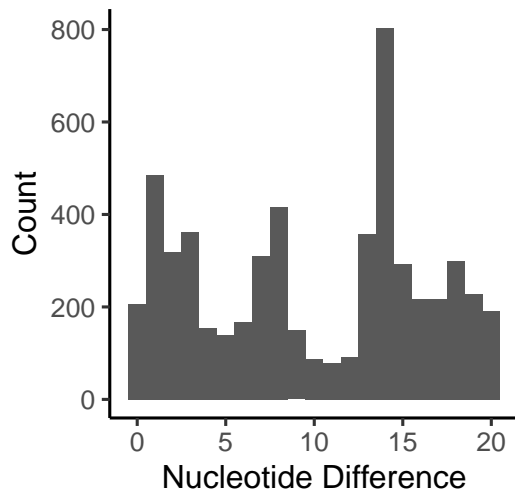


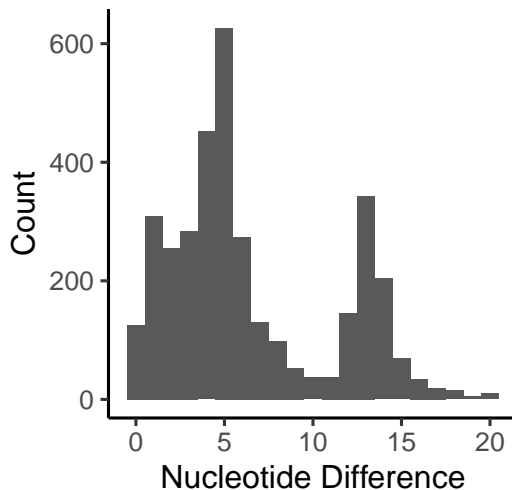
### IGHV1-2\*06

6634 sequences assigned  
207 (3.1%) exact matches, in which:  
129 unique CDR3  
7 unique J



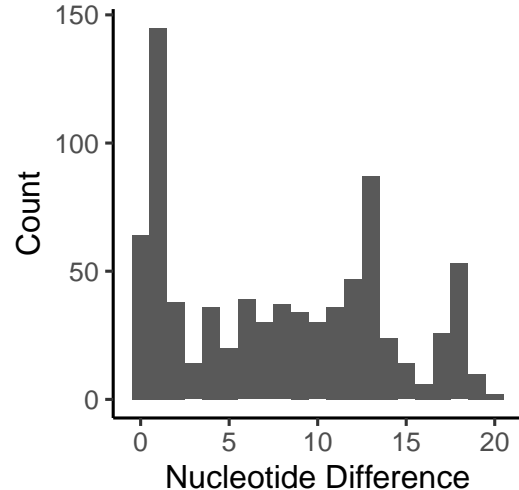
### IGHV1-18\*01

3729 sequences assigned  
125 (3.4%) exact matches, in which:  
78 unique CDR3  
6 unique J



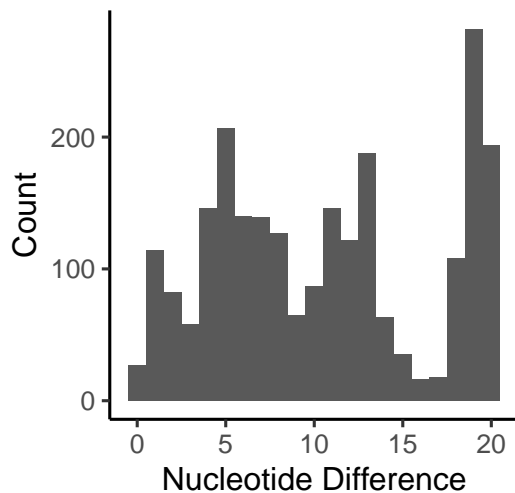
### IGHV1-46\*01

804 sequences assigned  
64 (8%) exact matches, in which:  
37 unique CDR3  
5 unique J



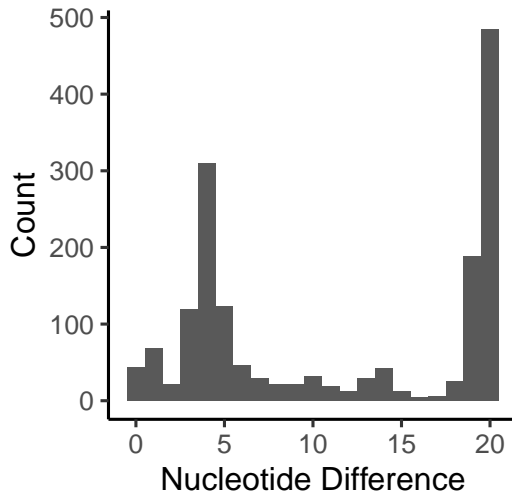
### IGHV1-3\*01\_05

3193 sequences assigned  
27 (0.8%) exact matches, in which:  
18 unique CDR3  
4 unique J



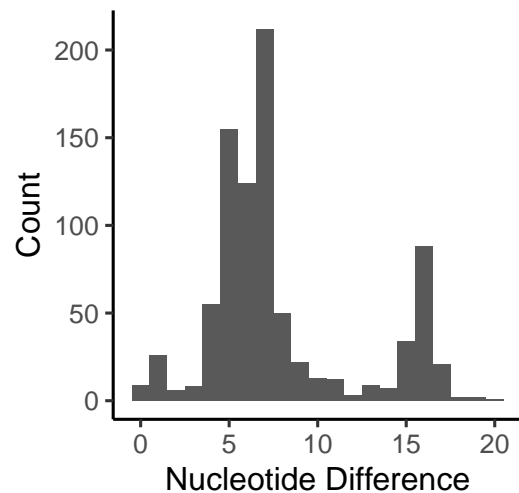
### IGHV1-18\*04

2756 sequences assigned  
44 (1.6%) exact matches, in which:  
33 unique CDR3  
5 unique J



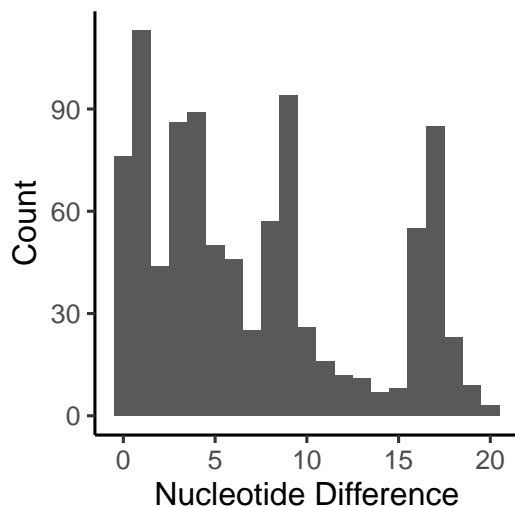
### IGHV1-46\*03

1145 sequences assigned  
9 (0.8%) exact matches, in which:  
7 unique CDR3  
4 unique J



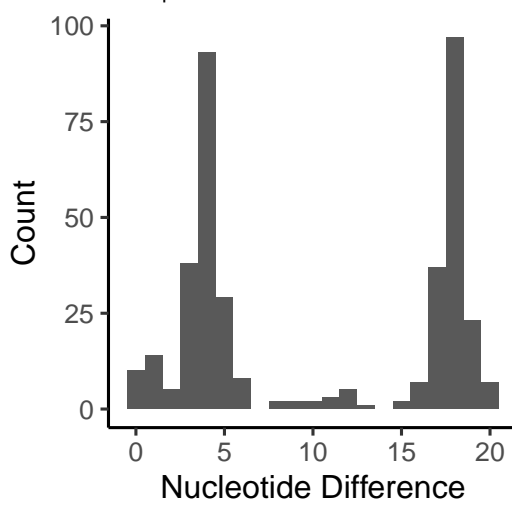
### IGHV1-8\*01

1073 sequences assigned  
76 (7.1%) exact matches, in which:  
53 unique CDR3  
6 unique J



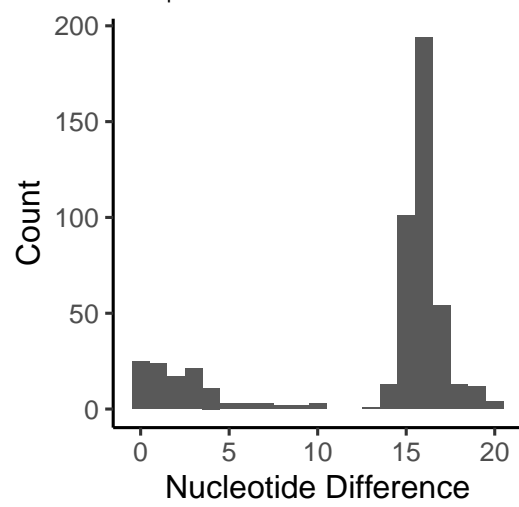
### IGHV1-24\*01

392 sequences assigned  
10 (2.6%) exact matches, in which:  
9 unique CDR3  
3 unique J



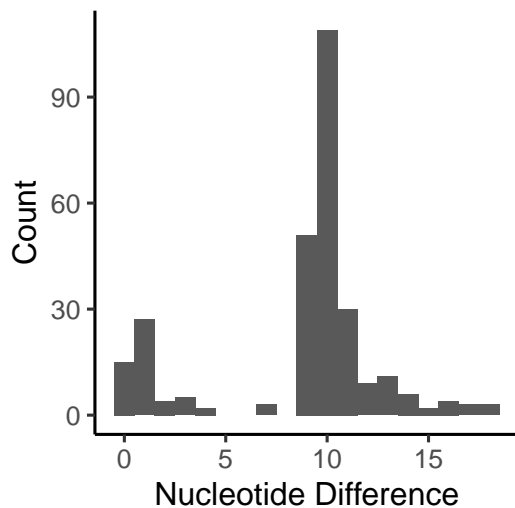
### IGHV1-58\*02

709 sequences assigned  
25 (3.5%) exact matches, in which:  
16 unique CDR3  
3 unique J



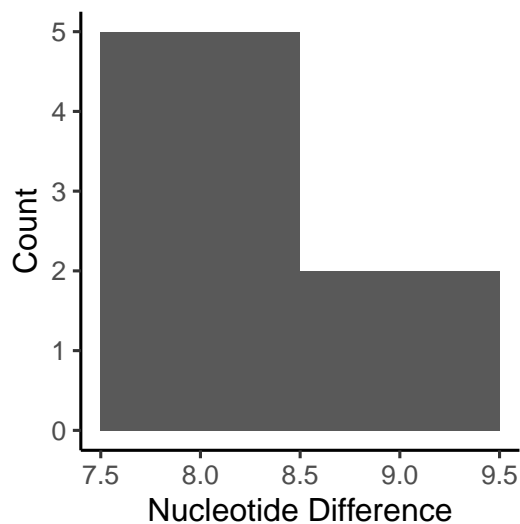
### IGHV1-58\*01\_03

285 sequences assigned  
15 (5.3%) exact matches, in which:  
10 unique CDR3  
4 unique J



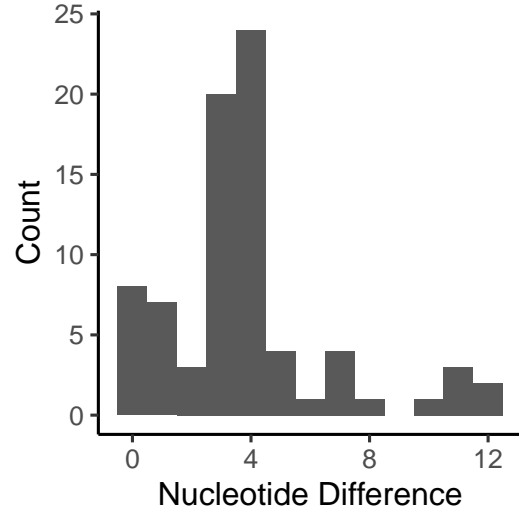
### IGHV1-NL1\*01

7 sequences assigned  
No exact matches.



