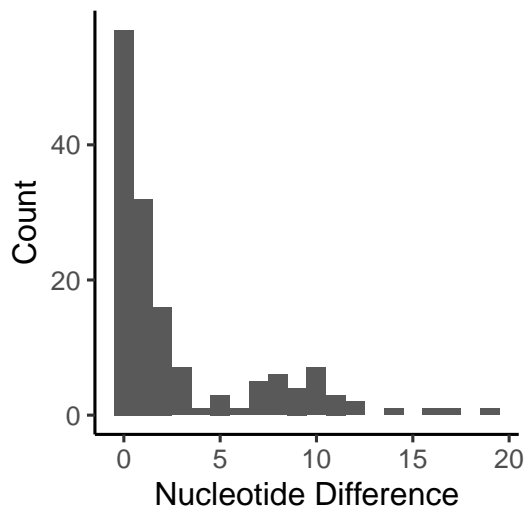


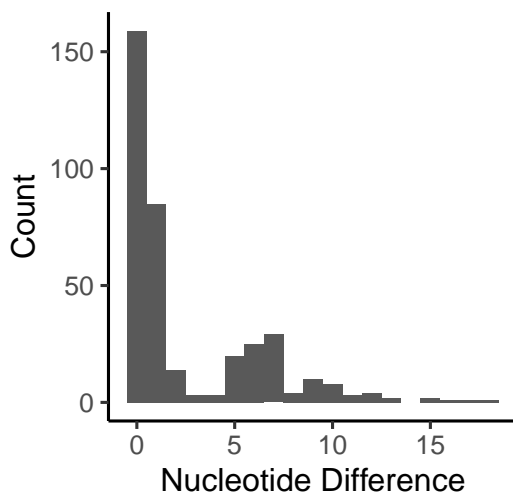
IGHV1-2*04

152 sequences assigned
57 (37.5%) exact matches, in which:
51 unique CDR3
7 unique J



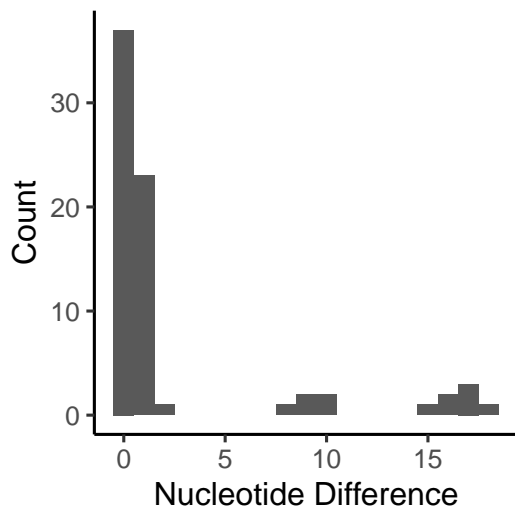
IGHV1-8*01

397 sequences assigned
159 (40.1%) exact matches, in which:
139 unique CDR3
7 unique J



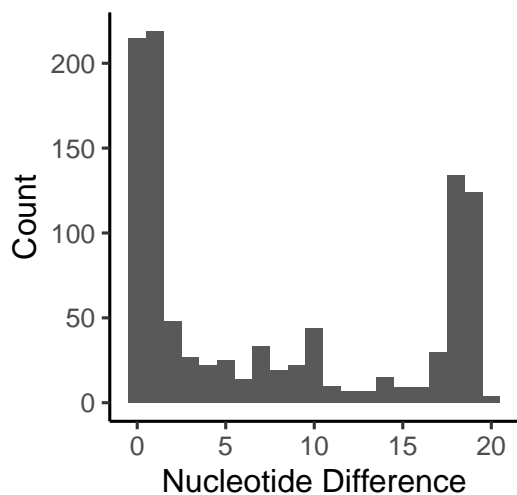
IGHV1-24*01

79 sequences assigned
37 (46.8%) exact matches, in which:
33 unique CDR3
4 unique J



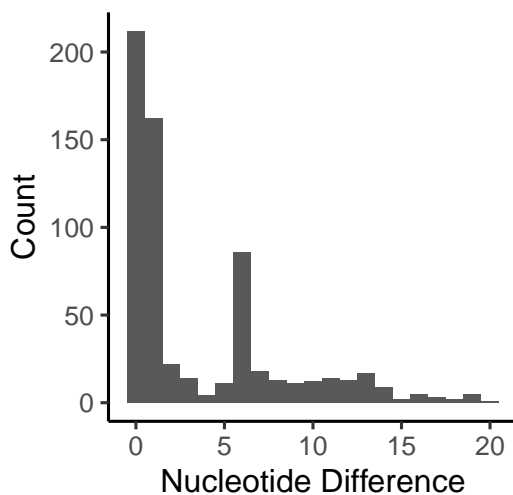
IGHV1-2*06

1051 sequences assigned
215 (20.5%) exact matches, in which:
176 unique CDR3
7 unique J



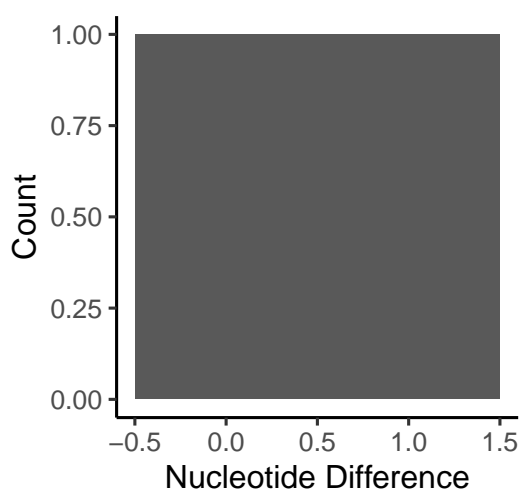
IGHV1-18*01

1082 sequences assigned
212 (19.6%) exact matches, in which:
177 unique CDR3
7 unique J



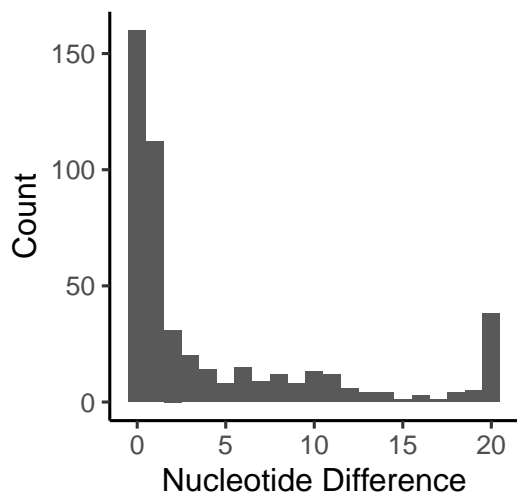
IGHV1-45*02

2 sequences assigned
1 (50%) exact matches, in which:
1 unique CDR3
0 unique J



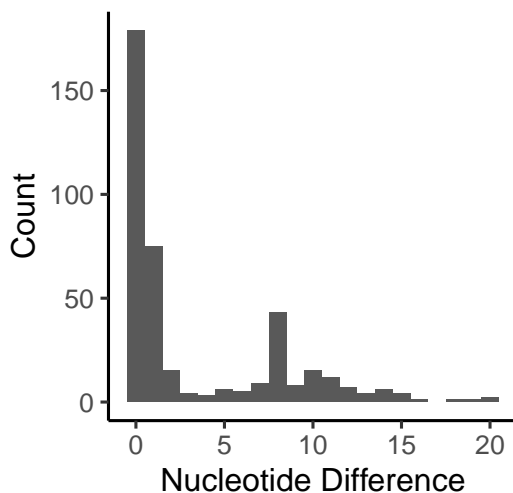
IGHV1-3*01_05

1082 sequences assigned
160 (14.8%) exact matches, in which:
127 unique CDR3
7 unique J



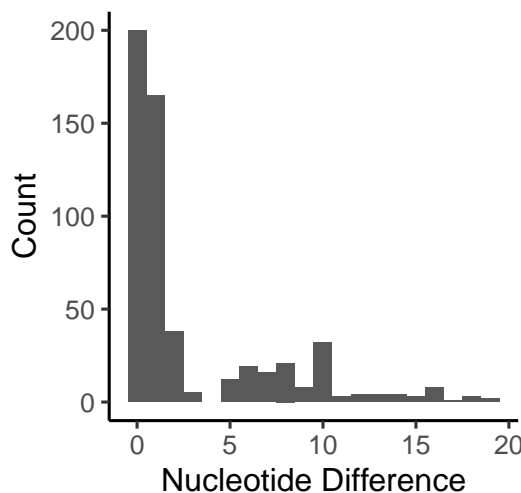
IGHV1-18*04

533 sequences assigned
179 (33.6%) exact matches, in which:
159 unique CDR3
7 unique J



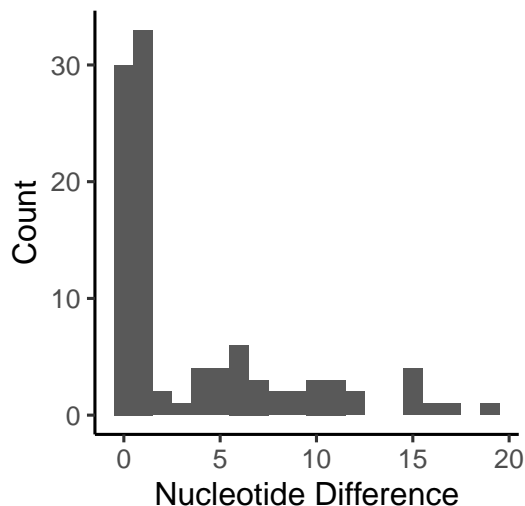
IGHV1-46*01

841 sequences assigned
200 (23.8%) exact matches, in which:
170 unique CDR3
7 unique J



