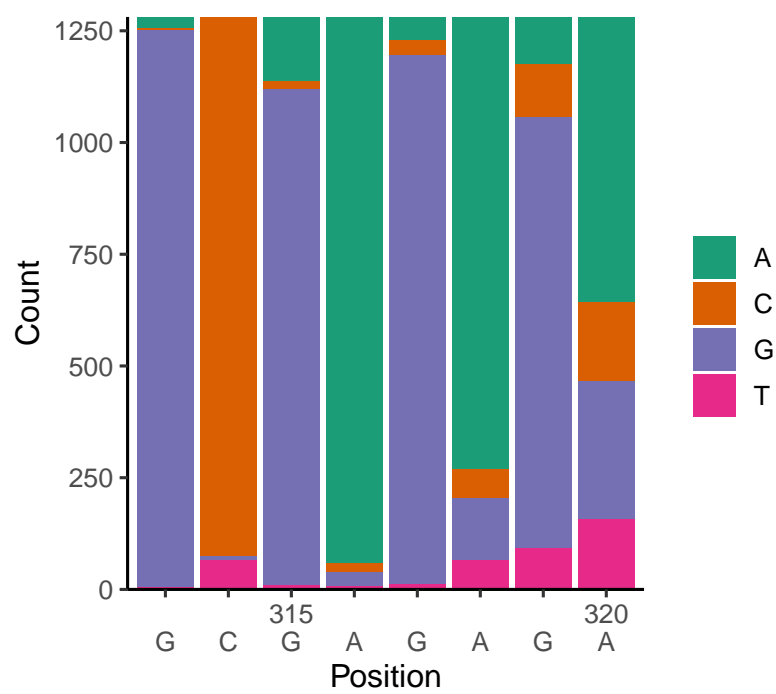


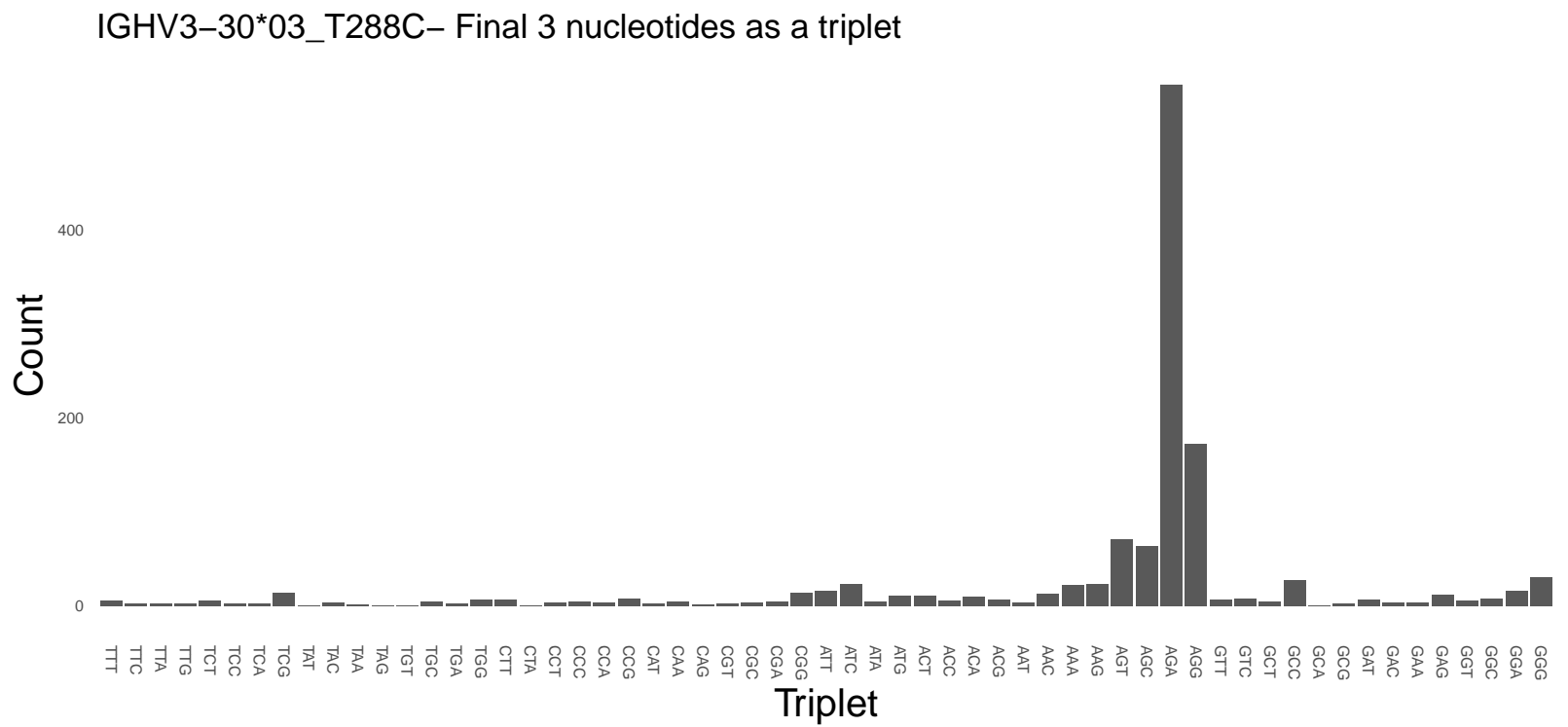
Gene IGHV3-30*03_T288C



Gene IGHV3-30*03_T288C

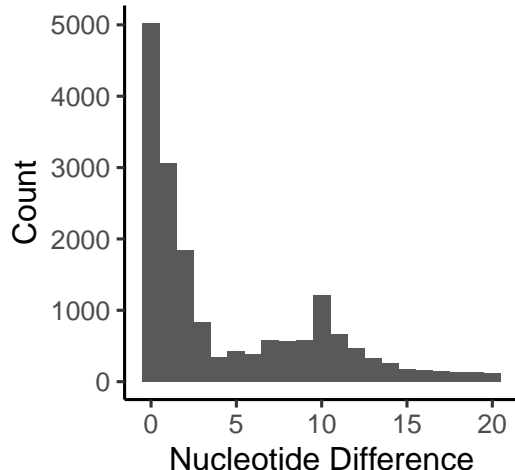


IGHV3-30*03_T288C- Final 3 nucleotides as a triplet



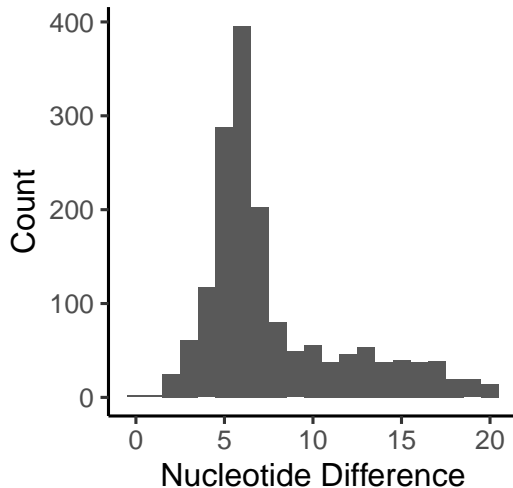
IGHV1-2*02

19865 sequences assigned
5020 (25.3%) exact matches, in which:
4810 unique CDR3
7 unique J



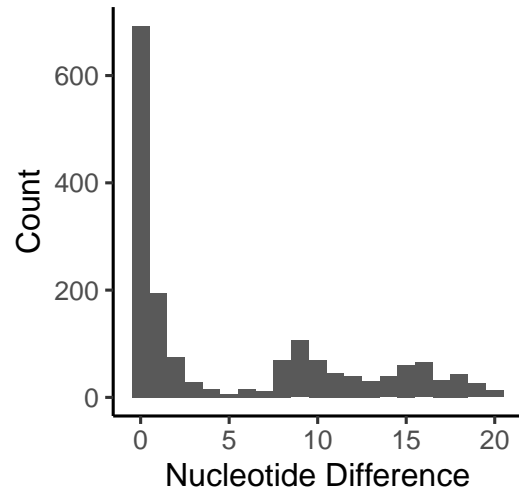
IGHV1-8*02

1753 sequences assigned
2 (0.1%) exact matches, in which:
2 unique CDR3
2 unique J



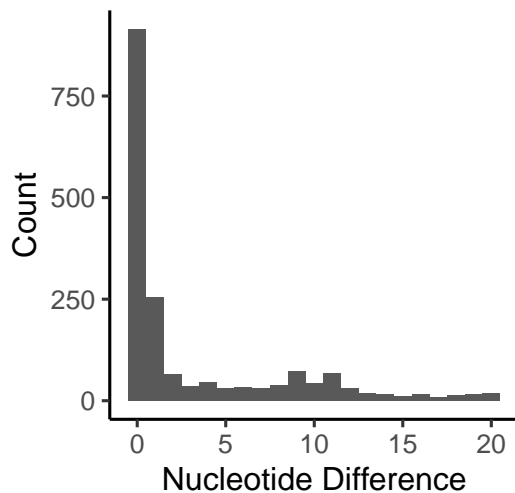
IGHV1-24*01

2013 sequences assigned
693 (34.4%) exact matches, in which:
674 unique CDR3
7 unique J



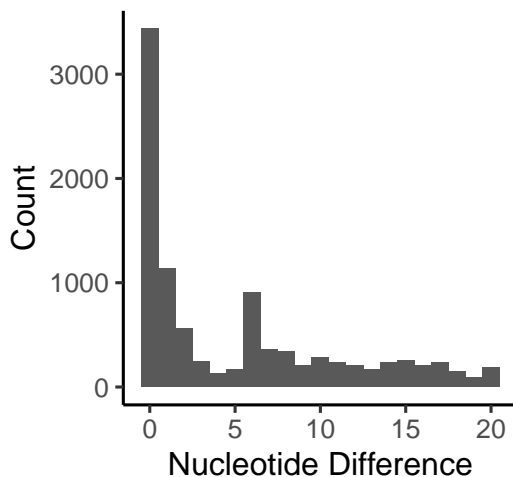
IGHV1-3*01_05

2074 sequences assigned
915 (44.1%) exact matches, in which:
875 unique CDR3
7 unique J



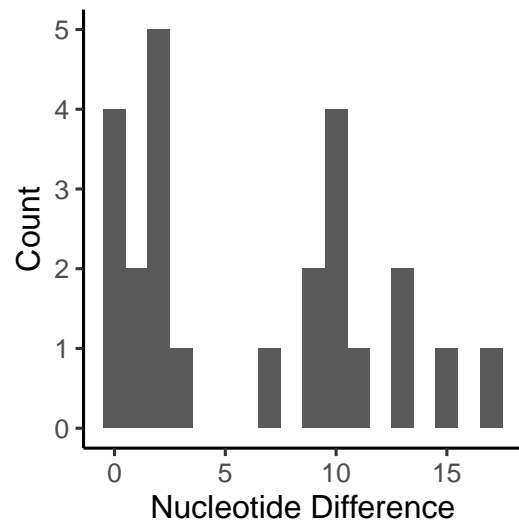
IGHV1-18*01

11571 sequences assigned
3436 (29.7%) exact matches, in which:
3346 unique CDR3
7 unique J



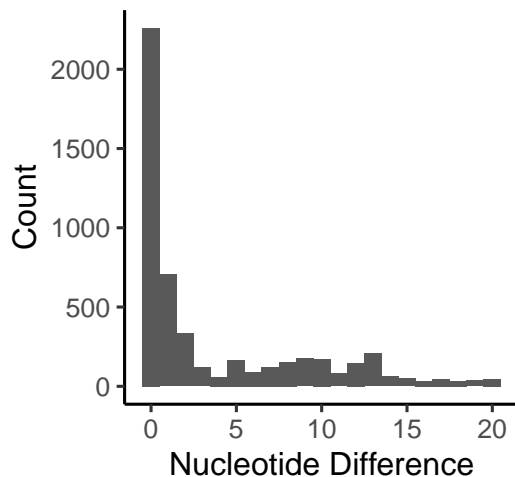
IGHV1-45*02

31 sequences assigned
4 (12.9%) exact matches, in which:
4 unique CDR3
3 unique J



