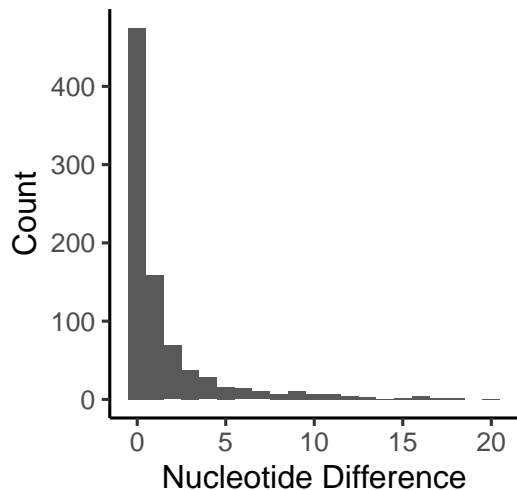


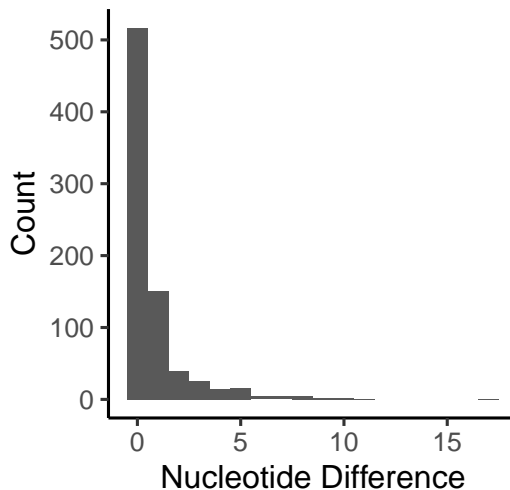
IGHV1-2*02

862 sequences assigned
475 (55.1%) exact matches, in which:
426 unique CDR3
6 unique J



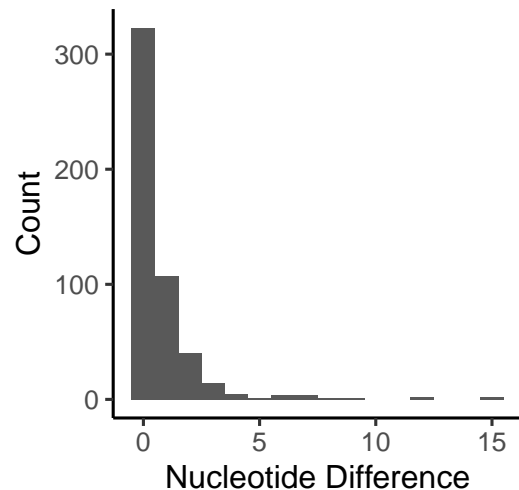
IGHV1-8*01

784 sequences assigned
517 (65.9%) exact matches, in which:
449 unique CDR3
6 unique J



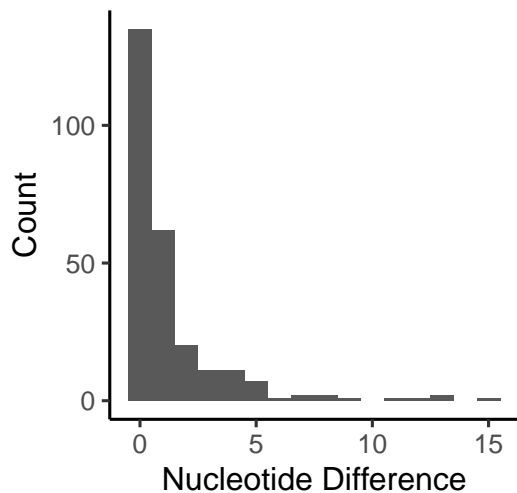
IGHV1-24*01

505 sequences assigned
323 (64%) exact matches, in which:
284 unique CDR3
6 unique J



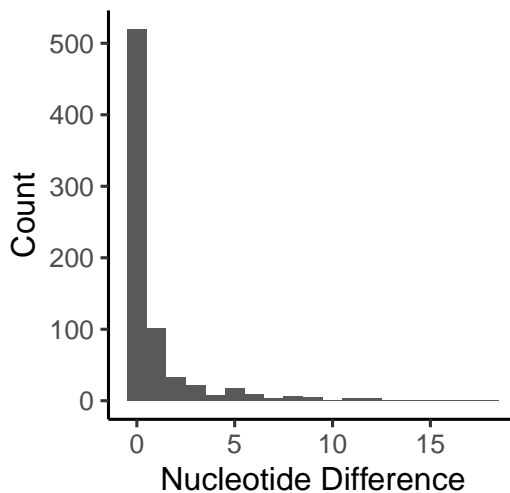
IGHV1-2*04

257 sequences assigned
135 (52.5%) exact matches, in which:
127 unique CDR3
6 unique J



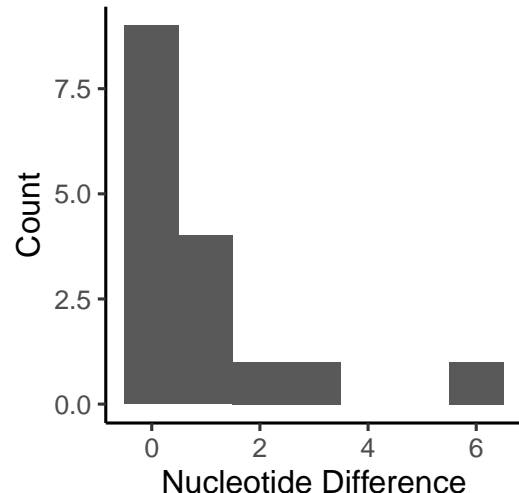
IGHV1-18*01

739 sequences assigned
520 (70.4%) exact matches, in which:
480 unique CDR3
6 unique J



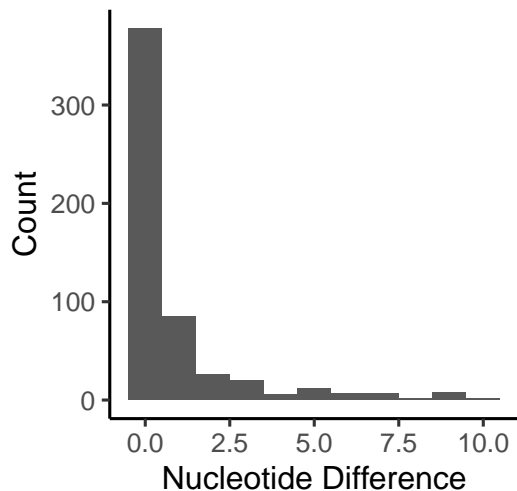
IGHV1-45*02

16 sequences assigned
9 (56.2%) exact matches, in which:
9 unique CDR3
3 unique J



