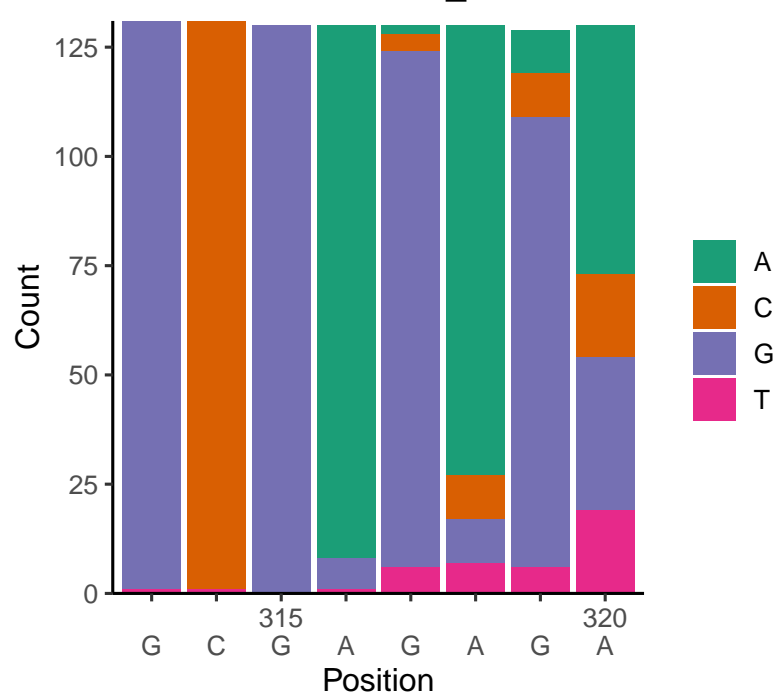
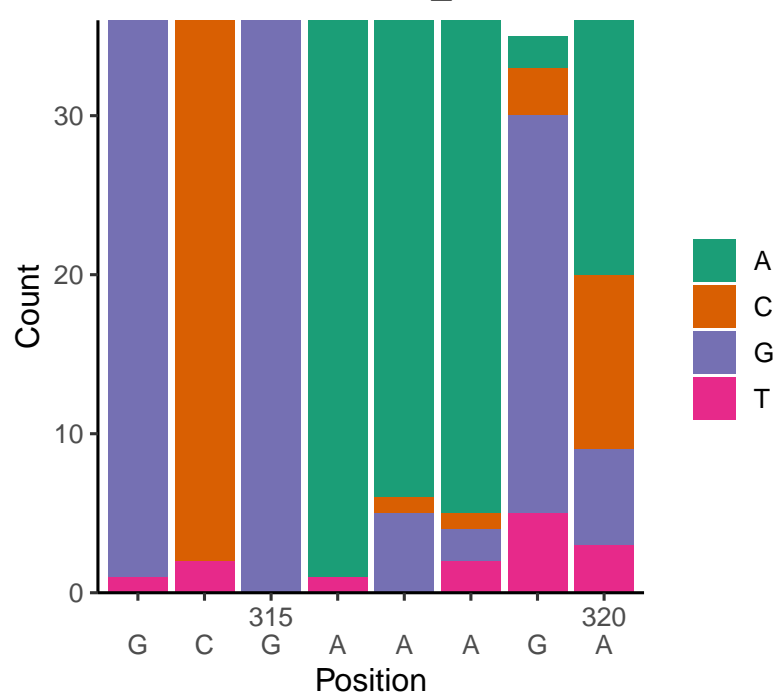


