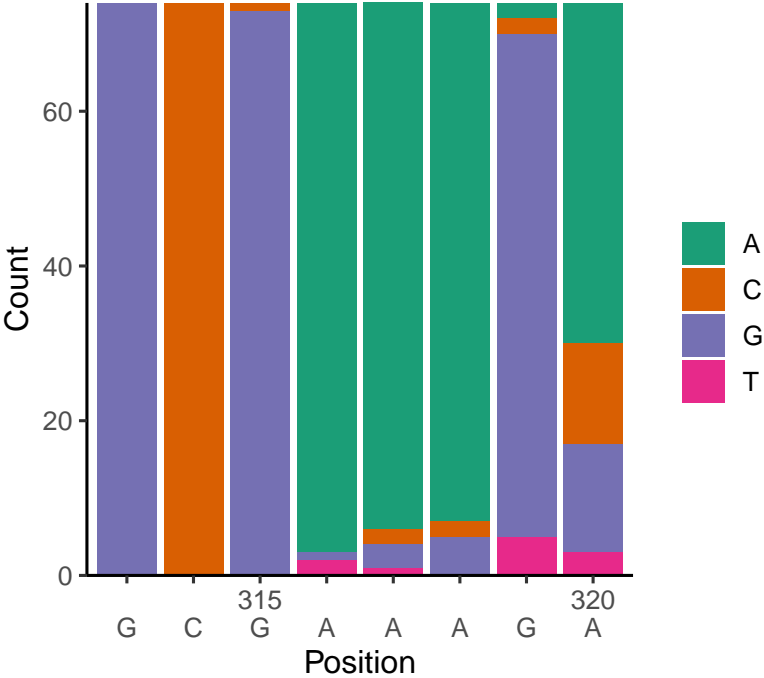
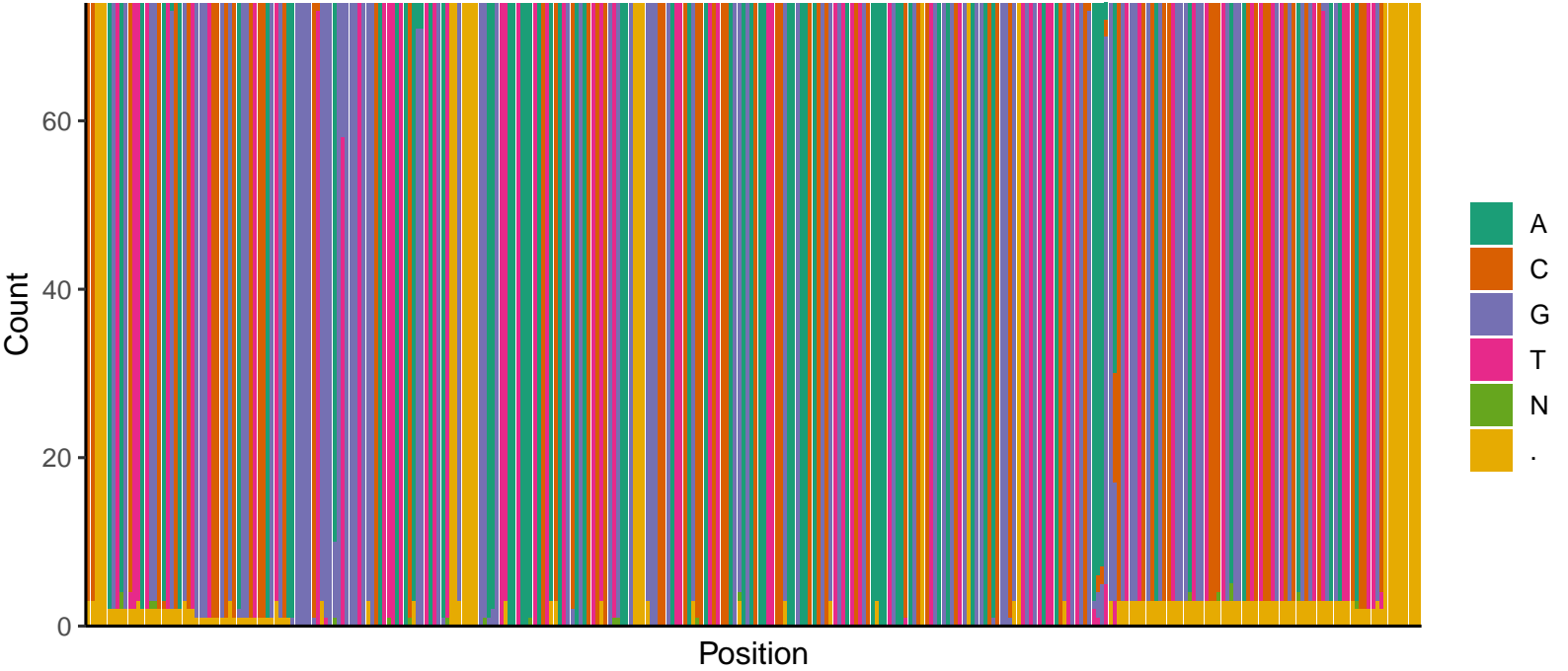


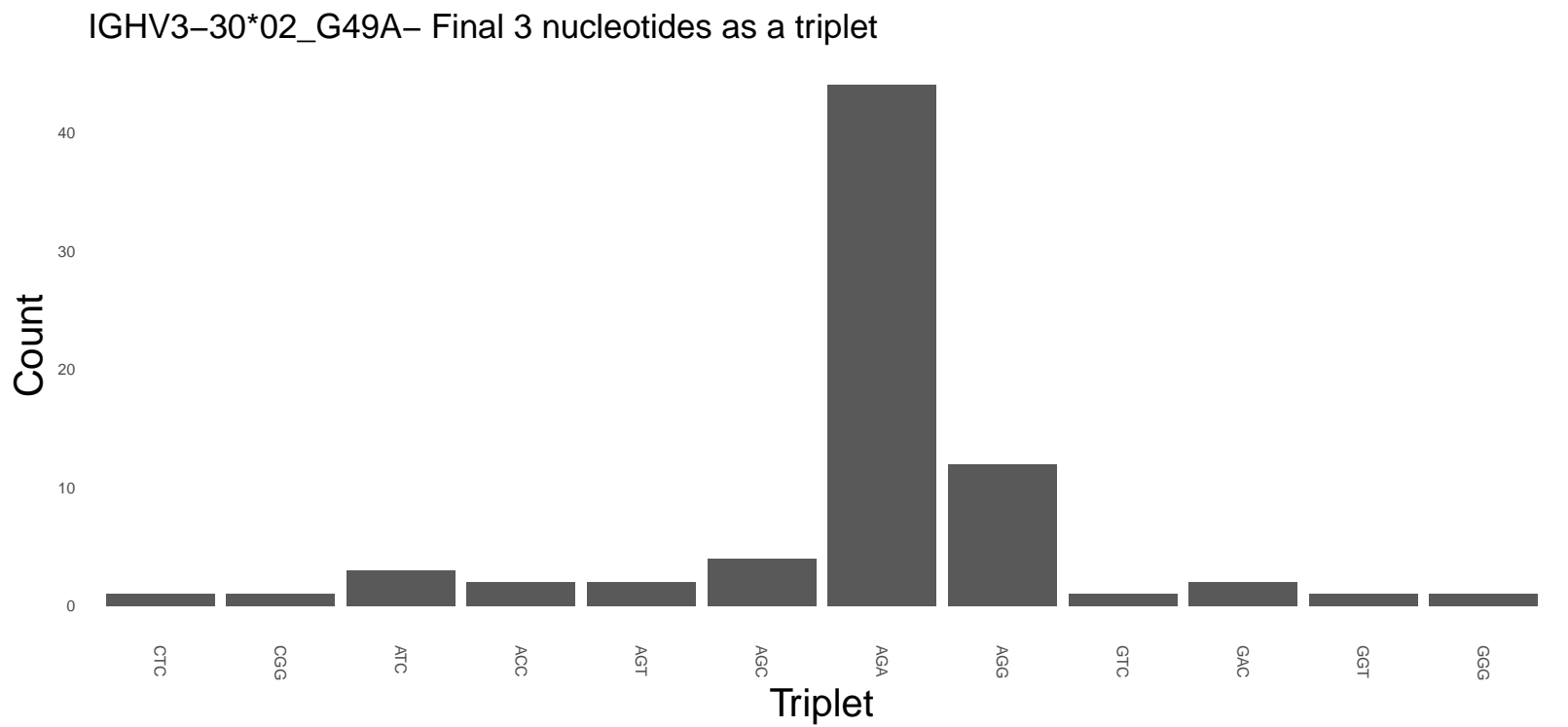
Gene IGHV3-30*02_G49A



Gene IGHV3-30*02_G49A

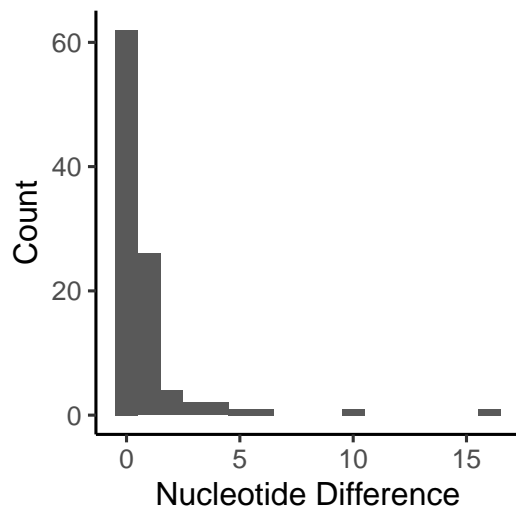


IGHV3-30*02_G49A- Final 3 nucleotides as a triplet



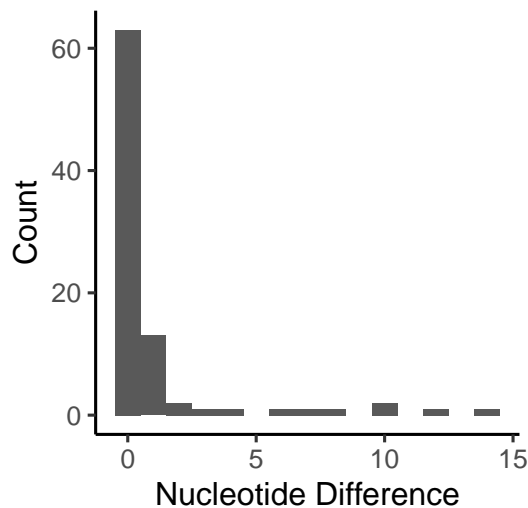
IGHV1-2*02

100 sequences assigned
62 (62%) exact matches, in which:
62 unique CDR3
4 unique J



