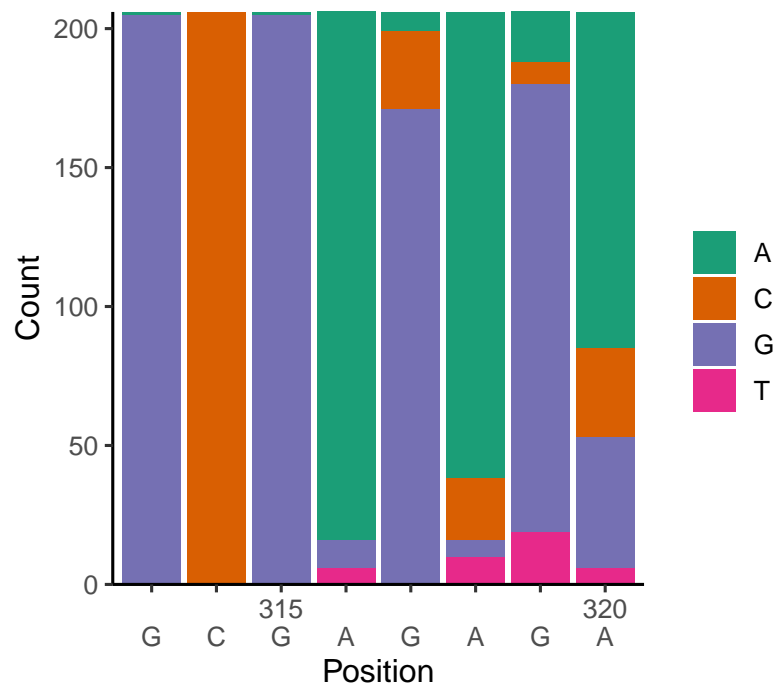
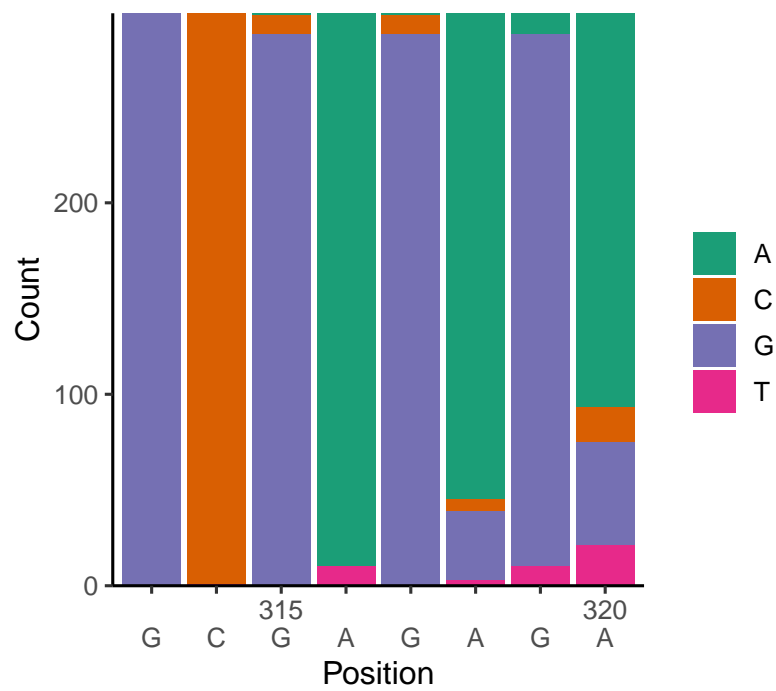


