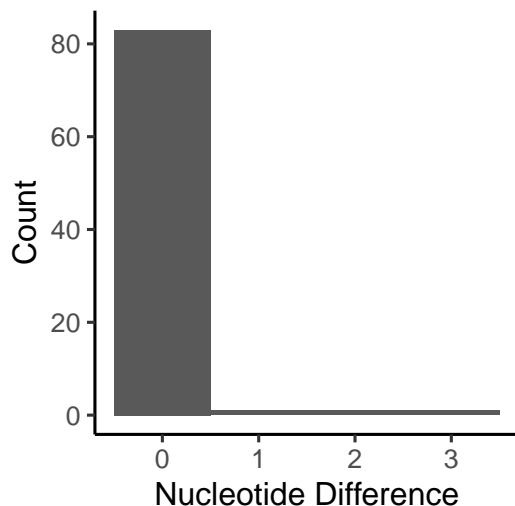


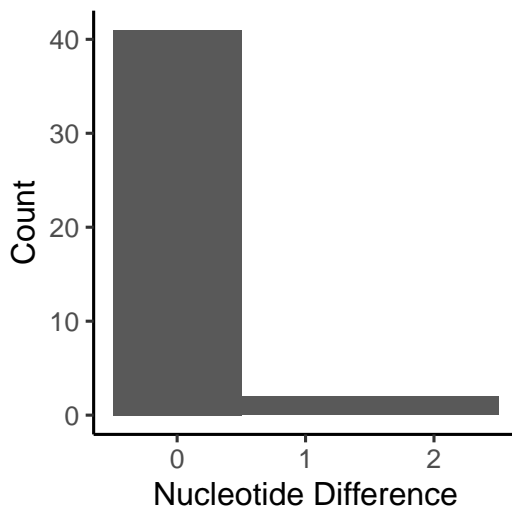
IGHV1-2*04

87 sequences assigned
83 (95.4%) exact matches, in which:
83 unique CDR3
7 unique J



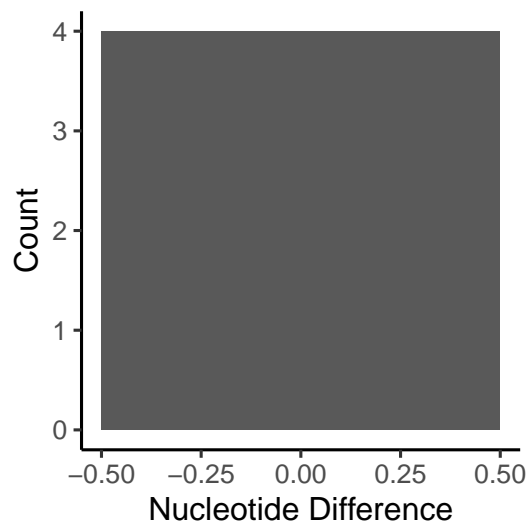
IGHV1-24*01

45 sequences assigned
41 (91.1%) exact matches, in which:
41 unique CDR3
5 unique J



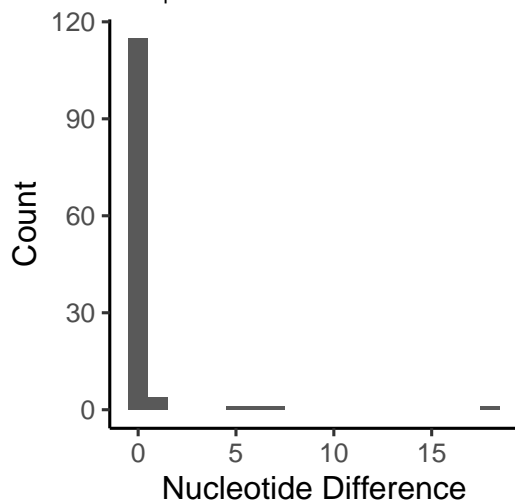
IGHV1-58*02

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



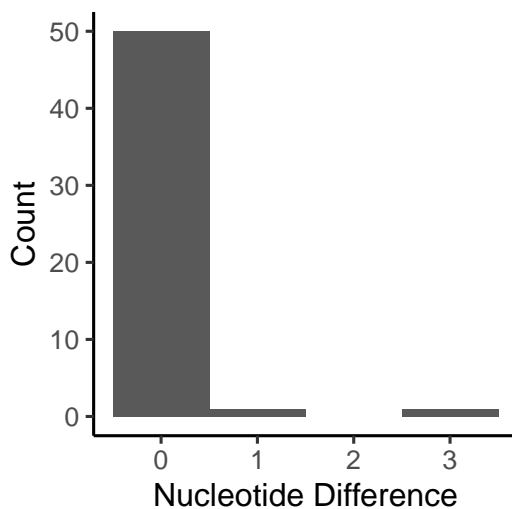
IGHV1-3*01

124 sequences assigned
115 (92.7%) exact matches, in which:
115 unique CDR3
7 unique J



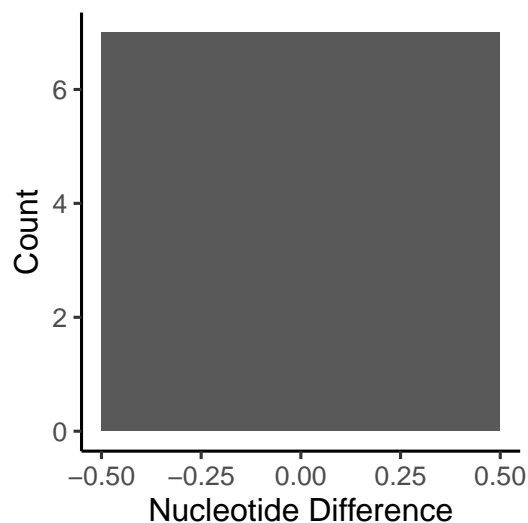
IGHV1-46*01

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



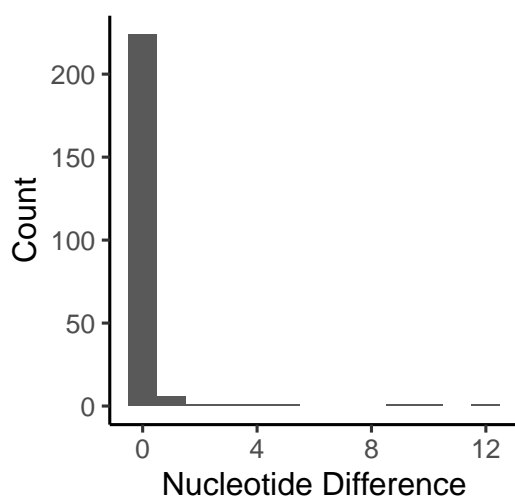
IGHV1-69-2*01

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



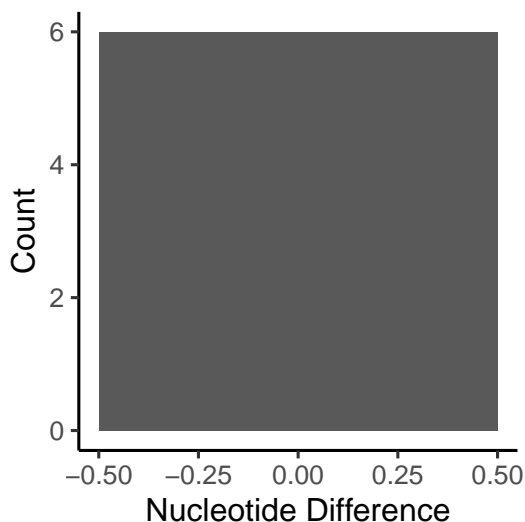
IGHV1-18*04

238 sequences assigned
224 (94.1%) exact matches, in which:
224 unique CDR3
7 unique J



