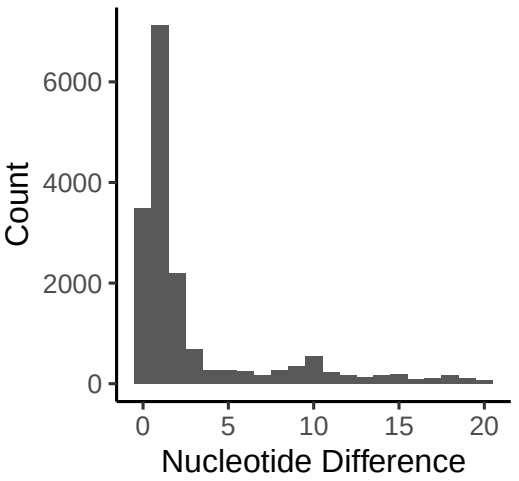
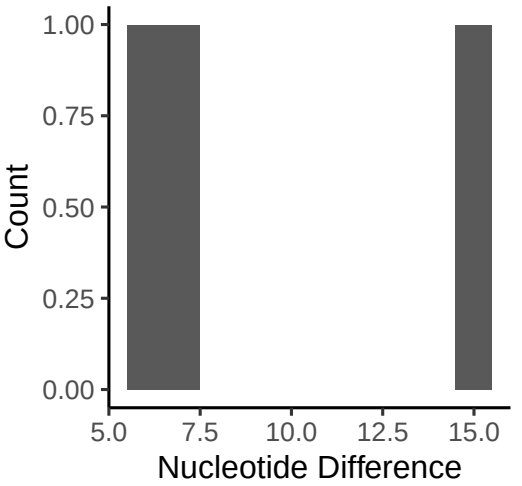
IGHV1−2*02

17120 sequences assigned
3491 (20.4%) exact matches, in which:
2325 unique CDR3
6 unique J



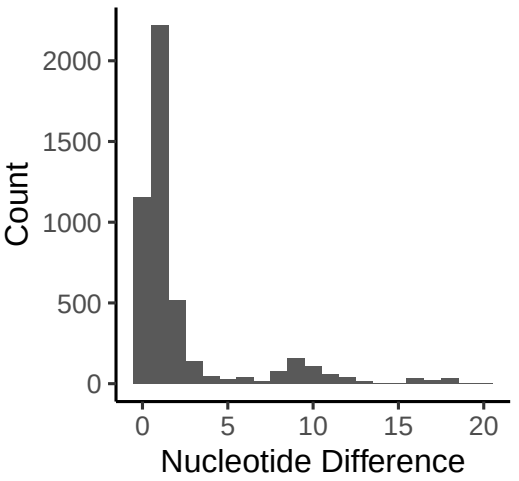
IGHV1−8*02

3 sequences assigned
No exact matches.



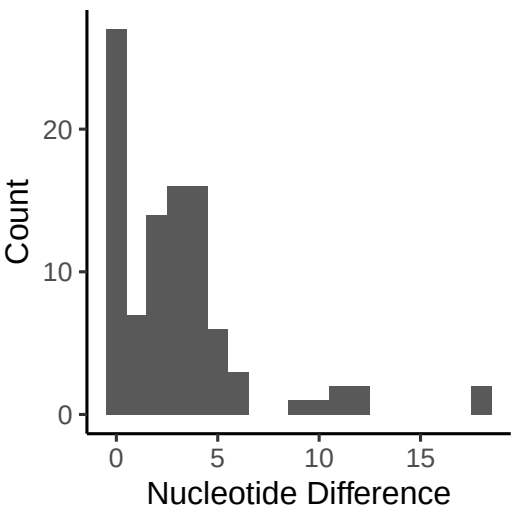
IGHV1−24*01

4729 sequences assigned
1153 (24.4%) exact matches, in which:
792 unique CDR3
6 unique J



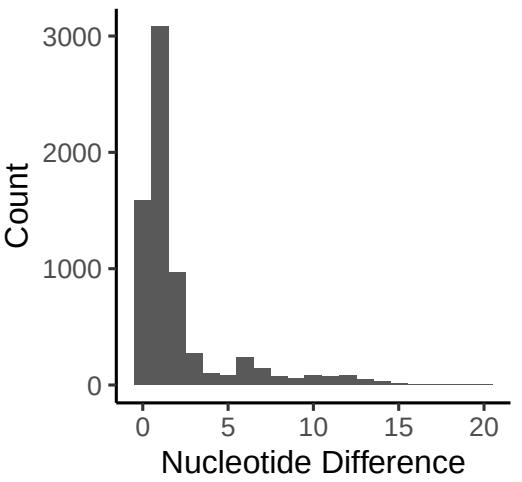
IGHV1−3*02

104 sequences assigned
27 (26%) exact matches, in which:
25 unique CDR3
4 unique J



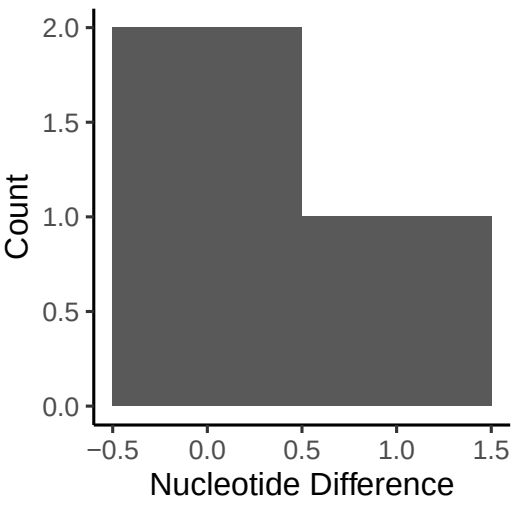
IGHV1−18*01

6991 sequences assigned
1589 (22.7%) exact matches, in which:
1163 unique CDR3
6 unique J



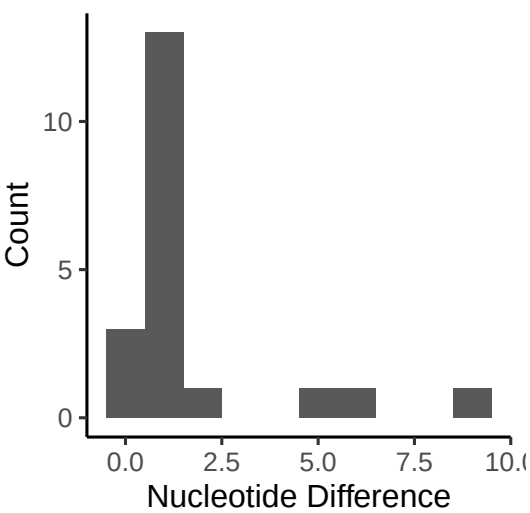
IGHV1−45*02

3 sequences assigned
2 (66.7%) exact matches, in which:
2 unique CDR3
1 unique J



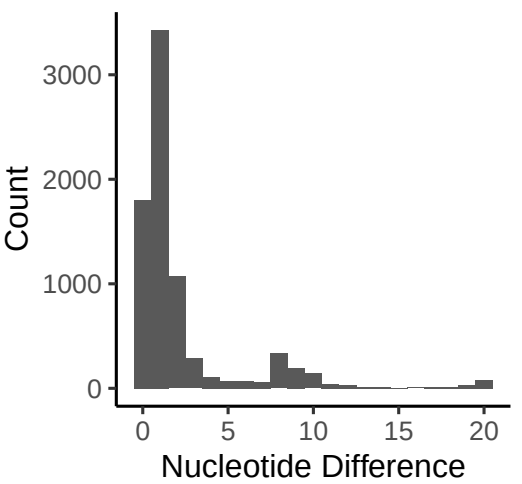
IGHV1−8*01

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



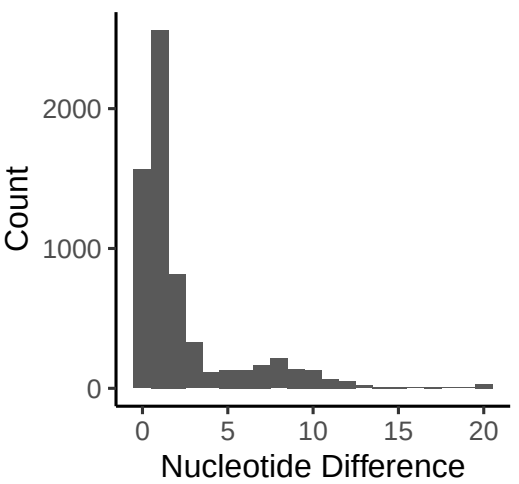
IGHV1−18*04

7861 sequences assigned
1799 (22.9%) exact matches, in which:
1259 unique CDR3
6 unique J



