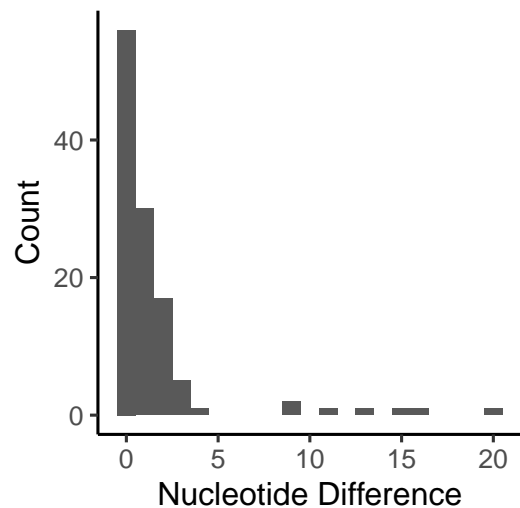


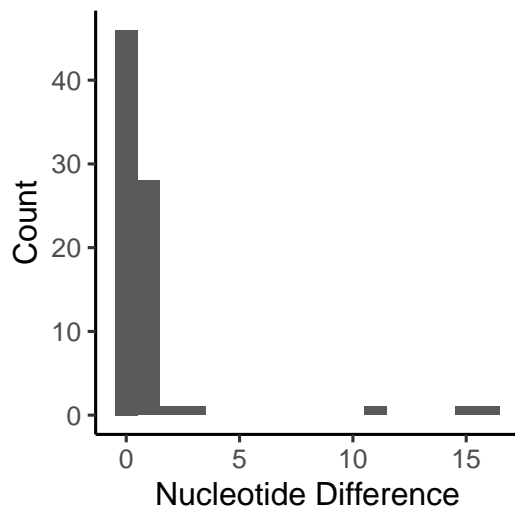
IGHV1-2*06

123 sequences assigned
56 (45.5%) exact matches, in which:
56 unique CDR3
6 unique J



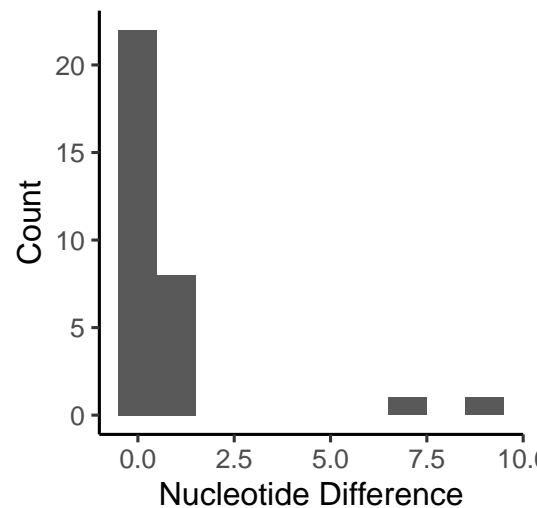
IGHV1-18*01

83 sequences assigned
46 (55.4%) exact matches, in which:
46 unique CDR3
6 unique J



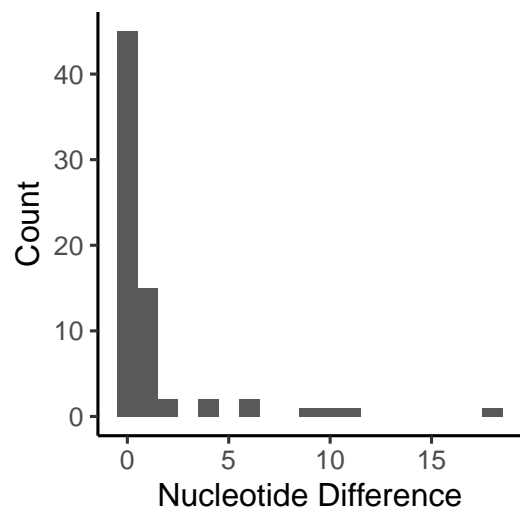
IGHV1-46*01

34 sequences assigned
22 (64.7%) exact matches, in which:
22 unique CDR3
4 unique J



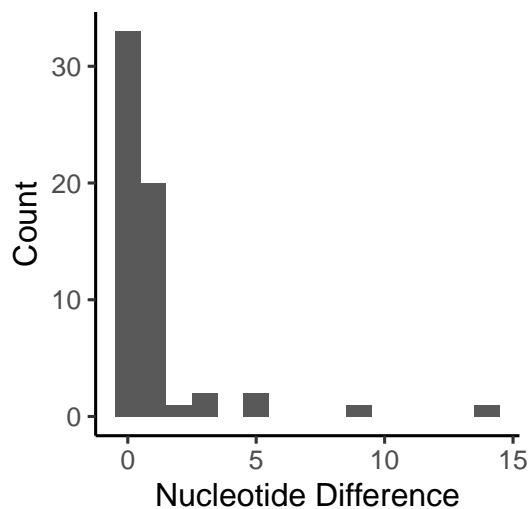
IGHV1-3*01

73 sequences assigned
45 (61.6%) exact matches, in which:
45 unique CDR3
6 unique J



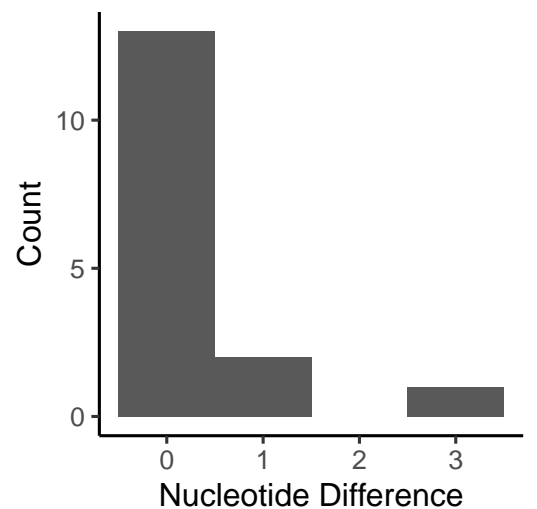
IGHV1-18*04

61 sequences assigned
33 (54.1%) exact matches, in which:
33 unique CDR3
4 unique J



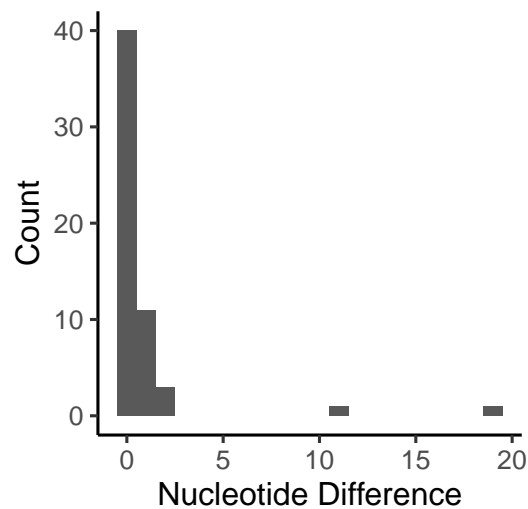
IGHV1-46*03

19 sequences assigned
13 (68.4%) exact matches, in which:
13 unique CDR3
5 unique J