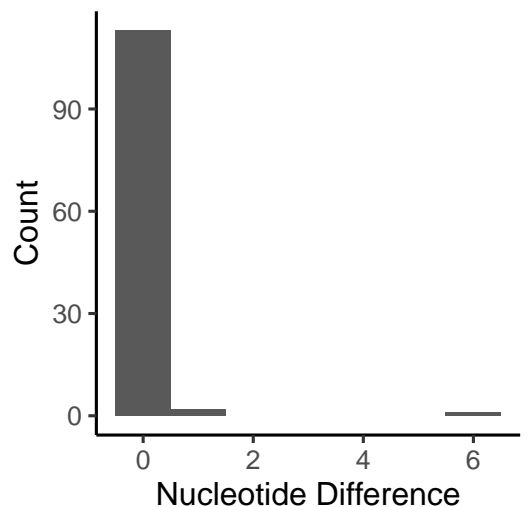
IGHV1-58*01

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



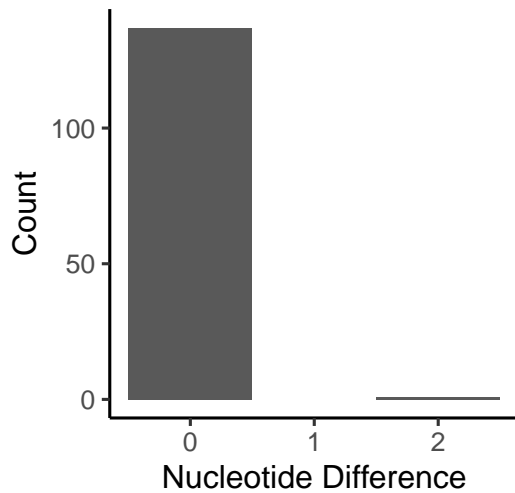
IGHV1-69*06

116 sequences assigned
113 (97.4%) exact matches, in which:
113 unique CDR3
7 unique J



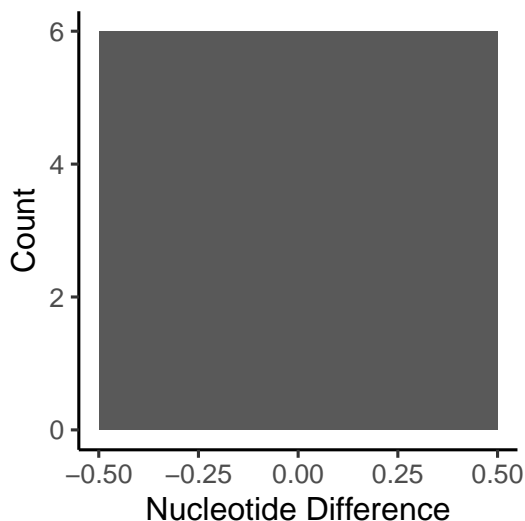
IGHV1–69*04_A163G

138 sequences assigned
137 (99.3%) exact matches, in which:
137 unique CDR3
7 unique J



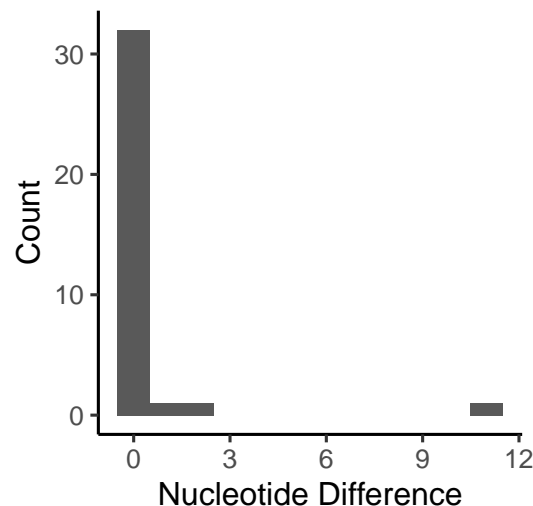
IGHV2–70*01

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



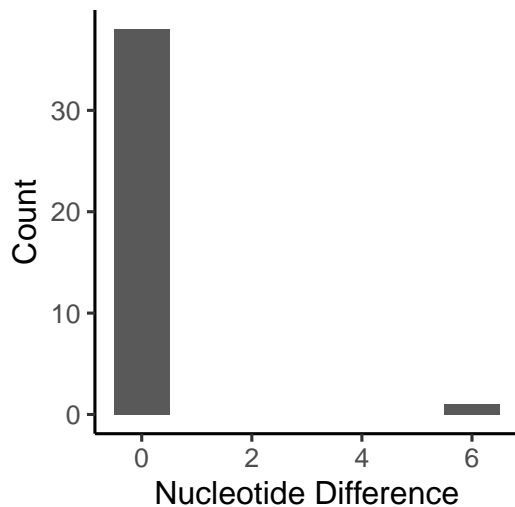
IGHV3–7*05

35 sequences assigned
32 (91.4%) exact matches, in which:
32 unique CDR3
4 unique J



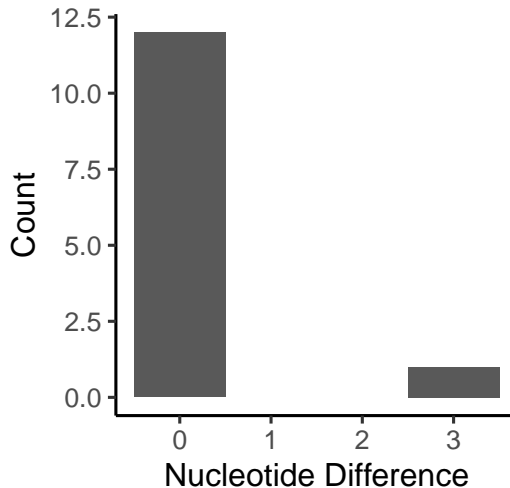
IGHV2–5*02

39 sequences assigned
38 (97.4%) exact matches, in which:
38 unique CDR3
5 unique J



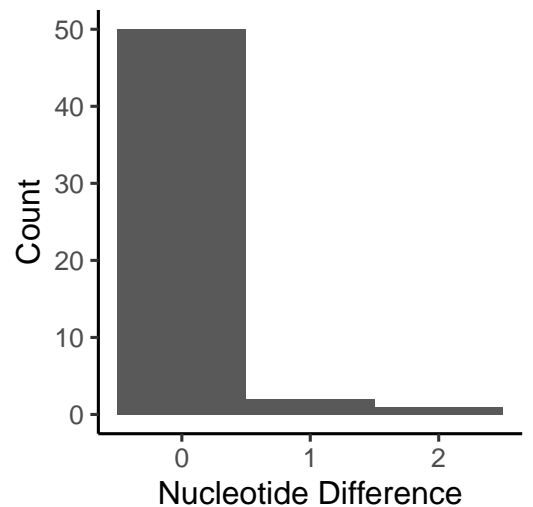
IGHV2–70*15

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



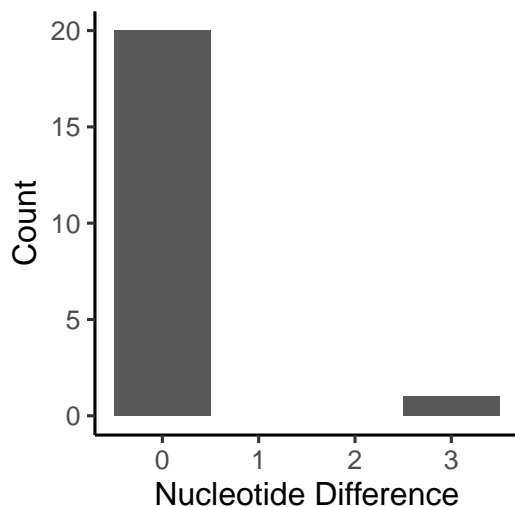
IGHV3–11*05

53 sequences assigned
50 (94.3%) exact matches, in which:
50 unique CDR3
5 unique J