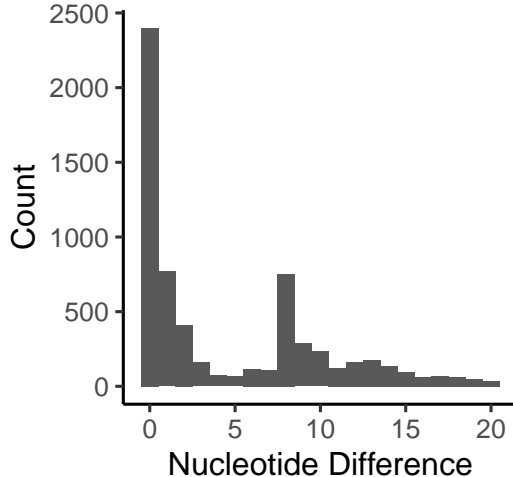
IGHV1-8*01

5737 sequences assigned
2260 (39.4%) exact matches, in which:
2193 unique CDR3
7 unique J



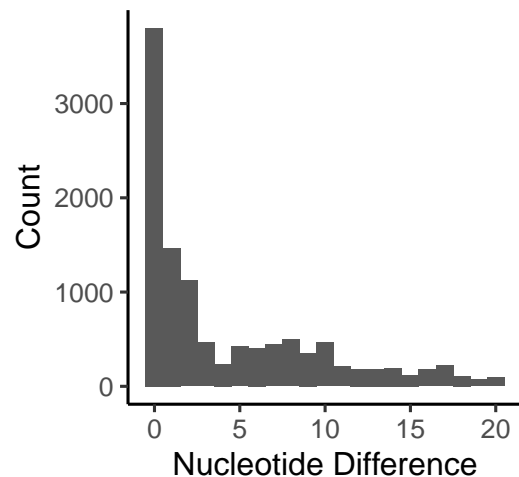
IGHV1-18*04

6895 sequences assigned
2399 (34.8%) exact matches, in which:
2349 unique CDR3
7 unique J



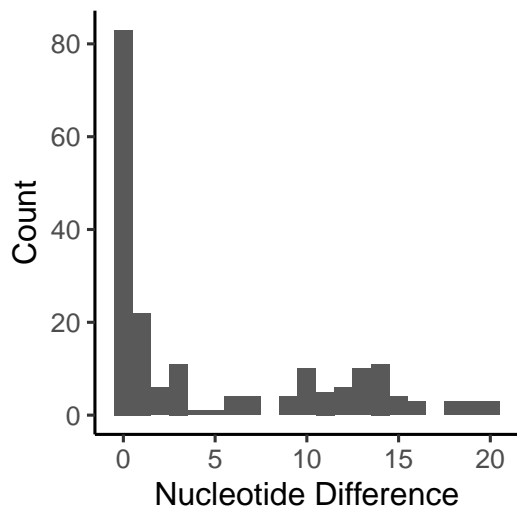
IGHV1-46*01

12610 sequences assigned
3801 (30.1%) exact matches, in which:
3681 unique CDR3
7 unique J



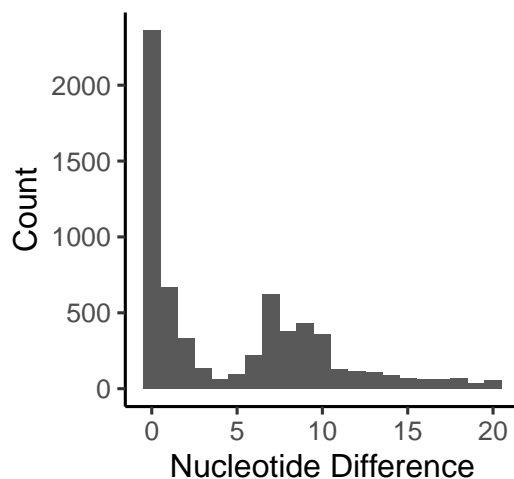
IGHV1-58*02

212 sequences assigned
83 (39.2%) exact matches, in which:
82 unique CDR3
7 unique J



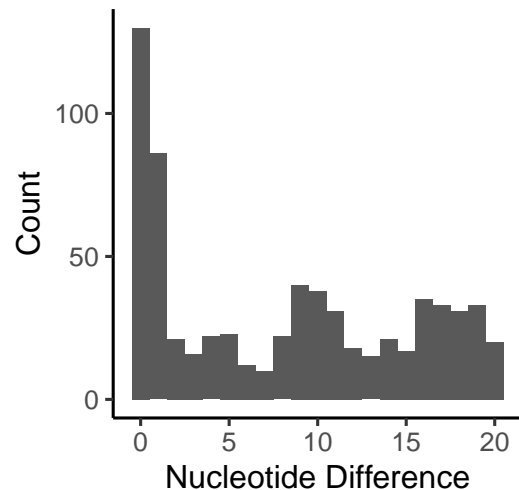
IGHV1-69*06_14

6970 sequences assigned
2361 (33.9%) exact matches, in which:
2315 unique CDR3
7 unique J



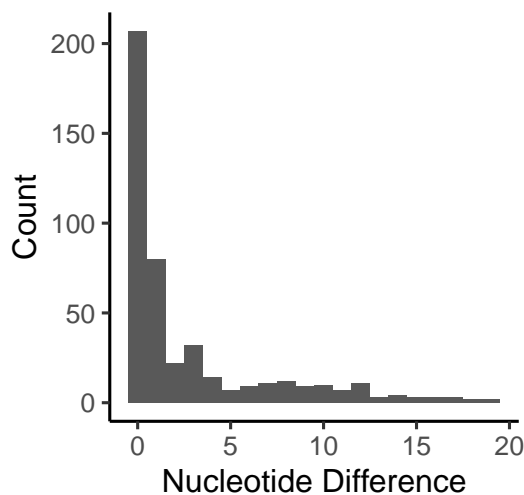
IGHV2-5*02

936 sequences assigned
130 (13.9%) exact matches, in which:
124 unique CDR3
7 unique J



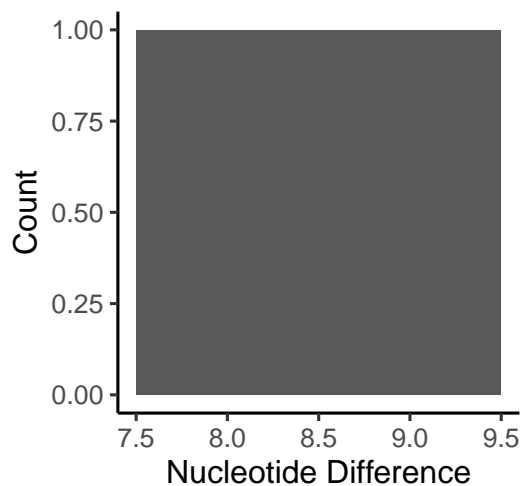
IGHV1-58*01_03

556 sequences assigned
207 (37.2%) exact matches, in which:
201 unique CDR3
7 unique J



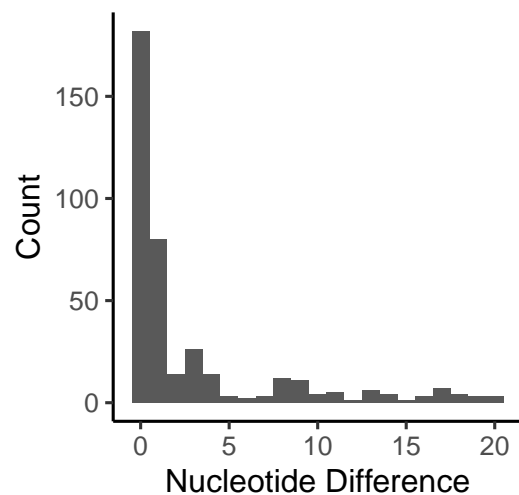
IGHV1-NL1*01

2 sequences assigned
No exact matches.



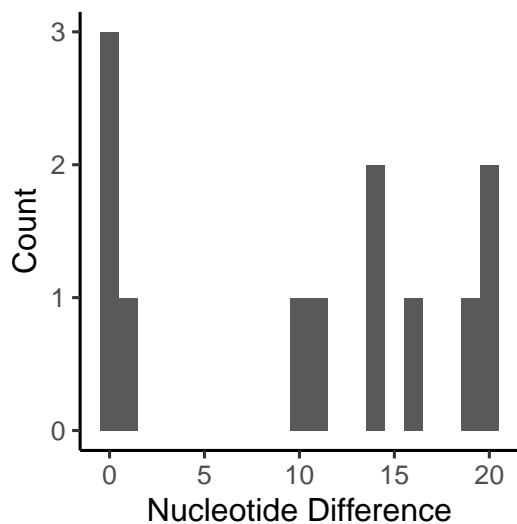
IGHV2-26*01

413 sequences assigned
182 (44.1%) exact matches, in which:
176 unique CDR3
6 unique J



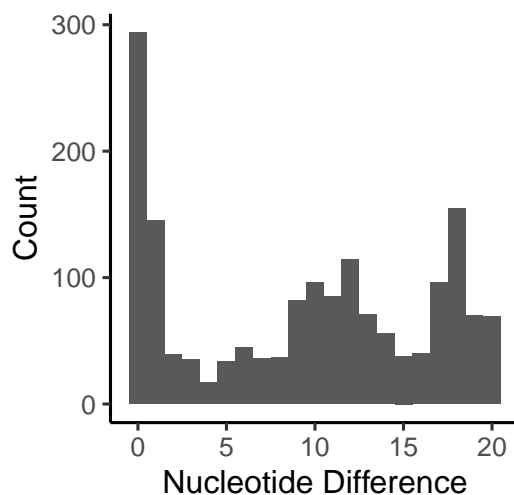
IGHV1-69-2*01

66 sequences assigned
3 (4.5%) exact matches, in which:
3 unique CDR3
2 unique J



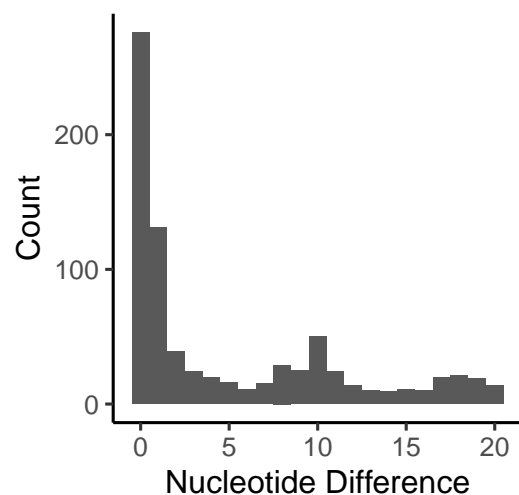
IGHV2-5*01

1960 sequences assigned
294 (15%) exact matches, in which:
285 unique CDR3
7 unique J



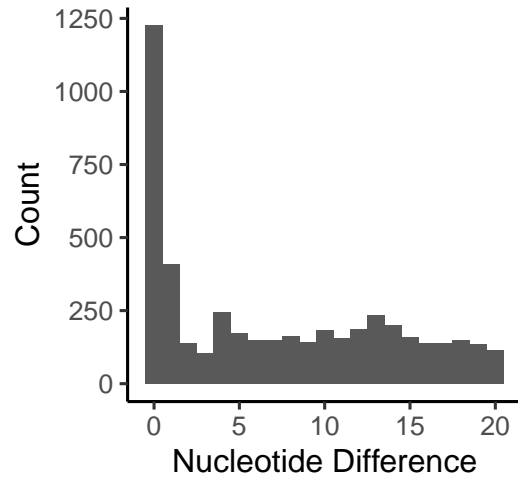
IGHV2-70*01

856 sequences assigned
276 (32.2%) exact matches, in which:
270 unique CDR3
7 unique J



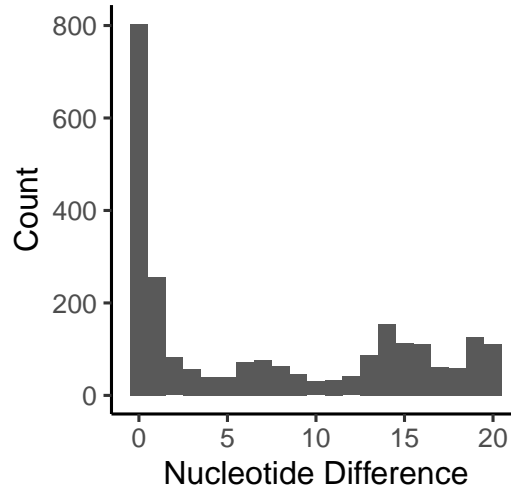
IGHV3-7*01

6050 sequences assigned
1226 (20.3%) exact matches, in which:
1136 unique CDR3
7 unique J



