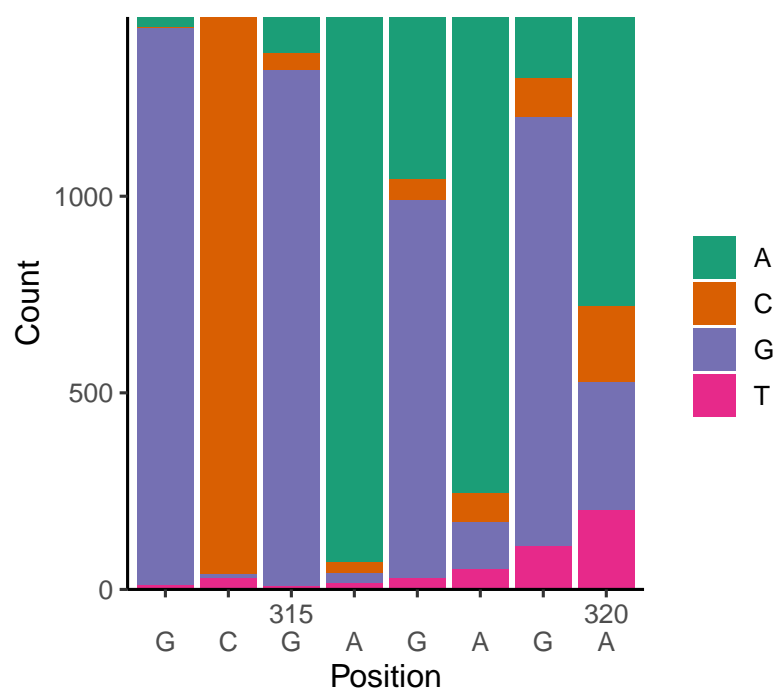
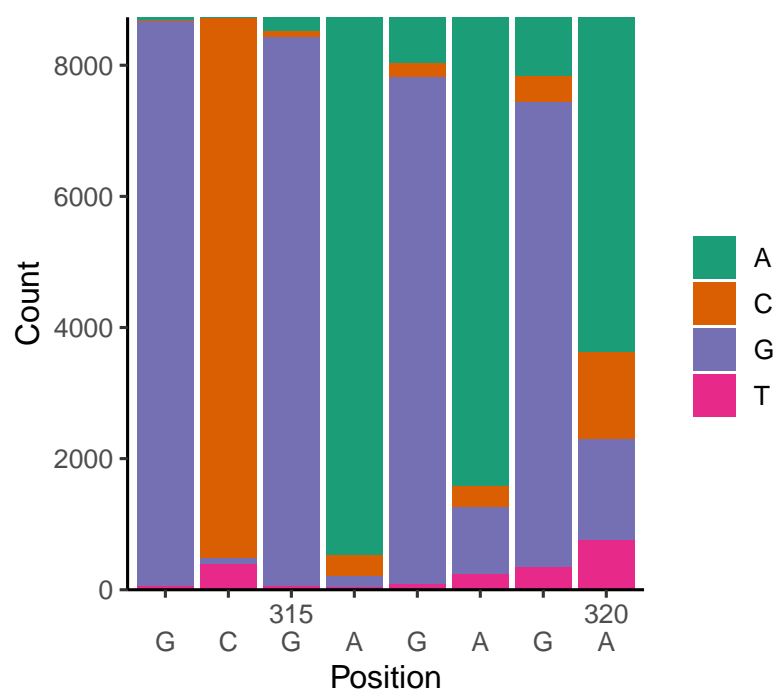


