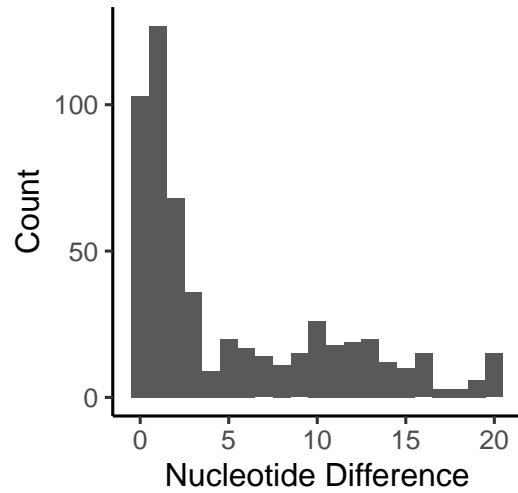


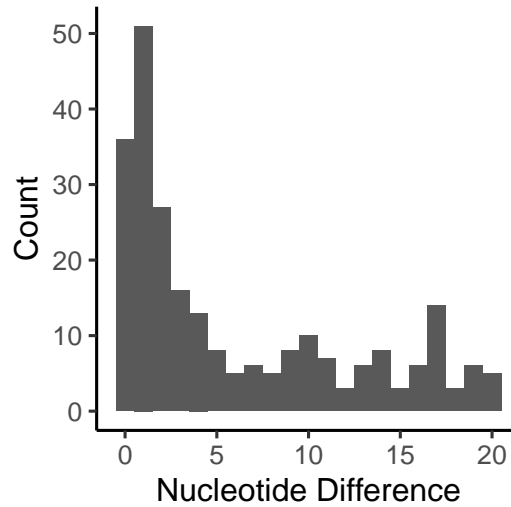
### IGHV1-2\*02

616 sequences assigned  
103 (16.7%) exact matches, in which:  
92 unique CDR3  
6 unique J



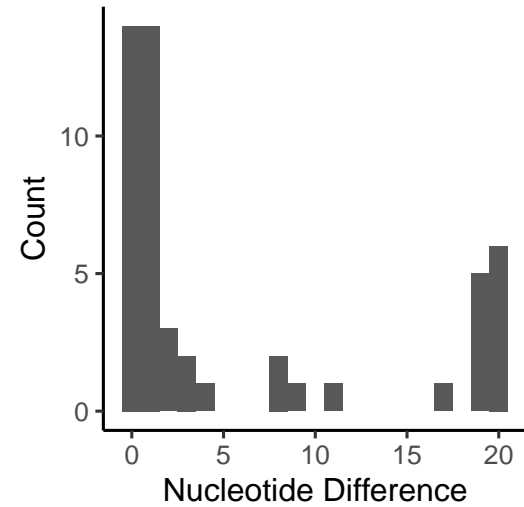
### IGHV1-3\*01\_05

282 sequences assigned  
36 (12.8%) exact matches, in which:  
34 unique CDR3  
4 unique J



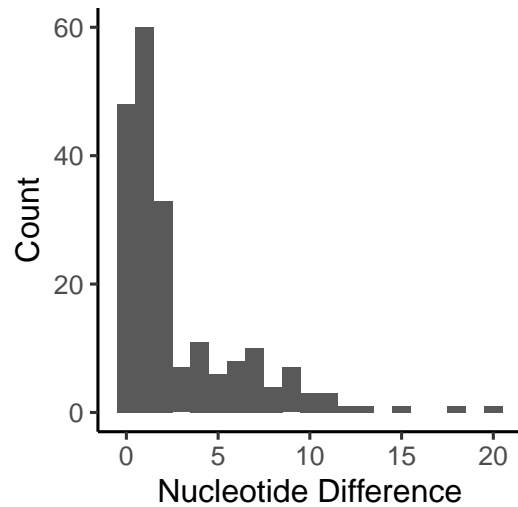
### IGHV1-24\*01

52 sequences assigned  
14 (26.9%) exact matches, in which:  
13 unique CDR3  
4 unique J



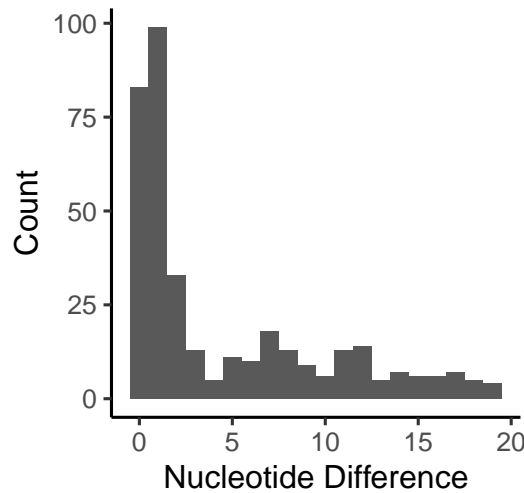
### IGHV1-2\*04

206 sequences assigned  
48 (23.3%) exact matches, in which:  
43 unique CDR3  
5 unique J



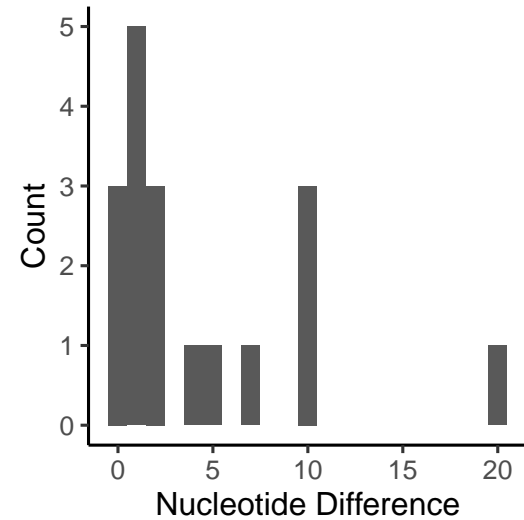
### IGHV1-8\*01

372 sequences assigned  
83 (22.3%) exact matches, in which:  
72 unique CDR3  
4 unique J



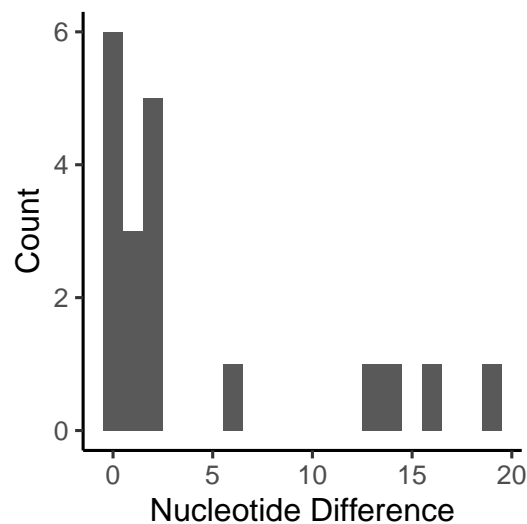
### IGHV1-45\*02

18 sequences assigned  
3 (16.7%) exact matches, in which:  
3 unique CDR3  
1 unique J



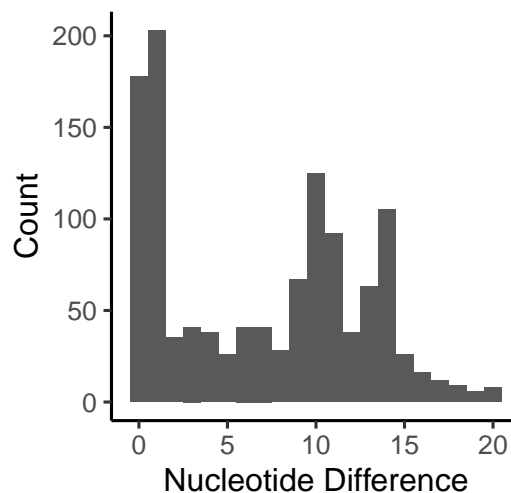
### IGHV1-2\*06

22 sequences assigned  
6 (27.3%) exact matches, in which:  
6 unique CDR3  
3 unique J



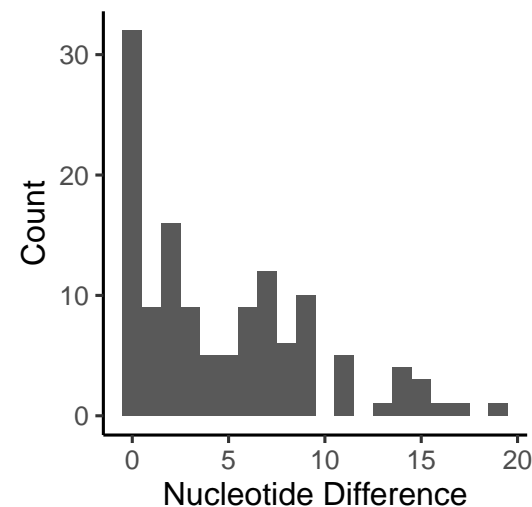
### IGHV1-18\*01

1210 sequences assigned  
178 (14.7%) exact matches, in which:  
148 unique CDR3  
4 unique J



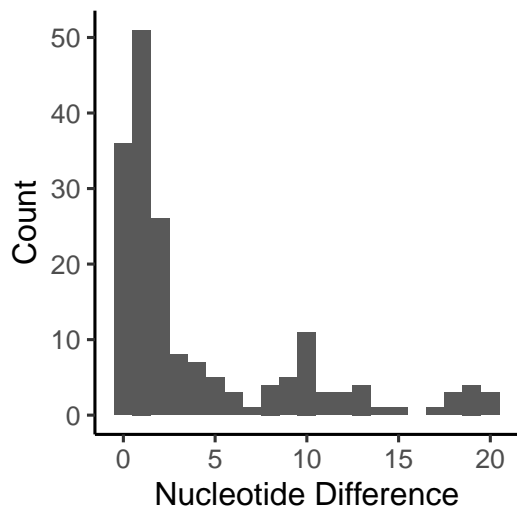
### IGHV1-46\*01

133 sequences assigned  
32 (24.1%) exact matches, in which:  
32 unique CDR3  
5 unique J