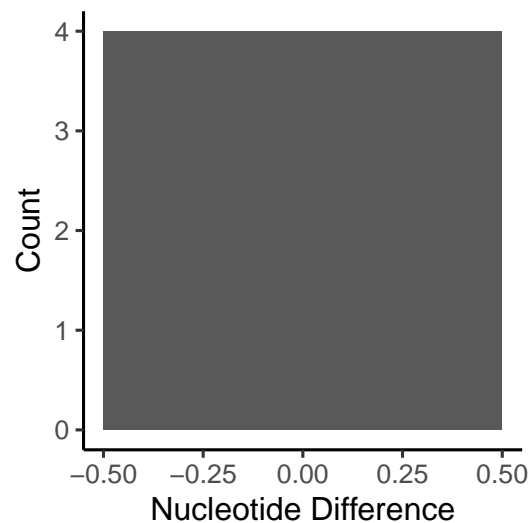
IGHV1-18*04

87 sequences assigned
63 (72.4%) exact matches, in which:
61 unique CDR3
7 unique J



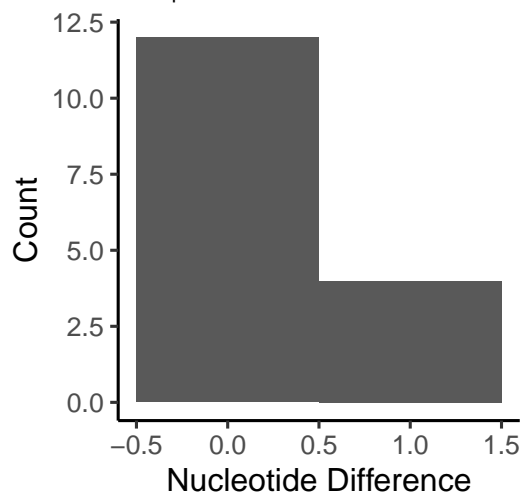
IGHV1-58*01

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



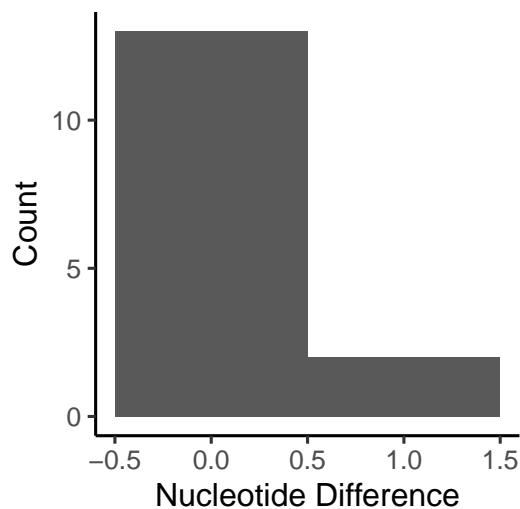
IGHV1-3*01

16 sequences assigned
12 (75%) exact matches, in which:
12 unique CDR3
3 unique J



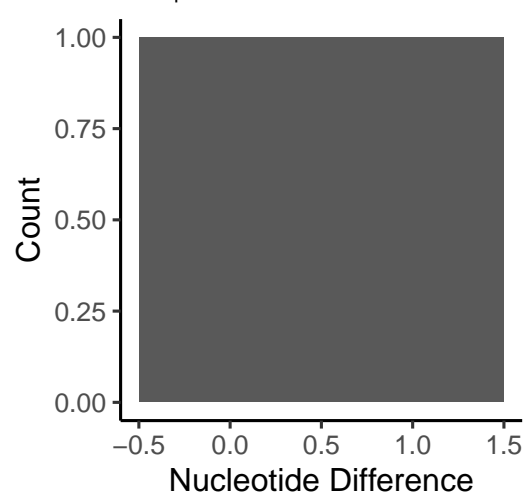
IGHV1-24*01

15 sequences assigned
13 (86.7%) exact matches, in which:
13 unique CDR3
5 unique J



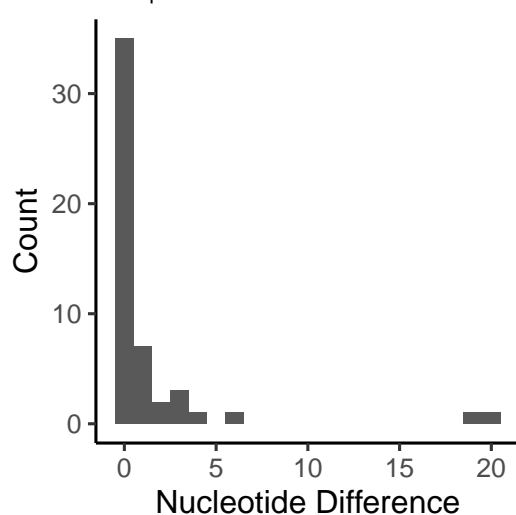
IGHV1-58*02

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



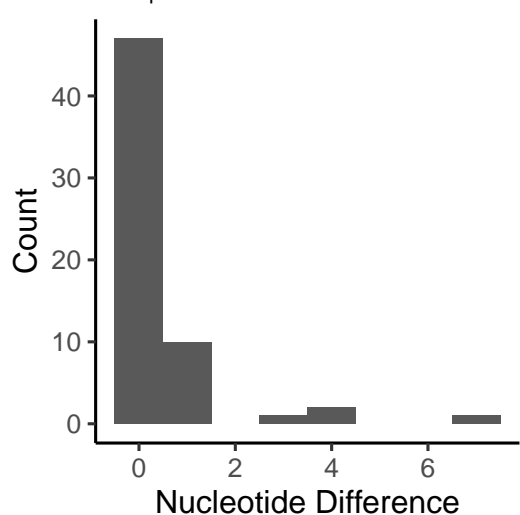
IGHV1-8*01

52 sequences assigned
35 (67.3%) exact matches, in which:
35 unique CDR3
4 unique J



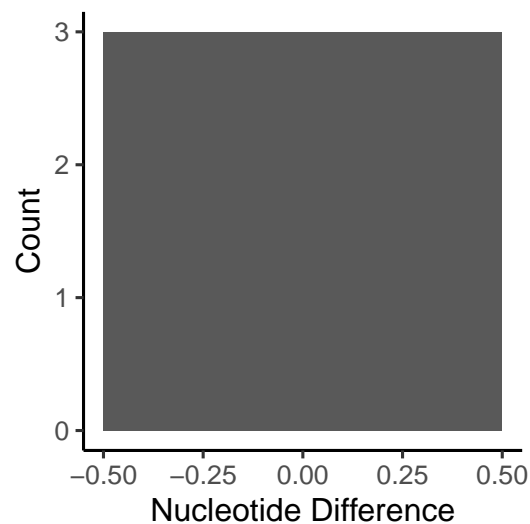
IGHV1-46*01

62 sequences assigned
47 (75.8%) exact matches, in which:
47 unique CDR3
6 unique J



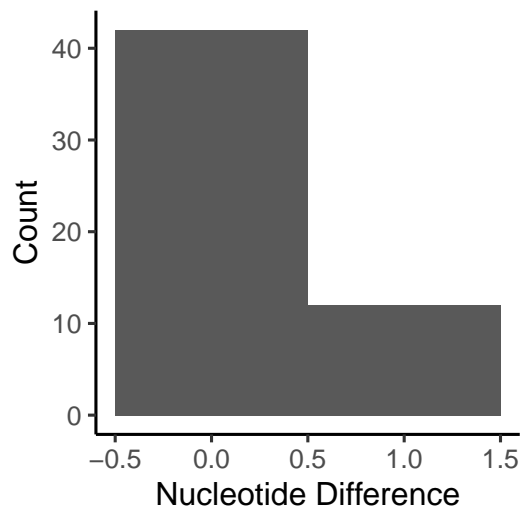
IGHV1-69-2*01

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



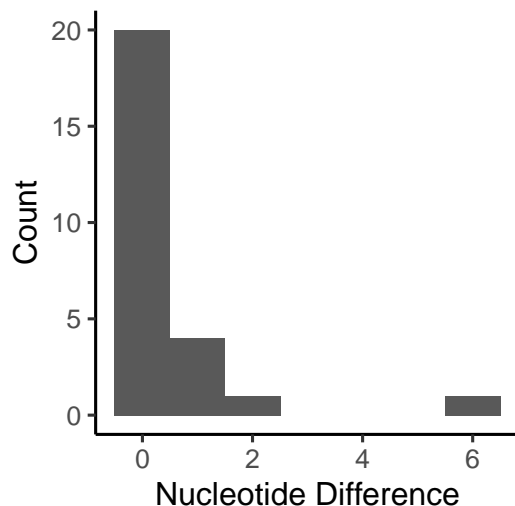
IGHV1-69*06

54 sequences assigned
42 (77.8%) exact matches, in which:
42 unique CDR3
6 unique J