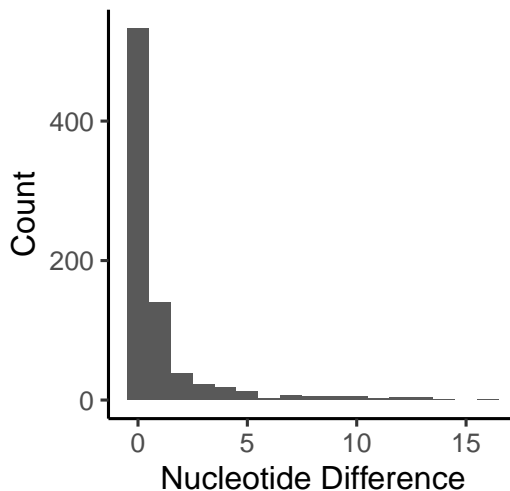
IGHV1-3*01

555 sequences assigned
378 (68.1%) exact matches, in which:
346 unique CDR3
6 unique J



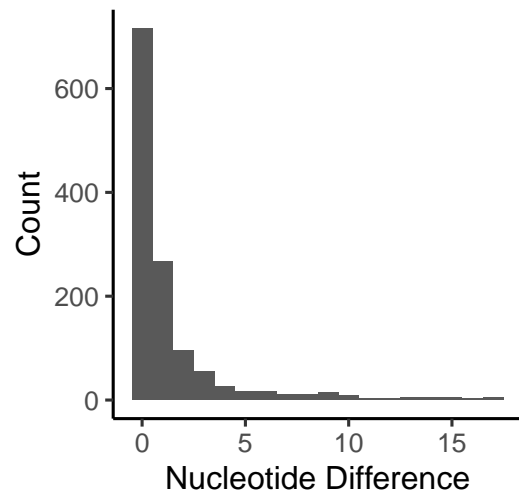
IGHV1-18*04

797 sequences assigned
533 (66.9%) exact matches, in which:
505 unique CDR3
6 unique J



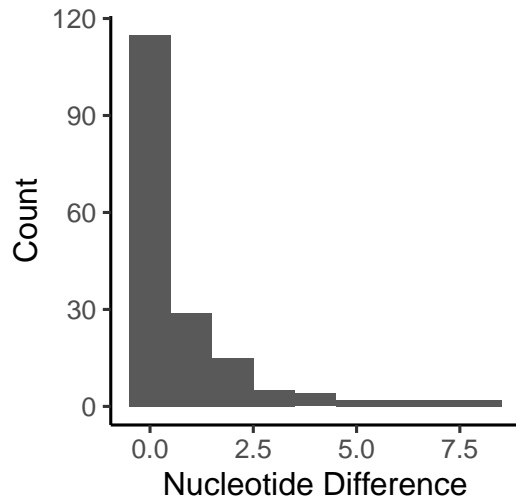
IGHV1-46*01

1263 sequences assigned
716 (56.7%) exact matches, in which:
648 unique CDR3
6 unique J



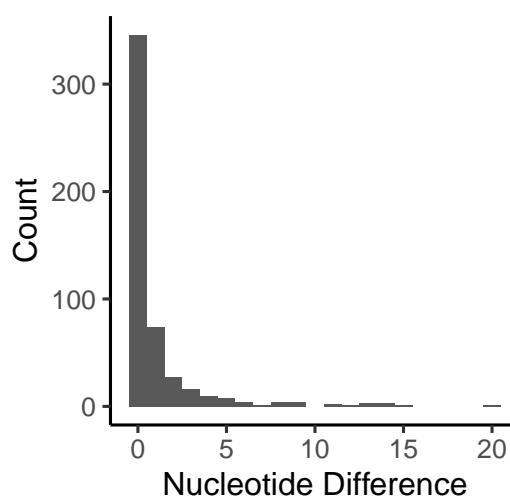
IGHV1–58*01

176 sequences assigned
115 (65.3%) exact matches, in which:
106 unique CDR3
6 unique J



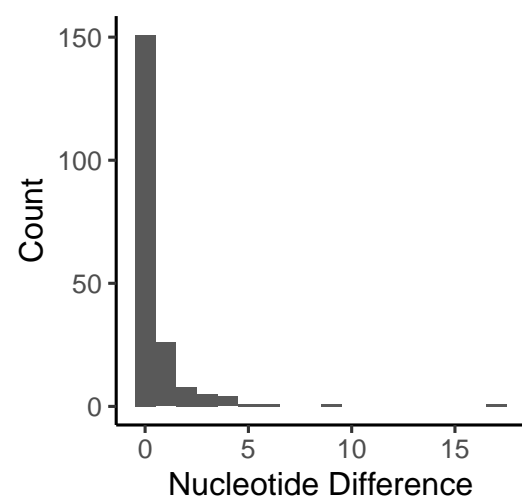
IGHV2–5*01

505 sequences assigned
346 (68.5%) exact matches, in which:
308 unique CDR3
6 unique J



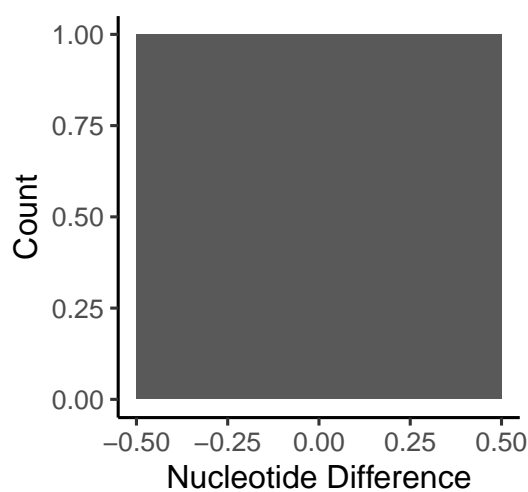
IGHV2–70*01

198 sequences assigned
151 (76.3%) exact matches, in which:
142 unique CDR3
6 unique J