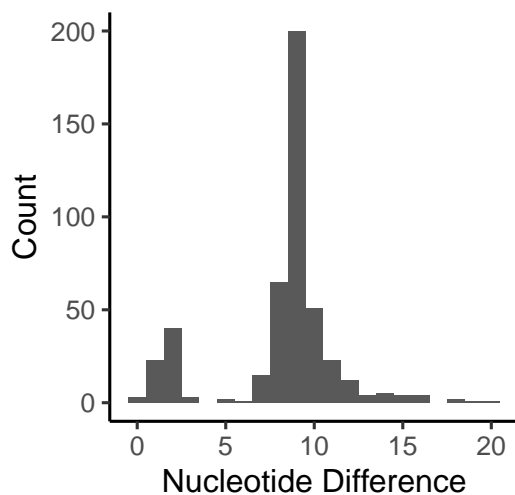
### IGHV2-26\*01

78 sequences assigned  
8 (10.3%) exact matches, in which:  
7 unique CDR3  
3 unique J



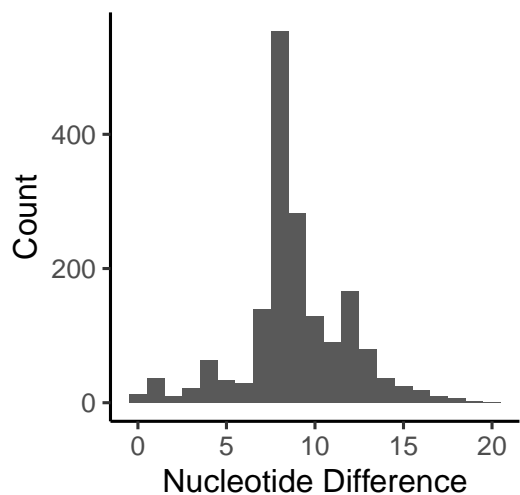
### IGHV1-69\*02

860 sequences assigned  
3 (0.3%) exact matches, in which:  
2 unique CDR3  
1 unique J



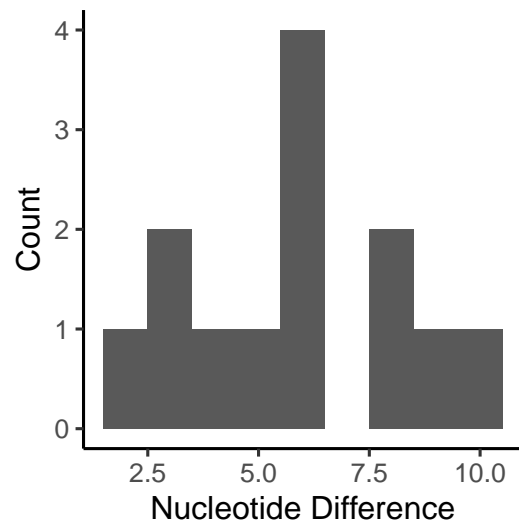
### IGHV2-5\*01

1946 sequences assigned  
13 (0.7%) exact matches, in which:  
9 unique CDR3  
2 unique J



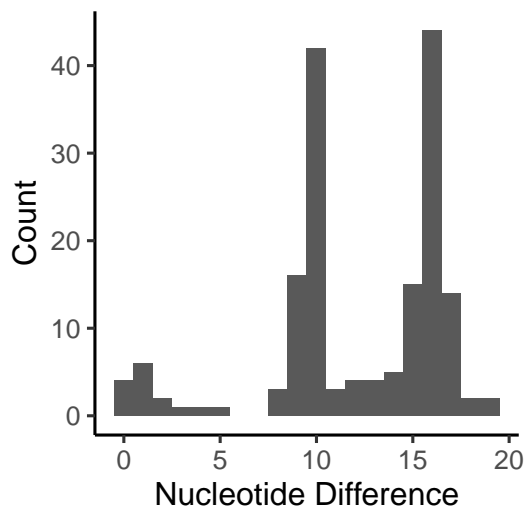
### IGHV2-70\*12

13 sequences assigned  
No exact matches.



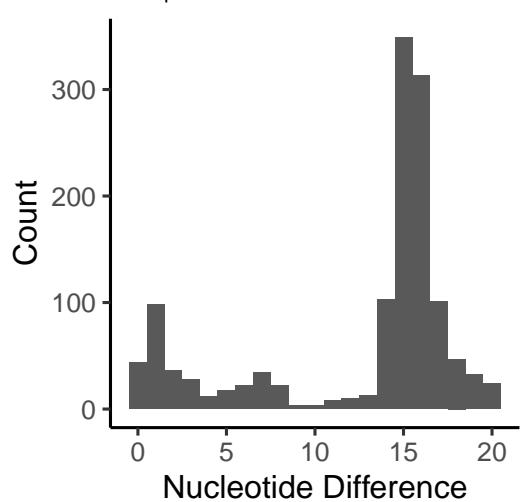
### IGHV1-69\*04\_09

177 sequences assigned  
4 (2.3%) exact matches, in which:  
4 unique CDR3  
2 unique J



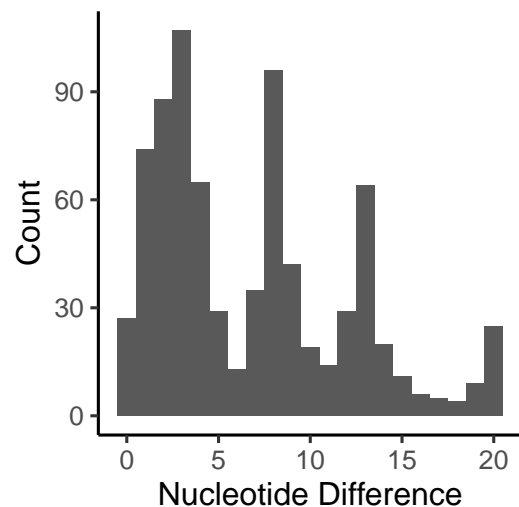
### IGHV2-5\*02

1706 sequences assigned  
44 (2.6%) exact matches, in which:  
25 unique CDR3  
5 unique J



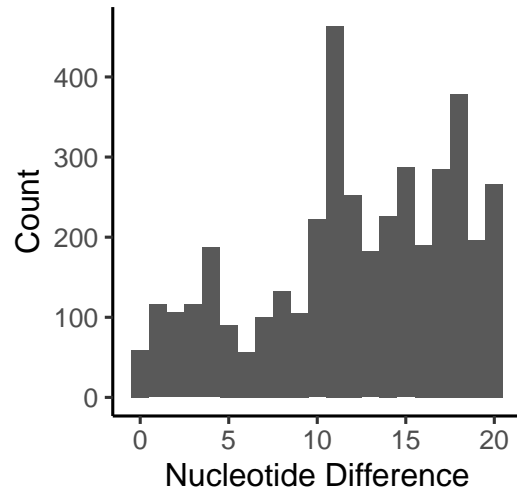
### IGHV2-70\*11\_15

797 sequences assigned  
27 (3.4%) exact matches, in which:  
16 unique CDR3  
3 unique J



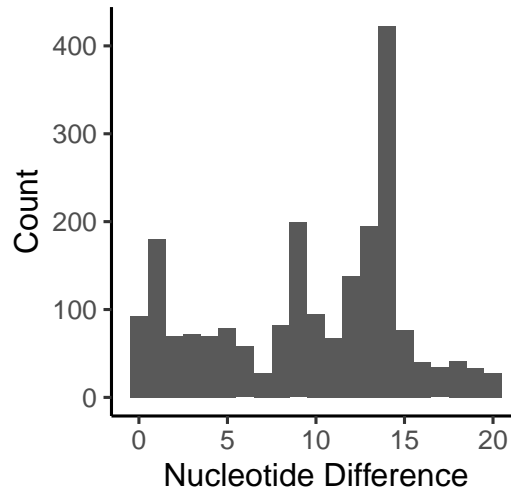
### IGHV3-7\*01

4592 sequences assigned  
59 (1.3%) exact matches, in which:  
37 unique CDR3  
6 unique J



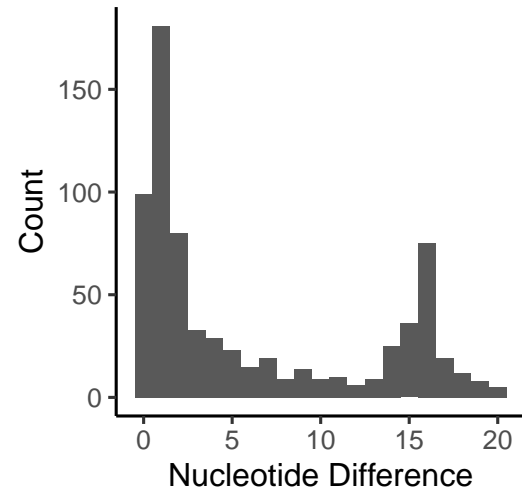
### IGHV3-11\*01

2433 sequences assigned  
93 (3.8%) exact matches, in which:  
51 unique CDR3  
6 unique J



