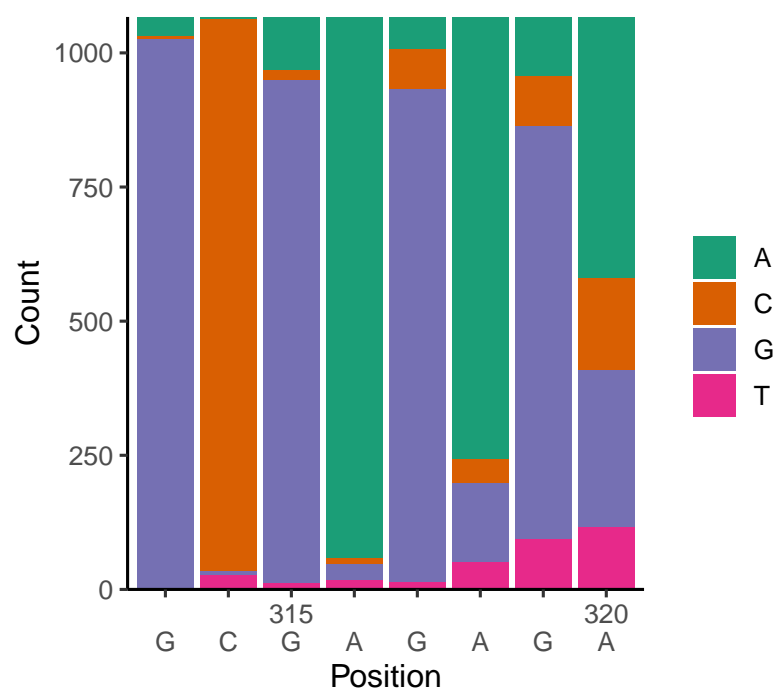
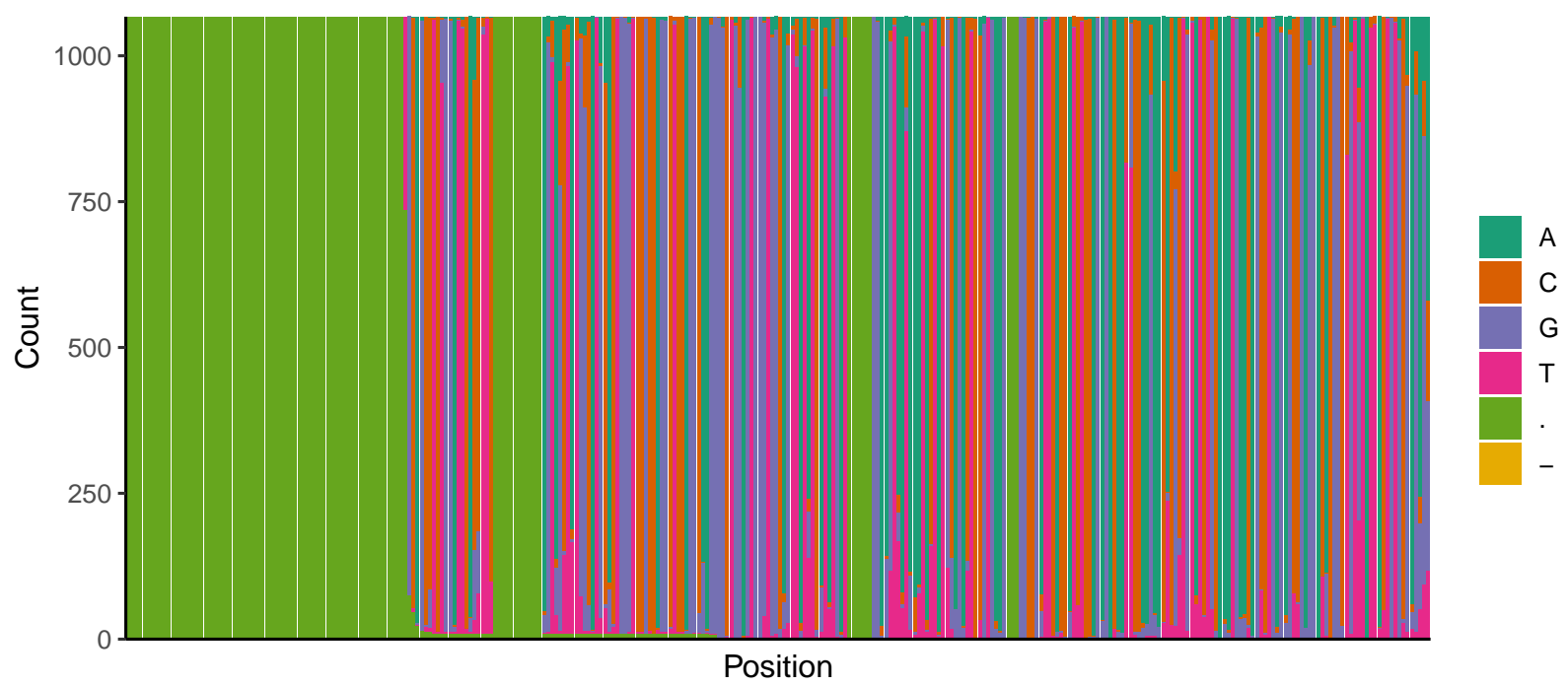


# Gene IGHV3-30\*03\_T288C



# Gene IGHV3-30\*03\_T288C



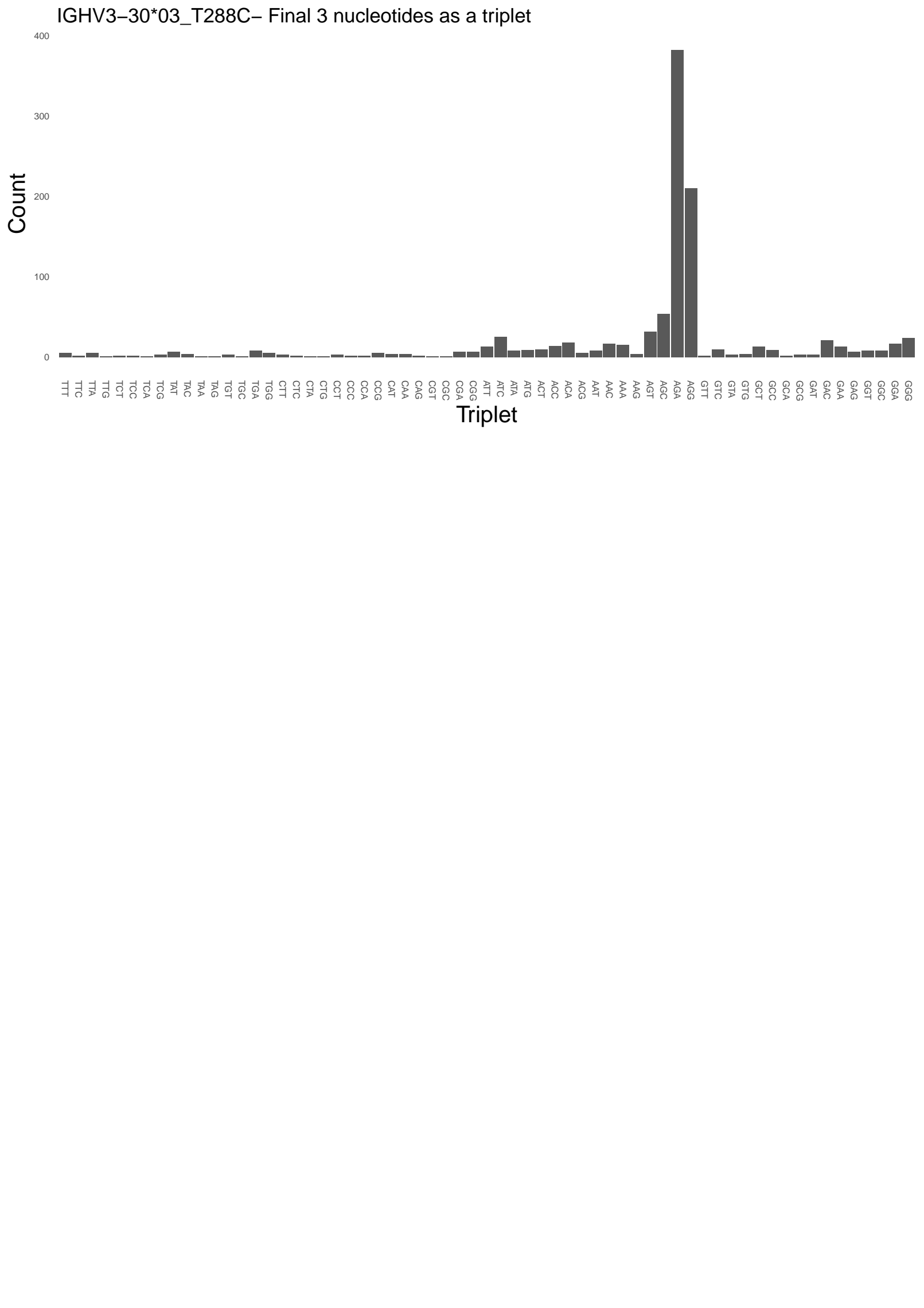
IGHV3-30\*03\_T288C- Final 3 nucleotides as a triplet

Count

400  
300  
200  
100  
0

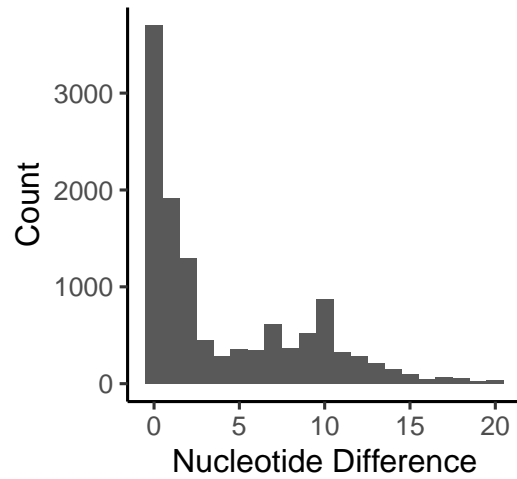
Triplet

TTT  
TTC  
TTA  
TTG  
TCT  
TCC  
TCA  
TCG  
TAT  
TAC  
TAA  
TAG  
TGT  
TGC  
TGA  
TGG  
CTT  
CTC  
CTA  
CTG  
CCT  
CCC  
CCA  
CCG  
CAT  
CAA  
CAG  
CGT  
CGC  
CGA  
CGG  
ATT  
ATC  
ATA  
ATG  
ACT  
ACC  
ACA  
ACG  
AAT  
AAC  
AAA  
AAG  
AGT  
AGC  
AGA  
AGG  
GTT  
GTC  
GTA  
GTG  
GCT  
GCC  
GCA  
GCG  
GAT  
GAC  
GAA  
GAG  
GGT  
GGC  
GGA  
GGG



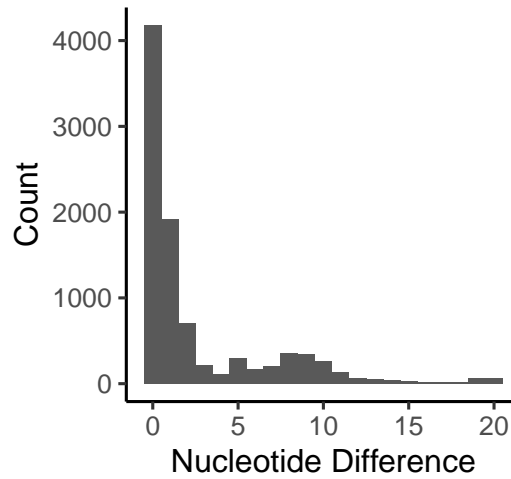
### IGHV1-2\*02

12702 sequences assigned  
3699 (29.1%) exact matches, in which:  
3472 unique CDR3  
7 unique J



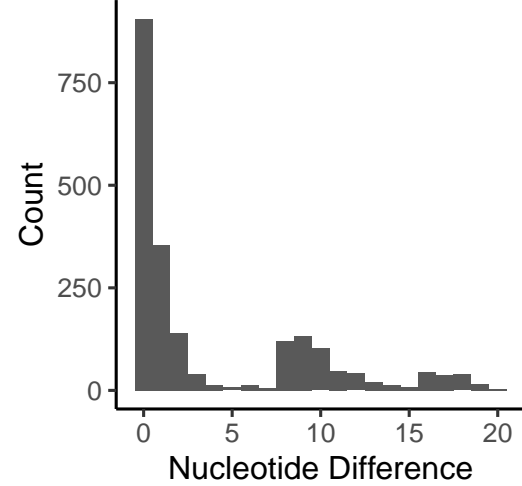
### IGHV1-8\*01

9424 sequences assigned  
4177 (44.3%) exact matches, in which:  
3970 unique CDR3  
7 unique J