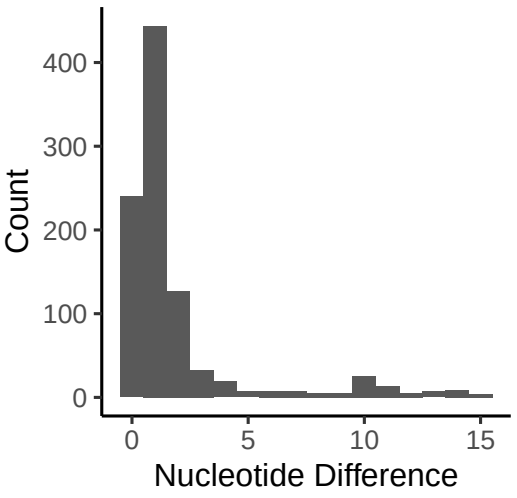
IGHV1−46*01

6673 sequences assigned
1564 (23.4%) exact matches, in which:
1148 unique CDR3
6 unique J



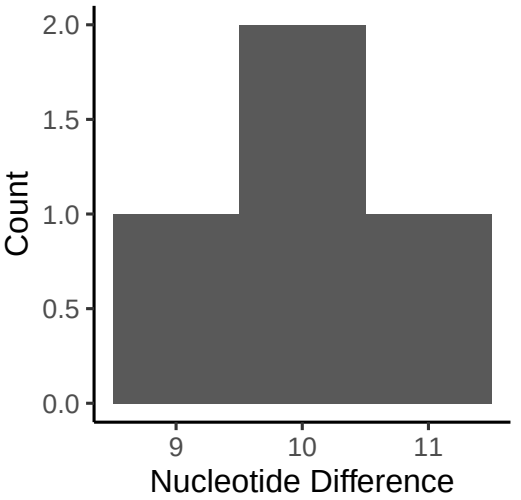
IGHV1−58*01_03

966 sequences assigned
240 (24.8%) exact matches, in which:
172 unique CDR3
5 unique J



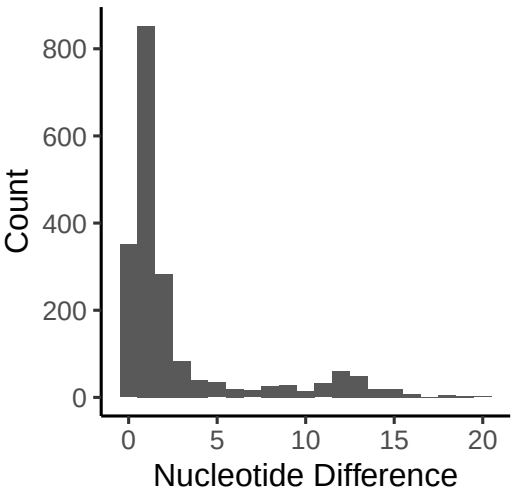
IGHV1−NL1*01

4 sequences assigned
No exact matches.



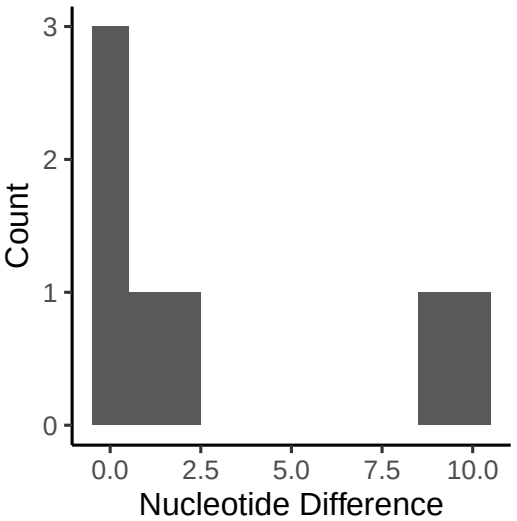
IGHV2−70*01

1991 sequences assigned
351 (17.6%) exact matches, in which:
200 unique CDR3
5 unique J



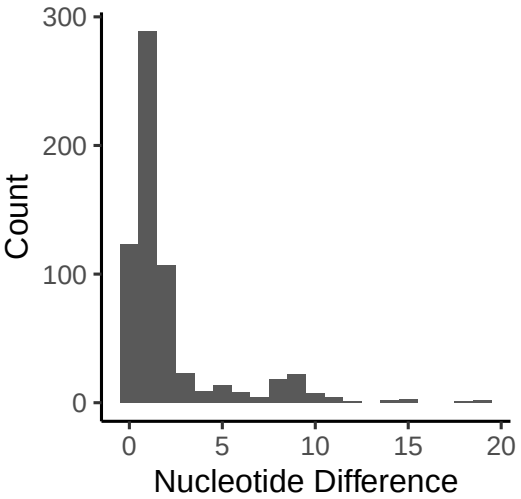
IGHV1−69−2*01

7 sequences assigned
3 (42.9%) exact matches, in which:
3 unique CDR3
3 unique J



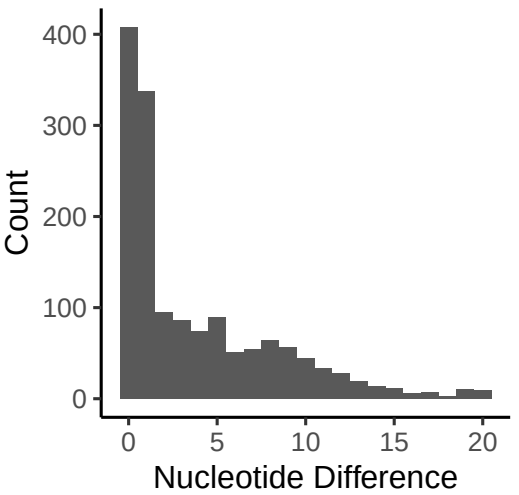
IGHV2−5*02

638 sequences assigned
123 (19.3%) exact matches, in which:
90 unique CDR3
5 unique J



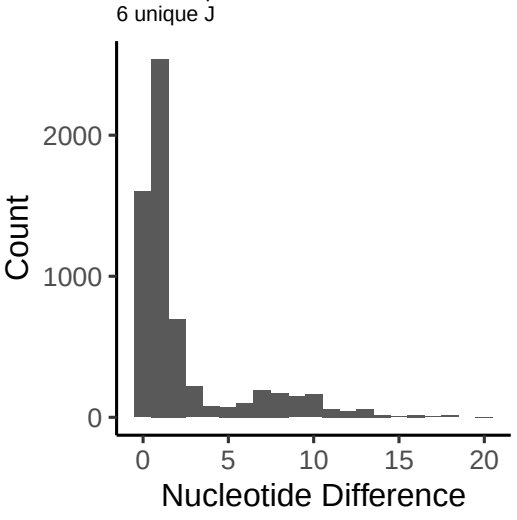
IGHV3−7*01

1515 sequences assigned
408 (26.9%) exact matches, in which:
333 unique CDR3
6 unique J



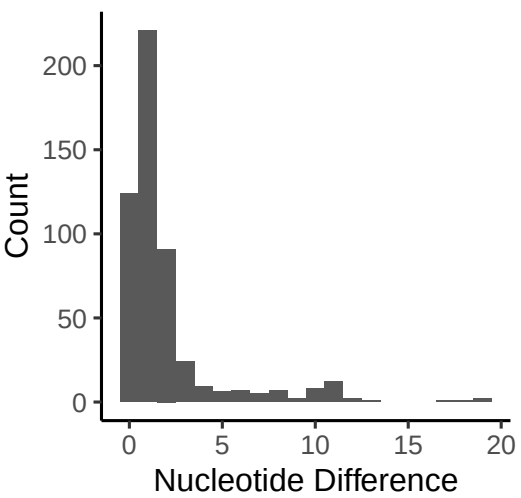
IGHV1−69*06_14

6221 sequences assigned
1602 (25.8%) exact matches, in which:
1184 unique CDR3
6 unique J



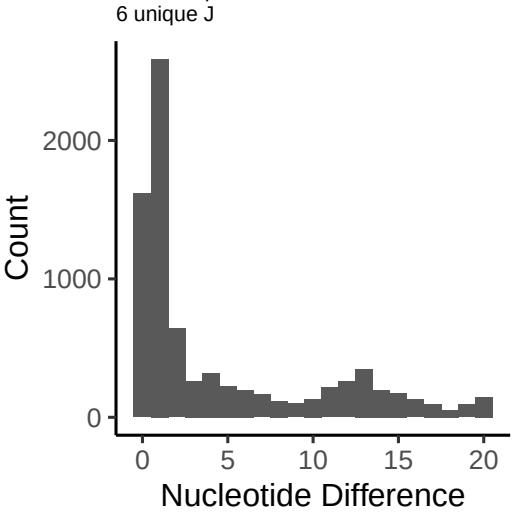
IGHV2−26*01

524 sequences assigned
124 (23.7%) exact matches, in which:
88 unique CDR3
5 unique J