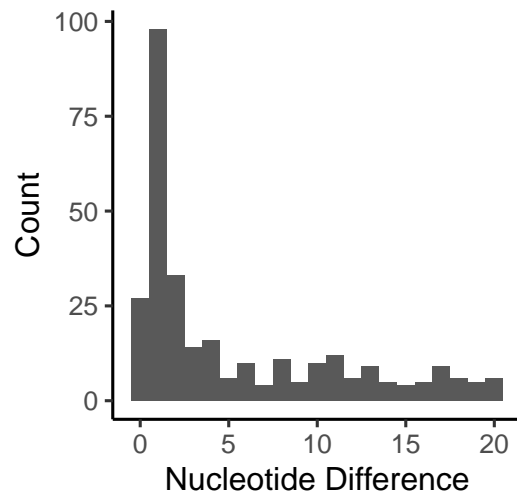
### IGHV3-15\*01\_02

851 sequences assigned  
99 (11.6%) exact matches, in which:  
56 unique CDR3  
6 unique J



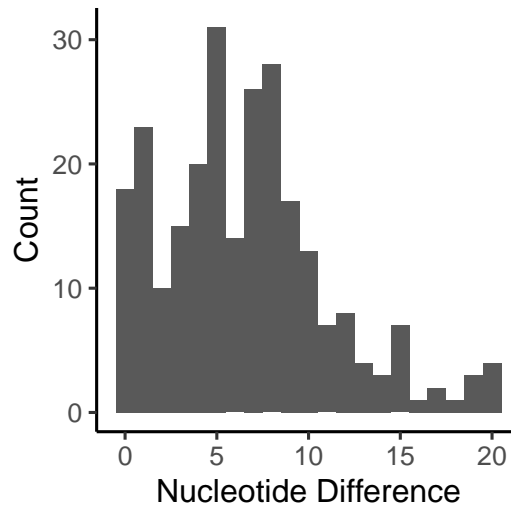
### IGHV3-7\*03

632 sequences assigned  
27 (4.3%) exact matches, in which:  
15 unique CDR3  
2 unique J



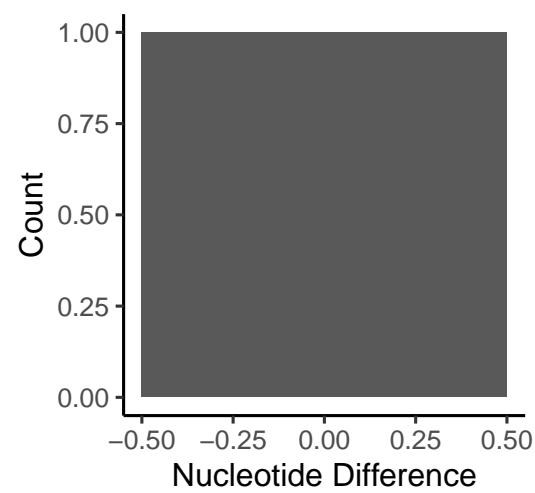
### IGHV3-11\*04

267 sequences assigned  
18 (6.7%) exact matches, in which:  
15 unique CDR3  
4 unique J



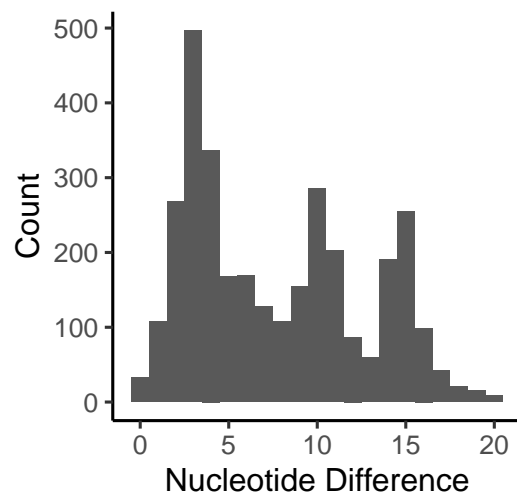
### IGHV3-19\*01

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



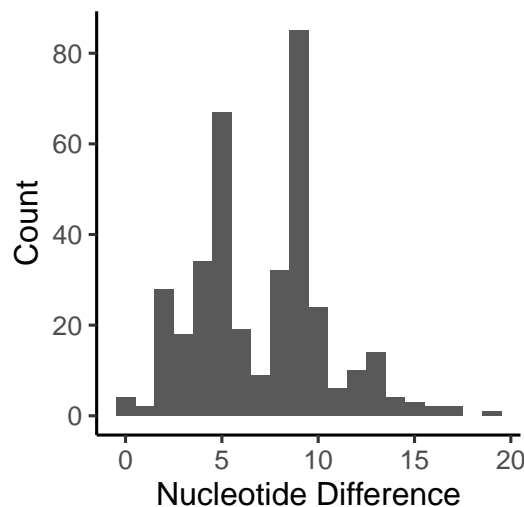
### IGHV3-9\*01

3289 sequences assigned  
33 (1%) exact matches, in which:  
20 unique CDR3  
5 unique J



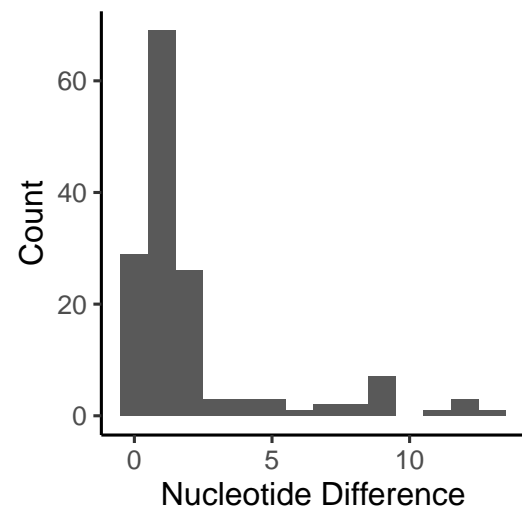
### IGHV3-13\*01

368 sequences assigned  
4 (1.1%) exact matches, in which:  
2 unique CDR3  
2 unique J



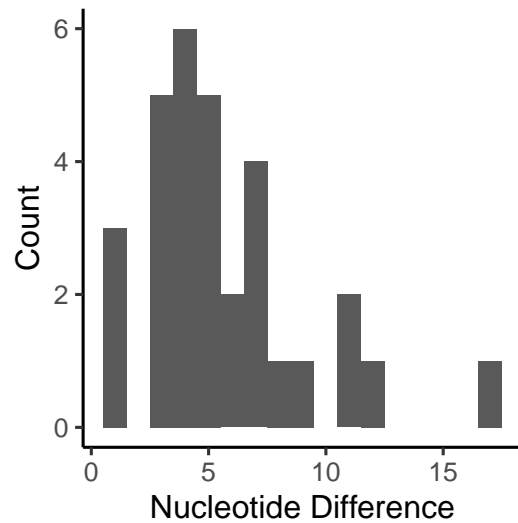
### IGHV3-20\*01\_02

150 sequences assigned  
29 (19.3%) exact matches, in which:  
14 unique CDR3  
3 unique J



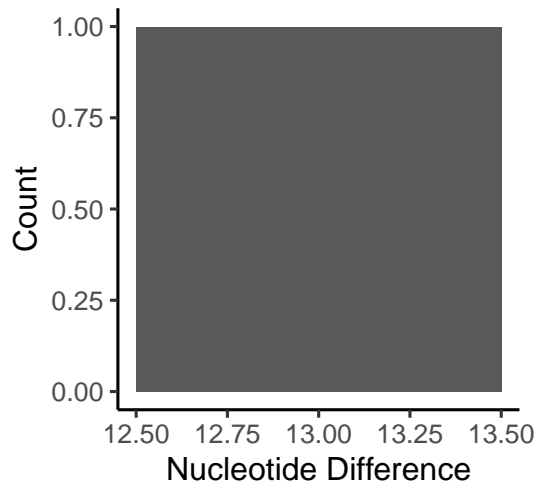
### IGHV3-20\*03\_04

32 sequences assigned  
No exact matches.



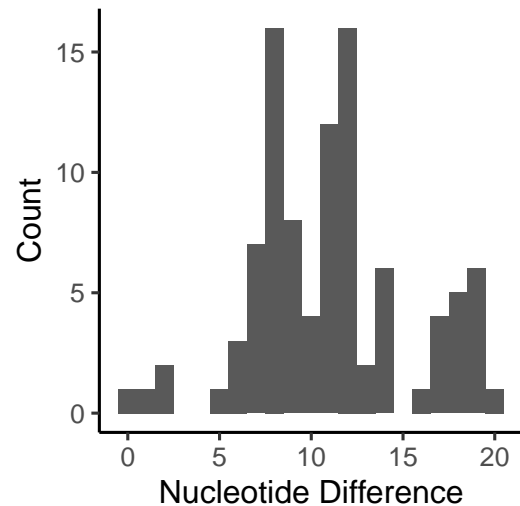
### IGHV3-22\*01\_02

1 sequences assigned  
No exact matches.