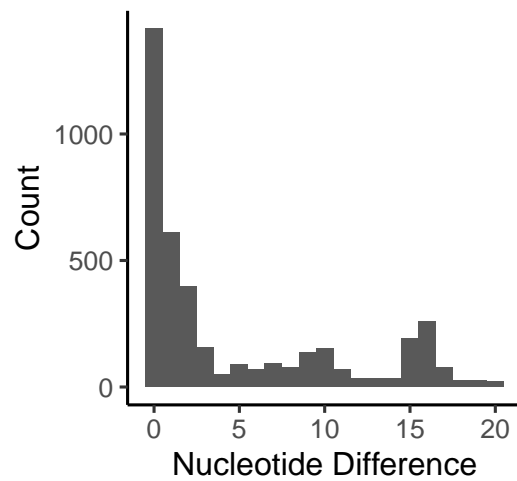
### IGHV1-24\*01

2262 sequences assigned  
906 (40.1%) exact matches, in which:  
863 unique CDR3  
7 unique J



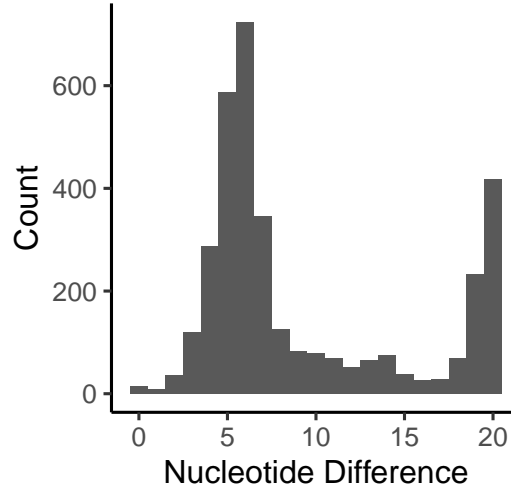
### IGHV1-2\*04

4440 sequences assigned  
1416 (31.9%) exact matches, in which:  
1353 unique CDR3  
7 unique J



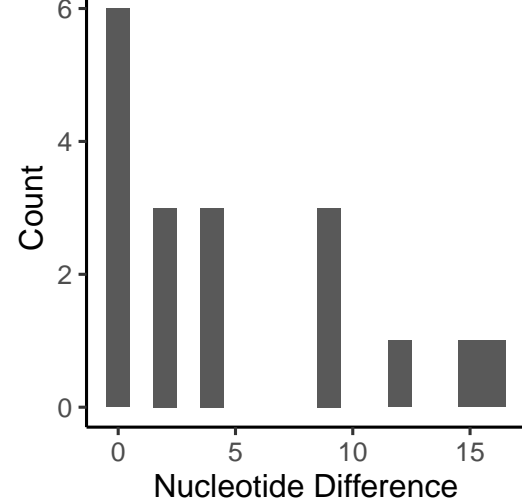
### IGHV1-8\*02

3833 sequences assigned  
15 (0.4%) exact matches, in which:  
15 unique CDR3  
5 unique J



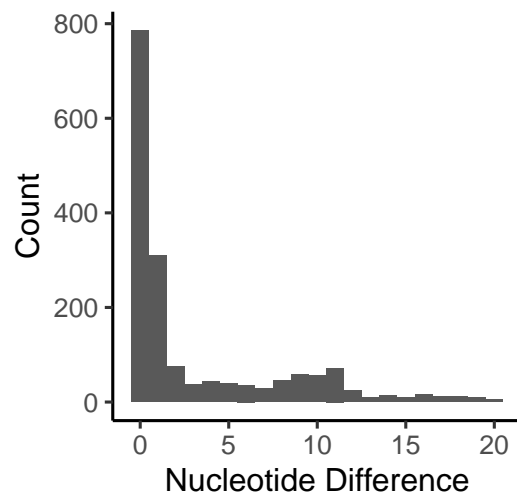
### IGHV1-45\*02

18 sequences assigned  
6 (33.3%) exact matches, in which:  
6 unique CDR3  
3 unique J



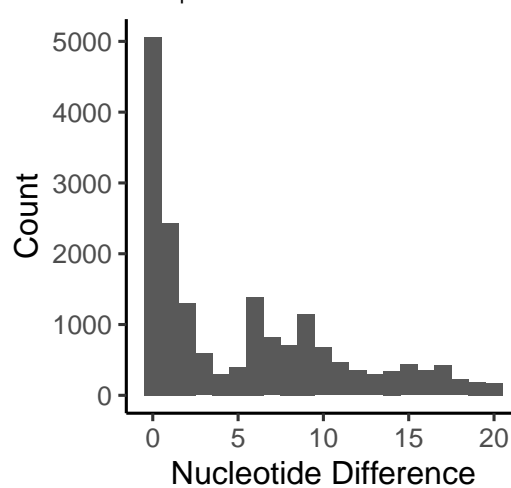
### IGHV1-3\*01\_05

1832 sequences assigned  
786 (42.9%) exact matches, in which:  
732 unique CDR3  
7 unique J



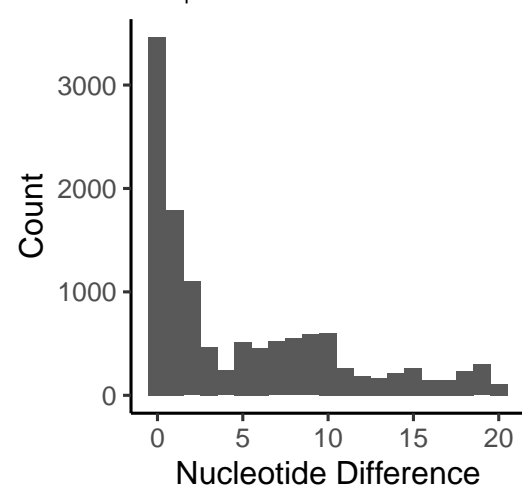
### IGHV1-18\*01

20279 sequences assigned  
5061 (25%) exact matches, in which:  
4749 unique CDR3  
7 unique J



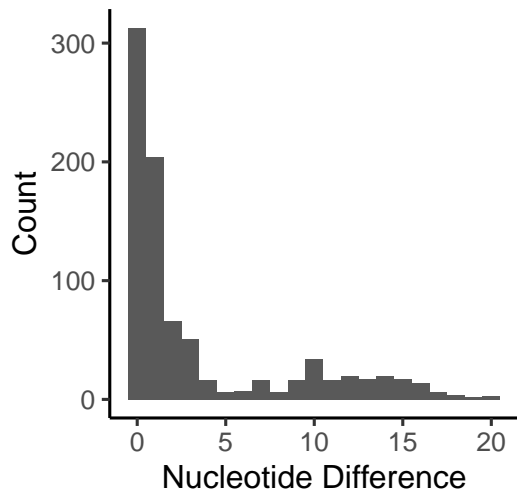
### IGHV1-46\*01

13652 sequences assigned  
3464 (25.4%) exact matches, in which:  
3283 unique CDR3  
7 unique J



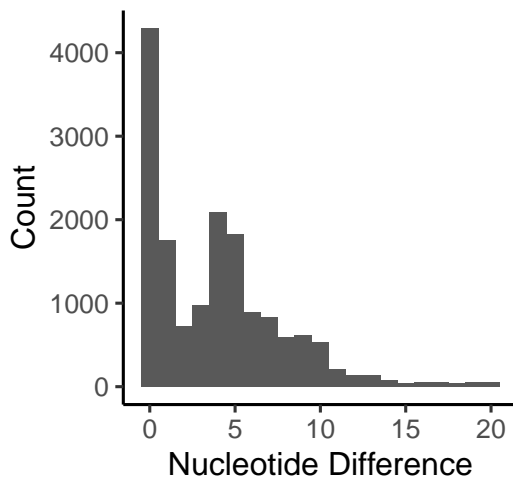
### IGHV1–58\*01\_03

876 sequences assigned  
313 (35.7%) exact matches, in which:  
301 unique CDR3  
7 unique J



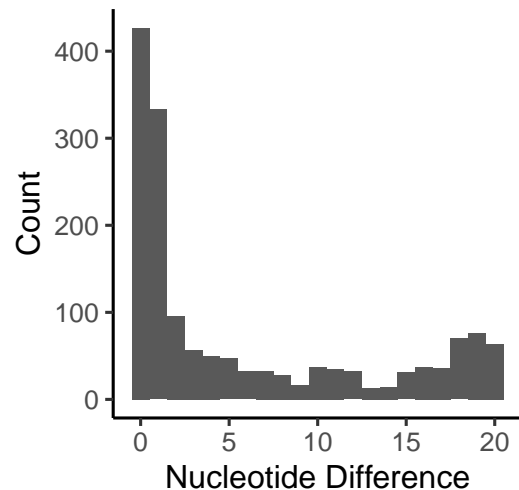
### IGHV1–69\*06\_14

16284 sequences assigned  
4291 (26.4%) exact matches, in which:  
4135 unique CDR3  
7 unique J



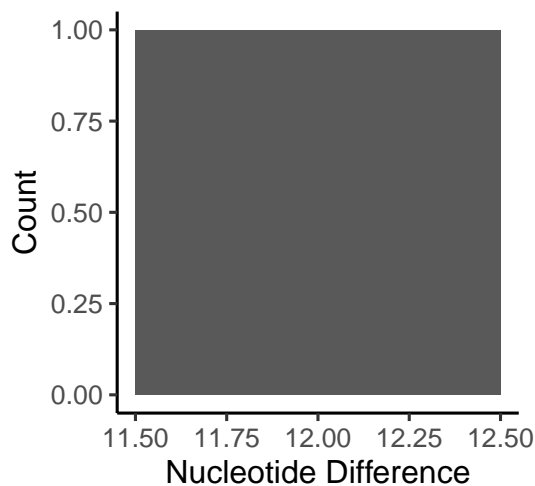
### IGHV2–5\*02

2213 sequences assigned  
427 (19.3%) exact matches, in which:  
404 unique CDR3  
7 unique J



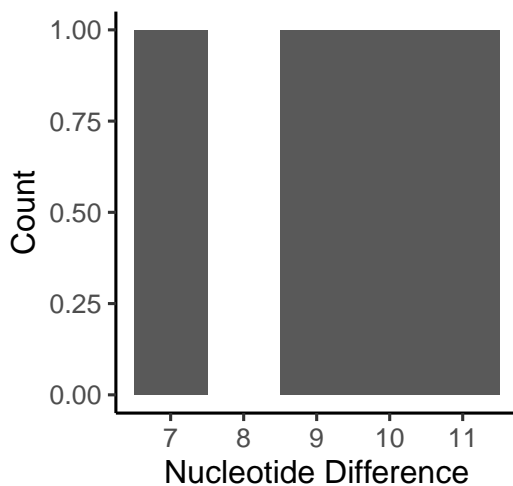
### IGHV1–68\*01

1 sequences assigned  
No exact matches.



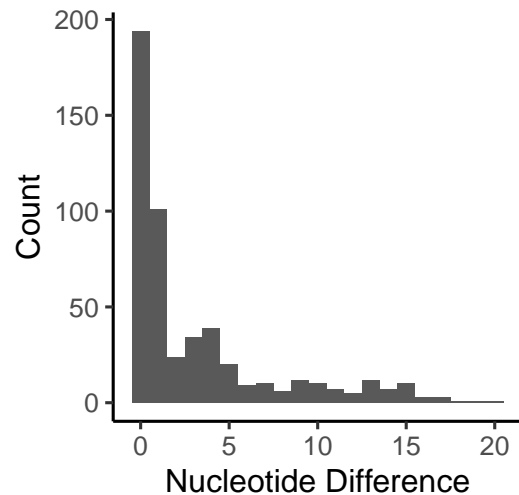
### IGHV1–NL1\*01

4 sequences assigned  
No exact matches.



