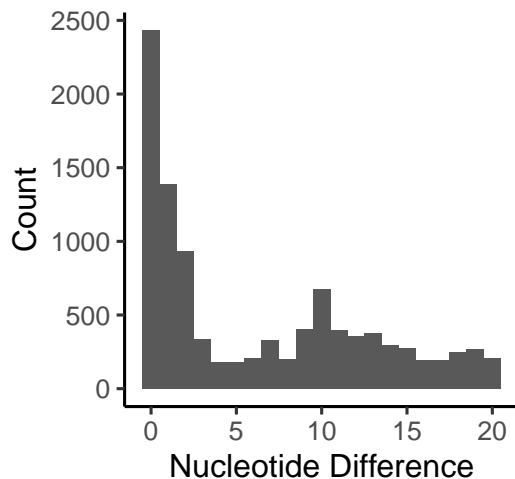


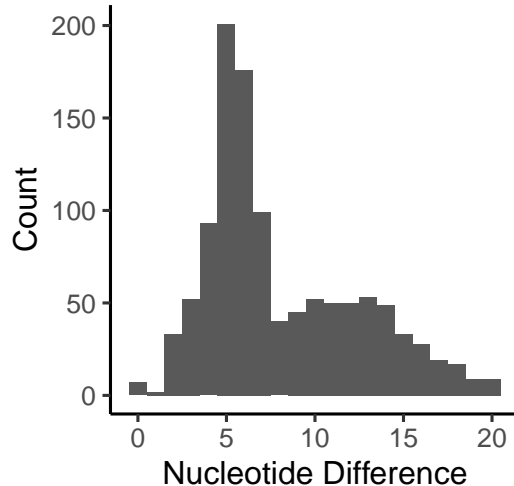
IGHV1-2*02

11170 sequences assigned
2432 (21.8%) exact matches, in which:
2284 unique CDR3
7 unique J



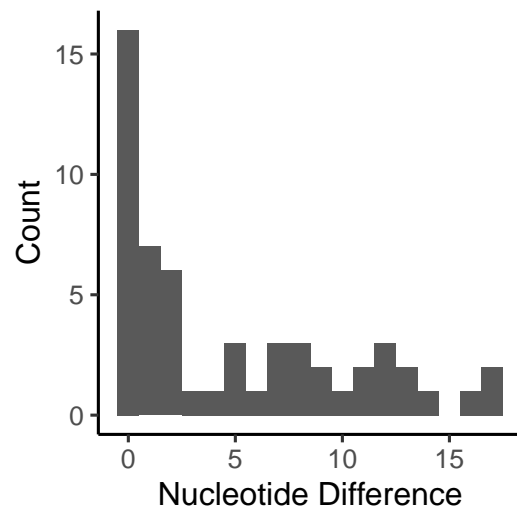
IGHV1-8*02

1194 sequences assigned
7 (0.6%) exact matches, in which:
7 unique CDR3
5 unique J



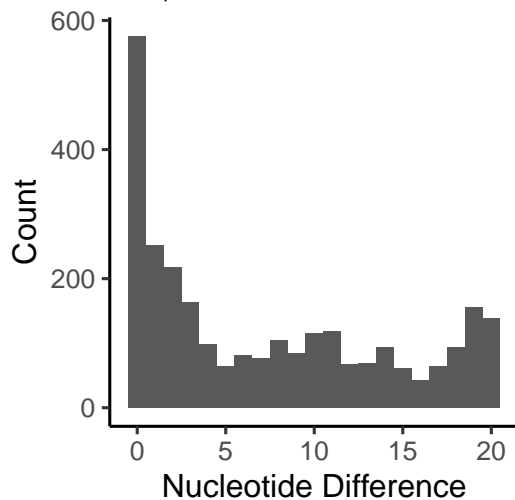
IGHV1-45*02

56 sequences assigned
16 (28.6%) exact matches, in which:
16 unique CDR3
4 unique J



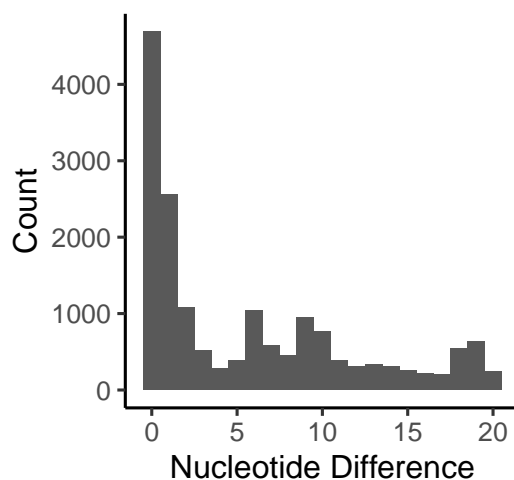
IGHV1-3*01_05

3689 sequences assigned
576 (15.6%) exact matches, in which:
534 unique CDR3
7 unique J



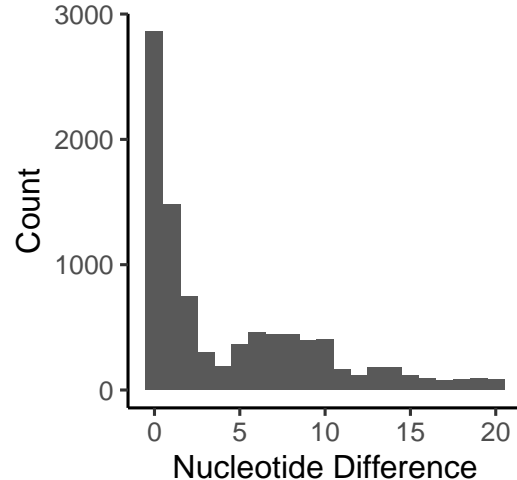
IGHV1-18*01

23939 sequences assigned
4689 (19.6%) exact matches, in which:
4324 unique CDR3
7 unique J



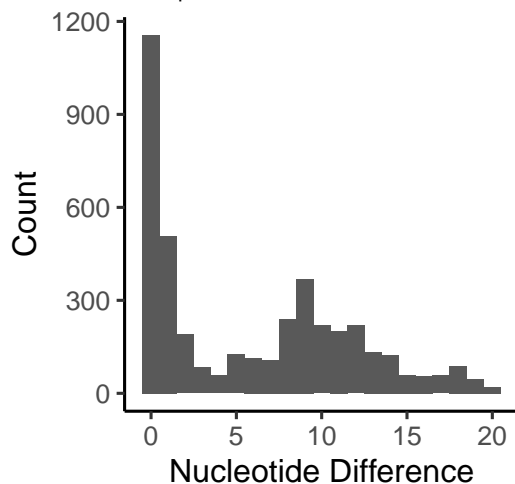
IGHV1-46*01

10450 sequences assigned
2859 (27.4%) exact matches, in which:
2694 unique CDR3
7 unique J



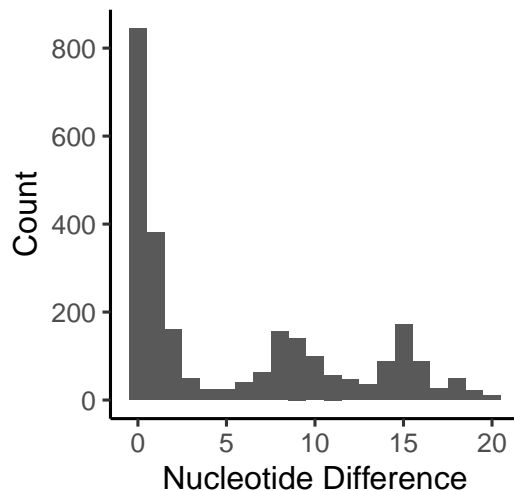
IGHV1-8*01

4690 sequences assigned
1156 (24.6%) exact matches, in which:
1107 unique CDR3
7 unique J



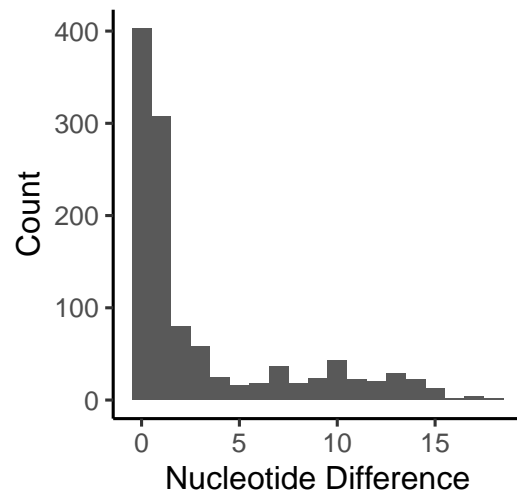
IGHV1-24*01

2636 sequences assigned
845 (32.1%) exact matches, in which:
800 unique CDR3
7 unique J



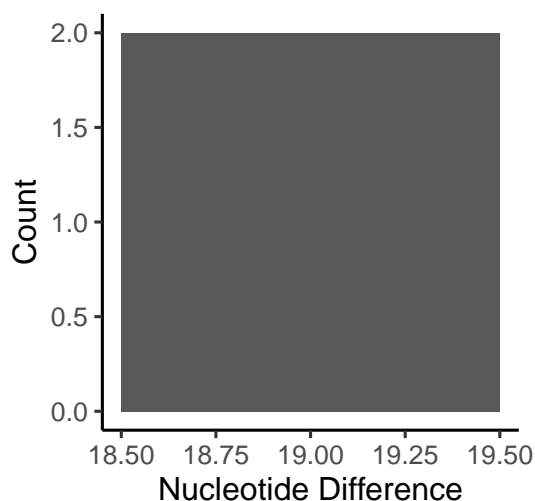
IGHV1-58*01_03

1166 sequences assigned
403 (34.6%) exact matches, in which:
377 unique CDR3
7 unique J



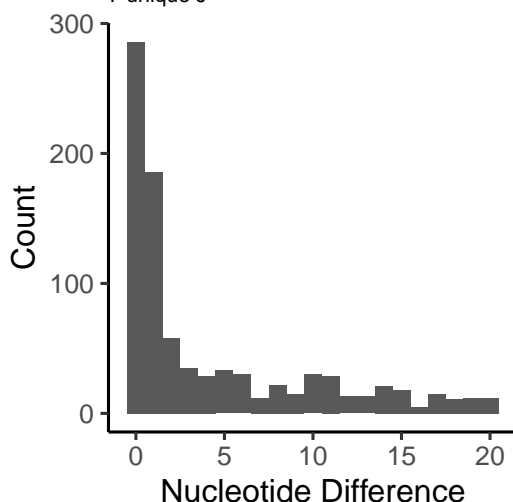
IGHV1-69-2*01

2 sequences assigned
No exact matches.



