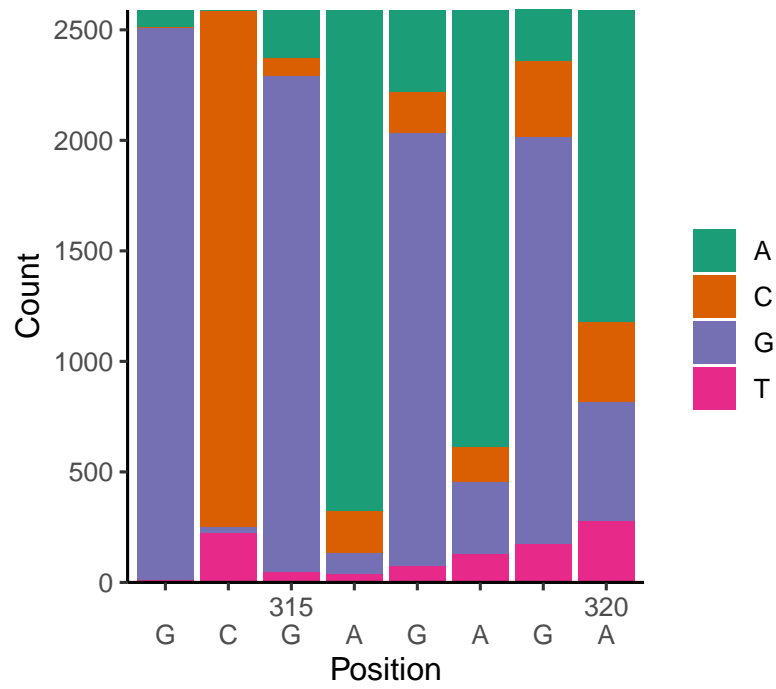
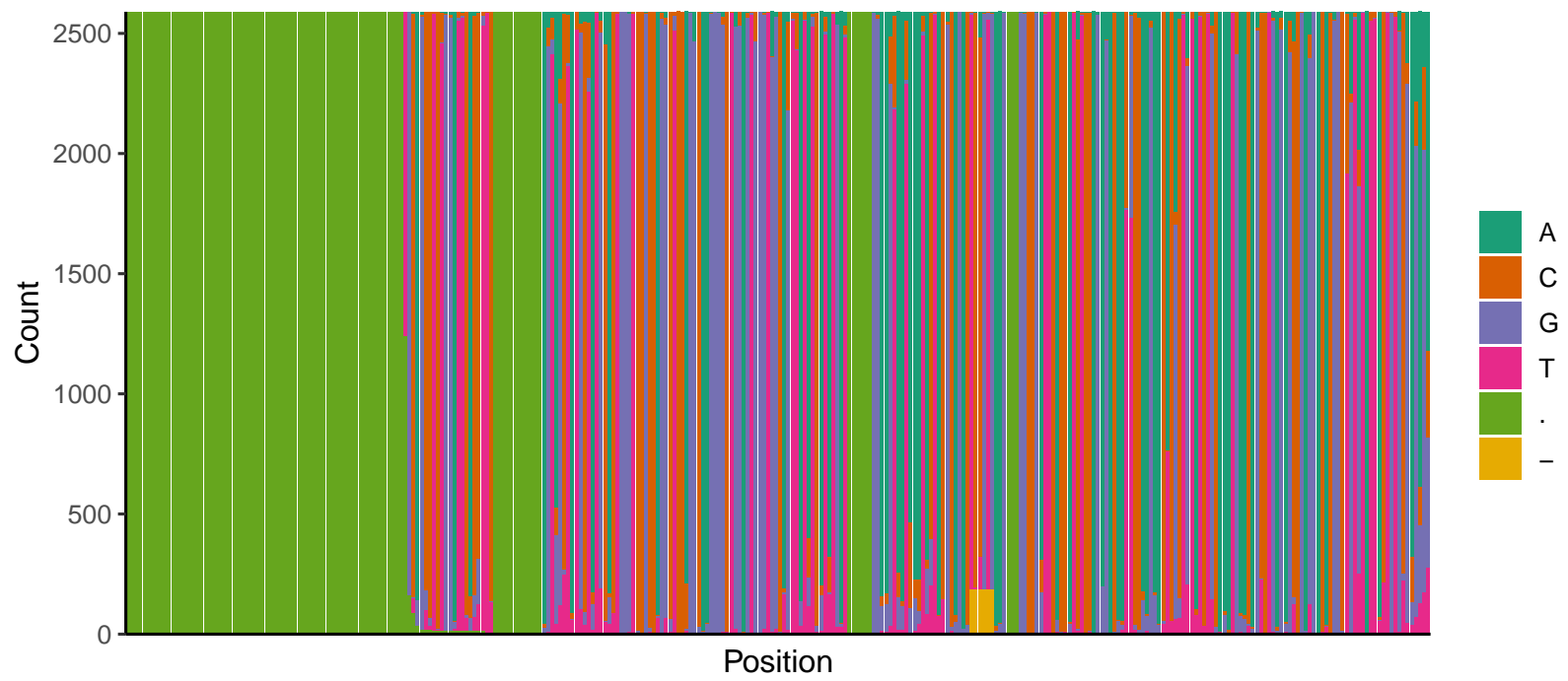


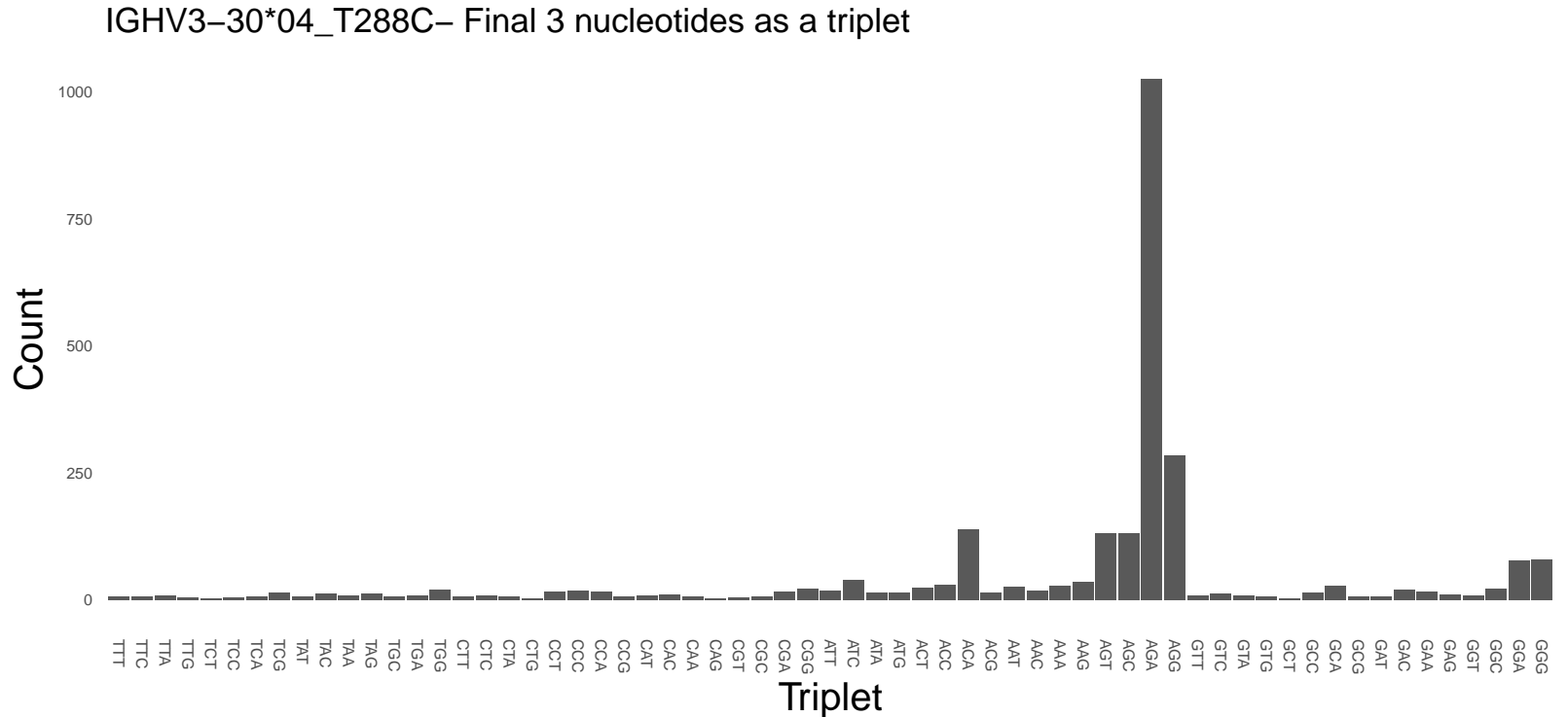
Gene IGHV3-30*04_T288C



Gene IGHV3-30*04_T288C

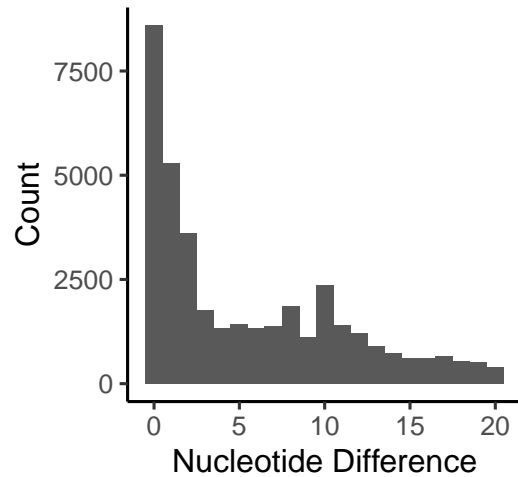


IGHV3-30*04_T288C- Final 3 nucleotides as a triplet



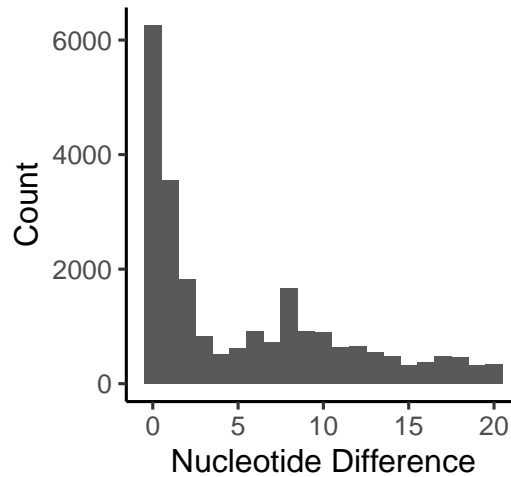
IGHV1-2*02

40659 sequences assigned
8594 (21.1%) exact matches, in which:
7850 unique CDR3
7 unique J



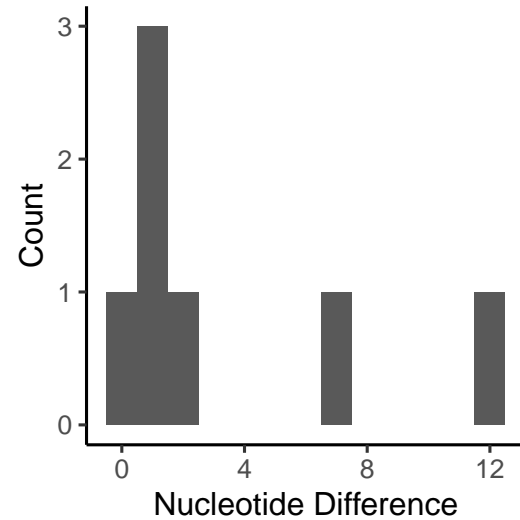
IGHV1-18*04

26346 sequences assigned
6256 (23.7%) exact matches, in which:
5692 unique CDR3
7 unique J