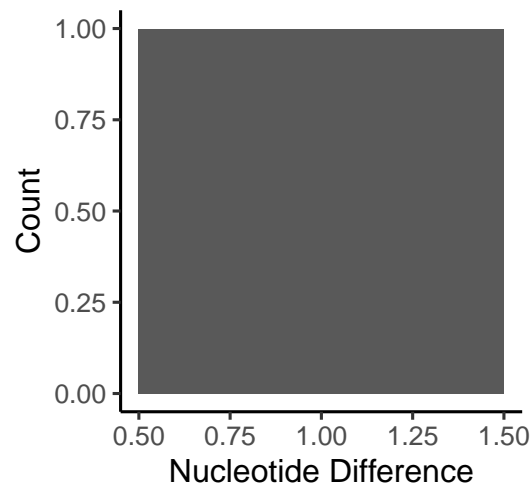
IGHV2-26*01

26 sequences assigned
20 (76.9%) exact matches, in which:
20 unique CDR3
5 unique J



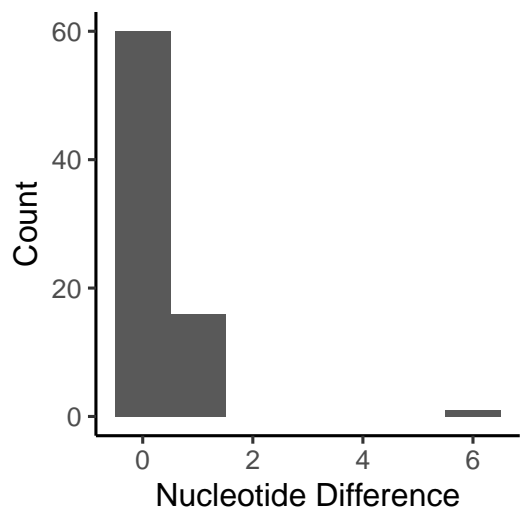
IGHV2-70D*04

1 sequences assigned
No exact matches.



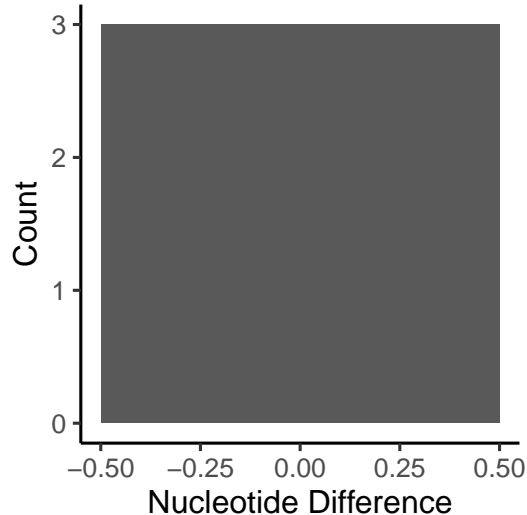
IGHV1-69*12

77 sequences assigned
60 (77.9%) exact matches, in which:
60 unique CDR3
5 unique J



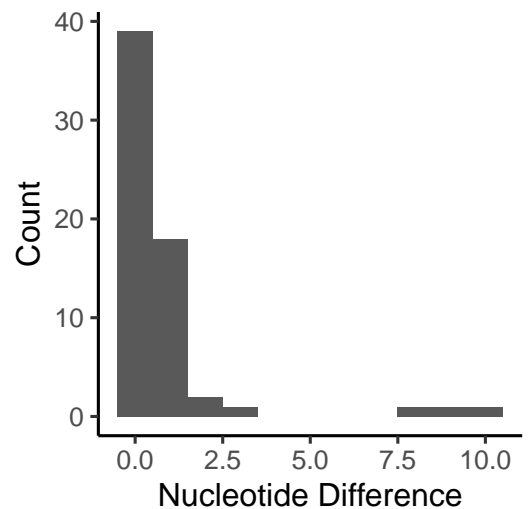
IGHV2-70*01

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



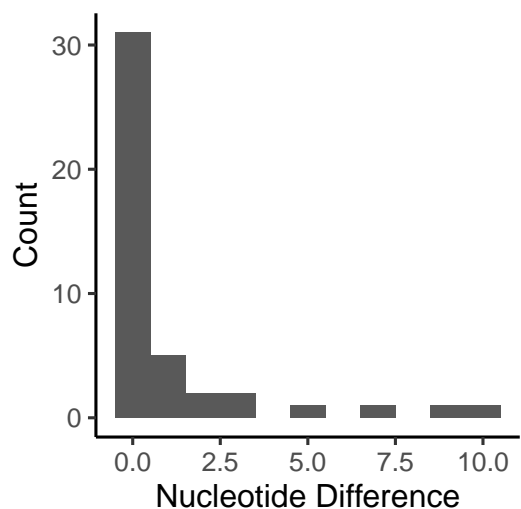
IGHV3-7*01

63 sequences assigned
39 (61.9%) exact matches, in which:
39 unique CDR3
6 unique J



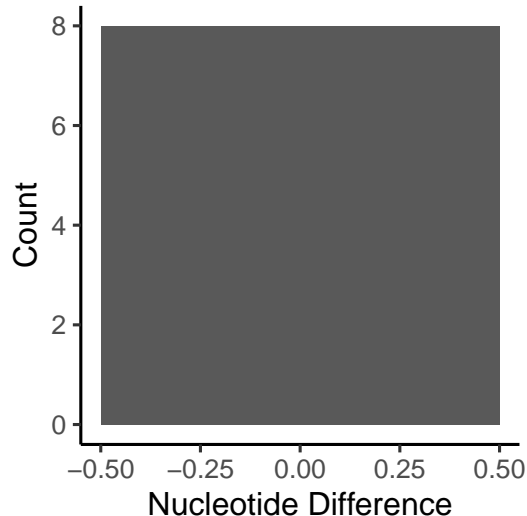
IGHV2-5*02

44 sequences assigned
31 (70.5%) exact matches, in which:
31 unique CDR3
6 unique J



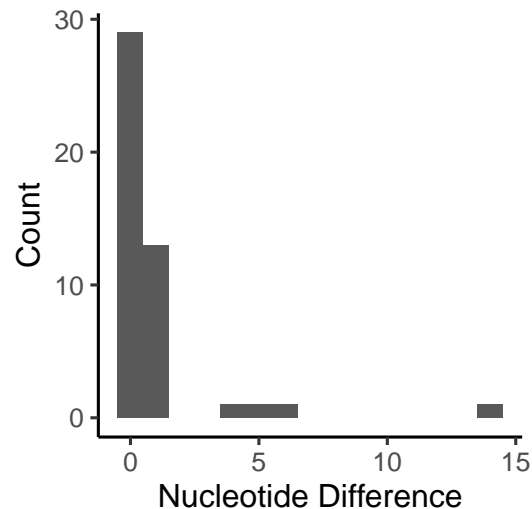
IGHV2-70*15

8 sequences assigned
8 (100%) exact matches, in which:
8 unique CDR3
2 unique J



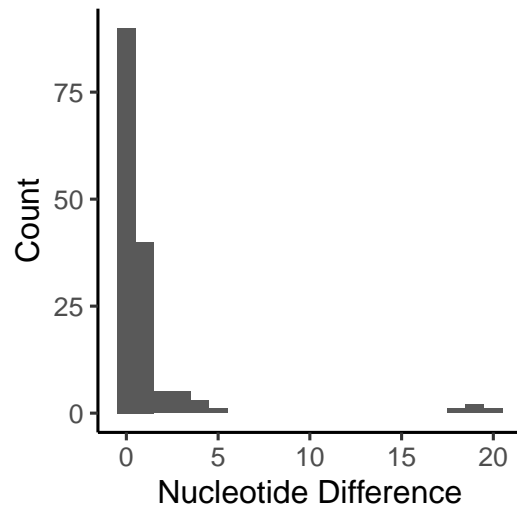
IGHV3-7*03

46 sequences assigned
29 (63%) exact matches, in which:
29 unique CDR3
5 unique J



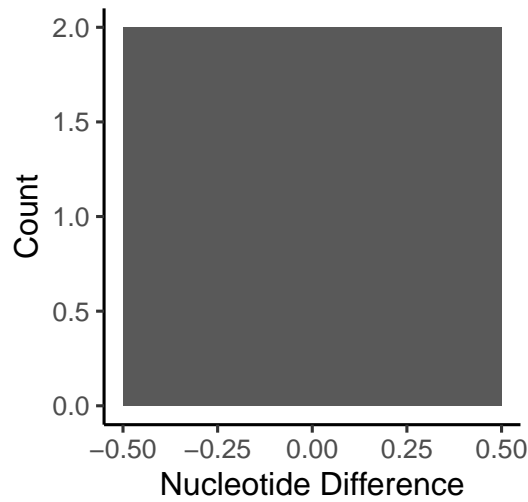
IGHV3-9*01

148 sequences assigned
90 (60.8%) exact matches, in which:
90 unique CDR3
6 unique J