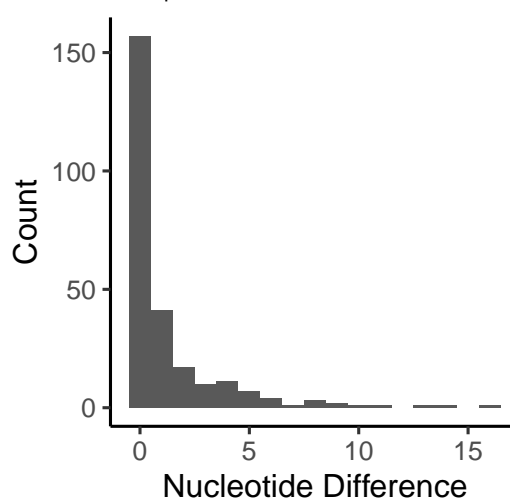
IGHV1–68*01

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



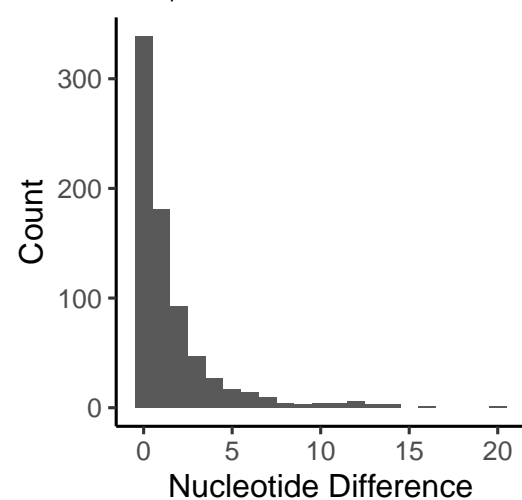
IGHV2–5*02

258 sequences assigned
157 (60.9%) exact matches, in which:
141 unique CDR3
6 unique J



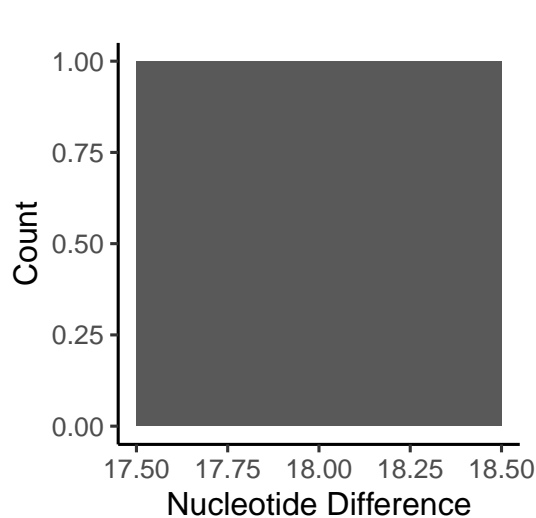
IGHV3–7*01

758 sequences assigned
339 (44.7%) exact matches, in which:
325 unique CDR3
6 unique J



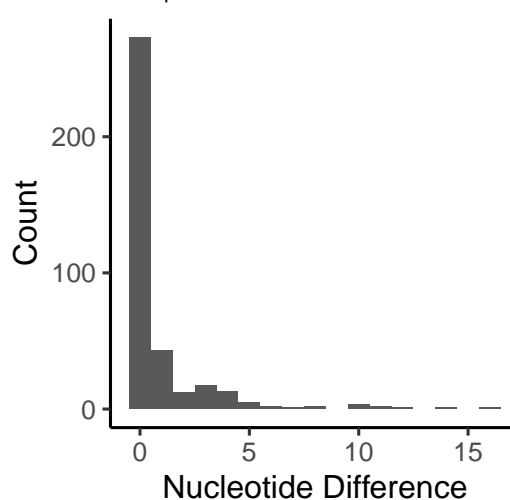
IGHV1–NL1*01

1 sequences assigned
No exact matches.



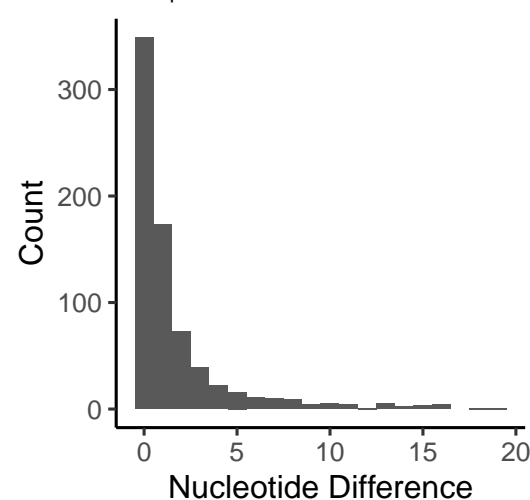
IGHV2–26*01

376 sequences assigned
273 (72.6%) exact matches, in which:
258 unique CDR3
6 unique J



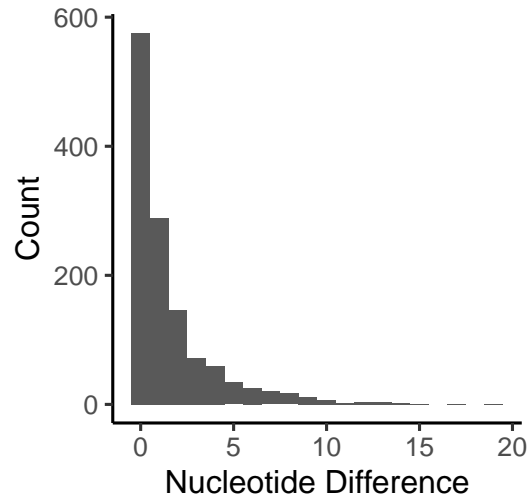
IGHV3–7*03

734 sequences assigned
349 (47.5%) exact matches, in which:
319 unique CDR3
6 unique J



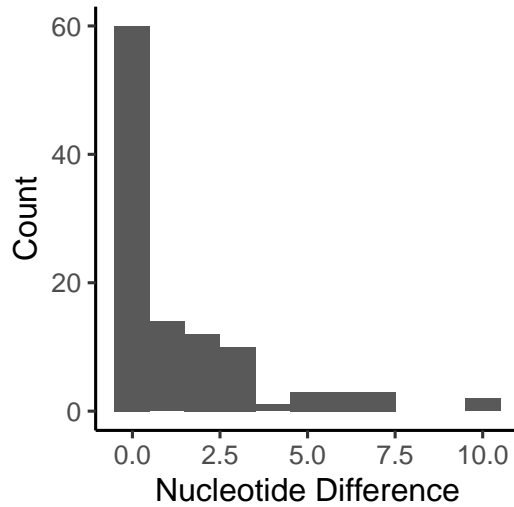
IGHV3-9*01

1274 sequences assigned
576 (45.2%) exact matches, in which:
522 unique CDR3
6 unique J



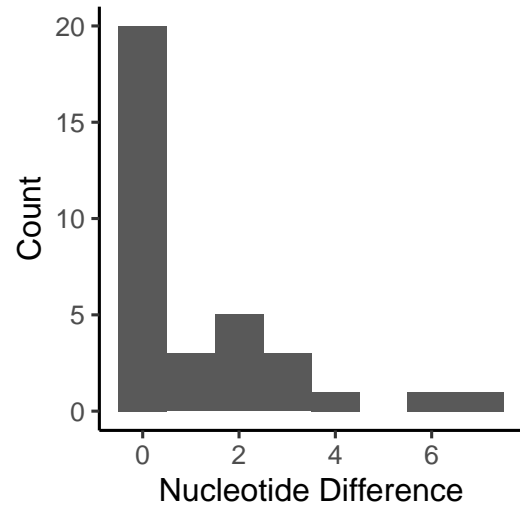
IGHV3-13*01

108 sequences assigned
60 (55.6%) exact matches, in which:
52 unique CDR3
5 unique J