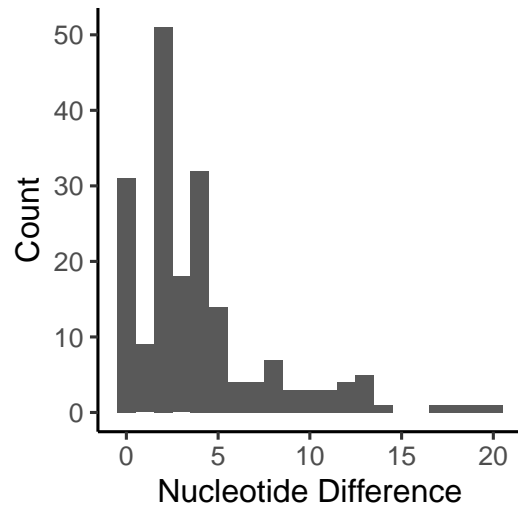
IGHV1-45*03

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



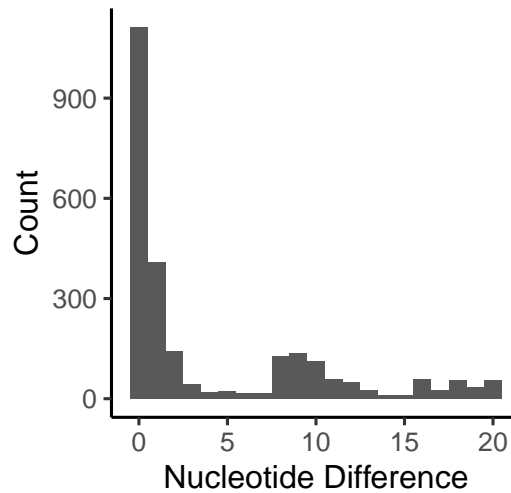
IGHV1-3*02

195 sequences assigned
31 (15.9%) exact matches, in which:
30 unique CDR3
4 unique J



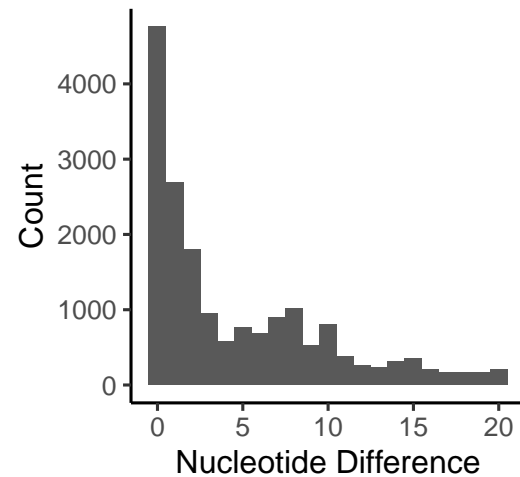
IGHV1-24*01

2712 sequences assigned
1113 (41%) exact matches, in which:
1058 unique CDR3
7 unique J



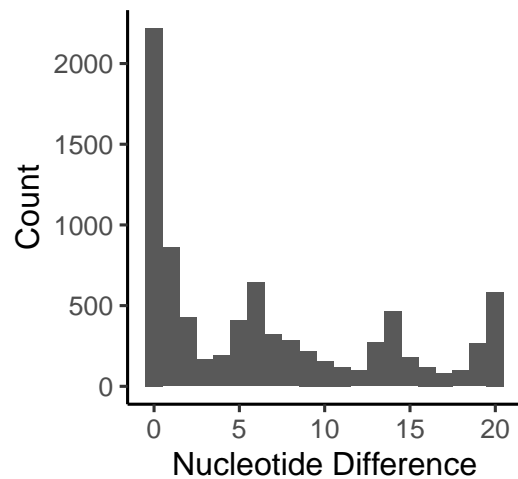
IGHV1-46*01

20228 sequences assigned
4759 (23.5%) exact matches, in which:
4457 unique CDR3
7 unique J



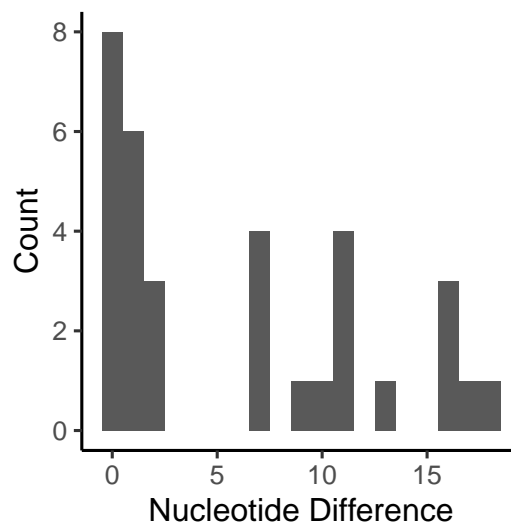
IGHV1-8*03

8975 sequences assigned
2220 (24.7%) exact matches, in which:
2096 unique CDR3
7 unique J



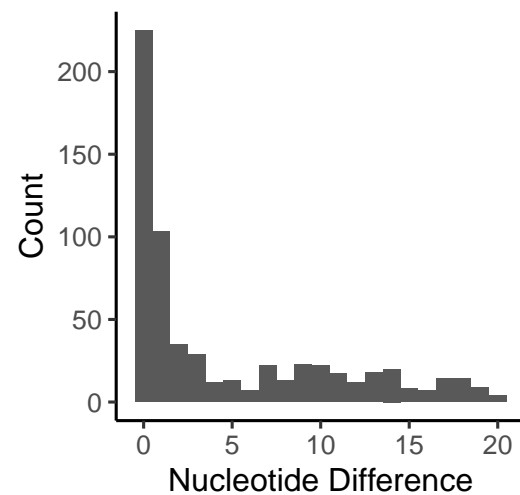
IGHV1-45*02

33 sequences assigned
8 (24.2%) exact matches, in which:
7 unique CDR3
3 unique J



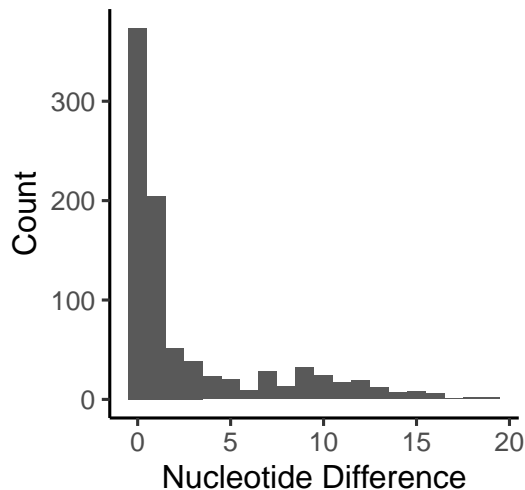
IGHV1-58*02

663 sequences assigned
225 (33.9%) exact matches, in which:
211 unique CDR3
7 unique J



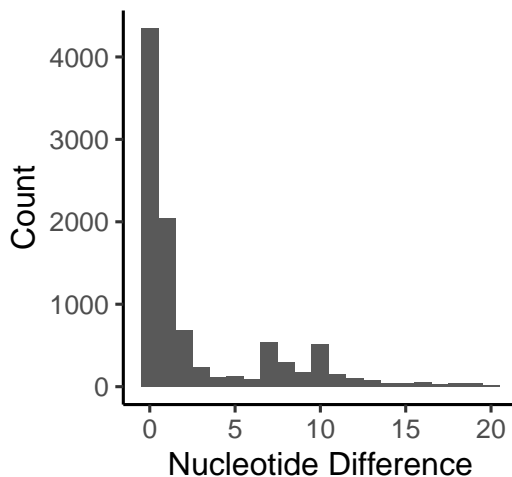
IGHV1–58*01_03

1317 sequences assigned
374 (28.4%) exact matches, in which:
350 unique CDR3
7 unique J



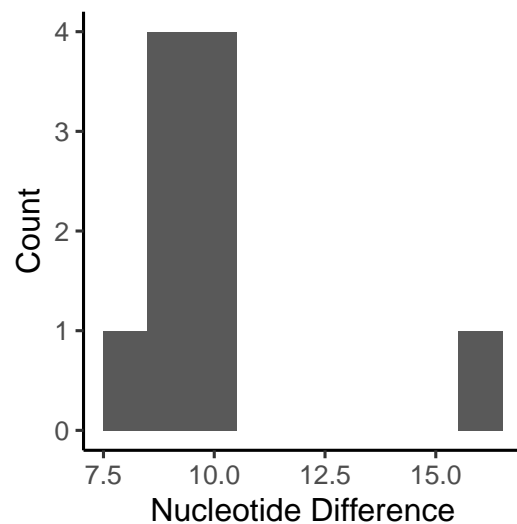
IGHV1–69*10

10041 sequences assigned
4346 (43.3%) exact matches, in which:
4156 unique CDR3
7 unique J



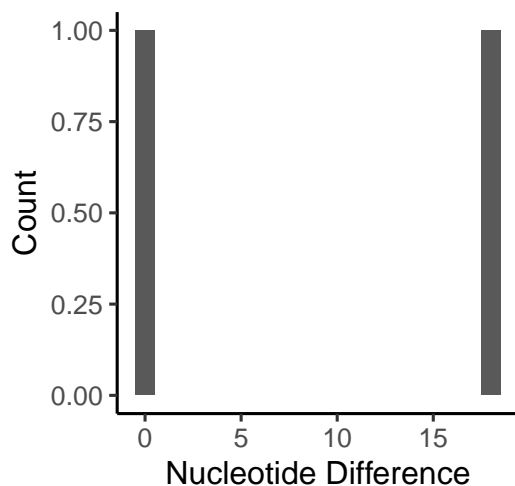
IGHV1–NL1*01

10 sequences assigned
No exact matches.



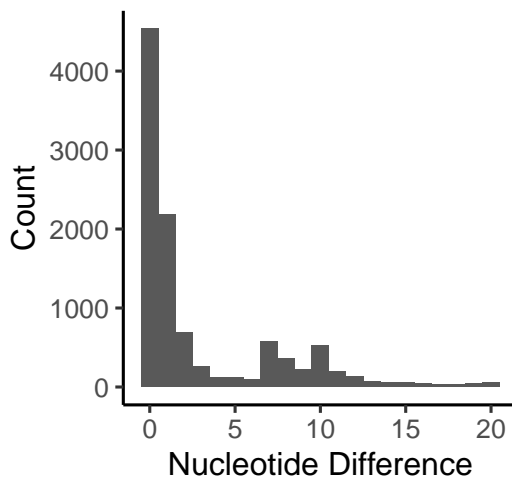
IGHV1–68*01

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



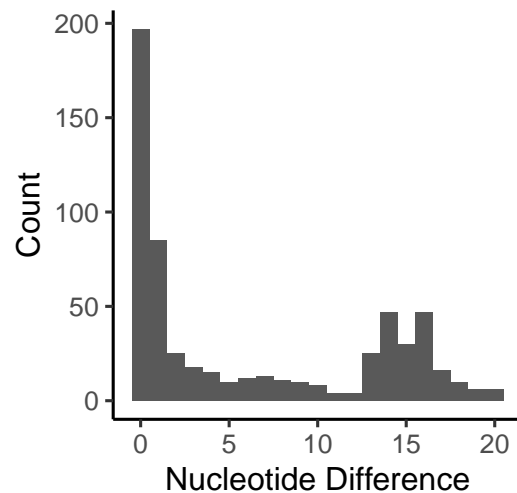
IGHV1–69*04_09

10636 sequences assigned
4536 (42.6%) exact matches, in which:
4329 unique CDR3
7 unique J



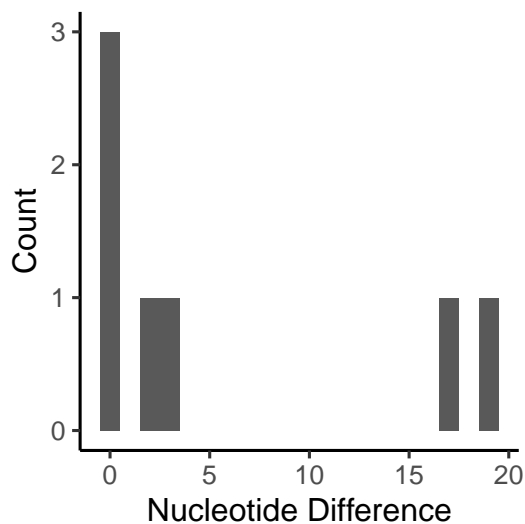
IGHV2–5*01

625 sequences assigned
197 (31.5%) exact matches, in which:
189 unique CDR3
7 unique J



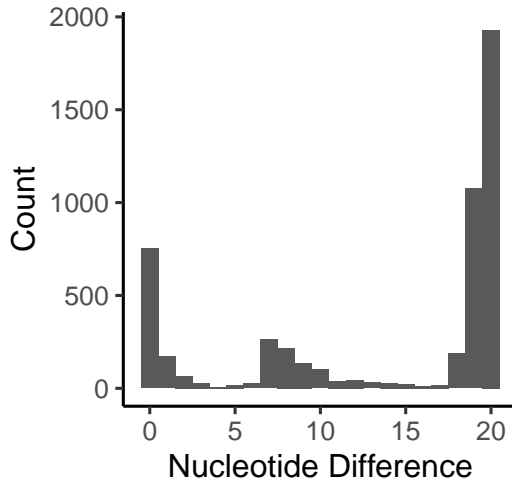
IGHV1–69–2*01

16 sequences assigned
3 (18.8%) exact matches, in which:
3 unique CDR3
2 unique J