Gene IGHV1-69*04_C184T



Gene IGHV3-33*01_G75C



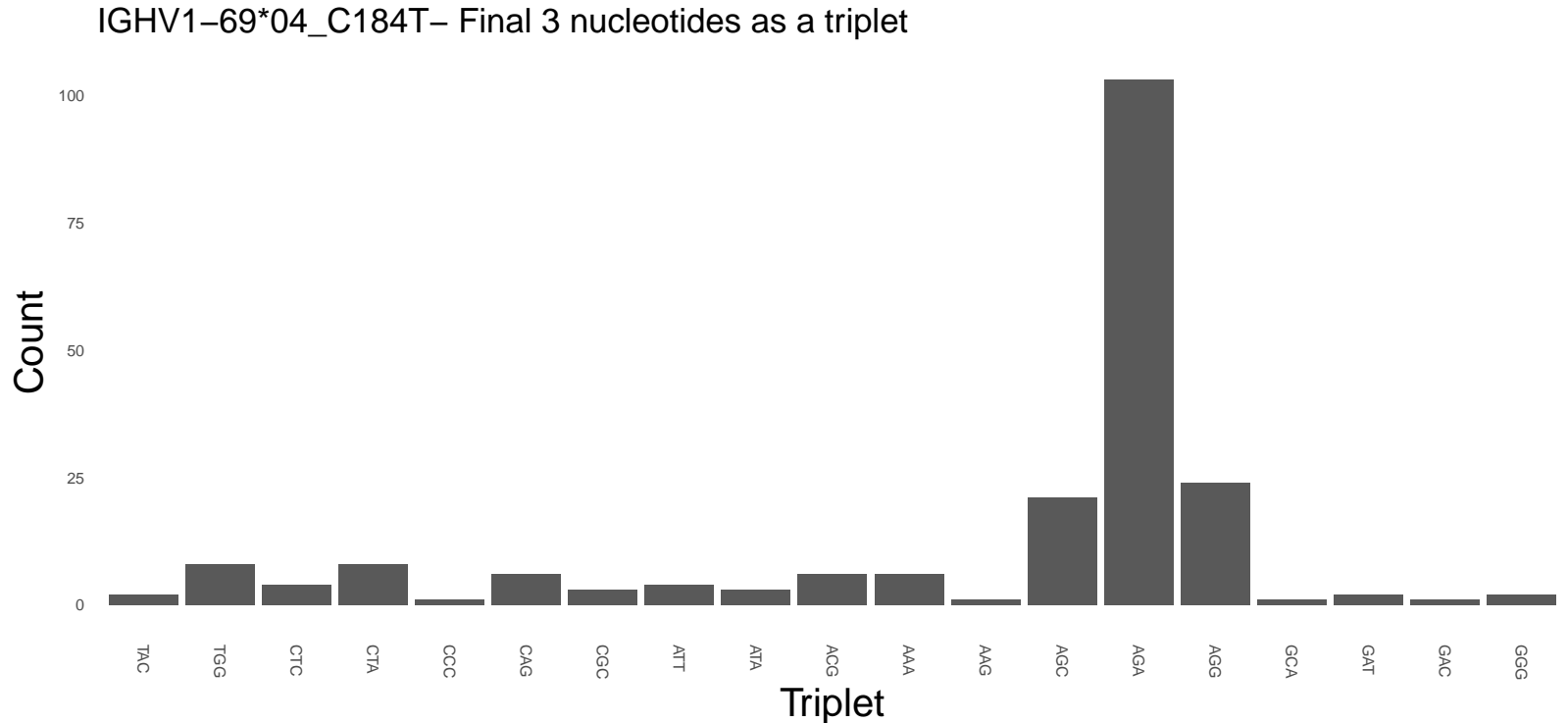
Gene IGHV1-69*04_C184T



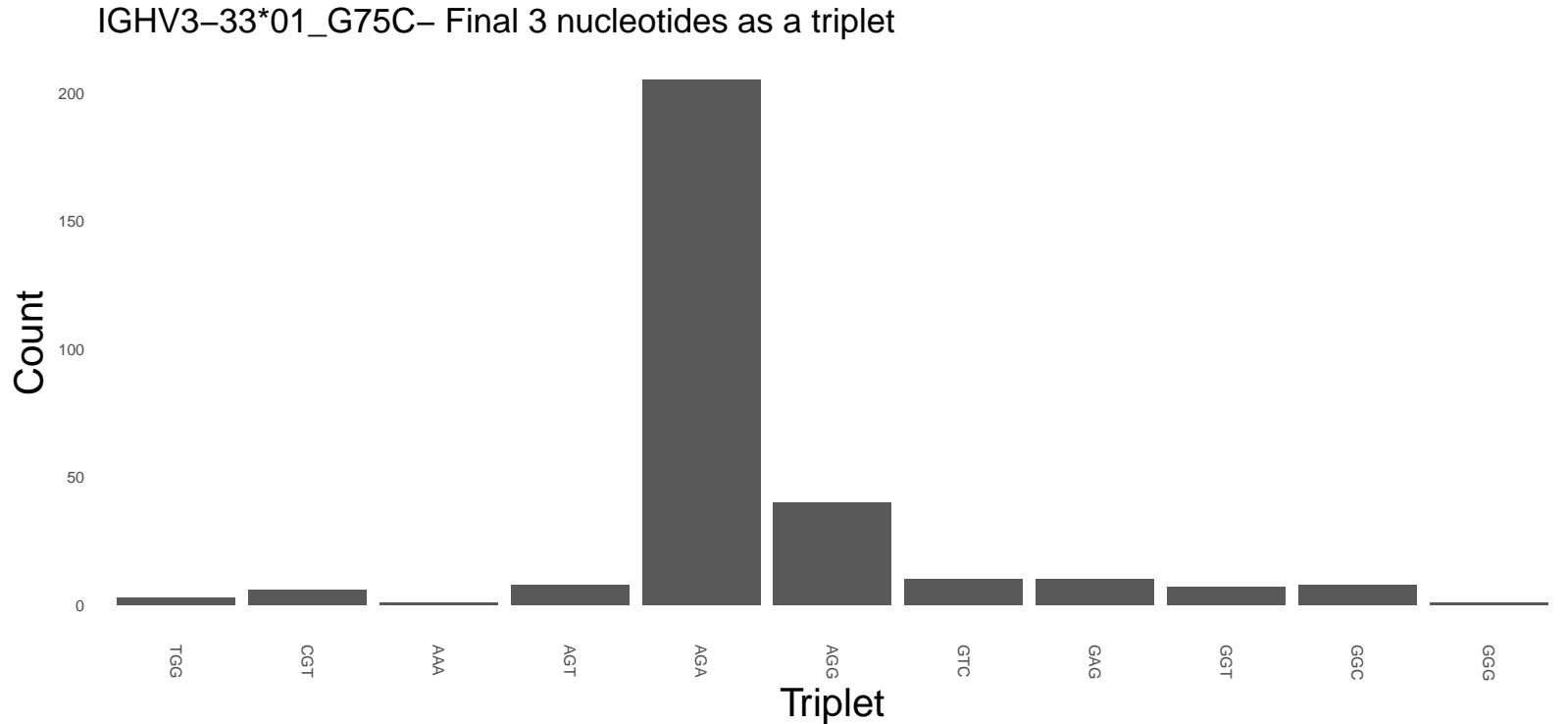
Gene IGHV3-33*01_G75C



IGHV1-69*04_C184T- Final 3 nucleotides as a triplet

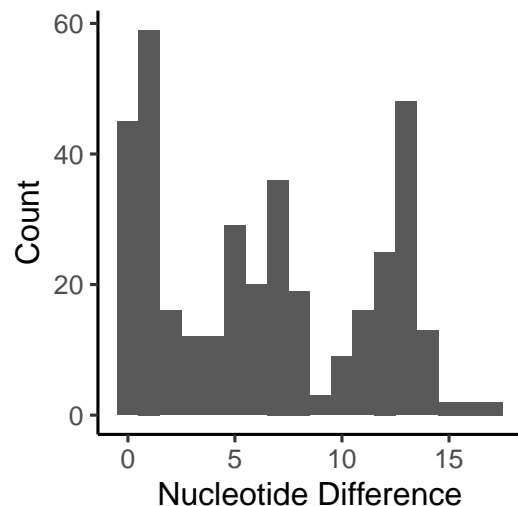


IGHV3-33*01_G75C- Final 3 nucleotides as a triplet



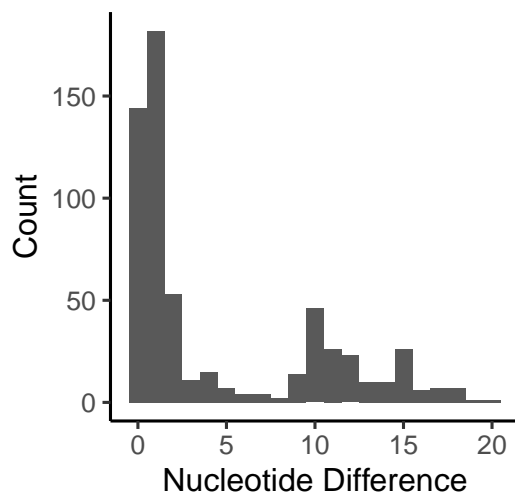
IGHV1-2*02

404 sequences assigned
45 (11.1%) exact matches, in which:
34 unique CDR3
4 unique J



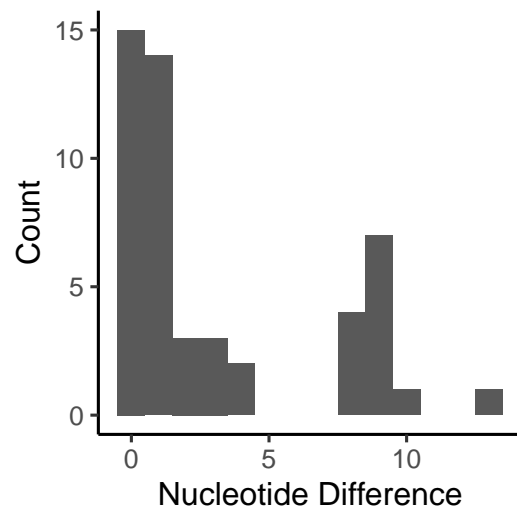
IGHV1-18*01

601 sequences assigned
144 (24%) exact matches, in which:
92 unique CDR3
7 unique J



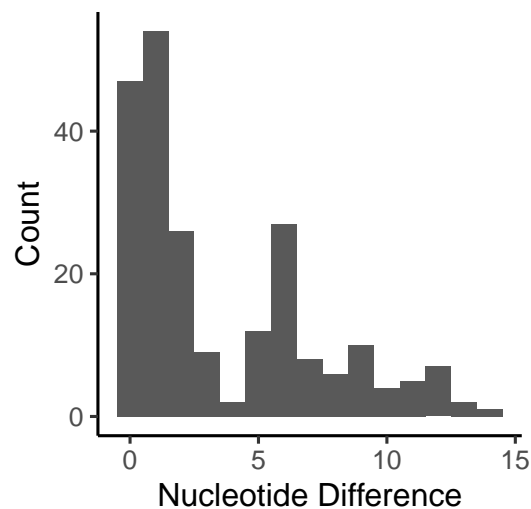
IGHV1-46*03

50 sequences assigned
15 (30%) exact matches, in which:
10 unique CDR3
2 unique J



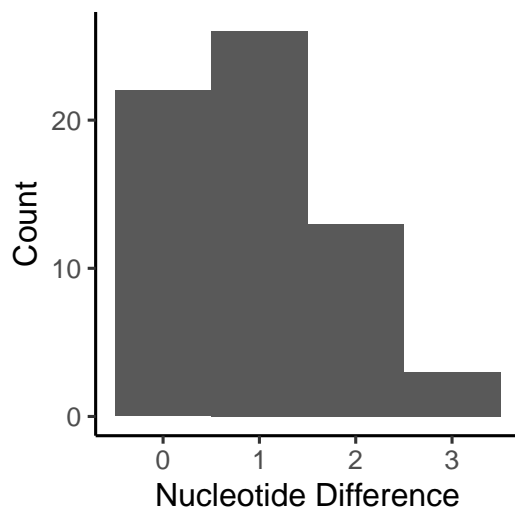
IGHV1-3*01

220 sequences assigned
47 (21.4%) exact matches, in which:
29 unique CDR3
4 unique J