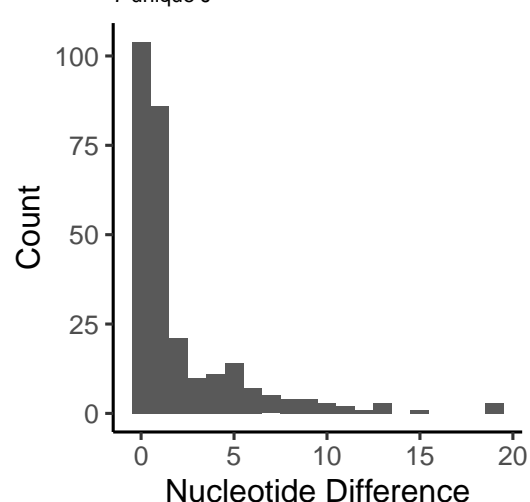
IGHV2-5*02

990 sequences assigned
286 (28.9%) exact matches, in which:
261 unique CDR3
7 unique J



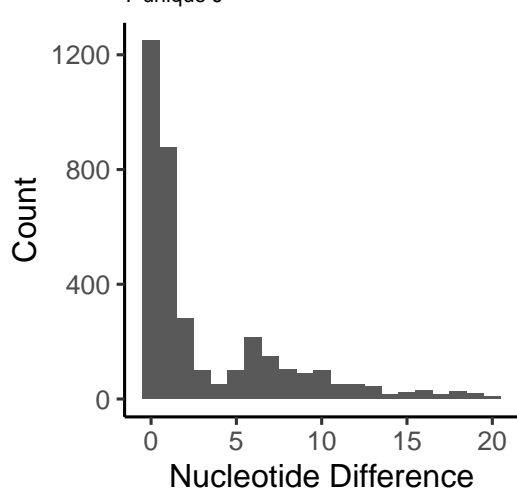
IGHV2-70*11_15

281 sequences assigned
104 (37%) exact matches, in which:
100 unique CDR3
7 unique J



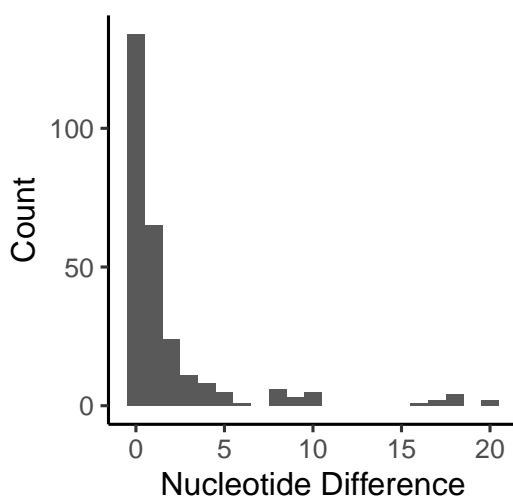
IGHV1-69*04_09

3724 sequences assigned
1249 (33.5%) exact matches, in which:
1188 unique CDR3
7 unique J



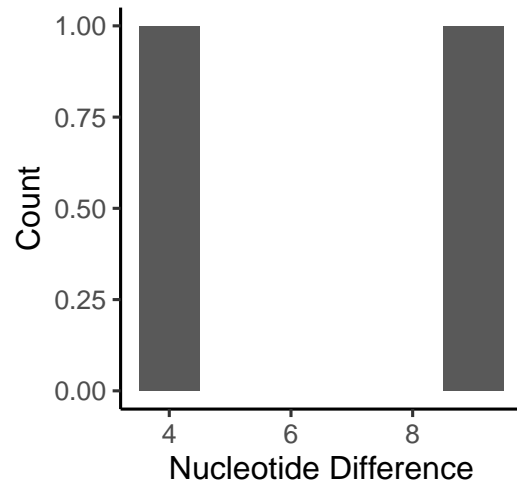
IGHV2-26*01

281 sequences assigned
134 (47.7%) exact matches, in which:
124 unique CDR3
6 unique J



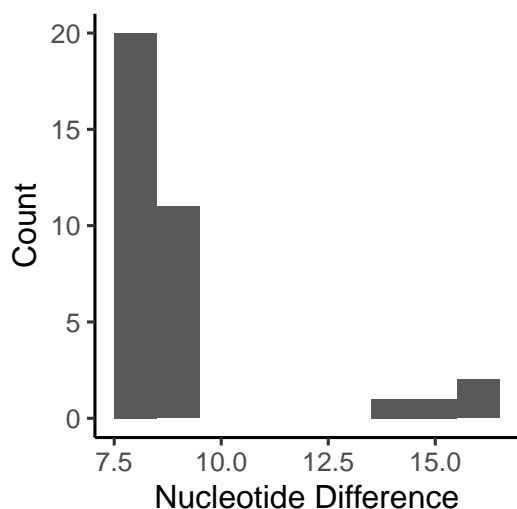
IGHV2-70D*04

2 sequences assigned
No exact matches.



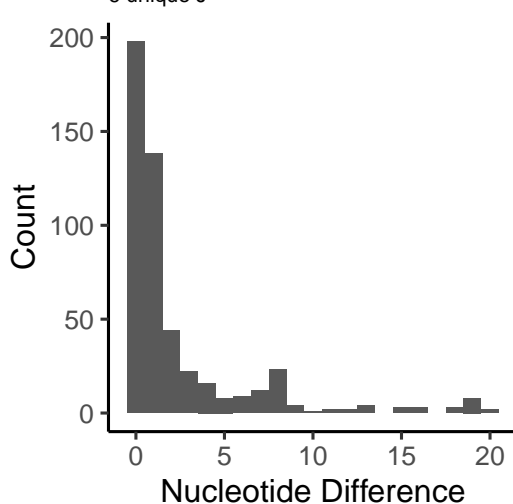
IGHV1-NL1*01

35 sequences assigned
No exact matches.



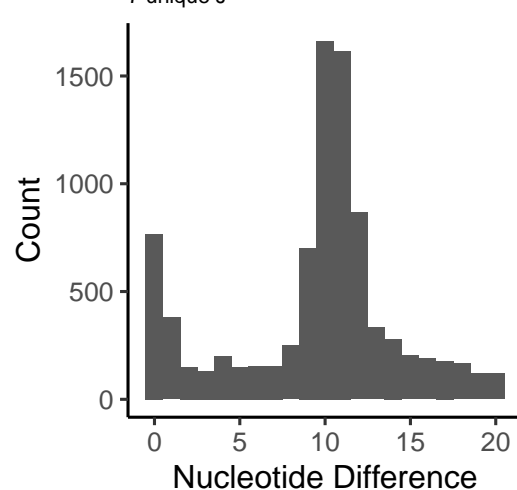
IGHV2-70*01

509 sequences assigned
198 (38.9%) exact matches, in which:
178 unique CDR3
6 unique J



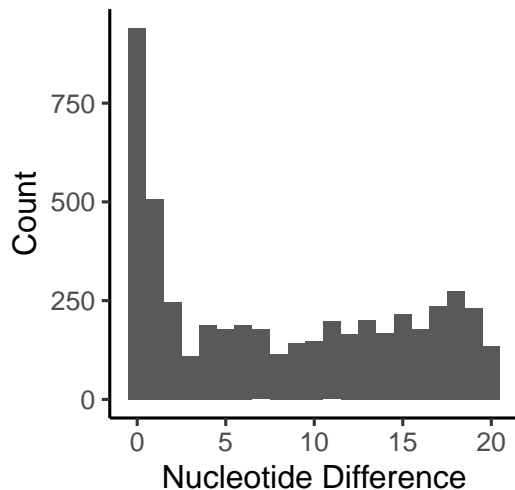
IGHV3-7*01

9319 sequences assigned
768 (8.2%) exact matches, in which:
629 unique CDR3
7 unique J



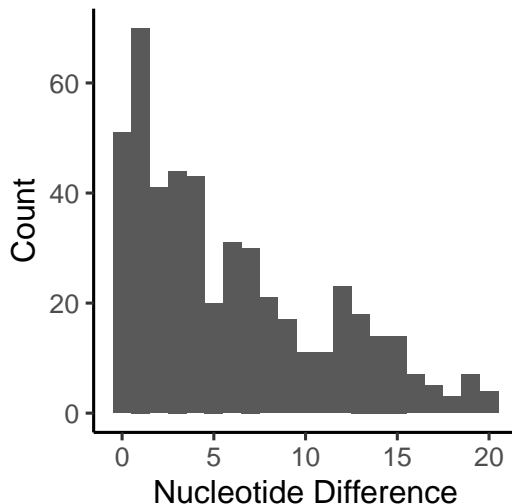
IGHV3-7*03

5750 sequences assigned
941 (16.4%) exact matches, in which:
752 unique CDR3
7 unique J



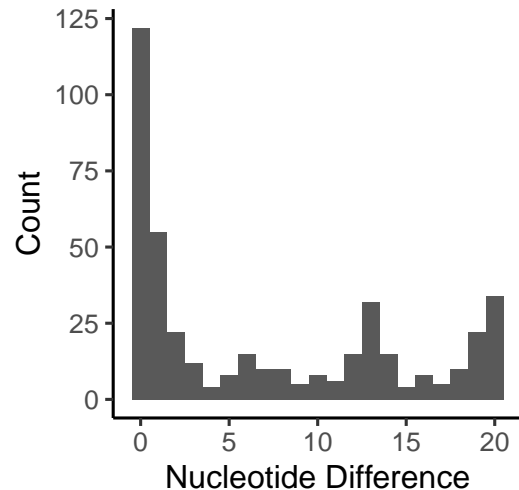
IGHV3-11*04

523 sequences assigned
51 (9.8%) exact matches, in which:
51 unique CDR3
7 unique J



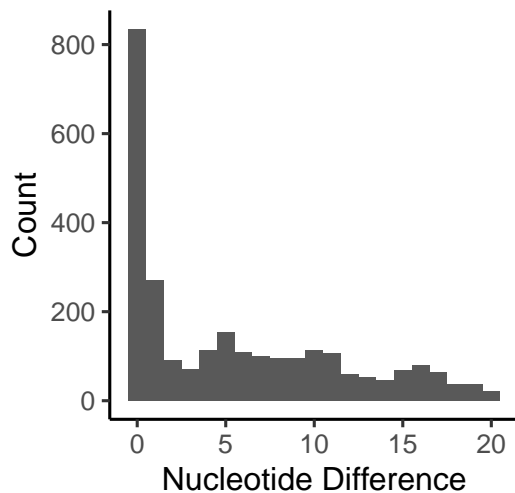
IGHV3-13*01

516 sequences assigned
122 (23.6%) exact matches, in which:
91 unique CDR3
6 unique J