Gene IGHV3-30*04_T288C



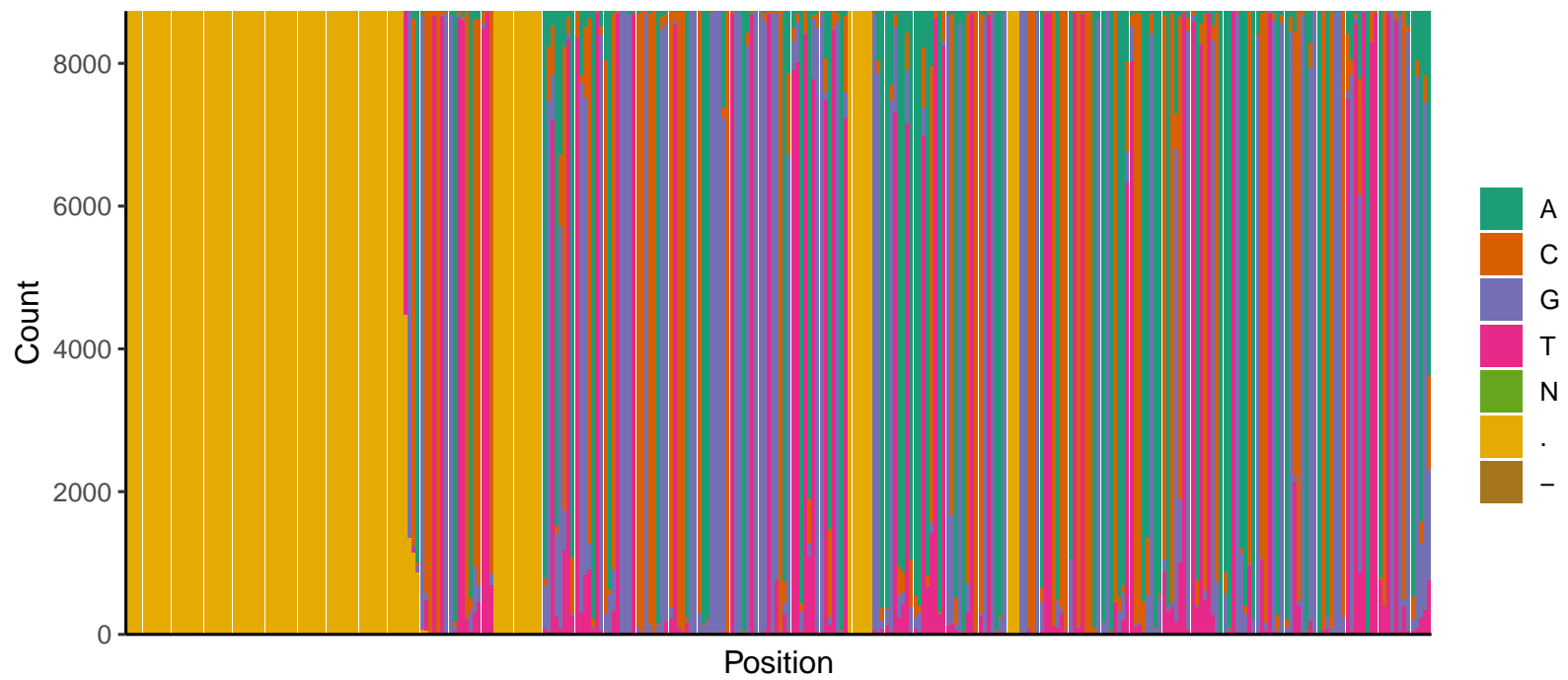
Gene IGHV3-33*01_G75C



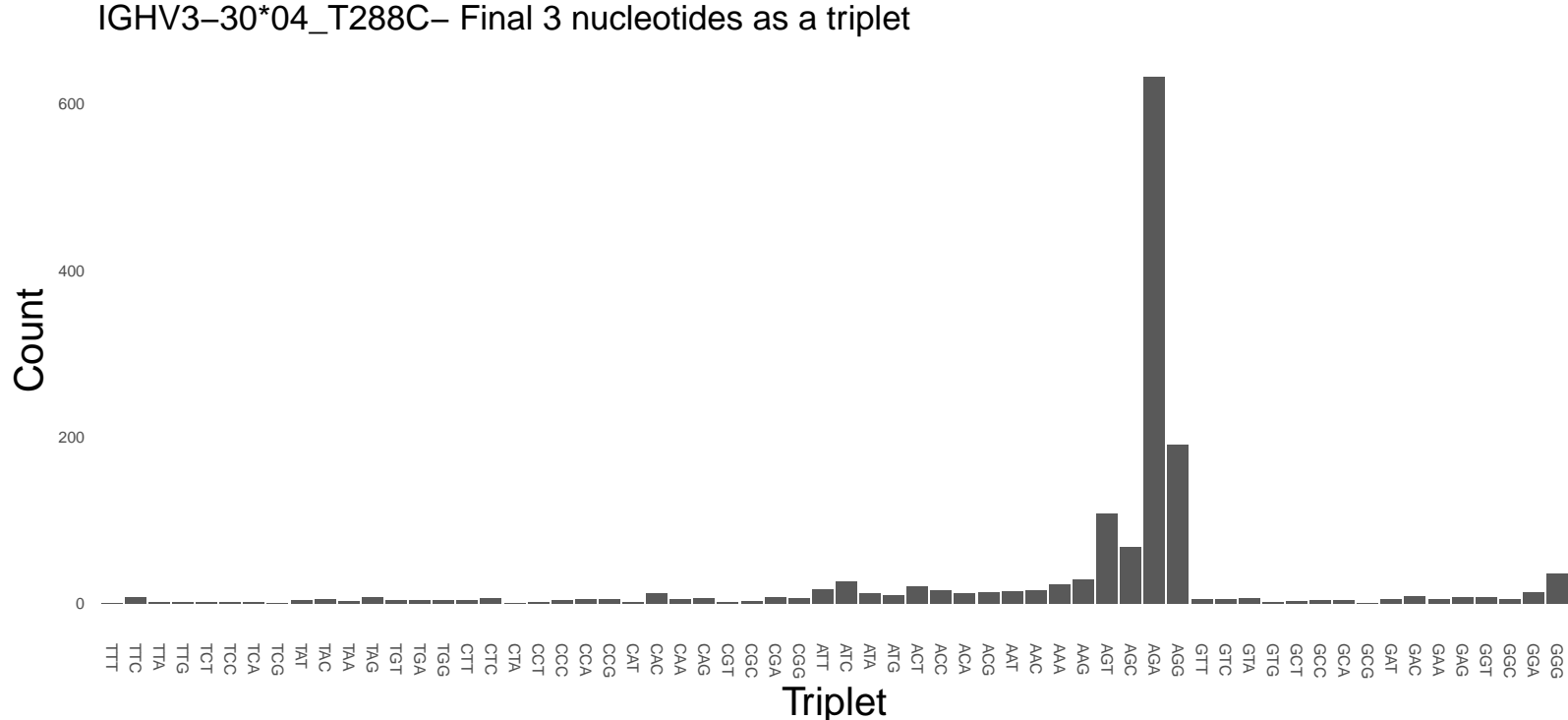
Gene IGHV3-30*04_T288C



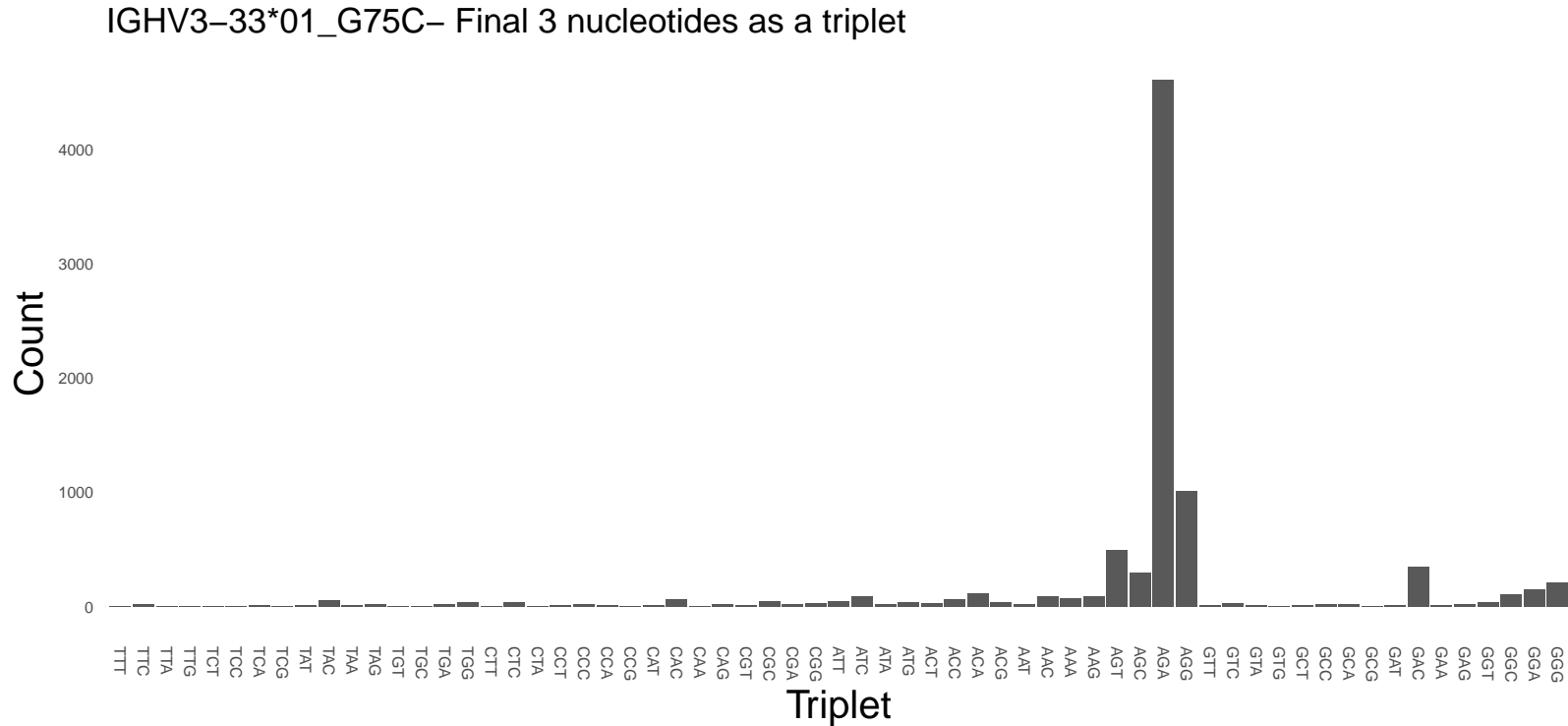
Gene IGHV3-33*01_G75C



IGHV3-30*04_T288C- Final 3 nucleotides as a triplet

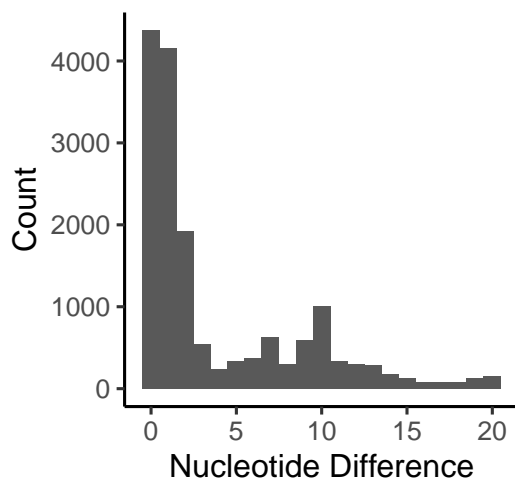


IGHV3-33*01_G75C- Final 3 nucleotides as a triplet



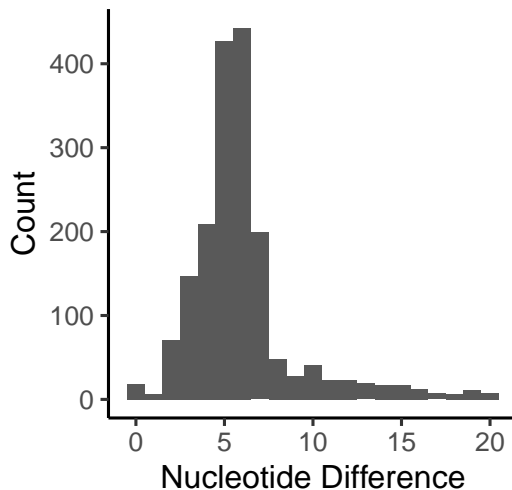
IGHV1-2*02

20762 sequences assigned
4373 (21.1%) exact matches, in which:
3792 unique CDR3
7 unique J



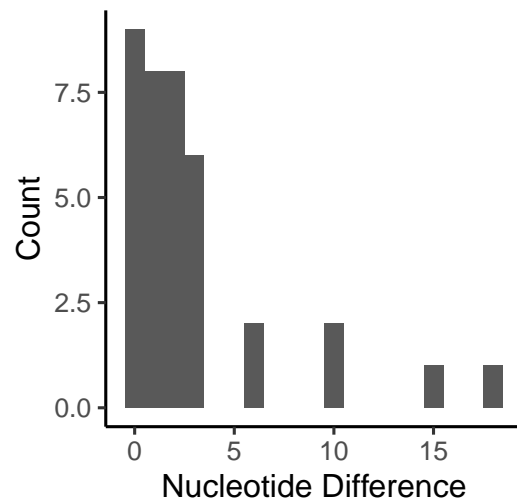
IGHV1-8*02

1957 sequences assigned
18 (0.9%) exact matches, in which:
18 unique CDR3
5 unique J



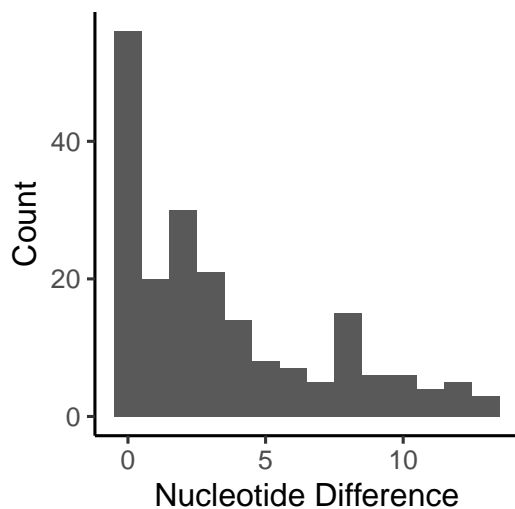
IGHV1-45*02

37 sequences assigned
9 (24.3%) exact matches, in which:
9 unique CDR3
2 unique J



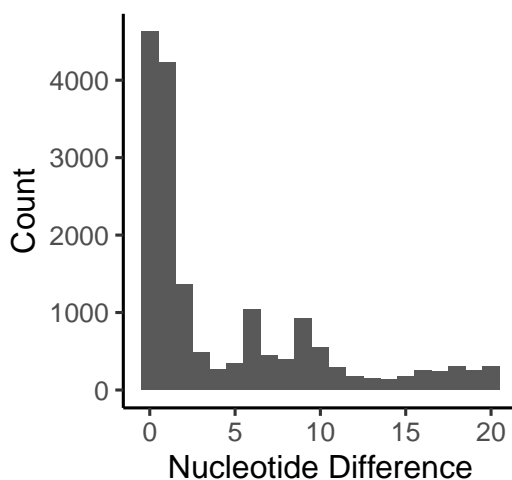
IGHV1-3*02

202 sequences assigned
56 (27.7%) exact matches, in which:
54 unique CDR3
6 unique J



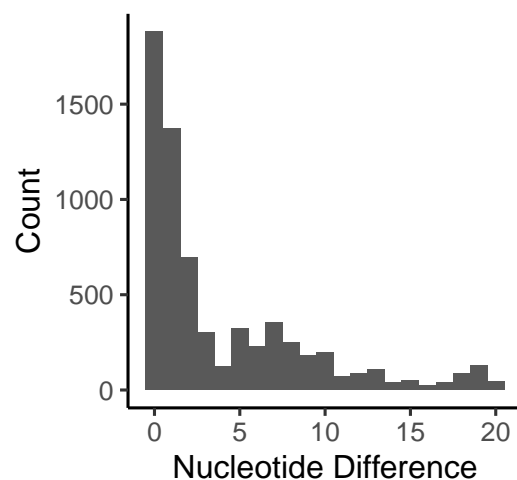
IGHV1-18*01

25295 sequences assigned
4626 (18.3%) exact matches, in which:
3981 unique CDR3
7 unique J



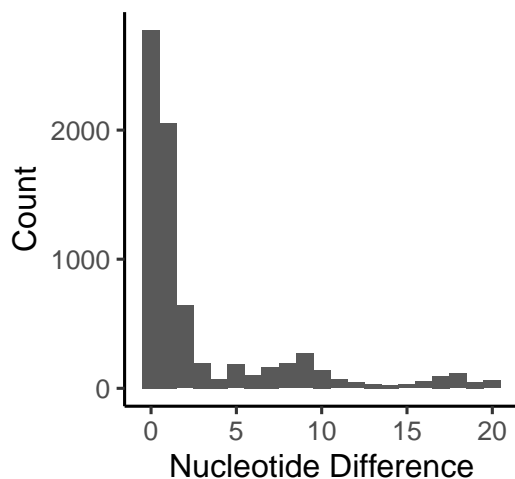
IGHV1-46*01

8176 sequences assigned
1880 (23%) exact matches, in which:
1717 unique CDR3
7 unique J



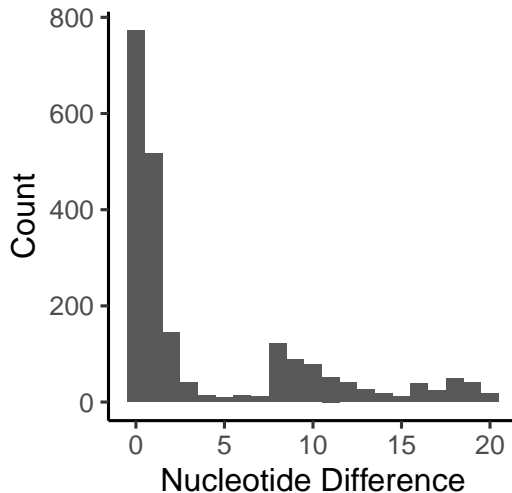
IGHV1-8*01

9653 sequences assigned
2775 (28.7%) exact matches, in which:
2477 unique CDR3
7 unique J



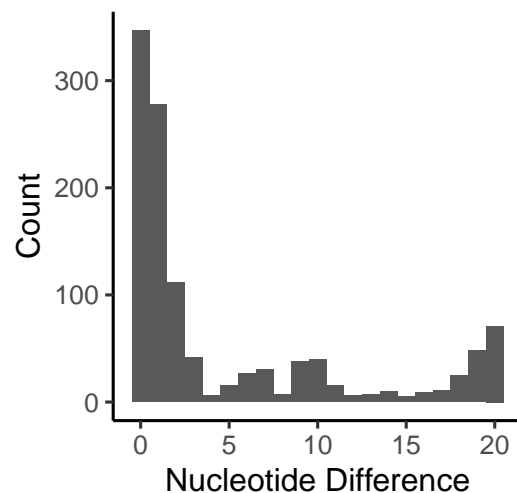
IGHV1-24*01

2326 sequences assigned
773 (33.2%) exact matches, in which:
711 unique CDR3
7 unique J



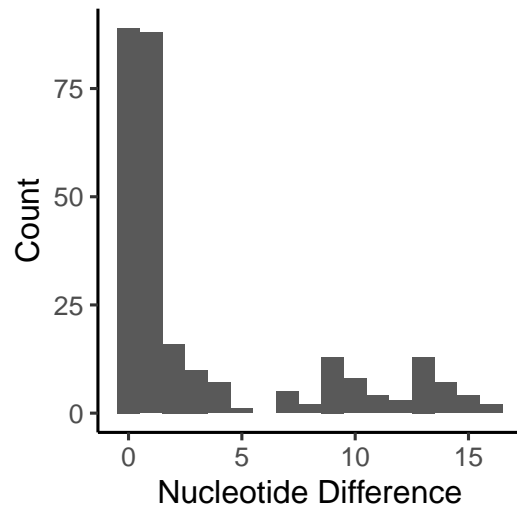
IGHV1-46*03

1217 sequences assigned
347 (28.5%) exact matches, in which:
287 unique CDR3
6 unique J



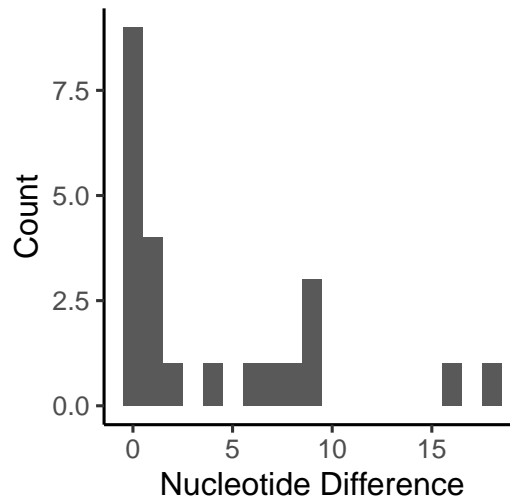
IGHV1-58*02

272 sequences assigned
89 (32.7%) exact matches, in which:
81 unique CDR3
6 unique J



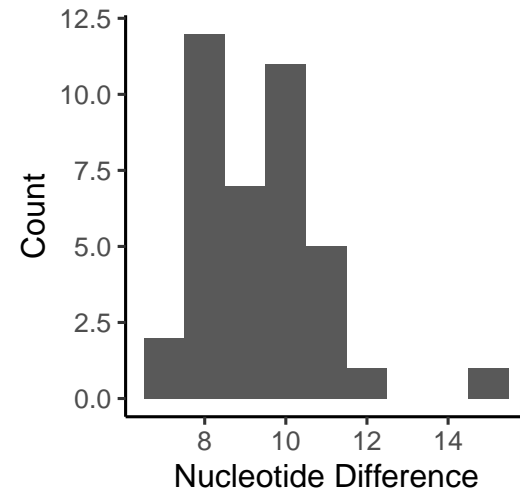
IGHV1-69-2*01

44 sequences assigned
9 (20.5%) exact matches, in which:
9 unique CDR3
3 unique J



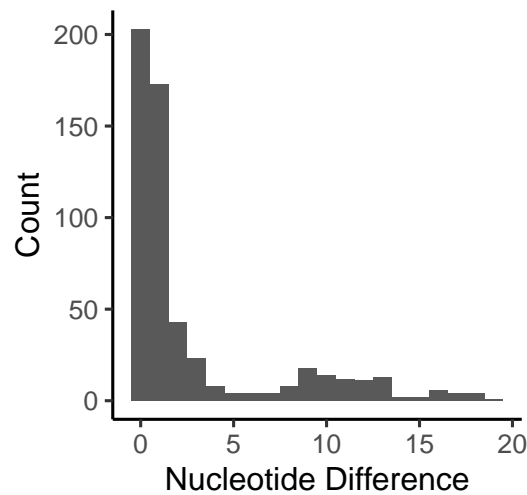
IGHV1-NL1*01

40 sequences assigned
No exact matches.