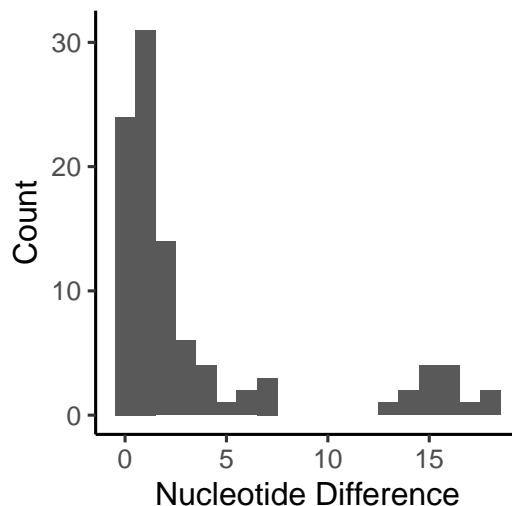
### IGHV1-46\*03

181 sequences assigned  
36 (19.9%) exact matches, in which:  
31 unique CDR3  
4 unique J



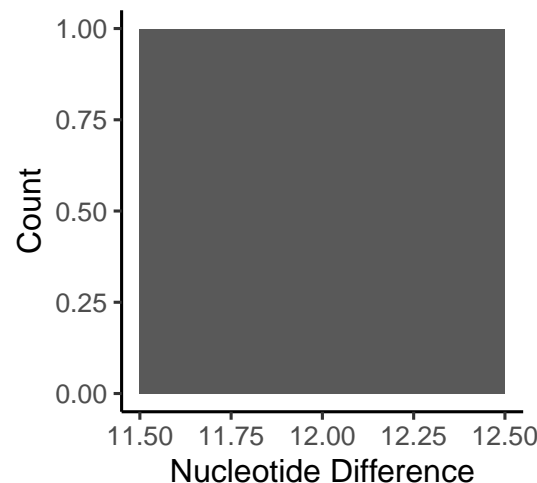
### IGHV1-69\*02

99 sequences assigned  
24 (24.2%) exact matches, in which:  
24 unique CDR3  
4 unique J



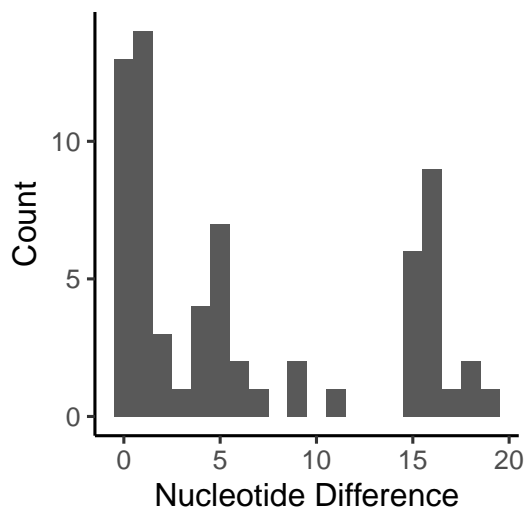
### IGHV1-NL1\*01

1 sequences assigned  
No exact matches.



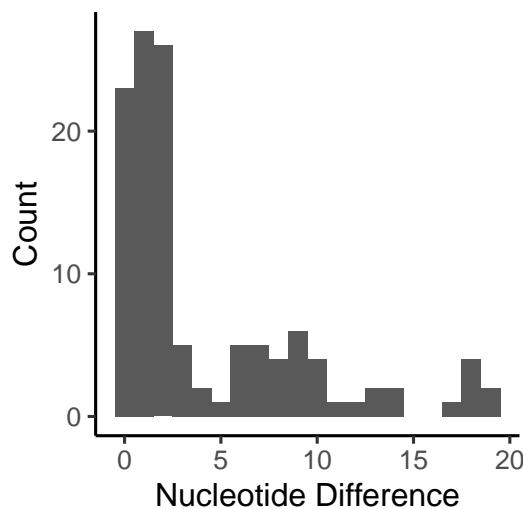
### IGHV1-58\*02

69 sequences assigned  
13 (18.8%) exact matches, in which:  
9 unique CDR3  
3 unique J



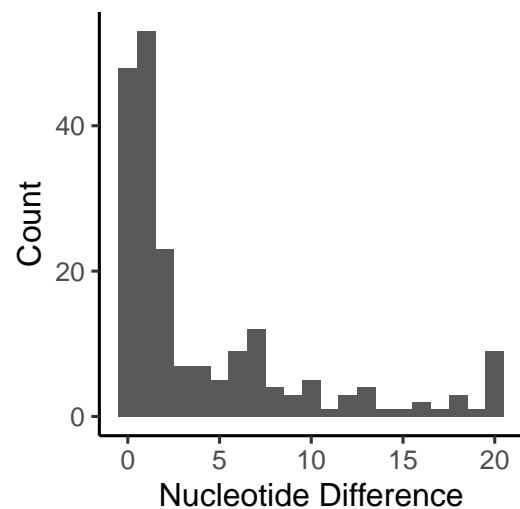
### IGHV1-69\*04\_09

121 sequences assigned  
23 (19%) exact matches, in which:  
18 unique CDR3  
4 unique J



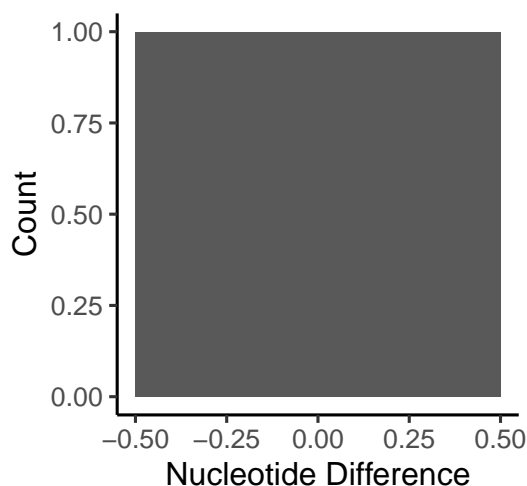
### IGHV2-5\*02

226 sequences assigned  
48 (21.2%) exact matches, in which:  
40 unique CDR3  
4 unique J



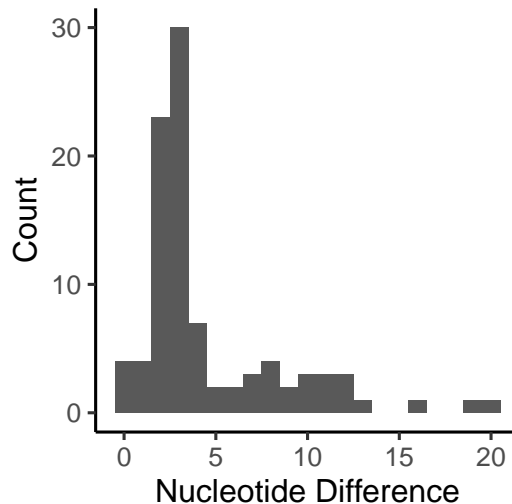
### IGHV1-69-2\*01

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



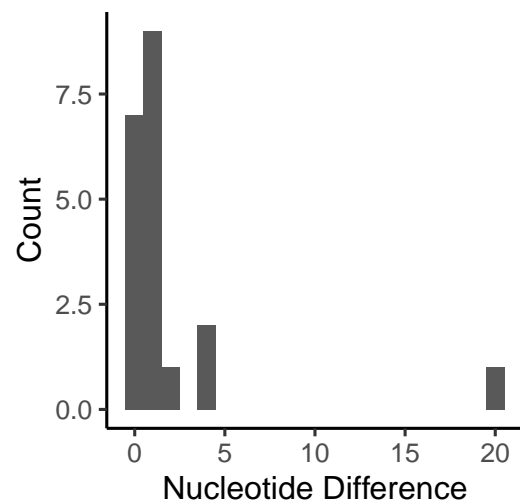
### IGHV1-69\*06\_14

97 sequences assigned  
4 (4.1%) exact matches, in which:  
4 unique CDR3  
2 unique J



### IGHV2-26\*01

20 sequences assigned  
7 (35%) exact matches, in which:  
6 unique CDR3  
3 unique J



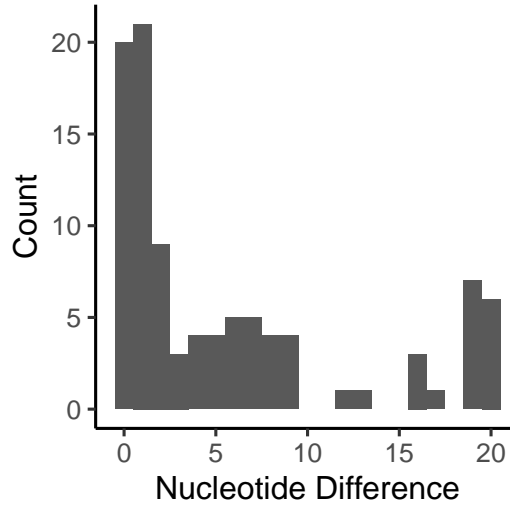
### IGHV2-70\*01

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



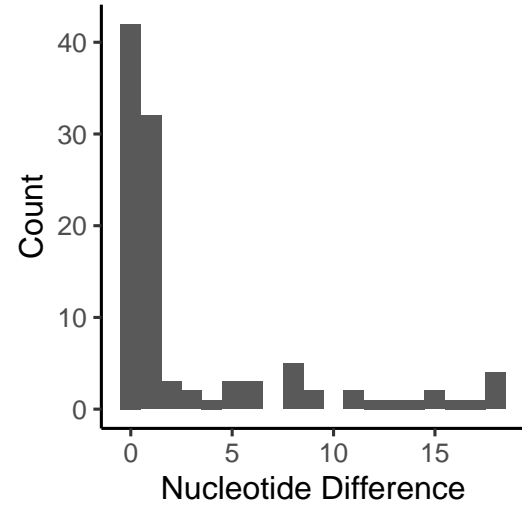
### IGHV3-7\*03

145 sequences assigned  
20 (13.8%) exact matches, in which:  
16 unique CDR3  
3 unique J



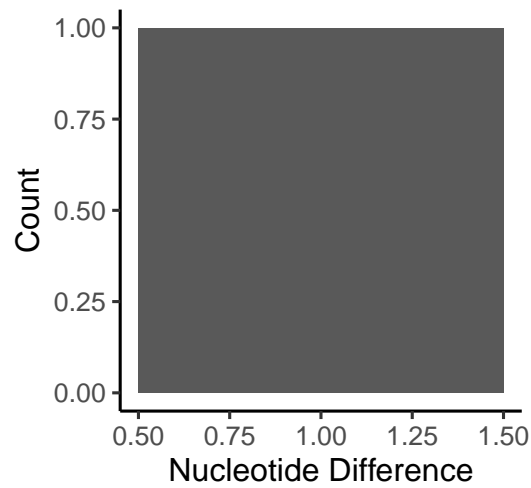
### IGHV3-11\*01

106 sequences assigned  
42 (39.6%) exact matches, in which:  
26 unique CDR3  
4 unique J



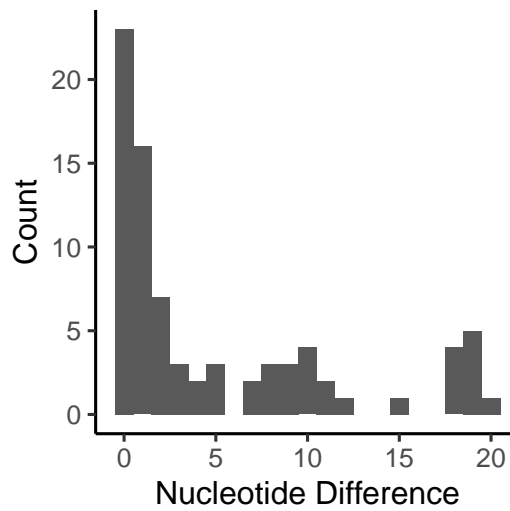
### IGHV2-70\*12

1 sequences assigned  
No exact matches.