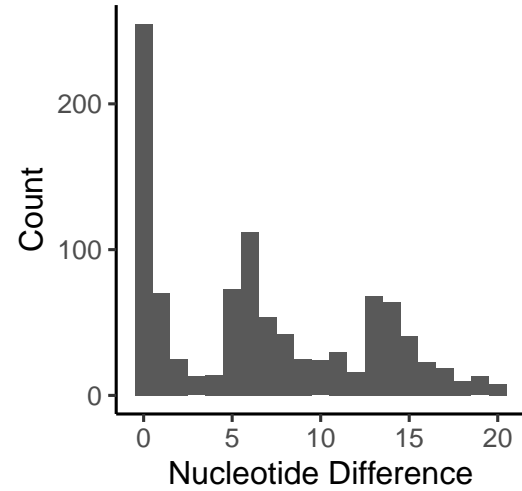
IGHV3-11*01

14205 sequences assigned
804 (5.7%) exact matches, in which:
739 unique CDR3
7 unique J



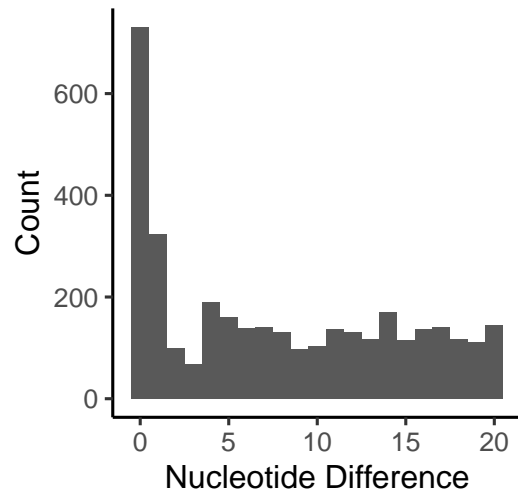
IGHV3-13*01

1118 sequences assigned
255 (22.8%) exact matches, in which:
232 unique CDR3
6 unique J



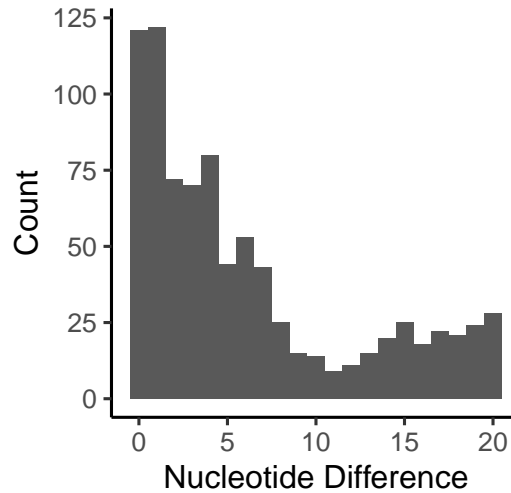
IGHV3-7*03

4726 sequences assigned
731 (15.5%) exact matches, in which:
648 unique CDR3
7 unique J



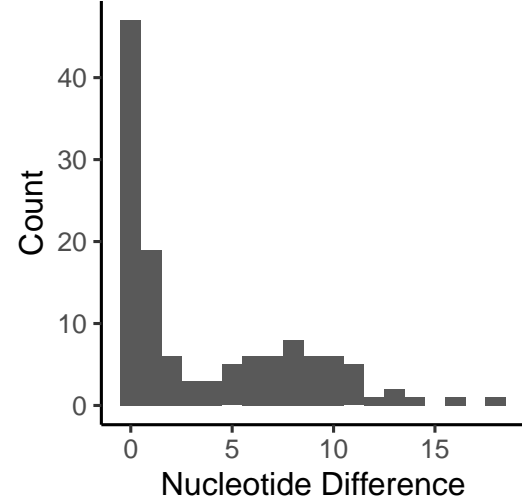
IGHV3-11*04

1034 sequences assigned
121 (11.7%) exact matches, in which:
121 unique CDR3
7 unique J



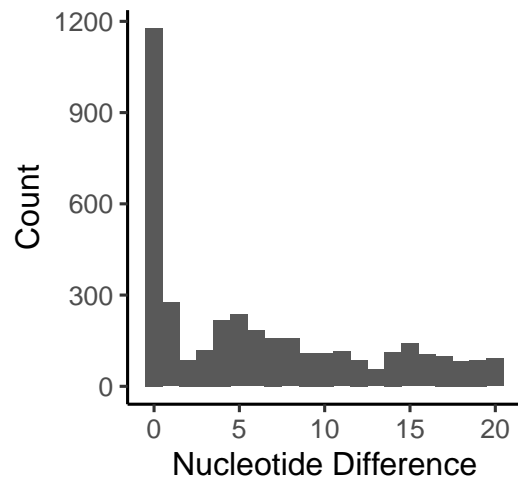
IGHV3-13*05

127 sequences assigned
47 (37%) exact matches, in which:
43 unique CDR3
6 unique J



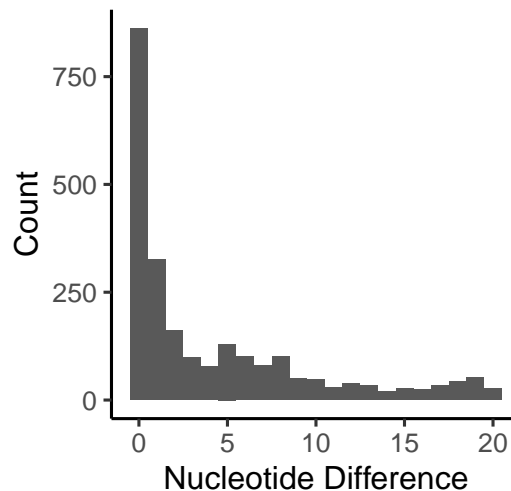
IGHV3-9*01

5036 sequences assigned
1178 (23.4%) exact matches, in which:
1062 unique CDR3
7 unique J



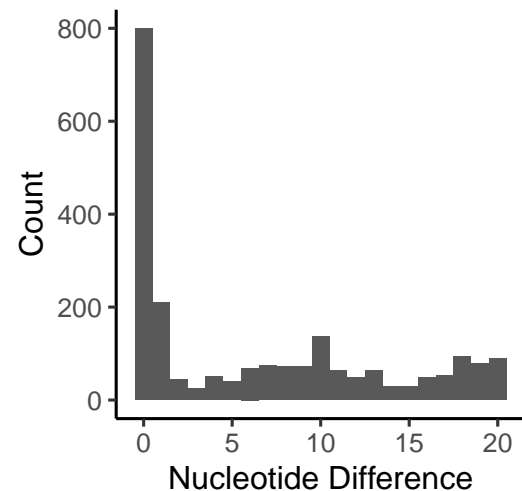
IGHV3-11*06

3387 sequences assigned
862 (25.5%) exact matches, in which:
775 unique CDR3
7 unique J



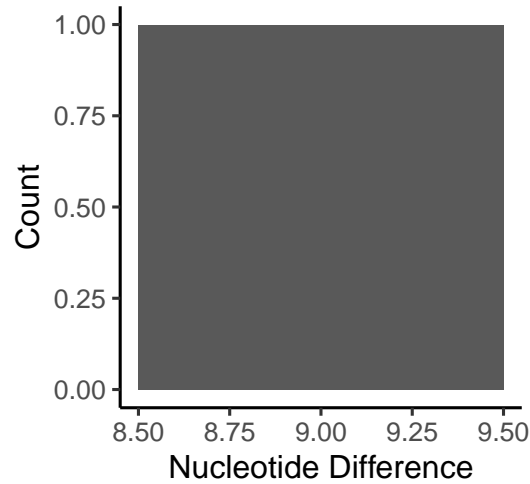
IGHV3-15*01_02

3047 sequences assigned
800 (26.3%) exact matches, in which:
709 unique CDR3
7 unique J



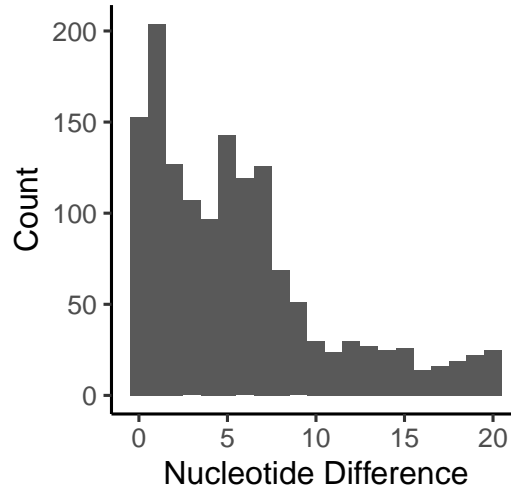
IGHV3-19*01

1 sequences assigned
No exact matches.



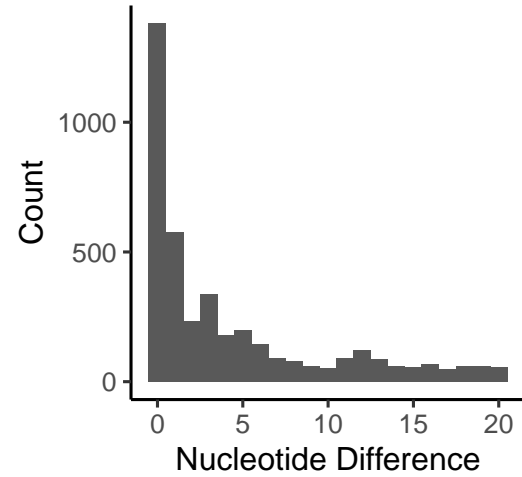
IGHV3-21*04

1740 sequences assigned
153 (8.8%) exact matches, in which:
153 unique CDR3
7 unique J



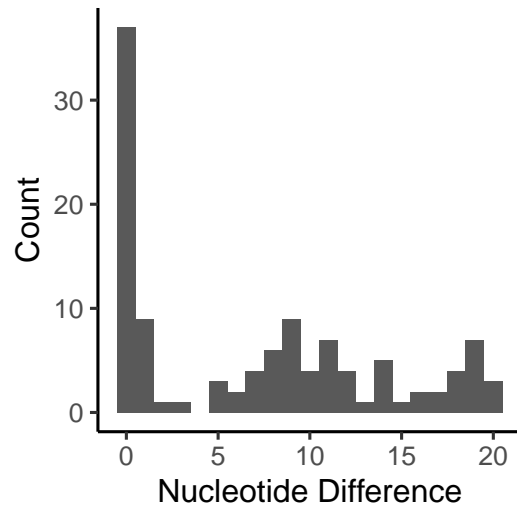
IGHV3-30-3*01

4504 sequences assigned
1381 (30.7%) exact matches, in which:
1278 unique CDR3
7 unique J



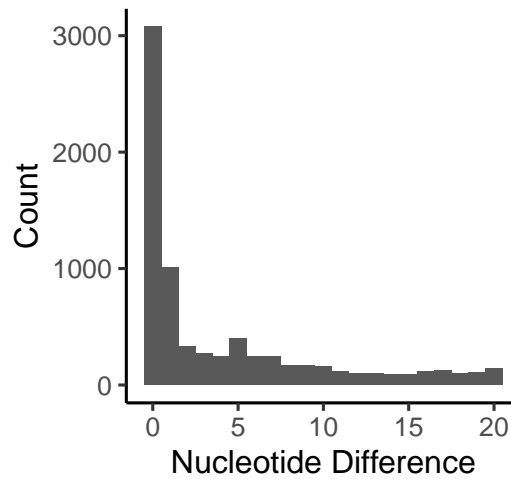
IGHV3-20*01_02

132 sequences assigned
37 (28%) exact matches, in which:
34 unique CDR3
5 unique J



