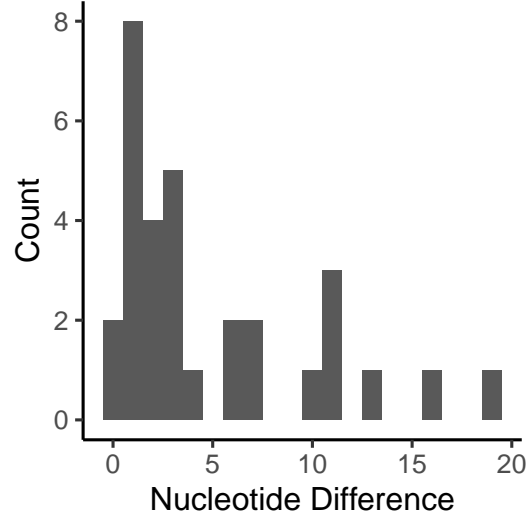


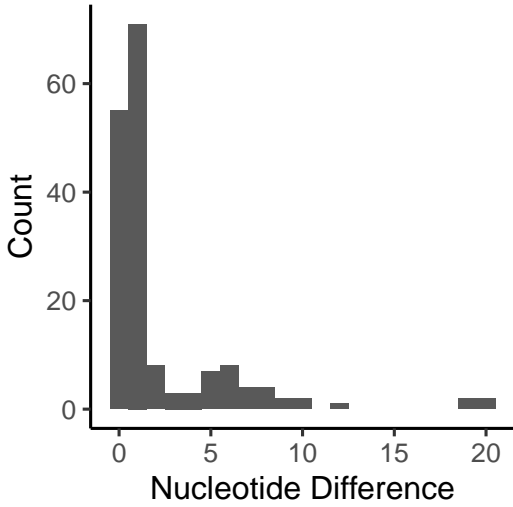
### IGHV1-2\*02

31 sequences assigned  
2 (6.5%) exact matches, in which:  
1 unique CDR3  
1 unique J



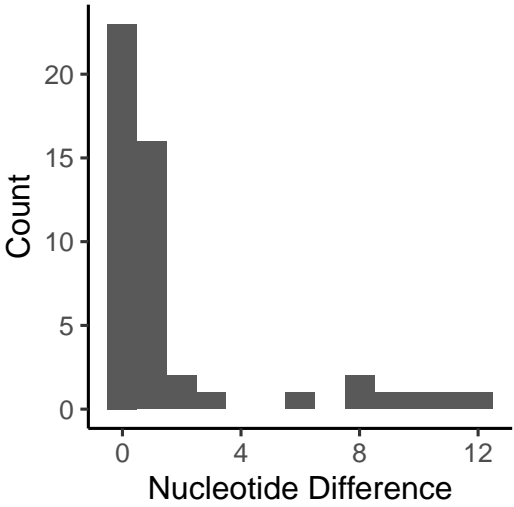
### IGHV1-8\*01

175 sequences assigned  
55 (31.4%) exact matches, in which:  
50 unique CDR3  
5 unique J



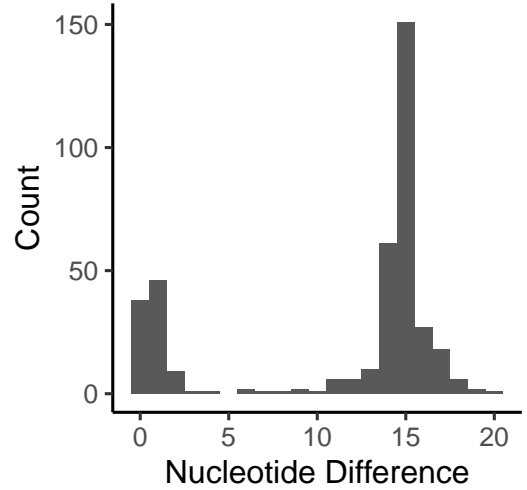
### IGHV1-24\*01

49 sequences assigned  
23 (46.9%) exact matches, in which:  
23 unique CDR3  
6 unique J



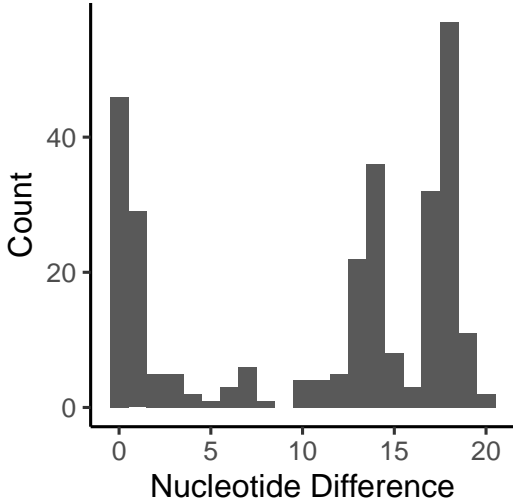
### IGHV1-2\*04

392 sequences assigned  
38 (9.7%) exact matches, in which:  
37 unique CDR3  
6 unique J



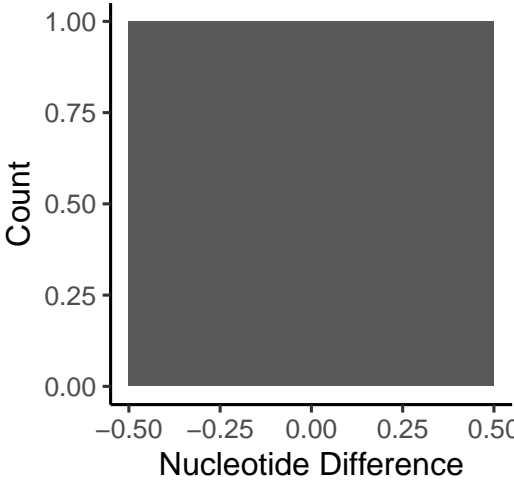
### IGHV1-18\*01

287 sequences assigned  
46 (16%) exact matches, in which:  
46 unique CDR3  
7 unique J



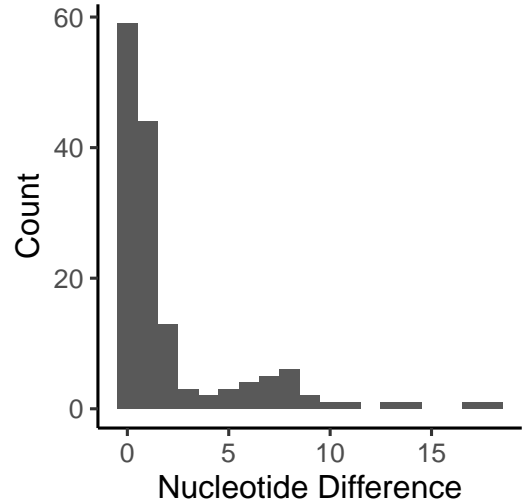
### IGHV1-38-4\*01

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



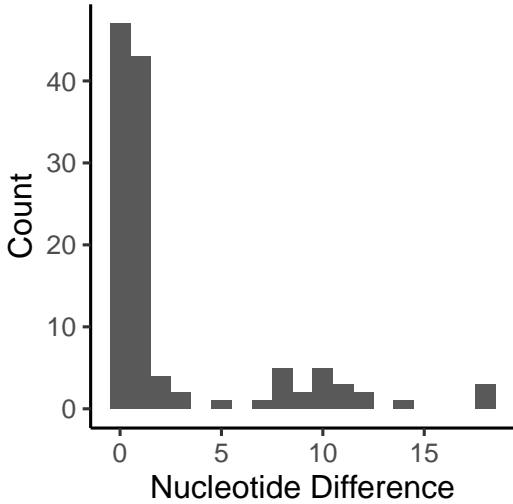
### IGHV1-3\*01\_05

147 sequences assigned  
59 (40.1%) exact matches, in which:  
52 unique CDR3  
6 unique J



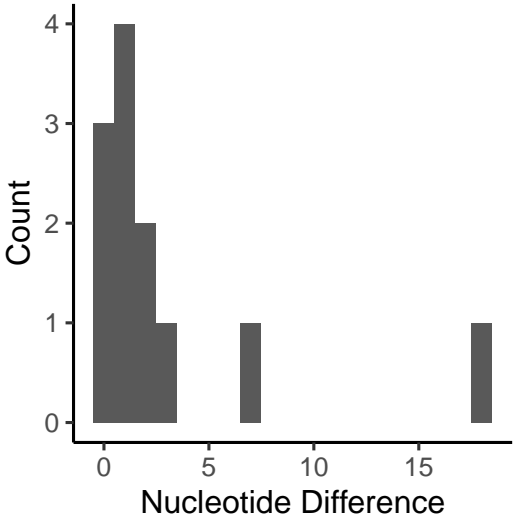
### IGHV1-18\*04

121 sequences assigned  
47 (38.8%) exact matches, in which:  
46 unique CDR3  
5 unique J



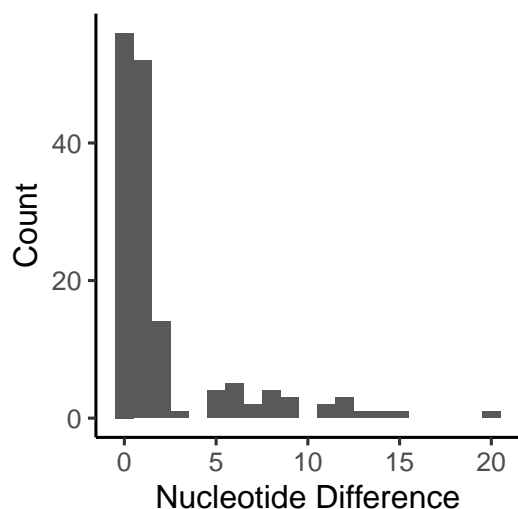
### IGHV1-45\*02

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



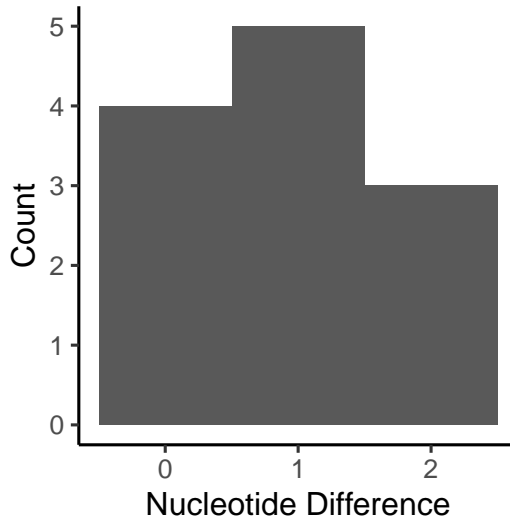
### IGHV1-46\*01

151 sequences assigned  
56 (37.1%) exact matches, in which:  
52 unique CDR3  
6 unique J



