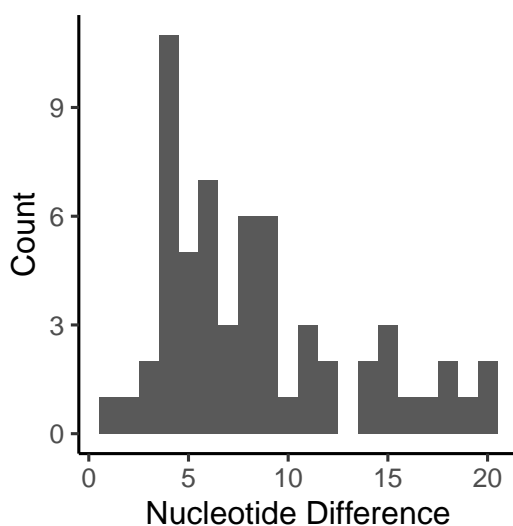
IGHV3-74*01_02

11298 sequences assigned
1367 (12.1%) exact matches, in which:
972 unique CDR3
6 unique J



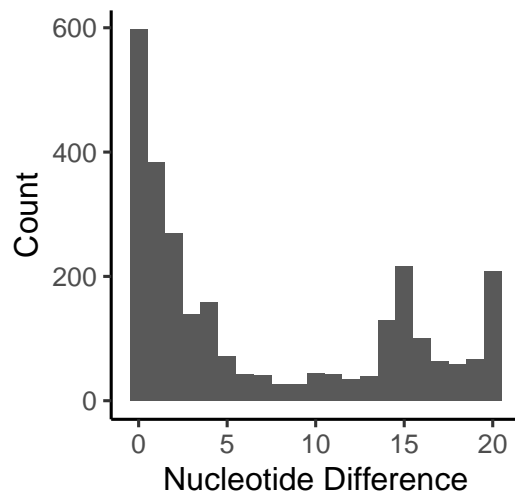
IGHV3-NL1*01

76 sequences assigned
No exact matches.



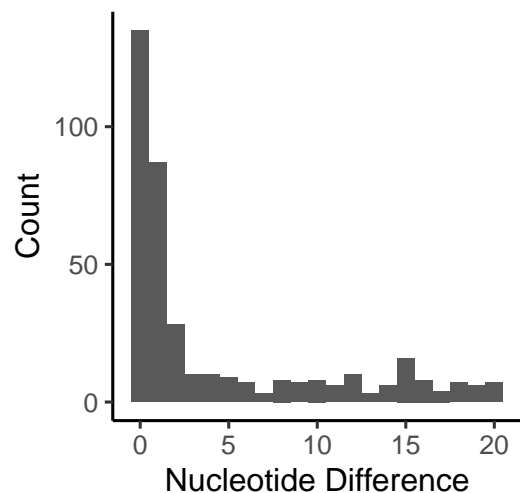
IGHV4-30-2*01

3557 sequences assigned
598 (16.8%) exact matches, in which:
541 unique CDR3
6 unique J



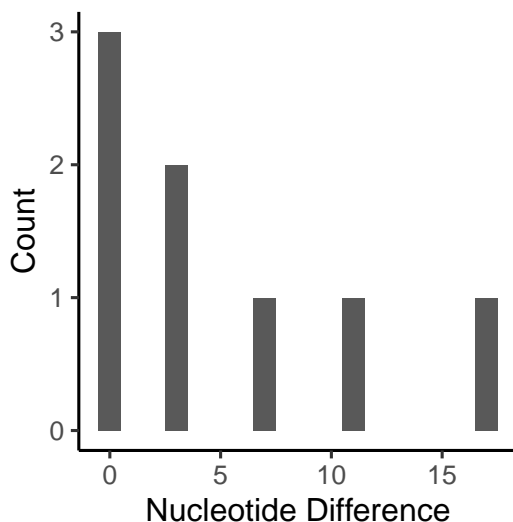
IGHV3-43D*04

412 sequences assigned
135 (32.8%) exact matches, in which:
92 unique CDR3
4 unique J



