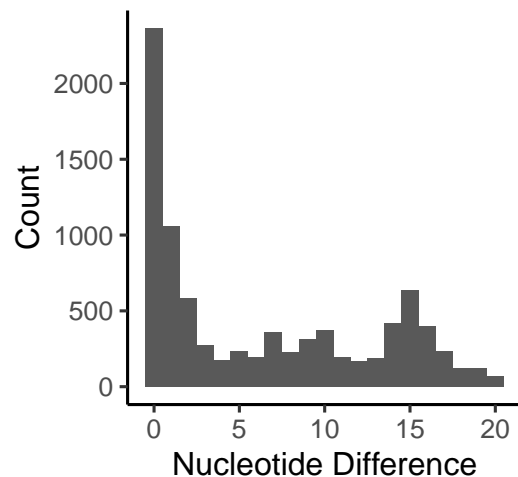


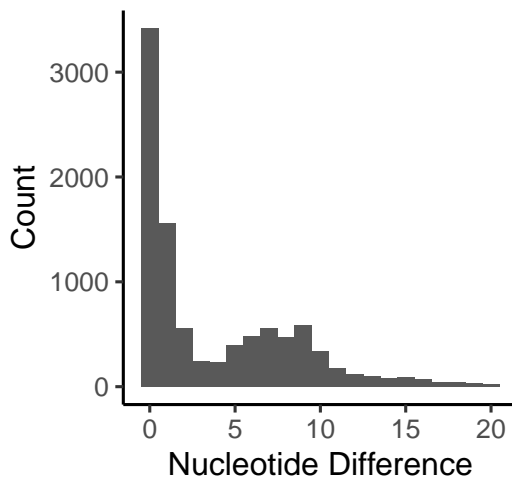
IGHV1-2*02

9161 sequences assigned
2363 (25.8%) exact matches, in which:
2243 unique CDR3
6 unique J



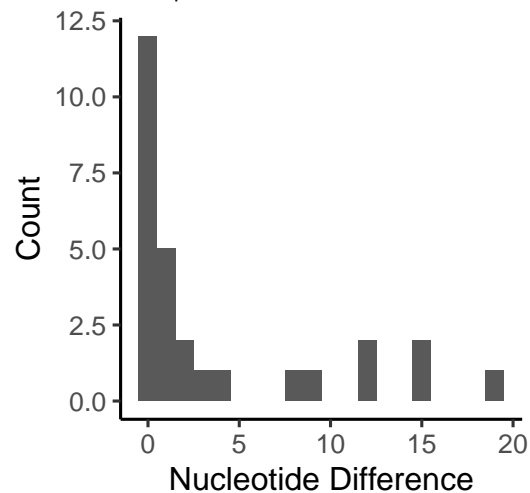
IGHV1-8*01

9780 sequences assigned
3417 (34.9%) exact matches, in which:
3208 unique CDR3
6 unique J



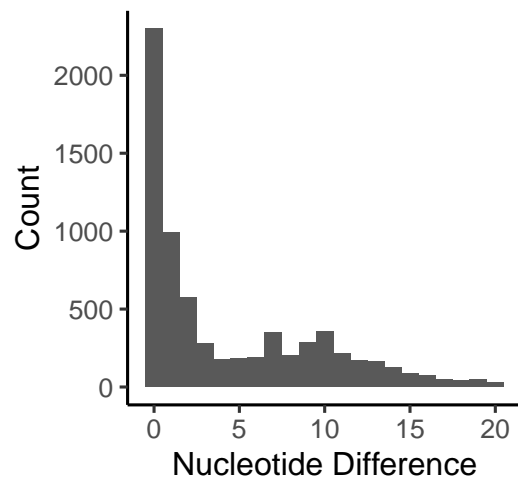
IGHV1-45*02

28 sequences assigned
12 (42.9%) exact matches, in which:
11 unique CDR3
4 unique J



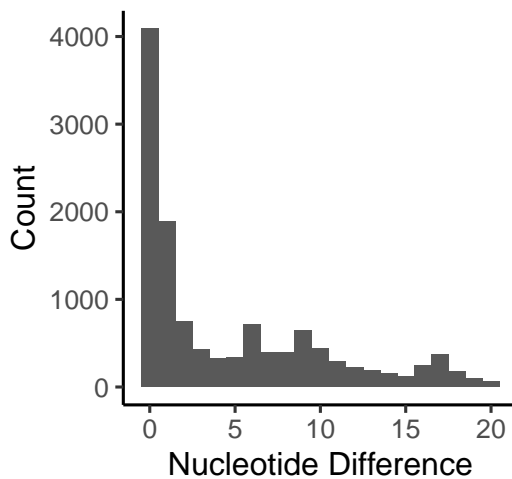
IGHV1-2*06

7081 sequences assigned
2299 (32.5%) exact matches, in which:
2180 unique CDR3
6 unique J



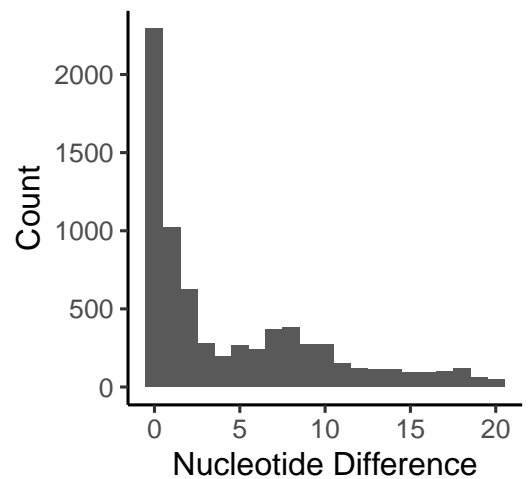
IGHV1-18*01

12763 sequences assigned
4089 (32%) exact matches, in which:
3825 unique CDR3
6 unique J



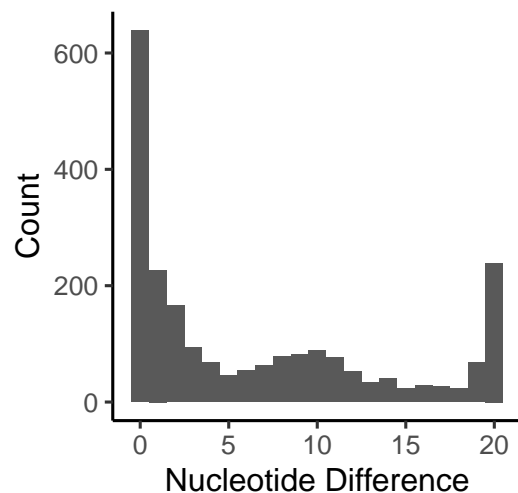
IGHV1-46*01

7692 sequences assigned
2293 (29.8%) exact matches, in which:
2171 unique CDR3
6 unique J



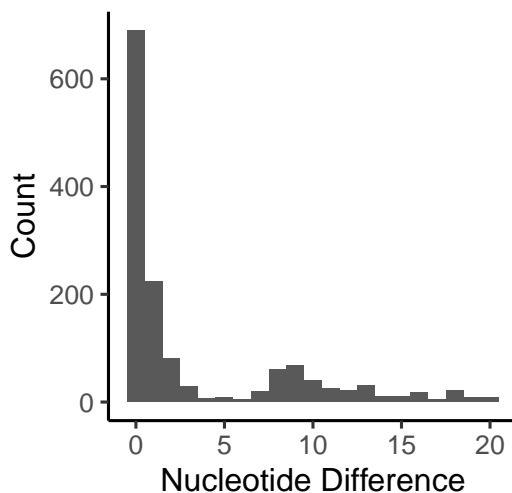
IGHV1-3*01_05

3214 sequences assigned
639 (19.9%) exact matches, in which:
594 unique CDR3
6 unique J



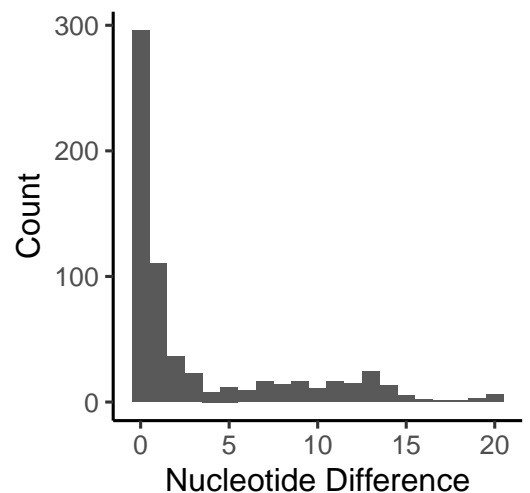
IGHV1-24*01

1483 sequences assigned
690 (46.5%) exact matches, in which:
644 unique CDR3
6 unique J



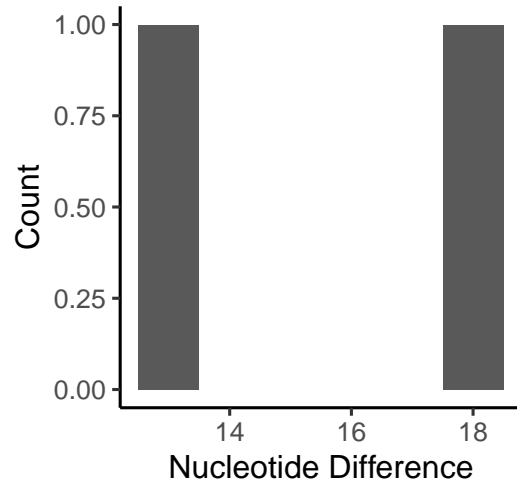
IGHV1-58*01_03

649 sequences assigned
296 (45.6%) exact matches, in which:
279 unique CDR3
6 unique J



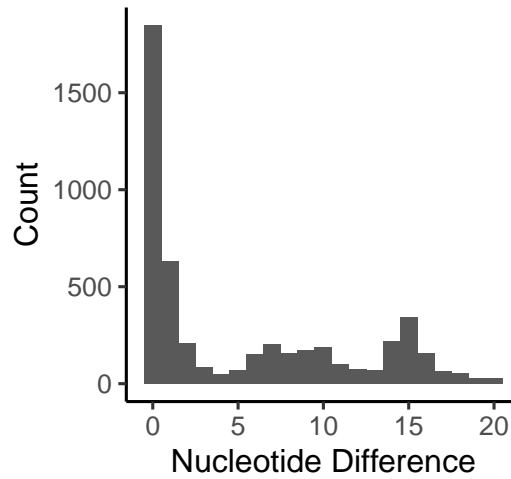
IGHV1-68*02

2 sequences assigned
No exact matches.



