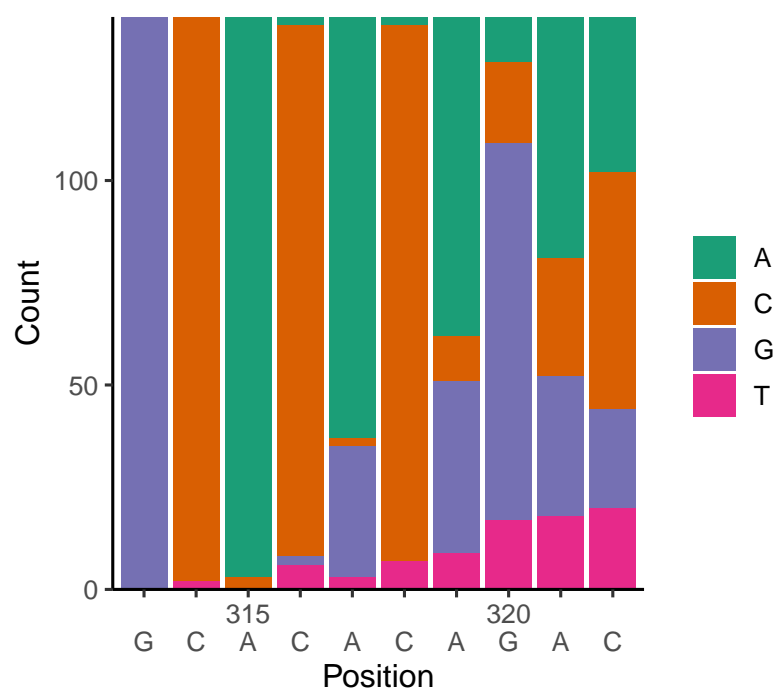
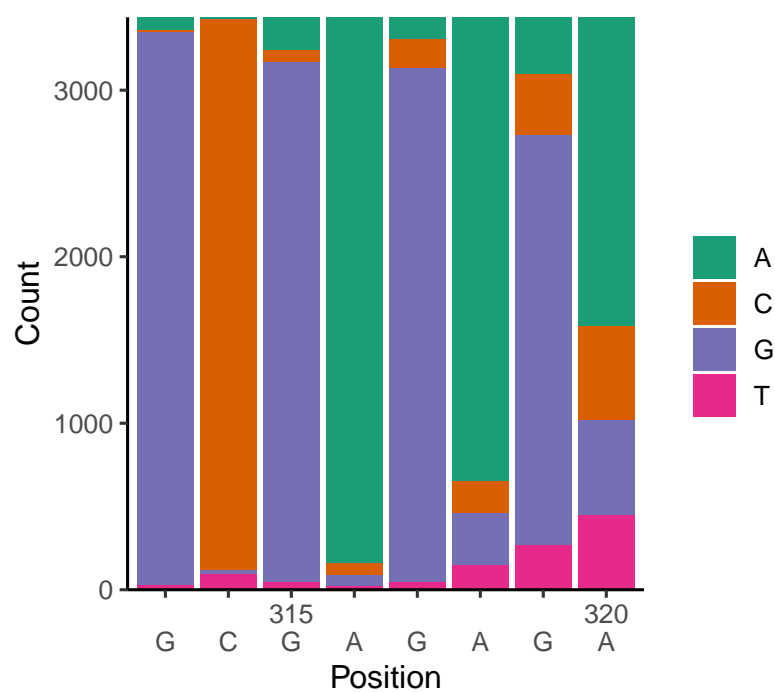


