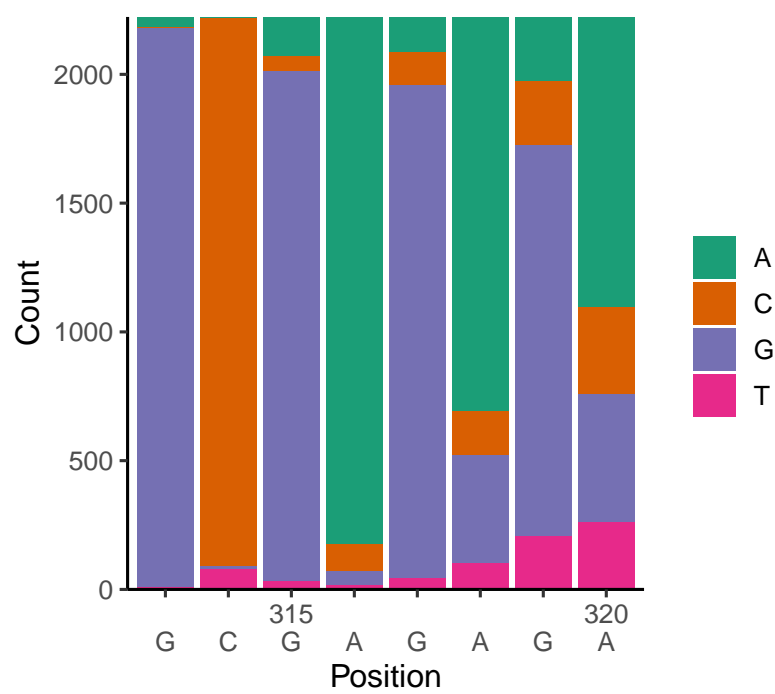
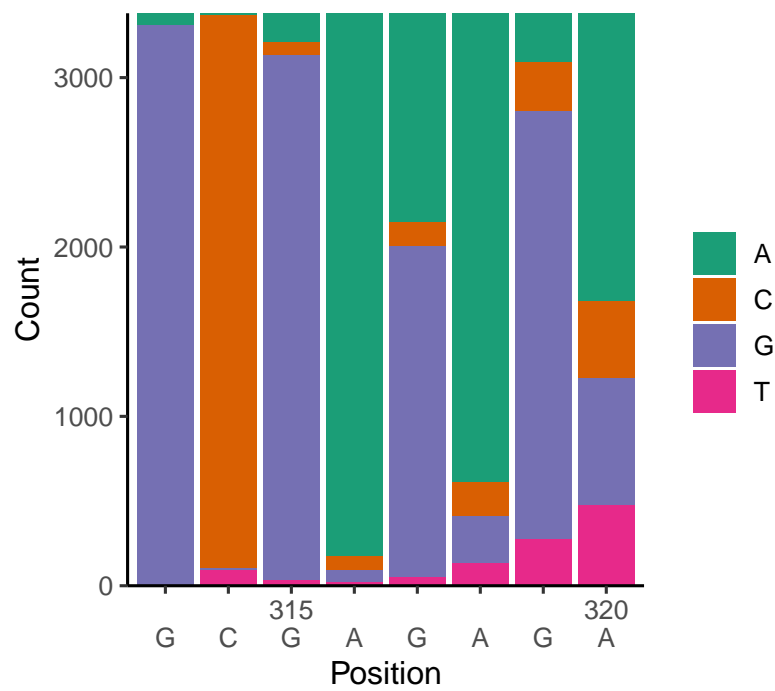


Gene IGHV3-30*03_T288C



Gene IGHV3-30-3*01_T288C



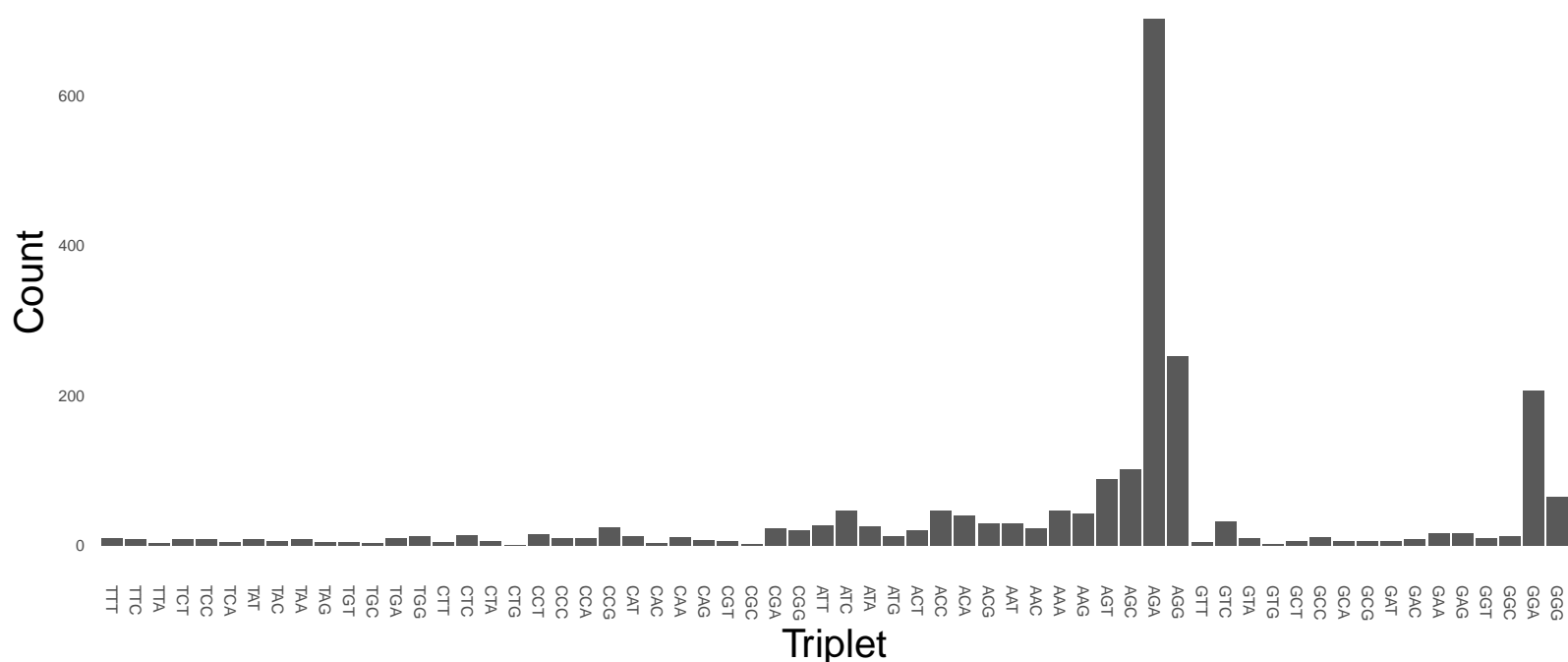
Gene IGHV3-30*03_T288C



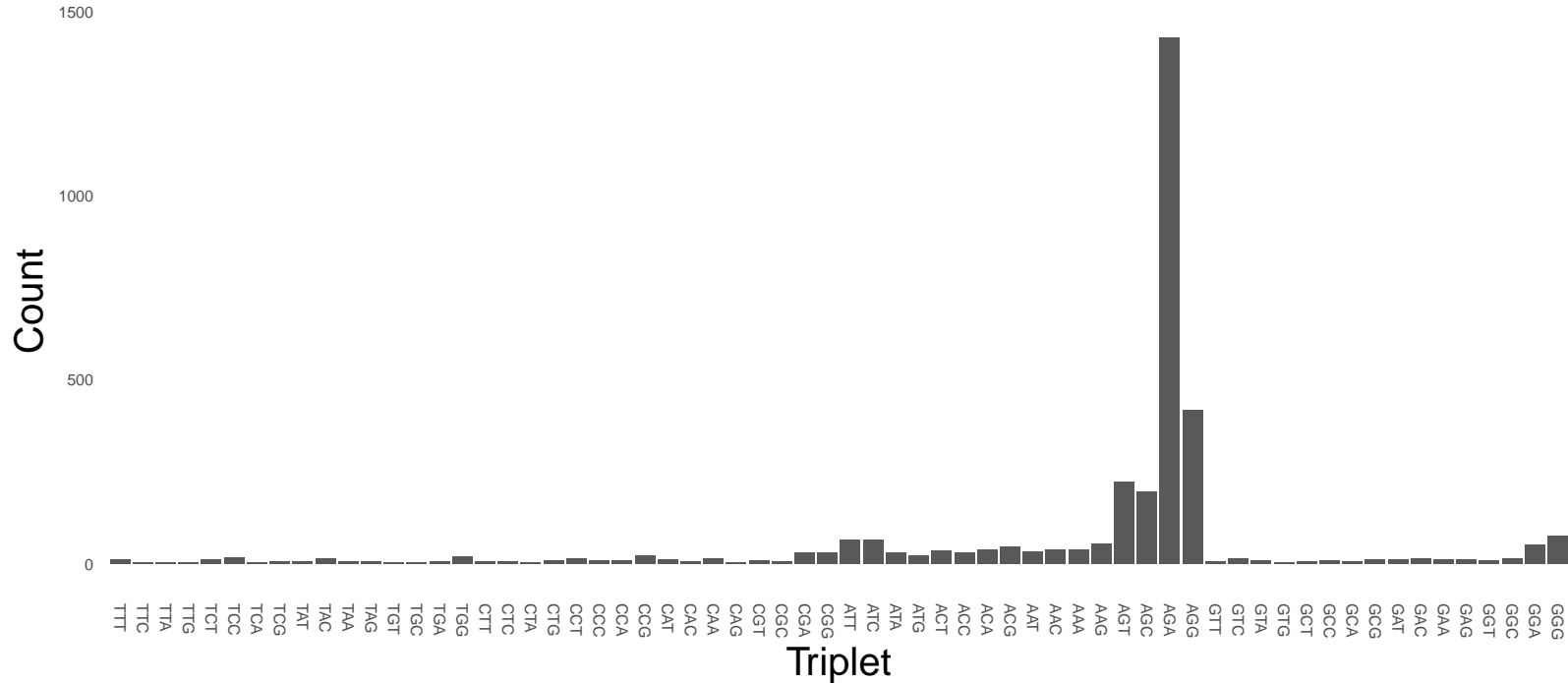
Gene IGHV3-30-3*01_T288C



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

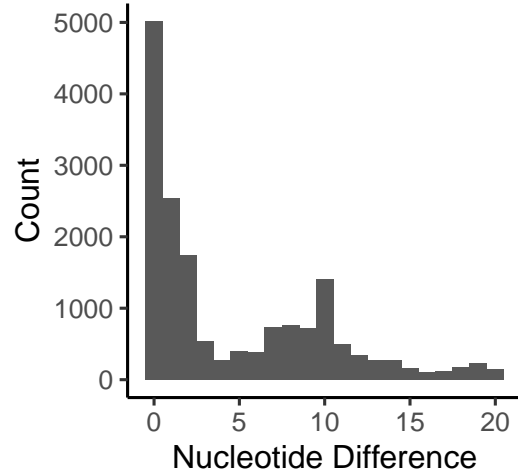


IGHV3-30-3*01_T288C- Final 3 nucleotides as a triplet



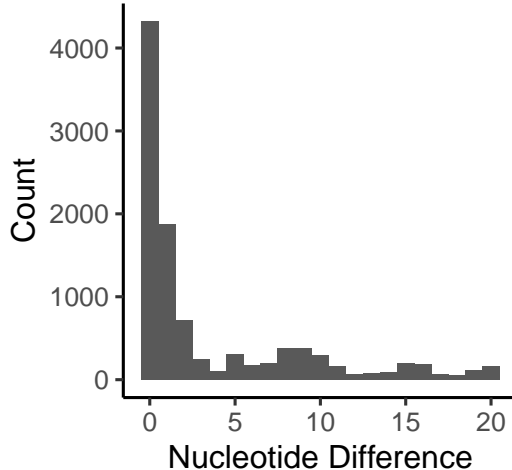
IGHV1-2*02

19274 sequences assigned
5014 (26%) exact matches, in which:
4707 unique CDR3
6 unique J