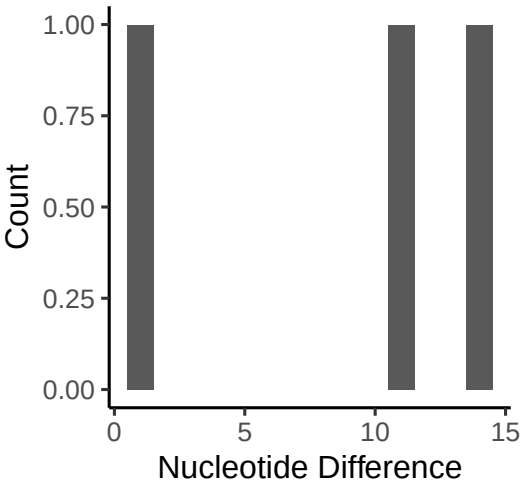
IGHV3−7*03

8660 sequences assigned
1616 (18.7%) exact matches, in which:
1025 unique CDR3
6 unique J



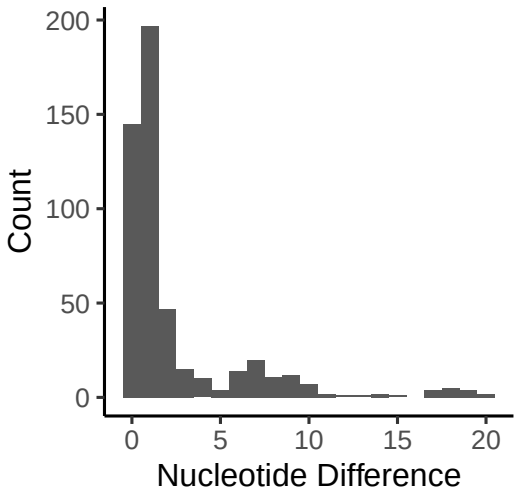
IGHV3−9*01

6 sequences assigned
No exact matches.



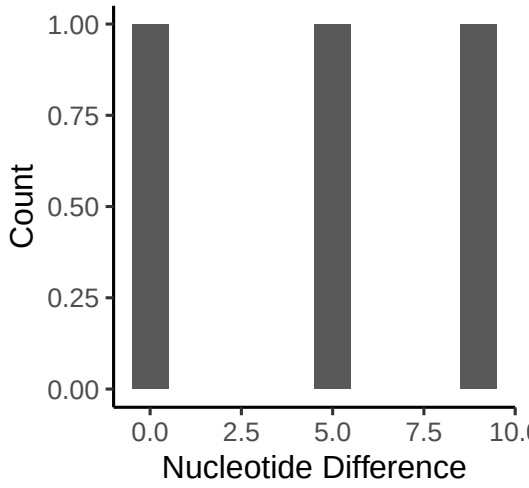
IGHV3−13*05

516 sequences assigned
145 (28.1%) exact matches, in which:
98 unique CDR3
6 unique J



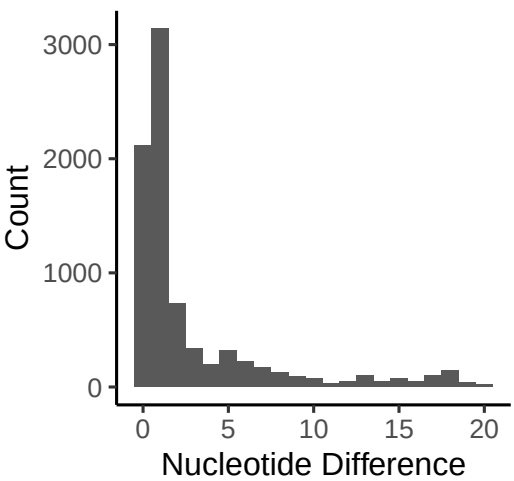
IGHV3−19*01

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



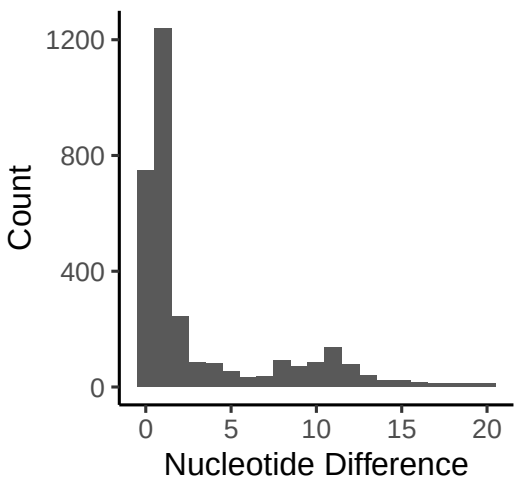
IGHV3−11*06

8225 sequences assigned
2119 (25.8%) exact matches, in which:
1246 unique CDR3
6 unique J



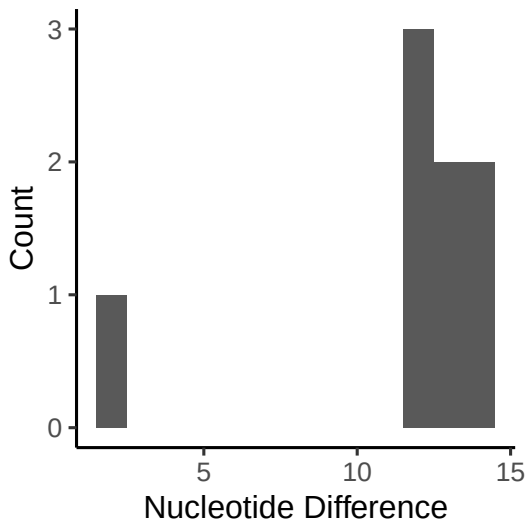
IGHV3−15*07

3223 sequences assigned
749 (23.2%) exact matches, in which:
405 unique CDR3
6 unique J



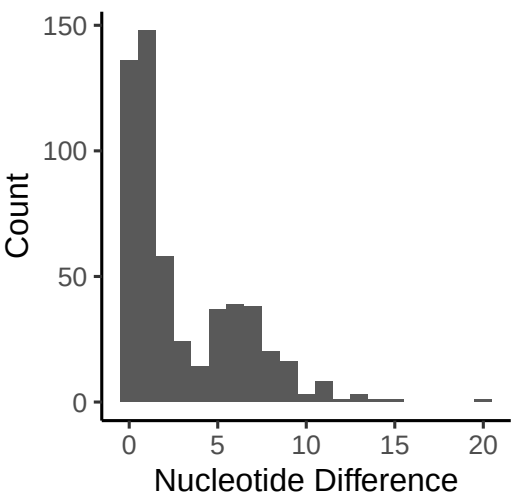
IGHV3−20*03_04

9 sequences assigned
No exact matches.



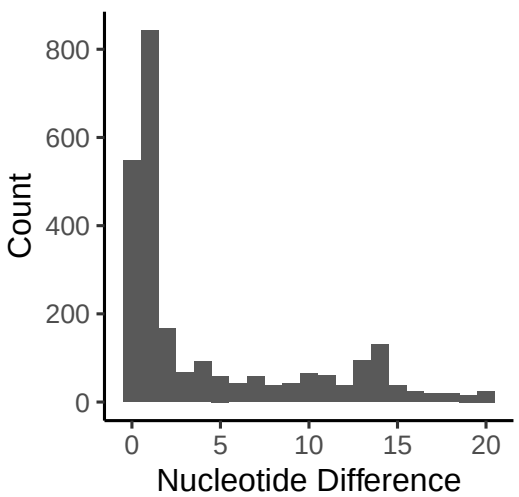
IGHV3−11*03_05

552 sequences assigned
136 (24.6%) exact matches, in which:
108 unique CDR3
6 unique J



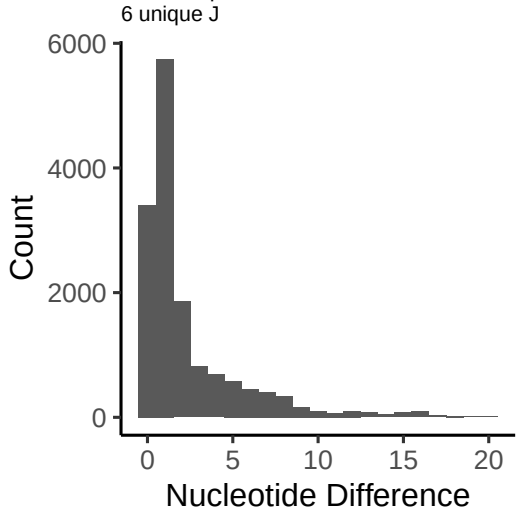
IGHV3−15*01_02

2629 sequences assigned
548 (20.8%) exact matches, in which:
301 unique CDR3
6 unique J