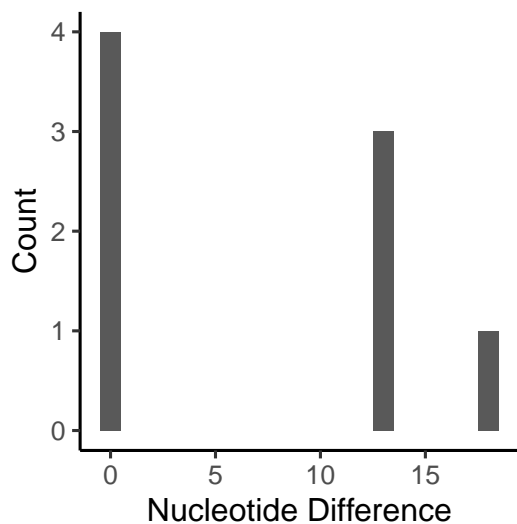
### IGHV2–26\*01

536 sequences assigned  
194 (36.2%) exact matches, in which:  
188 unique CDR3  
7 unique J



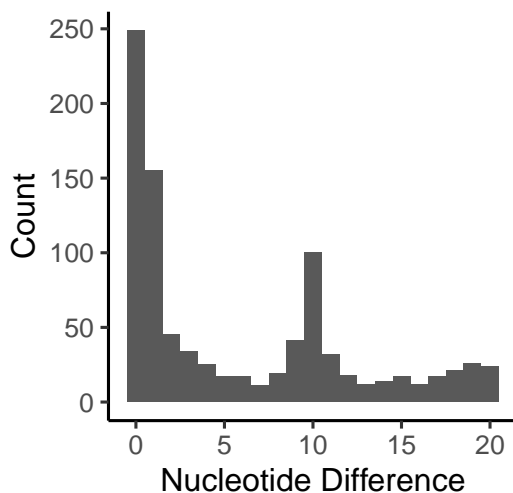
### IGHV1–69–2\*01

87 sequences assigned  
4 (4.6%) exact matches, in which:  
3 unique CDR3  
2 unique J



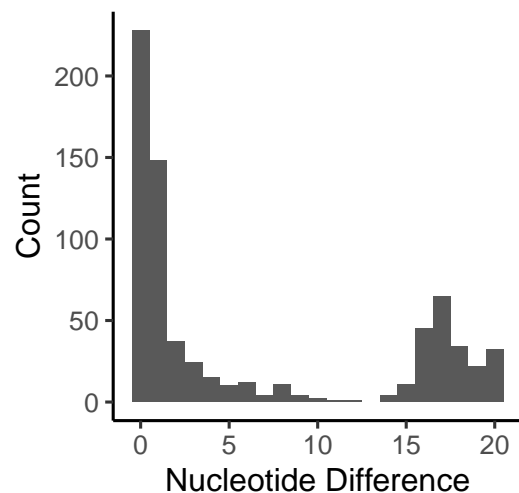
### IGHV2–5\*01

1200 sequences assigned  
249 (20.8%) exact matches, in which:  
238 unique CDR3  
7 unique J



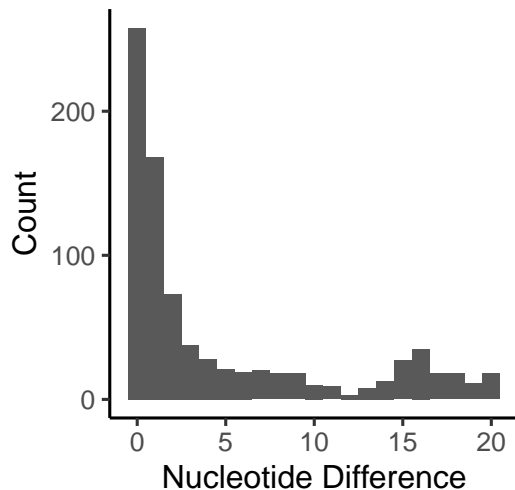
### IGHV2–70\*01

769 sequences assigned  
228 (29.6%) exact matches, in which:  
215 unique CDR3  
7 unique J



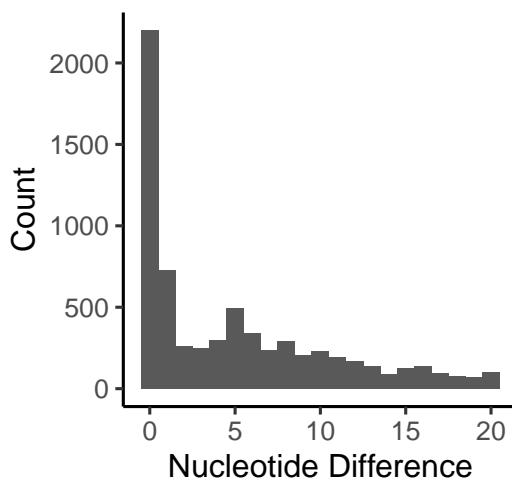
### IGHV2–70\*11\_15

1189 sequences assigned  
258 (21.7%) exact matches, in which:  
242 unique CDR3  
7 unique J



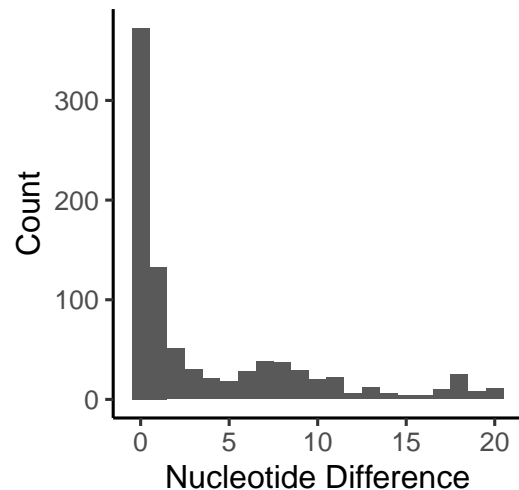
### IGHV3–9\*01

8096 sequences assigned  
2200 (27.2%) exact matches, in which:  
1746 unique CDR3  
7 unique J



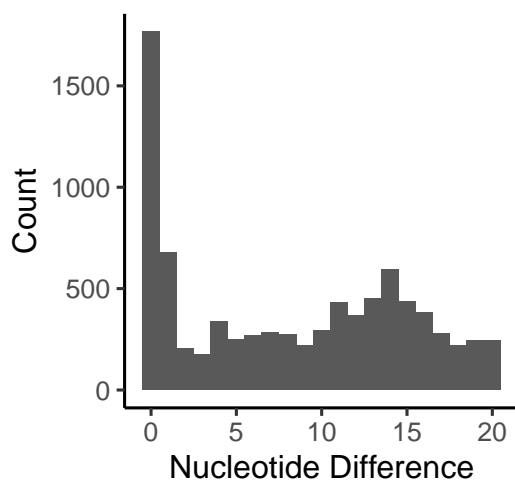
### IGHV3–13\*01

1164 sequences assigned  
373 (32%) exact matches, in which:  
303 unique CDR3  
7 unique J



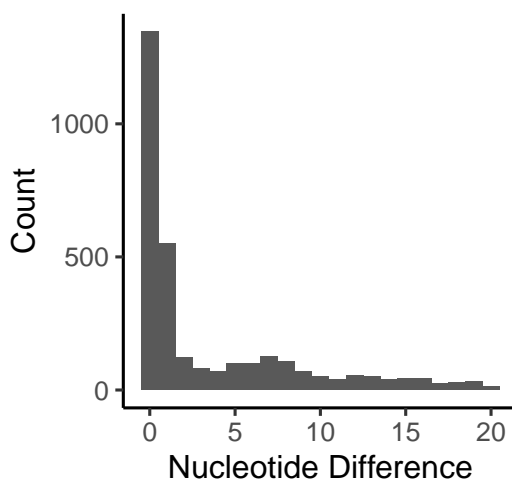
### IGHV3–7\*01

11167 sequences assigned  
1767 (15.8%) exact matches, in which:  
1465 unique CDR3  
7 unique J



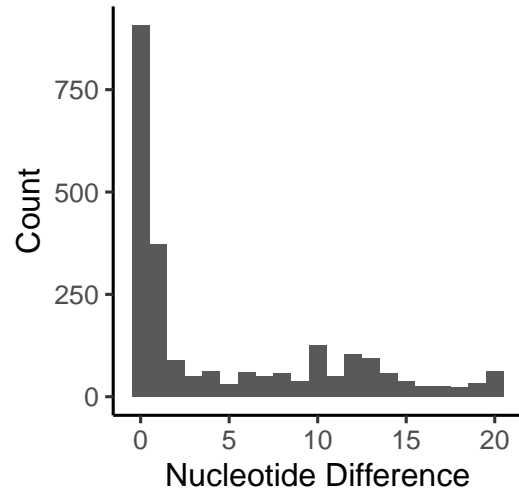
### IGHV3–11\*01

3887 sequences assigned  
1346 (34.6%) exact matches, in which:  
1145 unique CDR3  
7 unique J



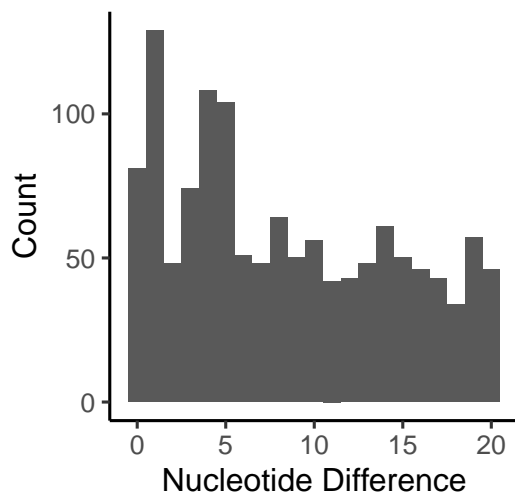
### IGHV3–15\*01\_02

2963 sequences assigned  
908 (30.6%) exact matches, in which:  
740 unique CDR3  
7 unique J



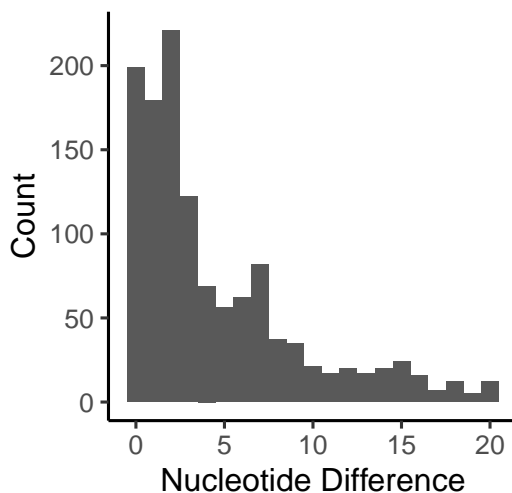
### IGHV3–7\*03

2235 sequences assigned  
81 (3.6%) exact matches, in which:  
74 unique CDR3  
7 unique J



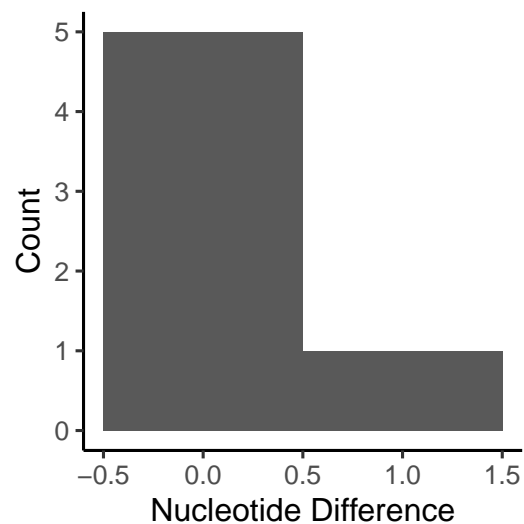
### IGHV3–11\*04

1410 sequences assigned  
199 (14.1%) exact matches, in which:  
198 unique CDR3  
7 unique J



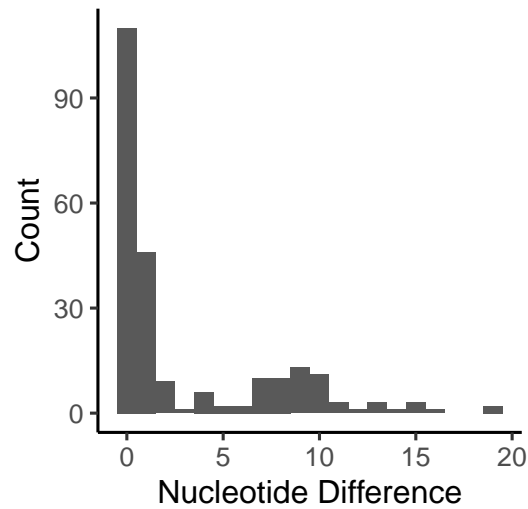
### IGHV3–19\*01

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



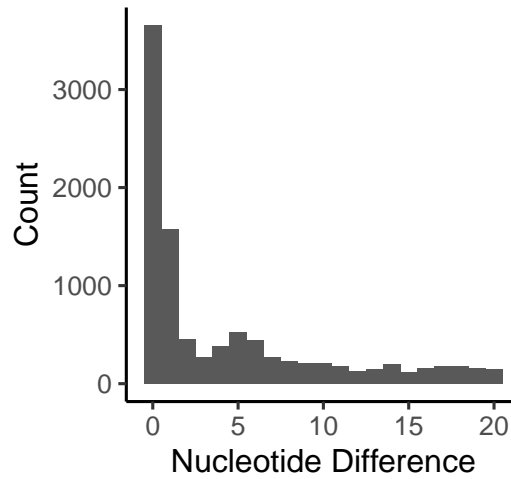
### IGHV3-20\*01\_02

238 sequences assigned  
110 (46.2%) exact matches, in which:  
87 unique CDR3  
6 unique J