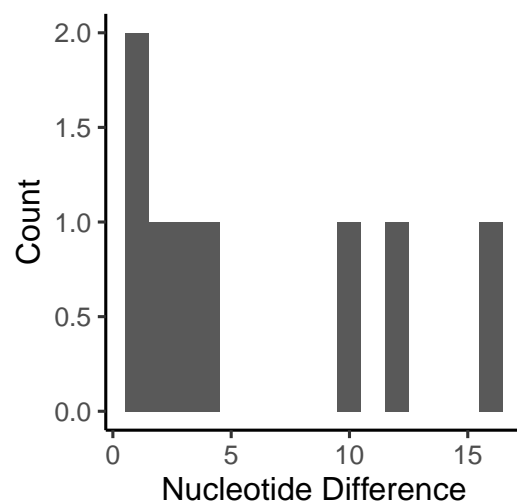
### IGHV1-58\*01\_03

12 sequences assigned  
4 (33.3%) exact matches, in which:  
4 unique CDR3  
2 unique J



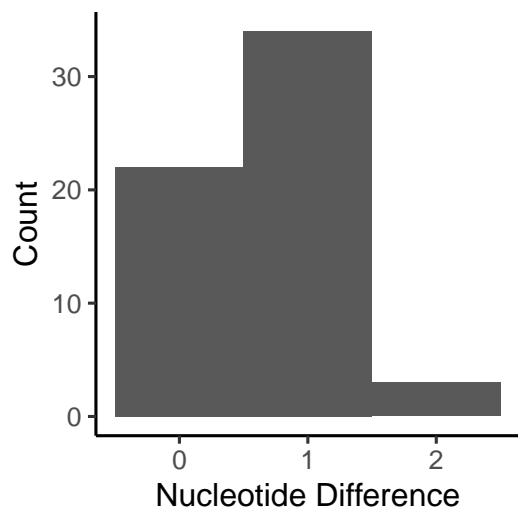
### IGHV1-69D\*01

8 sequences assigned  
No exact matches.



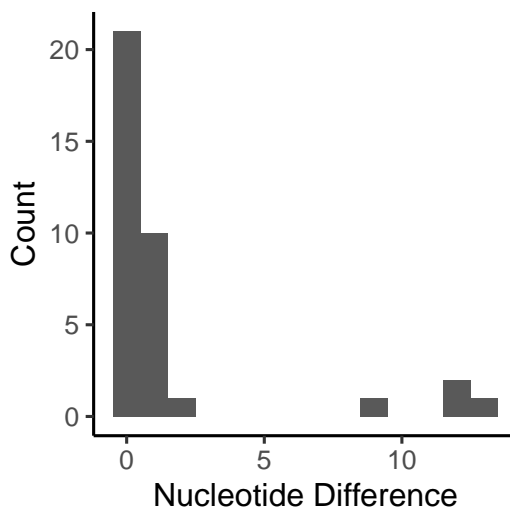
### IGHV1-46\*03

59 sequences assigned  
22 (37.3%) exact matches, in which:  
20 unique CDR3  
5 unique J



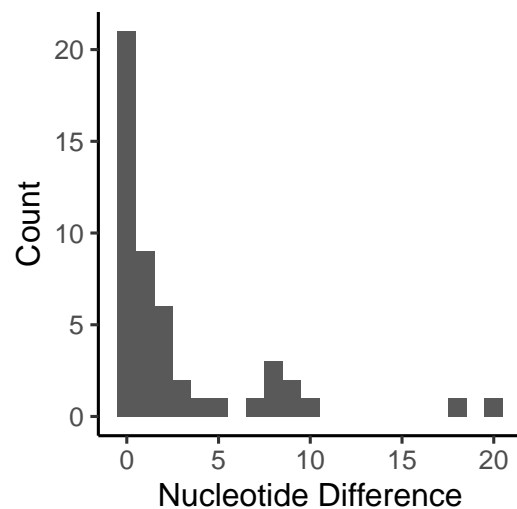
### IGHV1-69\*02

36 sequences assigned  
21 (58.3%) exact matches, in which:  
20 unique CDR3  
5 unique J



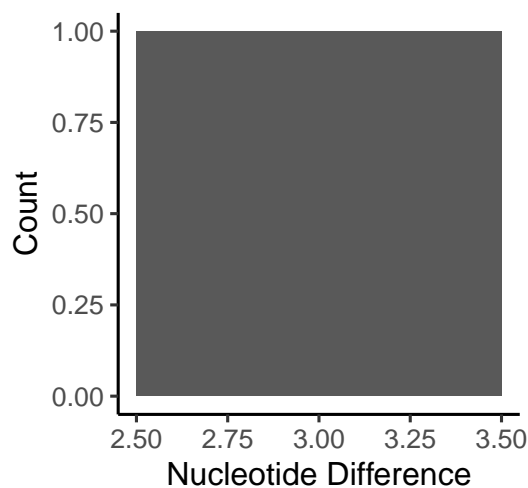
### IGHV2-5\*02

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



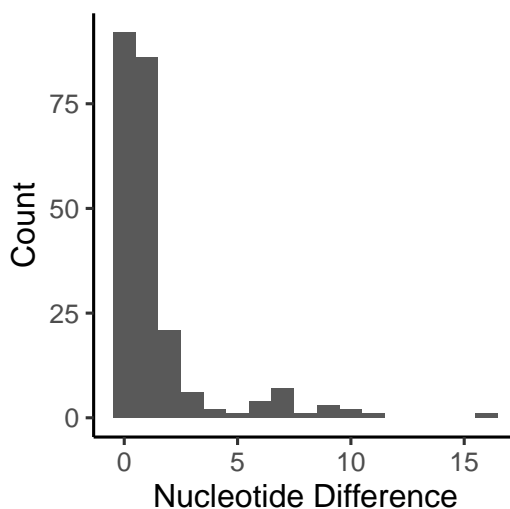
### IGHV1-58\*02

1 sequences assigned  
No exact matches.



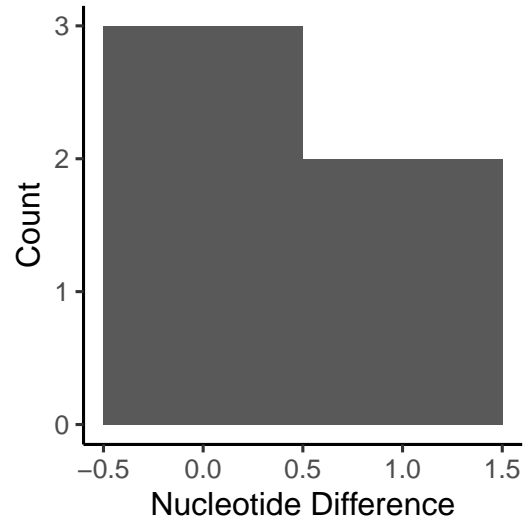
### IGHV1-69\*04\_09

227 sequences assigned  
92 (40.5%) exact matches, in which:  
87 unique CDR3  
7 unique J



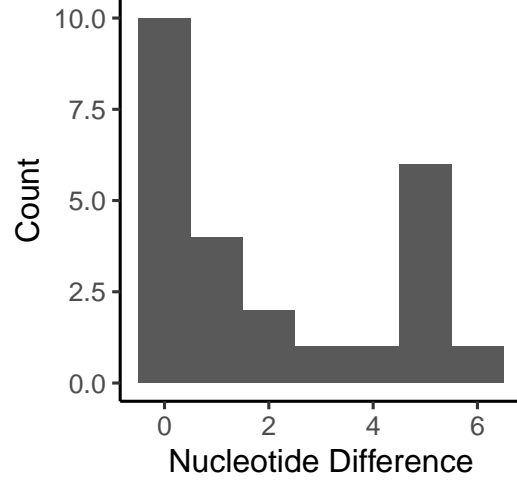
### IGHV2-26\*01

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



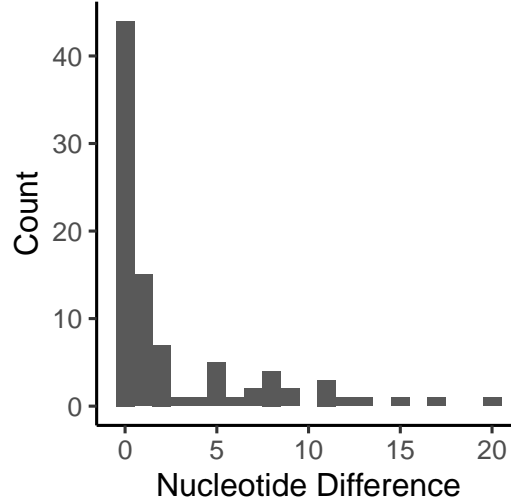
### IGHV2-70\*11\_15

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



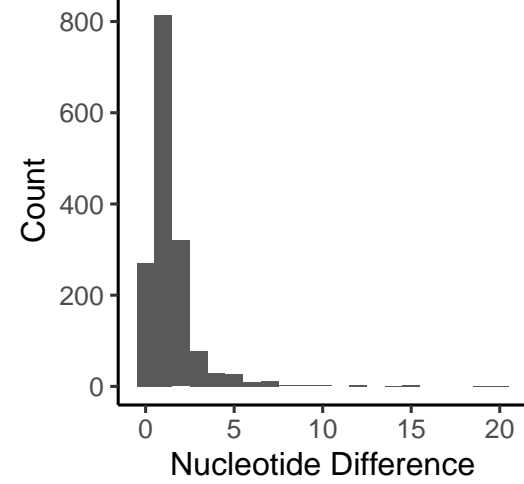
### IGHV3-9\*01

90 sequences assigned  
44 (48.9%) exact matches, in which:  
30 unique CDR3  
5 unique J