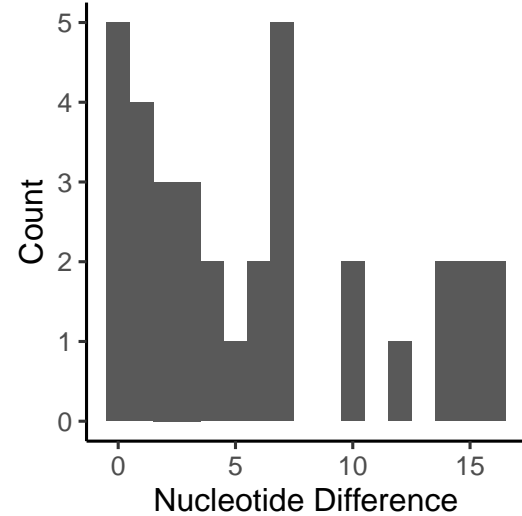
### IGHV3-7\*04

89 sequences assigned  
23 (25.8%) exact matches, in which:  
15 unique CDR3  
4 unique J



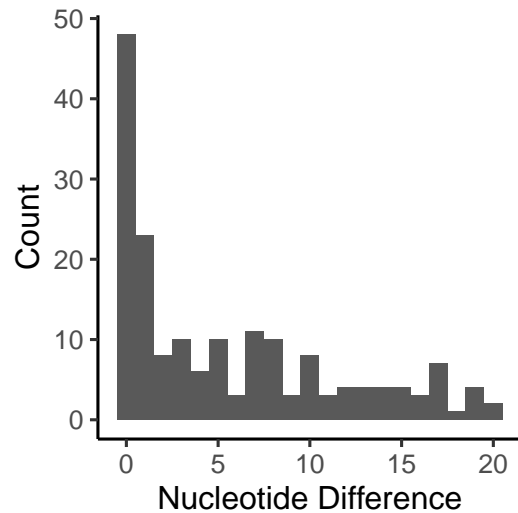
### IGHV3-11\*04

34 sequences assigned  
5 (14.7%) exact matches, in which:  
5 unique CDR3  
2 unique J



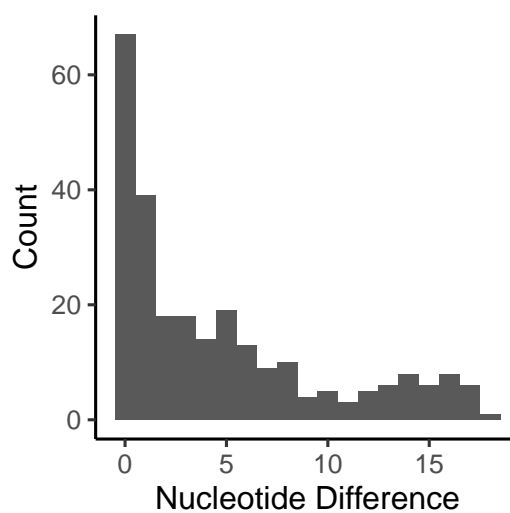
### IGHV3-7\*01

214 sequences assigned  
48 (22.4%) exact matches, in which:  
40 unique CDR3  
4 unique J



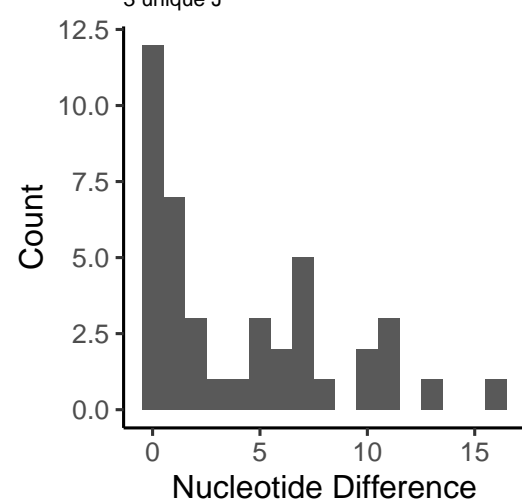
### IGHV3-9\*01

275 sequences assigned  
67 (24.4%) exact matches, in which:  
48 unique CDR3  
5 unique J



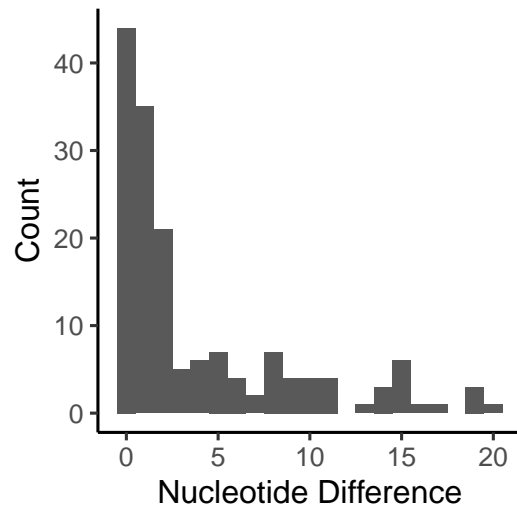
### IGHV3-11\*06

42 sequences assigned  
12 (28.6%) exact matches, in which:  
11 unique CDR3  
3 unique J



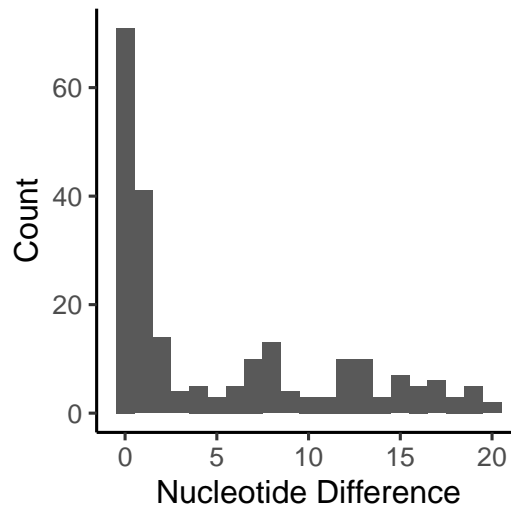
### IGHV3-11\*03\_05

162 sequences assigned  
44 (27.2%) exact matches, in which:  
31 unique CDR3  
4 unique J



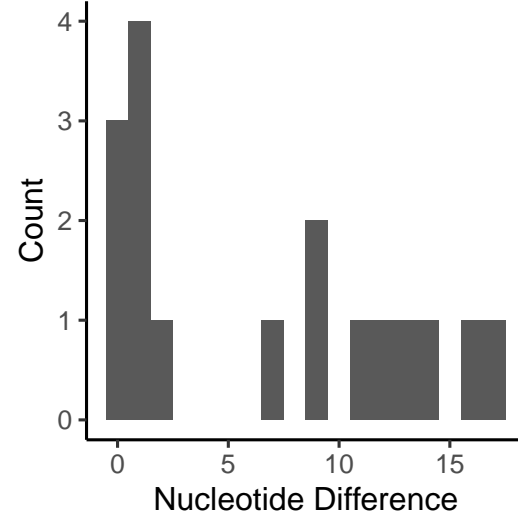
### IGHV3-15\*07

253 sequences assigned  
71 (28.1%) exact matches, in which:  
49 unique CDR3  
5 unique J



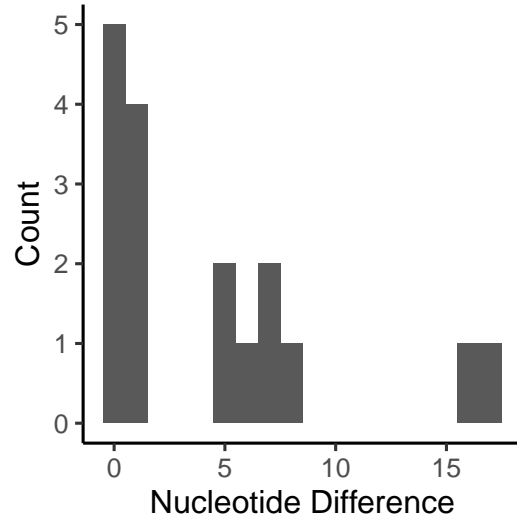
### IGHV3-20\*03\_04

19 sequences assigned  
3 (15.8%) exact matches, in which:  
2 unique CDR3  
2 unique J



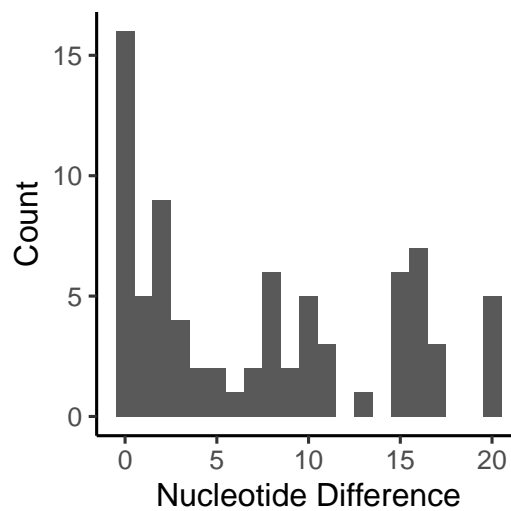
### IGHV3-13\*01

17 sequences assigned  
5 (29.4%) exact matches, in which:  
4 unique CDR3  
2 unique J



