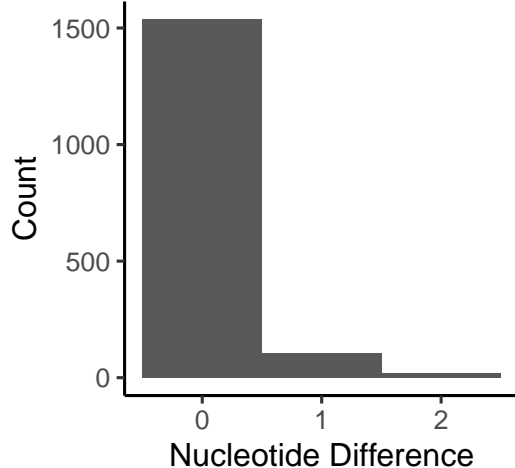


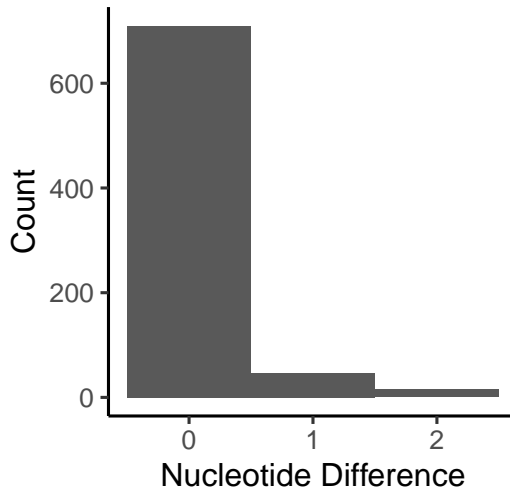
### IGHV1-2\*02

1664 sequences assigned  
1537 (92.4%) exact matches, in which:  
1528 unique CDR3  
6 unique J



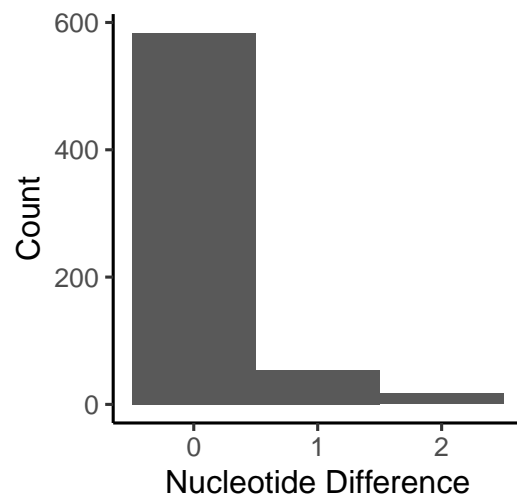
### IGHV1-8\*01

771 sequences assigned  
710 (92.1%) exact matches, in which:  
710 unique CDR3  
6 unique J



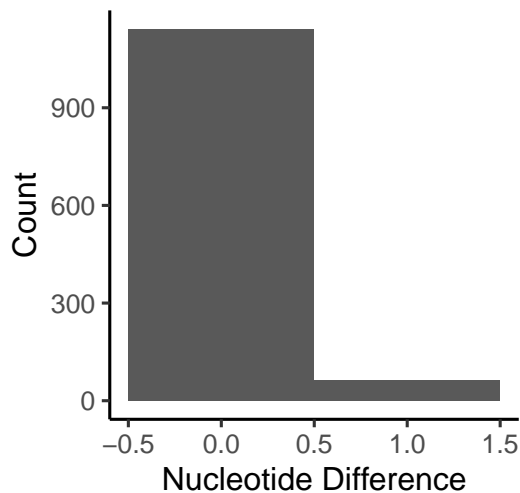
### IGHV1-46\*01

655 sequences assigned  
584 (89.2%) exact matches, in which:  
583 unique CDR3  
6 unique J



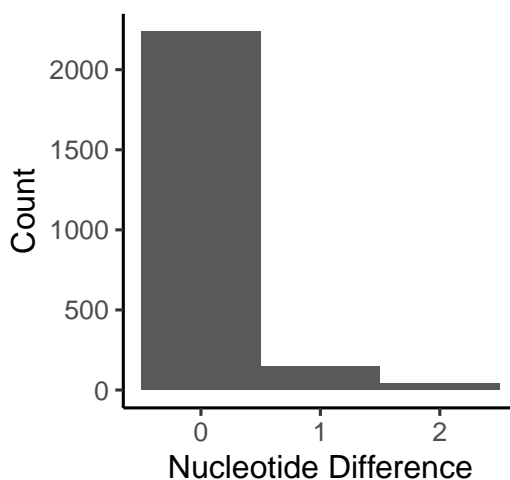
### IGHV1-2\*06

1204 sequences assigned  
1142 (94.9%) exact matches, in which:  
1141 unique CDR3  
6 unique J



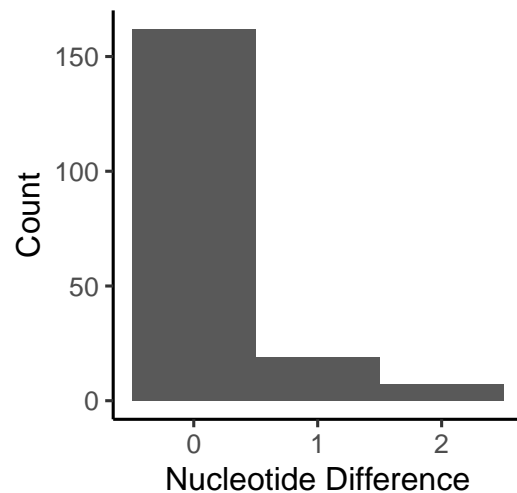
### IGHV1-18\*01

2424 sequences assigned  
2237 (92.3%) exact matches, in which:  
2228 unique CDR3  
6 unique J



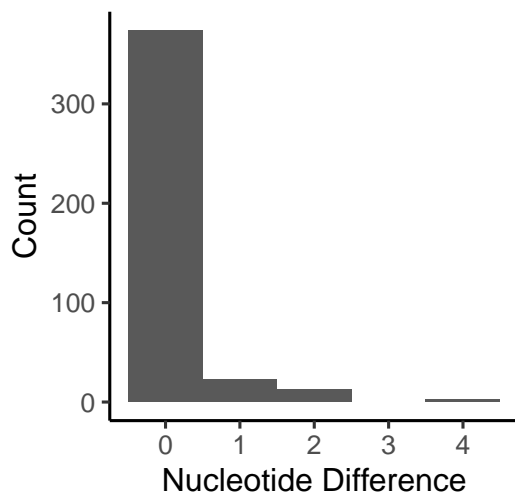
### IGHV1-58\*01\_03

188 sequences assigned  
162 (86.2%) exact matches, in which:  
161 unique CDR3  
6 unique J