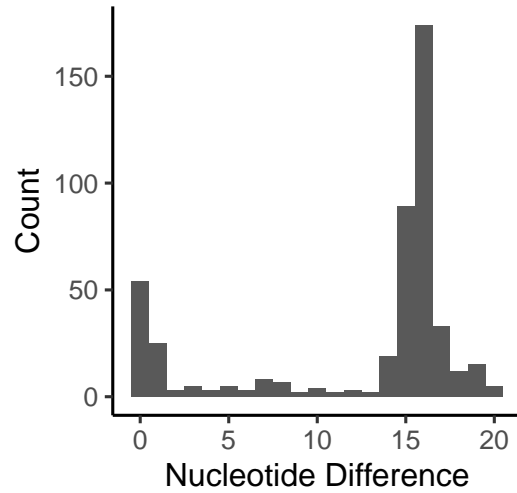
### IGHV3-11\*06

1581 sequences assigned  
271 (17.1%) exact matches, in which:  
104 unique CDR3  
7 unique J



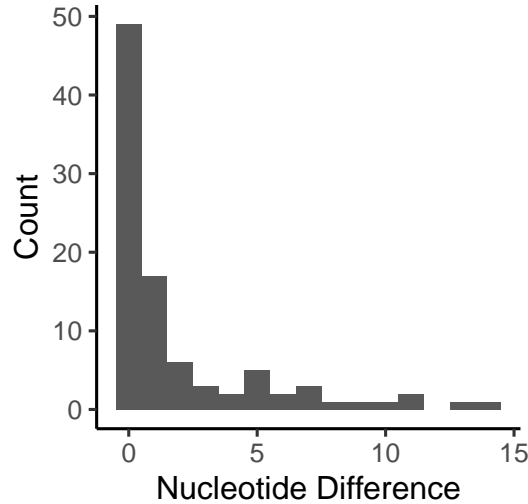
### IGHV3-7\*01

491 sequences assigned  
54 (11%) exact matches, in which:  
37 unique CDR3  
7 unique J



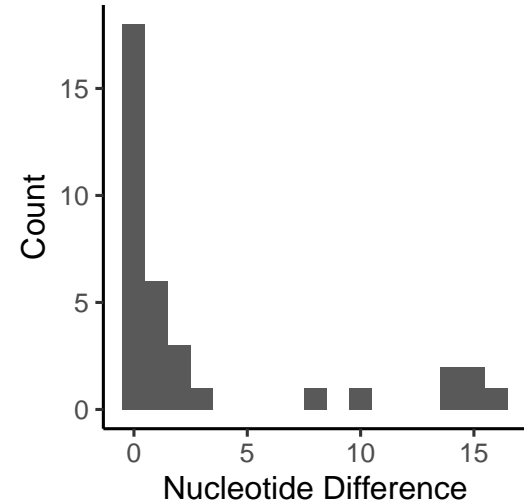
### IGHV3-11\*01

96 sequences assigned  
49 (51%) exact matches, in which:  
31 unique CDR3  
3 unique J



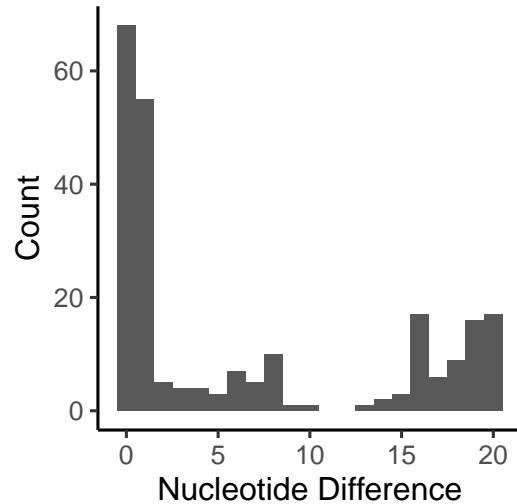
### IGHV3-13\*01

35 sequences assigned  
18 (51.4%) exact matches, in which:  
13 unique CDR3  
4 unique J



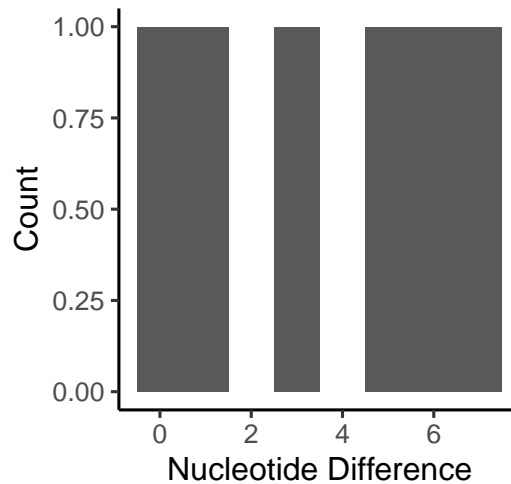
### IGHV3-7\*03

551 sequences assigned  
68 (12.3%) exact matches, in which:  
46 unique CDR3  
5 unique J



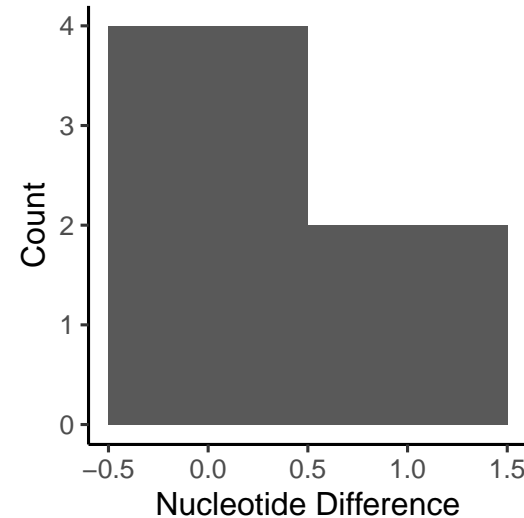
### IGHV3-11\*04

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



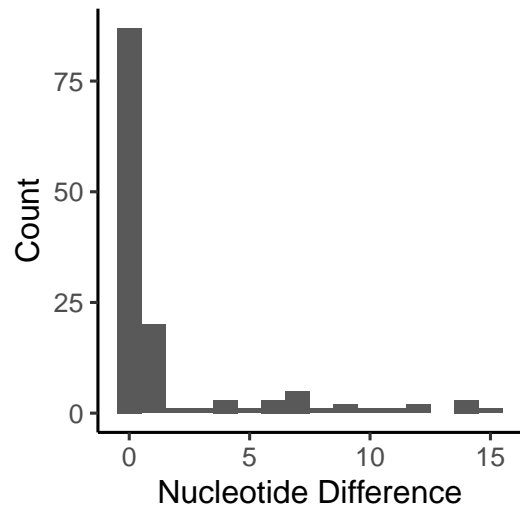
### IGHV3-13\*05

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



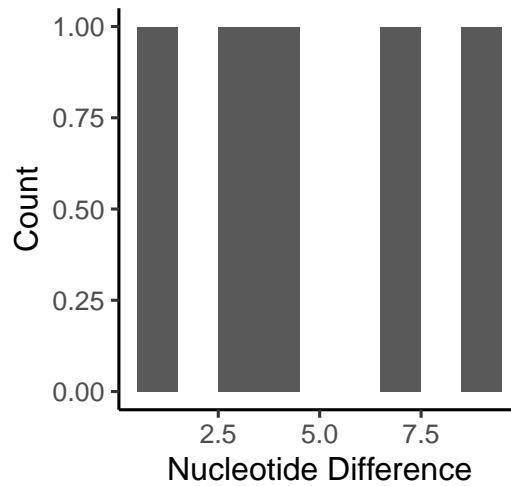
### IGHV3-15\*01\_02

133 sequences assigned  
87 (65.4%) exact matches, in which:  
61 unique CDR3  
6 unique J



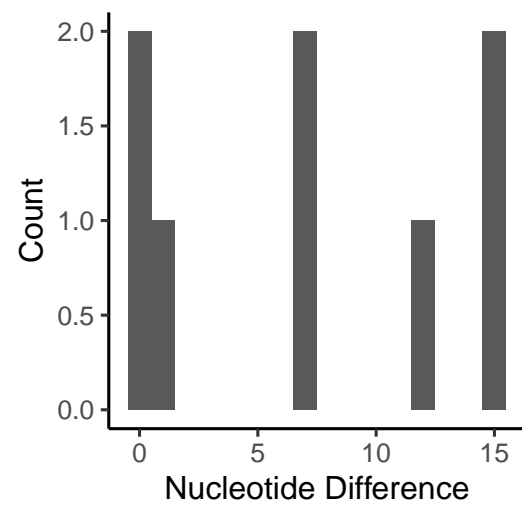
### IGHV3-20\*03\_04

5 sequences assigned  
No exact matches.



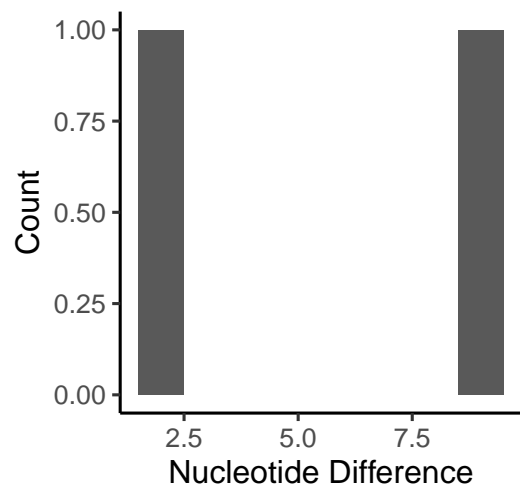
### IGHV3-30-5\*01

10 sequences assigned  
2 (20%) exact matches, in which:  
2 unique CDR3  
2 unique J



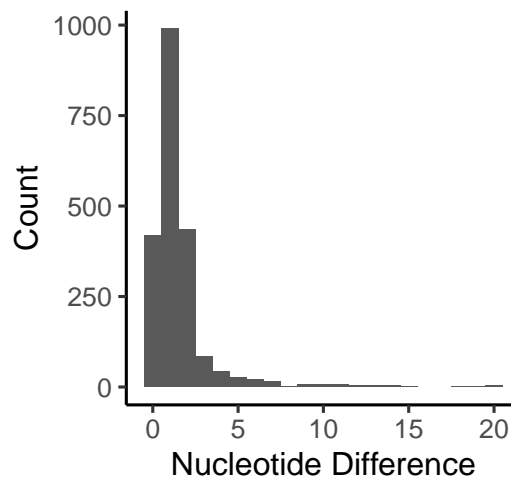
### IGHV3-19\*01

2 sequences assigned  
No exact matches.