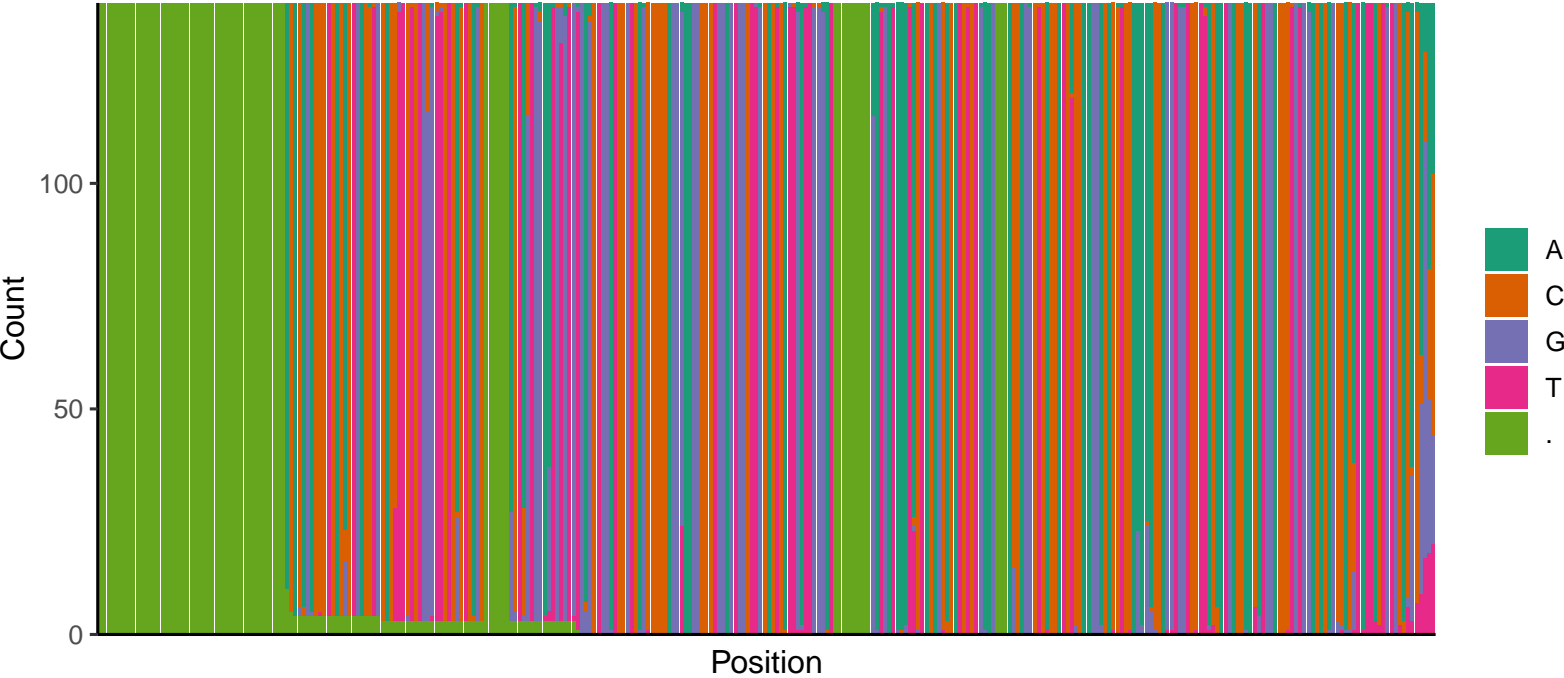
Gene IGHV2-70*12_G60A



Gene IGHV3-30*03_T288C



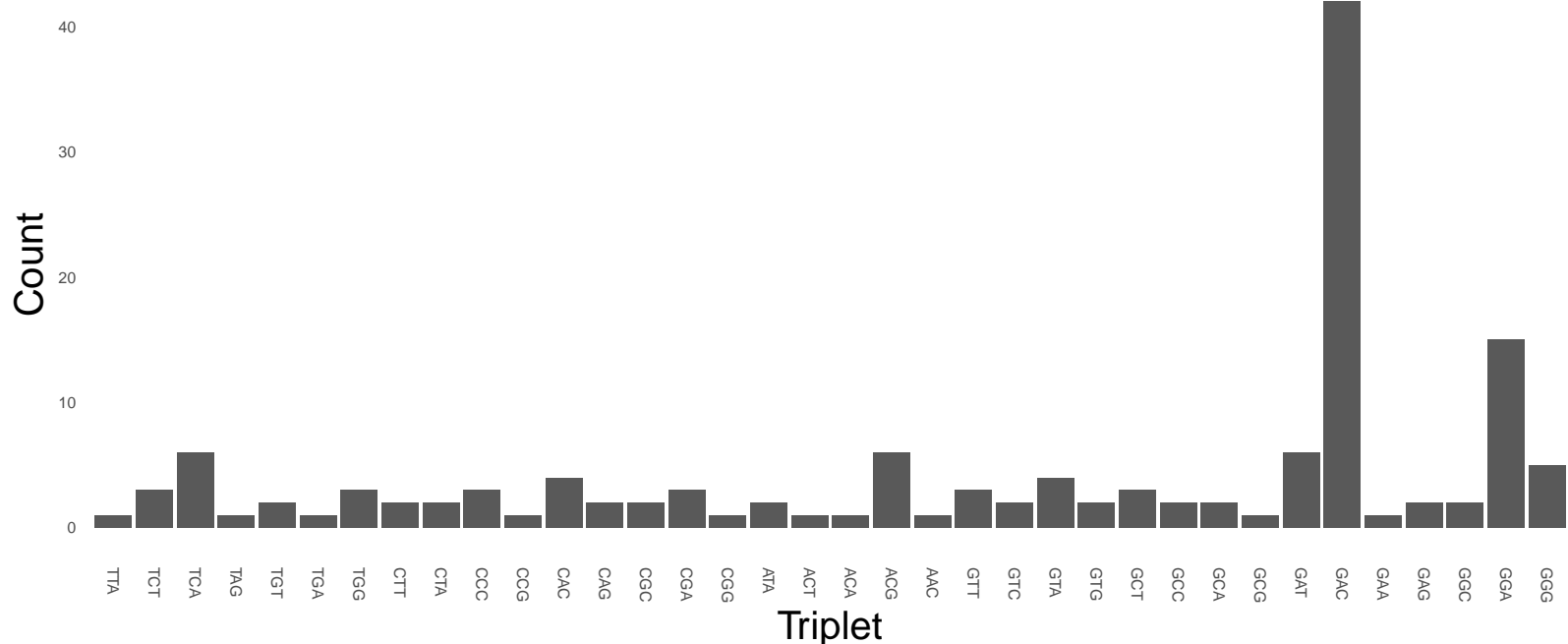
Gene IGHV2-70*12_G60A



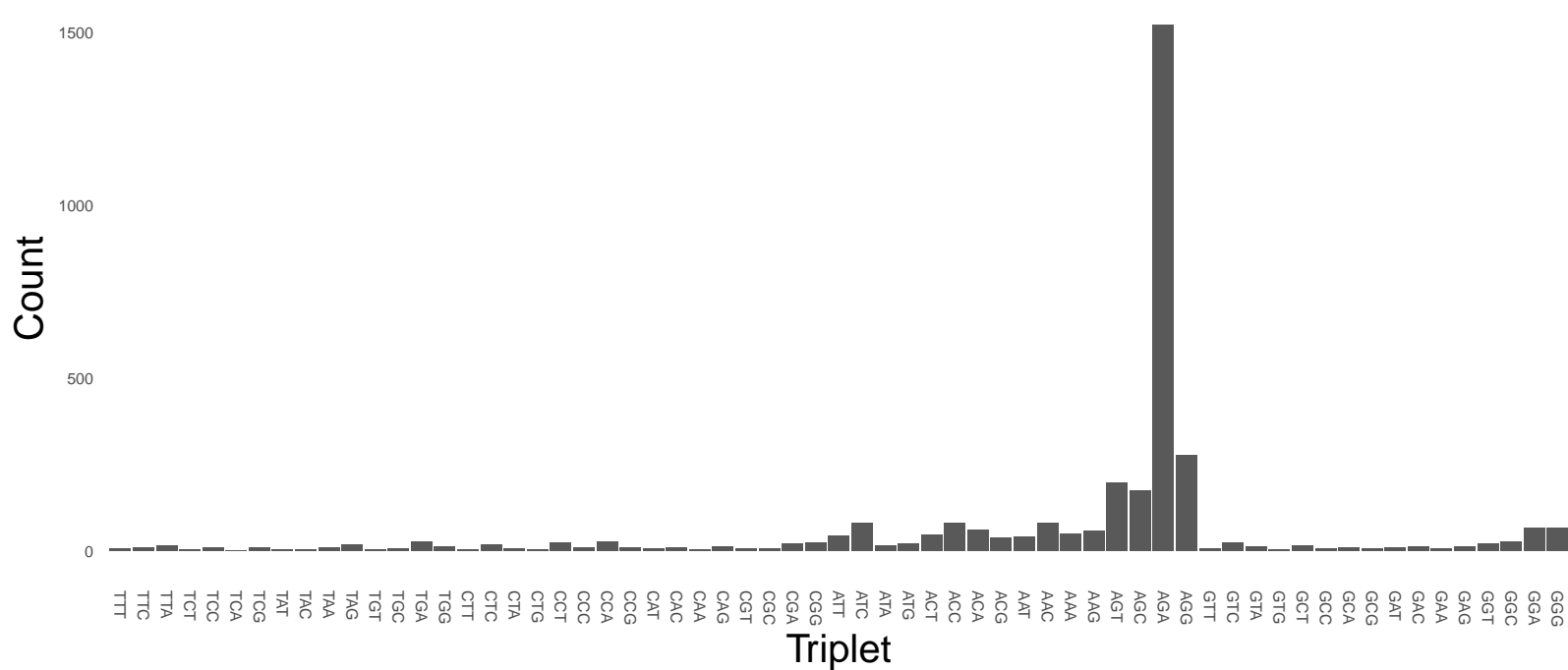
Gene IGHV3-30*03_T288C



IGHV2-70*12_G60A- Final 3 nucleotides as a triplet

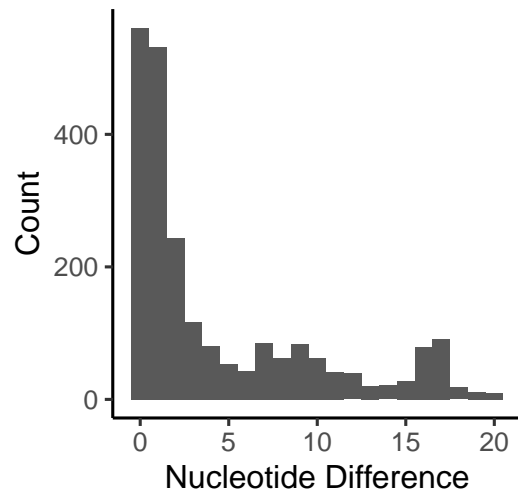


IGHV3-30*03_T288C- Final 3 nucleotides as a triplet



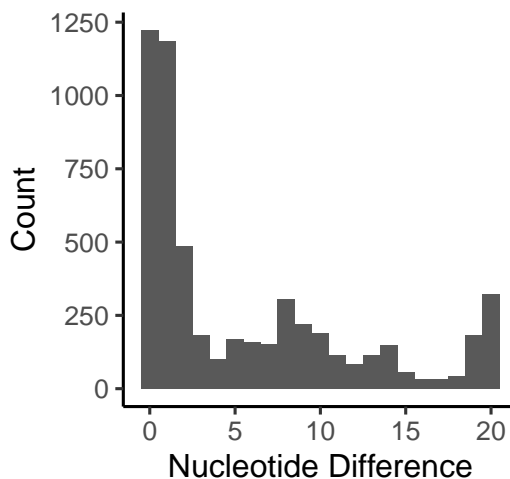
IGHV1-2*04

2410 sequences assigned
561 (23.3%) exact matches, in which:
472 unique CDR3
7 unique J



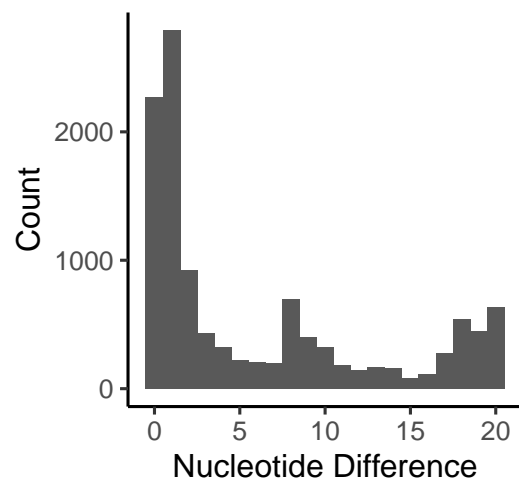
IGHV1-8*01

6176 sequences assigned
1222 (19.8%) exact matches, in which:
1027 unique CDR3
7 unique J



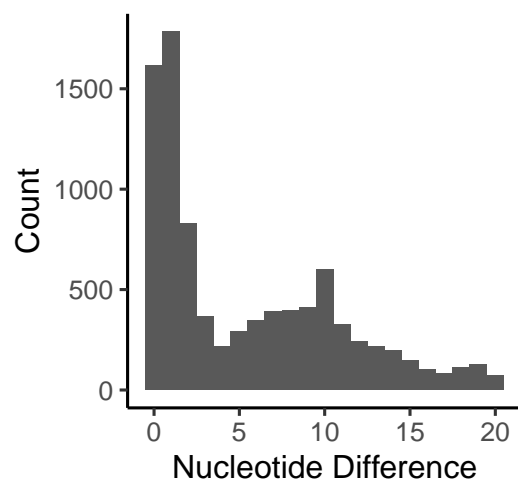
IGHV1-18*04

12348 sequences assigned
2274 (18.4%) exact matches, in which:
1777 unique CDR3
7 unique J



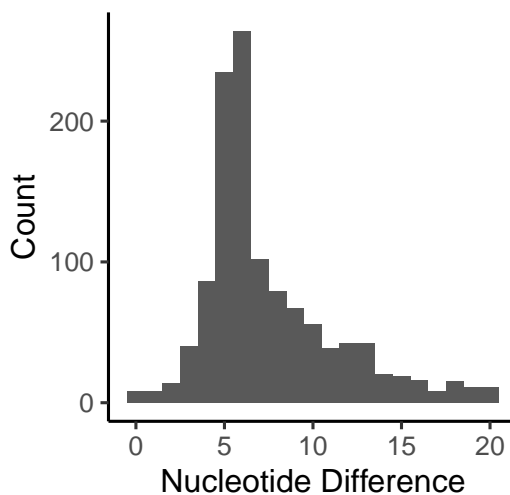
IGHV1-2*06

10684 sequences assigned
1616 (15.1%) exact matches, in which:
1264 unique CDR3
7 unique J



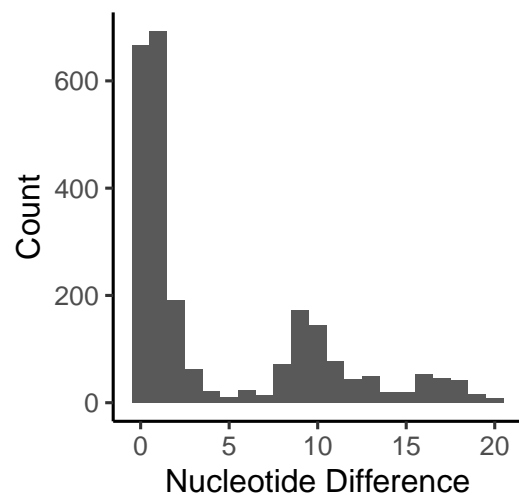
IGHV1-8*02

1283 sequences assigned
8 (0.6%) exact matches, in which:
7 unique CDR3
3 unique J



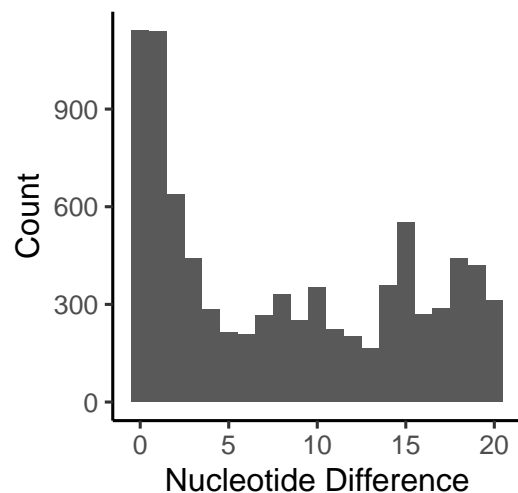
IGHV1-24*01

2914 sequences assigned
666 (22.9%) exact matches, in which:
535 unique CDR3
7 unique J



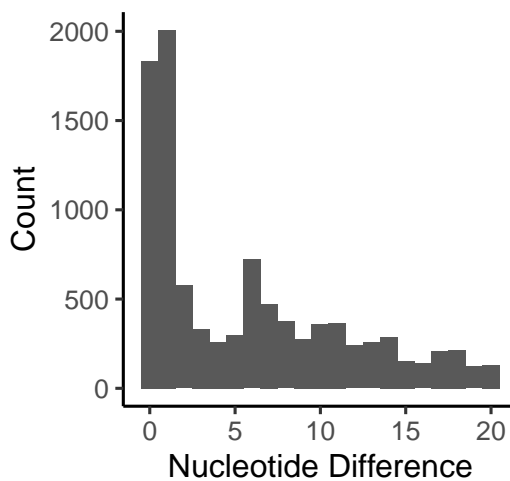
IGHV1-3*01_05

11931 sequences assigned
1142 (9.6%) exact matches, in which:
876 unique CDR3
7 unique J



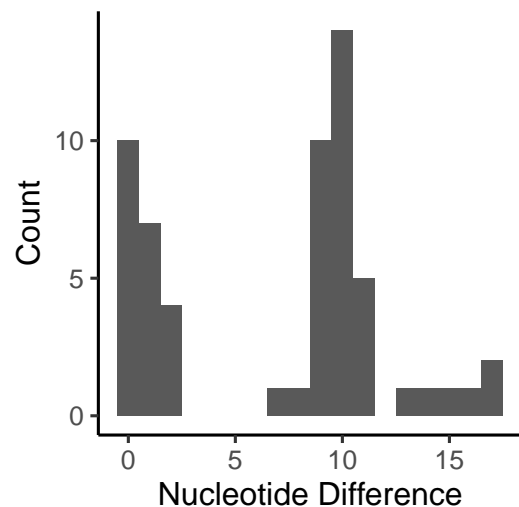
IGHV1-18*01

12293 sequences assigned
1832 (14.9%) exact matches, in which:
1484 unique CDR3
7 unique J



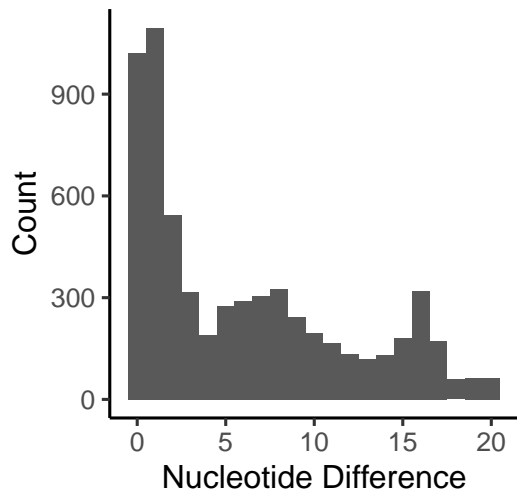
IGHV1-45*02

61 sequences assigned
10 (16.4%) exact matches, in which:
3 unique CDR3
2 unique J



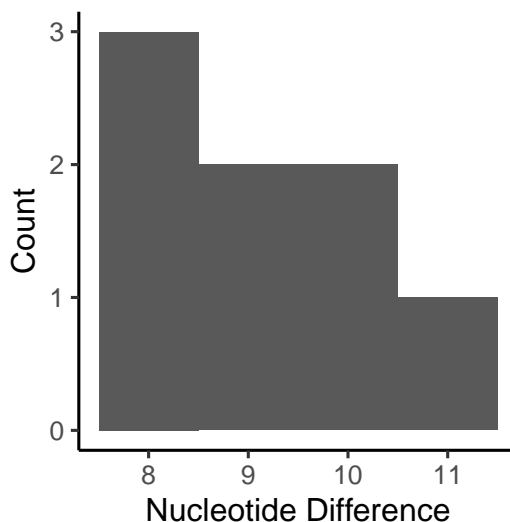
IGHV1-46*01

6894 sequences assigned
1021 (14.8%) exact matches, in which:
870 unique CDR3
7 unique J



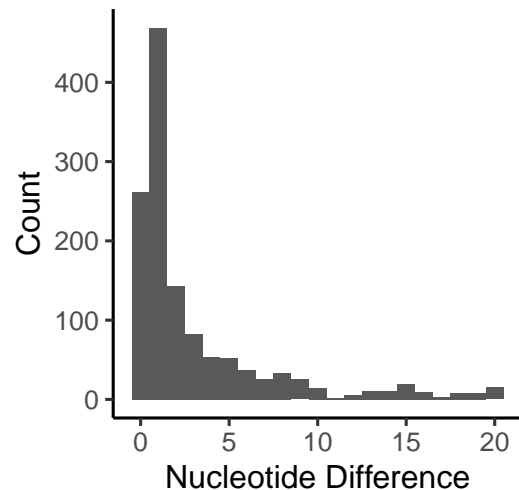
IGHV1-NL1*01

8 sequences assigned
No exact matches.



