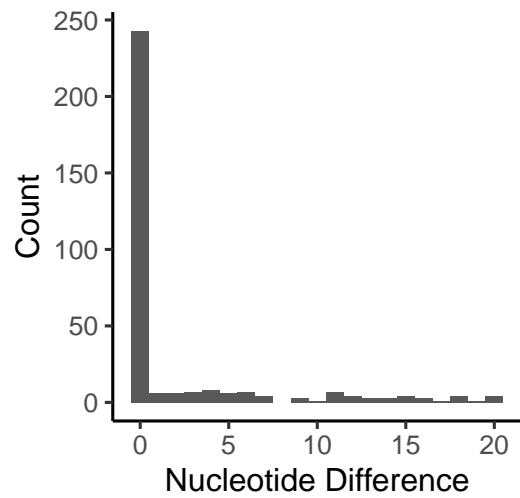


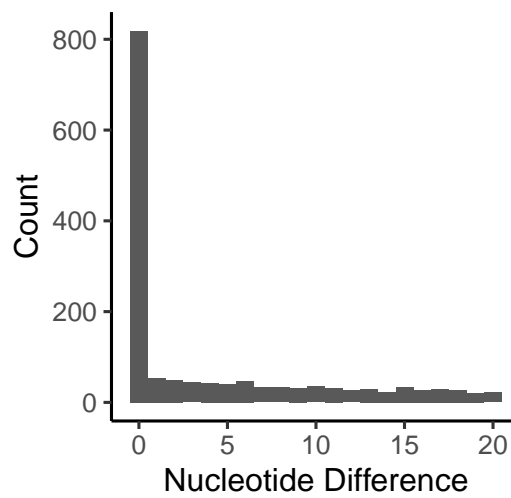
IGHV1-2*04

348 sequences assigned
243 (69.8%) exact matches, in which:
243 unique CDR3
5 unique J



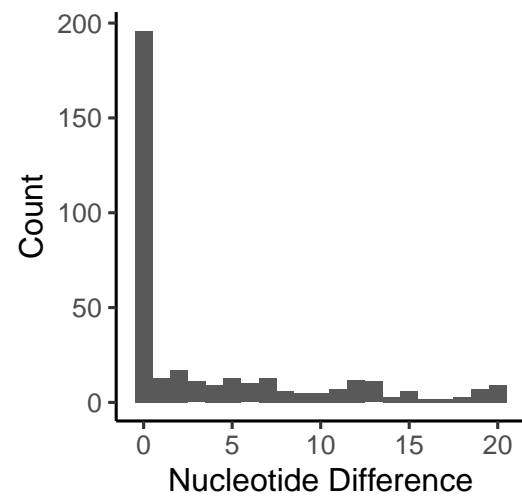
IGHV1-18*04

1845 sequences assigned
819 (44.4%) exact matches, in which:
818 unique CDR3
6 unique J



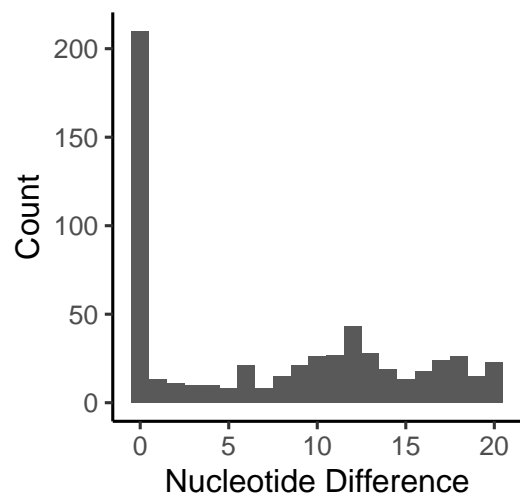
IGHV1-46*01

450 sequences assigned
196 (43.6%) exact matches, in which:
196 unique CDR3
6 unique J



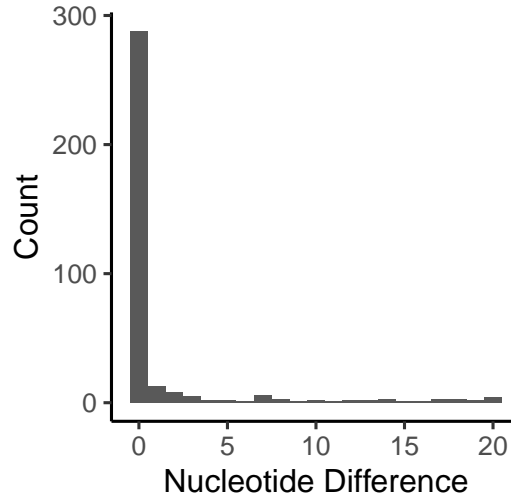
IGHV1-3*01_05

688 sequences assigned
210 (30.5%) exact matches, in which:
210 unique CDR3
6 unique J