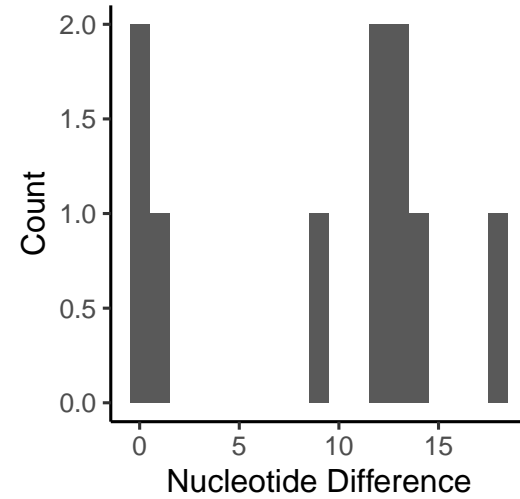
### IGHV3-21\*01\_02

11339 sequences assigned  
3654 (32.2%) exact matches, in which:  
2983 unique CDR3  
7 unique J



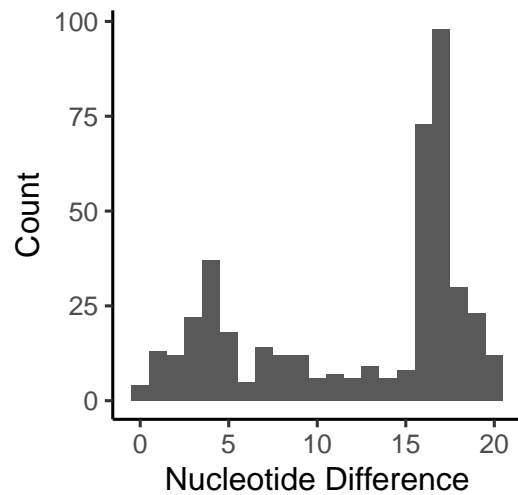
### IGHV3-30-3\*01

14 sequences assigned  
2 (14.3%) exact matches, in which:  
1 unique CDR3  
1 unique J



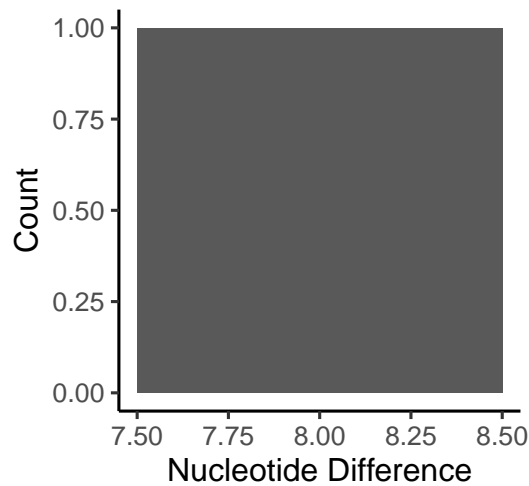
### IGHV3-20\*03\_04

532 sequences assigned  
4 (0.8%) exact matches, in which:  
4 unique CDR3  
3 unique J



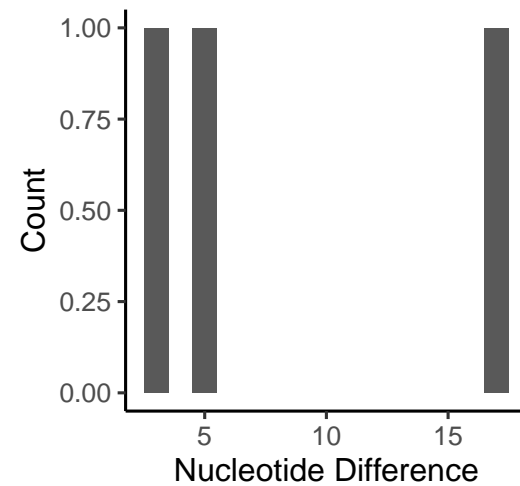
### IGHV3-22\*01\_02

5 sequences assigned  
No exact matches.



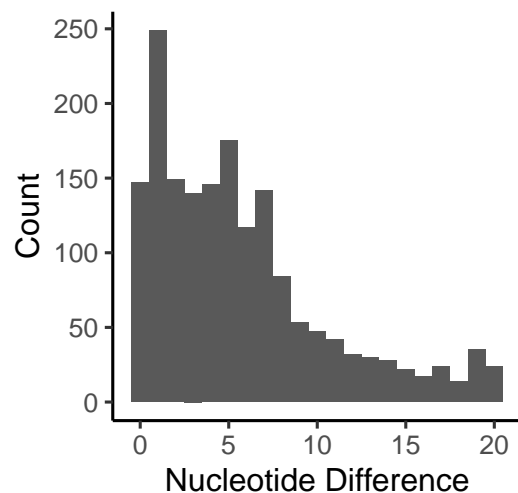
### IGHV3-30-3\*02

5 sequences assigned  
No exact matches.



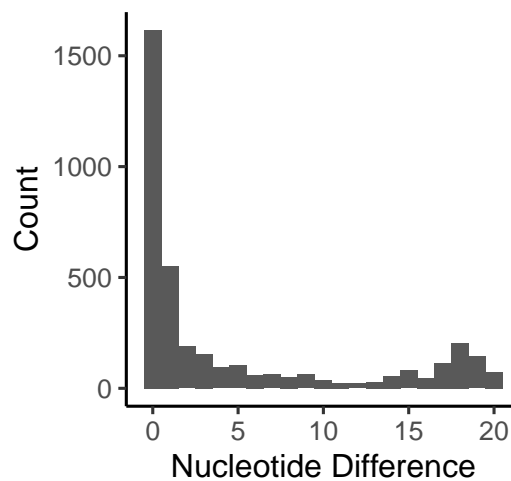
### IGHV3-21\*04

1991 sequences assigned  
147 (7.4%) exact matches, in which:  
145 unique CDR3  
7 unique J



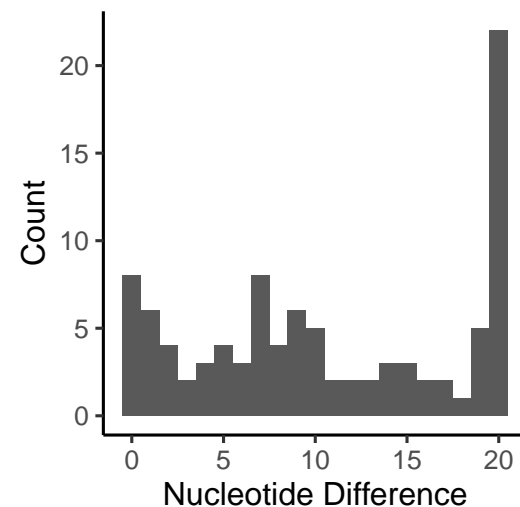
### IGHV3-30\*01

4071 sequences assigned  
1616 (39.7%) exact matches, in which:  
1379 unique CDR3  
7 unique J



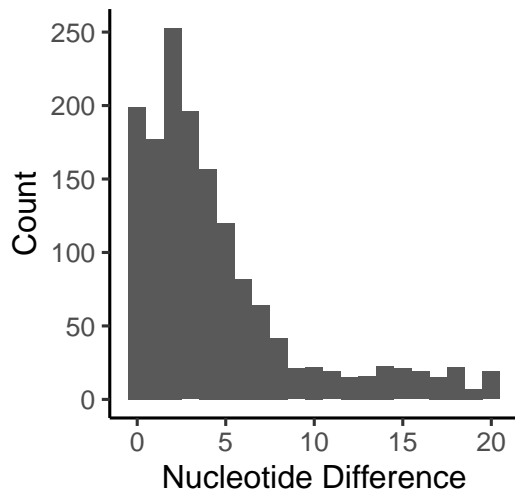
### IGHV3-30-3\*03

279 sequences assigned  
8 (2.9%) exact matches, in which:  
8 unique CDR3  
3 unique J



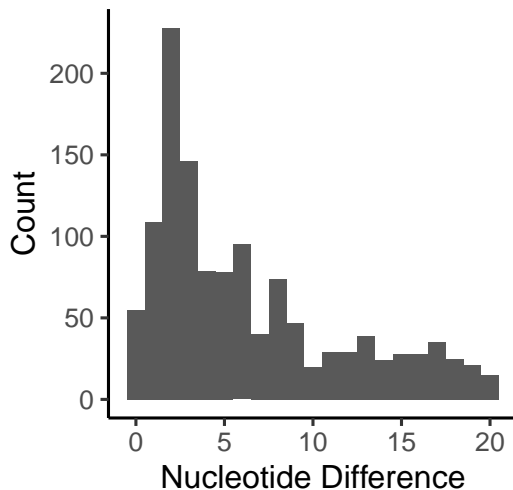
### IGHV3–30\*07

1592 sequences assigned  
199 (12.5%) exact matches, in which:  
197 unique CDR3  
7 unique J



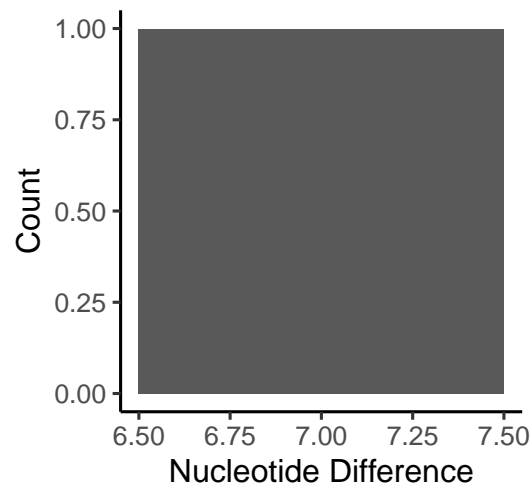
### IGHV3–33\*06

1582 sequences assigned  
55 (3.5%) exact matches, in which:  
54 unique CDR3  
6 unique J



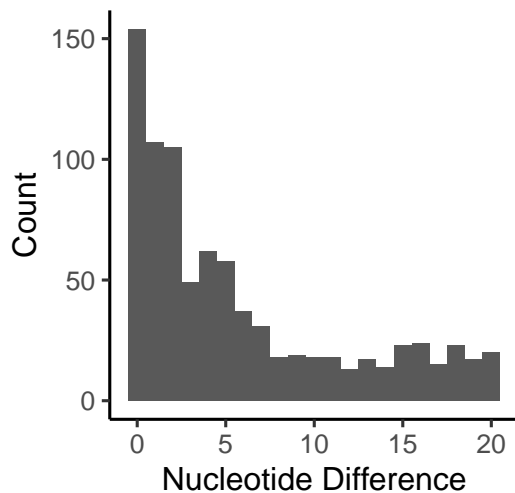
### IGHV3–47\*02

3 sequences assigned  
No exact matches.



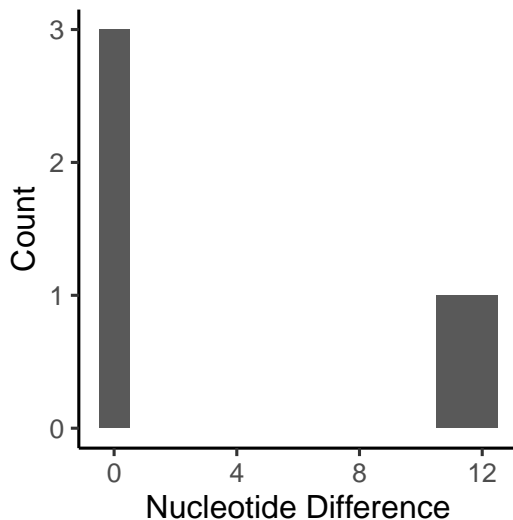
### IGHV3–30\*03\_T288C

1067 sequences assigned  
154 (14.4%) exact matches, in which:  
153 unique CDR3  
7 unique J



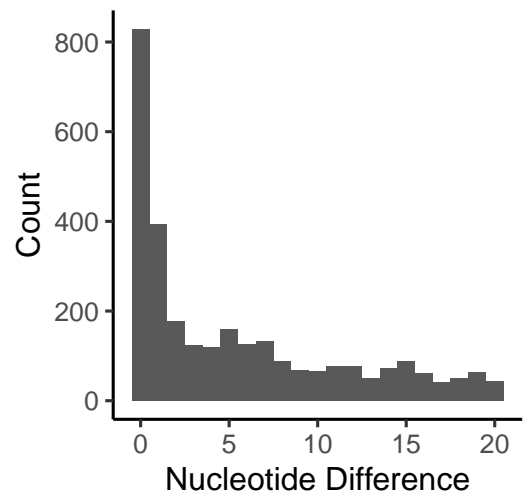
### IGHV3–35\*01

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



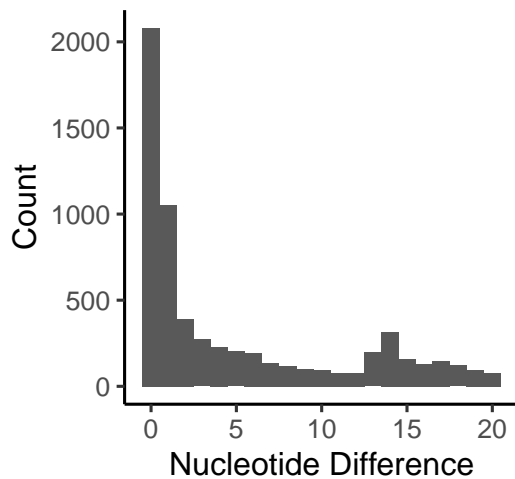
### IGHV3–48\*01

5142 sequences assigned  
829 (16.1%) exact matches, in which:  
690 unique CDR3  
7 unique J