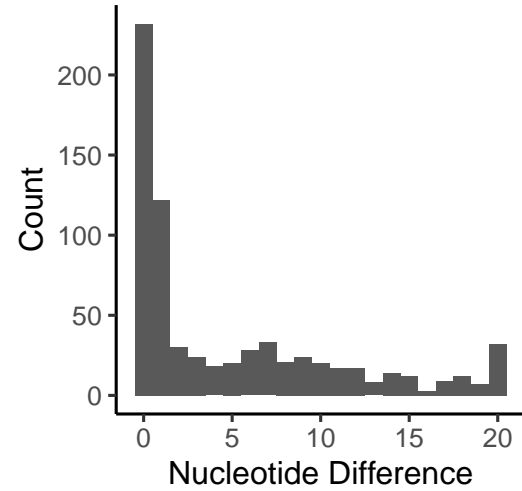
IGHV1-69*06_14

5034 sequences assigned
1847 (36.7%) exact matches, in which:
1796 unique CDR3
6 unique J



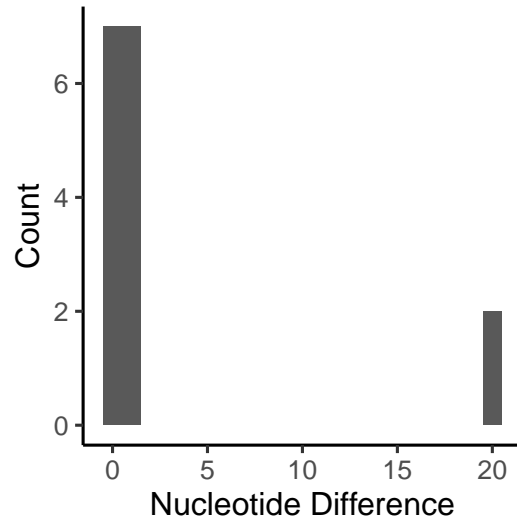
IGHV2-5*02

823 sequences assigned
232 (28.2%) exact matches, in which:
221 unique CDR3
6 unique J



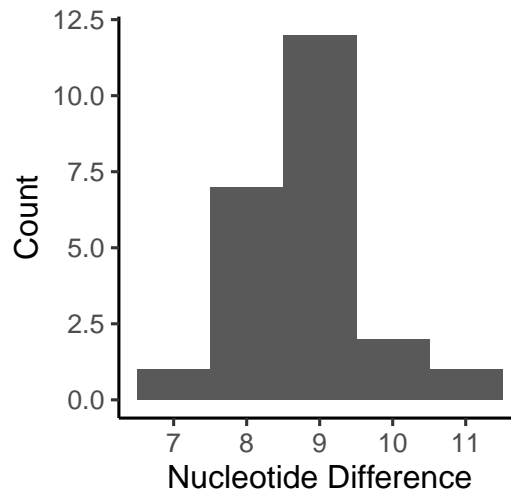
IGHV1-69-2*01

19 sequences assigned
7 (36.8%) exact matches, in which:
7 unique CDR3
2 unique J



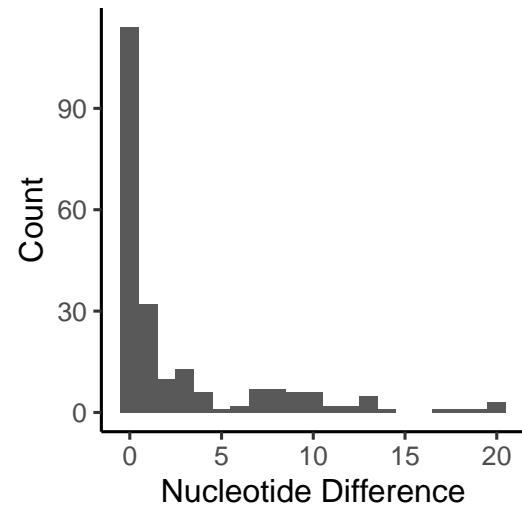
IGHV1-NL1*01

23 sequences assigned
No exact matches.



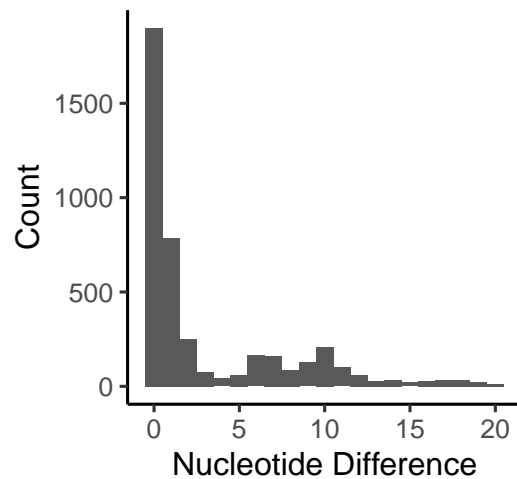
IGHV2-26*01

228 sequences assigned
114 (50%) exact matches, in which:
107 unique CDR3
5 unique J



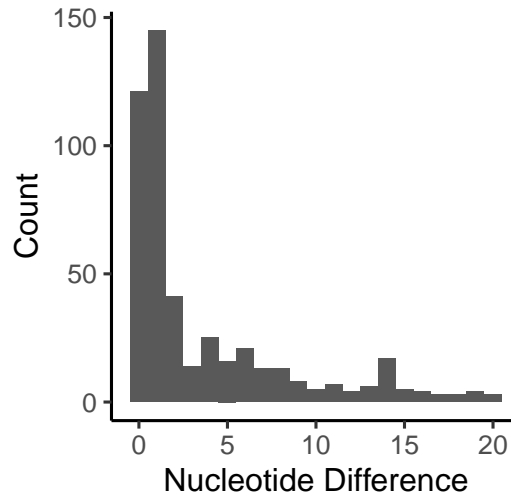
IGHV1-69*04_09

4407 sequences assigned
1899 (43.1%) exact matches, in which:
1829 unique CDR3
6 unique J



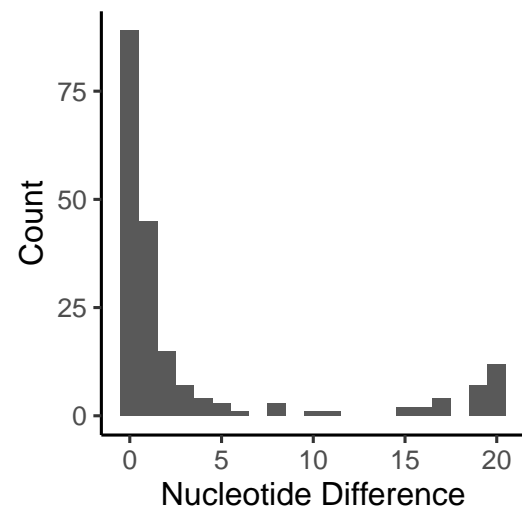
IGHV2-5*01

498 sequences assigned
121 (24.3%) exact matches, in which:
108 unique CDR3
5 unique J



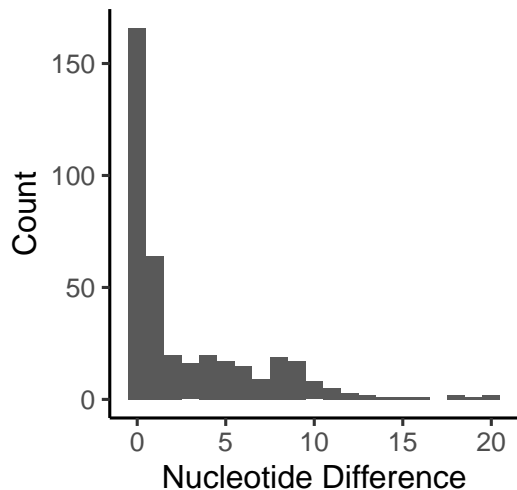
IGHV2-70*01

200 sequences assigned
89 (44.5%) exact matches, in which:
84 unique CDR3
4 unique J



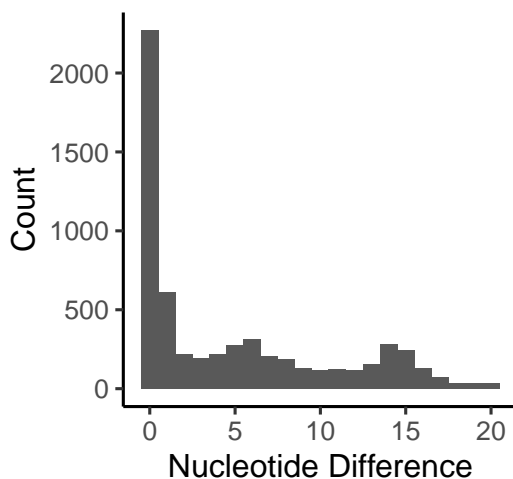
IGHV2-70*11_15

402 sequences assigned
166 (41.3%) exact matches, in which:
158 unique CDR3
5 unique J