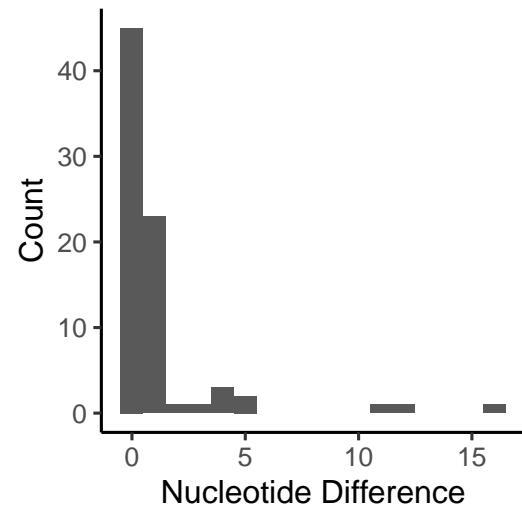
IGHV3-13*05

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



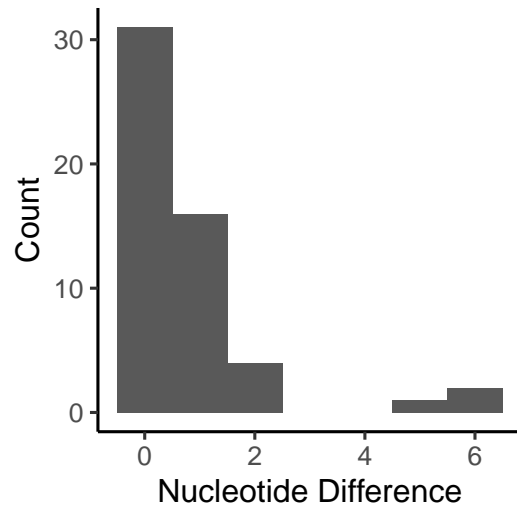
IGHV3-30-3*01

78 sequences assigned
45 (57.7%) exact matches, in which:
45 unique CDR3
6 unique J



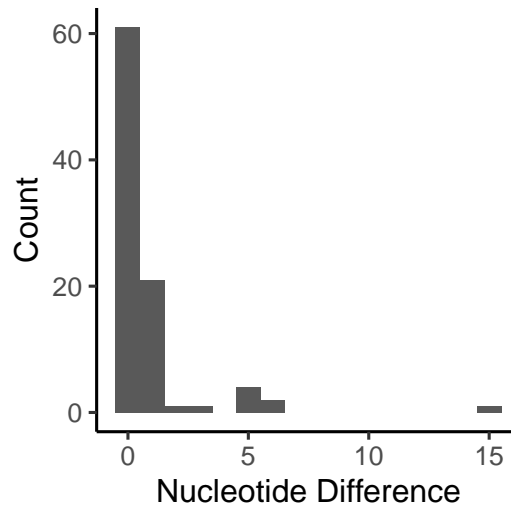
IGHV3-11*01

54 sequences assigned
31 (57.4%) exact matches, in which:
31 unique CDR3
5 unique J



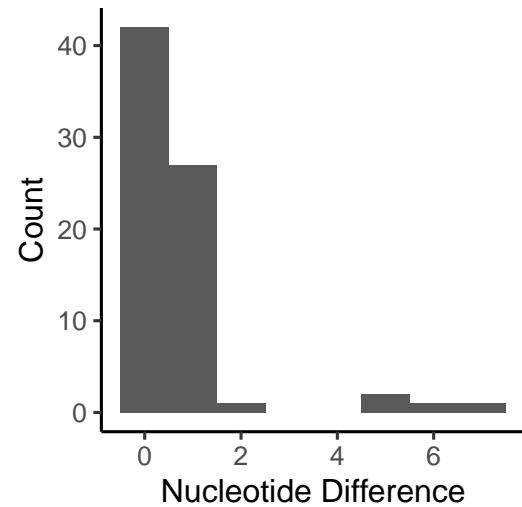
IGHV3-15*01

92 sequences assigned
61 (66.3%) exact matches, in which:
61 unique CDR3
5 unique J



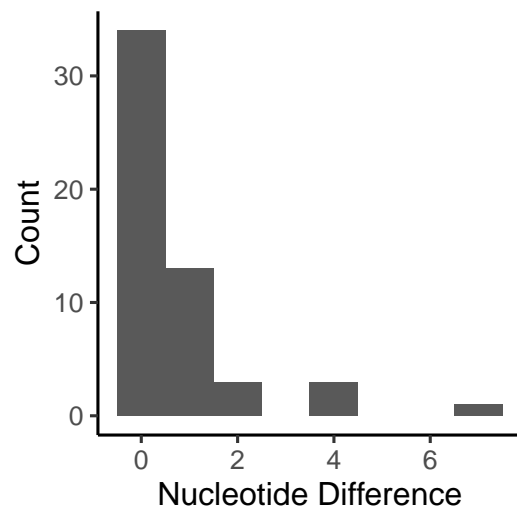
IGHV3-30*02_G49A

74 sequences assigned
42 (56.8%) exact matches, in which:
42 unique CDR3
5 unique J



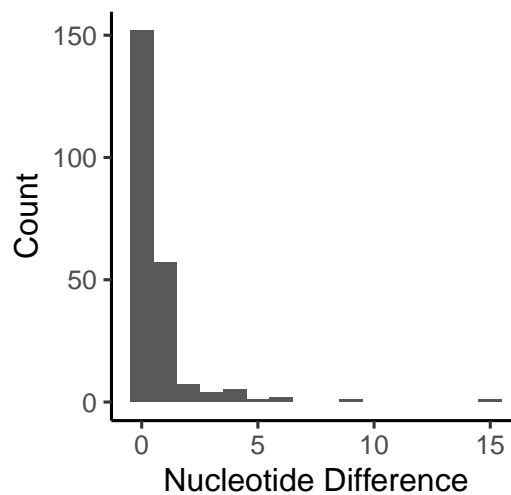
IGHV3-11*06

54 sequences assigned
34 (63%) exact matches, in which:
34 unique CDR3
5 unique J



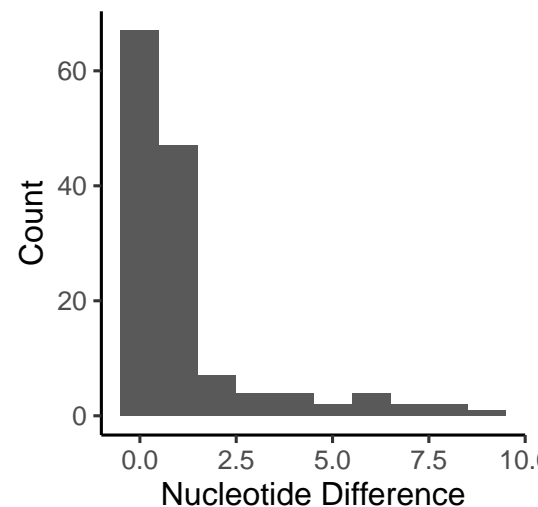
IGHV3-21*01

230 sequences assigned
152 (66.1%) exact matches, in which:
151 unique CDR3
7 unique J



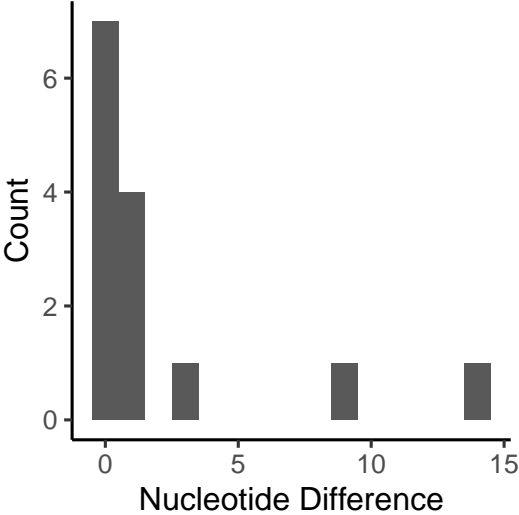
IGHV3-33*01

140 sequences assigned
67 (47.9%) exact matches, in which:
66 unique CDR3
6 unique J



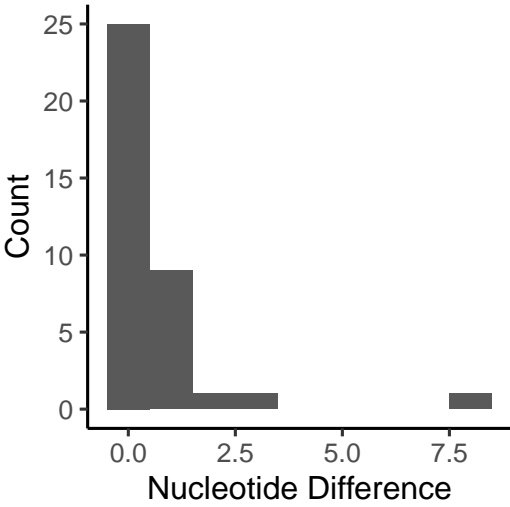
IGHV3-43*01

14 sequences assigned
7 (50%) exact matches, in which:
7 unique CDR3
3 unique J



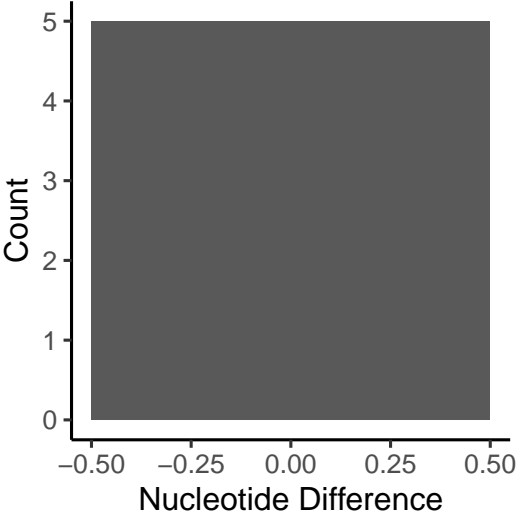
IGHV3-49*03

37 sequences assigned
25 (67.6%) exact matches, in which:
25 unique CDR3
4 unique J