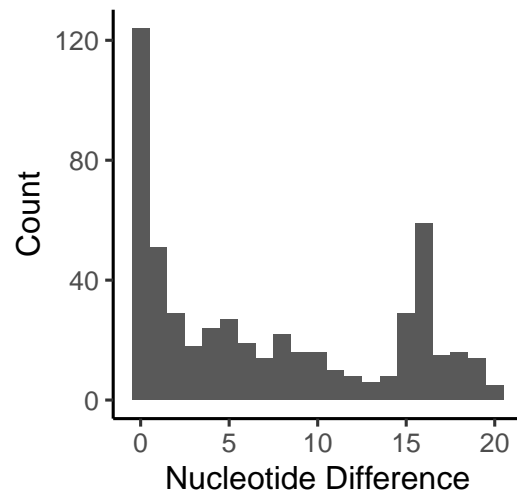
IGHV1–69*06_14

6834 sequences assigned
753 (11%) exact matches, in which:
747 unique CDR3
7 unique J



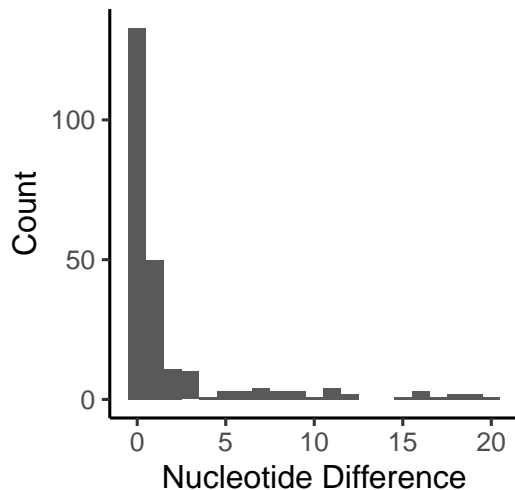
IGHV2–5*02

802 sequences assigned
124 (15.5%) exact matches, in which:
116 unique CDR3
7 unique J



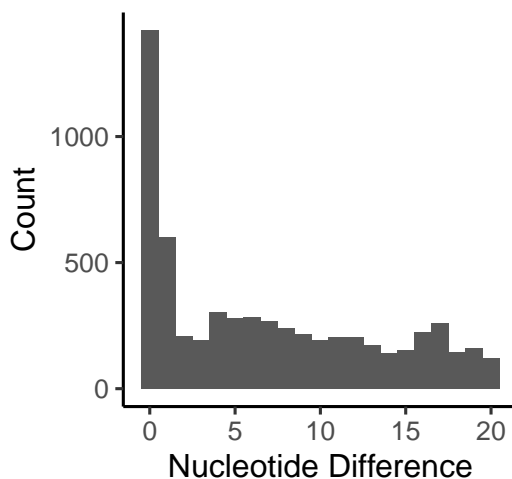
IGHV2-26*01

449 sequences assigned
133 (29.6%) exact matches, in which:
128 unique CDR3
6 unique J



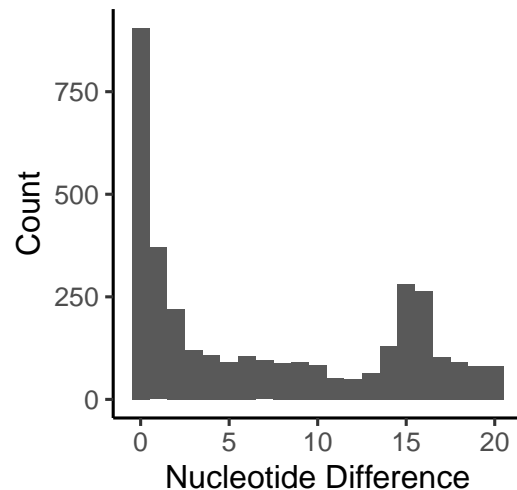
IGHV3-7*03

7974 sequences assigned
1421 (17.8%) exact matches, in which:
1101 unique CDR3
7 unique J



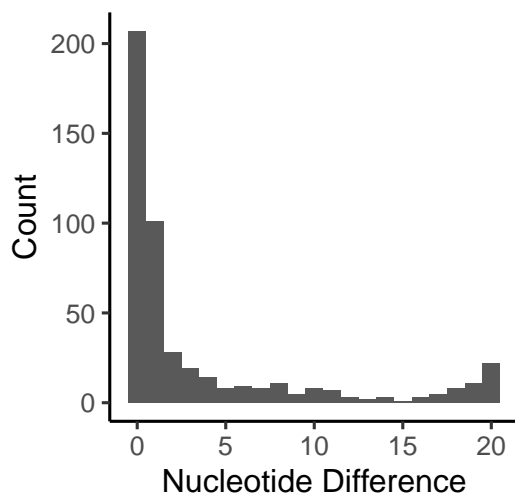
IGHV3-11*04

5925 sequences assigned
906 (15.3%) exact matches, in which:
749 unique CDR3
7 unique J



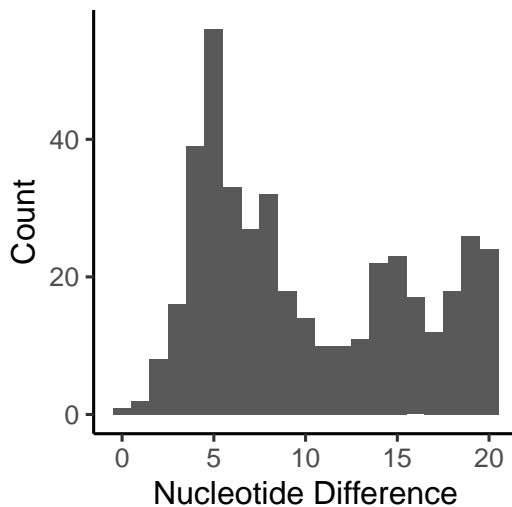
IGHV2-70*01

571 sequences assigned
207 (36.3%) exact matches, in which:
194 unique CDR3
6 unique J



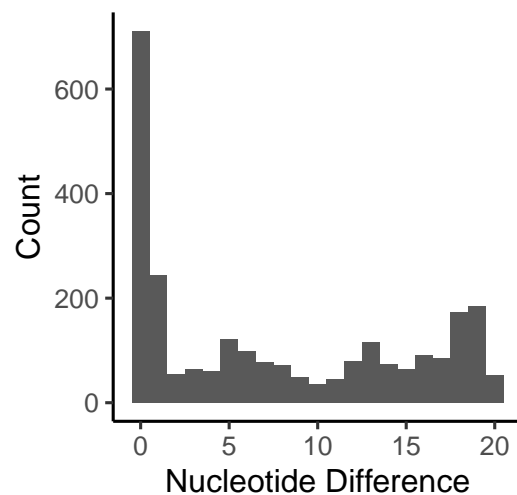
IGHV3-9*01

583 sequences assigned
1 (0.2%) exact matches, in which:
1 unique CDR3
1 unique J



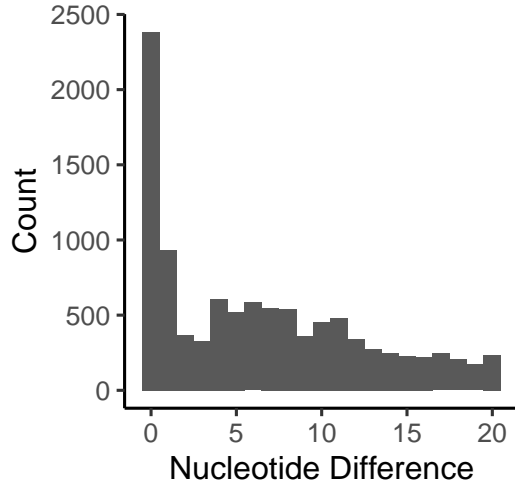
IGHV3-11*06

2985 sequences assigned
711 (23.8%) exact matches, in which:
572 unique CDR3
7 unique J



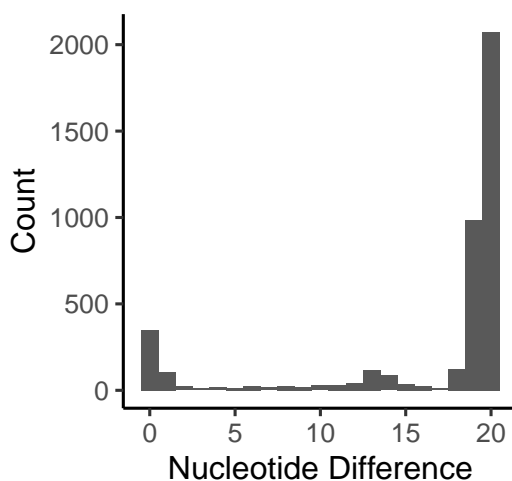
IGHV3-7*01

11982 sequences assigned
2383 (19.9%) exact matches, in which:
1893 unique CDR3
7 unique J



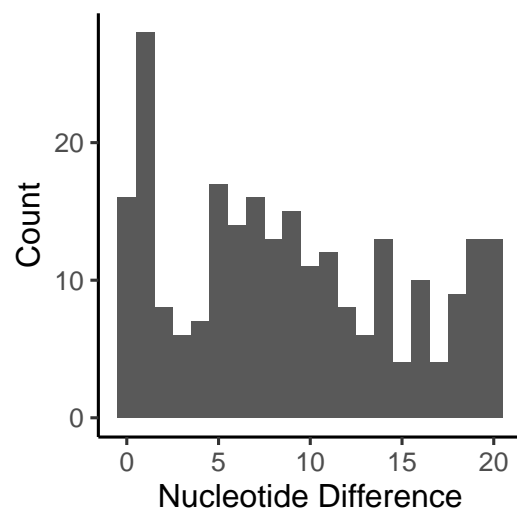
IGHV3-9*03

6158 sequences assigned
348 (5.7%) exact matches, in which:
265 unique CDR3
6 unique J



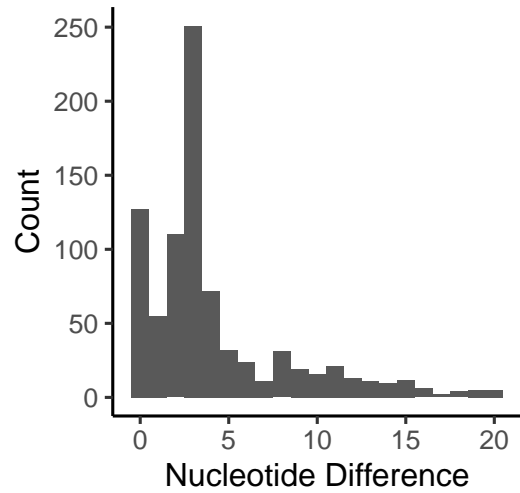
IGHV3-11*03_05

586 sequences assigned
16 (2.7%) exact matches, in which:
16 unique CDR3
6 unique J



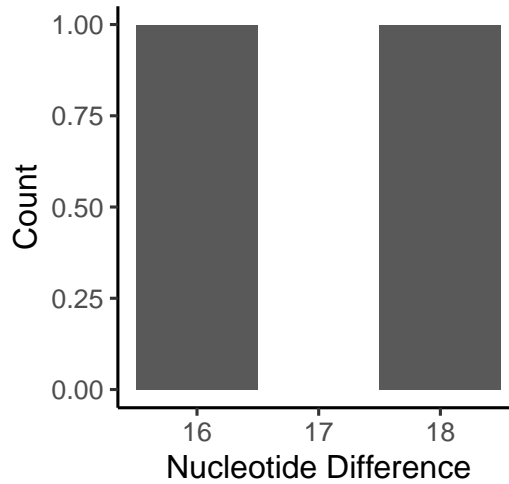
IGHV3-13*05

867 sequences assigned
127 (14.6%) exact matches, in which:
91 unique CDR3
7 unique J



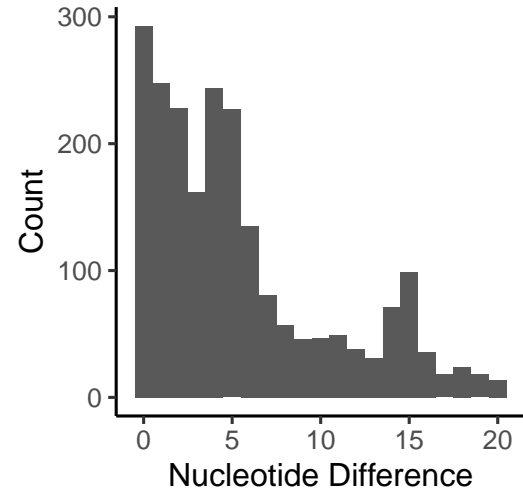
IGHV3-20*03_04

17 sequences assigned
No exact matches.