Gene IGHV1-69*04_A163G



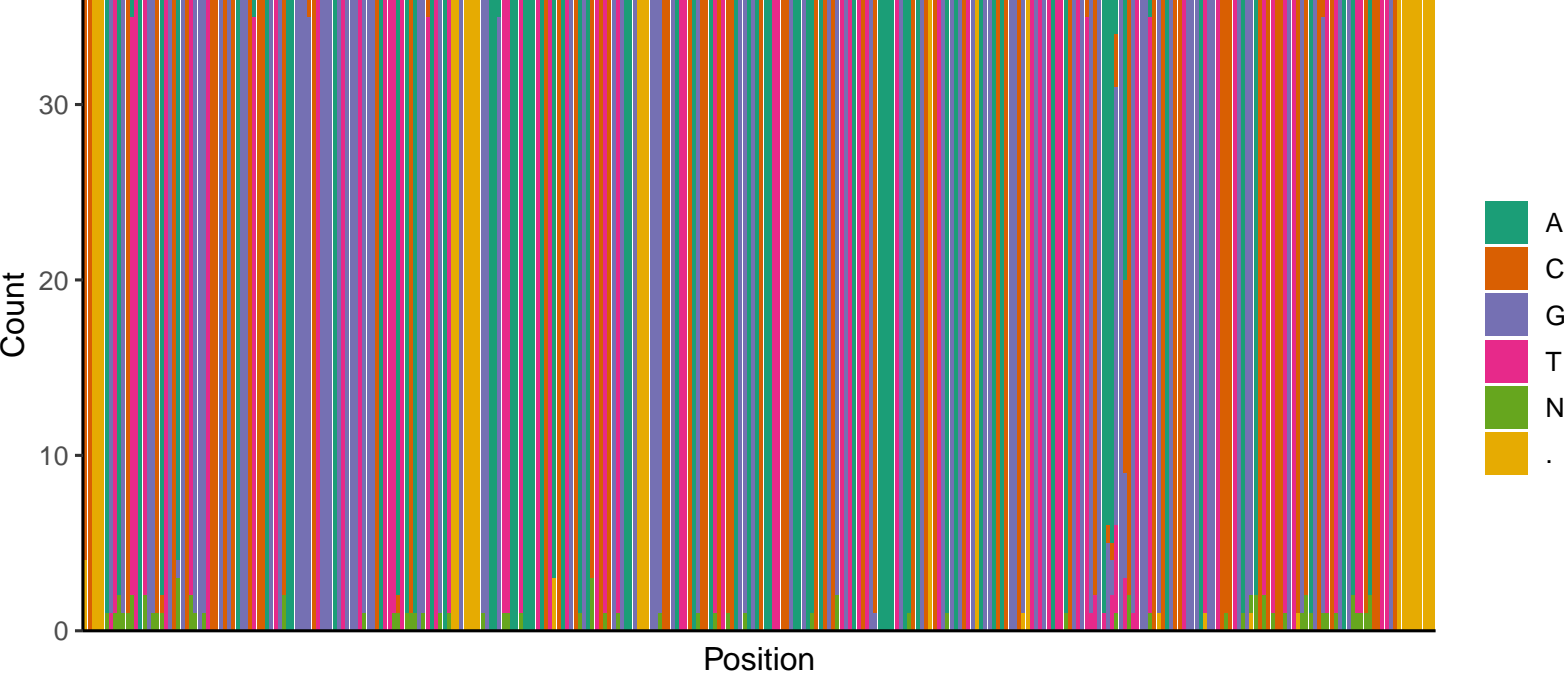
Gene IGHV3-30*02_G49A



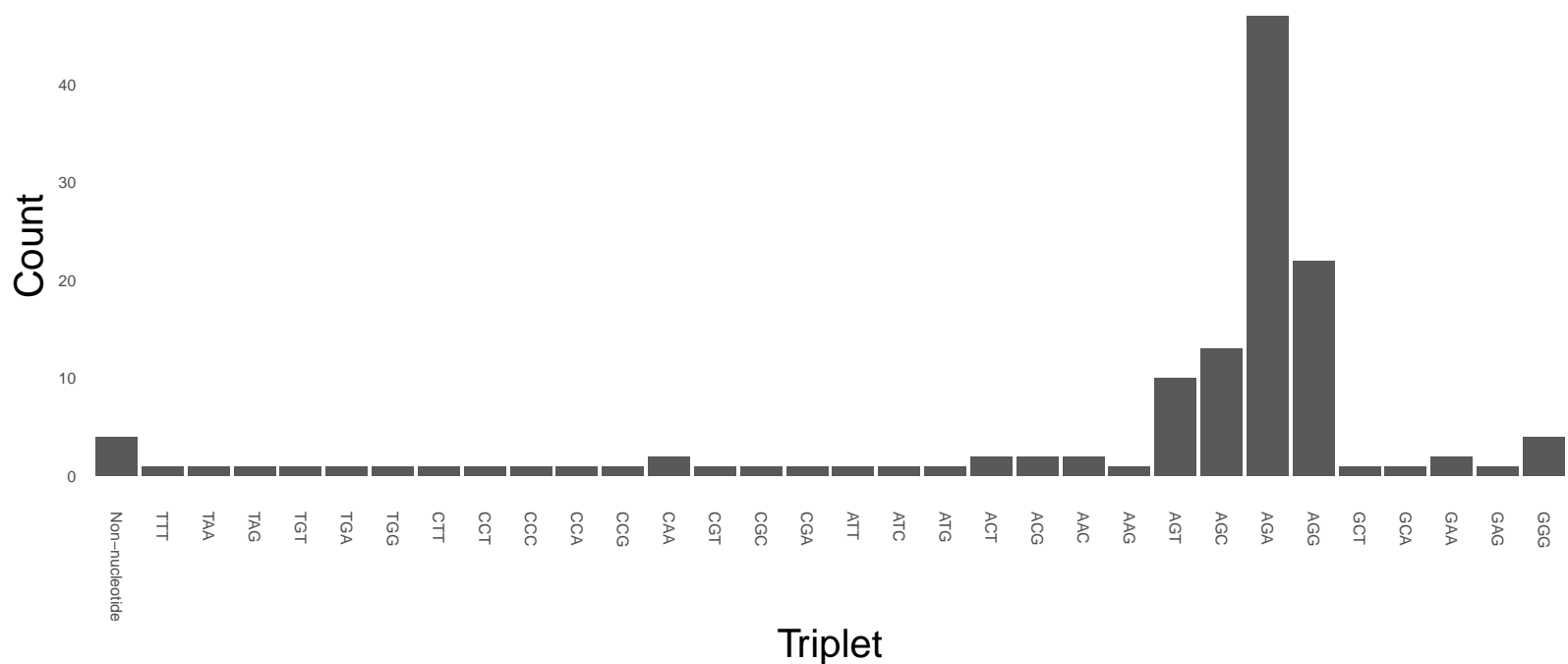
Gene IGHV1-69*04_A163G



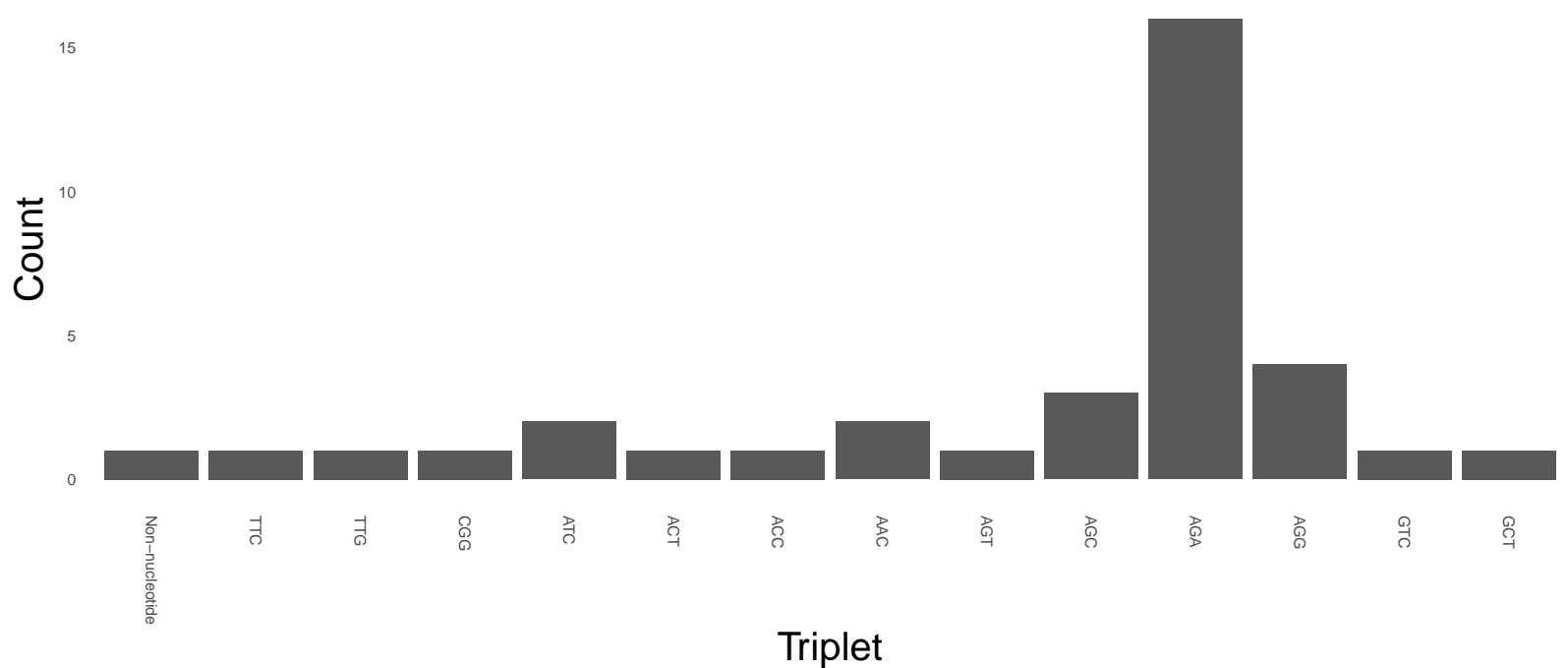
Gene IGHV3-30*02_G49A



IGHV1-69*04_A163G- Final 3 nucleotides as a triplet

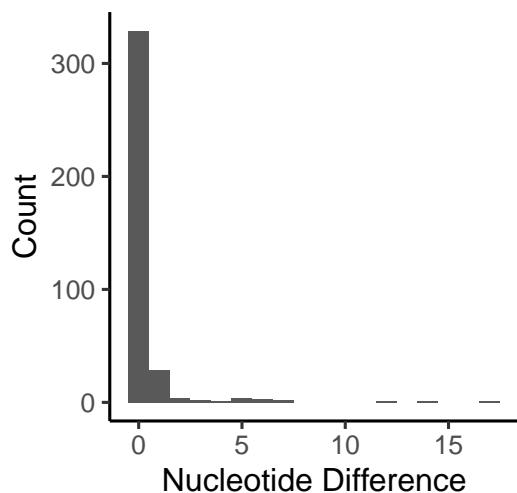


IGHV3-30*02_G49A- Final 3 nucleotides as a triplet



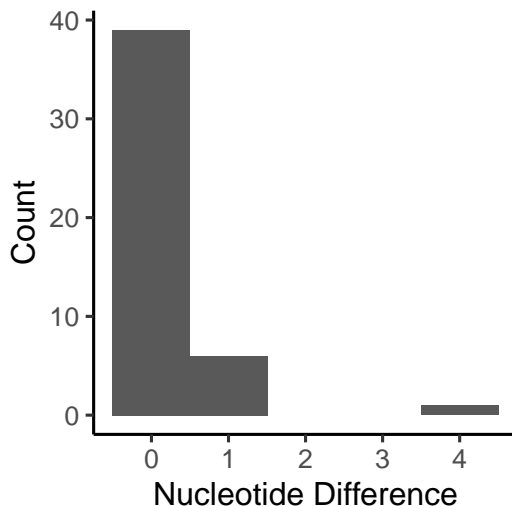
IGHV1-2*02

377 sequences assigned
329 (87.3%) exact matches, in which:
329 unique CDR3
7 unique J



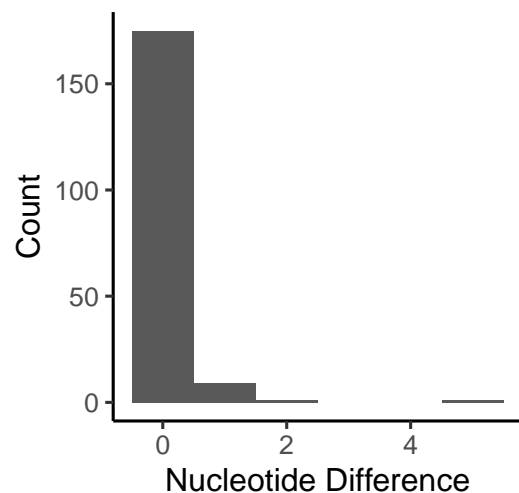
IGHV1-8*03

46 sequences assigned
39 (84.8%) exact matches, in which:
39 unique CDR3
4 unique J



IGHV1-24*01

186 sequences assigned
175 (94.1%) exact matches, in which:
175 unique CDR3
7 unique J



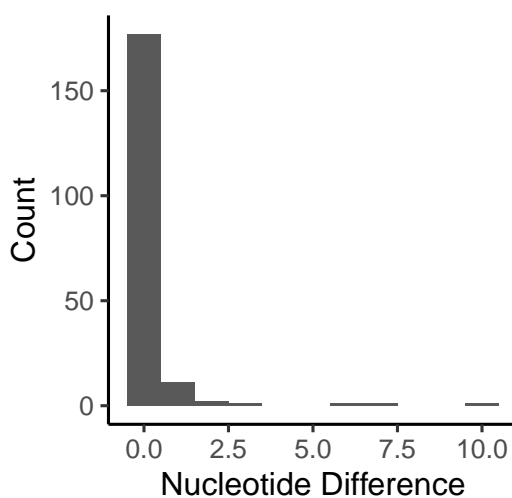
IGHV1-3*02

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



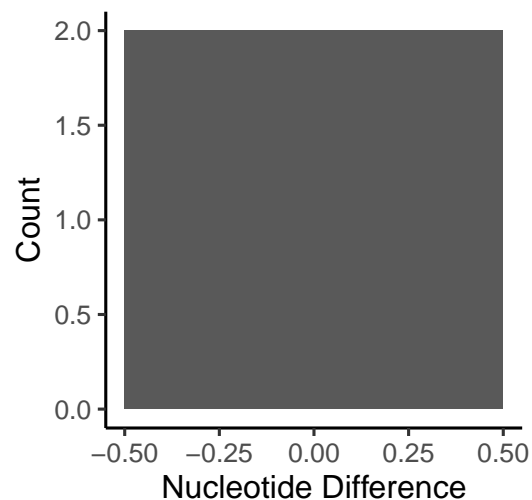
IGHV1-18*01

194 sequences assigned
177 (91.2%) exact matches, in which:
177 unique CDR3
7 unique J