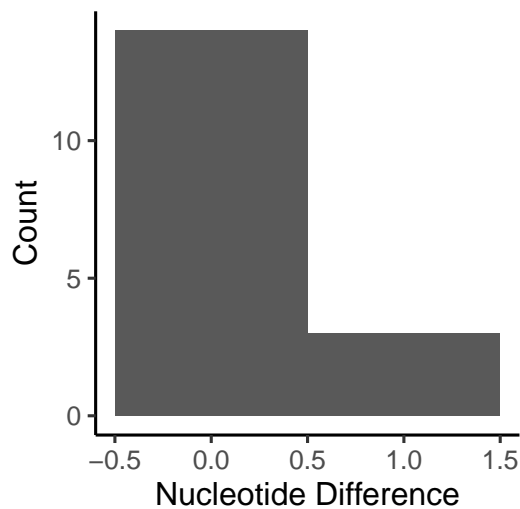
IGHV1-8*01

56 sequences assigned
40 (71.4%) exact matches, in which:
40 unique CDR3
5 unique J



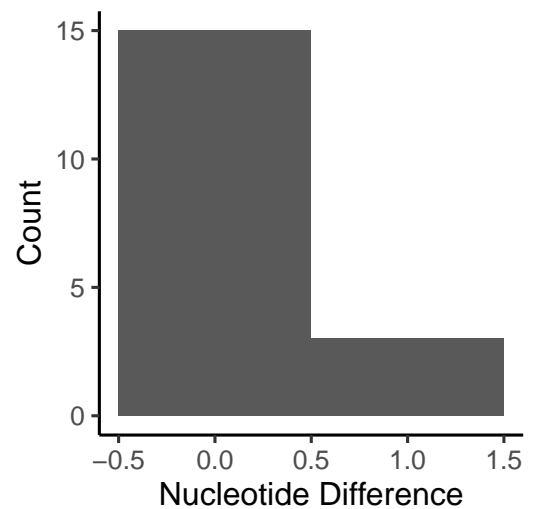
IGHV1-24*01

17 sequences assigned
14 (82.4%) exact matches, in which:
14 unique CDR3
4 unique J



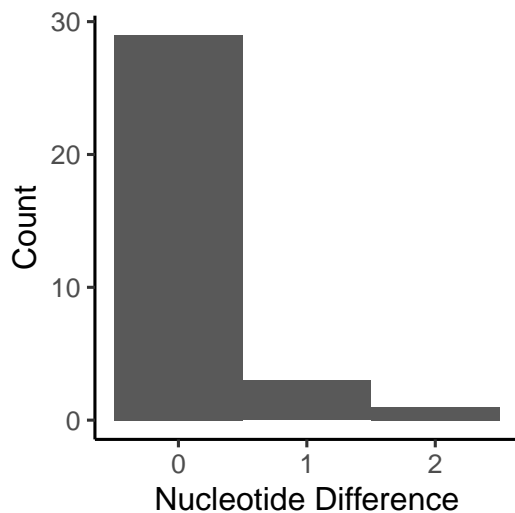
IGHV1-58*01

18 sequences assigned
15 (83.3%) exact matches, in which:
15 unique CDR3
5 unique J



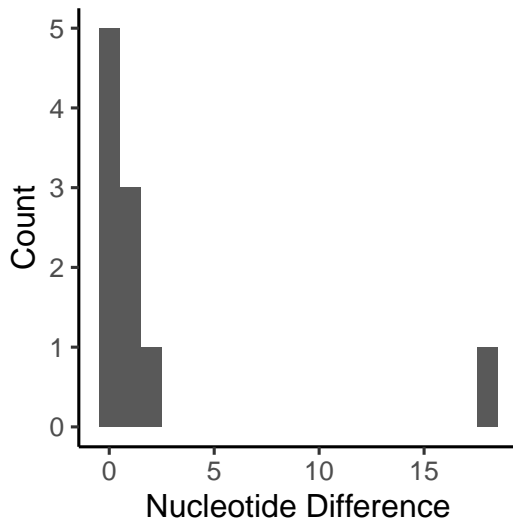
IGHV2-5*01

33 sequences assigned
29 (87.9%) exact matches, in which:
29 unique CDR3
5 unique J



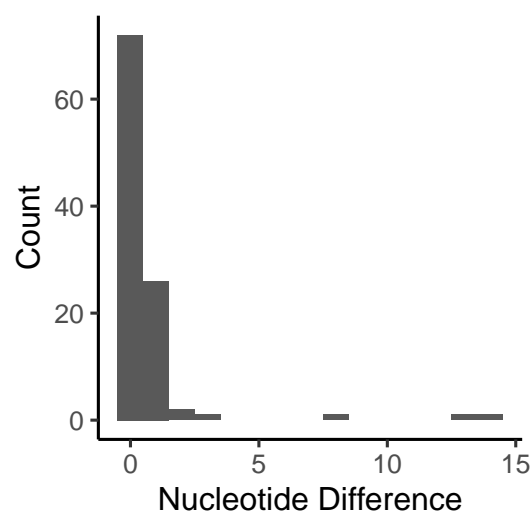
IGHV2-70*01

10 sequences assigned
5 (50%) exact matches, in which:
5 unique CDR3
4 unique J



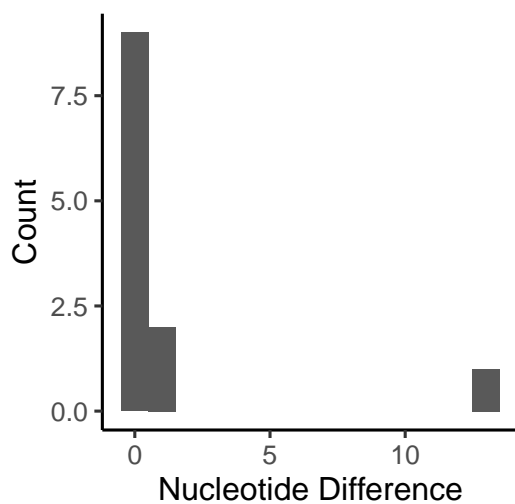
IGHV3-9*01

105 sequences assigned
72 (68.6%) exact matches, in which:
72 unique CDR3
5 unique J



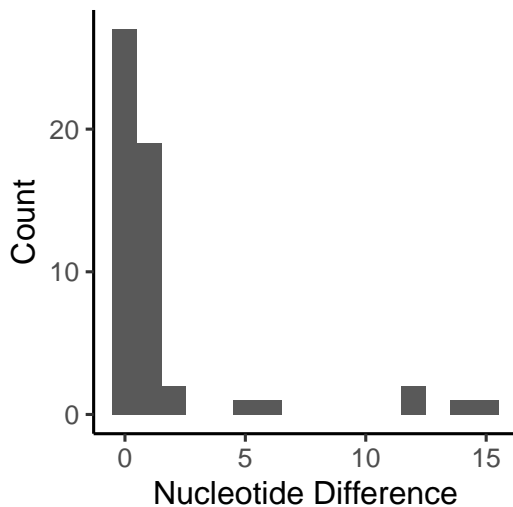
IGHV2-5*02

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



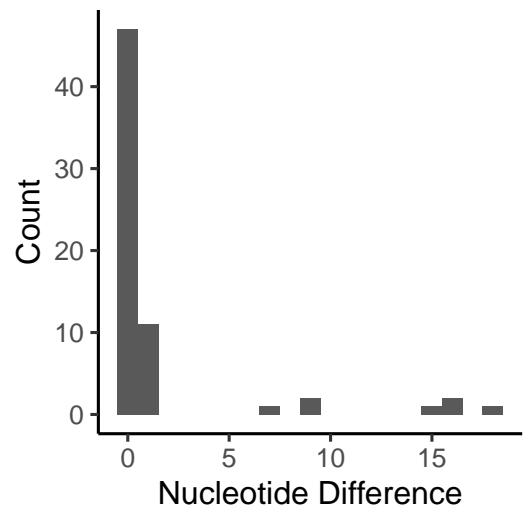
IGHV3-7*01

56 sequences assigned
27 (48.2%) exact matches, in which:
27 unique CDR3
4 unique J