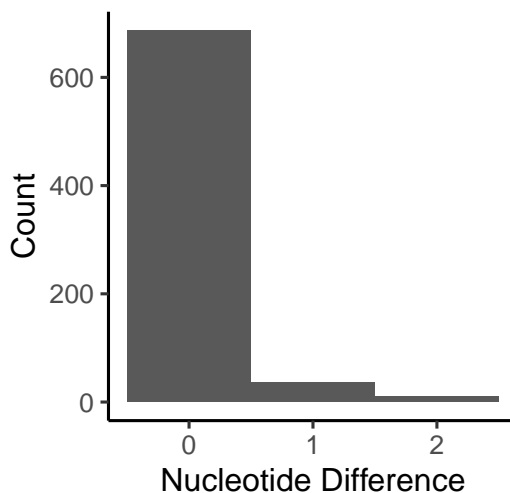
### IGHV1-3\*01\_05

413 sequences assigned  
374 (90.6%) exact matches, in which:  
372 unique CDR3  
6 unique J



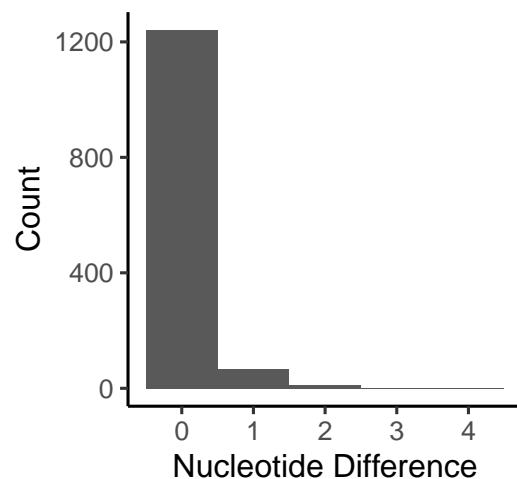
### IGHV1-24\*01

734 sequences assigned  
687 (93.6%) exact matches, in which:  
687 unique CDR3  
6 unique J



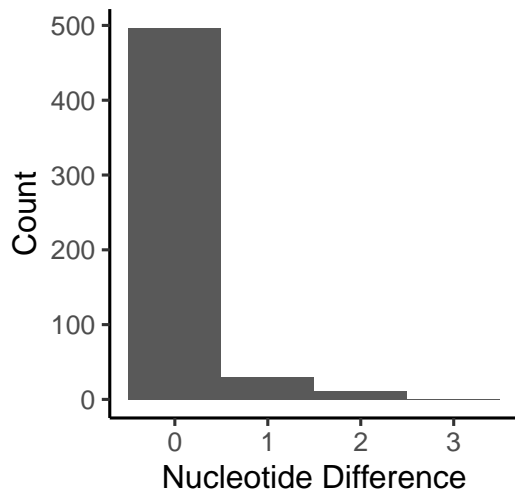
### IGHV1-69\*06\_14

1320 sequences assigned  
1241 (94%) exact matches, in which:  
1237 unique CDR3  
6 unique J



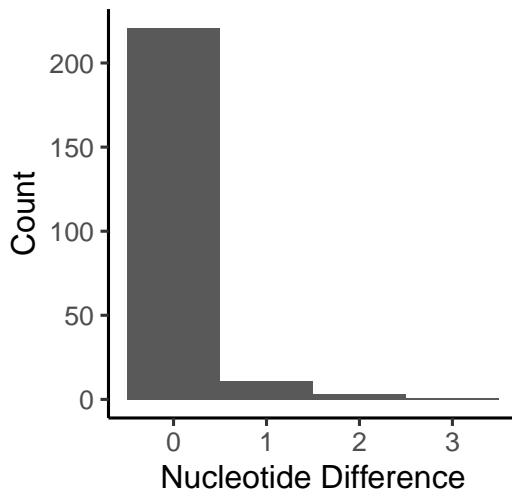
### IGHV2-5\*01

539 sequences assigned  
497 (92.2%) exact matches, in which:  
494 unique CDR3  
6 unique J



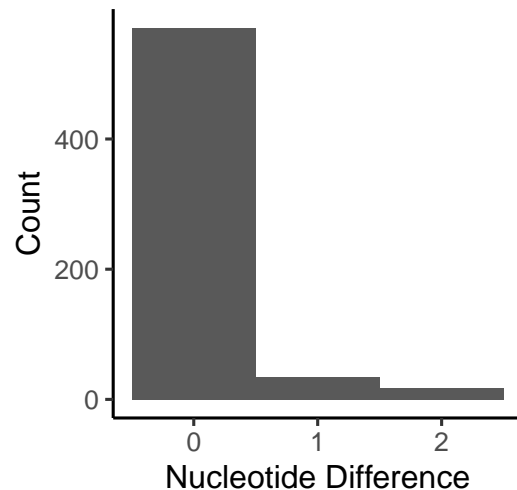
### IGHV2-70\*01

236 sequences assigned  
221 (93.6%) exact matches, in which:  
220 unique CDR3  
5 unique J



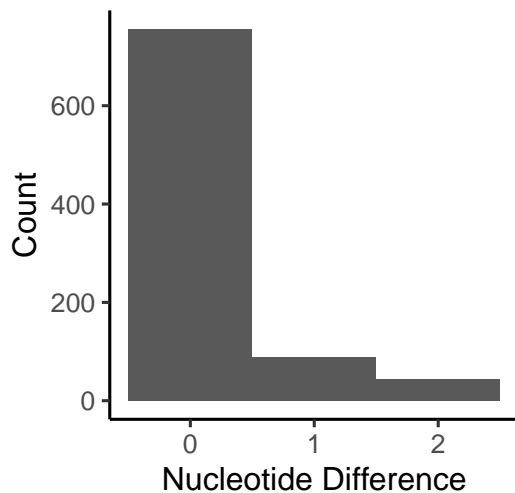
### IGHV3-11\*01

624 sequences assigned  
571 (91.5%) exact matches, in which:  
557 unique CDR3  
6 unique J



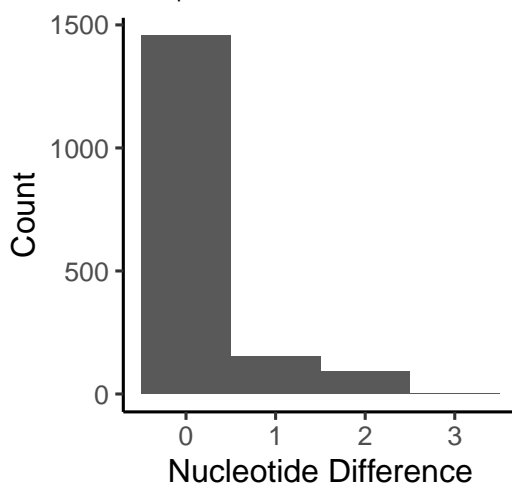
### IGHV2-5\*02

888 sequences assigned  
756 (85.1%) exact matches, in which:  
752 unique CDR3  
6 unique J



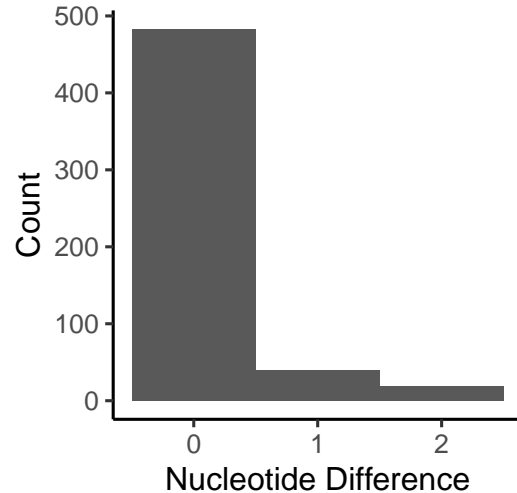
### IGHV3-7\*01

1703 sequences assigned  
1456 (85.5%) exact matches, in which:  
1407 unique CDR3  
6 unique J