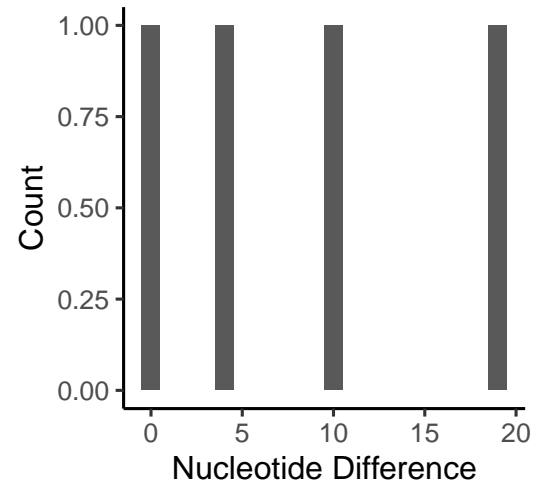
### IGHV3-21\*01\_02

2079 sequences assigned  
420 (20.2%) exact matches, in which:  
172 unique CDR3  
6 unique J



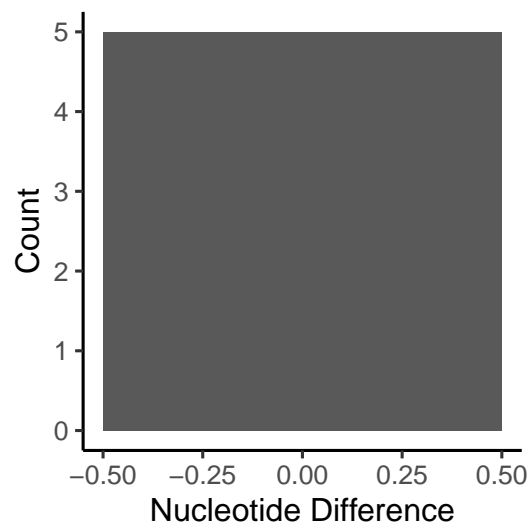
### IGHV3-30-5\*02

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



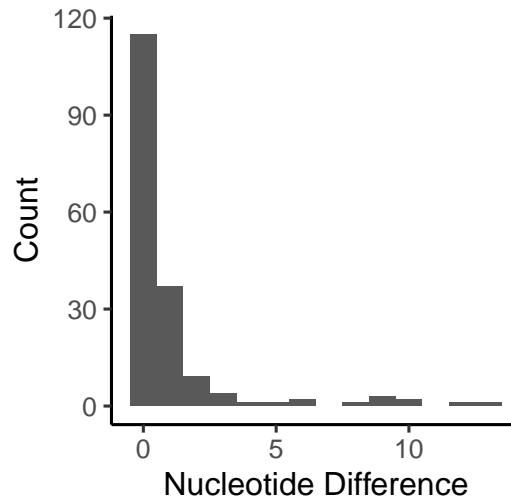
### IGHV3-20\*01\_02

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



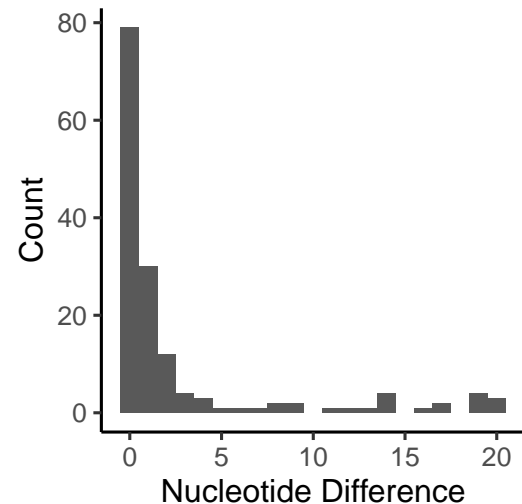
### IGHV3-30\*01

177 sequences assigned  
115 (65%) exact matches, in which:  
79 unique CDR3  
6 unique J



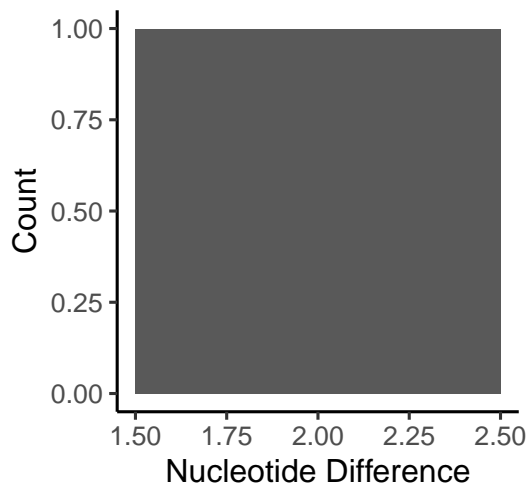
### IGHV3-33\*01

171 sequences assigned  
79 (46.2%) exact matches, in which:  
52 unique CDR3  
5 unique J



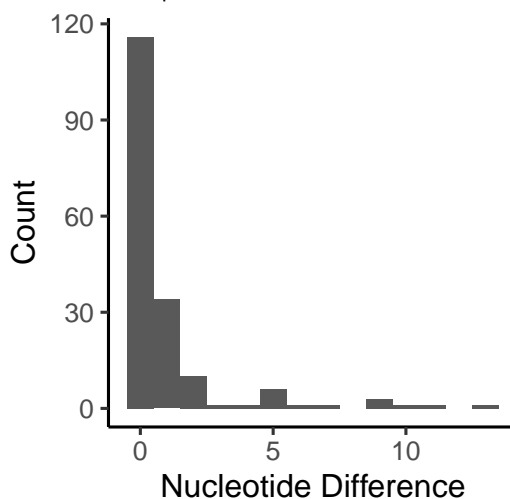
### IGHV3-38-3\*01

1 sequences assigned  
No exact matches.



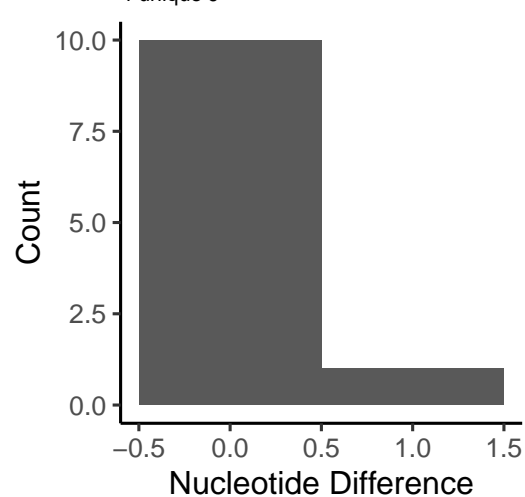
### IGHV3-48\*02

180 sequences assigned  
116 (64.4%) exact matches, in which:  
72 unique CDR3  
6 unique J



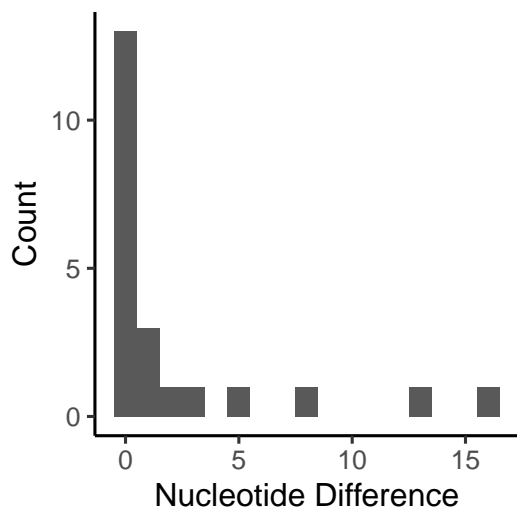
### IGHV3-49\*03\_05

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



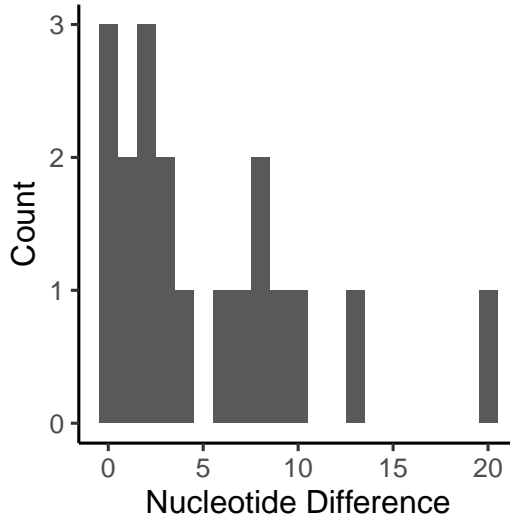
### IGHV3-43\*01

22 sequences assigned  
13 (59.1%) exact matches, in which:  
9 unique CDR3  
4 unique J