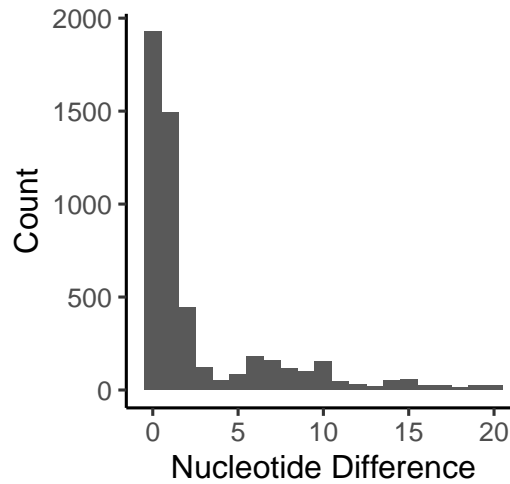
IGHV1-58*01_03

599 sequences assigned
203 (33.9%) exact matches, in which:
168 unique CDR3
6 unique J



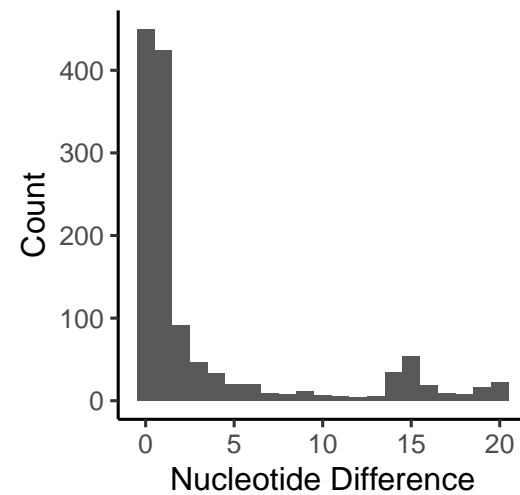
IGHV1-69*04_09

6941 sequences assigned
1927 (27.8%) exact matches, in which:
1792 unique CDR3
7 unique J



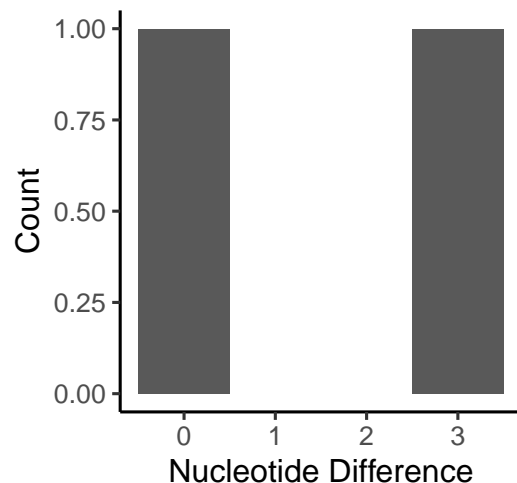
IGHV2-5*01

1946 sequences assigned
450 (23.1%) exact matches, in which:
384 unique CDR3
6 unique J



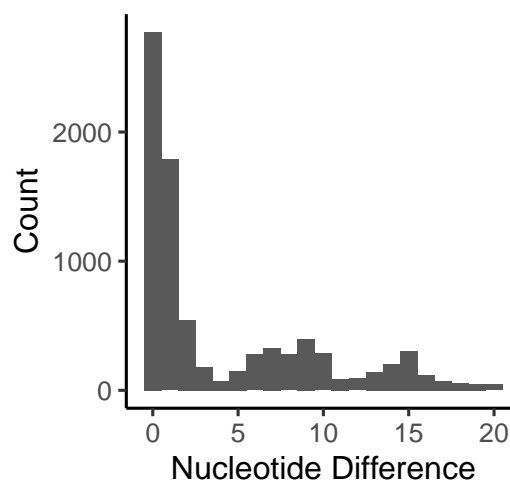
IGHV1-68*01

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



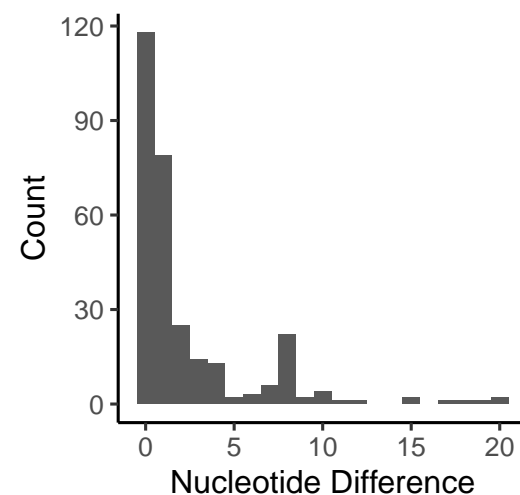
IGHV1-69*06_14

8853 sequences assigned
2774 (31.3%) exact matches, in which:
2556 unique CDR3
7 unique J



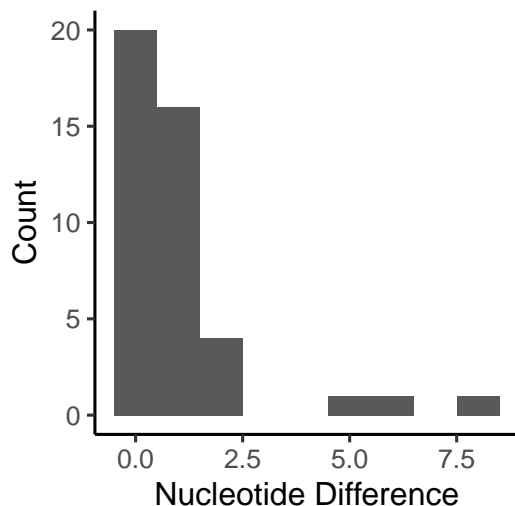
IGHV2-26*01

300 sequences assigned
118 (39.3%) exact matches, in which:
99 unique CDR3
5 unique J



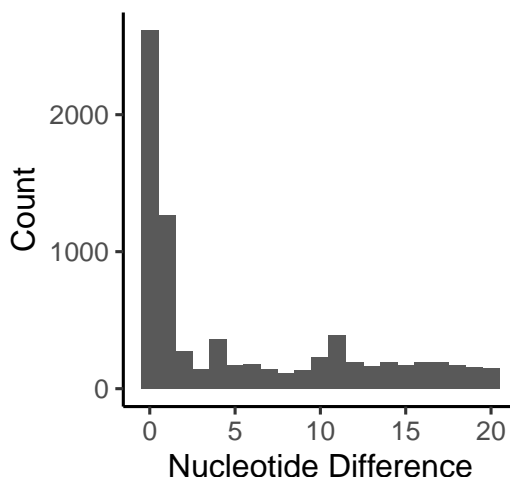
IGHV2-26*02

47 sequences assigned
20 (42.6%) exact matches, in which:
17 unique CDR3
5 unique J



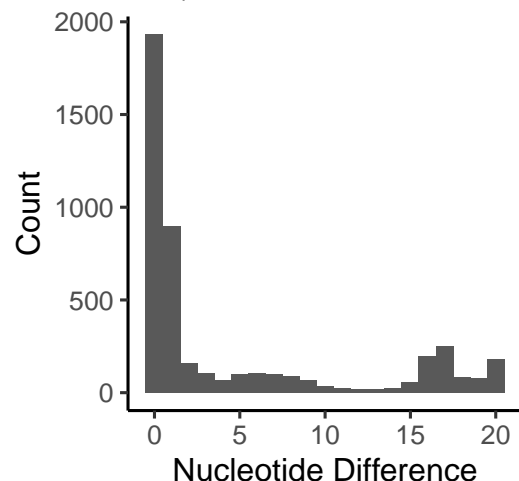
IGHV3-7*01

11419 sequences assigned
2615 (22.9%) exact matches, in which:
1794 unique CDR3
7 unique J



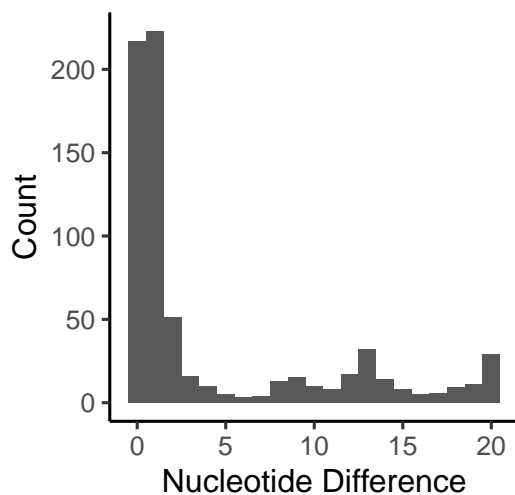
IGHV3-11*01

6095 sequences assigned
1932 (31.7%) exact matches, in which:
1294 unique CDR3
7 unique J



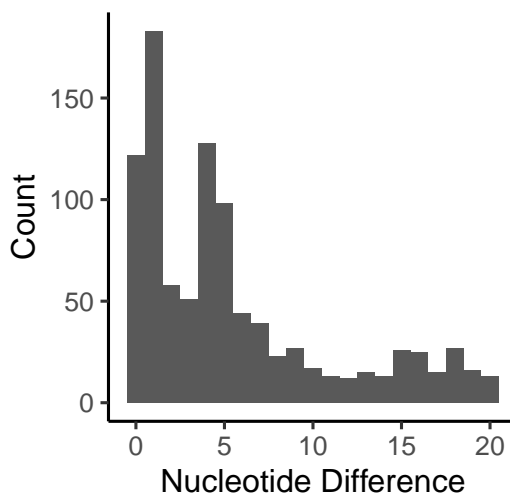
IGHV2-70*01

1518 sequences assigned
217 (14.3%) exact matches, in which:
182 unique CDR3
6 unique J



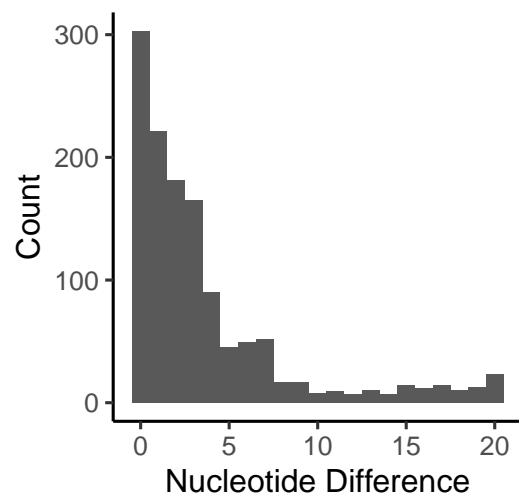
IGHV3-7*03

1265 sequences assigned
122 (9.6%) exact matches, in which:
115 unique CDR3
7 unique J



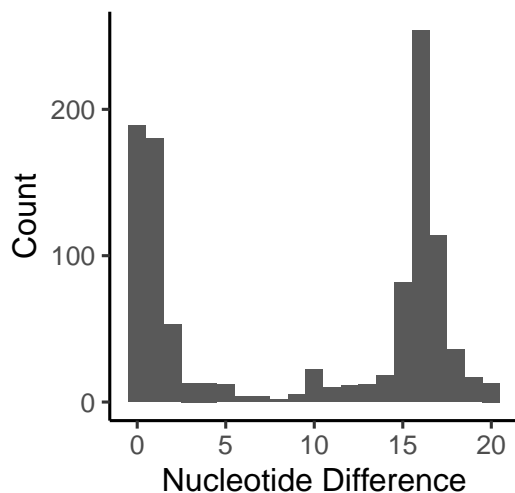
IGHV3-11*04

1422 sequences assigned
303 (21.3%) exact matches, in which:
297 unique CDR3
7 unique J



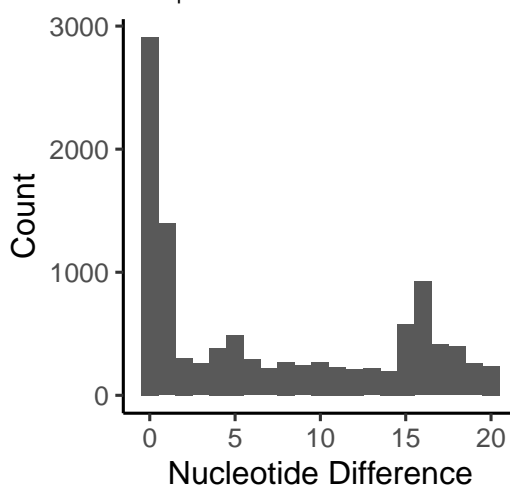
IGHV2-70*11_15

1104 sequences assigned
189 (17.1%) exact matches, in which:
156 unique CDR3
6 unique J