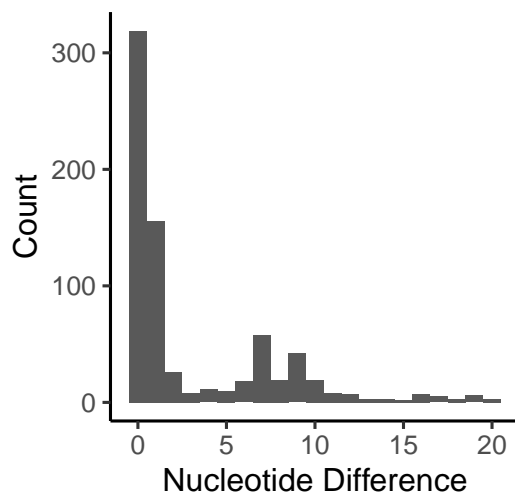
IGHV1-58*01_03

102 sequences assigned
30 (29.4%) exact matches, in which:
19 unique CDR3
5 unique J



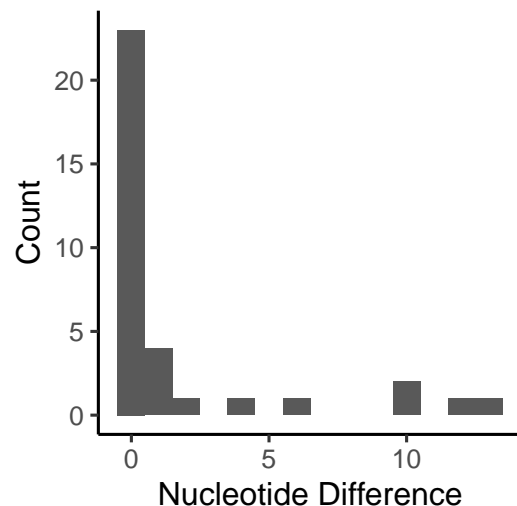
IGHV1-69*06_14

918 sequences assigned
319 (34.7%) exact matches, in which:
296 unique CDR3
7 unique J



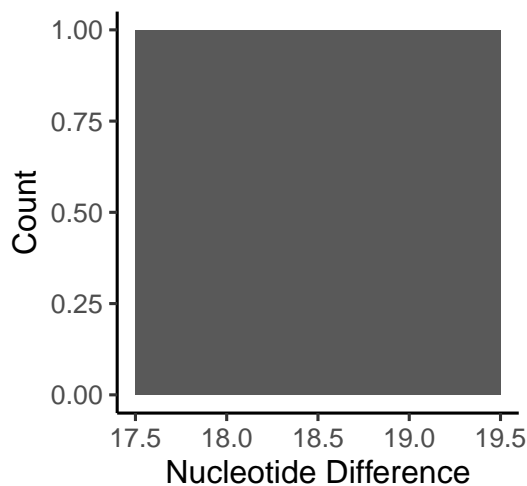
IGHV2-26*01

36 sequences assigned
23 (63.9%) exact matches, in which:
21 unique CDR3
5 unique J



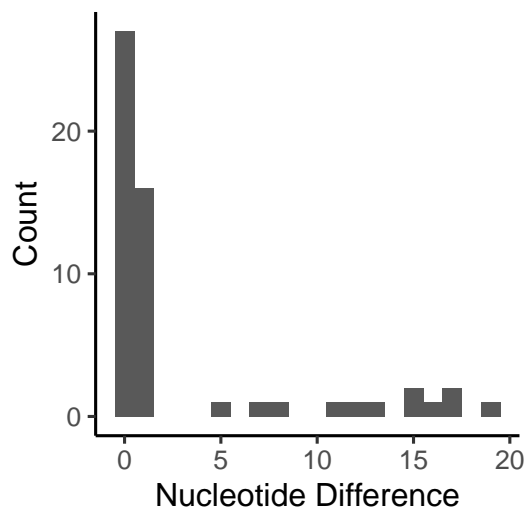
IGHV1-69-2*01

2 sequences assigned
No exact matches.



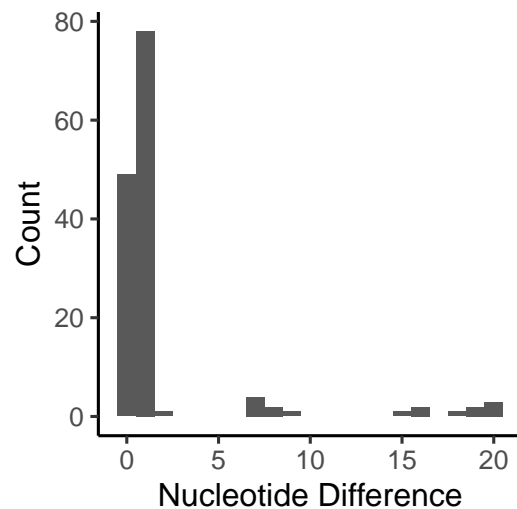
IGHV2-5*01

63 sequences assigned
27 (42.9%) exact matches, in which:
21 unique CDR3
5 unique J



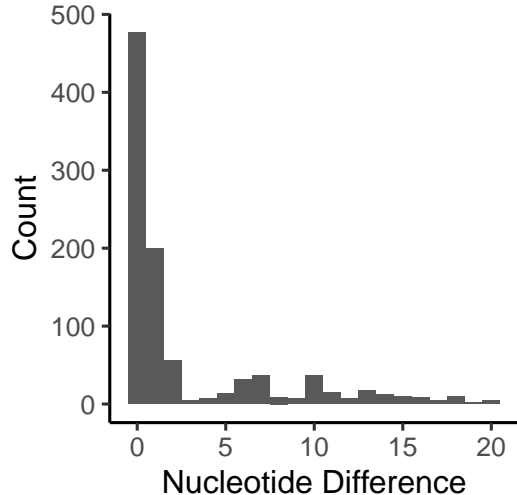
IGHV2-70*01

154 sequences assigned
49 (31.8%) exact matches, in which:
31 unique CDR3
5 unique J



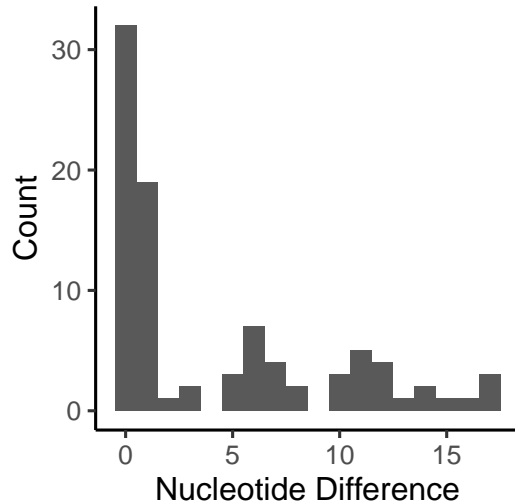
IGHV1-69*01_12_13

1044 sequences assigned
477 (45.7%) exact matches, in which:
439 unique CDR3
7 unique J



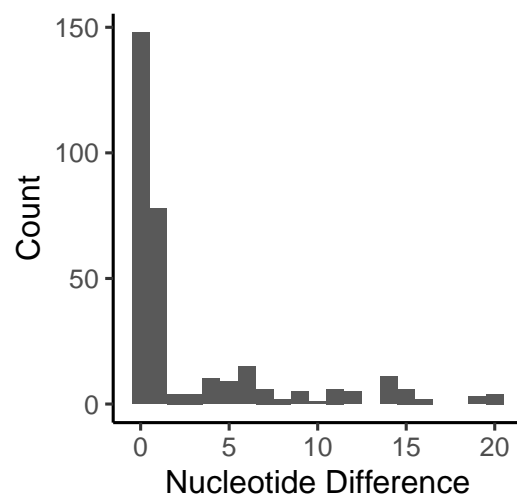
IGHV2-5*02

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



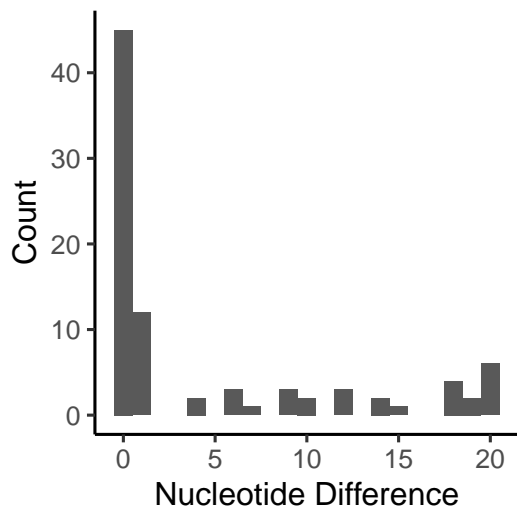
IGHV3-7*01

350 sequences assigned
148 (42.3%) exact matches, in which:
81 unique CDR3
6 unique J