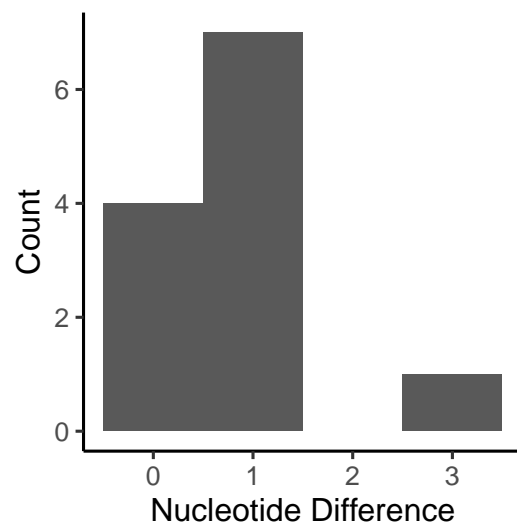
IGHV1-24*01

64 sequences assigned
22 (34.4%) exact matches, in which:
20 unique CDR3
5 unique J



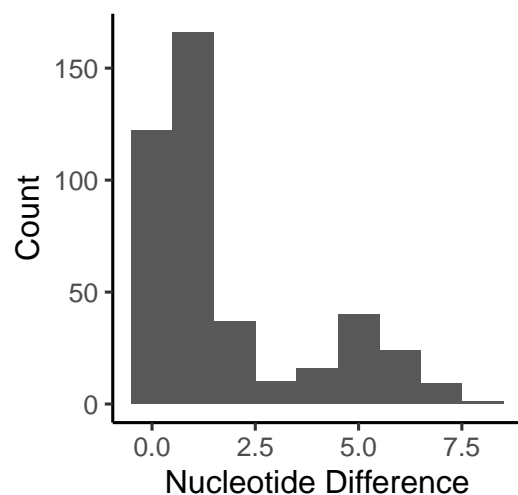
IGHV1-58*01

12 sequences assigned
4 (33.3%) exact matches, in which:
3 unique CDR3
2 unique J



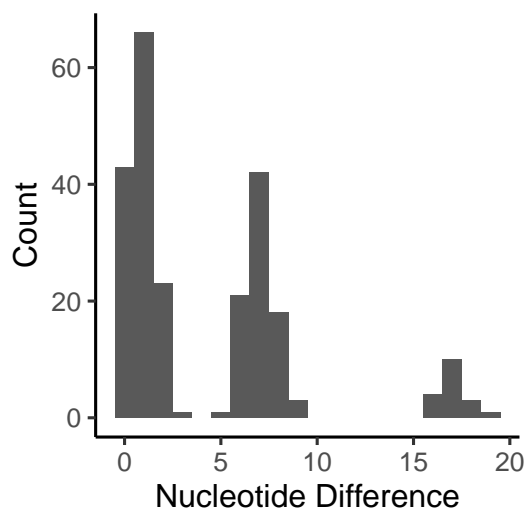
IGHV1-8*01

425 sequences assigned
122 (28.7%) exact matches, in which:
85 unique CDR3
6 unique J



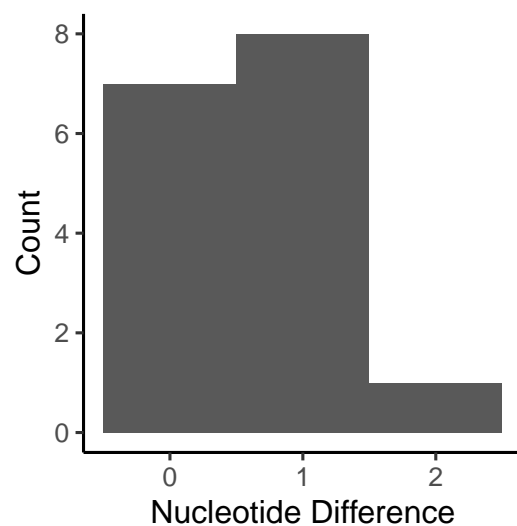
IGHV1-46*01

236 sequences assigned
43 (18.2%) exact matches, in which:
25 unique CDR3
5 unique J



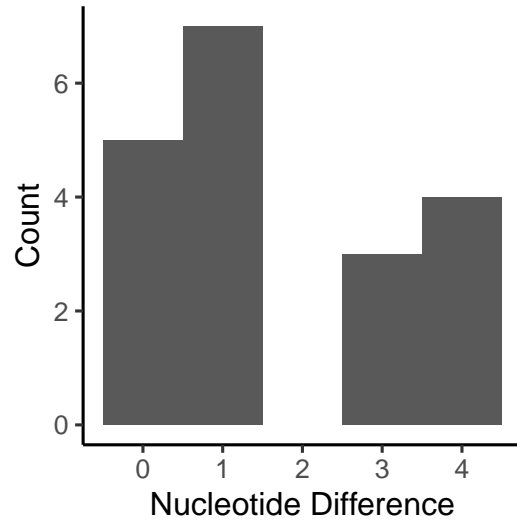
IGHV1-58*02

16 sequences assigned
7 (43.8%) exact matches, in which:
4 unique CDR3
3 unique J



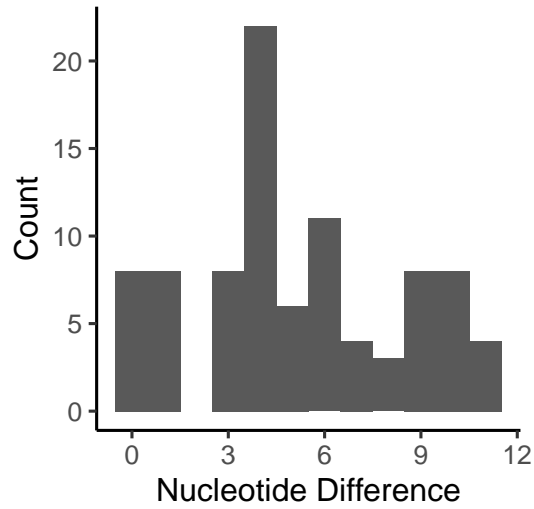
IGHV1-69-2*01

19 sequences assigned
5 (26.3%) exact matches, in which:
5 unique CDR3
1 unique J



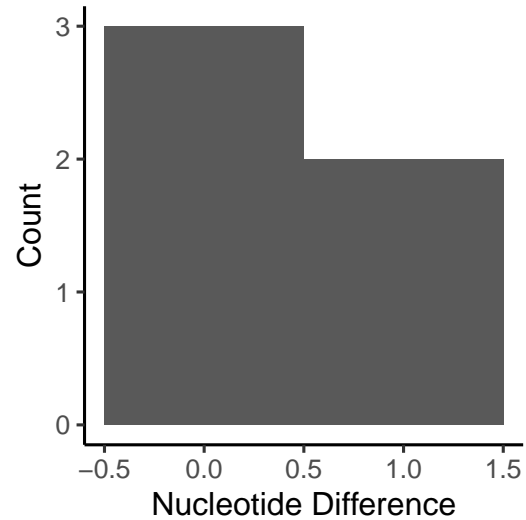
IGHV2-5*01

90 sequences assigned
8 (8.9%) exact matches, in which:
6 unique CDR3
4 unique J



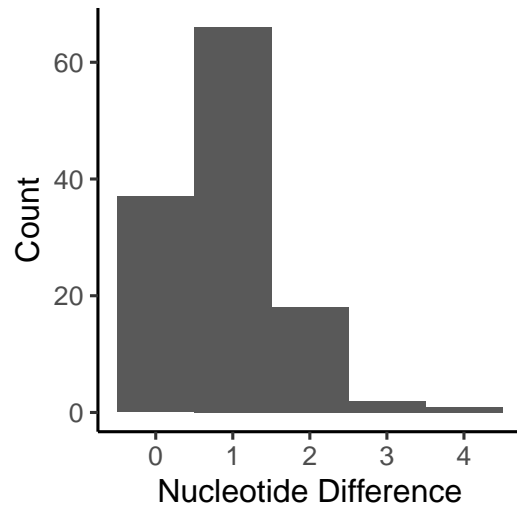
IGHV2-70*01

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



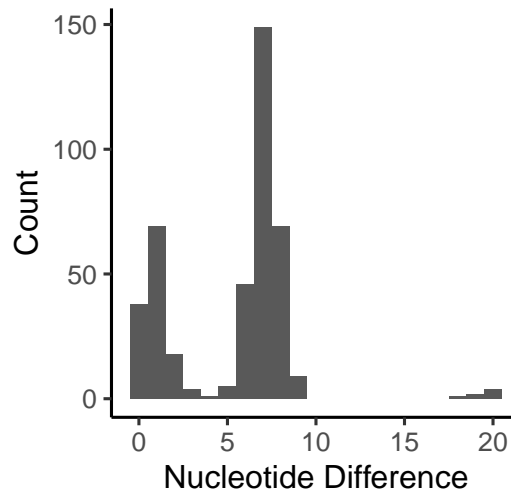
IGHV1-69*02

124 sequences assigned
37 (29.8%) exact matches, in which:
30 unique CDR3
4 unique J