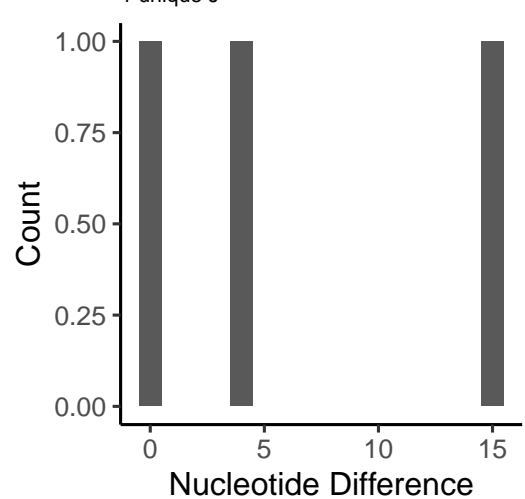
### IGHV3-48\*04

21 sequences assigned  
3 (14.3%) exact matches, in which:  
3 unique CDR3  
3 unique J



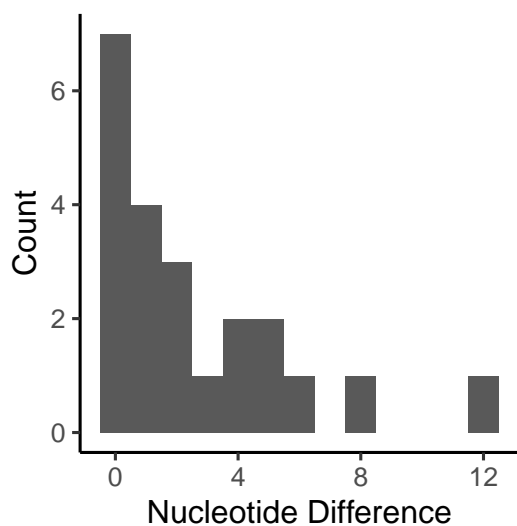
### IGHV3-52\*01\_03

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



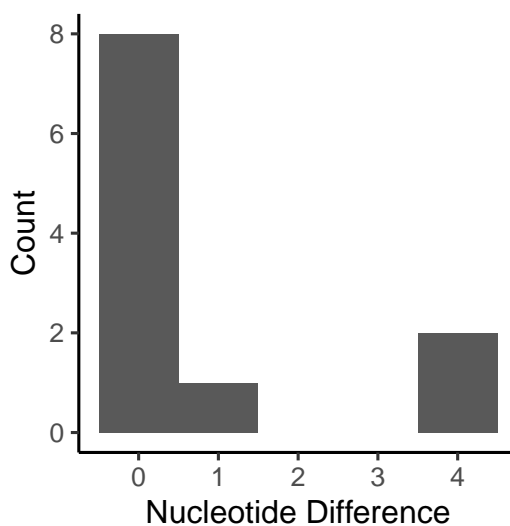
### IGHV3-48\*01

22 sequences assigned  
7 (31.8%) exact matches, in which:  
7 unique CDR3  
5 unique J



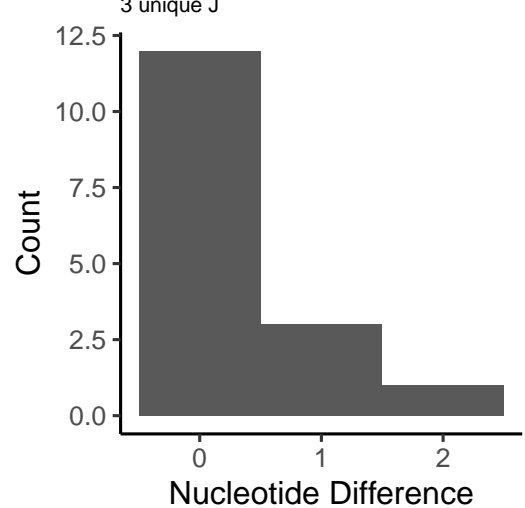
### IGHV3-49\*04

11 sequences assigned  
8 (72.7%) exact matches, in which:  
6 unique CDR3  
4 unique J



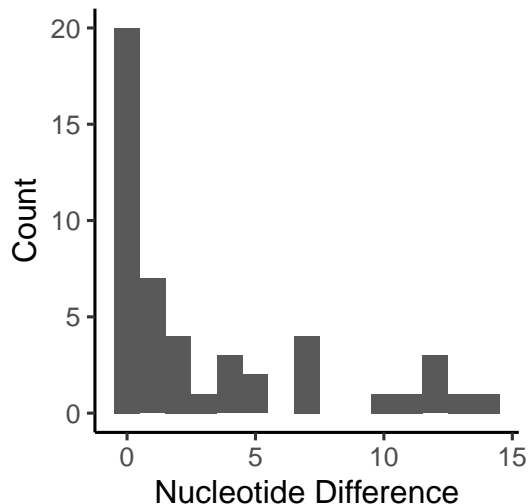
### IGHV3-53\*04

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



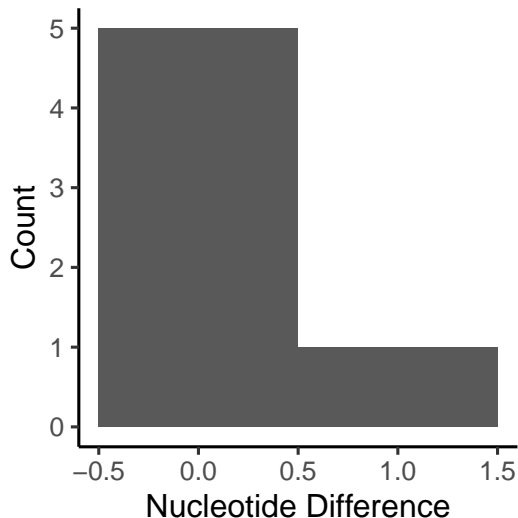
### IGHV3-53\*01\_02

48 sequences assigned  
20 (41.7%) exact matches, in which:  
15 unique CDR3  
5 unique J



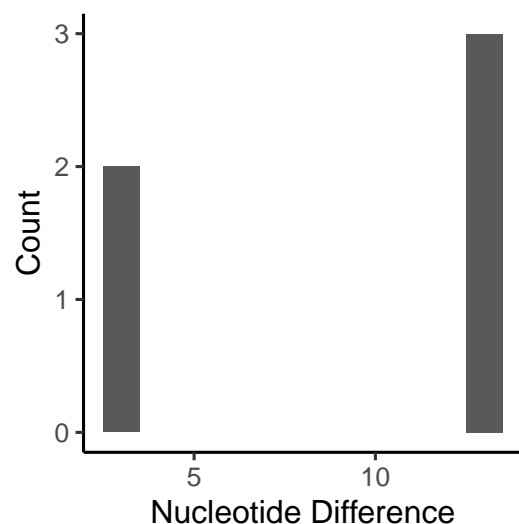
### IGHV3-64\*02\_07

6 sequences assigned  
5 (83.3%) exact matches, in which:  
2 unique CDR3  
1 unique J



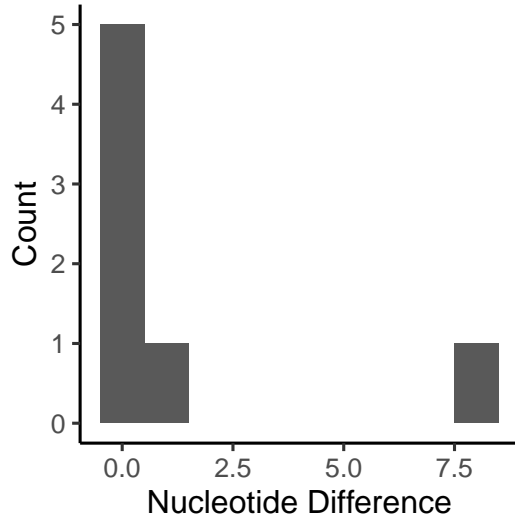
### IGHV3-69-1\*01

5 sequences assigned  
No exact matches.



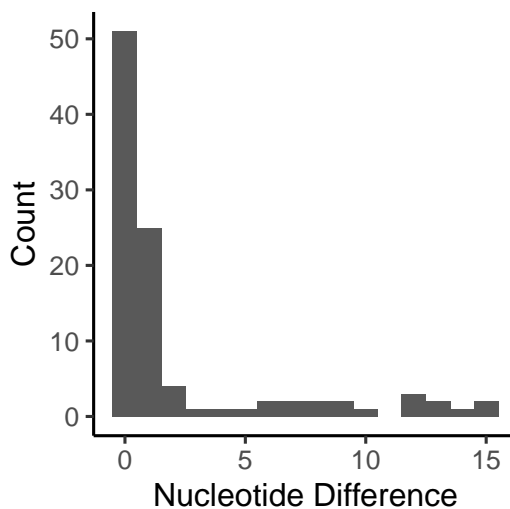
### IGHV3-64\*01

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



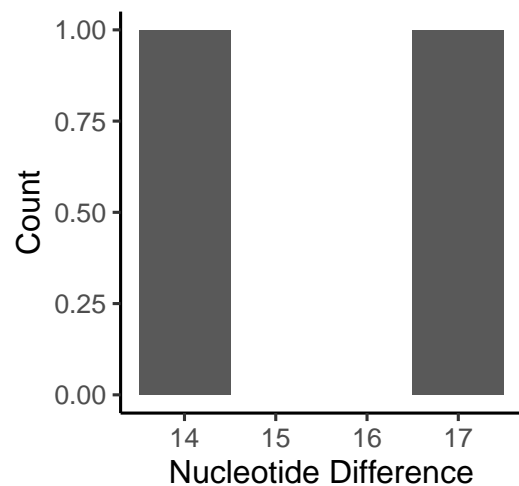
### IGHV3-66\*01

101 sequences assigned  
51 (50.5%) exact matches, in which:  
31 unique CDR3  
5 unique J



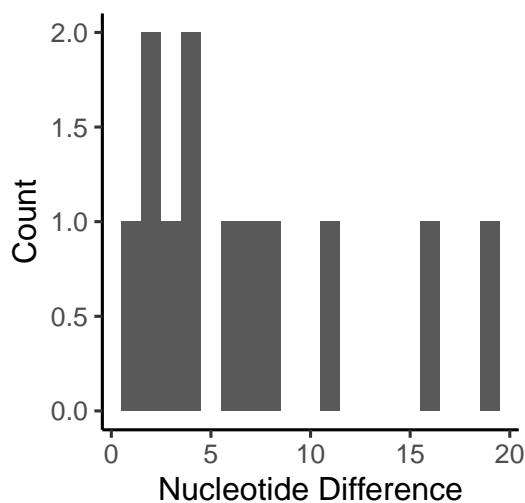
### IGHV3-69-1\*02

2 sequences assigned  
No exact matches.