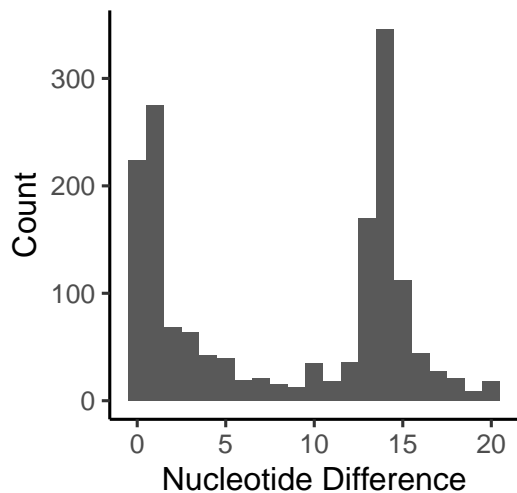
IGHV2-70*01

1299 sequences assigned
262 (20.2%) exact matches, in which:
172 unique CDR3
6 unique J



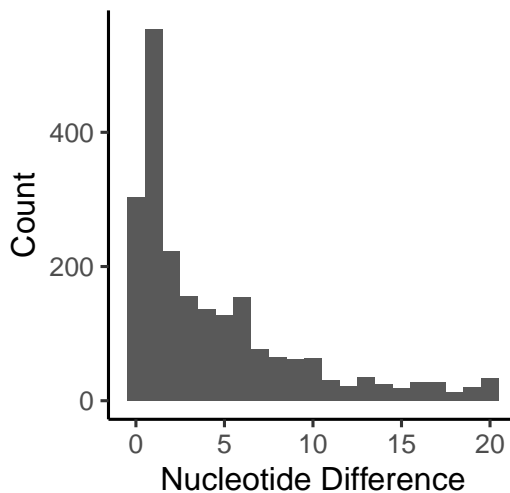
IGHV1-58*01_03

1646 sequences assigned
224 (13.6%) exact matches, in which:
184 unique CDR3
7 unique J



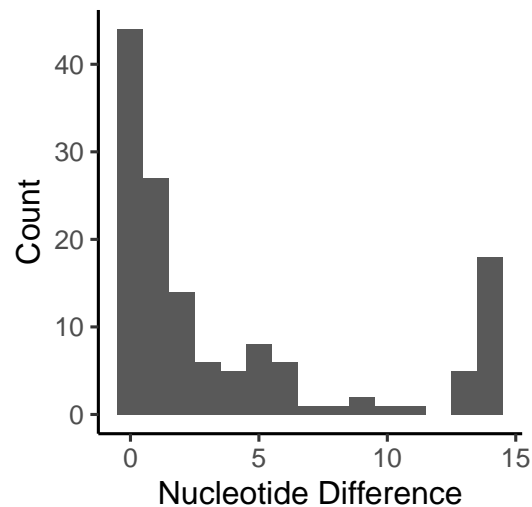
IGHV2-5*02

3505 sequences assigned
304 (8.7%) exact matches, in which:
232 unique CDR3
7 unique J



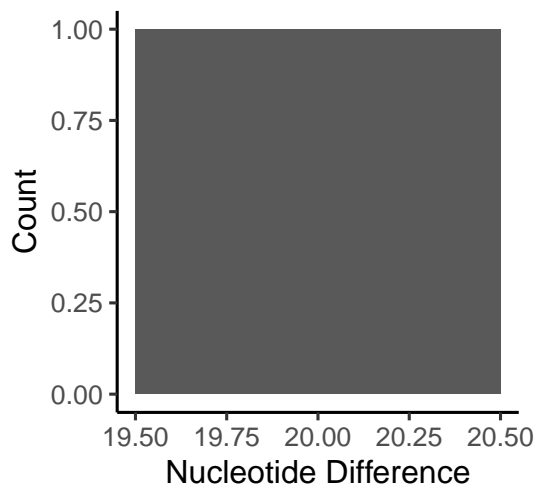
IGHV2-70*12_G60A

140 sequences assigned
44 (31.4%) exact matches, in which:
40 unique CDR3
6 unique J



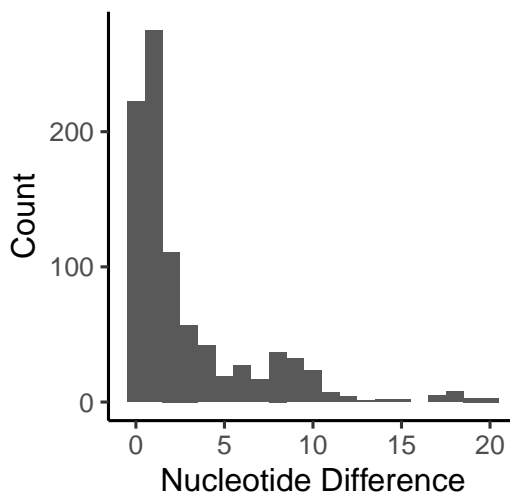
IGHV1-69-2*01

2 sequences assigned
No exact matches.



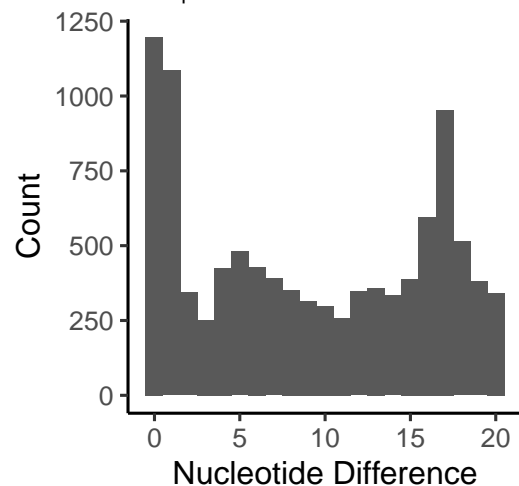
IGHV2-26*01

957 sequences assigned
222 (23.2%) exact matches, in which:
177 unique CDR3
7 unique J



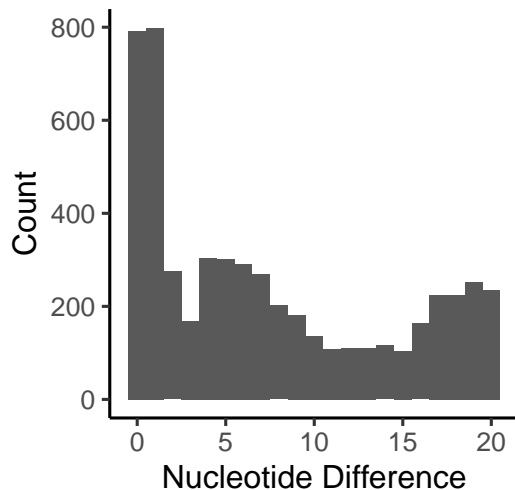
IGHV3-7*01

11345 sequences assigned
1197 (10.6%) exact matches, in which:
863 unique CDR3
7 unique J



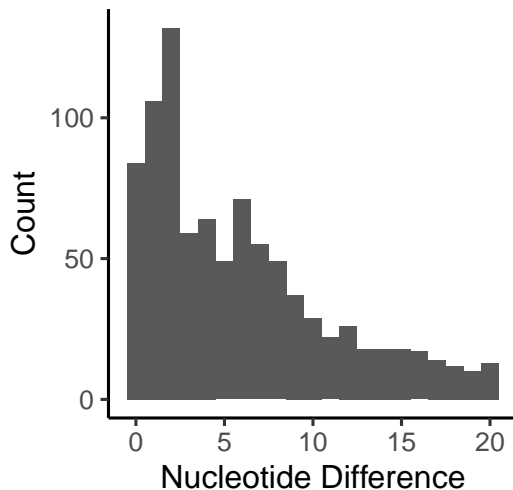
IGHV3-7*03

10380 sequences assigned
792 (7.6%) exact matches, in which:
529 unique CDR3
7 unique J



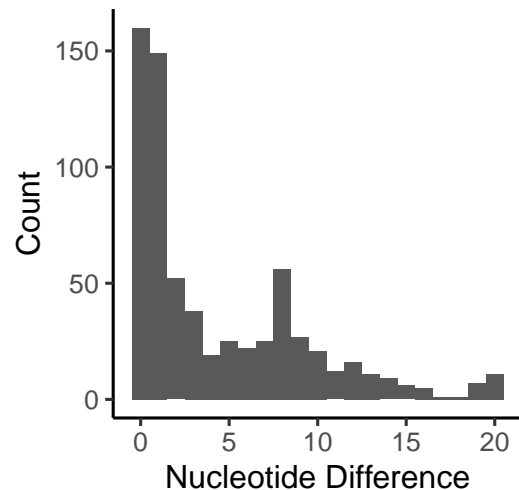
IGHV3-11*04

969 sequences assigned
84 (8.7%) exact matches, in which:
83 unique CDR3
7 unique J



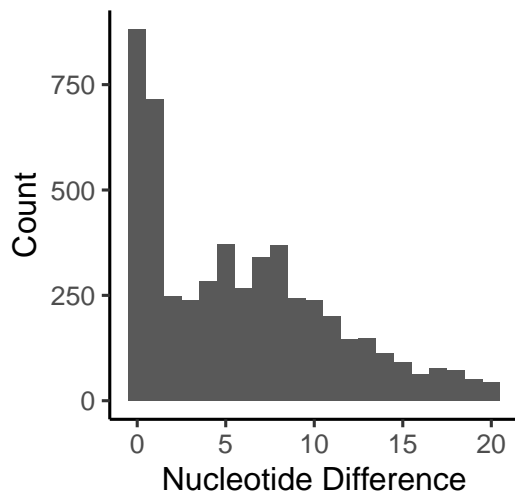
IGHV3-13*01

704 sequences assigned
160 (22.7%) exact matches, in which:
107 unique CDR3
6 unique J



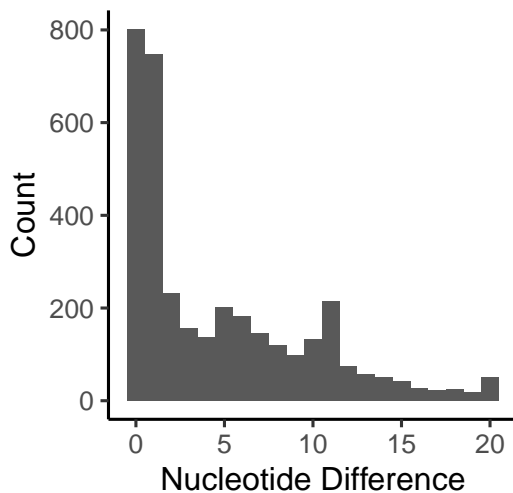
IGHV3-9*01

5358 sequences assigned
882 (16.5%) exact matches, in which:
528 unique CDR3
7 unique J



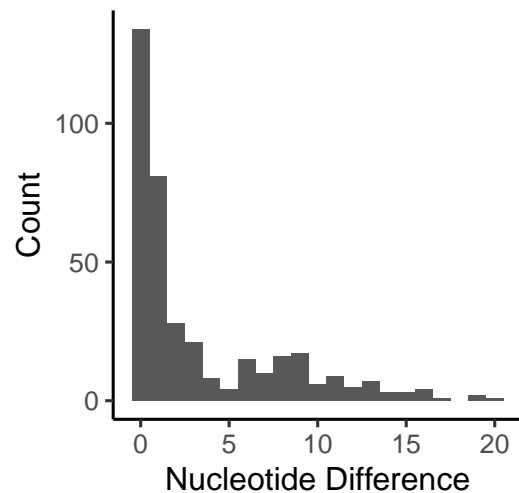
IGHV3-11*06

3734 sequences assigned
802 (21.5%) exact matches, in which:
539 unique CDR3
7 unique J



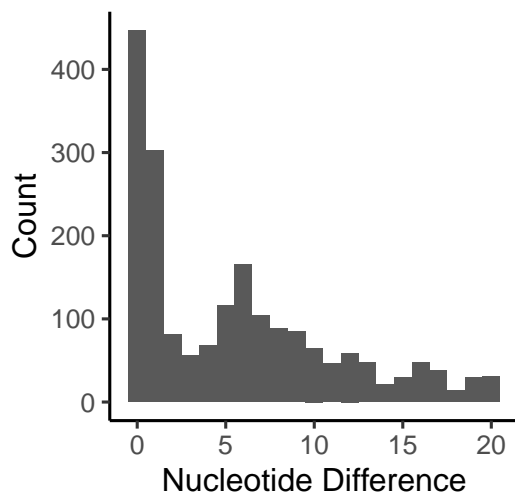
IGHV3-13*05

944 sequences assigned
134 (14.2%) exact matches, in which:
88 unique CDR3
7 unique J