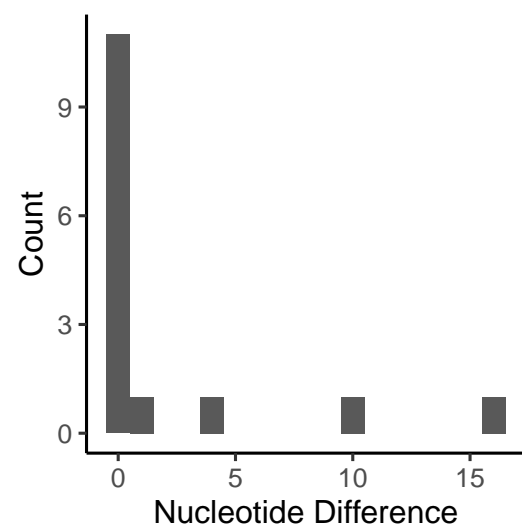
IGHV1-24*01

363 sequences assigned
288 (79.3%) exact matches, in which:
288 unique CDR3
6 unique J



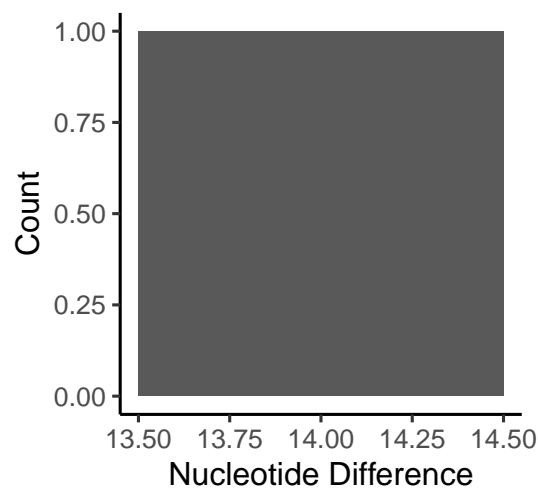
IGHV1-58*02

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



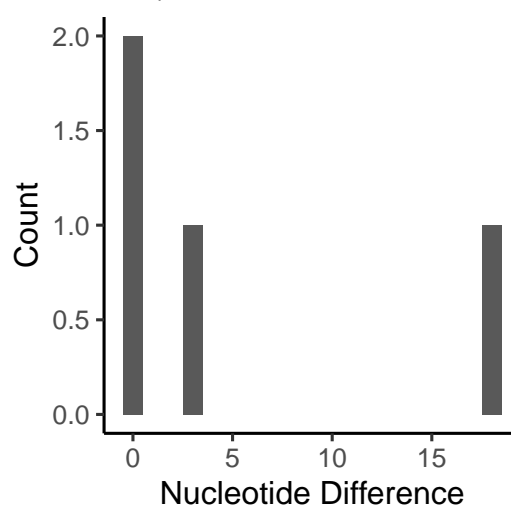
IGHV1-8*01

1 sequences assigned
No exact matches.



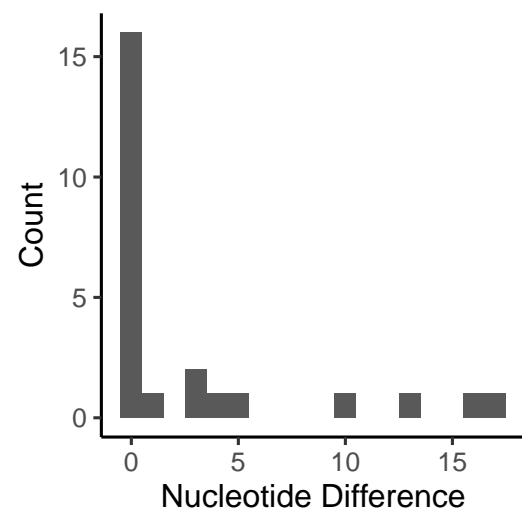
IGHV1-45*02

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



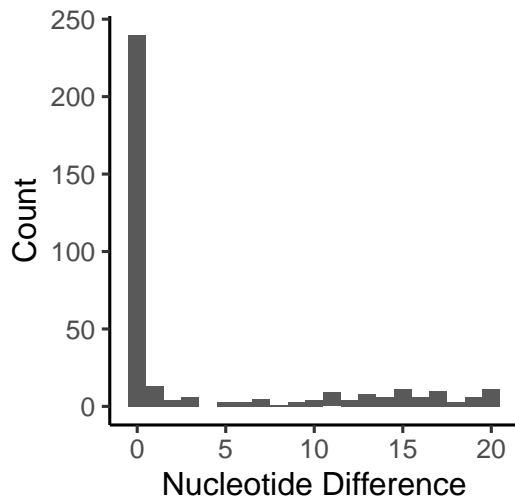
IGHV1-58*01_03

28 sequences assigned
16 (57.1%) exact matches, in which:
16 unique CDR3
4 unique J