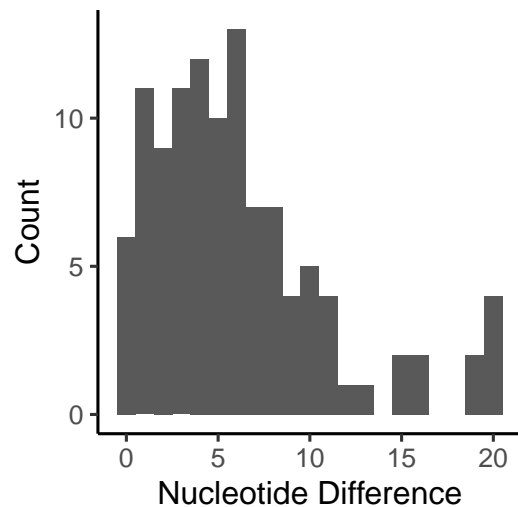
### IGHV3-30-3\*03

1349 sequences assigned  
1 (0.1%) exact matches, in which:  
1 unique CDR3  
1 unique J



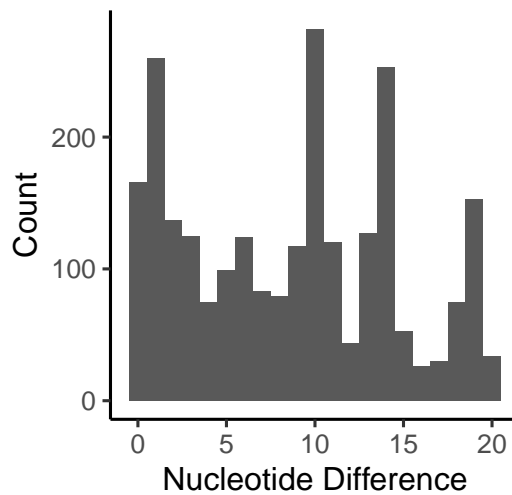
### IGHV3-21\*04

492 sequences assigned  
6 (1.2%) exact matches, in which:  
6 unique CDR3  
5 unique J



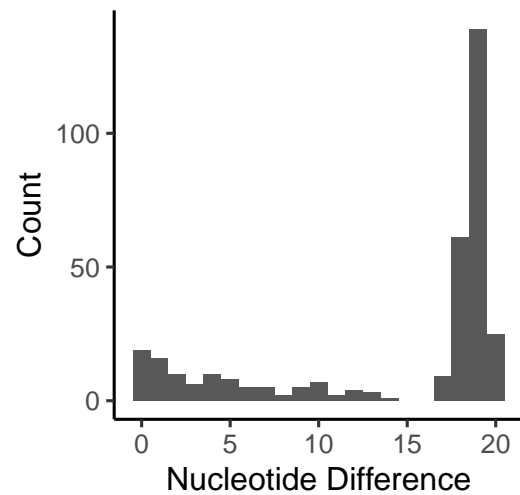
### IGHV3-30-3\*01

3110 sequences assigned  
166 (5.3%) exact matches, in which:  
100 unique CDR3  
6 unique J



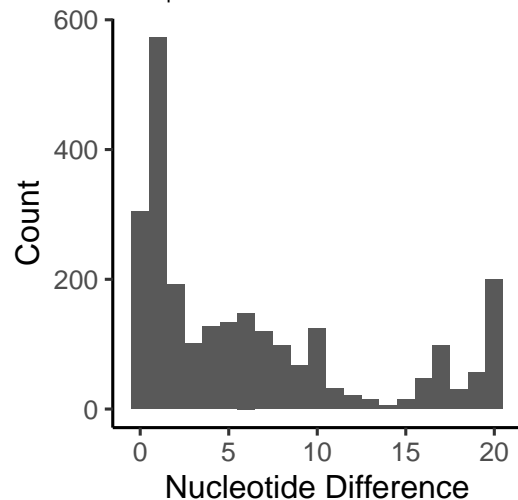
### IGHV3-30\*03

398 sequences assigned  
19 (4.8%) exact matches, in which:  
16 unique CDR3  
5 unique J



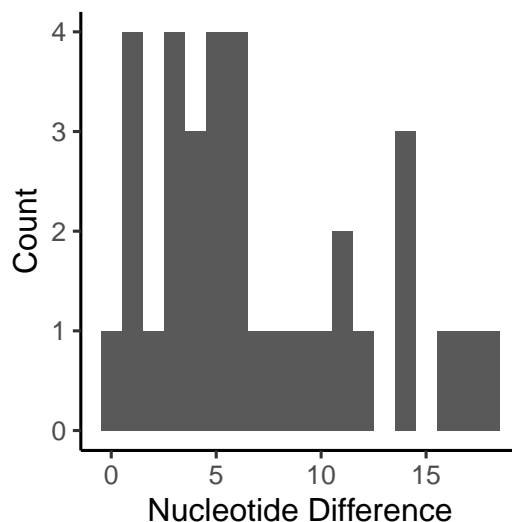
### IGHV3-21\*01\_02

3335 sequences assigned  
305 (9.1%) exact matches, in which:  
177 unique CDR3  
7 unique J



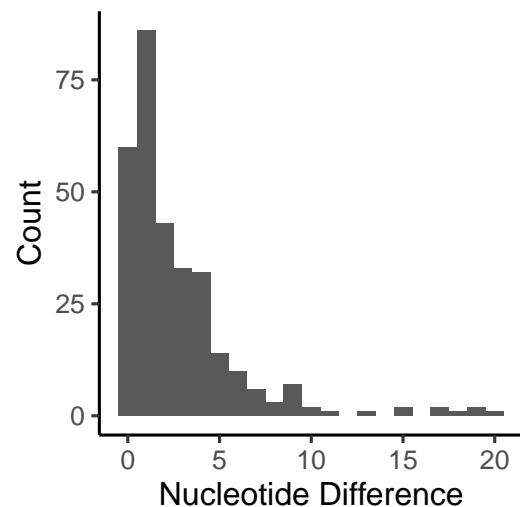
### IGHV3-30-3\*02

36 sequences assigned  
1 (2.8%) exact matches, in which:  
1 unique CDR3  
1 unique J



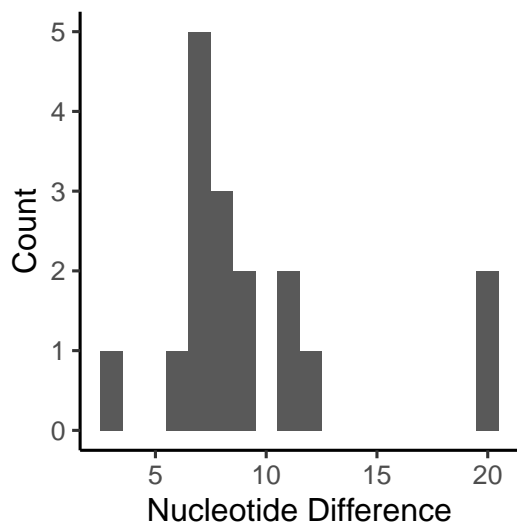
### IGHV3-33\*01

320 sequences assigned  
60 (18.8%) exact matches, in which:  
38 unique CDR3  
6 unique J



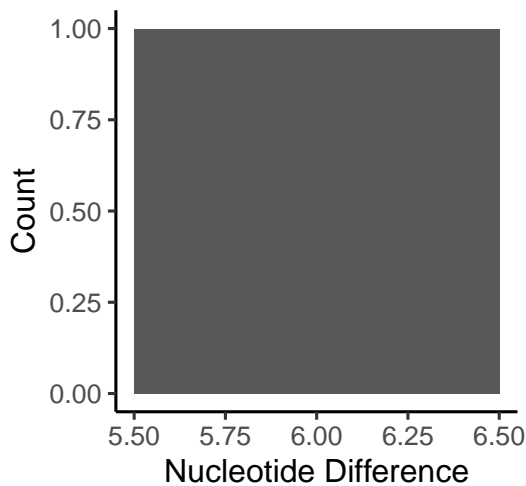
### IGHV3-33\*05

105 sequences assigned  
No exact matches.



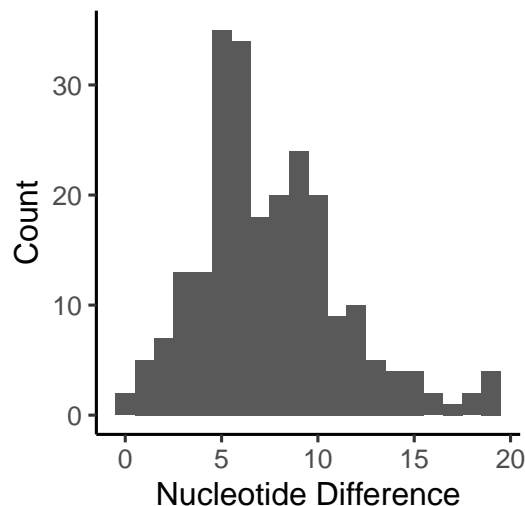
### IGHV3-43\*02

2 sequences assigned  
No exact matches.



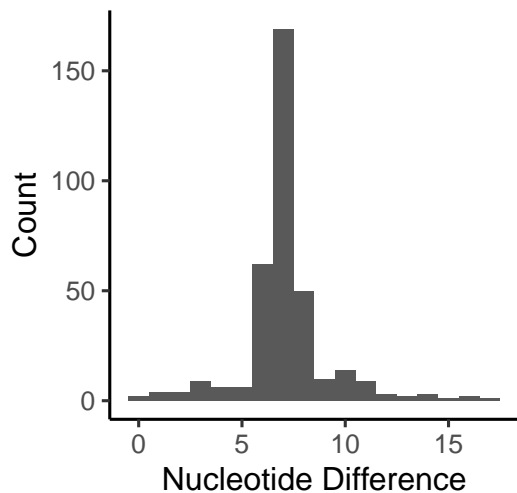
### IGHV3-48\*04

241 sequences assigned  
2 (0.8%) exact matches, in which:  
2 unique CDR3  
2 unique J



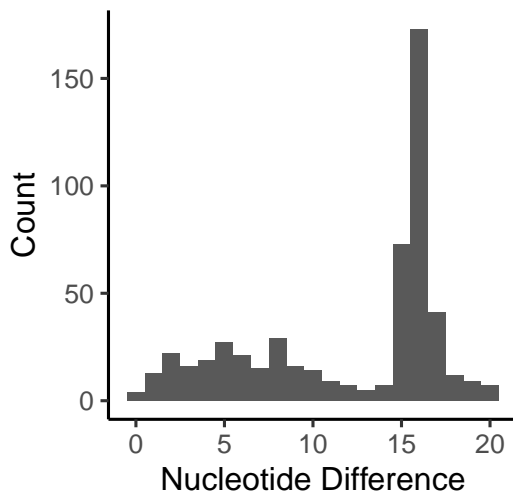
### IGHV3-33\*06

359 sequences assigned  
2 (0.6%) exact matches, in which:  
2 unique CDR3  
2 unique J



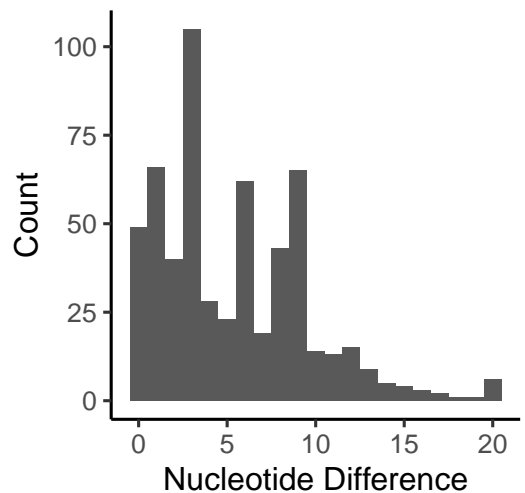
### IGHV3-48\*01

903 sequences assigned  
4 (0.4%) exact matches, in which:  
4 unique CDR3  
2 unique J



