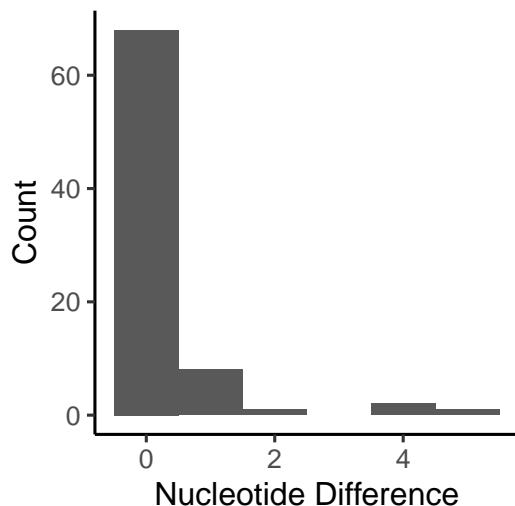


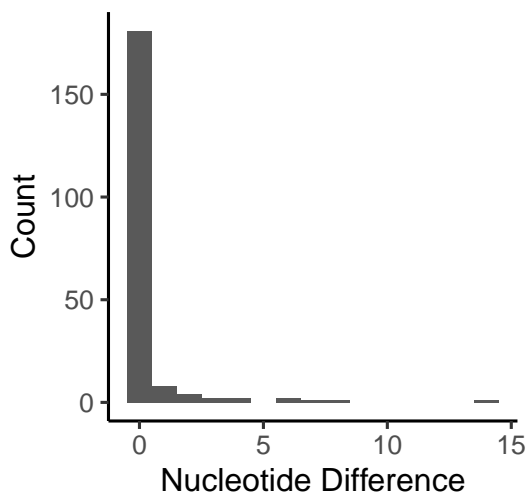
IGHV1-2*04

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



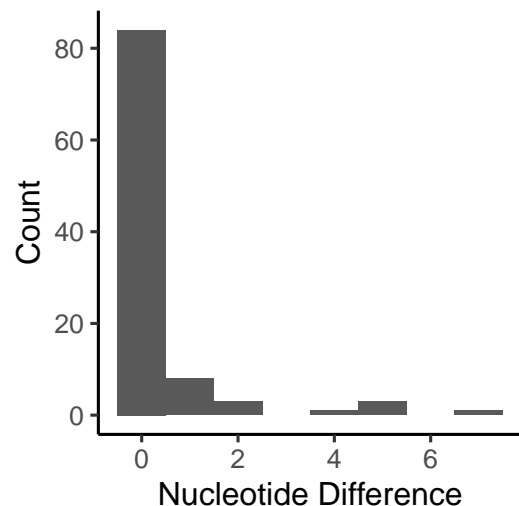
IGHV1-18*04

202 sequences assigned
181 (89.6%) exact matches, in which:
181 unique CDR3
7 unique J



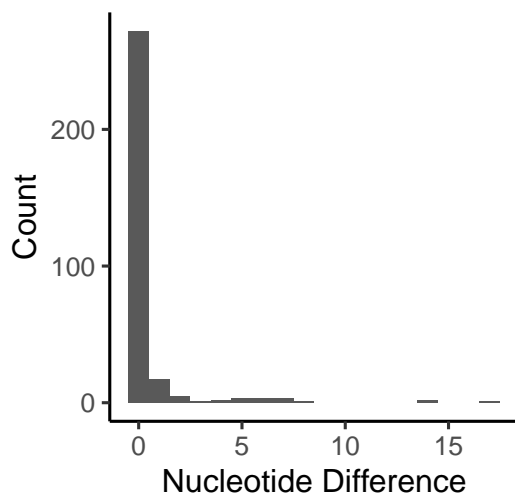
IGHV1-46*01

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



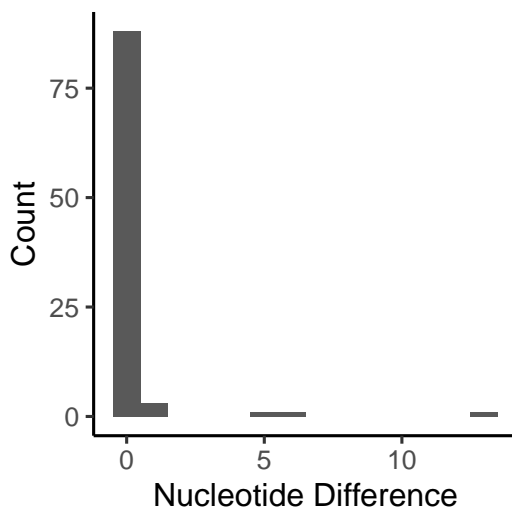
IGHV1-3*01

311 sequences assigned
272 (87.5%) exact matches, in which:
272 unique CDR3
7 unique J



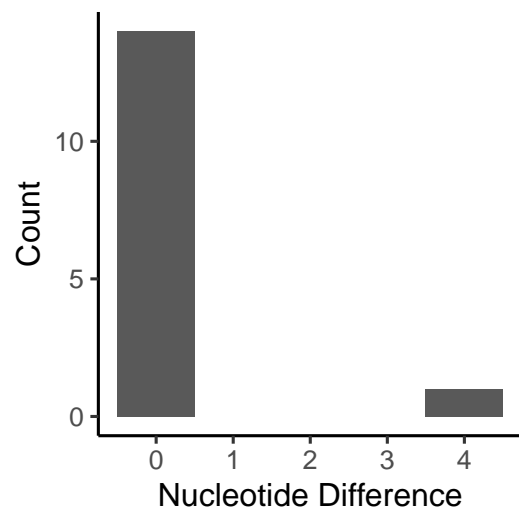
IGHV1-24*01

94 sequences assigned
88 (93.6%) exact matches, in which:
86 unique CDR3
7 unique J



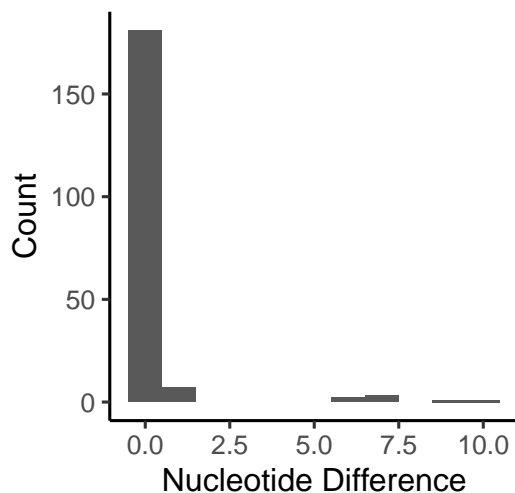
IGHV1-58*01

15 sequences assigned
14 (93.3%) exact matches, in which:
14 unique CDR3
5 unique J