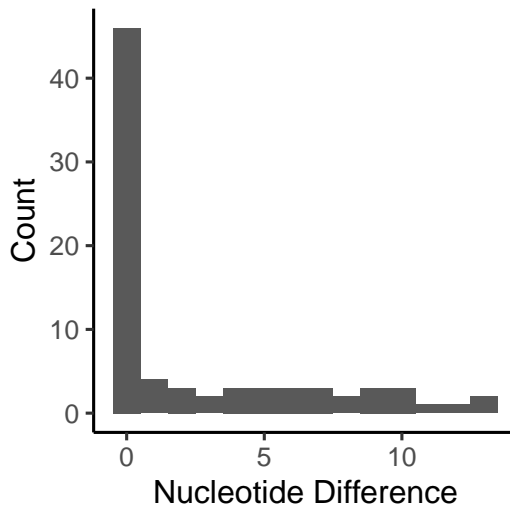
IGHV1–69*04_09

430 sequences assigned
240 (55.8%) exact matches, in which:
239 unique CDR3
6 unique J



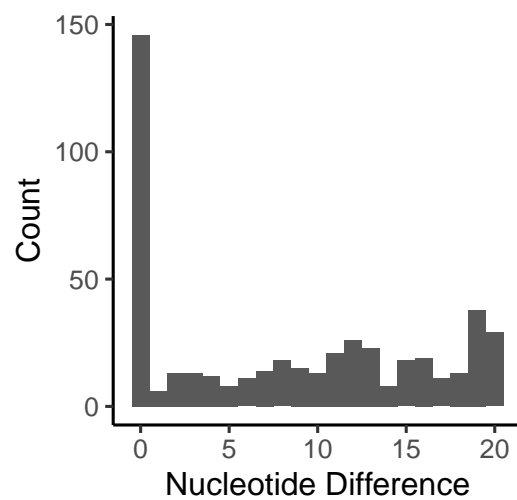
IGHV2–70*01

84 sequences assigned
46 (54.8%) exact matches, in which:
45 unique CDR3
6 unique J



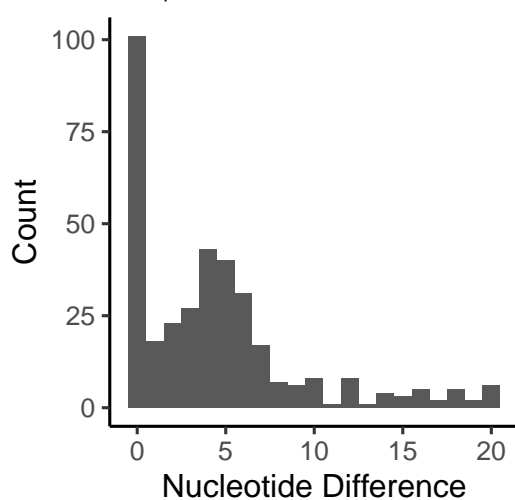
IGHV3–11*06

652 sequences assigned
146 (22.4%) exact matches, in which:
141 unique CDR3
6 unique J



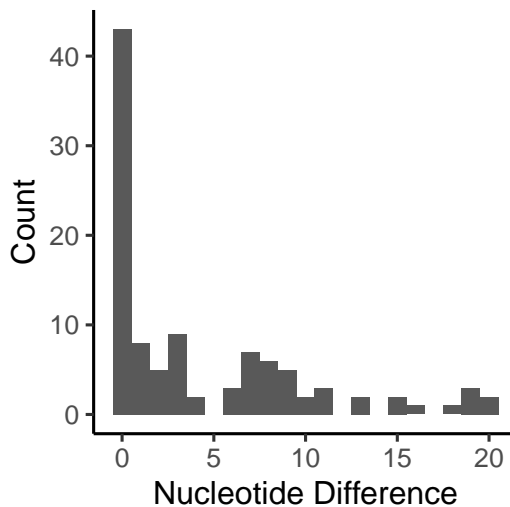
IGHV2–5*02

374 sequences assigned
101 (27%) exact matches, in which:
99 unique CDR3
6 unique J



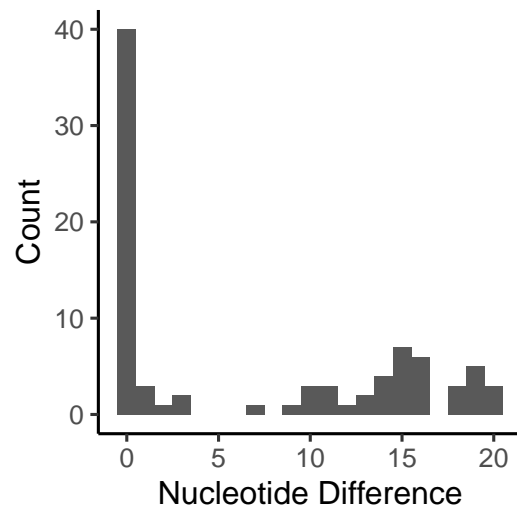
IGHV2–70*11_15

112 sequences assigned
43 (38.4%) exact matches, in which:
42 unique CDR3
4 unique J