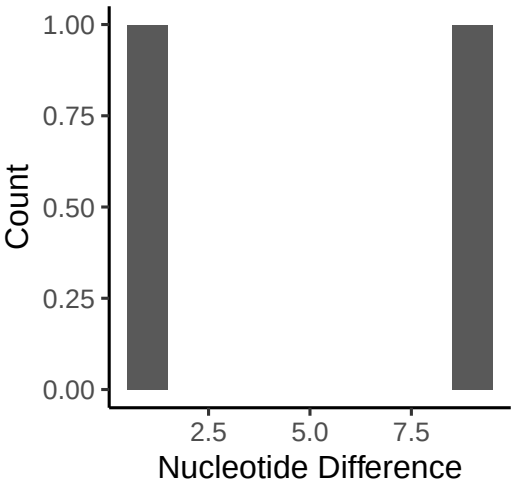
IGHV3−21*01_02

15273 sequences assigned
3403 (22.3%) exact matches, in which:
1932 unique CDR3
6 unique J



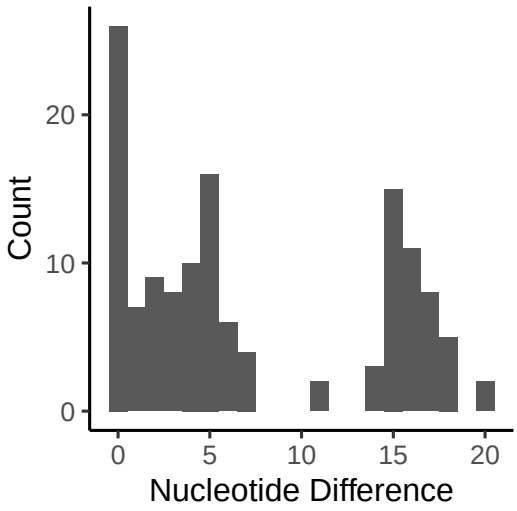
IGHV3−22*01_02

2 sequences assigned
No exact matches.



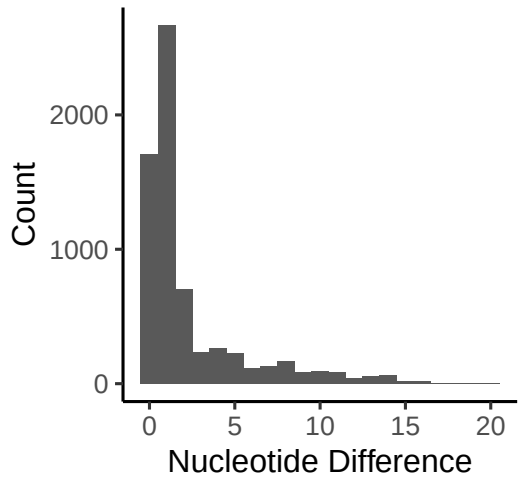
IGHV3−33*05

135 sequences assigned
26 (19.3%) exact matches, in which:
24 unique CDR3
4 unique J



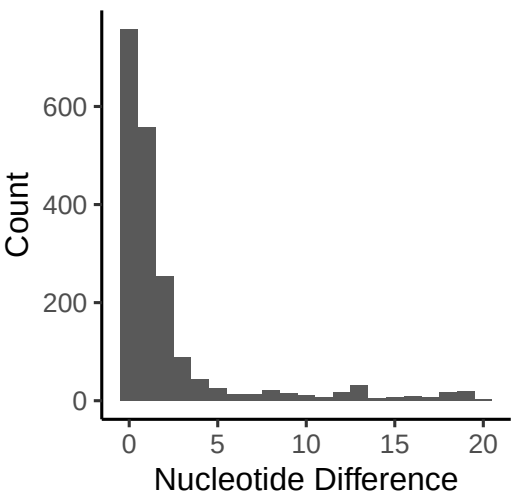
IGHV3−48*01

6740 sequences assigned
1710 (25.4%) exact matches, in which:
1015 unique CDR3
6 unique J



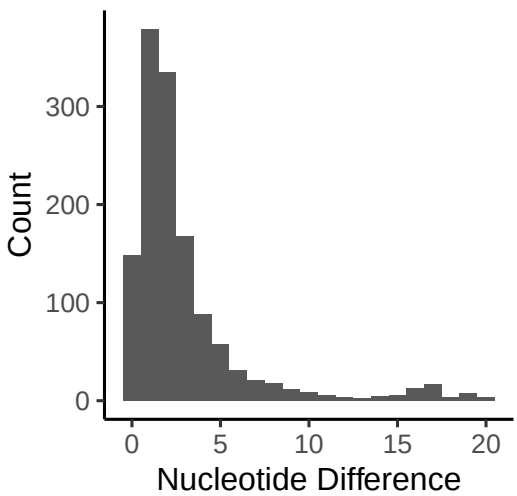
IGHV3−30*03

1954 sequences assigned
758 (38.8%) exact matches, in which:
569 unique CDR3
6 unique J



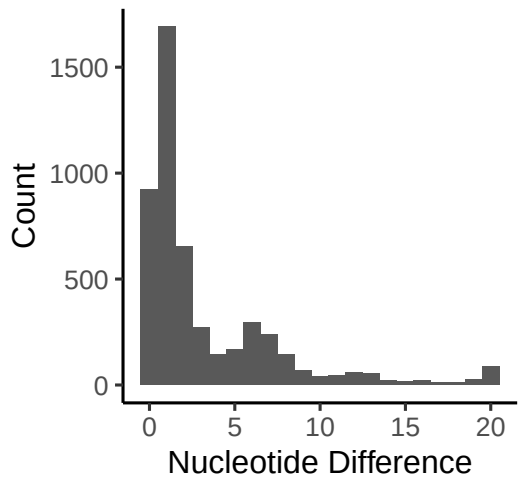
IGHV3−33*06

1344 sequences assigned
148 (11%) exact matches, in which:
125 unique CDR3
6 unique J



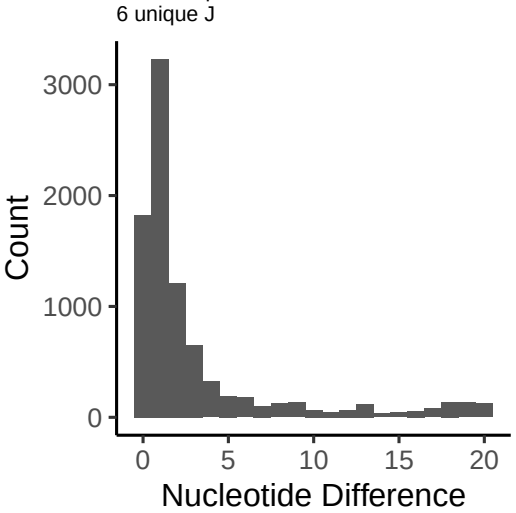
IGHV3−48*03

8012 sequences assigned
922 (11.5%) exact matches, in which:
516 unique CDR3
6 unique J



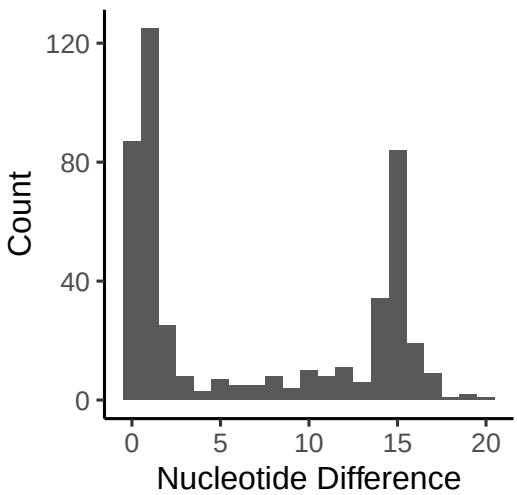
IGHV3−33*01

9089 sequences assigned
1826 (20.1%) exact matches, in which:
1112 unique CDR3
6 unique J



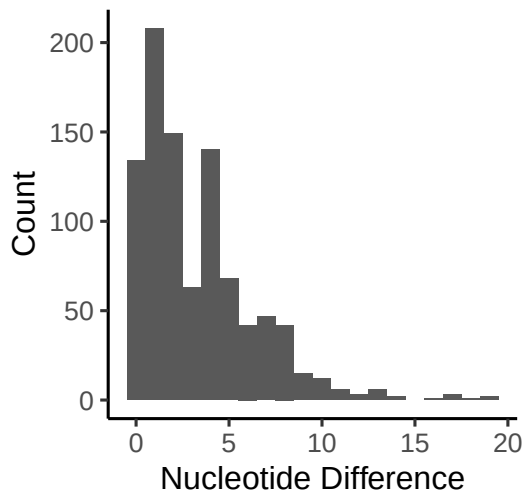
IGHV3−43*01

467 sequences assigned
87 (18.6%) exact matches, in which:
48 unique CDR3
3 unique J



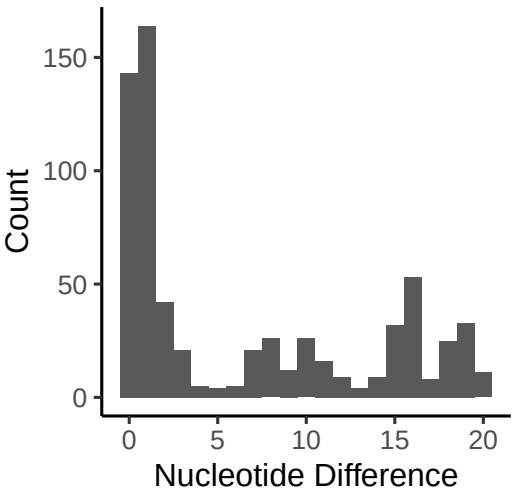
IGHV3−48*04

951 sequences assigned
134 (14.1%) exact matches, in which:
117 unique CDR3
5 unique J