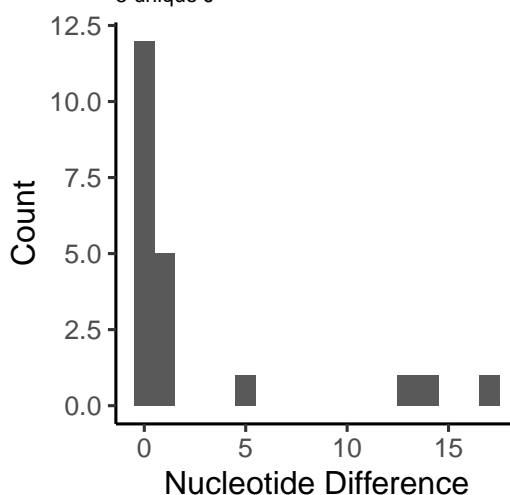
### IGHV3-64\*04

16 sequences assigned  
No exact matches.



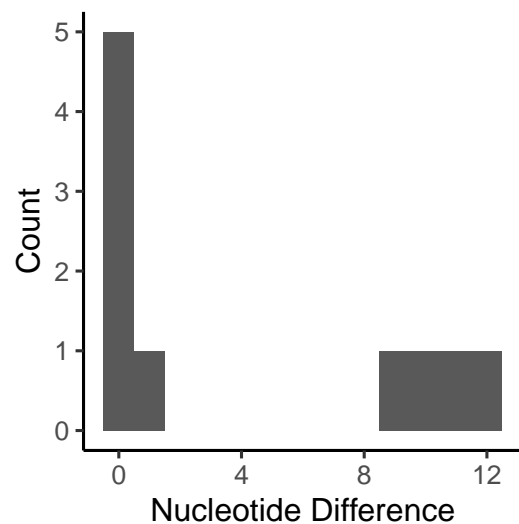
### IGHV3-66\*02

22 sequences assigned  
12 (54.5%) exact matches, in which:  
9 unique CDR3  
5 unique J



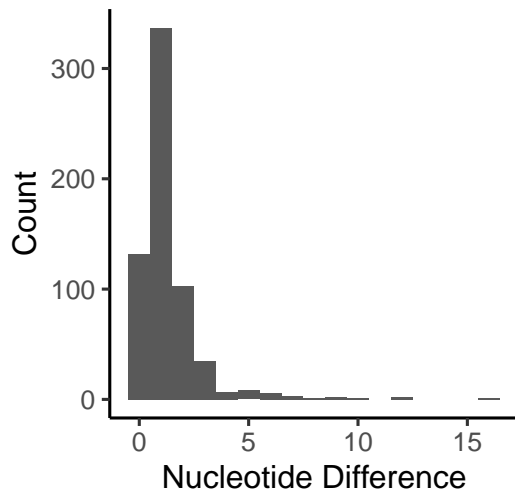
### IGHV3-72\*01

11 sequences assigned  
5 (45.5%) exact matches, in which:  
3 unique CDR3  
3 unique J



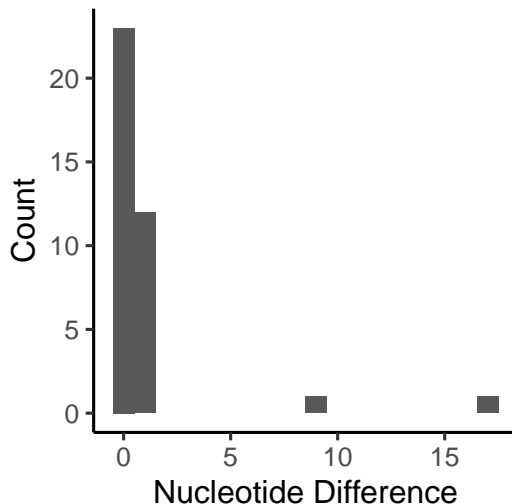
### IGHV3-73\*01\_02

638 sequences assigned  
132 (20.7%) exact matches, in which:  
67 unique CDR3  
4 unique J



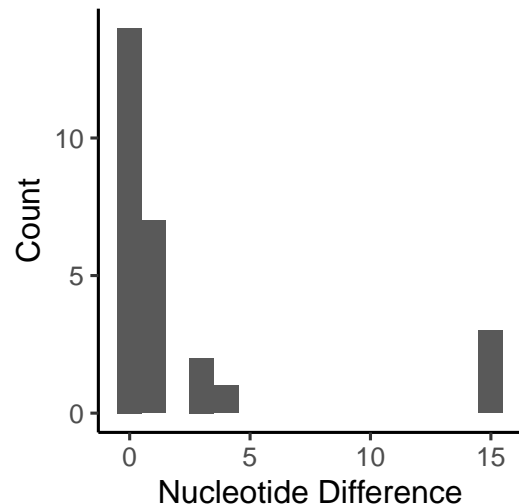
### IGHV3-64D\*06

88 sequences assigned  
23 (26.1%) exact matches, in which:  
13 unique CDR3  
4 unique J



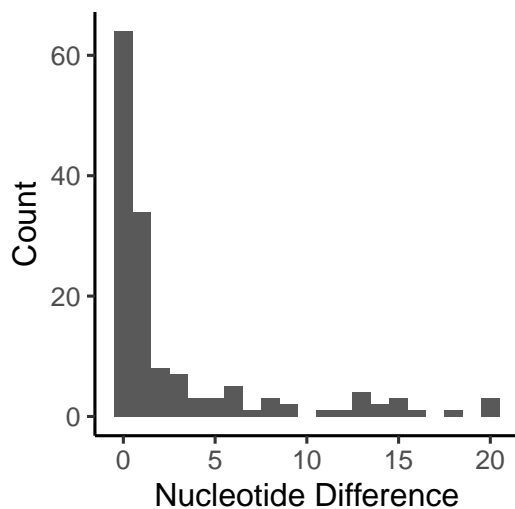
### IGHV4-31\*01

27 sequences assigned  
14 (51.9%) exact matches, in which:  
11 unique CDR3  
3 unique J



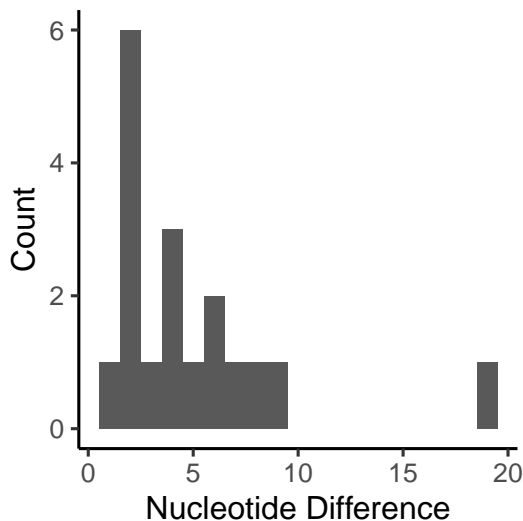
### IGHV3-74\*01\_02

158 sequences assigned  
64 (40.5%) exact matches, in which:  
41 unique CDR3  
5 unique J



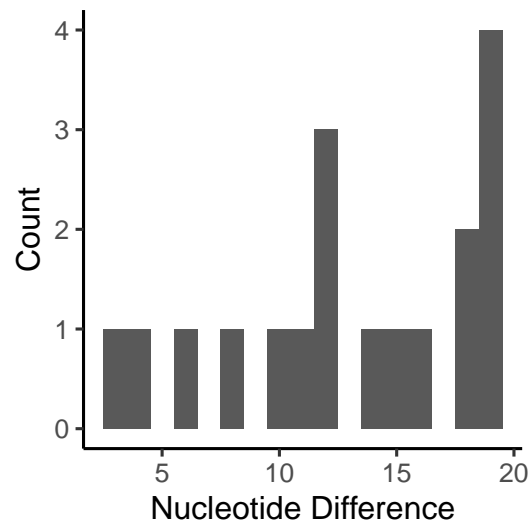
### IGHV4-4\*07

24 sequences assigned  
No exact matches.



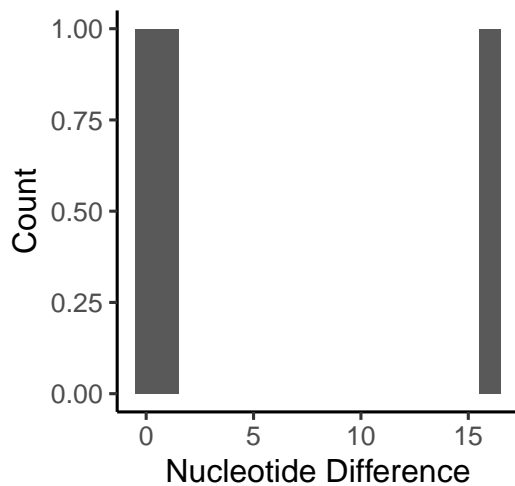
### IGHV4-31\*03\_04

20 sequences assigned  
No exact matches.