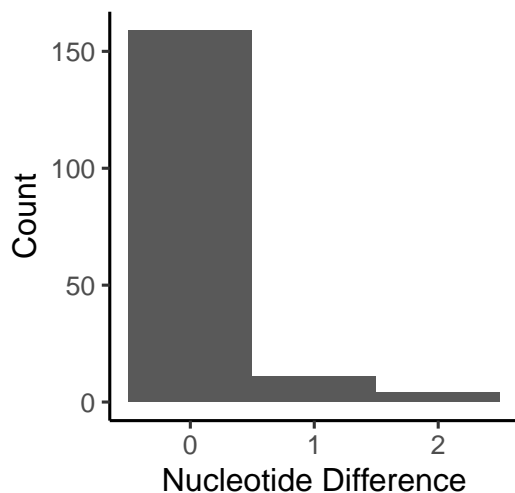
### IGHV3-11\*03\_05

542 sequences assigned  
483 (89.1%) exact matches, in which:  
470 unique CDR3  
6 unique J



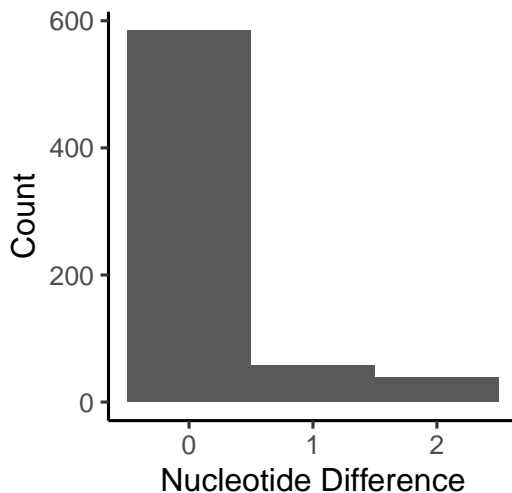
### IGHV2-26\*01

174 sequences assigned  
159 (91.4%) exact matches, in which:  
159 unique CDR3  
5 unique J



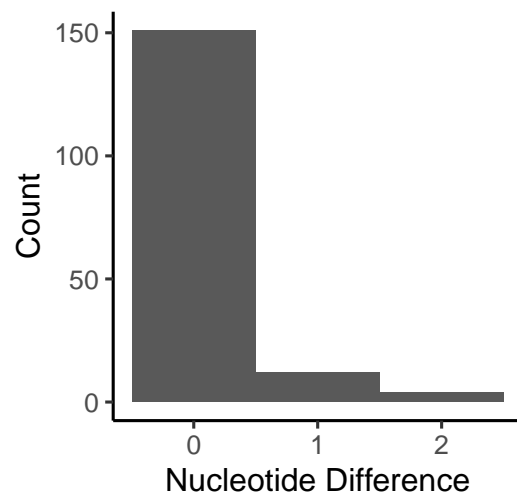
### IGHV3-9\*01

681 sequences assigned  
585 (85.9%) exact matches, in which:  
570 unique CDR3  
6 unique J



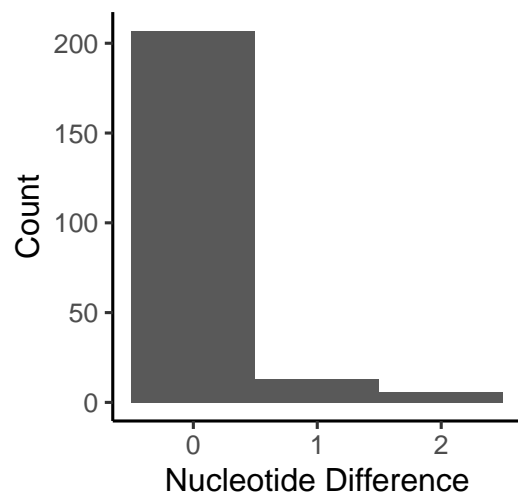
### IGHV3-13\*01

167 sequences assigned  
151 (90.4%) exact matches, in which:  
144 unique CDR3  
5 unique J



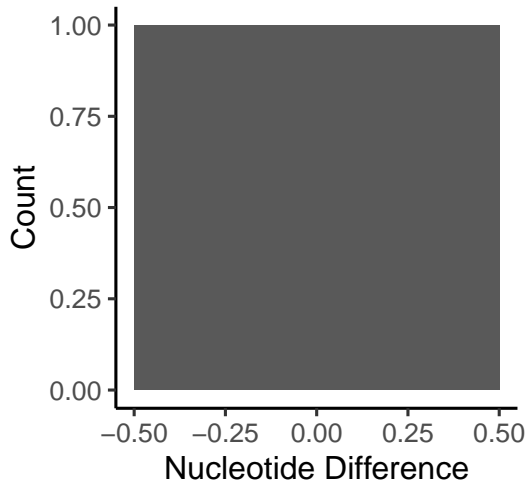
### IGHV3-13\*04

226 sequences assigned  
207 (91.6%) exact matches, in which:  
201 unique CDR3  
5 unique J



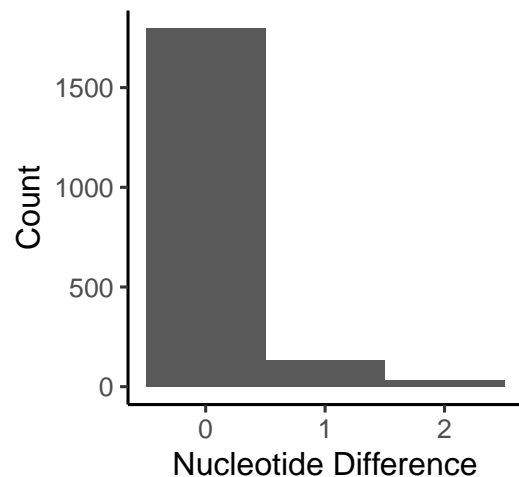
### IGHV3-19\*01

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



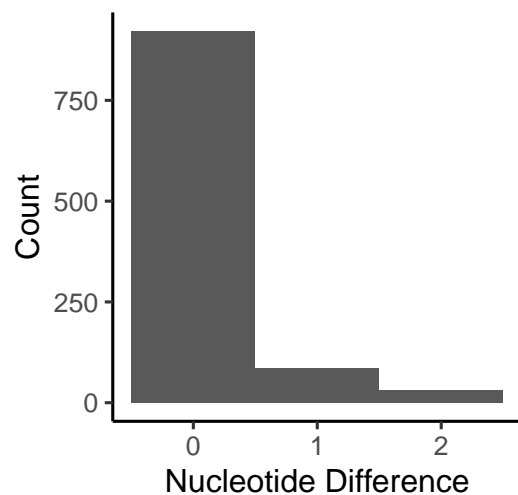
### IGHV3-30-3\*01

1961 sequences assigned  
1797 (91.6%) exact matches, in which:  
1760 unique CDR3  
6 unique J