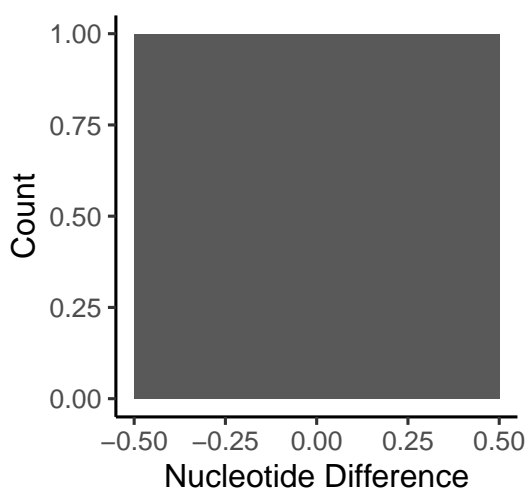
IGHV1-18*01

195 sequences assigned
181 (92.8%) exact matches, in which:
181 unique CDR3
7 unique J



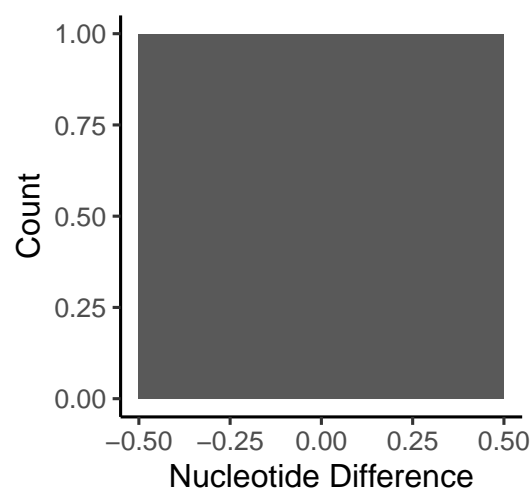
IGHV1-45*02

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



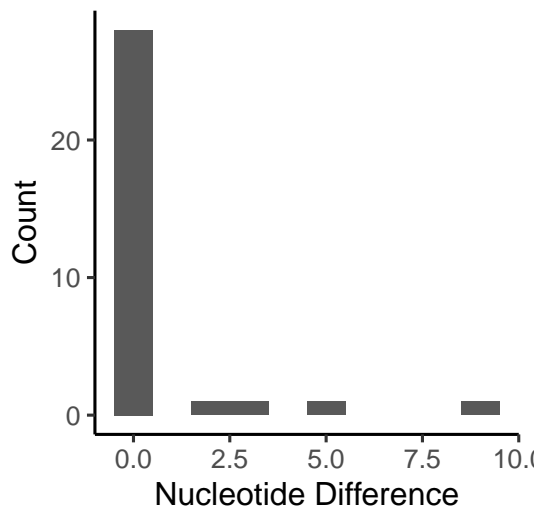
IGHV1-68*02

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



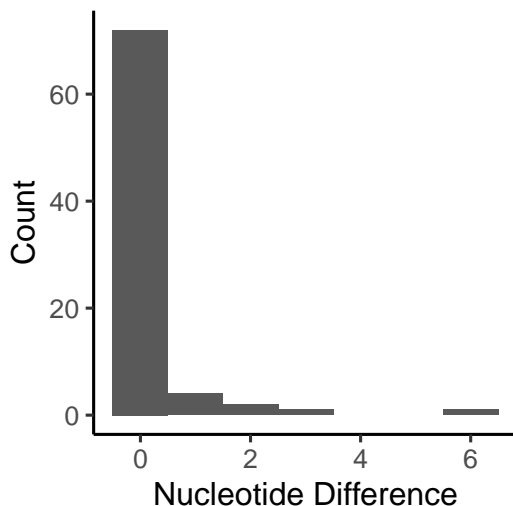
IGHV1-69-2*01

32 sequences assigned
28 (87.5%) exact matches, in which:
28 unique CDR3
6 unique J



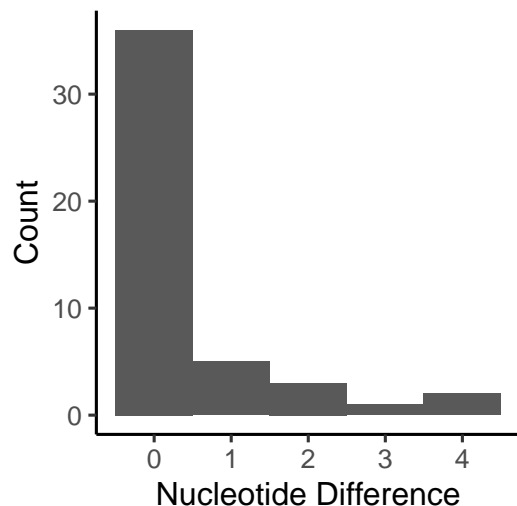
IGHV2-26*01

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



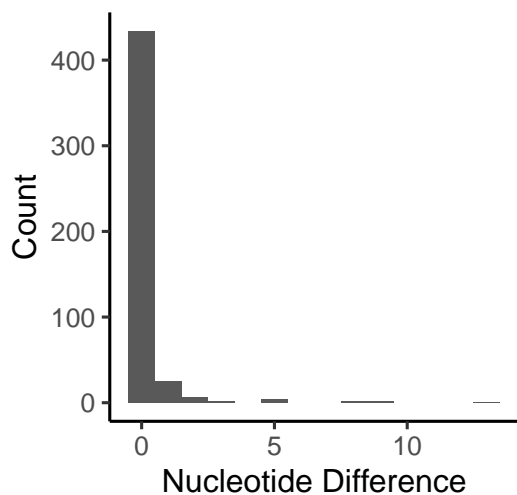
IGHV3-7*03

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



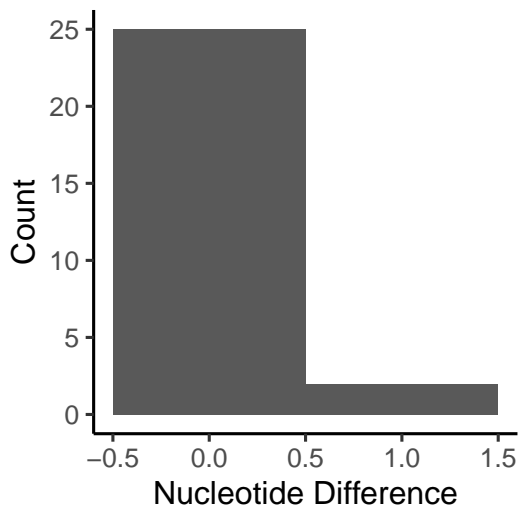
IGHV1-69*06

476 sequences assigned
434 (91.2%) exact matches, in which:
434 unique CDR3
7 unique J



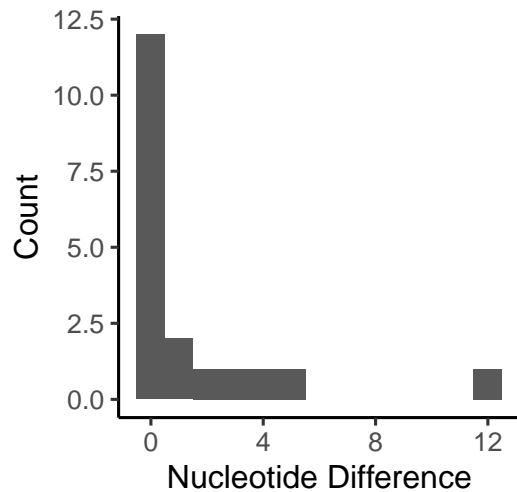
IGHV2-70*01

27 sequences assigned
25 (92.6%) exact matches, in which:
25 unique CDR3
5 unique J