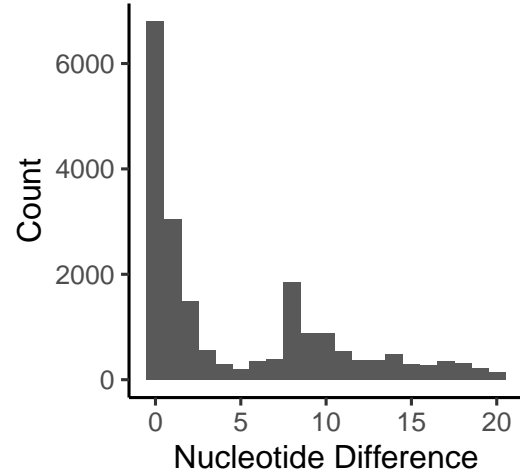
IGHV1-8*01

10470 sequences assigned
4321 (41.3%) exact matches, in which:
4065 unique CDR3
6 unique J



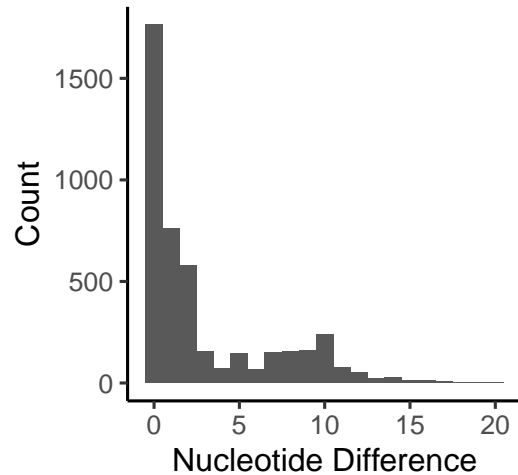
IGHV1-18*04

21116 sequences assigned
6799 (32.2%) exact matches, in which:
6397 unique CDR3
6 unique J



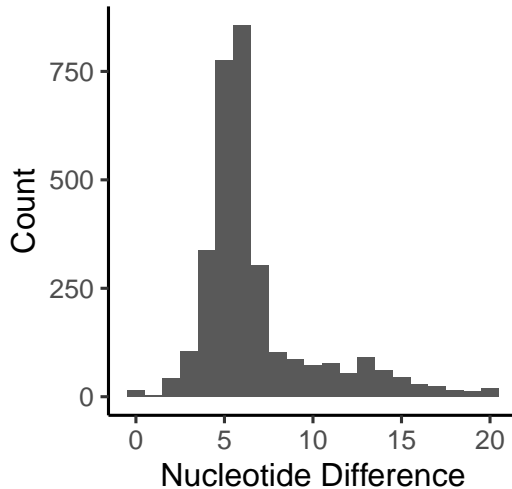
IGHV1-2*04

4497 sequences assigned
1764 (39.2%) exact matches, in which:
1659 unique CDR3
6 unique J



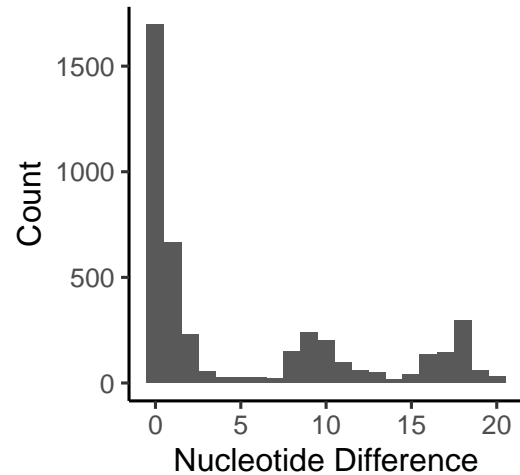
IGHV1-8*02

3234 sequences assigned
16 (0.5%) exact matches, in which:
16 unique CDR3
4 unique J



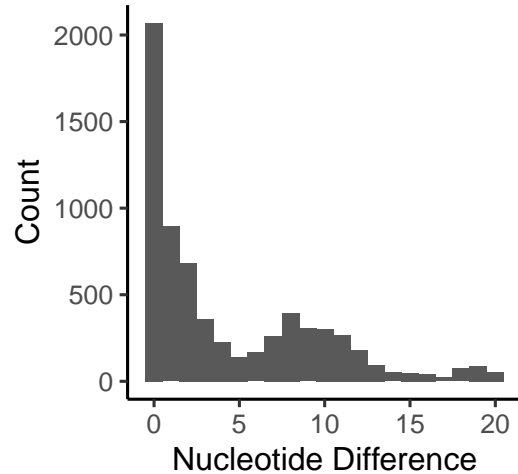
IGHV1-24*01

4678 sequences assigned
1696 (36.3%) exact matches, in which:
1593 unique CDR3
6 unique J



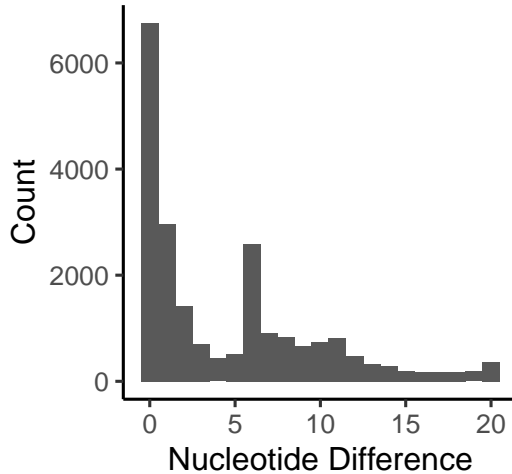
IGHV1-3*01_05

8145 sequences assigned
2069 (25.4%) exact matches, in which:
1890 unique CDR3
6 unique J



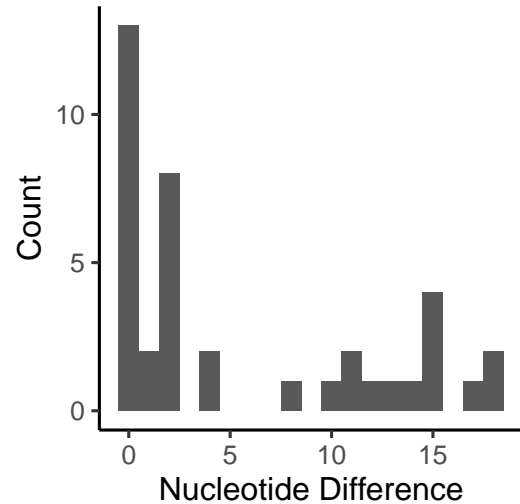
IGHV1-18*01

23697 sequences assigned
6752 (28.5%) exact matches, in which:
6372 unique CDR3
6 unique J



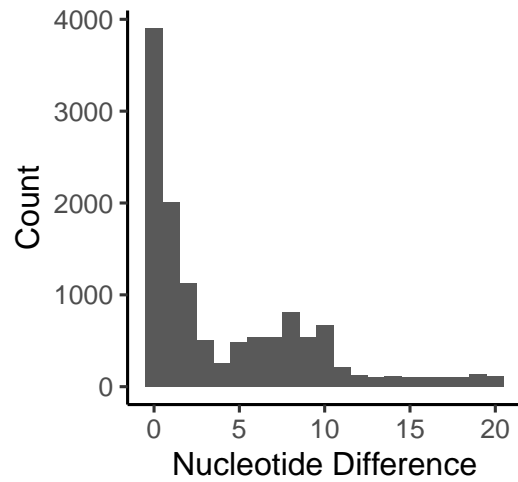
IGHV1-45*02

39 sequences assigned
13 (33.3%) exact matches, in which:
12 unique CDR3
3 unique J



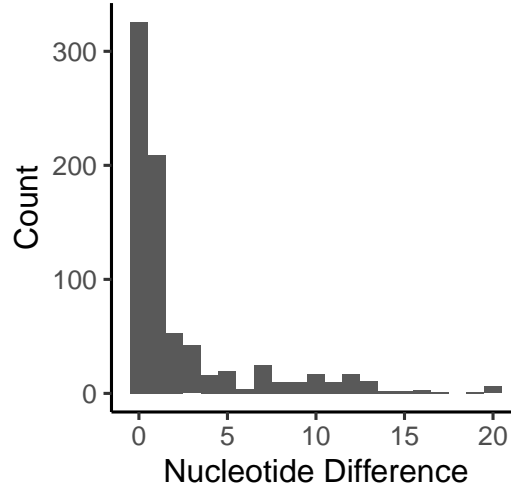
IGHV1-46*01

13740 sequences assigned
3901 (28.4%) exact matches, in which:
3688 unique CDR3
6 unique J



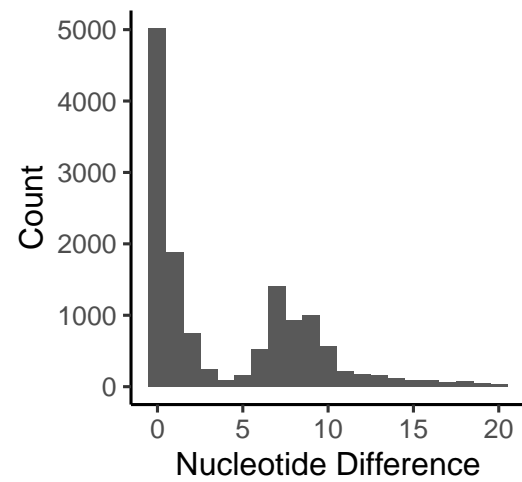
IGHV1-58*01_03

794 sequences assigned
326 (41.1%) exact matches, in which:
311 unique CDR3
6 unique J



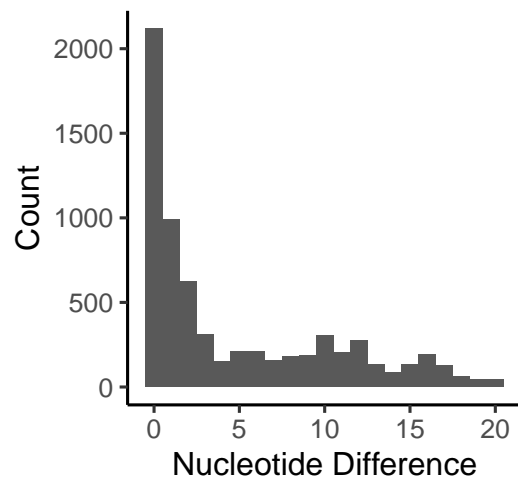
IGHV1-69*06_14

14301 sequences assigned
5017 (35.1%) exact matches, in which:
4776 unique CDR3
6 unique J



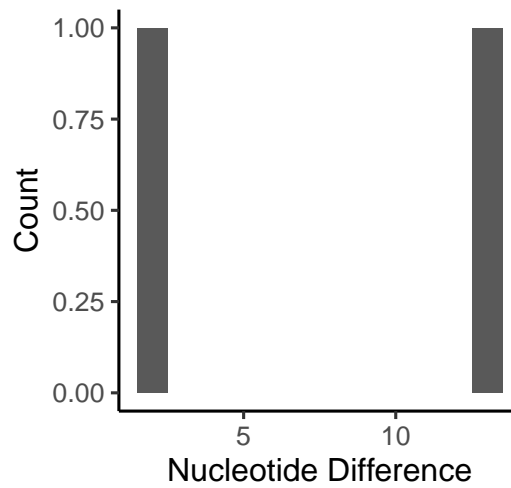
IGHV1-46*04

7436 sequences assigned
2118 (28.5%) exact matches, in which:
2011 unique CDR3
6 unique J



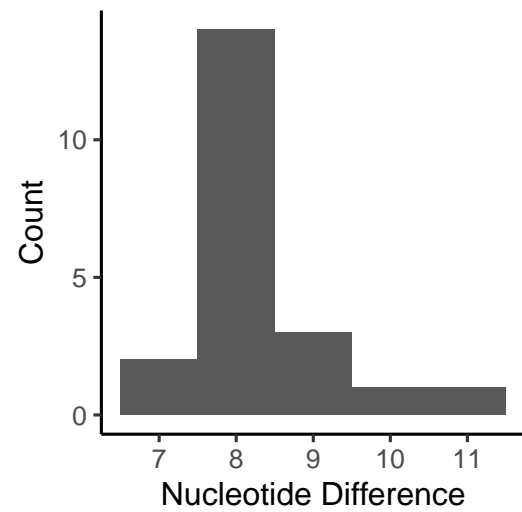
IGHV1-68*01

2 sequences assigned
No exact matches.



