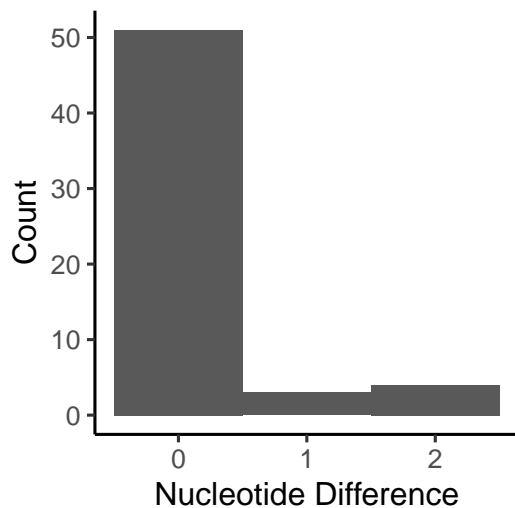


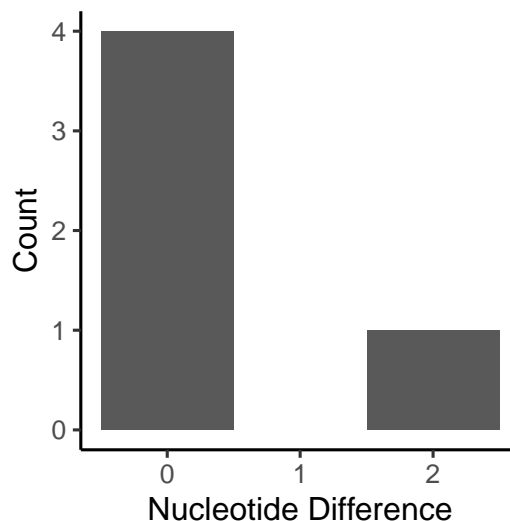
IGHV1-2*02

58 sequences assigned
51 (87.9%) exact matches, in which:
49 unique CDR3
6 unique J



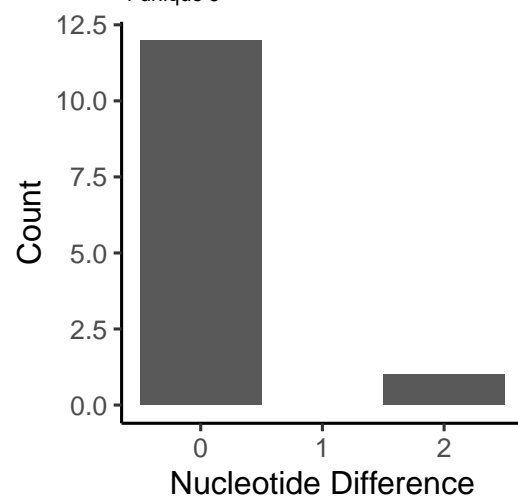
IGHV1-3*01_05

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



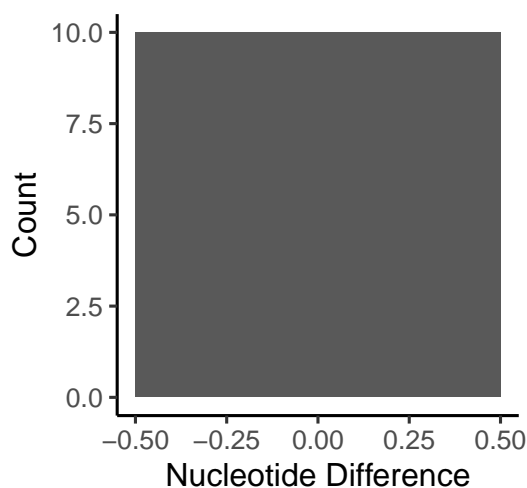
IGHV1-24*01

13 sequences assigned
12 (92.3%) exact matches, in which:
12 unique CDR3
4 unique J



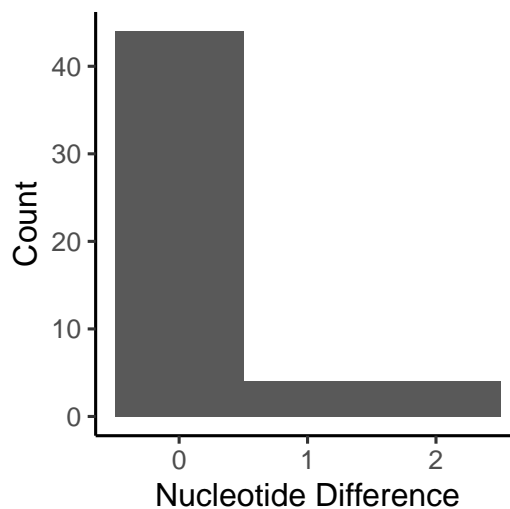
IGHV1-2*04

10 sequences assigned
10 (100%) exact matches, in which:
10 unique CDR3
4 unique J



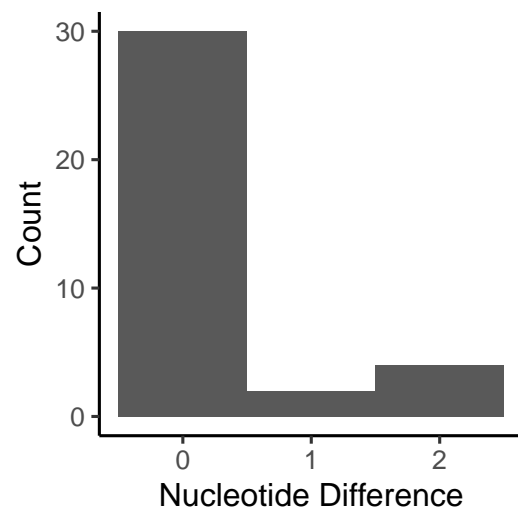
IGHV1-8*01

52 sequences assigned
44 (84.6%) exact matches, in which:
44 unique CDR3
6 unique J



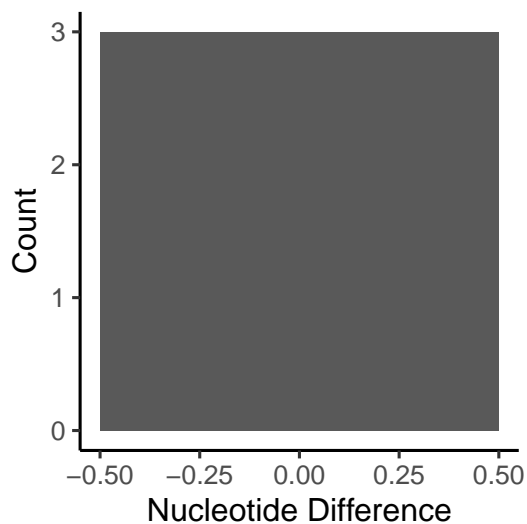
IGHV1-46*01

36 sequences assigned
30 (83.3%) exact matches, in which:
30 unique CDR3
6 unique J