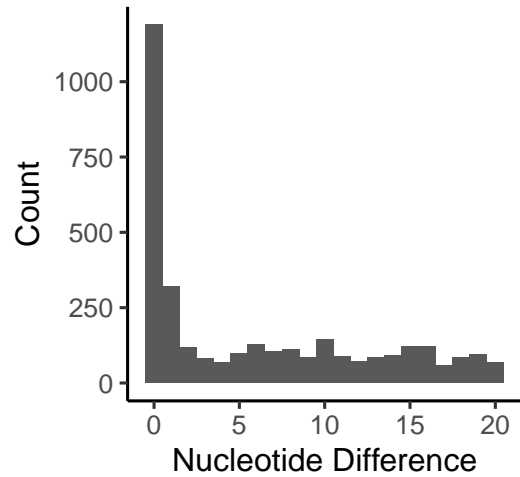
IGHV3-30*04_T288C

2590 sequences assigned
293 (11.3%) exact matches, in which:
290 unique CDR3
7 unique J



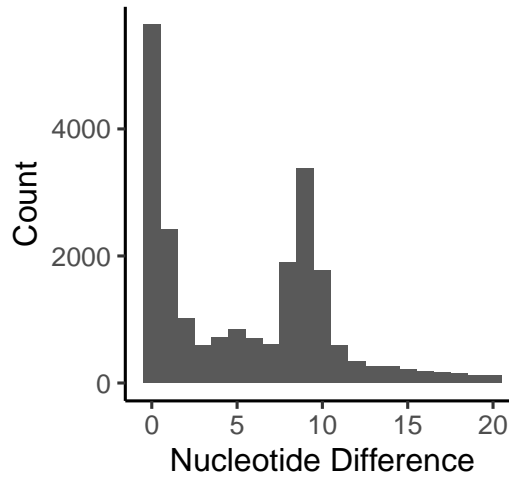
IGHV3-15*01_02

4417 sequences assigned
1189 (26.9%) exact matches, in which:
943 unique CDR3
7 unique J



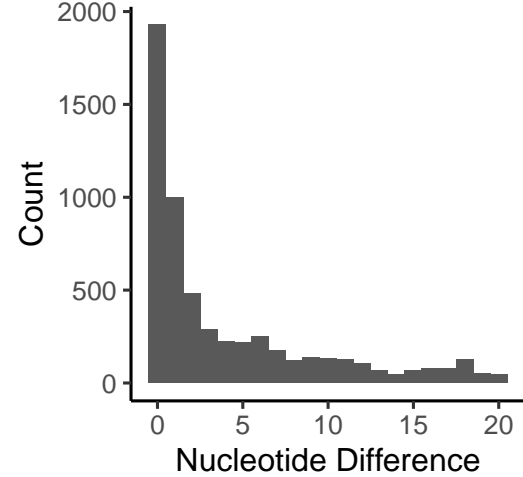
IGHV3-21*01_02

23786 sequences assigned
5640 (23.7%) exact matches, in which:
4175 unique CDR3
7 unique J



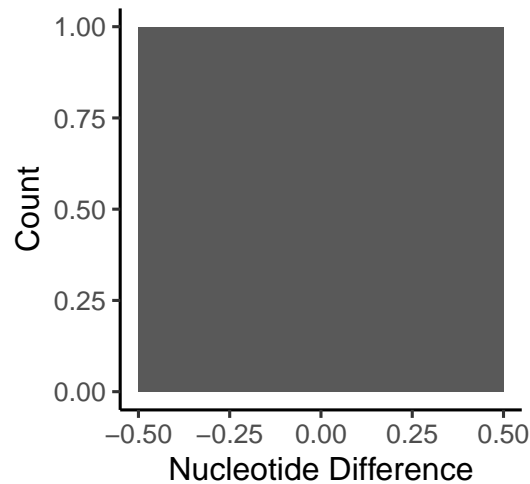
IGHV3-33*01

6554 sequences assigned
1929 (29.4%) exact matches, in which:
1558 unique CDR3
7 unique J



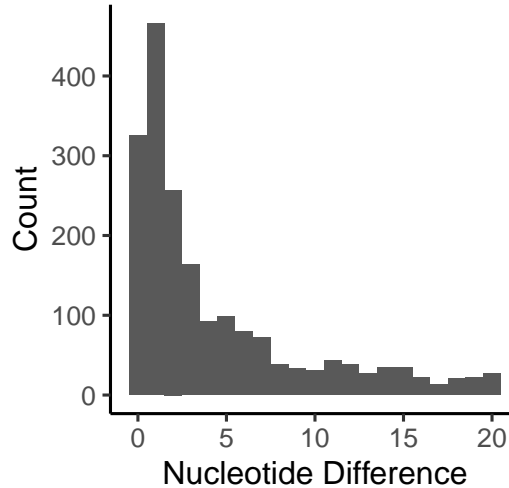
IGHV3-19*01

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



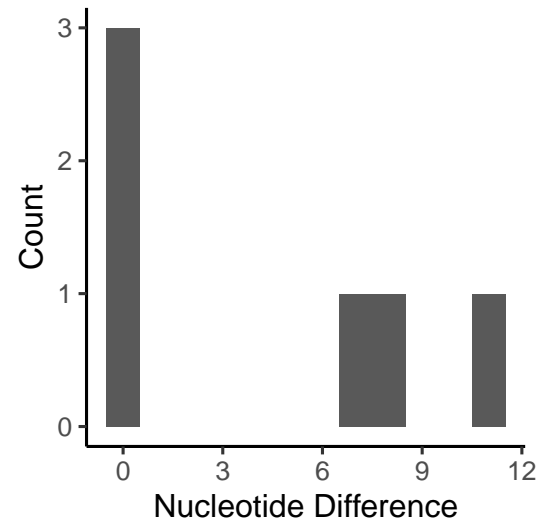
IGHV3-30*03

2338 sequences assigned
325 (13.9%) exact matches, in which:
317 unique CDR3
7 unique J



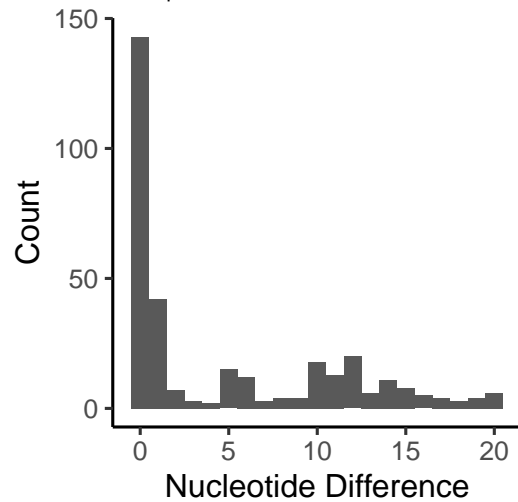
IGHV3-35*01

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



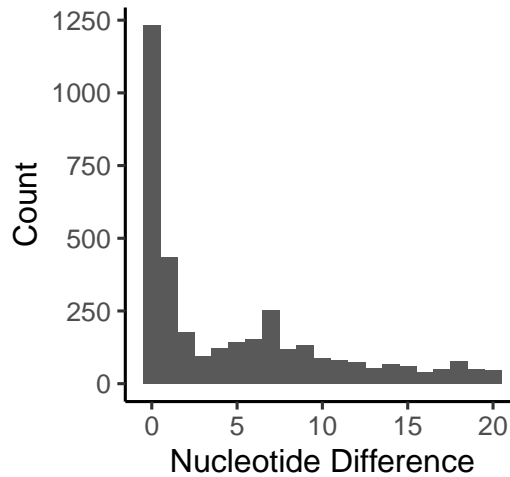
IGHV3-43*01

381 sequences assigned
143 (37.5%) exact matches, in which:
115 unique CDR3
7 unique J



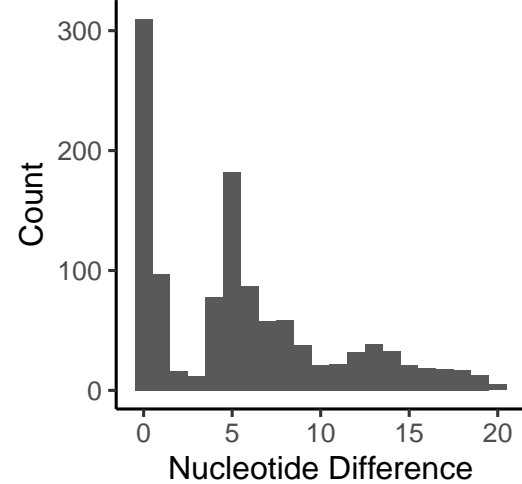
IGHV3-48*02

4024 sequences assigned
1232 (30.6%) exact matches, in which:
945 unique CDR3
7 unique J



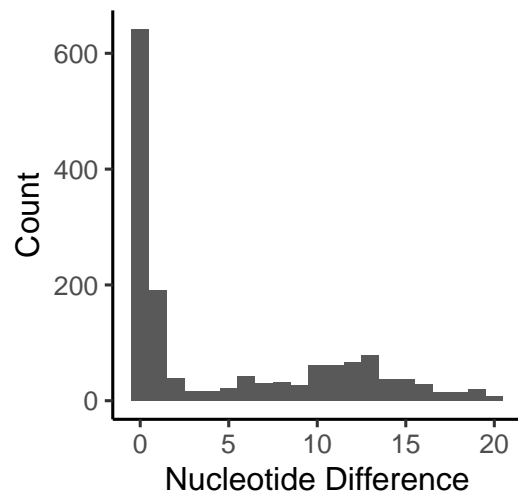
IGHV3-49*04

1411 sequences assigned
310 (22%) exact matches, in which:
263 unique CDR3
7 unique J



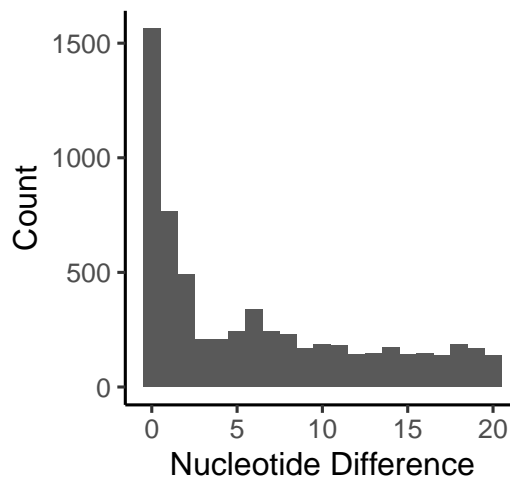
IGHV3-43*02

2025 sequences assigned
642 (31.7%) exact matches, in which:
470 unique CDR3
6 unique J



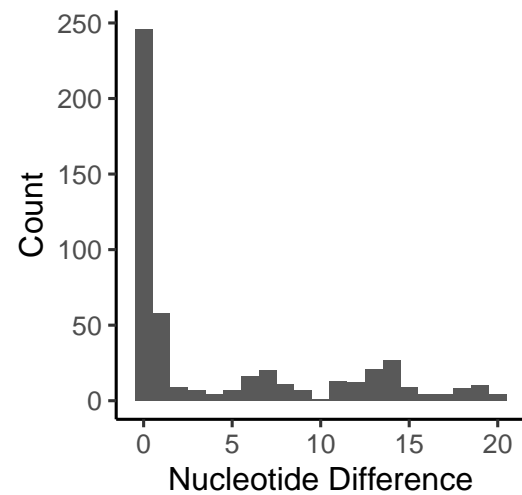
IGHV3-48*03

7284 sequences assigned
1563 (21.5%) exact matches, in which:
1198 unique CDR3
7 unique J



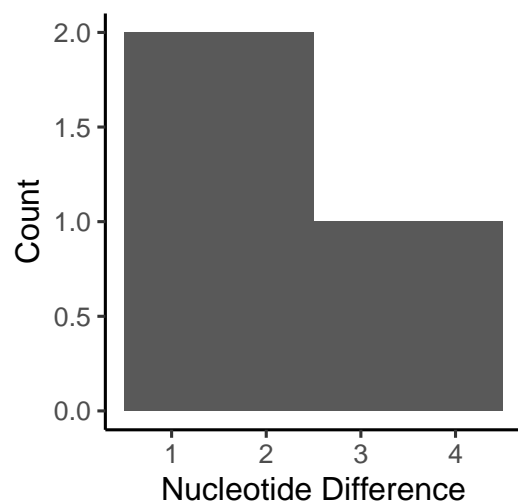
IGHV3-49*03_05

507 sequences assigned
246 (48.5%) exact matches, in which:
208 unique CDR3
7 unique J



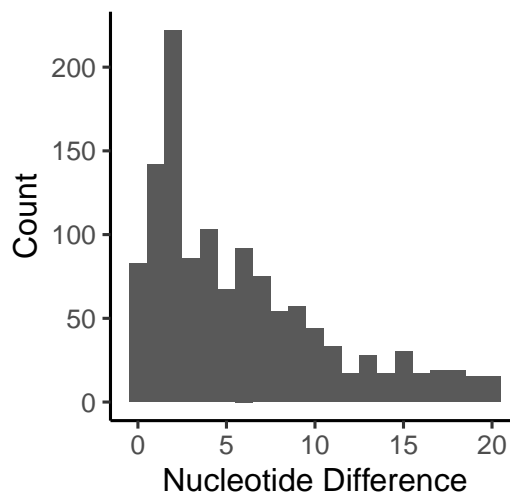
IGHV3-47*02

8 sequences assigned
No exact matches.