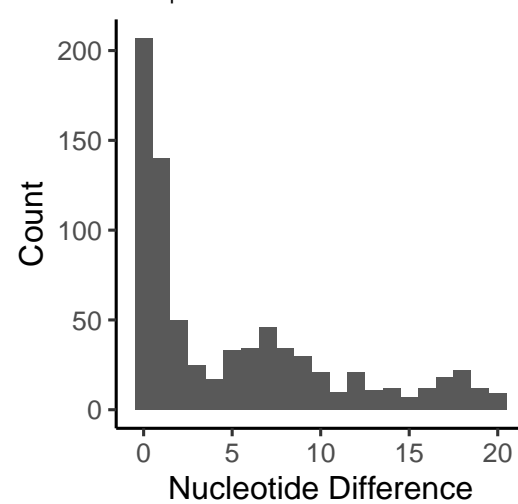
### IGHV3-15\*01\_02

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



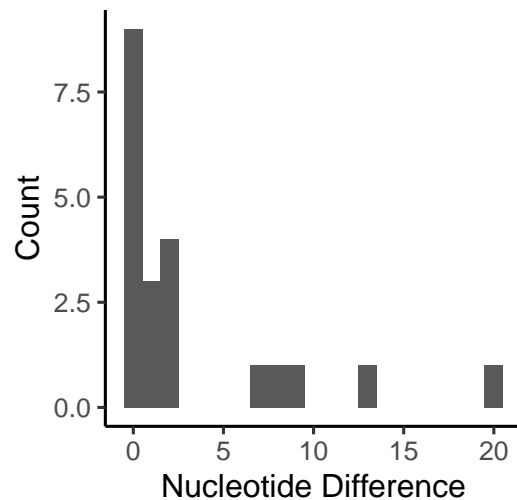
### IGHV3-21\*01\_02

848 sequences assigned  
207 (24.4%) exact matches, in which:  
148 unique CDR3  
6 unique J



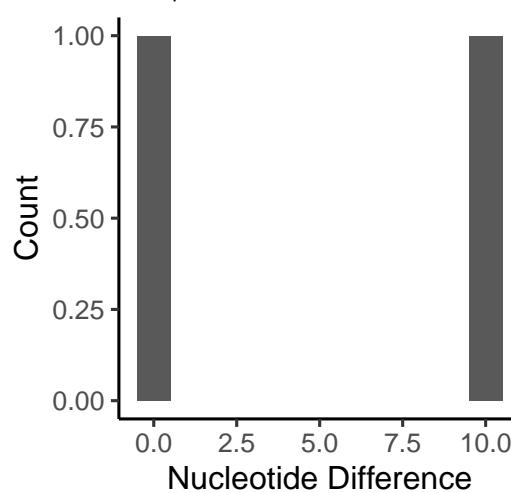
### IGHV3-13\*04

22 sequences assigned  
9 (40.9%) exact matches, in which:  
7 unique CDR3  
4 unique J



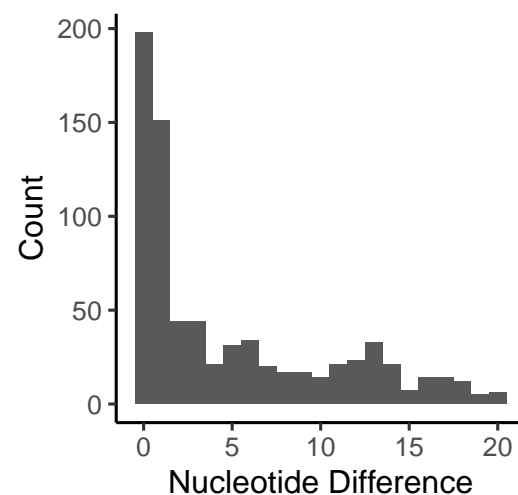
### IGHV3-19\*01

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



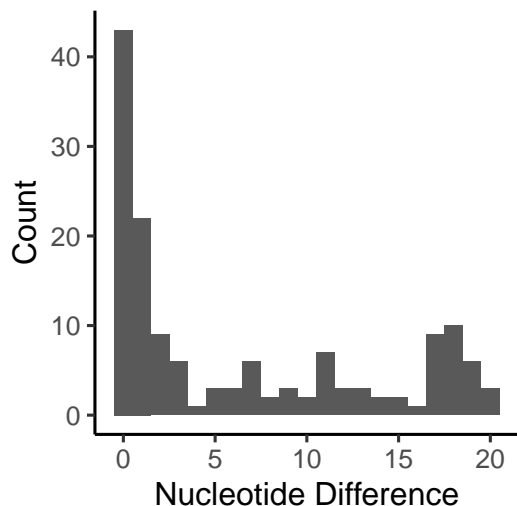
### IGHV3-30-3\*01

806 sequences assigned  
198 (24.6%) exact matches, in which:  
135 unique CDR3  
5 unique J



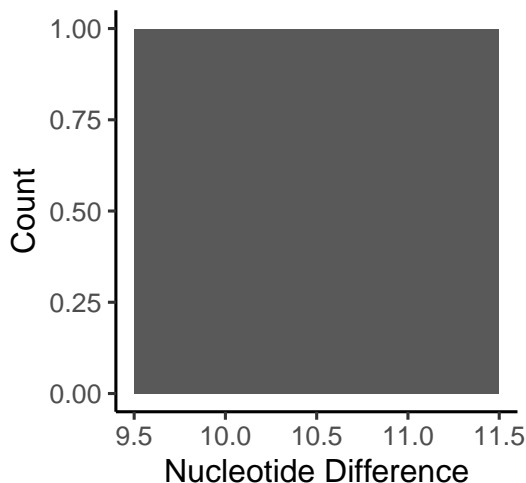
### IGHV3-30\*03

206 sequences assigned  
43 (20.9%) exact matches, in which:  
42 unique CDR3  
5 unique J



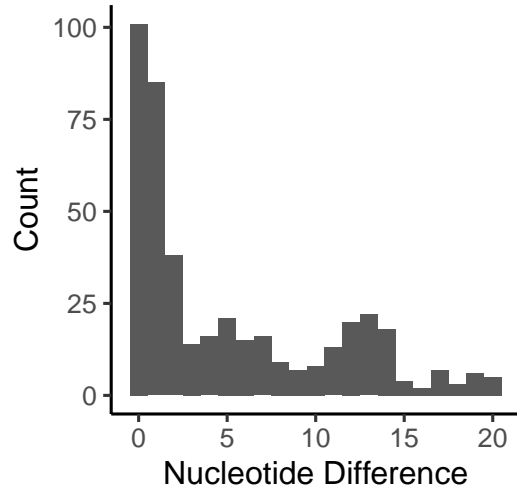
### IGHV3-35\*01

2 sequences assigned  
No exact matches.



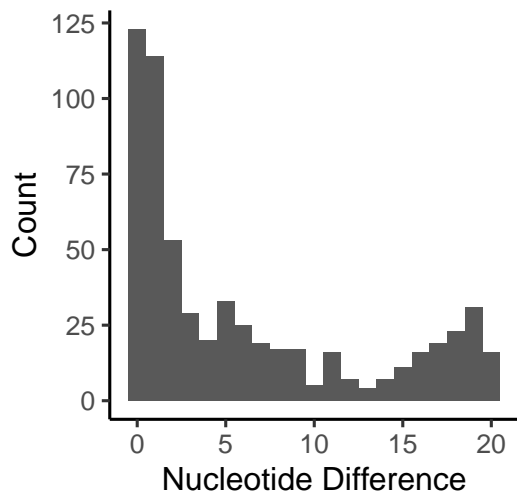
### IGHV3-48\*01

440 sequences assigned  
101 (23%) exact matches, in which:  
70 unique CDR3  
6 unique J



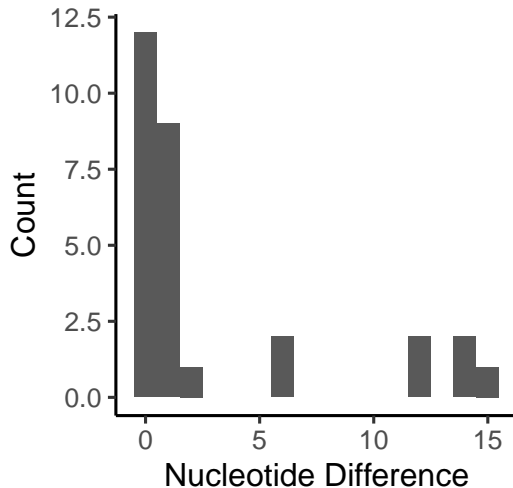
### IGHV3-33\*01

636 sequences assigned  
123 (19.3%) exact matches, in which:  
91 unique CDR3  
6 unique J



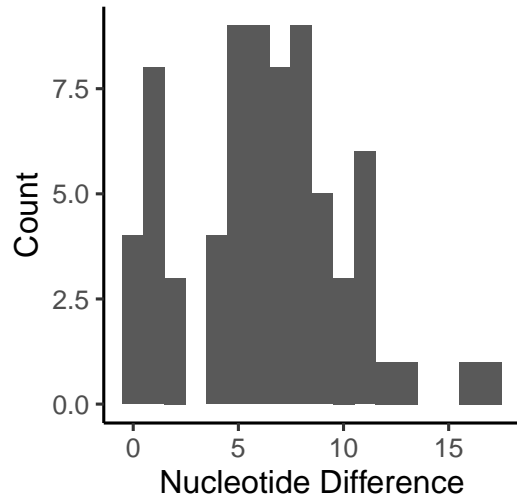
### IGHV3-43\*01

29 sequences assigned  
12 (41.4%) exact matches, in which:  
7 unique CDR3  
2 unique J



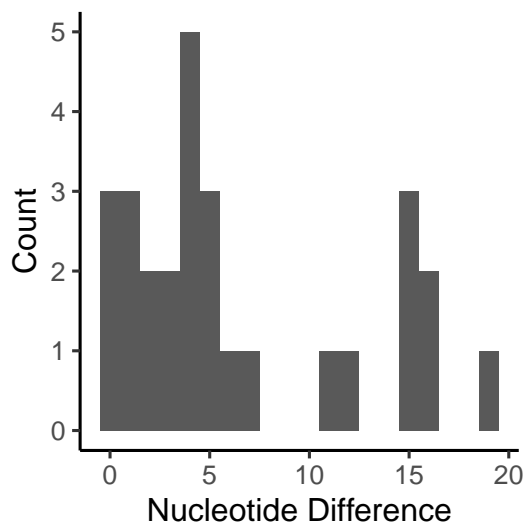
### IGHV3-48\*04

76 sequences assigned  
4 (5.3%) exact matches, in which:  
4 unique CDR3  
2 unique J