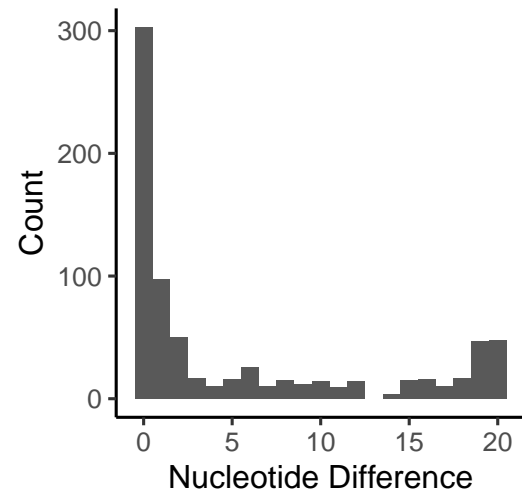
IGHV3-21*01_02

9176 sequences assigned
3077 (33.5%) exact matches, in which:
2754 unique CDR3
7 unique J



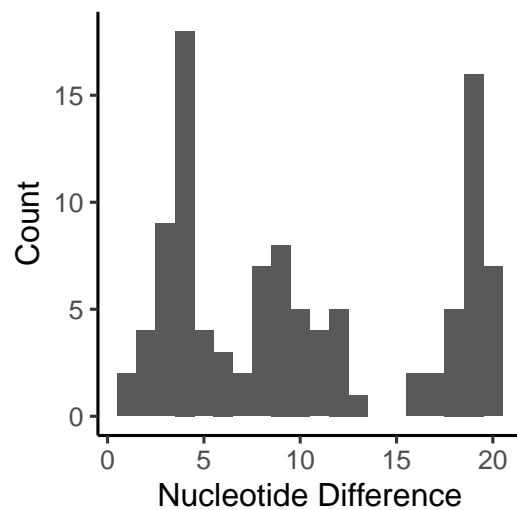
IGHV3-30*03

945 sequences assigned
303 (32.1%) exact matches, in which:
301 unique CDR3
7 unique J



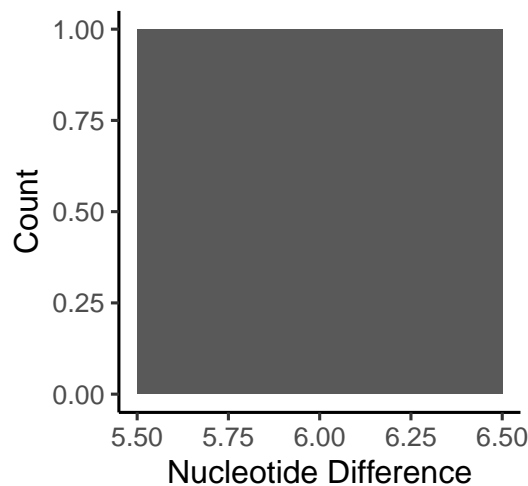
IGHV3-20*03_04

182 sequences assigned
No exact matches.



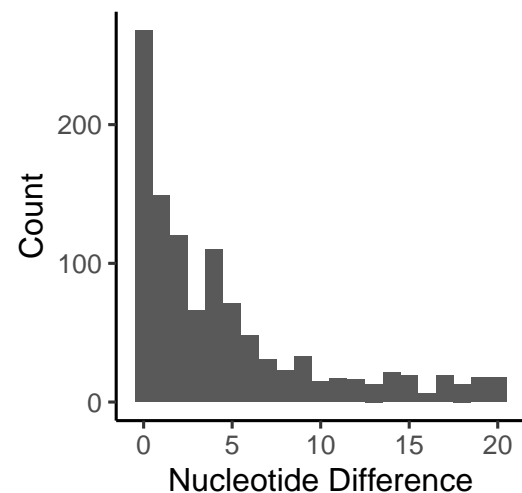
IGHV3-25*04

1 sequences assigned
No exact matches.



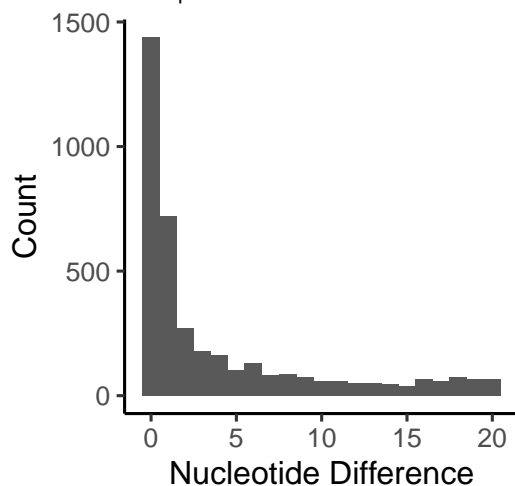
IGHV3-30*03_T288C

1281 sequences assigned
268 (20.9%) exact matches, in which:
268 unique CDR3
7 unique J



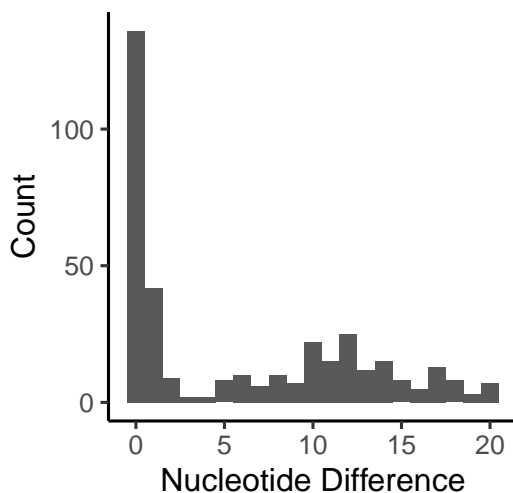
IGHV3-33*01

4753 sequences assigned
1438 (30.3%) exact matches, in which:
1317 unique CDR3
7 unique J



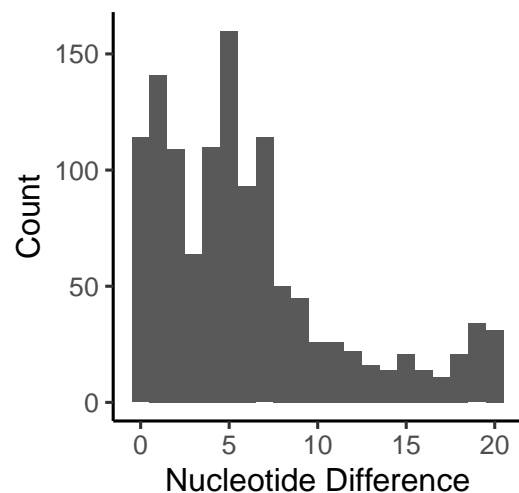
IGHV3-43*01

461 sequences assigned
136 (29.5%) exact matches, in which:
126 unique CDR3
7 unique J



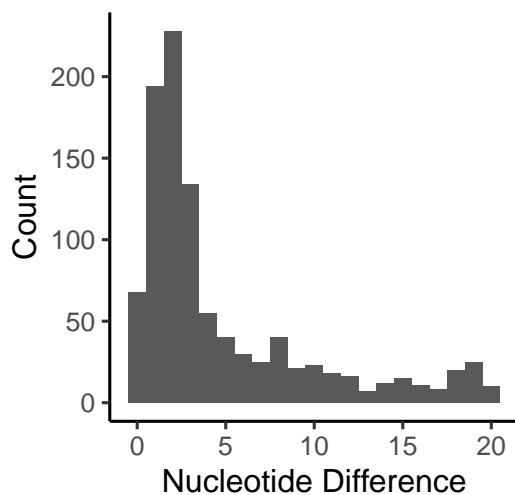
IGHV3-48*01

1437 sequences assigned
114 (7.9%) exact matches, in which:
114 unique CDR3
7 unique J



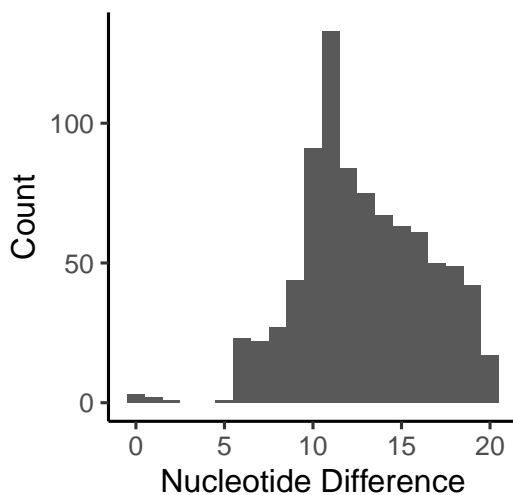
IGHV3-33*06

1121 sequences assigned
68 (6.1%) exact matches, in which:
68 unique CDR3
7 unique J



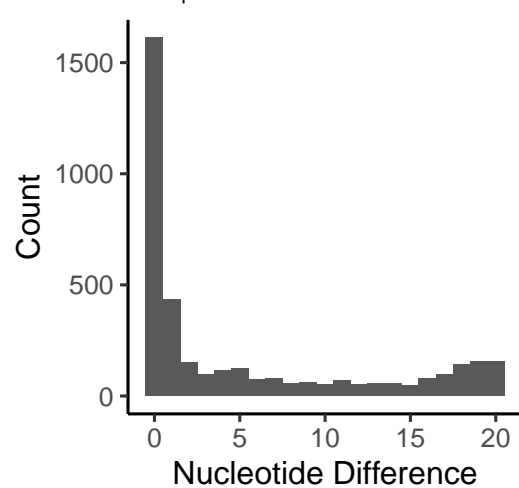
IGHV3-43*02

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



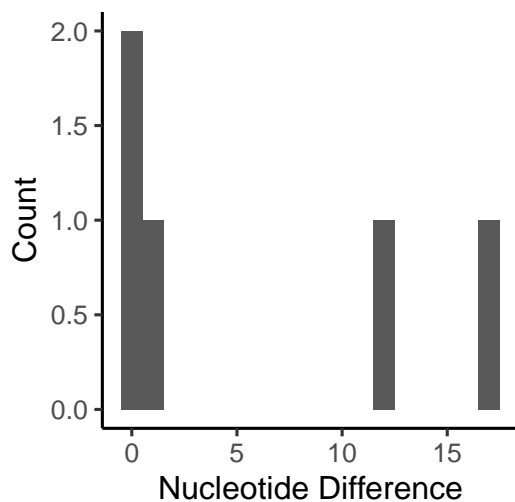
IGHV3-48*02

5011 sequences assigned
1612 (32.2%) exact matches, in which:
1442 unique CDR3
7 unique J



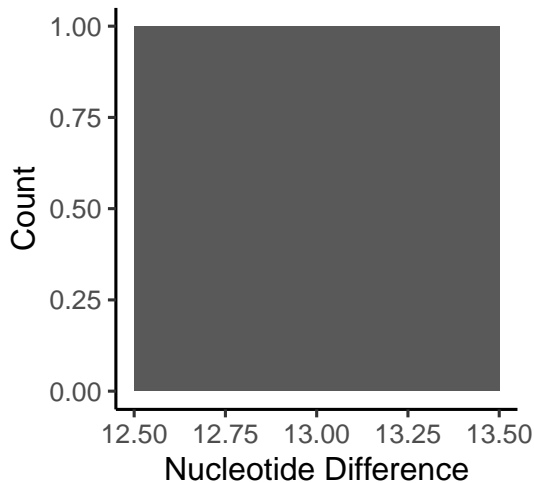
IGHV3-35*01

5 sequences assigned
2 (40%) exact matches, in which:
2 unique CDR3
1 unique J



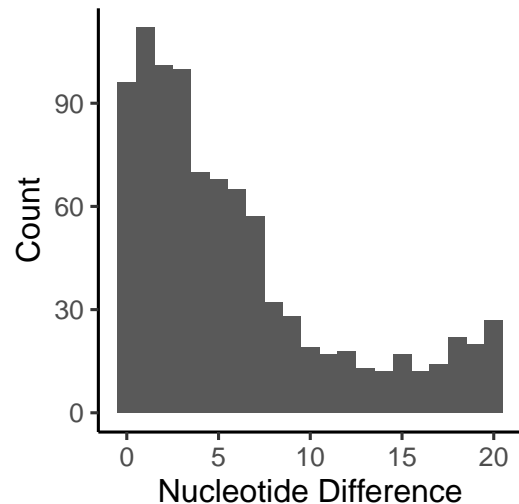
IGHV3-47*02

1 sequences assigned
No exact matches.