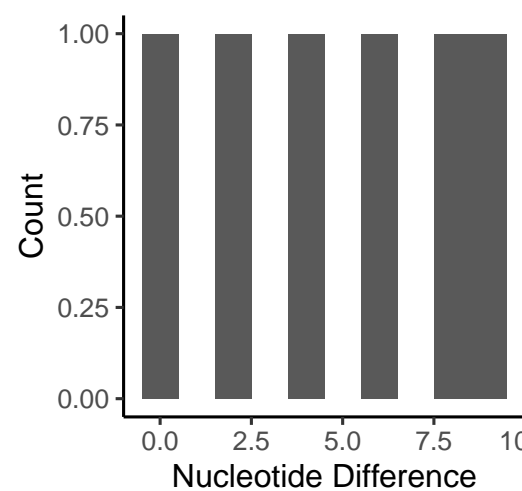
IGHV3-48*04

1492 sequences assigned
83 (5.6%) exact matches, in which:
82 unique CDR3
6 unique J



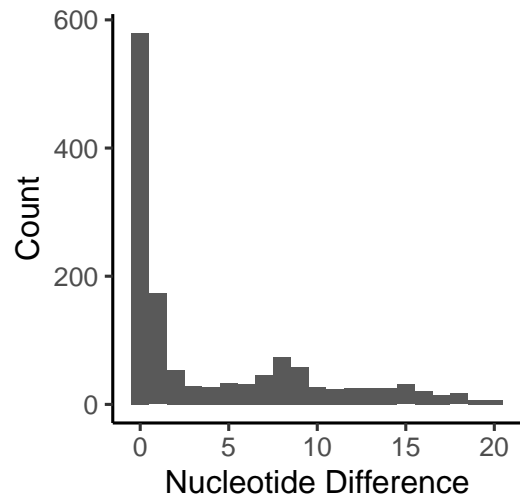
IGHV3-52*01_03

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



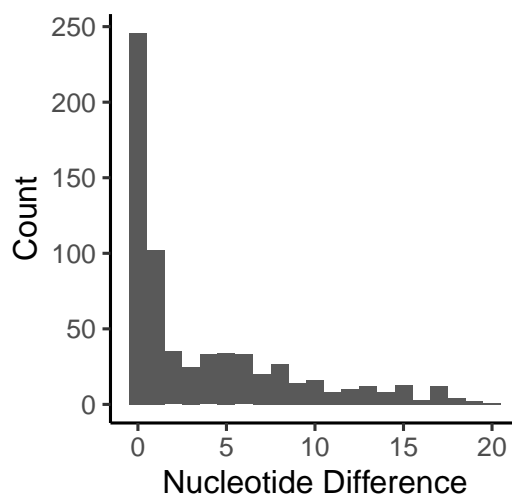
IGHV3-53*04

1528 sequences assigned
580 (38%) exact matches, in which:
446 unique CDR3
7 unique J



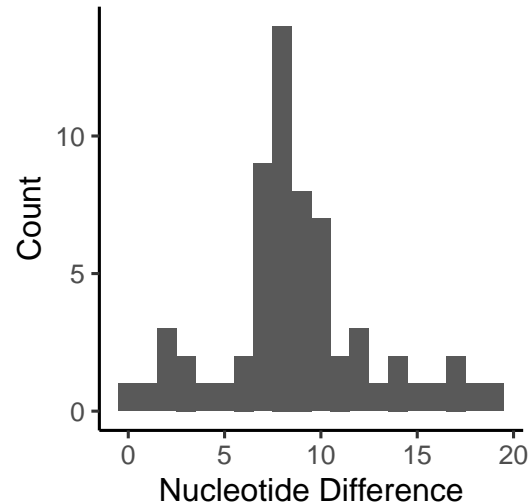
IGHV3-64*01

793 sequences assigned
246 (31%) exact matches, in which:
184 unique CDR3
7 unique J



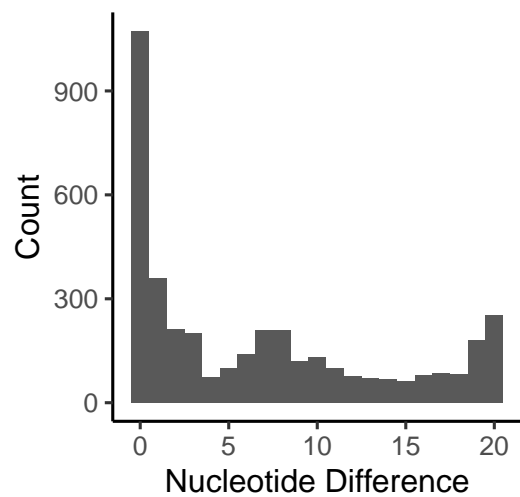
IGHV3-66*02

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



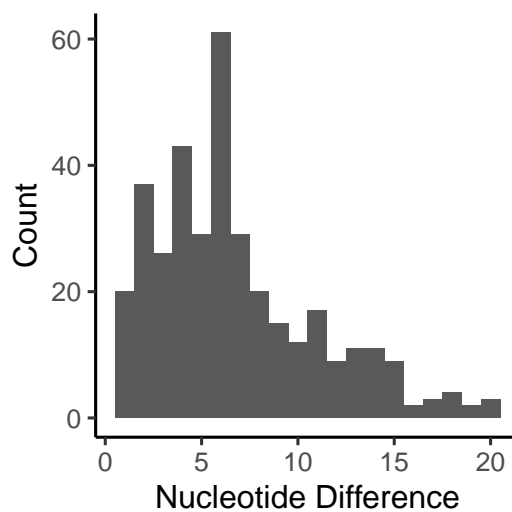
IGHV3-53*01_02

5772 sequences assigned
1073 (18.6%) exact matches, in which:
858 unique CDR3
7 unique J



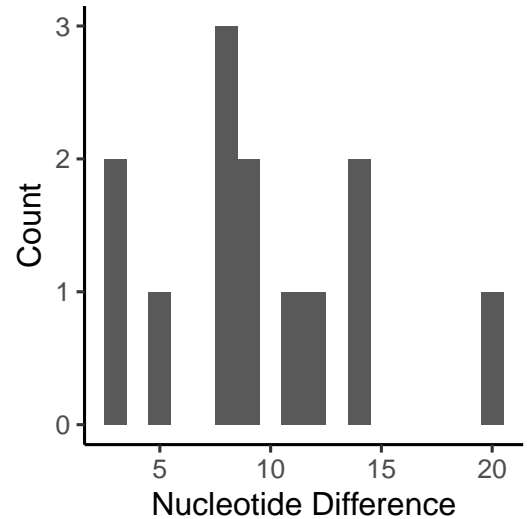
IGHV3-64*04

374 sequences assigned
No exact matches.



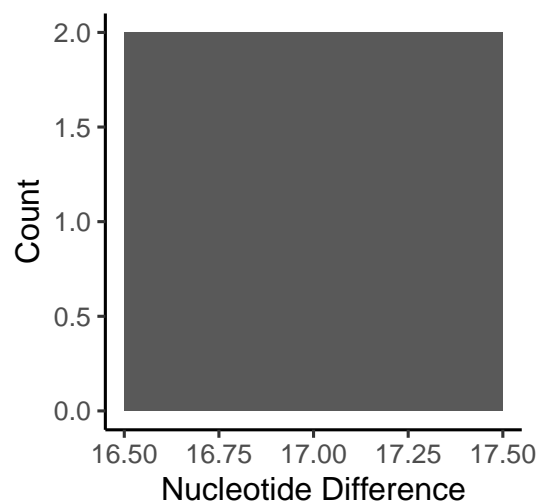
IGHV3-66*04

25 sequences assigned
No exact matches.



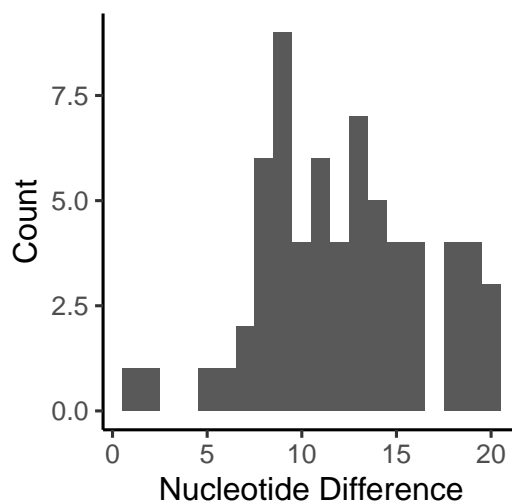
IGHV3-62*04

2 sequences assigned
No exact matches.



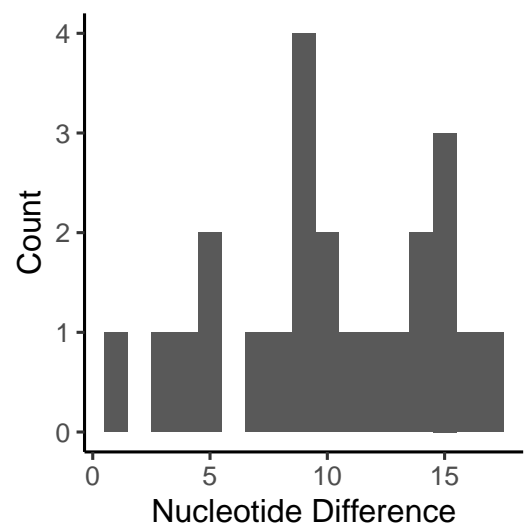
IGHV3-66*01

82 sequences assigned
No exact matches.



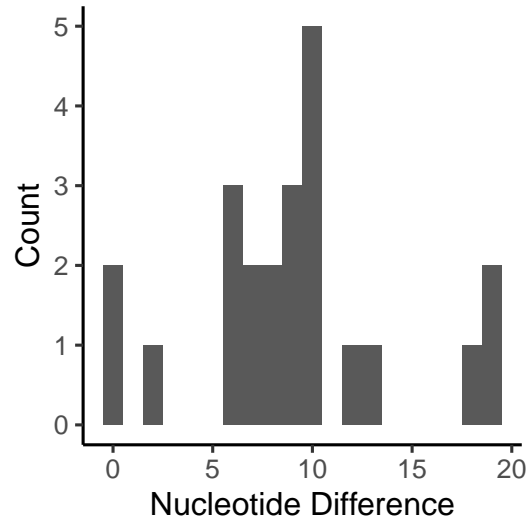
IGHV3-69-1*01

37 sequences assigned
No exact matches.