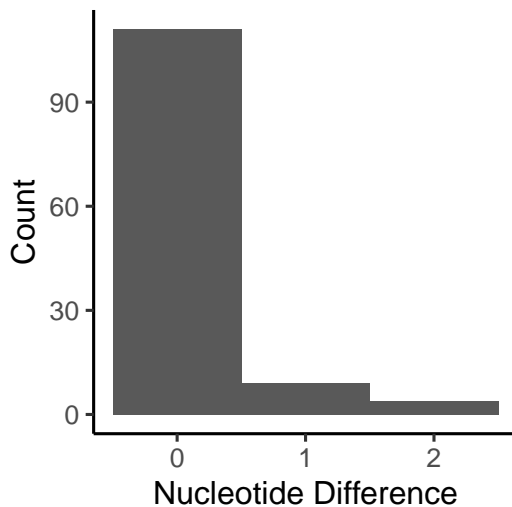
### IGHV3-15\*07

1039 sequences assigned  
922 (88.7%) exact matches, in which:  
887 unique CDR3  
6 unique J



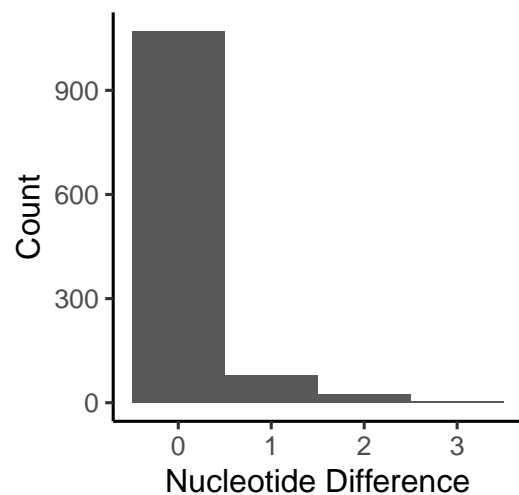
### IGHV3-20\*01\_02

124 sequences assigned  
111 (89.5%) exact matches, in which:  
104 unique CDR3  
5 unique J



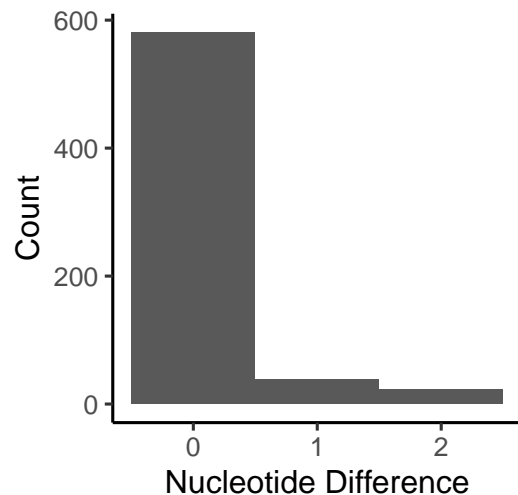
### IGHV3-33\*01

1176 sequences assigned  
1071 (91.1%) exact matches, in which:  
1046 unique CDR3  
6 unique J



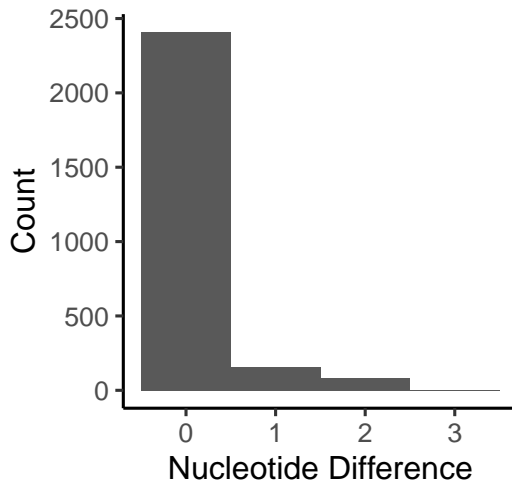
### IGHV3-15\*01\_02

643 sequences assigned  
581 (90.4%) exact matches, in which:  
564 unique CDR3  
6 unique J



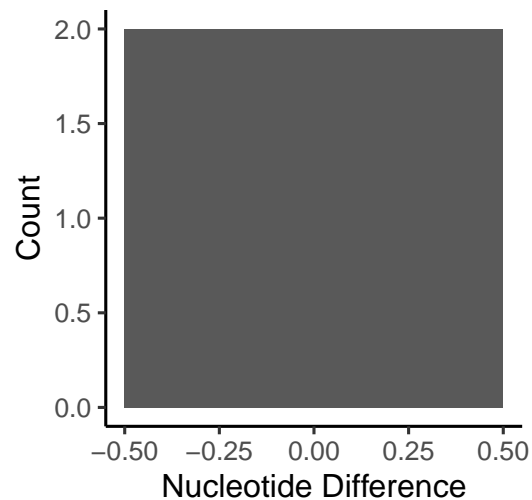
### IGHV3-21\*01\_02

2652 sequences assigned  
2409 (90.8%) exact matches, in which:  
2295 unique CDR3  
6 unique J



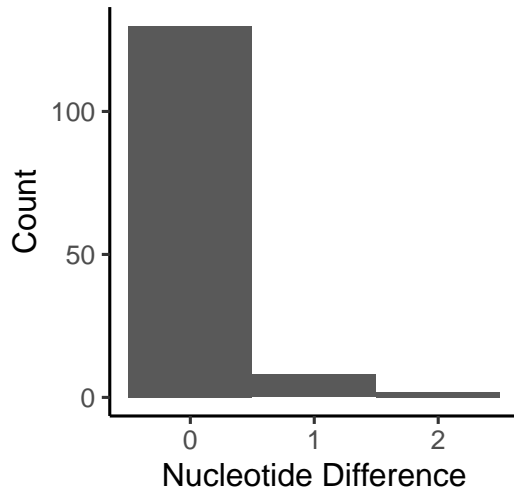
### IGHV3-35\*01

2 sequences assigned  
2 (100%) exact matches, in which:  
2 unique CDR3  
1 unique J



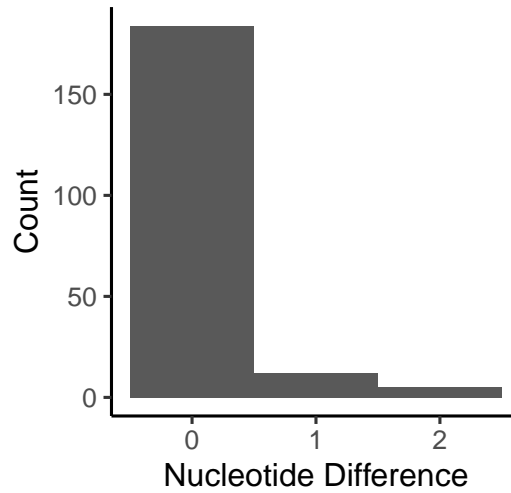
### IGHV3-43\*01

140 sequences assigned  
130 (92.9%) exact matches, in which:  
126 unique CDR3  
6 unique J