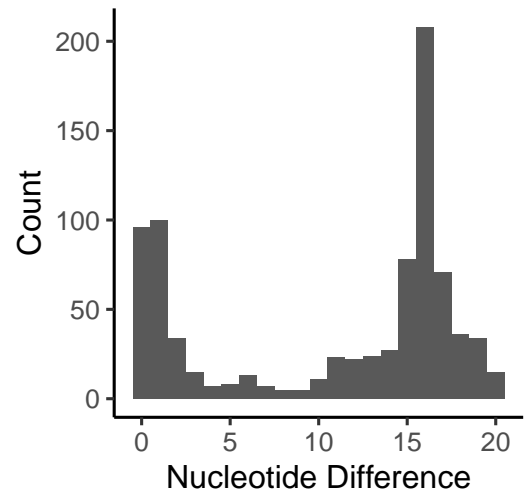
IGHV2-5*02

423 sequences assigned
38 (9%) exact matches, in which:
22 unique CDR3
3 unique J



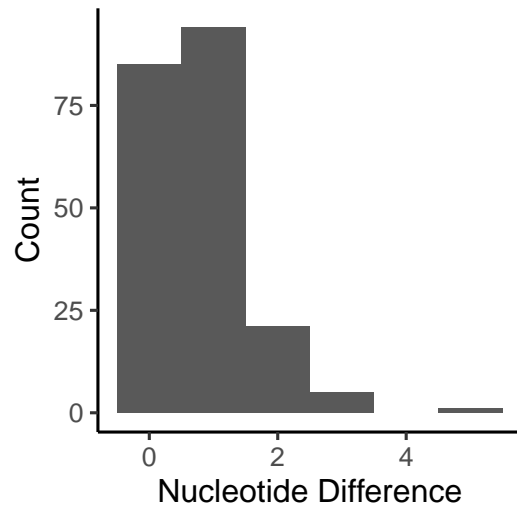
IGHV3-7*01

888 sequences assigned
96 (10.8%) exact matches, in which:
70 unique CDR3
7 unique J



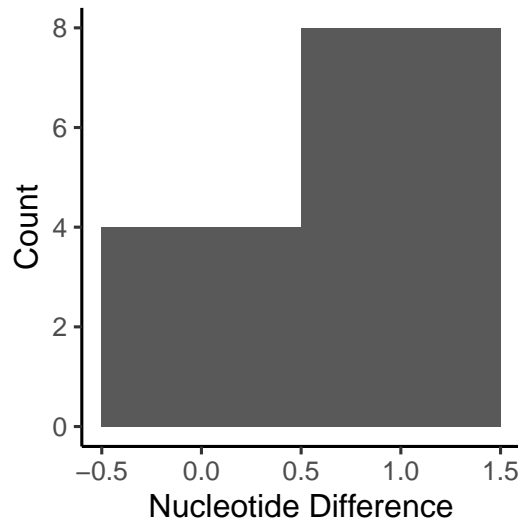
IGHV1-69*04_C184T

206 sequences assigned
85 (41.3%) exact matches, in which:
68 unique CDR3
6 unique J



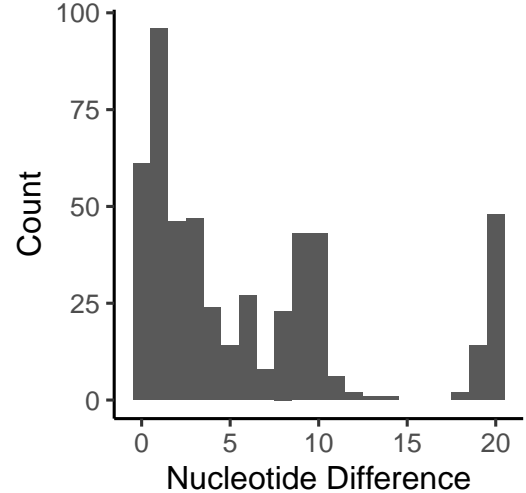
IGHV2-26*01

12 sequences assigned
4 (33.3%) exact matches, in which:
3 unique CDR3
1 unique J



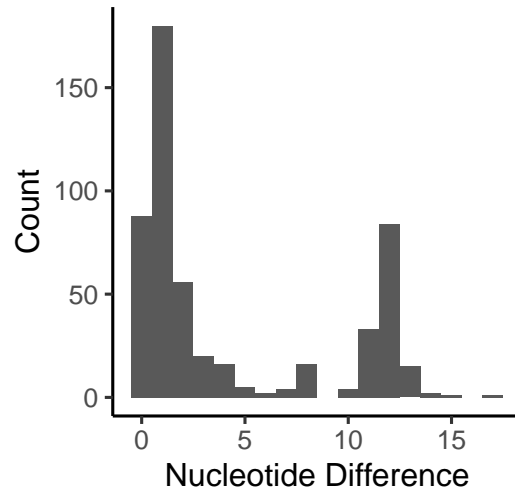
IGHV3-9*01

726 sequences assigned
61 (8.4%) exact matches, in which:
48 unique CDR3
5 unique J



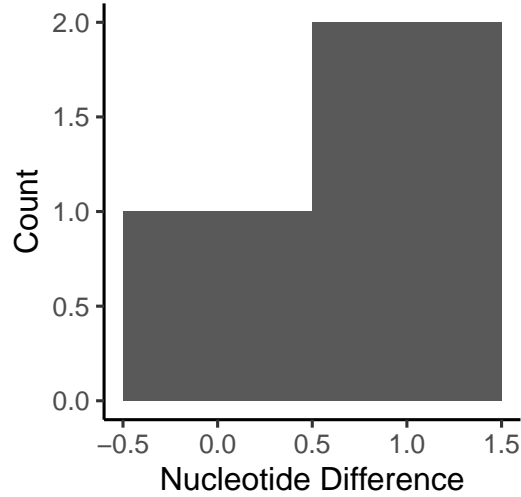
IGHV3-11*01

527 sequences assigned
88 (16.7%) exact matches, in which:
57 unique CDR3
5 unique J



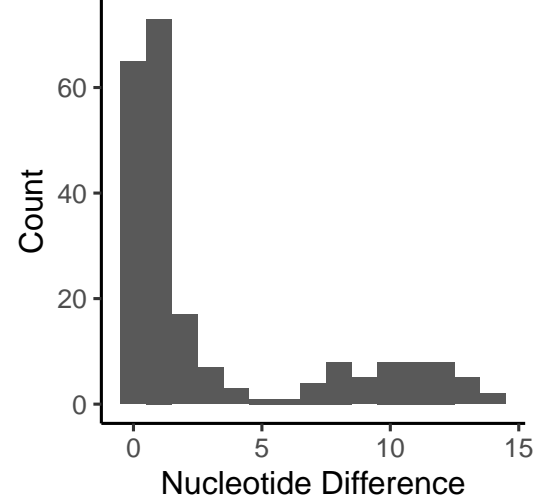
IGHV3-20*01

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



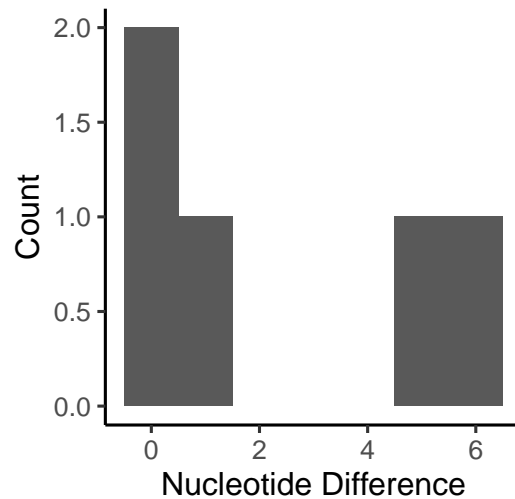
IGHV3-33*01

215 sequences assigned
65 (30.2%) exact matches, in which:
43 unique CDR3
4 unique J