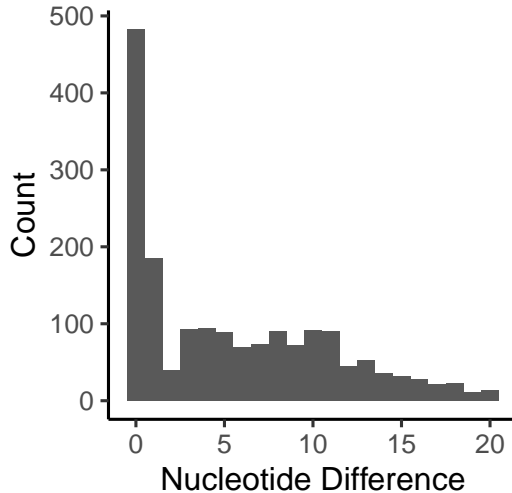
IGHV3-9*01

3098 sequences assigned
835 (27%) exact matches, in which:
656 unique CDR3
7 unique J



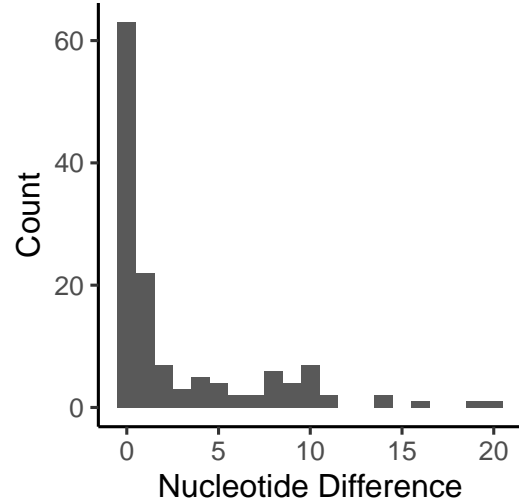
IGHV3-11*06

2003 sequences assigned
483 (24.1%) exact matches, in which:
391 unique CDR3
6 unique J



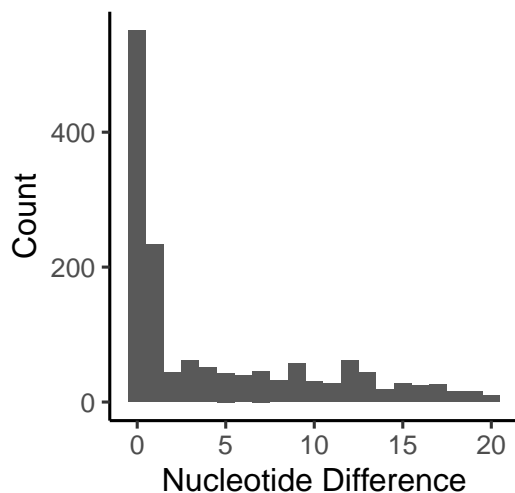
IGHV3-13*05

141 sequences assigned
63 (44.7%) exact matches, in which:
50 unique CDR3
6 unique J



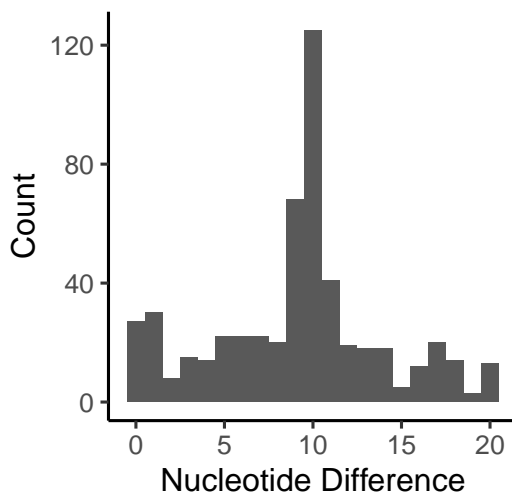
IGHV3-11*01

1547 sequences assigned
551 (35.6%) exact matches, in which:
425 unique CDR3
7 unique J



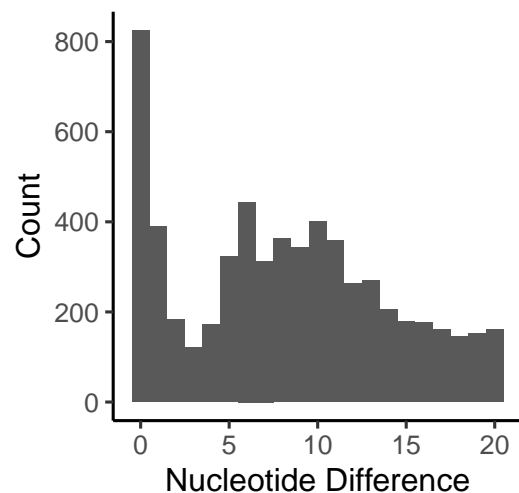
IGHV3-11*03_05

574 sequences assigned
27 (4.7%) exact matches, in which:
27 unique CDR3
5 unique J



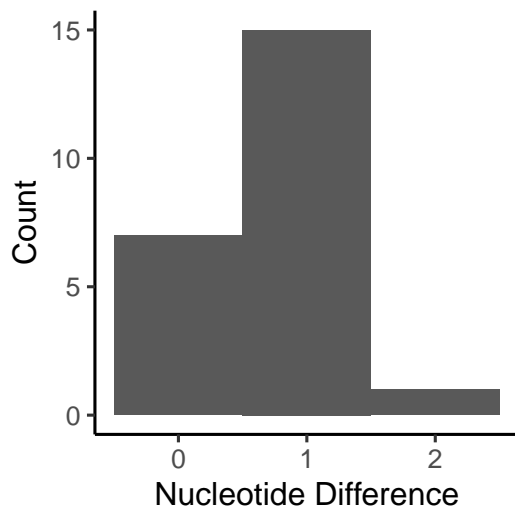
IGHV3-15*01_02

6821 sequences assigned
825 (12.1%) exact matches, in which:
626 unique CDR3
7 unique J



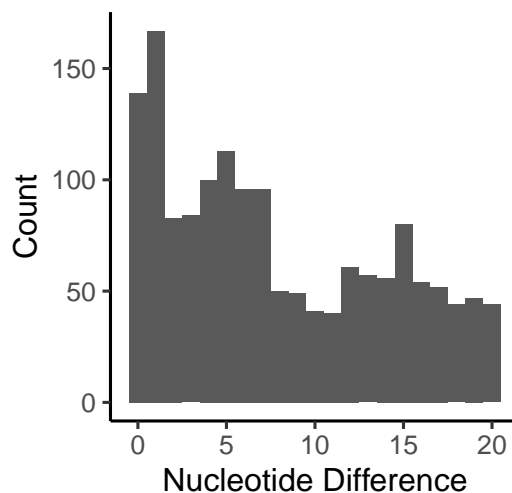
IGHV3-19*01

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



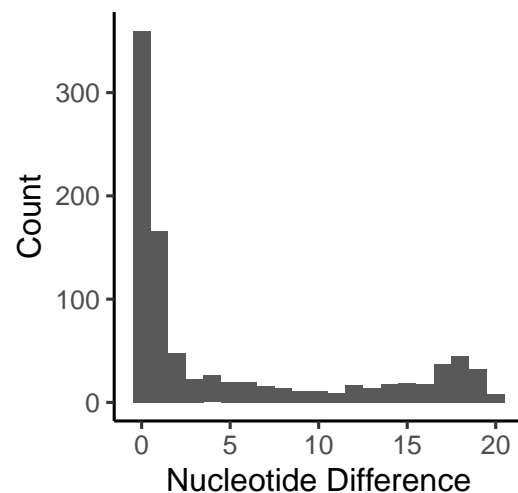
IGHV3-21*04

1790 sequences assigned
139 (7.8%) exact matches, in which:
135 unique CDR3
6 unique J



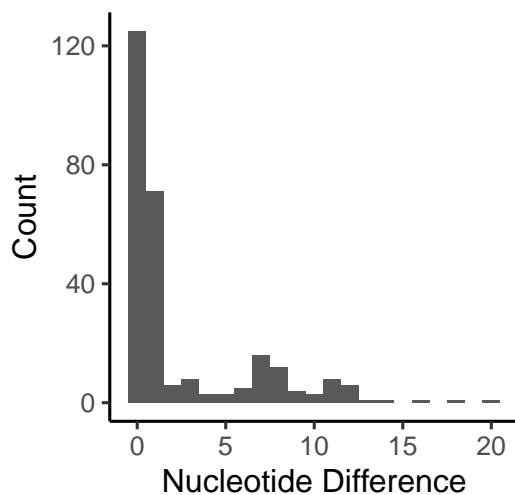
IGHV3-30*03

1217 sequences assigned
360 (29.6%) exact matches, in which:
342 unique CDR3
7 unique J



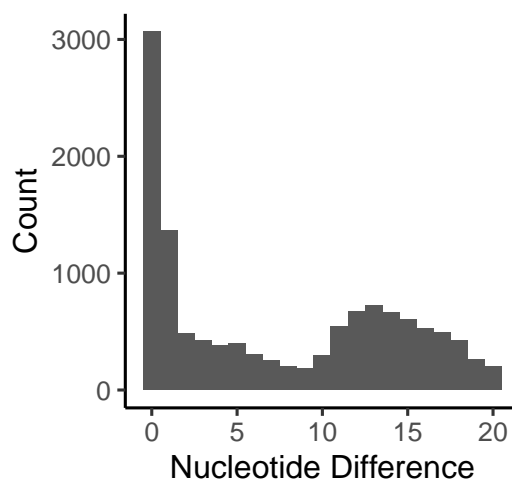
IGHV3-20*01_02

295 sequences assigned
125 (42.4%) exact matches, in which:
91 unique CDR3
6 unique J



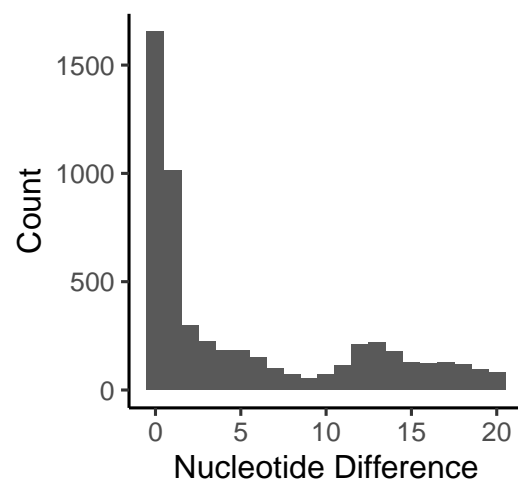
IGHV3-21*01_02

13512 sequences assigned
3066 (22.7%) exact matches, in which:
2410 unique CDR3
7 unique J



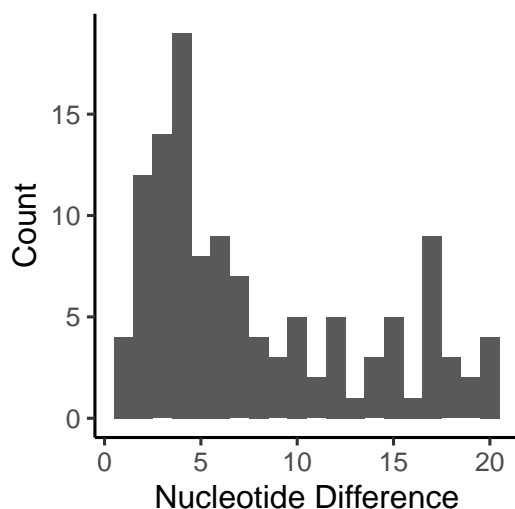
IGHV3-33*01

6003 sequences assigned
1654 (27.6%) exact matches, in which:
1363 unique CDR3
7 unique J



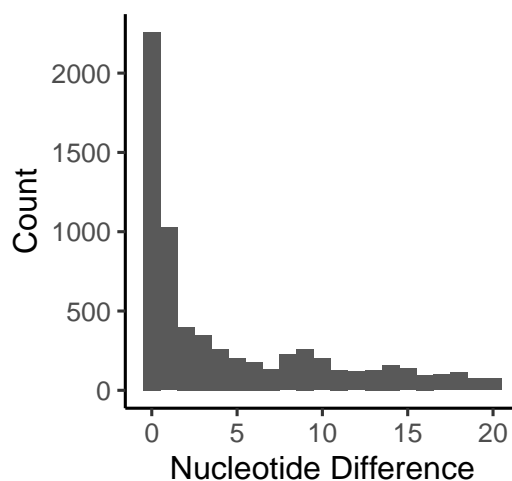
IGHV3-20*03_04

138 sequences assigned
No exact matches.