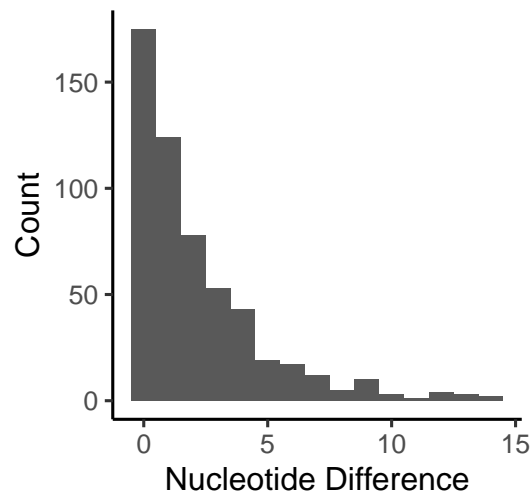
IGHV3-20*01

34 sequences assigned
20 (58.8%) exact matches, in which:
19 unique CDR3
5 unique J



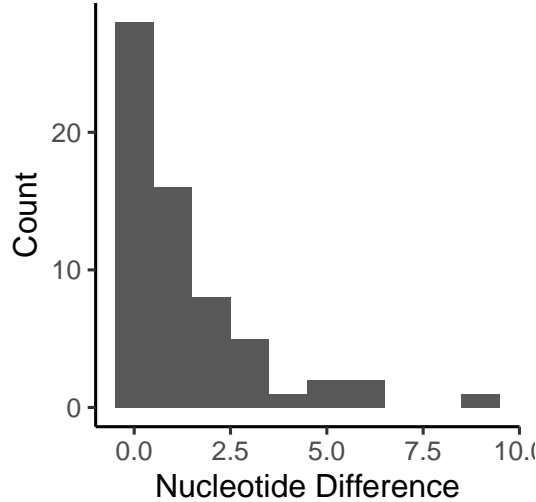
IGHV3-11*01

551 sequences assigned
175 (31.8%) exact matches, in which:
162 unique CDR3
6 unique J



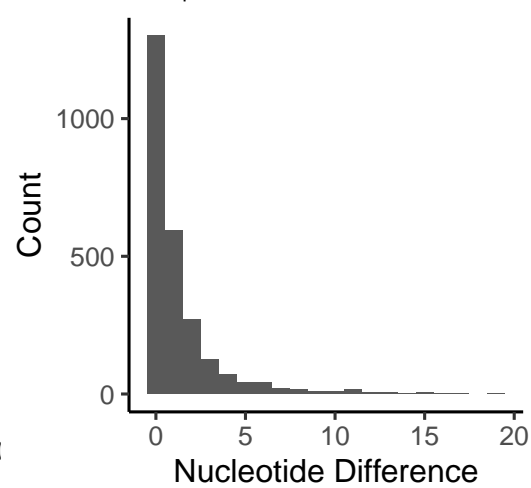
IGHV3-13*05

63 sequences assigned
28 (44.4%) exact matches, in which:
26 unique CDR3
4 unique J



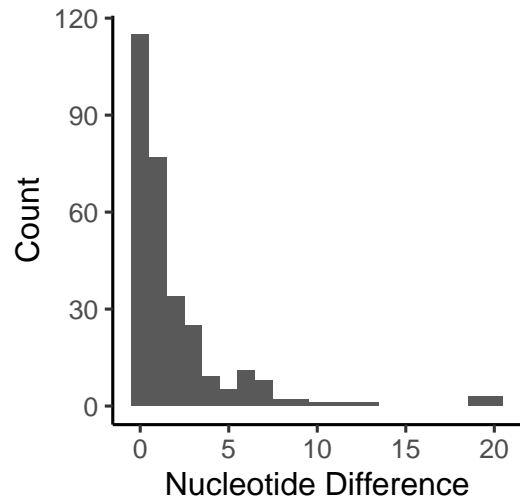
IGHV3-21*01

2539 sequences assigned
1301 (51.2%) exact matches, in which:
1158 unique CDR3
6 unique J



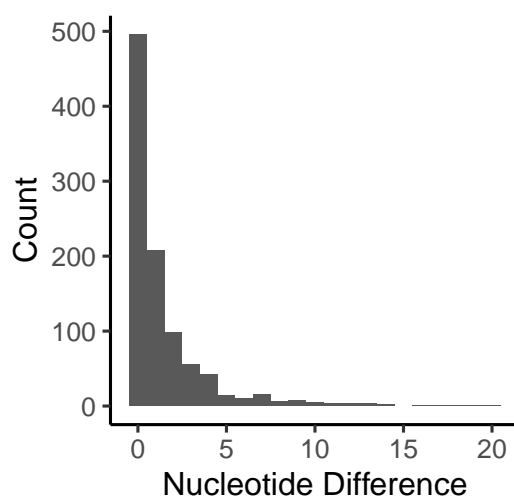
IGHV3-11*06

306 sequences assigned
115 (37.6%) exact matches, in which:
108 unique CDR3
5 unique J



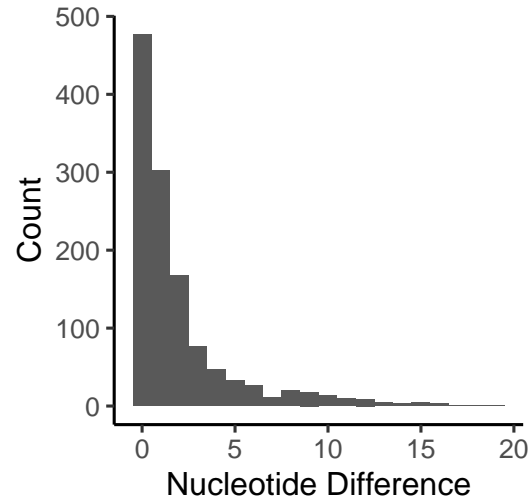
IGHV3-15*01

973 sequences assigned
496 (51%) exact matches, in which:
472 unique CDR3
6 unique J