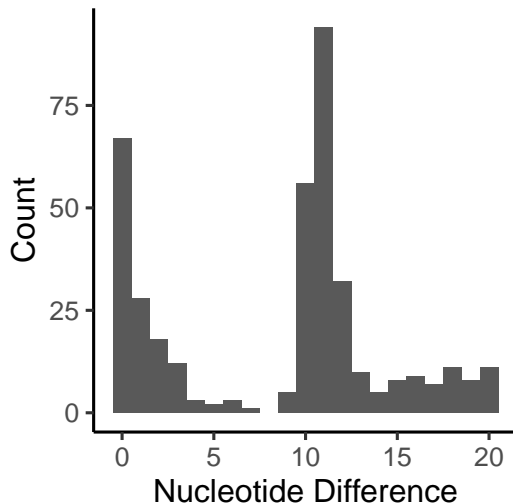
### IGHV3–33\*01

6689 sequences assigned  
2080 (31.1%) exact matches, in which:  
1730 unique CDR3  
7 unique J



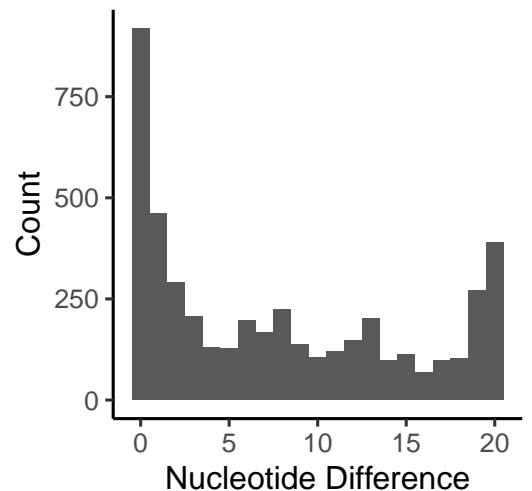
### IGHV3–43\*01

524 sequences assigned  
67 (12.8%) exact matches, in which:  
56 unique CDR3  
5 unique J



### IGHV3–48\*03

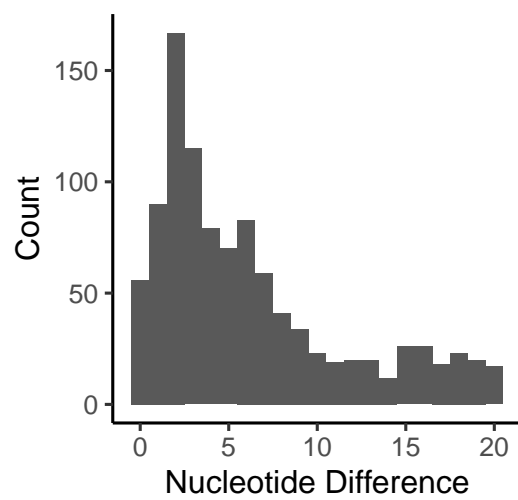
5696 sequences assigned  
919 (16.1%) exact matches, in which:  
754 unique CDR3  
7 unique J





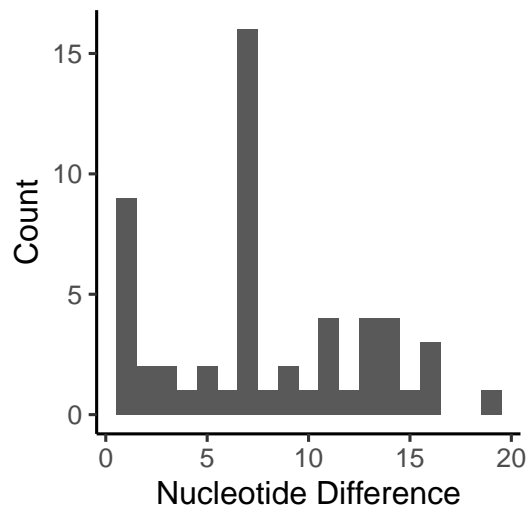
### IGHV3-48\*04

1383 sequences assigned  
56 (4%) exact matches, in which:  
56 unique CDR3  
6 unique J



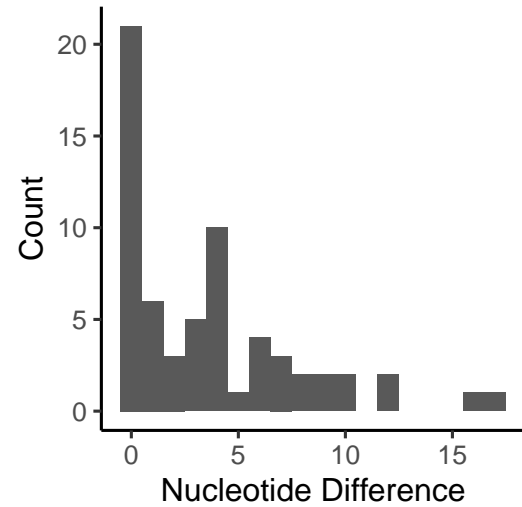
### IGHV3-53\*05

67 sequences assigned  
No exact matches.



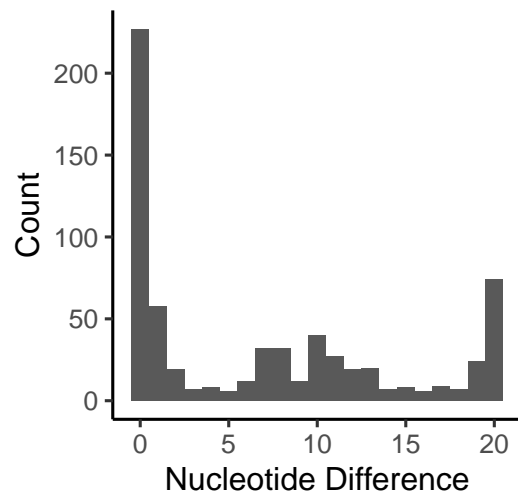
### IGHV3-64\*02\_07

64 sequences assigned  
21 (32.8%) exact matches, in which:  
20 unique CDR3  
6 unique J



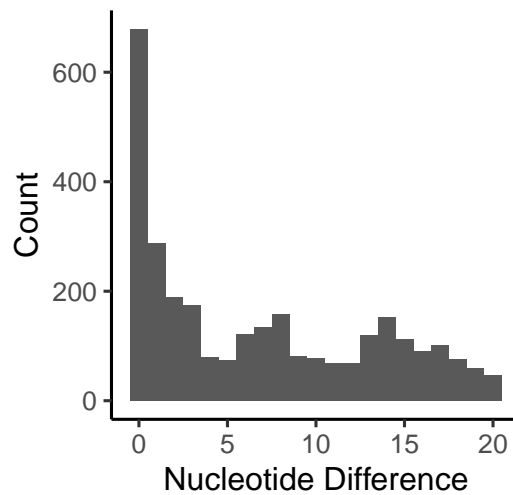
### IGHV3-49\*04

1015 sequences assigned  
227 (22.4%) exact matches, in which:  
198 unique CDR3  
7 unique J



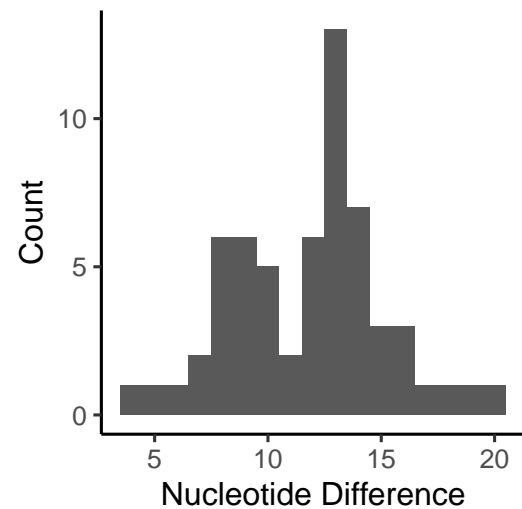
### IGHV3-53\*01\_02

3709 sequences assigned  
679 (18.3%) exact matches, in which:  
578 unique CDR3  
7 unique J



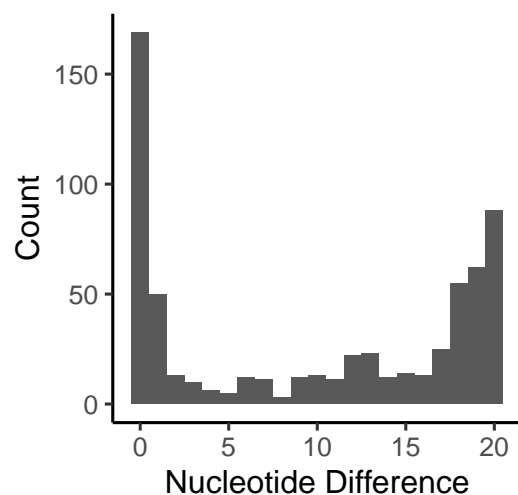
### IGHV3-66\*01

74 sequences assigned  
No exact matches.



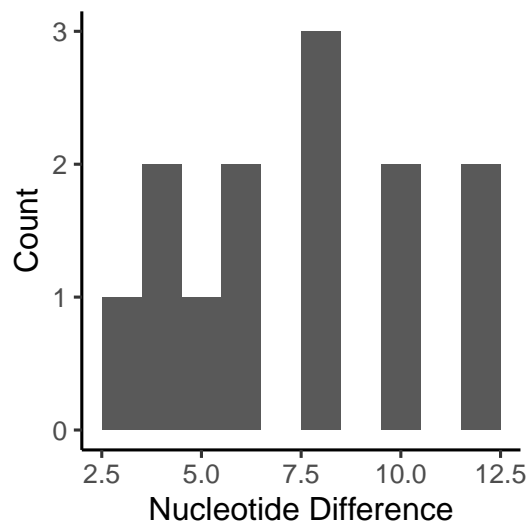
### IGHV3-49\*03\_05

1059 sequences assigned  
169 (16%) exact matches, in which:  
141 unique CDR3  
7 unique J



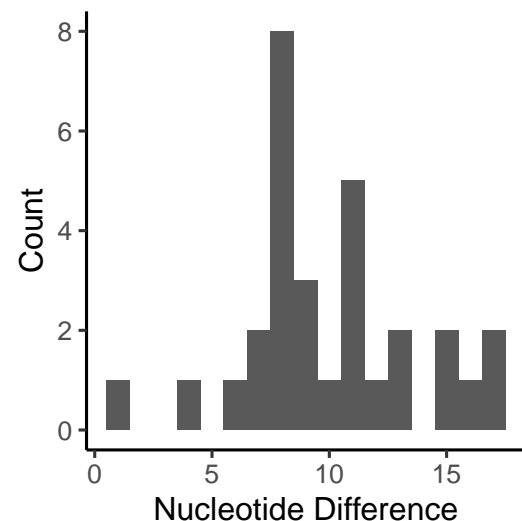
### IGHV3-64\*04

19 sequences assigned  
No exact matches.



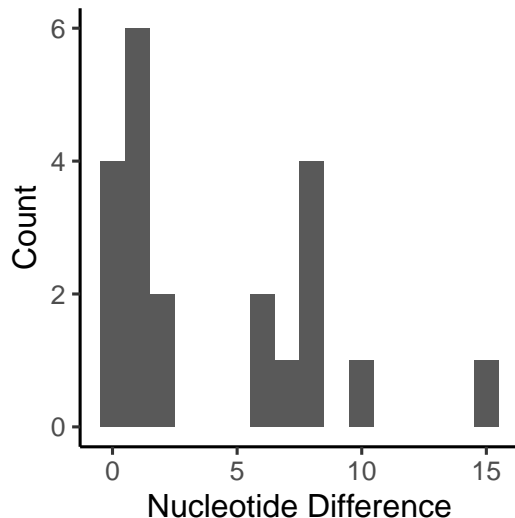
### IGHV3-66\*02

40 sequences assigned  
No exact matches.