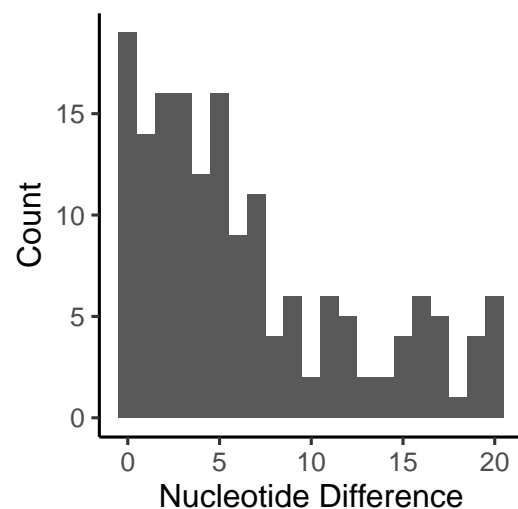
IGHV3-30-3*01

7265 sequences assigned
2259 (31.1%) exact matches, in which:
1810 unique CDR3
7 unique J



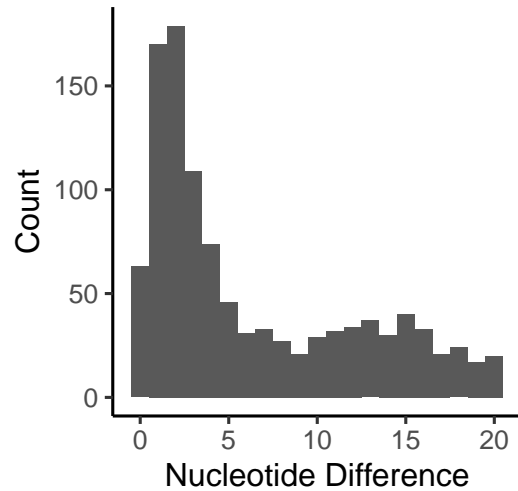
IGHV3-33*05

223 sequences assigned
19 (8.5%) exact matches, in which:
19 unique CDR3
5 unique J



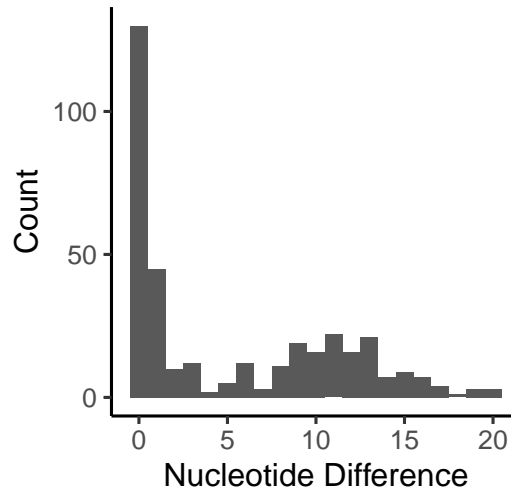
IGHV3–33*06

1166 sequences assigned
63 (5.4%) exact matches, in which:
60 unique CDR3
6 unique J



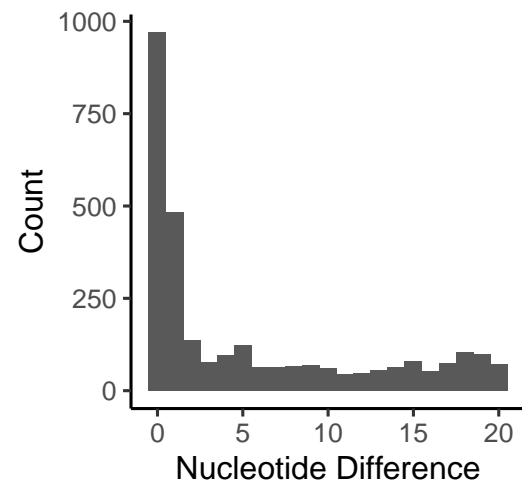
IGHV3–43*01

386 sequences assigned
130 (33.7%) exact matches, in which:
104 unique CDR3
7 unique J



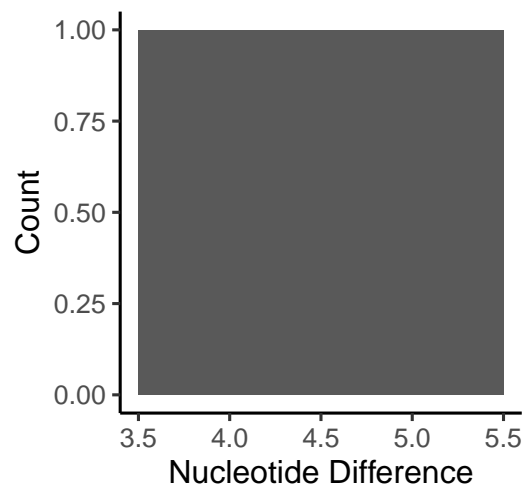
IGHV3–48*02

3970 sequences assigned
970 (24.4%) exact matches, in which:
752 unique CDR3
7 unique J



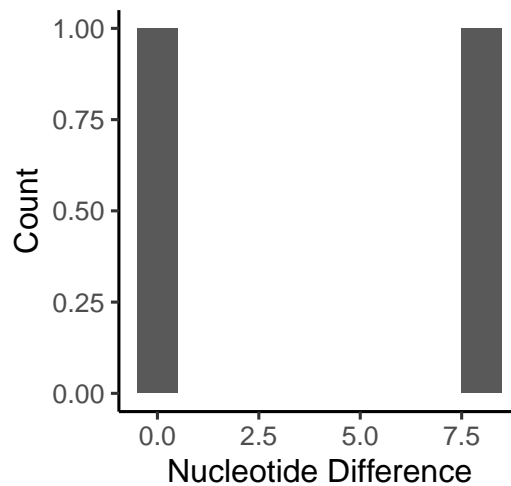
IGHV3–35*01

2 sequences assigned
No exact matches.



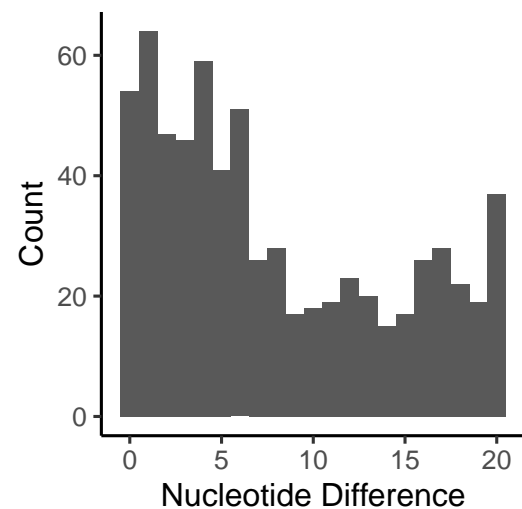
IGHV3–47*02

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



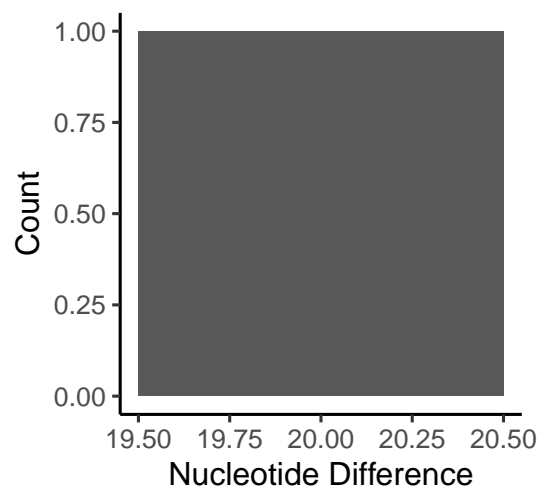
IGHV3–48*04

927 sequences assigned
54 (5.8%) exact matches, in which:
53 unique CDR3
6 unique J



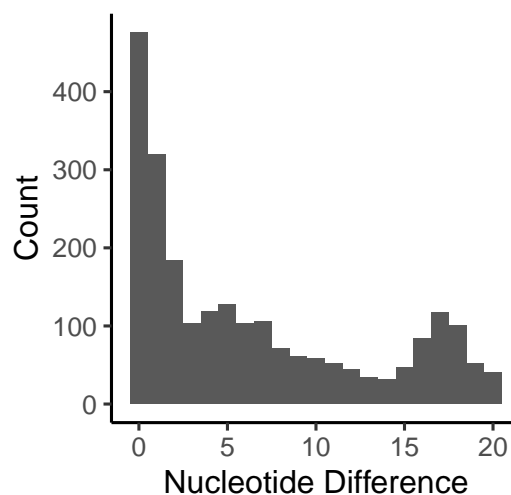
IGHV3–38–3*01

1 sequences assigned
No exact matches.