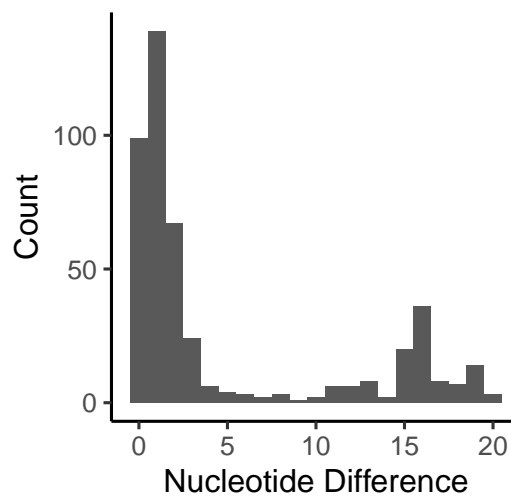
IGHV3-13*01

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



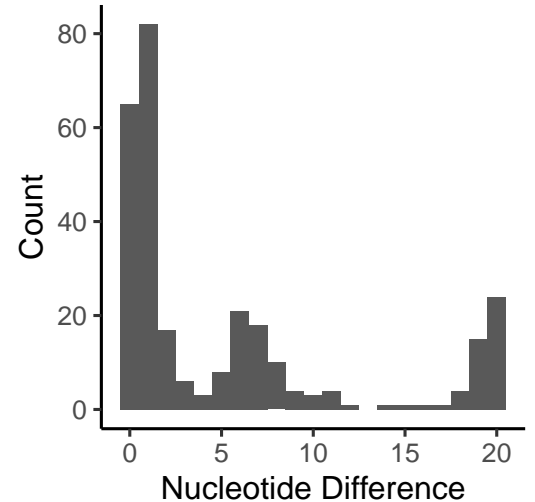
IGHV3-21*01

462 sequences assigned
99 (21.4%) exact matches, in which:
57 unique CDR3
6 unique J



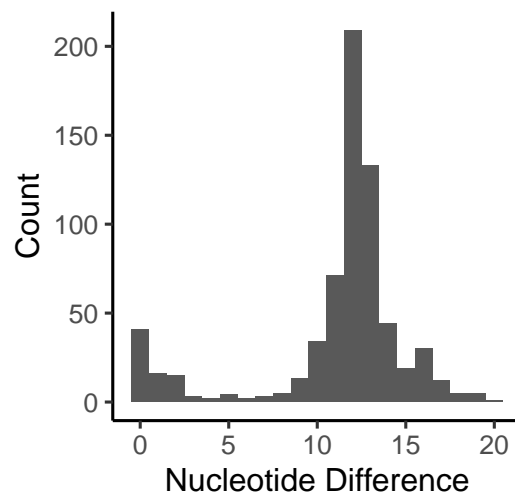
IGHV3-33*01_G75C

299 sequences assigned
65 (21.7%) exact matches, in which:
44 unique CDR3
4 unique J



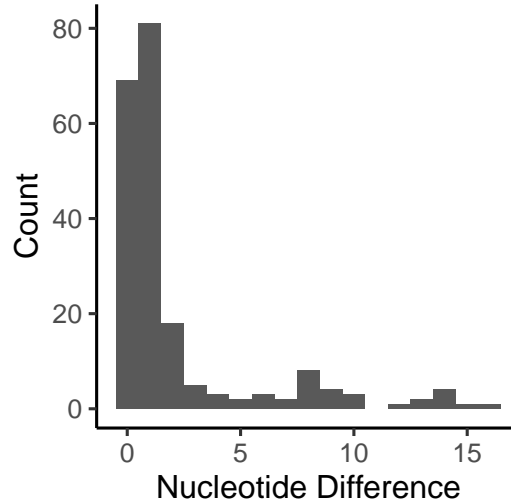
IGHV3-15*01

667 sequences assigned
41 (6.1%) exact matches, in which:
36 unique CDR3
5 unique J



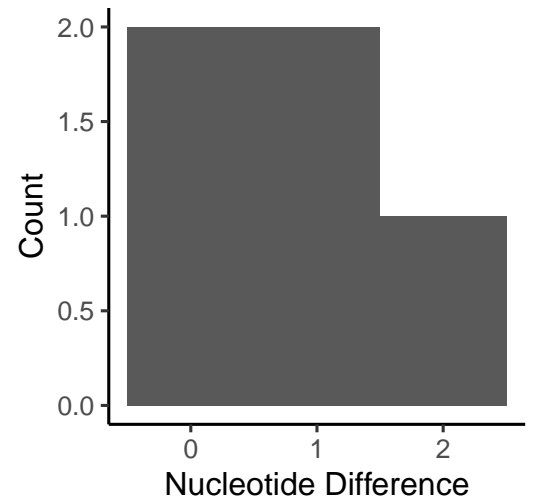
IGHV3-30-3*01

207 sequences assigned
69 (33.3%) exact matches, in which:
39 unique CDR3
6 unique J



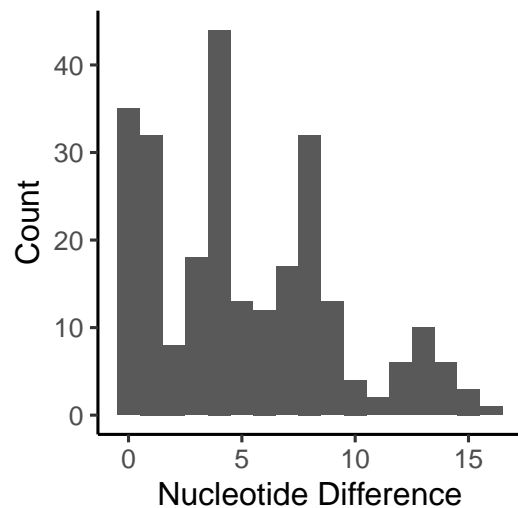
IGHV3-43*01

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



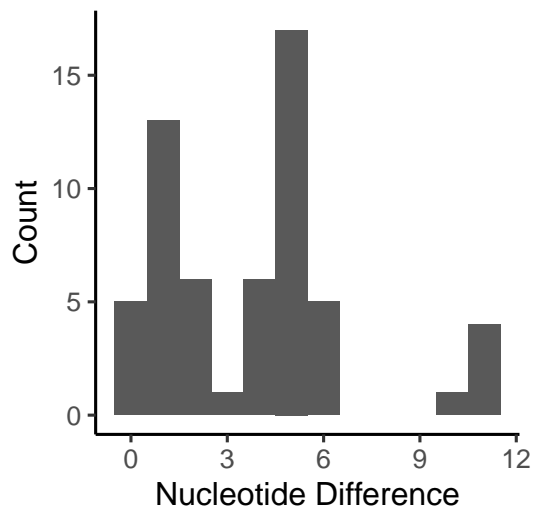
IGHV3-48*01

256 sequences assigned
35 (13.7%) exact matches, in which:
22 unique CDR3
4 unique J