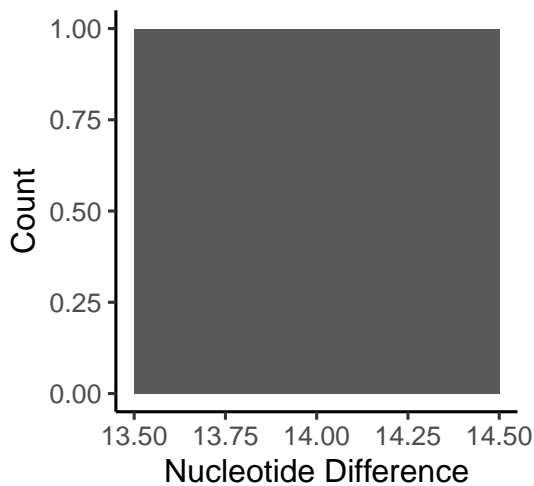
### IGHV3-66\*03

22 sequences assigned  
4 (18.2%) exact matches, in which:  
4 unique CDR3  
2 unique J



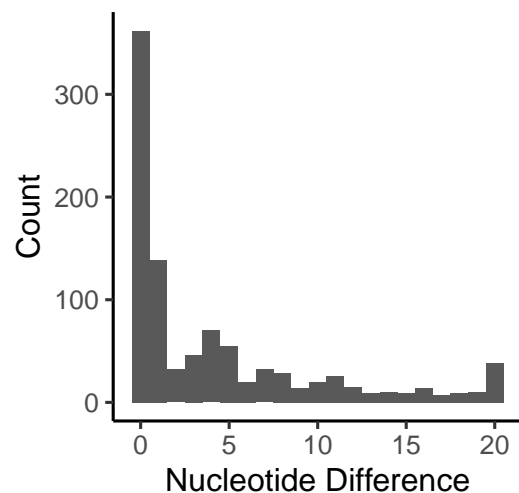
### IGHV3-71\*03

1 sequences assigned  
No exact matches.



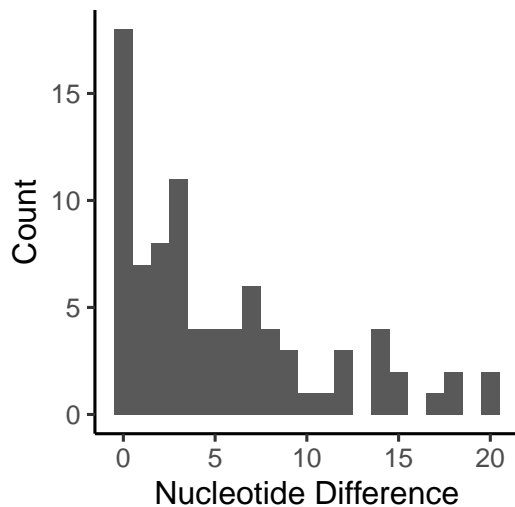
### IGHV3-73\*01\_02

1163 sequences assigned  
362 (31.1%) exact matches, in which:  
307 unique CDR3  
7 unique J



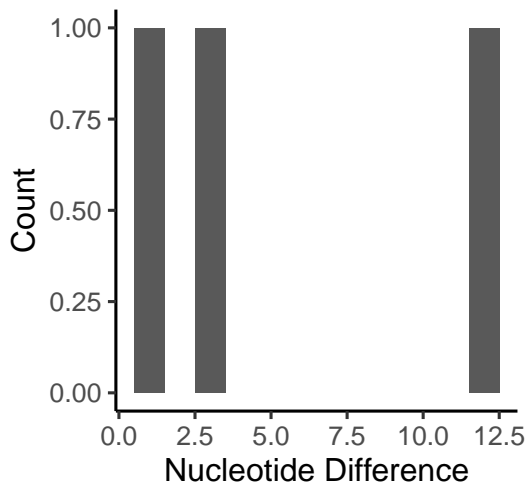
### IGHV3-69-1\*01

115 sequences assigned  
18 (15.7%) exact matches, in which:  
17 unique CDR3  
6 unique J



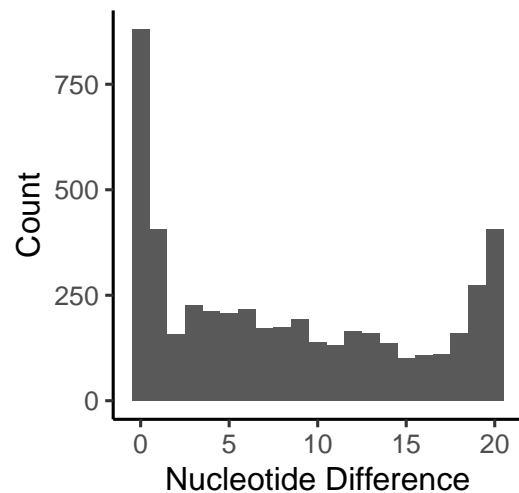
### IGHV3-71\*01\_04

5 sequences assigned  
No exact matches.



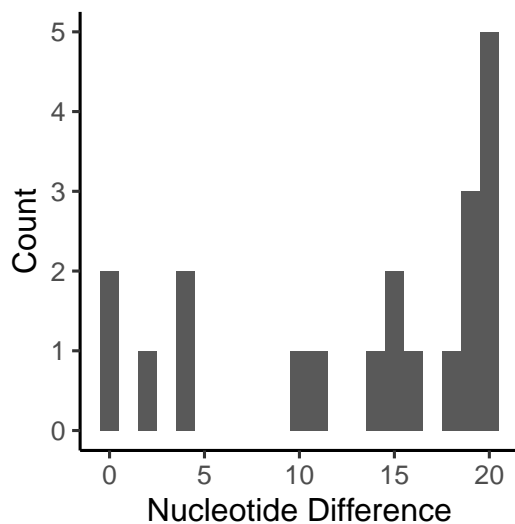
### IGHV3-74\*01\_02

7325 sequences assigned  
881 (12%) exact matches, in which:  
709 unique CDR3  
7 unique J



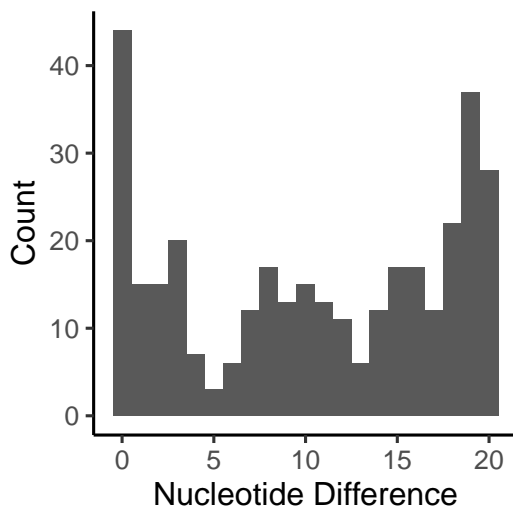
### IGHV3-69-1\*02

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



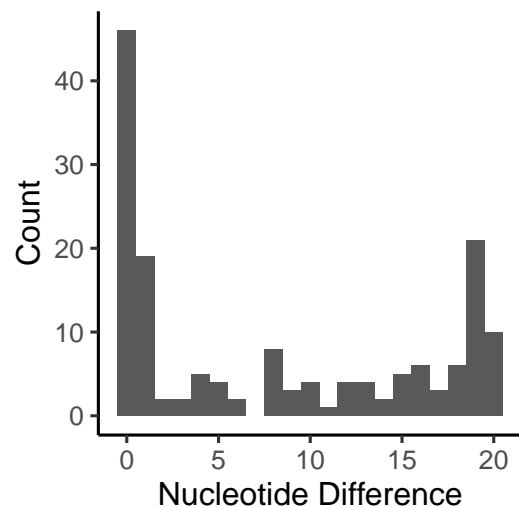
### IGHV3-72\*01

454 sequences assigned  
44 (9.7%) exact matches, in which:  
38 unique CDR3  
6 unique J



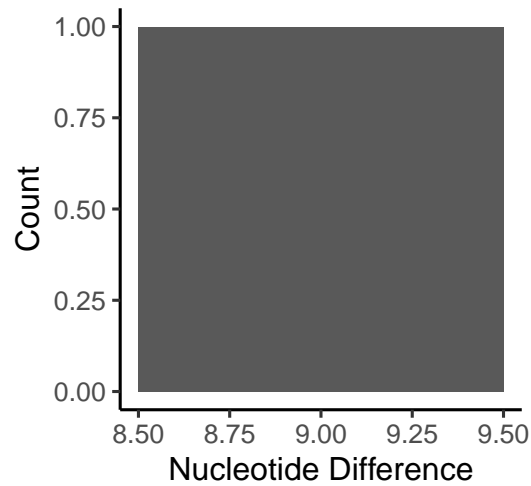
### IGHV3-43D\*04

186 sequences assigned  
46 (24.7%) exact matches, in which:  
41 unique CDR3  
3 unique J



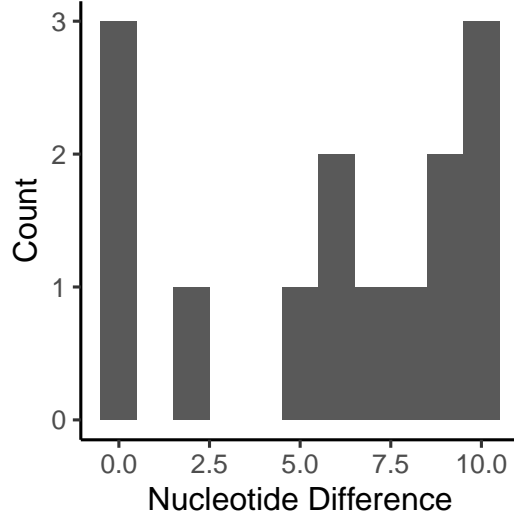
### IGHV3-64D\*06

6 sequences assigned  
No exact matches.



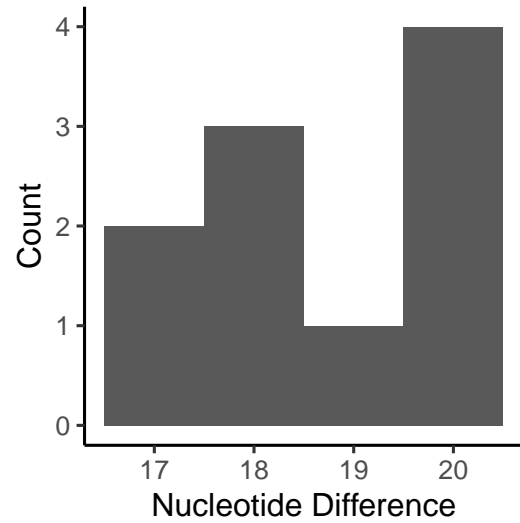
### IGHV4-28\*03

15 sequences assigned  
3 (20%) exact matches, in which:  
3 unique CDR3  
2 unique J



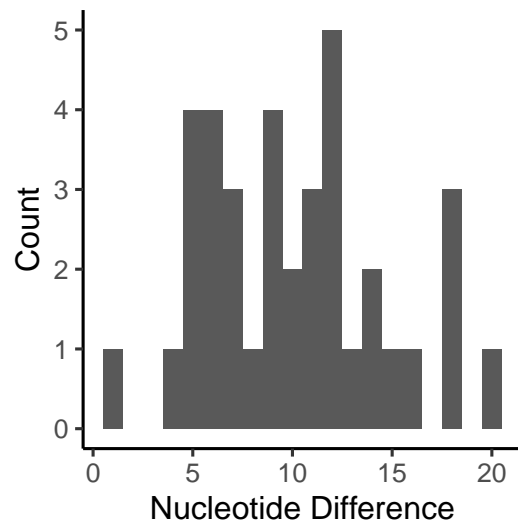
### IGHV4-30-4\*01

23 sequences assigned  
No exact matches.



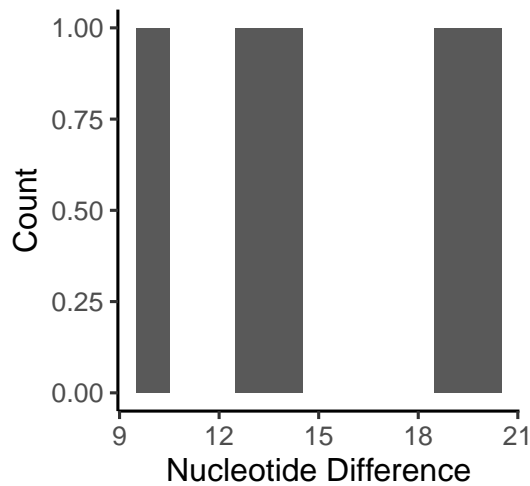
### IGHV3-NL1\*01

51 sequences assigned  
No exact matches.



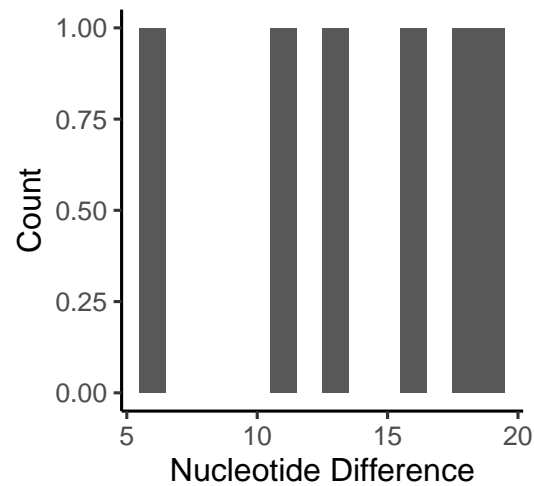
### IGHV4-28\*01\_07

5 sequences assigned  
No exact matches.