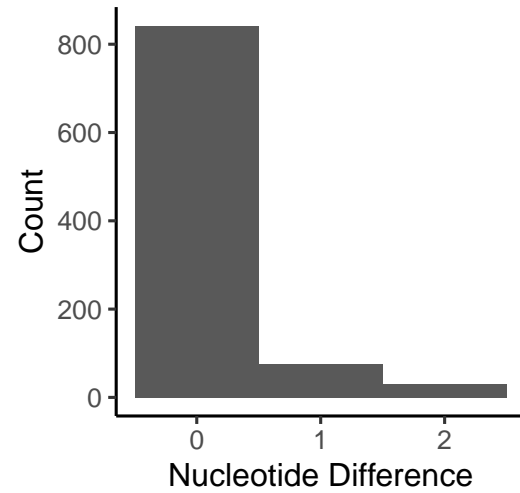
### IGHV3-49\*04

201 sequences assigned  
184 (91.5%) exact matches, in which:  
184 unique CDR3  
6 unique J



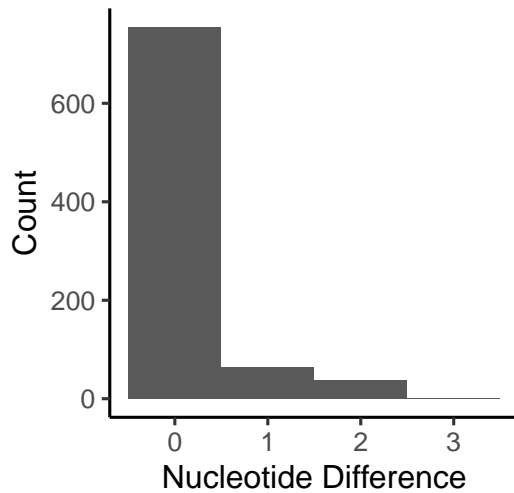
### IGHV3-53\*01\_02

948 sequences assigned  
842 (88.8%) exact matches, in which:  
802 unique CDR3  
6 unique J



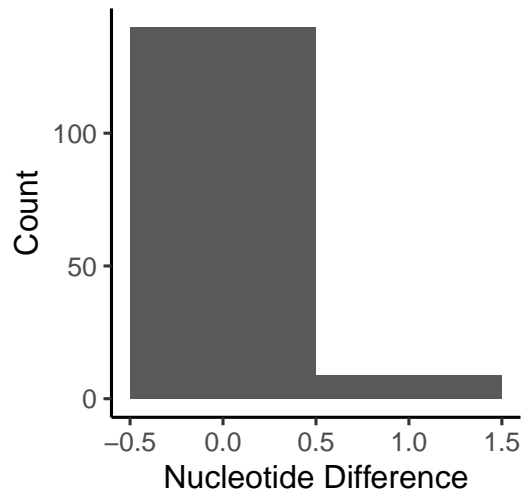
### IGHV3-48\*02

857 sequences assigned  
755 (88.1%) exact matches, in which:  
725 unique CDR3  
6 unique J



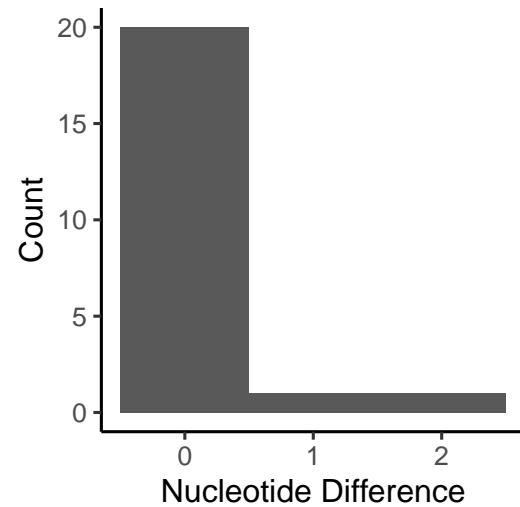
### IGHV3-49\*03\_05

149 sequences assigned  
140 (94%) exact matches, in which:  
138 unique CDR3  
5 unique J



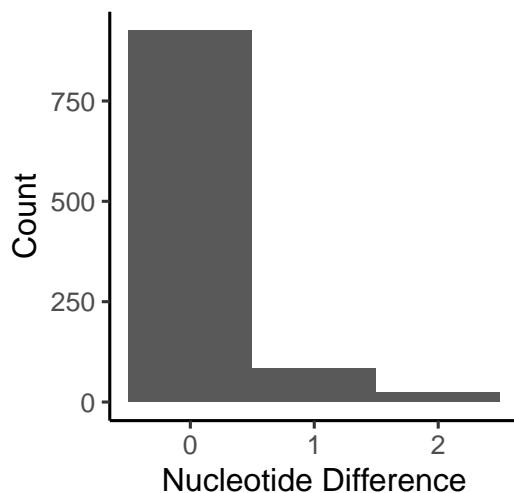
### IGHV3-64\*02\_07

22 sequences assigned  
20 (90.9%) exact matches, in which:  
19 unique CDR3  
4 unique J



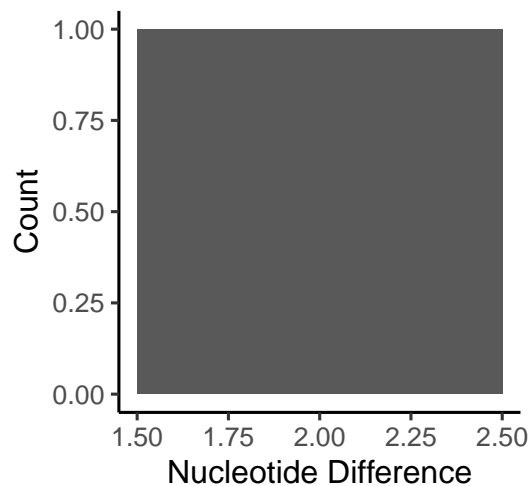
### IGHV3-48\*03

1033 sequences assigned  
926 (89.6%) exact matches, in which:  
894 unique CDR3  
6 unique J



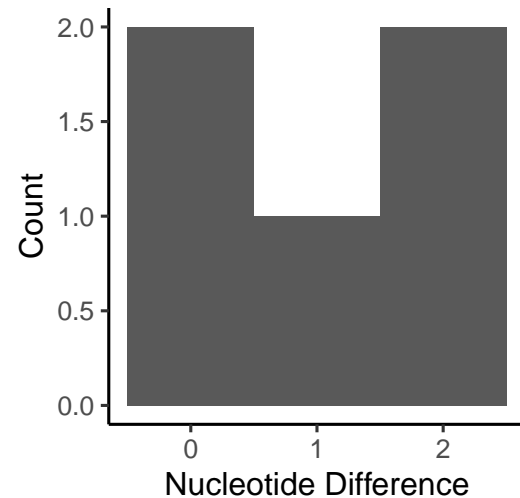
### IGHV3-52\*01\_03

1 sequences assigned  
No exact matches.