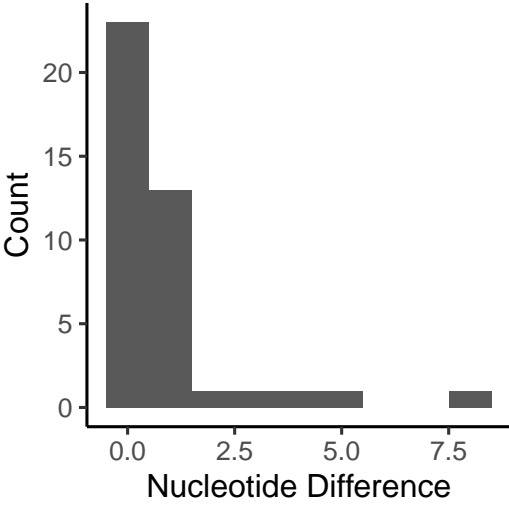
IGHV3-53*04

5 sequences assigned
5 (100%) exact matches, in which:
5 unique CDR3
3 unique J



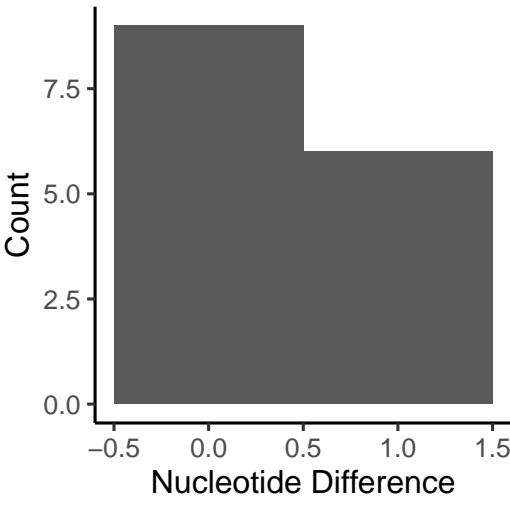
IGHV3-48*02

41 sequences assigned
23 (56.1%) exact matches, in which:
22 unique CDR3
3 unique J



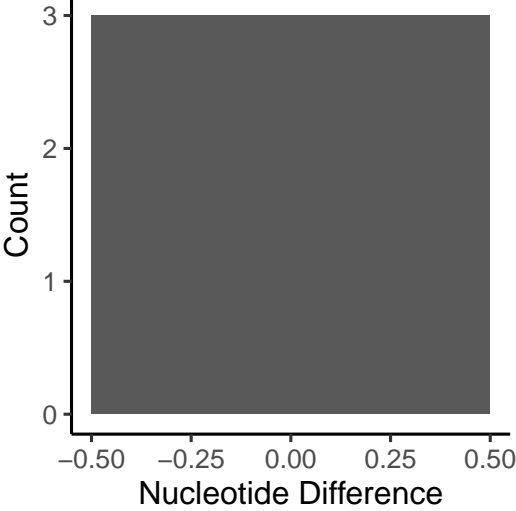
IGHV3-49*05

15 sequences assigned
9 (60%) exact matches, in which:
9 unique CDR3
4 unique J



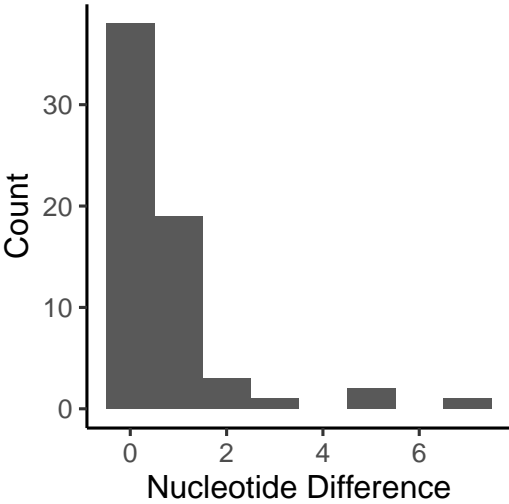
IGHV3-64*01

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



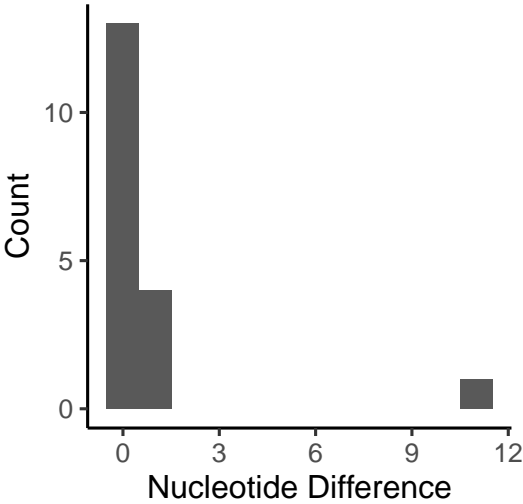
IGHV3-48*04

64 sequences assigned
38 (59.4%) exact matches, in which:
38 unique CDR3
6 unique J



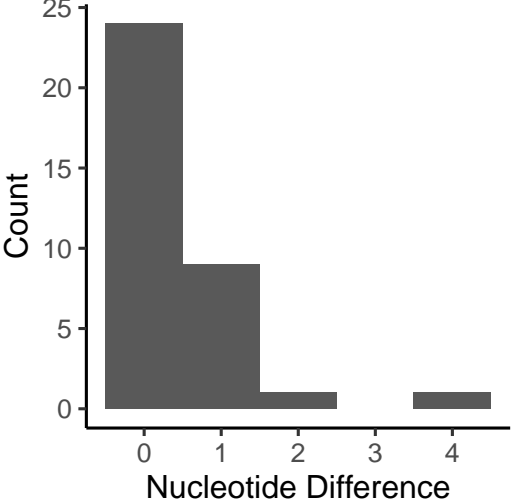
IGHV3-53*01

18 sequences assigned
13 (72.2%) exact matches, in which:
13 unique CDR3
4 unique J



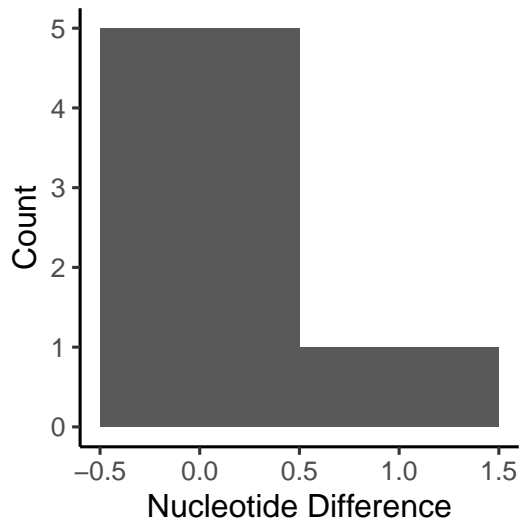
IGHV3-66*01

35 sequences assigned
24 (68.6%) exact matches, in which:
24 unique CDR3
6 unique J



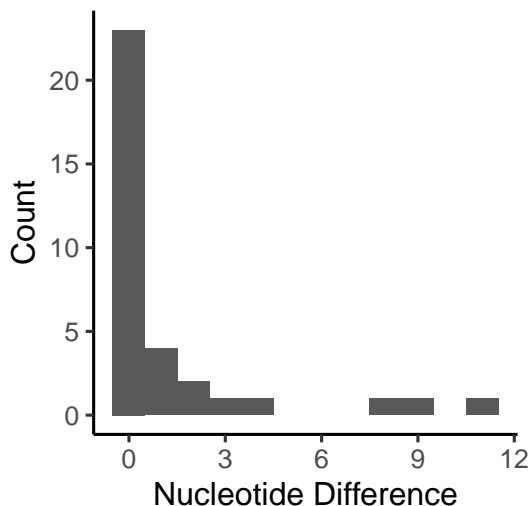
IGHV3-72*01

6 sequences assigned
5 (83.3%) exact matches, in which:
5 unique CDR3
4 unique J



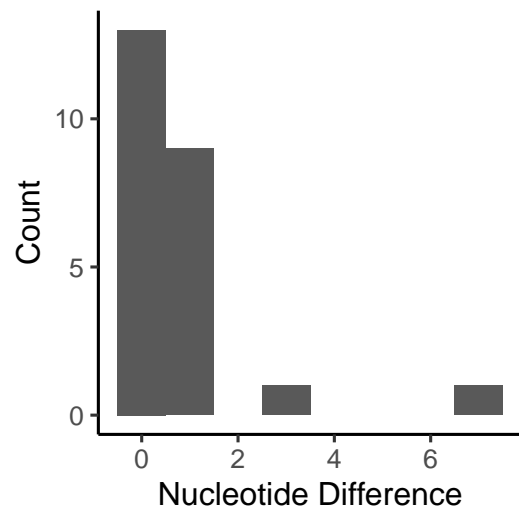
IGHV3-74*01

34 sequences assigned
23 (67.6%) exact matches, in which:
23 unique CDR3
3 unique J



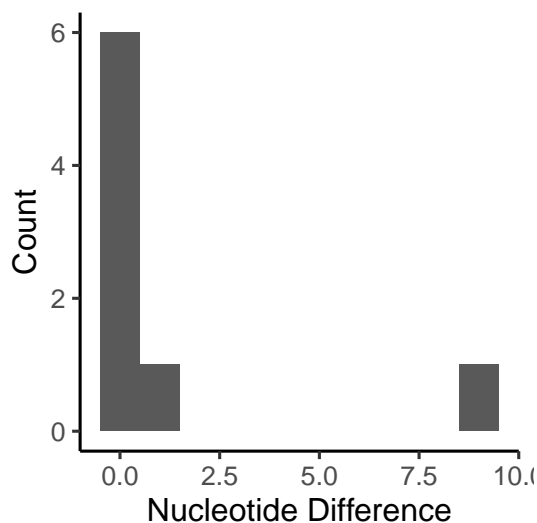
IGHV4-4*02

24 sequences assigned
13 (54.2%) exact matches, in which:
13 unique CDR3
5 unique J