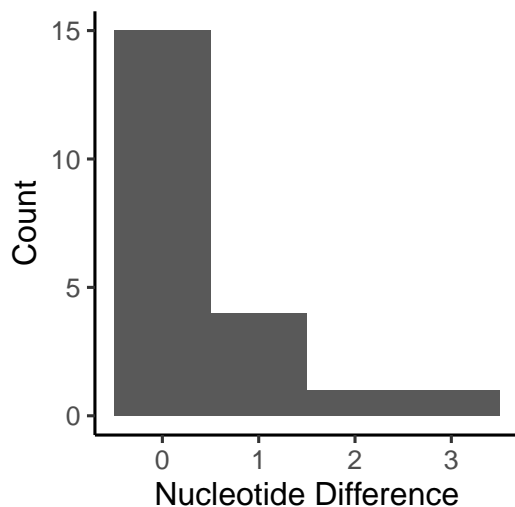
IGHV3-11*01

74 sequences assigned
47 (63.5%) exact matches, in which:
47 unique CDR3
5 unique J



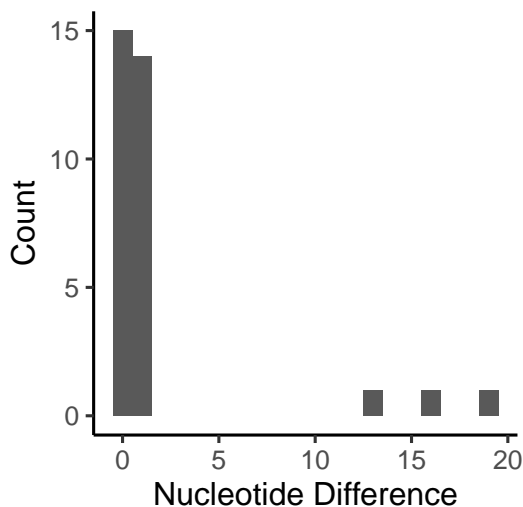
IGHV2-26*01

21 sequences assigned
15 (71.4%) exact matches, in which:
15 unique CDR3
4 unique J



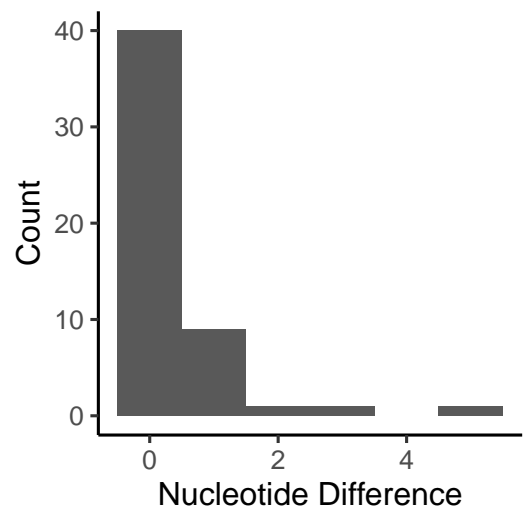
IGHV3-7*03

37 sequences assigned
15 (40.5%) exact matches, in which:
15 unique CDR3
4 unique J



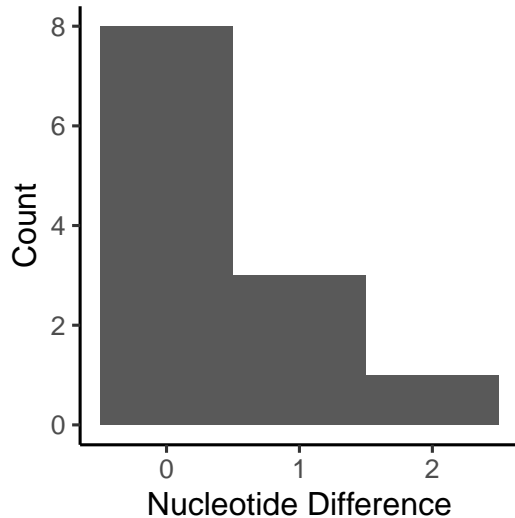
IGHV3-11*06

53 sequences assigned
40 (75.5%) exact matches, in which:
40 unique CDR3
5 unique J



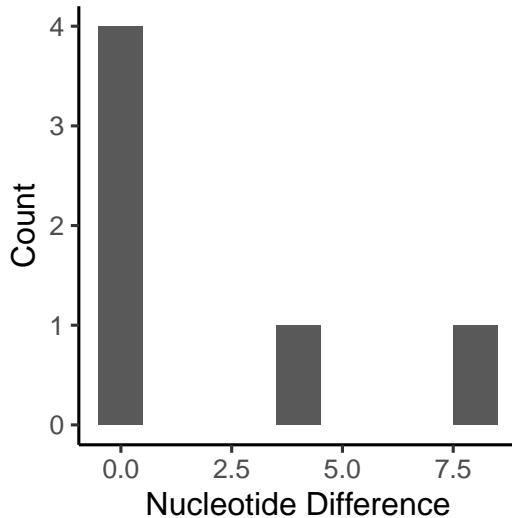
IGHV3-13*01

13 sequences assigned
8 (61.5%) exact matches, in which:
8 unique CDR3
2 unique J



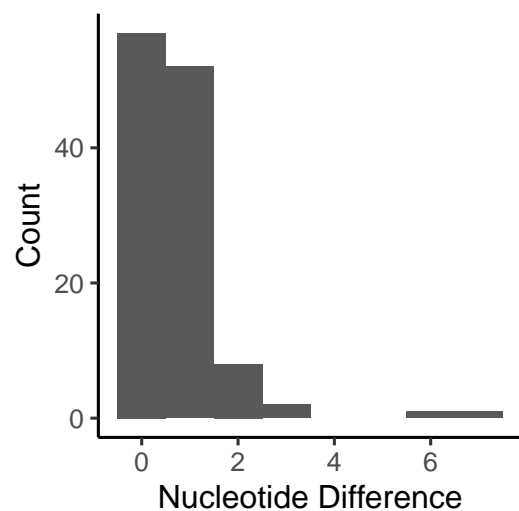
IGHV3-20*01

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



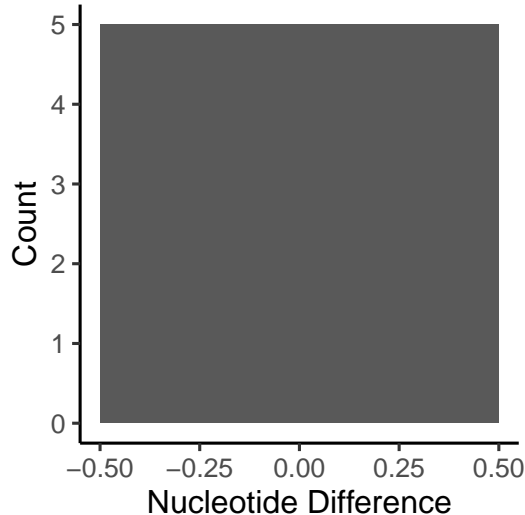
IGHV3-30-3*01

128 sequences assigned
57 (44.5%) exact matches, in which:
56 unique CDR3
5 unique J