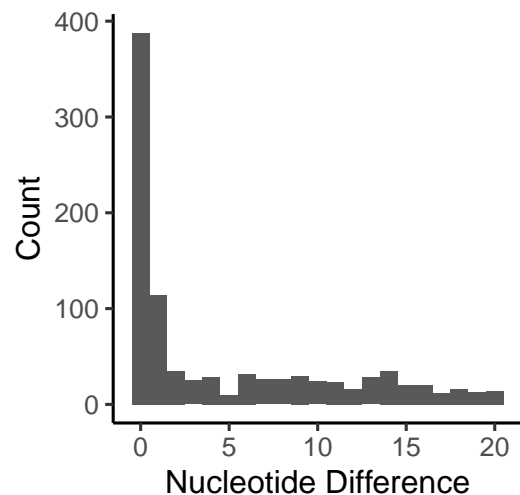
IGHV3-9*01

6137 sequences assigned
2270 (37%) exact matches, in which:
1829 unique CDR3
6 unique J



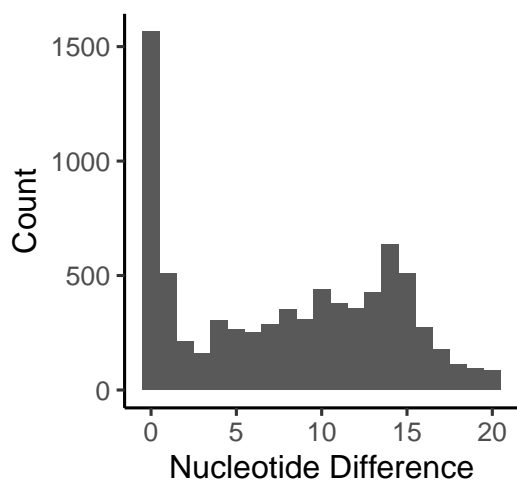
IGHV3-13*01

1048 sequences assigned
388 (37%) exact matches, in which:
301 unique CDR3
5 unique J



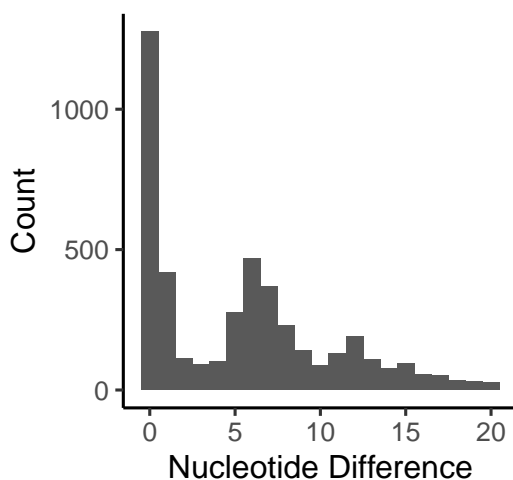
IGHV3-7*01

8010 sequences assigned
1565 (19.5%) exact matches, in which:
1258 unique CDR3
6 unique J



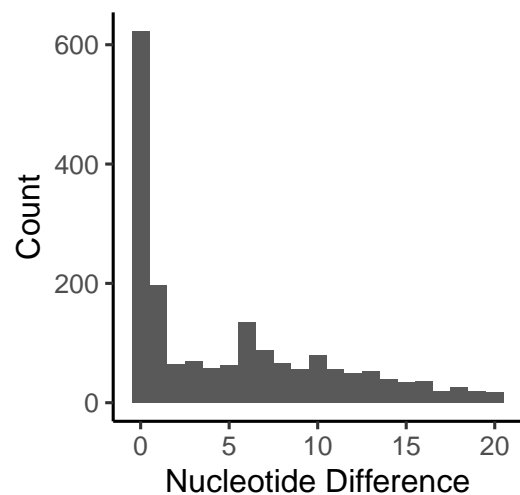
IGHV3-11*01

4589 sequences assigned
1276 (27.8%) exact matches, in which:
1044 unique CDR3
6 unique J



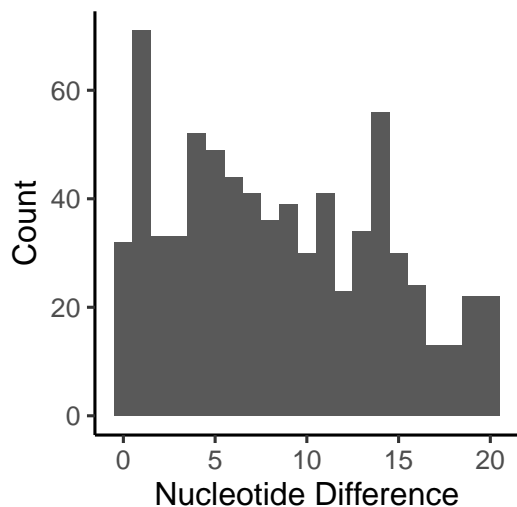
IGHV3-15*01_02

2024 sequences assigned
623 (30.8%) exact matches, in which:
522 unique CDR3
6 unique J



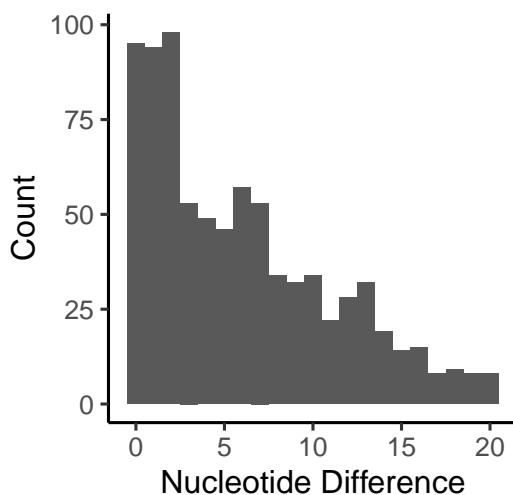
IGHV3-7*03

781 sequences assigned
32 (4.1%) exact matches, in which:
31 unique CDR3
3 unique J



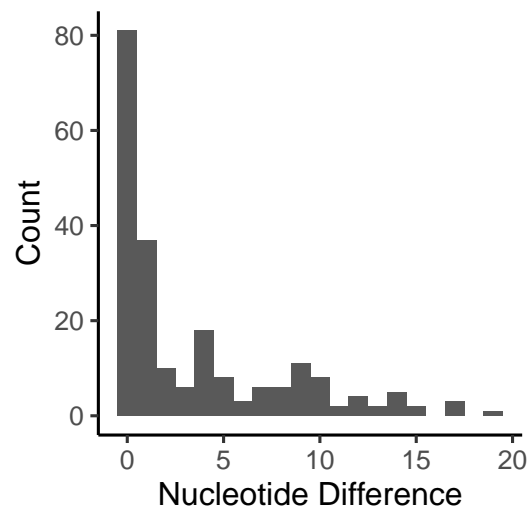
IGHV3-11*04

828 sequences assigned
95 (11.5%) exact matches, in which:
95 unique CDR3
5 unique J



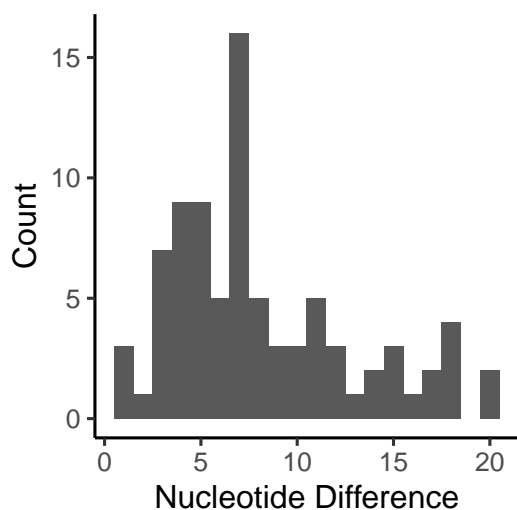
IGHV3-20*01_02

236 sequences assigned
81 (34.3%) exact matches, in which:
69 unique CDR3
5 unique J



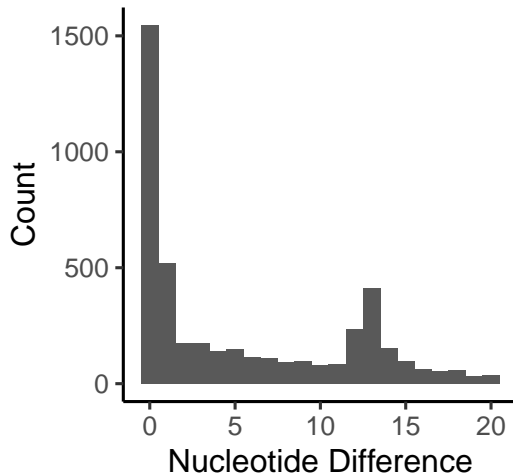
IGHV3-20*03_04

103 sequences assigned
No exact matches.