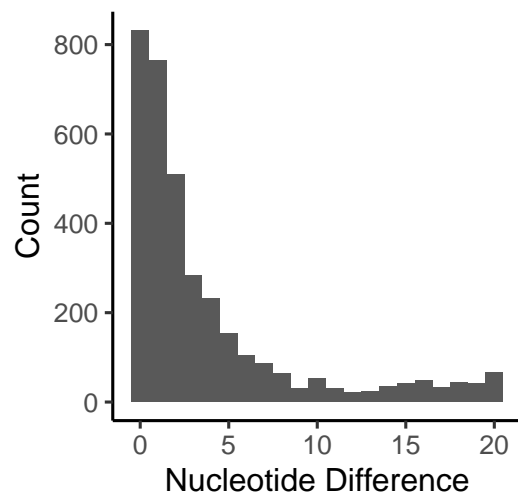
### IGHV4-30-2\*03

10 sequences assigned  
No exact matches.



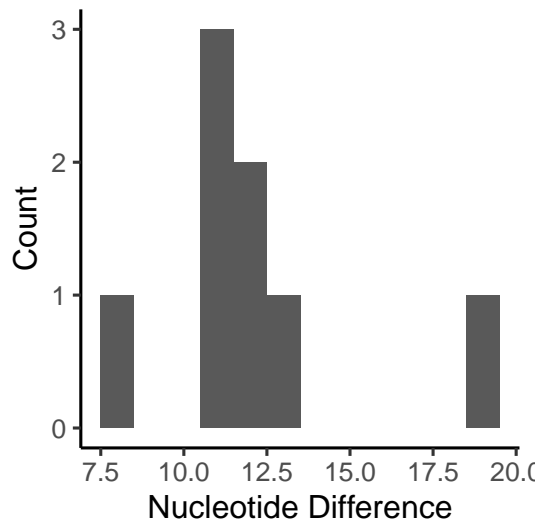
### IGHV4-4\*07

5442 sequences assigned  
832 (15.3%) exact matches, in which:  
788 unique CDR3  
7 unique J



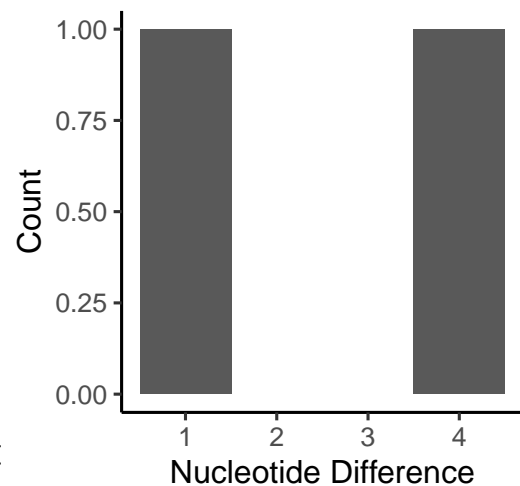
### IGHV4-30-2\*01

11 sequences assigned  
No exact matches.



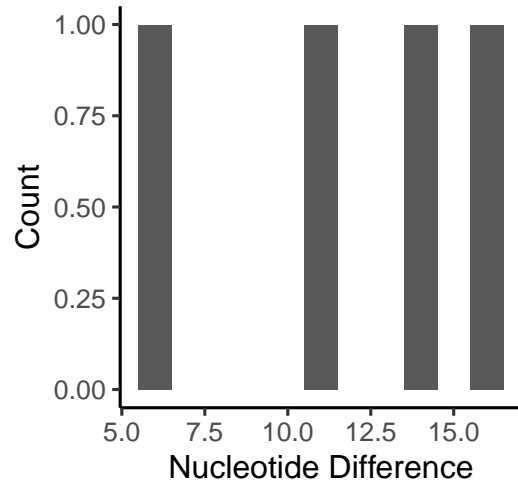
### IGHV4-30-2\*04

5 sequences assigned  
No exact matches.



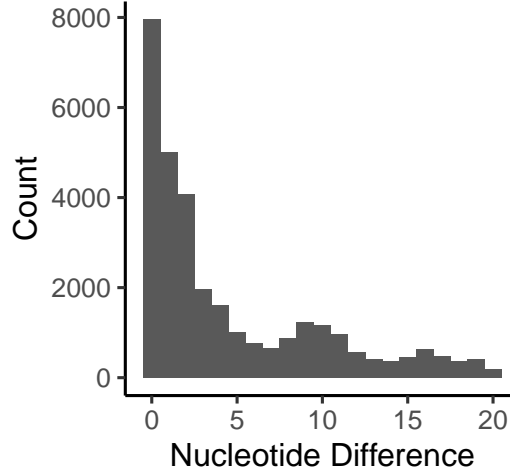
### IGHV4-30-4\*08

9 sequences assigned  
No exact matches.



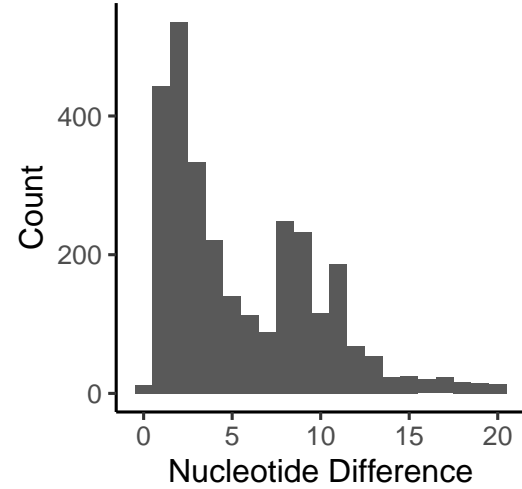
### IGHV4-34\*01\_02

46547 sequences assigned  
7957 (17.1%) exact matches, in which:  
6836 unique CDR3  
7 unique J



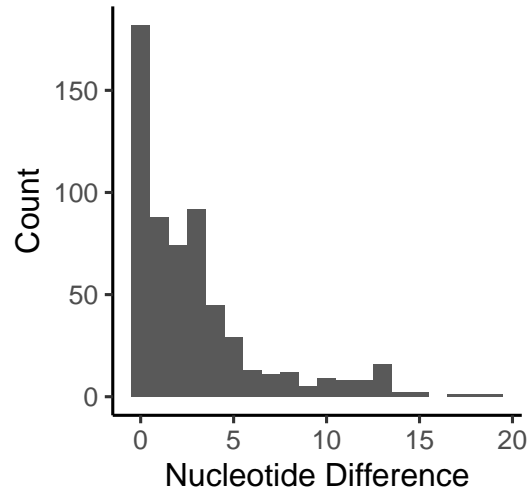
### IGHV4-39\*07

3108 sequences assigned  
12 (0.4%) exact matches, in which:  
12 unique CDR3  
6 unique J



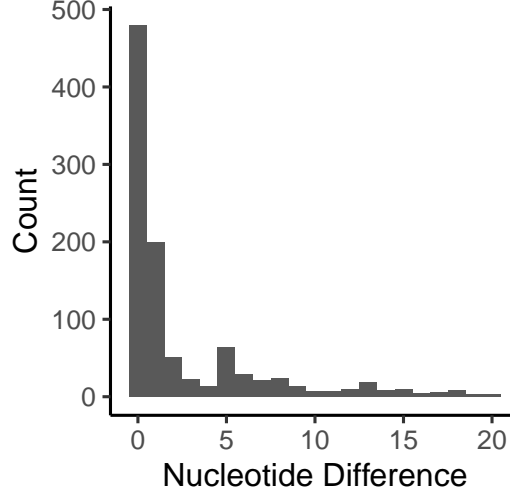
### IGHV4-31\*01

609 sequences assigned  
182 (29.9%) exact matches, in which:  
173 unique CDR3  
7 unique J



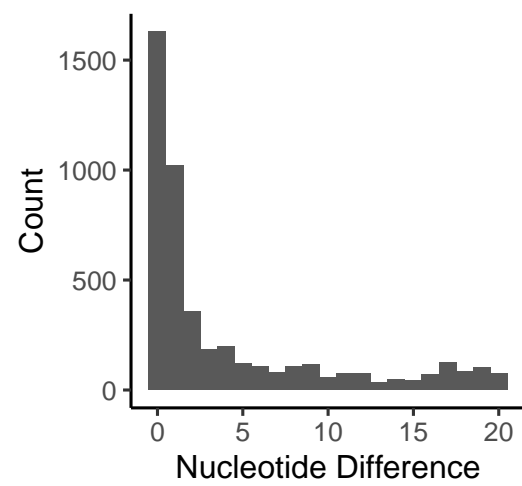
### IGHV4-38-2\*01

1394 sequences assigned  
480 (34.4%) exact matches, in which:  
465 unique CDR3  
7 unique J



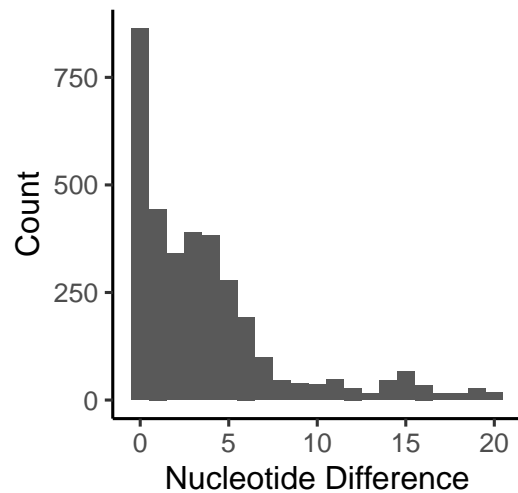
### IGHV4-39\*01\_05

6578 sequences assigned  
1629 (24.8%) exact matches, in which:  
1508 unique CDR3  
7 unique J



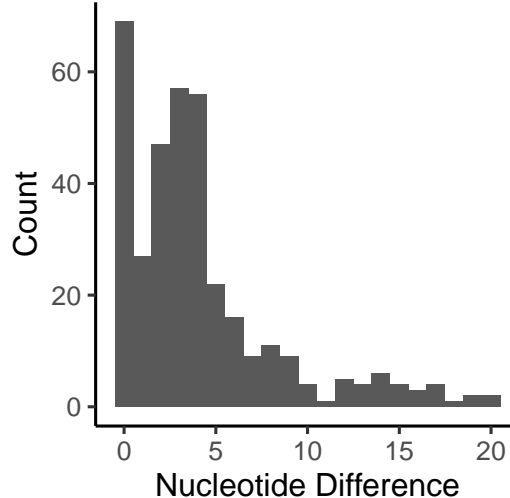
### IGHV4-31\*03\_04

5119 sequences assigned  
864 (16.9%) exact matches, in which:  
809 unique CDR3  
7 unique J



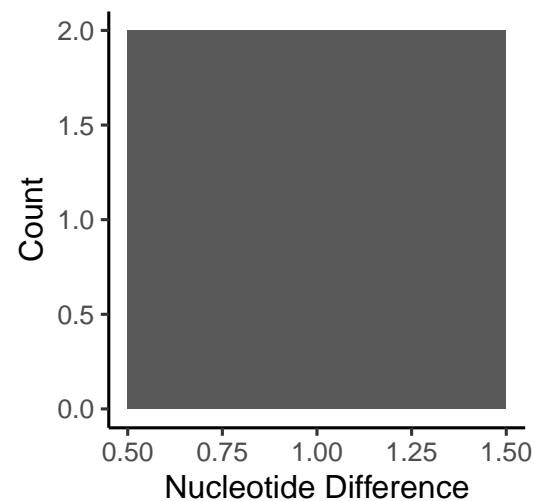
### IGHV4-38-2\*02

685 sequences assigned  
69 (10.1%) exact matches, in which:  
66 unique CDR3  
7 unique J



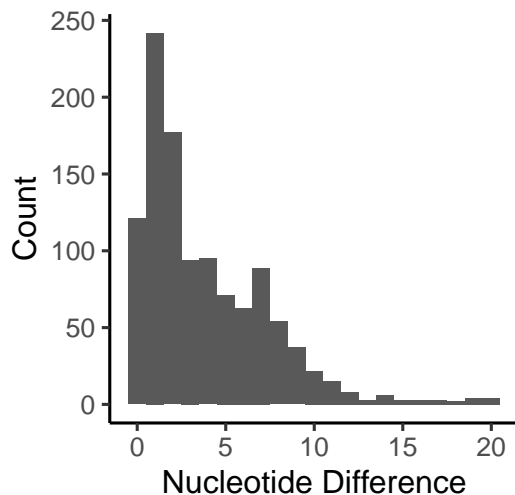
### IGHV4-55\*01\_05

3 sequences assigned  
No exact matches.