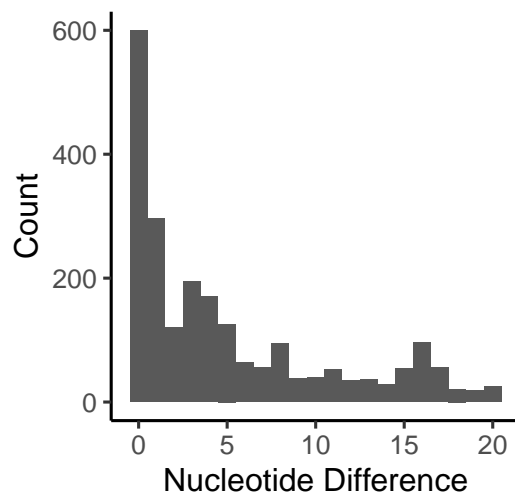
IGHV4-28*03

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



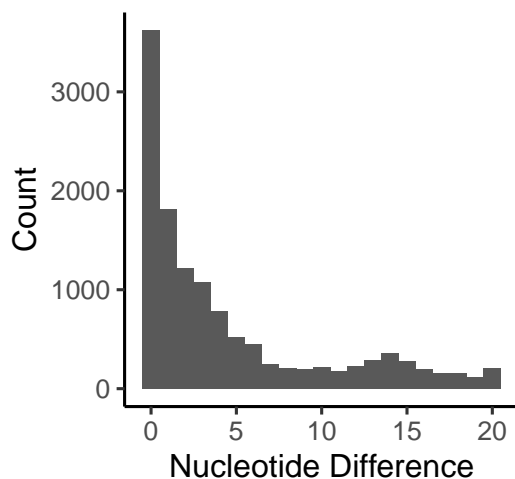
IGHV4-30-4*01

2342 sequences assigned
600 (25.6%) exact matches, in which:
565 unique CDR3
6 unique J



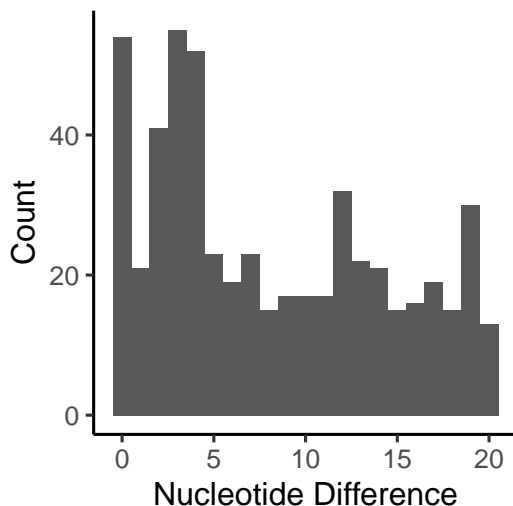
IGHV4-31*03_04

14147 sequences assigned
3621 (25.6%) exact matches, in which:
3378 unique CDR3
6 unique J



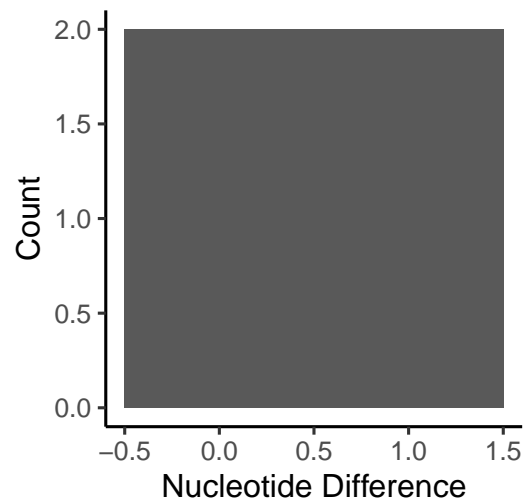
IGHV4-38-2*02

1314 sequences assigned
54 (4.1%) exact matches, in which:
53 unique CDR3
6 unique J