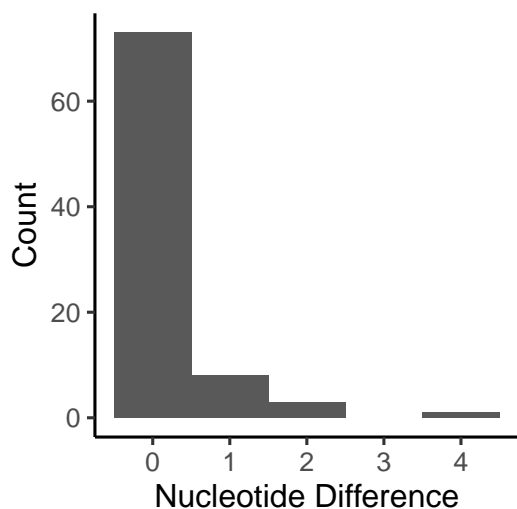
IGHV1-45*02

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



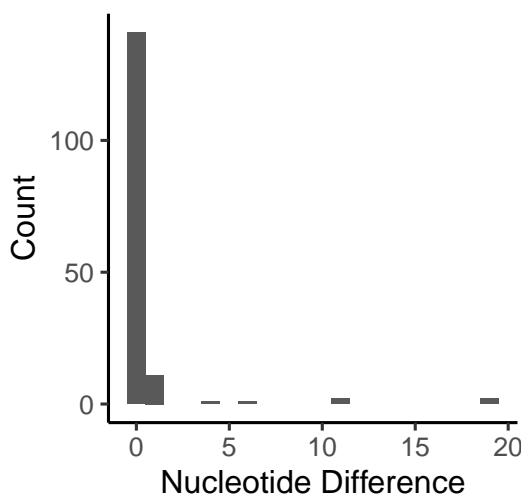
IGHV1-8*01

85 sequences assigned
73 (85.9%) exact matches, in which:
73 unique CDR3
5 unique J



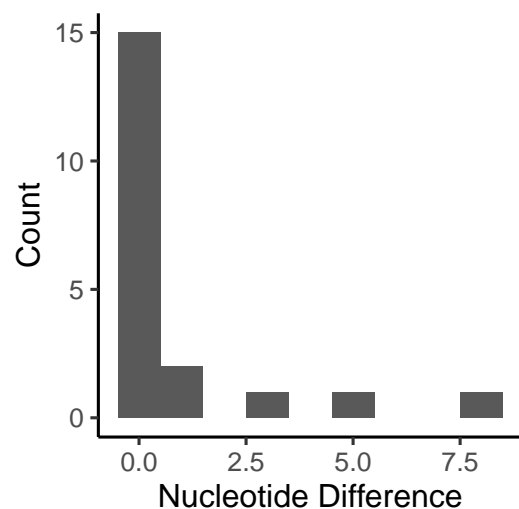
IGHV1-18*04

158 sequences assigned
141 (89.2%) exact matches, in which:
140 unique CDR3
6 unique J



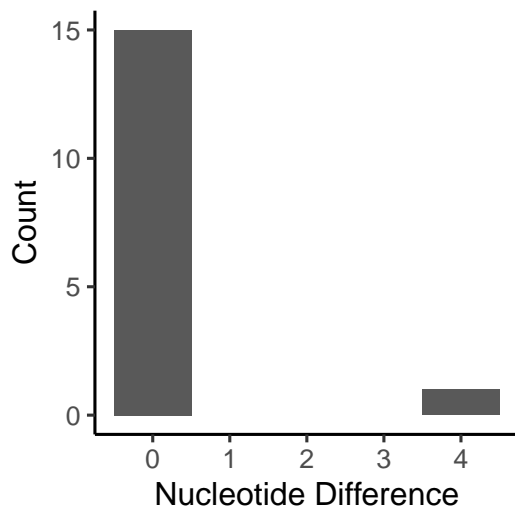
IGHV1-46*01

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



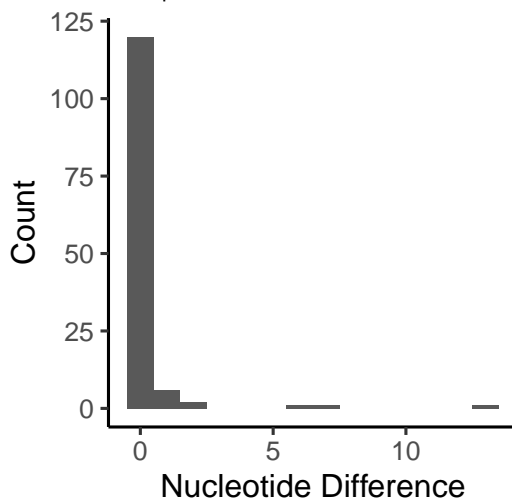
IGHV1-46*03

16 sequences assigned
15 (93.8%) exact matches, in which:
15 unique CDR3
6 unique J



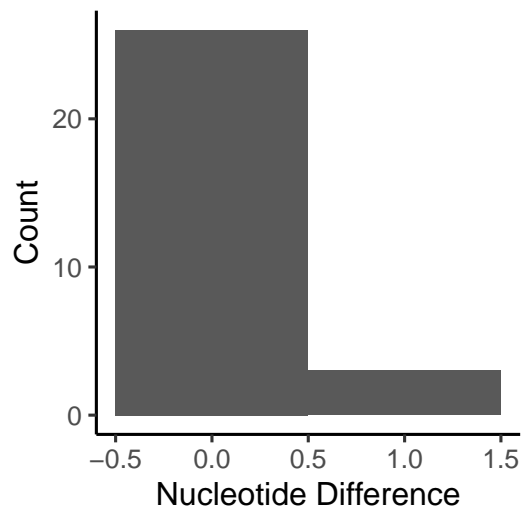
IGHV1-69*04_A163G

131 sequences assigned
120 (91.6%) exact matches, in which:
120 unique CDR3
7 unique J



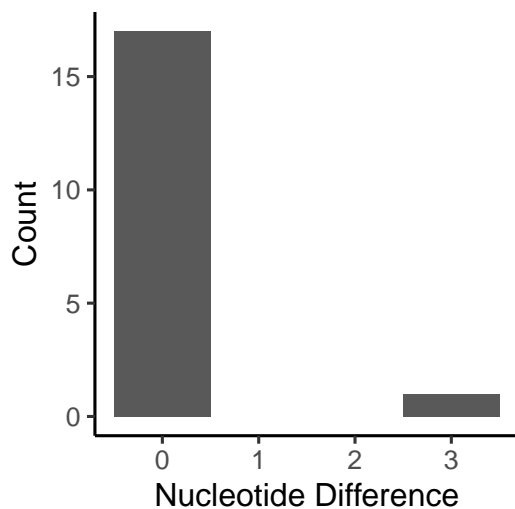
IGHV2-70*01

29 sequences assigned
26 (89.7%) exact matches, in which:
26 unique CDR3
4 unique J



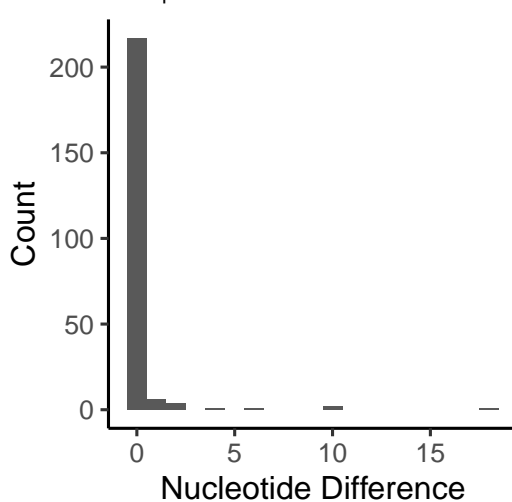
IGHV1-58*01

18 sequences assigned
17 (94.4%) exact matches, in which:
17 unique CDR3
4 unique J