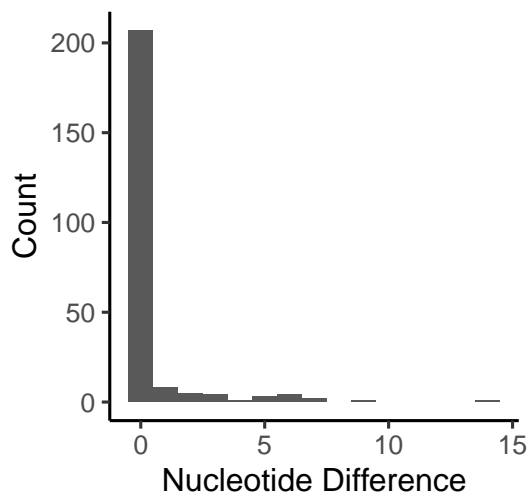
IGHV3-7*04

19 sequences assigned
12 (63.2%) exact matches, in which:
12 unique CDR3
4 unique J



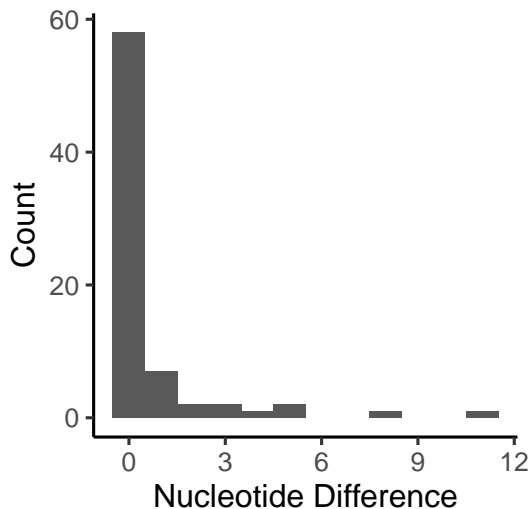
IGHV2-5*02

236 sequences assigned
207 (87.7%) exact matches, in which:
206 unique CDR3
7 unique J



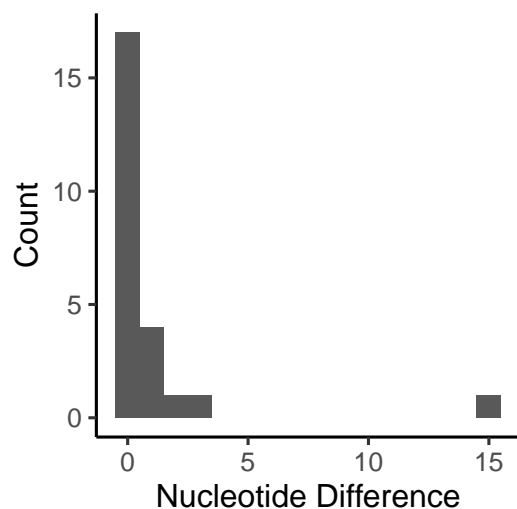
IGHV2-70*15

74 sequences assigned
58 (78.4%) exact matches, in which:
58 unique CDR3
5 unique J



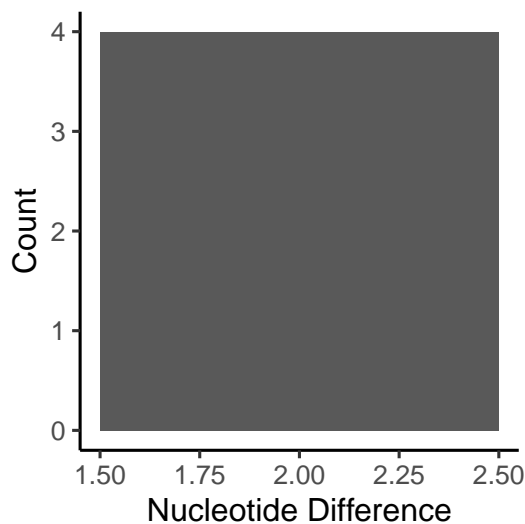
IGHV3-11*06

24 sequences assigned
17 (70.8%) exact matches, in which:
17 unique CDR3
6 unique J



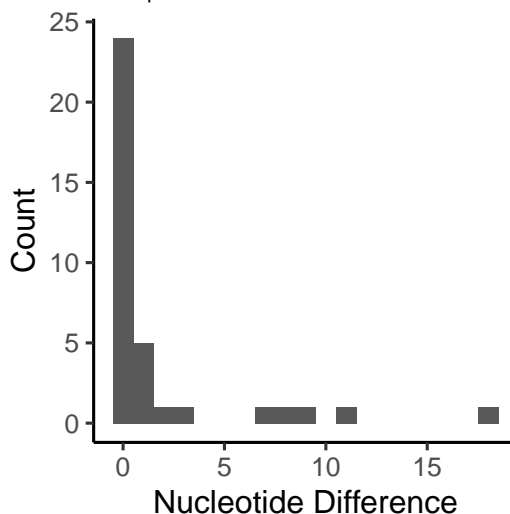
IGHV3-13*01

4 sequences assigned
No exact matches.



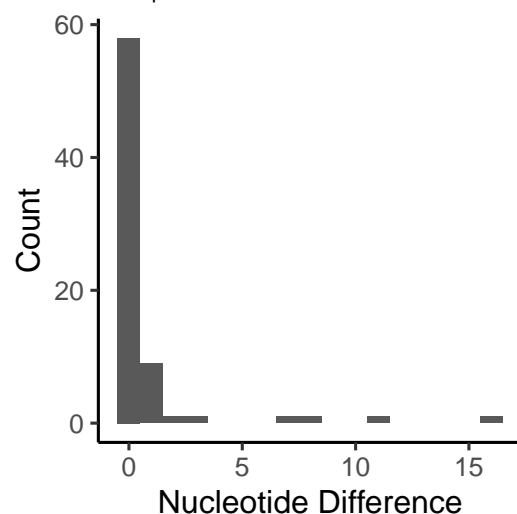
IGHV3-15*07

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



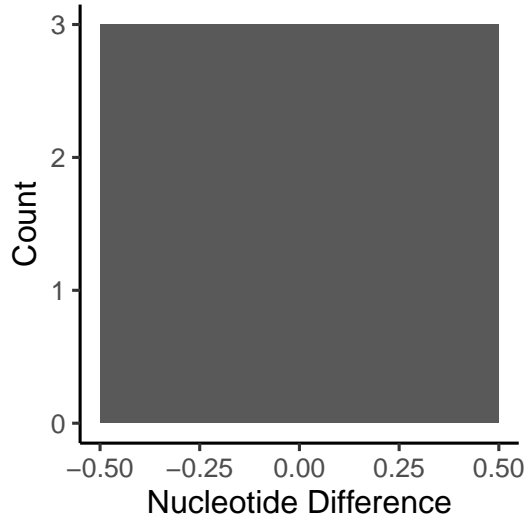
IGHV3-33*01

73 sequences assigned
58 (79.5%) exact matches, in which:
58 unique CDR3
4 unique J