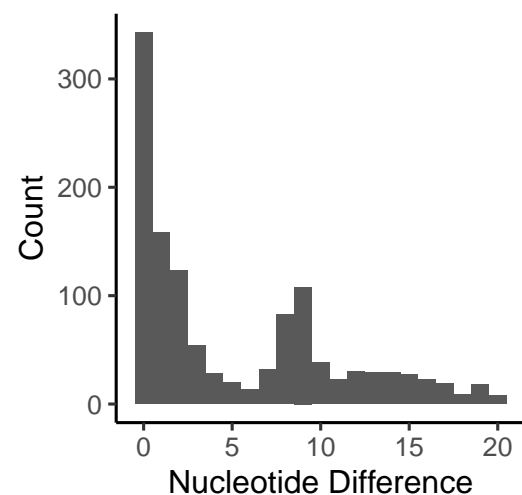
IGHV3–48*01

2703 sequences assigned
476 (17.6%) exact matches, in which:
384 unique CDR3
7 unique J



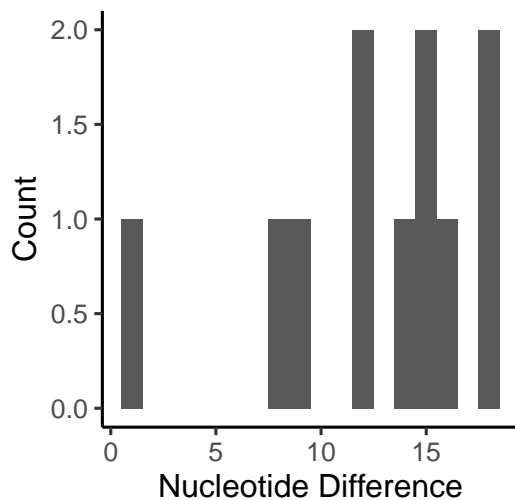
IGHV3–49*03_05

1275 sequences assigned
343 (26.9%) exact matches, in which:
277 unique CDR3
7 unique J



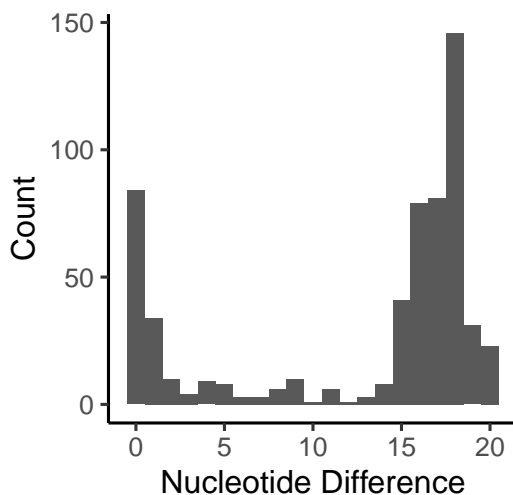
IGHV3-52*01_03

11 sequences assigned
No exact matches.



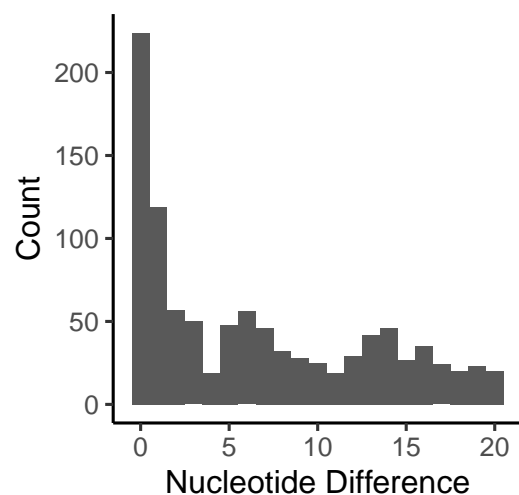
IGHV3-64*01

643 sequences assigned
84 (13.1%) exact matches, in which:
64 unique CDR3
7 unique J



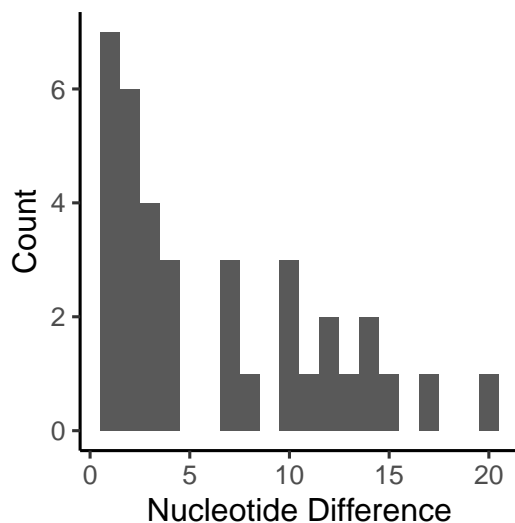
IGHV3-66*01

1154 sequences assigned
224 (19.4%) exact matches, in which:
183 unique CDR3
7 unique J



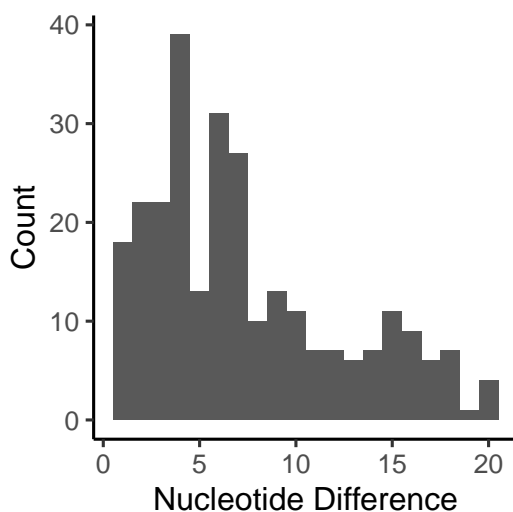
IGHV3-53*05

48 sequences assigned
No exact matches.



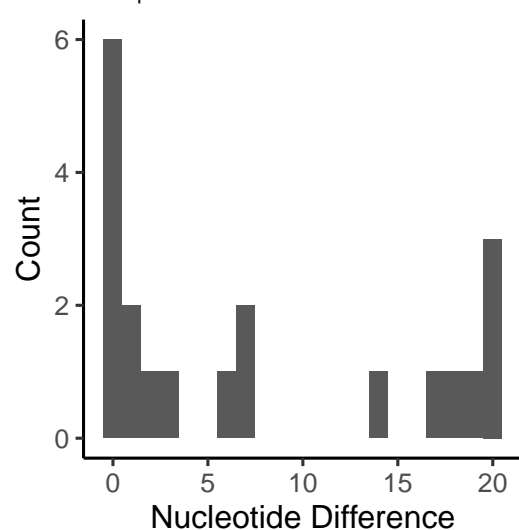
IGHV3-64*04

301 sequences assigned
No exact matches.



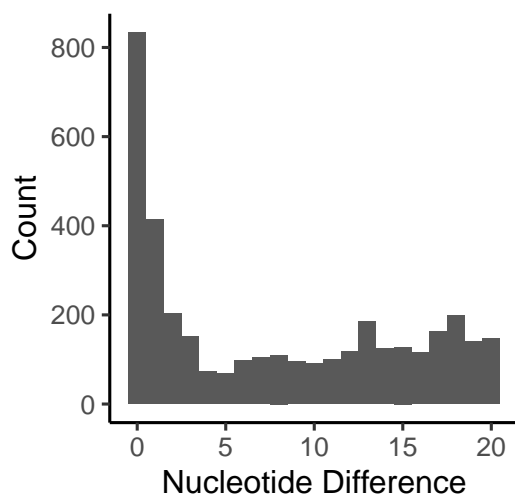
IGHV3-66*03

24 sequences assigned
6 (25%) exact matches, in which:
5 unique CDR3
2 unique J



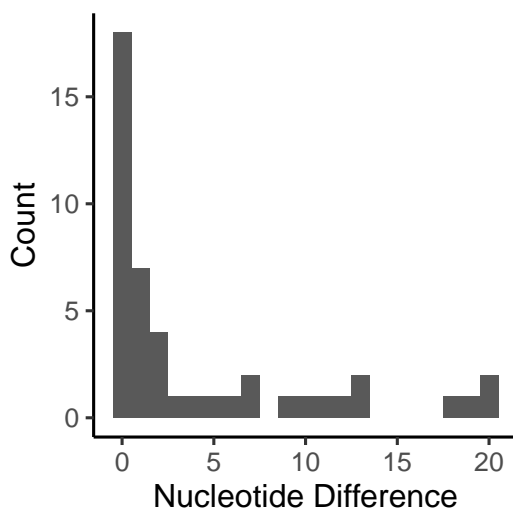
IGHV3-53*01_02

5127 sequences assigned
834 (16.3%) exact matches, in which:
676 unique CDR3
7 unique J



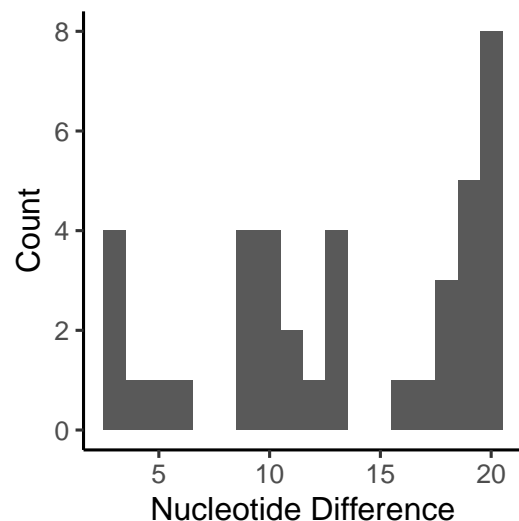
IGHV3-64*02_07

50 sequences assigned
18 (36%) exact matches, in which:
13 unique CDR3
4 unique J



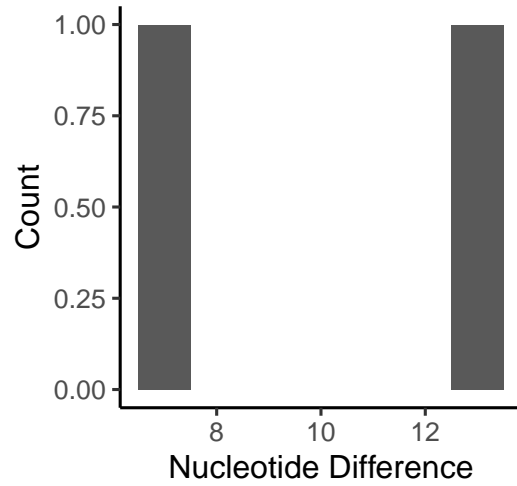
IGHV3-69-1*01

111 sequences assigned
No exact matches.



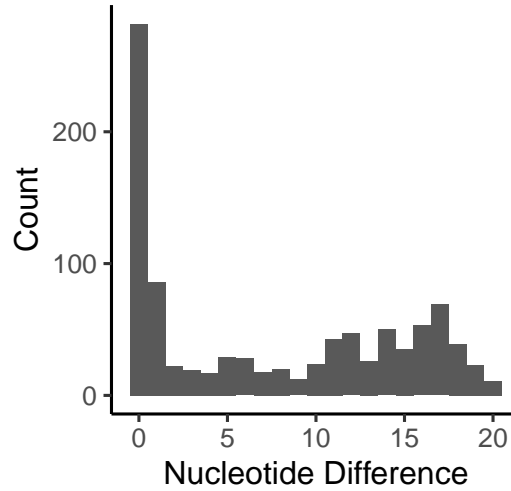
IGHV3-69-1*02

36 sequences assigned
No exact matches.