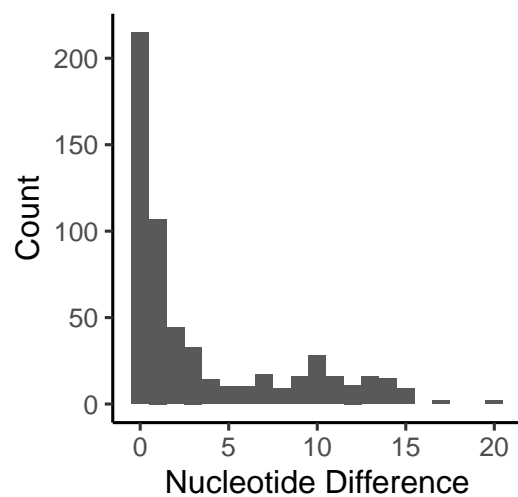
IGHV1-NL1*01

21 sequences assigned
No exact matches.



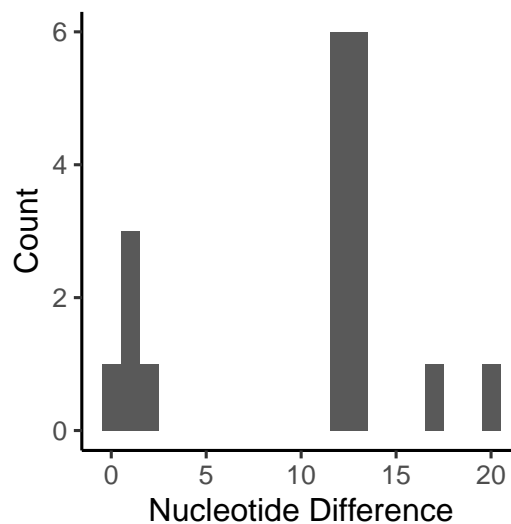
IGHV1-58*02

582 sequences assigned
215 (36.9%) exact matches, in which:
207 unique CDR3
6 unique J



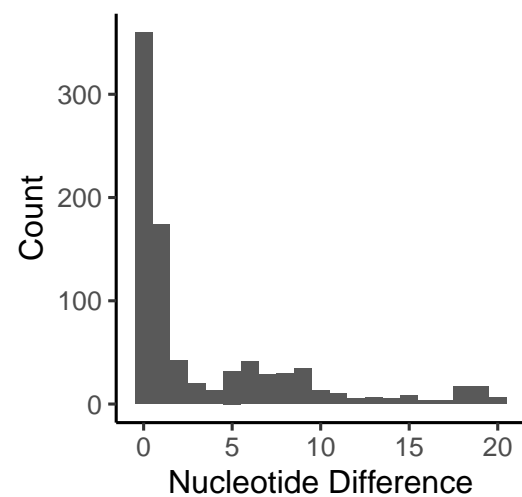
IGHV1-69-2*01

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



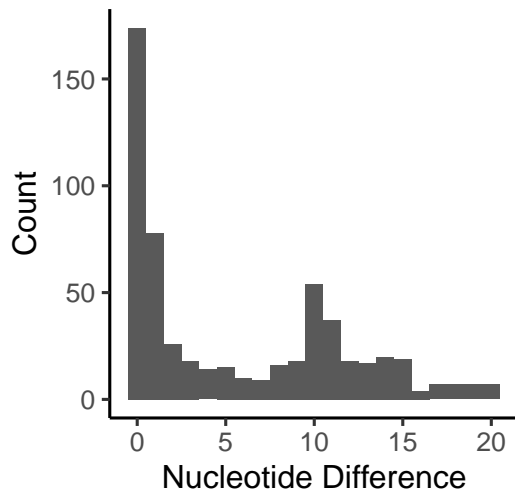
IGHV2-5*01

1034 sequences assigned
360 (34.8%) exact matches, in which:
336 unique CDR3
6 unique J



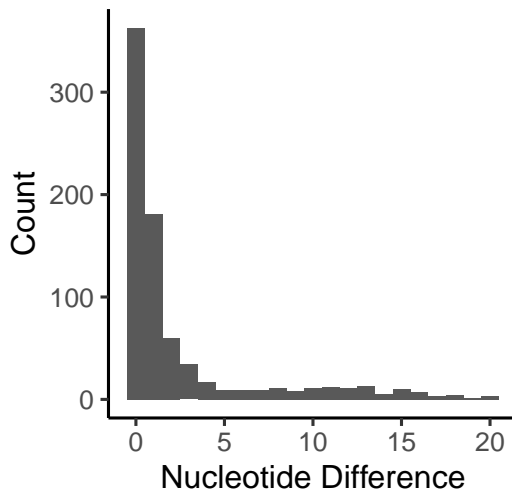
IGHV2-5*02

748 sequences assigned
174 (23.3%) exact matches, in which:
166 unique CDR3
6 unique J



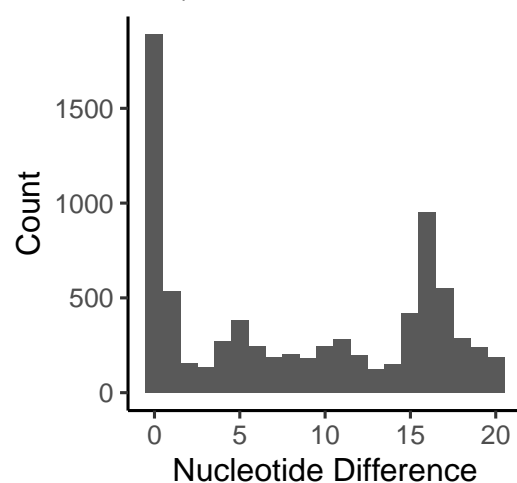
IGHV2-70*11_15

806 sequences assigned
363 (45%) exact matches, in which:
338 unique CDR3
5 unique J



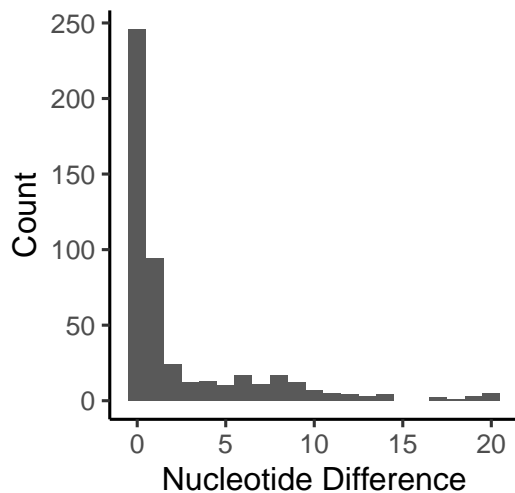
IGHV3-9*01

9401 sequences assigned
1890 (20.1%) exact matches, in which:
1424 unique CDR3
6 unique J



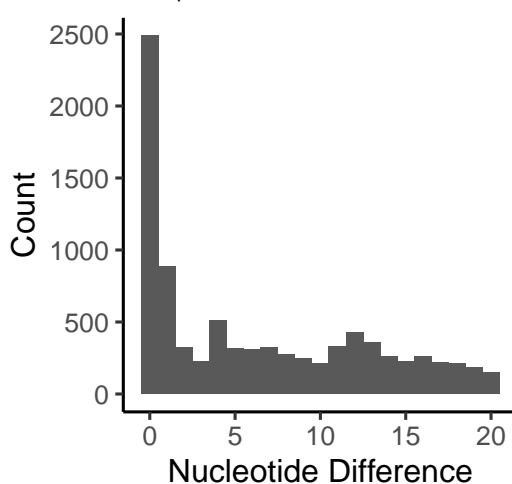
IGHV2-26*01

520 sequences assigned
246 (47.3%) exact matches, in which:
235 unique CDR3
5 unique J



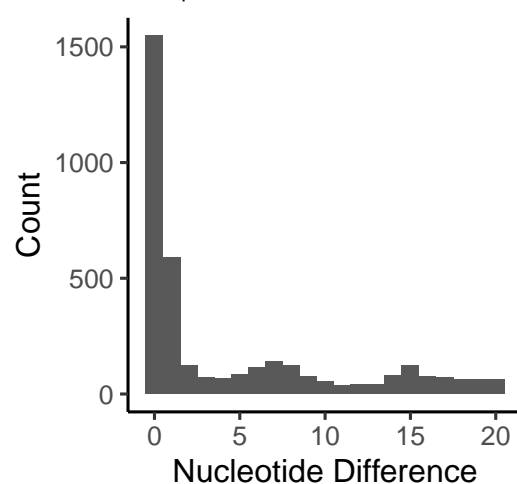
IGHV3-7*01

10584 sequences assigned
2488 (23.5%) exact matches, in which:
2035 unique CDR3
6 unique J



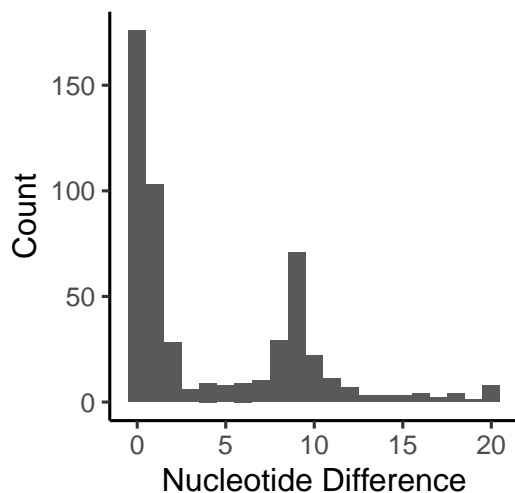
IGHV3-11*01

5979 sequences assigned
1548 (25.9%) exact matches, in which:
1231 unique CDR3
6 unique J



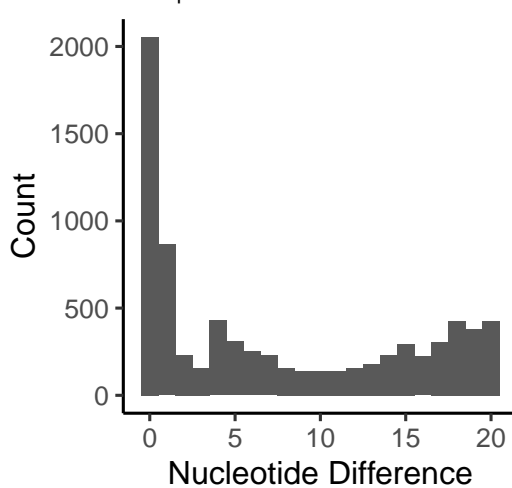
IGHV2-70*01

640 sequences assigned
176 (27.5%) exact matches, in which:
164 unique CDR3
6 unique J



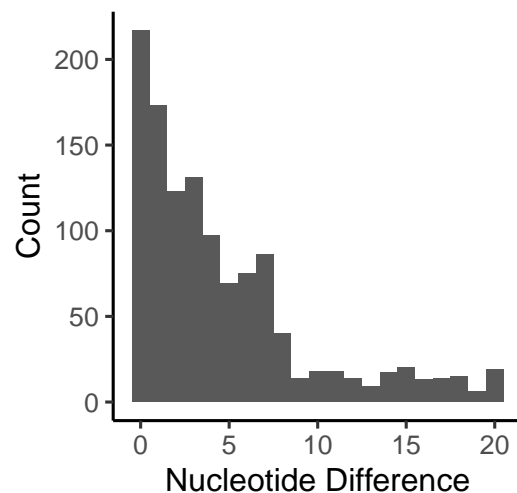
IGHV3-7*03

10318 sequences assigned
2054 (19.9%) exact matches, in which:
1600 unique CDR3
6 unique J