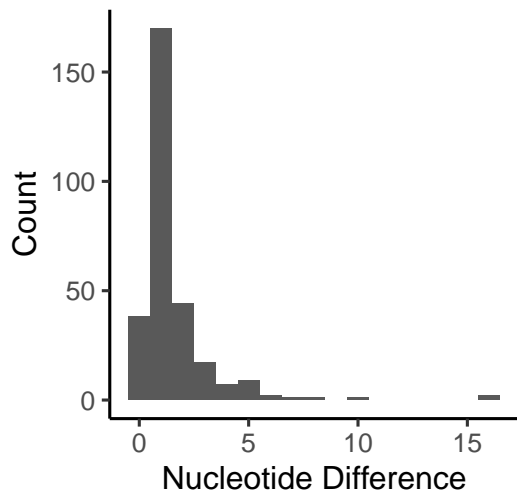
### IGHV3-49\*04

580 sequences assigned  
49 (8.4%) exact matches, in which:  
26 unique CDR3  
4 unique J



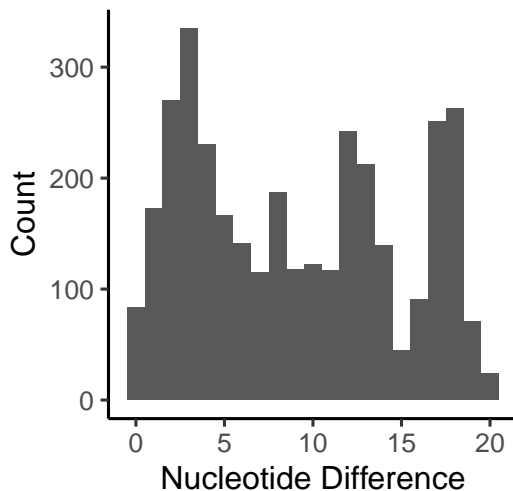
### IGHV3-43\*01

293 sequences assigned  
38 (13%) exact matches, in which:  
20 unique CDR3  
1 unique J



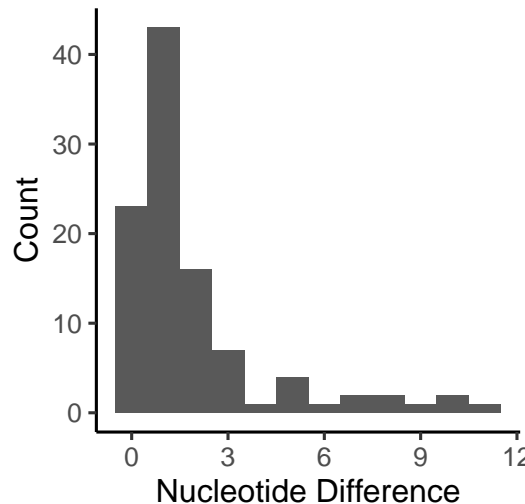
### IGHV3-48\*02

3922 sequences assigned  
83 (2.1%) exact matches, in which:  
44 unique CDR3  
5 unique J



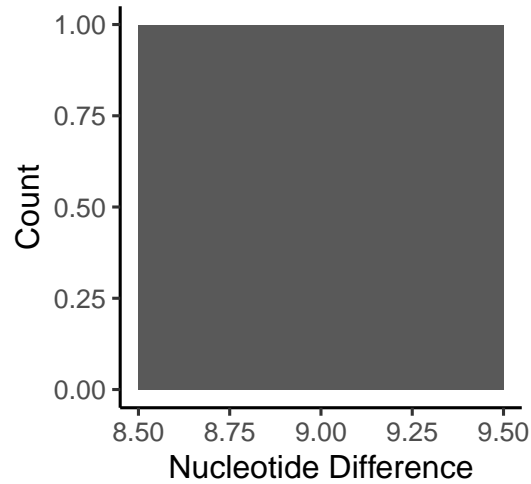
### IGHV3-53\*04

103 sequences assigned  
23 (22.3%) exact matches, in which:  
16 unique CDR3  
3 unique J



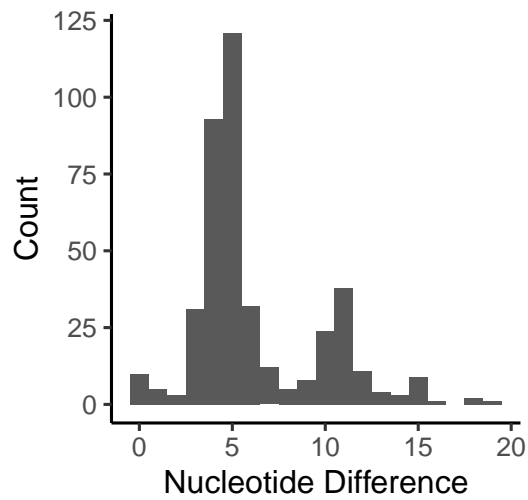
### IGHV3-53\*05

2 sequences assigned  
No exact matches.



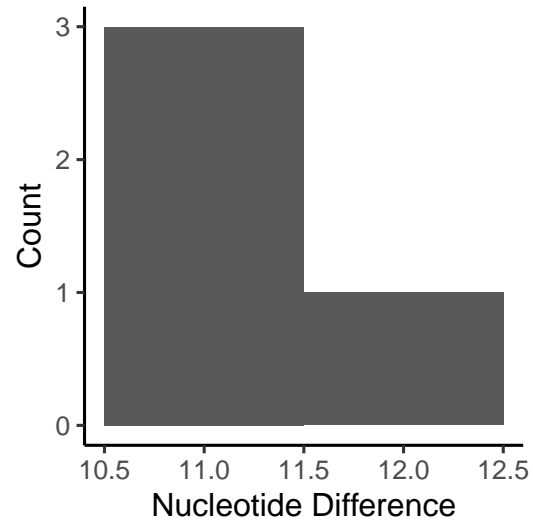
### IGHV3-64\*01

413 sequences assigned  
10 (2.4%) exact matches, in which:  
5 unique CDR3  
2 unique J



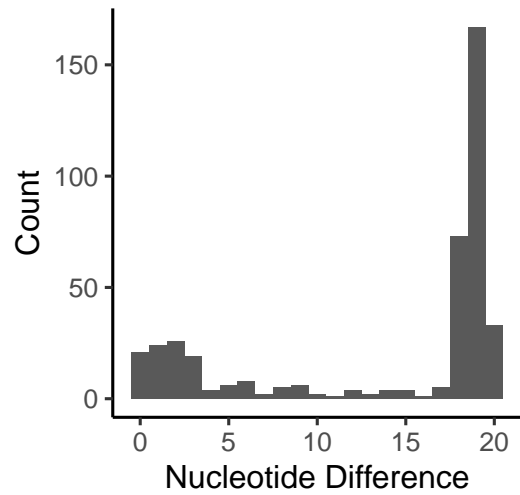
### IGHV3-71\*03

4 sequences assigned  
No exact matches.



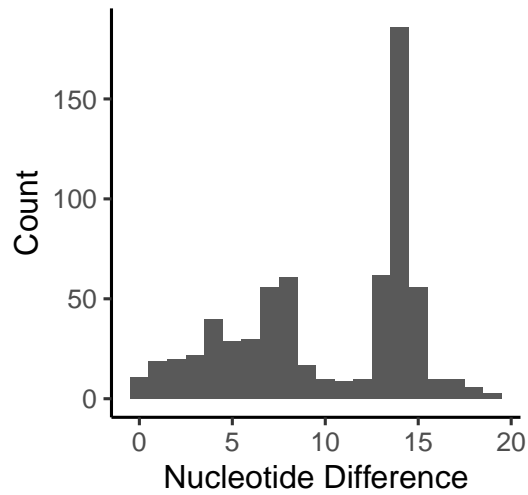
### IGHV3-53\*01\_02

455 sequences assigned  
21 (4.6%) exact matches, in which:  
11 unique CDR3  
3 unique J



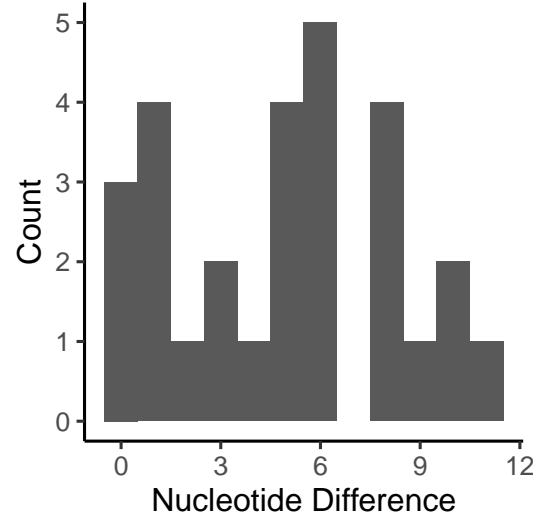
### IGHV3-66\*01

1704 sequences assigned  
11 (0.6%) exact matches, in which:  
7 unique CDR3  
2 unique J



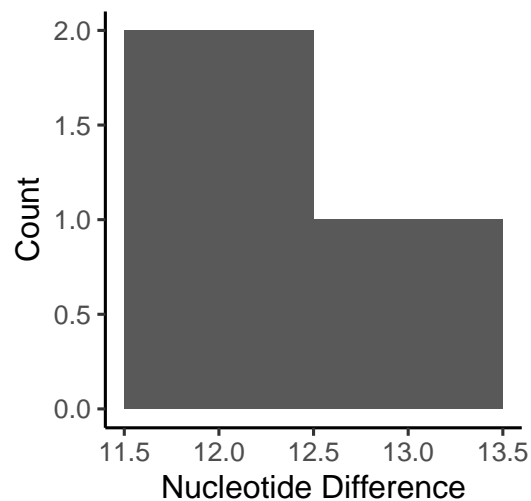
### IGHV3-72\*01

94 sequences assigned  
3 (3.2%) exact matches, in which:  
1 unique CDR3  
1 unique J



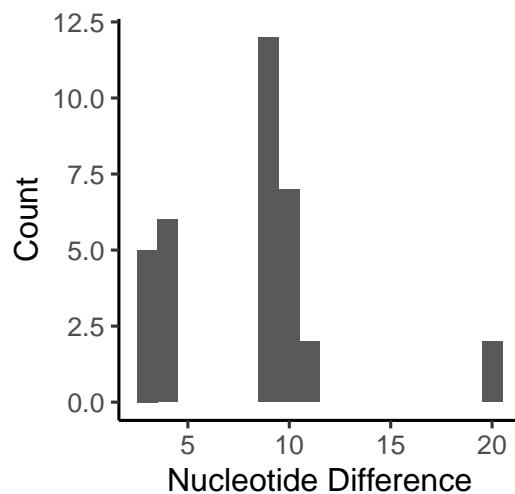
### IGHV3-62\*04

3 sequences assigned  
No exact matches.