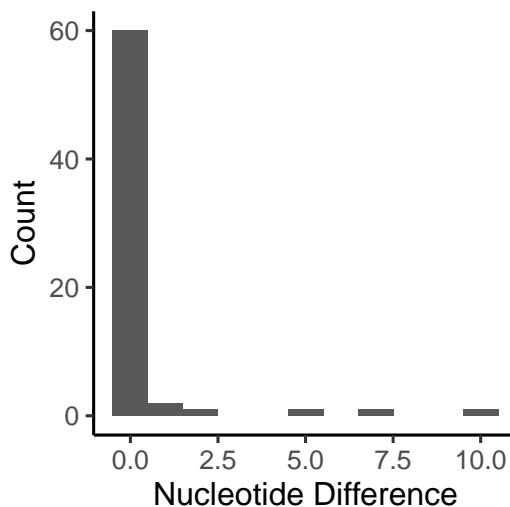
IGHV2–26*01

21 sequences assigned
20 (95.2%) exact matches, in which:
20 unique CDR3
5 unique J



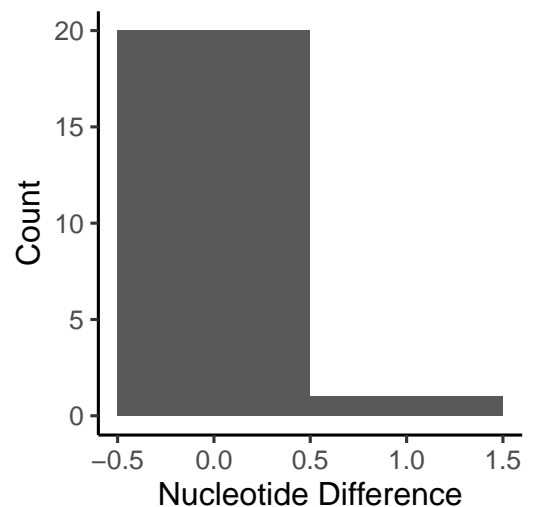
IGHV3–7*03

66 sequences assigned
60 (90.9%) exact matches, in which:
60 unique CDR3
5 unique J



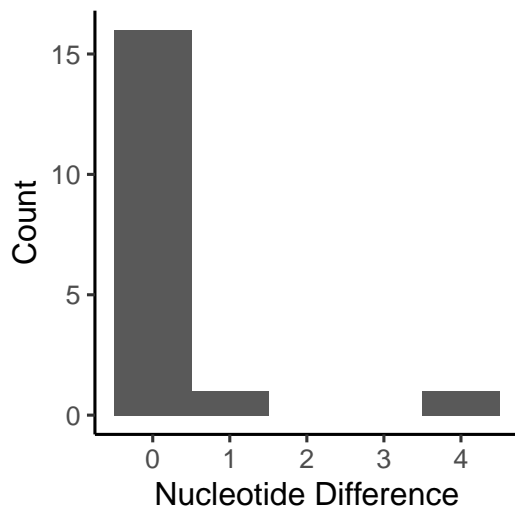
IGHV3–11*06

21 sequences assigned
20 (95.2%) exact matches, in which:
20 unique CDR3
5 unique J



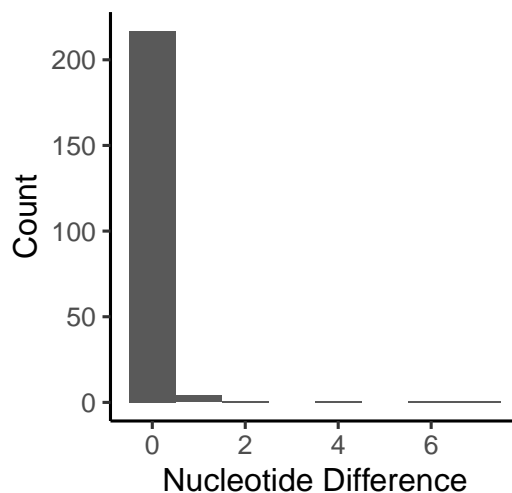
IGHV3-13*04

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



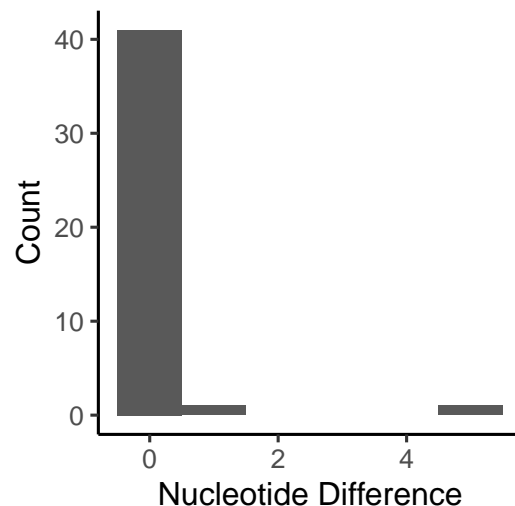
IGHV3-21*01

228 sequences assigned
217 (95.2%) exact matches, in which:
217 unique CDR3
6 unique J



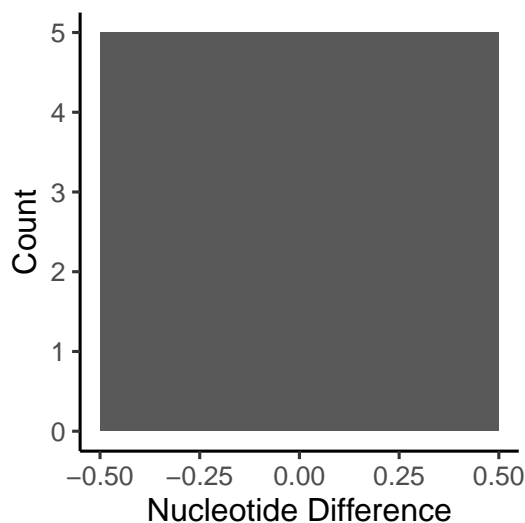
IGHV3-48*02

43 sequences assigned
41 (95.3%) exact matches, in which:
41 unique CDR3
4 unique J