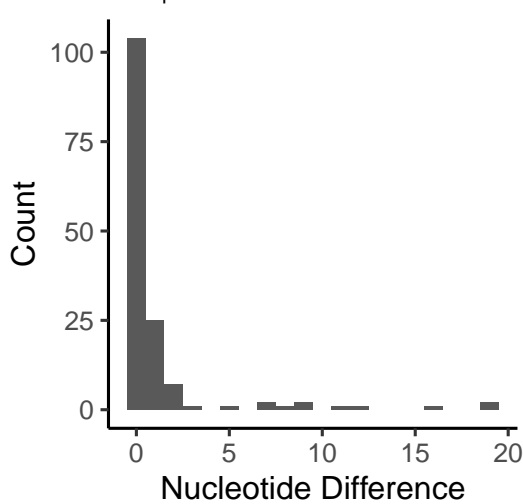
IGHV3-13*05

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



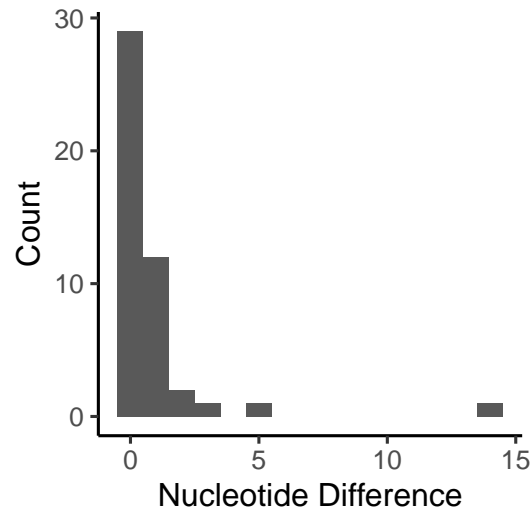
IGHV3-21*01

149 sequences assigned
104 (69.8%) exact matches, in which:
104 unique CDR3
7 unique J



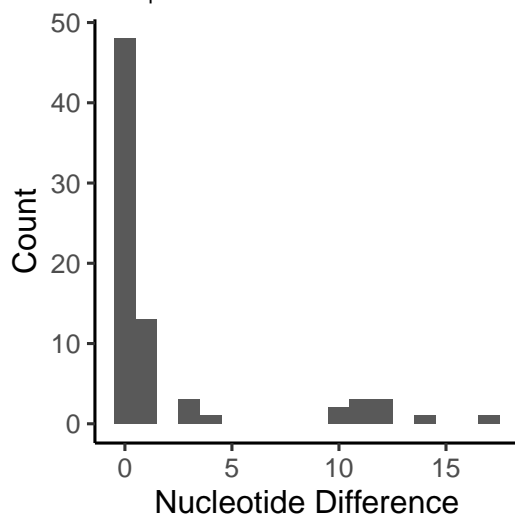
IGHV3-30*18_T158G

48 sequences assigned
29 (60.4%) exact matches, in which:
29 unique CDR3
5 unique J



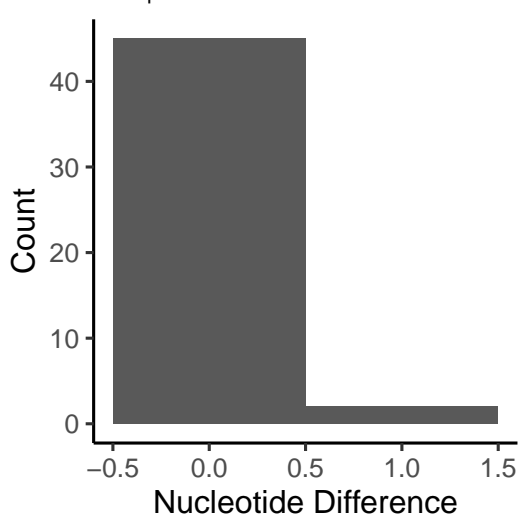
IGHV3-15*01

78 sequences assigned
48 (61.5%) exact matches, in which:
48 unique CDR3
5 unique J



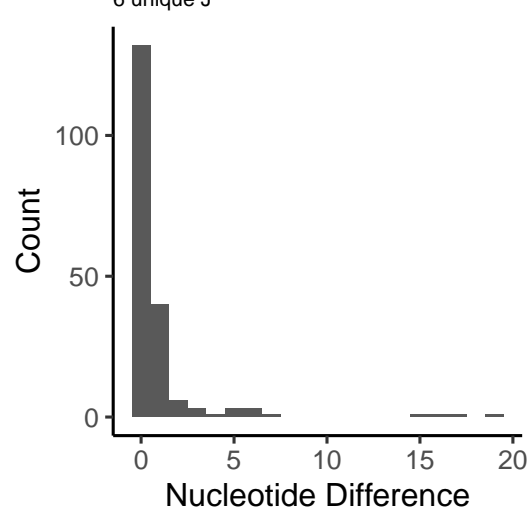
IGHV3-21*01_T158G

47 sequences assigned
45 (95.7%) exact matches, in which:
45 unique CDR3
6 unique J



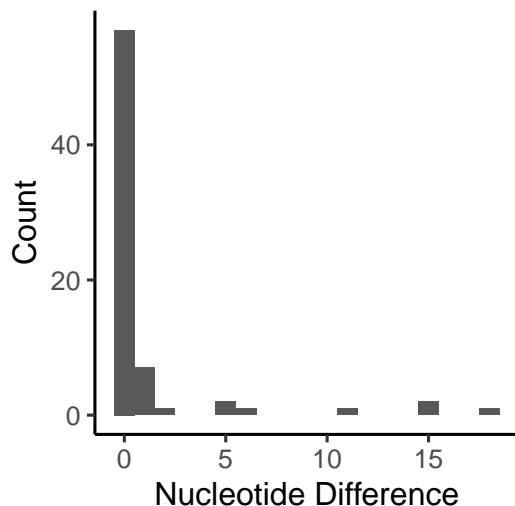
IGHV3-33*01

198 sequences assigned
132 (66.7%) exact matches, in which:
128 unique CDR3
6 unique J



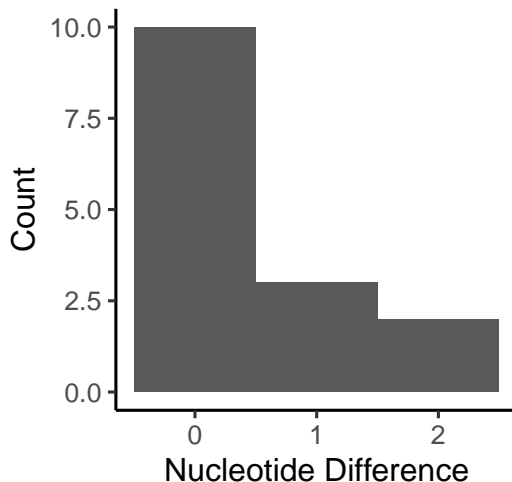
IGHV3-33*01_T158G

73 sequences assigned
57 (78.1%) exact matches, in which:
57 unique CDR3
6 unique J



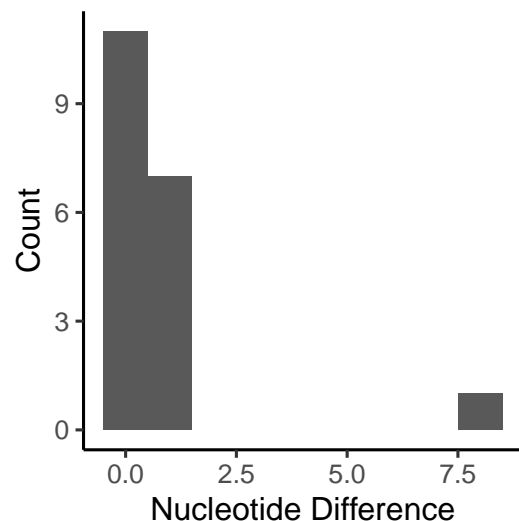
IGHV3-48*02

16 sequences assigned
10 (62.5%) exact matches, in which:
10 unique CDR3
4 unique J