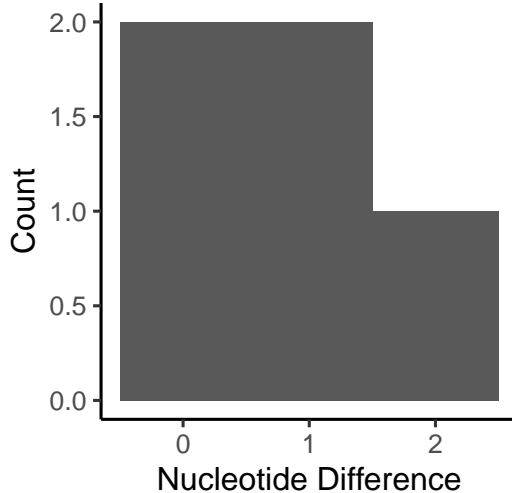
### IGHV3-43D\*03

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



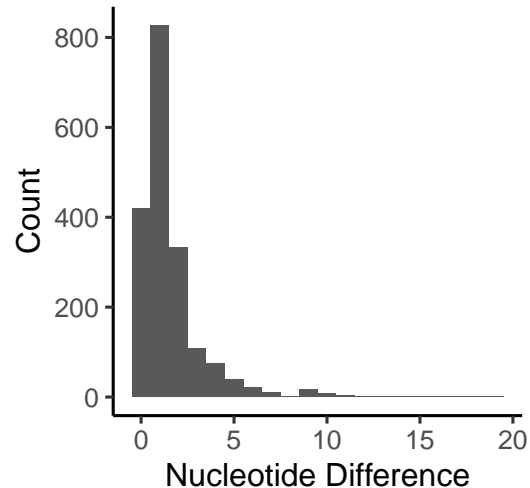
### IGHV4-28\*02\_05

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



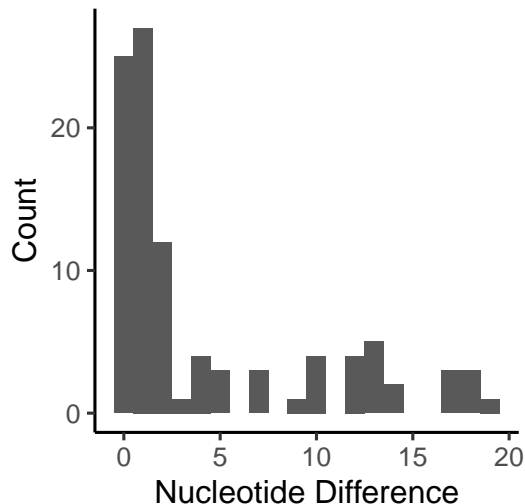
### IGHV4-34\*01\_02

1883 sequences assigned  
420 (22.3%) exact matches, in which:  
282 unique CDR3  
6 unique J



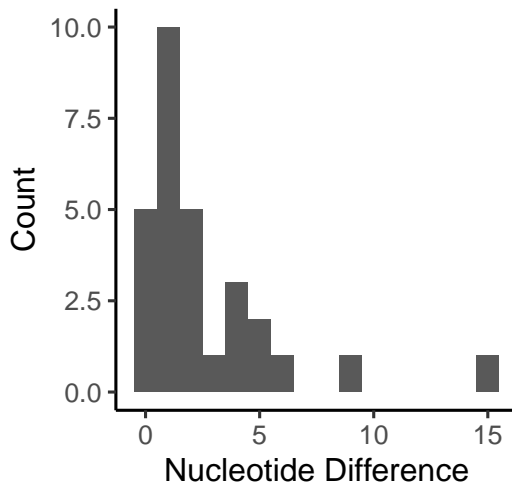
## IGHV4-38-2\*02

99 sequences assigned  
25 (25.3%) exact matches, in which:  
22 unique CDR3  
6 unique J



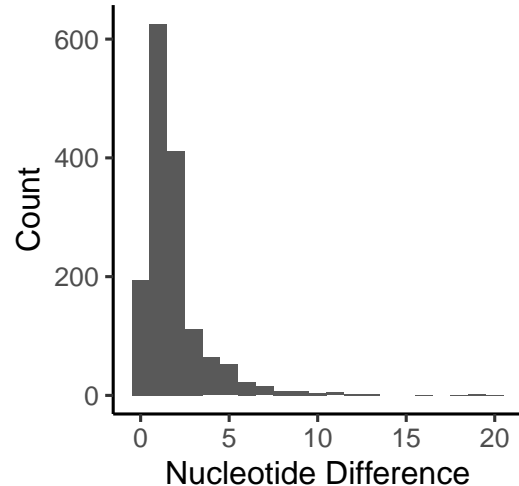
## IGHV4-59\*08

29 sequences assigned  
5 (17.2%) exact matches, in which:  
5 unique CDR3  
4 unique J



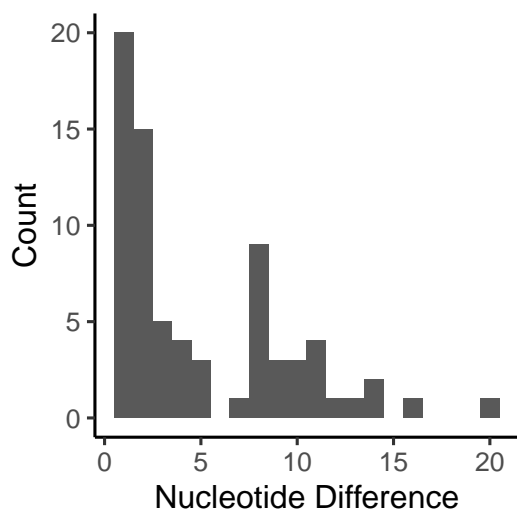
## IGHV4-61\*01

1532 sequences assigned  
194 (12.7%) exact matches, in which:  
102 unique CDR3  
5 unique J



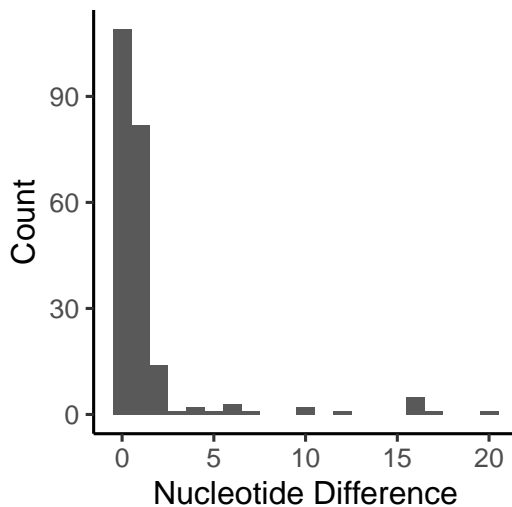
## IGHV4-39\*07

73 sequences assigned  
No exact matches.



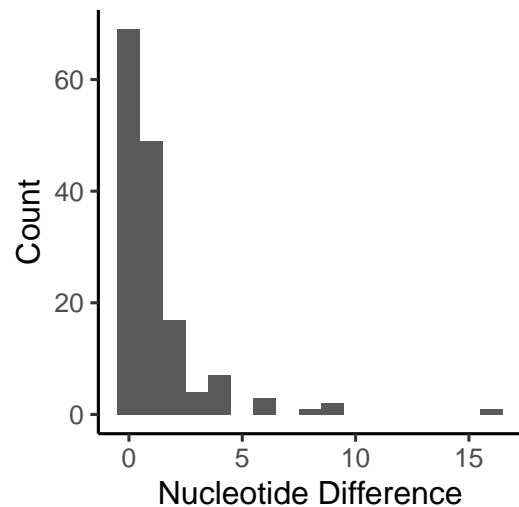
## IGHV4-59\*01\_07

234 sequences assigned  
109 (46.6%) exact matches, in which:  
101 unique CDR3  
6 unique J



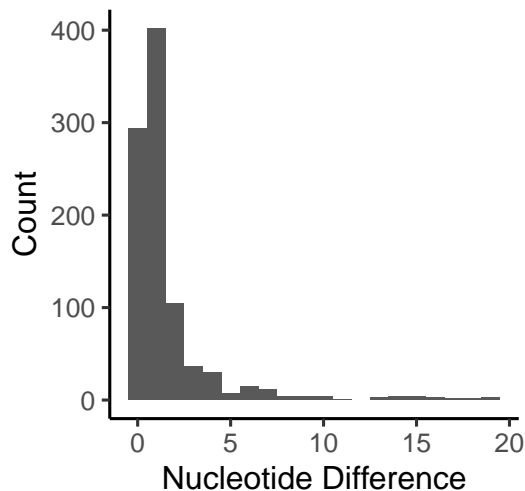
## IGHV4-61\*02

162 sequences assigned  
69 (42.6%) exact matches, in which:  
64 unique CDR3  
5 unique J



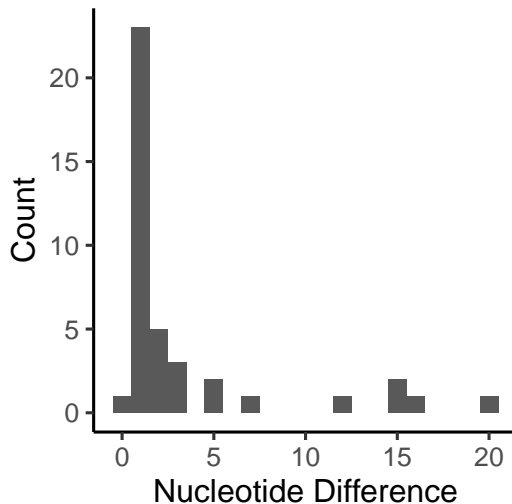
## IGHV4-39\*01\_05

945 sequences assigned  
294 (31.1%) exact matches, in which:  
232 unique CDR3  
6 unique J



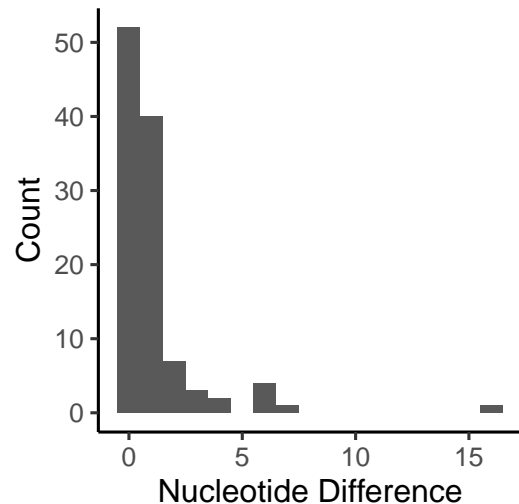
## IGHV4-59\*12

40 sequences assigned  
1 (2.5%) exact matches, in which:  
1 unique CDR3  
1 unique J