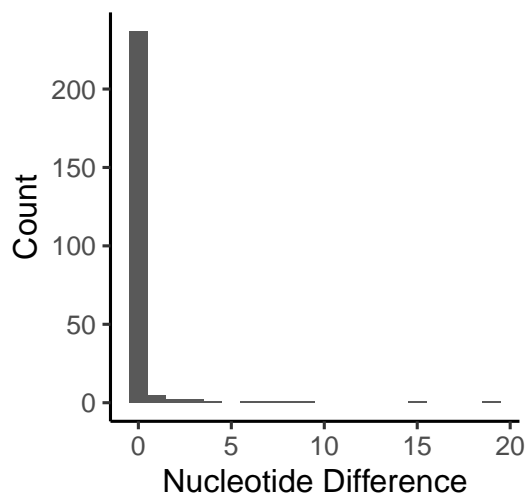
IGHV3-13*05

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



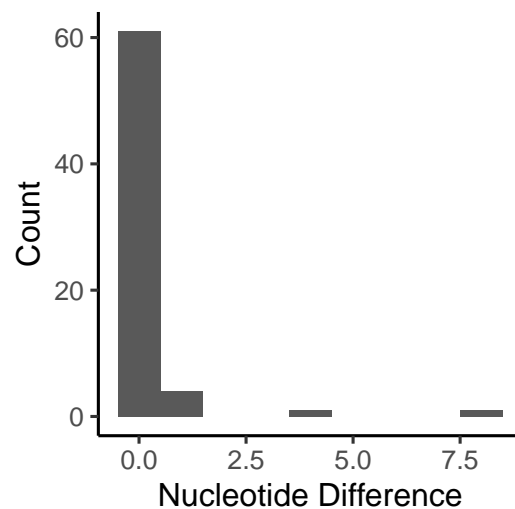
IGHV3-30-3*01

254 sequences assigned
237 (93.3%) exact matches, in which:
237 unique CDR3
7 unique J



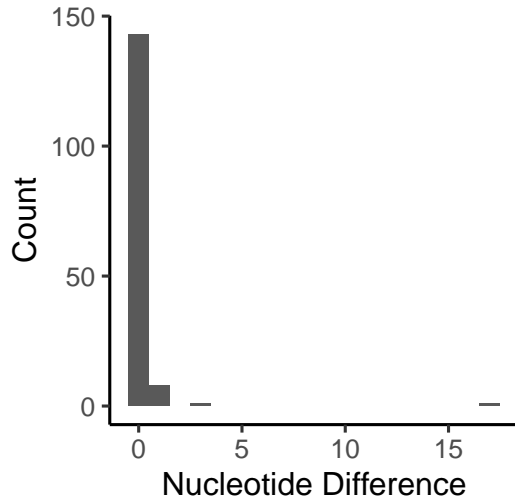
IGHV3-48*04

67 sequences assigned
61 (91%) exact matches, in which:
61 unique CDR3
7 unique J



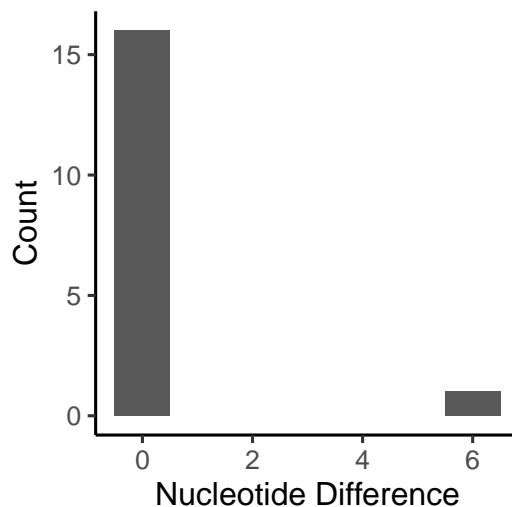
IGHV3-15*01

154 sequences assigned
143 (92.9%) exact matches, in which:
143 unique CDR3
6 unique J



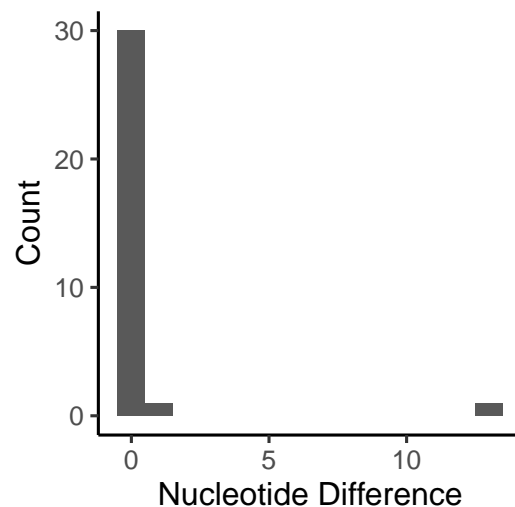
IGHV3-43*01

17 sequences assigned
16 (94.1%) exact matches, in which:
16 unique CDR3
5 unique J



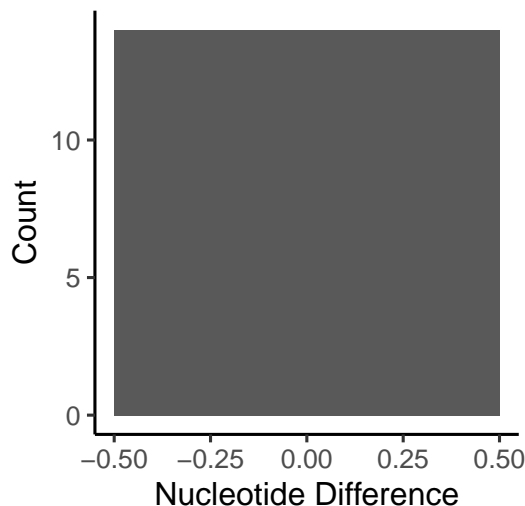
IGHV3-49*03

32 sequences assigned
30 (93.8%) exact matches, in which:
30 unique CDR3
4 unique J



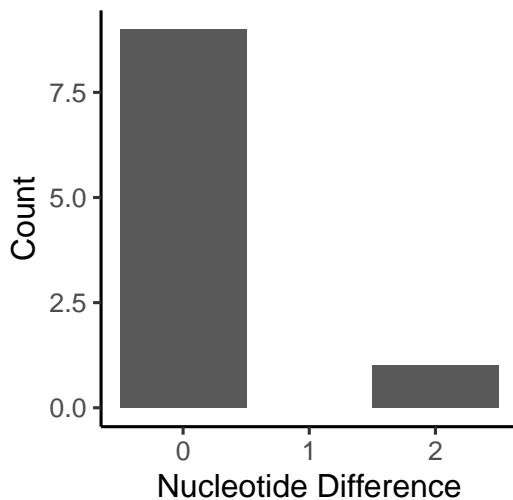
IGHV3-49*05

14 sequences assigned
14 (100%) exact matches, in which:
14 unique CDR3
4 unique J