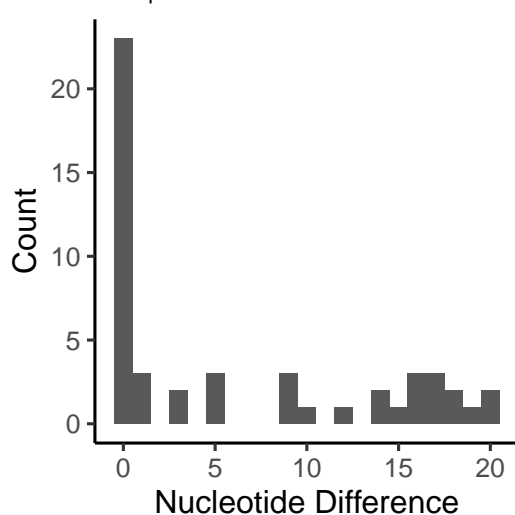
IGHV3–13*05

106 sequences assigned
40 (37.7%) exact matches, in which:
38 unique CDR3
5 unique J



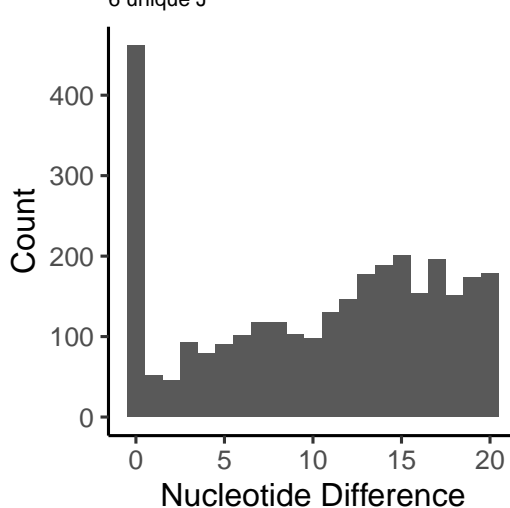
IGHV2–26*01

51 sequences assigned
23 (45.1%) exact matches, in which:
23 unique CDR3
5 unique J



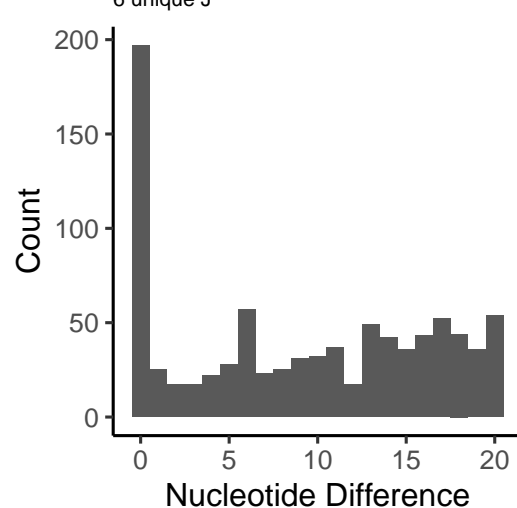
IGHV3–7*03

4155 sequences assigned
462 (11.1%) exact matches, in which:
455 unique CDR3
6 unique J



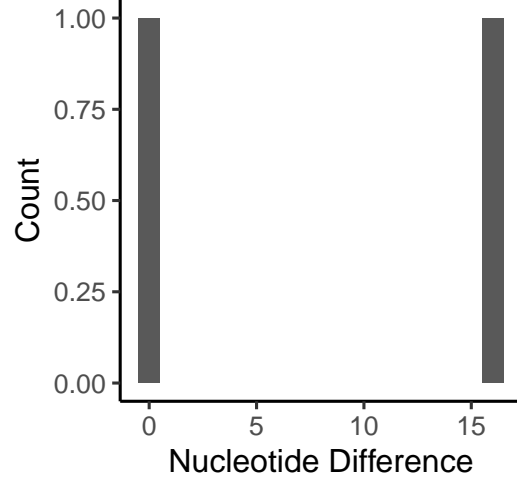
IGHV3–15*01_02

1266 sequences assigned
197 (15.6%) exact matches, in which:
192 unique CDR3
6 unique J