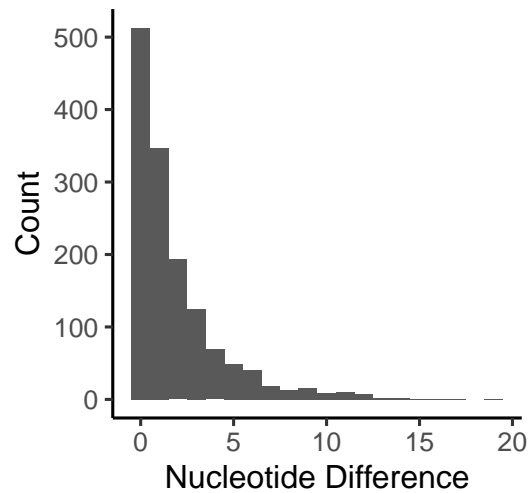
IGHV3-30-3*01

1229 sequences assigned
477 (38.8%) exact matches, in which:
458 unique CDR3
6 unique J



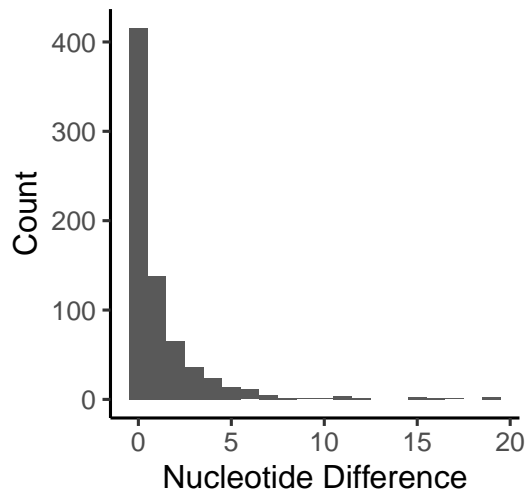
IGHV3-33*01

1422 sequences assigned
513 (36.1%) exact matches, in which:
475 unique CDR3
6 unique J



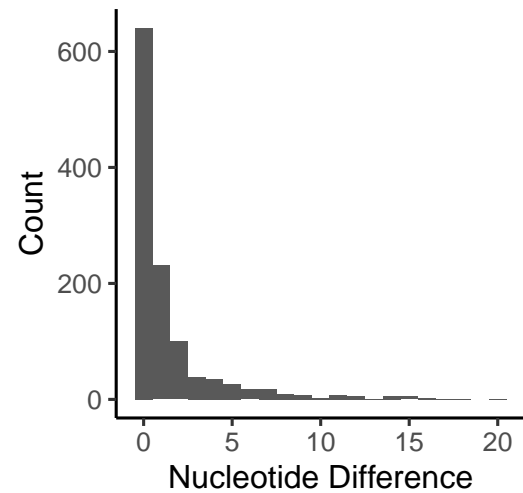
IGHV3-48*02

728 sequences assigned
416 (57.1%) exact matches, in which:
389 unique CDR3
6 unique J



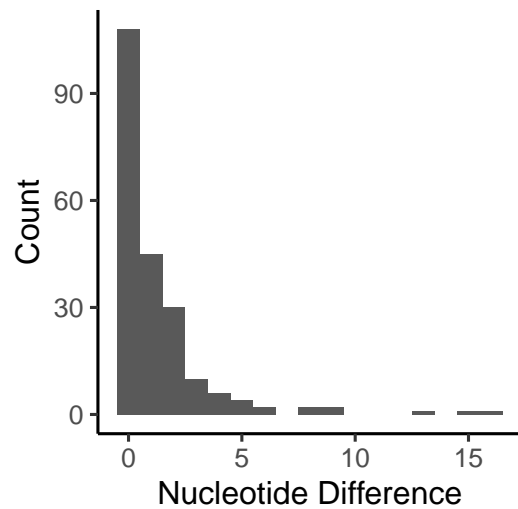
IGHV3-53*01

1157 sequences assigned
641 (55.4%) exact matches, in which:
579 unique CDR3
6 unique J



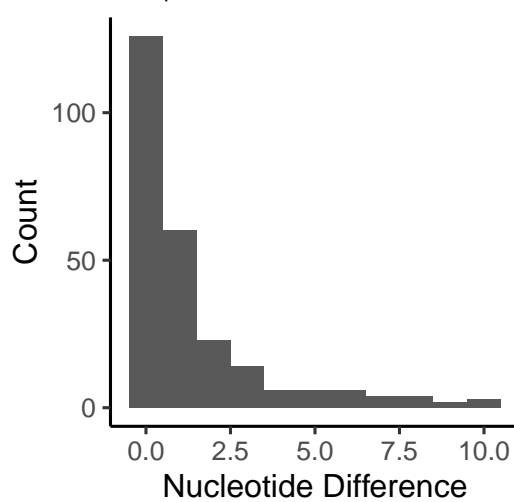
IGHV3-43*01

212 sequences assigned
108 (50.9%) exact matches, in which:
103 unique CDR3
5 unique J



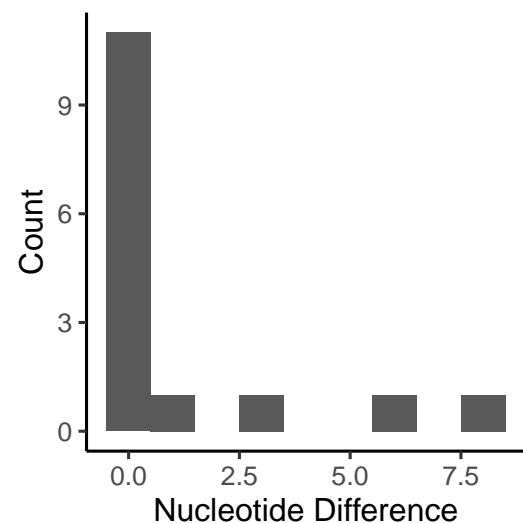
IGHV3-49*03

254 sequences assigned
126 (49.6%) exact matches, in which:
124 unique CDR3
5 unique J



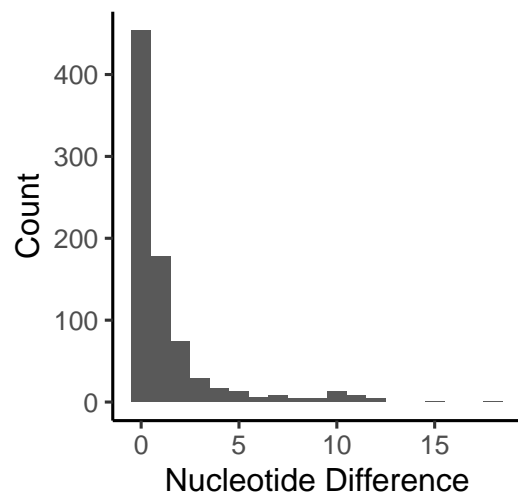
IGHV3-64*02

15 sequences assigned
11 (73.3%) exact matches, in which:
10 unique CDR3
2 unique J