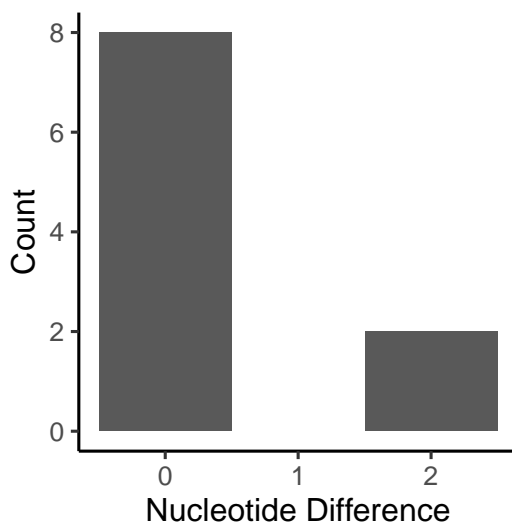
IGHV3-73*01

8 sequences assigned
6 (75%) exact matches, in which:
6 unique CDR3
1 unique J



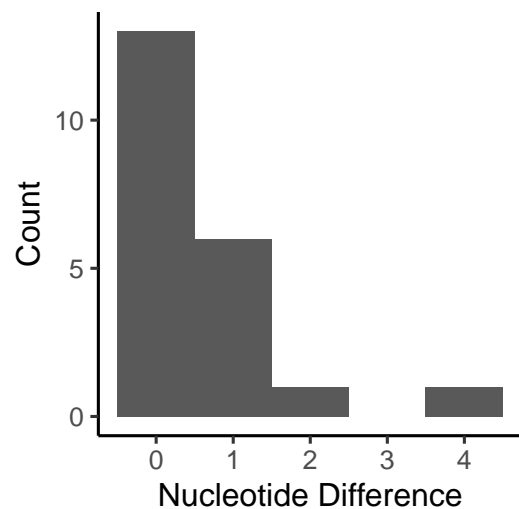
IGHV3-43D*03

10 sequences assigned
8 (80%) exact matches, in which:
8 unique CDR3
3 unique J



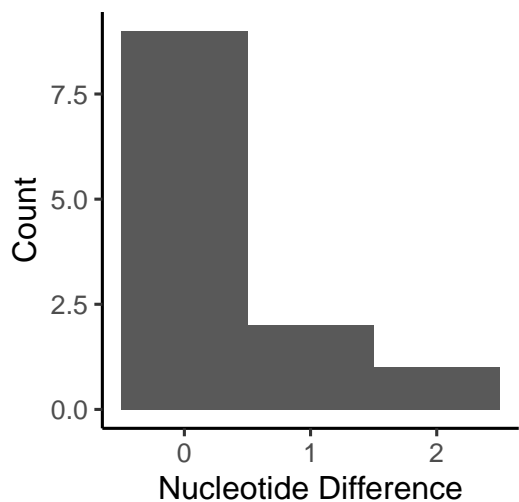
IGHV4-4*07

21 sequences assigned
13 (61.9%) exact matches, in which:
13 unique CDR3
5 unique J



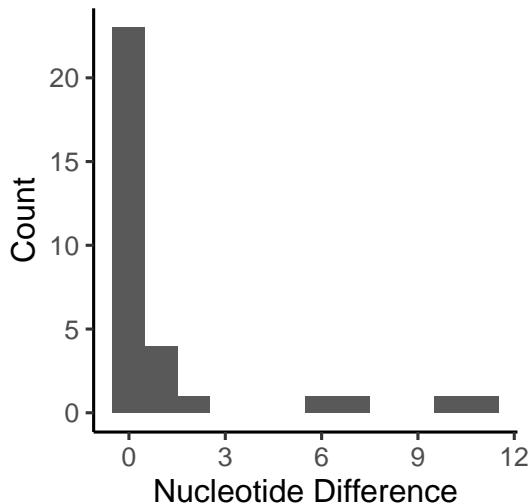
IGHV3-73*02

12 sequences assigned
9 (75%) exact matches, in which:
9 unique CDR3
4 unique J



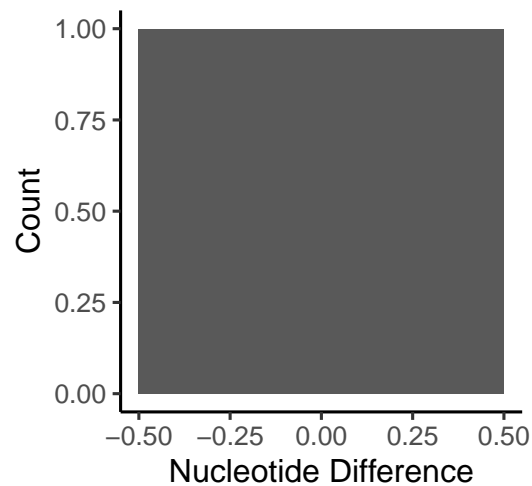
IGHV3-64D*06

32 sequences assigned
23 (71.9%) exact matches, in which:
22 unique CDR3
4 unique J



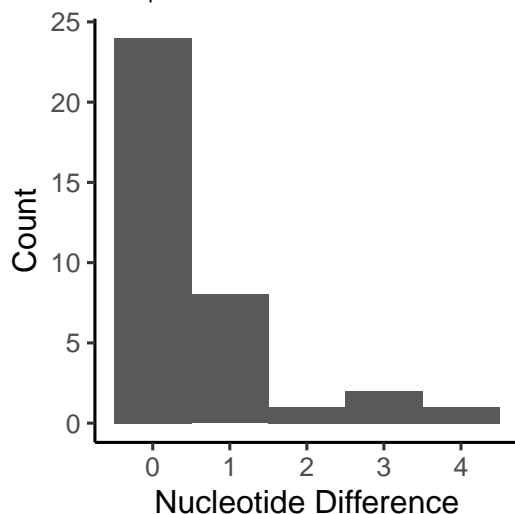
IGHV4-28*07

1 sequences assigned
1 (100%) exact matches, in which:
1 unique CDR3
1 unique J



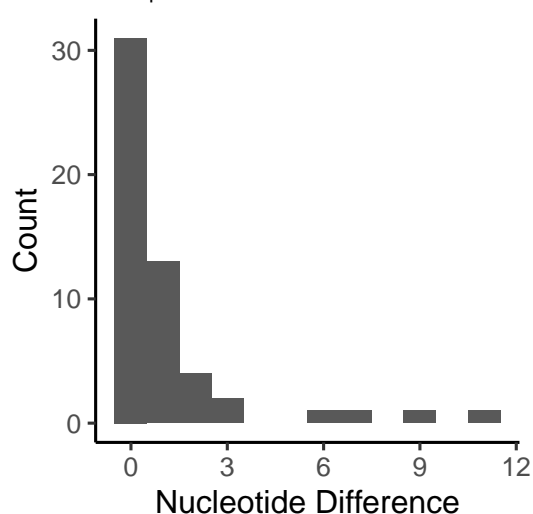
IGHV4-30-2*01

36 sequences assigned
24 (66.7%) exact matches, in which:
24 unique CDR3
6 unique J



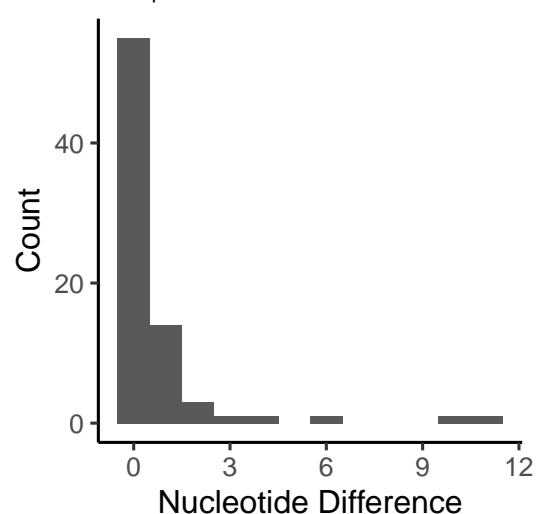
IGHV4-31*03

54 sequences assigned
31 (57.4%) exact matches, in which:
31 unique CDR3
5 unique J



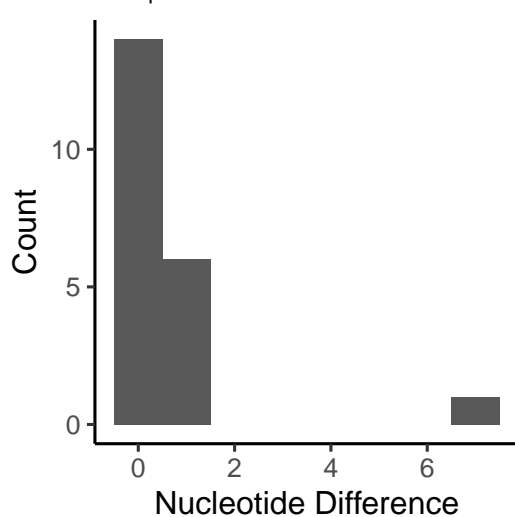
IGHV4-39*01

77 sequences assigned
55 (71.4%) exact matches, in which:
54 unique CDR3
6 unique J