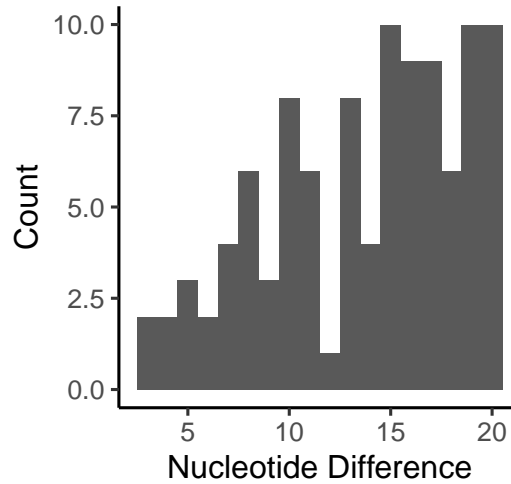
IGHV3-20*01_02

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



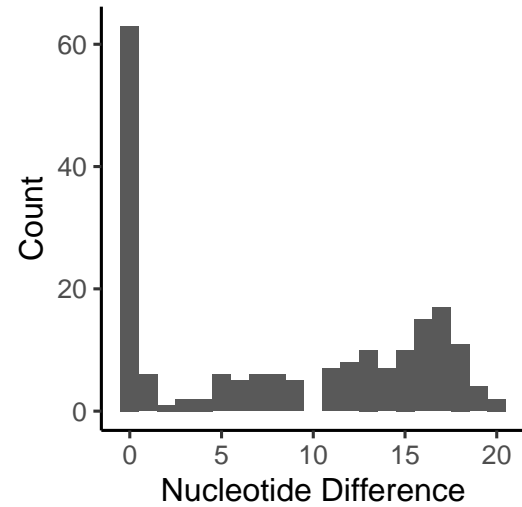
IGHV3-30*04

137 sequences assigned
No exact matches.



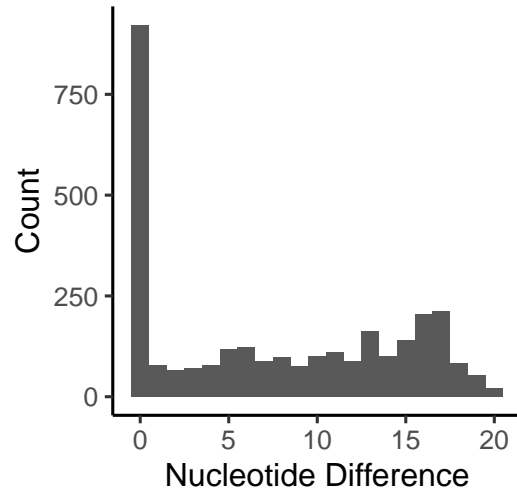
IGHV3-43*01

211 sequences assigned
63 (29.9%) exact matches, in which:
61 unique CDR3
5 unique J



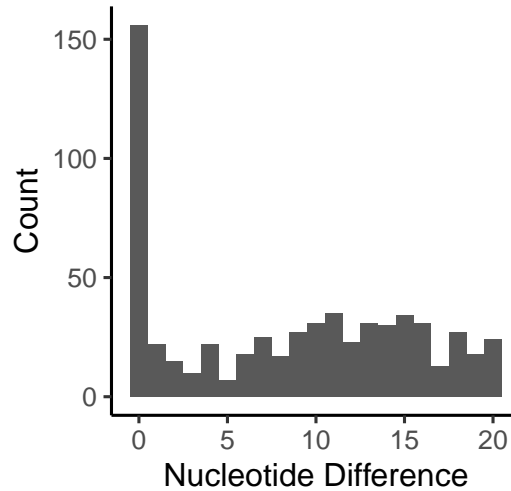
IGHV3-21*01_02

3167 sequences assigned
922 (29.1%) exact matches, in which:
882 unique CDR3
6 unique J



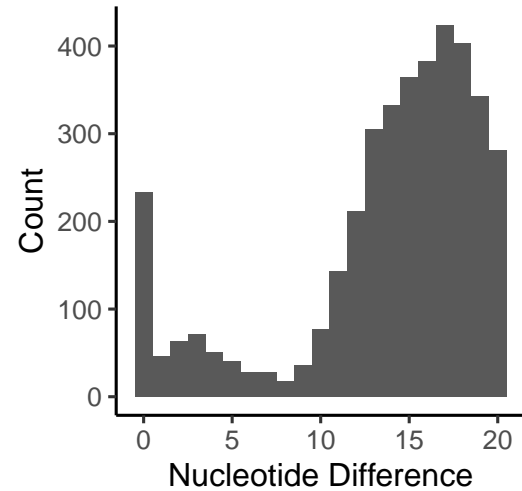
IGHV3-33*01

772 sequences assigned
156 (20.2%) exact matches, in which:
150 unique CDR3
6 unique J