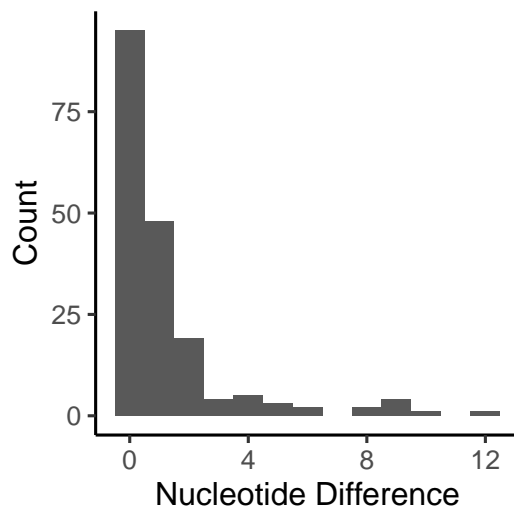
IGHV3-48*01

817 sequences assigned
454 (55.6%) exact matches, in which:
422 unique CDR3
6 unique J



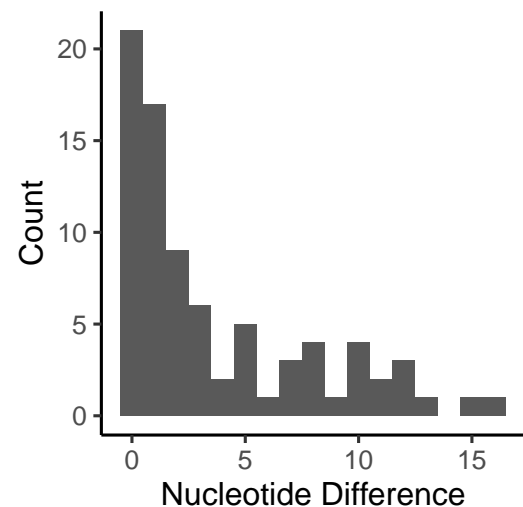
IGHV3-49*05

184 sequences assigned
95 (51.6%) exact matches, in which:
86 unique CDR3
6 unique J



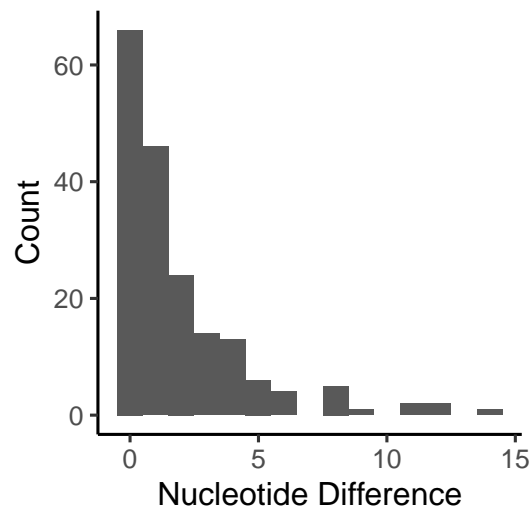
IGHV3-72*01

82 sequences assigned
21 (25.6%) exact matches, in which:
20 unique CDR3
5 unique J



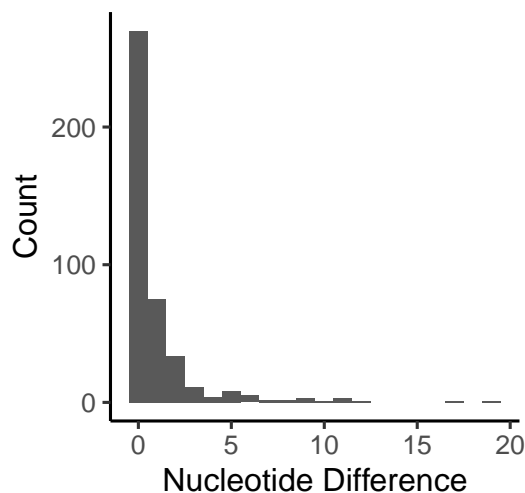
IGHV3-73*02

184 sequences assigned
66 (35.9%) exact matches, in which:
61 unique CDR3
5 unique J



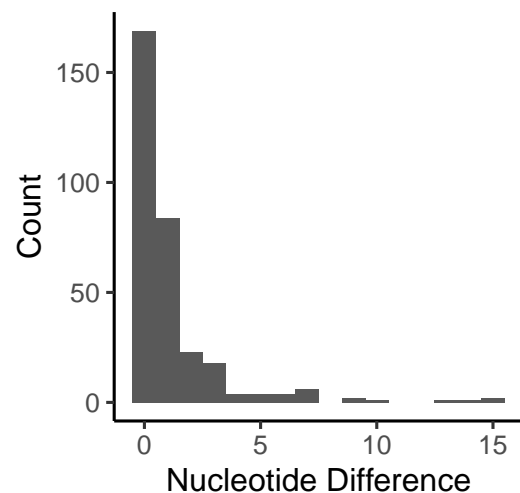
IGHV4-4*02

422 sequences assigned
270 (64%) exact matches, in which:
245 unique CDR3
6 unique J



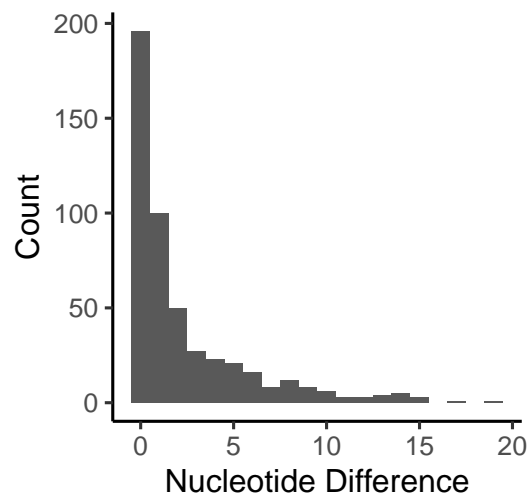
IGHV4-30-2*01

319 sequences assigned
169 (53%) exact matches, in which:
152 unique CDR3
6 unique J



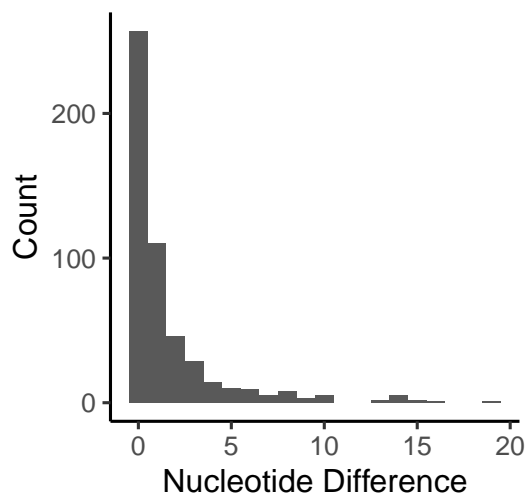
IGHV3-74*01

491 sequences assigned
196 (39.9%) exact matches, in which:
181 unique CDR3
6 unique J