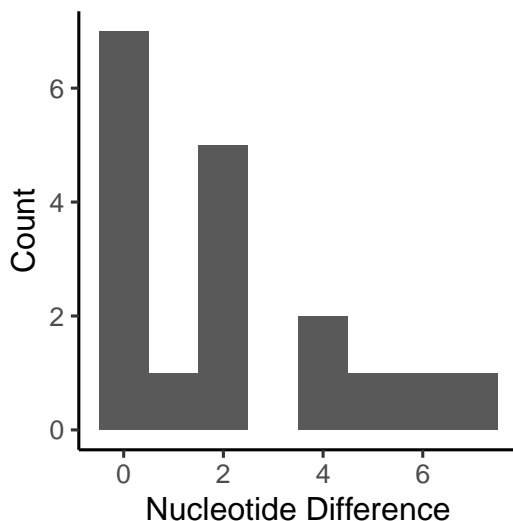
IGHV3-7*05

98 sequences assigned
45 (45.9%) exact matches, in which:
23 unique CDR3
5 unique J



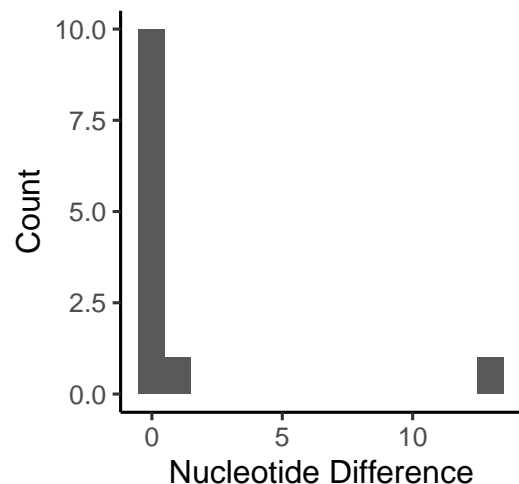
IGHV3-11*04

18 sequences assigned
7 (38.9%) exact matches, in which:
6 unique CDR3
3 unique J



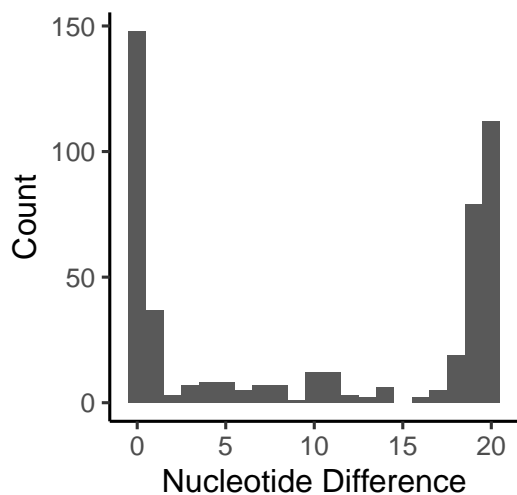
IGHV3-13*05

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



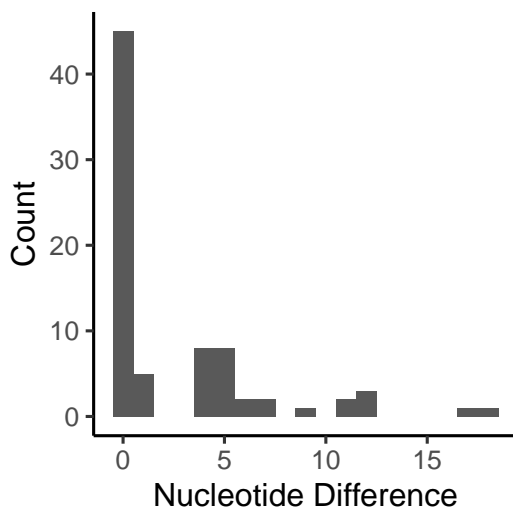
IGHV3-9*01

707 sequences assigned
148 (20.9%) exact matches, in which:
72 unique CDR3
7 unique J



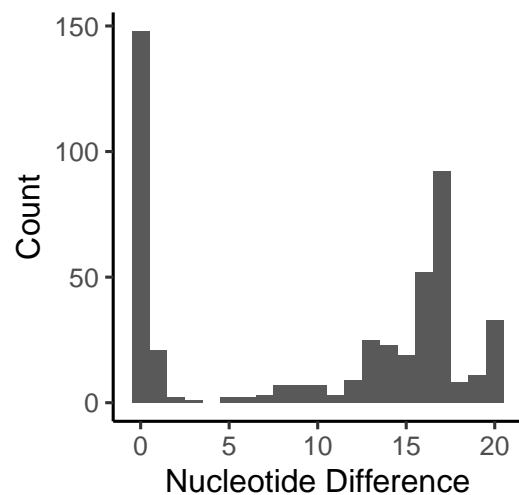
IGHV3-11*06

87 sequences assigned
45 (51.7%) exact matches, in which:
25 unique CDR3
5 unique J



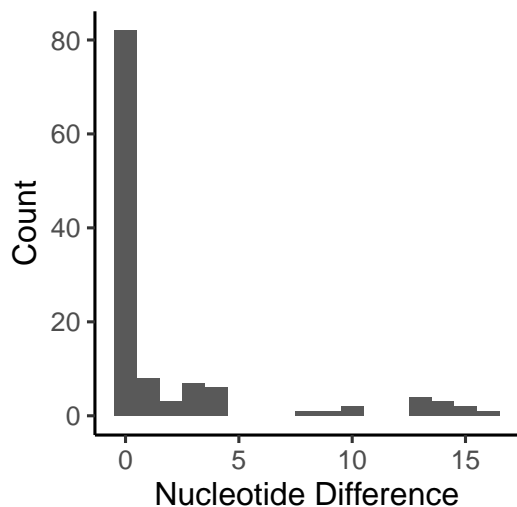
IGHV3-15*01_02

556 sequences assigned
148 (26.6%) exact matches, in which:
72 unique CDR3
6 unique J



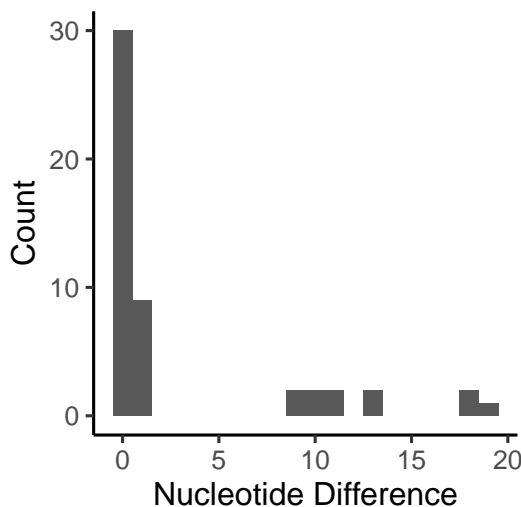
IGHV3-11*01

126 sequences assigned
82 (65.1%) exact matches, in which:
44 unique CDR3
6 unique J



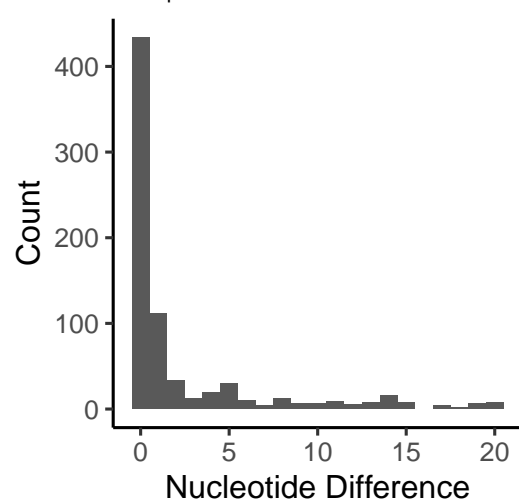
IGHV3-13*01

54 sequences assigned
30 (55.6%) exact matches, in which:
15 unique CDR3
5 unique J



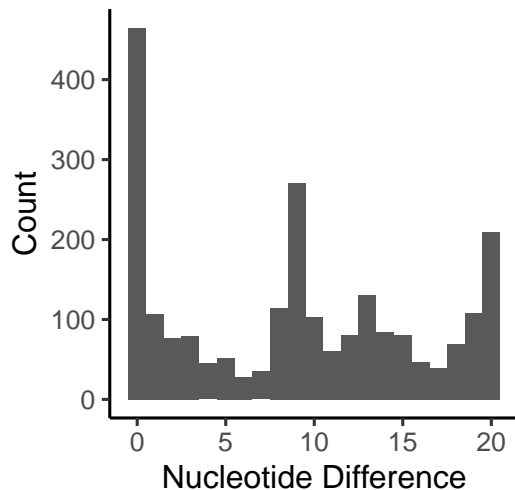
IGHV3-21*01_02

771 sequences assigned
434 (56.3%) exact matches, in which:
216 unique CDR3
7 unique J



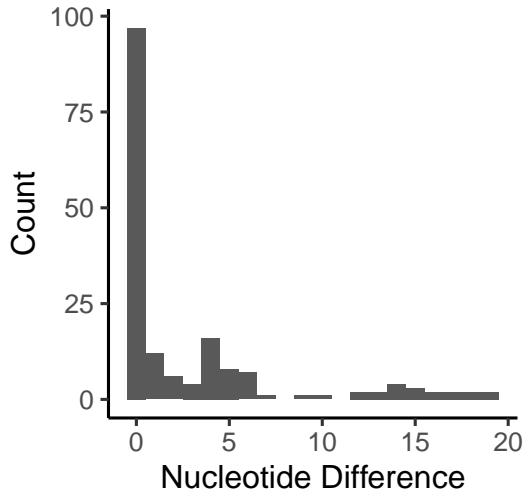
IGHV3-23*01_04

2784 sequences assigned
465 (16.7%) exact matches, in which:
239 unique CDR3
7 unique J