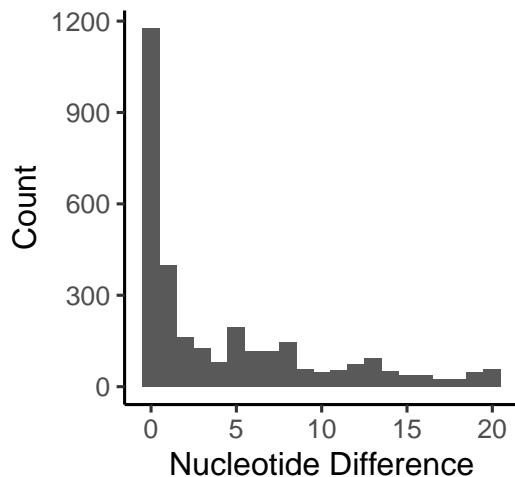
IGHV3-11*04

1314 sequences assigned
217 (16.5%) exact matches, in which:
215 unique CDR3
6 unique J



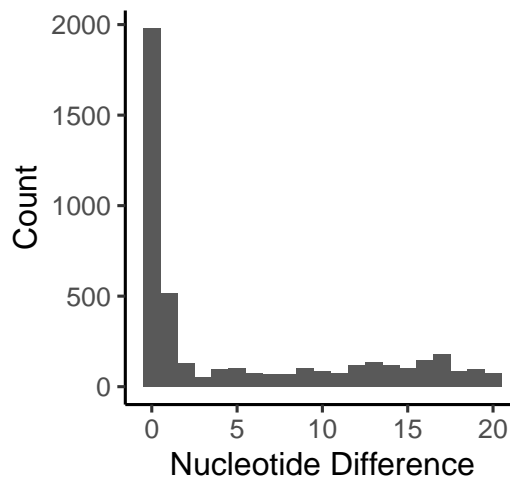
IGHV3-11*06

3754 sequences assigned
1176 (31.3%) exact matches, in which:
947 unique CDR3
6 unique J



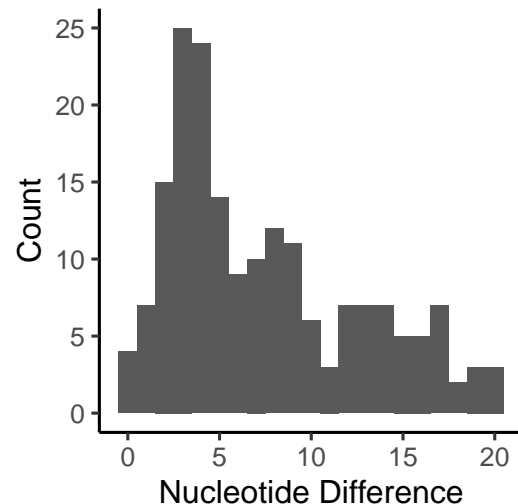
IGHV3-15*01_02

5221 sequences assigned
1979 (37.9%) exact matches, in which:
1630 unique CDR3
6 unique J



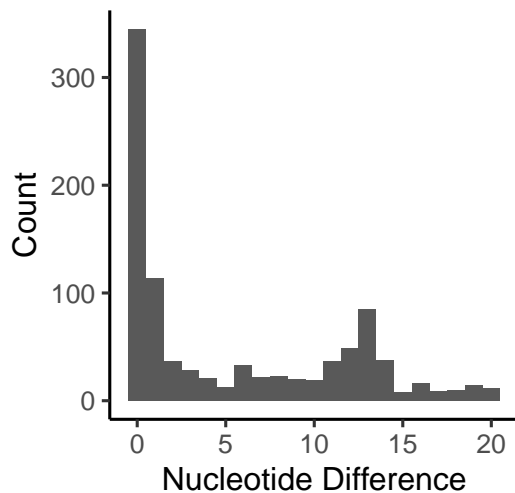
IGHV3-20*03_04

355 sequences assigned
4 (1.1%) exact matches, in which:
4 unique CDR3
3 unique J



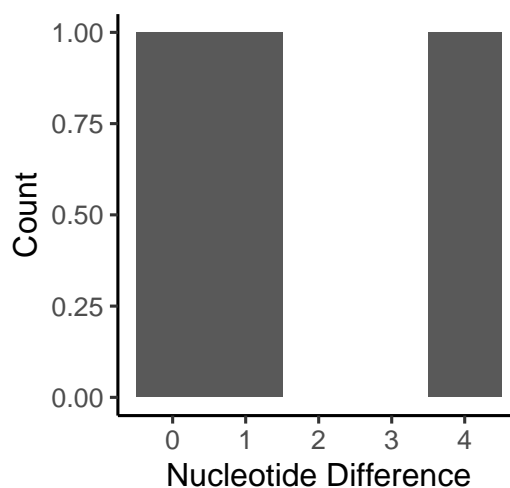
IGHV3-13*01

1339 sequences assigned
345 (25.8%) exact matches, in which:
263 unique CDR3
5 unique J



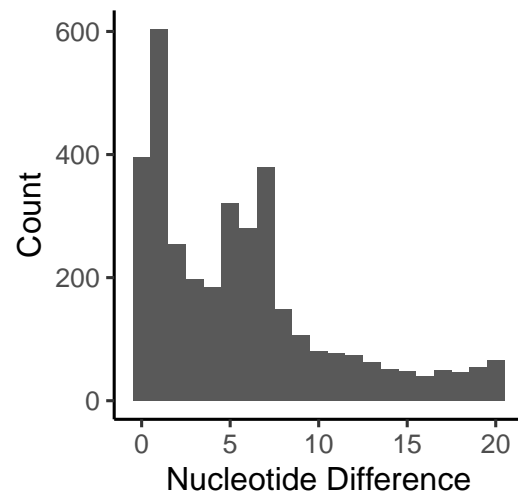
IGHV3-19*01

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



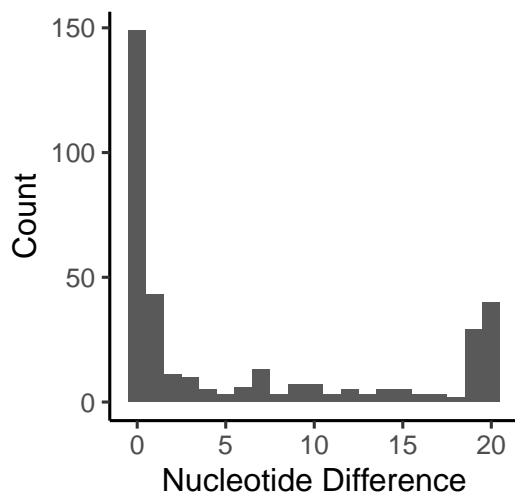
IGHV3-21*04

4149 sequences assigned
395 (9.5%) exact matches, in which:
382 unique CDR3
6 unique J



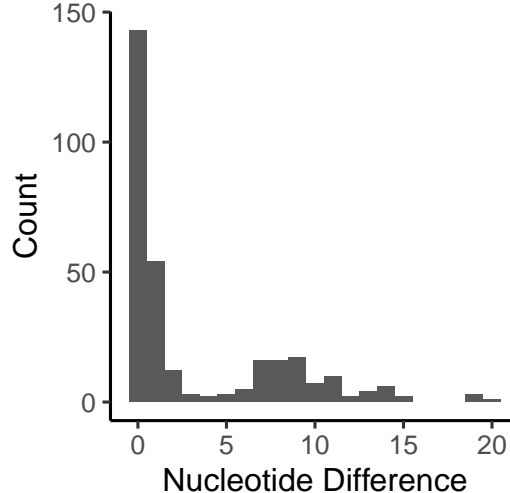
IGHV3-13*05

391 sequences assigned
149 (38.1%) exact matches, in which:
111 unique CDR3
5 unique J



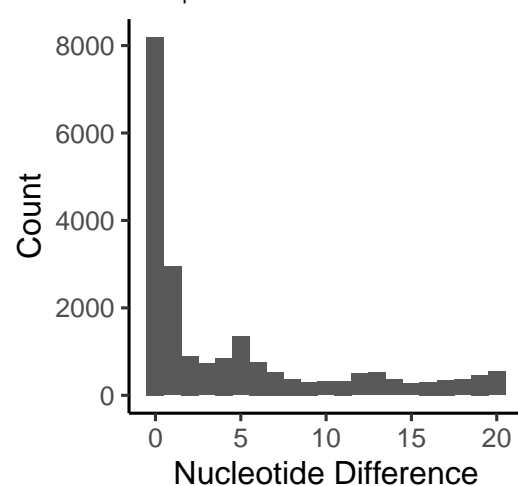
IGHV3-20*01_02

363 sequences assigned
143 (39.4%) exact matches, in which:
110 unique CDR3
5 unique J



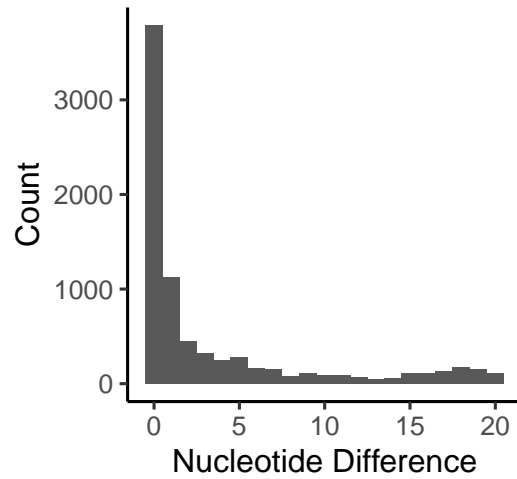
IGHV3-21*01_02

25151 sequences assigned
8195 (32.6%) exact matches, in which:
6170 unique CDR3
6 unique J



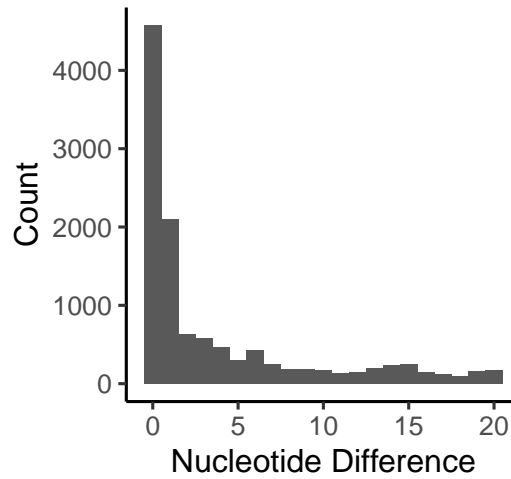
IGHV3-30-3*01

10393 sequences assigned
3787 (36.4%) exact matches, in which:
2972 unique CDR3
6 unique J



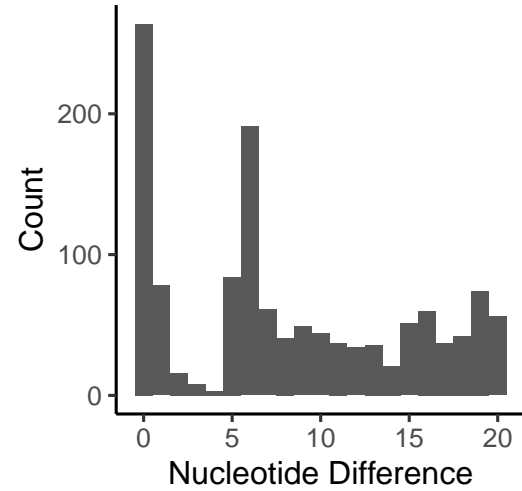
IGHV3-33*01

13517 sequences assigned
4574 (33.8%) exact matches, in which:
3705 unique CDR3
6 unique J