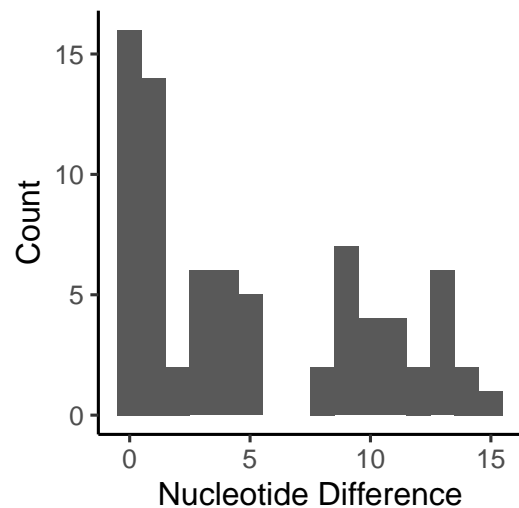
IGHV3-49*05

58 sequences assigned
5 (8.6%) exact matches, in which:
3 unique CDR3
2 unique J



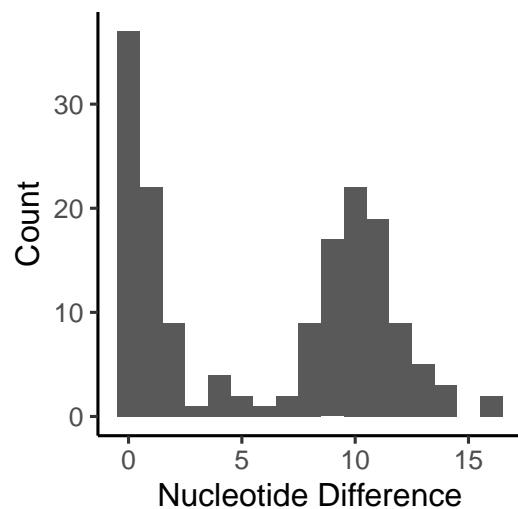
IGHV3-66*02

77 sequences assigned
16 (20.8%) exact matches, in which:
13 unique CDR3
5 unique J



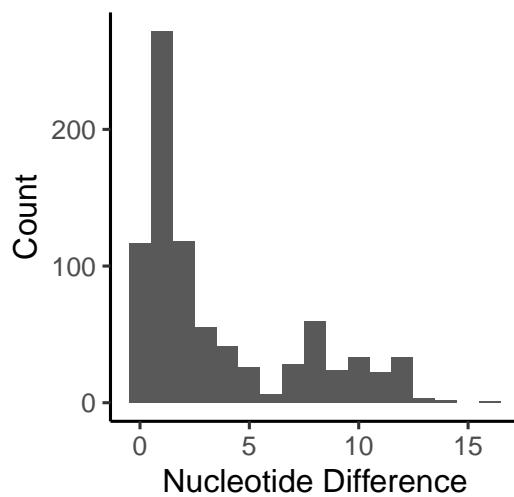
IGHV3-48*02

164 sequences assigned
37 (22.6%) exact matches, in which:
24 unique CDR3
6 unique J



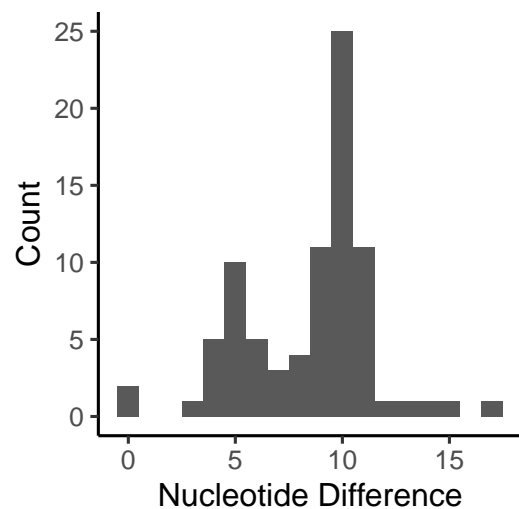
IGHV3-53*01

844 sequences assigned
117 (13.9%) exact matches, in which:
81 unique CDR3
6 unique J



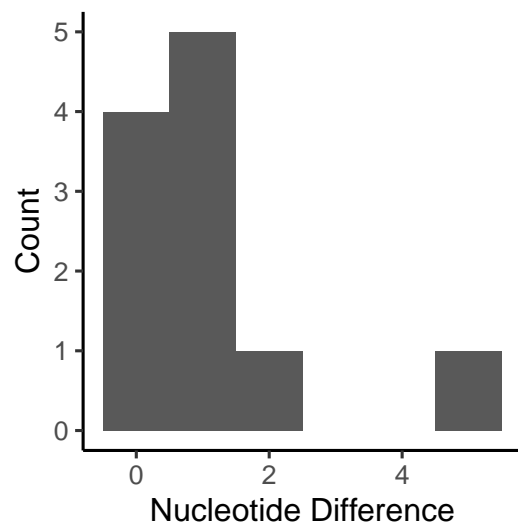
IGHV3-72*01

82 sequences assigned
2 (2.4%) exact matches, in which:
1 unique CDR3
1 unique J



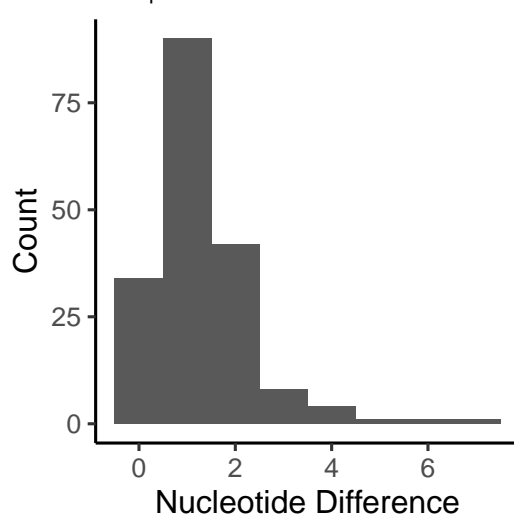
IGHV3-49*03

11 sequences assigned
4 (36.4%) exact matches, in which:
4 unique CDR3
3 unique J



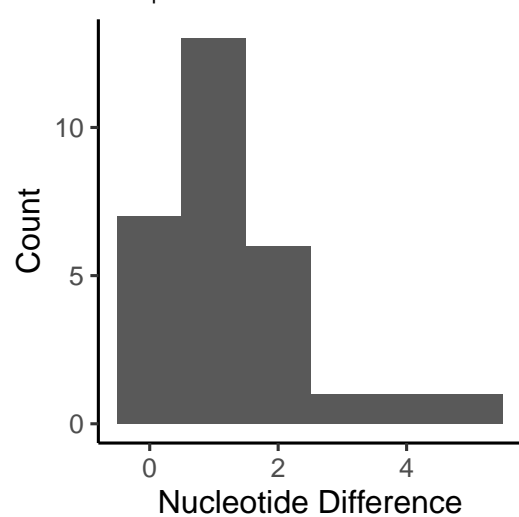
IGHV3-64*01

181 sequences assigned
34 (18.8%) exact matches, in which:
19 unique CDR3
2 unique J



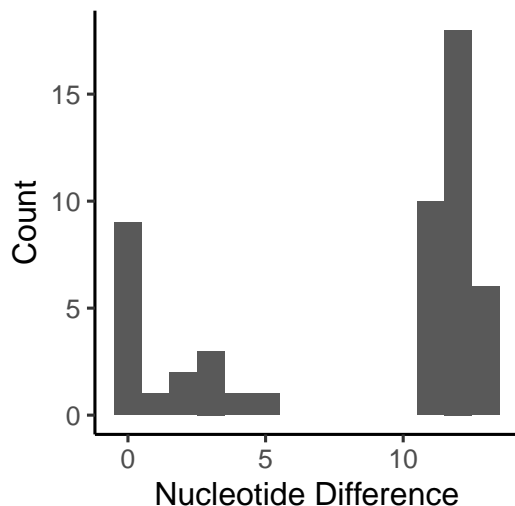
IGHV3-73*01

29 sequences assigned
7 (24.1%) exact matches, in which:
5 unique CDR3
2 unique J



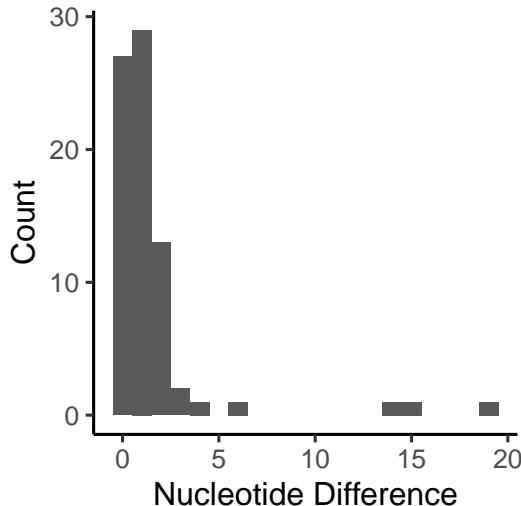
IGHV3-73*02

51 sequences assigned
9 (17.6%) exact matches, in which:
7 unique CDR3
2 unique J