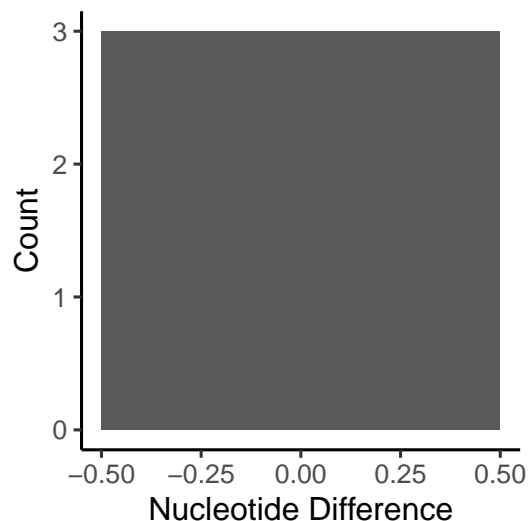
IGHV3-64*01

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



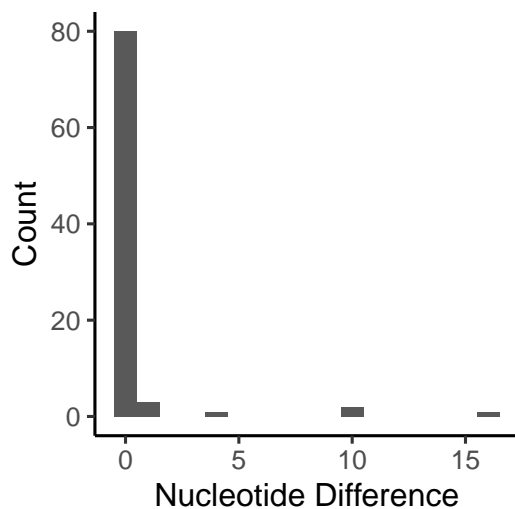
IGHV3-72*01

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



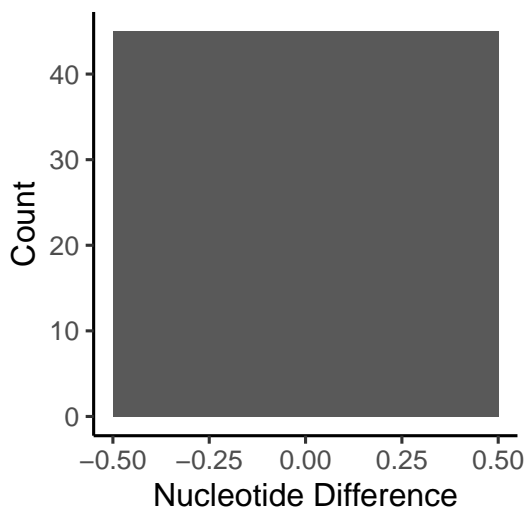
IGHV3-53*01

87 sequences assigned
80 (92%) exact matches, in which:
80 unique CDR3
6 unique J



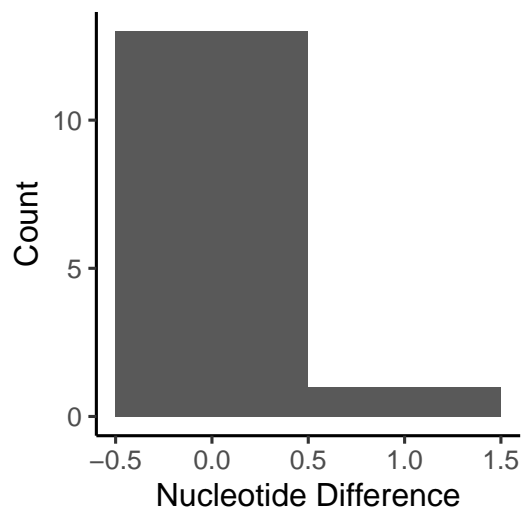
IGHV3-66*01

45 sequences assigned
45 (100%) exact matches, in which:
45 unique CDR3
5 unique J



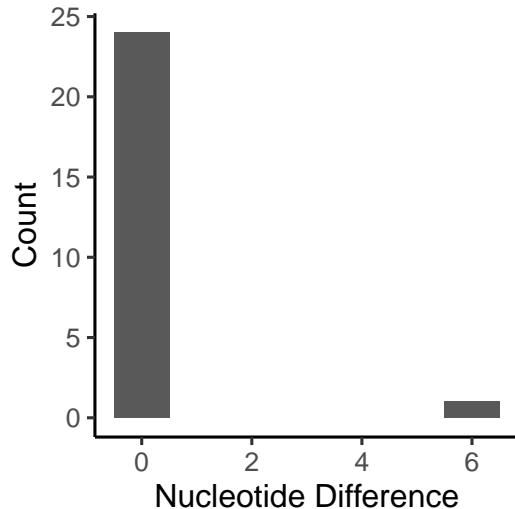
IGHV3-73*01

14 sequences assigned
13 (92.9%) exact matches, in which:
13 unique CDR3
4 unique J



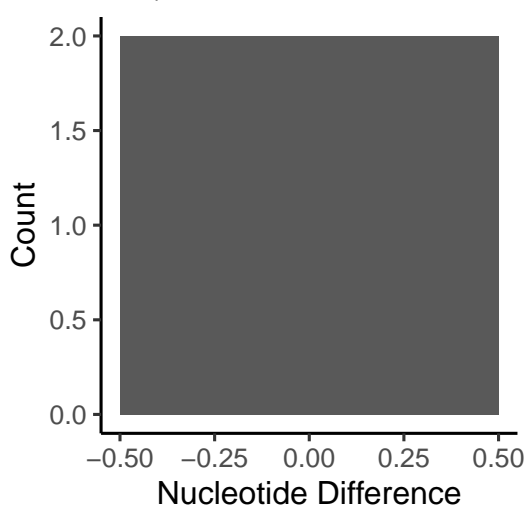
IGHV3-53*04

25 sequences assigned
24 (96%) exact matches, in which:
24 unique CDR3
4 unique J



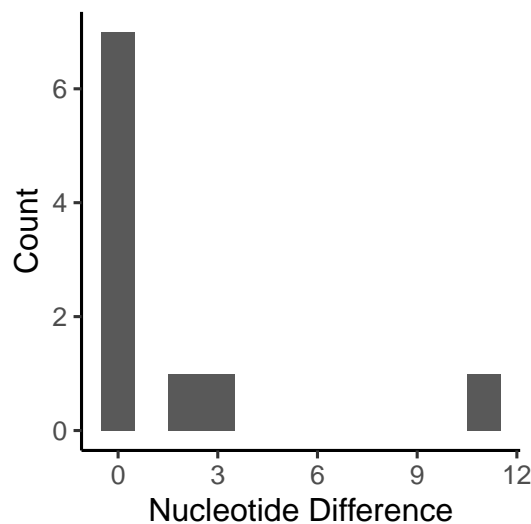
IGHV3-69-1*01

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



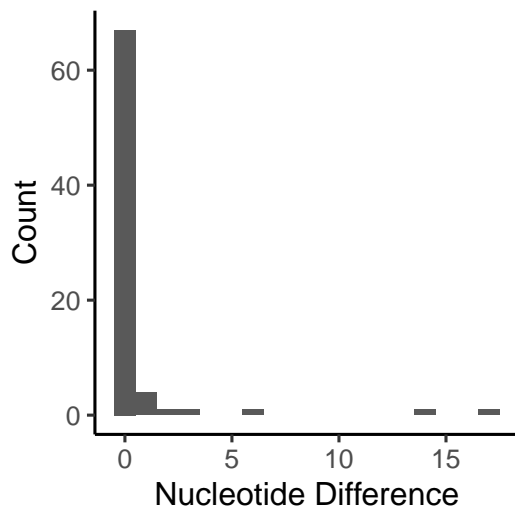
IGHV3-73*02

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



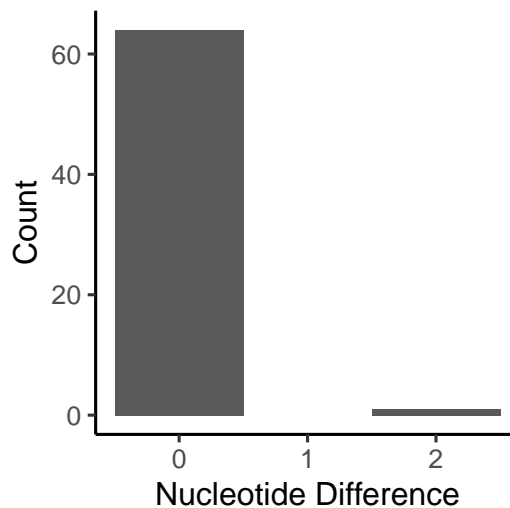
IGHV3-74*01

76 sequences assigned
67 (88.2%) exact matches, in which:
67 unique CDR3
7 unique J