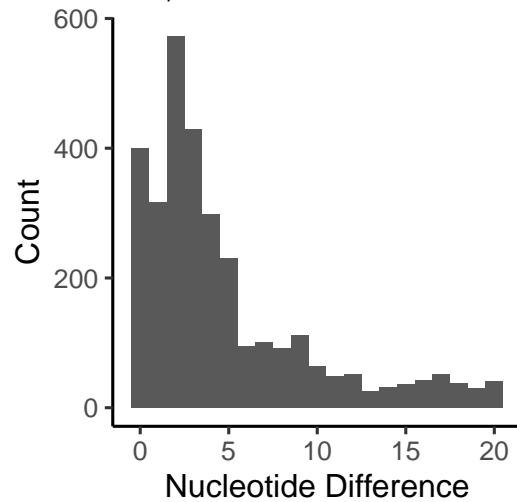
IGHV3-43*01

1856 sequences assigned
264 (14.2%) exact matches, in which:
202 unique CDR3
6 unique J



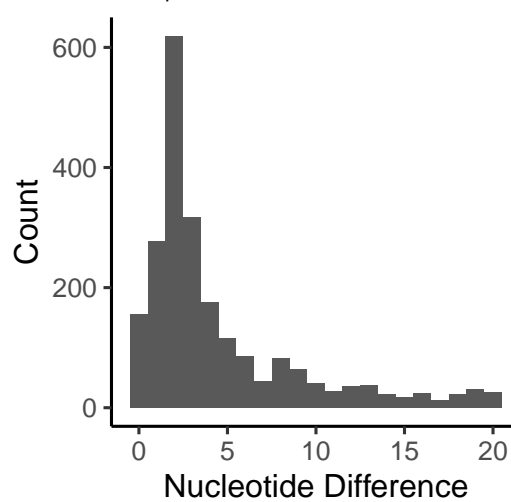
IGHV3-30-3*01_T288C

3380 sequences assigned
400 (11.8%) exact matches, in which:
394 unique CDR3
6 unique J



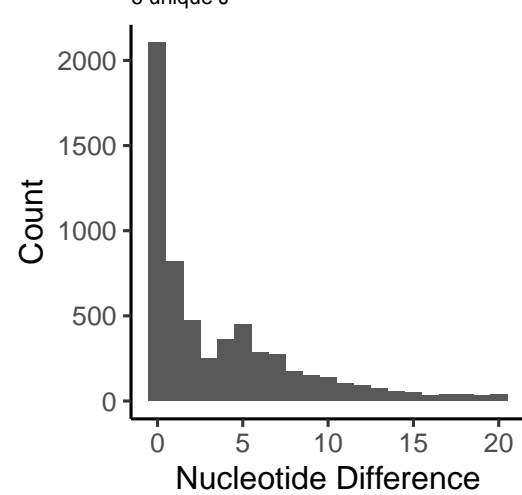
IGHV3-33*06

2441 sequences assigned
155 (6.3%) exact matches, in which:
147 unique CDR3
5 unique J



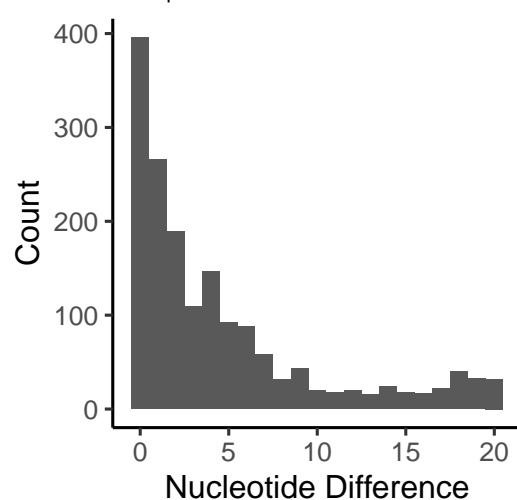
IGHV3-48*01

6726 sequences assigned
2104 (31.3%) exact matches, in which:
1677 unique CDR3
6 unique J



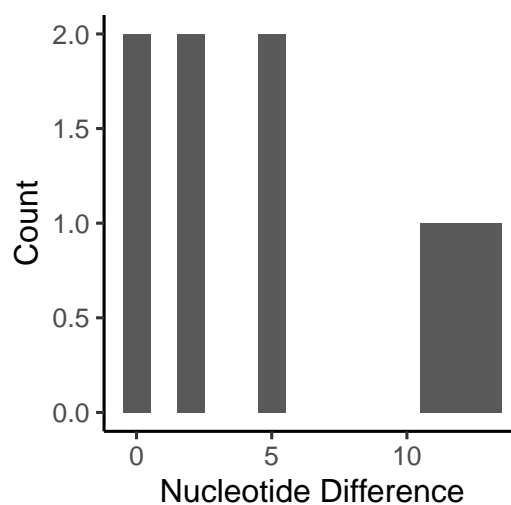
IGHV3-30*03_T288C

2223 sequences assigned
396 (17.8%) exact matches, in which:
385 unique CDR3
6 unique J



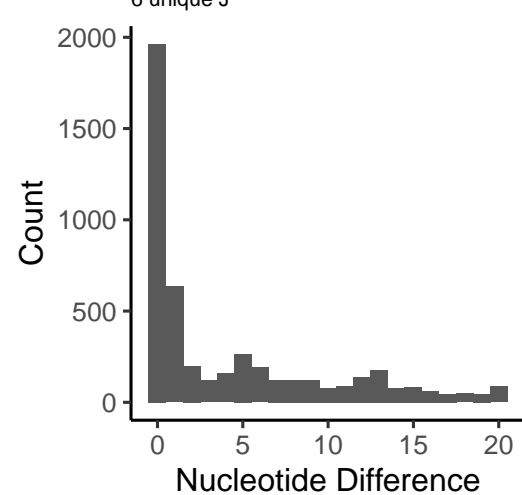
IGHV3-35*01

9 sequences assigned
2 (22.2%) exact matches, in which:
2 unique CDR3
2 unique J



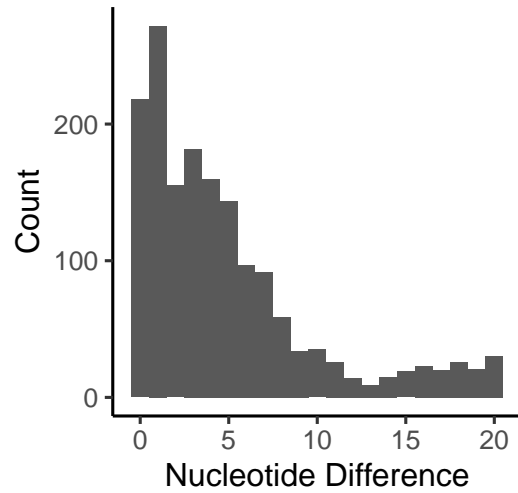
IGHV3-48*02

5994 sequences assigned
1963 (32.7%) exact matches, in which:
1459 unique CDR3
6 unique J



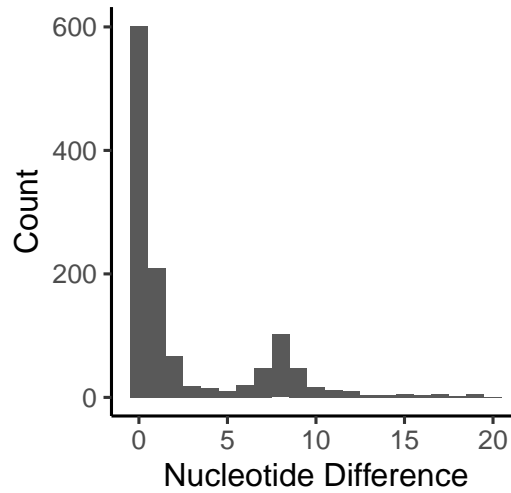
IGHV3-48*04

2083 sequences assigned
218 (10.5%) exact matches, in which:
218 unique CDR3
6 unique J



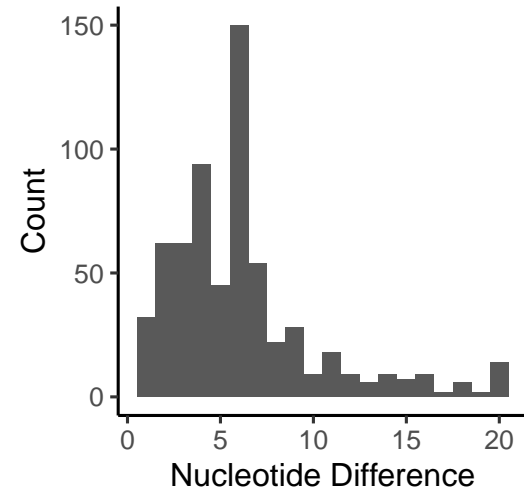
IGHV3-53*04

1241 sequences assigned
602 (48.5%) exact matches, in which:
488 unique CDR3
6 unique J



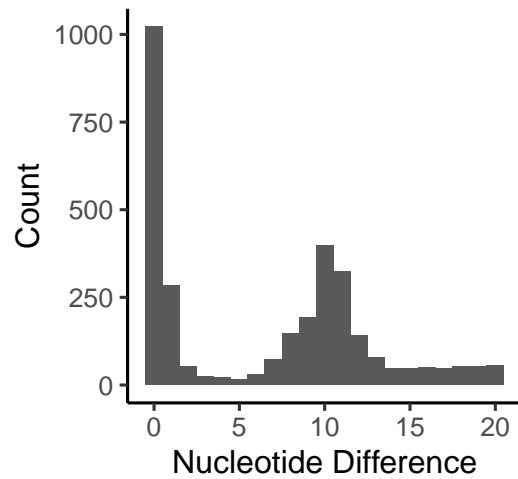
IGHV3-64*04

717 sequences assigned
No exact matches.



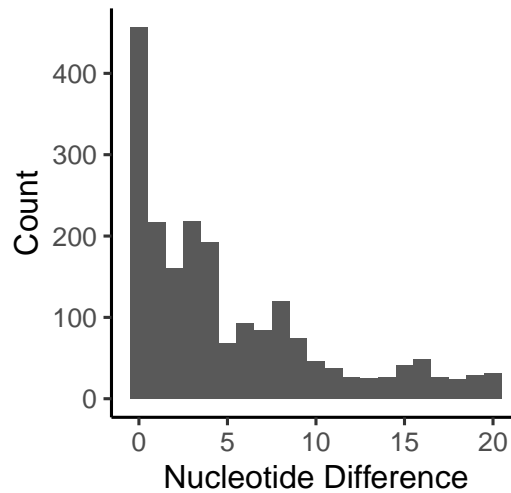
IGHV3-49*03_05

3499 sequences assigned
1022 (29.2%) exact matches, in which:
816 unique CDR3
6 unique J



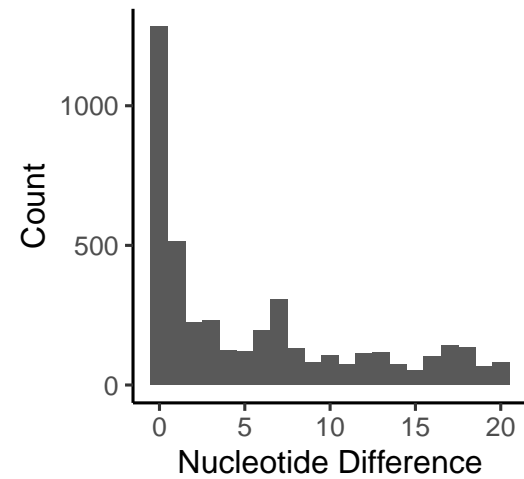
IGHV3-53*01_02

2366 sequences assigned
457 (19.3%) exact matches, in which:
363 unique CDR3
6 unique J



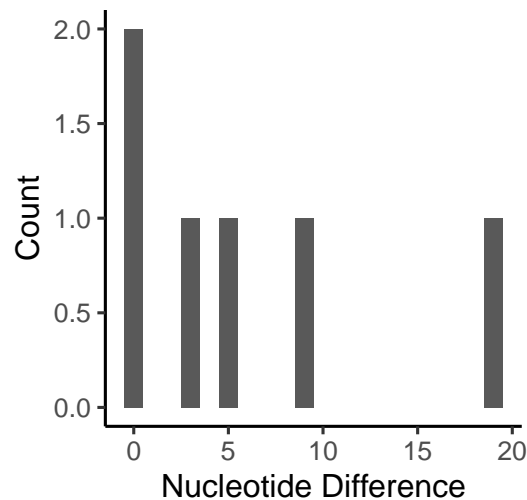
IGHV3-66*01

6858 sequences assigned
1283 (18.7%) exact matches, in which:
1020 unique CDR3
6 unique J