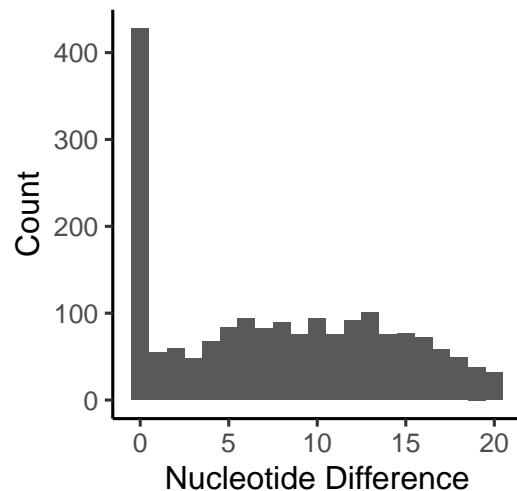
IGHV3-48*02

5203 sequences assigned
233 (4.5%) exact matches, in which:
222 unique CDR3
6 unique J



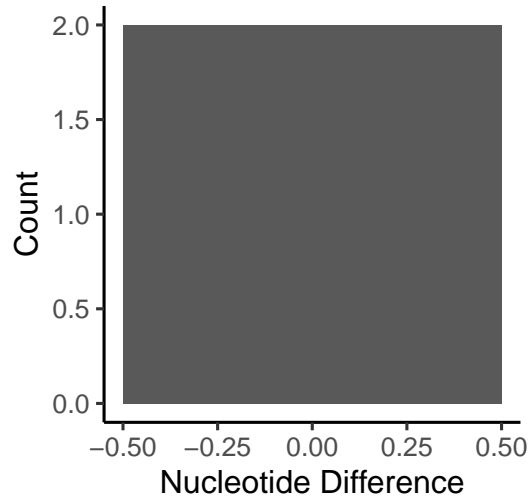
IGHV3-30-3*01

2033 sequences assigned
428 (21.1%) exact matches, in which:
422 unique CDR3
6 unique J



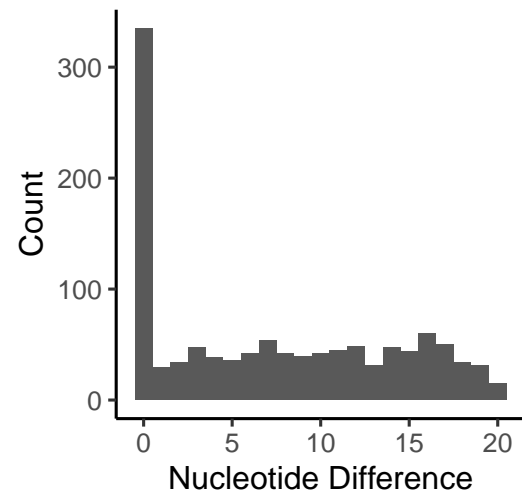
IGHV3-38-3*01

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



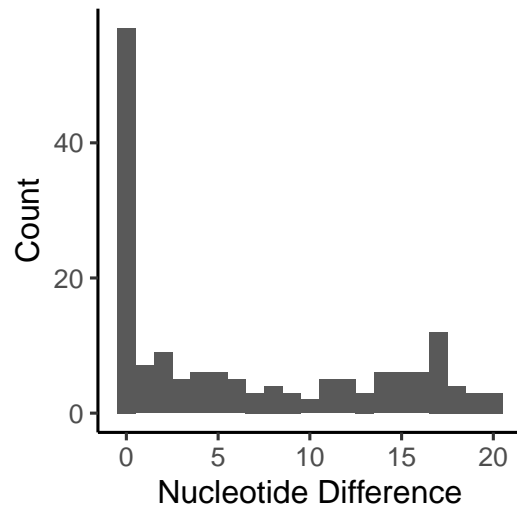
IGHV3-48*04

1322 sequences assigned
335 (25.3%) exact matches, in which:
322 unique CDR3
6 unique J



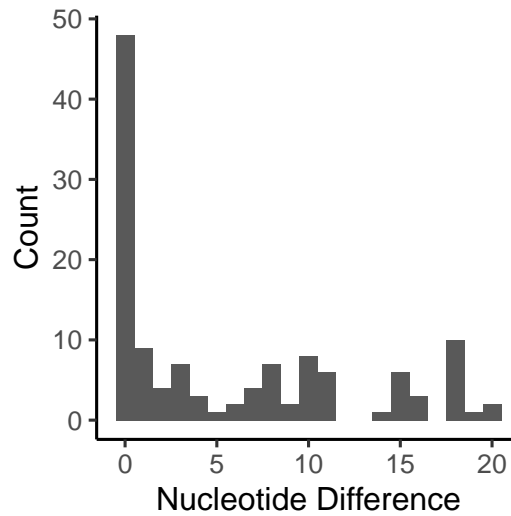
IGHV3-49*03_05

182 sequences assigned
57 (31.3%) exact matches, in which:
56 unique CDR3
5 unique J