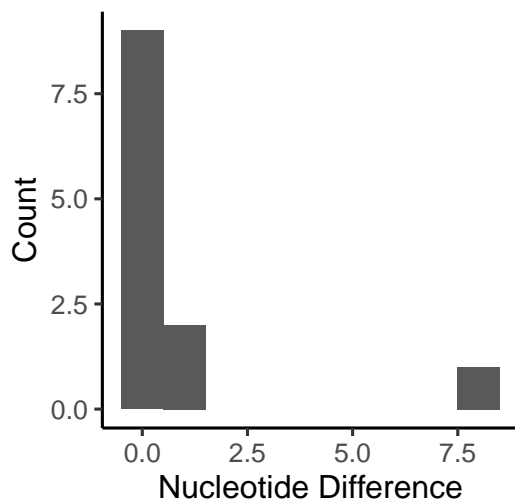
IGHV3-53*02

19 sequences assigned
11 (57.9%) exact matches, in which:
11 unique CDR3
5 unique J



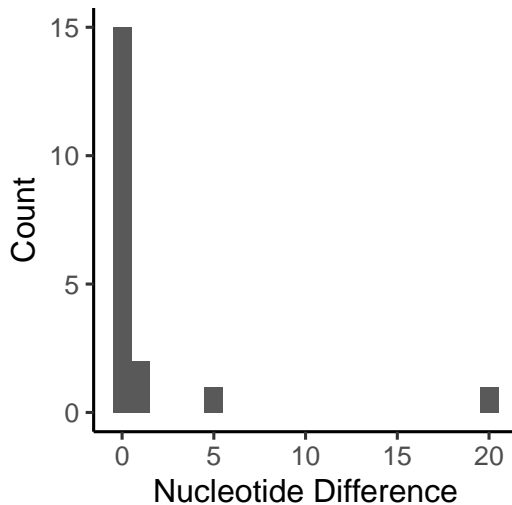
IGHV3-43*01

14 sequences assigned
9 (64.3%) exact matches, in which:
9 unique CDR3
2 unique J



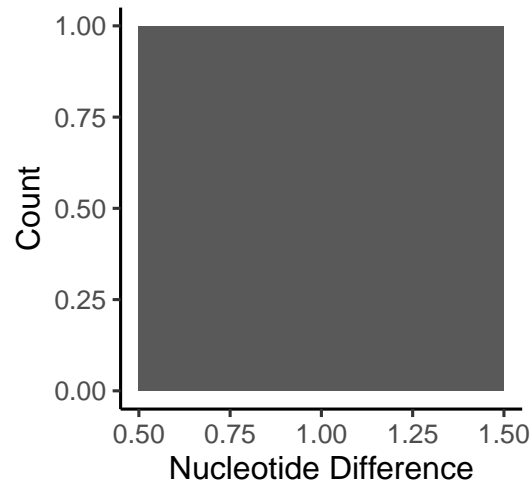
IGHV3-49*05

19 sequences assigned
15 (78.9%) exact matches, in which:
15 unique CDR3
6 unique J



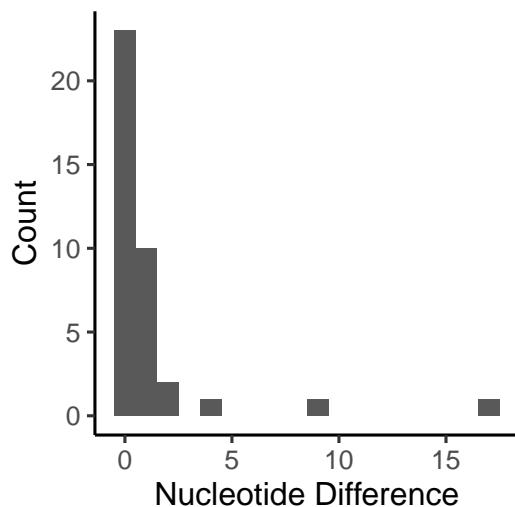
IGHV3-72*01

1 sequences assigned
No exact matches.



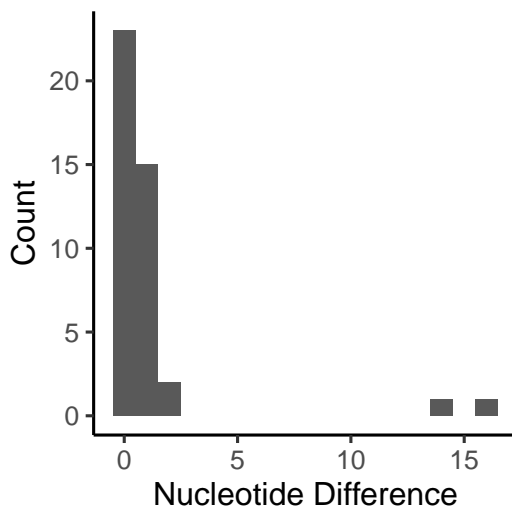
IGHV3-48*01

39 sequences assigned
23 (59%) exact matches, in which:
23 unique CDR3
5 unique J



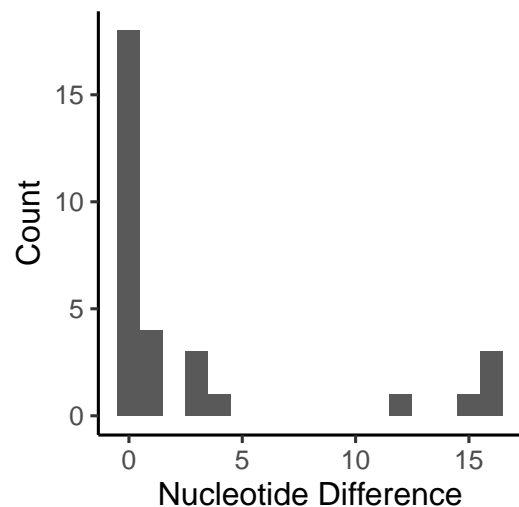
IGHV3-53*01

48 sequences assigned
23 (47.9%) exact matches, in which:
23 unique CDR3
5 unique J



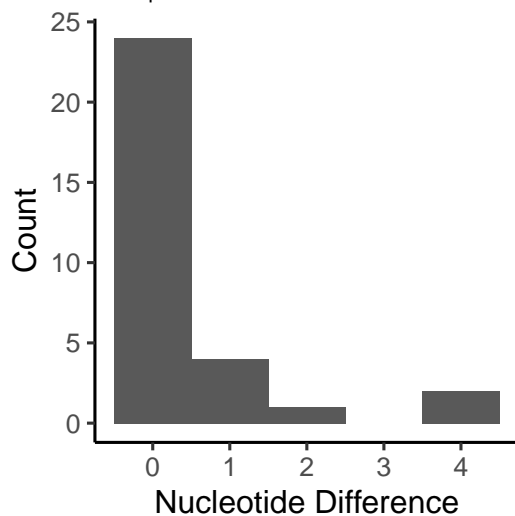
IGHV3-73*02

32 sequences assigned
18 (56.2%) exact matches, in which:
18 unique CDR3
5 unique J