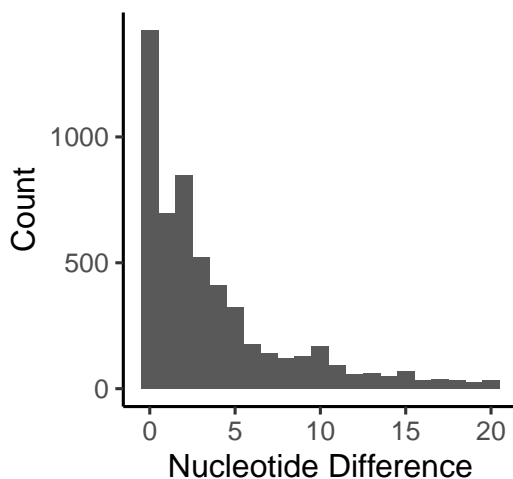
### IGHV4–59\*08

1162 sequences assigned  
121 (10.4%) exact matches, in which:  
116 unique CDR3  
7 unique J



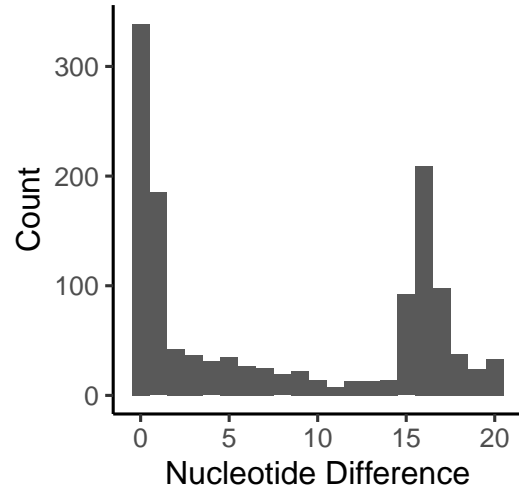
### IGHV4–61\*01

6263 sequences assigned  
1423 (22.7%) exact matches, in which:  
1383 unique CDR3  
7 unique J



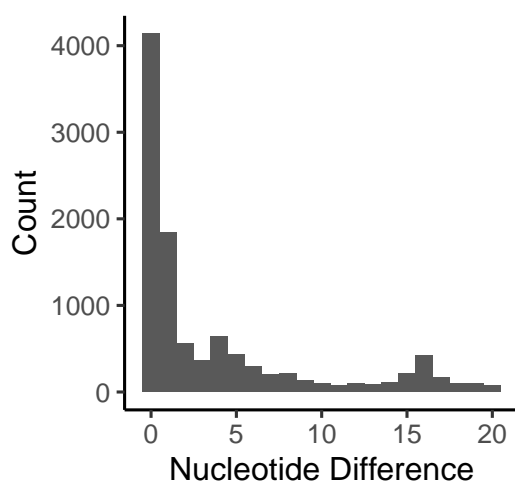
### IGHV6–1\*01\_02

1531 sequences assigned  
339 (22.1%) exact matches, in which:  
318 unique CDR3  
7 unique J



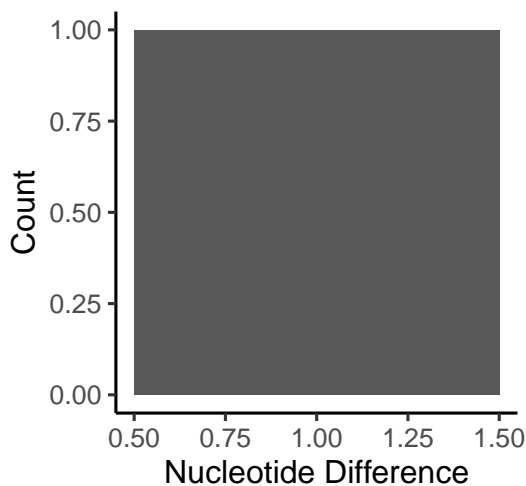
### IGHV4–59\*01\_07

12178 sequences assigned  
4138 (34%) exact matches, in which:  
3868 unique CDR3  
7 unique J



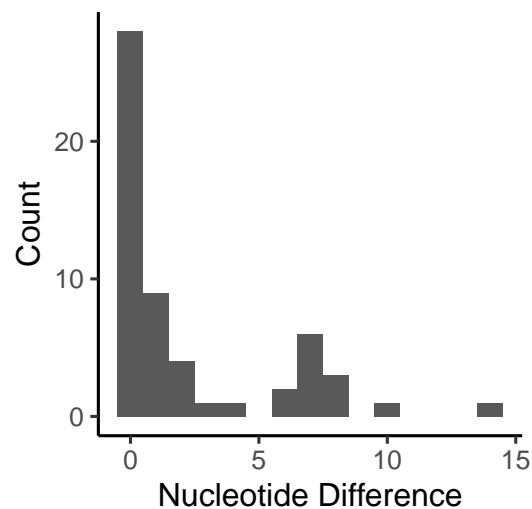
### IGHV5–10–1\*01\_03

1 sequences assigned  
No exact matches.



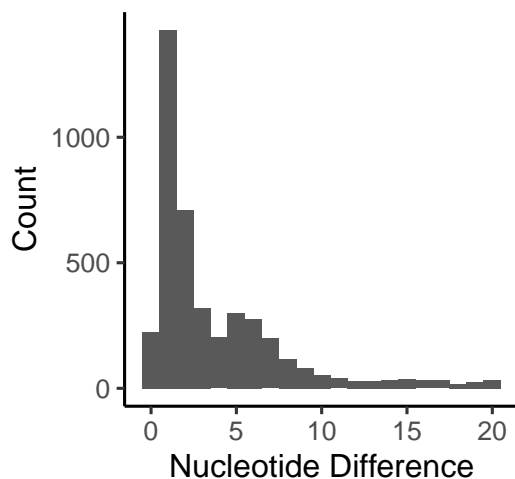
### IGHV7–4–1\*01

56 sequences assigned  
28 (50%) exact matches, in which:  
26 unique CDR3  
4 unique J



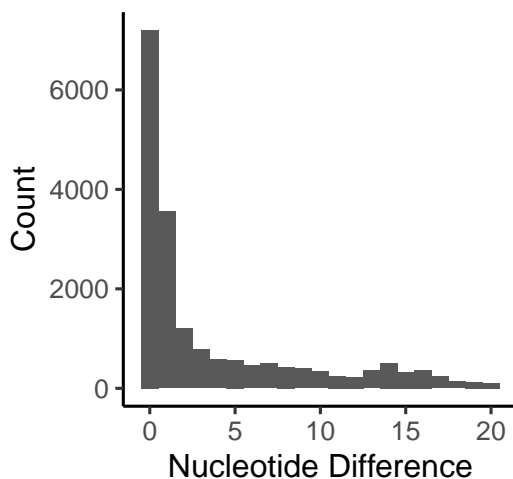
### IGHV4–59\*12

4400 sequences assigned  
224 (5.1%) exact matches, in which:  
223 unique CDR3  
7 unique J

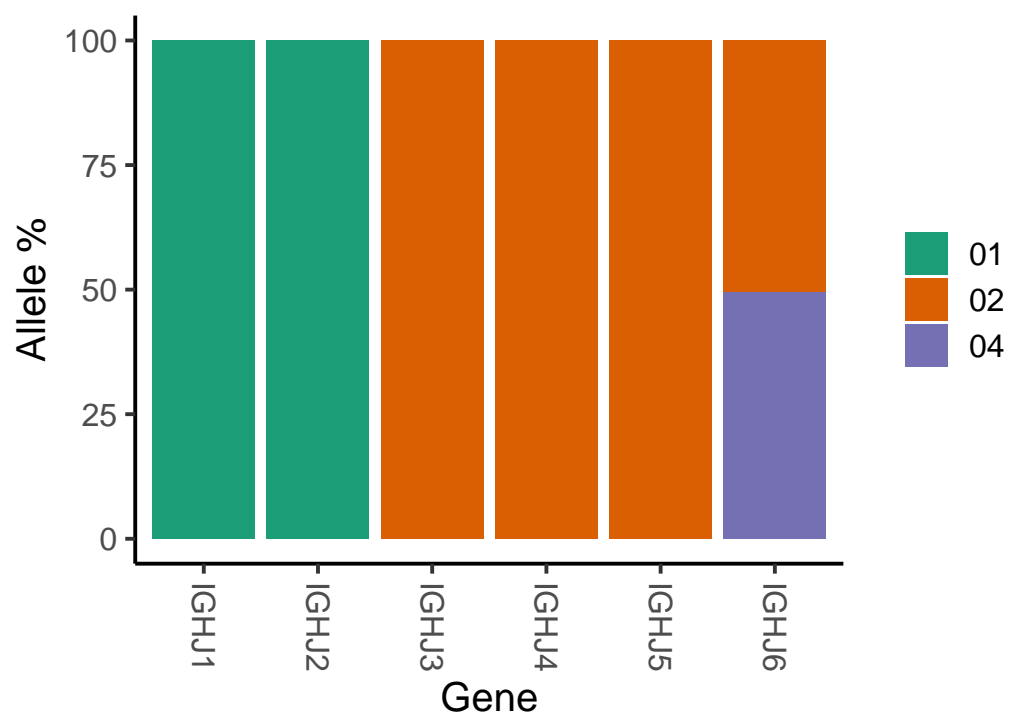


### IGHV5–51\*01\_03

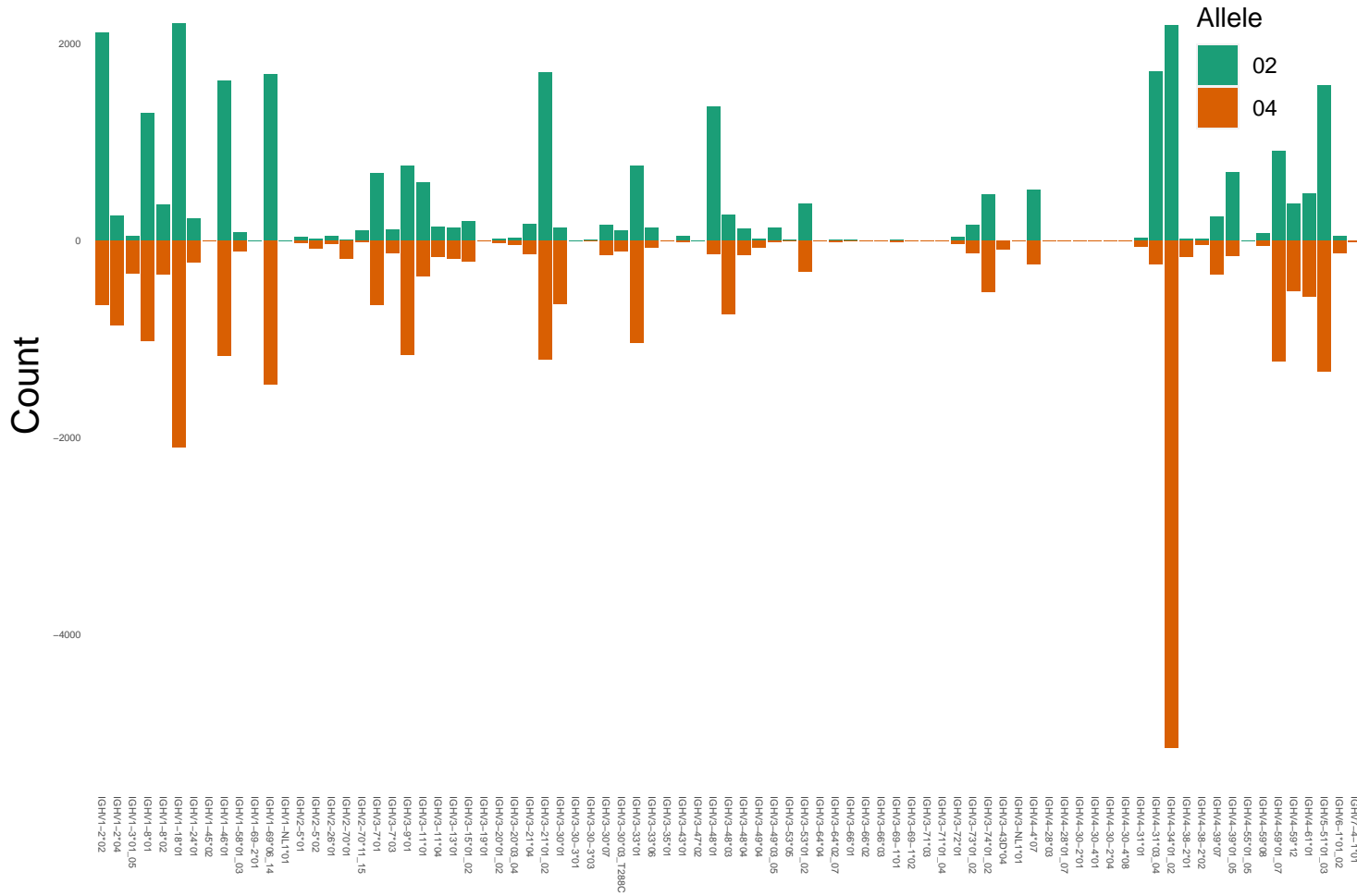
20315 sequences assigned  
7204 (35.5%) exact matches, in which:  
4957 unique CDR3  
7 unique J



Allele Usage



Sequence Count by IGHJ6 allele usage



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.

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.