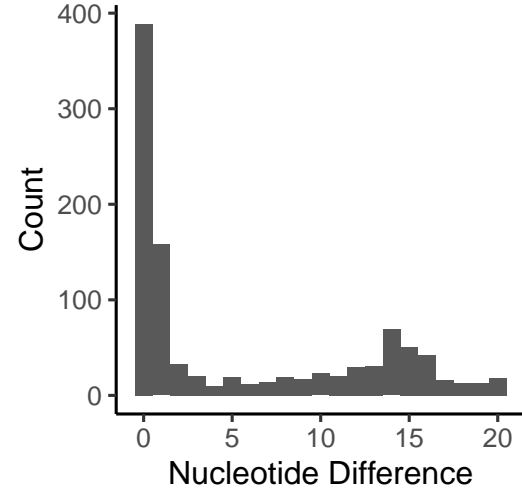
IGHV3-73*01_02

1021 sequences assigned
282 (27.6%) exact matches, in which:
233 unique CDR3
7 unique J



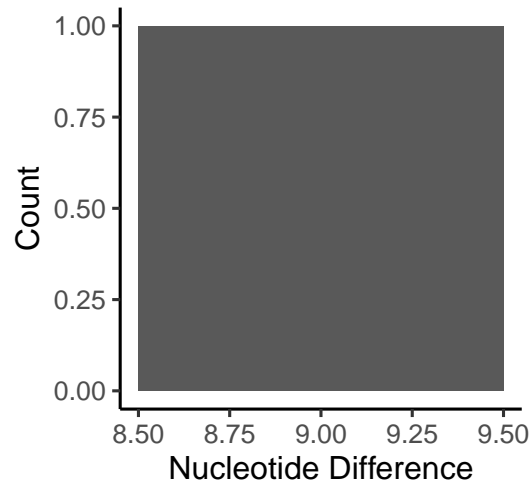
IGHV3-64D*06

1121 sequences assigned
389 (34.7%) exact matches, in which:
286 unique CDR3
7 unique J



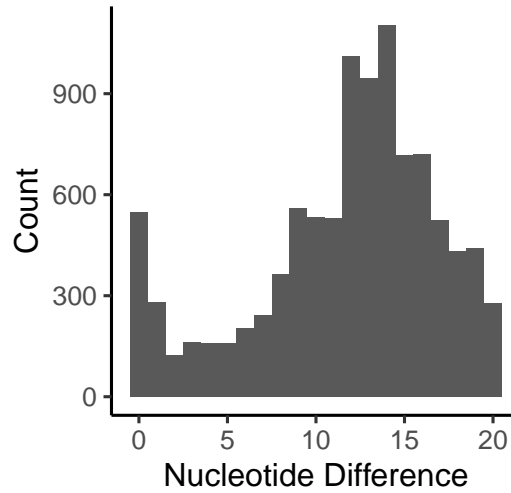
IGHV3-71*01_04

4 sequences assigned
No exact matches.



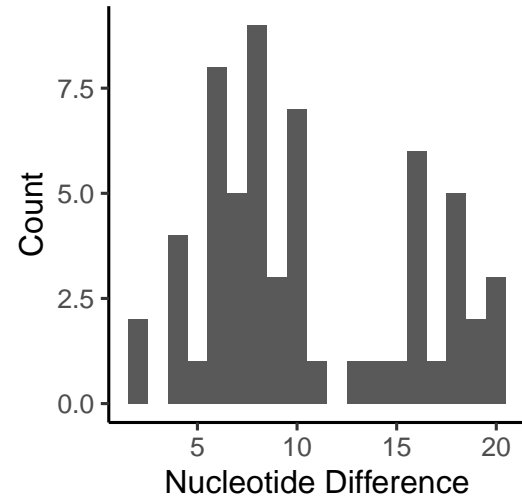
IGHV3-74*01_02

11740 sequences assigned
548 (4.7%) exact matches, in which:
421 unique CDR3
7 unique J



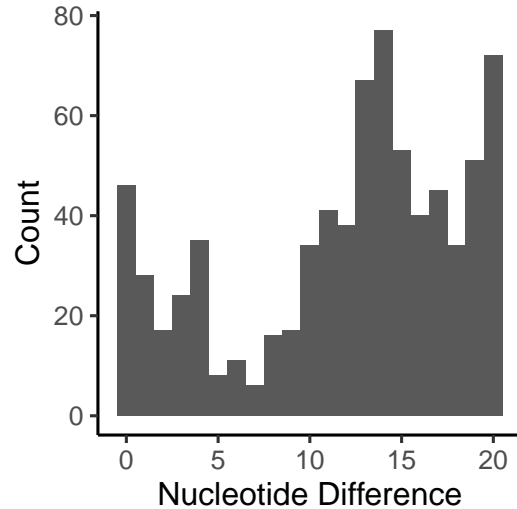
IGHV3-NL1*01

87 sequences assigned
No exact matches.



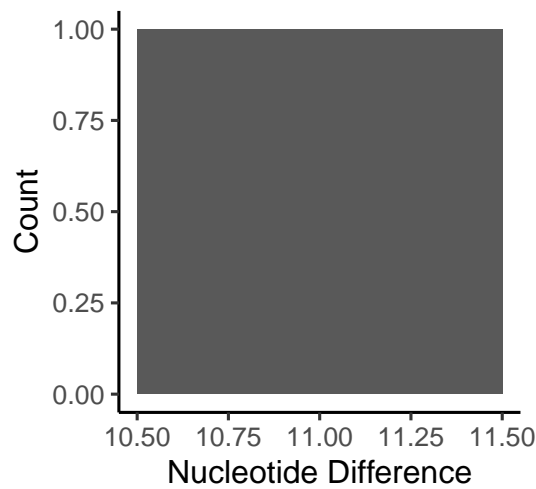
IGHV3-72*01

1070 sequences assigned
46 (4.3%) exact matches, in which:
32 unique CDR3
6 unique J



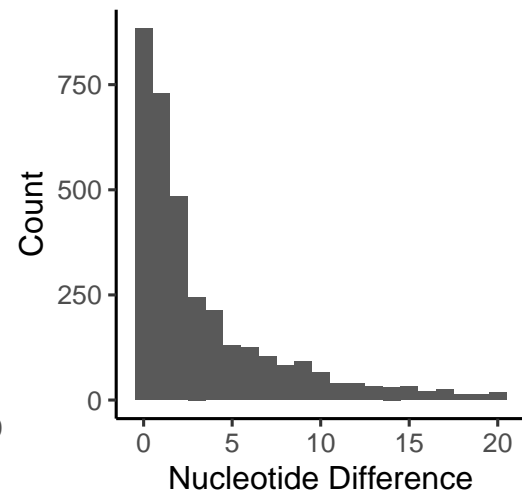
IGHV3-43D*04

4 sequences assigned
No exact matches.



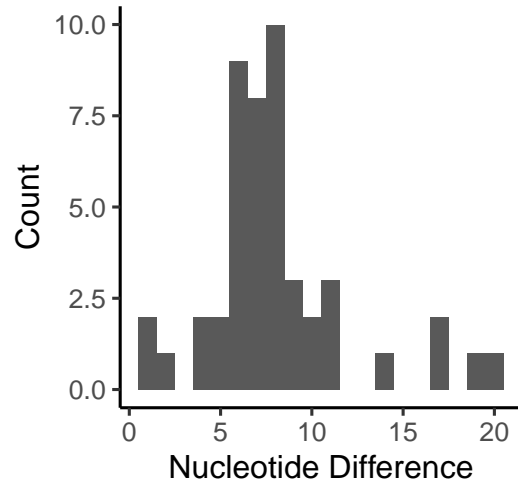
IGHV4-4*07

3984 sequences assigned
884 (22.2%) exact matches, in which:
823 unique CDR3
6 unique J



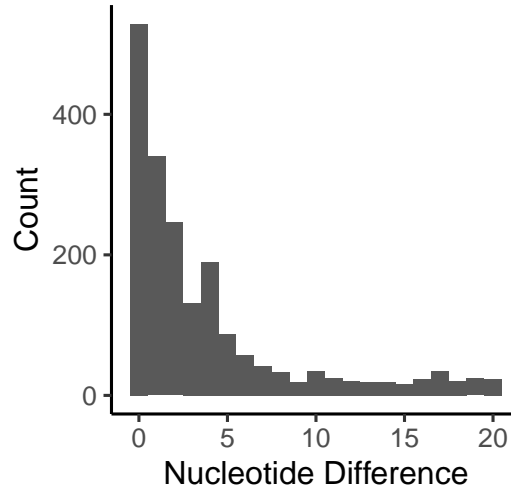
IGHV4-28*03

54 sequences assigned
No exact matches.



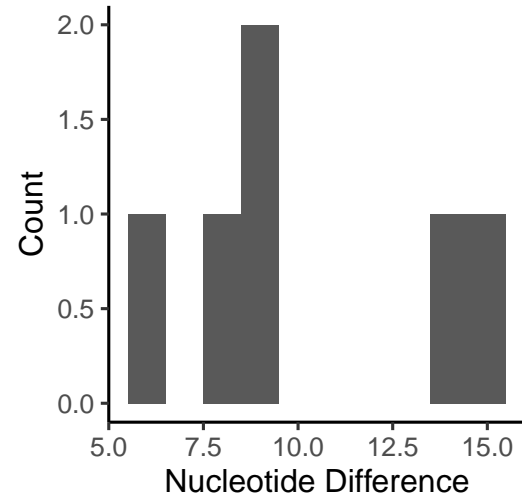
IGHV4-30-2*01

2481 sequences assigned
529 (21.3%) exact matches, in which:
443 unique CDR3
7 unique J



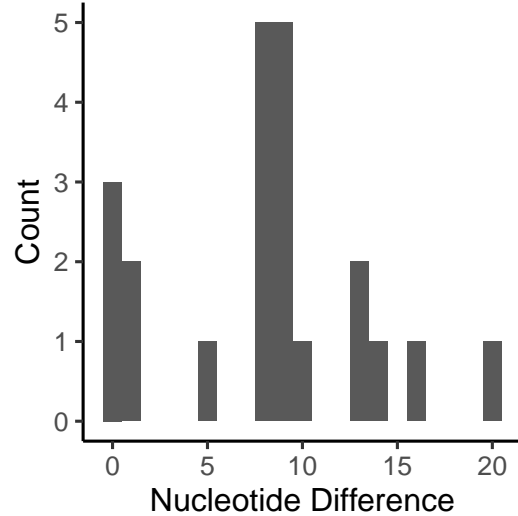
IGHV4-38-2*02

12 sequences assigned
No exact matches.