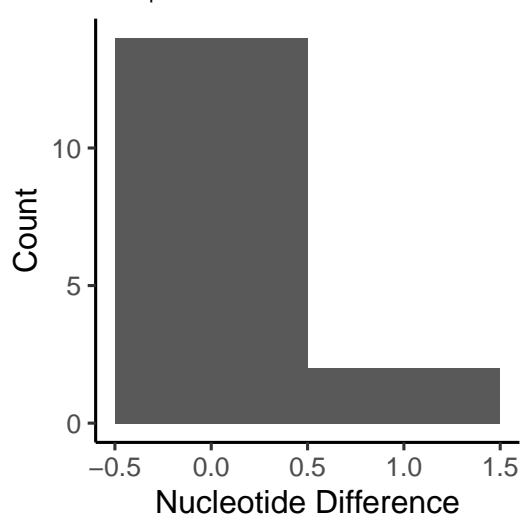
IGHV3-74*01

31 sequences assigned
24 (77.4%) exact matches, in which:
23 unique CDR3
6 unique J



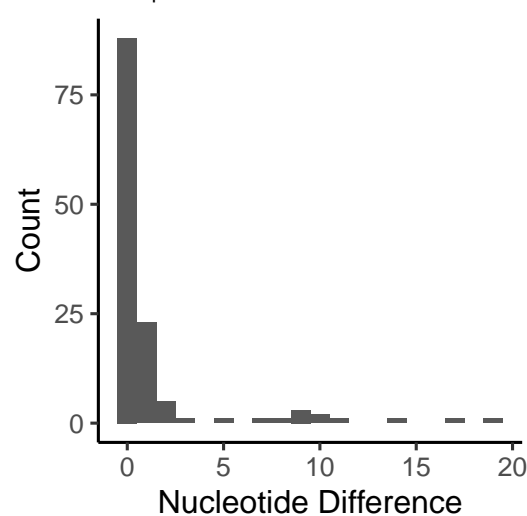
IGHV4-4*02_T208C

16 sequences assigned
14 (87.5%) exact matches, in which:
14 unique CDR3
4 unique J



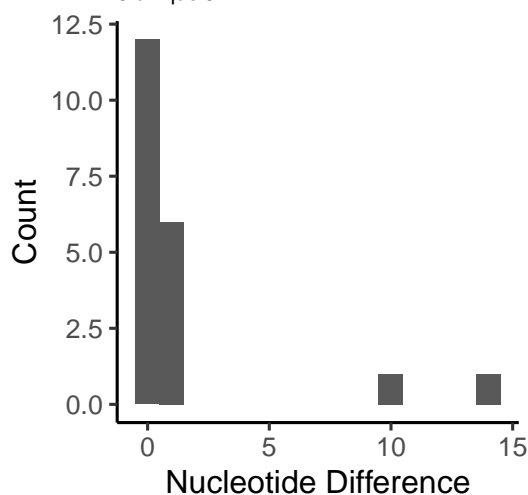
IGHV4-31*03

141 sequences assigned
88 (62.4%) exact matches, in which:
88 unique CDR3
6 unique J



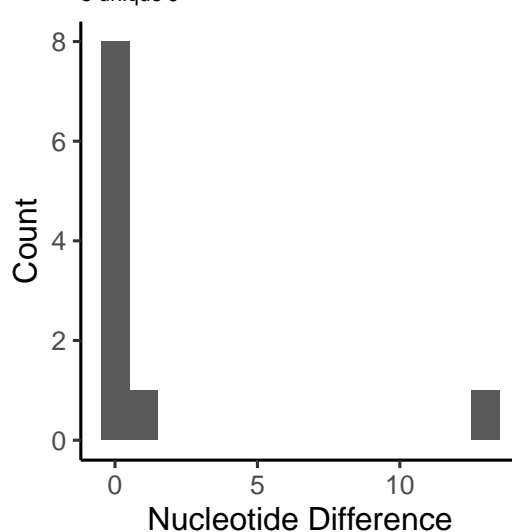
IGHV3-64D*06

20 sequences assigned
12 (60%) exact matches, in which:
12 unique CDR3
3 unique J



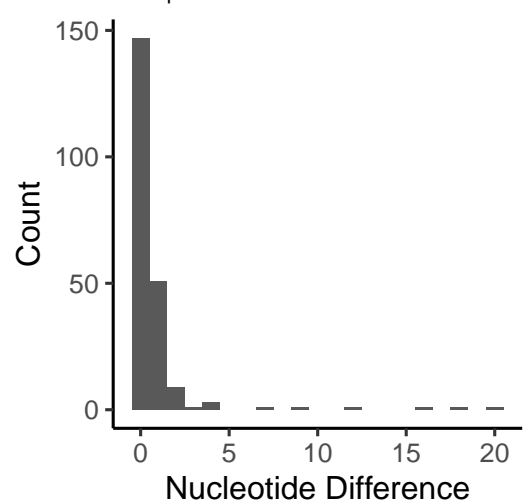
IGHV4-30-2*01

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



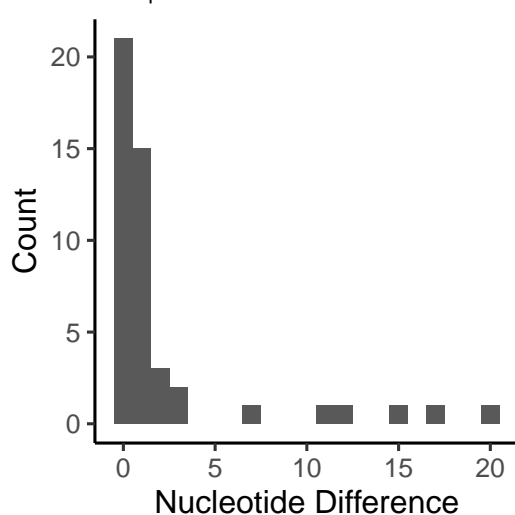
IGHV4-34*01

218 sequences assigned
147 (67.4%) exact matches, in which:
146 unique CDR3
7 unique J



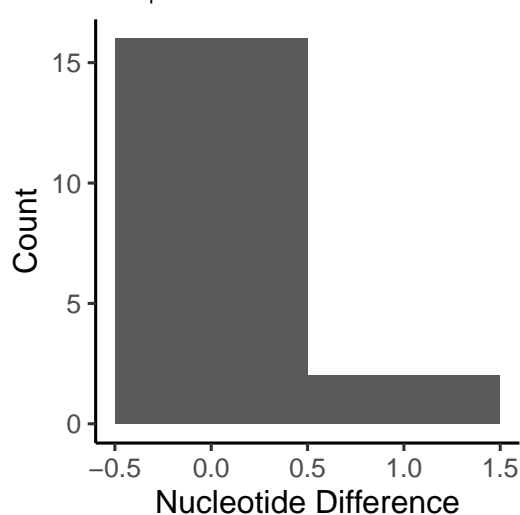
IGHV4-4*02

49 sequences assigned
21 (42.9%) exact matches, in which:
21 unique CDR3
6 unique J



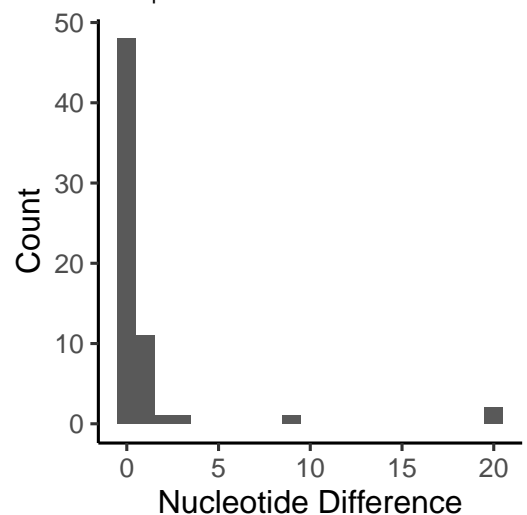
IGHV4-30-4*01

18 sequences assigned
16 (88.9%) exact matches, in which:
16 unique CDR3
5 unique J