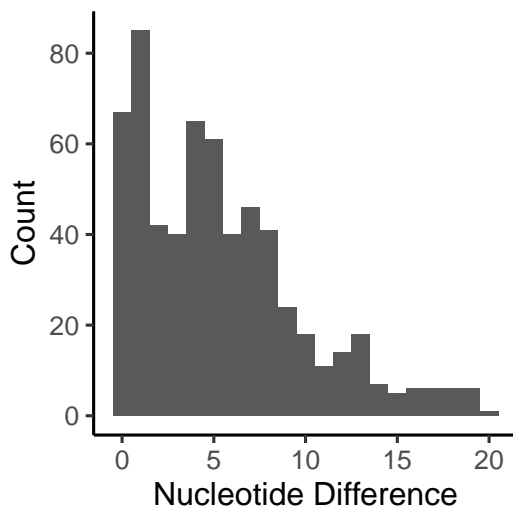
IGHV3-11*01

2682 sequences assigned
447 (16.7%) exact matches, in which:
313 unique CDR3
7 unique J



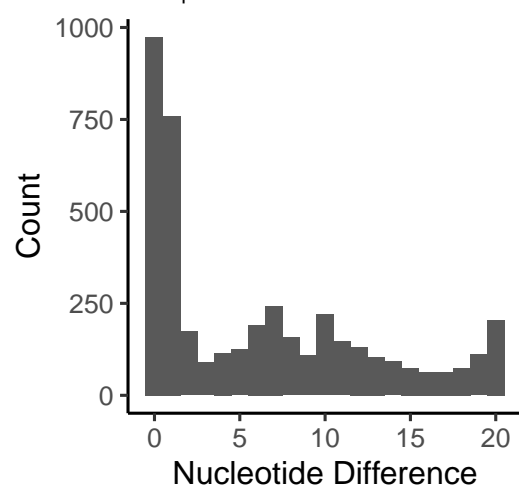
IGHV3-11*03_05

626 sequences assigned
67 (10.7%) exact matches, in which:
60 unique CDR3
7 unique J



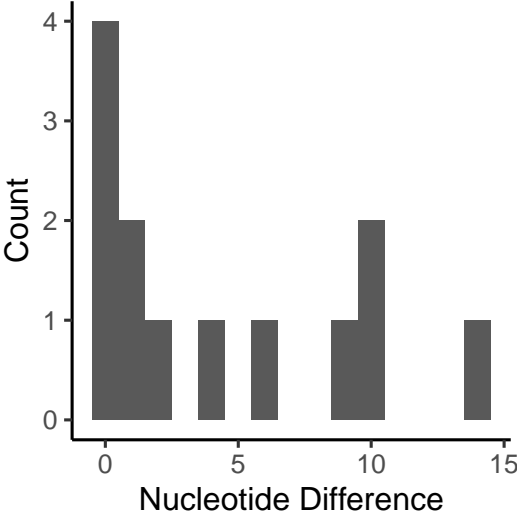
IGHV3-15*01_02

4736 sequences assigned
974 (20.6%) exact matches, in which:
558 unique CDR3
7 unique J



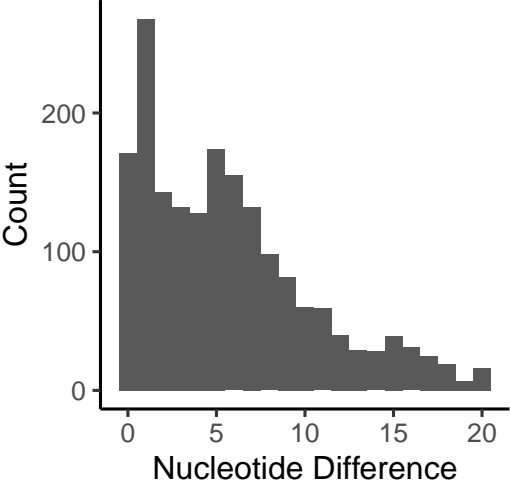
IGHV3-19*01

13 sequences assigned
4 (30.8%) exact matches, in which:
3 unique CDR3
3 unique J



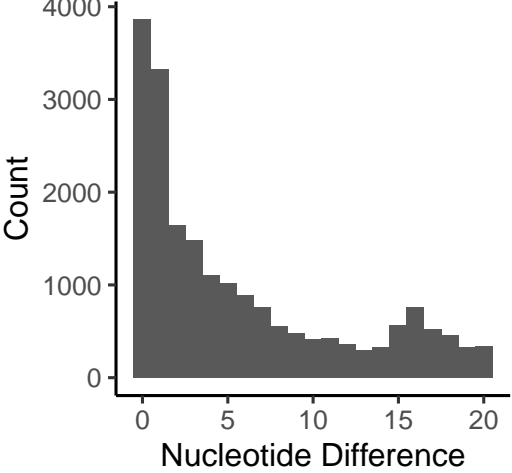
IGHV3-21*04

1961 sequences assigned
171 (8.7%) exact matches, in which:
147 unique CDR3
7 unique J



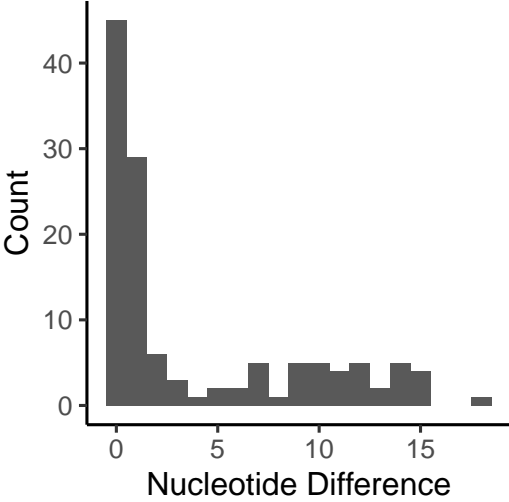
IGHV3-30-3*01

22351 sequences assigned
3863 (17.3%) exact matches, in which:
2414 unique CDR3
7 unique J



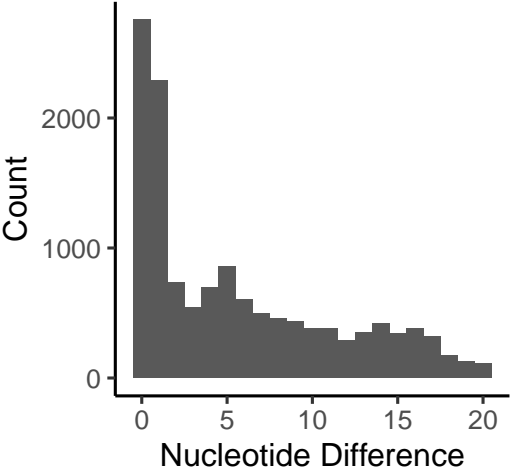
IGHV3-20*01_02

125 sequences assigned
45 (36%) exact matches, in which:
30 unique CDR3
4 unique J



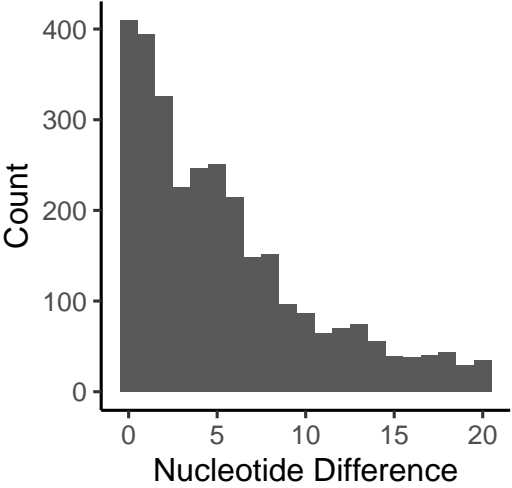
IGHV3-21*01_02

14580 sequences assigned
2756 (18.9%) exact matches, in which:
1749 unique CDR3
7 unique J



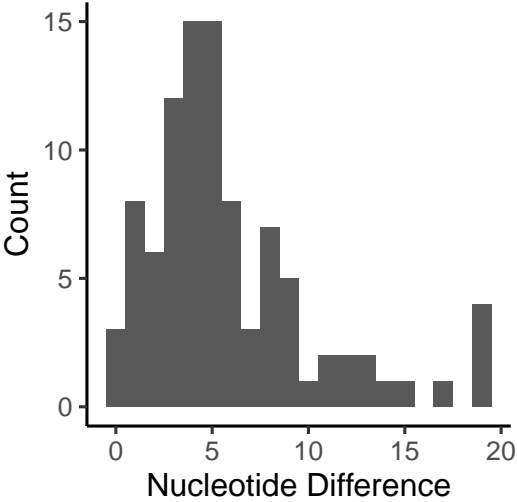
IGHV3-30*03_T288C

3438 sequences assigned
410 (11.9%) exact matches, in which:
345 unique CDR3
7 unique J



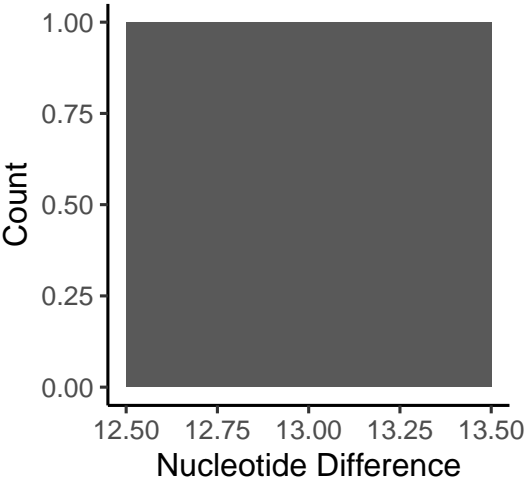
IGHV3-20*03_04

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



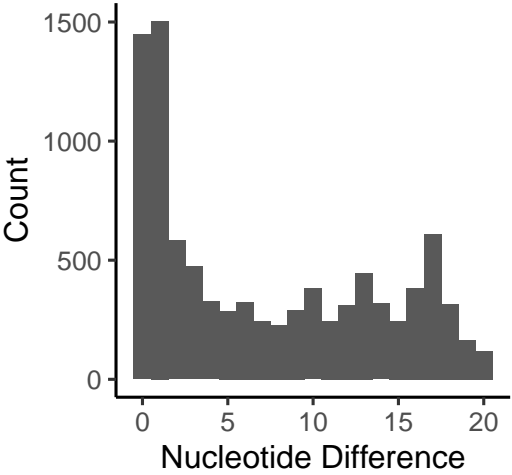
IGHV3-22*01_02

1 sequences assigned
No exact matches.



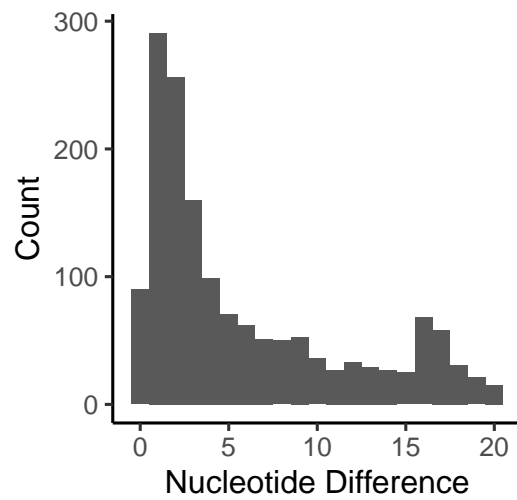
IGHV3-33*01

11611 sequences assigned
1448 (12.5%) exact matches, in which:
961 unique CDR3
7 unique J



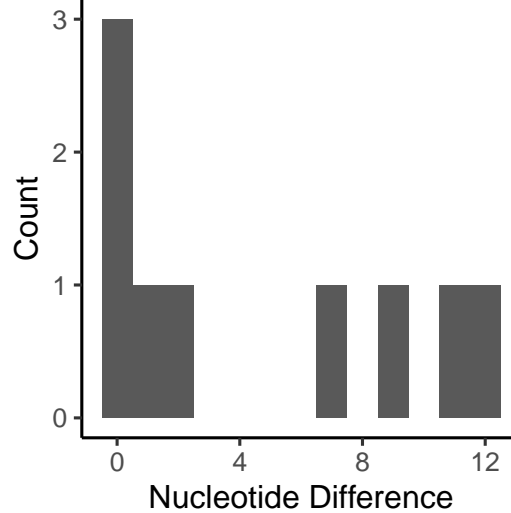
IGHV3-33*06

1675 sequences assigned
90 (5.4%) exact matches, in which:
87 unique CDR3
7 unique J