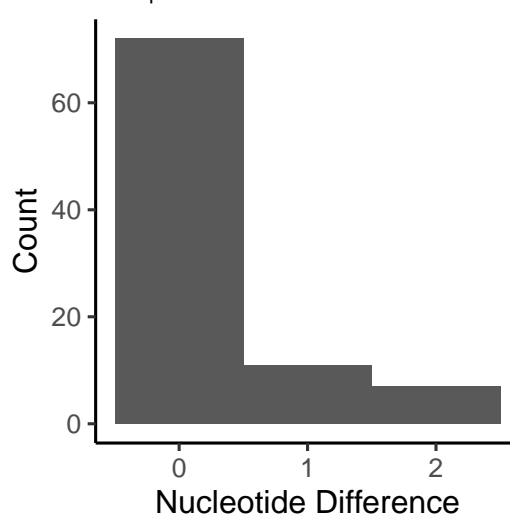
IGHV1-3*03

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



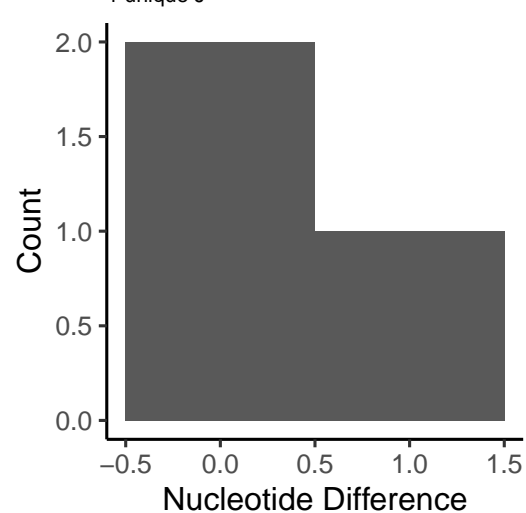
IGHV1-18*01

90 sequences assigned
72 (80%) exact matches, in which:
72 unique CDR3
7 unique J



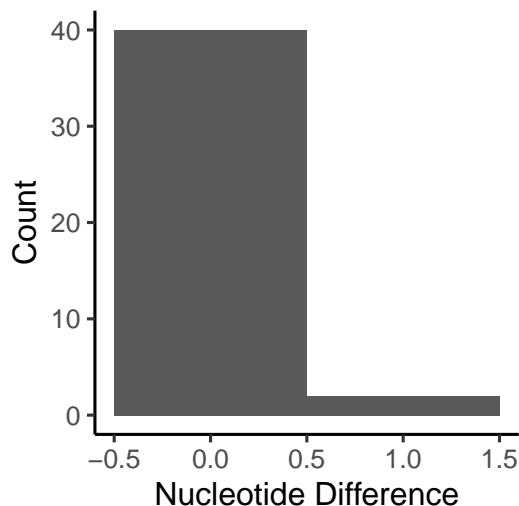
IGHV1-69-2*01

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



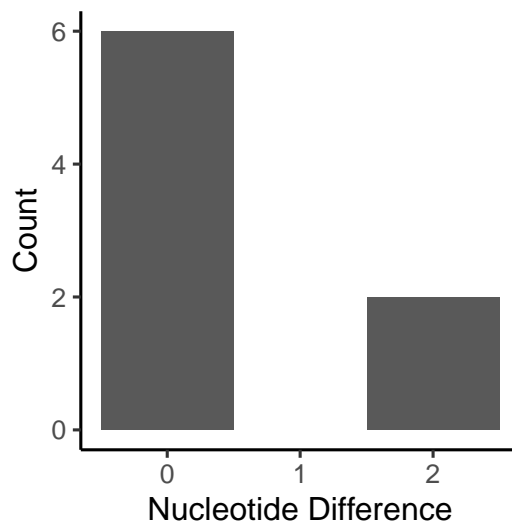
IGHV1-69*02

42 sequences assigned
40 (95.2%) exact matches, in which:
40 unique CDR3
6 unique J



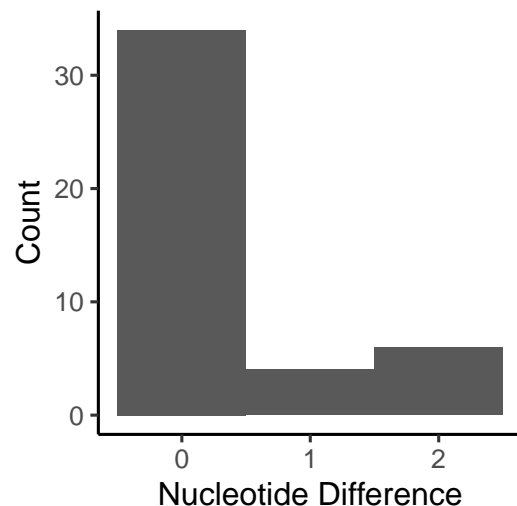
IGHV2-5*01

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



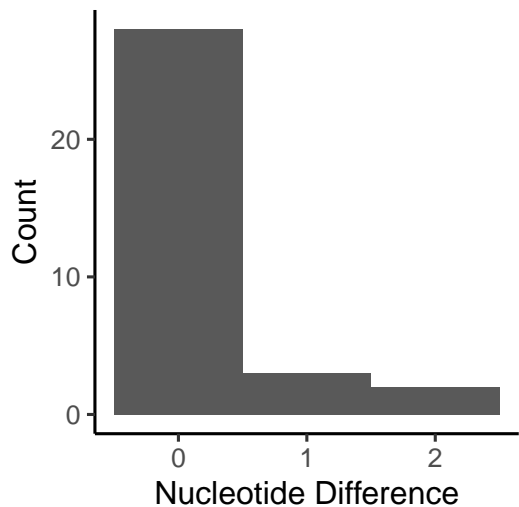
IGHV3-7*01

44 sequences assigned
34 (77.3%) exact matches, in which:
32 unique CDR3
4 unique J



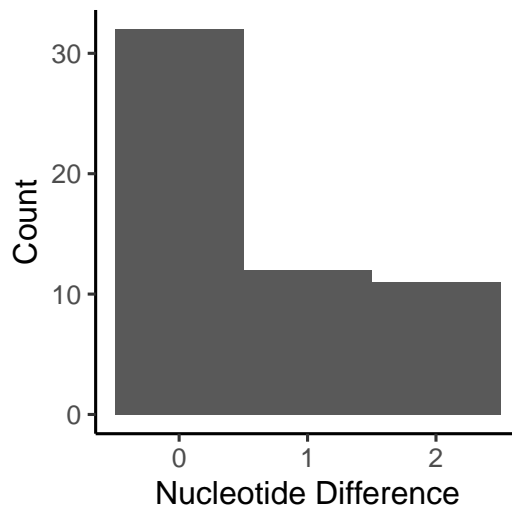
IGHV1-69*05

33 sequences assigned
28 (84.8%) exact matches, in which:
28 unique CDR3
4 unique J



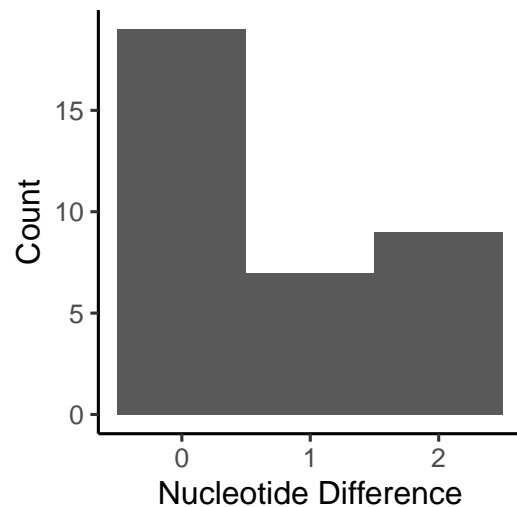
IGHV2-5*02

55 sequences assigned
32 (58.2%) exact matches, in which:
31 unique CDR3
4 unique J