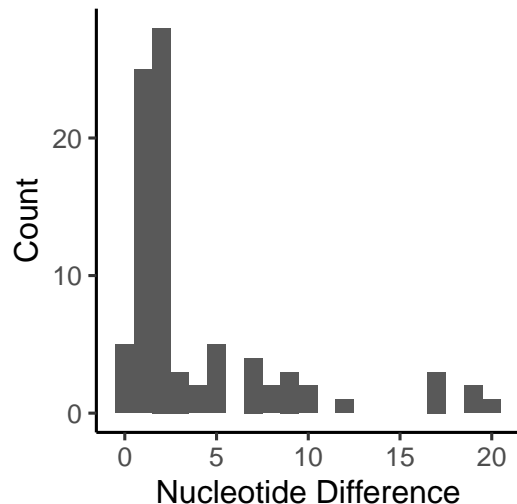
IGHV3-30*03_T288C

184 sequences assigned
97 (52.7%) exact matches, in which:
73 unique CDR3
7 unique J



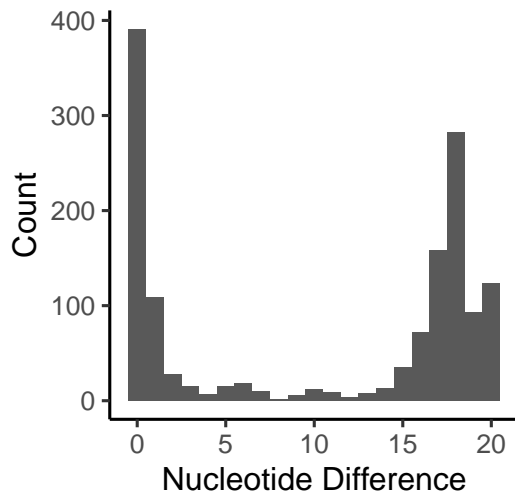
IGHV3-33*06

90 sequences assigned
5 (5.6%) exact matches, in which:
5 unique CDR3
3 unique J



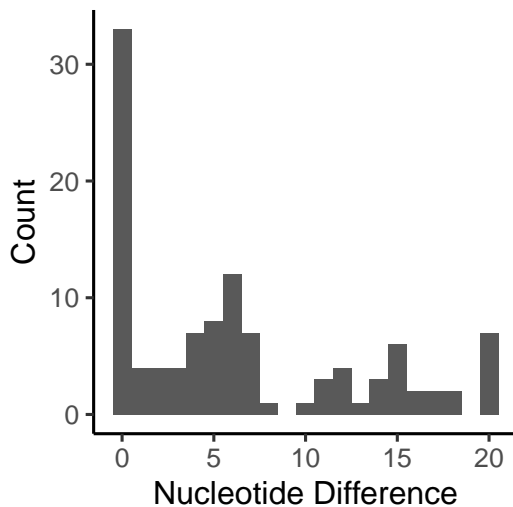
IGHV3-30-3*01

2111 sequences assigned
391 (18.5%) exact matches, in which:
226 unique CDR3
7 unique J



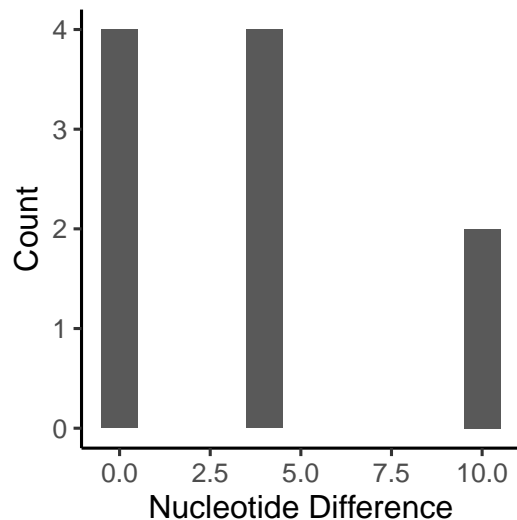
IGHV3-30*18_T288C_T30C

127 sequences assigned
33 (26%) exact matches, in which:
29 unique CDR3
6 unique J



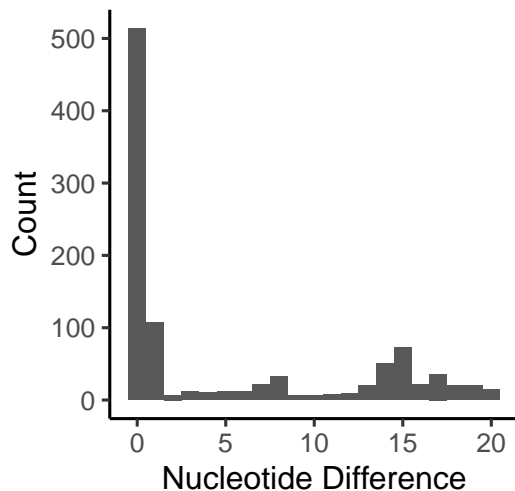
IGHV3-43*01

10 sequences assigned
4 (40%) exact matches, in which:
2 unique CDR3
1 unique J



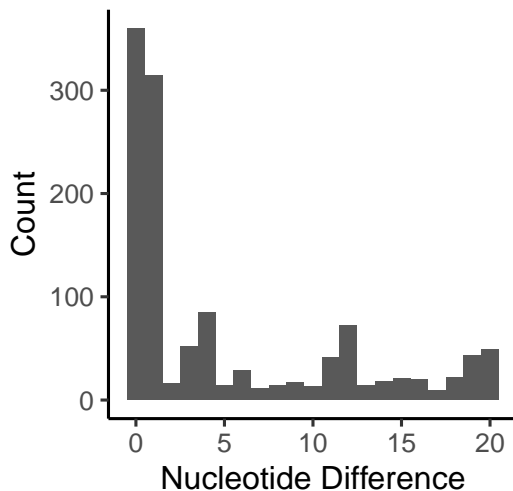
IGHV3-30*03

1395 sequences assigned
514 (36.8%) exact matches, in which:
294 unique CDR3
7 unique J



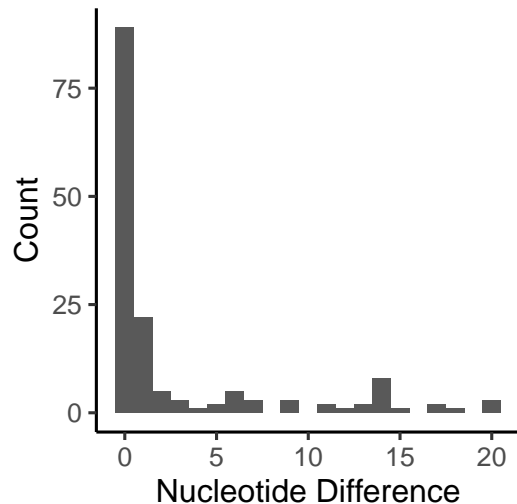
IGHV3-33*01

1279 sequences assigned
360 (28.1%) exact matches, in which:
196 unique CDR3
7 unique J



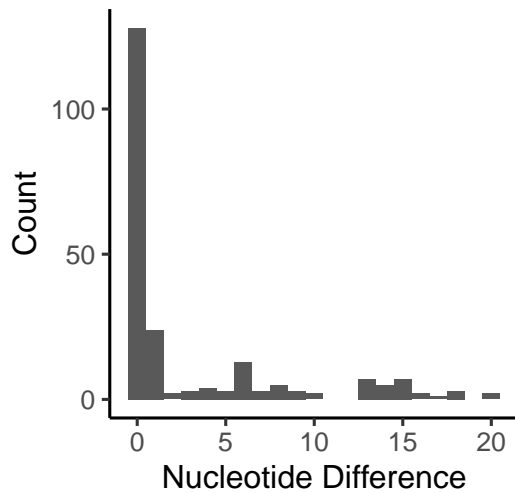
IGHV3-48*02

159 sequences assigned
89 (56%) exact matches, in which:
41 unique CDR3
5 unique J



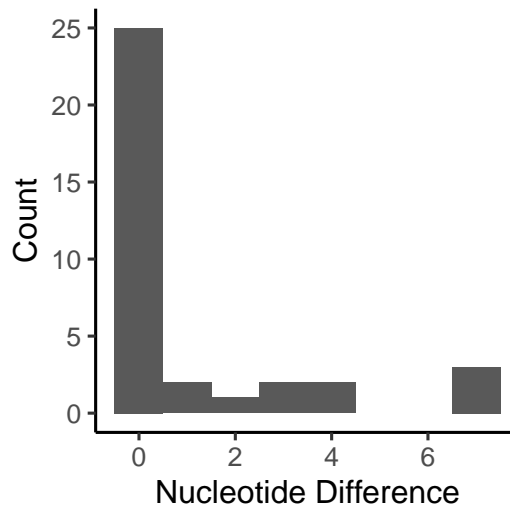
IGHV3-48*03

225 sequences assigned
128 (56.9%) exact matches, in which:
66 unique CDR3
4 unique J



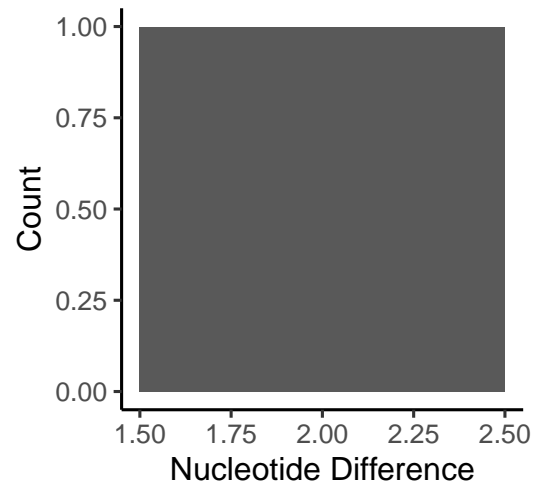
IGHV3-49*03_05

37 sequences assigned
25 (67.6%) exact matches, in which:
12 unique CDR3
3 unique J



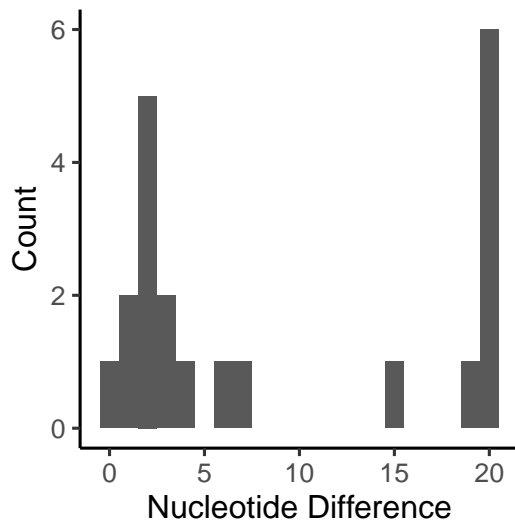
IGHV3-66*02

1 sequences assigned
No exact matches.