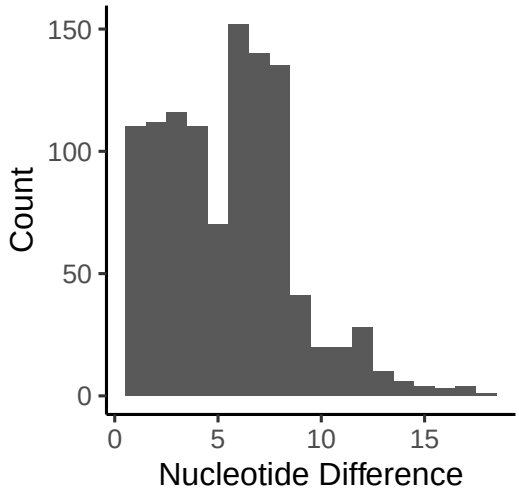
IGHV3−49*04

925 sequences assigned
143 (15.5%) exact matches, in which:
86 unique CDR3
5 unique J



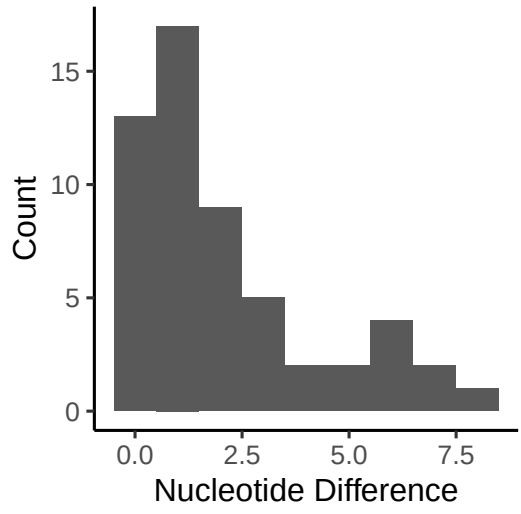
IGHV3−64*04

1084 sequences assigned
No exact matches.



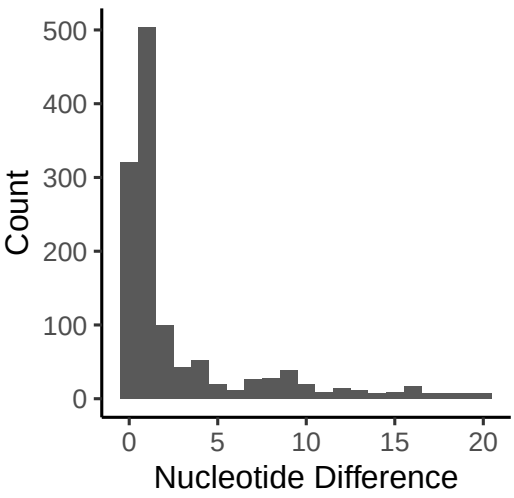
IGHV3−66*03

57 sequences assigned
13 (22.8%) exact matches, in which:
12 unique CDR3
3 unique J



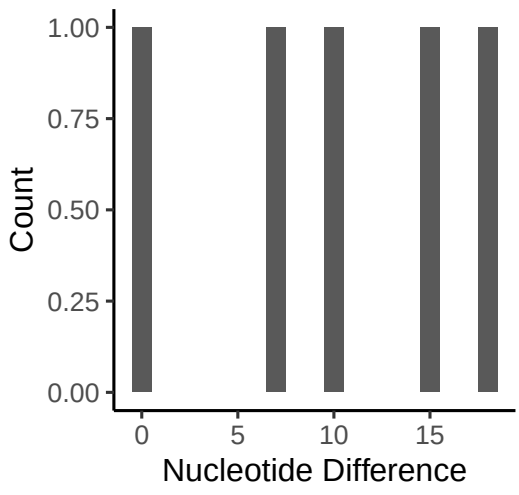
IGHV3−49*03_05

1295 sequences assigned
320 (24.7%) exact matches, in which:
176 unique CDR3
4 unique J



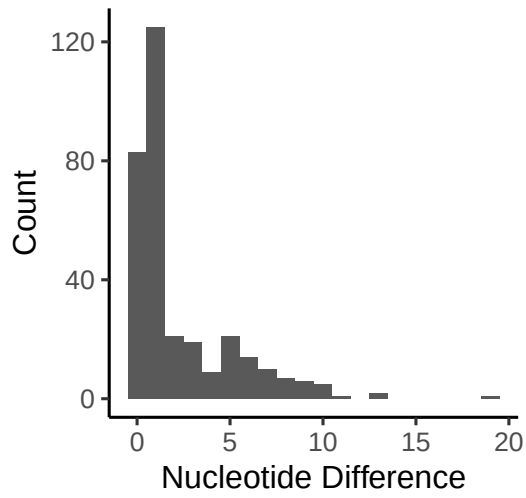
IGHV3−66*01

7 sequences assigned
1 (14.3%) exact matches, in which:
1 unique CDR3
1 unique J



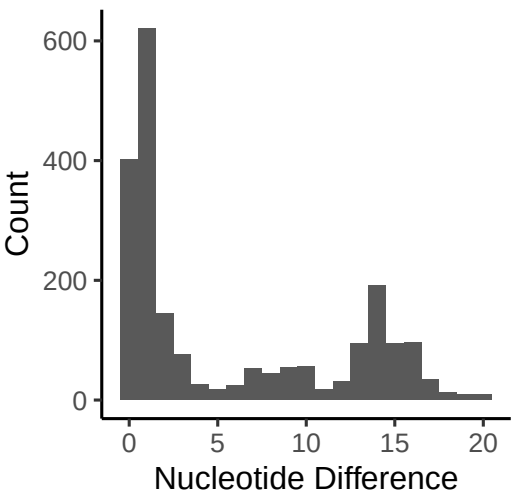
IGHV3−69−1*01

326 sequences assigned
83 (25.5%) exact matches, in which:
63 unique CDR3
5 unique J



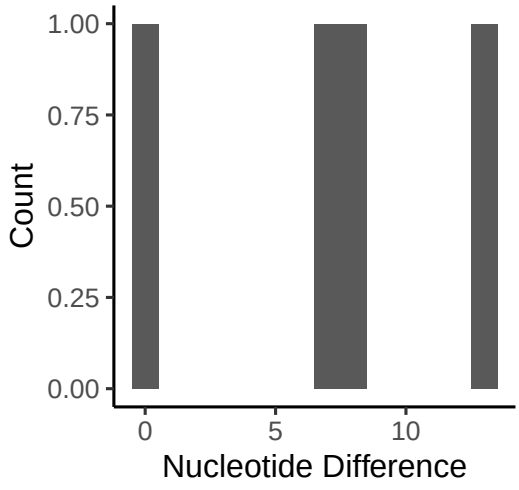
IGHV3−53*01_02

2201 sequences assigned
402 (18.3%) exact matches, in which:
262 unique CDR3
6 unique J



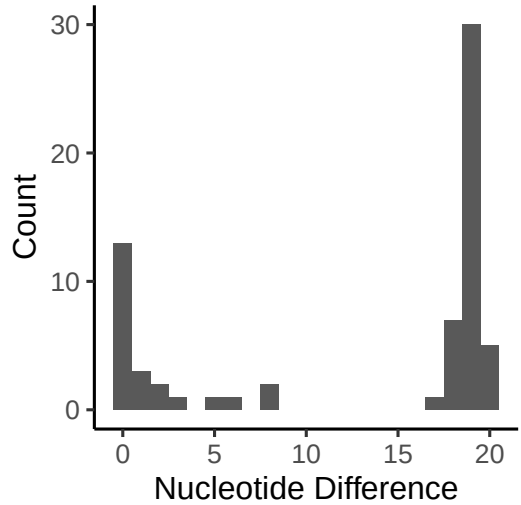
IGHV3−66*02

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



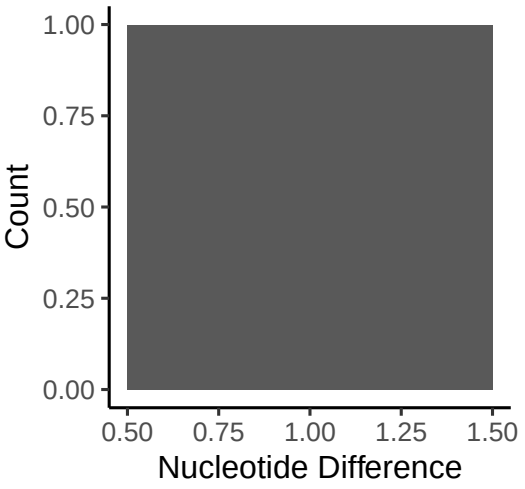
IGHV3−69−1*02

69 sequences assigned
13 (18.8%) exact matches, in which:
13 unique CDR3
4 unique J



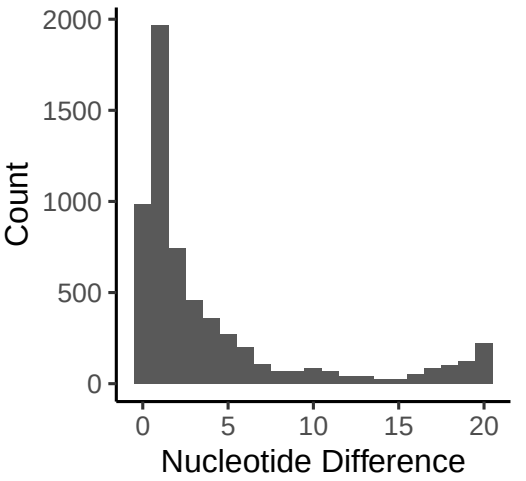
IGHV3−71*02

1 sequences assigned
No exact matches.