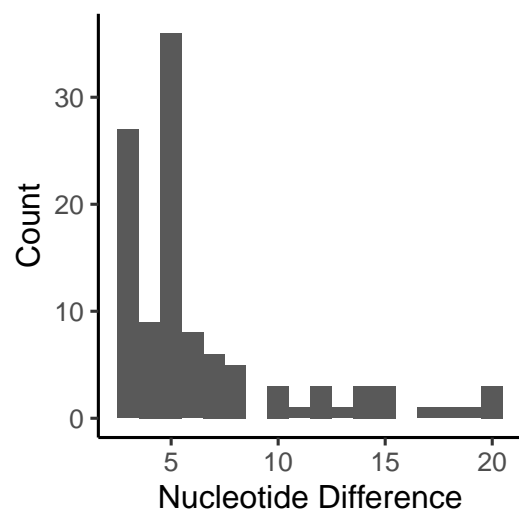
IGHV3-9*01

13231 sequences assigned
2911 (22%) exact matches, in which:
1792 unique CDR3
7 unique J



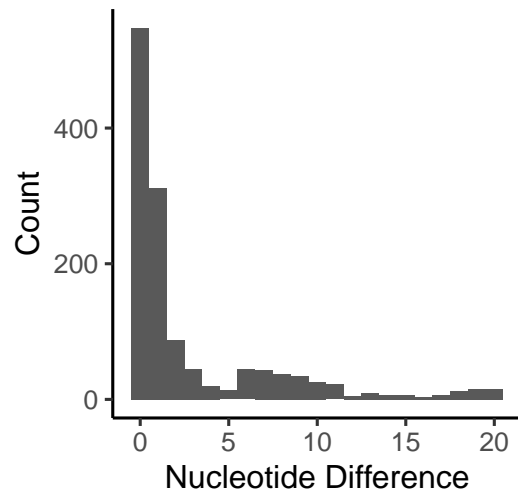
IGHV3-11*06

151 sequences assigned
No exact matches.



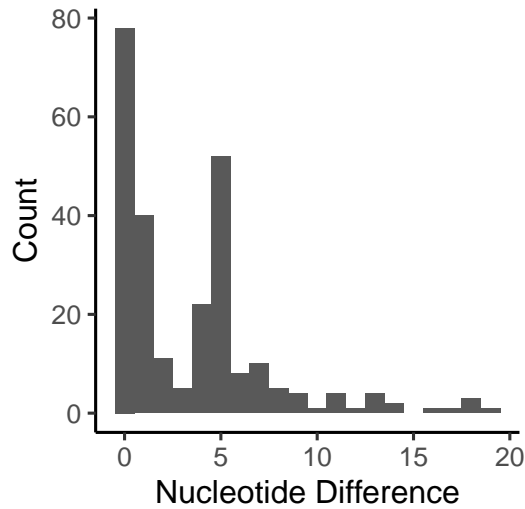
IGHV3-13*01

1469 sequences assigned
548 (37.3%) exact matches, in which:
372 unique CDR3
7 unique J



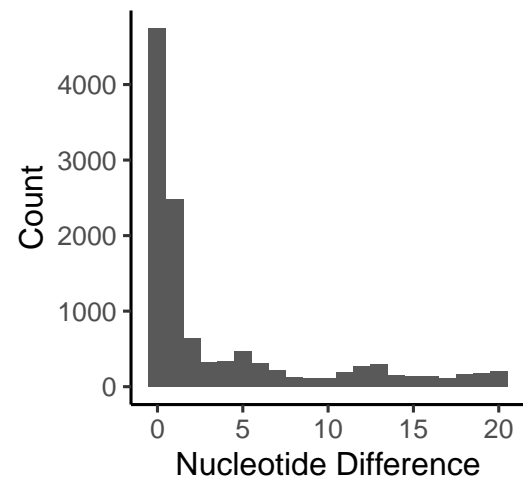
IGHV3-20*01_02

332 sequences assigned
78 (23.5%) exact matches, in which:
46 unique CDR3
6 unique J



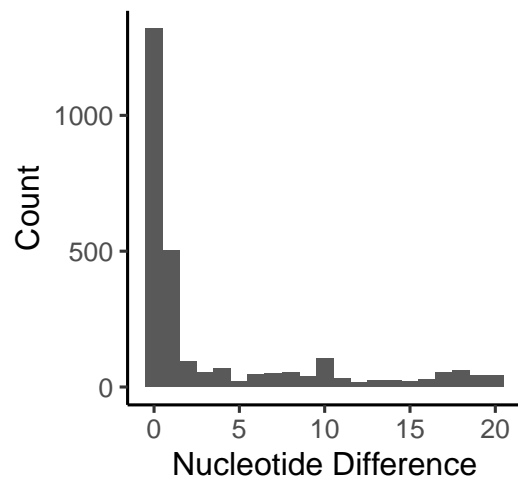
IGHV3-21*01_02

16186 sequences assigned
4743 (29.3%) exact matches, in which:
3073 unique CDR3
7 unique J



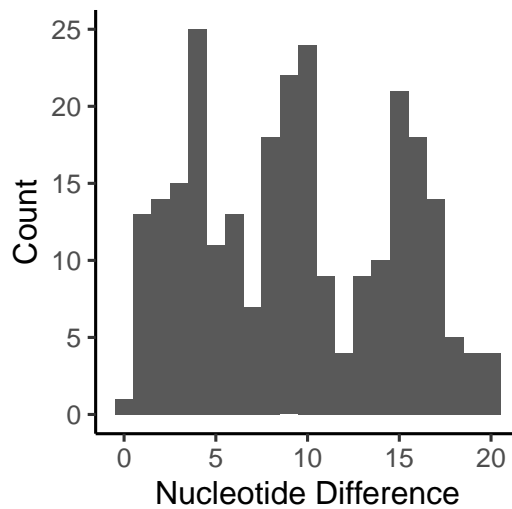
IGHV3-15*01_02

4315 sequences assigned
1319 (30.6%) exact matches, in which:
851 unique CDR3
7 unique J



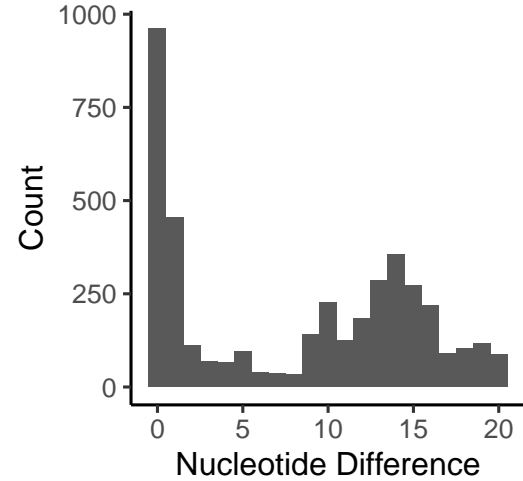
IGHV3-20*03_04

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



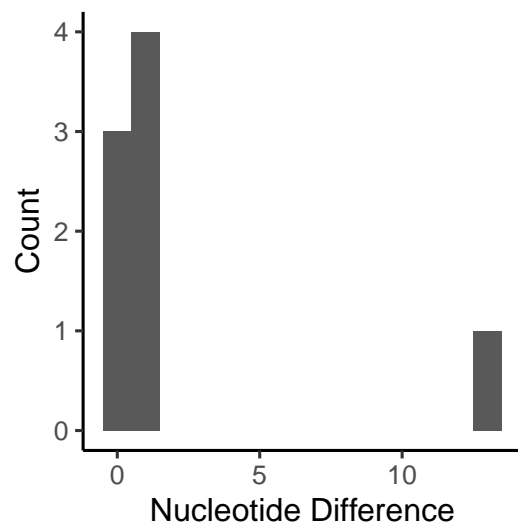
IGHV3-30*03

4732 sequences assigned
961 (20.3%) exact matches, in which:
657 unique CDR3
7 unique J



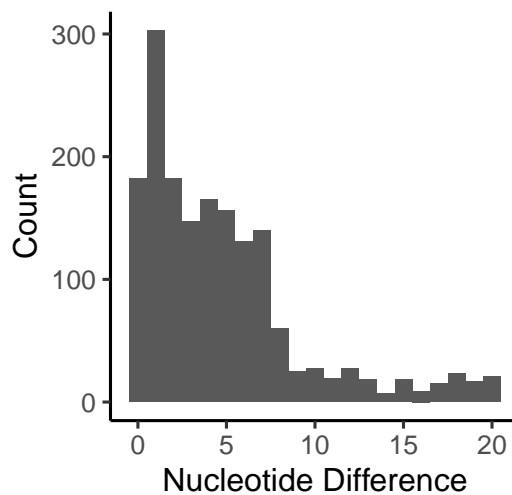
IGHV3-19*01

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



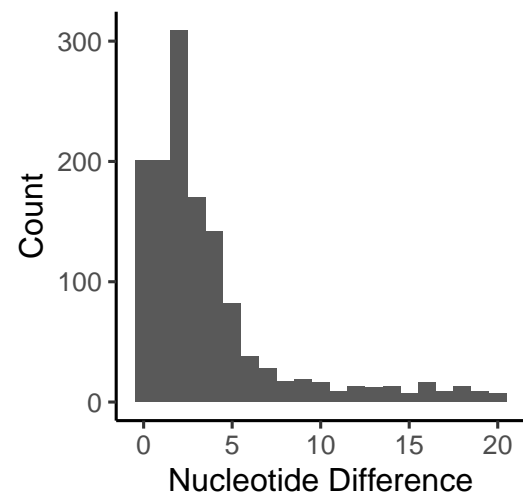
IGHV3-21*04

2063 sequences assigned
182 (8.8%) exact matches, in which:
177 unique CDR3
7 unique J



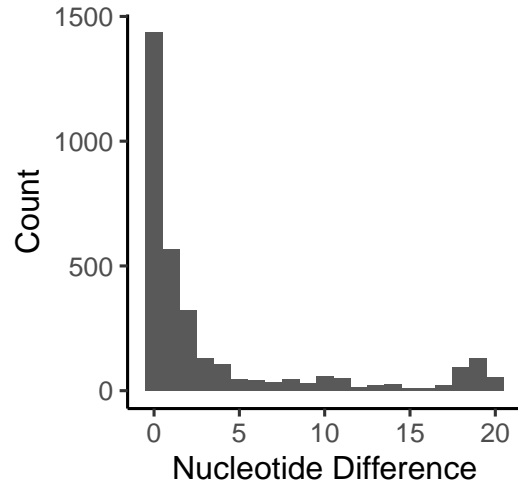
IGHV3-30*04_T288C

1456 sequences assigned
201 (13.8%) exact matches, in which:
199 unique CDR3
6 unique J



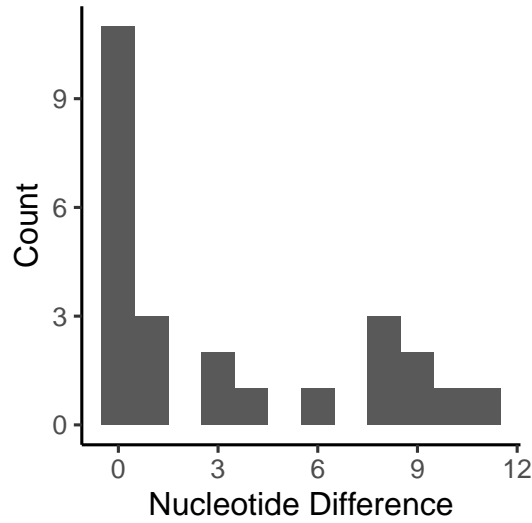
IGHV3-33*01

4855 sequences assigned
1436 (29.6%) exact matches, in which:
1051 unique CDR3
7 unique J



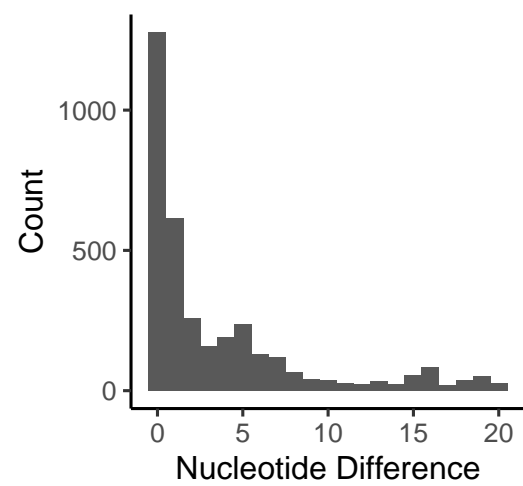
IGHV3-35*01

25 sequences assigned
11 (44%) exact matches, in which:
11 unique CDR3
4 unique J