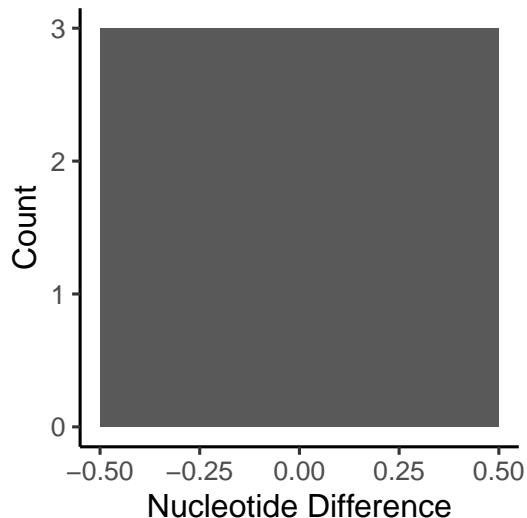
### IGHV3-66\*03

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



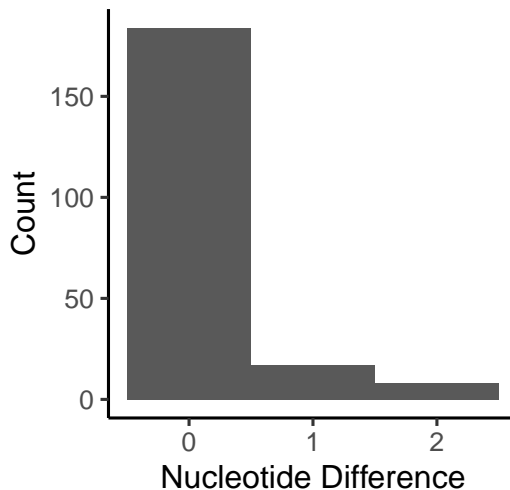
### IGHV3-69-1\*01

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



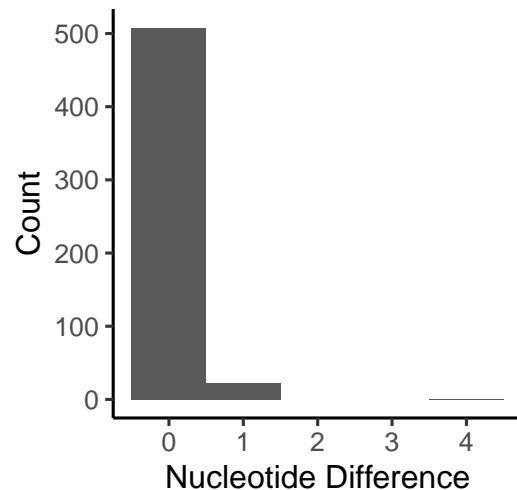
### IGHV3-73\*01\_02

209 sequences assigned  
184 (88%) exact matches, in which:  
183 unique CDR3  
6 unique J



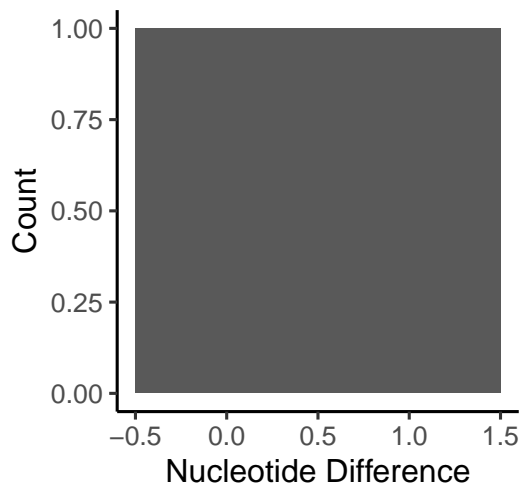
### IGHV3-64D\*09

531 sequences assigned  
508 (95.7%) exact matches, in which:  
499 unique CDR3  
6 unique J



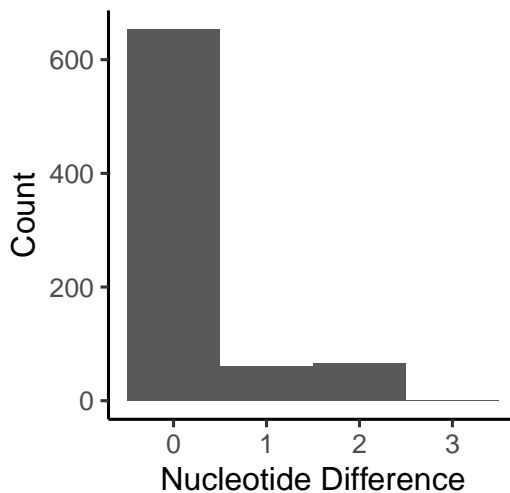
### IGHV3-69-1\*02

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



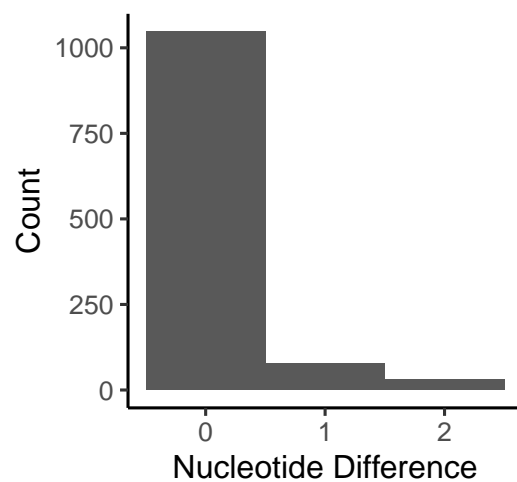
### IGHV3-74\*01\_02

781 sequences assigned  
654 (83.7%) exact matches, in which:  
624 unique CDR3  
6 unique J



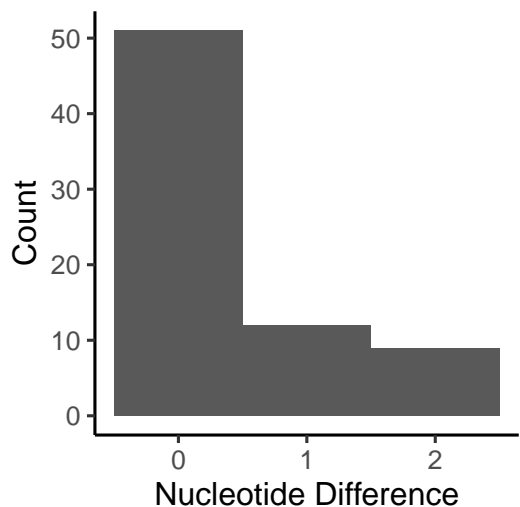
### IGHV4-4\*07

1154 sequences assigned  
1047 (90.7%) exact matches, in which:  
1019 unique CDR3  
6 unique J



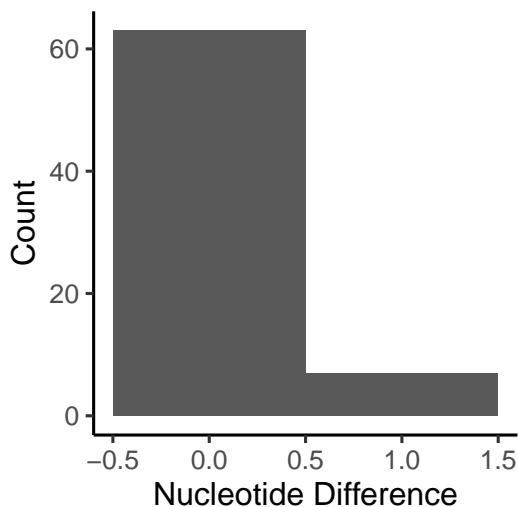
### IGHV3-72\*01

72 sequences assigned  
51 (70.8%) exact matches, in which:  
48 unique CDR3  
5 unique J