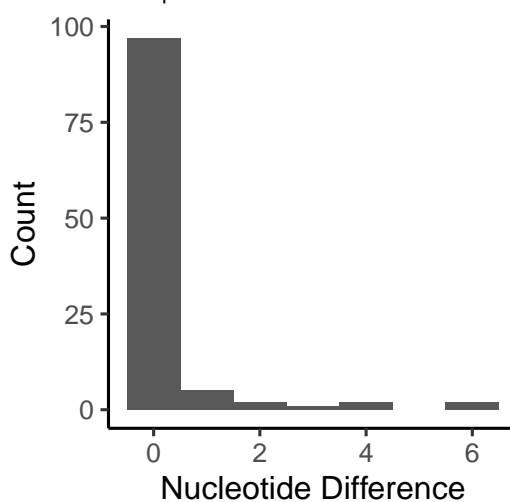
IGHV3-13*05

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



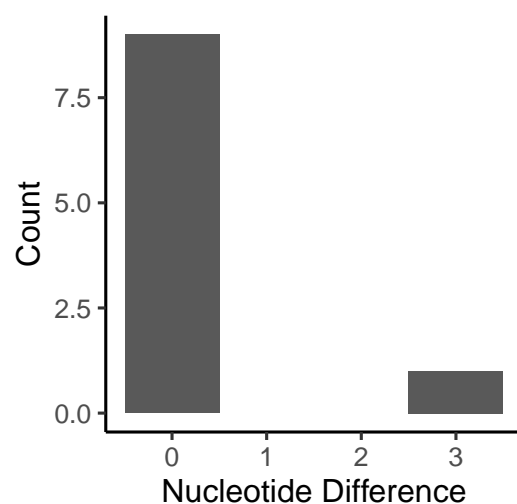
IGHV3-21*01

109 sequences assigned
97 (89%) exact matches, in which:
97 unique CDR3
7 unique J



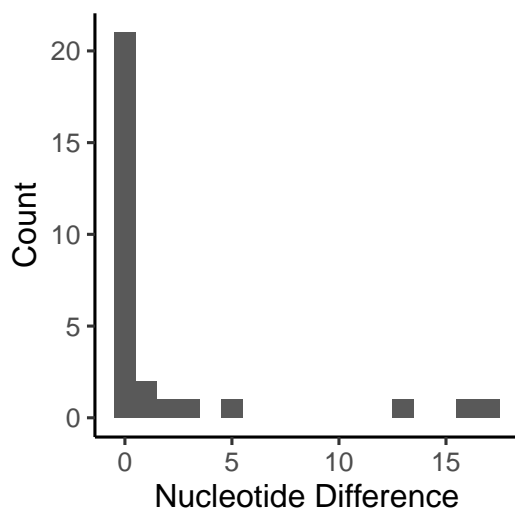
IGHV3-43*01

10 sequences assigned
9 (90%) exact matches, in which:
9 unique CDR3
3 unique J



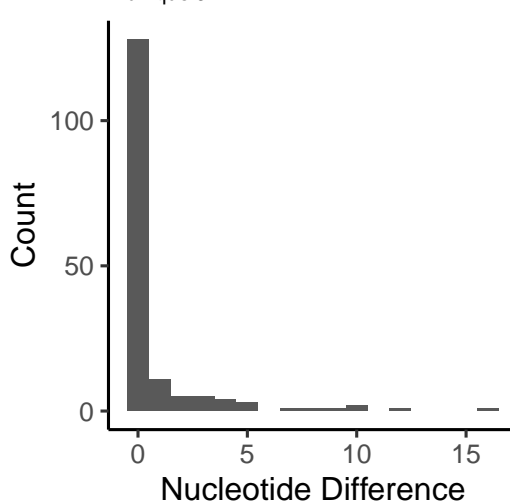
IGHV3-15*01

29 sequences assigned
21 (72.4%) exact matches, in which:
21 unique CDR3
5 unique J



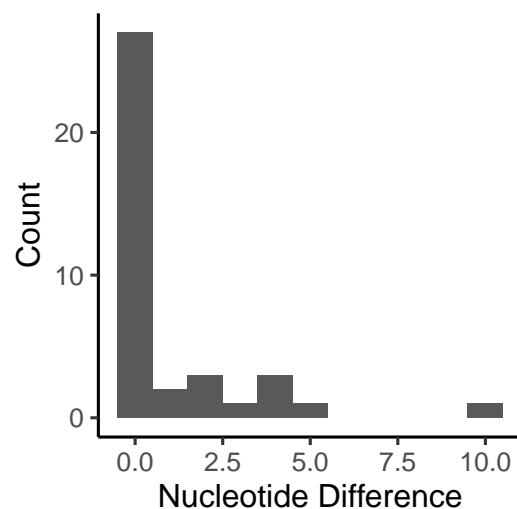
IGHV3-30-3*01

163 sequences assigned
128 (78.5%) exact matches, in which:
128 unique CDR3
7 unique J



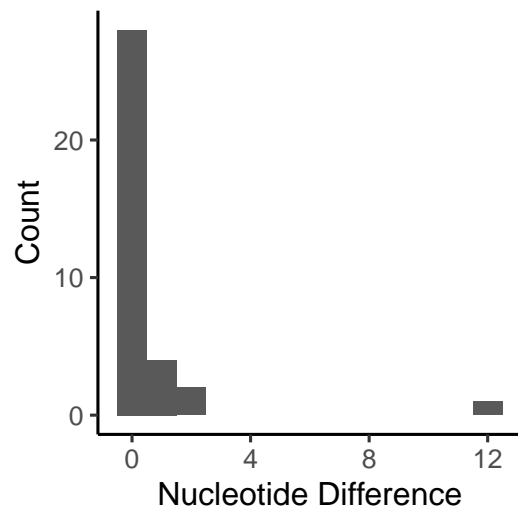
IGHV3-48*01

38 sequences assigned
27 (71.1%) exact matches, in which:
27 unique CDR3
4 unique J



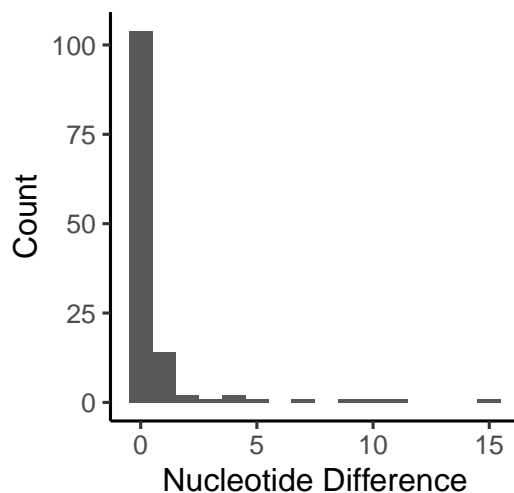
IGHV3-48*02

35 sequences assigned
28 (80%) exact matches, in which:
28 unique CDR3
6 unique J