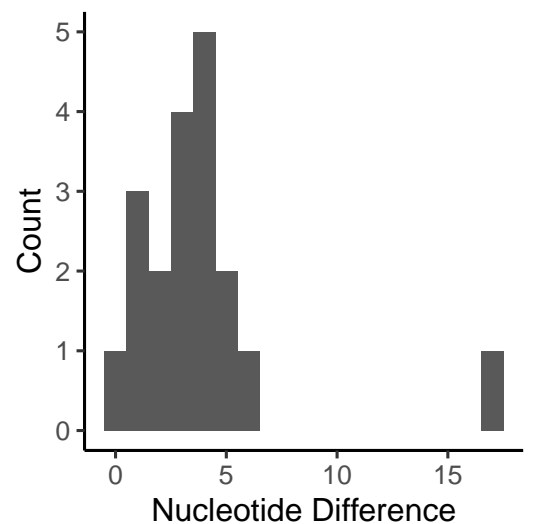
### IGHV3-69-1\*01

35 sequences assigned  
No exact matches.



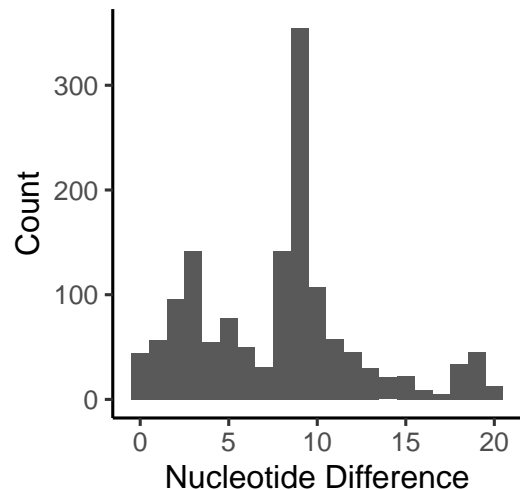
### IGHV3-73\*01\_02

146 sequences assigned  
1 (0.7%) exact matches, in which:  
1 unique CDR3  
1 unique J



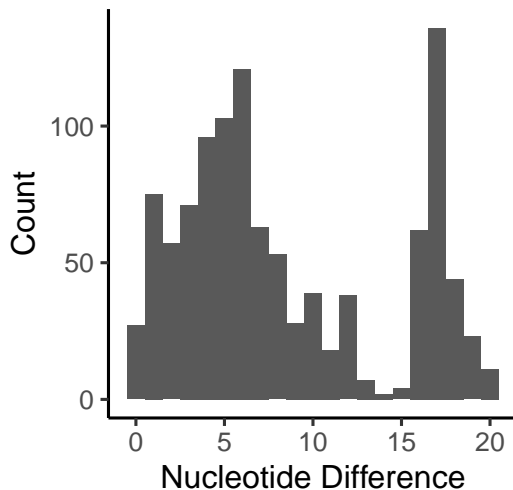
### IGHV3-74\*01\_02

2389 sequences assigned  
44 (1.8%) exact matches, in which:  
27 unique CDR3  
5 unique J



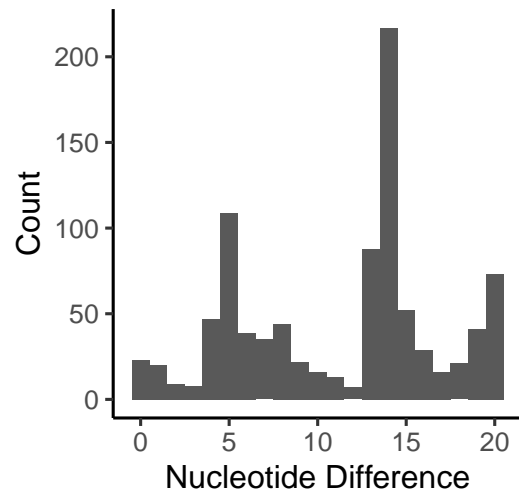
### IGHV4-4\*07

1146 sequences assigned  
27 (2.4%) exact matches, in which:  
22 unique CDR3  
3 unique J



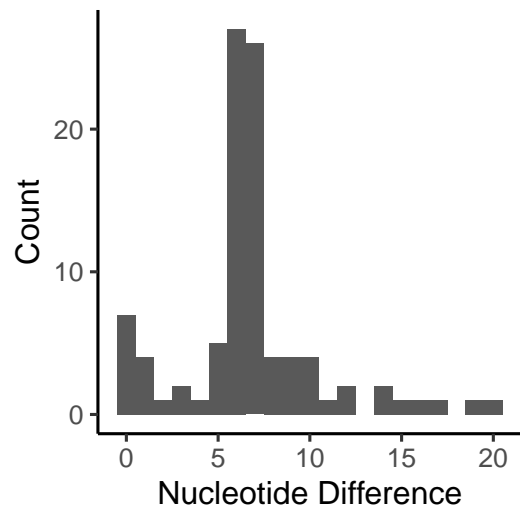
### IGHV4-30-2\*01

1136 sequences assigned  
23 (2%) exact matches, in which:  
17 unique CDR3  
3 unique J



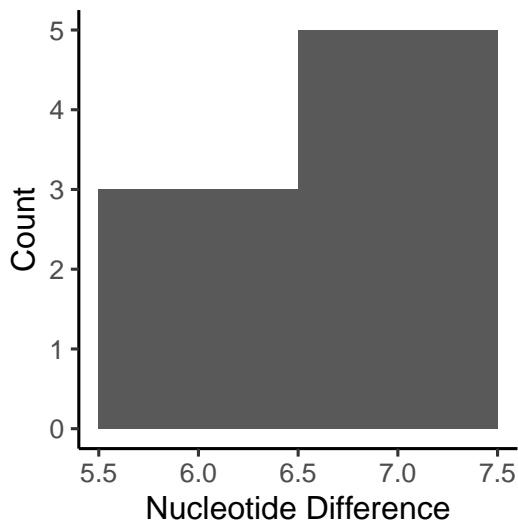
### IGHV3-43D\*03

196 sequences assigned  
7 (3.6%) exact matches, in which:  
5 unique CDR3  
2 unique J



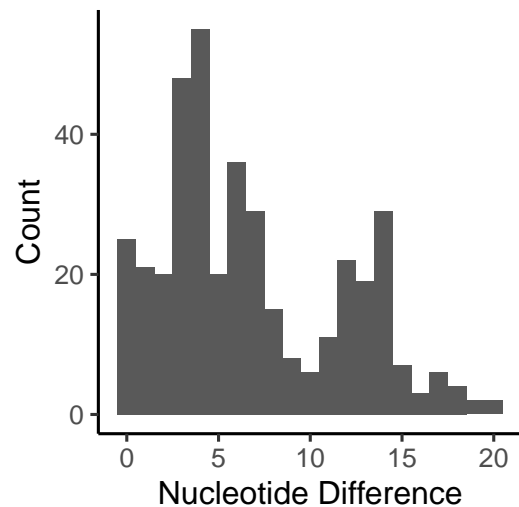
### IGHV4-28\*03

8 sequences assigned  
No exact matches.



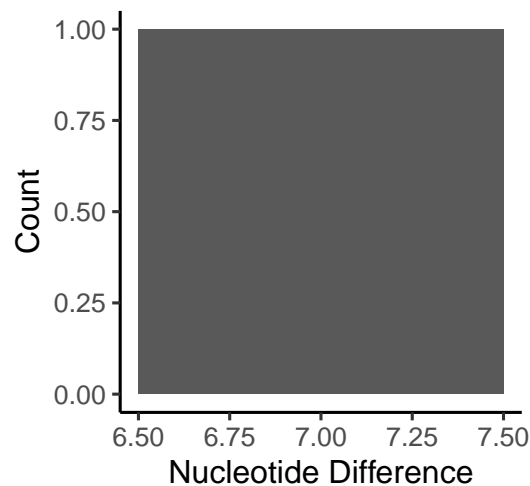
### IGHV4-31\*03\_04

420 sequences assigned  
25 (6%) exact matches, in which:  
17 unique CDR3  
4 unique J



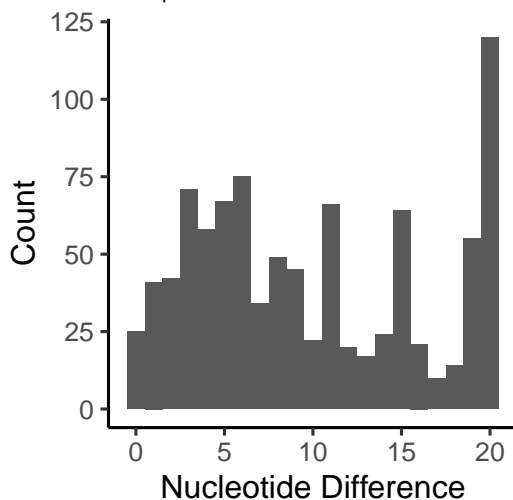
### IGHV3-NL1\*01

2 sequences assigned  
No exact matches.