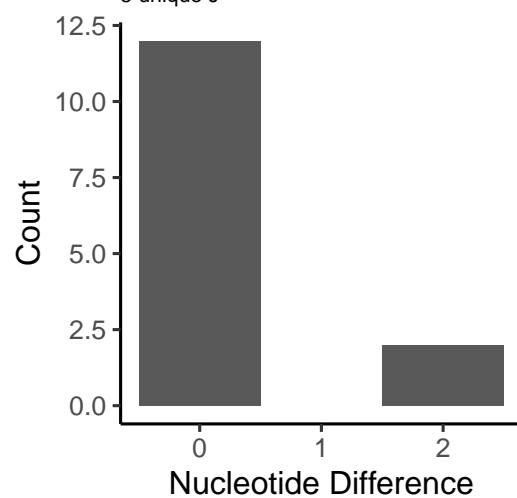
### IGHV3-43D\*04

70 sequences assigned  
63 (90%) exact matches, in which:  
61 unique CDR3  
6 unique J



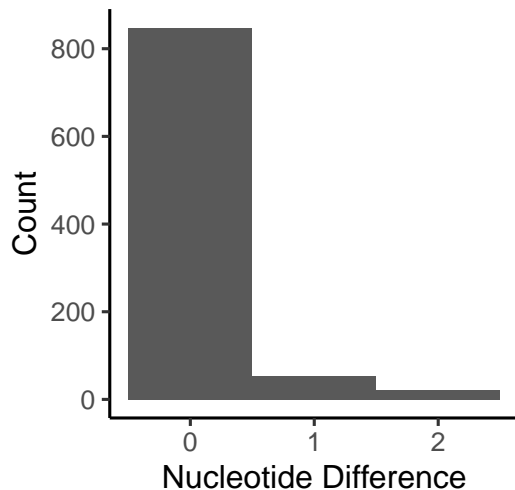
### IGHV4-28\*01\_07

14 sequences assigned  
12 (85.7%) exact matches, in which:  
11 unique CDR3  
5 unique J



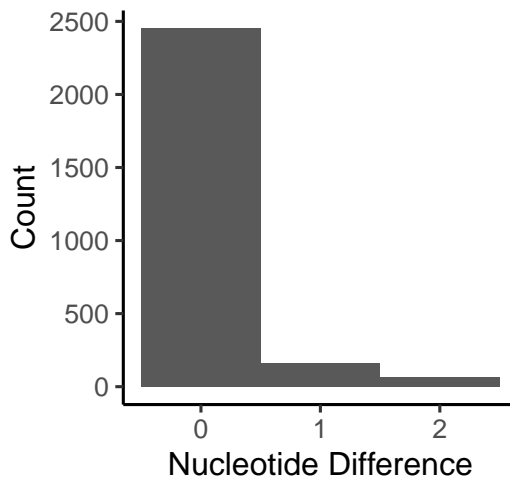
### IGHV4-30-4\*01

924 sequences assigned  
848 (91.8%) exact matches, in which:  
834 unique CDR3  
6 unique J



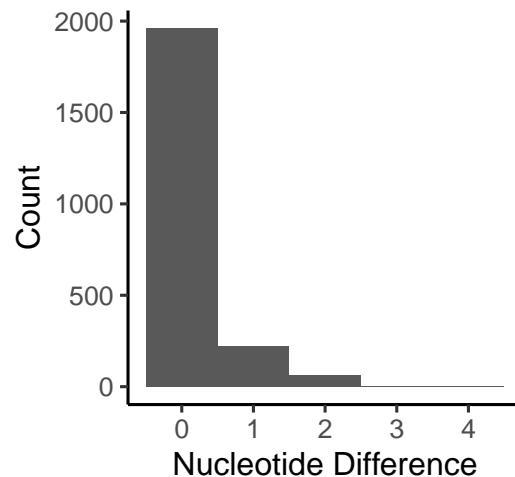
### IGHV4-34\*01\_02

2680 sequences assigned  
2452 (91.5%) exact matches, in which:  
2392 unique CDR3  
6 unique J



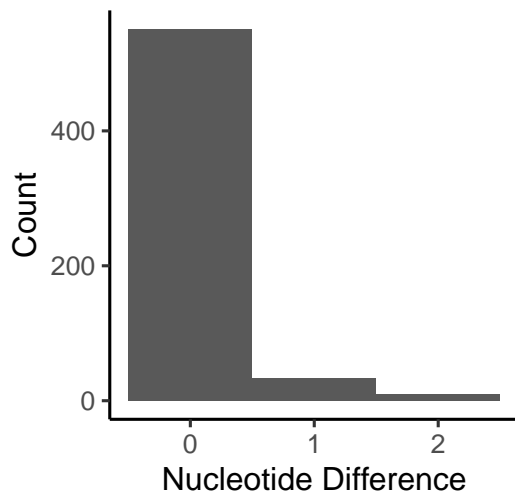
### IGHV4-39\*01\_05

2247 sequences assigned  
1960 (87.2%) exact matches, in which:  
1908 unique CDR3  
6 unique J



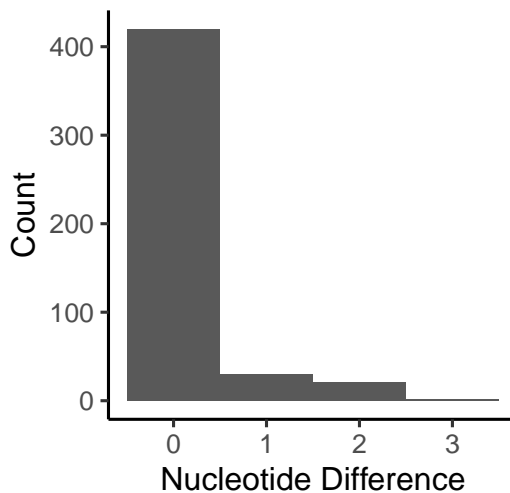
### IGHV4-30-2\*01

593 sequences assigned  
551 (92.9%) exact matches, in which:  
540 unique CDR3  
6 unique J



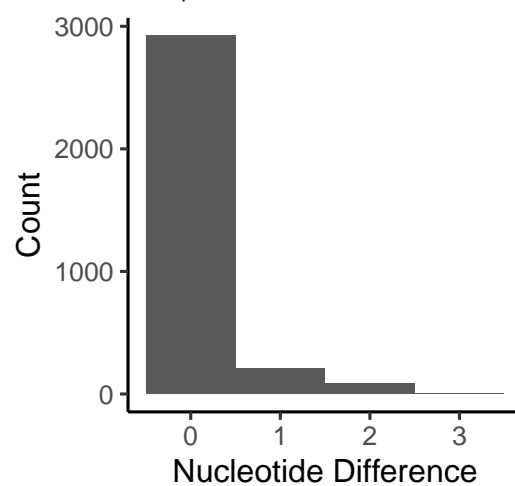
### IGHV4-38-2\*01

473 sequences assigned  
420 (88.8%) exact matches, in which:  
418 unique CDR3  
6 unique J