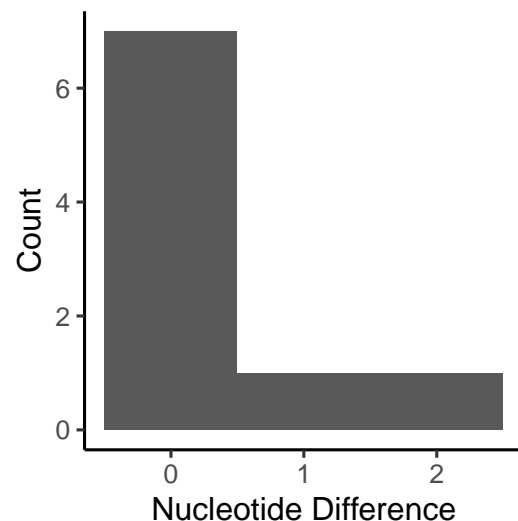
IGHV3-53*01

131 sequences assigned
104 (79.4%) exact matches, in which:
104 unique CDR3
6 unique J



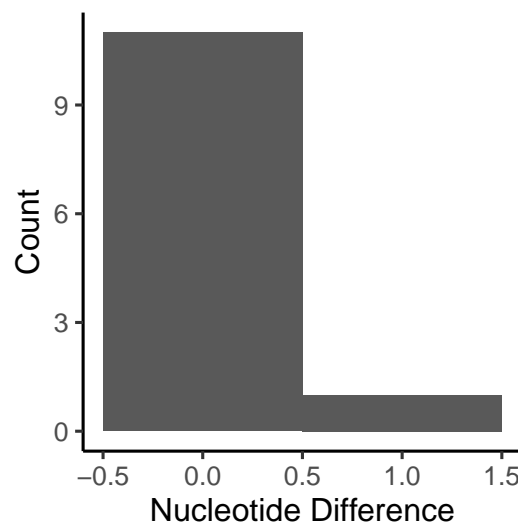
IGHV3-73*02

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



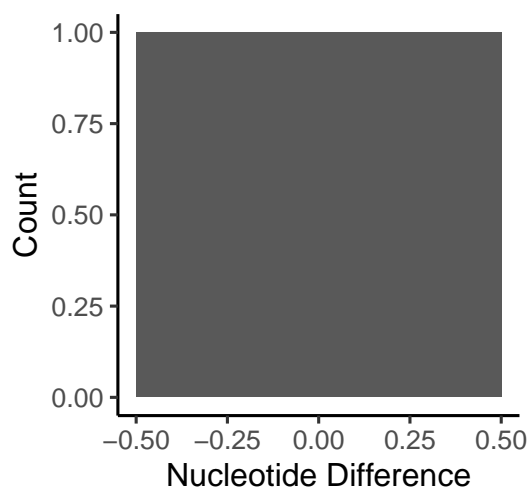
IGHV3-49*03

12 sequences assigned
11 (91.7%) exact matches, in which:
11 unique CDR3
4 unique J



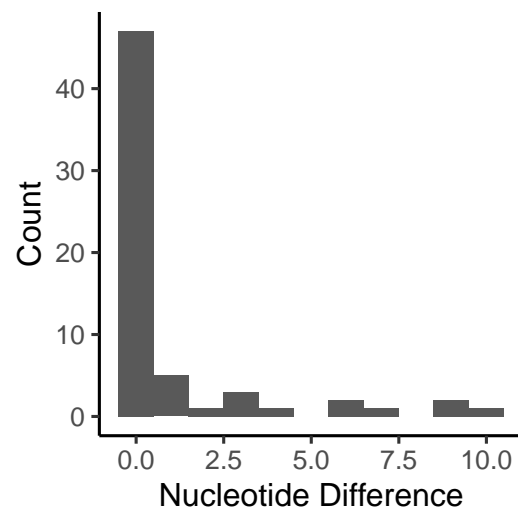
IGHV3-66*03

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



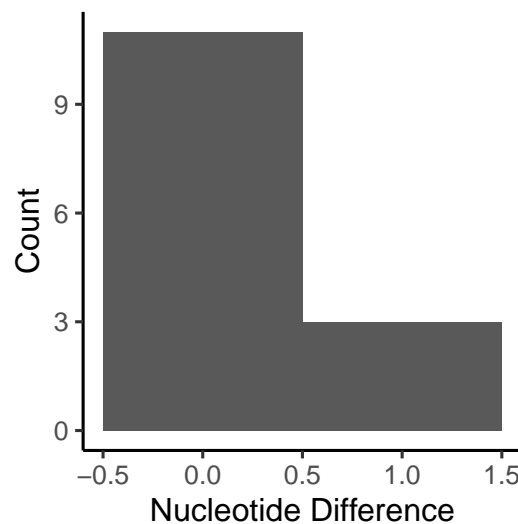
IGHV3-74*01

63 sequences assigned
47 (74.6%) exact matches, in which:
47 unique CDR3
6 unique J