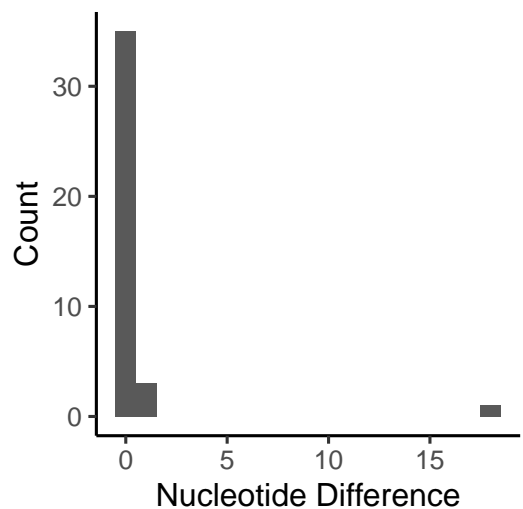
IGHV2-5*01

232 sequences assigned
217 (93.5%) exact matches, in which:
217 unique CDR3
7 unique J



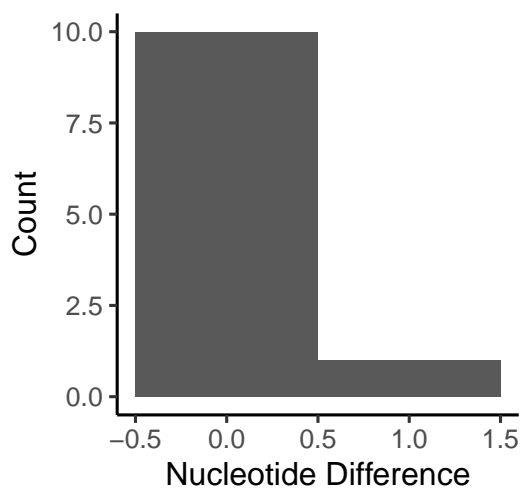
IGHV2-70*15

39 sequences assigned
35 (89.7%) exact matches, in which:
35 unique CDR3
3 unique J



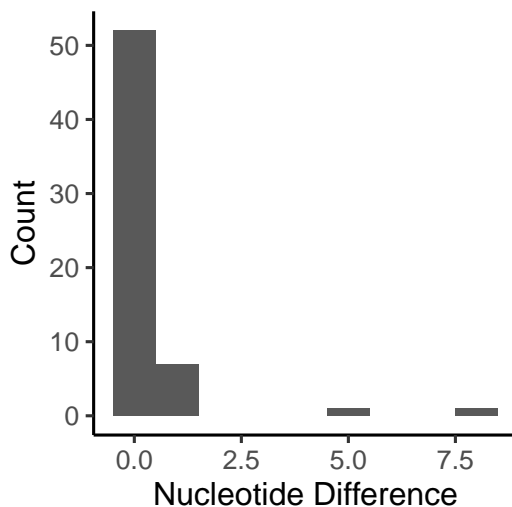
IGHV1-58*02

11 sequences assigned
10 (90.9%) exact matches, in which:
10 unique CDR3
4 unique J



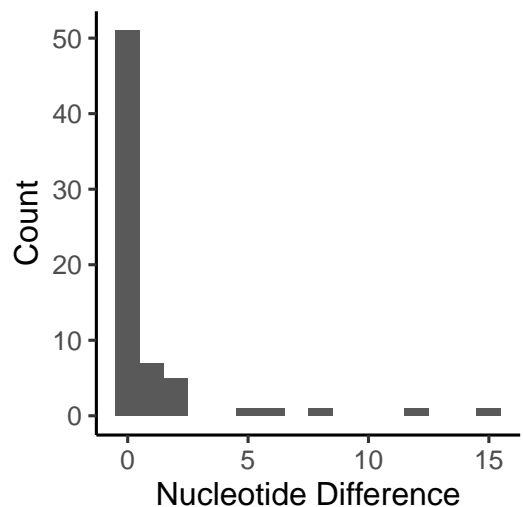
IGHV2-26*01

61 sequences assigned
52 (85.2%) exact matches, in which:
52 unique CDR3
6 unique J



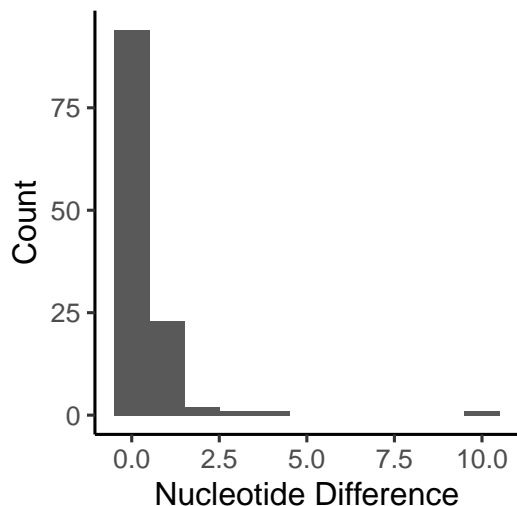
IGHV3-7*01

68 sequences assigned
51 (75%) exact matches, in which:
51 unique CDR3
6 unique J



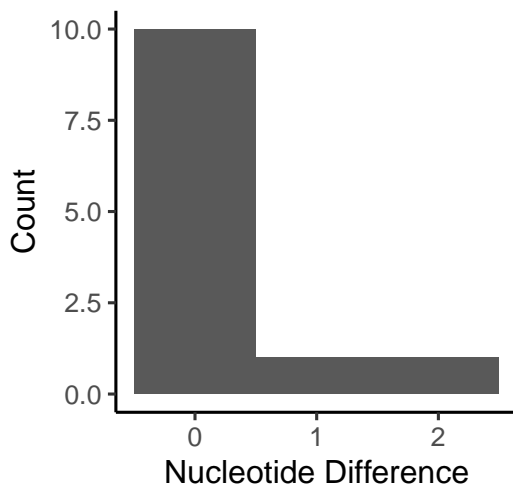
IGHV3-9*01

122 sequences assigned
94 (77%) exact matches, in which:
94 unique CDR3
6 unique J



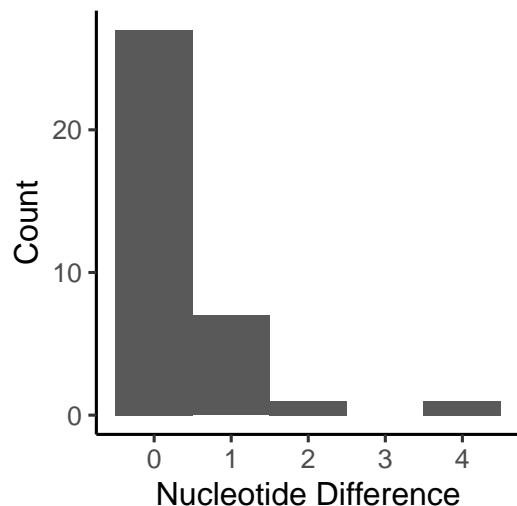
IGHV3-13*01

12 sequences assigned
10 (83.3%) exact matches, in which:
10 unique CDR3
3 unique J



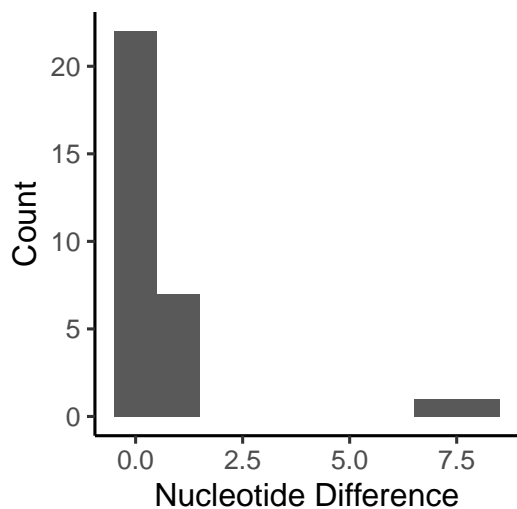
IGHV3-30*02_G49A

36 sequences assigned
27 (75%) exact matches, in which:
27 unique CDR3
4 unique J



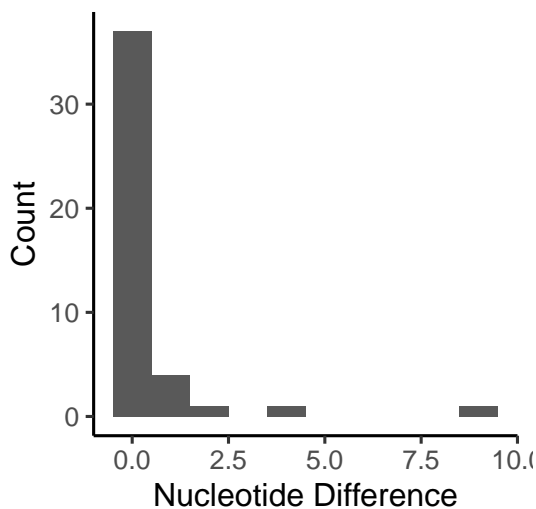
IGHV3-11*01

31 sequences assigned
22 (71%) exact matches, in which:
22 unique CDR3
6 unique J