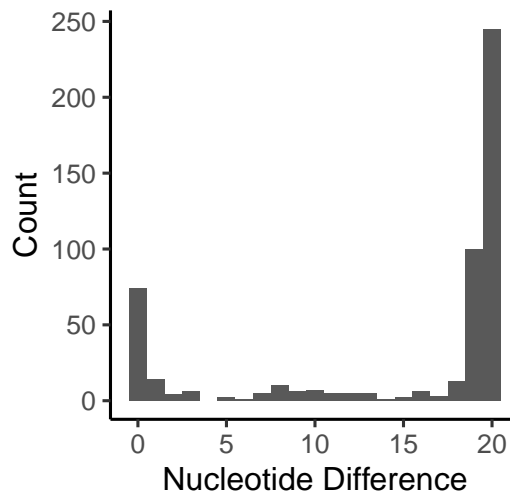
IGHV3-48*04

43 sequences assigned
1 (2.3%) exact matches, in which:
1 unique CDR3
1 unique J



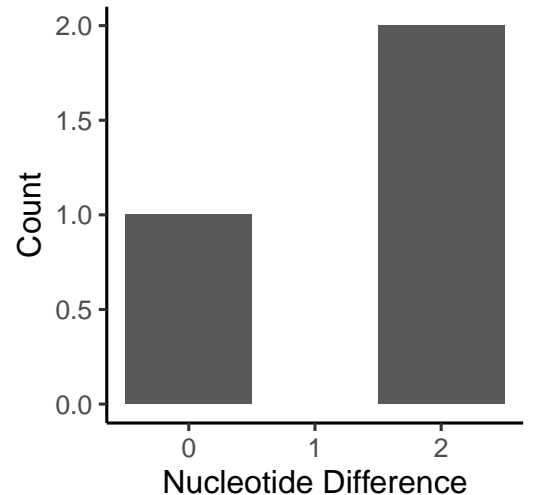
IGHV3-53*01_02

650 sequences assigned
74 (11.4%) exact matches, in which:
37 unique CDR3
7 unique J



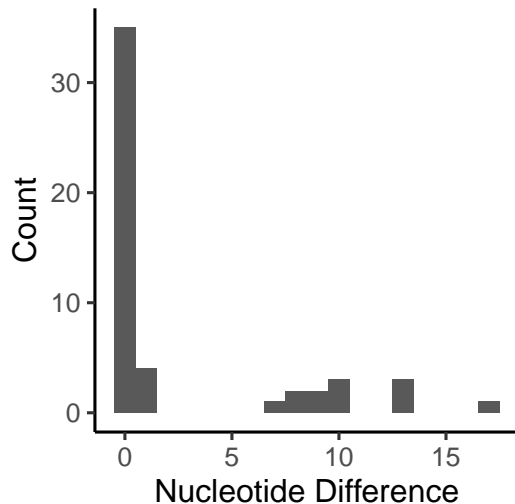
IGHV3-66*03

4 sequences assigned
1 (25%) exact matches, in which:
1 unique CDR3
1 unique J



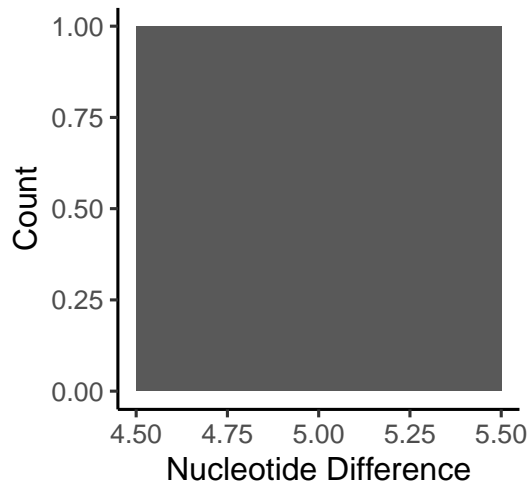
IGHV3-49*04

54 sequences assigned
35 (64.8%) exact matches, in which:
18 unique CDR3
4 unique J



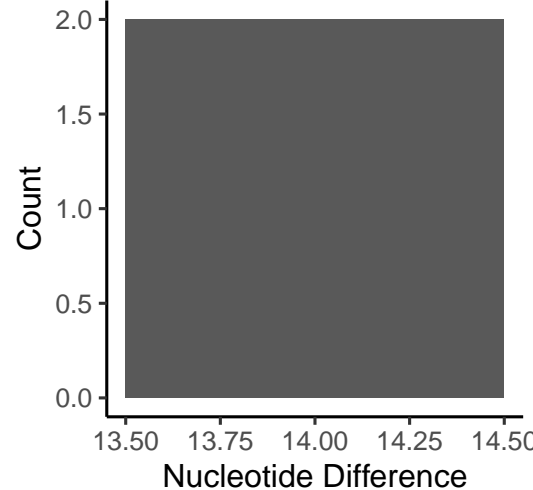
IGHV3-64*04

3 sequences assigned
No exact matches.



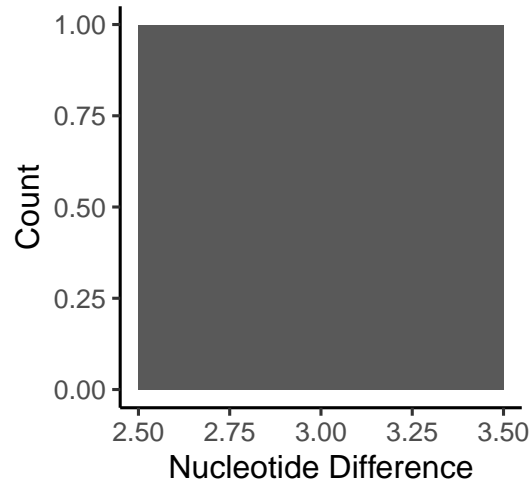
IGHV3-66*04

2 sequences assigned
No exact matches.



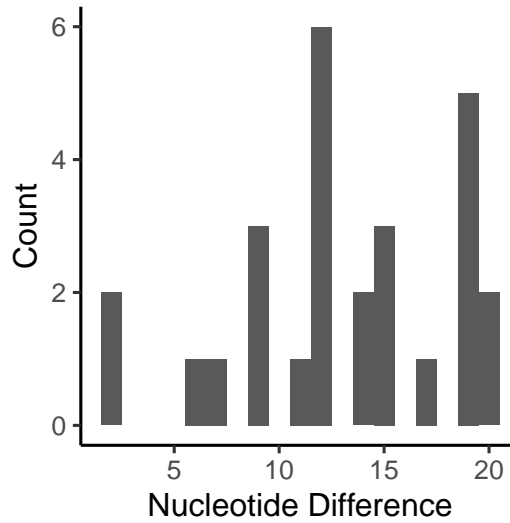
IGHV3-69-1*01

1 sequences assigned
No exact matches.



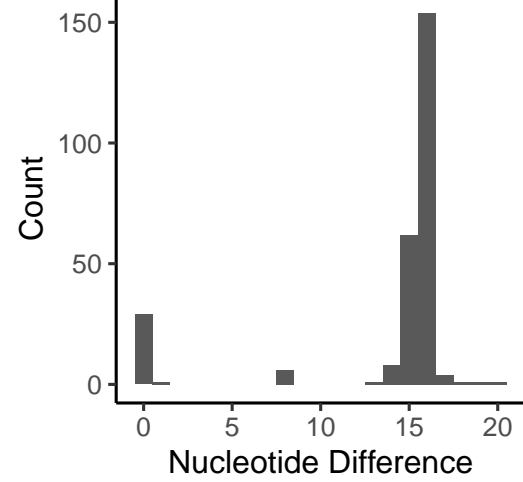
IGHV3-74*03

36 sequences assigned
No exact matches.