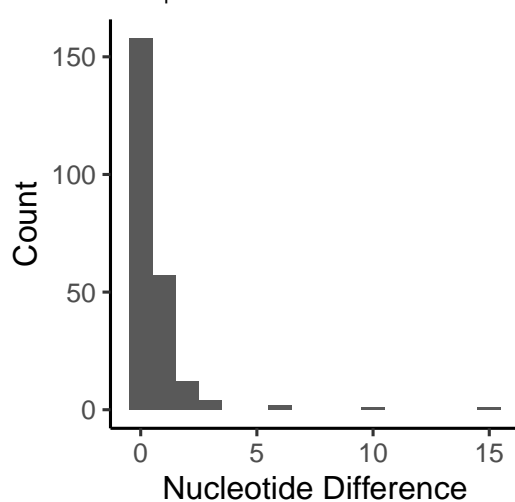
IGHV4-30-4*01

21 sequences assigned
14 (66.7%) exact matches, in which:
13 unique CDR3
5 unique J



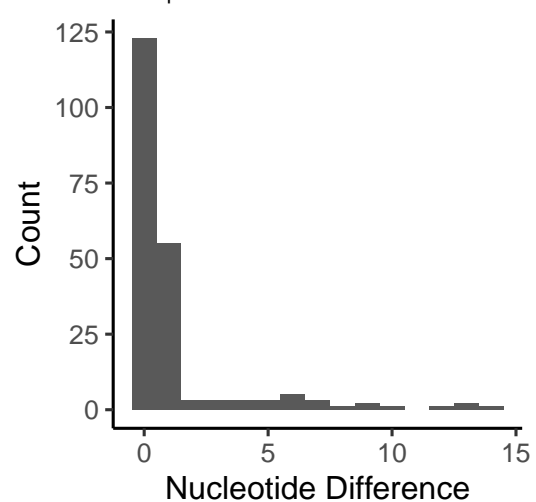
IGHV4-34*01

236 sequences assigned
158 (66.9%) exact matches, in which:
158 unique CDR3
6 unique J



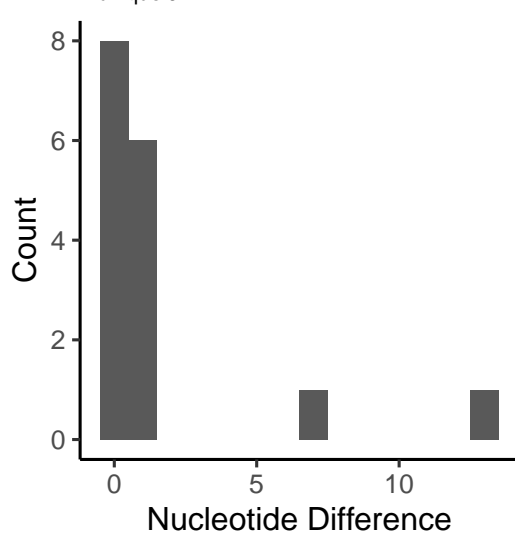
IGHV4-39*07

206 sequences assigned
123 (59.7%) exact matches, in which:
122 unique CDR3
5 unique J



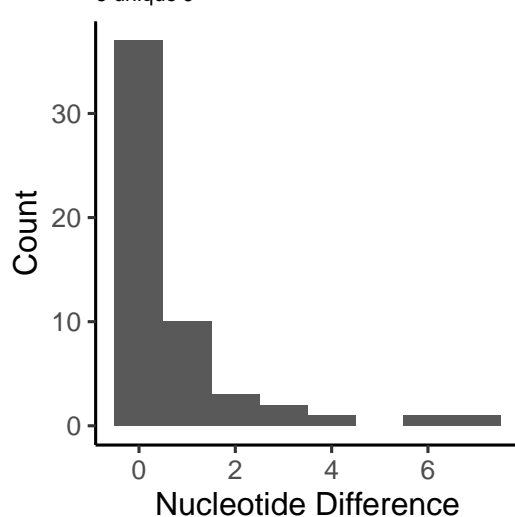
IGHV4-30-4*07

16 sequences assigned
8 (50%) exact matches, in which:
8 unique CDR3
4 unique J



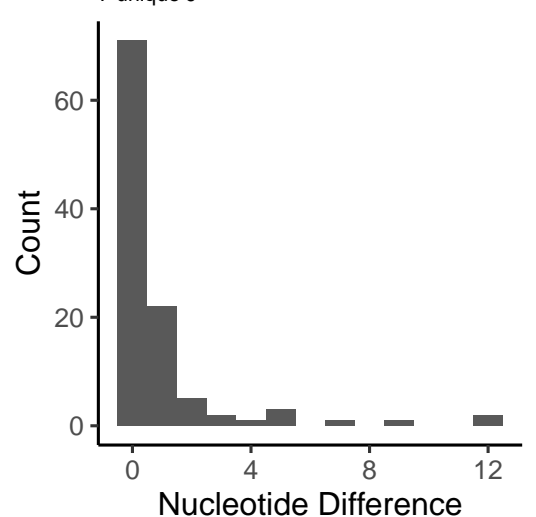
IGHV4-38-2*02

55 sequences assigned
37 (67.3%) exact matches, in which:
37 unique CDR3
6 unique J



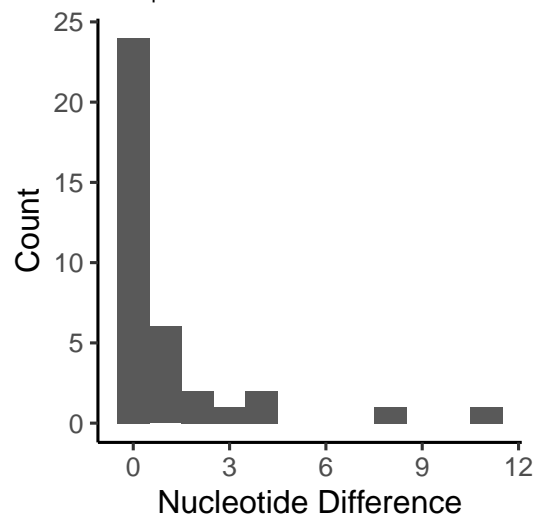
IGHV4-59*01

108 sequences assigned
71 (65.7%) exact matches, in which:
71 unique CDR3
7 unique J



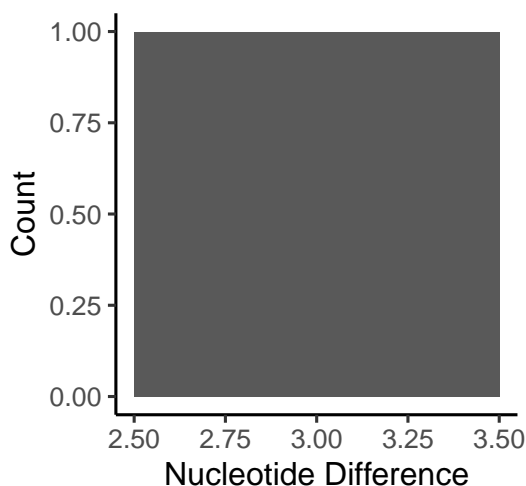
IGHV4–59*08

37 sequences assigned
24 (64.9%) exact matches, in which:
24 unique CDR3
5 unique J



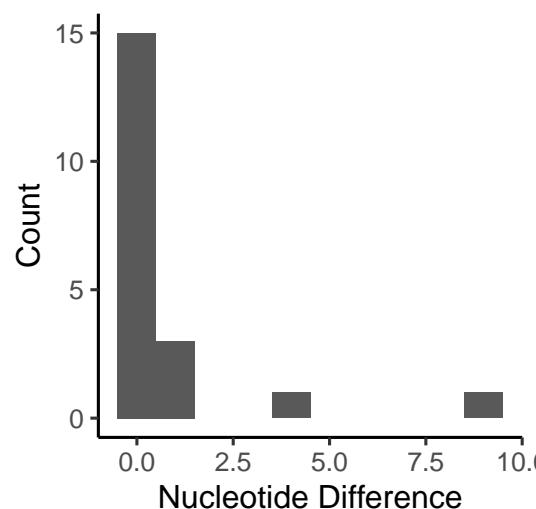
IGHV4/OR15–8*02

1 sequences assigned
No exact matches.



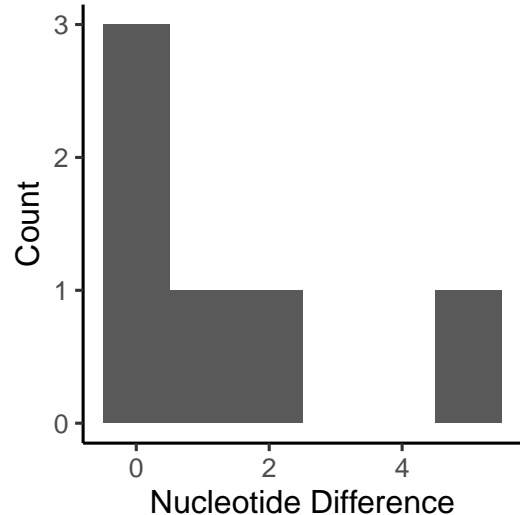
IGHV6–1*01

20 sequences assigned
15 (75%) exact matches, in which:
15 unique CDR3
6 unique J