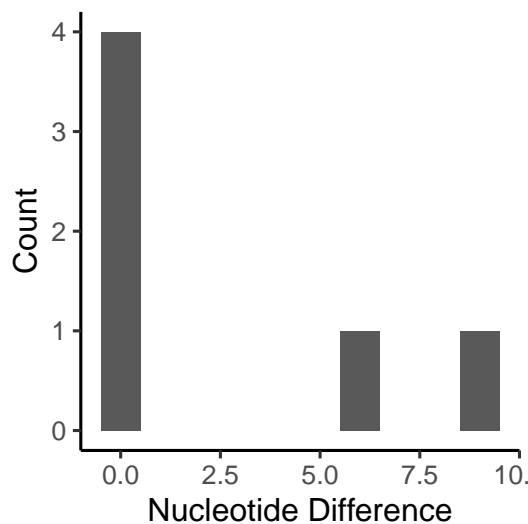
IGHV3-49*05

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



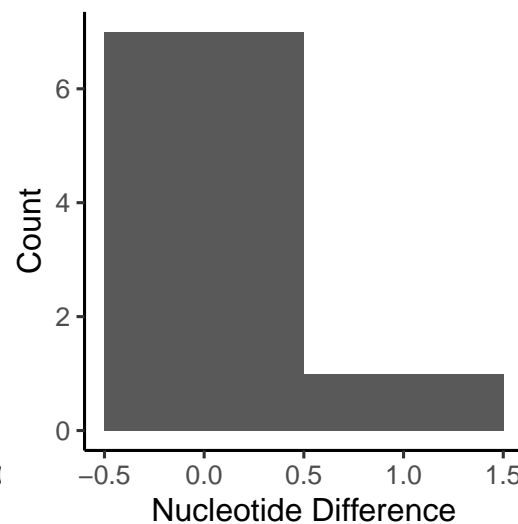
IGHV3-72*01

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



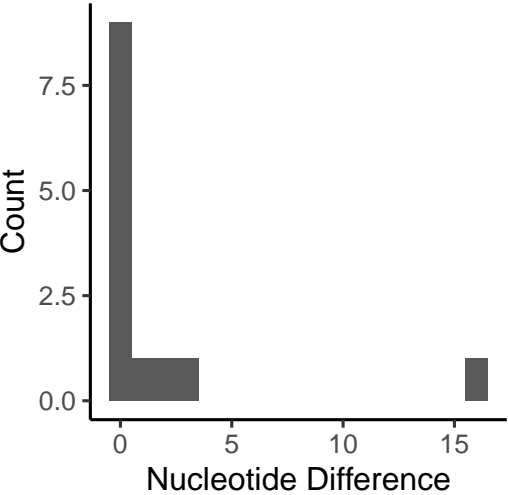
IGHV3-64D*06

8 sequences assigned
7 (87.5%) exact matches, in which:
7 unique CDR3
3 unique J



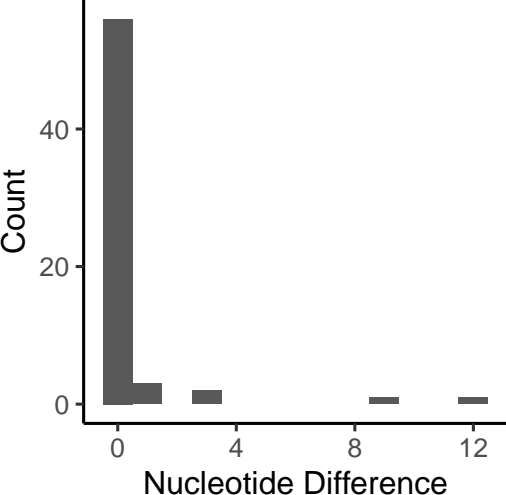
IGHV3–64D*09

13 sequences assigned
9 (69.2%) exact matches, in which:
9 unique CDR3
3 unique J



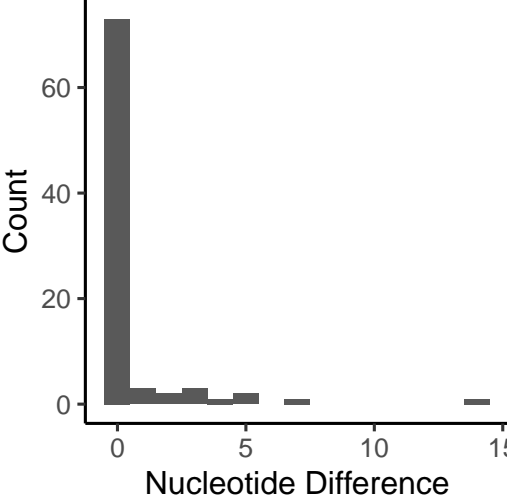
IGHV4–30–2*01

63 sequences assigned
56 (88.9%) exact matches, in which:
56 unique CDR3
7 unique J



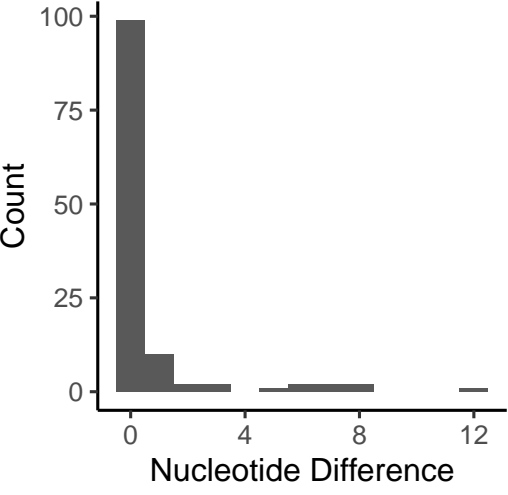
IGHV4–31*03

86 sequences assigned
73 (84.9%) exact matches, in which:
73 unique CDR3
6 unique J



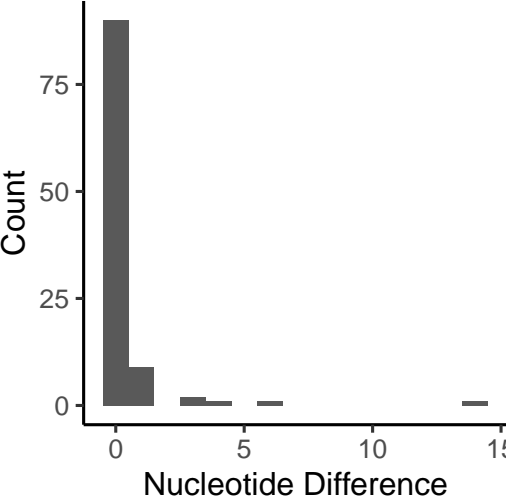
IGHV4–4*02

121 sequences assigned
99 (81.8%) exact matches, in which:
99 unique CDR3
6 unique J



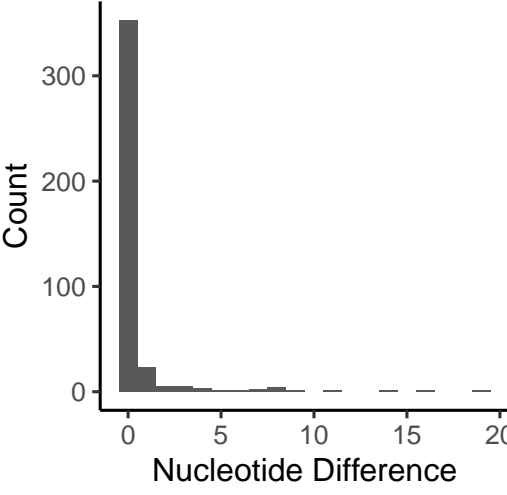
IGHV4–30–4*01

104 sequences assigned
90 (86.5%) exact matches, in which:
90 unique CDR3
7 unique J



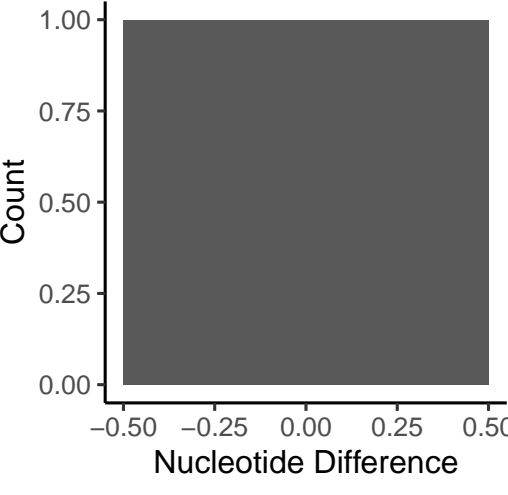
IGHV4–34*01

404 sequences assigned
353 (87.4%) exact matches, in which:
353 unique CDR3
7 unique J



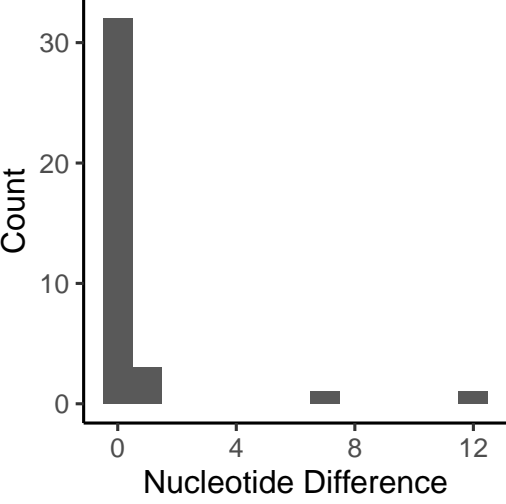
IGHV4–28*01

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



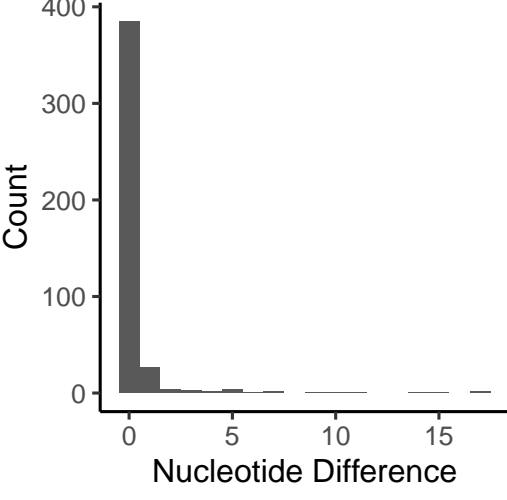
IGHV4–30–2*01_C285T

37 sequences assigned
32 (86.5%) exact matches, in which:
32 unique CDR3
5 unique J