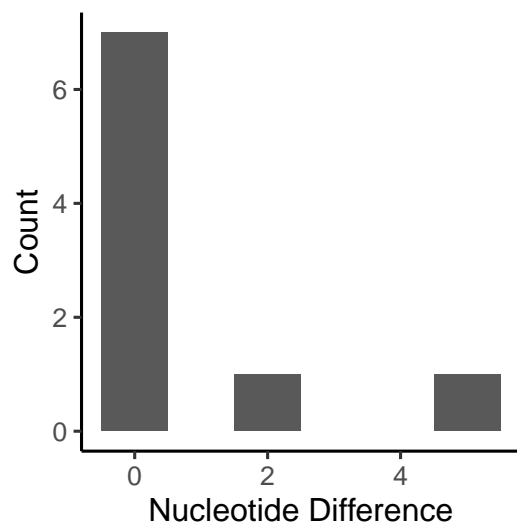
IGHV3-15*01

44 sequences assigned
37 (84.1%) exact matches, in which:
37 unique CDR3
5 unique J



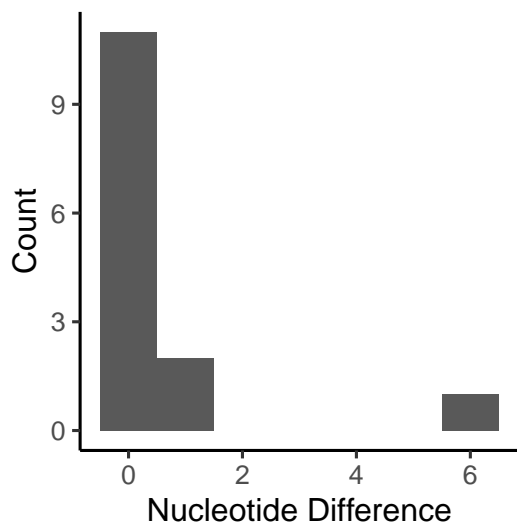
IGHV3-43*01

9 sequences assigned
7 (77.8%) exact matches, in which:
7 unique CDR3
3 unique J



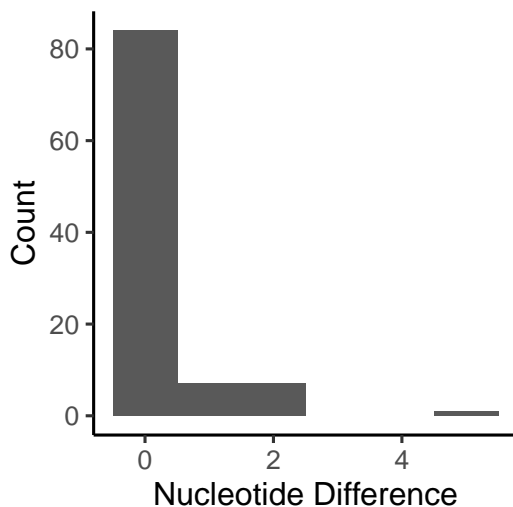
IGHV3-11*04

14 sequences assigned
11 (78.6%) exact matches, in which:
11 unique CDR3
3 unique J



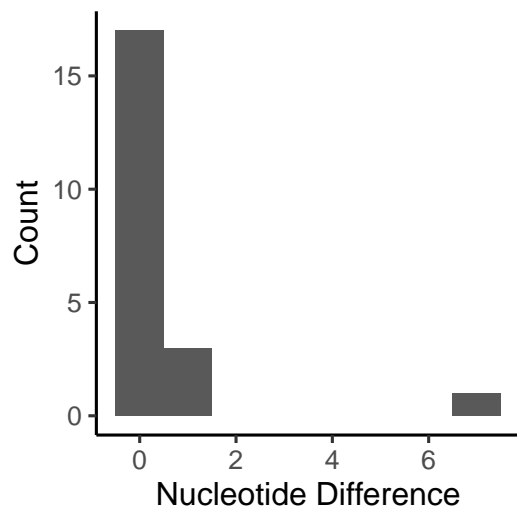
IGHV3-21*01

99 sequences assigned
84 (84.8%) exact matches, in which:
84 unique CDR3
7 unique J



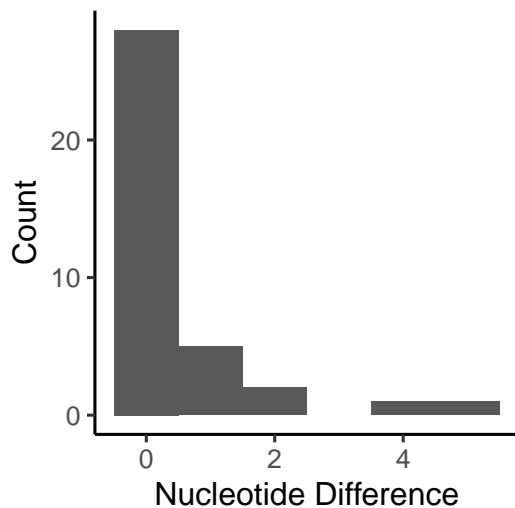
IGHV3-48*01

21 sequences assigned
17 (81%) exact matches, in which:
17 unique CDR3
4 unique J



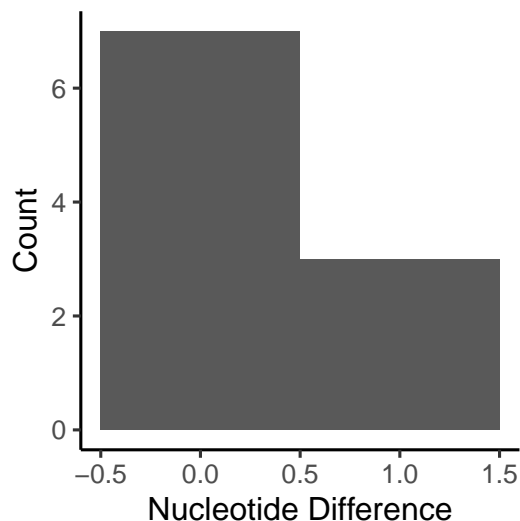
IGHV3-48*04

37 sequences assigned
28 (75.7%) exact matches, in which:
28 unique CDR3
5 unique J



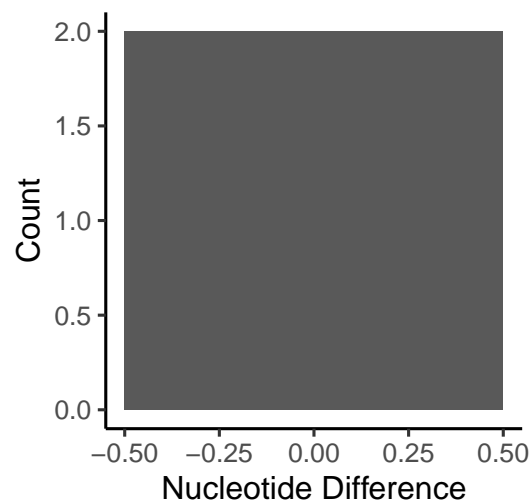
IGHV3-53*04

10 sequences assigned
7 (70%) exact matches, in which:
7 unique CDR3
3 unique J



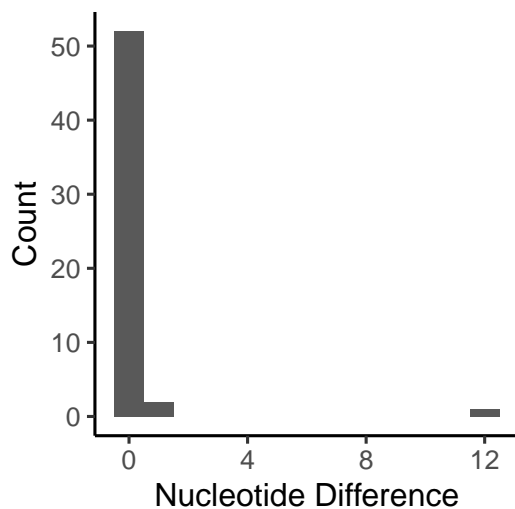
IGHV3-72*01

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



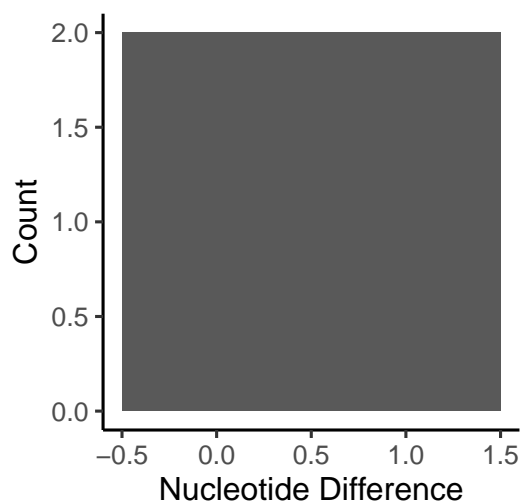
IGHV3-49*03

56 sequences assigned
52 (92.9%) exact matches, in which:
52 unique CDR3
6 unique J