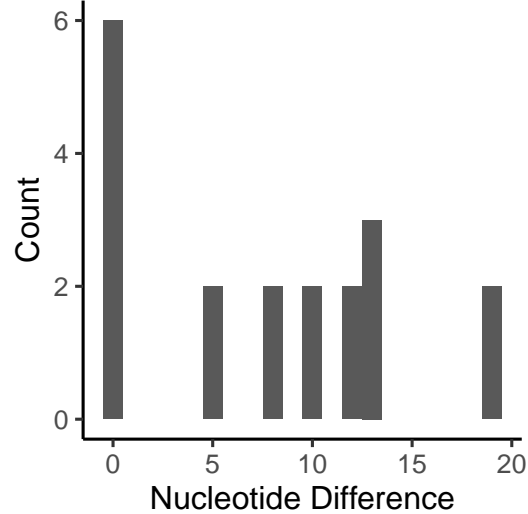
IGHV3-64D*08

275 sequences assigned
29 (10.5%) exact matches, in which:
12 unique CDR3
3 unique J



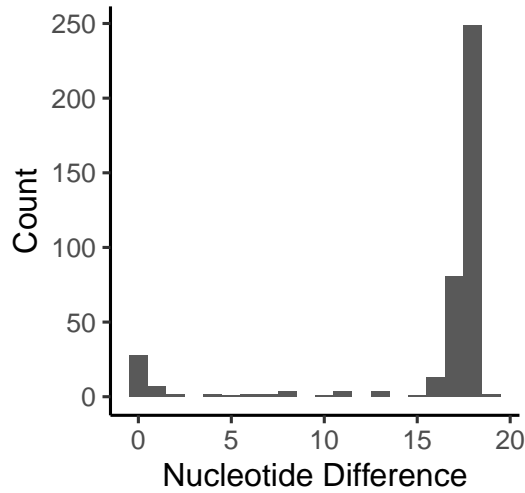
IGHV3-72*01

19 sequences assigned
6 (31.6%) exact matches, in which:
3 unique CDR3
3 unique J



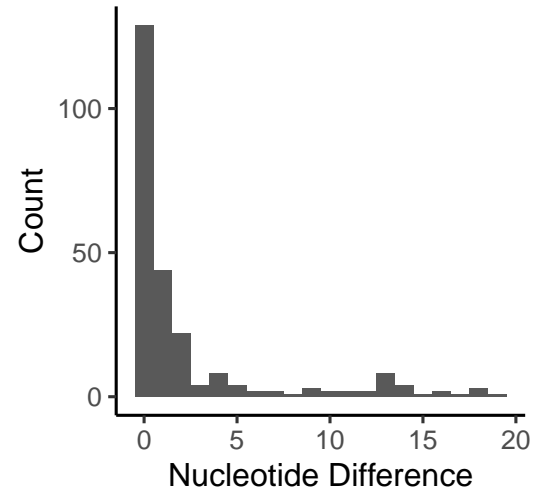
IGHV3-74*01_02

419 sequences assigned
28 (6.7%) exact matches, in which:
14 unique CDR3
5 unique J



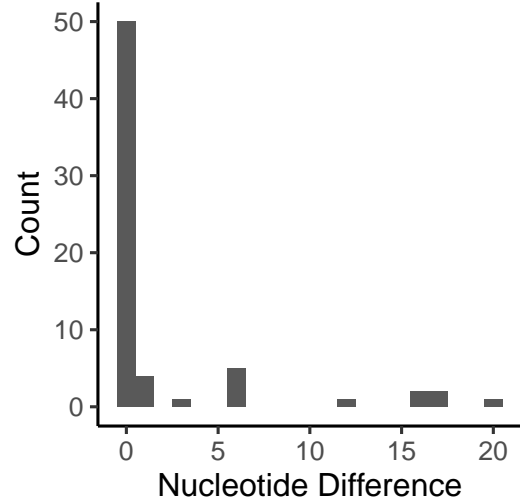
IGHV4-4*02_03

253 sequences assigned
129 (51%) exact matches, in which:
105 unique CDR3
7 unique J



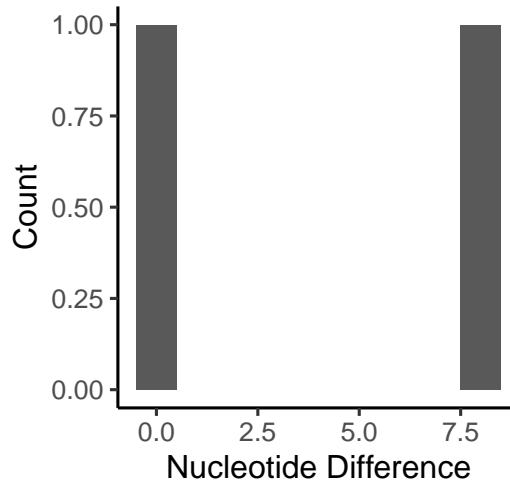
IGHV3-73*01_02

74 sequences assigned
50 (67.6%) exact matches, in which:
27 unique CDR3
6 unique J



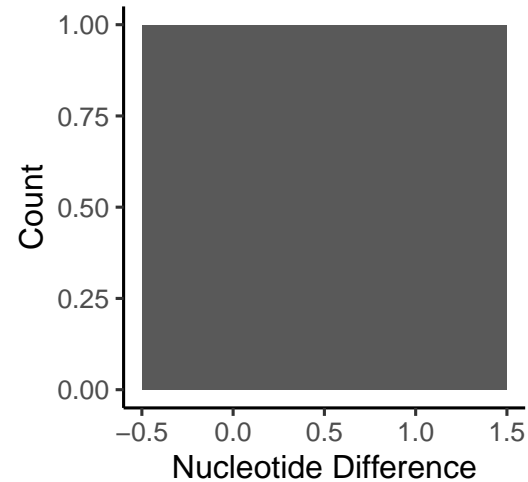
IGHV3-43D*04

2 sequences assigned
1 (50%) exact matches, in which:
1 unique CDR3
1 unique J



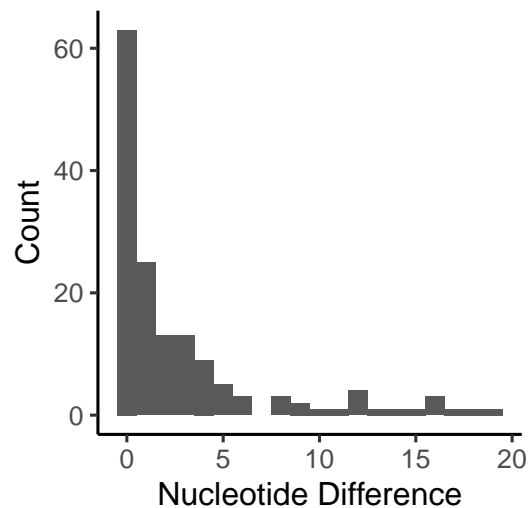
IGHV4-28*01_07

2 sequences assigned
1 (50%) exact matches, in which:
1 unique CDR3
1 unique J



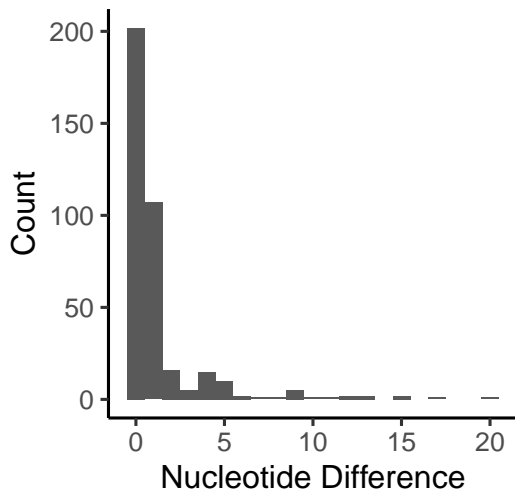
IGHV4-30-4*01

163 sequences assigned
63 (38.7%) exact matches, in which:
57 unique CDR3
6 unique J



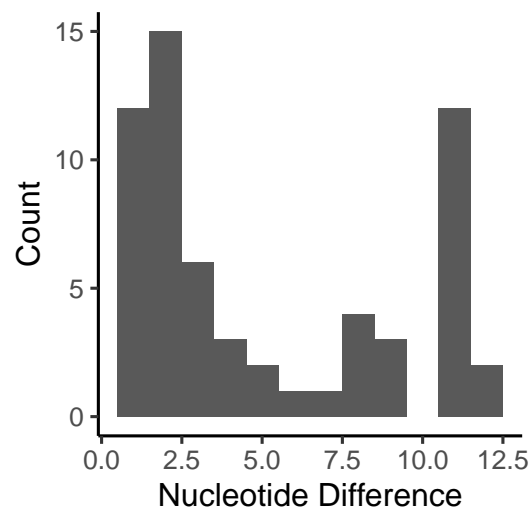
IGHV4-34*01_02

409 sequences assigned
202 (49.4%) exact matches, in which:
147 unique CDR3
7 unique J



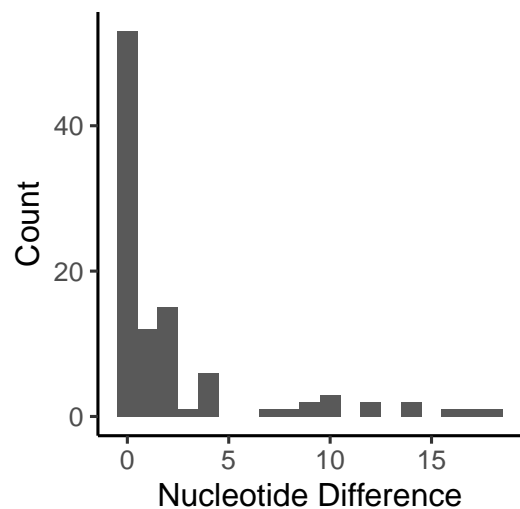
IGHV4-39*07

61 sequences assigned
No exact matches.