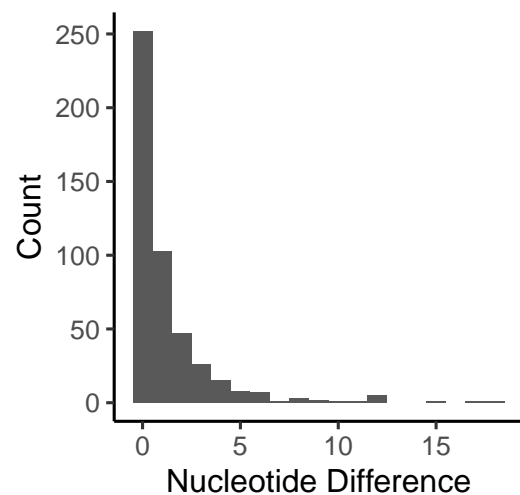
IGHV4-4*07

507 sequences assigned
257 (50.7%) exact matches, in which:
234 unique CDR3
6 unique J



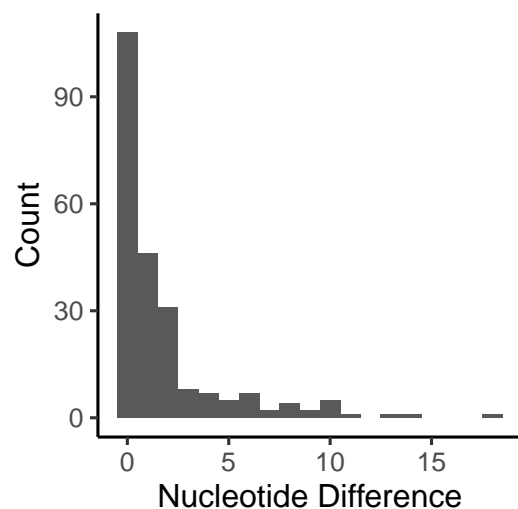
IGHV4-30-4*01

474 sequences assigned
252 (53.2%) exact matches, in which:
226 unique CDR3
6 unique J



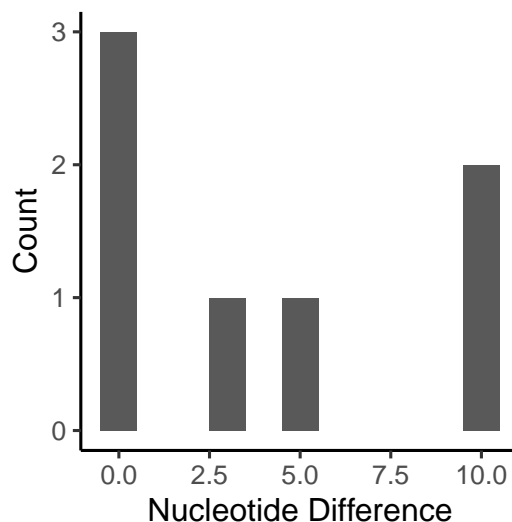
IGHV3-64D*06

231 sequences assigned
108 (46.8%) exact matches, in which:
98 unique CDR3
5 unique J



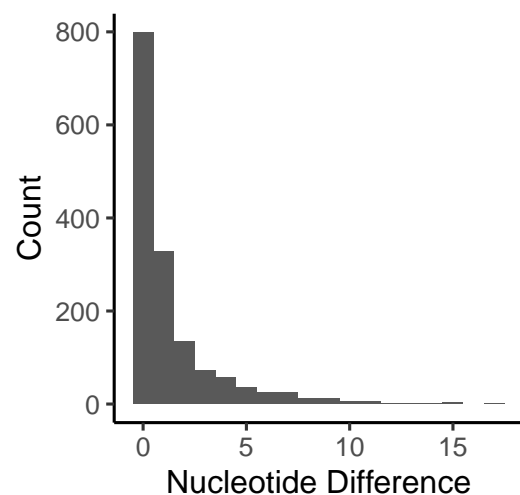
IGHV4-28*01

7 sequences assigned
3 (42.9%) exact matches, in which:
3 unique CDR3
2 unique J



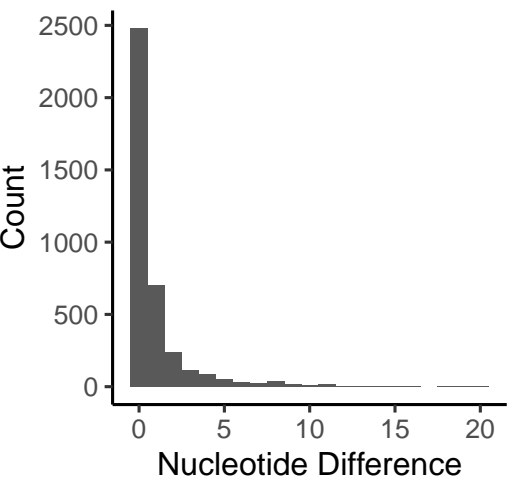
IGHV4-31*03

1522 sequences assigned
799 (52.5%) exact matches, in which:
722 unique CDR3
6 unique J



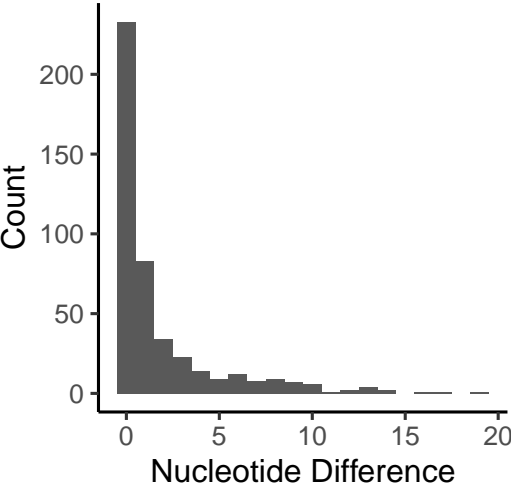
IGHV4-34*01

3836 sequences assigned
2479 (64.6%) exact matches, in which:
2105 unique CDR3
6 unique J