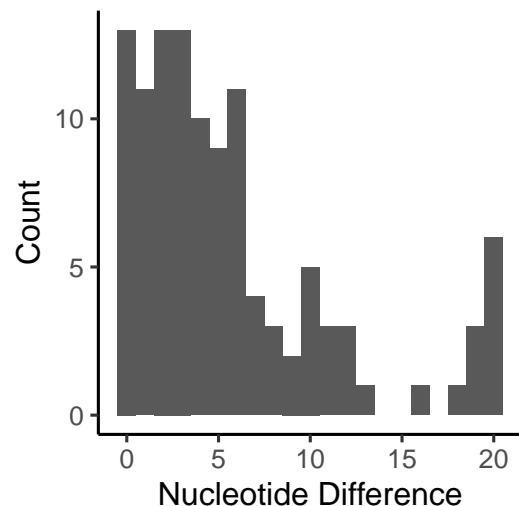
IGHV3-30-3*01

4679 sequences assigned
1545 (33%) exact matches, in which:
1281 unique CDR3
6 unique J



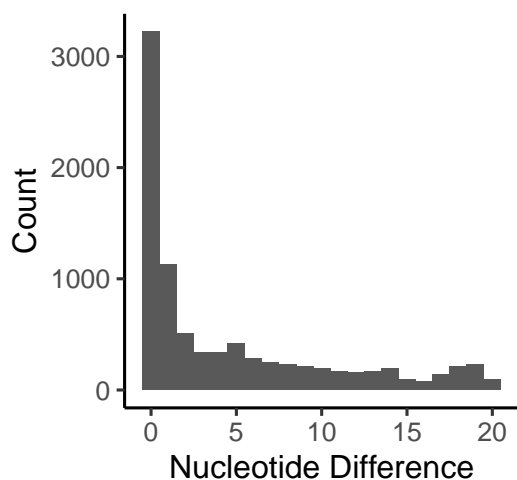
IGHV3-33*05

134 sequences assigned
13 (9.7%) exact matches, in which:
13 unique CDR3
4 unique J



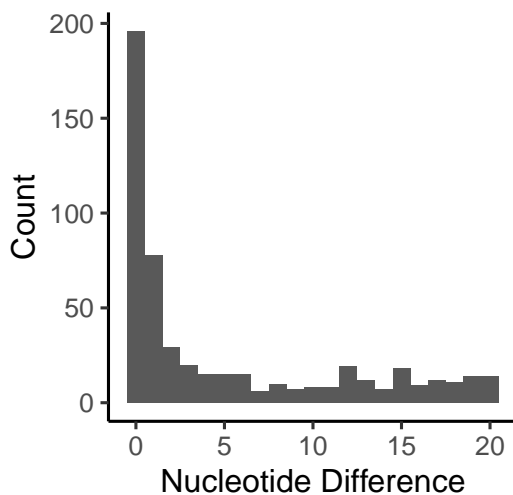
IGHV3-21*01_02

11788 sequences assigned
3222 (27.3%) exact matches, in which:
2582 unique CDR3
6 unique J



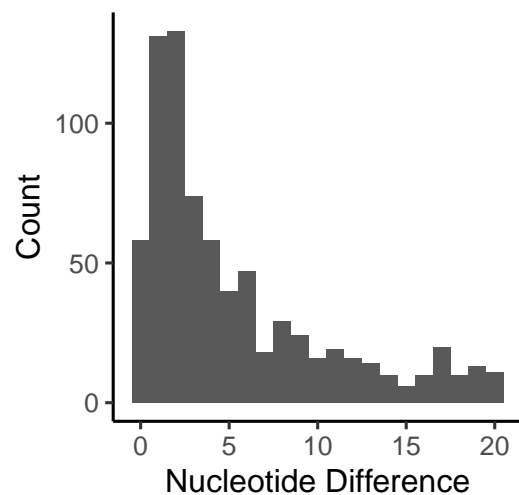
IGHV3-30*03

668 sequences assigned
196 (29.3%) exact matches, in which:
192 unique CDR3
6 unique J



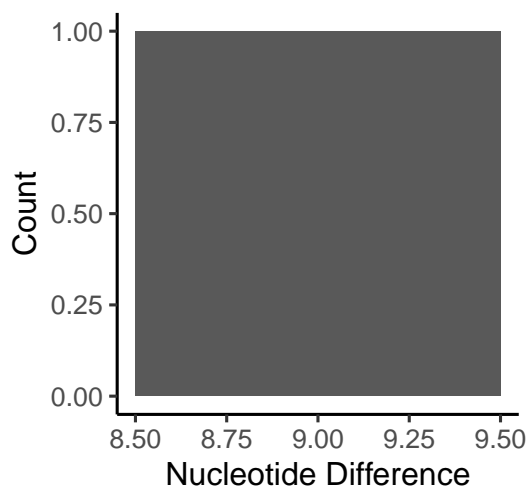
IGHV3-33*06

847 sequences assigned
58 (6.8%) exact matches, in which:
56 unique CDR3
4 unique J



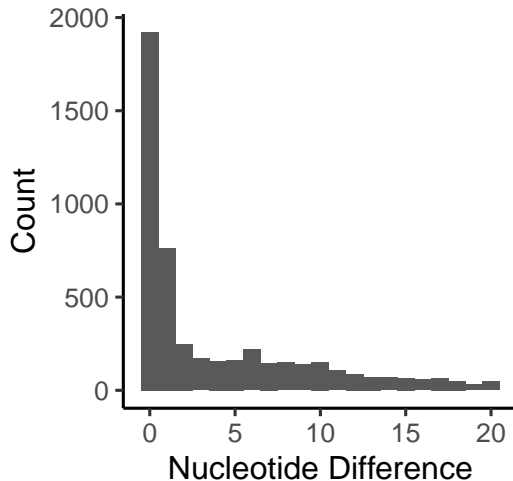
IGHV3-22*01_02

1 sequences assigned
No exact matches.



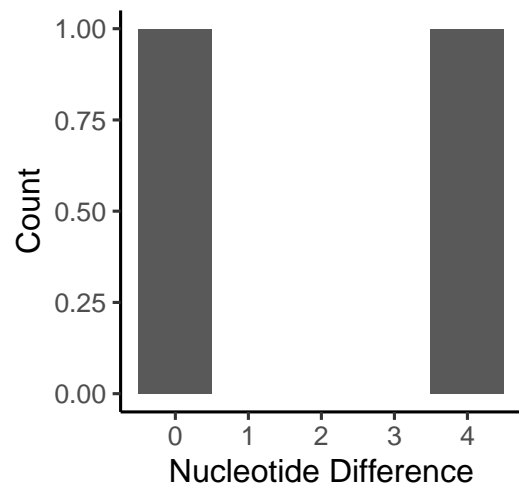
IGHV3-33*01

5777 sequences assigned
1922 (33.3%) exact matches, in which:
1613 unique CDR3
6 unique J



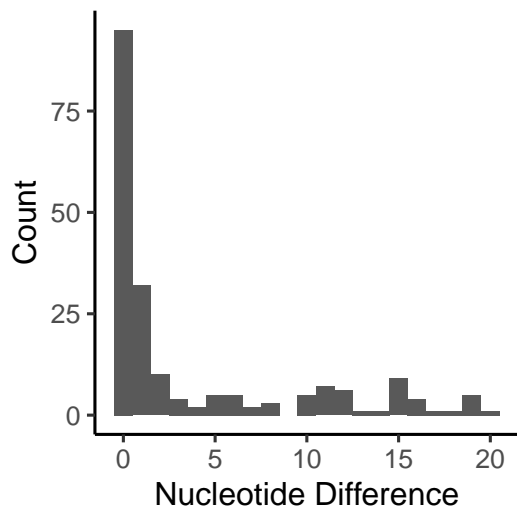
IGHV3-35*01

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



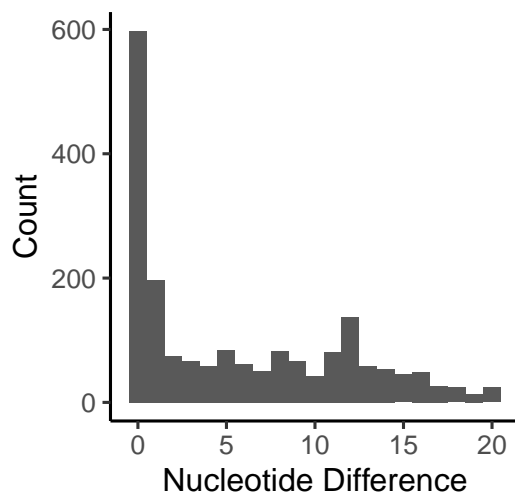
IGHV3-43*01

209 sequences assigned
95 (45.5%) exact matches, in which:
81 unique CDR3
6 unique J



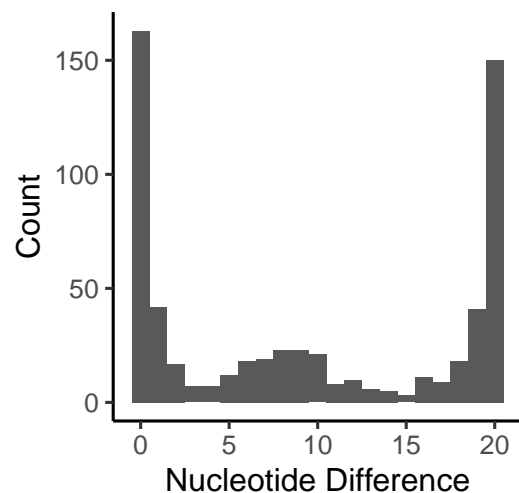
IGHV3-48*02

2036 sequences assigned
598 (29.4%) exact matches, in which:
495 unique CDR3
6 unique J



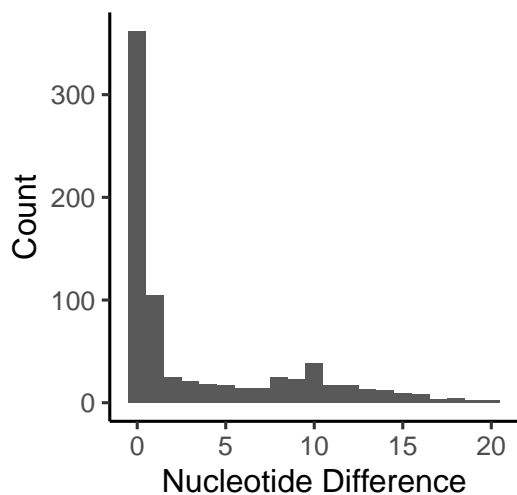
IGHV3-49*04

1187 sequences assigned
163 (13.7%) exact matches, in which:
136 unique CDR3
6 unique J