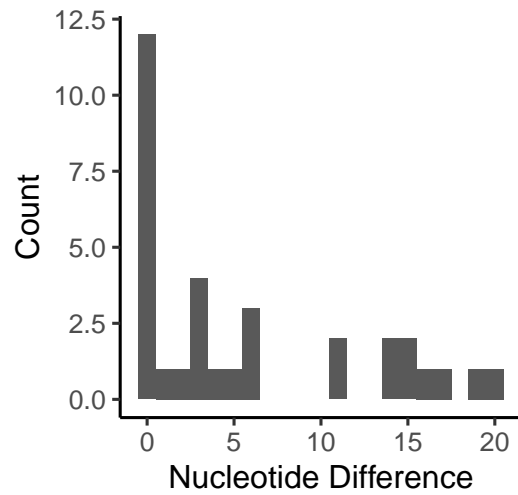
IGHV3-48*01

3719 sequences assigned
1277 (34.3%) exact matches, in which:
923 unique CDR3
7 unique J



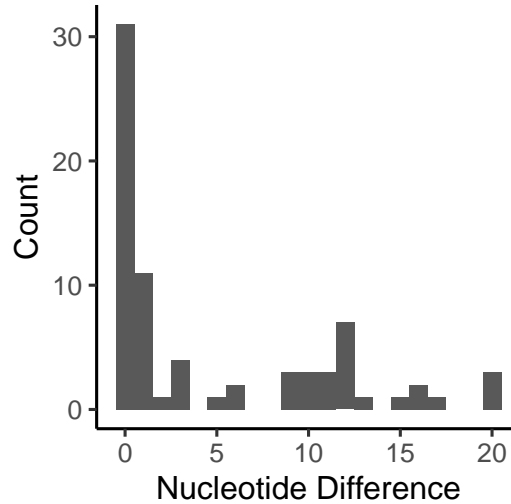
IGHV3-33*05

86 sequences assigned
12 (14%) exact matches, in which:
12 unique CDR3
3 unique J



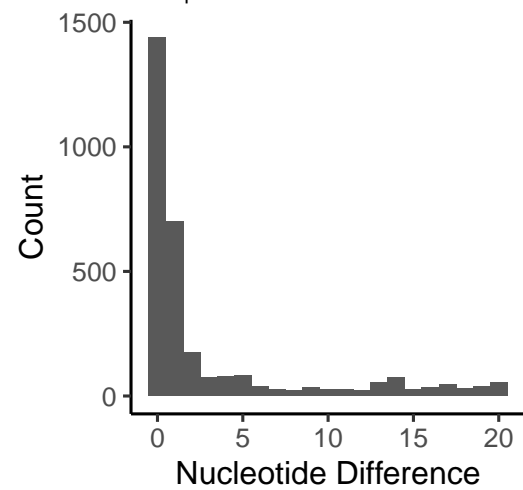
IGHV3-43*01

368 sequences assigned
31 (8.4%) exact matches, in which:
22 unique CDR3
4 unique J



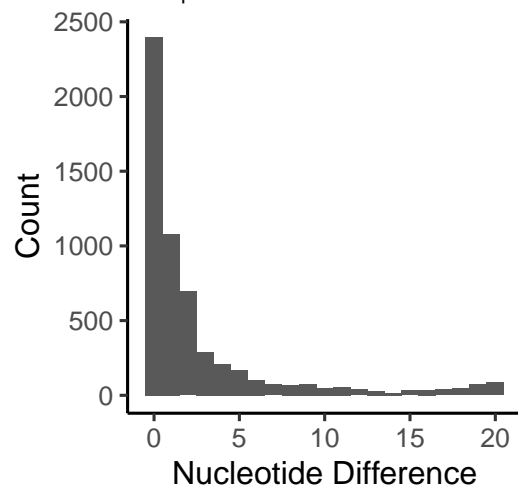
IGHV3-48*02

4075 sequences assigned
1438 (35.3%) exact matches, in which:
903 unique CDR3
7 unique J



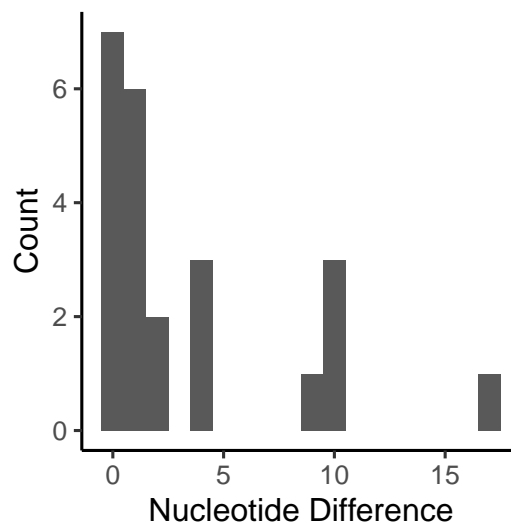
IGHV3-33*01_G75C

8732 sequences assigned
2398 (27.5%) exact matches, in which:
1700 unique CDR3
7 unique J



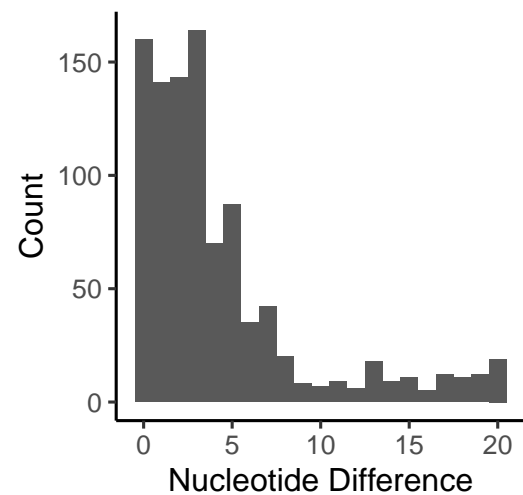
IGHV3-47*02

23 sequences assigned
7 (30.4%) exact matches, in which:
3 unique CDR3
2 unique J



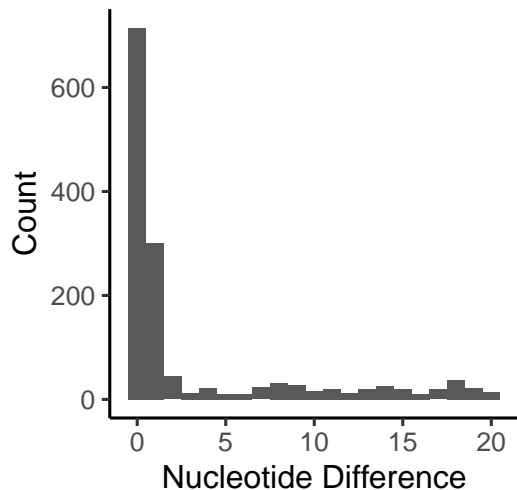
IGHV3-48*04

1161 sequences assigned
160 (13.8%) exact matches, in which:
156 unique CDR3
7 unique J



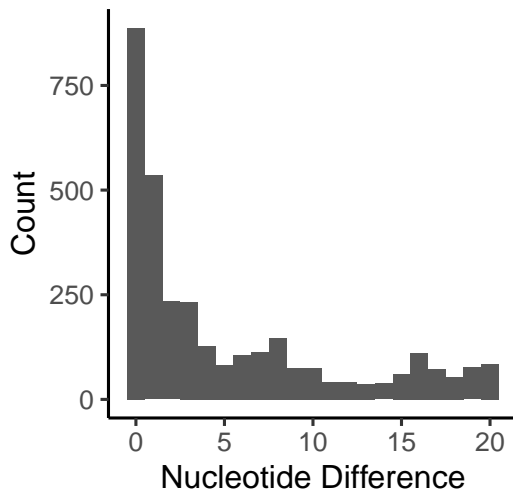
IGHV3-49*03_05

2570 sequences assigned
715 (27.8%) exact matches, in which:
450 unique CDR3
7 unique J



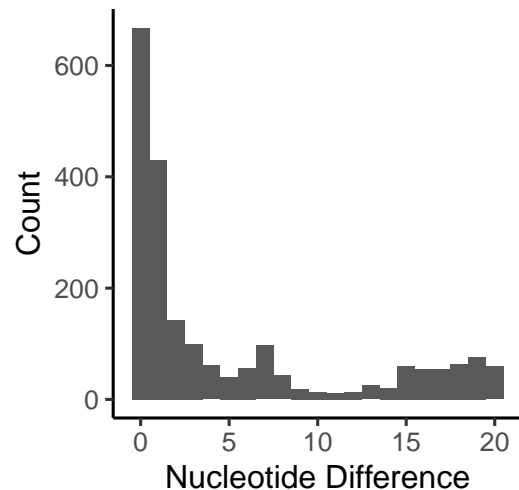
IGHV3-53*01_02

5103 sequences assigned
888 (17.4%) exact matches, in which:
581 unique CDR3
7 unique J



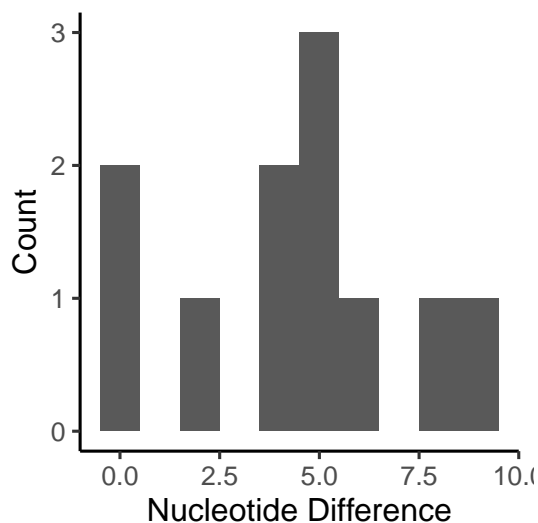
IGHV3-66*01

3276 sequences assigned
668 (20.4%) exact matches, in which:
451 unique CDR3
7 unique J



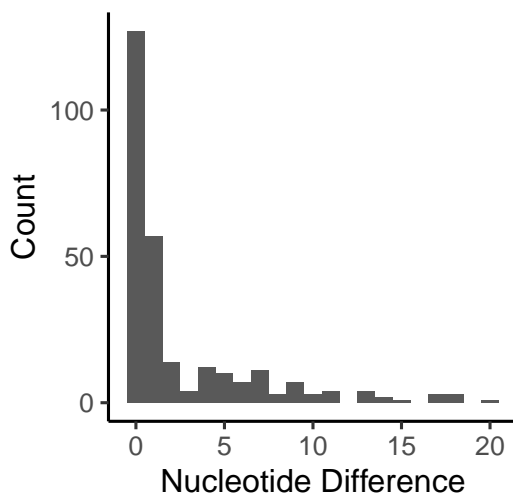
IGHV3-52*02

11 sequences assigned
2 (18.2%) exact matches, in which:
1 unique CDR3
1 unique J



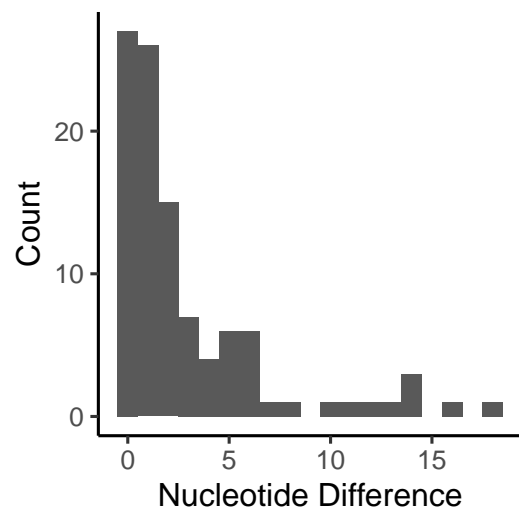
IGHV3-64*01

293 sequences assigned
127 (43.3%) exact matches, in which:
75 unique CDR3
5 unique J



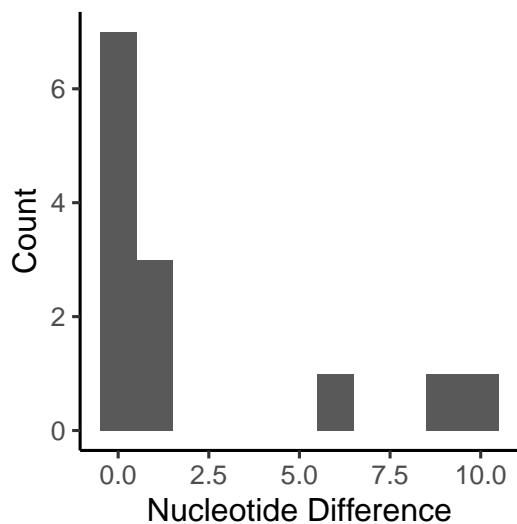
IGHV3-69-1*01

115 sequences assigned
27 (23.5%) exact matches, in which:
24 unique CDR3
5 unique J