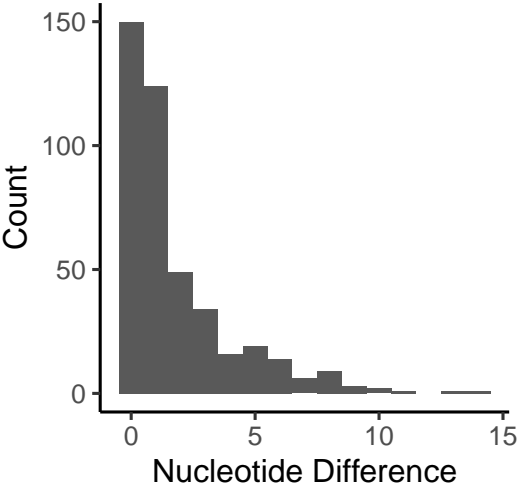
IGHV4-61*01

450 sequences assigned
233 (51.8%) exact matches, in which:
219 unique CDR3
6 unique J



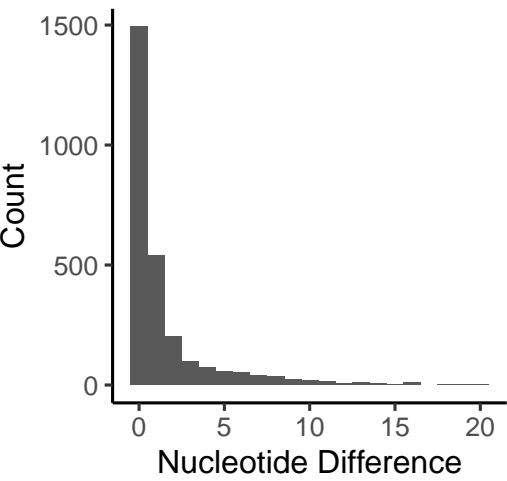
IGHV6-1*01

429 sequences assigned
150 (35%) exact matches, in which:
137 unique CDR3
5 unique J



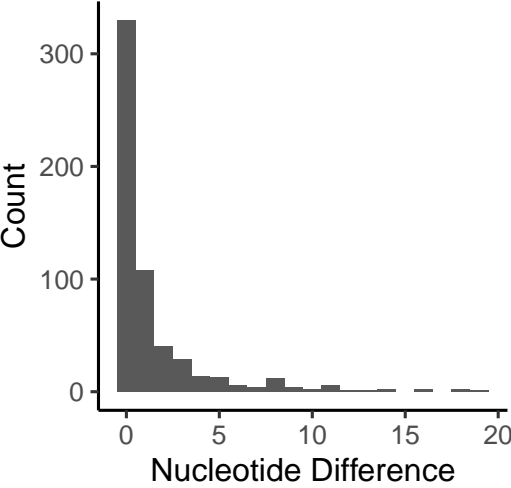
IGHV4-39*01

2702 sequences assigned
1493 (55.3%) exact matches, in which:
1341 unique CDR3
6 unique J



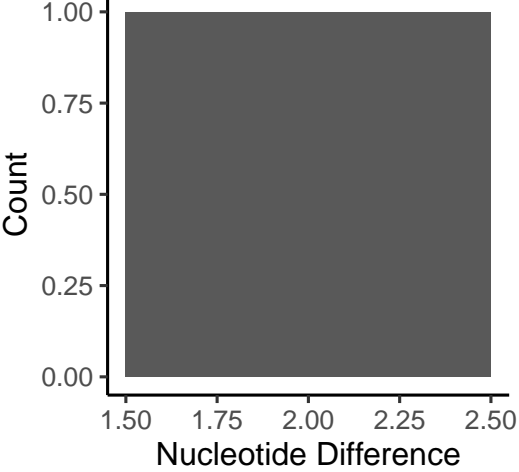
IGHV5-10-1*03

578 sequences assigned
330 (57.1%) exact matches, in which:
299 unique CDR3
6 unique J



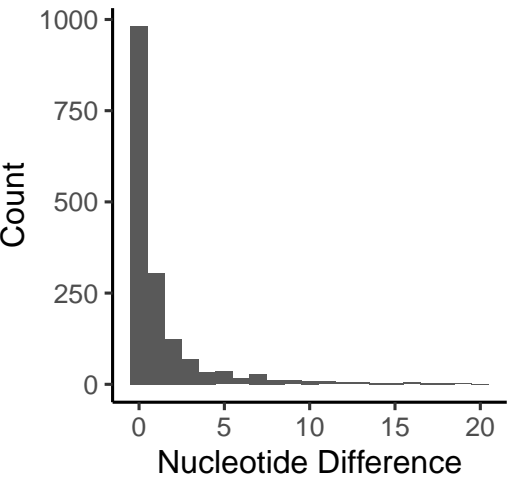
IGHV3/OR16-12*01

1 sequences assigned
No exact matches.



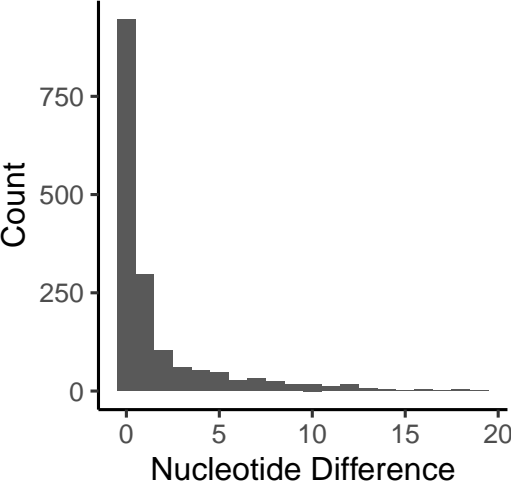
IGHV4-59*01

1665 sequences assigned
982 (59%) exact matches, in which:
899 unique CDR3
6 unique J



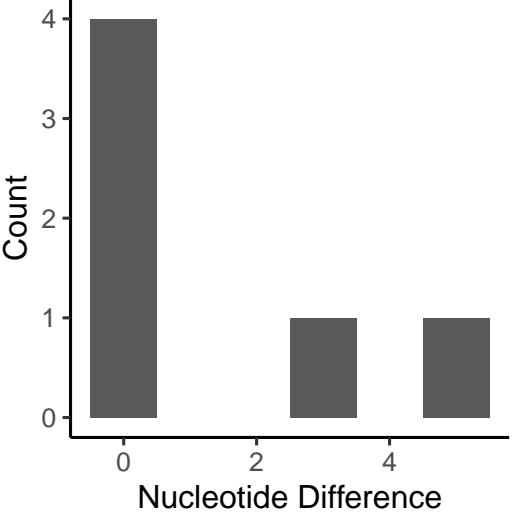
IGHV5-51*01

1675 sequences assigned
946 (56.5%) exact matches, in which:
853 unique CDR3
6 unique J



IGHV7-4-1*01

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





Novel sequence(s)IGHV6-1*01_T91C are not listed in the genotype and will be ignored.