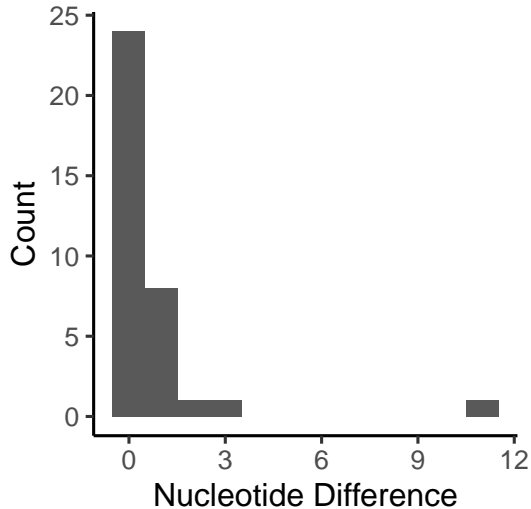
IGHV4-30-2*01

102 sequences assigned
53 (52%) exact matches, in which:
31 unique CDR3
6 unique J



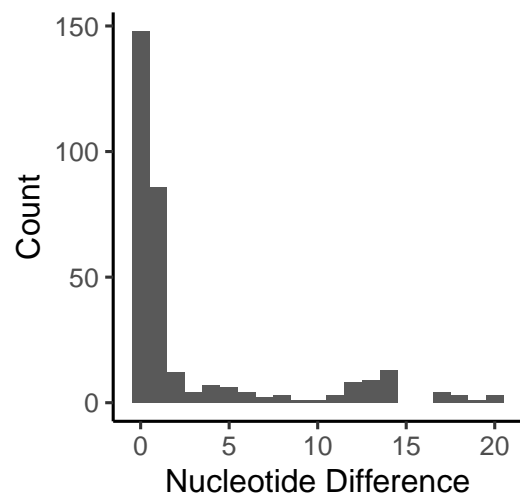
IGHV4-34*01_02_C288T_

35 sequences assigned
24 (68.6%) exact matches, in which:
24 unique CDR3
5 unique J



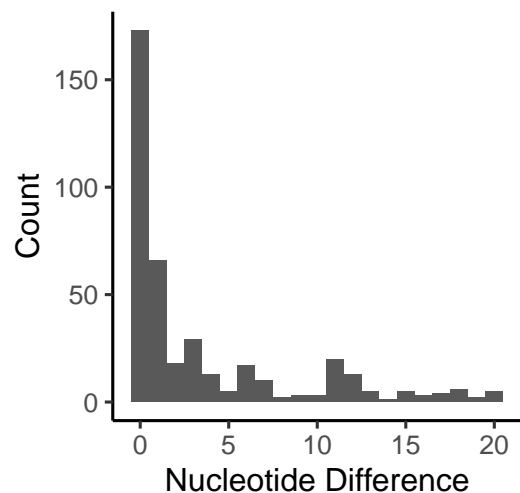
IGHV4-39*02_C258G

542 sequences assigned
148 (27.3%) exact matches, in which:
124 unique CDR3
6 unique J



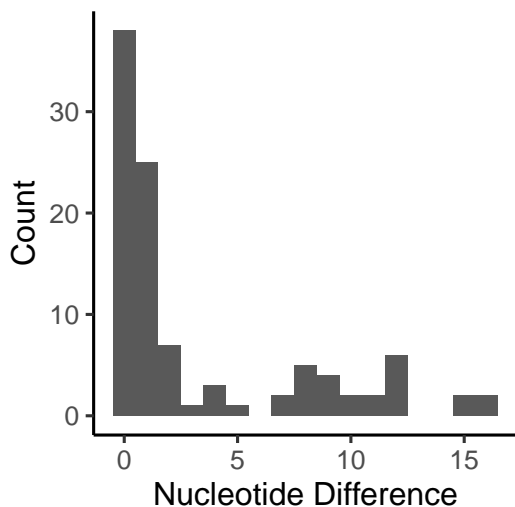
IGHV4-31*02

443 sequences assigned
173 (39.1%) exact matches, in which:
153 unique CDR3
7 unique J



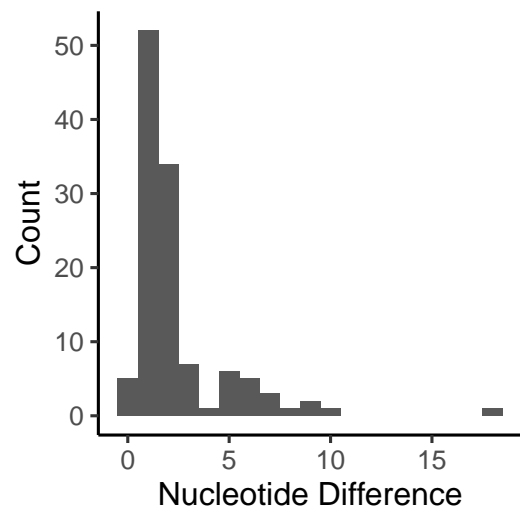
IGHV4-38-2*01

111 sequences assigned
38 (34.2%) exact matches, in which:
33 unique CDR3
4 unique J



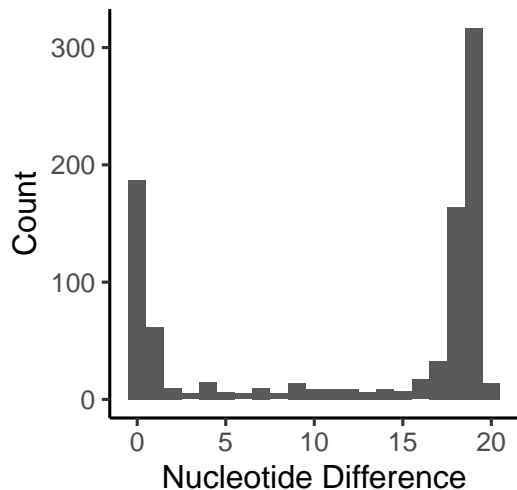
IGHV4-59*12

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



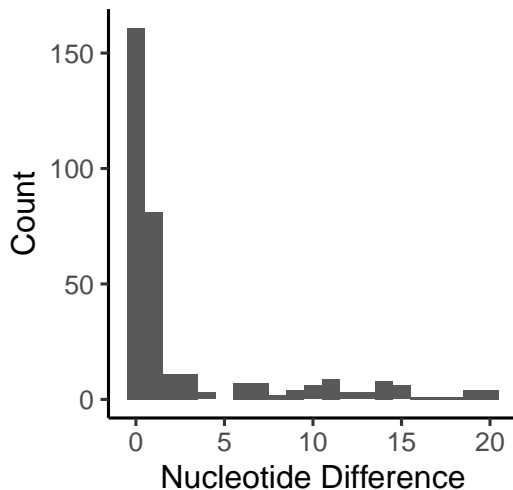
IGHV4–59*02_G88A

962 sequences assigned
187 (19.4%) exact matches, in which:
165 unique CDR3
7 unique J



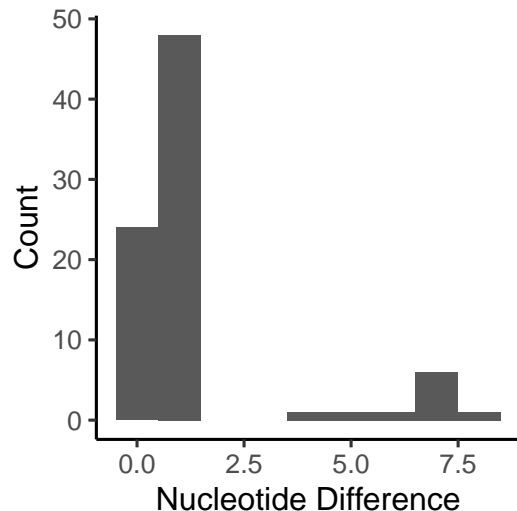
IGHV5–10–1*01_03

347 sequences assigned
161 (46.4%) exact matches, in which:
91 unique CDR3
7 unique J



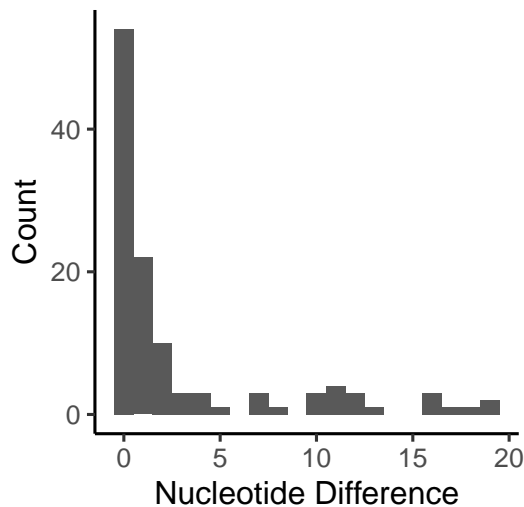
IGHV7–4–1*01

82 sequences assigned
24 (29.3%) exact matches, in which:
17 unique CDR3
5 unique J



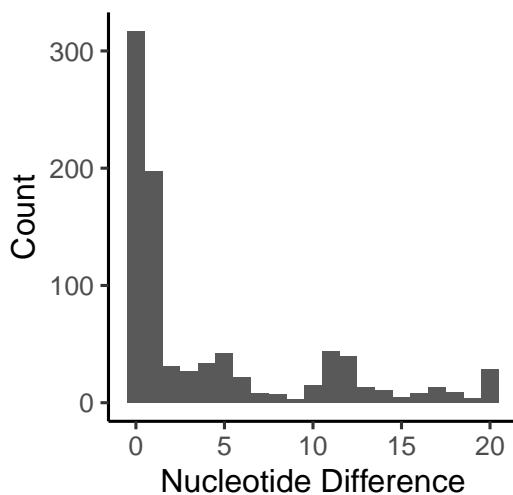
IGHV4–61*01

115 sequences assigned
54 (47%) exact matches, in which:
45 unique CDR3
6 unique J