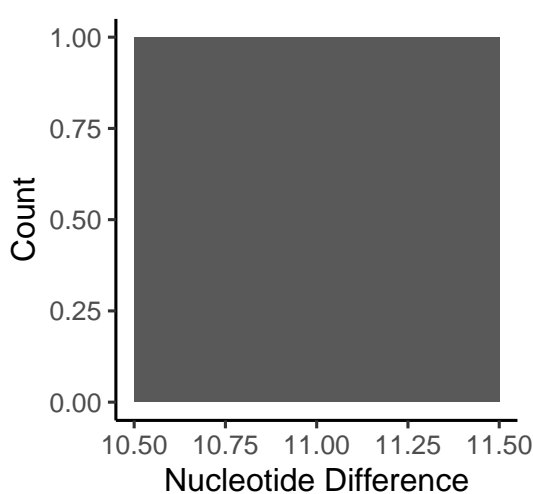
### IGHV3-33\*05

28 sequences assigned  
3 (10.7%) exact matches, in which:  
3 unique CDR3  
3 unique J



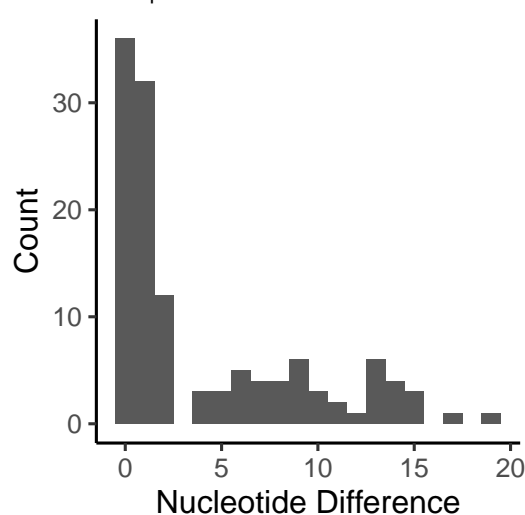
### IGHV3-47\*02

1 sequences assigned  
No exact matches.



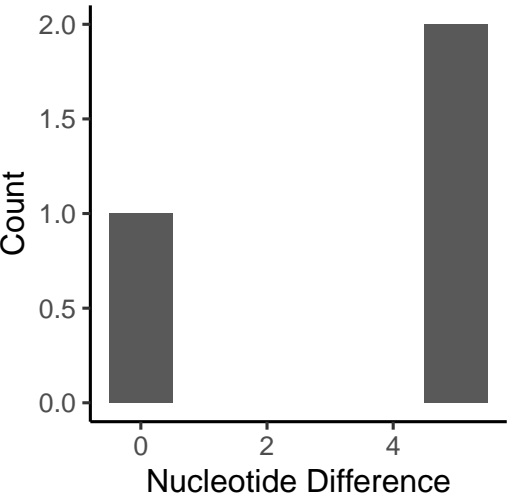
### IGHV3-49\*03\_05

149 sequences assigned  
36 (24.2%) exact matches, in which:  
20 unique CDR3  
3 unique J



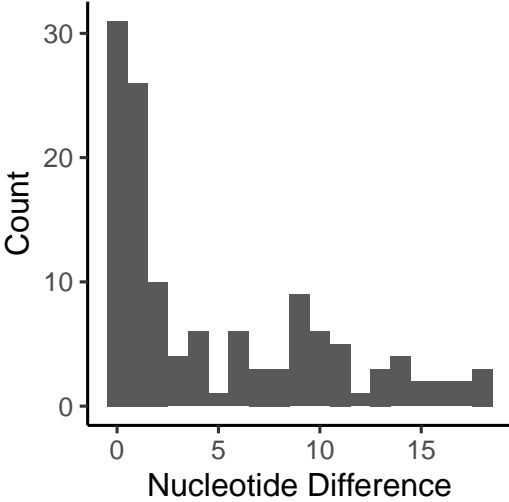
IGHV3-52\*02

3 sequences assigned  
1 (33.3%) exact matches, in which:  
1 unique CDR3  
1 unique J



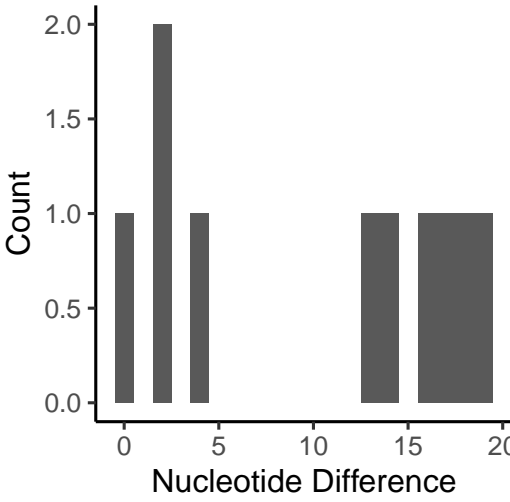
IGHV3-53\*01\_02

131 sequences assigned  
31 (23.7%) exact matches, in which:  
22 unique CDR3  
4 unique J



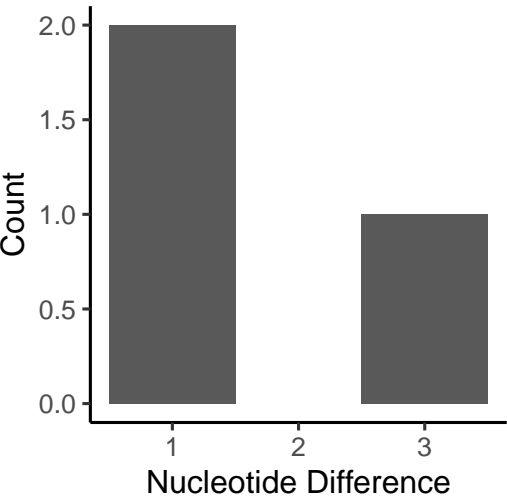
IGHV3-66\*01

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



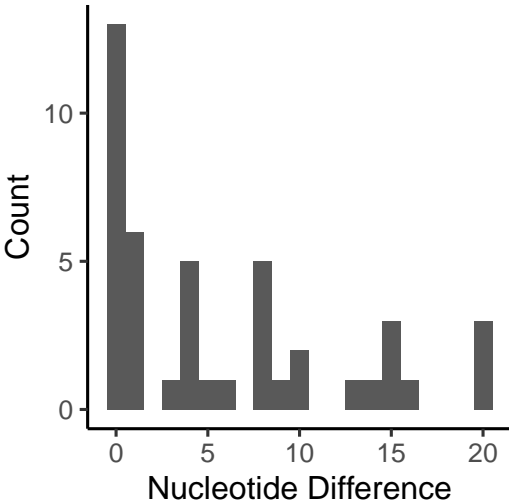
IGHV3-52\*01\_03

3 sequences assigned  
No exact matches.



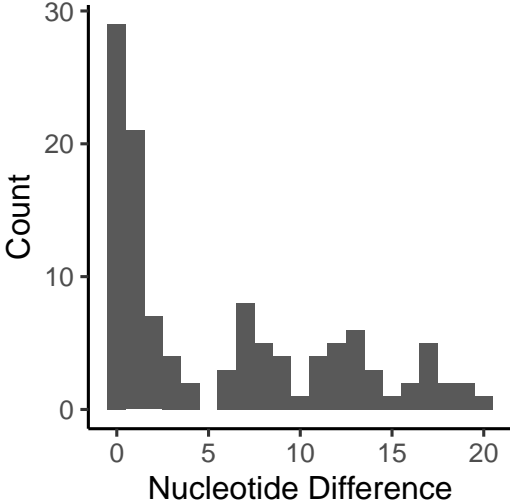
IGHV3-64\*01

60 sequences assigned  
13 (21.7%) exact matches, in which:  
10 unique CDR3  
3 unique J



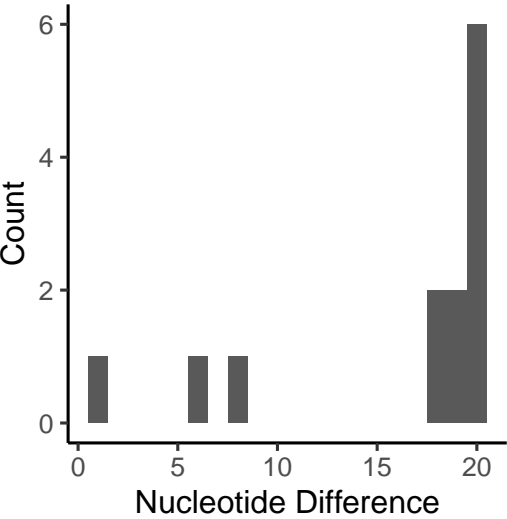
IGHV3-66\*02

125 sequences assigned  
29 (23.2%) exact matches, in which:  
18 unique CDR3  
4 unique J



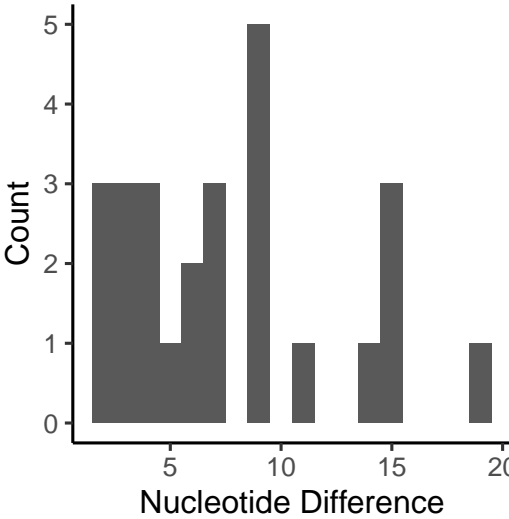
IGHV3-53\*05

21 sequences assigned  
No exact matches.



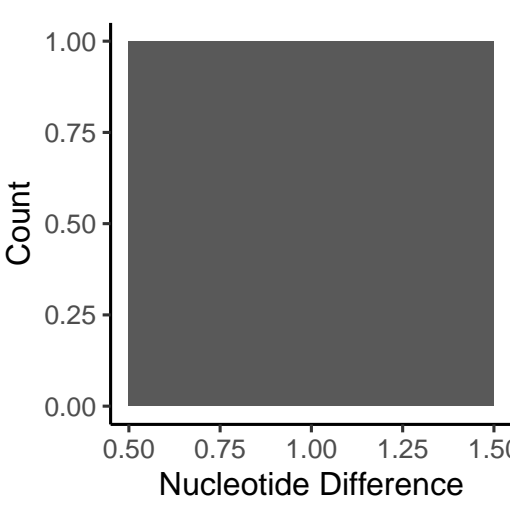
IGHV3-64\*04

28 sequences assigned  
No exact matches.