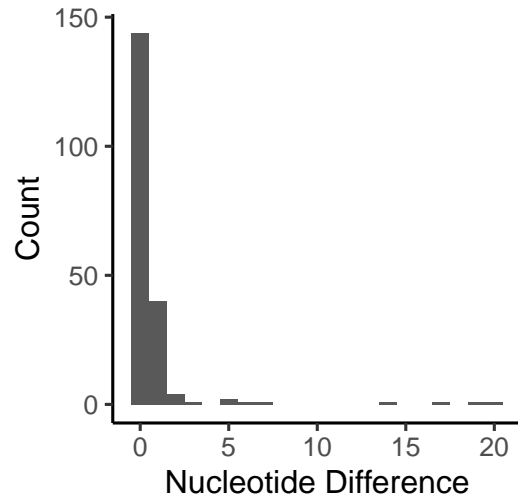
IGHV4-34*01_T208C

65 sequences assigned
48 (73.8%) exact matches, in which:
48 unique CDR3
7 unique J



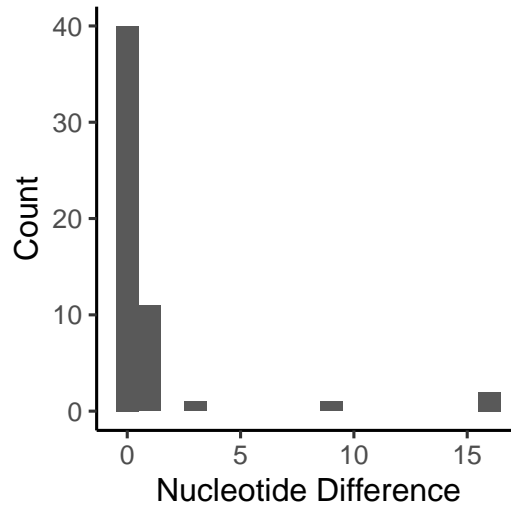
IGHV4-39*01

215 sequences assigned
144 (67%) exact matches, in which:
144 unique CDR3
7 unique J



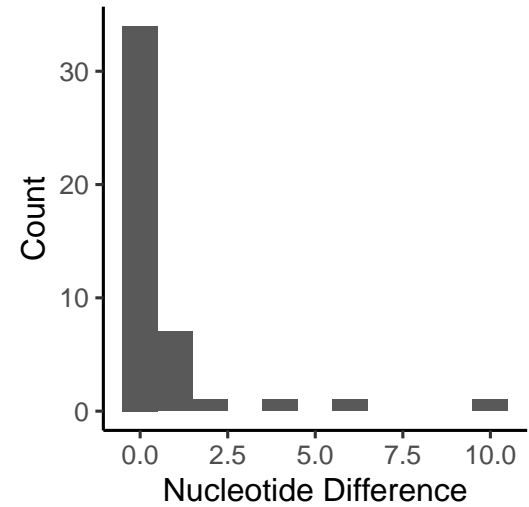
IGHV5-10-1*03

58 sequences assigned
40 (69%) exact matches, in which:
40 unique CDR3
5 unique J



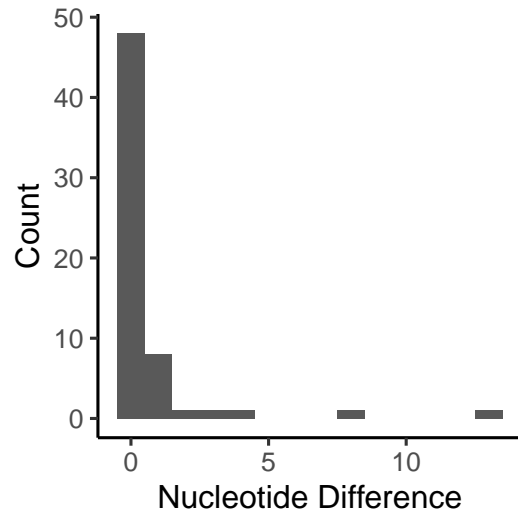
IGHV6-1*01

45 sequences assigned
34 (75.6%) exact matches, in which:
34 unique CDR3
6 unique J



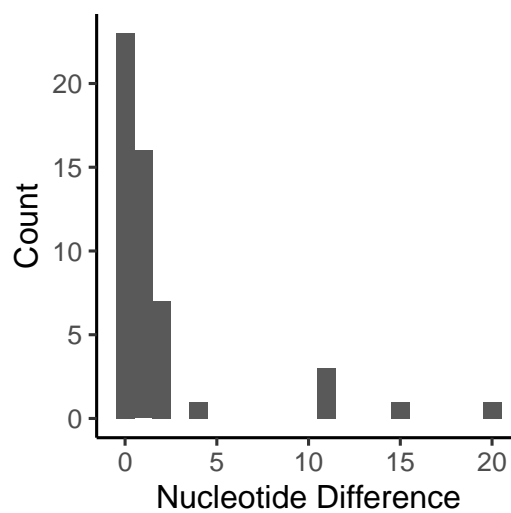
IGHV4-59*01

62 sequences assigned
48 (77.4%) exact matches, in which:
47 unique CDR3
6 unique J



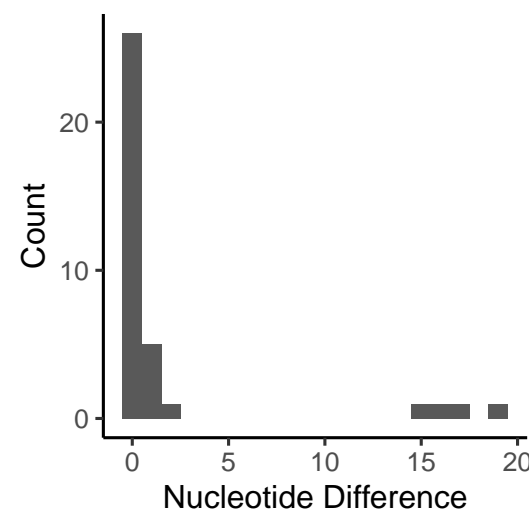
IGHV5-51*01

56 sequences assigned
23 (41.1%) exact matches, in which:
23 unique CDR3
5 unique J



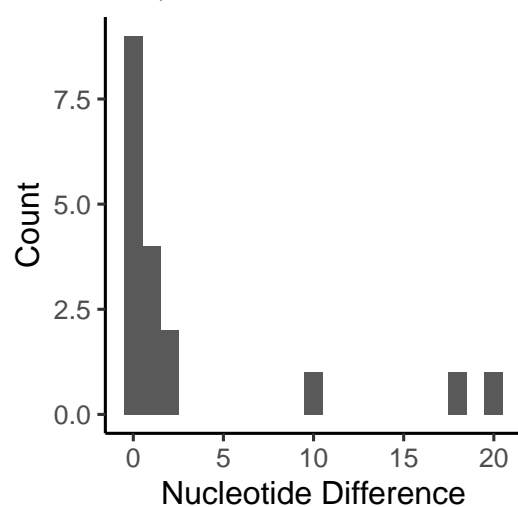
IGHV7-4-1*02

46 sequences assigned
26 (56.5%) exact matches, in which:
26 unique CDR3
5 unique J