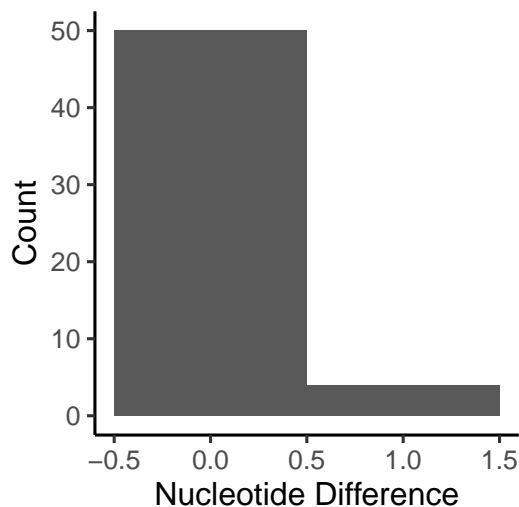
IGHV3-7*03

35 sequences assigned
19 (54.3%) exact matches, in which:
15 unique CDR3
3 unique J



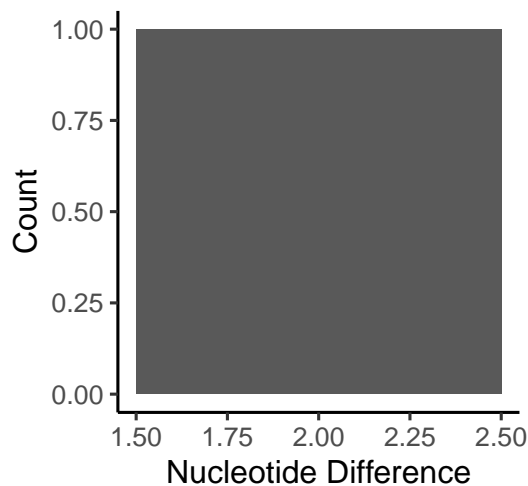
IGHV1-69*07_15_18

54 sequences assigned
50 (92.6%) exact matches, in which:
50 unique CDR3
6 unique J



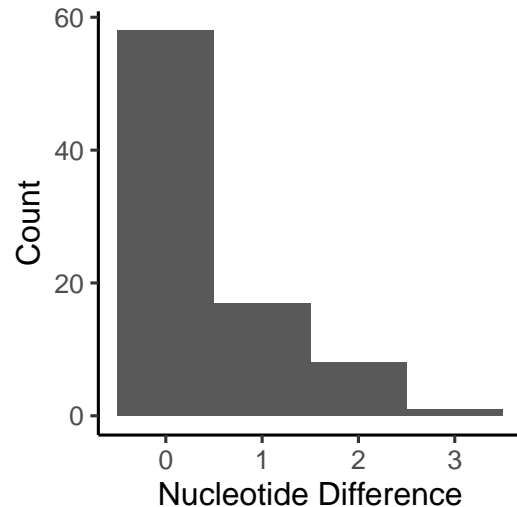
IGHV2-26*01

1 sequences assigned
No exact matches.



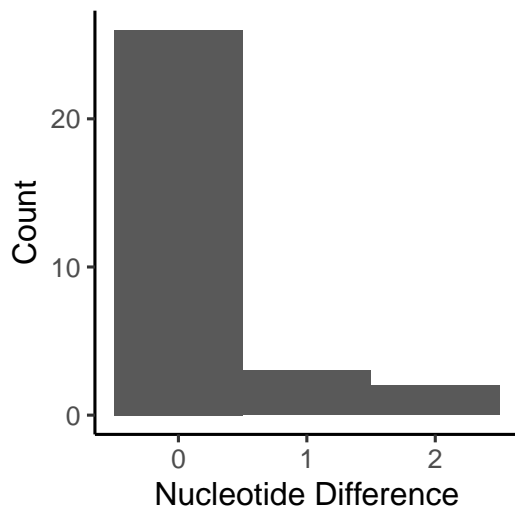
IGHV3-9*01

84 sequences assigned
58 (69%) exact matches, in which:
52 unique CDR3
6 unique J



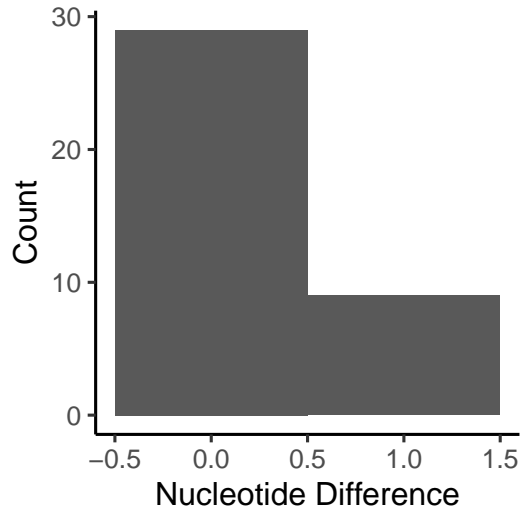
IGHV3-11*01

31 sequences assigned
26 (83.9%) exact matches, in which:
25 unique CDR3
5 unique J



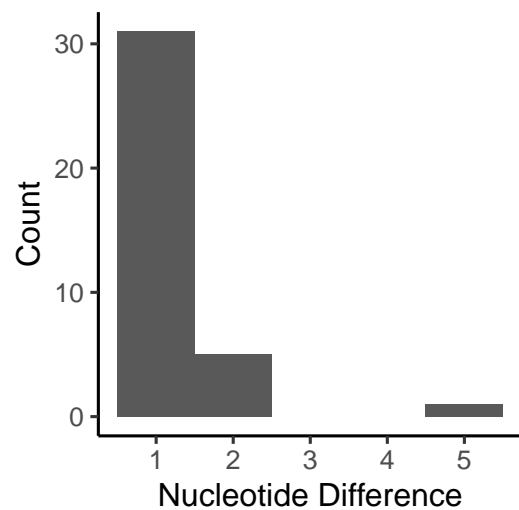
IGHV3-20*03_04

38 sequences assigned
29 (76.3%) exact matches, in which:
28 unique CDR3
6 unique J



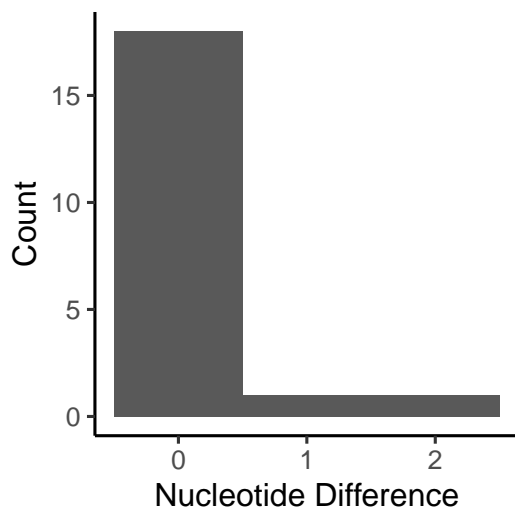
IGHV3-33*06

37 sequences assigned
No exact matches.