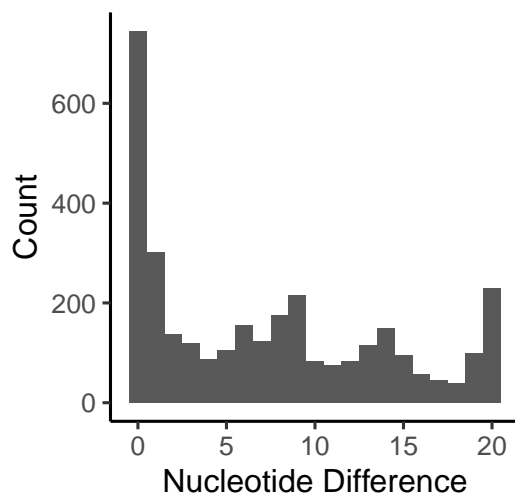
IGHV3-43*02

780 sequences assigned
362 (46.4%) exact matches, in which:
298 unique CDR3
6 unique J



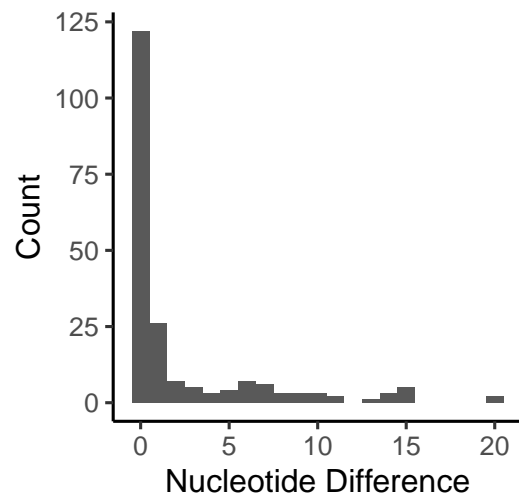
IGHV3-48*03

3516 sequences assigned
745 (21.2%) exact matches, in which:
609 unique CDR3
6 unique J



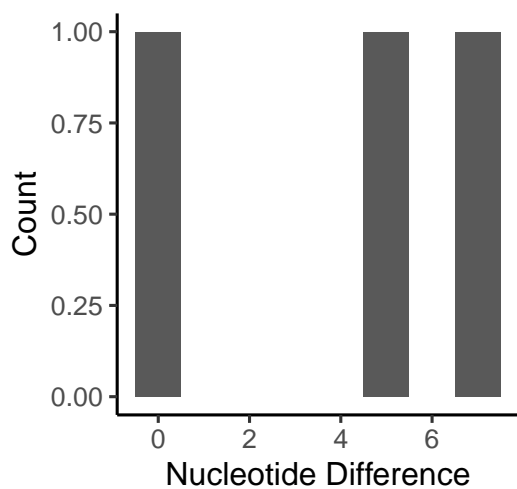
IGHV3-49*03_05

206 sequences assigned
122 (59.2%) exact matches, in which:
105 unique CDR3
4 unique J



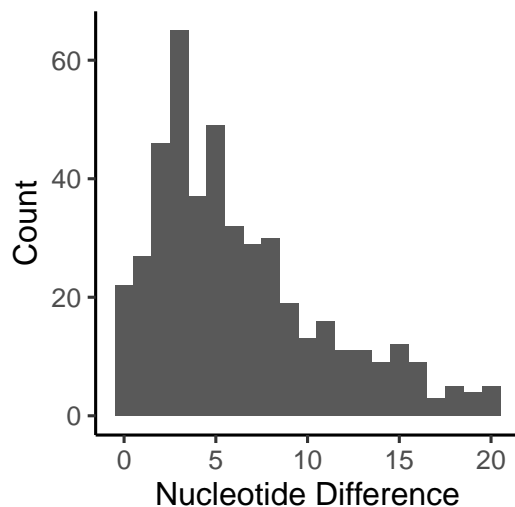
IGHV3-47*02

3 sequences assigned
1 (33.3%) exact matches, in which:
1 unique CDR3
1 unique J



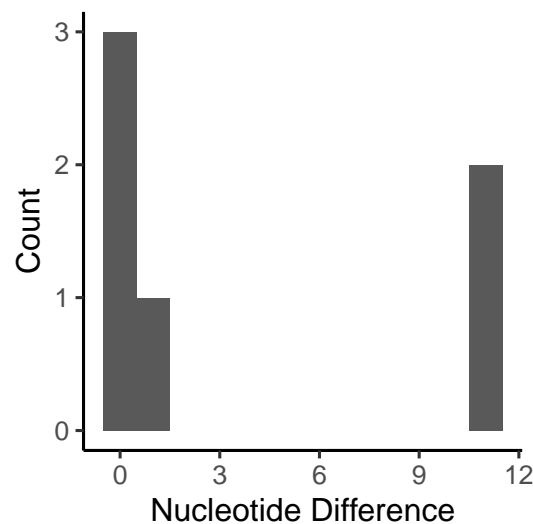
IGHV3-48*04

464 sequences assigned
22 (4.7%) exact matches, in which:
22 unique CDR3
4 unique J



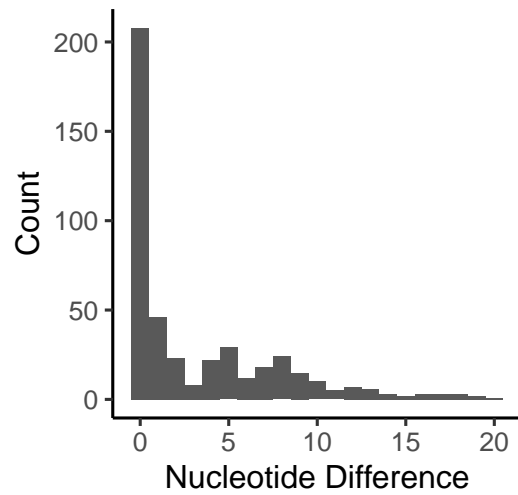
IGHV3-52*01_03

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



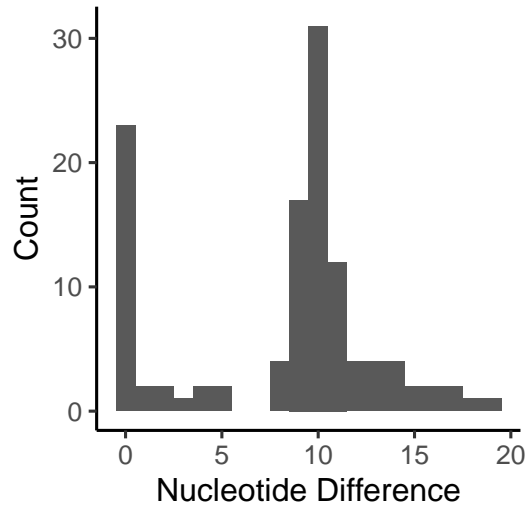
IGHV3-53*04

464 sequences assigned
208 (44.8%) exact matches, in which:
168 unique CDR3
5 unique J



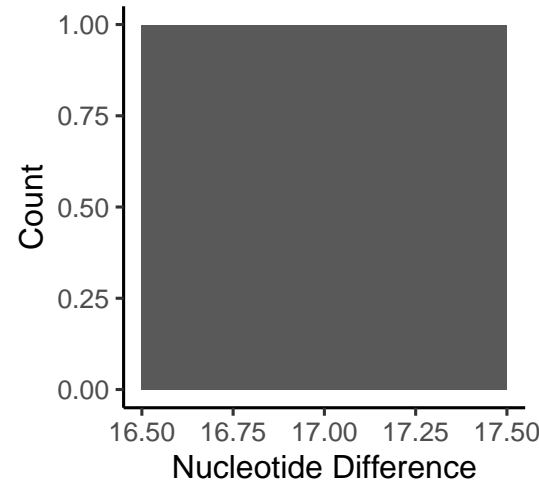
IGHV3-64*02_07

119 sequences assigned
23 (19.3%) exact matches, in which:
18 unique CDR3
5 unique J



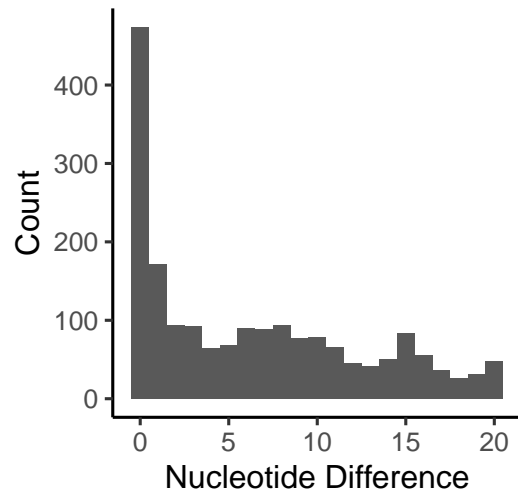
IGHV3-69-1*02

15 sequences assigned
No exact matches.