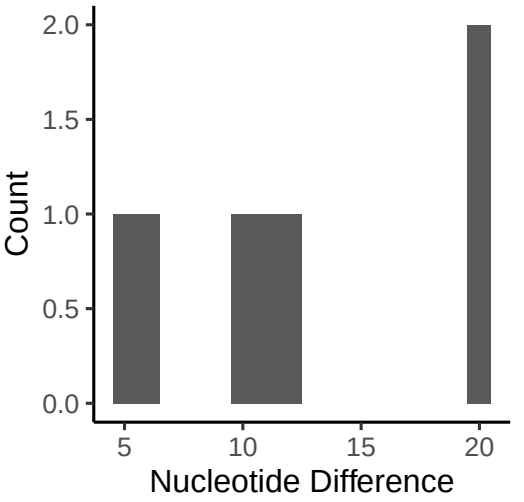
IGHV3−74*01_02

9383 sequences assigned
983 (10.5%) exact matches, in which:
596 unique CDR3
6 unique J



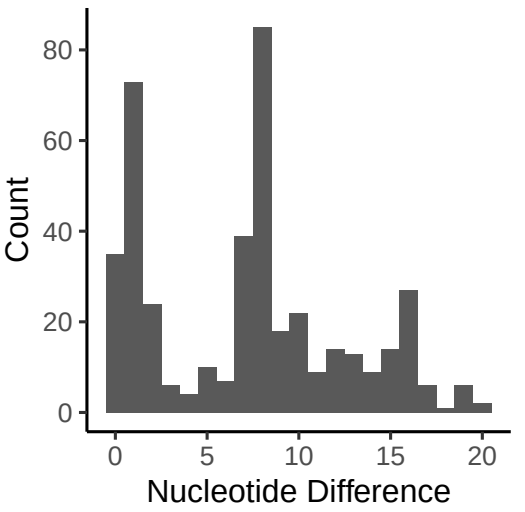
IGHV3−NL1*01

8 sequences assigned
No exact matches.



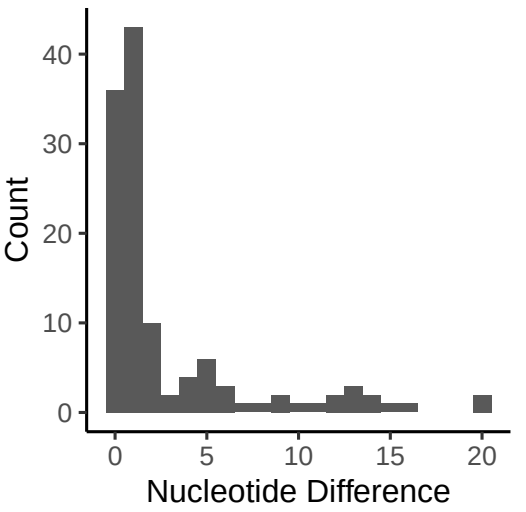
IGHV3−72*01

694 sequences assigned
35 (5%) exact matches, in which:
18 unique CDR3
3 unique J



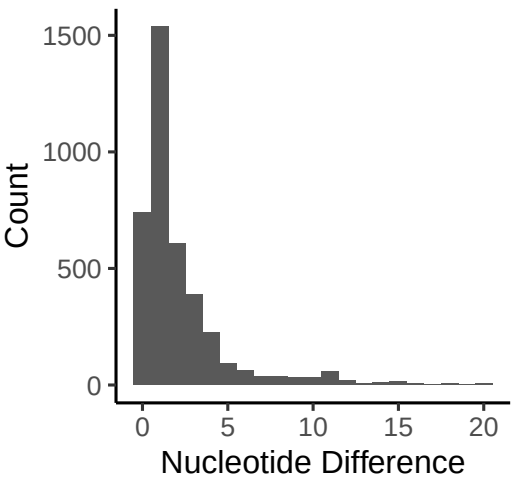
IGHV3−43D*04

148 sequences assigned
36 (24.3%) exact matches, in which:
24 unique CDR3
2 unique J



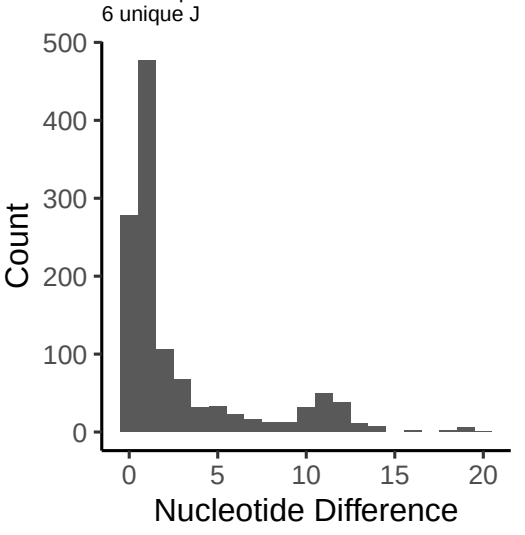
IGHV4−4*07

4030 sequences assigned
742 (18.4%) exact matches, in which:
513 unique CDR3
6 unique J



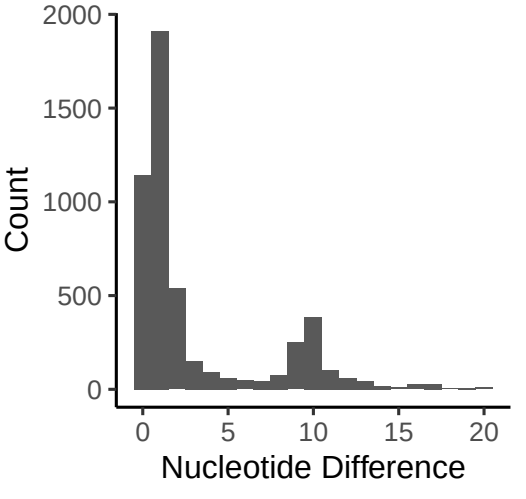
IGHV3−73*01_02

1205 sequences assigned
278 (23.1%) exact matches, in which:
160 unique CDR3
6 unique J



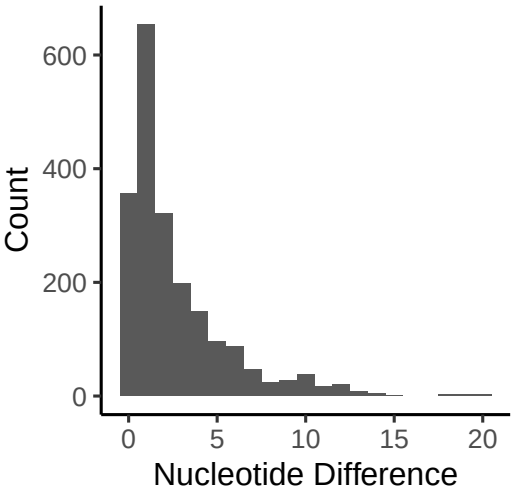
IGHV3−64D*06

5116 sequences assigned
1144 (22.4%) exact matches, in which:
676 unique CDR3
6 unique J



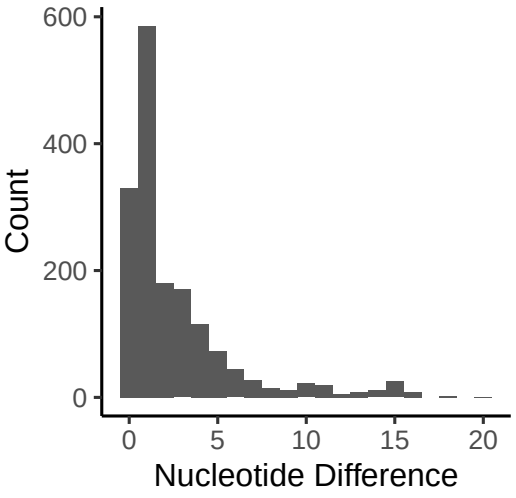
IGHV4−30−2*01

2303 sequences assigned
357 (15.5%) exact matches, in which:
255 unique CDR3
6 unique J