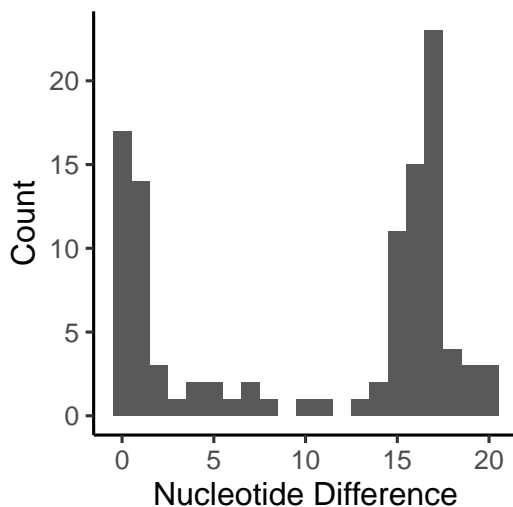
IGHV3-52*01_03

13 sequences assigned
7 (53.8%) exact matches, in which:
6 unique CDR3
3 unique J



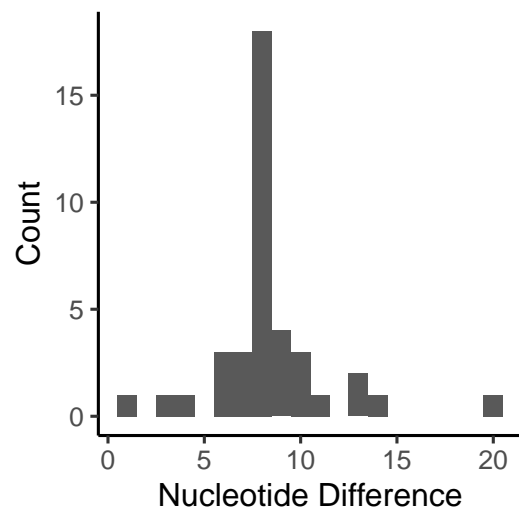
IGHV3-64*02_07

113 sequences assigned
17 (15%) exact matches, in which:
11 unique CDR3
4 unique J



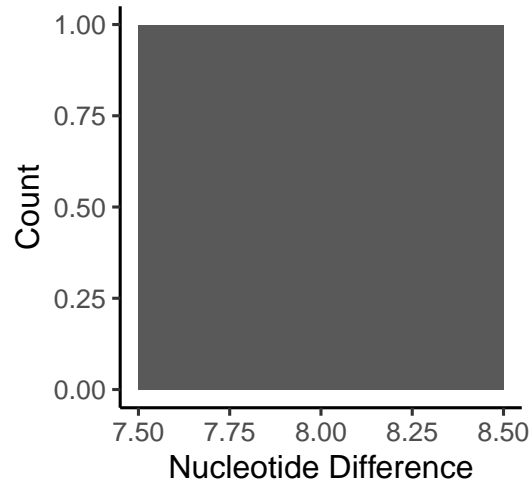
IGHV3-69-1*02

55 sequences assigned
No exact matches.



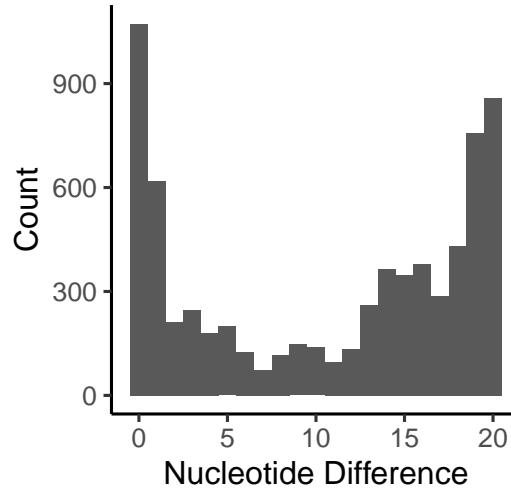
IGHV3-71*01_04

3 sequences assigned
No exact matches.



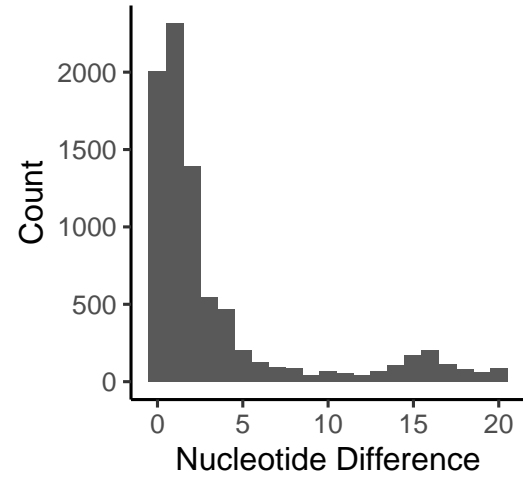
IGHV3-74*01_02

17031 sequences assigned
1073 (6.3%) exact matches, in which:
697 unique CDR3
7 unique J



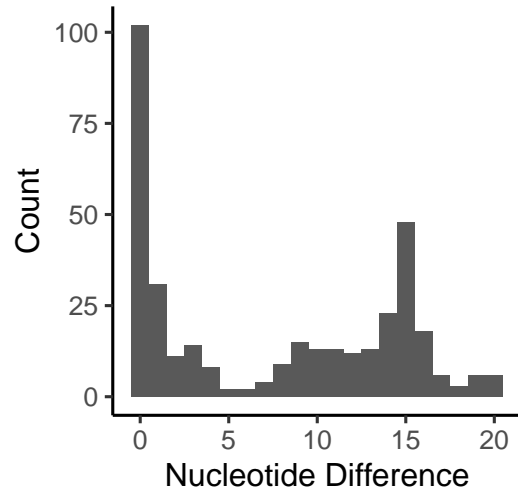
IGHV4-4*07

11163 sequences assigned
2004 (18%) exact matches, in which:
1767 unique CDR3
7 unique J



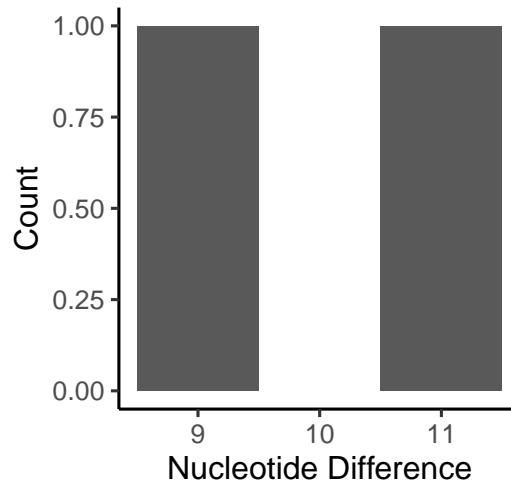
IGHV3-72*01

725 sequences assigned
102 (14.1%) exact matches, in which:
65 unique CDR3
6 unique J



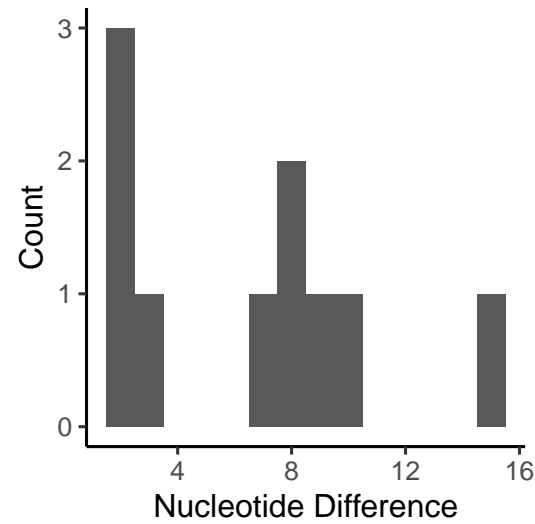
IGHV3-64D*06

4 sequences assigned
No exact matches.



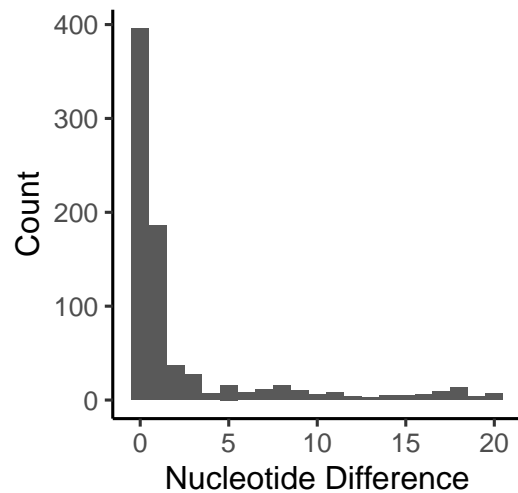
IGHV4-28*03

13 sequences assigned
No exact matches.



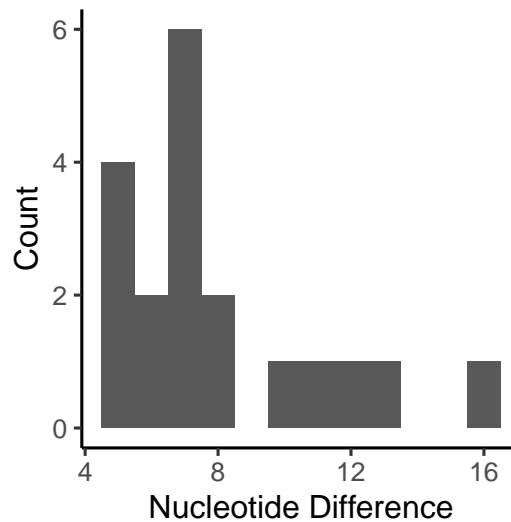
IGHV3-73*01_02

968 sequences assigned
396 (40.9%) exact matches, in which:
259 unique CDR3
7 unique J



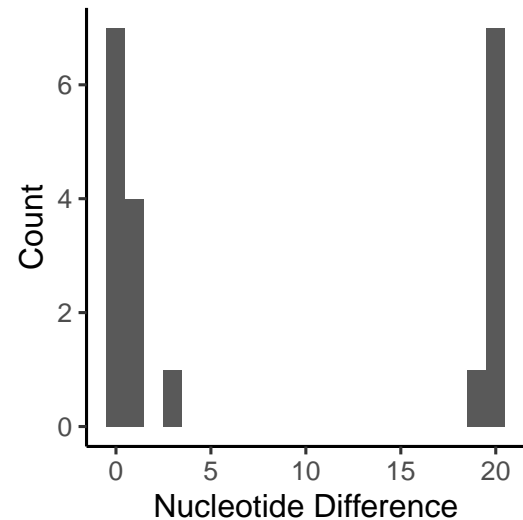
IGHV3-NL1*01

60 sequences assigned
No exact matches.



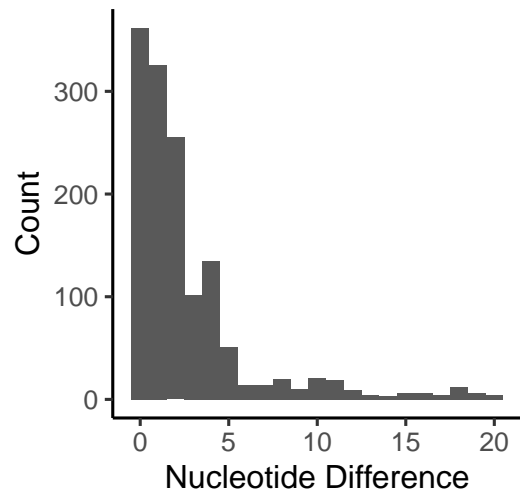
IGHV4-28*01_07

65 sequences assigned
7 (10.8%) exact matches, in which:
6 unique CDR3
4 unique J



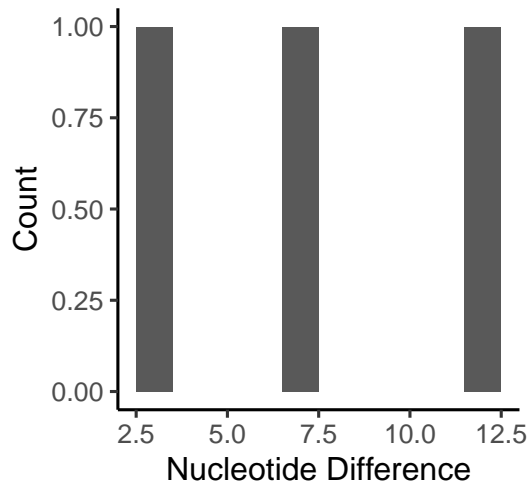
IGHV4-30-2*01

1434 sequences assigned
362 (25.2%) exact matches, in which:
291 unique CDR3
7 unique J



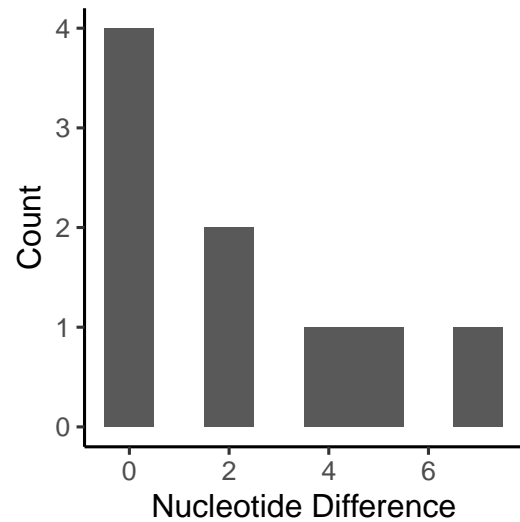
IGHV4-30-4*08

7 sequences assigned
No exact matches.