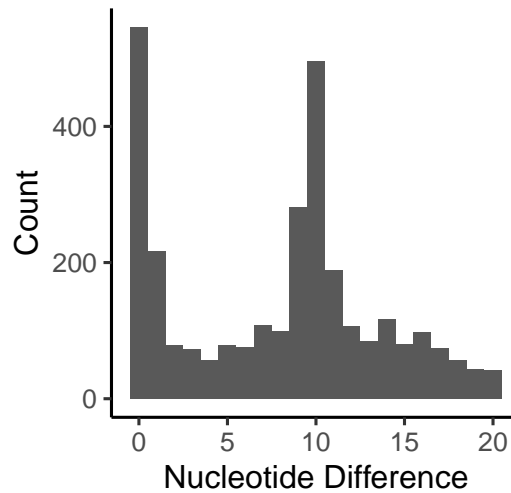
IGHV3-53*01_02

3438 sequences assigned
474 (13.8%) exact matches, in which:
392 unique CDR3
5 unique J



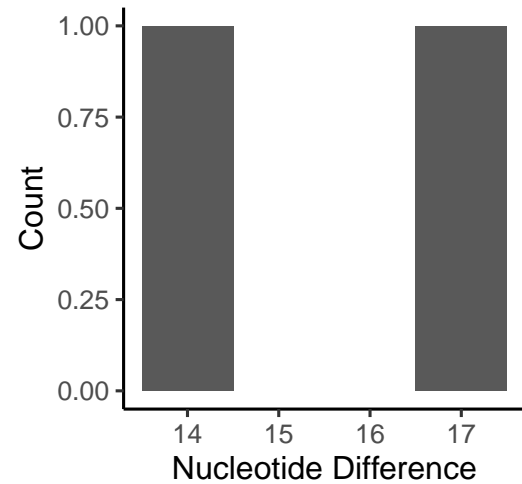
IGHV3-66*01

3433 sequences assigned
546 (15.9%) exact matches, in which:
440 unique CDR3
6 unique J



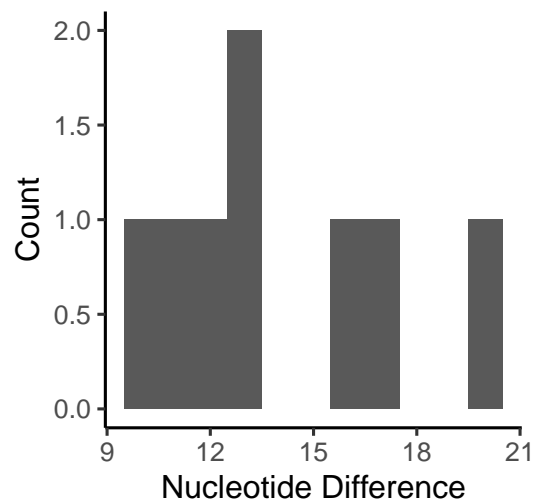
IGHV3-71*01_04

8 sequences assigned
No exact matches.



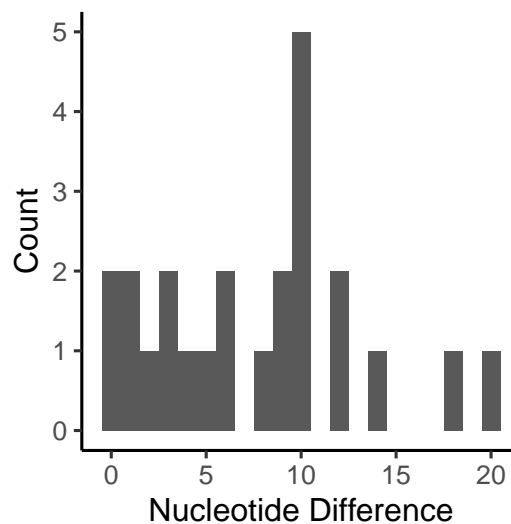
IGHV3-64*04

8 sequences assigned
No exact matches.



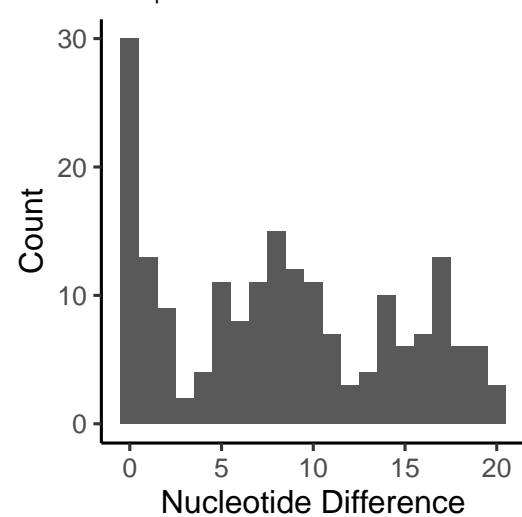
IGHV3-69-1*01

30 sequences assigned
2 (6.7%) exact matches, in which:
2 unique CDR3
2 unique J



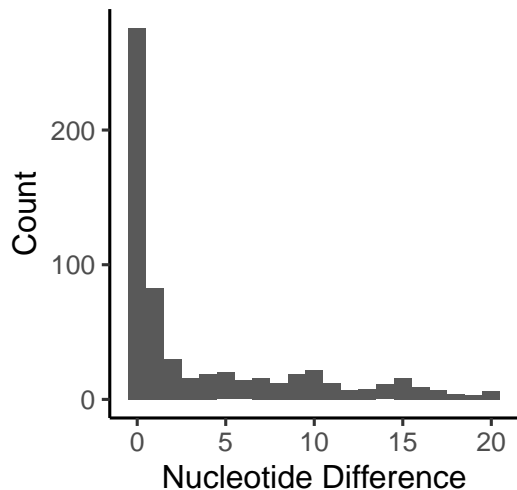
IGHV3-72*01

336 sequences assigned
30 (8.9%) exact matches, in which:
24 unique CDR3
4 unique J



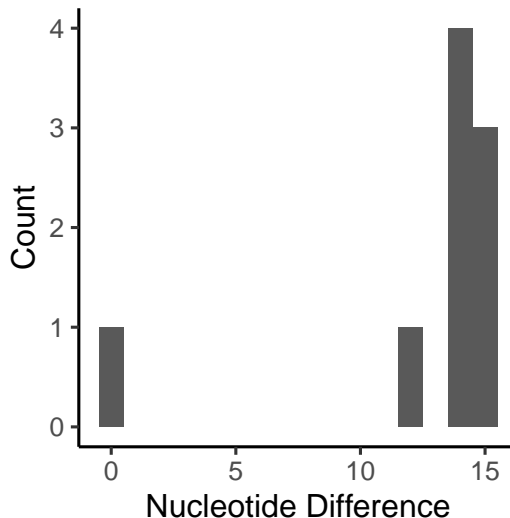
IGHV3-73*01_02

632 sequences assigned
276 (43.7%) exact matches, in which:
221 unique CDR3
6 unique J



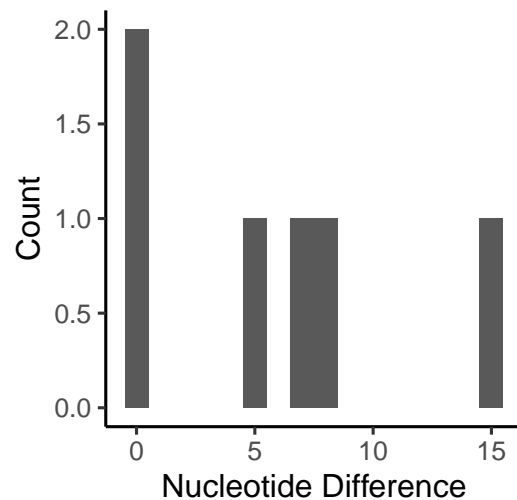
IGHV3-64D*06

19 sequences assigned
1 (5.3%) exact matches, in which:
1 unique CDR3
1 unique J



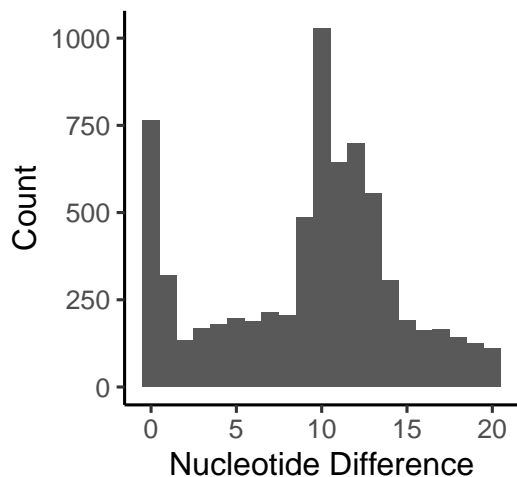
IGHV4-28*03

6 sequences assigned
2 (33.3%) exact matches, in which:
2 unique CDR3
2 unique J



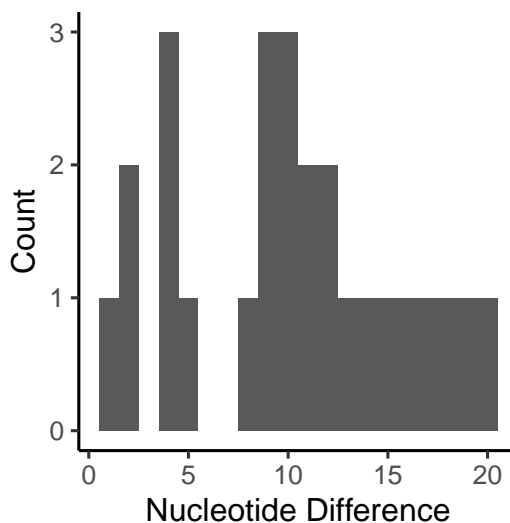
IGHV3-74*01_02

7300 sequences assigned
763 (10.5%) exact matches, in which:
602 unique CDR3
6 unique J



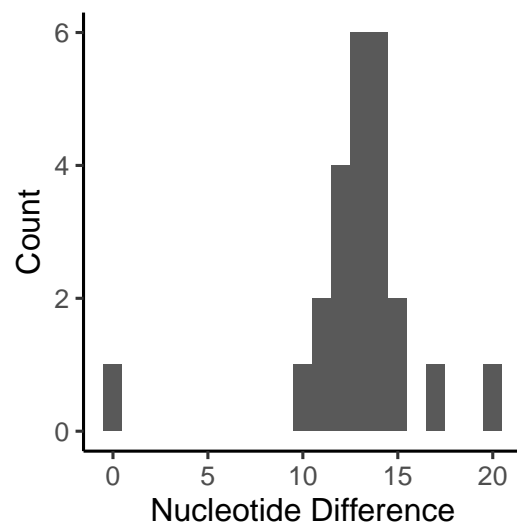
IGHV3-NL1*01

38 sequences assigned
No exact matches.