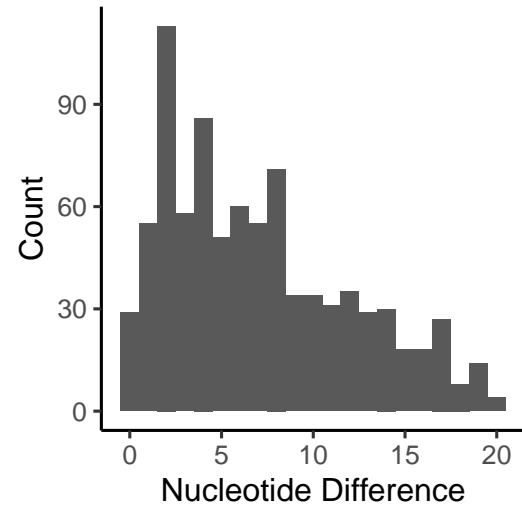
IGHV3-47*02

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



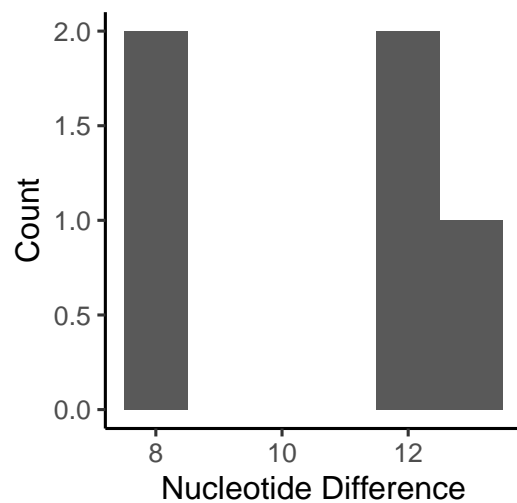
IGHV3-48*04

901 sequences assigned
29 (3.2%) exact matches, in which:
29 unique CDR3
5 unique J



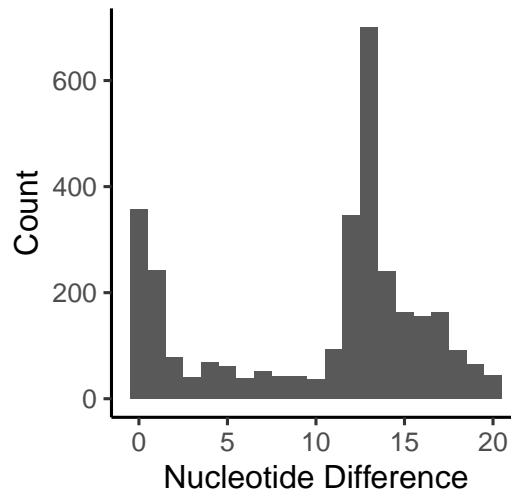
IGHV3-35*01

5 sequences assigned
No exact matches.



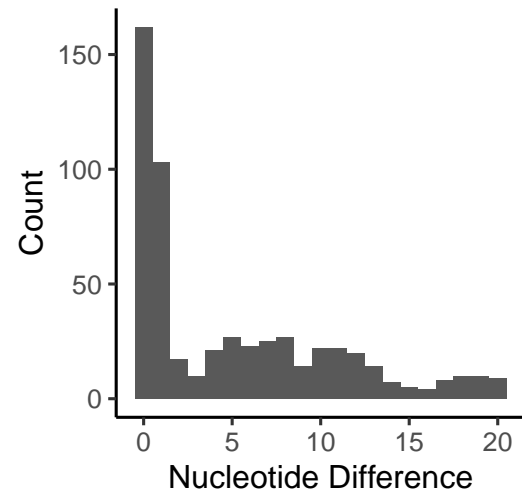
IGHV3-48*02

3369 sequences assigned
357 (10.6%) exact matches, in which:
242 unique CDR3
7 unique J



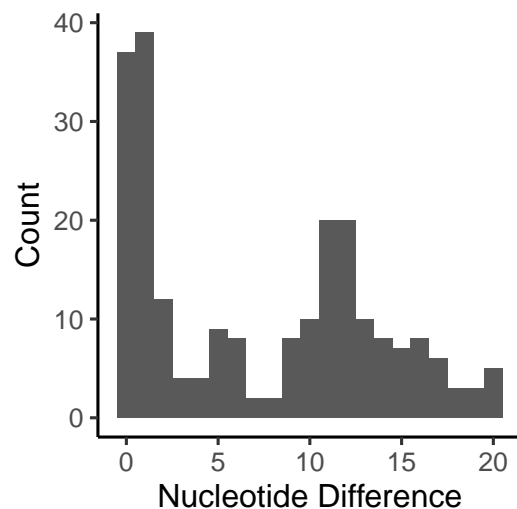
IGHV3-49*04

1122 sequences assigned
162 (14.4%) exact matches, in which:
104 unique CDR3
7 unique J



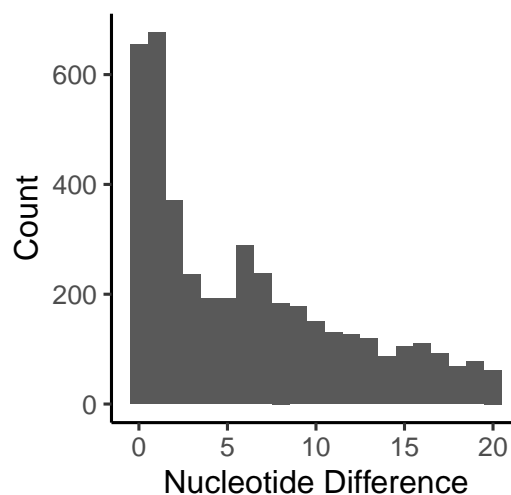
IGHV3-43*01

254 sequences assigned
37 (14.6%) exact matches, in which:
26 unique CDR3
5 unique J



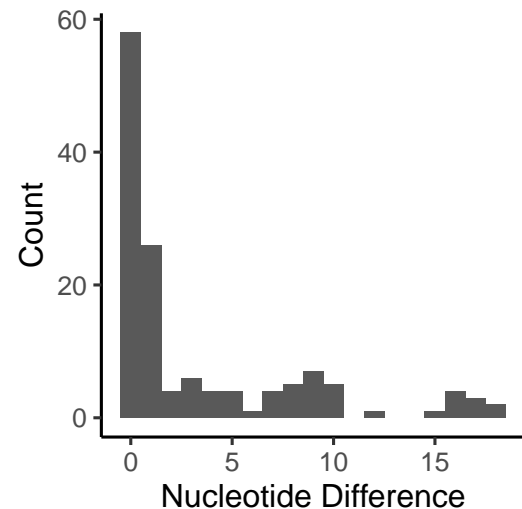
IGHV3-48*03

4869 sequences assigned
654 (13.4%) exact matches, in which:
421 unique CDR3
7 unique J



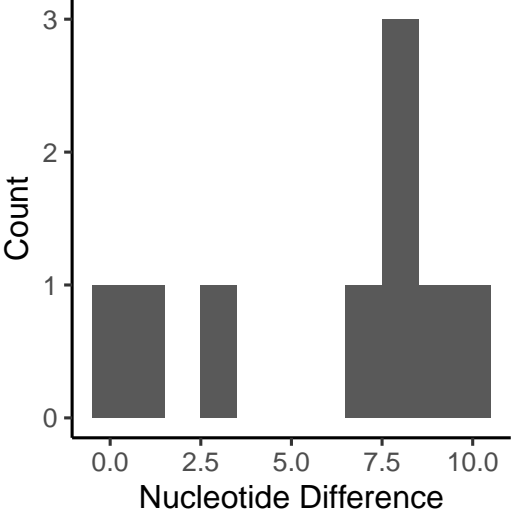
IGHV3-49*03_05

291 sequences assigned
58 (19.9%) exact matches, in which:
43 unique CDR3
5 unique J



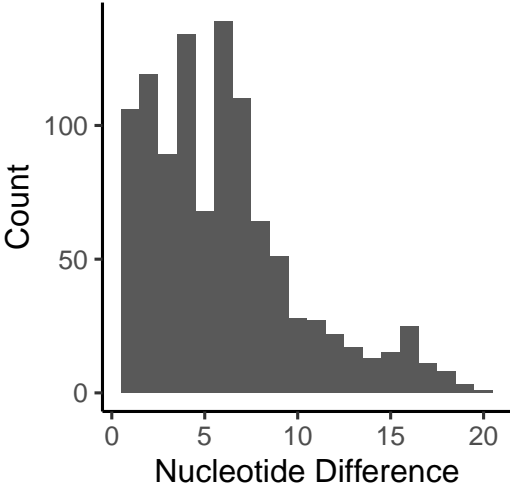
IGHV3-52*01_03

9 sequences assigned
1 (11.1%) exact matches, in which:
1 unique CDR3
1 unique J



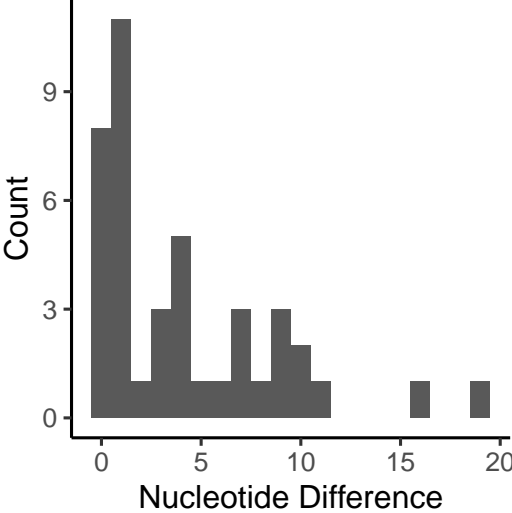
IGHV3-64*04

1076 sequences assigned
No exact matches.



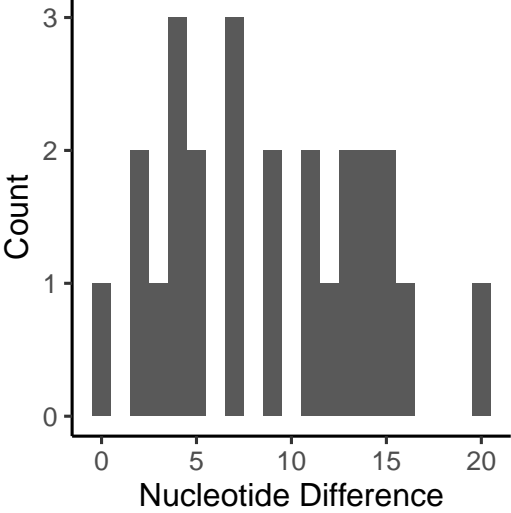
IGHV3-66*03

44 sequences assigned
8 (18.2%) exact matches, in which:
8 unique CDR3
4 unique J



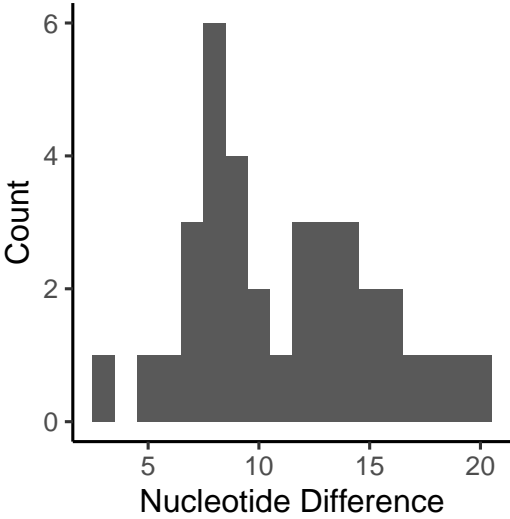
IGHV3-53*05

26 sequences assigned
1 (3.8%) exact matches, in which:
1 unique CDR3
1 unique J



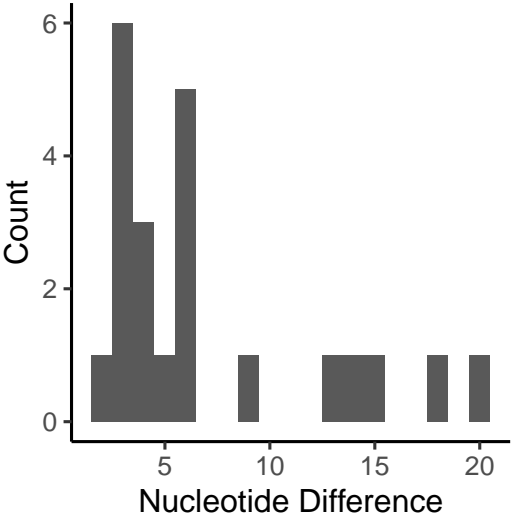
IGHV3-66*01

41 sequences assigned
No exact matches.