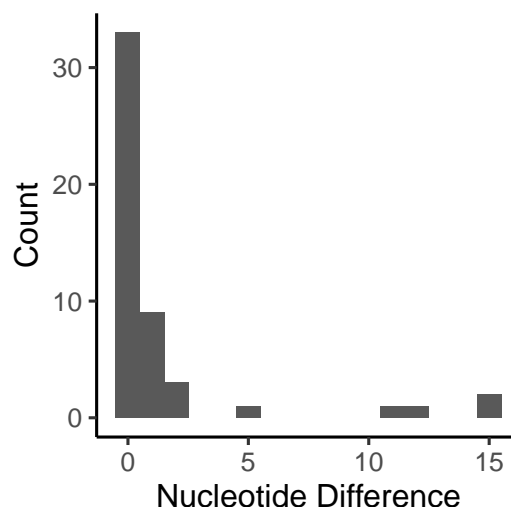
IGHV4-61*01

19 sequences assigned
9 (47.4%) exact matches, in which:
9 unique CDR3
4 unique J

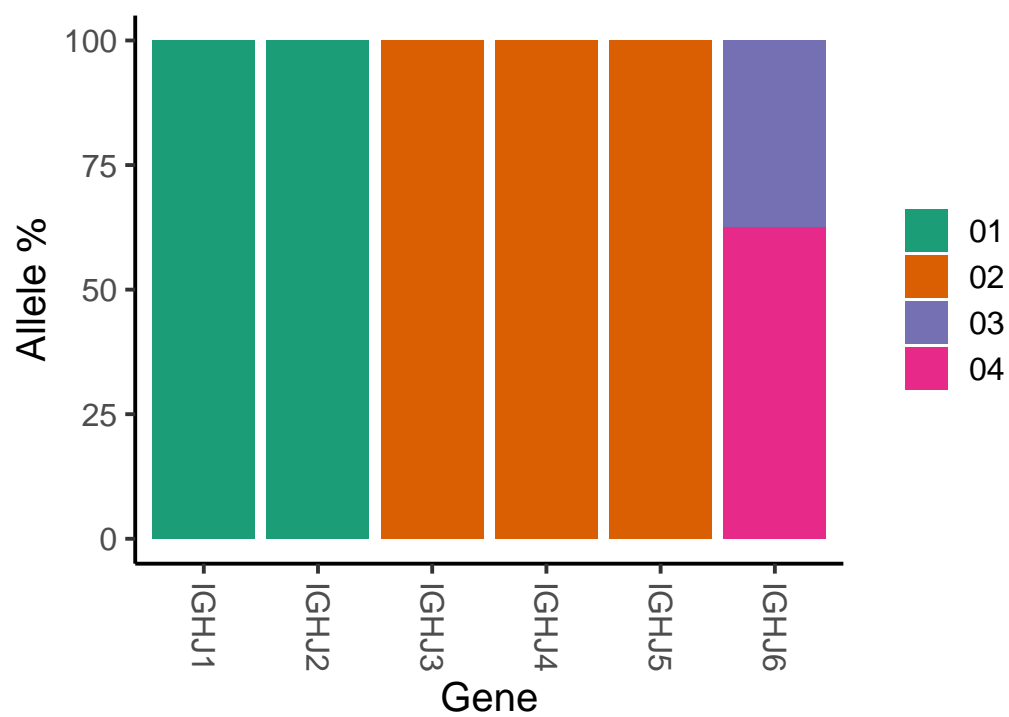


IGHV5-51*03

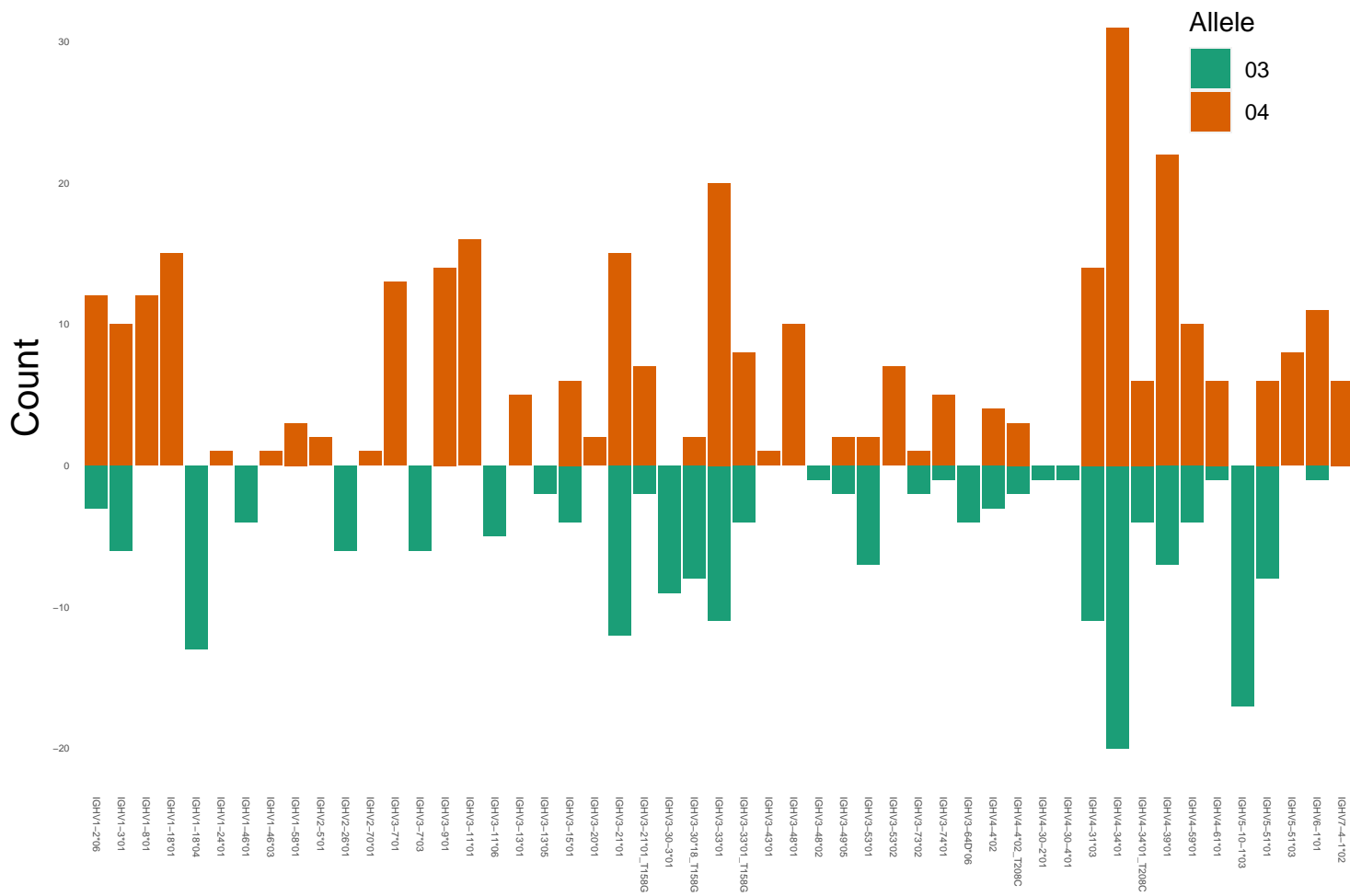
56 sequences assigned
33 (58.9%) exact matches, in which:
33 unique CDR3
6 unique J



Allele Usage



Sequence Count by IGHJ6 allele usage



Warning – no inferred sequences found.