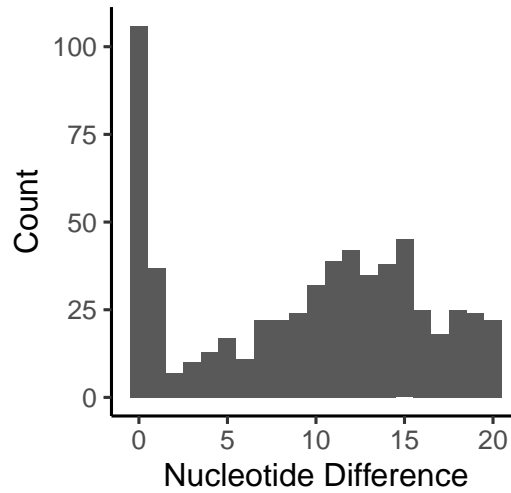
IGHV3-69-1*02

134 sequences assigned
2 (1.5%) exact matches, in which:
1 unique CDR3
1 unique J



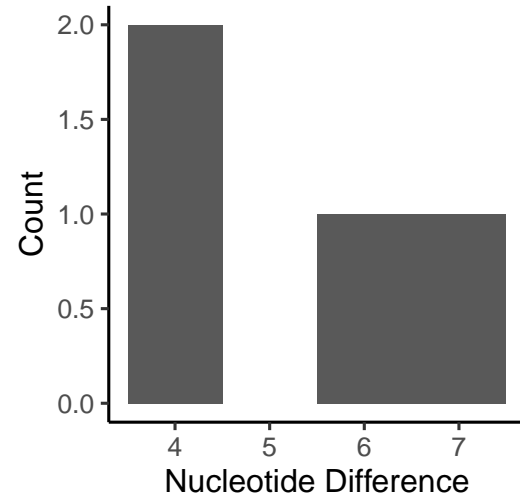
IGHV3-72*01

718 sequences assigned
106 (14.8%) exact matches, in which:
79 unique CDR3
6 unique J



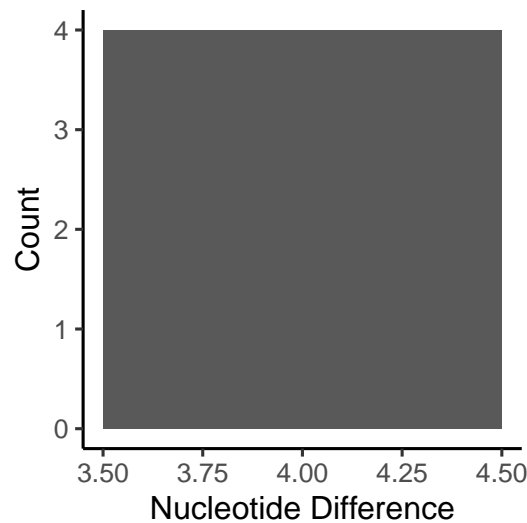
IGHV3-43D*04

4 sequences assigned
No exact matches.



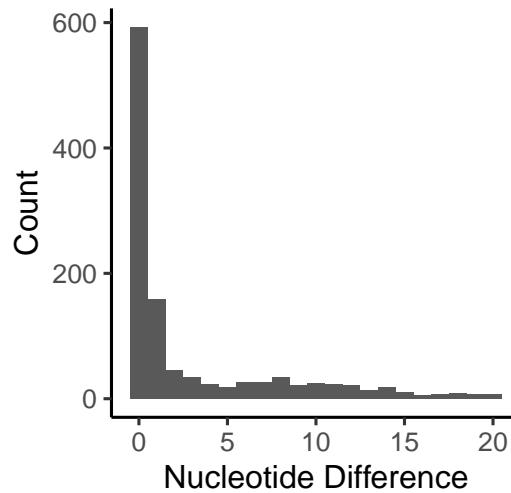
IGHV3-71*03

4 sequences assigned
No exact matches.



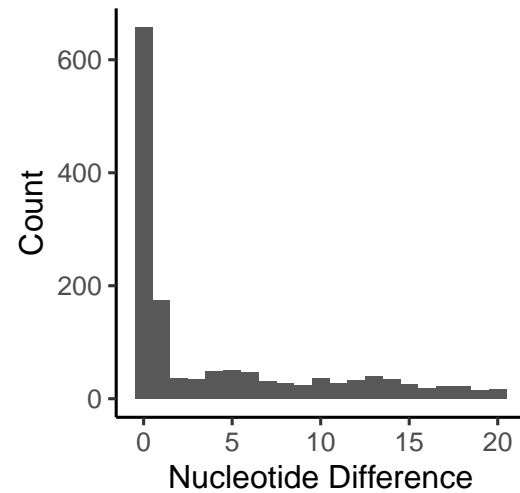
IGHV3-73*01_02

1391 sequences assigned
593 (42.6%) exact matches, in which:
466 unique CDR3
7 unique J



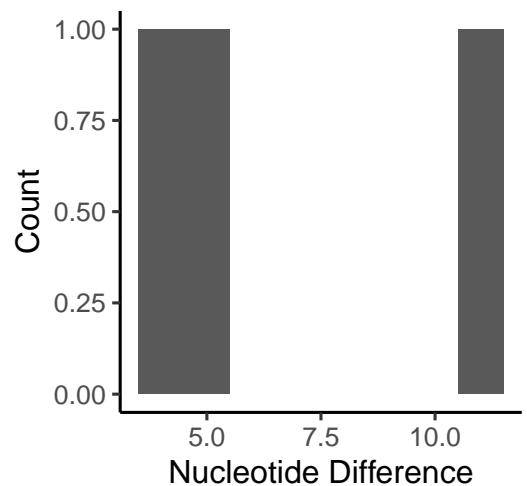
IGHV3-64D*06

1712 sequences assigned
658 (38.4%) exact matches, in which:
464 unique CDR3
7 unique J



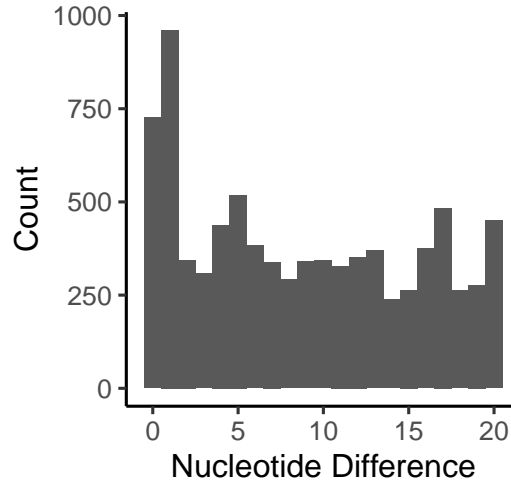
IGHV3-71*01_04

5 sequences assigned
No exact matches.



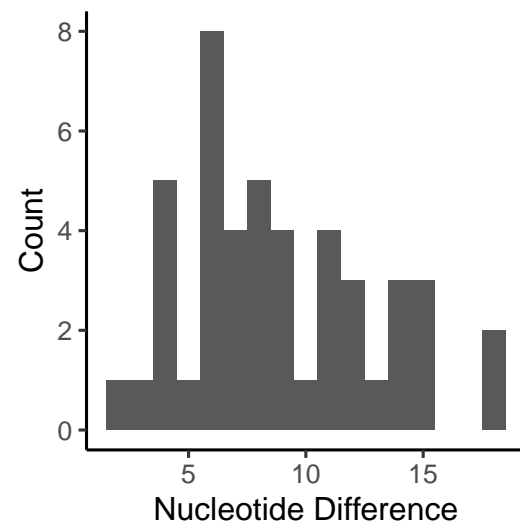
IGHV3-74*01_02

13408 sequences assigned
726 (5.4%) exact matches, in which:
563 unique CDR3
7 unique J



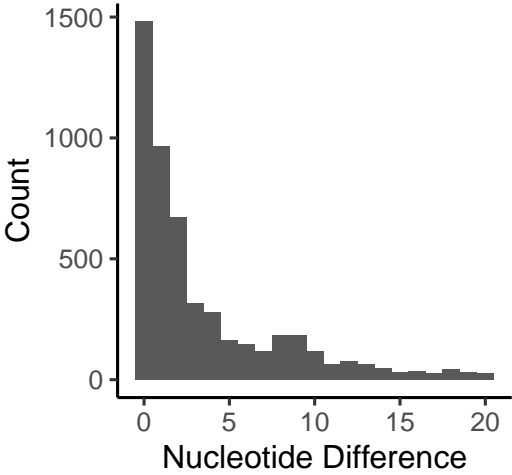
IGHV3-NL1*01

68 sequences assigned
No exact matches.



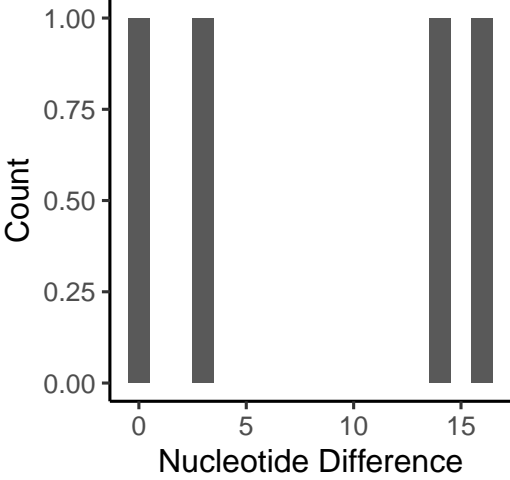
IGHV4-4*07

6843 sequences assigned
1482 (21.7%) exact matches, in which:
1389 unique CDR3
7 unique J



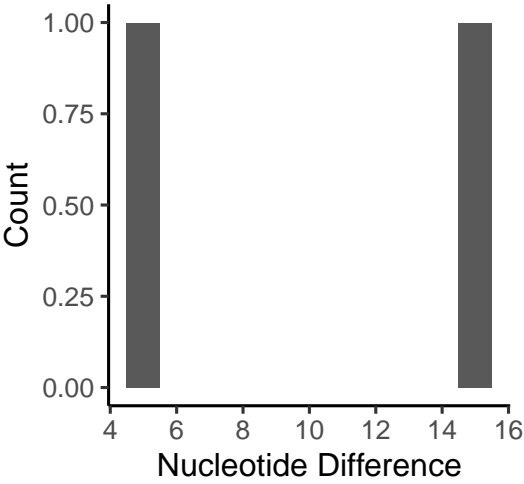
IGHV4-28*02_05

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



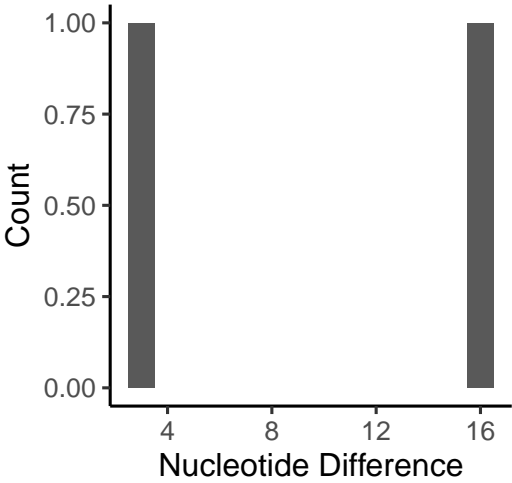
IGHV4-30-2*03

2 sequences assigned
No exact matches.



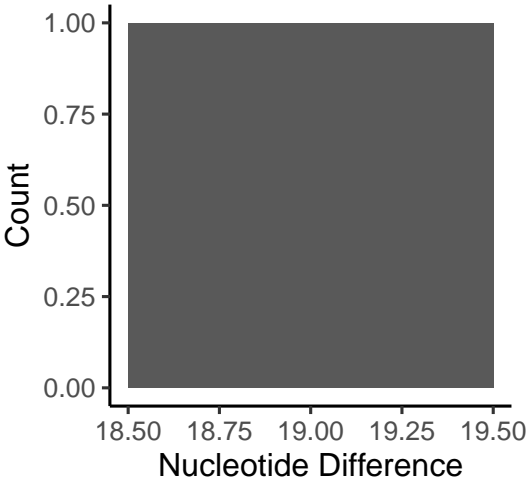
IGHV4-28*03

2 sequences assigned
No exact matches.