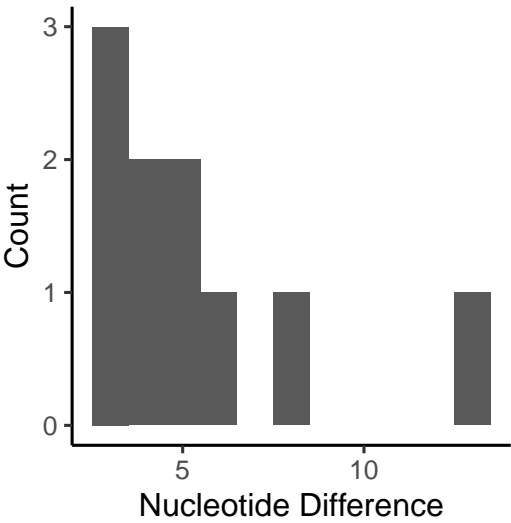
IGHV3-66\*03

1 sequences assigned  
No exact matches.



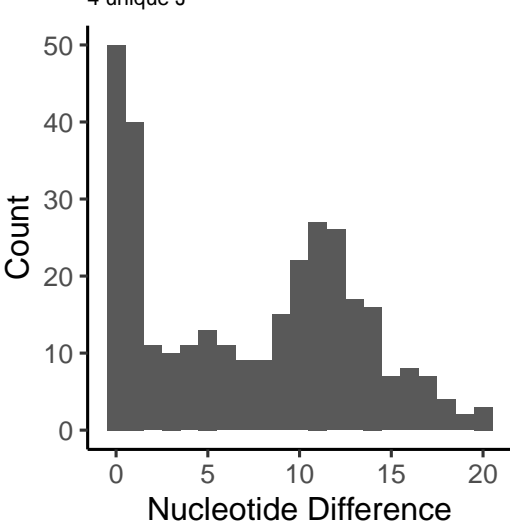
IGHV3-69-1\*01

10 sequences assigned  
No exact matches.



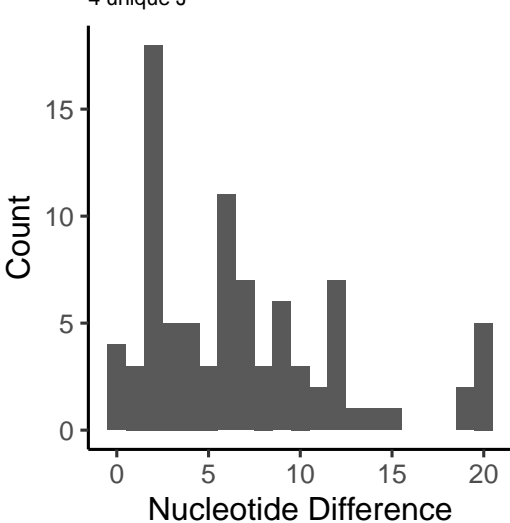
IGHV3-74\*01\_02

360 sequences assigned  
50 (13.9%) exact matches, in which:  
34 unique CDR3  
4 unique J



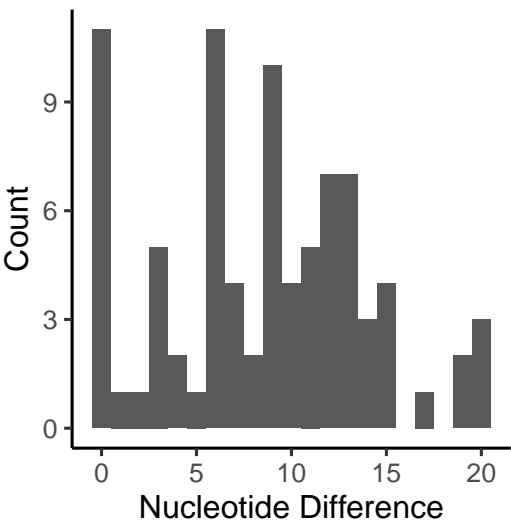
IGHV4-4\*07

94 sequences assigned  
4 (4.3%) exact matches, in which:  
4 unique CDR3  
4 unique J



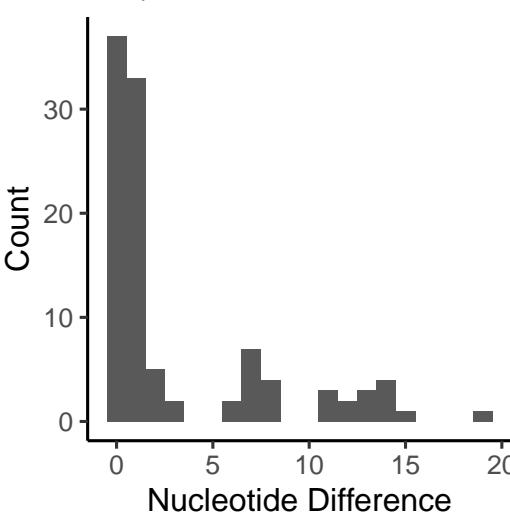
IGHV3-72\*01

84 sequences assigned  
11 (13.1%) exact matches, in which:  
8 unique CDR3  
3 unique J



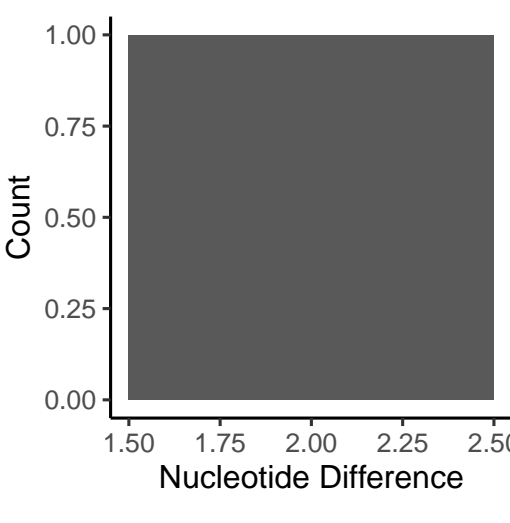
IGHV3-64D\*06

150 sequences assigned  
37 (24.7%) exact matches, in which:  
22 unique CDR3  
3 unique J



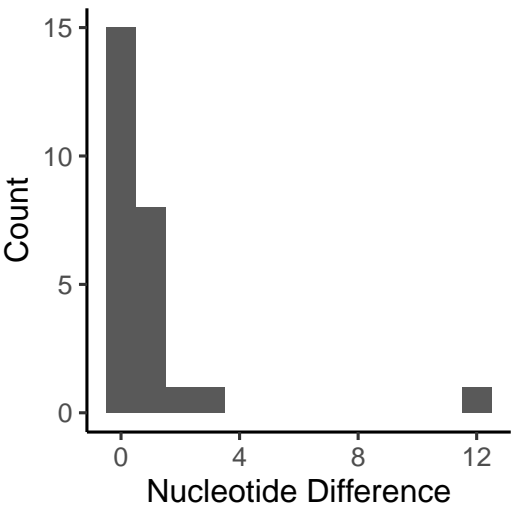
IGHV4-28\*03

1 sequences assigned  
No exact matches.



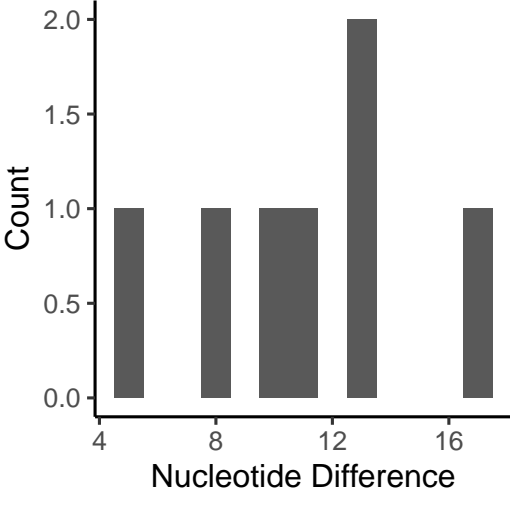
IGHV3-73\*01\_02

28 sequences assigned  
15 (53.6%) exact matches, in which:  
11 unique CDR3  
3 unique J



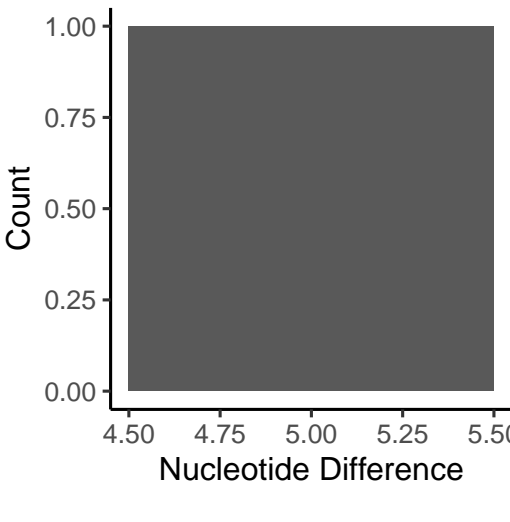
IGHV3-NL1\*01

7 sequences assigned  
No exact matches.



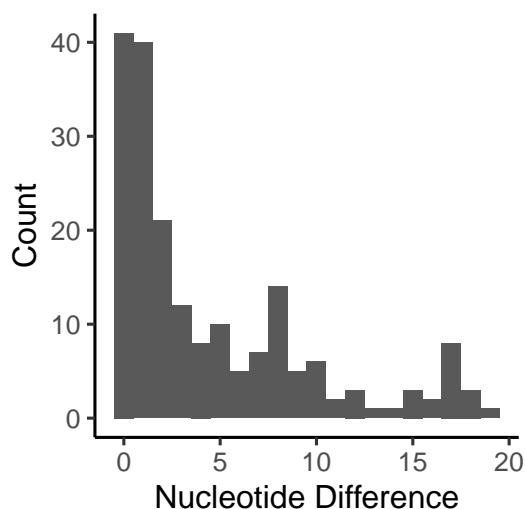
IGHV4-28\*01\_07

1 sequences assigned  
No exact matches.