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

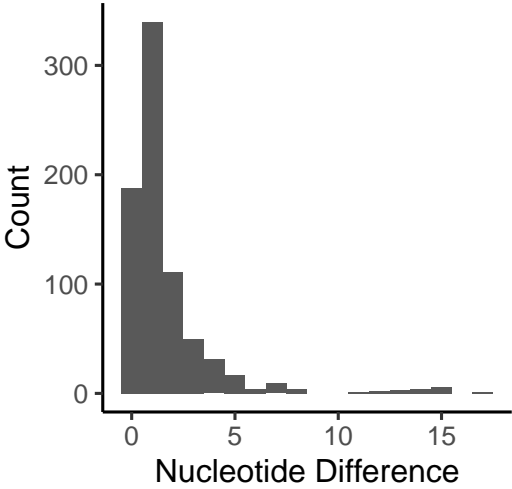
110 sequences assigned  
52 (47.3%) exact matches, in which:  
41 unique CDR3  
4 unique J





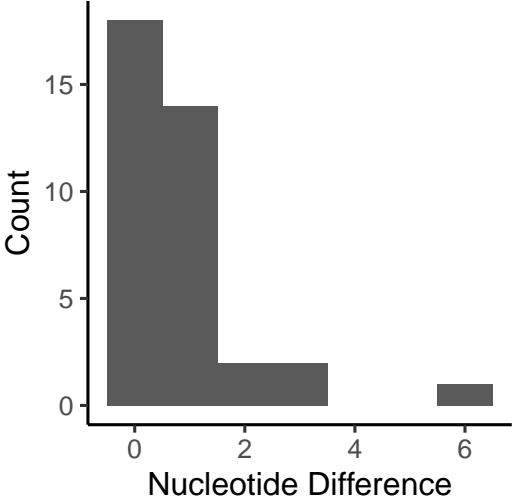
### IGHV5–51\*01\_03

771 sequences assigned  
188 (24.4%) exact matches, in which:  
129 unique CDR3  
7 unique J



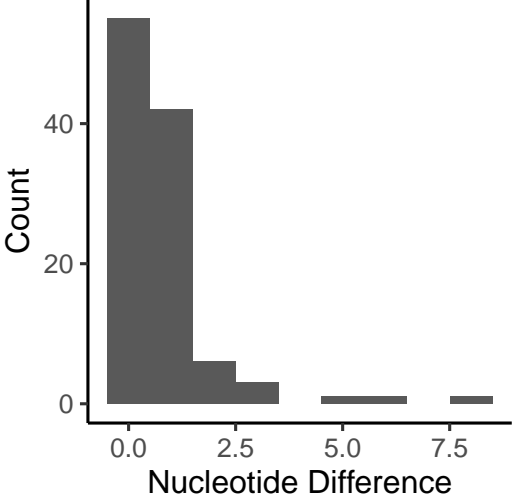
### IGHV6–1\*01\_02

38 sequences assigned  
18 (47.4%) exact matches, in which:  
17 unique CDR3  
4 unique J

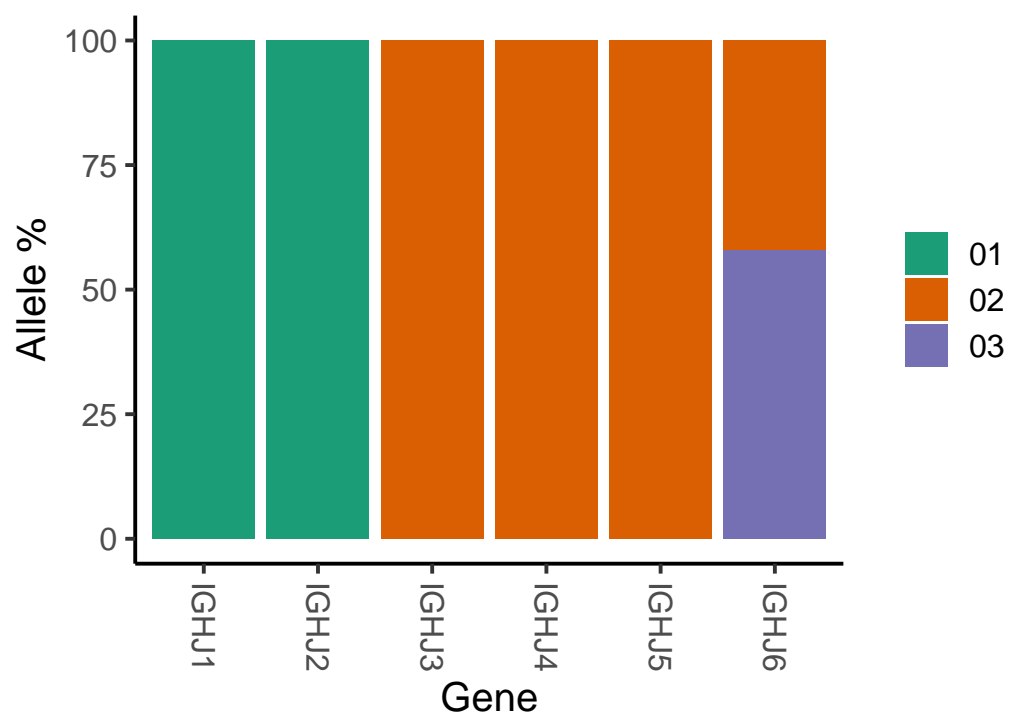


### IGHV7–4–1\*02

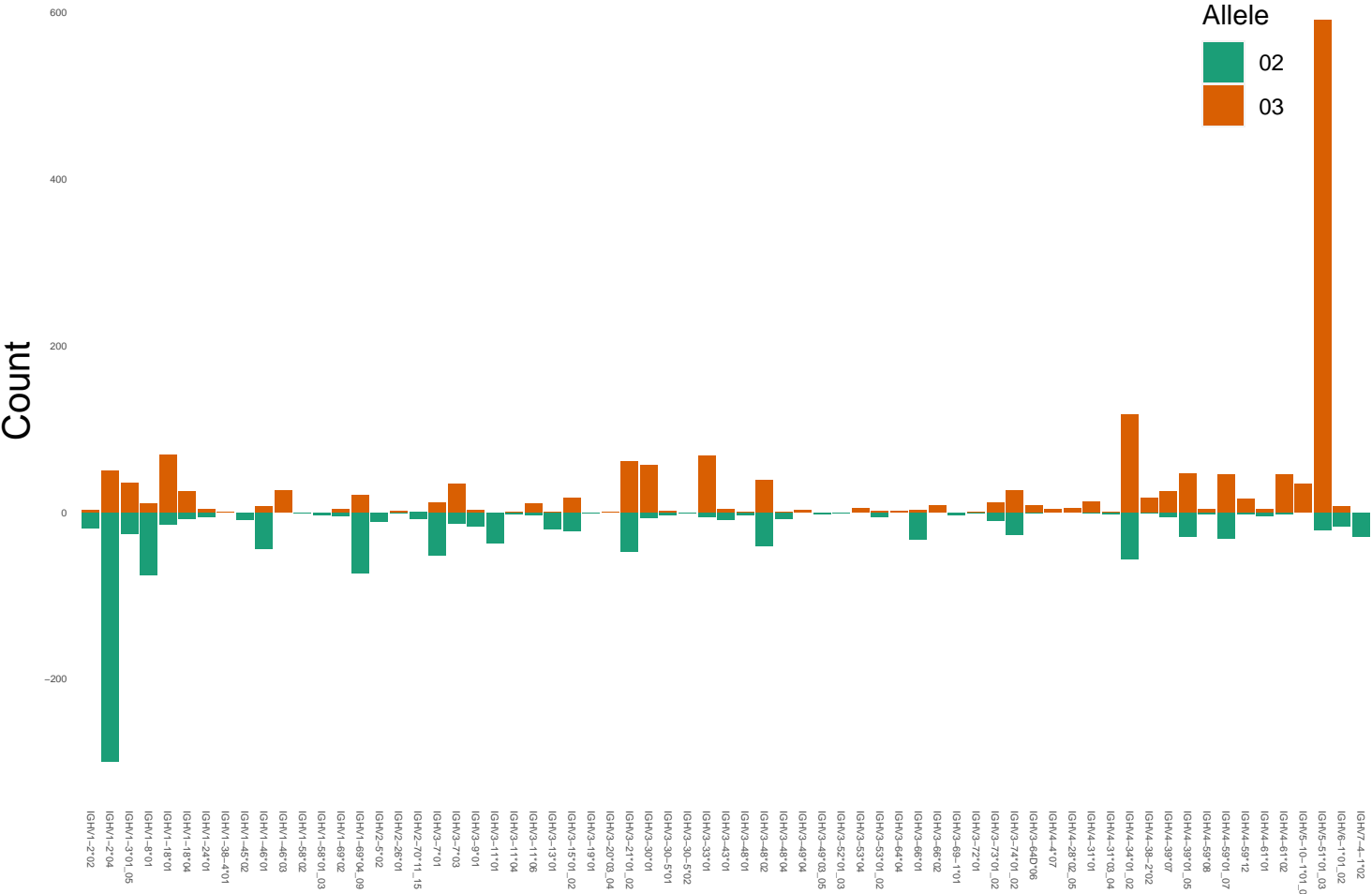
109 sequences assigned  
55 (50.5%) exact matches, in which:  
49 unique CDR3  
5 unique J



Allele Usage



Sequence Count by IGHJ6 allele usage



Novel sequence(s)IGHV3-31\*01\_T128C 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.

Novel sequence(s)IGHV3-30-3\*01\_T288CIGHV4-59\*02\_G88AIGHV5-51\*07\_A128G are not listed in the genotype and will be ignored.

Novel sequence(s)IGHV3-30\*03\_T288C 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)IGHV3-33\*01\_G75CIGHV4-59\*02\_G88AIGHV5-51\*07\_A128G are not listed in the genotype and will be ignored.

Novel sequence(s)IGHV3-33\*01\_G75CIGHV4-59\*02\_G88AIGHV5-51\*07\_A128G are not listed in the genotype and will be ignored.

Novel sequence(s)IGHV3-30\*03\_T288CIGHV4-59\*02\_G88AIGHV5-51\*07\_A128G are not listed in the genotype and will be ignored.

Warning – no inferred sequences found.

Warning – no inferred sequences found.

Warning – no inferred sequences found.