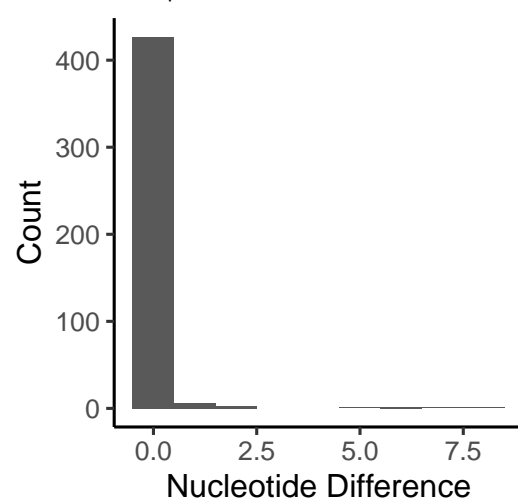
IGHV4-4*02

65 sequences assigned
64 (98.5%) exact matches, in which:
64 unique CDR3
7 unique J



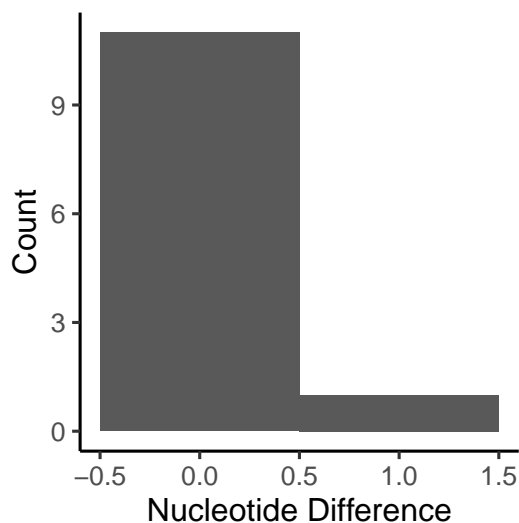
IGHV4-34*01

441 sequences assigned
427 (96.8%) exact matches, in which:
427 unique CDR3
7 unique J



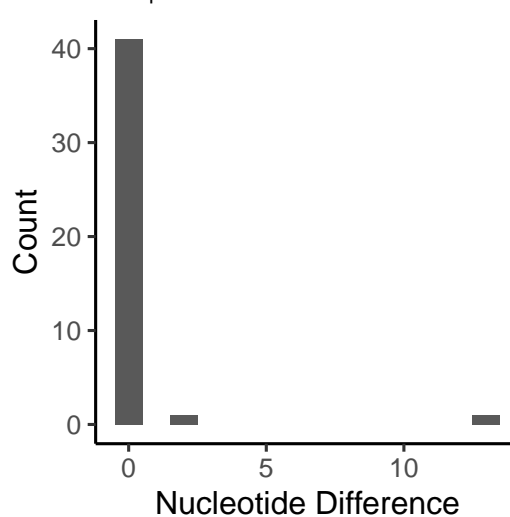
IGHV3-43D*03

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



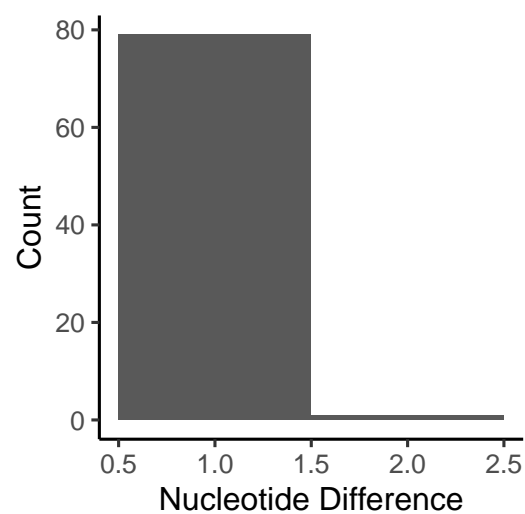
IGHV4-30-4*01

43 sequences assigned
41 (95.3%) exact matches, in which:
41 unique CDR3
6 unique J



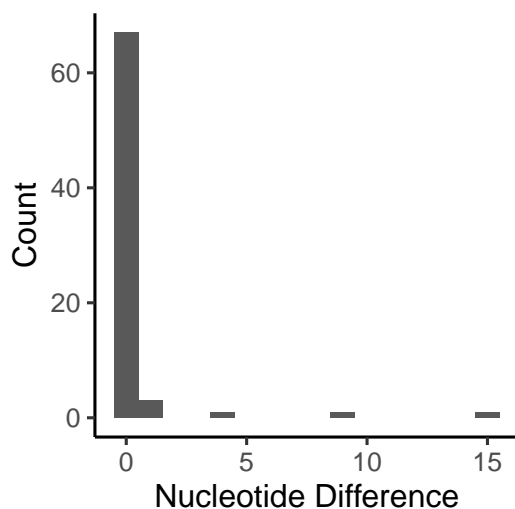
IGHV4-38-2*02

80 sequences assigned
No exact matches.



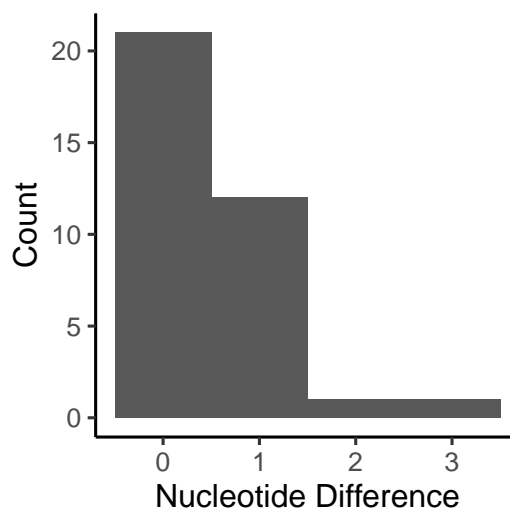
IGHV3-64D*09

73 sequences assigned
67 (91.8%) exact matches, in which:
67 unique CDR3
6 unique J



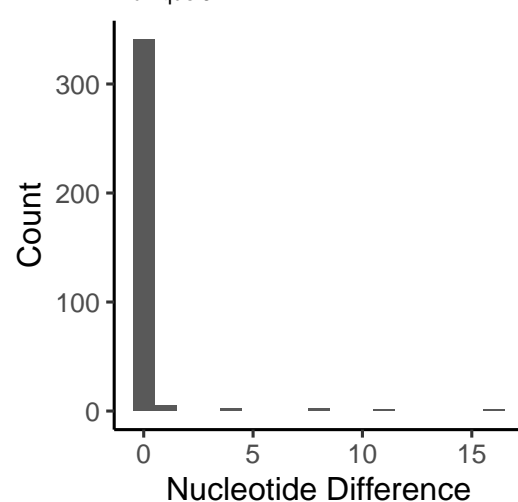
IGHV4-30-2*01

35 sequences assigned
21 (60%) exact matches, in which:
21 unique CDR3
7 unique J