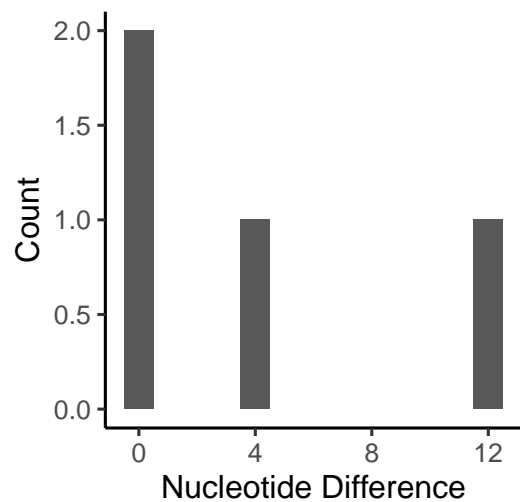
IGHV4-38-2*01

15 sequences assigned
4 (26.7%) exact matches, in which:
4 unique CDR3
4 unique J



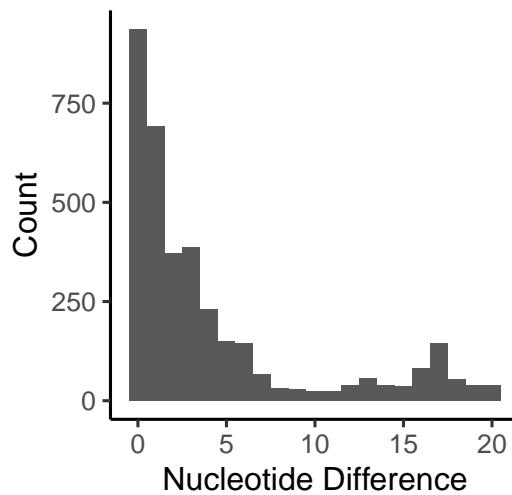
IGHV4-30-4*01

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



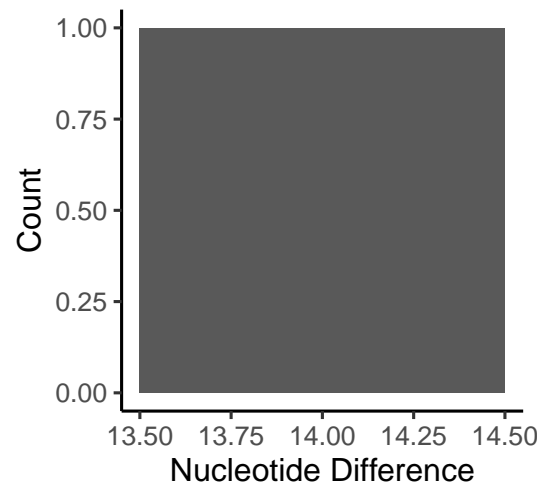
IGHV4-31*03_04

4651 sequences assigned
937 (20.1%) exact matches, in which:
830 unique CDR3
7 unique J



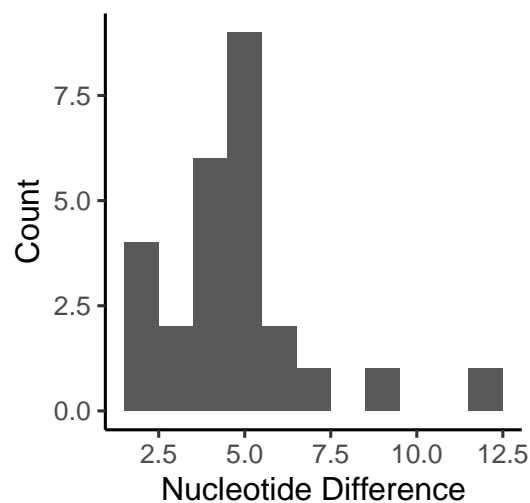
IGHV4-38-2*02

5 sequences assigned
No exact matches.



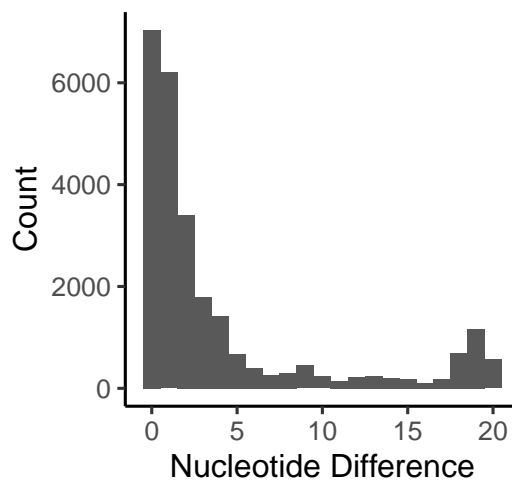
IGHV4-30-4*07

26 sequences assigned
No exact matches.



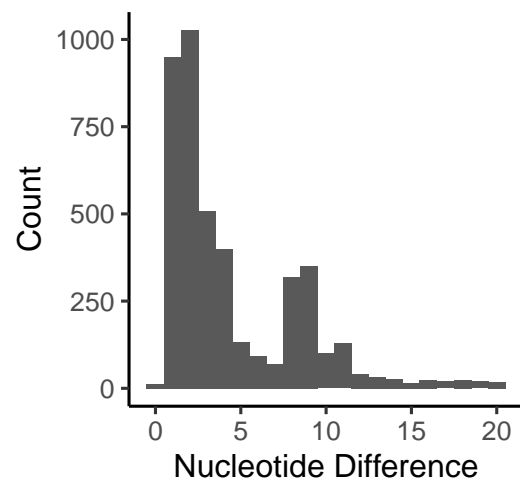
IGHV4-34*01_02

29789 sequences assigned
7036 (23.6%) exact matches, in which:
5862 unique CDR3
7 unique J



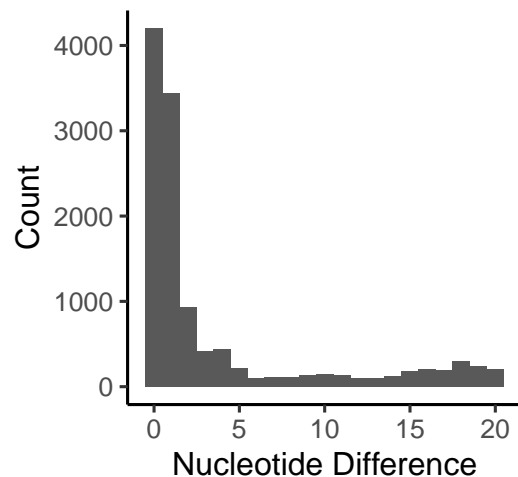
IGHV4-39*07

4502 sequences assigned
13 (0.3%) exact matches, in which:
13 unique CDR3
5 unique J



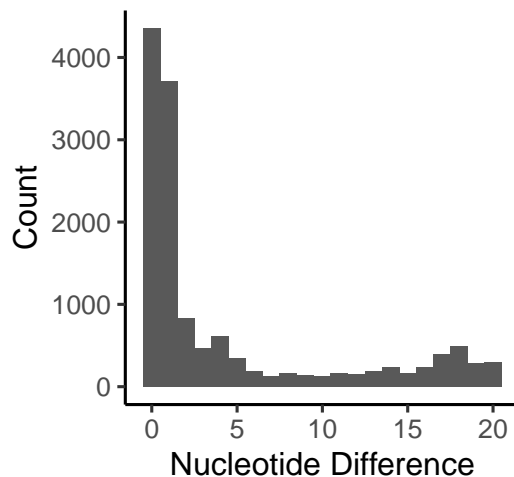
IGHV4-39*01_05

17675 sequences assigned
4200 (23.8%) exact matches, in which:
3408 unique CDR3
7 unique J



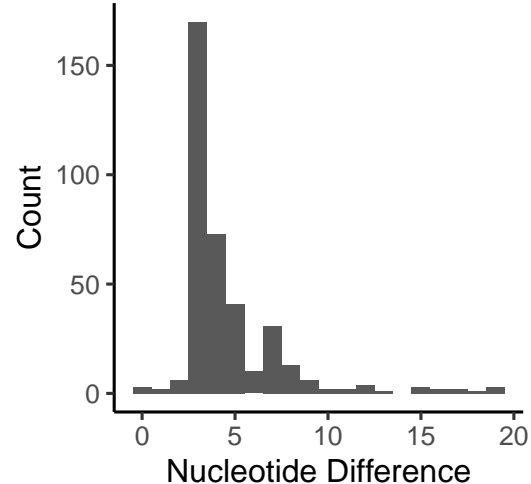
IGHV4-59*01_07

17937 sequences assigned
4353 (24.3%) exact matches, in which:
3742 unique CDR3
7 unique J



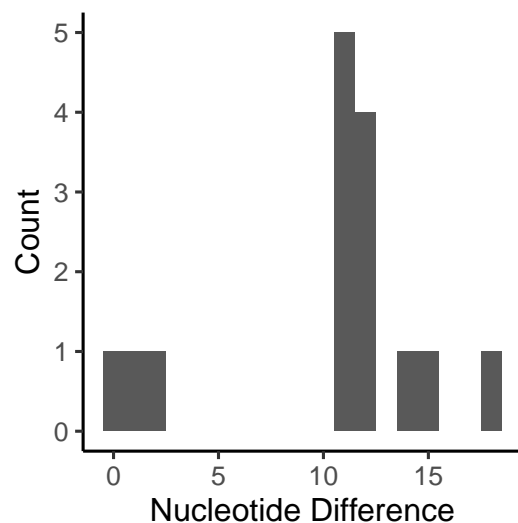
IGHV4-61*02

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



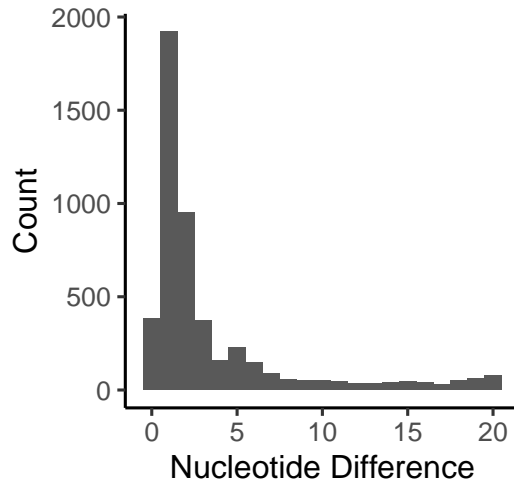
IGHV4-55*02_04_08

15 sequences assigned
1 (6.7%) exact matches, in which:
1 unique CDR3
1 unique J



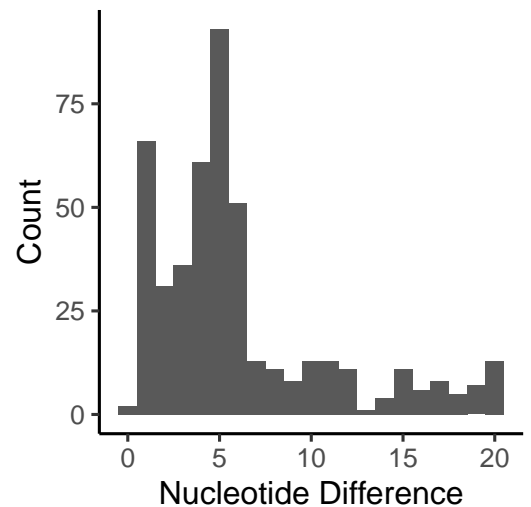
IGHV4-59*12

5404 sequences assigned
382 (7.1%) exact matches, in which:
371 unique CDR3
7 unique J



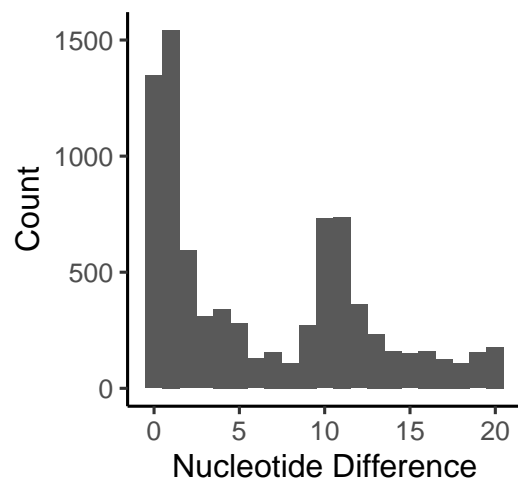
IGHV4-61*08

745 sequences assigned
2 (0.3%) exact matches, in which:
2 unique CDR3
1 unique J