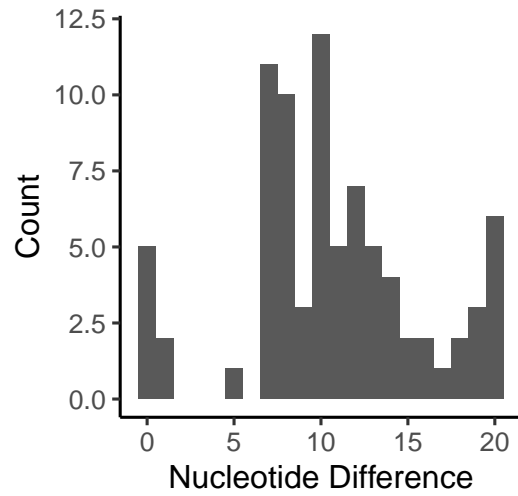
IGHV3-48*04

1263 sequences assigned
96 (7.6%) exact matches, in which:
96 unique CDR3
6 unique J



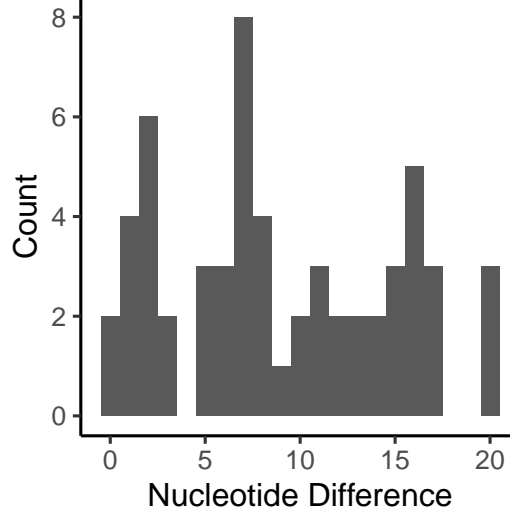
IGHV3-49*04

261 sequences assigned
5 (1.9%) exact matches, in which:
3 unique CDR3
2 unique J



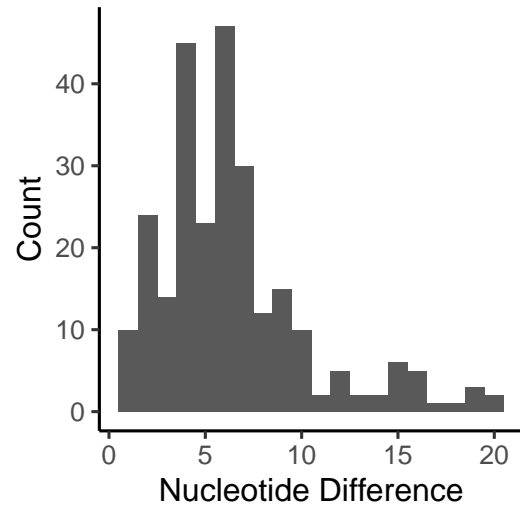
IGHV3-53*05

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



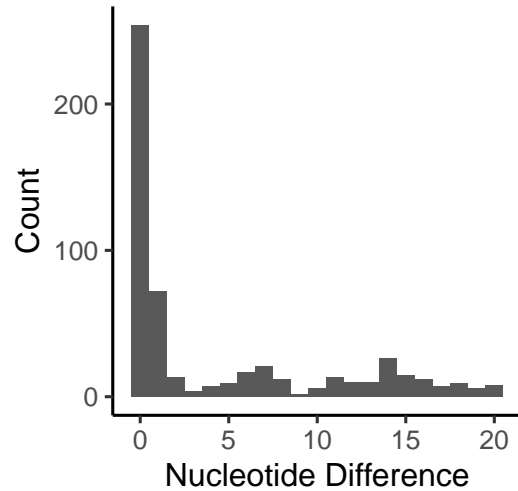
IGHV3-64*04

287 sequences assigned
No exact matches.



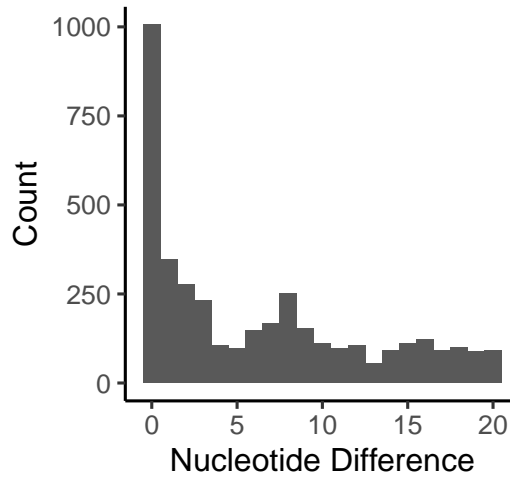
IGHV3-49*03_05

630 sequences assigned
254 (40.3%) exact matches, in which:
241 unique CDR3
7 unique J



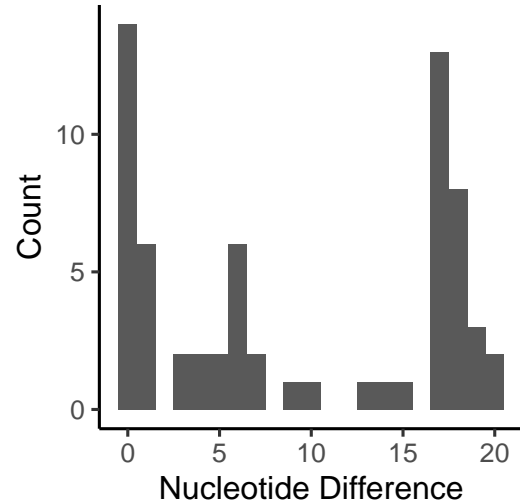
IGHV3-53*01_02

5042 sequences assigned
1006 (20%) exact matches, in which:
914 unique CDR3
7 unique J



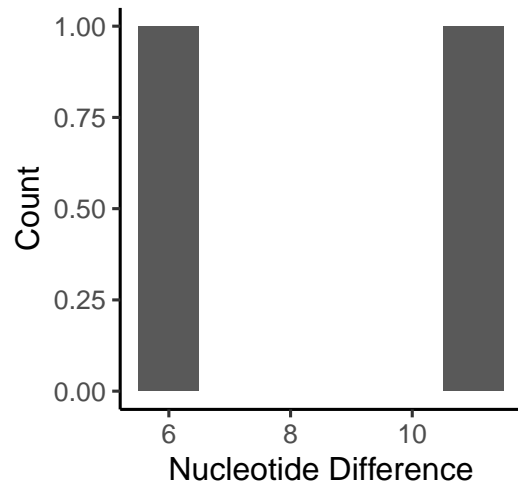
IGHV3-64*02_07

99 sequences assigned
14 (14.1%) exact matches, in which:
13 unique CDR3
4 unique J



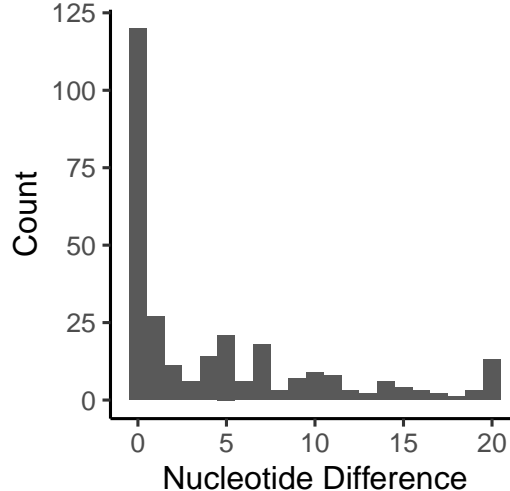
IGHV3-52*01_03

2 sequences assigned
No exact matches.



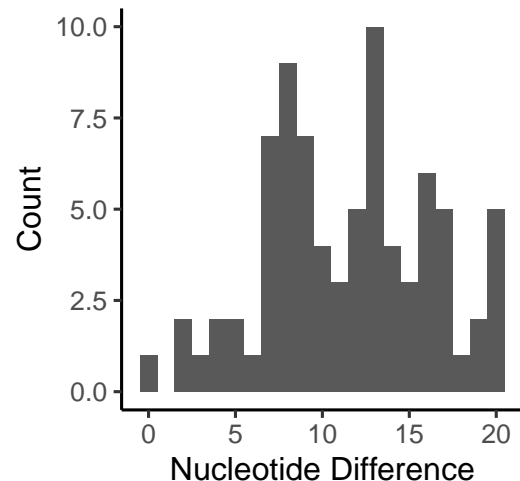
IGHV3-64*01

332 sequences assigned
120 (36.1%) exact matches, in which:
107 unique CDR3
7 unique J



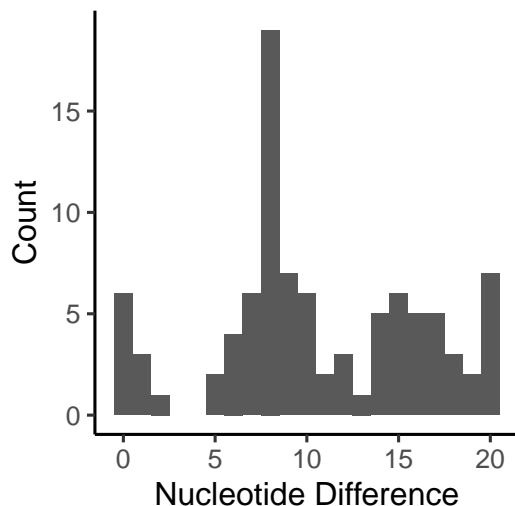
IGHV3-66*01

115 sequences assigned
1 (0.9%) exact matches, in which:
1 unique CDR3
1 unique J



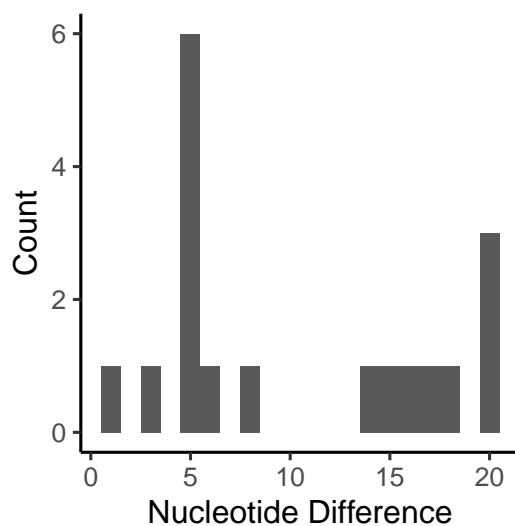
IGHV3-66*02

192 sequences assigned
6 (3.1%) exact matches, in which:
4 unique CDR3
2 unique J



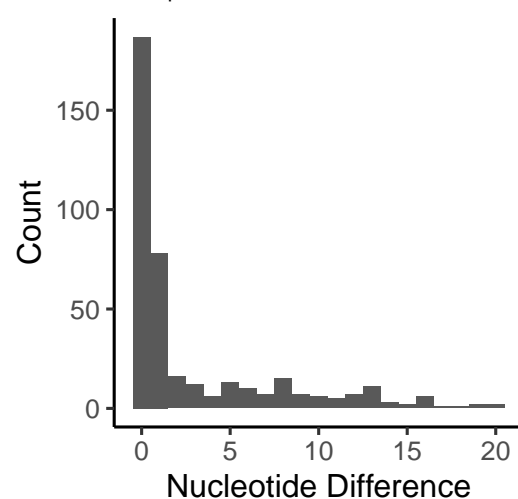
IGHV3-69-1*02

46 sequences assigned
No exact matches.