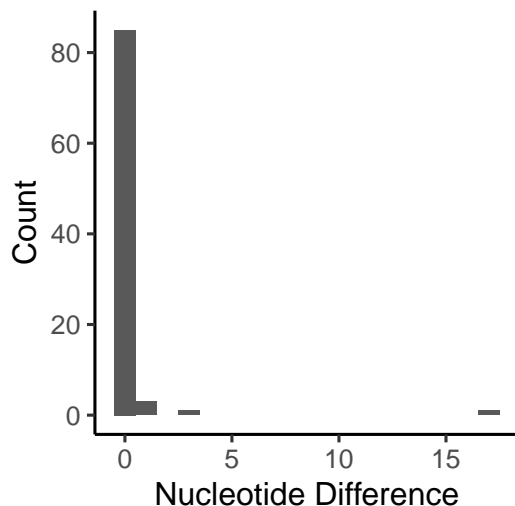
IGHV4-39*07

353 sequences assigned
341 (96.6%) exact matches, in which:
341 unique CDR3
7 unique J



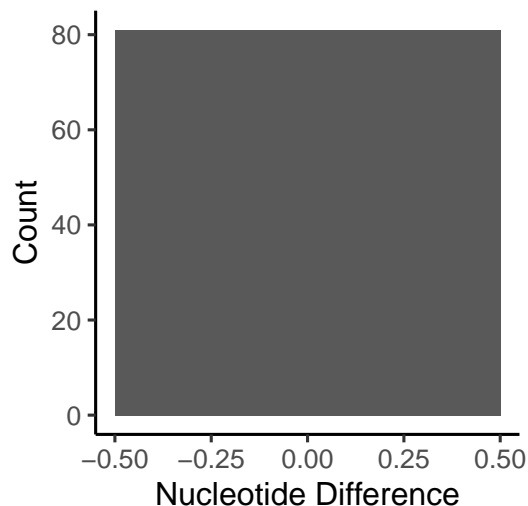
IGHV4–59*01

90 sequences assigned
85 (94.4%) exact matches, in which:
85 unique CDR3
7 unique J



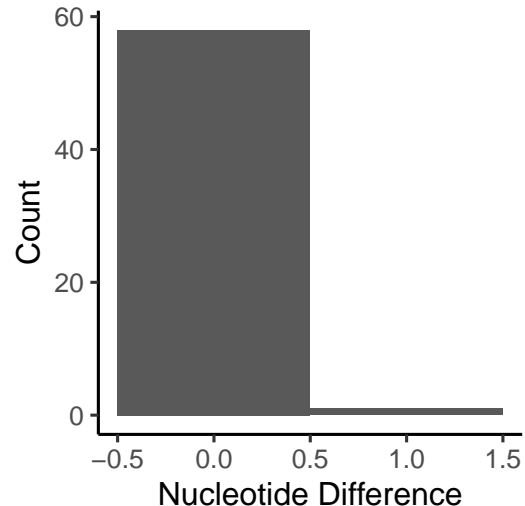
IGHV5–10–1*01

81 sequences assigned
81 (100%) exact matches, in which:
81 unique CDR3
5 unique J



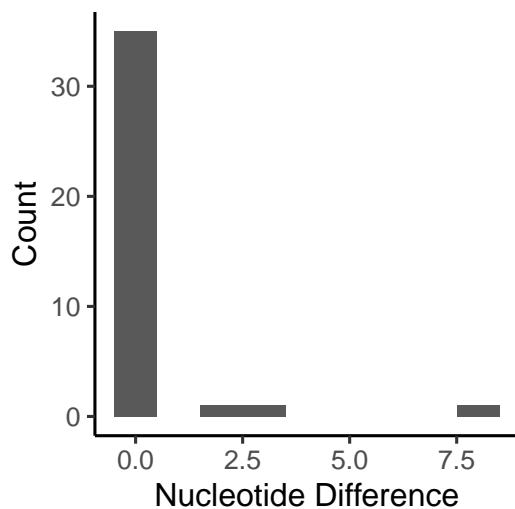
IGHV6–1*01

59 sequences assigned
58 (98.3%) exact matches, in which:
58 unique CDR3
5 unique J



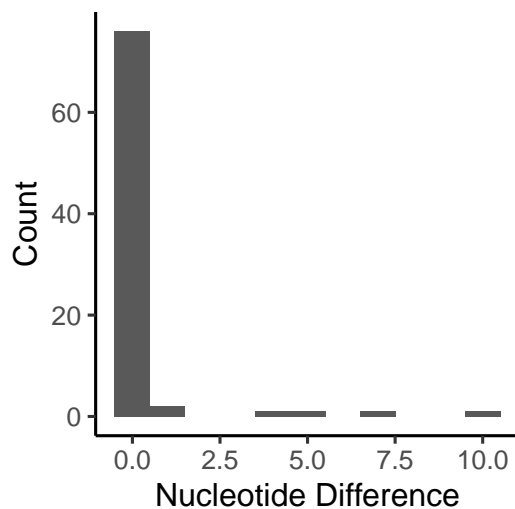
IGHV4–59*08

38 sequences assigned
35 (92.1%) exact matches, in which:
35 unique CDR3
5 unique J



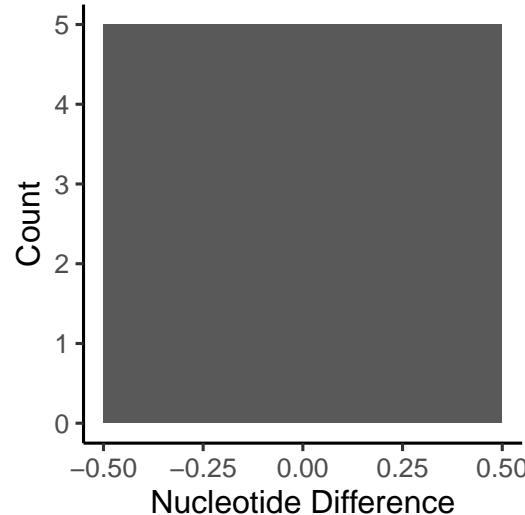
IGHV5–10–1*03

82 sequences assigned
76 (92.7%) exact matches, in which:
76 unique CDR3
6 unique J



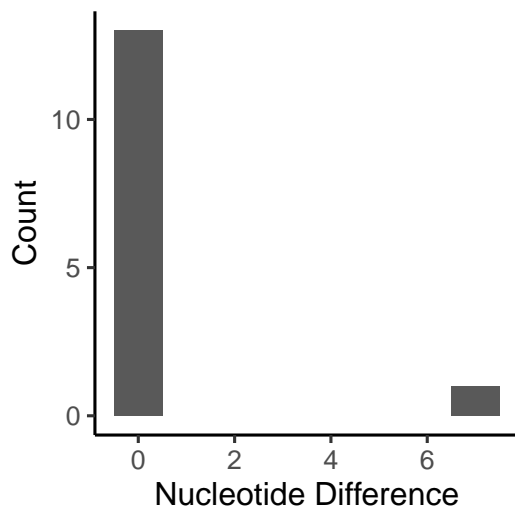
IGHV7–4–1*01

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



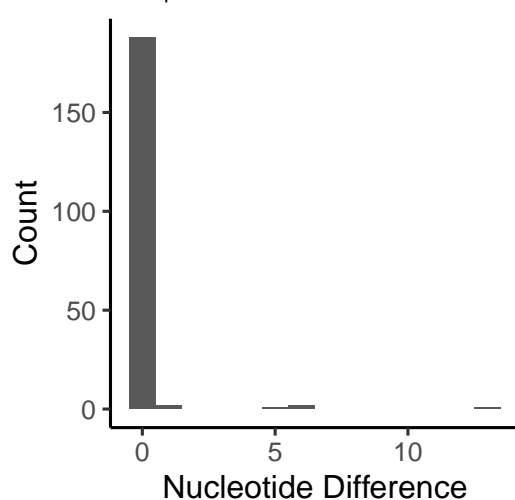
IGHV4–61*01

14 sequences assigned
13 (92.9%) exact matches, in which:
13 unique CDR3
4 unique J