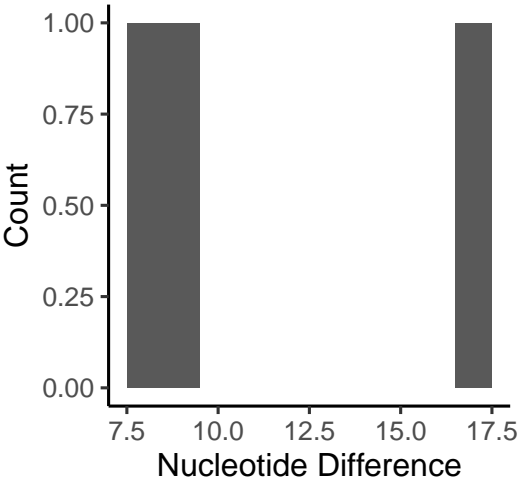
IGHV4-30-4*01

6 sequences assigned
No exact matches.



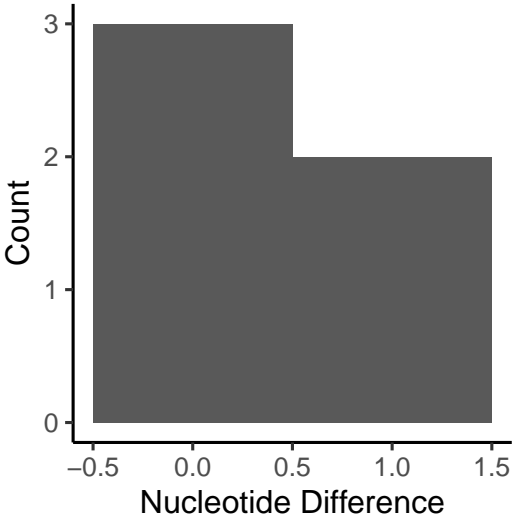
IGHV4-30-4*08

7 sequences assigned
No exact matches.



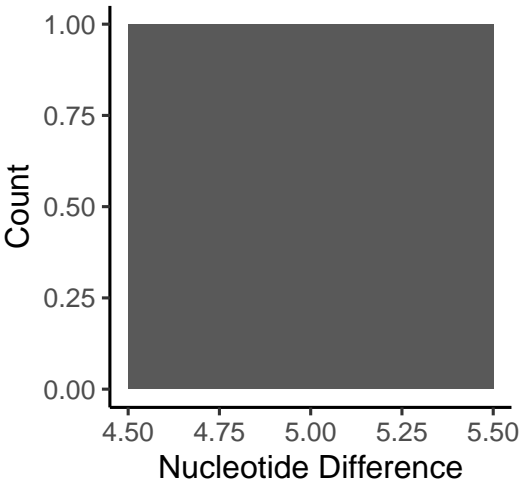
IGHV4-28*01_07

5 sequences assigned
3 (60%) exact matches, in which:
3 unique CDR3
3 unique J



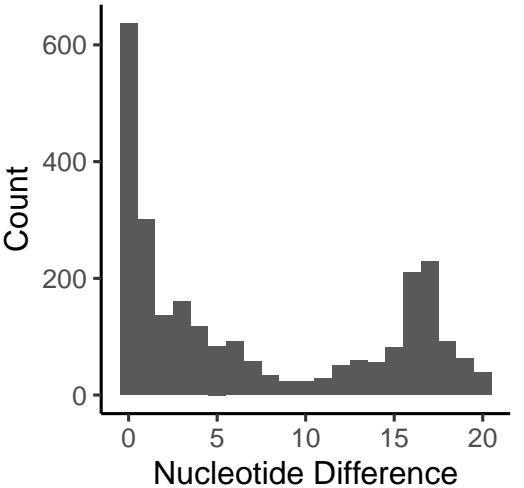
IGHV4-30-2*01

2 sequences assigned
No exact matches.



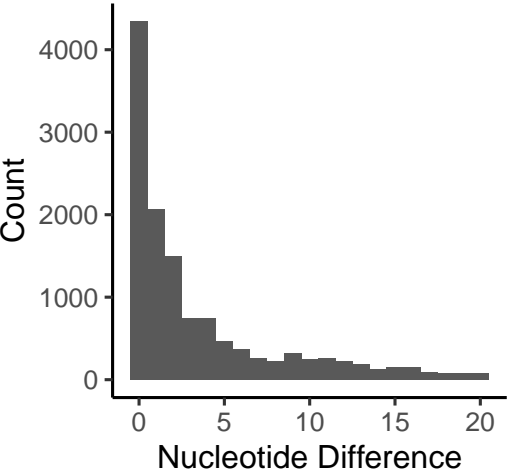
IGHV4-31*03_04

2861 sequences assigned
637 (22.3%) exact matches, in which:
614 unique CDR3
7 unique J



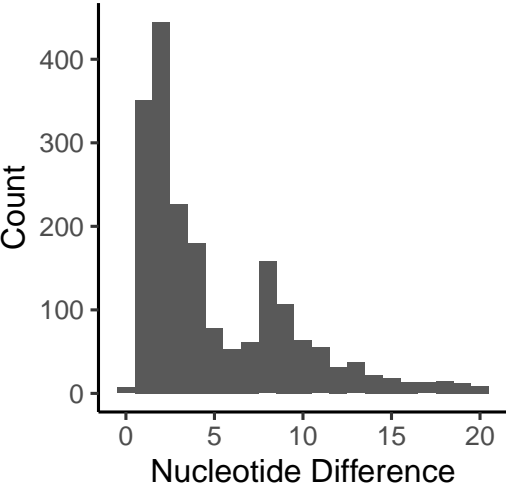
IGHV4-34*01_02

14692 sequences assigned
4343 (29.6%) exact matches, in which:
4084 unique CDR3
7 unique J



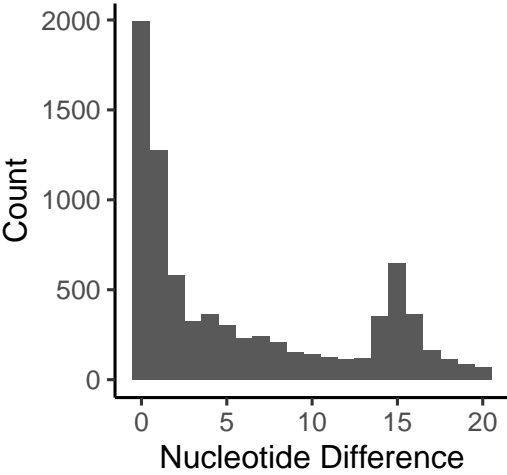
IGHV4-39*07

2046 sequences assigned
7 (0.3%) exact matches, in which:
7 unique CDR3
3 unique J



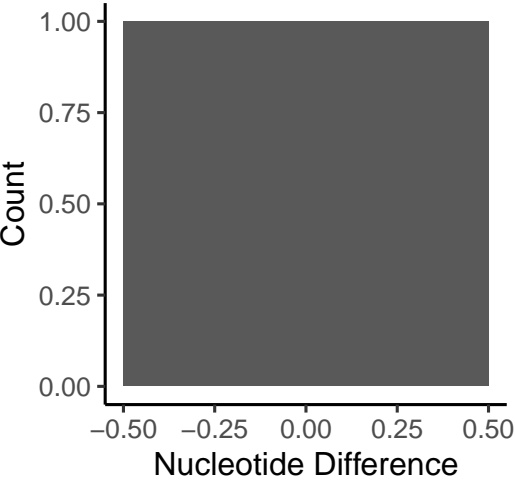
IGHV4-59*08

9176 sequences assigned
1992 (21.7%) exact matches, in which:
1852 unique CDR3
7 unique J



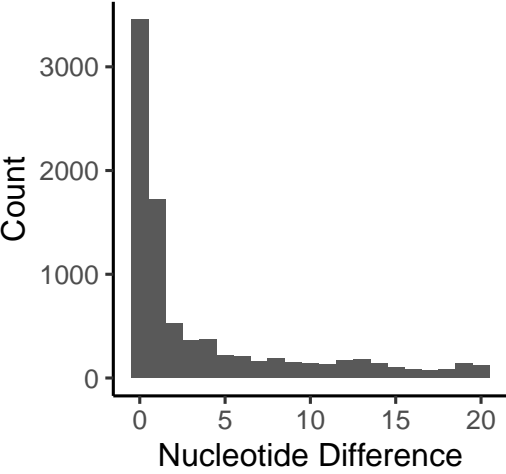
IGHV4-38-2*01

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



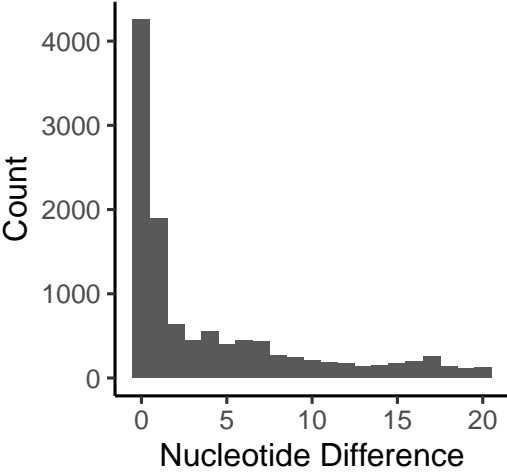
IGHV4-39*01_05

10345 sequences assigned
3454 (33.4%) exact matches, in which:
3220 unique CDR3
7 unique J



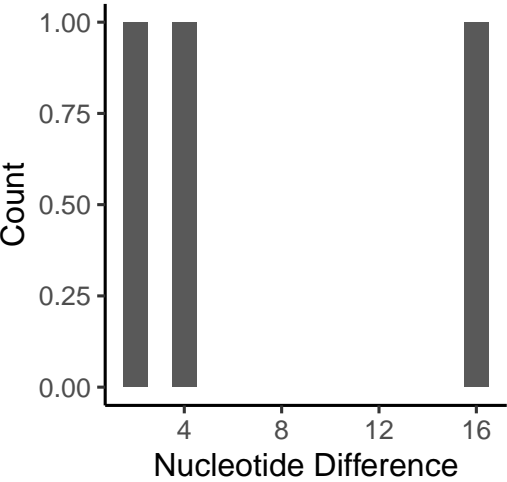
IGHV4-59*01_07

13088 sequences assigned
4254 (32.5%) exact matches, in which:
4008 unique CDR3
7 unique J



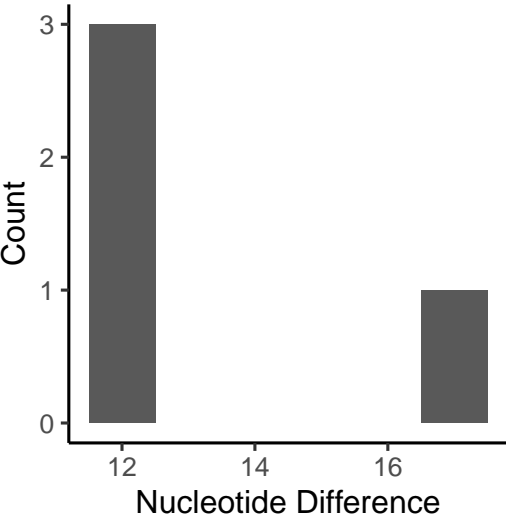
IGHV4-38-2*02

4 sequences assigned
No exact matches.



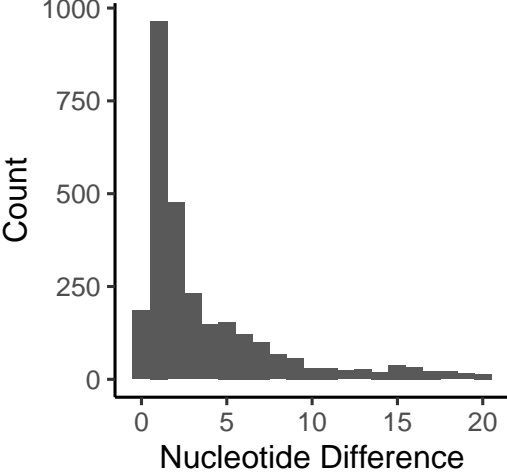
IGHV4-55*02_04_08

5 sequences assigned
No exact matches.