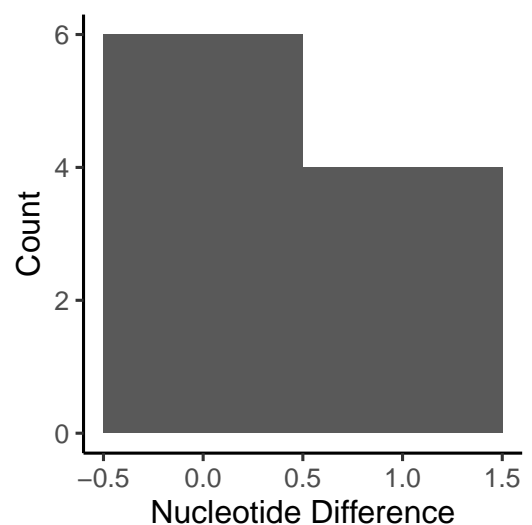
IGHV3-64*01

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



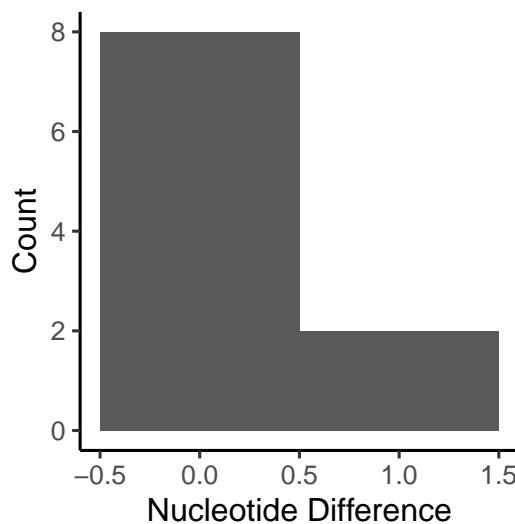
IGHV3-73*01

10 sequences assigned
6 (60%) exact matches, in which:
6 unique CDR3
3 unique J



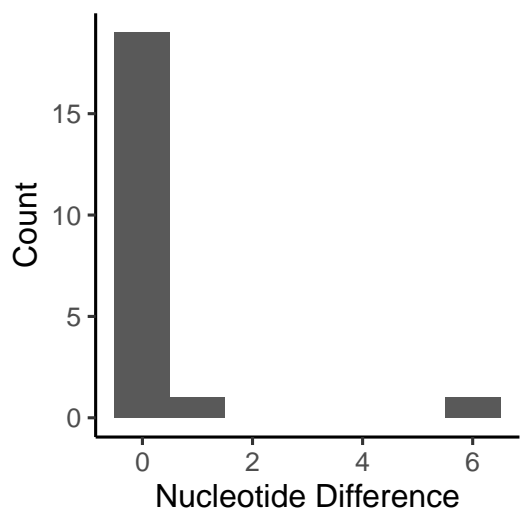
IGHV3-53*02

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



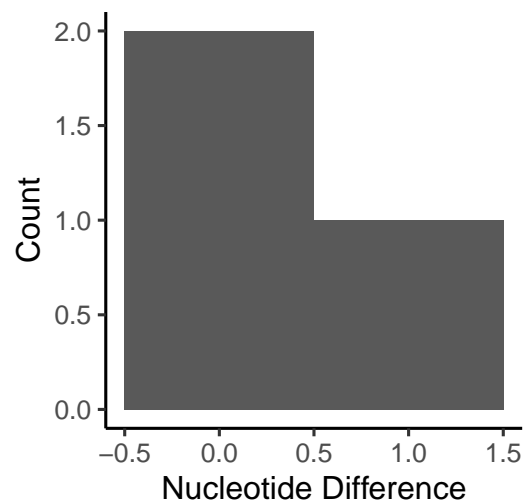
IGHV3-66*01

21 sequences assigned
19 (90.5%) exact matches, in which:
19 unique CDR3
4 unique J



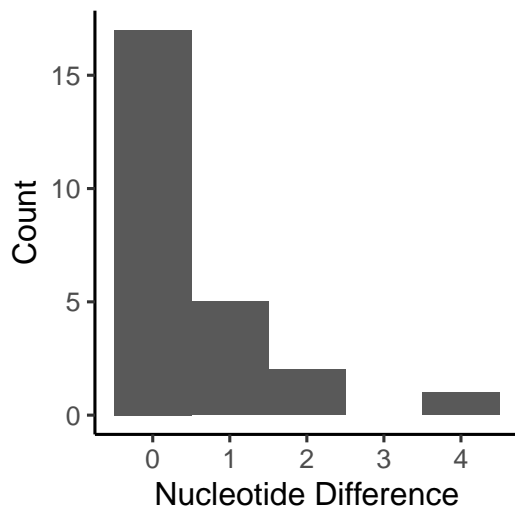
IGHV3-73*02

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



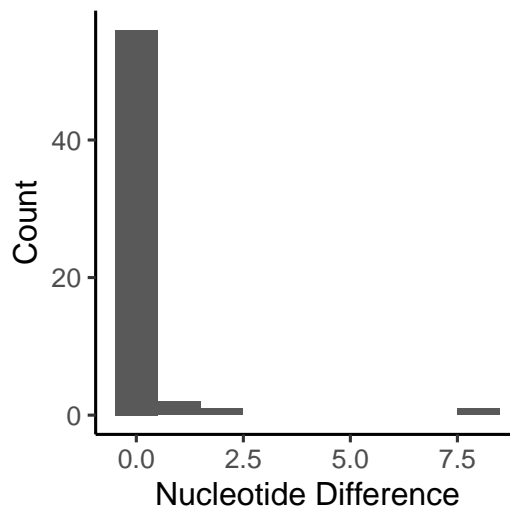
IGHV3-74*01

25 sequences assigned
17 (68%) exact matches, in which:
17 unique CDR3
6 unique J



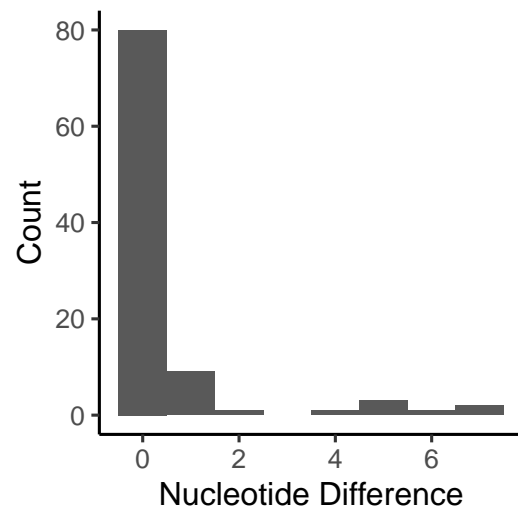
IGHV4-30-2*01

60 sequences assigned
56 (93.3%) exact matches, in which:
56 unique CDR3
7 unique J



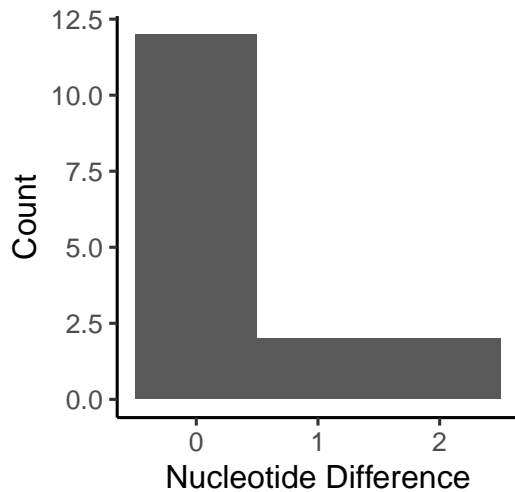
IGHV4-38-2*02

97 sequences assigned
80 (82.5%) exact matches, in which:
80 unique CDR3
6 unique J



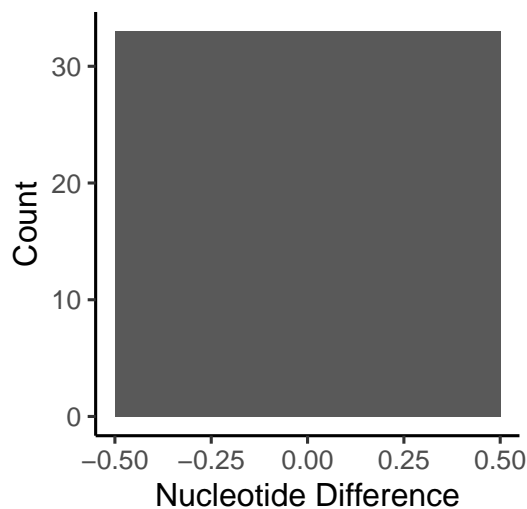
IGHV3-43D*03

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



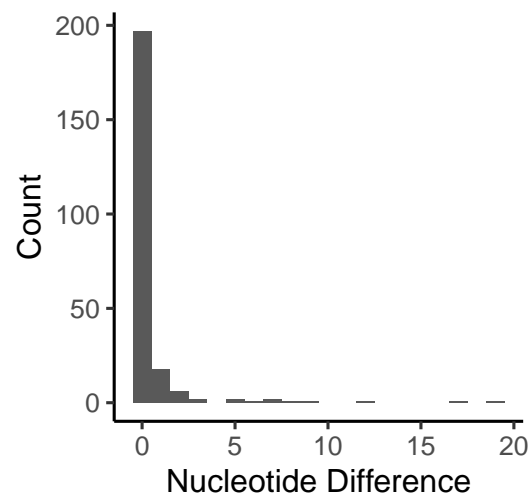
IGHV4-30-4*07

33 sequences assigned
33 (100%) exact matches, in which:
33 unique CDR3
6 unique J