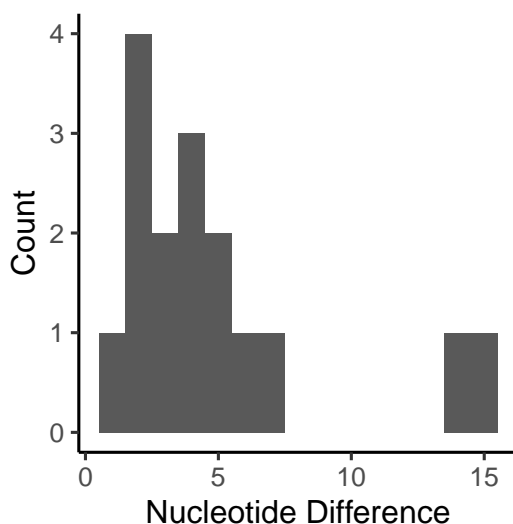
### IGHV4-30-2\*01

193 sequences assigned  
41 (21.2%) exact matches, in which:  
29 unique CDR3  
5 unique J



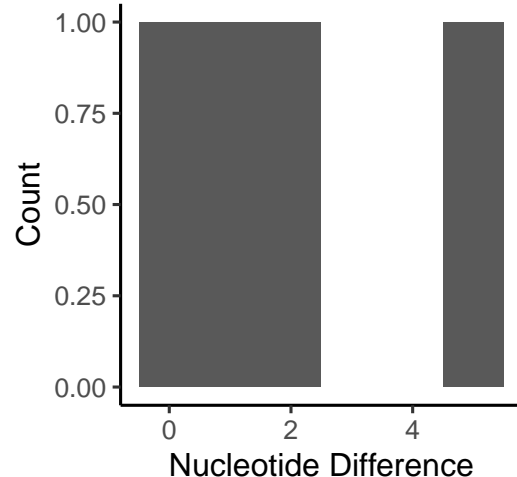
### IGHV4-30-2\*04

16 sequences assigned  
No exact matches.



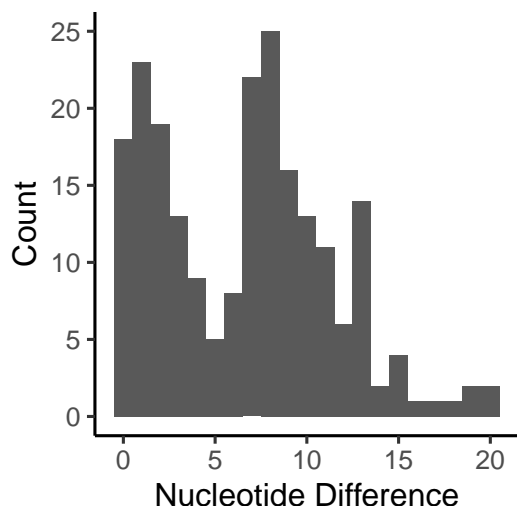
### IGHV4-38-2\*01

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



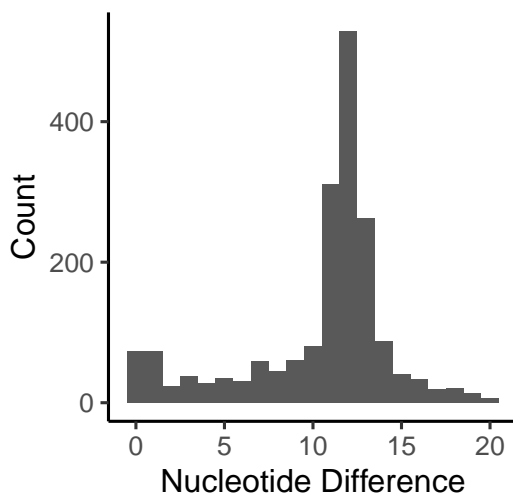
### IGHV4-30-4\*01

231 sequences assigned  
18 (7.8%) exact matches, in which:  
15 unique CDR3  
3 unique J



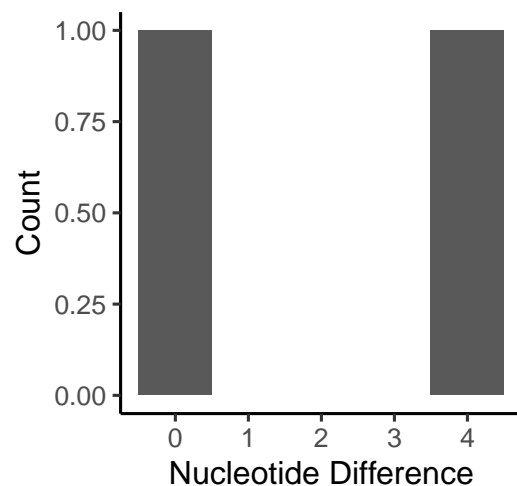
### IGHV4-31\*03\_04

1914 sequences assigned  
74 (3.9%) exact matches, in which:  
64 unique CDR3  
5 unique J



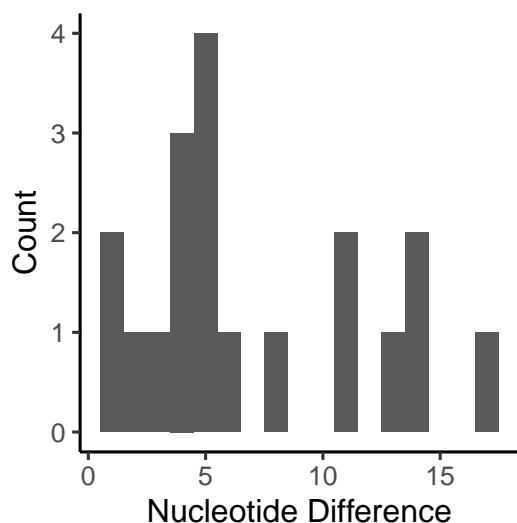
### IGHV4-38-2\*02

12 sequences assigned  
1 (8.3%) exact matches, in which:  
1 unique CDR3  
1 unique J



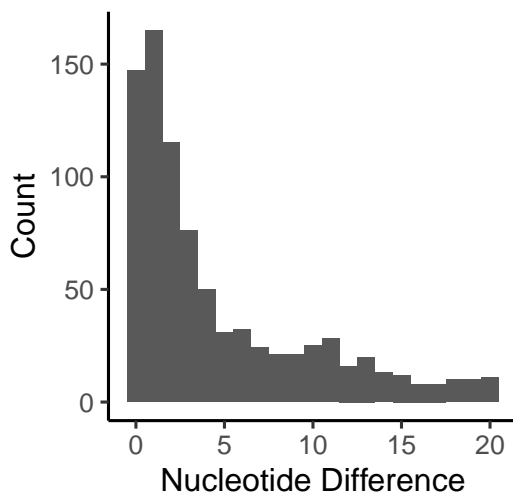
### IGHV4-30-2\*03

19 sequences assigned  
No exact matches.



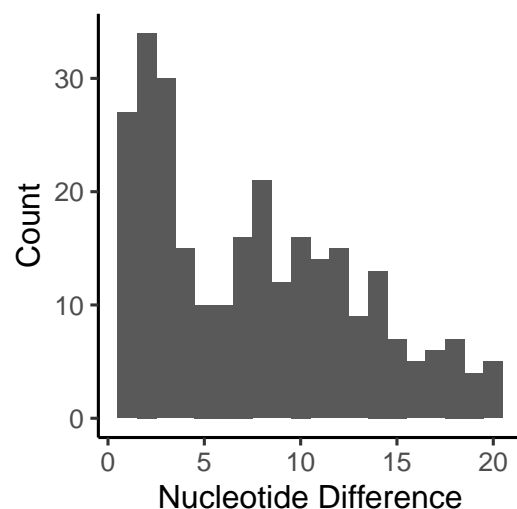
### IGHV4-34\*01\_02

873 sequences assigned  
147 (16.8%) exact matches, in which:  
102 unique CDR3  
4 unique J



### IGHV4-39\*07

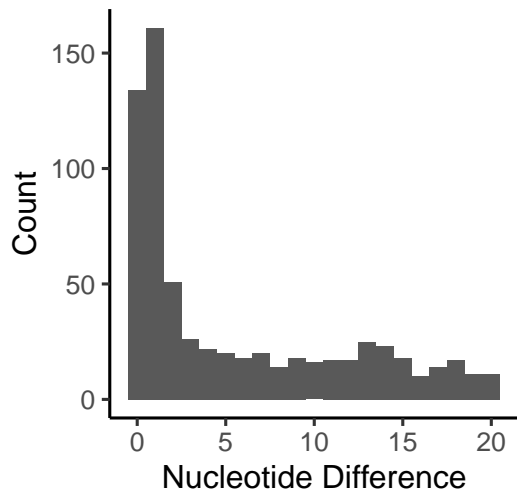
282 sequences assigned  
No exact matches.





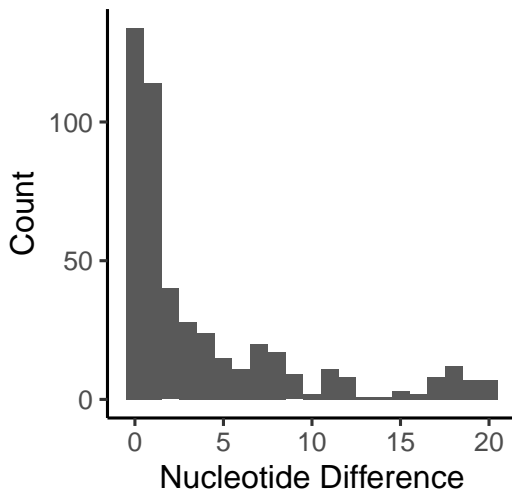
### IGHV4-39\*01\_05

724 sequences assigned  
134 (18.5%) exact matches, in which:  
107 unique CDR3  
6 unique J



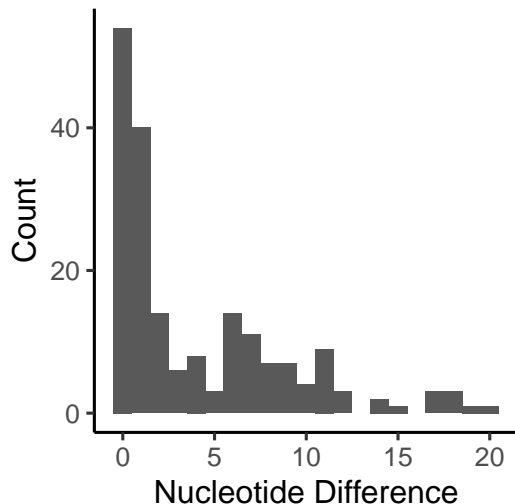
### IGHV4-59\*01\_07

514 sequences assigned  
134 (26.1%) exact matches, in which:  
115 unique CDR3  
5 unique J