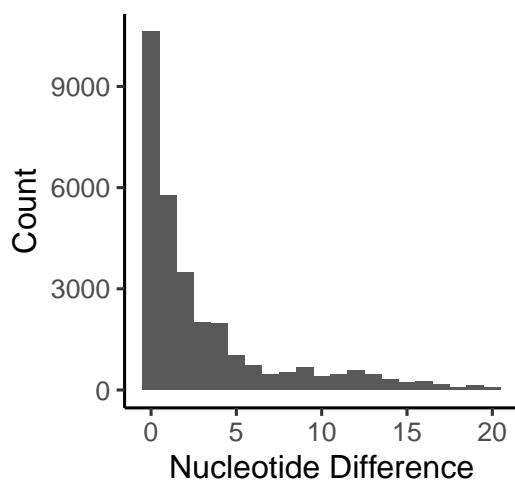
IGHV4-55*02_04_08

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



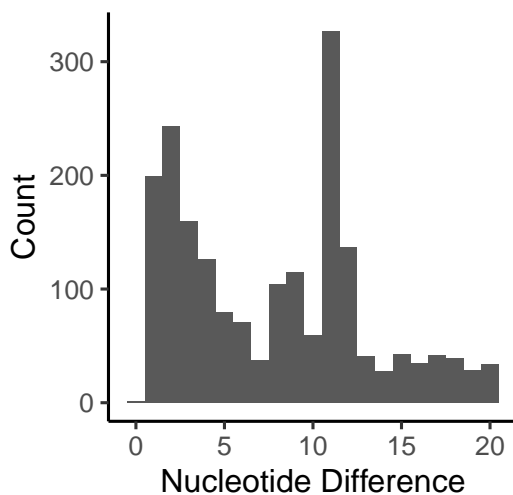
IGHV4-34*01_02

31094 sequences assigned
10622 (34.2%) exact matches, in which:
9531 unique CDR3
6 unique J



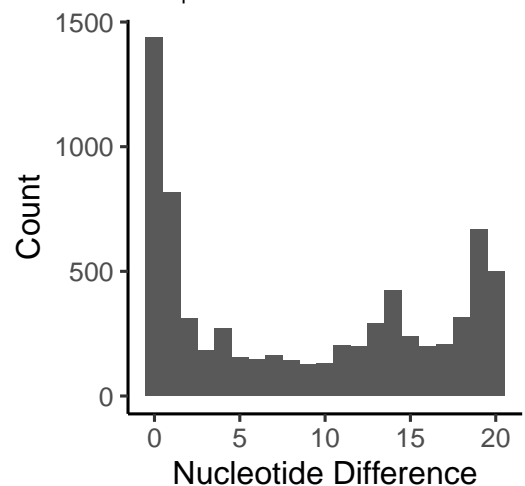
IGHV4-39*07

2106 sequences assigned
1 (0%) exact matches, in which:
1 unique CDR3
1 unique J



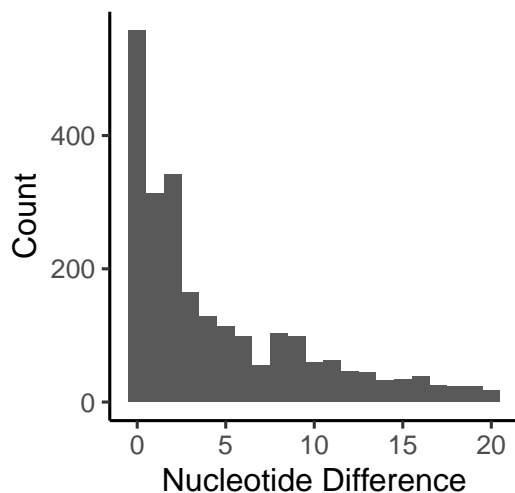
IGHV4-59*08

8352 sequences assigned
1437 (17.2%) exact matches, in which:
1354 unique CDR3
6 unique J



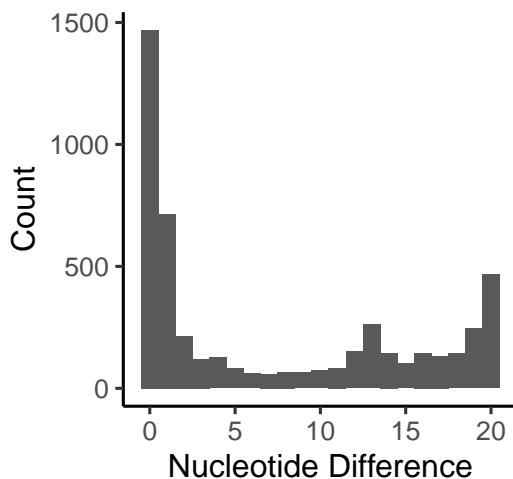
IGHV4-38-2*01

2767 sequences assigned
558 (20.2%) exact matches, in which:
538 unique CDR3
6 unique J