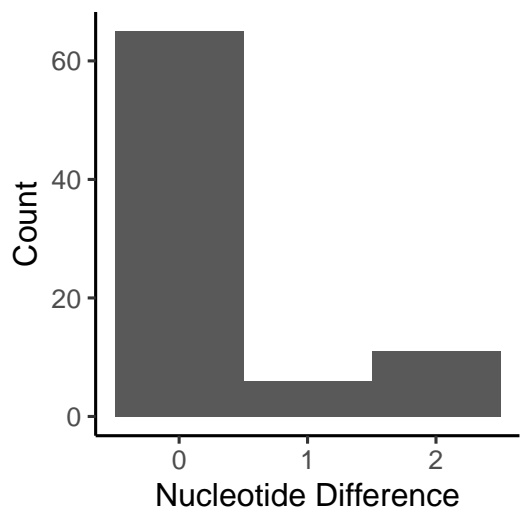
IGHV3-11*04

20 sequences assigned
18 (90%) exact matches, in which:
18 unique CDR3
4 unique J



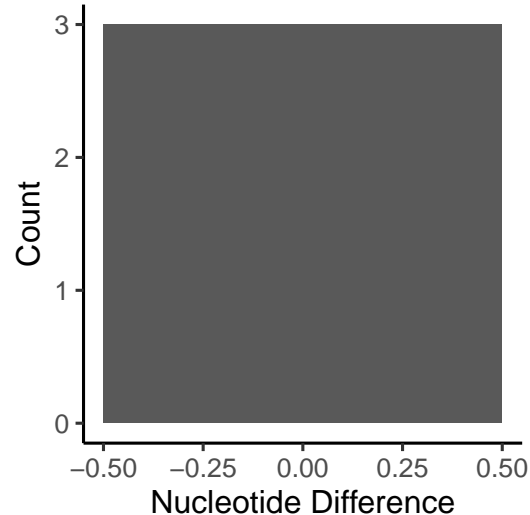
IGHV3-21*03

82 sequences assigned
65 (79.3%) exact matches, in which:
61 unique CDR3
6 unique J



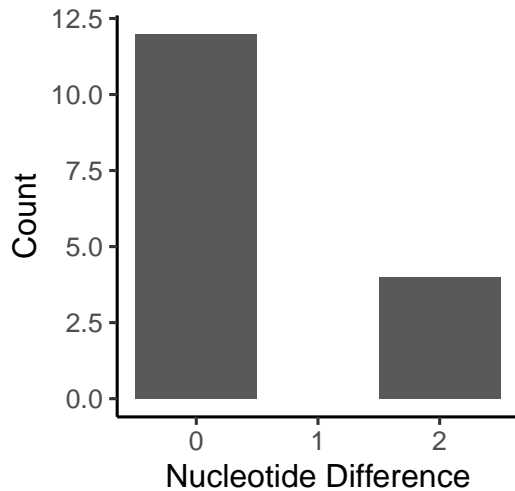
IGHV3-43*01

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



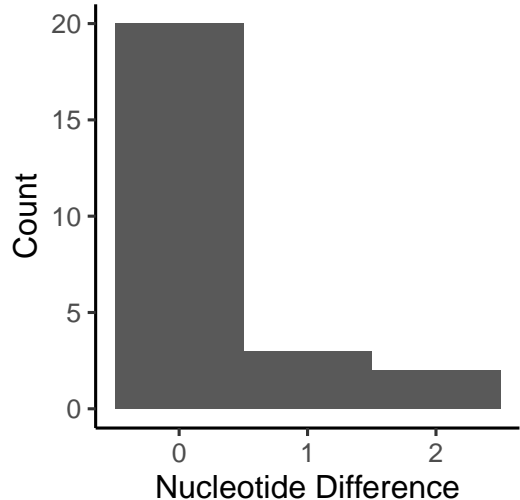
IGHV3-15*01_02

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



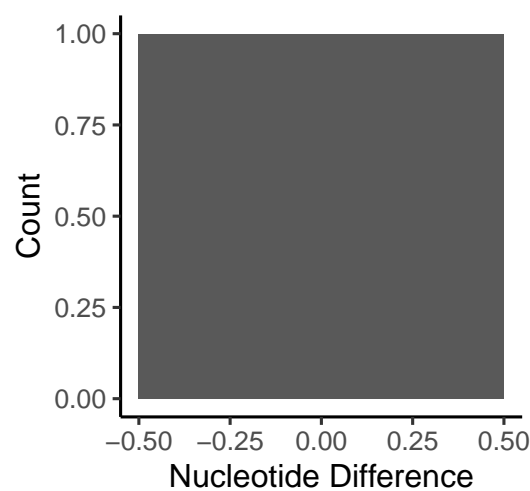
IGHV3-33*01

25 sequences assigned
20 (80%) exact matches, in which:
19 unique CDR3
3 unique J



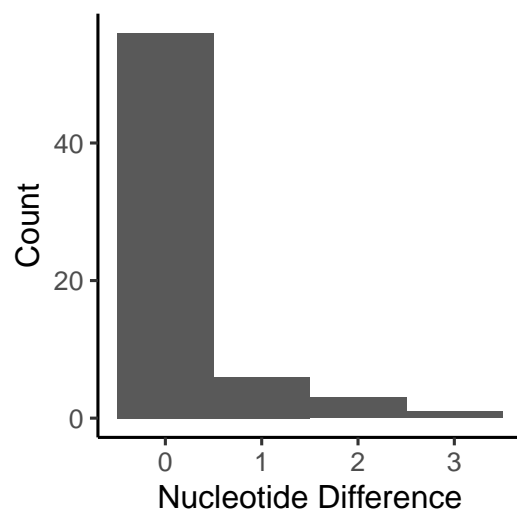
IGHV3-47*02

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



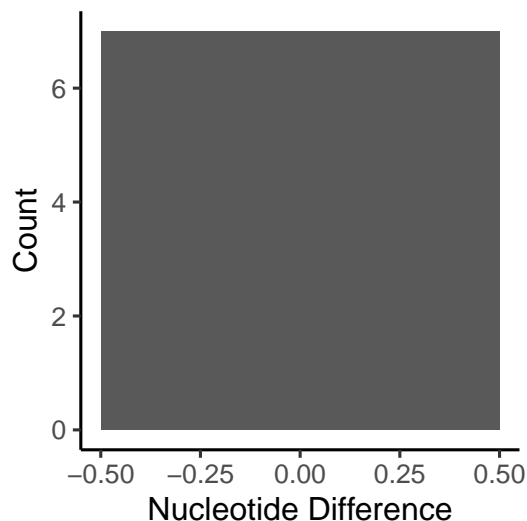
IGHV3-48*04

66 sequences assigned
56 (84.8%) exact matches, in which:
48 unique CDR3
5 unique J