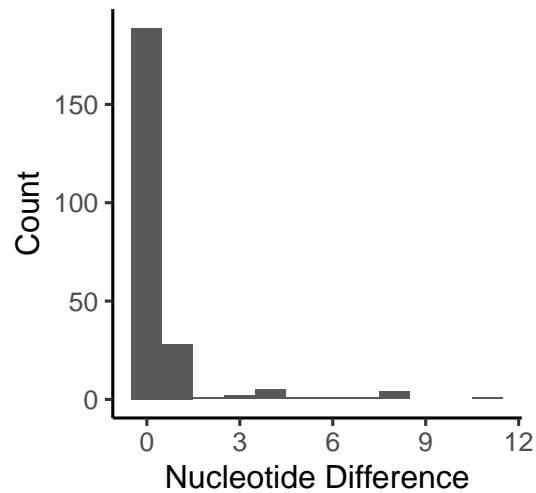
IGHV4–39*01

435 sequences assigned
385 (88.5%) exact matches, in which:
385 unique CDR3
7 unique J



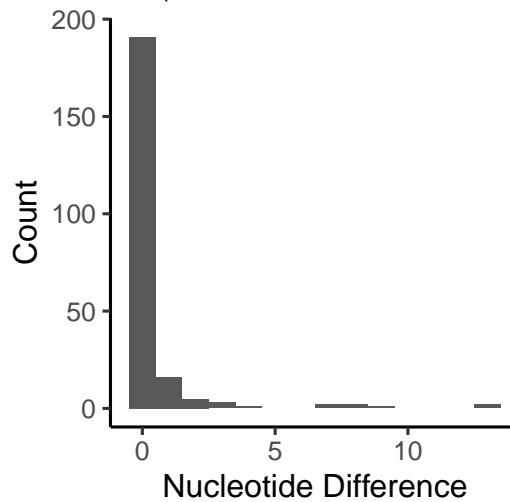
IGHV4–39*07

233 sequences assigned
189 (81.1%) exact matches, in which:
189 unique CDR3
7 unique J



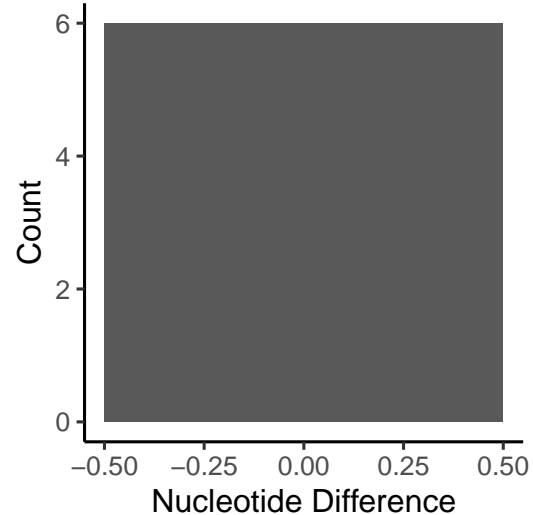
IGHV5–10–1*03

223 sequences assigned
191 (85.7%) exact matches, in which:
191 unique CDR3
7 unique J



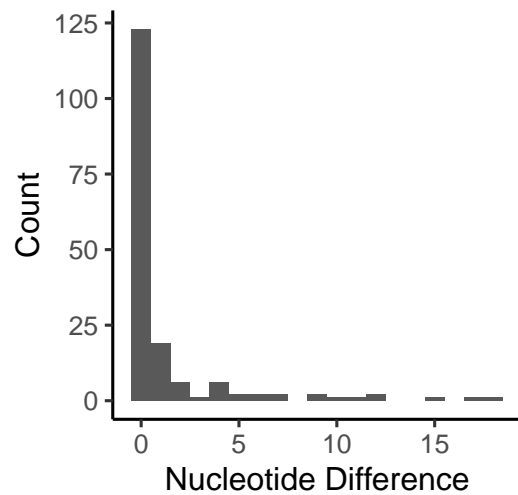
IGHV7–4–1*01

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



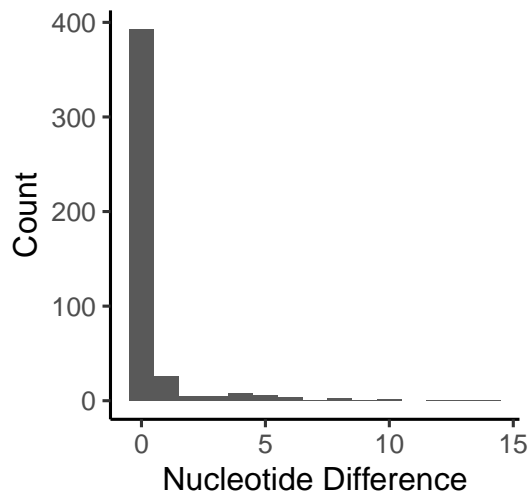
IGHV4–59*01

170 sequences assigned
123 (72.4%) exact matches, in which:
123 unique CDR3
7 unique J



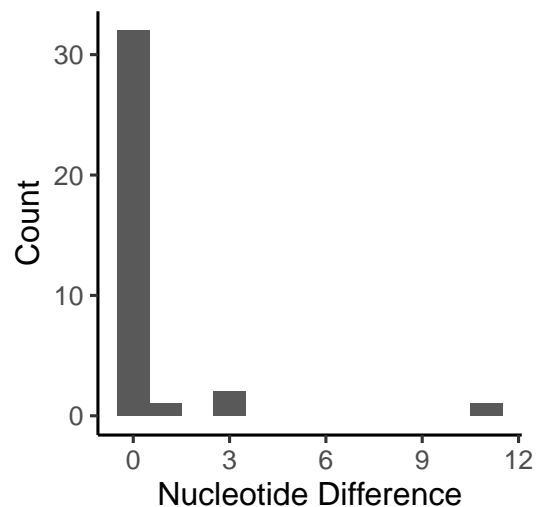
IGHV5–51*01

459 sequences assigned
393 (85.6%) exact matches, in which:
393 unique CDR3
7 unique J