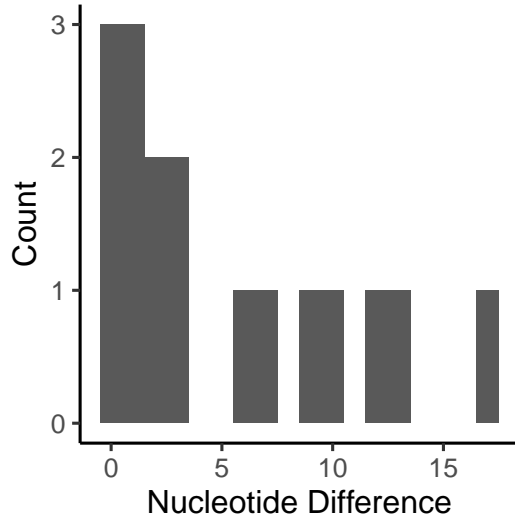
IGHV3-73*01_02

522 sequences assigned
187 (35.8%) exact matches, in which:
172 unique CDR3
7 unique J



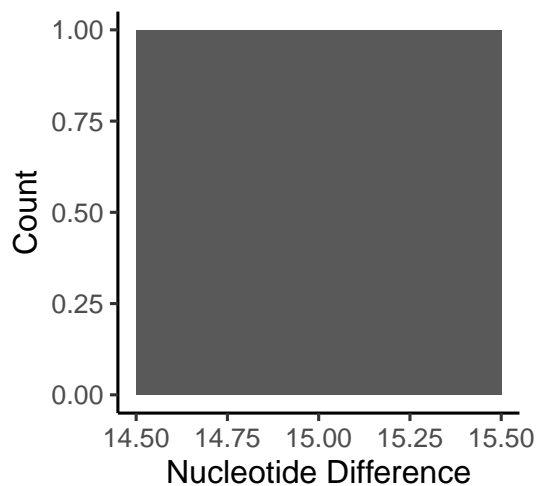
IGHV3-66*03

19 sequences assigned
3 (15.8%) exact matches, in which:
3 unique CDR3
2 unique J



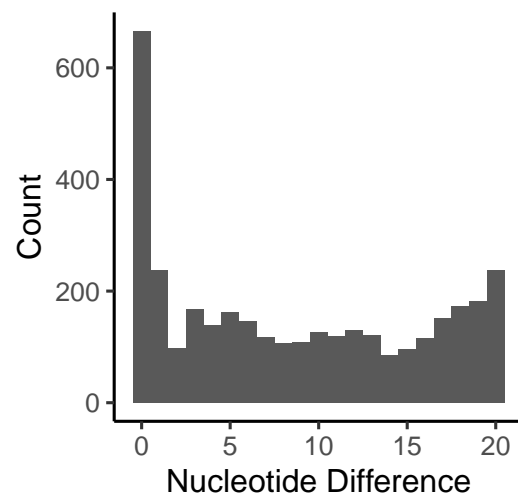
IGHV3-71*01_04

2 sequences assigned
No exact matches.



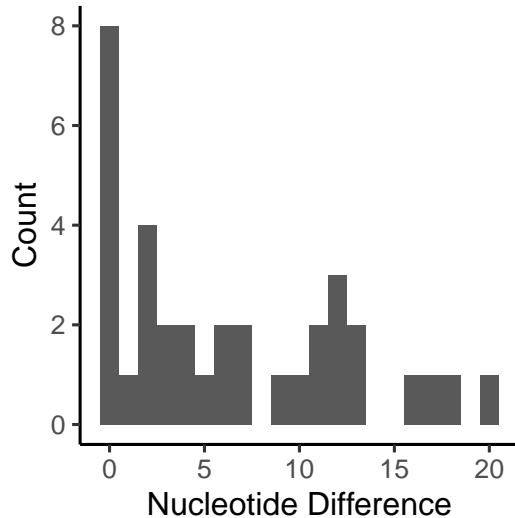
IGHV3-74*01_02

5659 sequences assigned
666 (11.8%) exact matches, in which:
595 unique CDR3
7 unique J



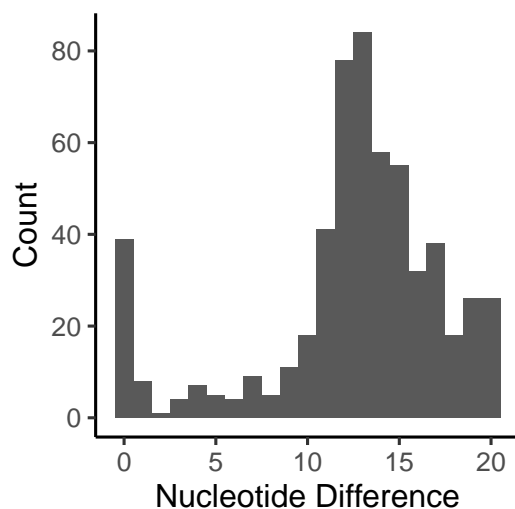
IGHV3-69-1*01

56 sequences assigned
8 (14.3%) exact matches, in which:
8 unique CDR3
6 unique J



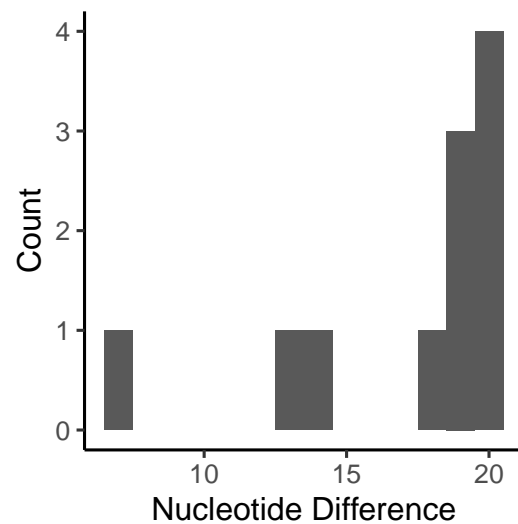
IGHV3-72*01

767 sequences assigned
39 (5.1%) exact matches, in which:
35 unique CDR3
5 unique J



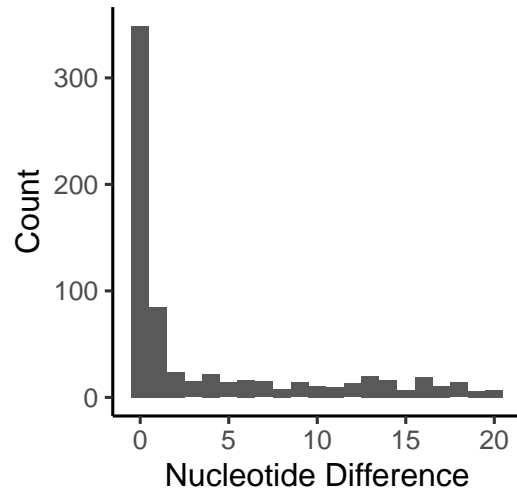
IGHV3-43D*04

17 sequences assigned
No exact matches.



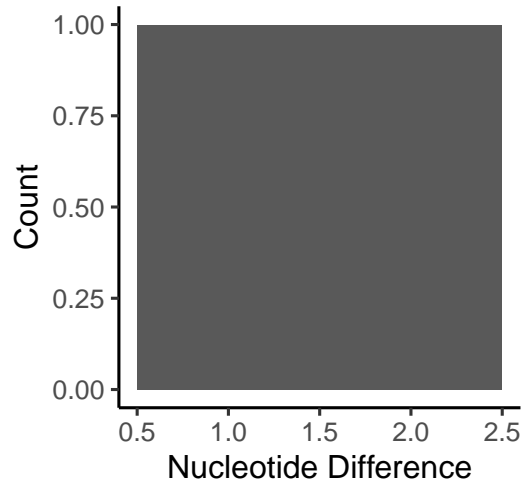
IGHV3-64D*06

785 sequences assigned
349 (44.5%) exact matches, in which:
309 unique CDR3
7 unique J



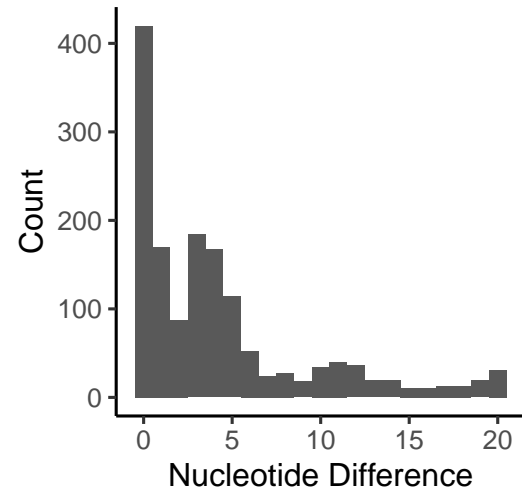
IGHV4-28*03

2 sequences assigned
No exact matches.



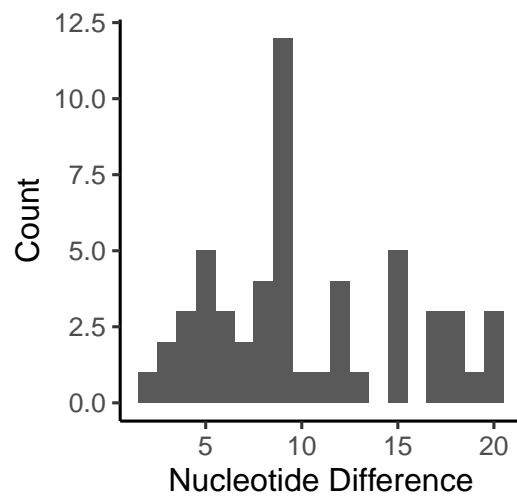
IGHV4-30-4*01

1871 sequences assigned
420 (22.4%) exact matches, in which:
410 unique CDR3
7 unique J



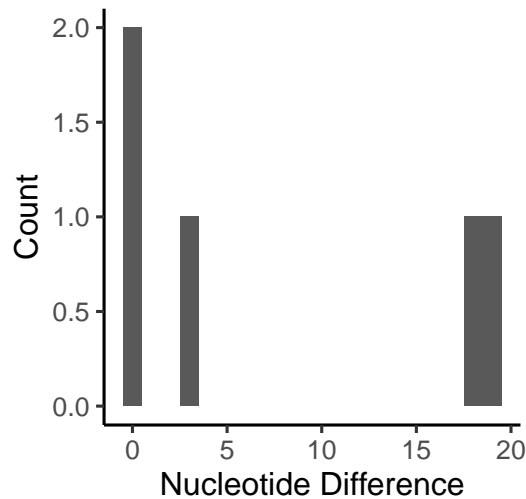
IGHV3-NL1*01

74 sequences assigned
No exact matches.



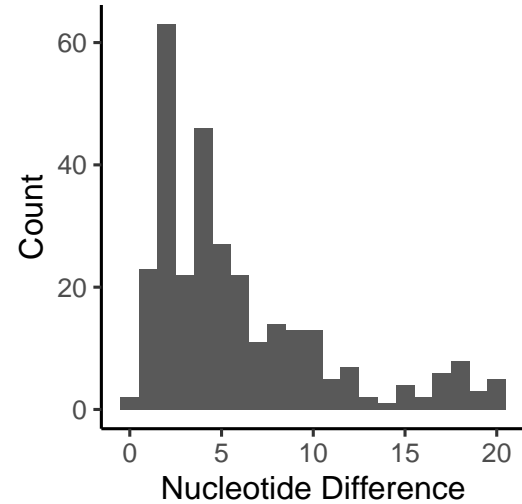
IGHV4-28*01_07

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



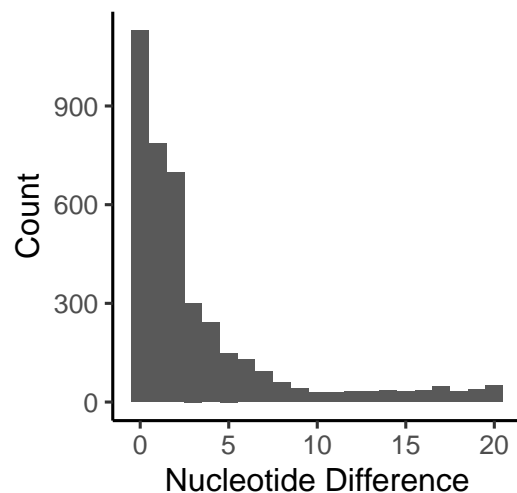
IGHV4-30-4*08

350 sequences assigned
2 (0.6%) exact matches, in which:
2 unique CDR3
2 unique J