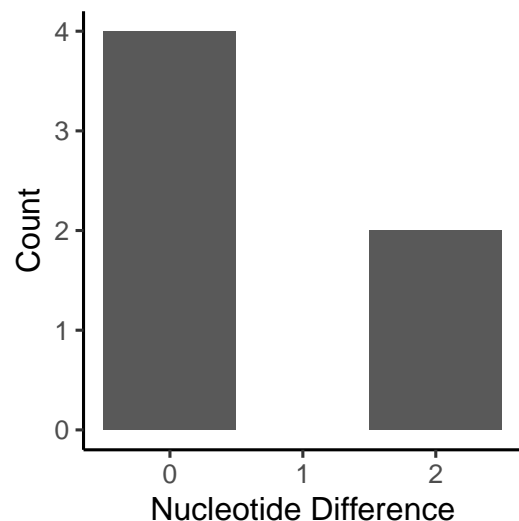
IGHV3-53*04

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



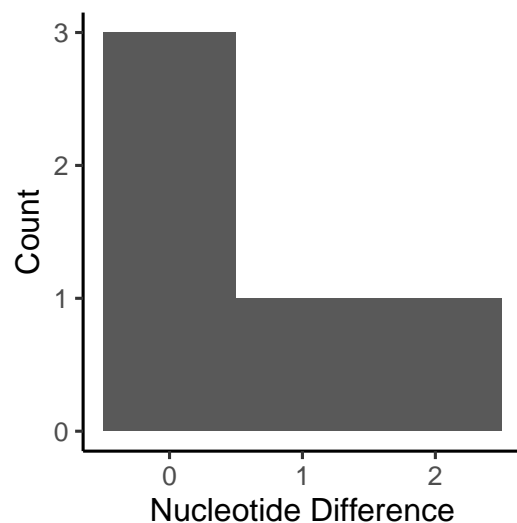
IGHV3-64*02_07

6 sequences assigned
4 (66.7%) exact matches, in which:
4 unique CDR3
3 unique J



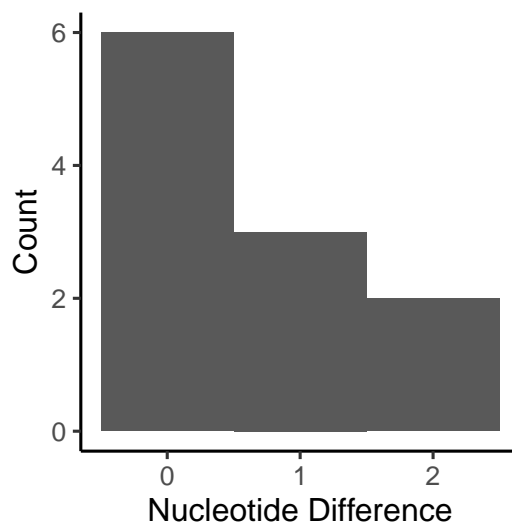
IGHV3-49*04

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



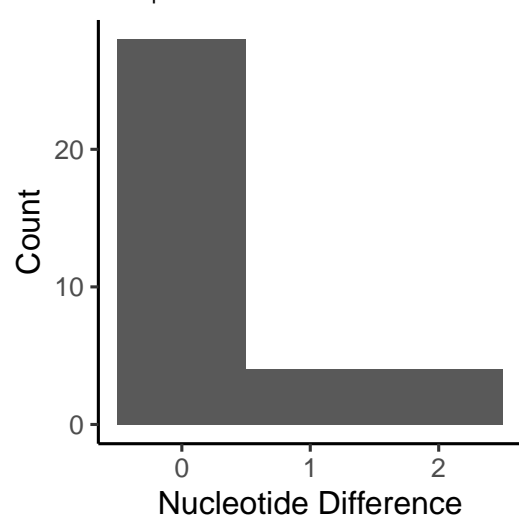
IGHV3-53*01_02

11 sequences assigned
6 (54.5%) exact matches, in which:
6 unique CDR3
3 unique J



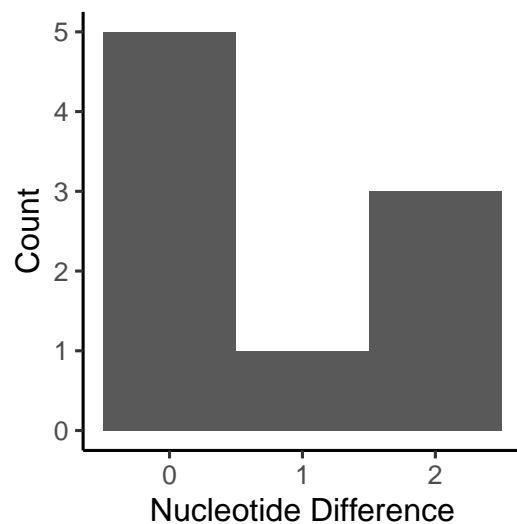
IGHV3-66*02

36 sequences assigned
28 (77.8%) exact matches, in which:
27 unique CDR3
6 unique J