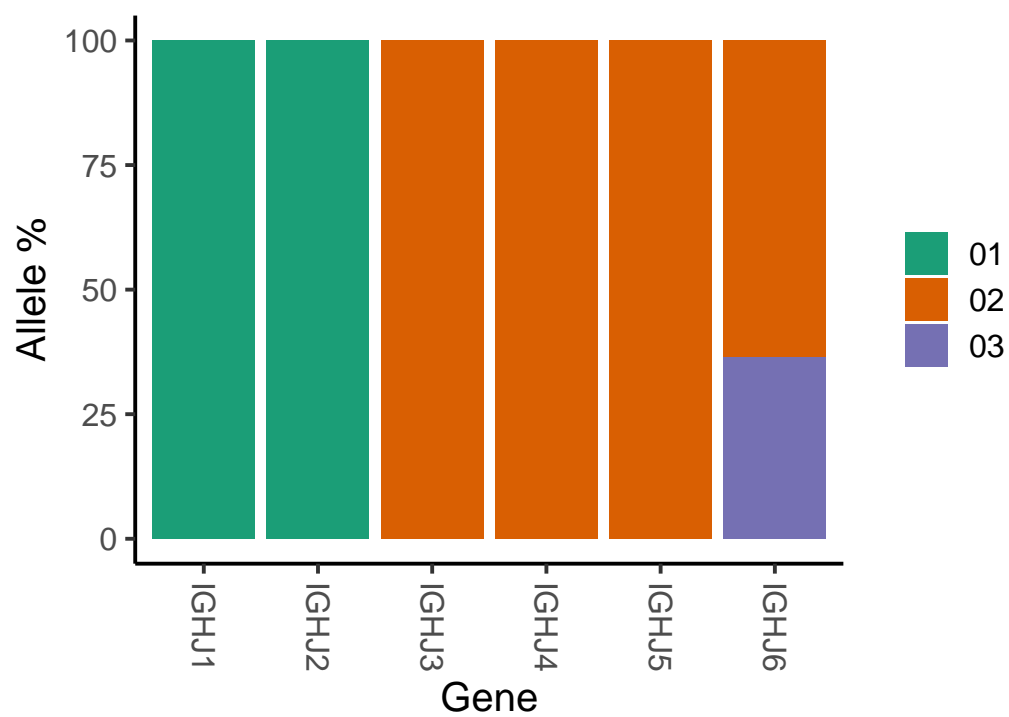


IGHV5–51*01

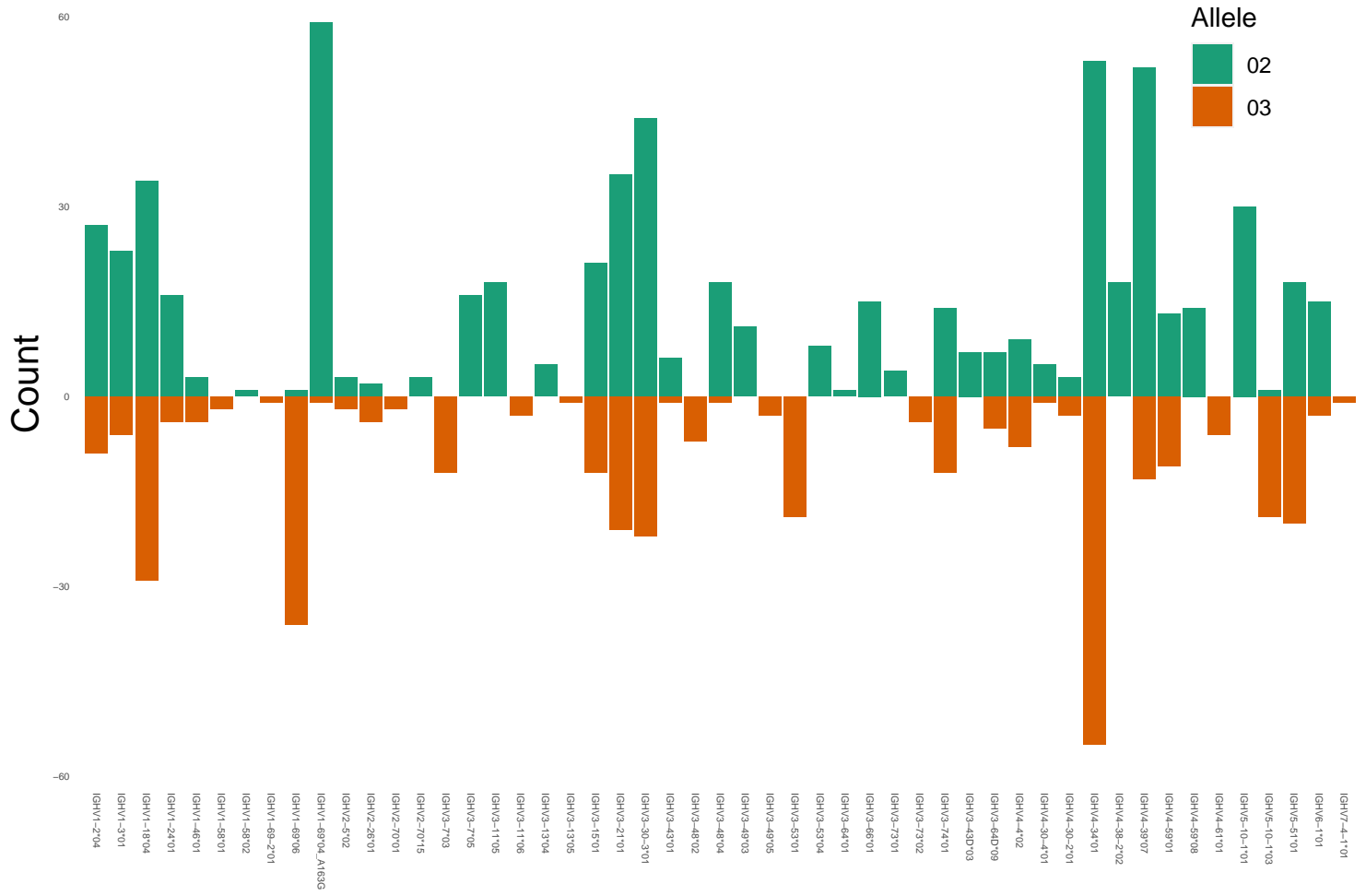
194 sequences assigned
188 (96.9%) exact matches, in which:
188 unique CDR3
7 unique J



Allele Usage



Sequence Count byIGHJ6 allele usage



Warning – no inferred sequences found.