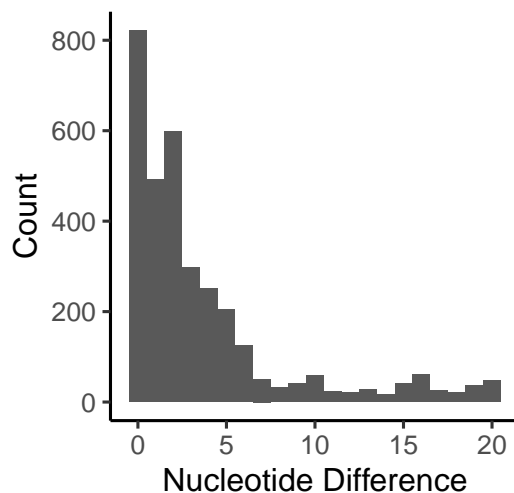
IGHV4-59*08

10411 sequences assigned
1347 (12.9%) exact matches, in which:
1171 unique CDR3
7 unique J



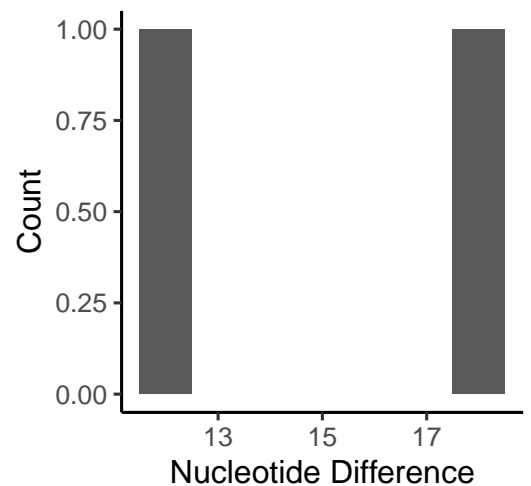
IGHV4-61*01

3611 sequences assigned
822 (22.8%) exact matches, in which:
777 unique CDR3
7 unique J



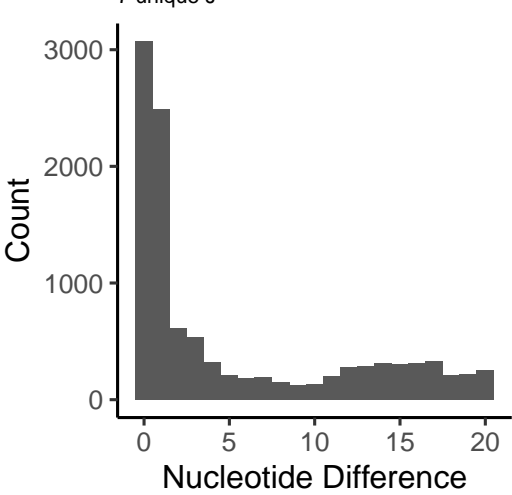
IGHV5-10-1*01_03

2 sequences assigned
No exact matches.



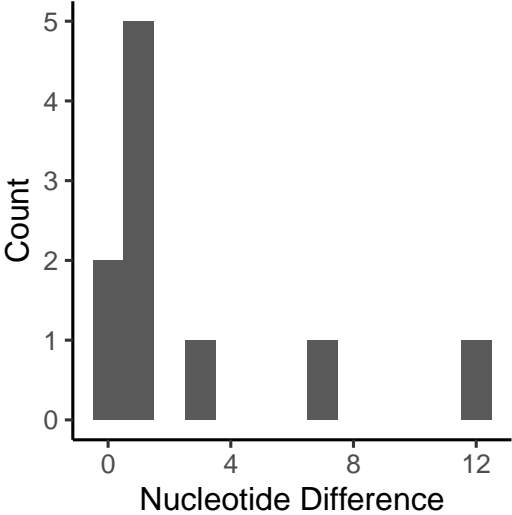
IGHV5-51*01_03

15987 sequences assigned
3071 (19.2%) exact matches, in which:
1867 unique CDR3
7 unique J



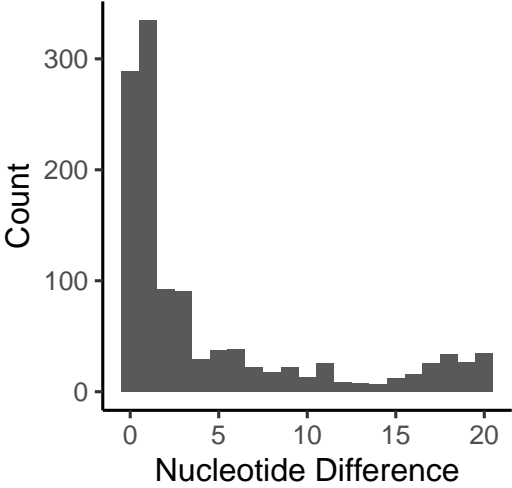
IGHV7-4-1*02

10 sequences assigned
2 (20%) exact matches, in which:
2 unique CDR3
2 unique J



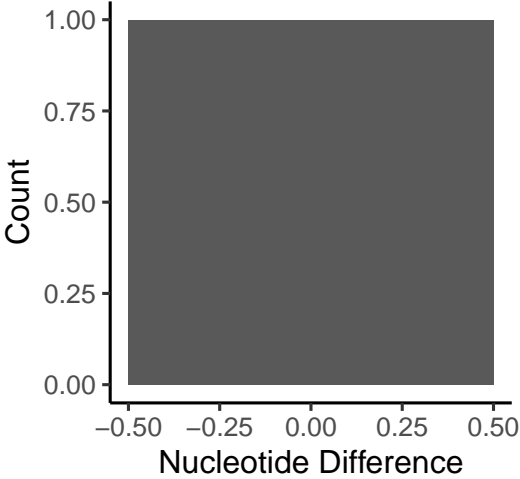
IGHV6-1*01_02

1385 sequences assigned
289 (20.9%) exact matches, in which:
259 unique CDR3
7 unique J

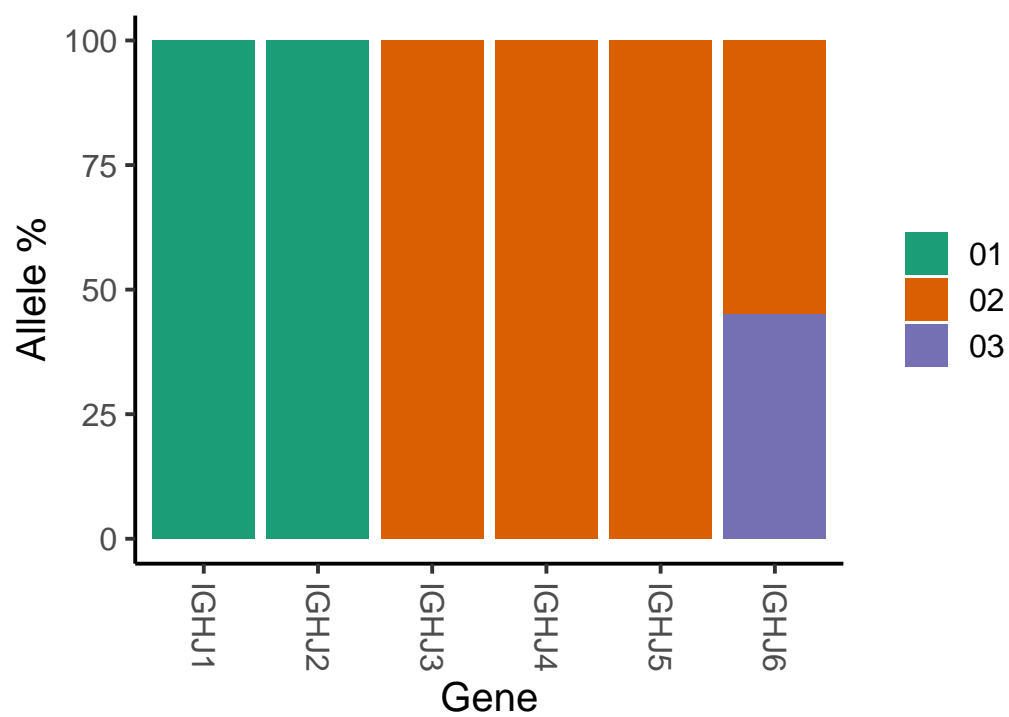


IGHV7-4-1*01

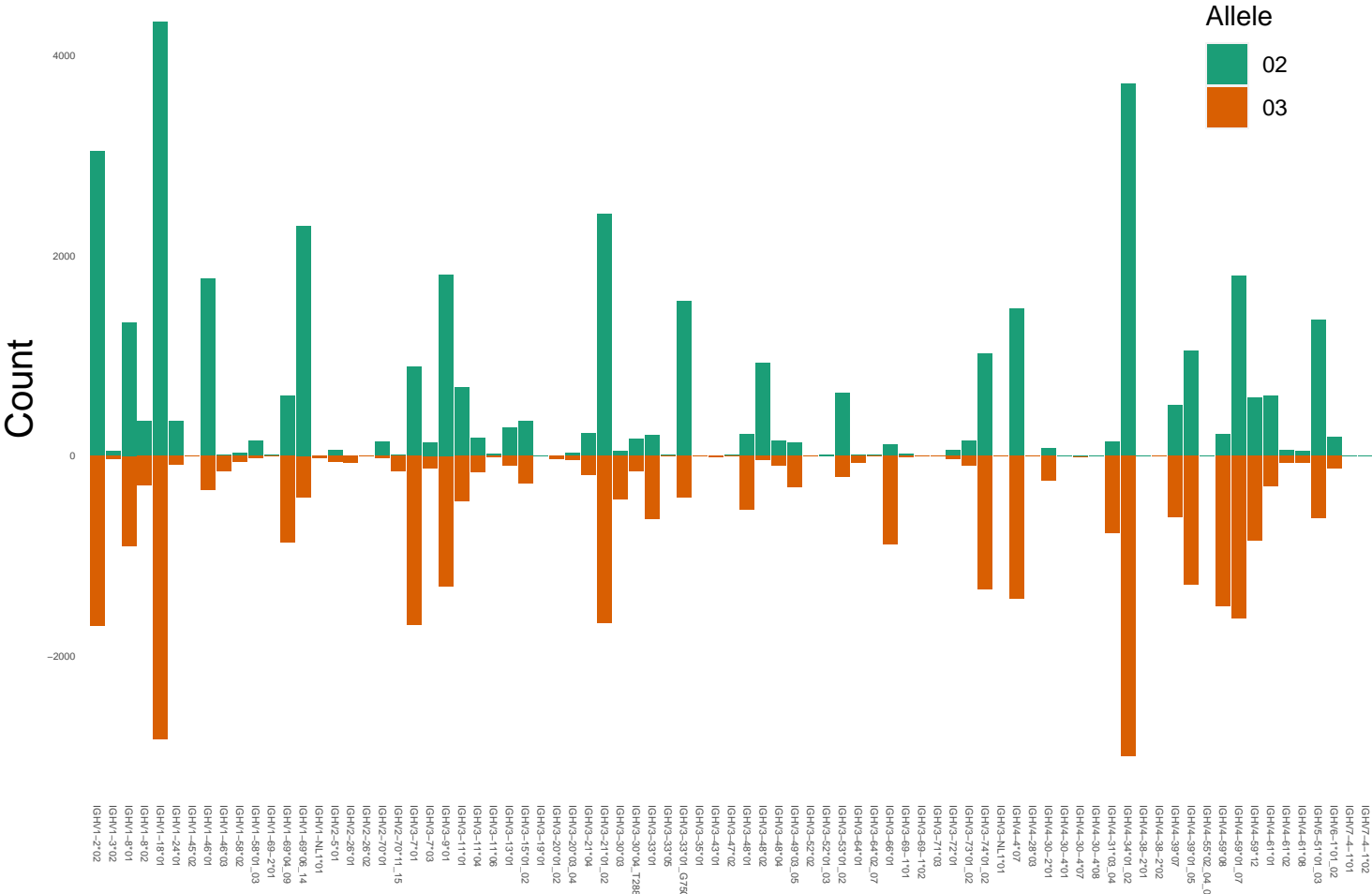
1 sequences assigned
1 (100%) exact matches, in which:
1 unique CDR3
1 unique J



Allele Usage



Sequence Count by IGHJ6 allele usage



Warning - no inferred sequences found.

Novel sequence(s)IGHV1-69*04_09_G112AIGHV4-59*02_G88AIGHV5-10-1*01_03_T258CIGHV5-51*07_A128G are not listed in the genotype and will be ignored.

Warning - no inferred sequences found.

Novel sequence(s)IGHV1-69*08_C191TIGHV3-48*03_T303GIGHV4-59*02_G88AIGHV5-51*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_T288CIGHV5-51*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_C191TIGHV3-30*03_T288CIGHV3-30-3*02_G75CIGHV4-59*02_G88AIGHV5-51*07_A128G are not listed in the genotype and will be ignored.

Novel sequence(s)IGHV4-59*02_G88AIGHV5-51*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_C300TIGHV5-51*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_C191TIGHV3-11*06_T300CIGHV3-30*03_T288CIGHV4-59*02_G88AIGHV5-51*07_A128G are not listed in the genotype and will be ignored.

Novel sequence(s)IGHV4-59*02_G88AIGHV5-51*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_T288CIGHV3-30-3*01_T288CIGHV4-59*02_G88AIGHV5-10-1*01_03_T258CIGHV5-51*07_A128G are not listed in the genotype and will be ignored.