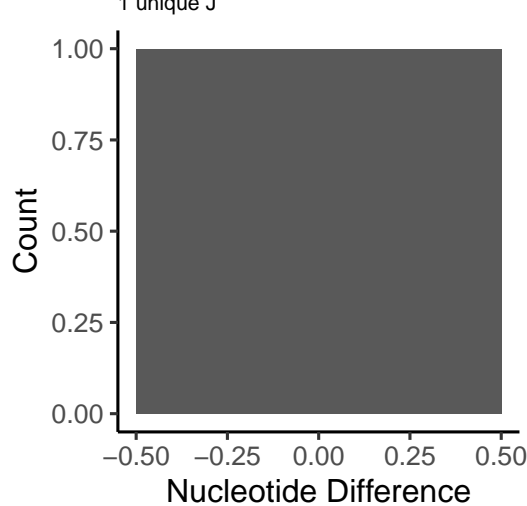
IGHV3-49*03_05

9 sequences assigned
5 (55.6%) exact matches, in which:
4 unique CDR3
3 unique J



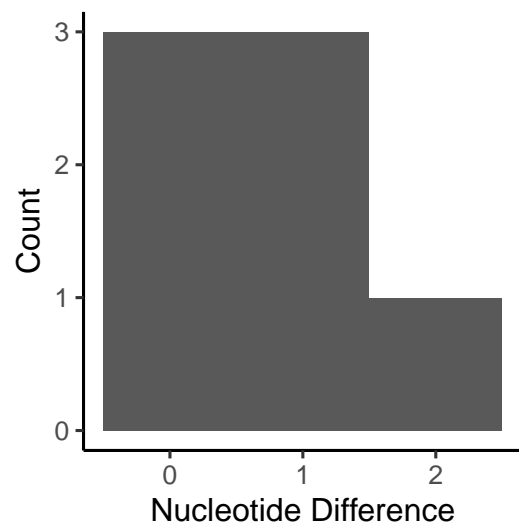
IGHV3-64*01

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



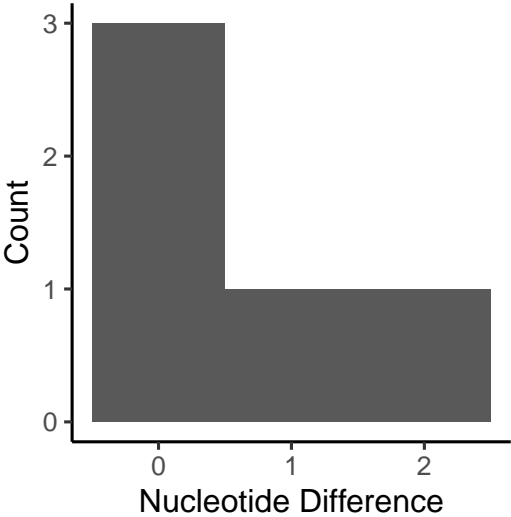
IGHV3-72*01

7 sequences assigned
3 (42.9%) exact matches, in which:
3 unique CDR3
2 unique J



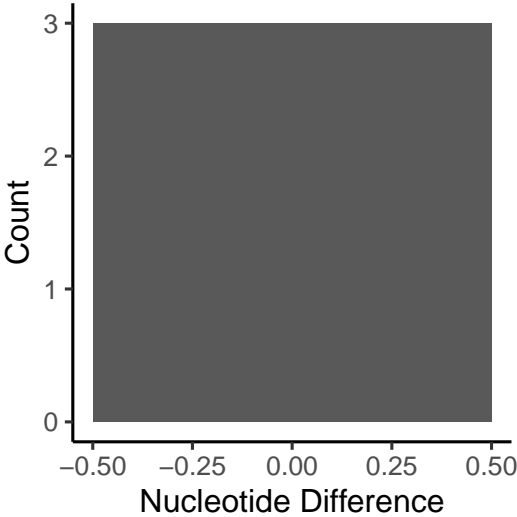
IGHV3-73*01_02

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



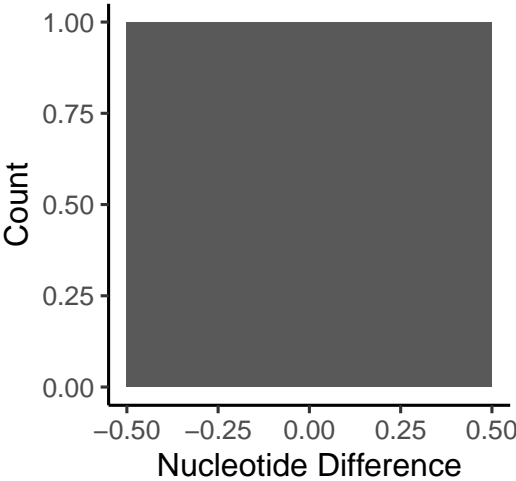
IGHV3-43D*04

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



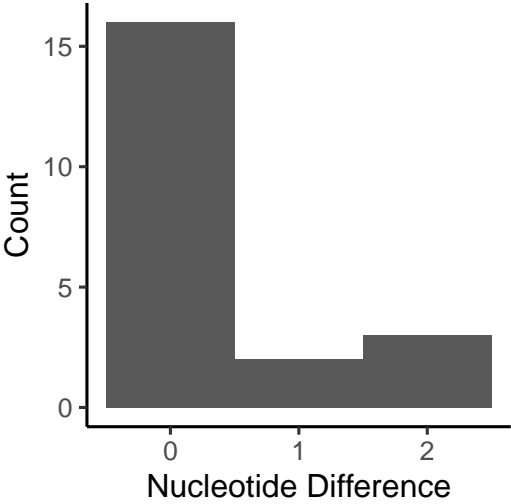
IGHV4-30-2*01

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



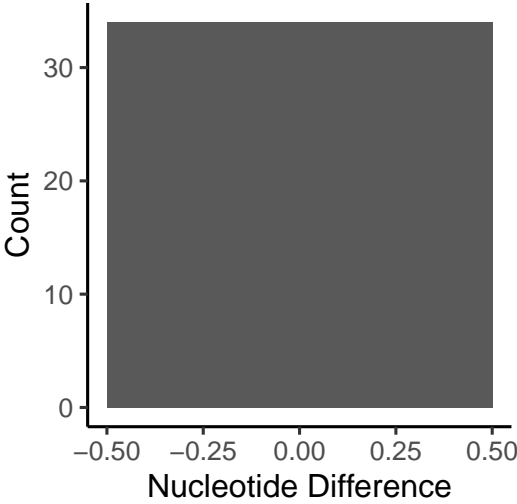
IGHV3-74*01_02

21 sequences assigned
16 (76.2%) exact matches, in which:
14 unique CDR3
5 unique J



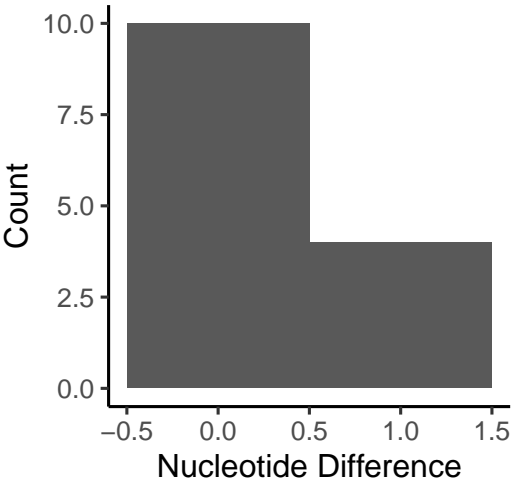
IGHV4-4*09

34 sequences assigned
34 (100%) exact matches, in which:
29 unique CDR3
6 unique J



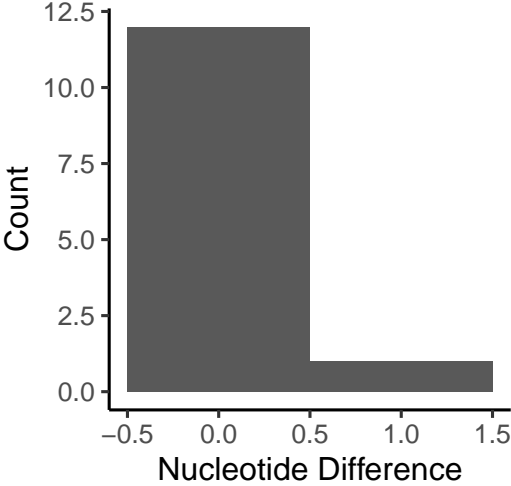
IGHV4-30-4*08

14 sequences assigned
10 (71.4%) exact matches, in which:
9 unique CDR3
4 unique J



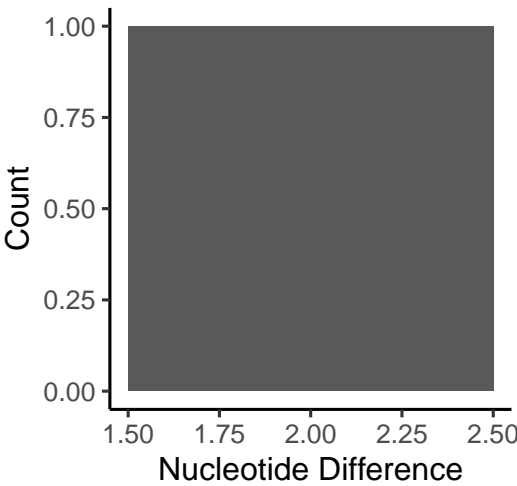
IGHV3-43D*03

13 sequences assigned
12 (92.3%) exact matches, in which:
8 unique CDR3
4 unique J



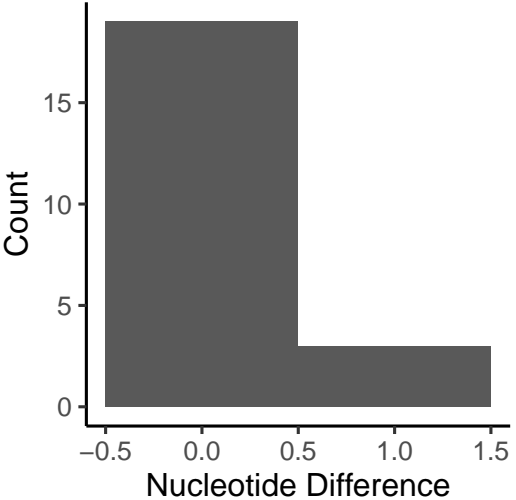
IGHV4-28*01_07

1 sequences assigned
No exact matches.