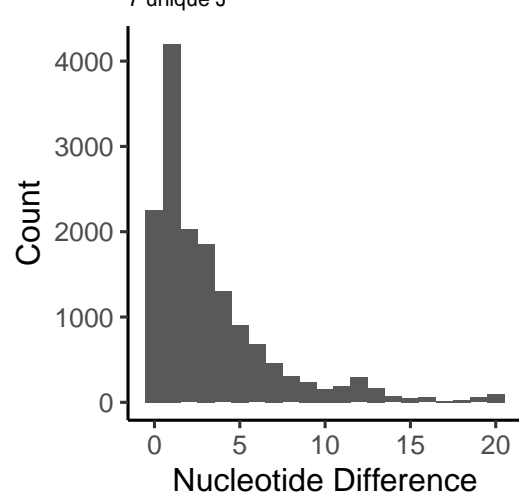
### IGHV4-30-4\*01

1226 sequences assigned  
25 (2%) exact matches, in which:  
19 unique CDR3  
5 unique J



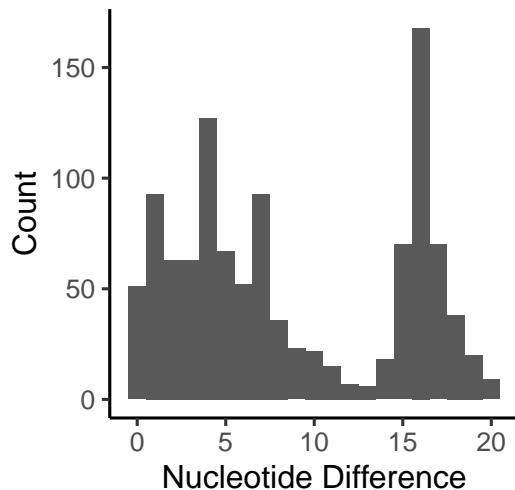
### IGHV4-34\*01\_02

15814 sequences assigned  
2257 (14.3%) exact matches, in which:  
1394 unique CDR3  
7 unique J



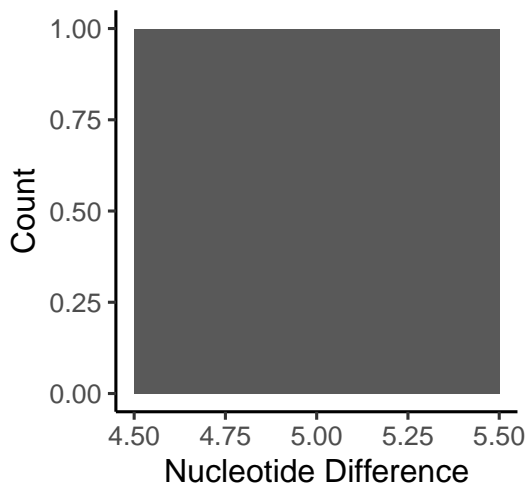
### IGHV4-38-2\*02

2502 sequences assigned  
51 (2%) exact matches, in which:  
35 unique CDR3  
4 unique J



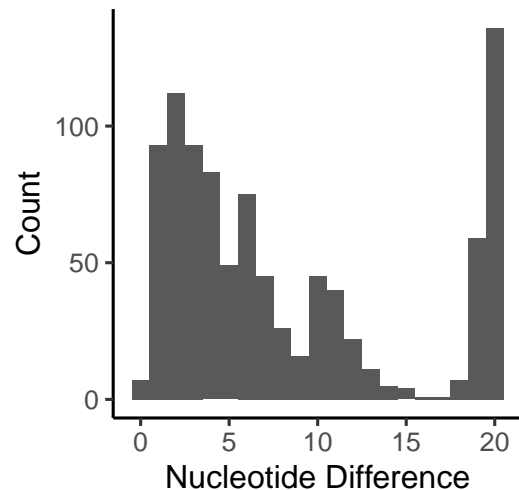
### IGHV4-55\*02\_04\_08

1 sequences assigned  
No exact matches.



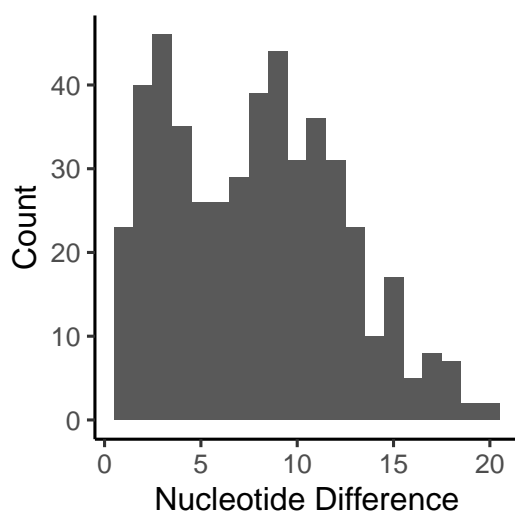
### IGHV4-59\*12

1008 sequences assigned  
7 (0.7%) exact matches, in which:  
6 unique CDR3  
4 unique J



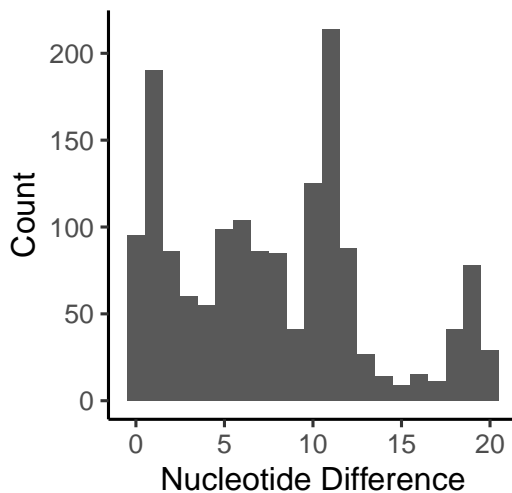
### IGHV4-39\*07

489 sequences assigned  
No exact matches.



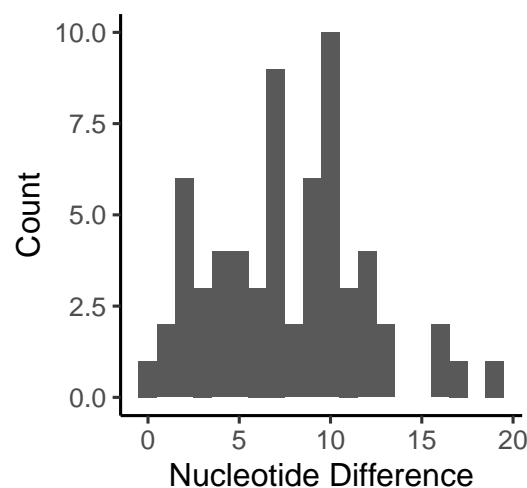
### IGHV4-59\*08

1814 sequences assigned  
95 (5.2%) exact matches, in which:  
72 unique CDR3  
5 unique J



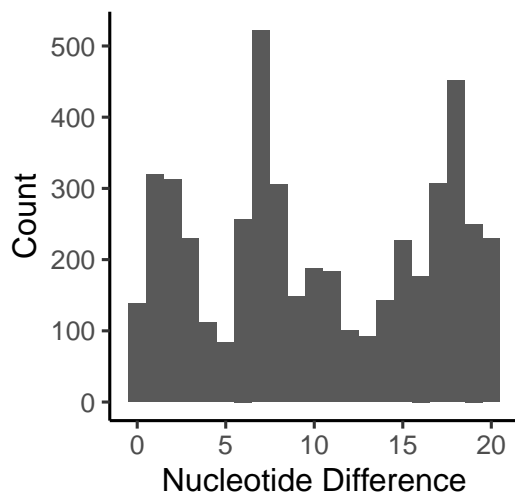
### IGHV4-61\*01

189 sequences assigned  
1 (0.5%) exact matches, in which:  
1 unique CDR3  
1 unique J



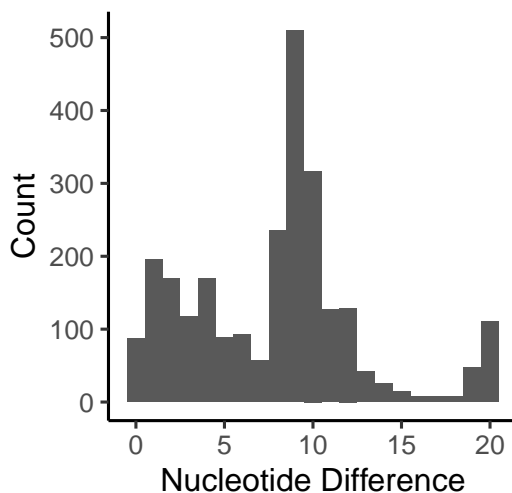
### IGHV4-39\*01\_05

5683 sequences assigned  
138 (2.4%) exact matches, in which:  
100 unique CDR3  
7 unique J



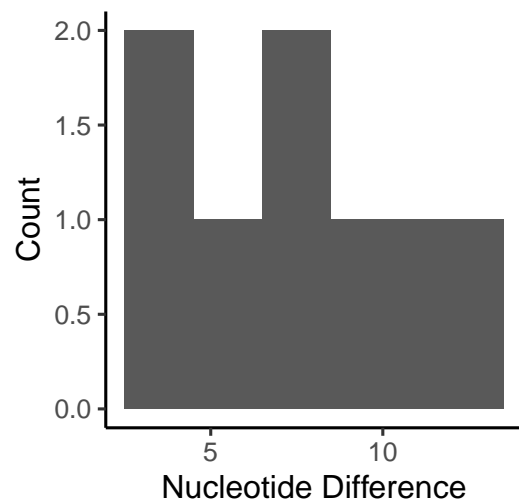
### IGHV4-59\*01\_07

3203 sequences assigned  
87 (2.7%) exact matches, in which:  
63 unique CDR3  
7 unique J



### IGHV4-61\*05

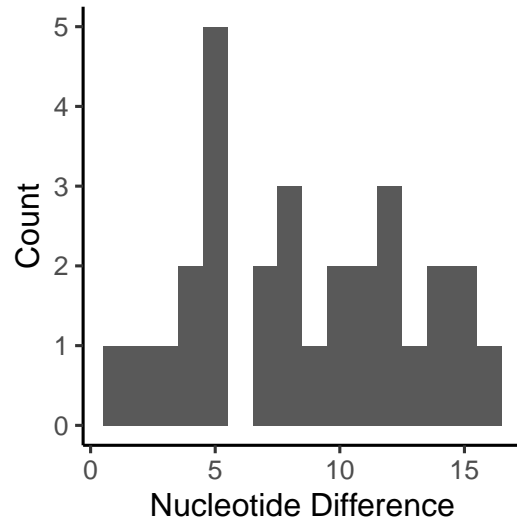
15 sequences assigned  
No exact matches.





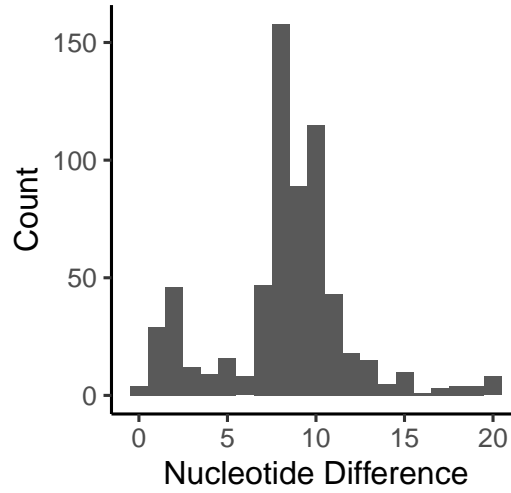
### IGHV4-61\*08

38 sequences assigned  
No exact matches.