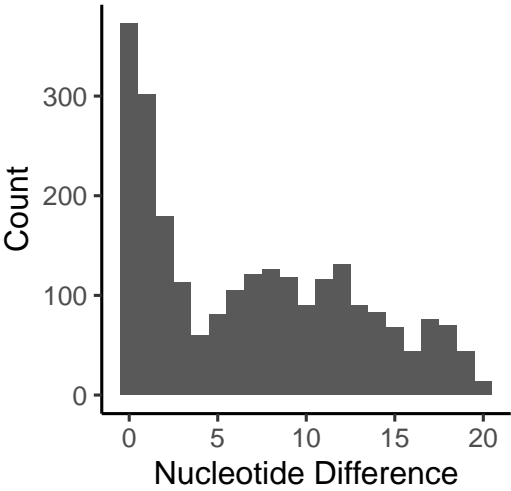
IGHV3-69-1*01

24 sequences assigned
No exact matches.



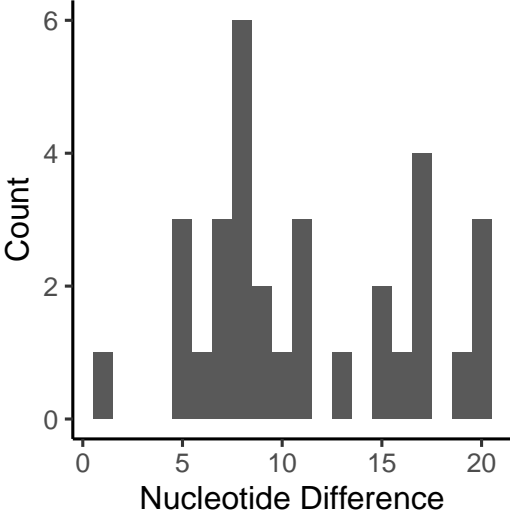
IGHV3-53*01_02

2834 sequences assigned
373 (13.2%) exact matches, in which:
235 unique CDR3
7 unique J



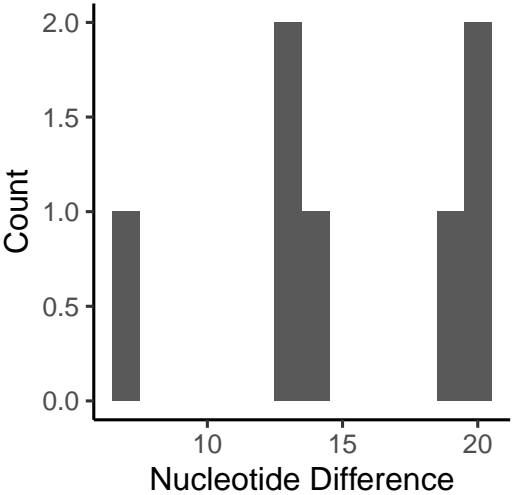
IGHV3-66*02

40 sequences assigned
No exact matches.



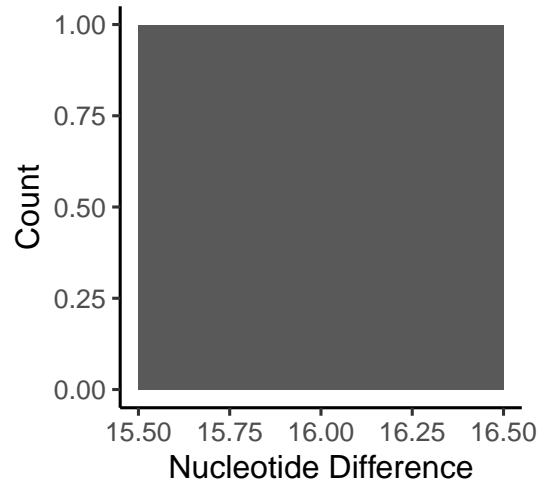
IGHV3-69-1*02

9 sequences assigned
No exact matches.



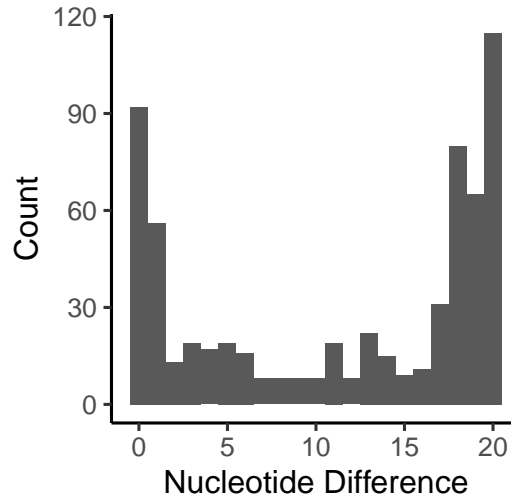
IGHV3-71*03

1 sequences assigned
No exact matches.



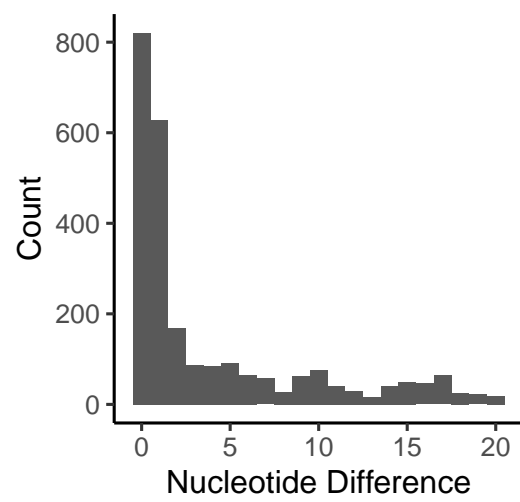
IGHV3-73*01_02

777 sequences assigned
92 (11.8%) exact matches, in which:
58 unique CDR3
6 unique J



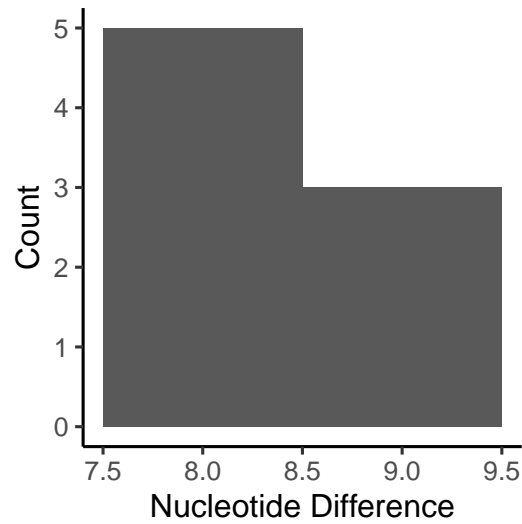
IGHV3-64D*06

2678 sequences assigned
821 (30.7%) exact matches, in which:
497 unique CDR3
7 unique J



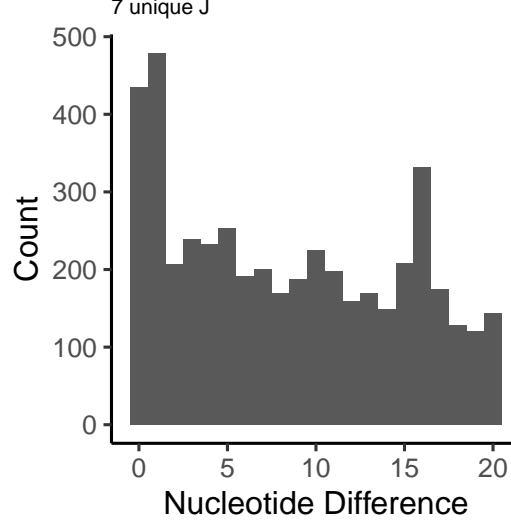
IGHV3-71*01_04

9 sequences assigned
No exact matches.



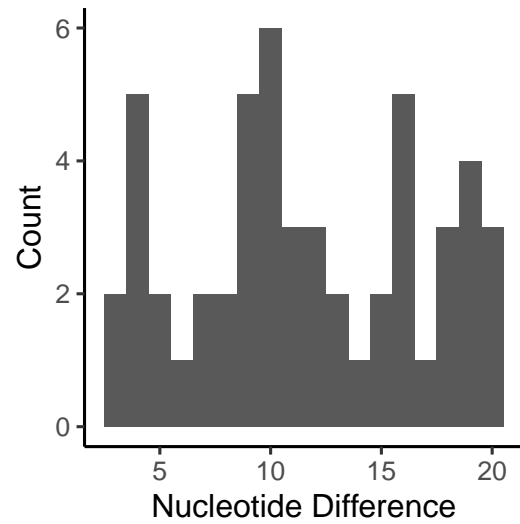
IGHV3-74*01_02

5389 sequences assigned
435 (8.1%) exact matches, in which:
294 unique CDR3
7 unique J



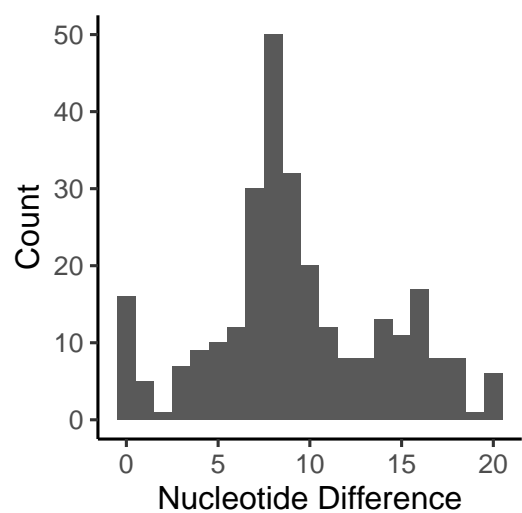
IGHV3-NL1*01

72 sequences assigned
No exact matches.



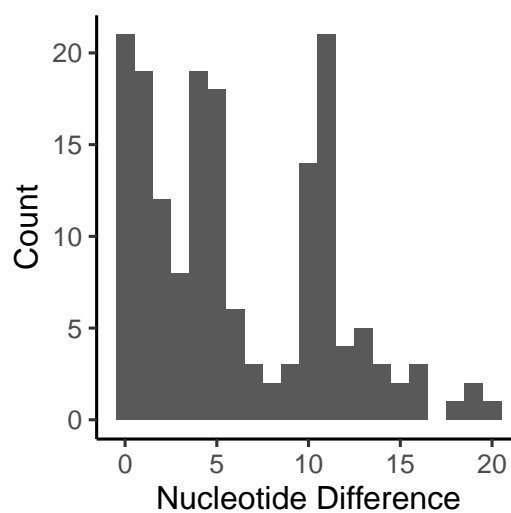
IGHV3-72*01

292 sequences assigned
16 (5.5%) exact matches, in which:
9 unique CDR3
4 unique J



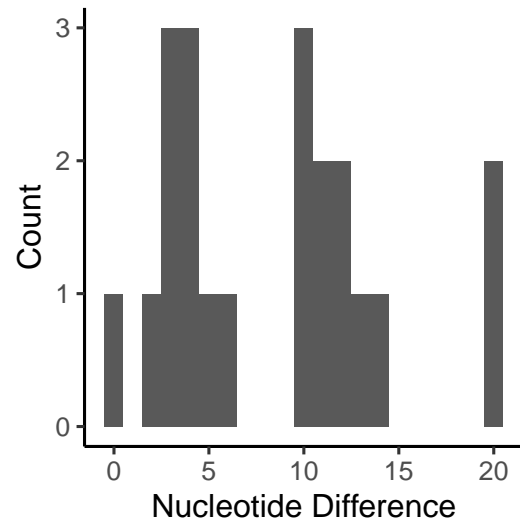
IGHV3-43D*04

172 sequences assigned
21 (12.2%) exact matches, in which:
14 unique CDR3
3 unique J