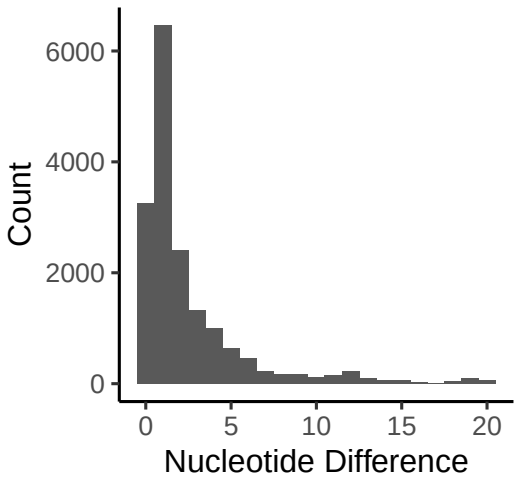
IGHV4−30−4*01

1677 sequences assigned
330 (19.7%) exact matches, in which:
236 unique CDR3
6 unique J



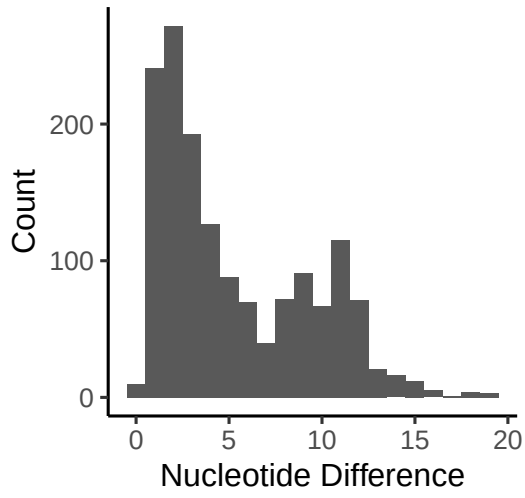
IGHV4−34*01_02

17303 sequences assigned
3249 (18.8%) exact matches, in which:
2094 unique CDR3
6 unique J



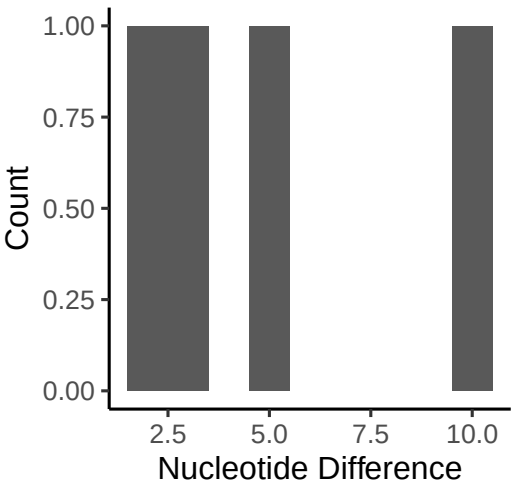
IGHV4−39*07

1521 sequences assigned
10 (0.7%) exact matches, in which:
10 unique CDR3
3 unique J



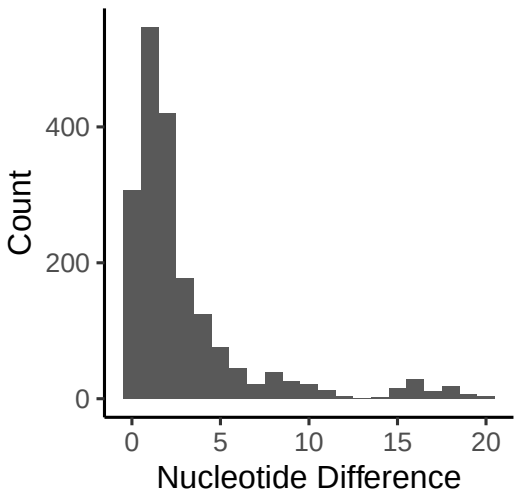
IGHV4−30−2*04

4 sequences assigned
No exact matches.



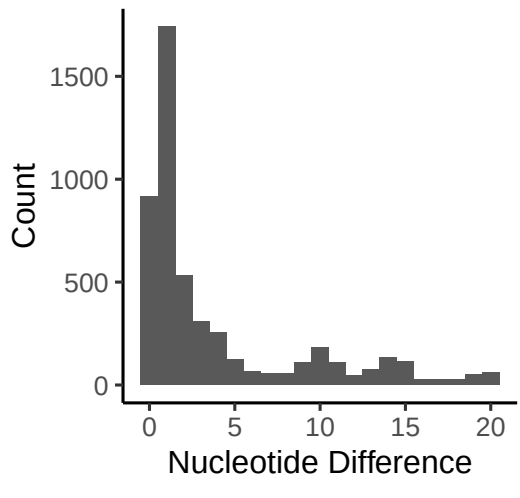
IGHV4−38−2*01

1941 sequences assigned
307 (15.8%) exact matches, in which:
249 unique CDR3
6 unique J



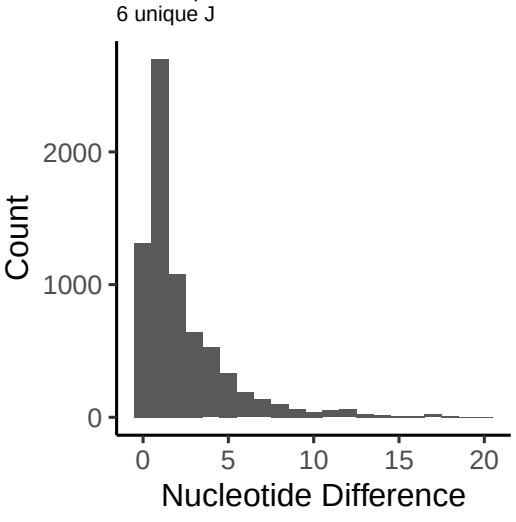
IGHV4−39*01_05

5168 sequences assigned
916 (17.7%) exact matches, in which:
622 unique CDR3
6 unique J



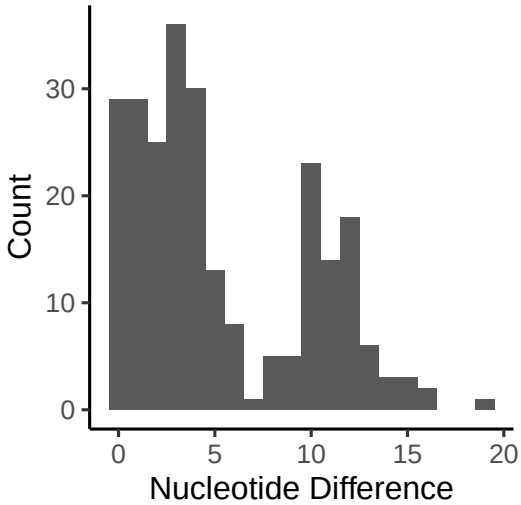
IGHV4−31*03_04

7384 sequences assigned
1314 (17.8%) exact matches, in which:
892 unique CDR3
6 unique J



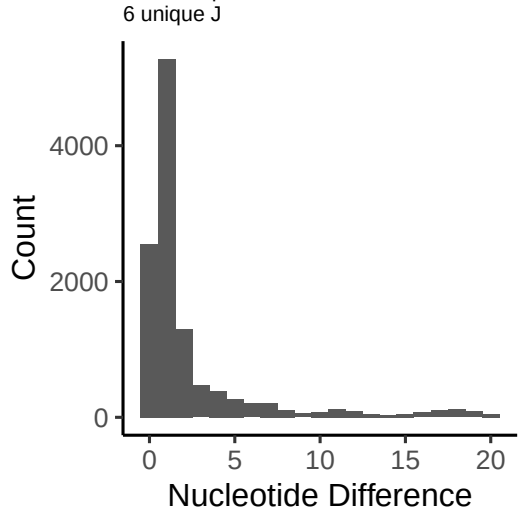
IGHV4−38−2*02

280 sequences assigned
29 (10.4%) exact matches, in which:
23 unique CDR3
6 unique J



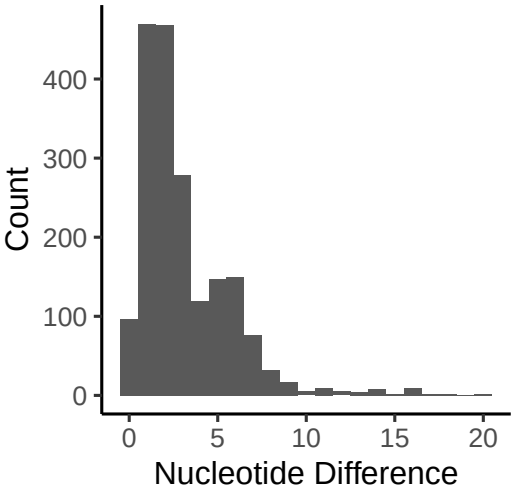
IGHV4−59*01_07

12689 sequences assigned
2549 (20.1%) exact matches, in which:
1727 unique CDR3
6 unique J