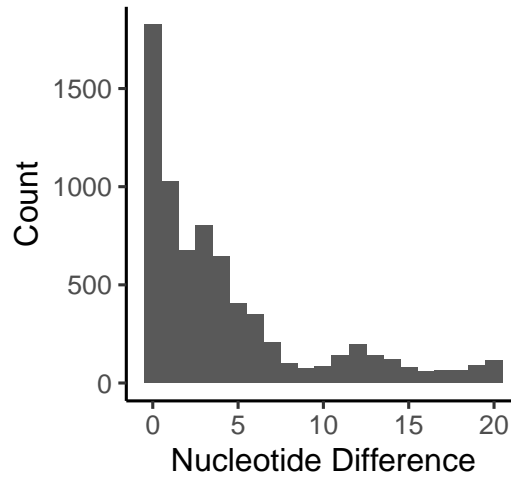
IGHV4-28*01_07

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



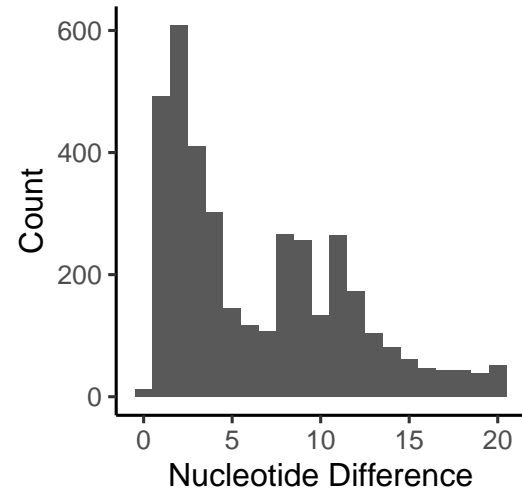
IGHV4-31*03_04

8372 sequences assigned
1825 (21.8%) exact matches, in which:
1698 unique CDR3
7 unique J



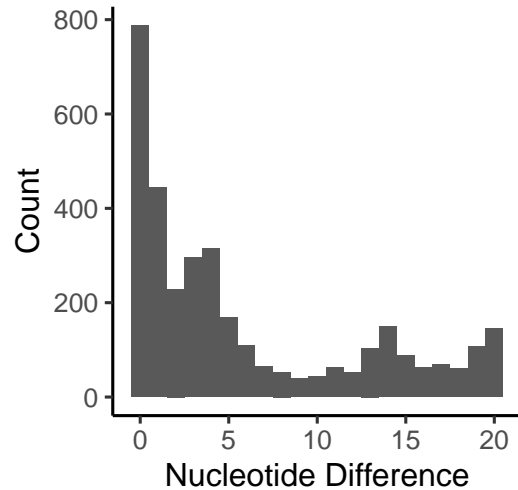
IGHV4-39*07

3944 sequences assigned
13 (0.3%) exact matches, in which:
13 unique CDR3
5 unique J



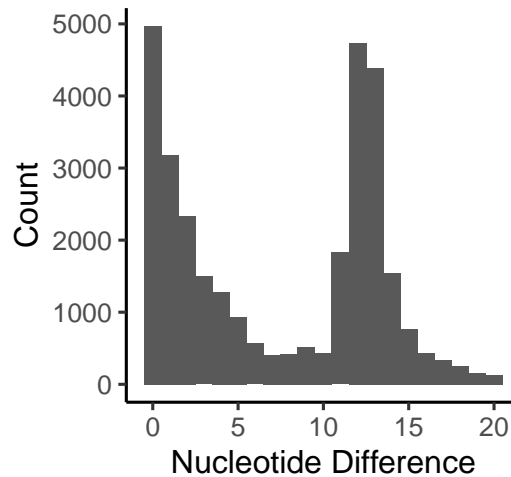
IGHV4-30-4*01

3944 sequences assigned
788 (20%) exact matches, in which:
745 unique CDR3
7 unique J



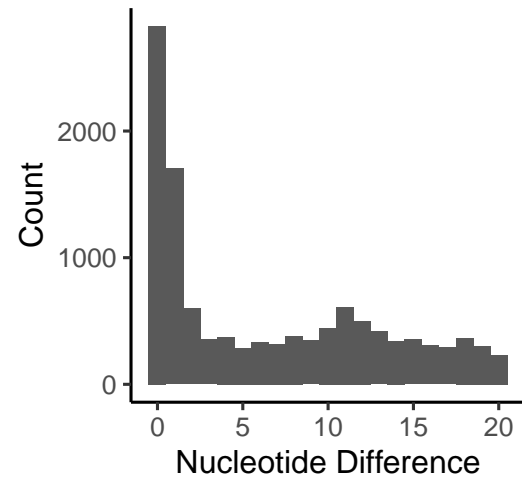
IGHV4-34*01_02

31917 sequences assigned
4970 (15.6%) exact matches, in which:
4490 unique CDR3
7 unique J



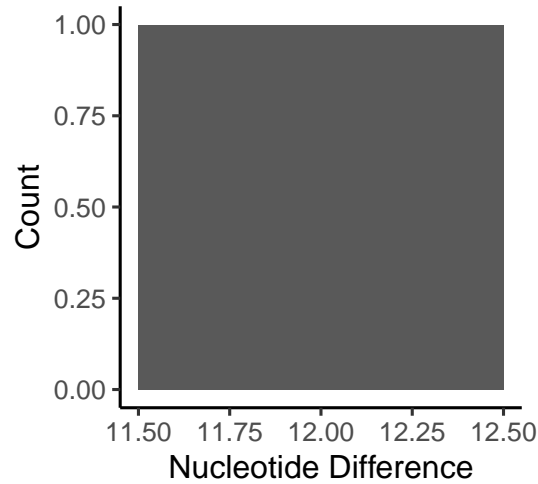
IGHV4-39*01_05

14035 sequences assigned
2829 (20.2%) exact matches, in which:
2542 unique CDR3
7 unique J



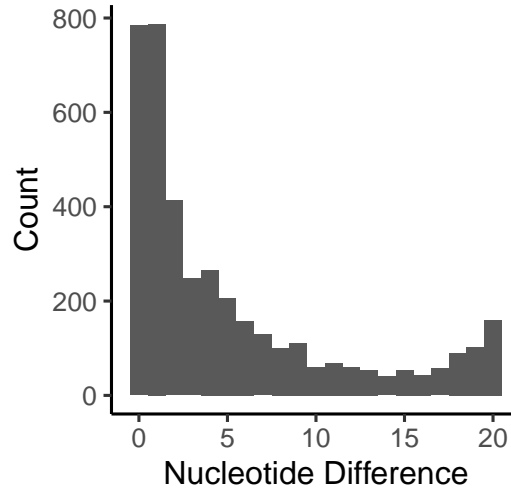
IGHV4-55*09

1 sequences assigned
No exact matches.



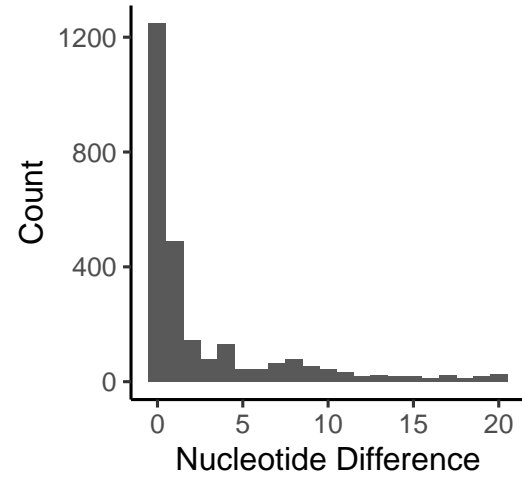
IGHV4-59*08

4501 sequences assigned
784 (17.4%) exact matches, in which:
722 unique CDR3
7 unique J



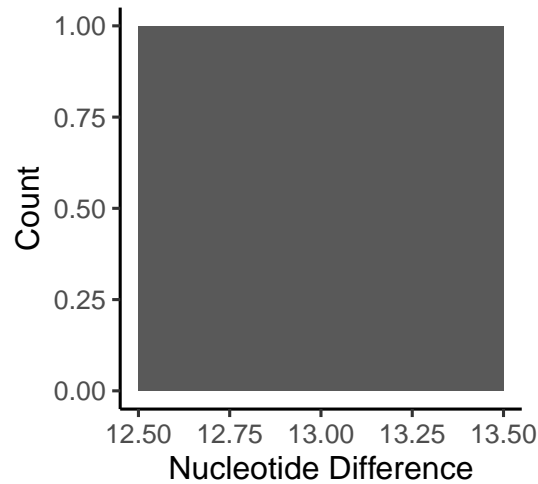
IGHV4-59*13

3460 sequences assigned
1248 (36.1%) exact matches, in which:
1208 unique CDR3
7 unique J



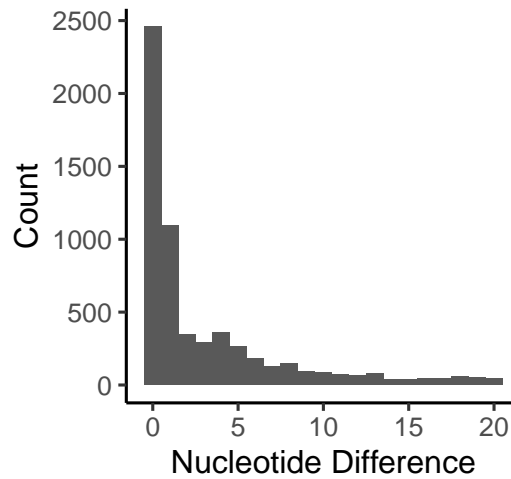
IGHV4-55*01_05

1 sequences assigned
No exact matches.