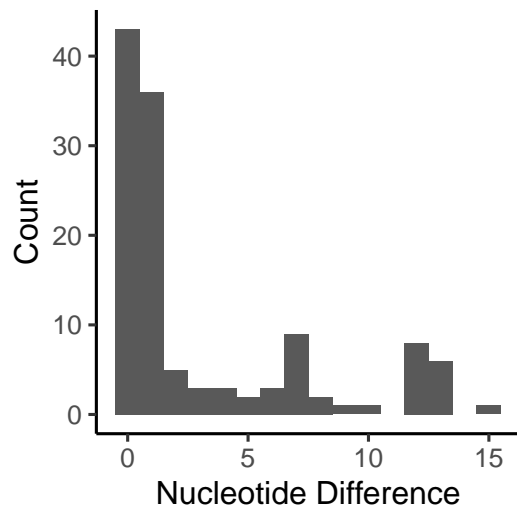
IGHV5–51*07_A128G

932 sequences assigned
317 (34%) exact matches, in which:
162 unique CDR3
7 unique J



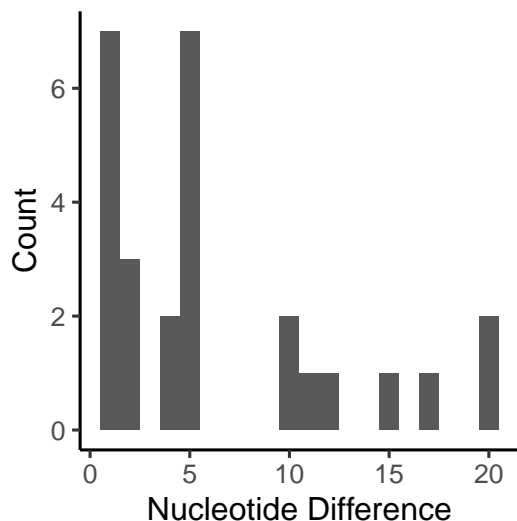
IGHV7–4–1*02

127 sequences assigned
43 (33.9%) exact matches, in which:
37 unique CDR3
6 unique J



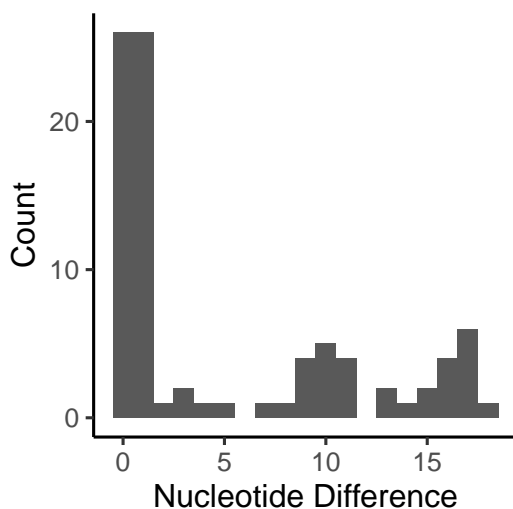
IGHV4–61*08

114 sequences assigned
No exact matches.

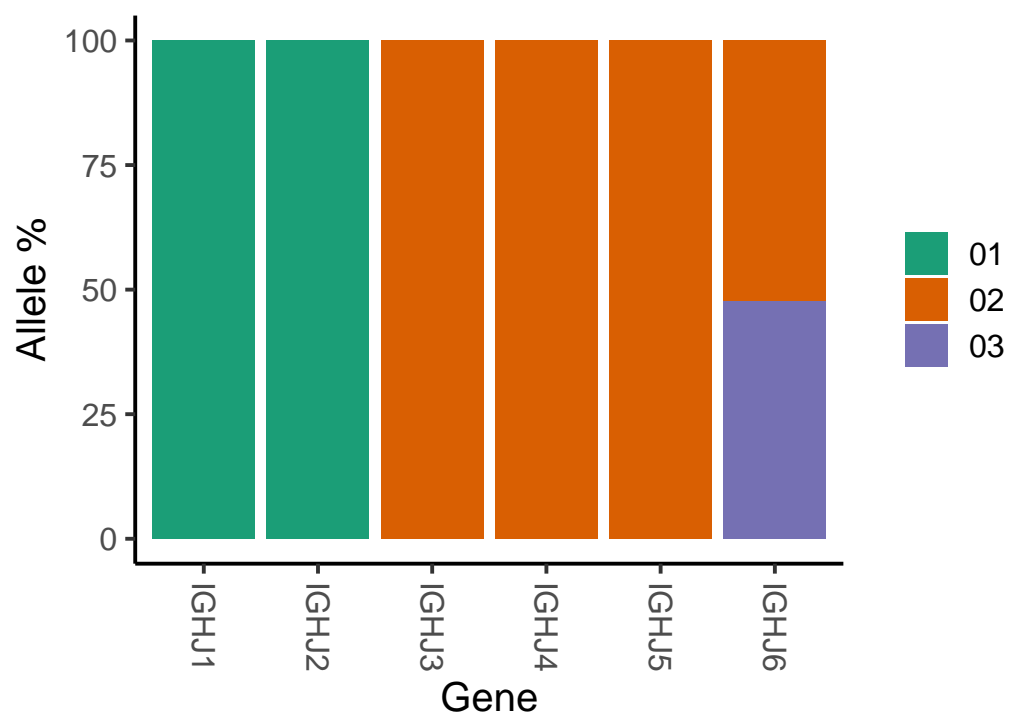


IGHV6–1*01_02

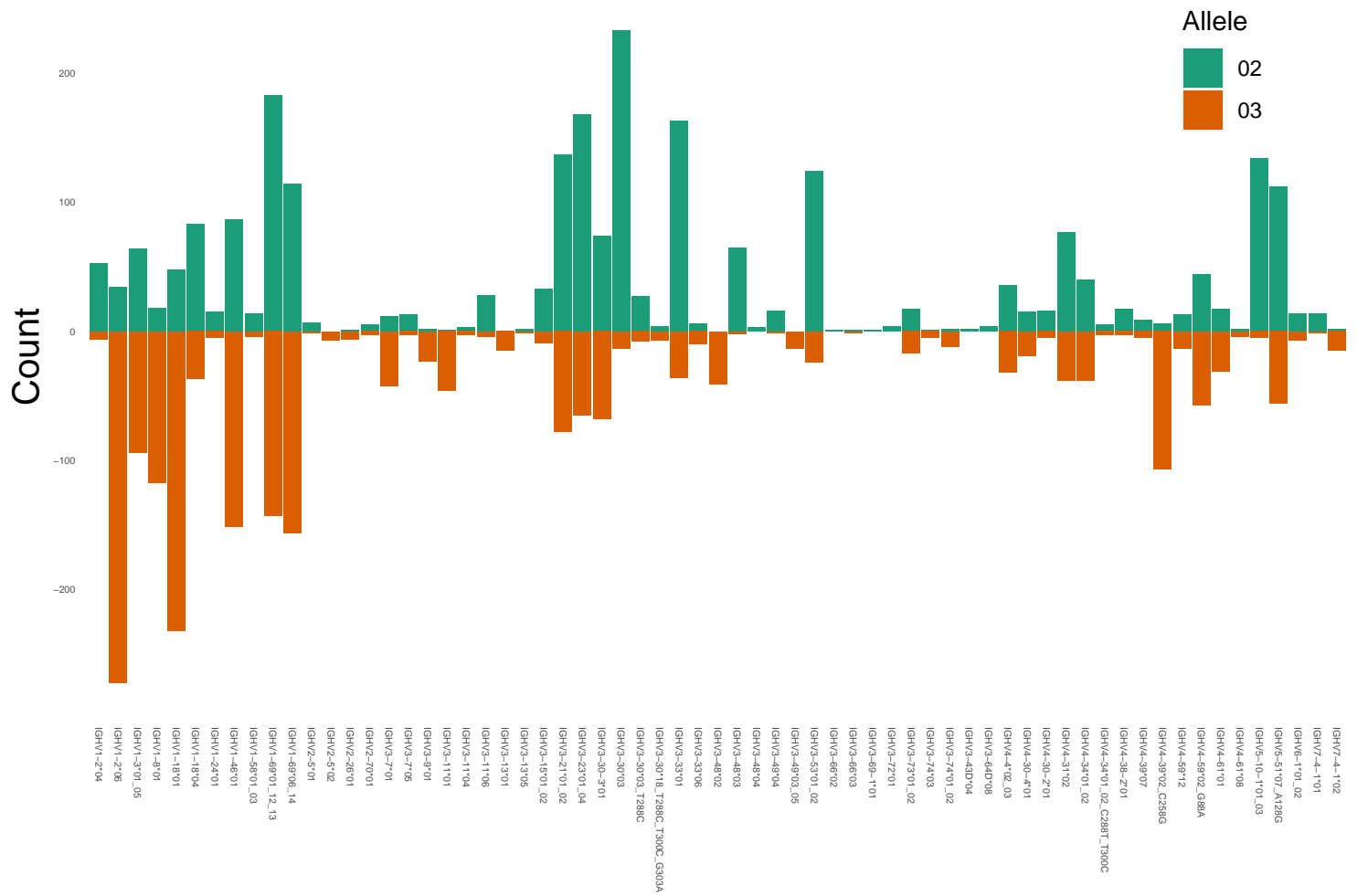
98 sequences assigned
26 (26.5%) exact matches, in which:
23 unique CDR3
5 unique J



Allele Usage



Sequence Count byIGHJ6 allele usage



Warning – no inferred sequences found.