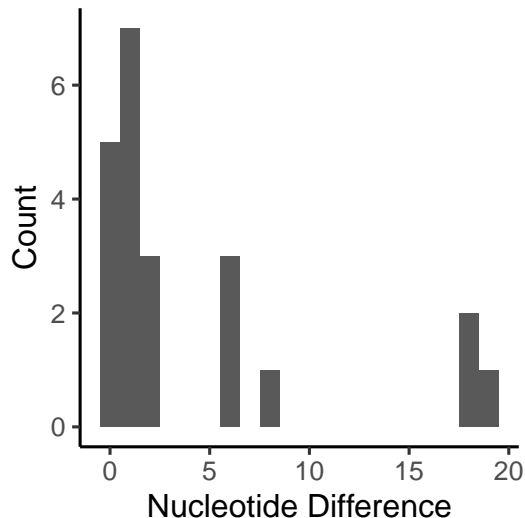
IGHV4-28*03

28 sequences assigned
1 (3.6%) exact matches, in which:
1 unique CDR3
1 unique J



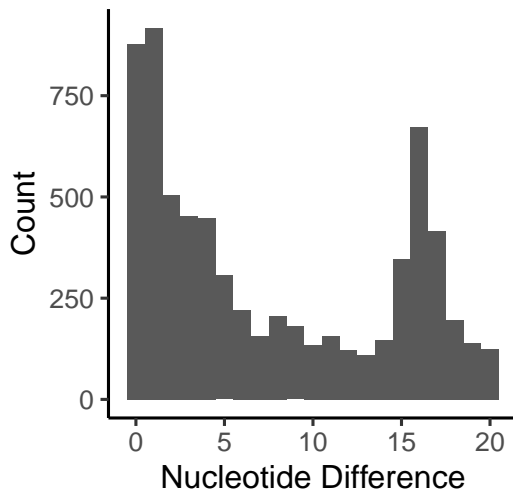
IGHV4-28*01_07

23 sequences assigned
5 (21.7%) exact matches, in which:
2 unique CDR3
2 unique J



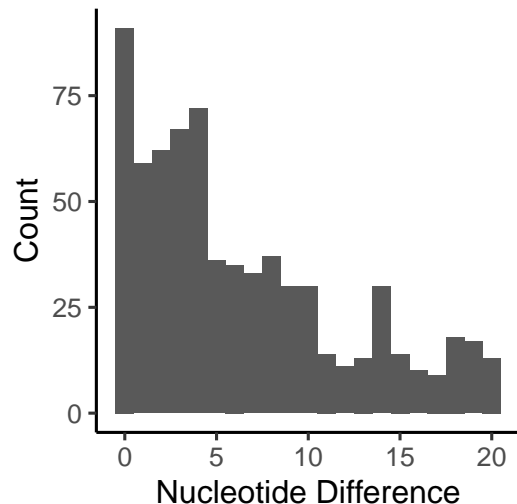
IGHV4-31*03_04

8347 sequences assigned
878 (10.5%) exact matches, in which:
666 unique CDR3
7 unique J



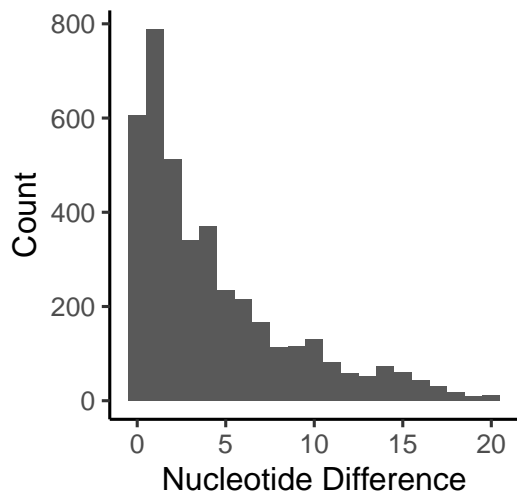
IGHV4-38-2*02

875 sequences assigned
91 (10.4%) exact matches, in which:
71 unique CDR3
6 unique J



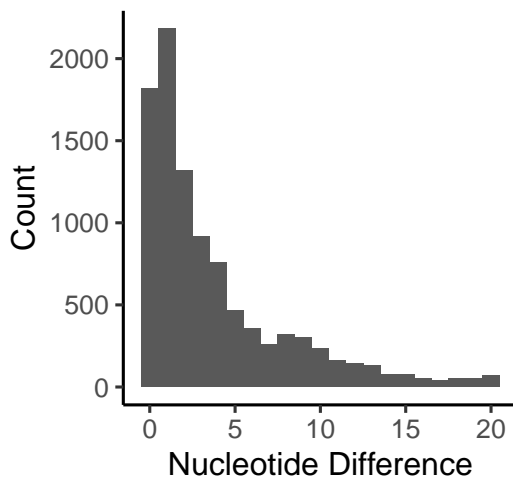
IGHV4-30-2*01

4176 sequences assigned
605 (14.5%) exact matches, in which:
412 unique CDR3
7 unique J



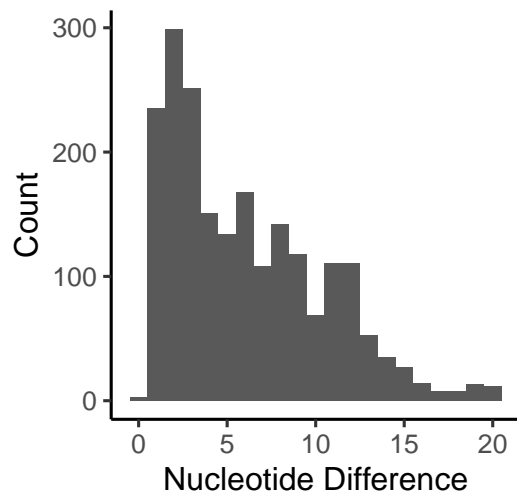
IGHV4-34*01_02

13202 sequences assigned
1817 (13.8%) exact matches, in which:
1222 unique CDR3
7 unique J



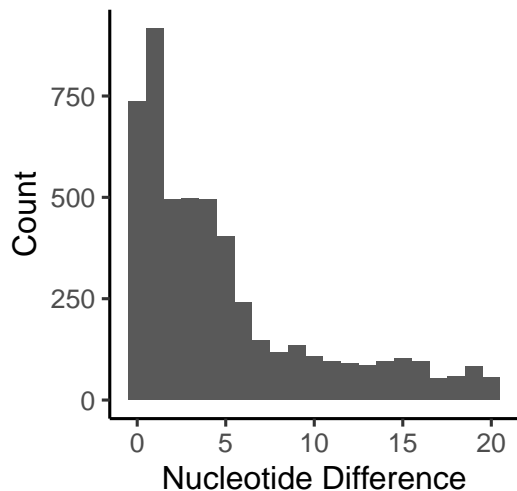
IGHV4-39*07

2143 sequences assigned
3 (0.1%) exact matches, in which:
3 unique CDR3
3 unique J



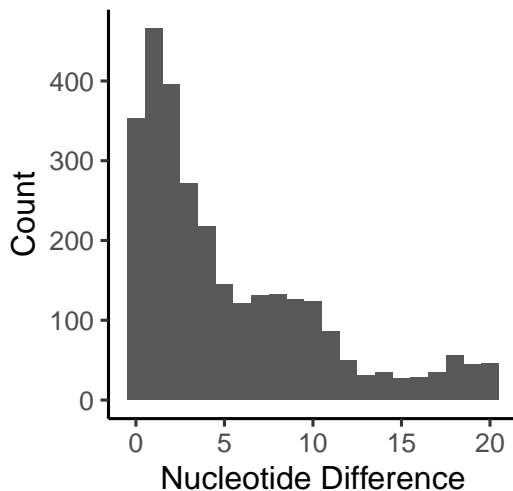
IGHV4-30-4*01

5664 sequences assigned
736 (13%) exact matches, in which:
554 unique CDR3
7 unique J



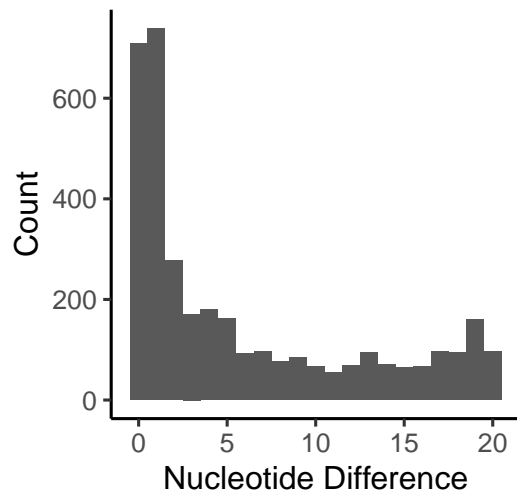
IGHV4-38-2*01

3813 sequences assigned
353 (9.3%) exact matches, in which:
296 unique CDR3
7 unique J



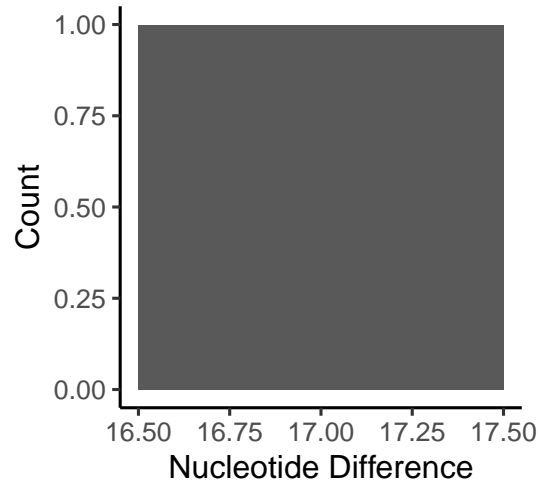
IGHV4-39*01_05

3844 sequences assigned
709 (18.4%) exact matches, in which:
516 unique CDR3
7 unique J



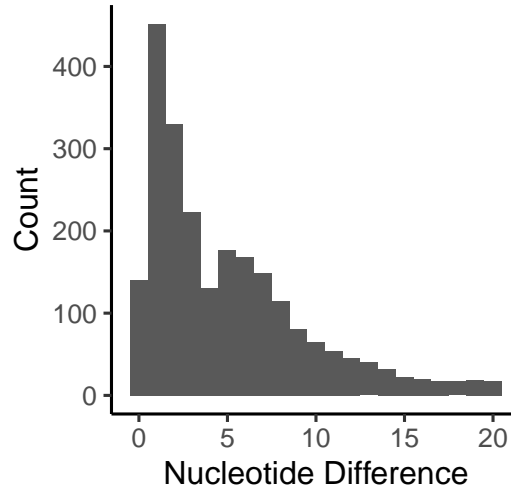
IGHV4-55*01_05

1 sequences assigned
No exact matches.



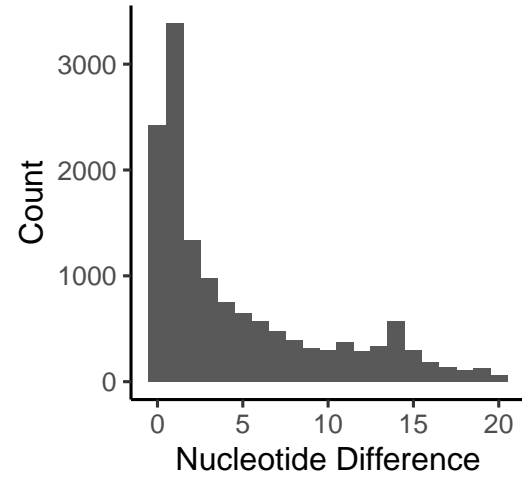
IGHV4-59*12

2383 sequences assigned
140 (5.9%) exact matches, in which:
135 unique CDR3
7 unique J



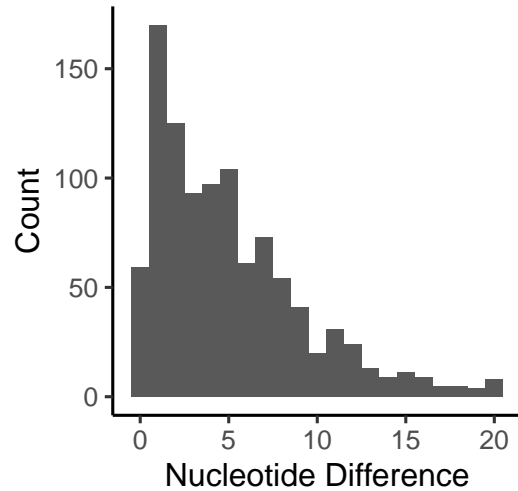
IGHV5-10-1*01_03

14249 sequences assigned
2428 (17%) exact matches, in which:
1340 unique CDR3
7 unique J



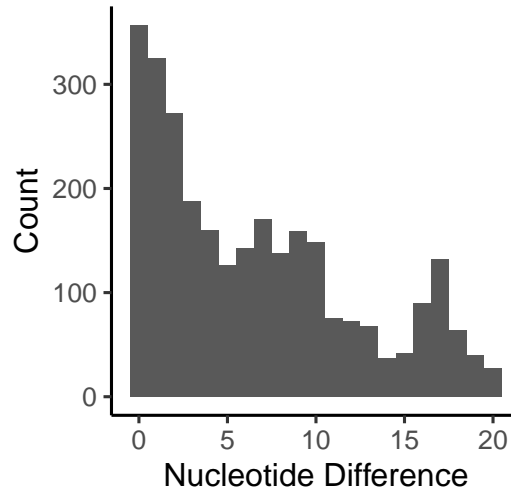
IGHV4-59*08

1053 sequences assigned
59 (5.6%) exact matches, in which:
57 unique CDR3
7 unique J