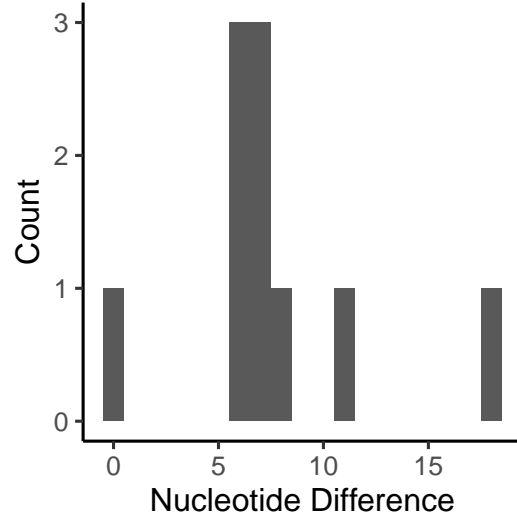
### IGHV6-1\*01\_02

844 sequences assigned  
4 (0.5%) exact matches, in which:  
3 unique CDR3  
2 unique J



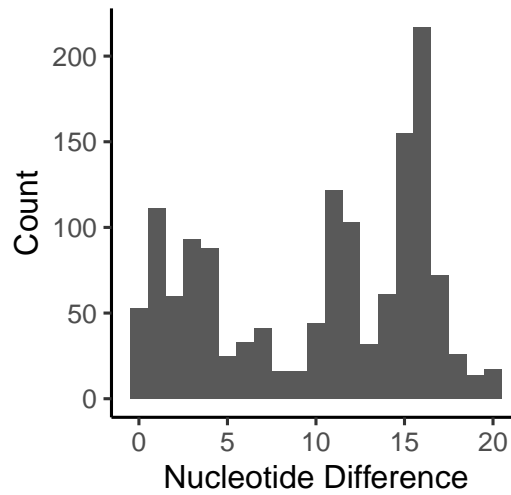
### IGHV5-10-1\*01\_03

13 sequences assigned  
1 (7.7%) exact matches, in which:  
1 unique CDR3  
1 unique J



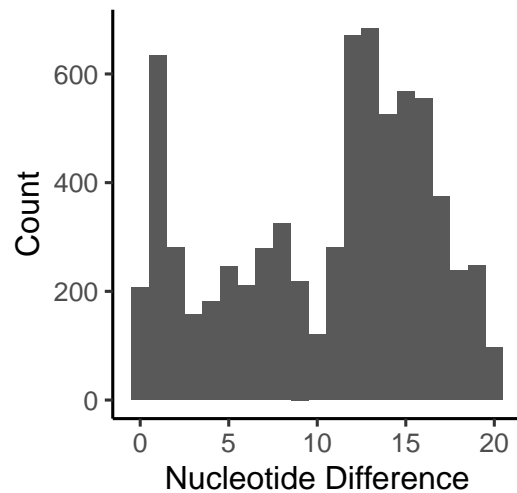
### IGHV7-4-1\*02

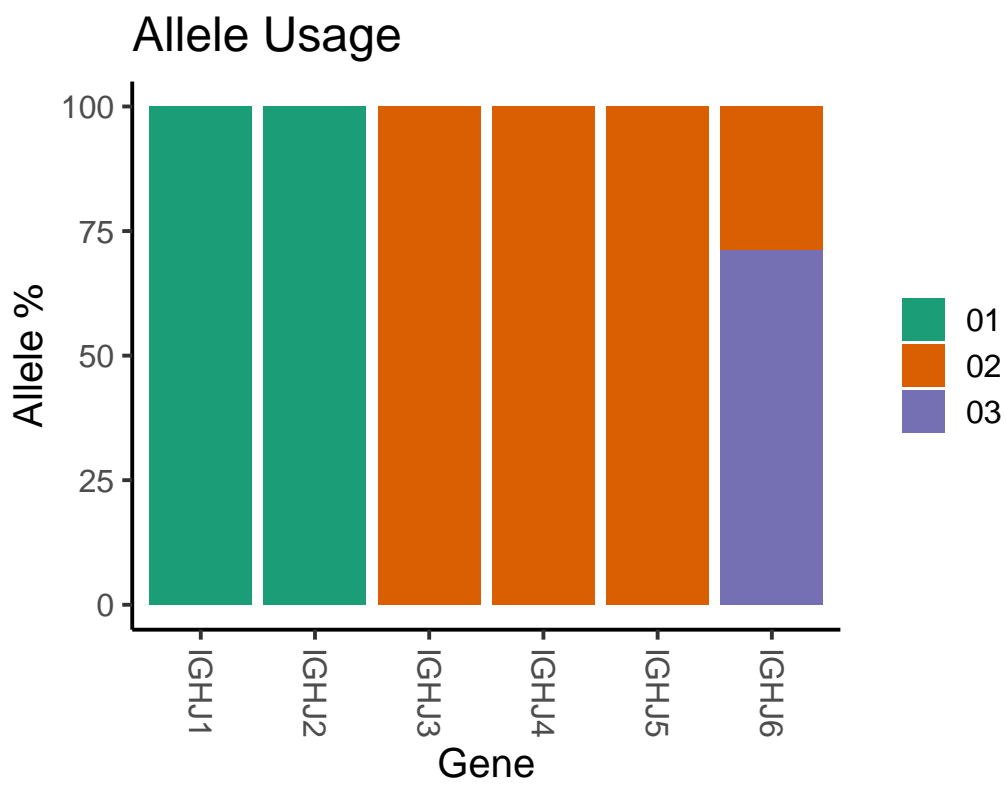
1580 sequences assigned  
53 (3.4%) exact matches, in which:  
36 unique CDR3  
4 unique J



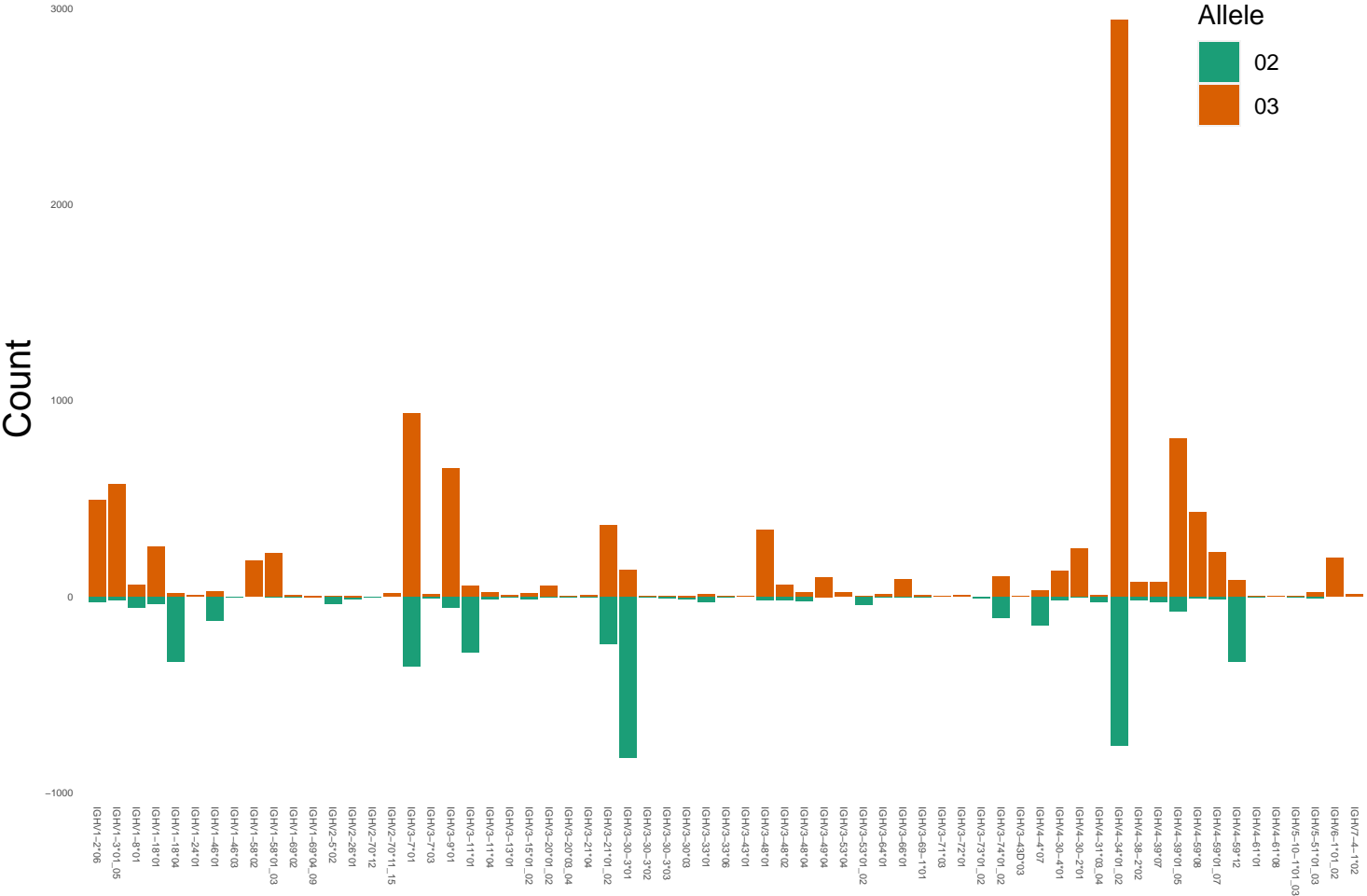
### IGHV5-51\*01\_03

7990 sequences assigned  
207 (2.6%) exact matches, in which:  
104 unique CDR3  
5 unique J





Sequence Count by IGHJ6 allele usage



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.

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

Novel sequence(s) IGHV3-33\*01\_C288T 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) IGHV3-33\*01\_T105C\_A173T\_T192G\_C288T are not listed in the genotype and will be ignored.

Novel sequence(s) IGHV3-30\*04\_T288C IGHV3-33\*01\_G75C IGHV4-30-2\*03\_T288C IGHV4-59\*02\_G88A are not listed in the genotype and will be ignored.

Novel sequence(s) IGHV3-11\*06\_T300C 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) 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) IGHV5-51\*07\_A128G are not listed in the genotype and will be ignored.

Warning – no inferred sequences found.