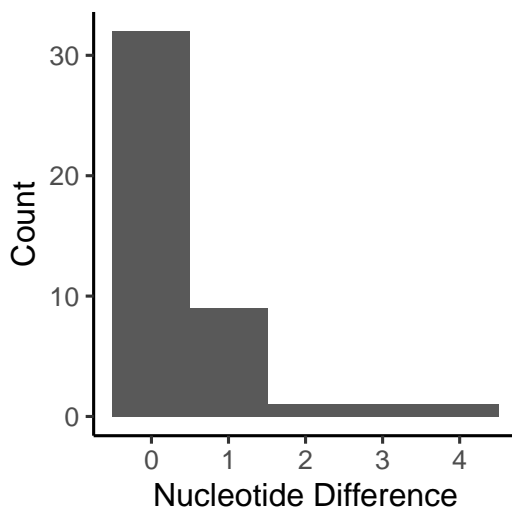
IGHV4–61*01

6 sequences assigned
3 (50%) exact matches, in which:
3 unique CDR3
3 unique J



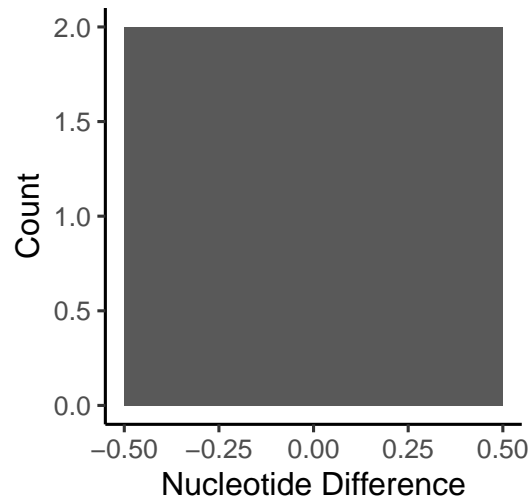
IGHV5–10–1*03

44 sequences assigned
32 (72.7%) exact matches, in which:
32 unique CDR3
5 unique J



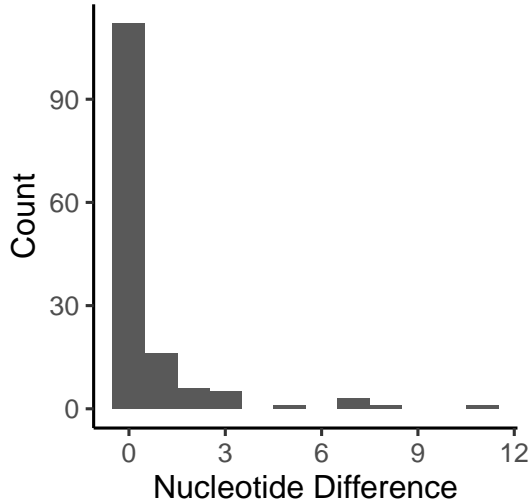
IGHV4–61*07

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

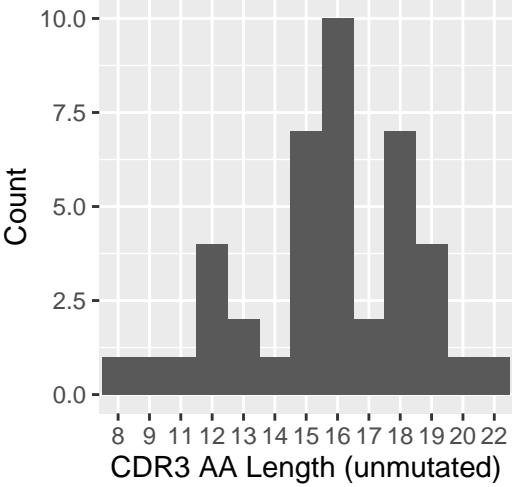


IGHV5–51*01

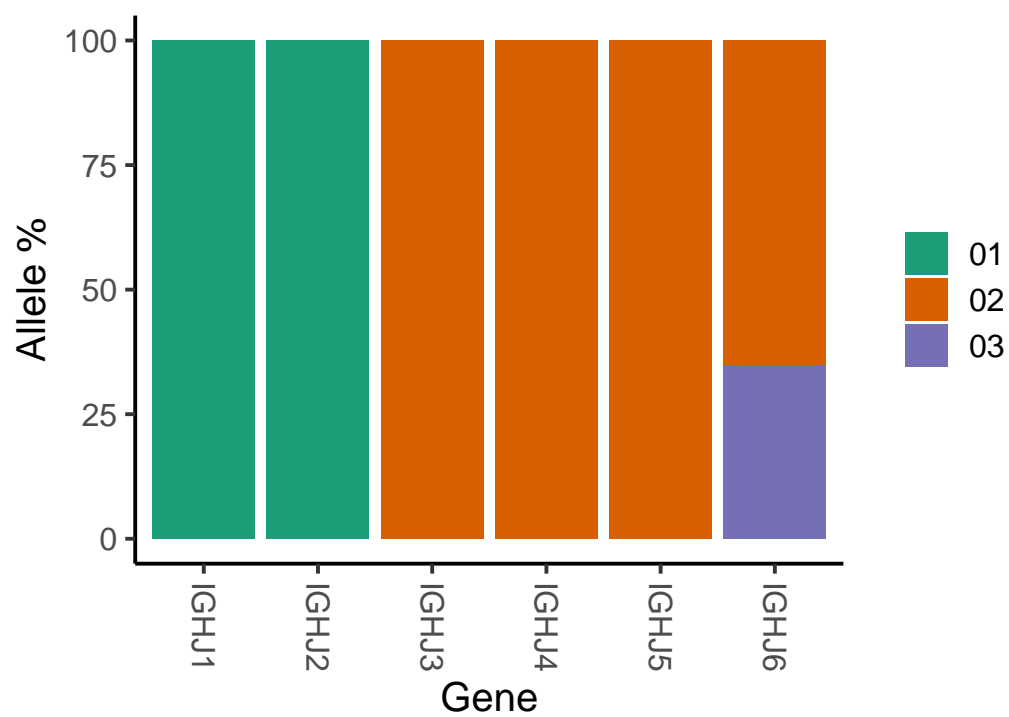
146 sequences assigned
112 (76.7%) exact matches, in which:
112 unique CDR3
7 unique J



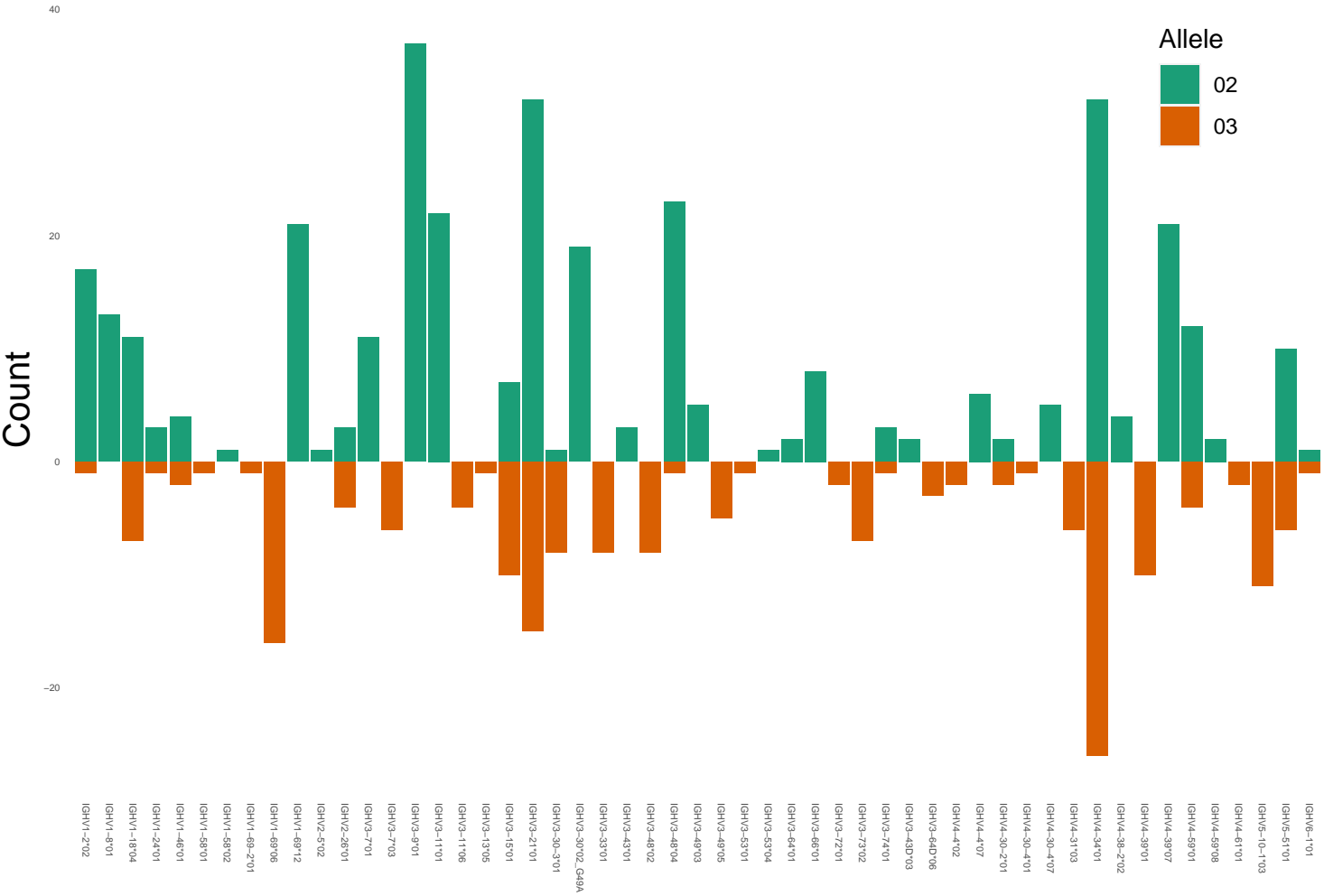
IGHV3-30*02_G49A



Allele Usage



Sequence Count by IGHJ6 allele usage



[illegible]