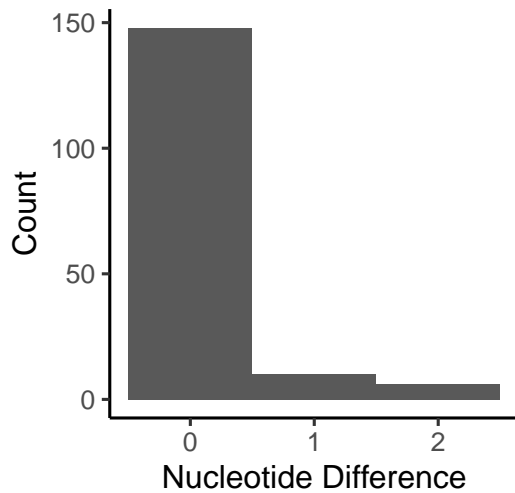
IGHV4-31*03_04

22 sequences assigned
19 (86.4%) exact matches, in which:
18 unique CDR3
4 unique J



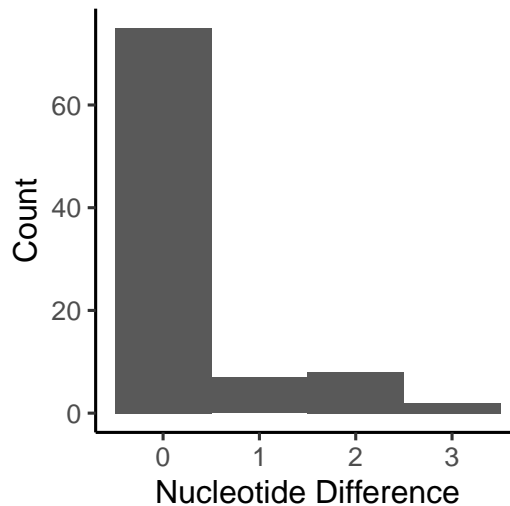
IGHV4-34*01_02

164 sequences assigned
148 (90.2%) exact matches, in which:
141 unique CDR3
7 unique J



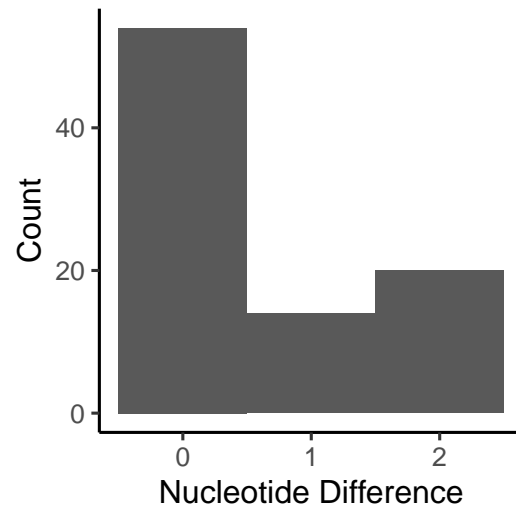
IGHV4-39*07

92 sequences assigned
75 (81.5%) exact matches, in which:
69 unique CDR3
5 unique J



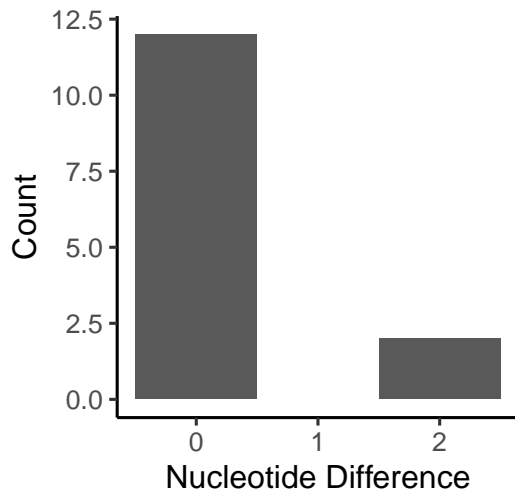
IGHV5-51*01_03

88 sequences assigned
54 (61.4%) exact matches, in which:
53 unique CDR3
7 unique J



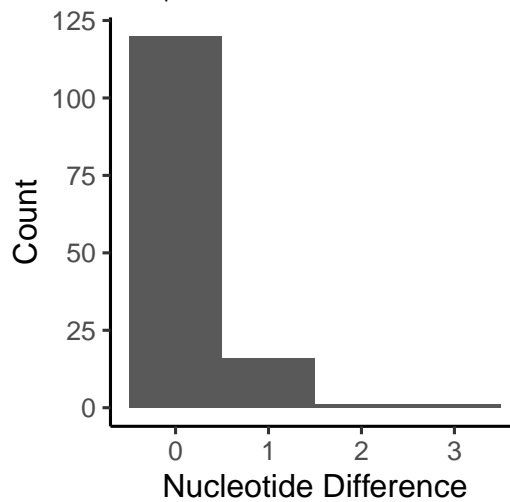
IGHV4-38-2*01

14 sequences assigned
12 (85.7%) exact matches, in which:
12 unique CDR3
3 unique J



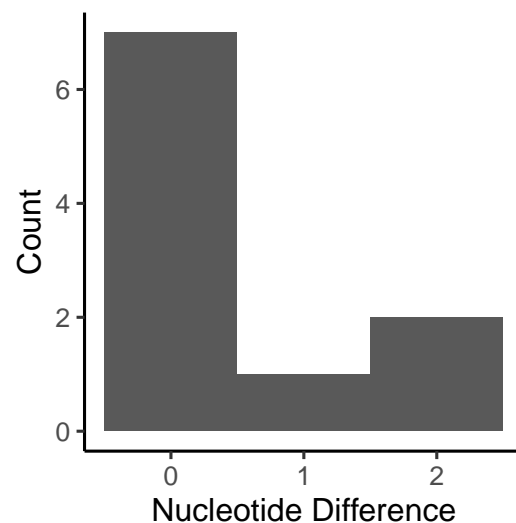
IGHV4-59*11

138 sequences assigned
120 (87%) exact matches, in which:
116 unique CDR3
7 unique J



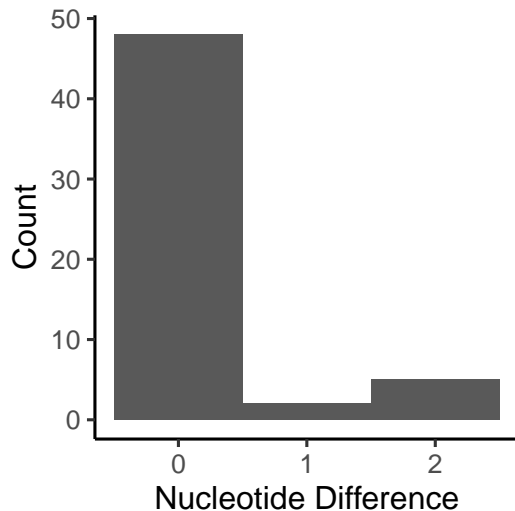
IGHV6-1*01_02

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



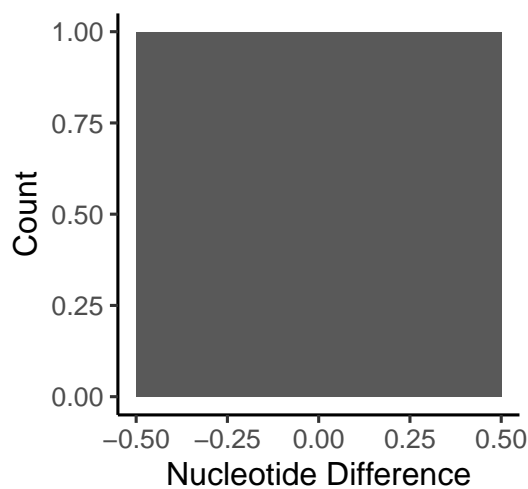
IGHV4-38-2*02

55 sequences assigned
48 (87.3%) exact matches, in which:
45 unique CDR3
6 unique J