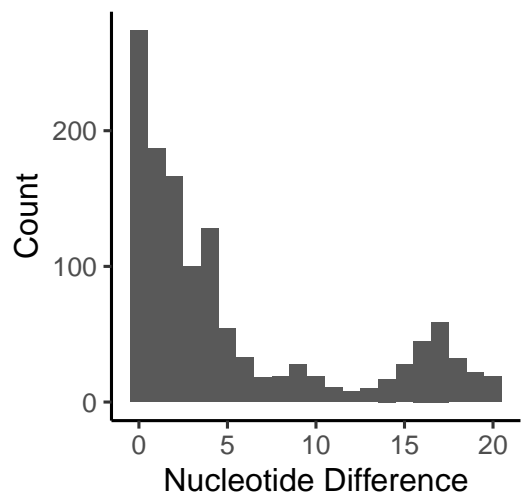
IGHV4-4*07

5263 sequences assigned
1130 (21.5%) exact matches, in which:
1106 unique CDR3
7 unique J



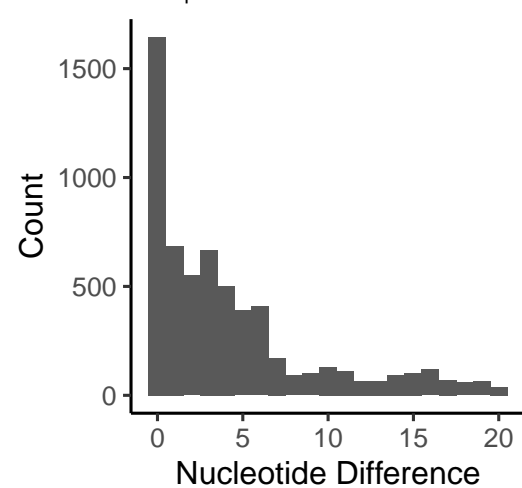
IGHV4-30-2*01

1377 sequences assigned
274 (19.9%) exact matches, in which:
262 unique CDR3
7 unique J



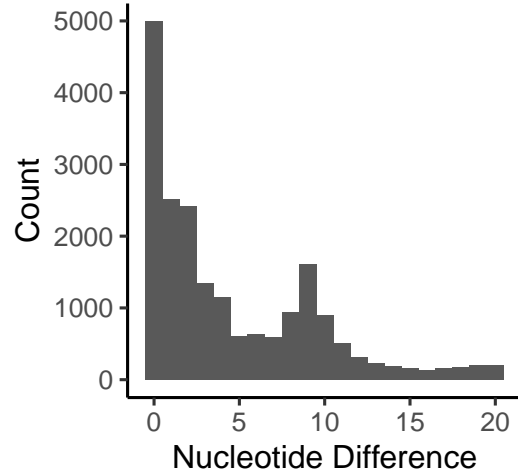
IGHV4-31*03_04

6974 sequences assigned
1645 (23.6%) exact matches, in which:
1606 unique CDR3
7 unique J



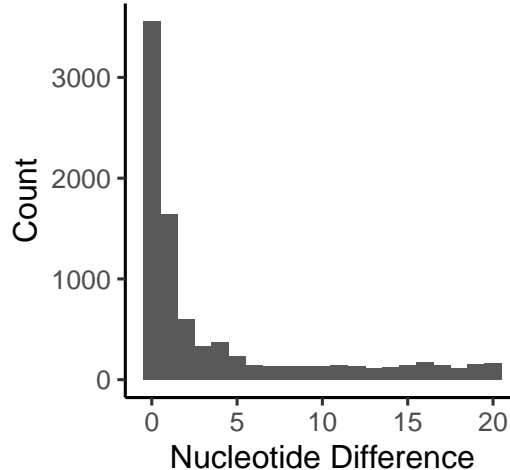
IGHV4-34*01_02

22502 sequences assigned
4993 (22.2%) exact matches, in which:
4751 unique CDR3
7 unique J



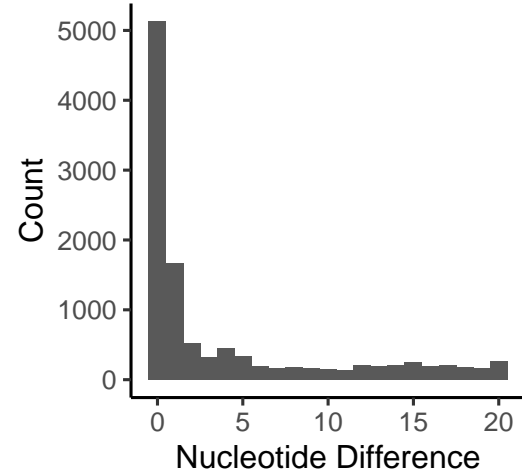
IGHV4-39*01_05

11426 sequences assigned
3556 (31.1%) exact matches, in which:
3415 unique CDR3
7 unique J



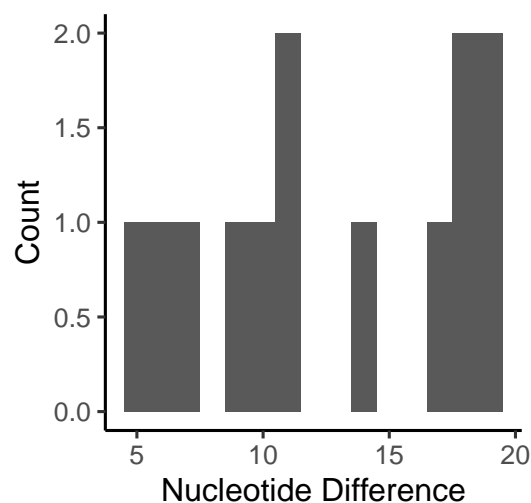
IGHV4-59*01_07

14408 sequences assigned
5129 (35.6%) exact matches, in which:
4958 unique CDR3
7 unique J



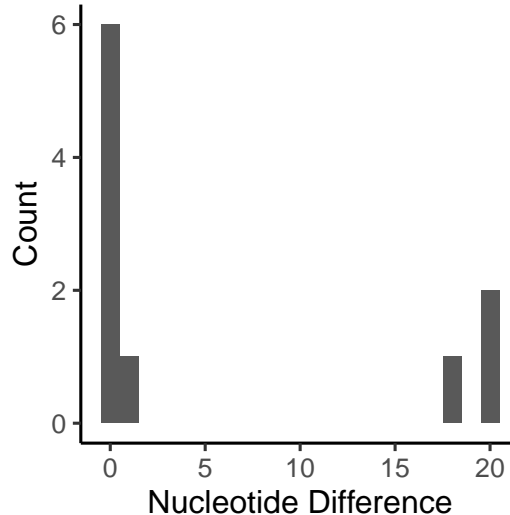
IGHV4-38-2*02

36 sequences assigned
No exact matches.



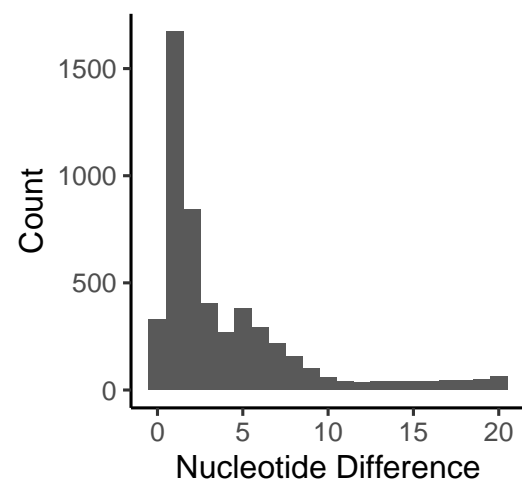
IGHV4-55*01_05

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



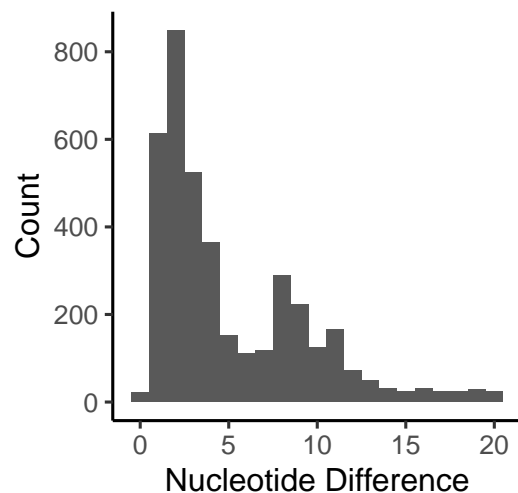
IGHV4-59*12

5885 sequences assigned
328 (5.6%) exact matches, in which:
326 unique CDR3
7 unique J



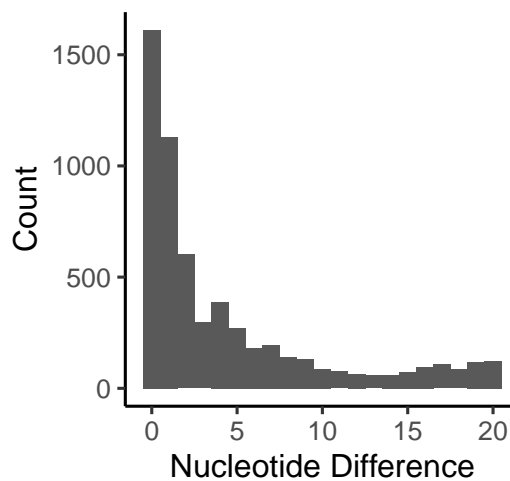
IGHV4-39*07

4082 sequences assigned
22 (0.5%) exact matches, in which:
22 unique CDR3
6 unique J



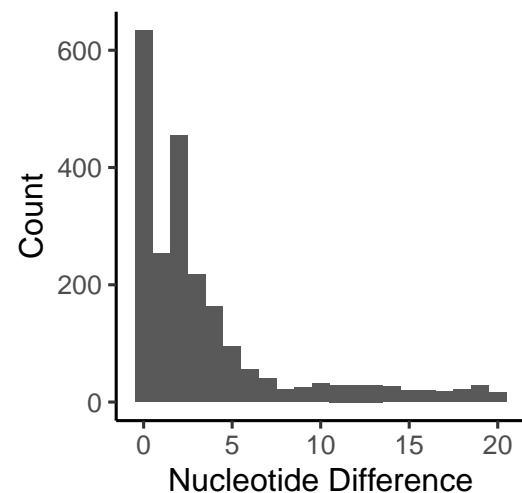
IGHV4-59*08

7814 sequences assigned
1611 (20.6%) exact matches, in which:
1573 unique CDR3
7 unique J



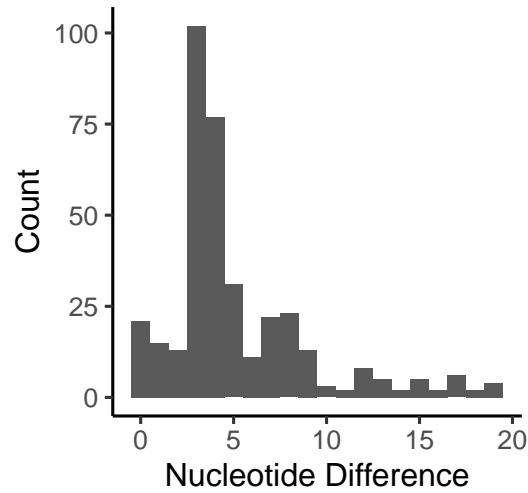
IGHV4-61*01

2580 sequences assigned
634 (24.6%) exact matches, in which:
626 unique CDR3
7 unique J



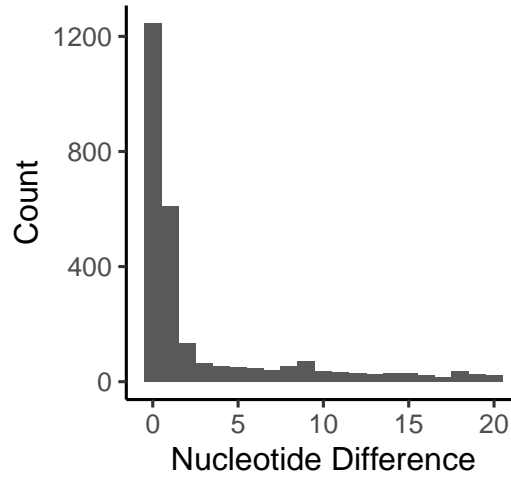
IGHV4-61*02

403 sequences assigned
21 (5.2%) exact matches, in which:
20 unique CDR3
4 unique J