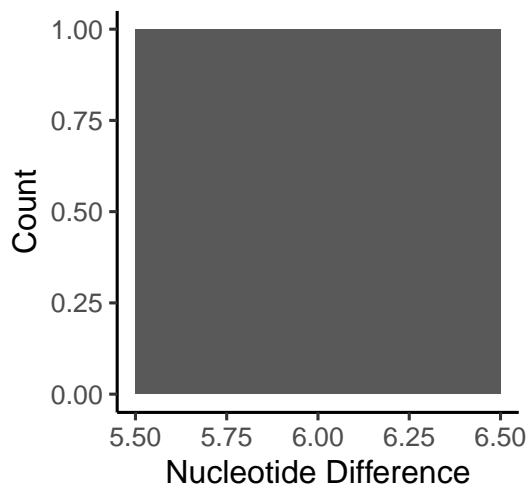
IGHV4-28*01_07

24 sequences assigned
1 (4.2%) exact matches, in which:
1 unique CDR3
1 unique J



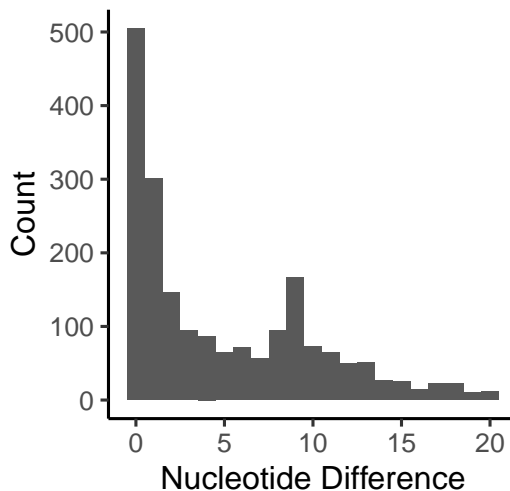
IGHV3-43D*03

1 sequences assigned
No exact matches.



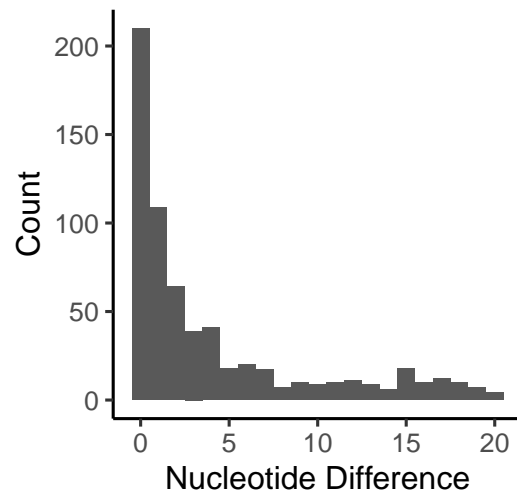
IGHV4-4*07

2024 sequences assigned
505 (25%) exact matches, in which:
470 unique CDR3
6 unique J



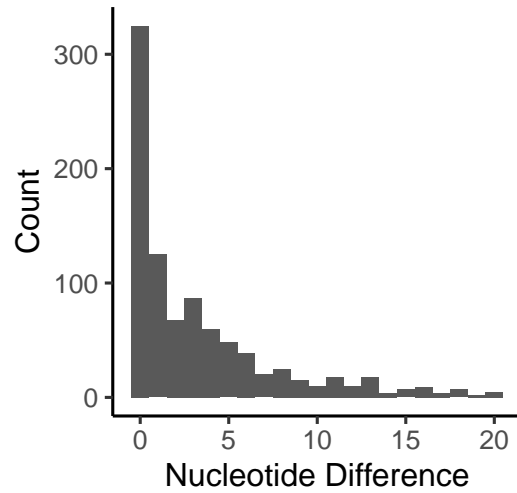
IGHV4-30-2*01

691 sequences assigned
210 (30.4%) exact matches, in which:
194 unique CDR3
6 unique J



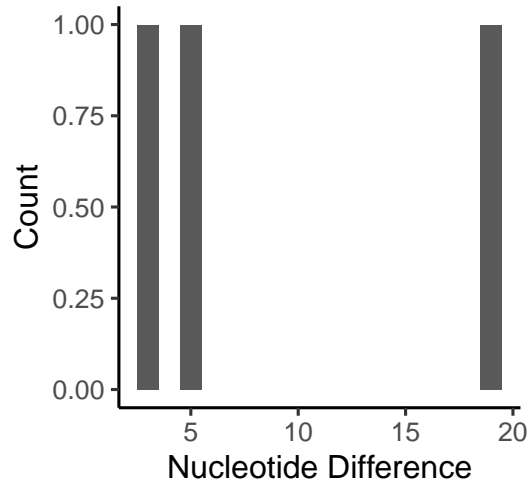
IGHV4-30-4*01

1205 sequences assigned
325 (27%) exact matches, in which:
310 unique CDR3
6 unique J



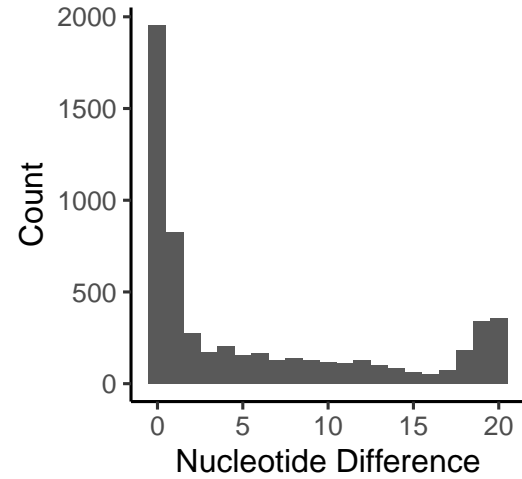
IGHV4-38-2*01

4 sequences assigned
No exact matches.



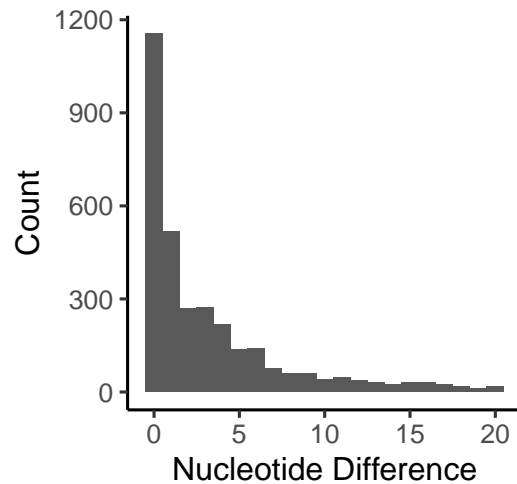
IGHV4-39*01_05

7116 sequences assigned
1953 (27.4%) exact matches, in which:
1857 unique CDR3
6 unique J



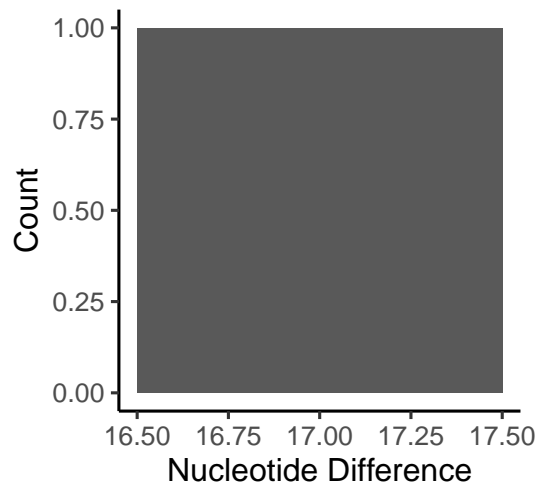
IGHV4-31*03_04

3575 sequences assigned
1155 (32.3%) exact matches, in which:
1109 unique CDR3
6 unique J



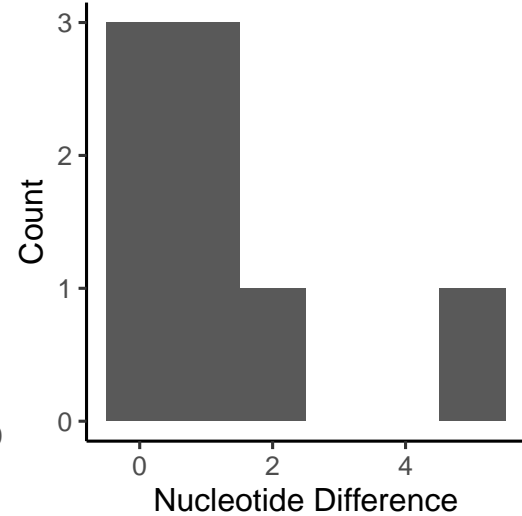
IGHV4-38-2*02

2 sequences assigned
No exact matches.