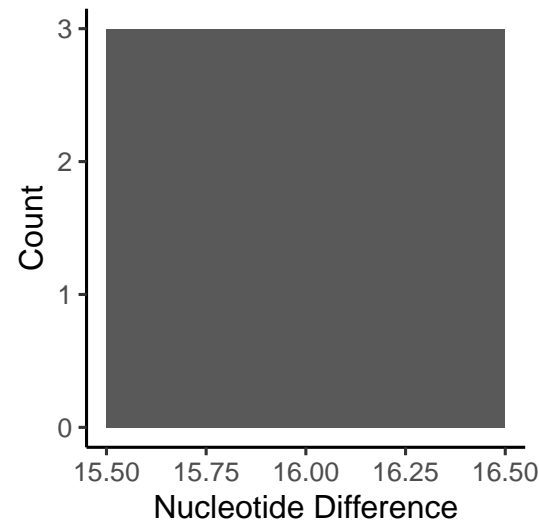
IGHV3-64*01

152 sequences assigned
48 (31.6%) exact matches, in which:
47 unique CDR3
5 unique J



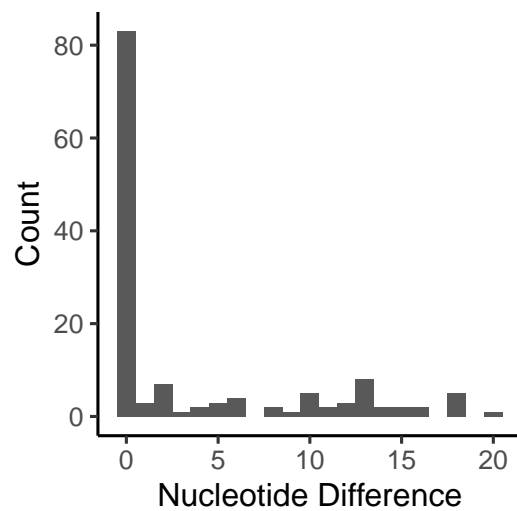
IGHV3-69-1*02

6 sequences assigned
No exact matches.



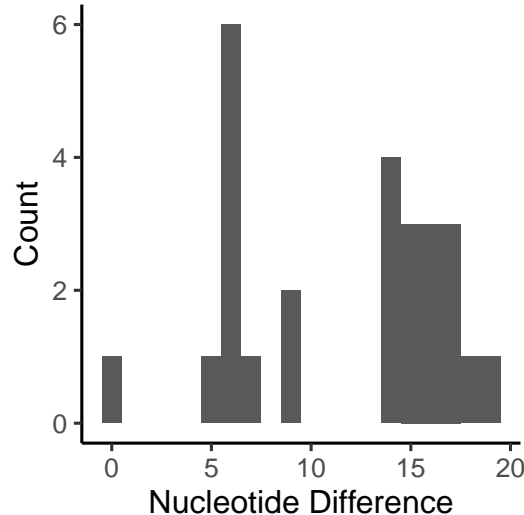
IGHV3-53*04

192 sequences assigned
83 (43.2%) exact matches, in which:
81 unique CDR3
6 unique J



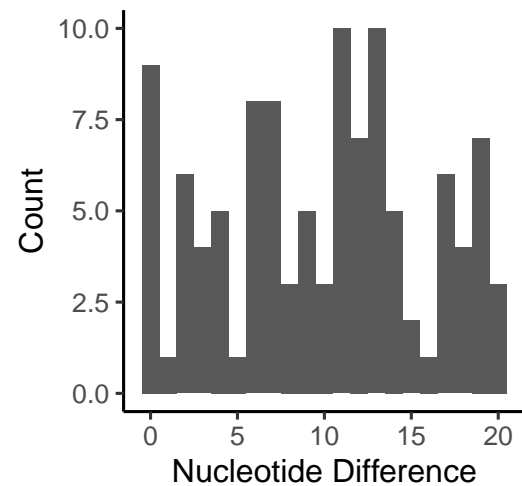
IGHV3-64*02_07

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



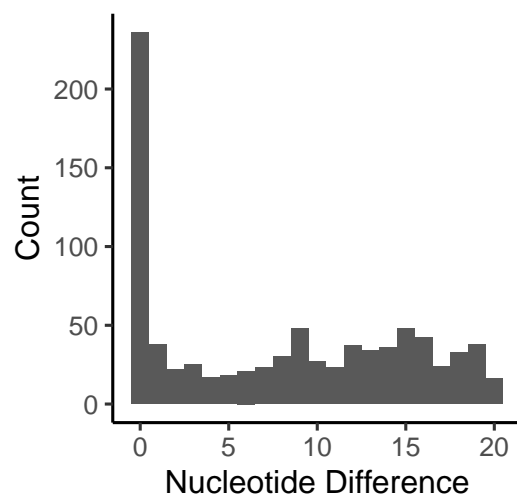
IGHV3-72*01

135 sequences assigned
9 (6.7%) exact matches, in which:
9 unique CDR3
4 unique J