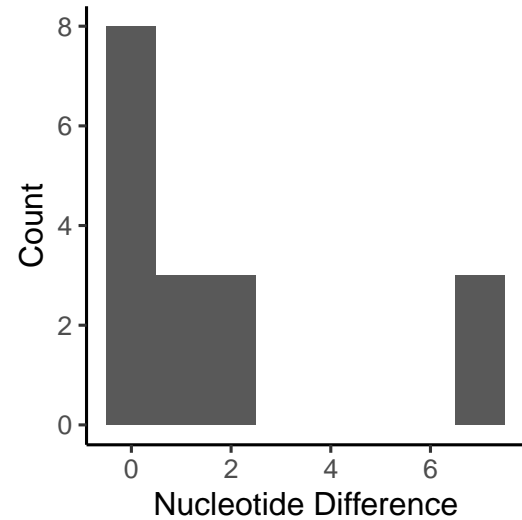
IGHV5-10-1*01_03

2918 sequences assigned
1245 (42.7%) exact matches, in which:
1119 unique CDR3
7 unique J



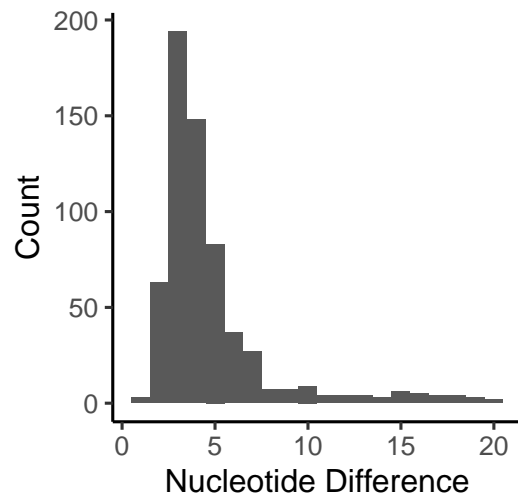
IGHV7-4-1*01

19 sequences assigned
8 (42.1%) exact matches, in which:
7 unique CDR3
3 unique J



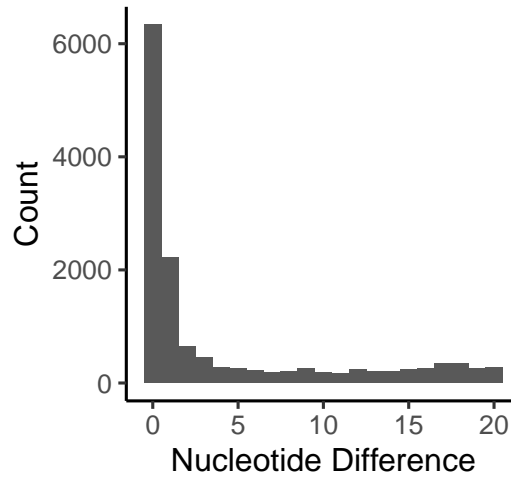
IGHV4-61*05

660 sequences assigned
No exact matches.



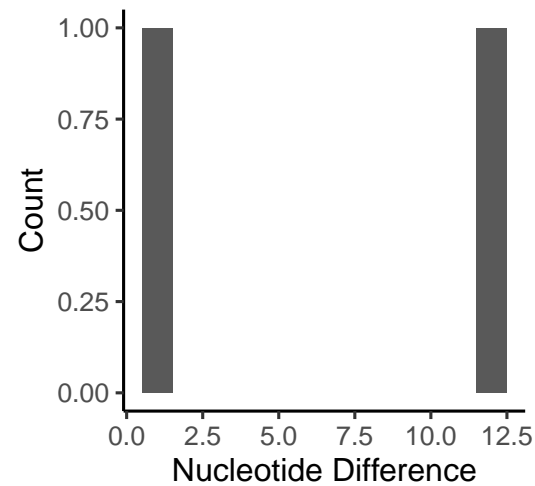
IGHV5-51*01_03

16409 sequences assigned
6336 (38.6%) exact matches, in which:
5126 unique CDR3
7 unique J



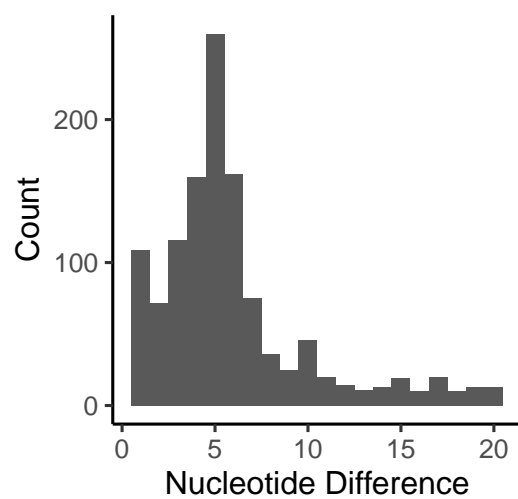
IGHV7-4-1*02

4 sequences assigned
No exact matches.



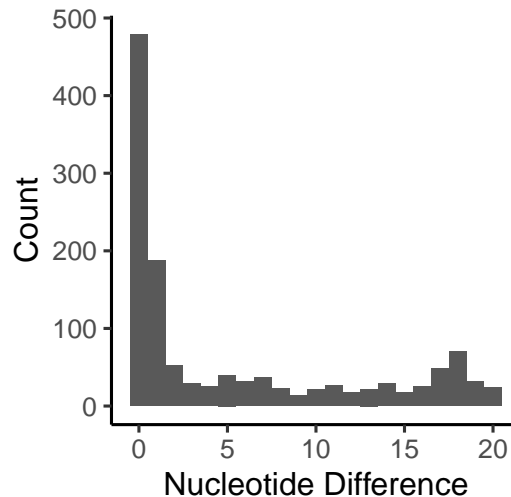
IGHV4-61*08

1387 sequences assigned
No exact matches.

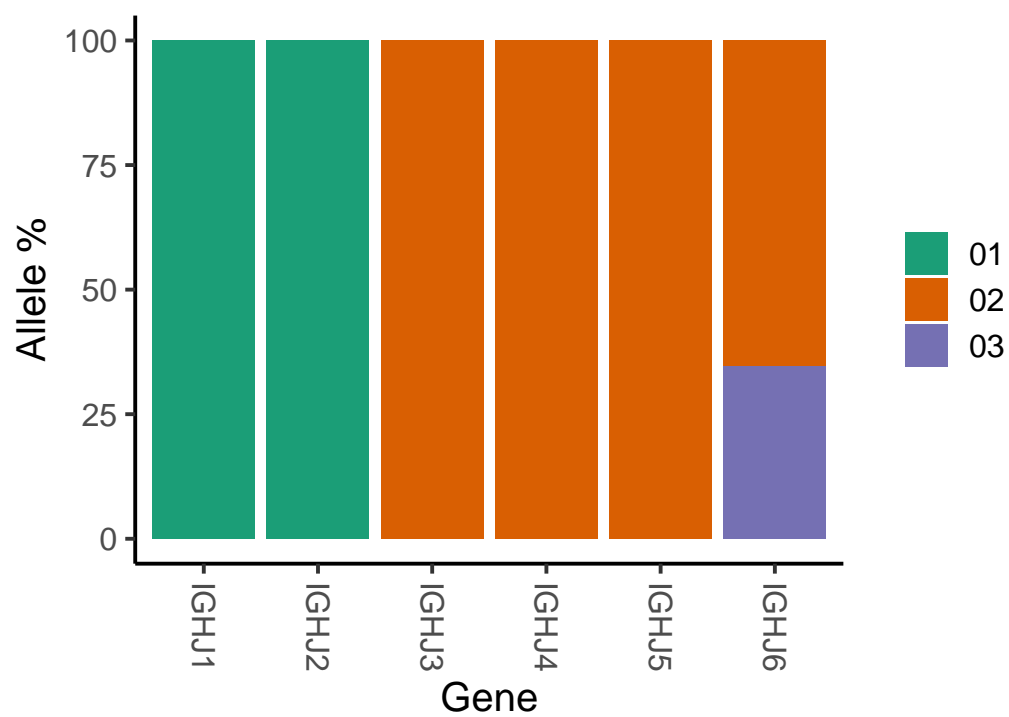


IGHV6-1*01_02

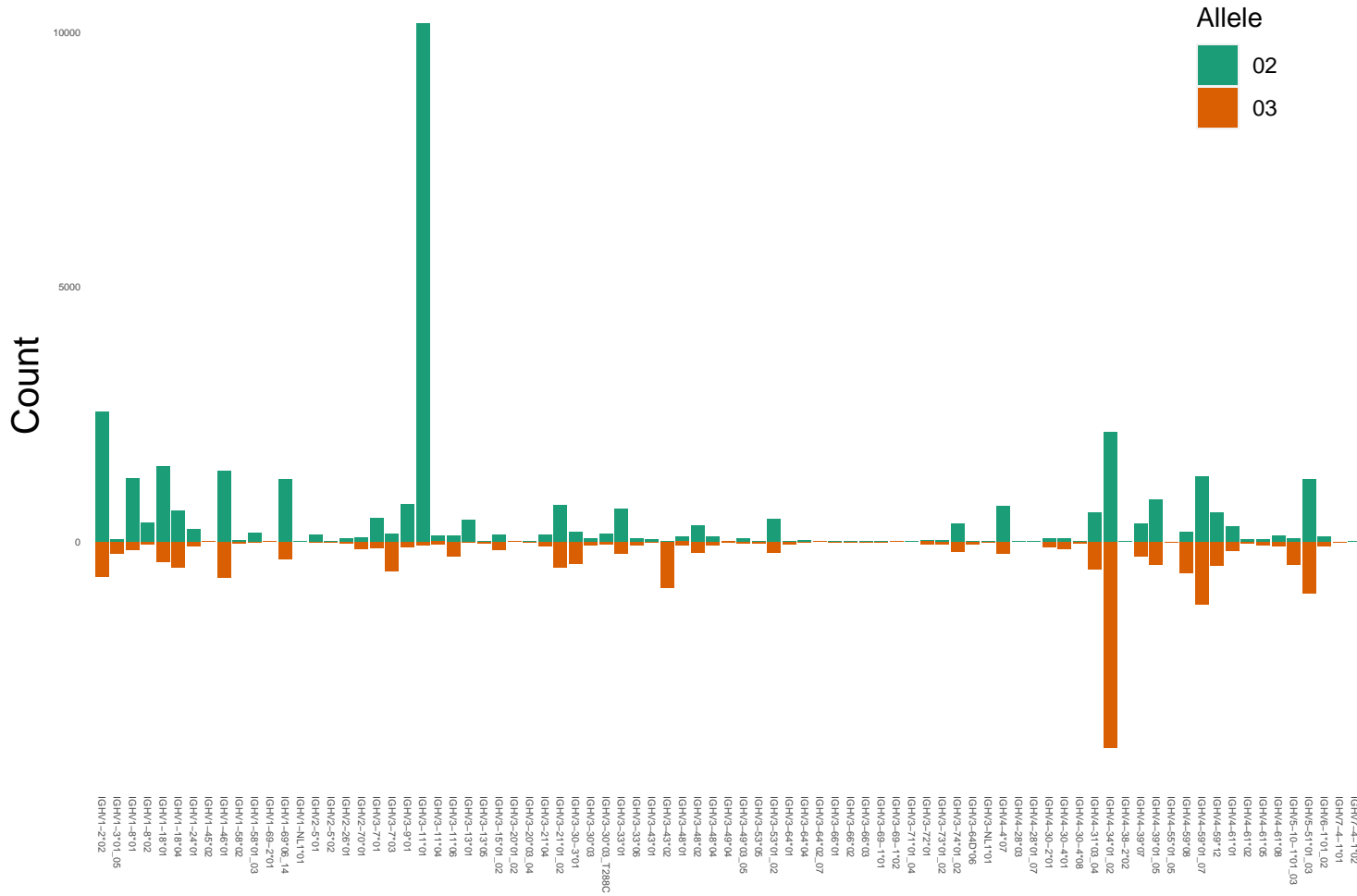
1725 sequences assigned
479 (27.8%) exact matches, in which:
469 unique CDR3
7 unique J



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.