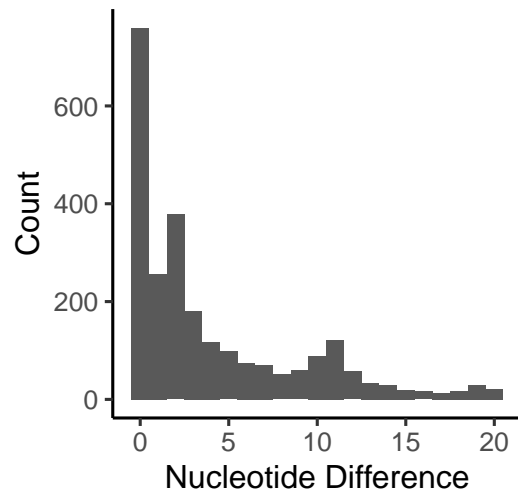
IGHV4-59*12

2933 sequences assigned
185 (6.3%) exact matches, in which:
185 unique CDR3
6 unique J



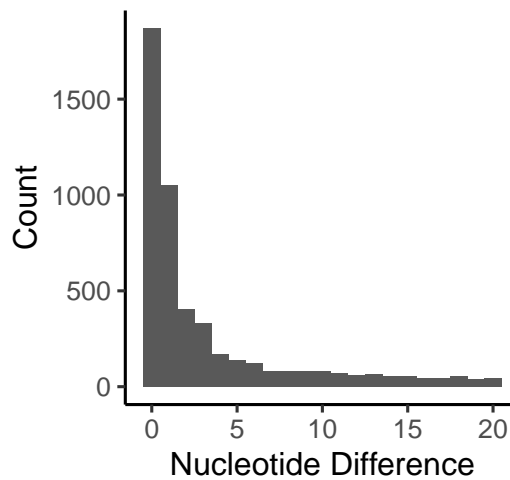
IGHV4-61*01

2759 sequences assigned
760 (27.5%) exact matches, in which:
736 unique CDR3
7 unique J



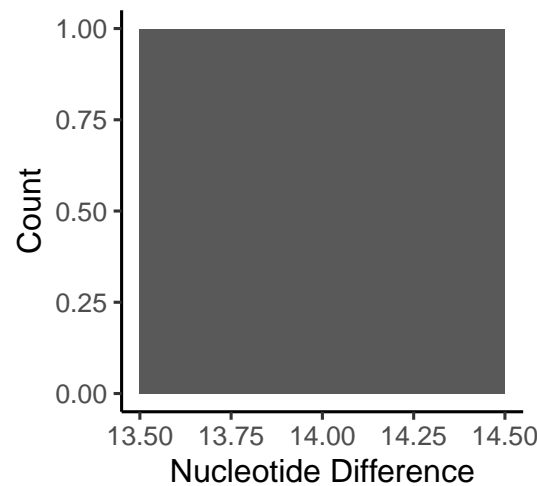
IGHV5-10-1*01_03

5740 sequences assigned
1869 (32.6%) exact matches, in which:
1512 unique CDR3
7 unique J



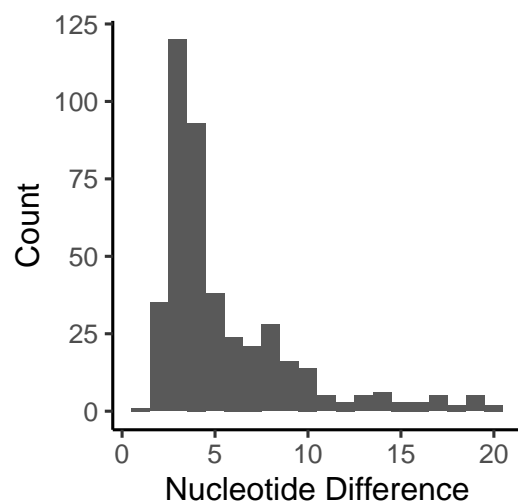
IGHV7-4-1*02

1 sequences assigned
No exact matches.



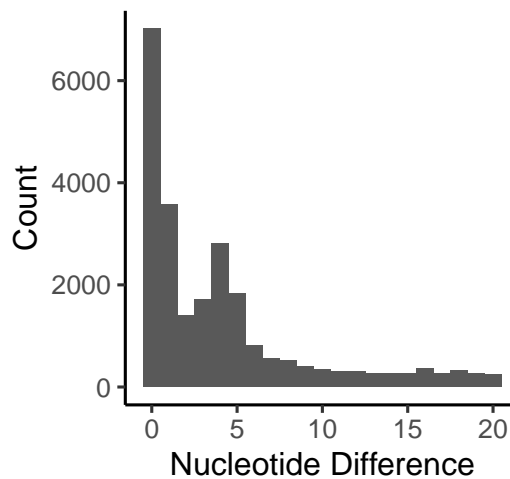
IGHV4-61*05

465 sequences assigned
No exact matches.



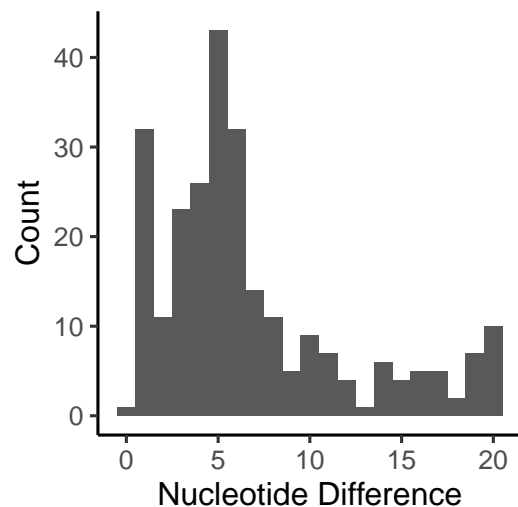
IGHV5-51*01_03

27844 sequences assigned
7017 (25.2%) exact matches, in which:
5065 unique CDR3
7 unique J



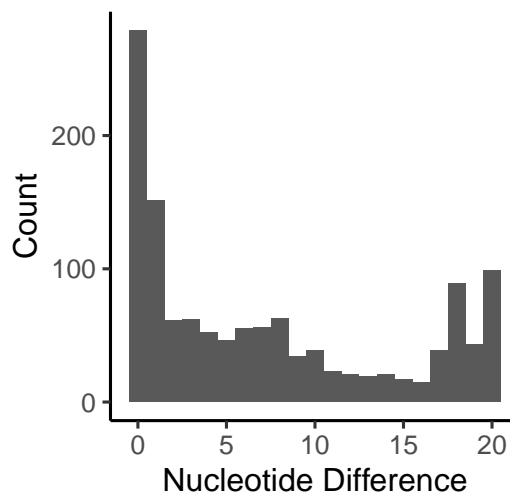
IGHV4-61*08

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

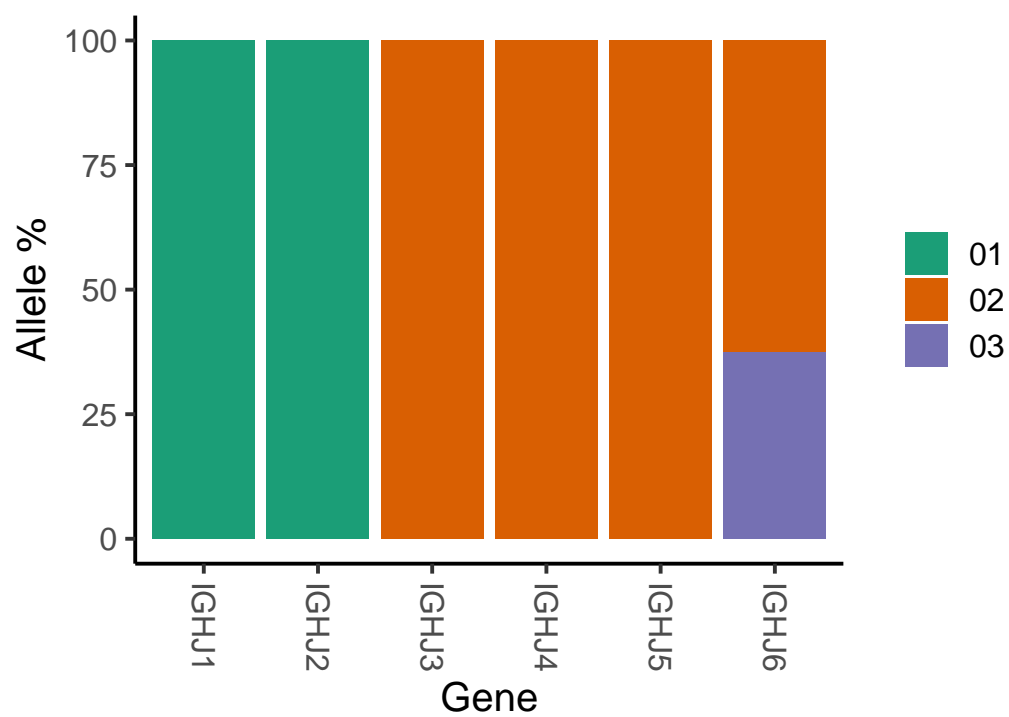


IGHV6-1*01_02

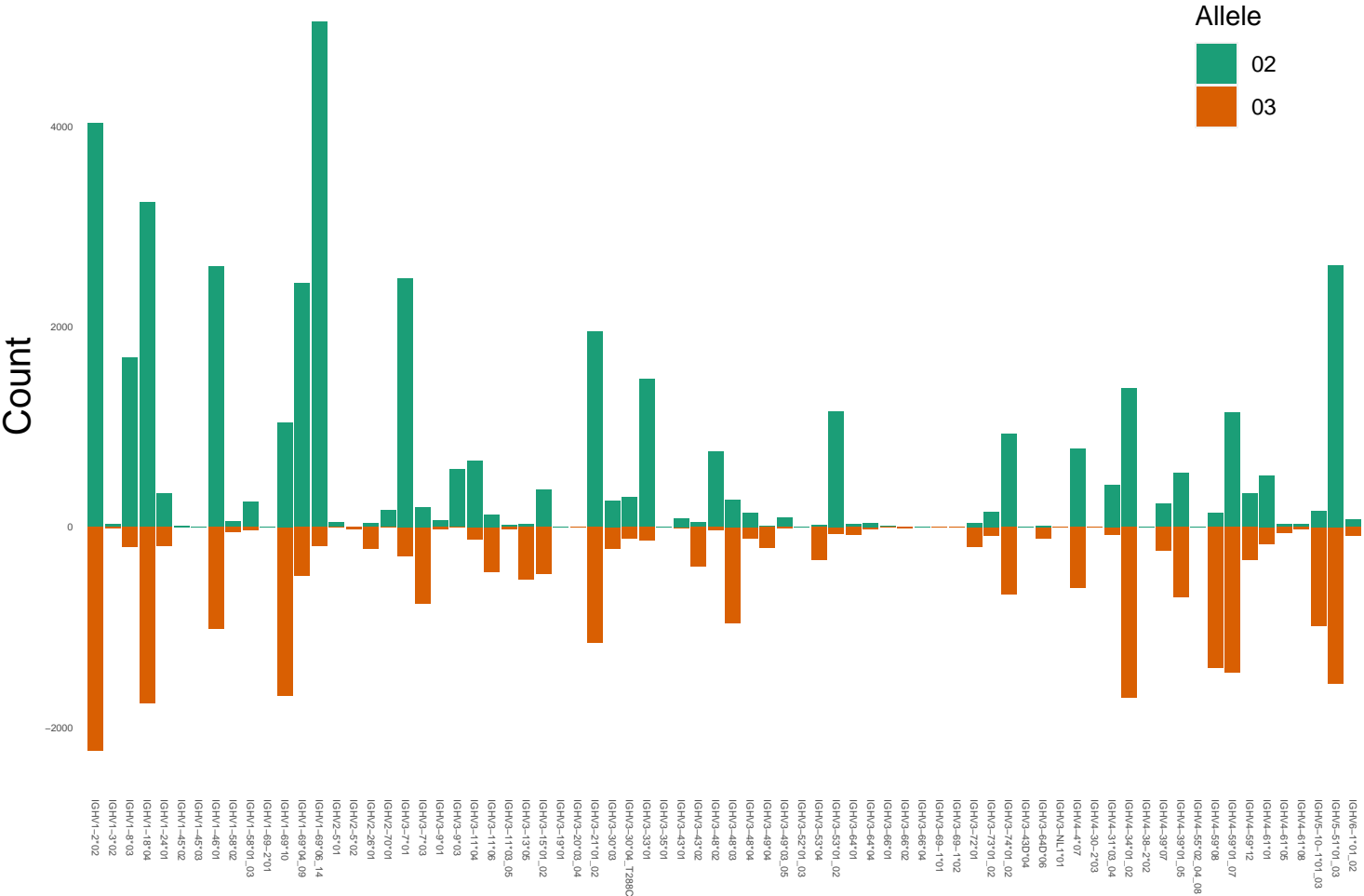
1737 sequences assigned
279 (16.1%) exact matches, in which:
268 unique CDR3
7 unique J



Allele Usage



Sequence Count by IGHJ6 allele usage



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.