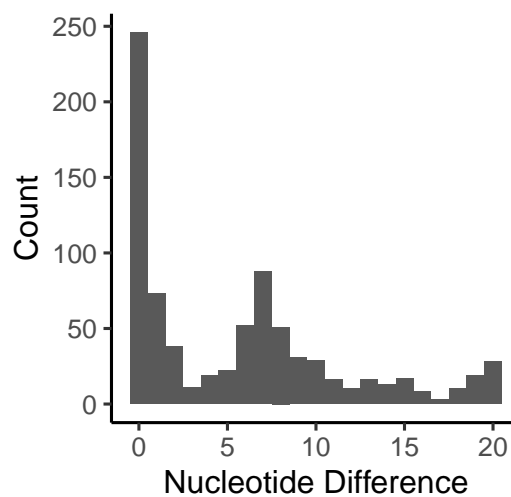
IGHV3-52*01_03

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



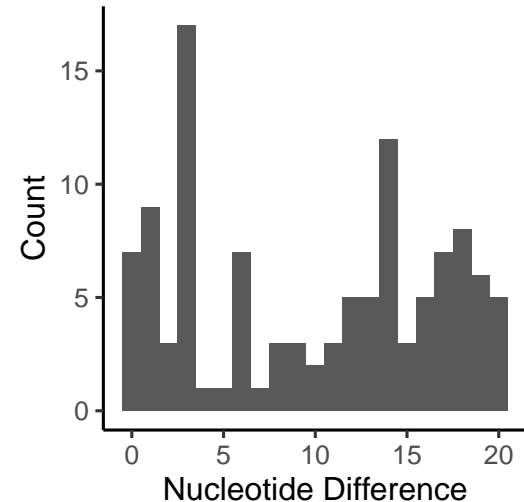
IGHV3-64*01

848 sequences assigned
246 (29%) exact matches, in which:
184 unique CDR3
6 unique J



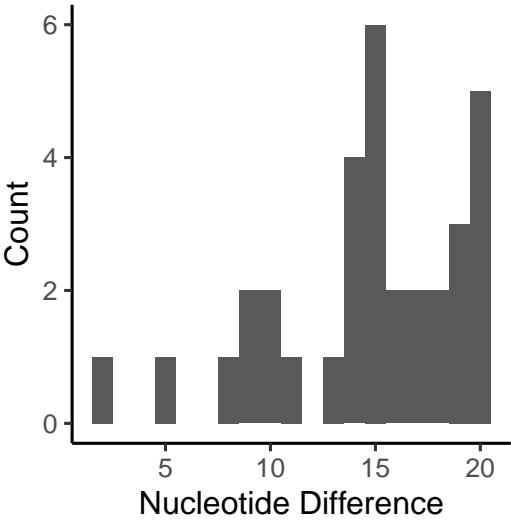
IGHV3-69-1*01

395 sequences assigned
7 (1.8%) exact matches, in which:
7 unique CDR3
3 unique J



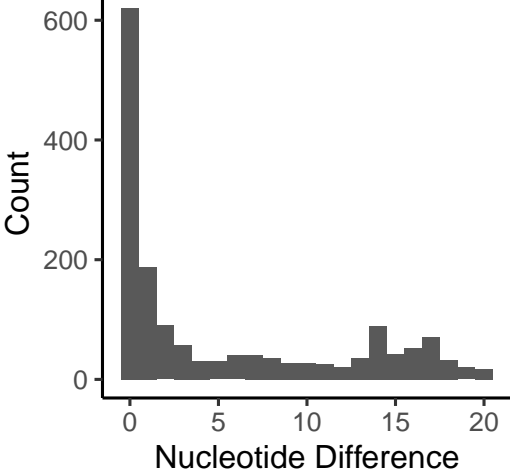
IGHV3-69-1*02

47 sequences assigned
No exact matches.



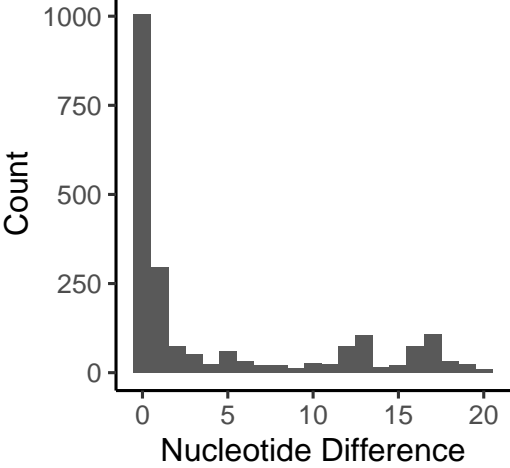
IGHV3-73*01_02

1684 sequences assigned
621 (36.9%) exact matches, in which:
487 unique CDR3
5 unique J



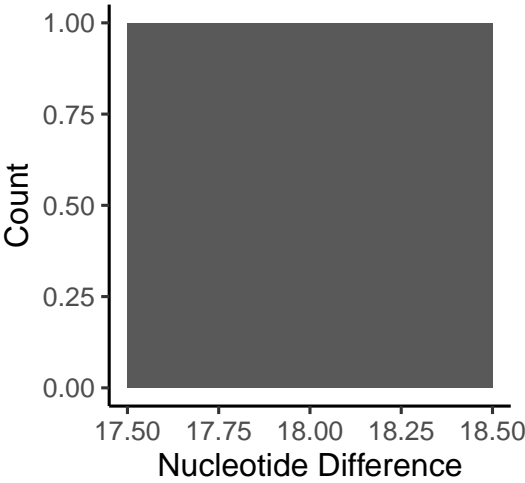
IGHV3-64D*06

2517 sequences assigned
1005 (39.9%) exact matches, in which:
697 unique CDR3
6 unique J



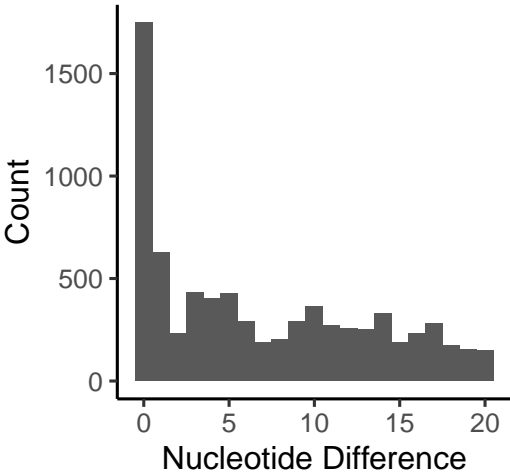
IGHV3-71*01_04

3 sequences assigned
No exact matches.



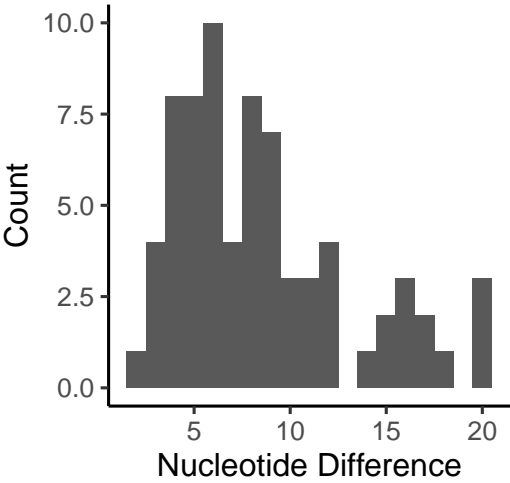
IGHV3-74*01_02

11454 sequences assigned
1748 (15.3%) exact matches, in which:
1312 unique CDR3
6 unique J



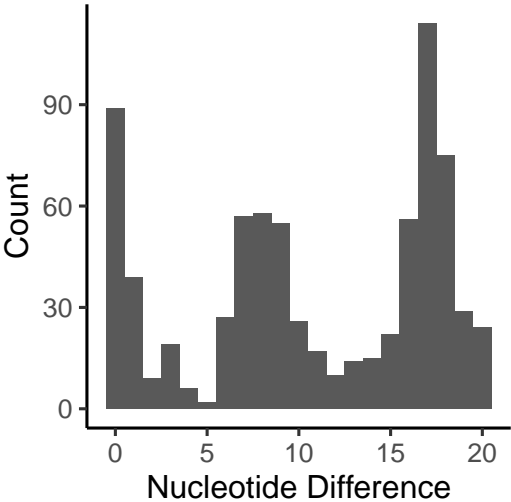
IGHV3-NL1*01

107 sequences assigned
No exact matches.



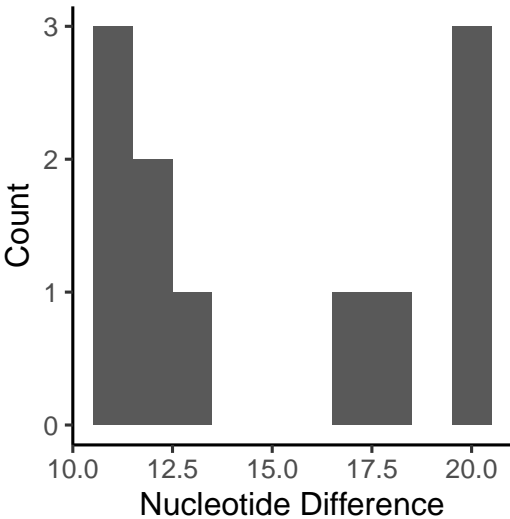
IGHV3-72*01

1029 sequences assigned
89 (8.6%) exact matches, in which:
69 unique CDR3
5 unique J



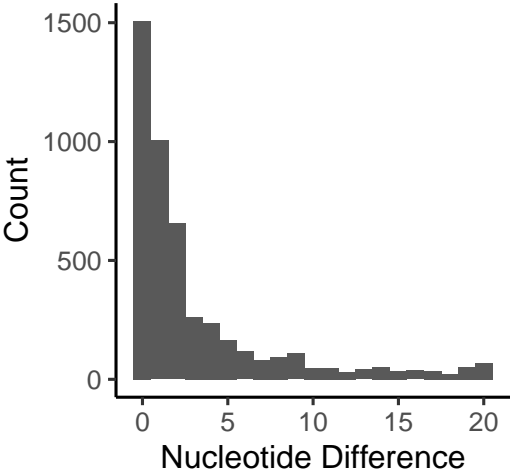
IGHV3-43D*04

20 sequences assigned
No exact matches.



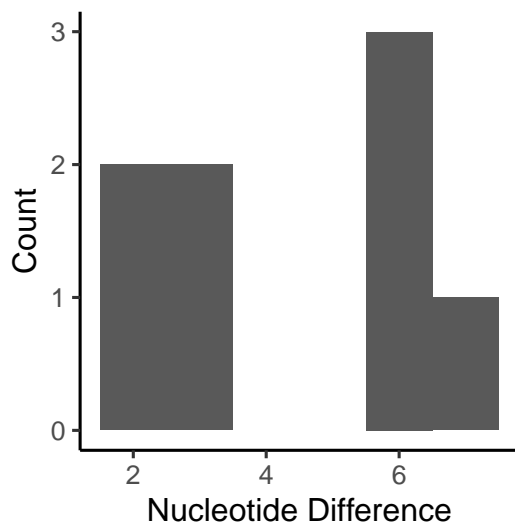
IGHV4-4*07

4938 sequences assigned
1507 (30.5%) exact matches, in which:
1401 unique CDR3
6 unique J



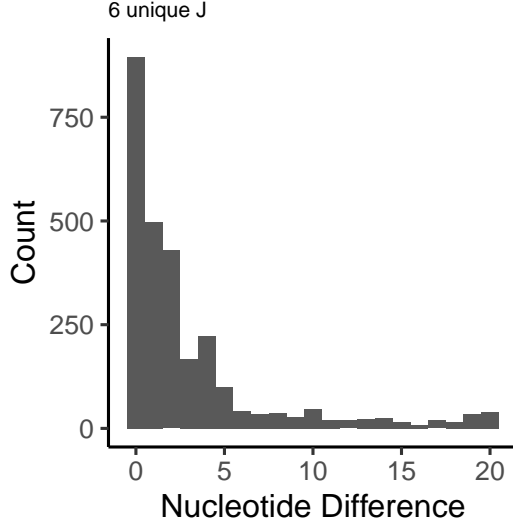
IGHV4-28*03

8 sequences assigned
No exact matches.