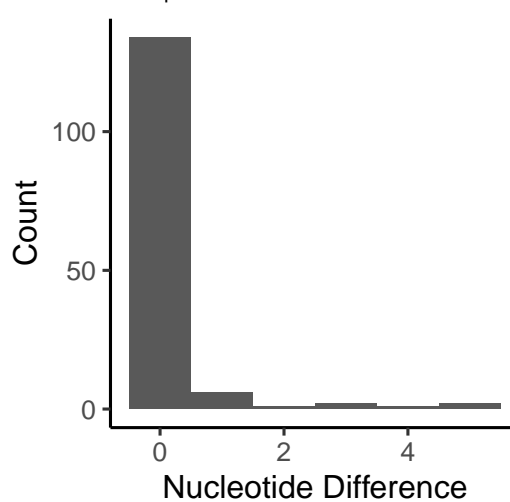
IGHV4–61*01

36 sequences assigned
32 (88.9%) exact matches, in which:
32 unique CDR3
6 unique J

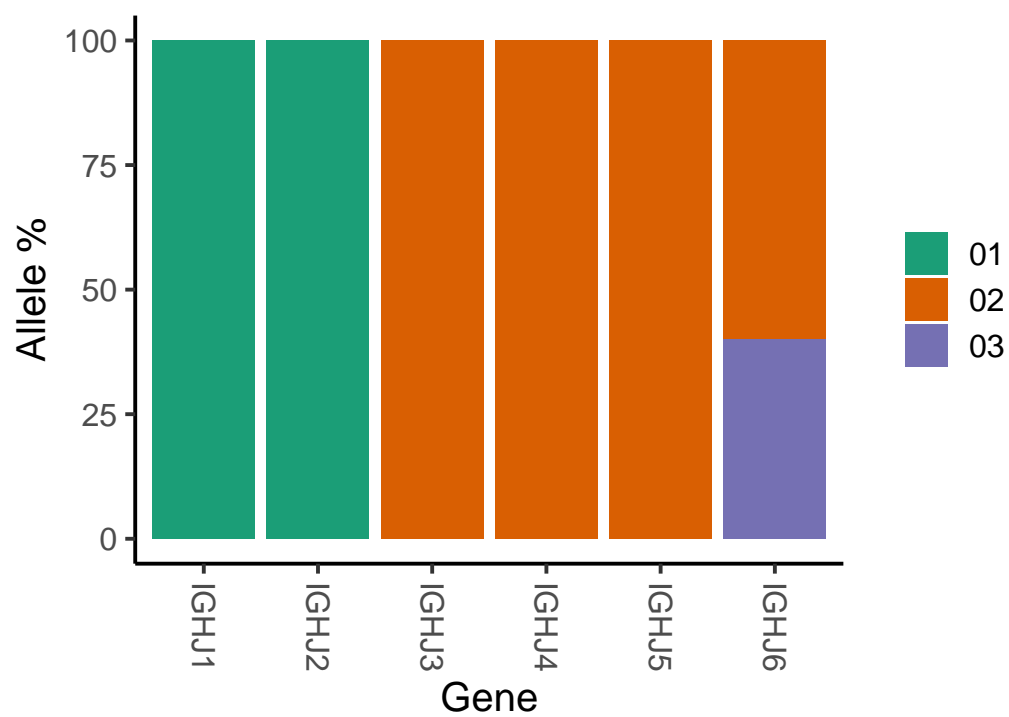


IGHV6–1*01

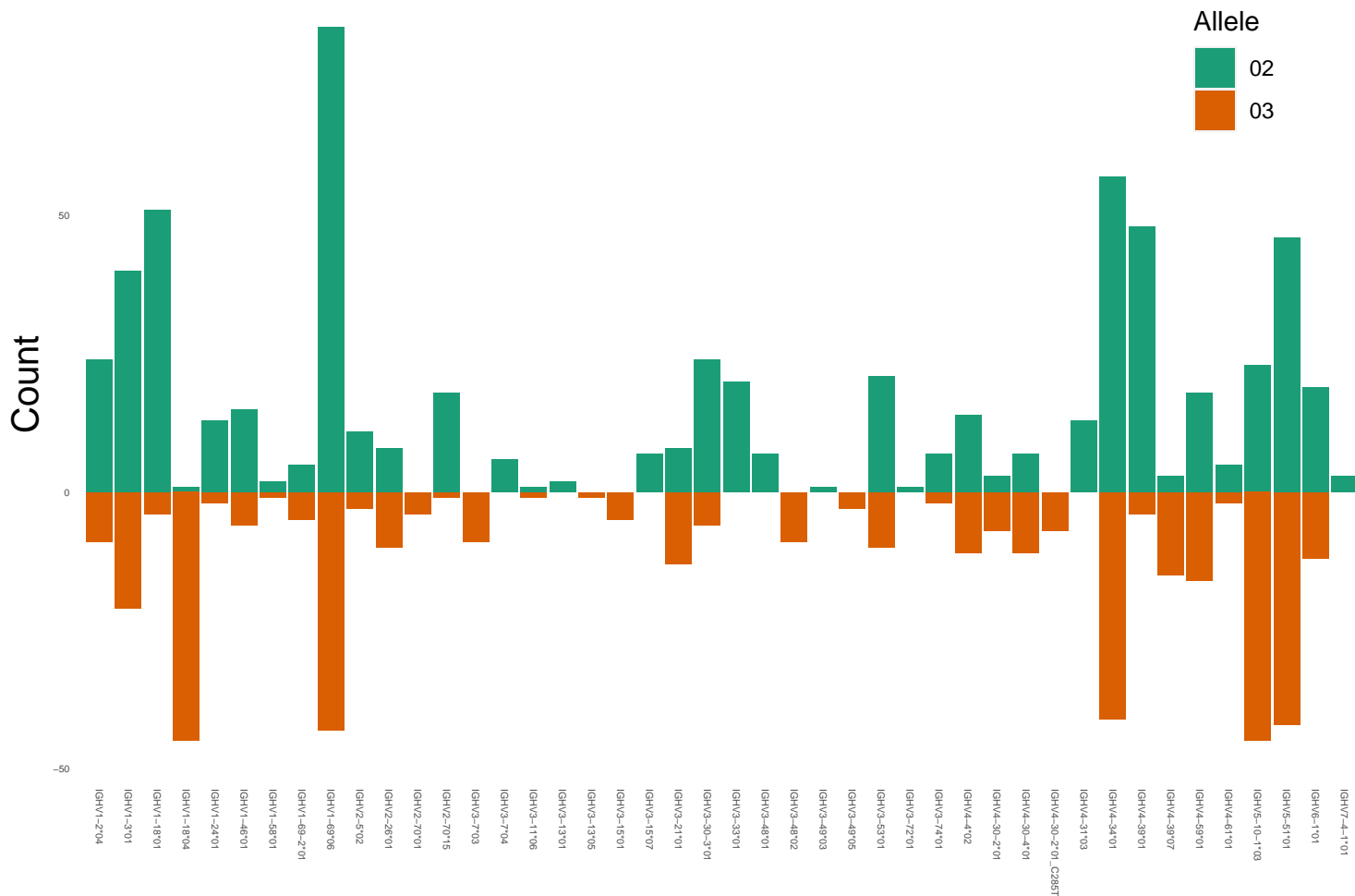
146 sequences assigned
134 (91.8%) exact matches, in which:
134 unique CDR3
6 unique J



Allele Usage



Sequence Count by IGHJ6 allele usage



Warning – no inferred sequences found.