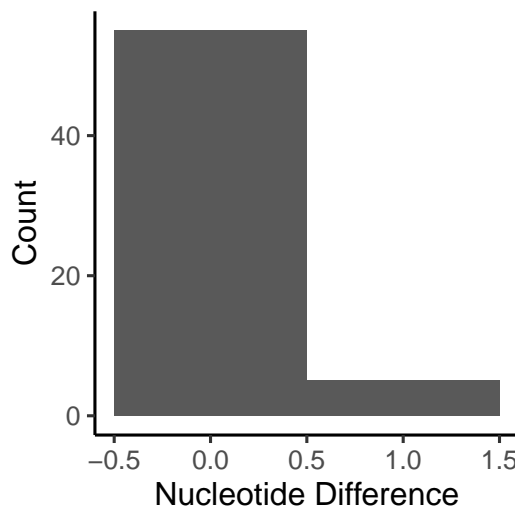
IGHV4-39*01

233 sequences assigned
197 (84.5%) exact matches, in which:
197 unique CDR3
7 unique J



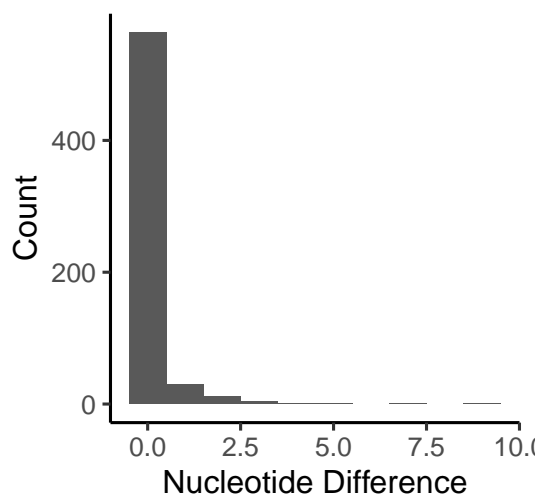
IGHV4-4*07

60 sequences assigned
55 (91.7%) exact matches, in which:
55 unique CDR3
6 unique J



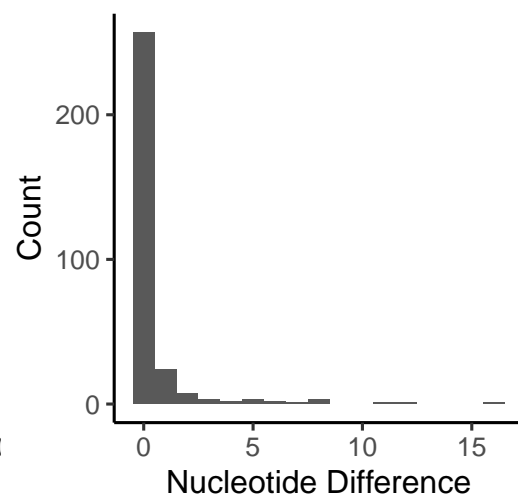
IGHV4-34*01

614 sequences assigned
564 (91.9%) exact matches, in which:
564 unique CDR3
7 unique J



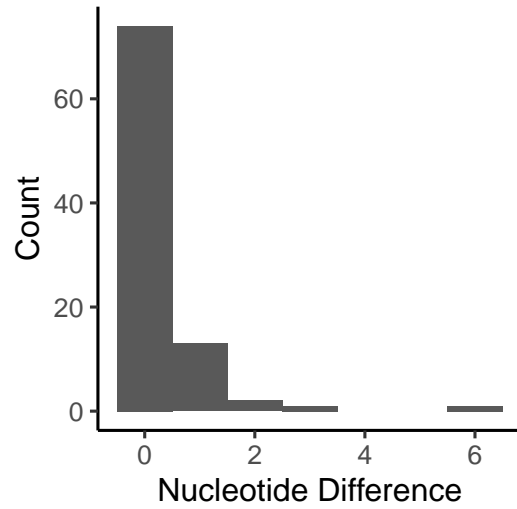
IGHV4-39*07

305 sequences assigned
257 (84.3%) exact matches, in which:
256 unique CDR3
6 unique J



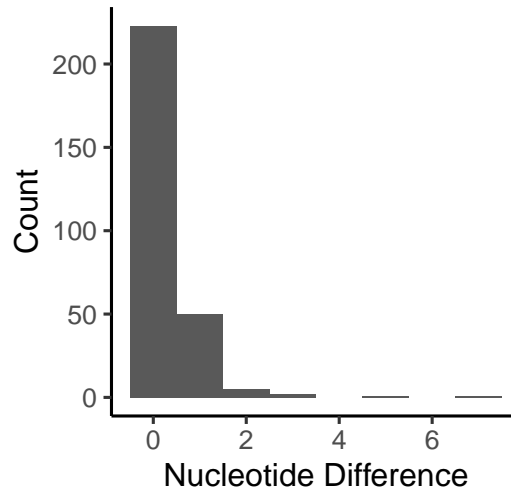
IGHV4-59*01

91 sequences assigned
74 (81.3%) exact matches, in which:
74 unique CDR3
6 unique J



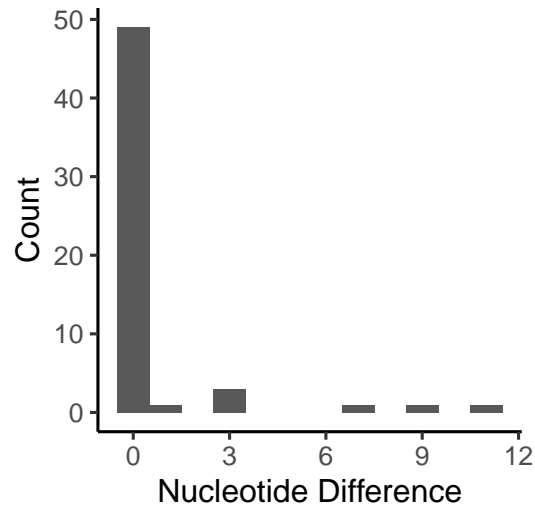
IGHV5-51*01

282 sequences assigned
223 (79.1%) exact matches, in which:
223 unique CDR3
7 unique J



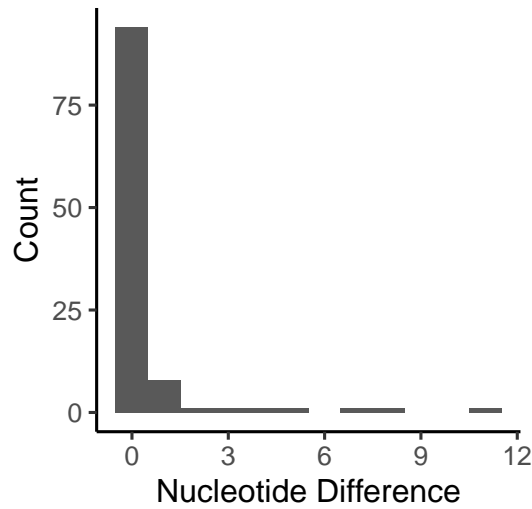
IGHV4-59*08

56 sequences assigned
49 (87.5%) exact matches, in which:
49 unique CDR3
5 unique J



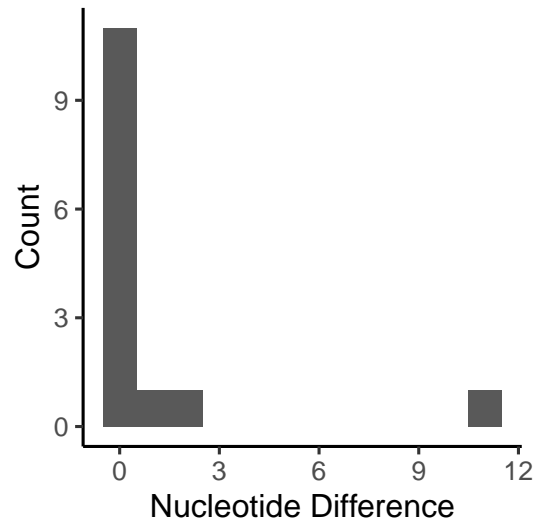
IGHV5-51*03

110 sequences assigned
94 (85.5%) exact matches, in which:
94 unique CDR3
6 unique J