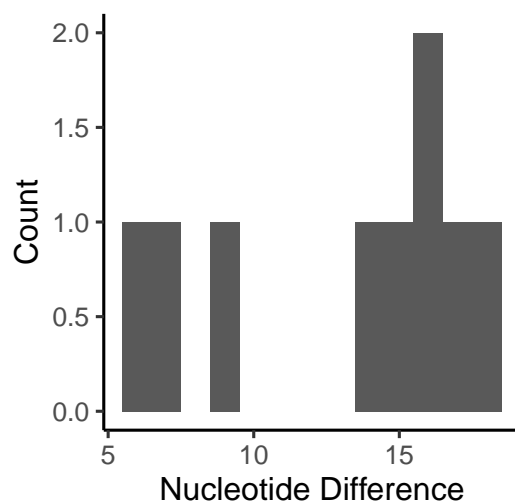
IGHV4-30-2*01

2933 sequences assigned
896 (30.5%) exact matches, in which:
829 unique CDR3
6 unique J



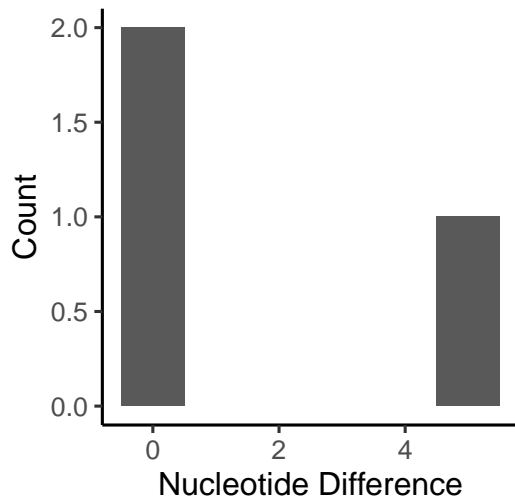
IGHV4-30-4*08

14 sequences assigned
No exact matches.



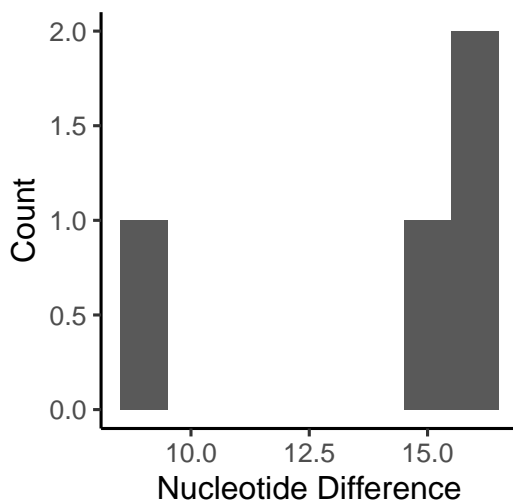
IGHV4-28*01_07

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



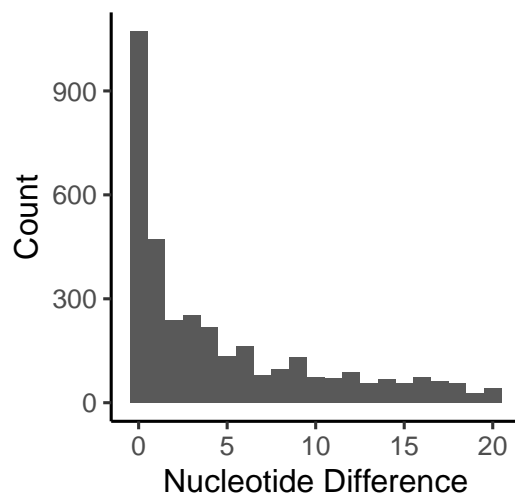
IGHV4-30-4*01

5 sequences assigned
No exact matches.



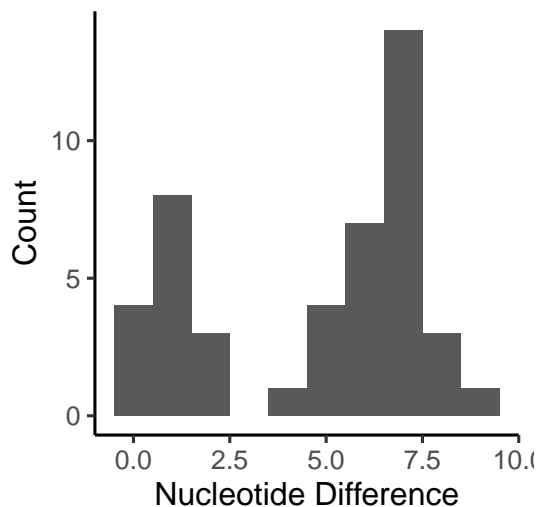
IGHV4-31*03_04

4409 sequences assigned
1073 (24.3%) exact matches, in which:
1024 unique CDR3
6 unique J



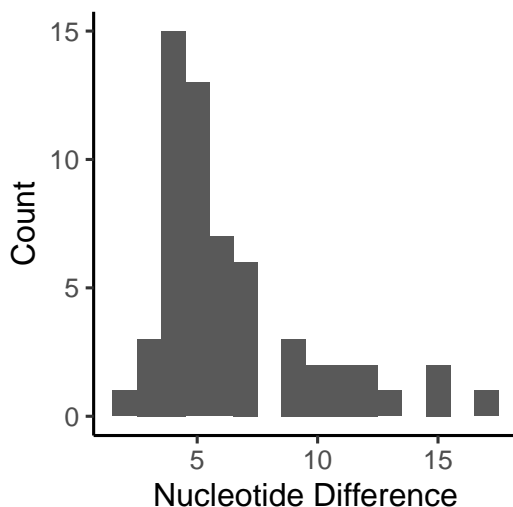
IGHV4-28*02_05

45 sequences assigned
4 (8.9%) exact matches, in which:
4 unique CDR3
3 unique J



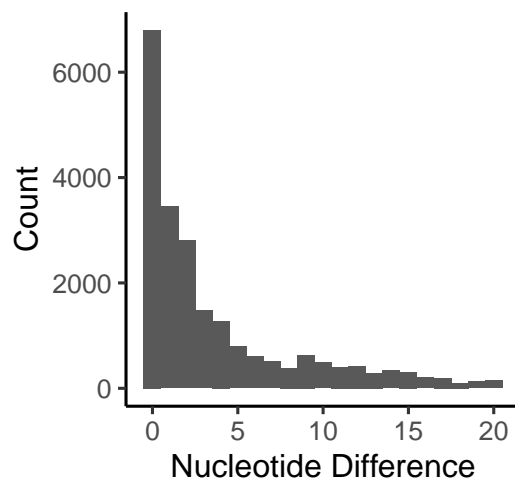
IGHV4-30-4*07

59 sequences assigned
No exact matches.



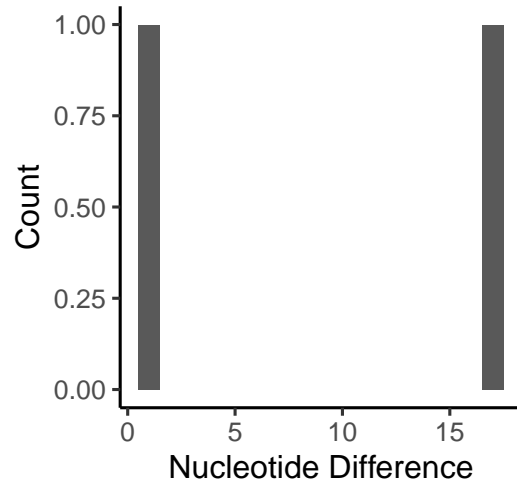
IGHV4-34*01_02

22866 sequences assigned
6800 (29.7%) exact matches, in which:
6351 unique CDR3
6 unique J



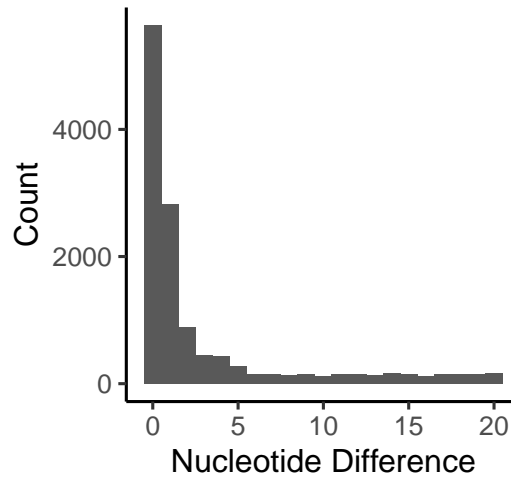
IGHV4-38-2*01

5 sequences assigned
No exact matches.



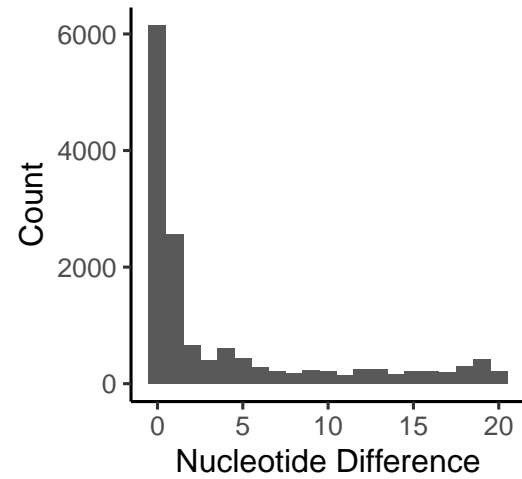
IGHV4-39*01_05

14161 sequences assigned
5636 (39.8%) exact matches, in which:
5166 unique CDR3
6 unique J



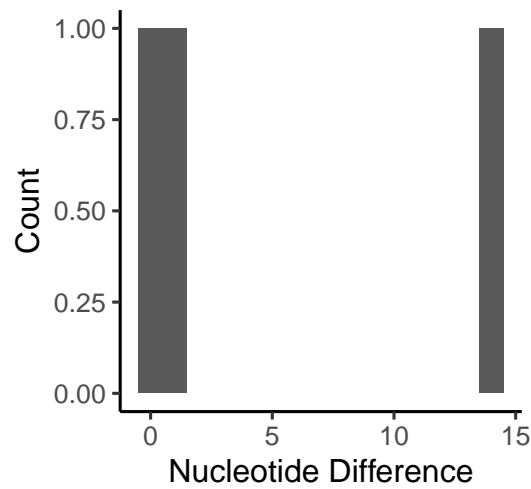
IGHV4-59*01_07

15433 sequences assigned
6147 (39.8%) exact matches, in which:
5743 unique CDR3
6 unique J