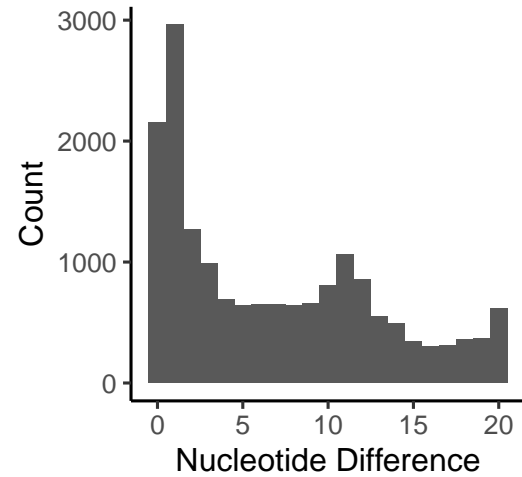
IGHV4-61*01

3064 sequences assigned
357 (11.7%) exact matches, in which:
301 unique CDR3
7 unique J



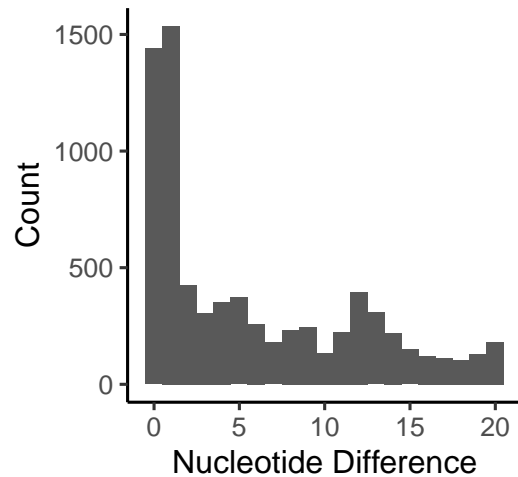
IGHV5-51*01_03

20507 sequences assigned
2154 (10.5%) exact matches, in which:
1181 unique CDR3
7 unique J



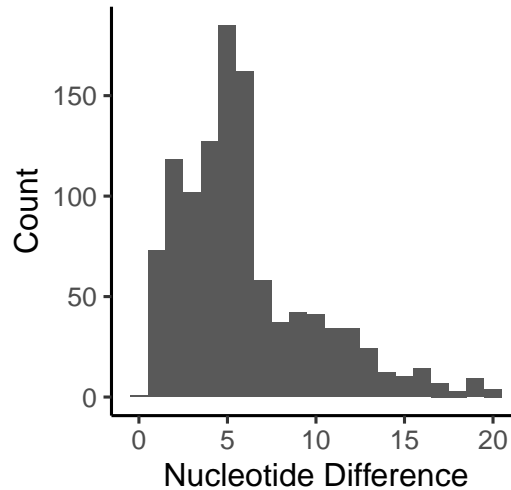
IGHV4-59*01_07

8656 sequences assigned
1440 (16.6%) exact matches, in which:
1125 unique CDR3
7 unique J



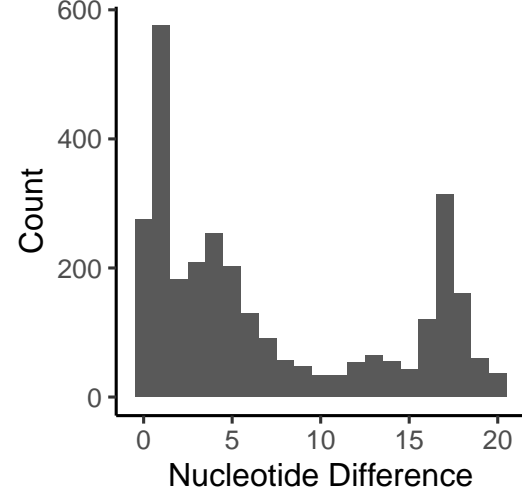
IGHV4-61*08

1155 sequences assigned
1 (0.1%) exact matches, in which:
1 unique CDR3
1 unique J



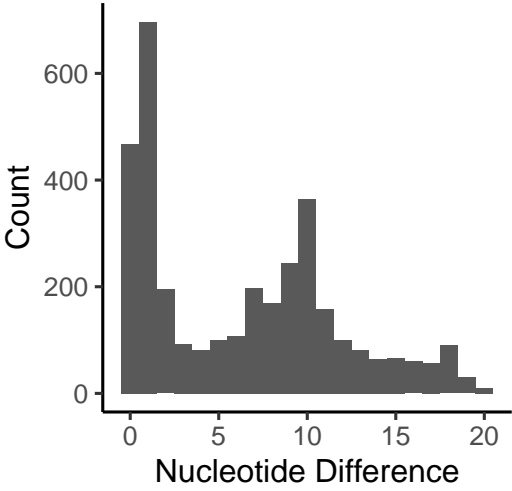
IGHV6-1*01_02

3113 sequences assigned
275 (8.8%) exact matches, in which:
227 unique CDR3
7 unique J



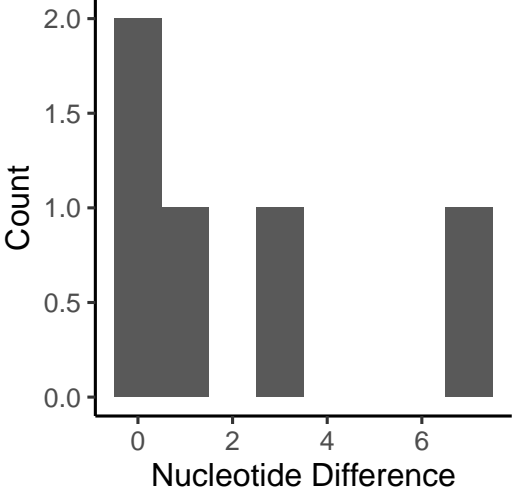
IGHV7-4-1*02

3618 sequences assigned
467 (12.9%) exact matches, in which:
360 unique CDR3
7 unique J

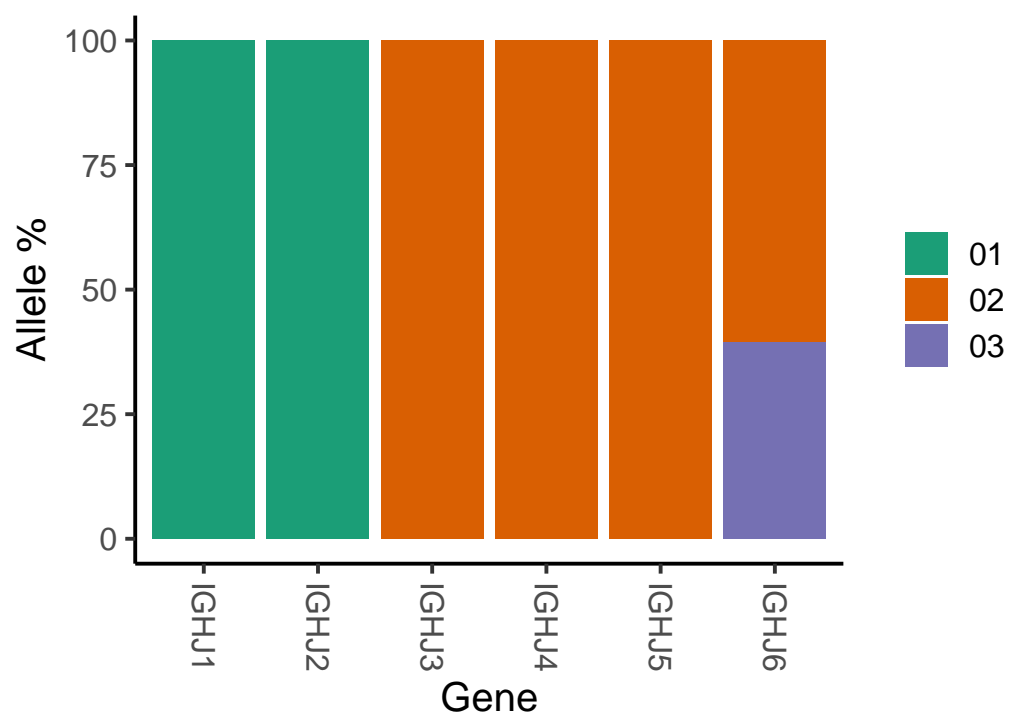


IGHV7-81*01

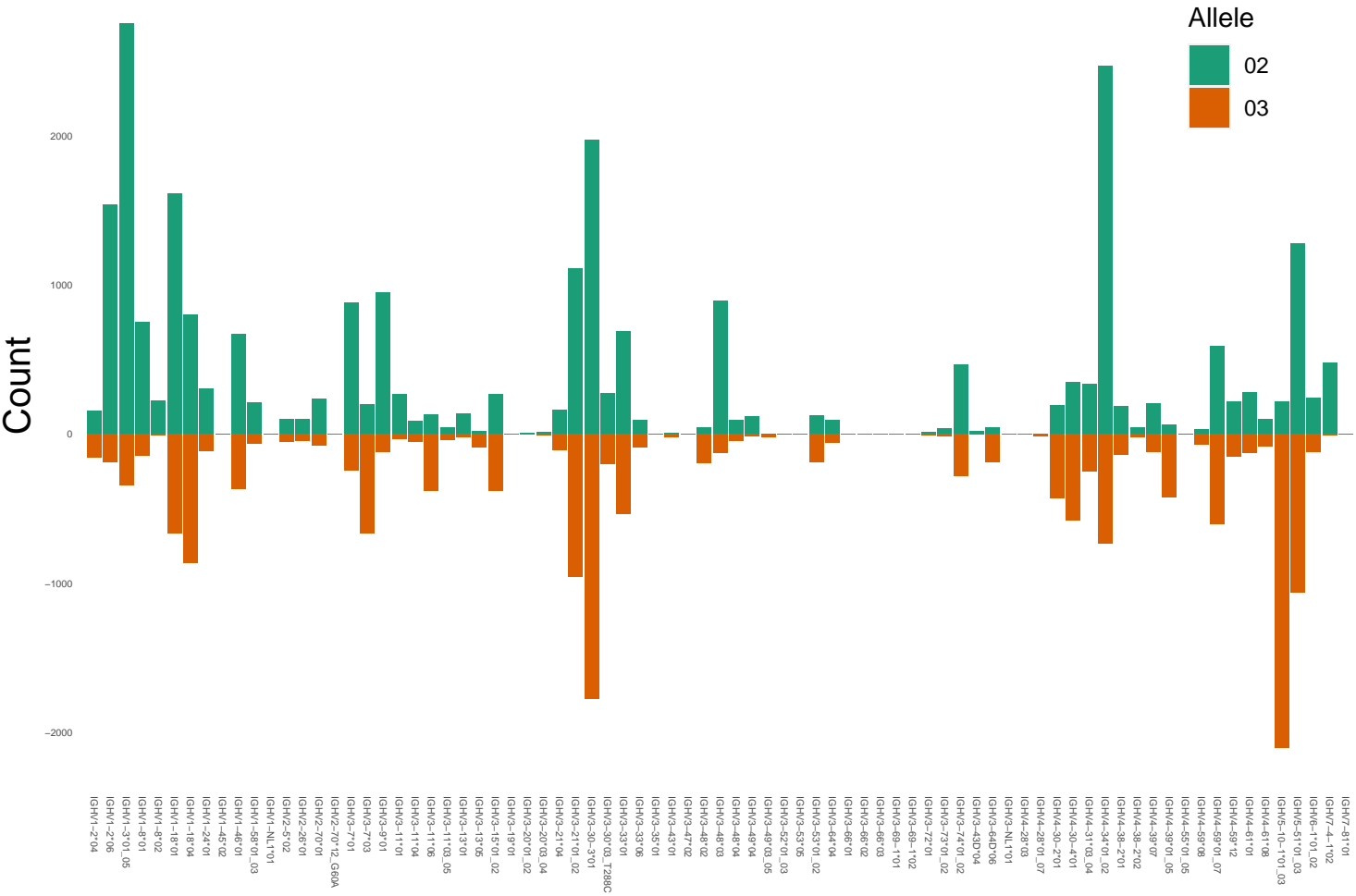
5 sequences assigned
2 (40%) exact matches, in which:
2 unique CDR3
2 unique J



Allele Usage



Sequence Count by IGHJ6 allele usage



Warning – no inferred sequences found.

Novel sequence(s) IGHV1–69*08_C191T IGHV3–48*03_T303G IGHV4–59*02_G88A 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 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.