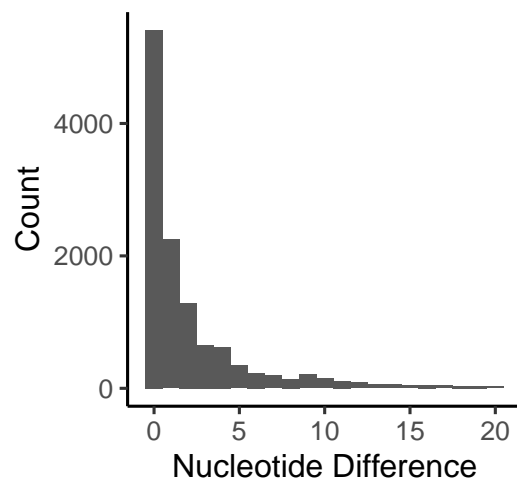
IGHV4-55*02_04_08

8 sequences assigned
3 (37.5%) exact matches, in which:
3 unique CDR3
2 unique J



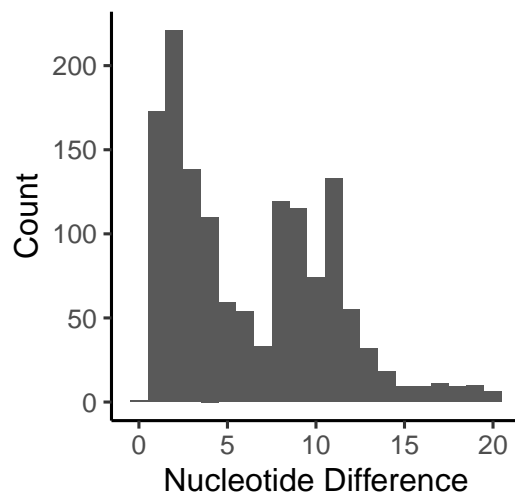
IGHV4-34*01_02

12216 sequences assigned
5411 (44.3%) exact matches, in which:
5022 unique CDR3
6 unique J



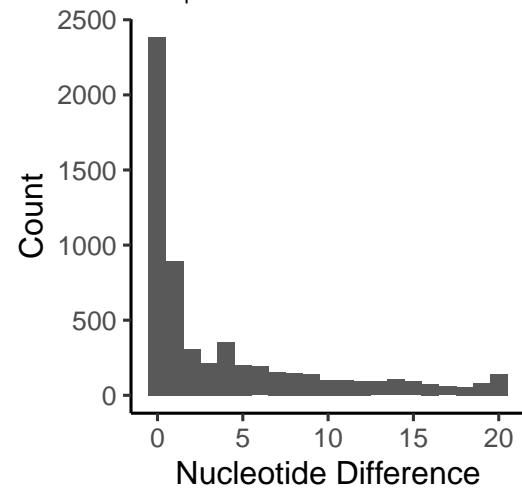
IGHV4-39*07

1418 sequences assigned
1 (0.1%) exact matches, in which:
1 unique CDR3
1 unique J



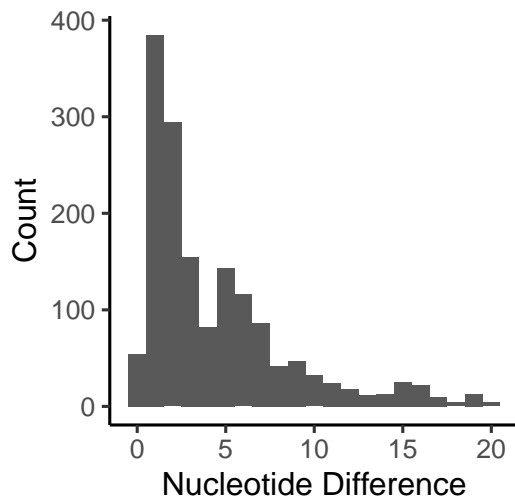
IGHV4-59*01_07

8883 sequences assigned
2385 (26.8%) exact matches, in which:
2263 unique CDR3
6 unique J



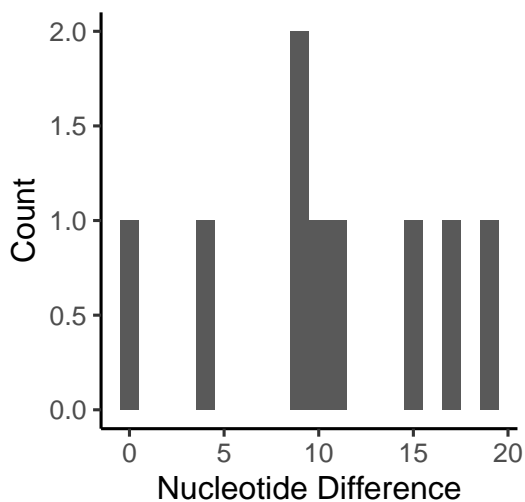
IGHV4-59*12

1646 sequences assigned
54 (3.3%) exact matches, in which:
54 unique CDR3
4 unique J



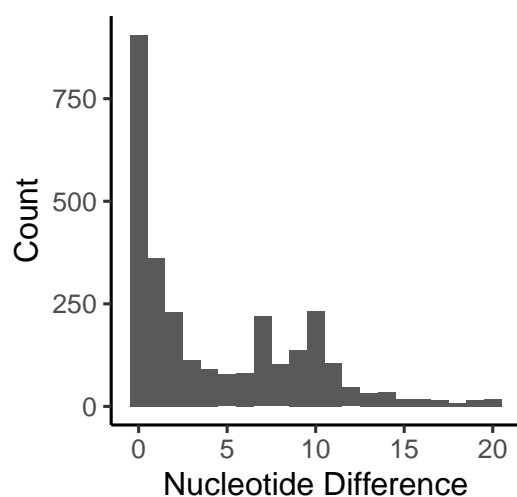
IGHV5-10-1*01_03

11 sequences assigned
1 (9.1%) exact matches, in which:
1 unique CDR3
1 unique J



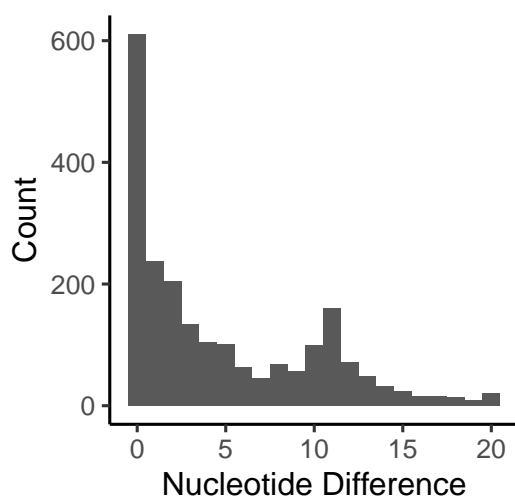
IGHV7-4-1*02

2939 sequences assigned
906 (30.8%) exact matches, in which:
856 unique CDR3
6 unique J



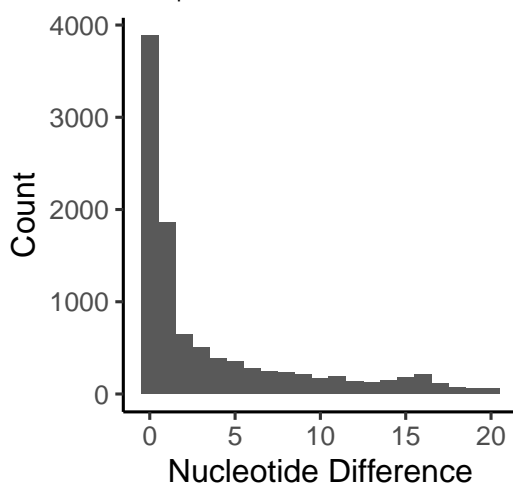
IGHV4-61*01

2280 sequences assigned
611 (26.8%) exact matches, in which:
592 unique CDR3
6 unique J



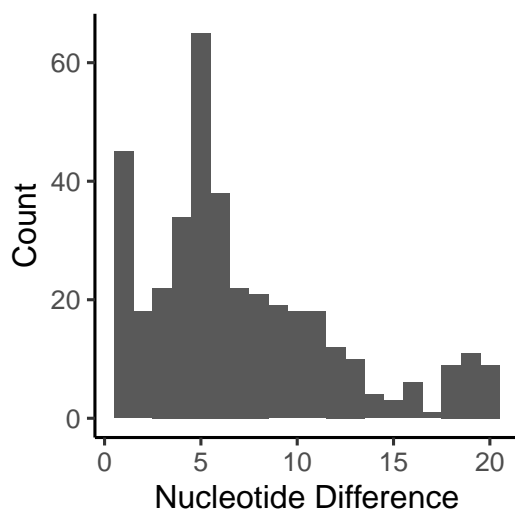
IGHV5-51*01_03

10352 sequences assigned
3884 (37.5%) exact matches, in which:
3149 unique CDR3
6 unique J



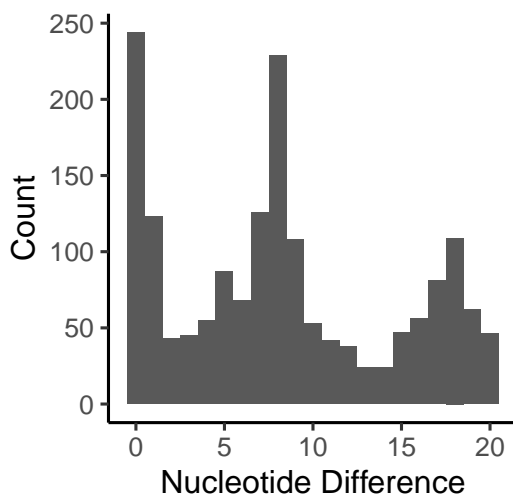
IGHV4-61*08

428 sequences assigned
No exact matches.



IGHV6-1*01_02

4434 sequences assigned
244 (5.5%) exact matches, in which:
233 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.