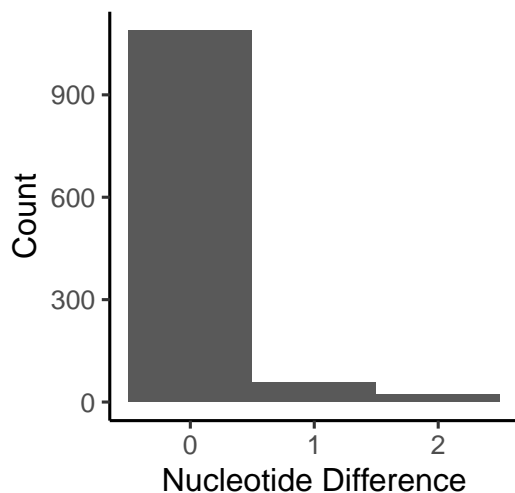
### IGHV4-59\*01\_07

3217 sequences assigned  
2923 (90.9%) exact matches, in which:  
2830 unique CDR3  
6 unique J



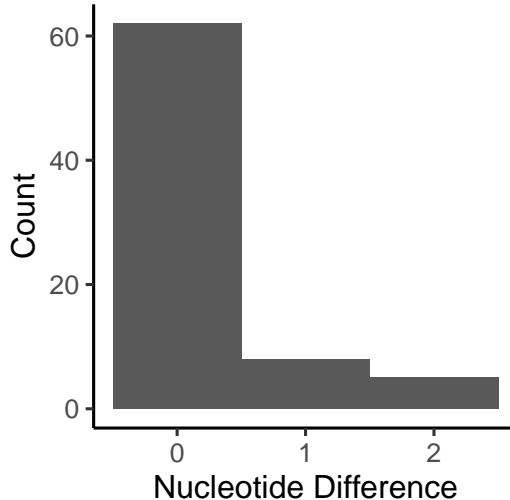
### IGHV4-31\*03\_04

1169 sequences assigned  
1089 (93.2%) exact matches, in which:  
1075 unique CDR3  
6 unique J



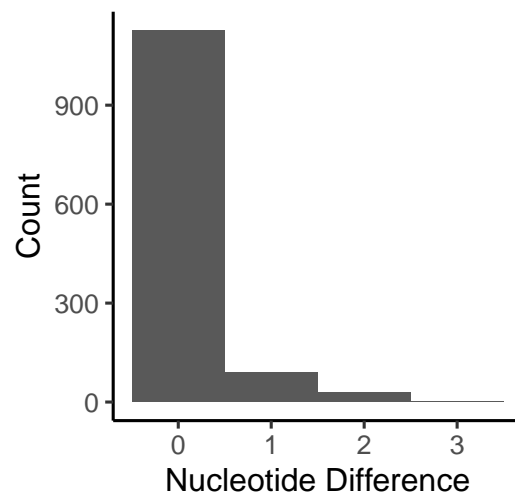
### IGHV4-38-2\*02

75 sequences assigned  
62 (82.7%) exact matches, in which:  
62 unique CDR3  
6 unique J



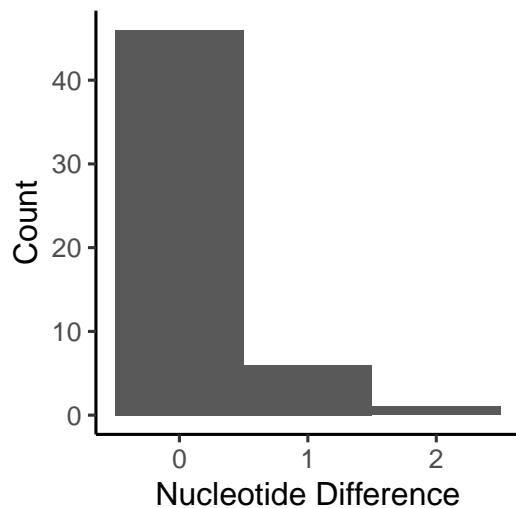
### IGHV4-61\*01

1249 sequences assigned  
1127 (90.2%) exact matches, in which:  
1094 unique CDR3  
6 unique J



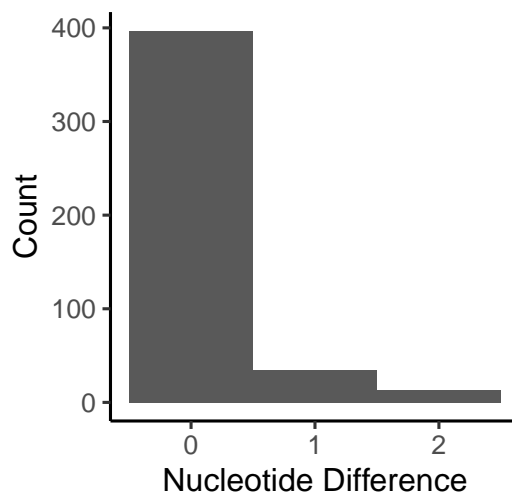
## IGHV5-10-1\*01\_03

53 sequences assigned  
46 (86.8%) exact matches, in which:  
46 unique CDR3  
5 unique J



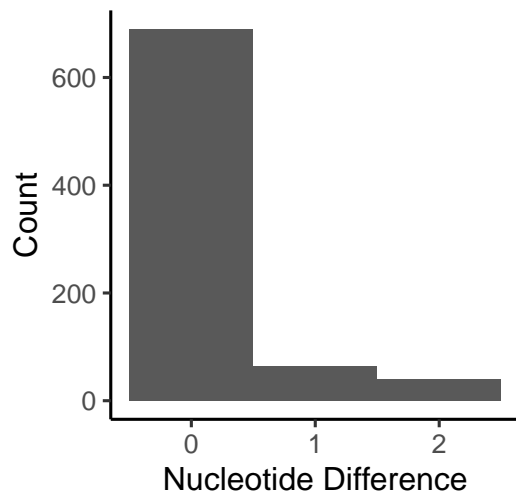
## IGHV7-4-1\*02

445 sequences assigned  
397 (89.2%) exact matches, in which:  
396 unique CDR3  
6 unique J



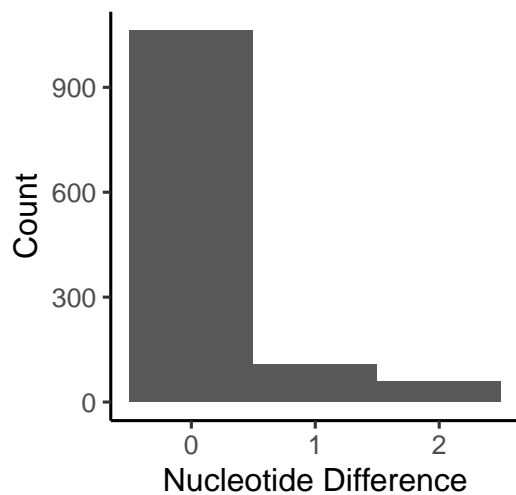
## IGHV5-51\*01\_03

793 sequences assigned  
690 (87%) exact matches, in which:  
688 unique CDR3  
6 unique J



## IGHV6-1\*01\_02

1230 sequences assigned  
1063 (86.4%) exact matches, in which:  
1058 unique CDR3  
6 unique J







Warning – no inferred sequences found.

Novel sequence(s)IGHV4–59\*02\_G88AIGHV5–51\*07\_A128G are not listed in the genotype and will be ignored.

Warning – no inferred sequences found.

Novel sequence(s)IGHV4–59\*02\_G88AIGHV5–51\*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.

Warning – no inferred sequences found.

Novel sequence(s)IGHV3–11\*06\_T300CIGHV4–38–2\*02\_A70GIGHV4–39\*02\_C258GIGHV5–51\*07\_A128G are not listed in the genotype and will be ignored.