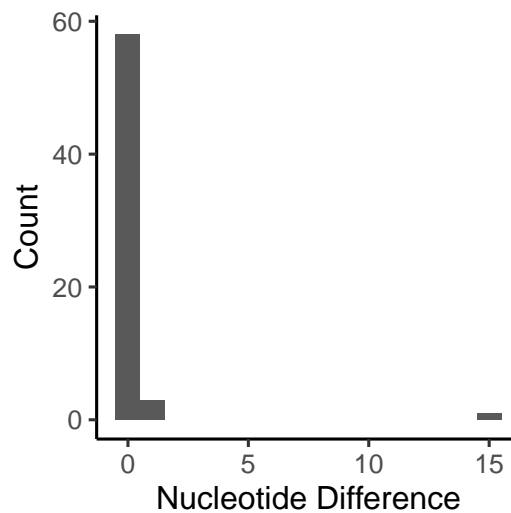
IGHV4-61*01

14 sequences assigned
11 (78.6%) exact matches, in which:
11 unique CDR3
5 unique J

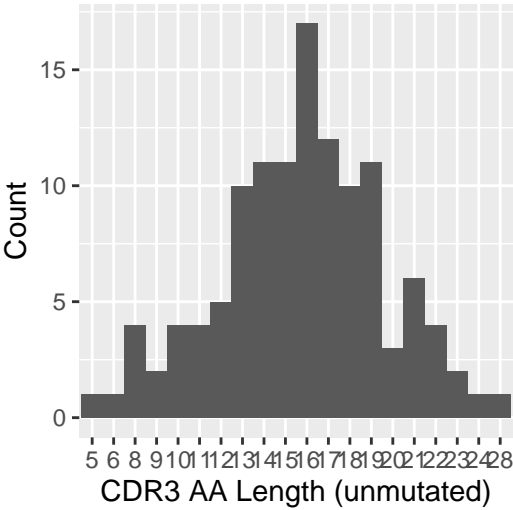


IGHV6-1*01

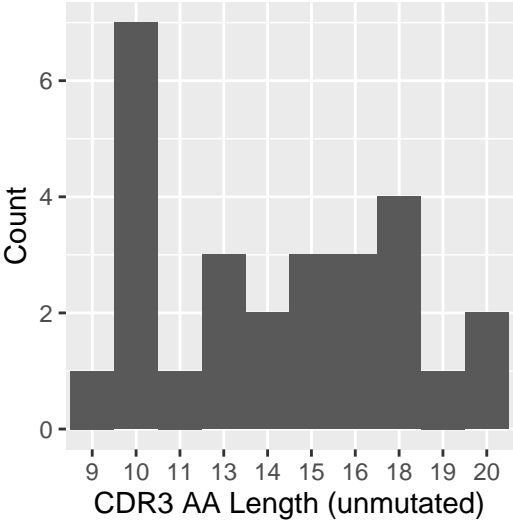
62 sequences assigned
58 (93.5%) exact matches, in which:
58 unique CDR3
6 unique J



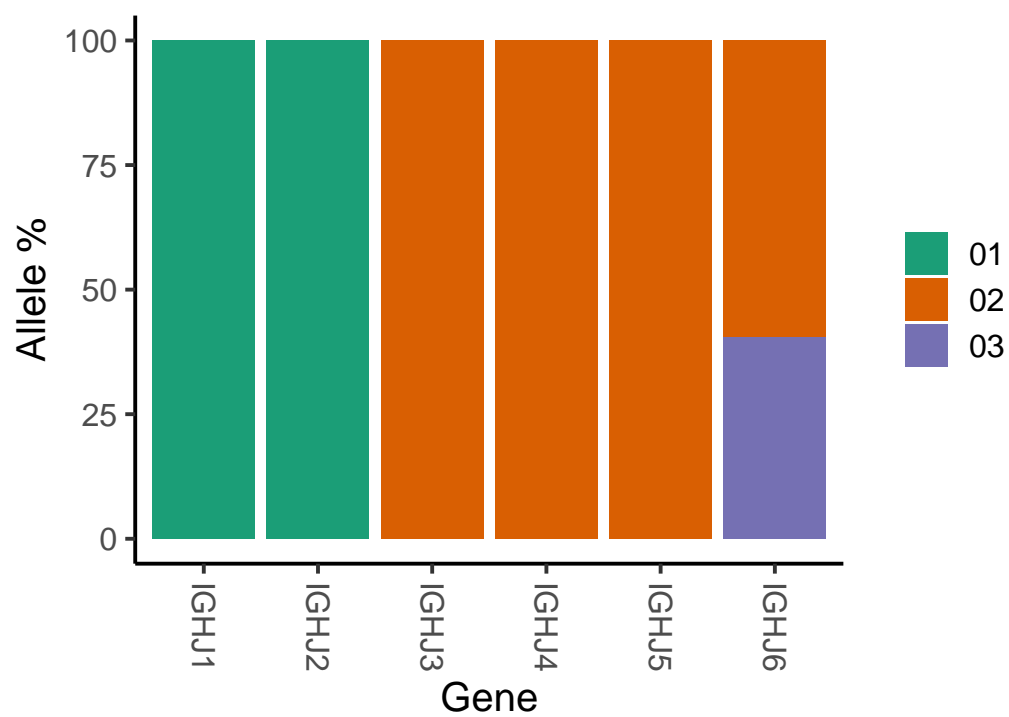
IGHV1-69*04_A163G



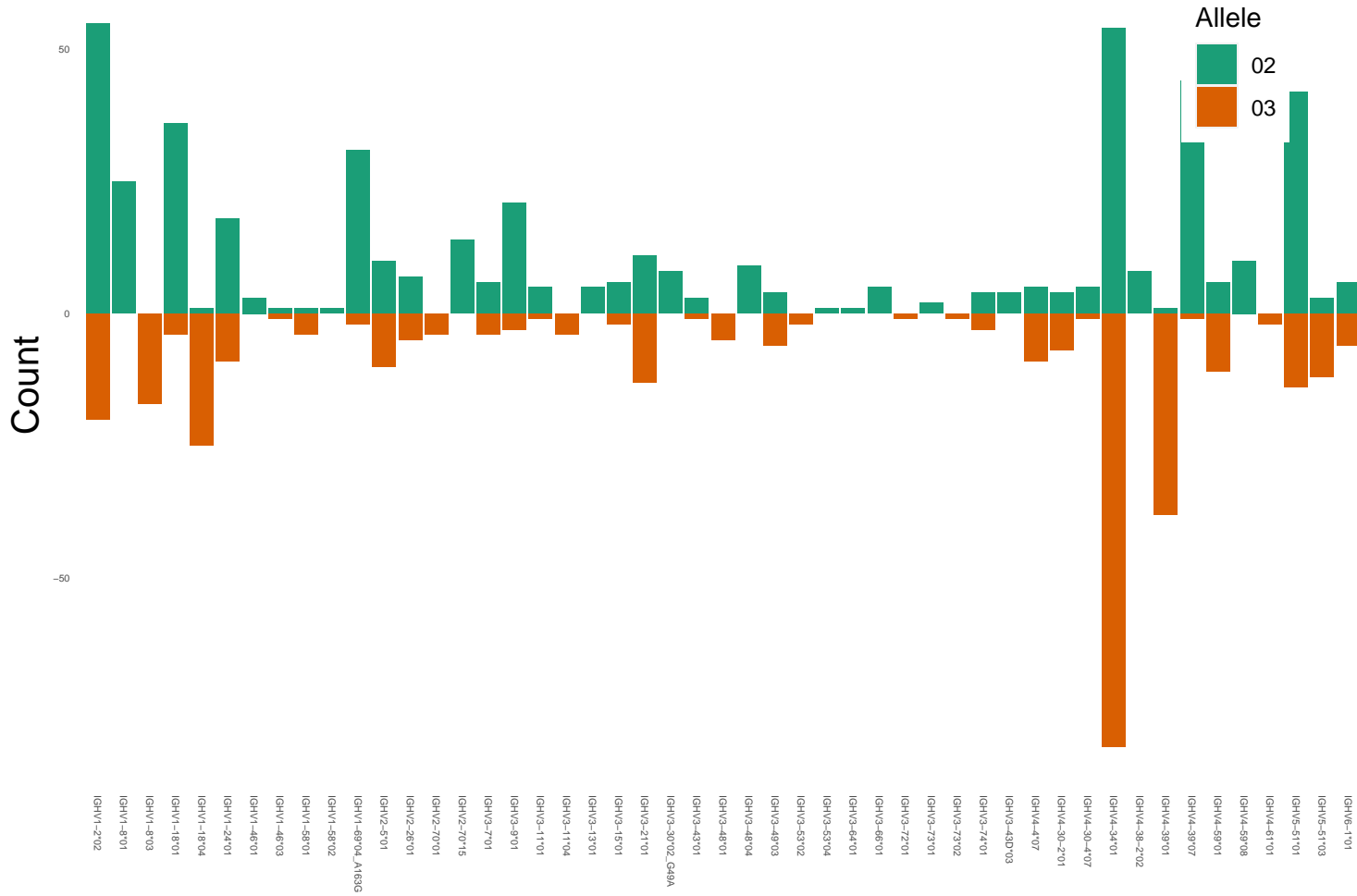
IGHV3-30*02_G49A



Allele Usage



Sequence Count by IGHJ6 allele usage



[illegible]