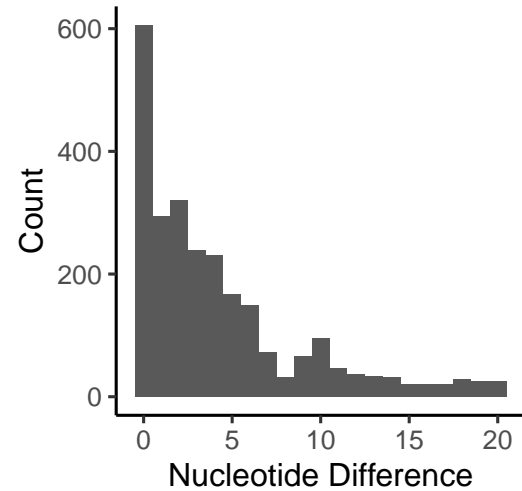
IGHV4-59*01_07

6955 sequences assigned
2458 (35.3%) exact matches, in which:
2296 unique CDR3
7 unique J



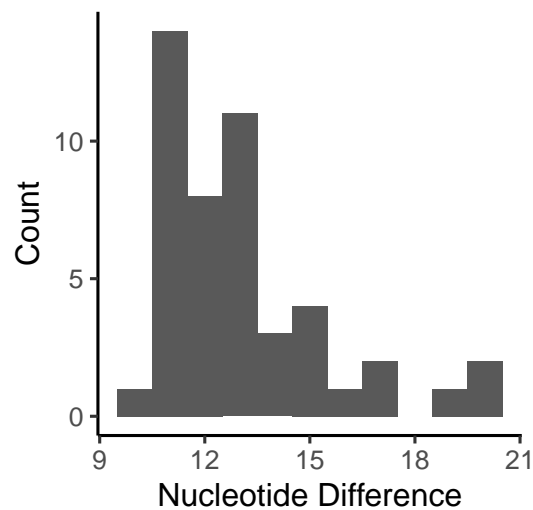
IGHV4-61*01

2929 sequences assigned
606 (20.7%) exact matches, in which:
587 unique CDR3
7 unique J



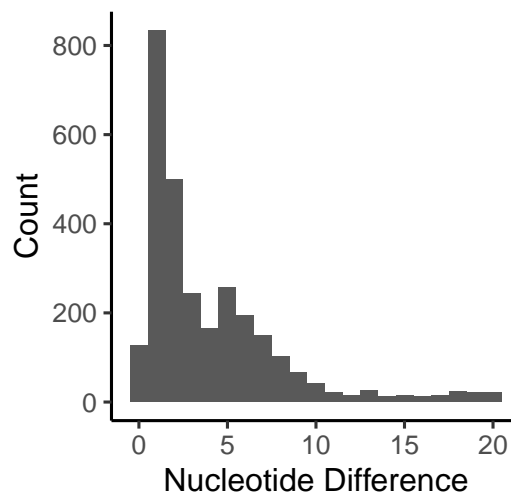
IGHV4-55*02_04_08

49 sequences assigned
No exact matches.



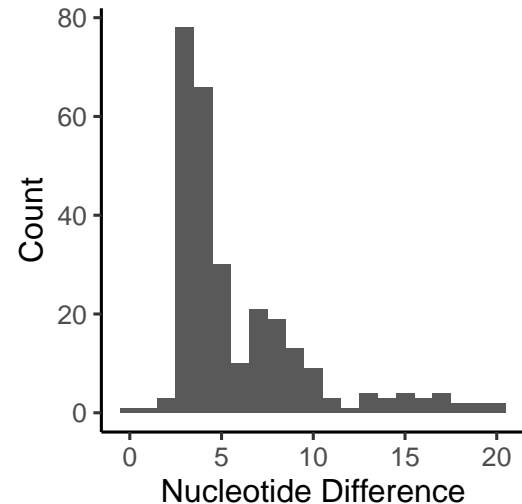
IGHV4-59*12

3010 sequences assigned
127 (4.2%) exact matches, in which:
127 unique CDR3
6 unique J



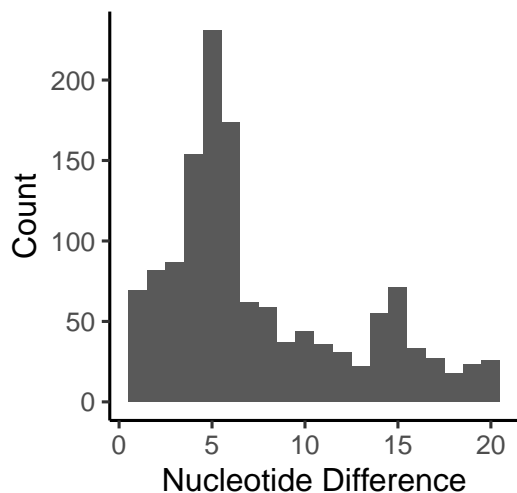
IGHV4-61*02

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



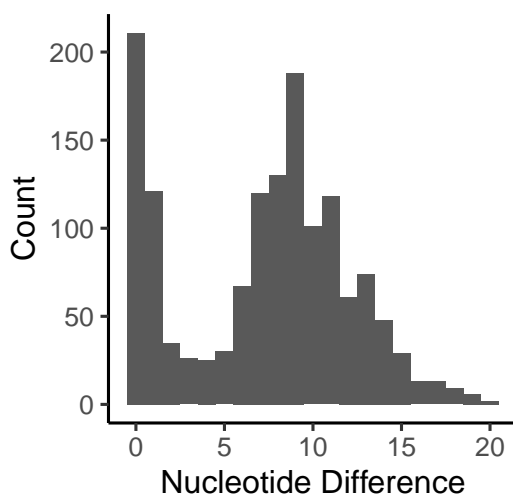
IGHV4-61*08

1711 sequences assigned
No exact matches.



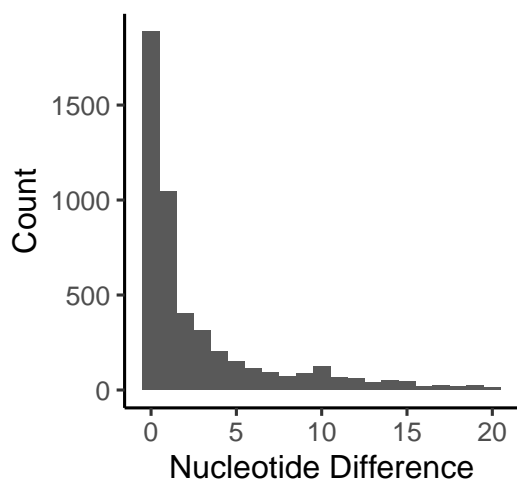
IGHV6-1*01_02

1466 sequences assigned
211 (14.4%) exact matches, in which:
196 unique CDR3
7 unique J



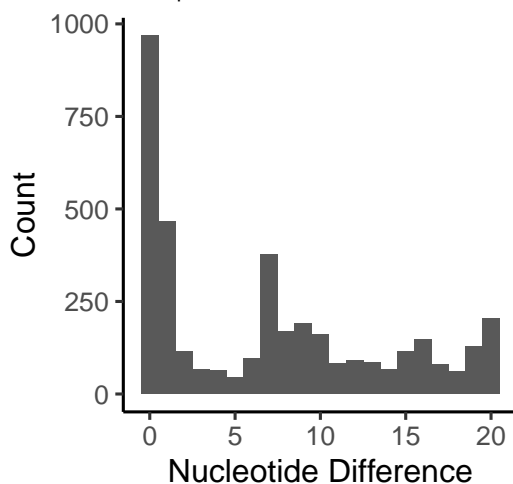
IGHV5-10-1*01_03

4959 sequences assigned
1886 (38%) exact matches, in which:
1476 unique CDR3
7 unique J



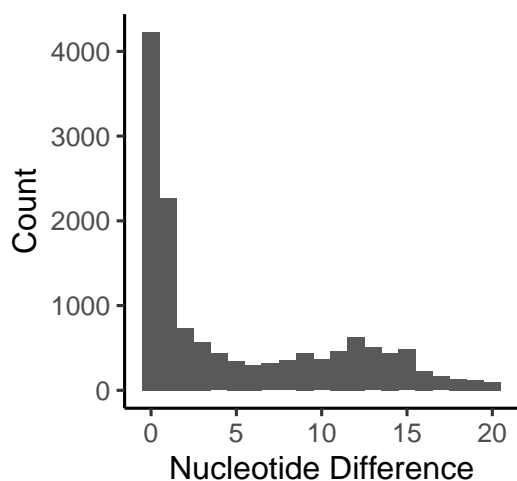
IGHV7-4-1*02

4158 sequences assigned
968 (23.3%) exact matches, in which:
910 unique CDR3
7 unique J



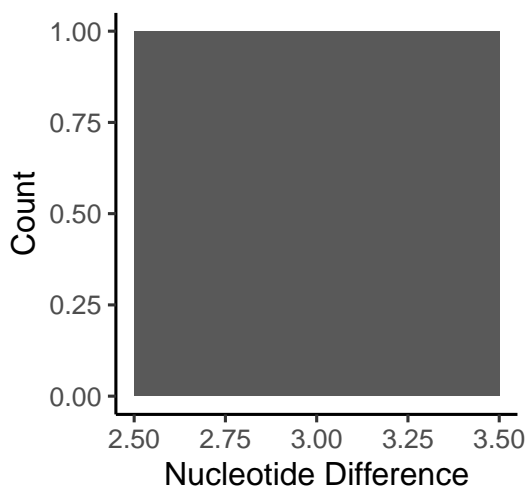
IGHV5-51*01_03

14088 sequences assigned
4228 (30%) exact matches, in which:
3083 unique CDR3
7 unique J

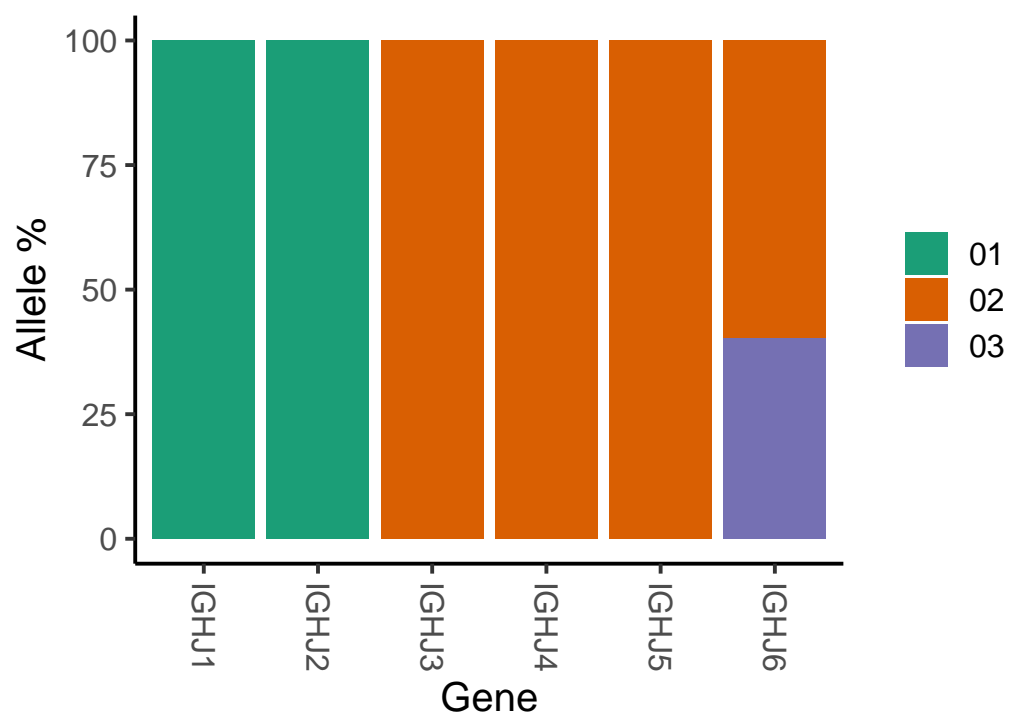


IGHV7-81*01

1 sequences assigned
No exact matches.



Allele Usage



Sequence Count by IGHJ6 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.