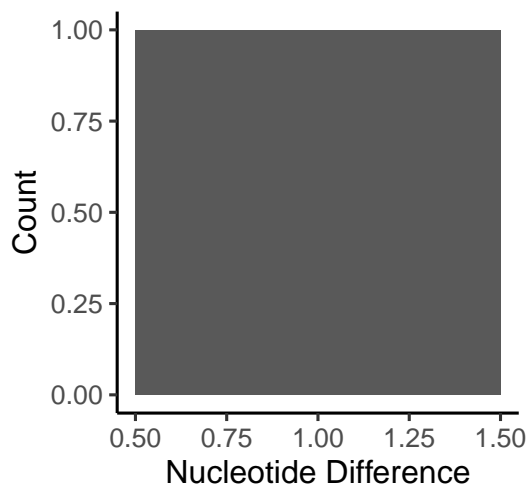
### IGHV5-10-1\*01\_03

193 sequences assigned  
54 (28%) exact matches, in which:  
38 unique CDR3  
4 unique J



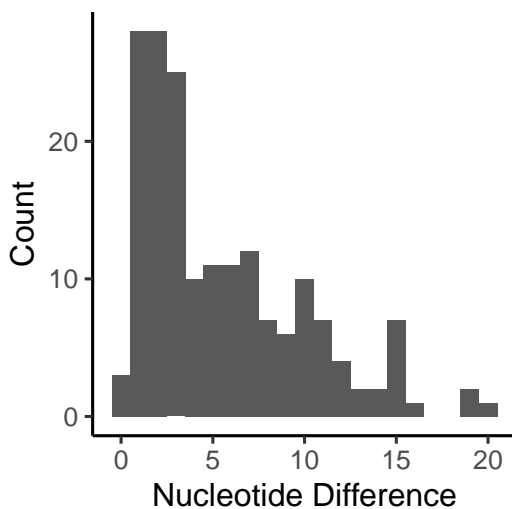
### IGHV4-55\*01\_05

1 sequences assigned  
No exact matches.



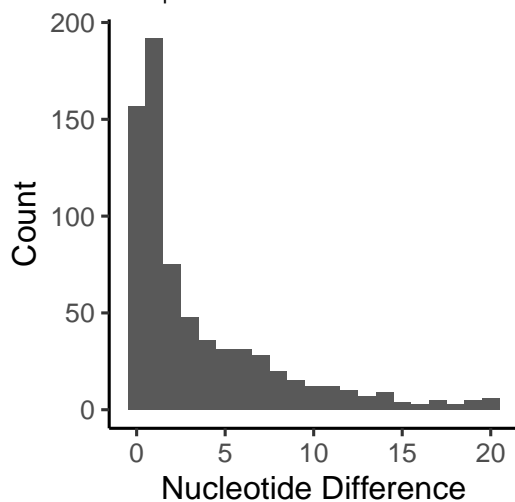
### IGHV4-59\*12

189 sequences assigned  
3 (1.6%) exact matches, in which:  
3 unique CDR3  
3 unique J



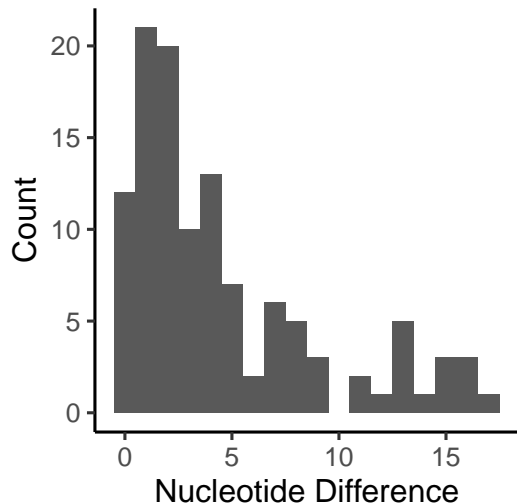
### IGHV5-51\*01\_03

732 sequences assigned  
157 (21.4%) exact matches, in which:  
114 unique CDR3  
5 unique J



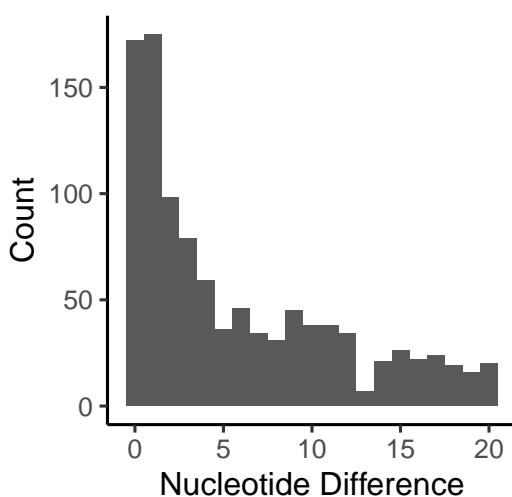
### IGHV4-59\*08

116 sequences assigned  
12 (10.3%) exact matches, in which:  
12 unique CDR3  
5 unique J



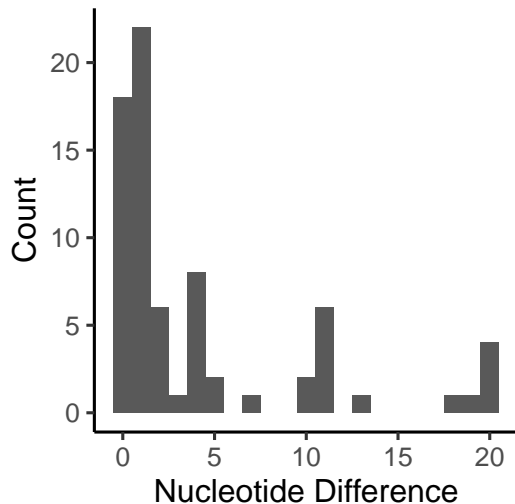
### IGHV4-61\*02

1090 sequences assigned  
172 (15.8%) exact matches, in which:  
143 unique CDR3  
6 unique J



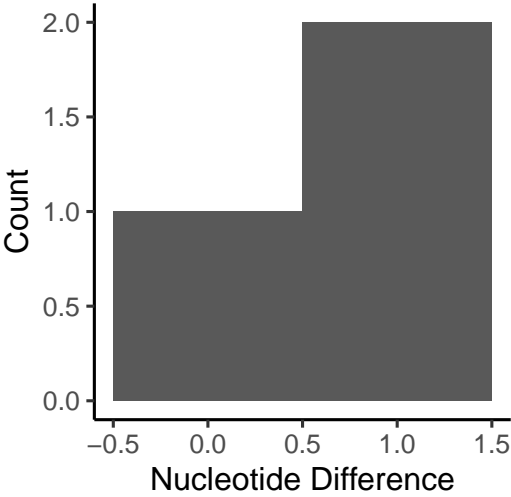
### IGHV6-1\*01\_02

87 sequences assigned  
18 (20.7%) exact matches, in which:  
15 unique CDR3  
3 unique J



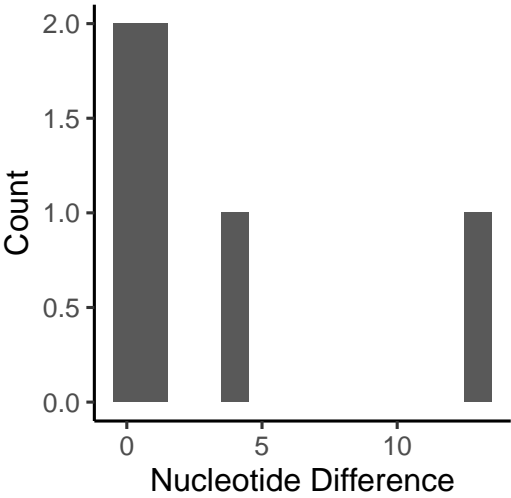
IGHV7-4-1\*01

3 sequences assigned  
1 (33.3%) exact matches, in which:  
1 unique CDR3  
1 unique J



IGHV7-4-1\*02

7 sequences assigned  
2 (28.6%) exact matches, in which:  
2 unique CDR3  
2 unique J





Novel sequence(s) IGHV1-69\*04\_09\_G112A IGHV4-59\*02\_G88A IGHV5-10-1\*01\_03\_T258C IGHV5-51\*07\_A128G are not listed in the genotype and will be ignored.

Warning – no inferred sequences found.

Novel sequence(s) IGHV1-69\*08\_C191T IGHV3-48\*03\_T303G IGHV4-59\*02\_G88A IGHV5-51\*07\_A128G are not listed in the genotype and will be ignored.

Warning – no inferred sequences found.

Warning – no inferred sequences found.

Novel sequence(s) IGHV3-30\*03\_T288C IGHV5-51\*07\_A128G are not listed in the genotype and will be ignored.

Warning: IGHV4-31\*02, IGHV4-31\*03\_04 have identical germline sequences.

Novel sequence(s) IGHV5-51\*07\_A128G are not listed in the genotype and will be ignored.

Novel sequence(s) IGHV1-69\*04\_09\_G112A 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.

Novel sequence(s) IGHV1-69\*08\_C191T IGHV3-30\*03\_T288C IGHV3-30-3\*02\_G75C IGHV4-59\*02\_G88A IGHV5-51\*07\_A128G are not listed in the genotype and will be ignored.

Novel sequence(s) IGHV4-59\*02\_G88A IGHV5-51\*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) IGHV4-4\*02\_03\_C300T IGHV5-51\*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.

Novel sequence(s) IGHV4-59\*02\_G88A are not listed in the genotype and will be ignored.

Novel sequence(s) IGHV1-69\*08\_C191T IGHV3-11\*06\_T300C IGHV3-30\*03\_T288C IGHV4-59\*02\_G88A IGHV5-51\*07\_A128G are not listed in the genotype and will be ignored.

Novel sequence(s) IGHV4-59\*02\_G88A IGHV5-51\*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.

Warning – no inferred sequences found.

Novel sequence(s) IGHV3-30\*03\_T288C IGHV3-30-3\*01\_T288C IGHV4-59\*02\_G88A IGHV5-10-1\*01\_03\_T258C IGHV5-51\*07\_A128G are not listed in the genotype and will be ignored.

Warning – no inferred sequences found.

Novel sequence(s) IGHV3-48\*04\_A193T\_C198T\_A200C\_C201T\_T210A are not listed in the genotype and will be ignored.

Novel sequence(s) IGHV4-59\*02\_G88A are not listed in the genotype and will be ignored.