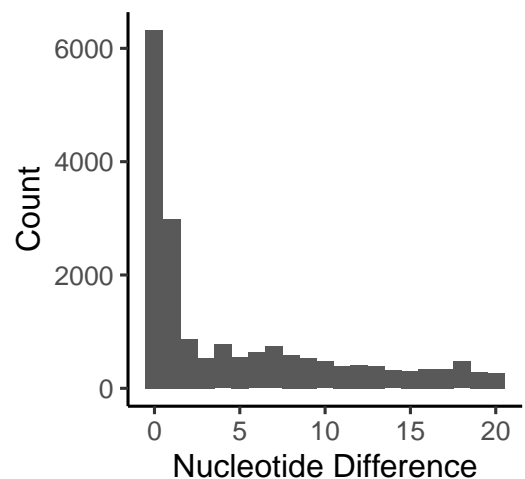
IGHV4-39*01_05

6643 sequences assigned
1469 (22.1%) exact matches, in which:
1342 unique CDR3
6 unique J



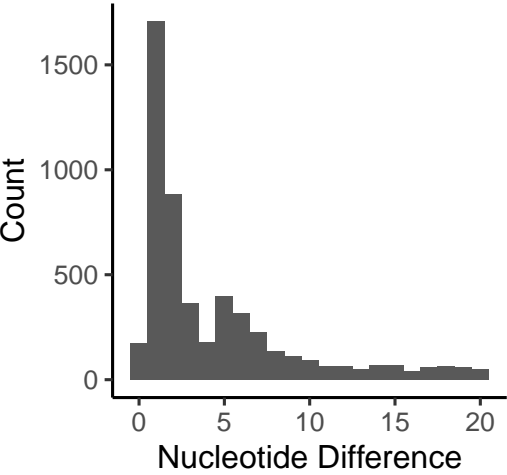
IGHV4-59*01_07

23478 sequences assigned
6323 (26.9%) exact matches, in which:
5843 unique CDR3
6 unique J



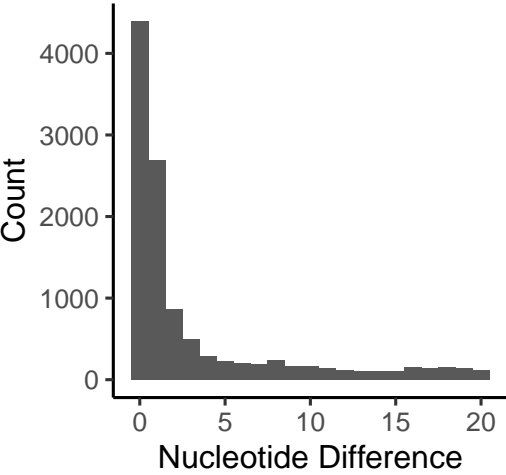
IGHV4-59*12

5697 sequences assigned
173 (3%) exact matches, in which:
172 unique CDR3
6 unique J



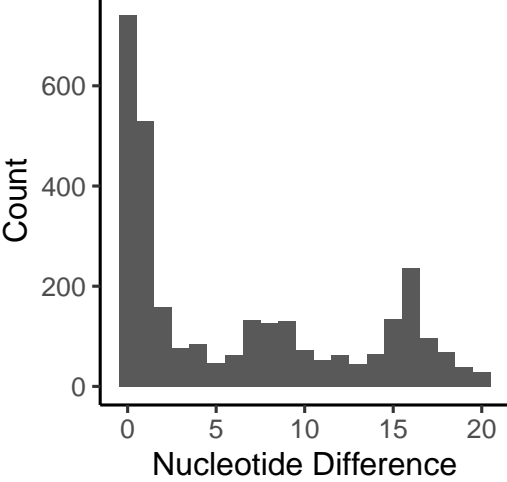
IGHV5-10-1*01_03

12582 sequences assigned
4392 (34.9%) exact matches, in which:
3659 unique CDR3
6 unique J



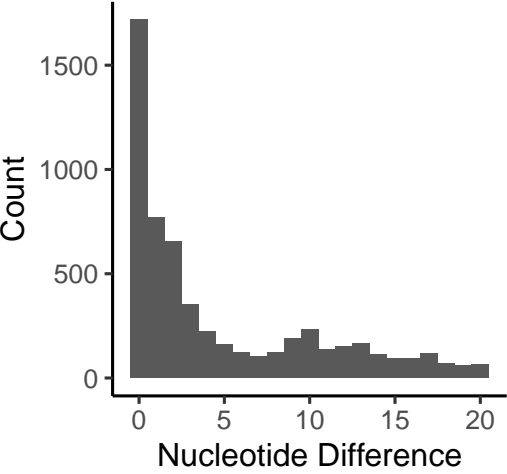
IGHV7-4-1*02

3279 sequences assigned
742 (22.6%) exact matches, in which:
681 unique CDR3
6 unique J