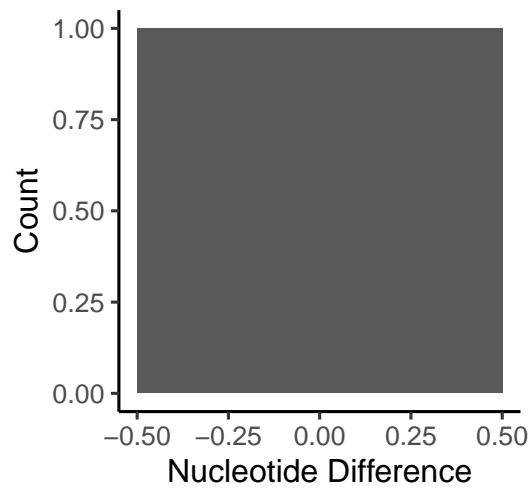
IGHV4-38-2*02

5 sequences assigned
1 (20%) exact matches, in which:
1 unique CDR3
1 unique J



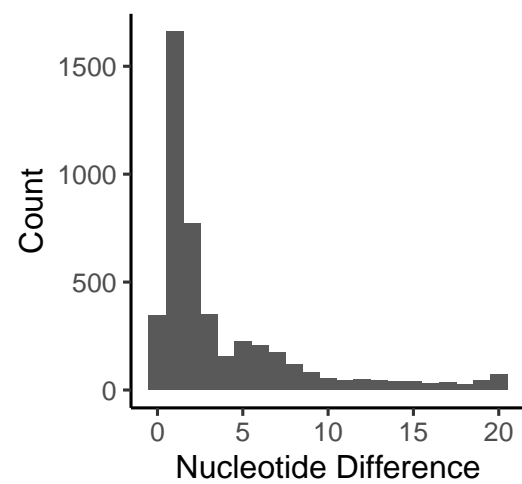
IGHV4-55*02_04_08

5 sequences assigned
1 (20%) exact matches, in which:
1 unique CDR3
1 unique J



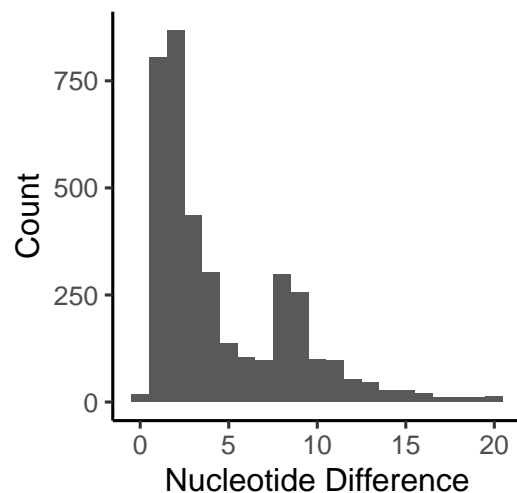
IGHV4-59*12

4794 sequences assigned
346 (7.2%) exact matches, in which:
344 unique CDR3
6 unique J



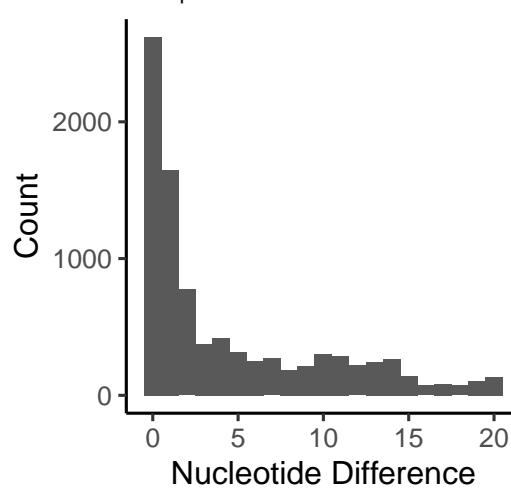
IGHV4-39*07

3814 sequences assigned
17 (0.4%) exact matches, in which:
17 unique CDR3
4 unique J



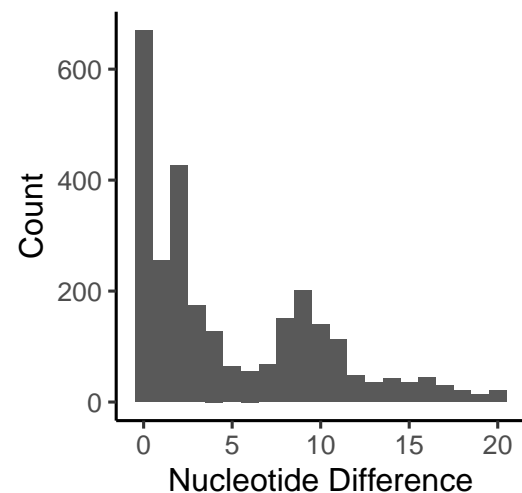
IGHV4-59*08

9864 sequences assigned
2620 (26.6%) exact matches, in which:
2450 unique CDR3
6 unique J



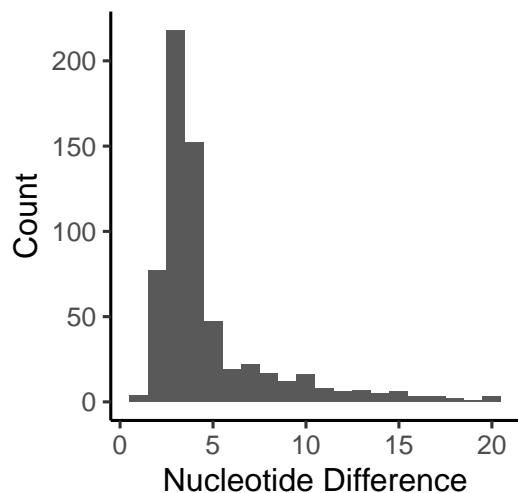
IGHV4-61*01

2842 sequences assigned
670 (23.6%) exact matches, in which:
651 unique CDR3
6 unique J



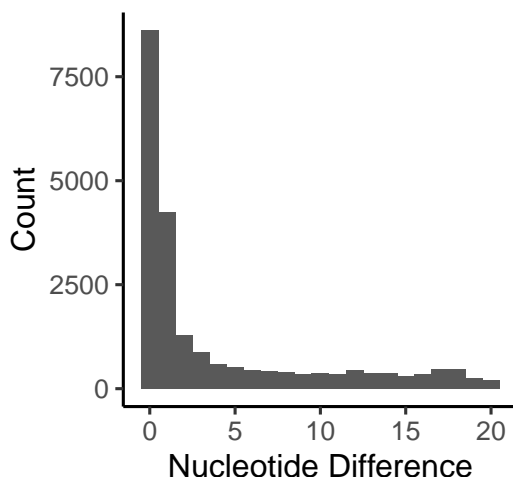
IGHV4-61*05

641 sequences assigned
No exact matches.



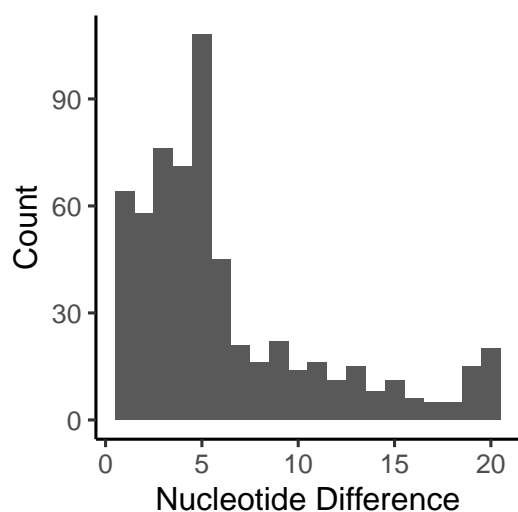
IGHV5-51*01_03

41471 sequences assigned
8613 (20.8%) exact matches, in which:
6264 unique CDR3
6 unique J



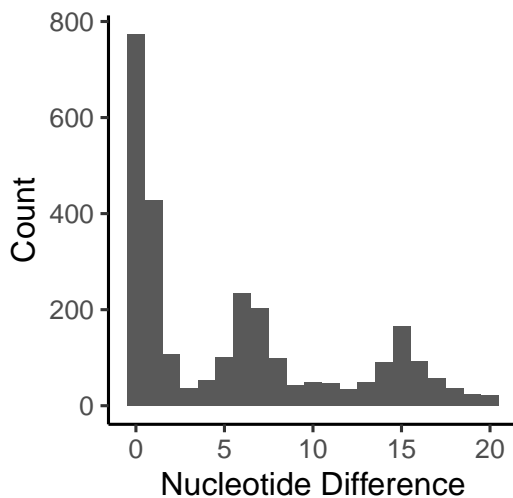
IGHV4-61*08

718 sequences assigned
No exact matches.



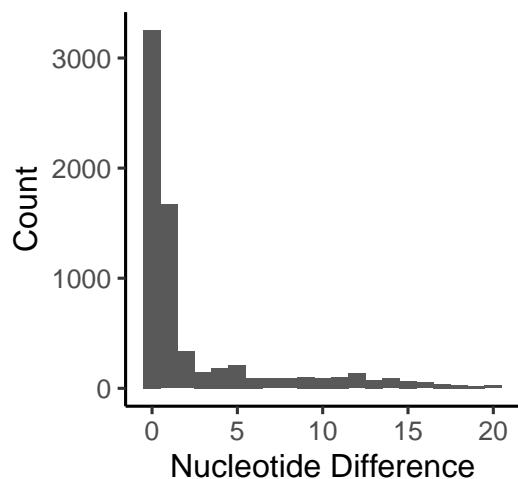
IGHV6-1*01_02

3050 sequences assigned
774 (25.4%) exact matches, in which:
737 unique CDR3
6 unique J



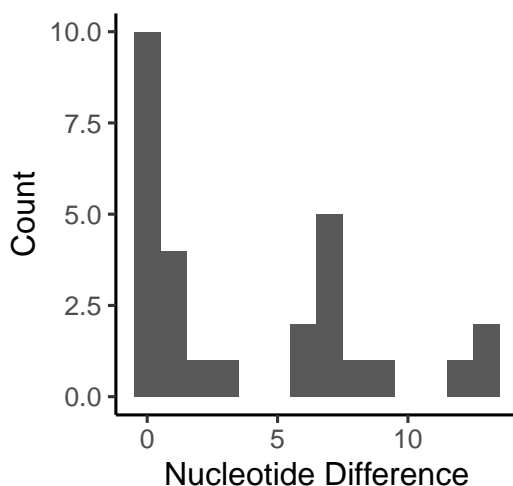
IGHV5-10-1*01_03

7124 sequences assigned
3254 (45.7%) exact matches, in which:
2584 unique CDR3
6 unique J

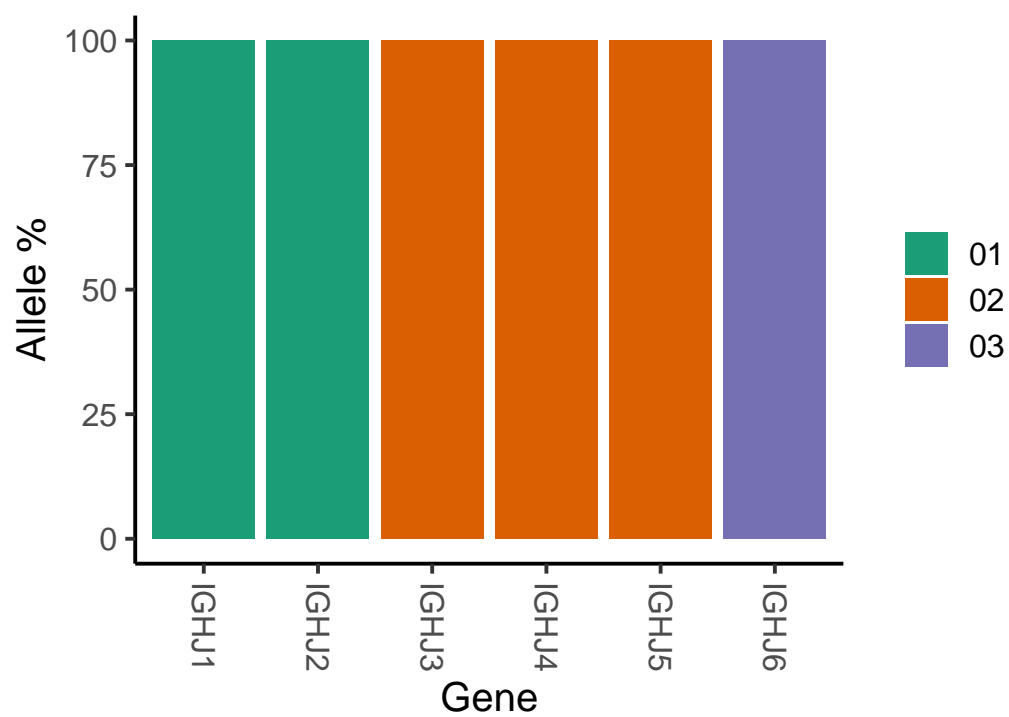


IGHV7-4-1*01

28 sequences assigned
10 (35.7%) exact matches, in which:
10 unique CDR3
4 unique J



Allele Usage



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.

Novel sequence(s) IGHV5-51*07_A128G are not listed in the genotype and will be ignored.