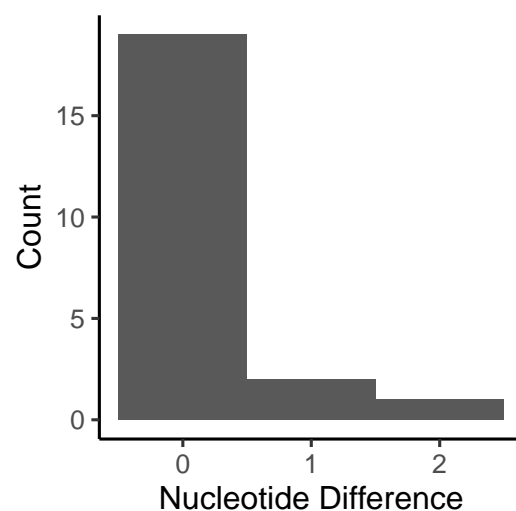
IGHV4-61*01

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

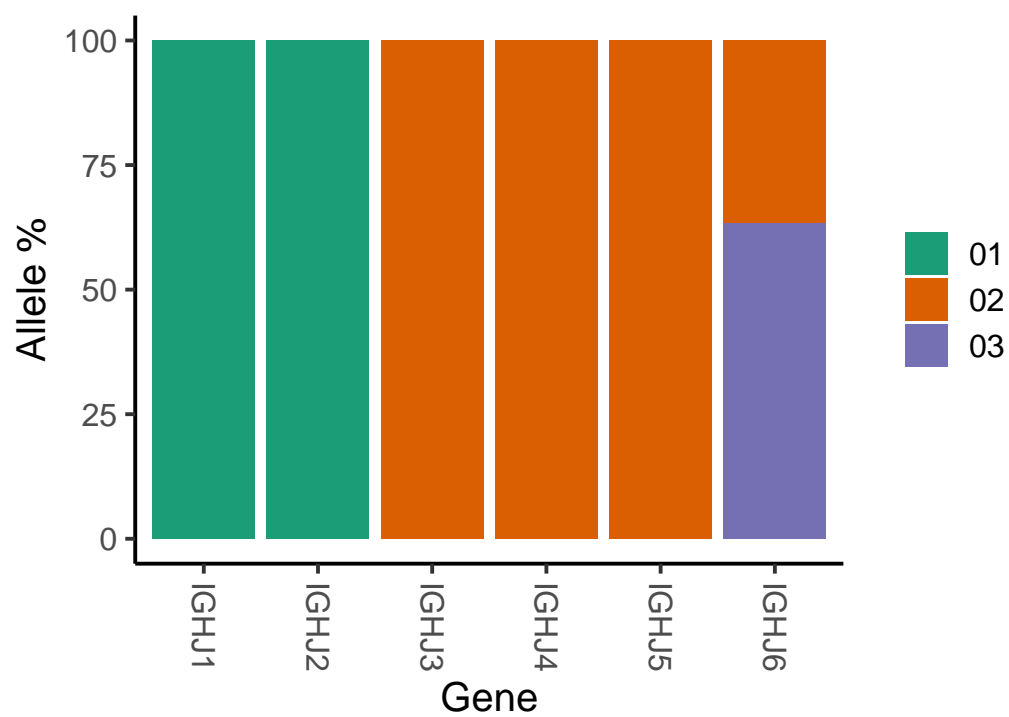


IGHV7-4-1*02

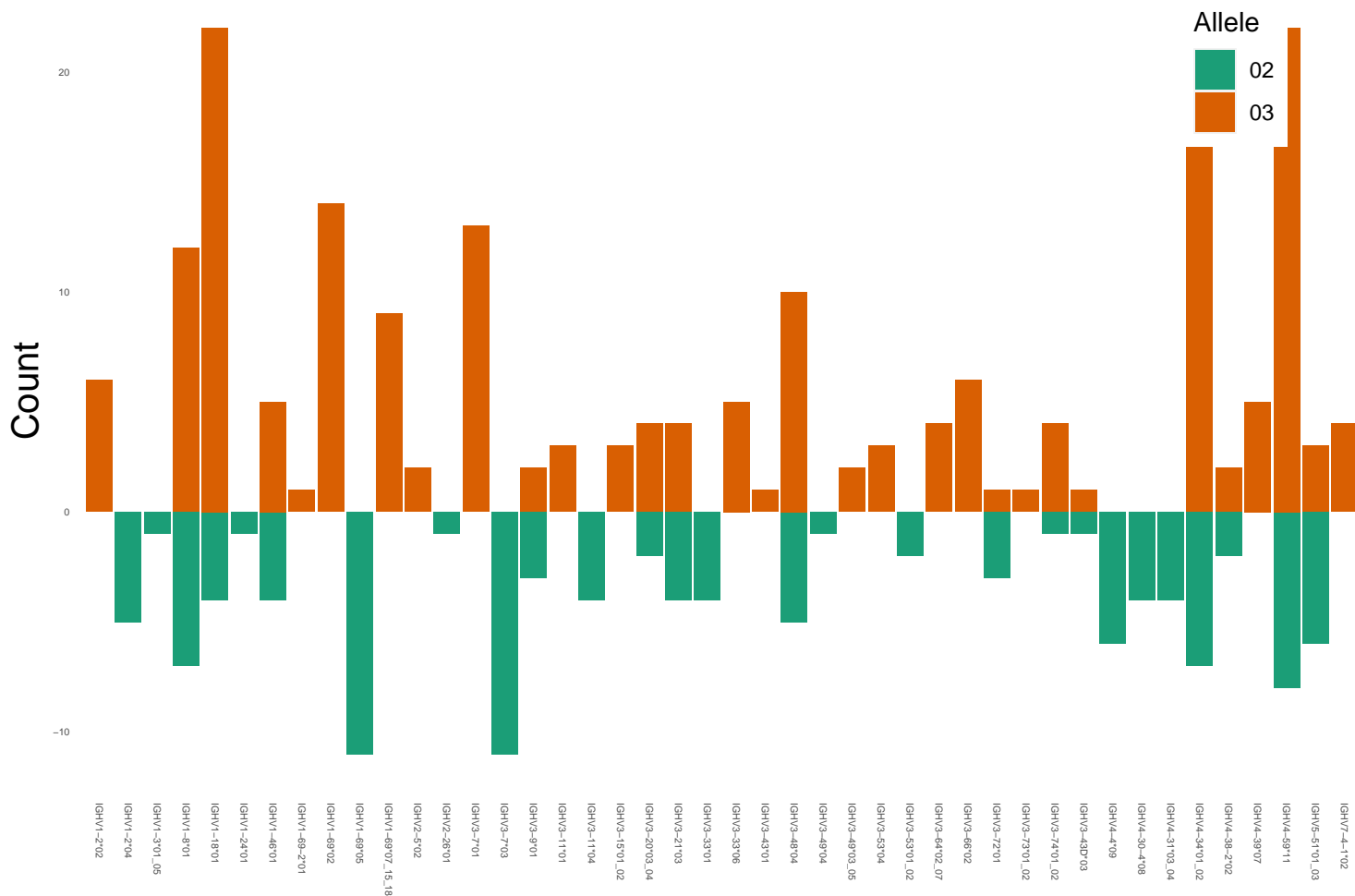
22 sequences assigned
19 (86.4%) exact matches, in which:
19 unique CDR3
4 unique J



Allele Usage



Sequence Count by IGHJ6 allele usage



Novel sequence(s)IGHV4-59*02_G88AIGHV5-51*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.

Warning – no inferred sequences found.

Novel sequence(s)IGHV3-11*06_T300CIGHV4-38-2*02_A70GIGHV4-39*02_C258GIGHV5-51*07_A128G are not listed in the genotype and will be ignored.

Warning – no inferred sequences found.

Novel sequence(s)IGHV4-39*02_C258GIGHV4-59*02_G88AIGHV5-51*07_A128G are not listed in the genotype and will be ignored.

Warning – no inferred sequences found.

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_G88AIGHV5-51*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_G88AIGHV5-51*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.