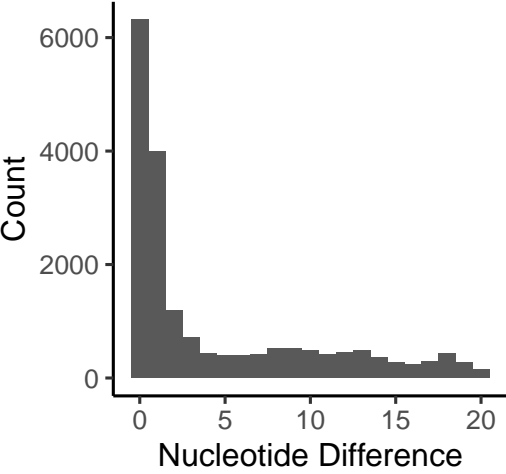
IGHV4-61*01

6642 sequences assigned
1718 (25.9%) exact matches, in which:
1641 unique CDR3
6 unique J



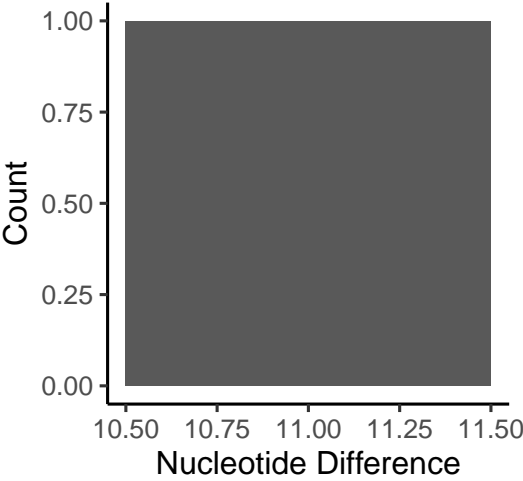
IGHV5-51*01_03

19335 sequences assigned
6315 (32.7%) exact matches, in which:
5067 unique CDR3
6 unique J



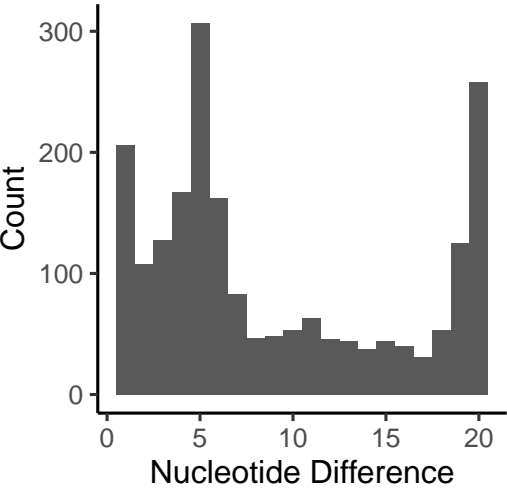
IGHV7-81*01

1 sequences assigned
No exact matches.



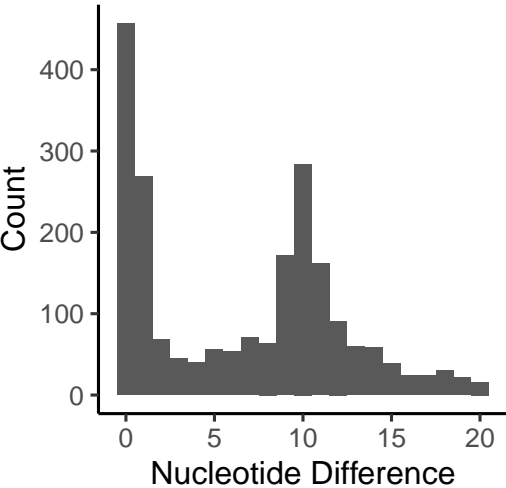
IGHV4-61*08

2590 sequences assigned
No exact matches.



IGHV6-1*01_02

2187 sequences assigned
457 (20.9%) exact matches, in which:
435 unique CDR3
6 unique J





Warning:IGHV4-51*02_IGHV4-51*02_G75C_IGHV4-51*02_G75C 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) 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.

Warning – no inferred sequences found.

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