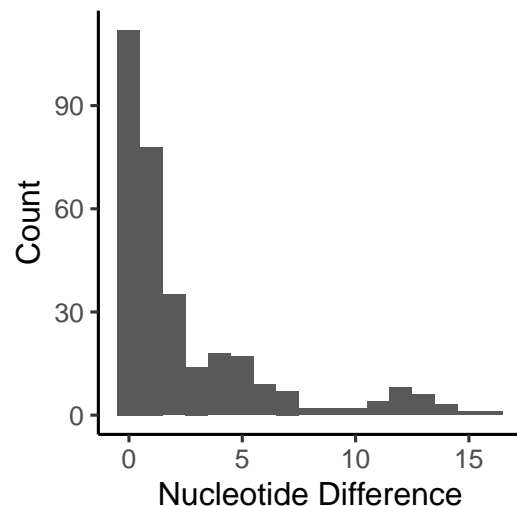
IGHV4-30-4*01

76 sequences assigned
27 (35.5%) exact matches, in which:
17 unique CDR3
3 unique J



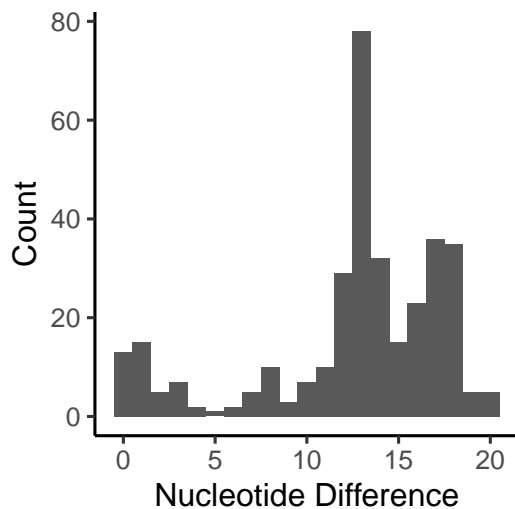
IGHV4-34*01

319 sequences assigned
112 (35.1%) exact matches, in which:
75 unique CDR3
6 unique J



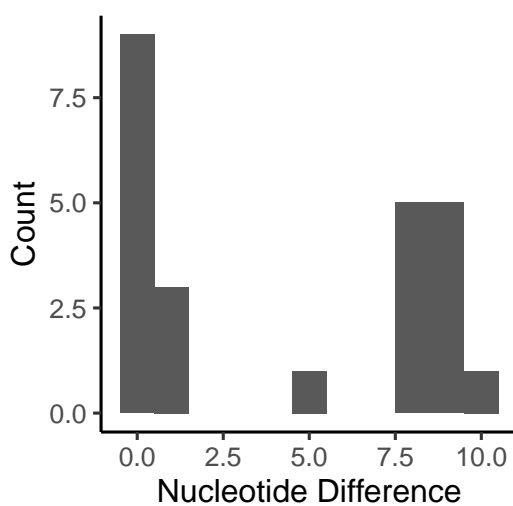
IGHV3-74*01

341 sequences assigned
13 (3.8%) exact matches, in which:
11 unique CDR3
4 unique J



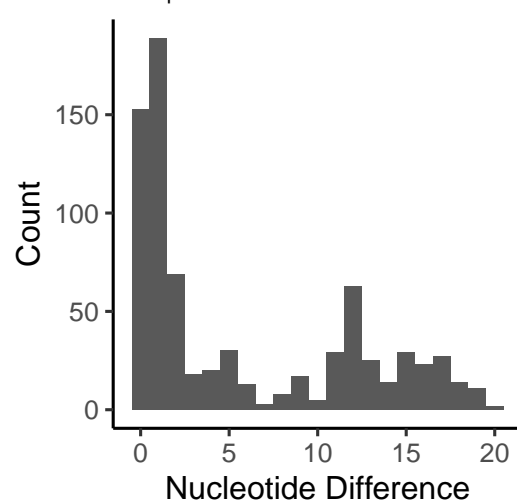
IGHV4-30-2*01

24 sequences assigned
9 (37.5%) exact matches, in which:
6 unique CDR3
3 unique J



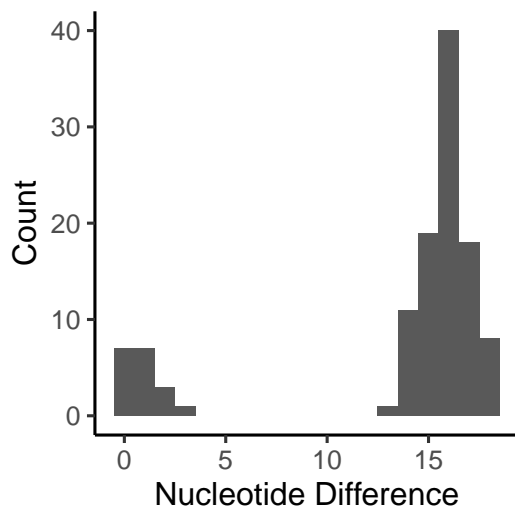
IGHV4-39*01

778 sequences assigned
153 (19.7%) exact matches, in which:
112 unique CDR3
7 unique J



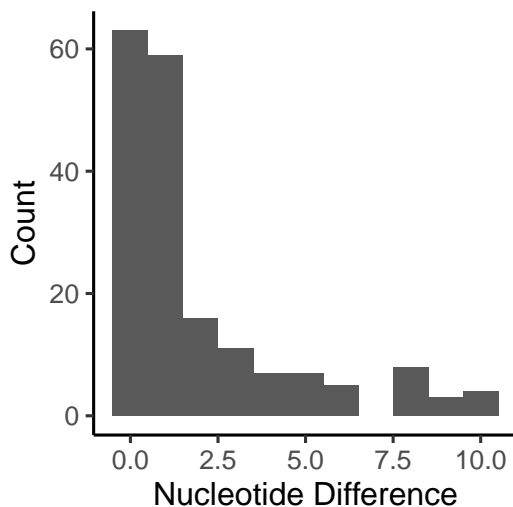
IGHV4-4*07

115 sequences assigned
7 (6.1%) exact matches, in which:
4 unique CDR3
3 unique J



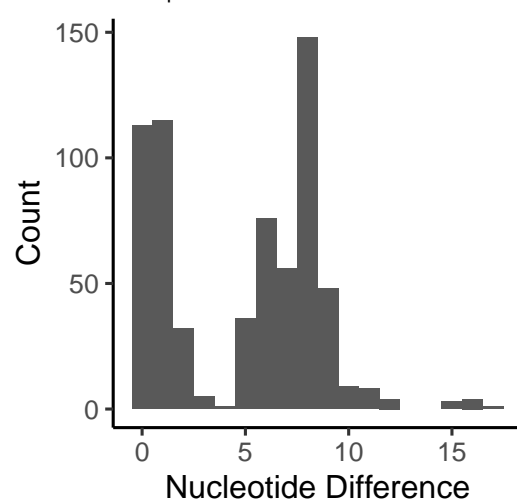
IGHV4-31*03

183 sequences assigned
63 (34.4%) exact matches, in which:
36 unique CDR3
5 unique J



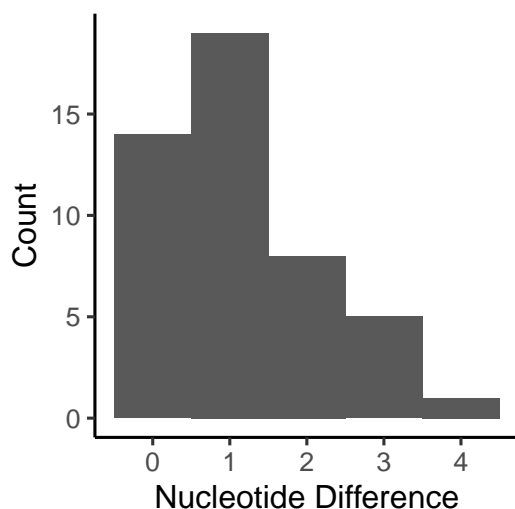
IGHV4-59*01

660 sequences assigned
113 (17.1%) exact matches, in which:
72 unique CDR3
6 unique J