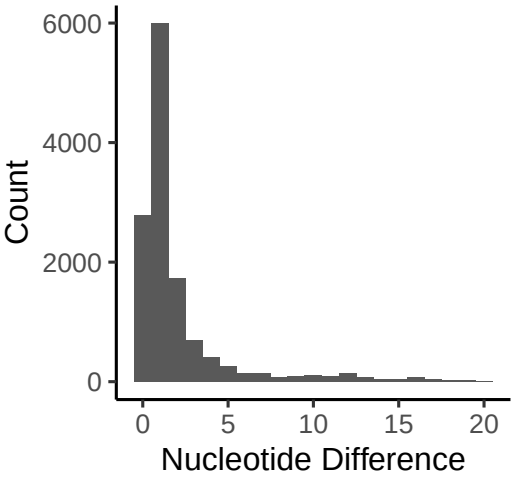
IGHV4−59*12

1958 sequences assigned
97 (5%) exact matches, in which:
94 unique CDR3
6 unique J



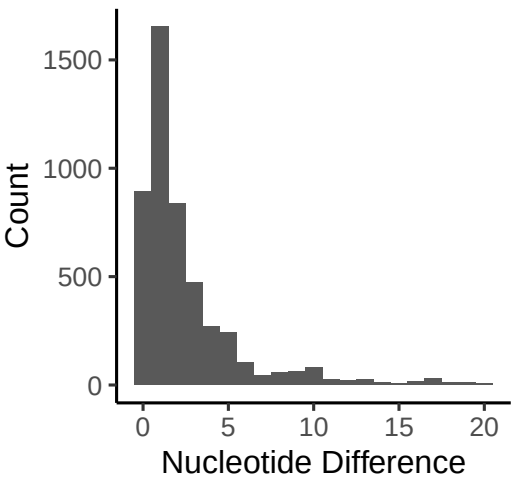
IGHV5−51*01_03

13081 sequences assigned
2781 (21.3%) exact matches, in which:
1455 unique CDR3
6 unique J



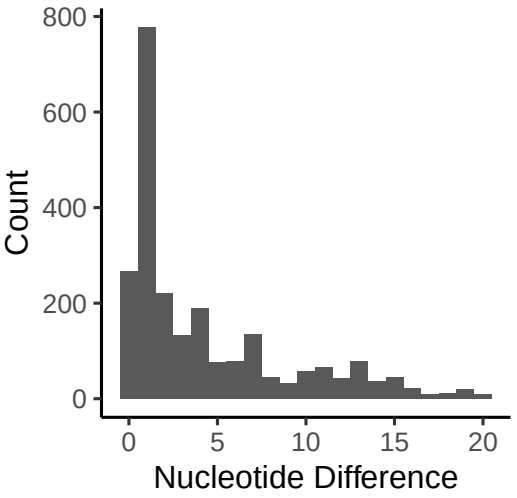
IGHV4−61*01

4986 sequences assigned
894 (17.9%) exact matches, in which:
692 unique CDR3
6 unique J



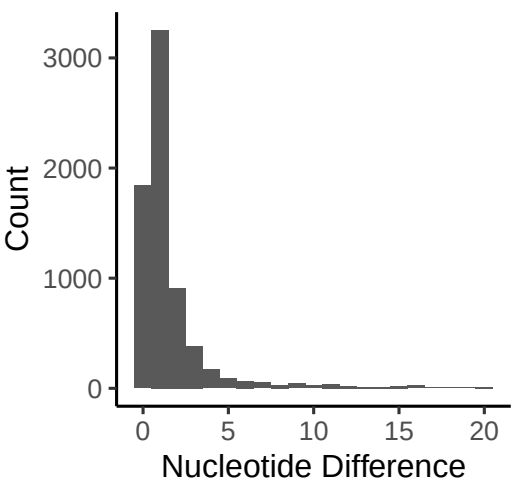
IGHV6−1*01_02

2463 sequences assigned
267 (10.8%) exact matches, in which:
169 unique CDR3
5 unique J



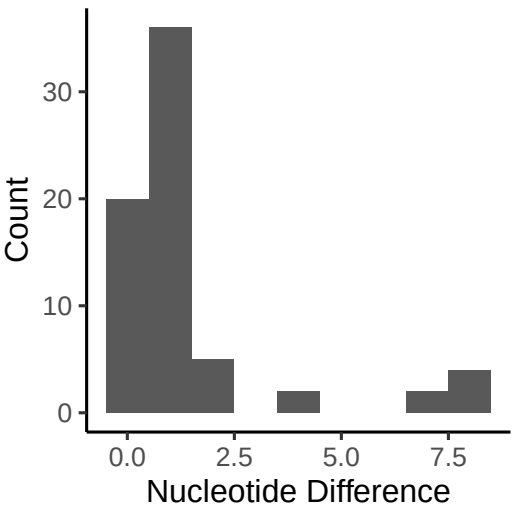
IGHV5−10−1*01_03

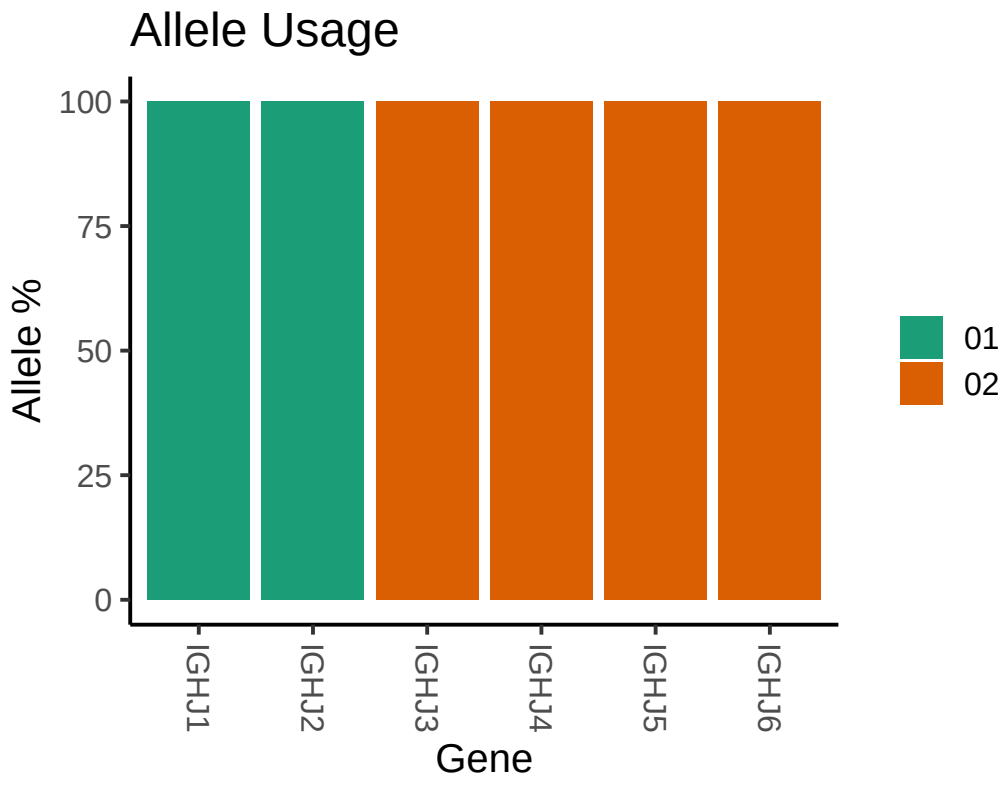
7067 sequences assigned
1842 (26.1%) exact matches, in which:
1024 unique CDR3
6 unique J



IGHV7−4−1*01

69 sequences assigned
20 (29%) exact matches, in which:
16 unique CDR3
4 unique J




Allele Usage
100
75
50
25
0
Allele %
IGHJ1
IGHJ2
IGHJ3
IGHJ4
IGHJ5
IGHJ6
Gene
01
02

Novel sequence(s) IGHV1−69*01_12_13_G238A IGHV3−48*03_T303G 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 are not listed in the genotype and will be ignored.

Novel sequence(s) IGHV3−30−3*01_T288C IGHV4−59*02_G88A IGHV5−51*07_A128G are not listed in the genotype and will be ignored.

Novel sequence(s) IGHV3−30*03_T288C 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) IGHV3−33*01_G75C IGHV4−59*02_G88A IGHV5−51*07_A128G are not listed in the genotype and will be ignored.

Novel sequence(s) IGHV3−33*01_G75C IGHV4−59*02_G88A IGHV5−51*07_A128G are not listed in the genotype and will be ignored.

Novel sequence(s) IGHV3−30*03_T288C IGHV4−59*02_G88A IGHV5−51*07_A128G are not listed in the genotype and will be ignored.