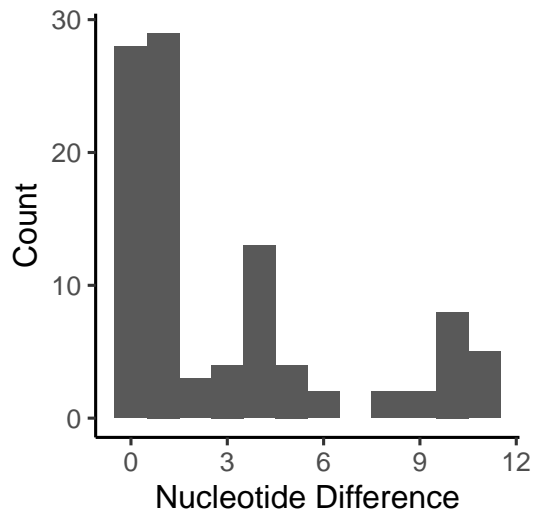
IGHV4-61*01

47 sequences assigned
14 (29.8%) exact matches, in which:
8 unique CDR3
3 unique J



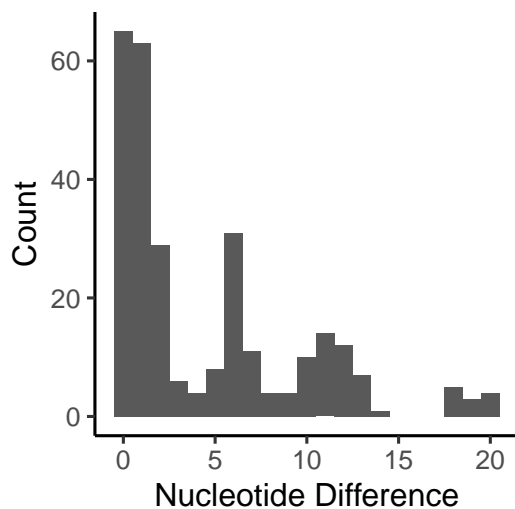
IGHV5-51*03

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



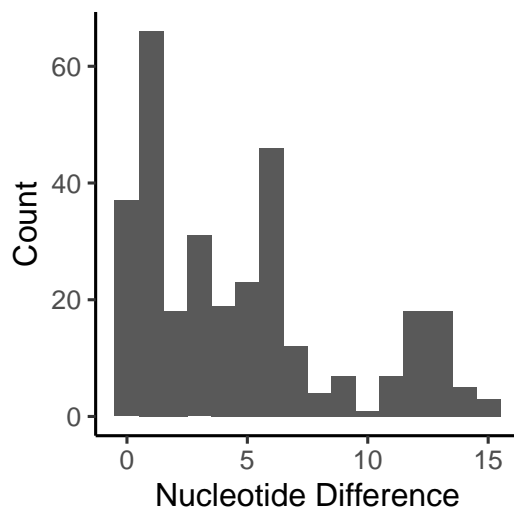
IGHV4-61*02

284 sequences assigned
65 (22.9%) exact matches, in which:
38 unique CDR3
6 unique J



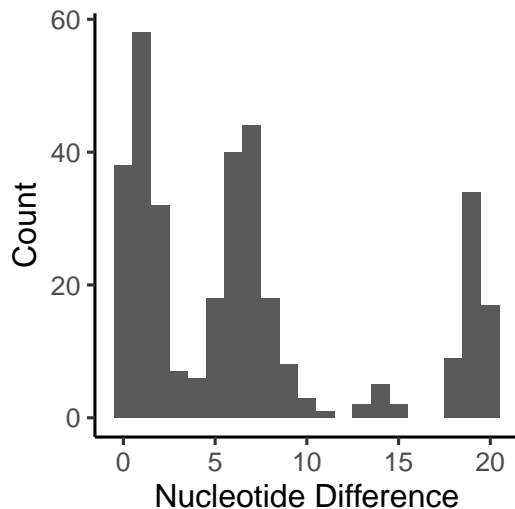
IGHV6-1*01

315 sequences assigned
37 (11.7%) exact matches, in which:
18 unique CDR3
4 unique J



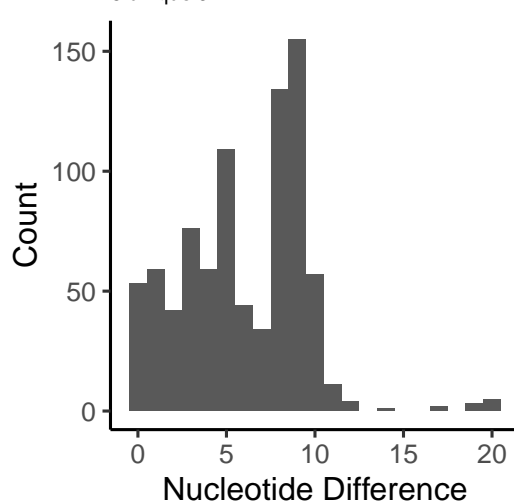
IGHV5-51*01

509 sequences assigned
38 (7.5%) exact matches, in which:
35 unique CDR3
4 unique J

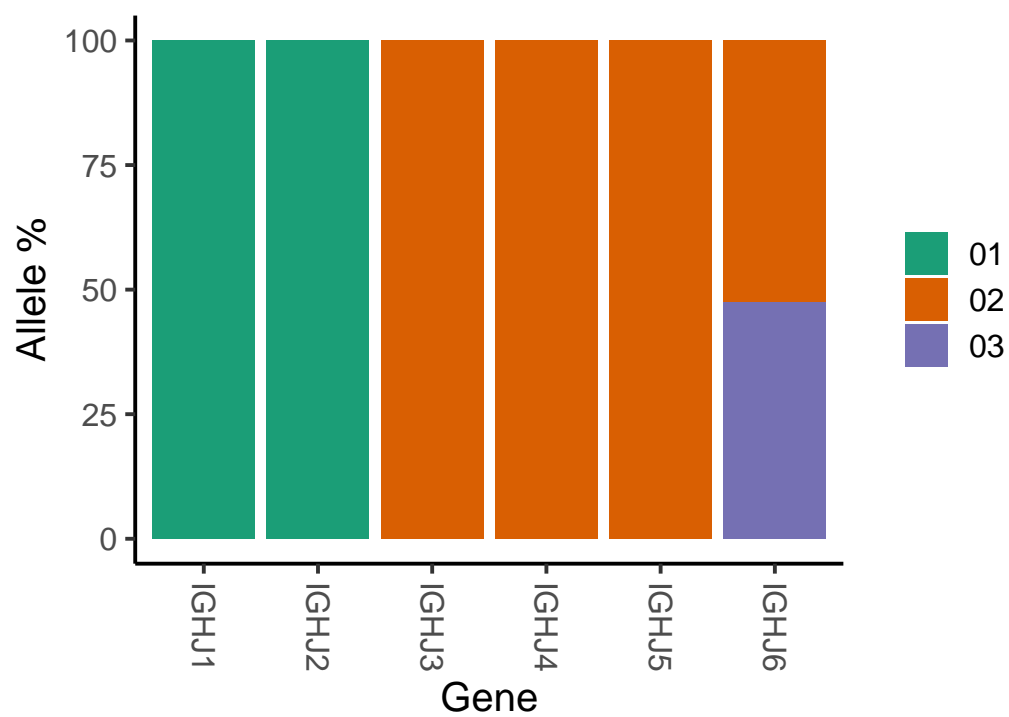


IGHV7-4-1*02

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



Allele Usage



Sequence Count by IGHJ6 allele usage



Warning – no inferred sequences found.

Warning – no inferred sequences found.

Warning – no inferred sequences found.

Warning – no inferred sequences found.