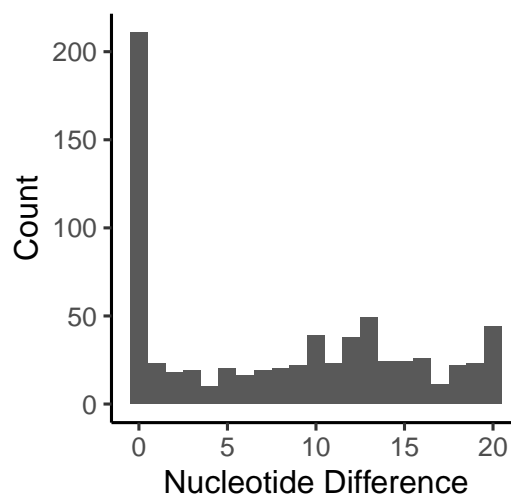
IGHV3-53*01_02

933 sequences assigned
236 (25.3%) exact matches, in which:
232 unique CDR3
6 unique J



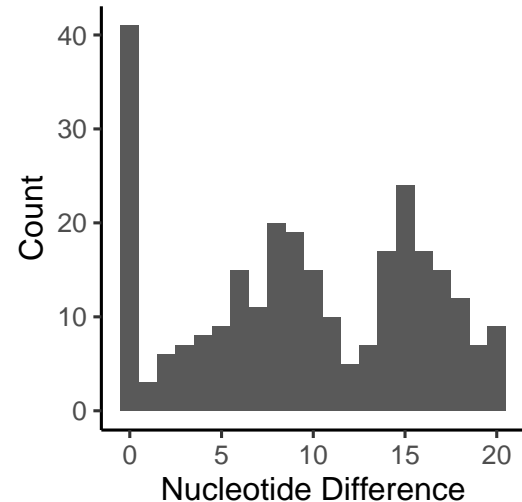
IGHV3-66*01

912 sequences assigned
211 (23.1%) exact matches, in which:
207 unique CDR3
6 unique J



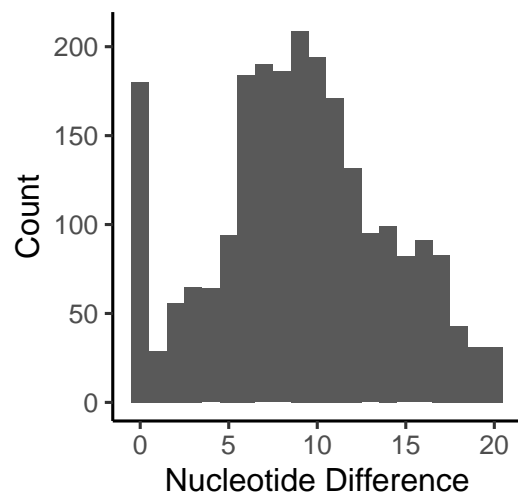
IGHV3-73*01_02

284 sequences assigned
41 (14.4%) exact matches, in which:
41 unique CDR3
4 unique J



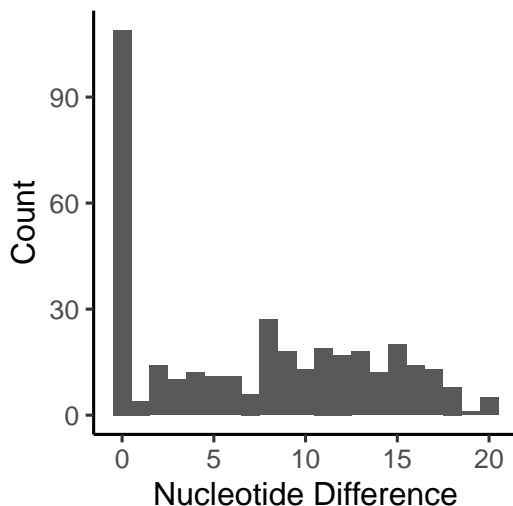
IGHV3-74*01_02

2443 sequences assigned
180 (7.4%) exact matches, in which:
169 unique CDR3
6 unique J



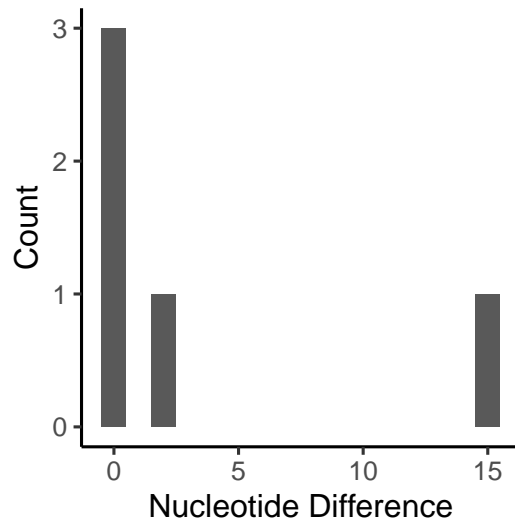
IGHV3-64D*09

404 sequences assigned
109 (27%) exact matches, in which:
108 unique CDR3
5 unique J



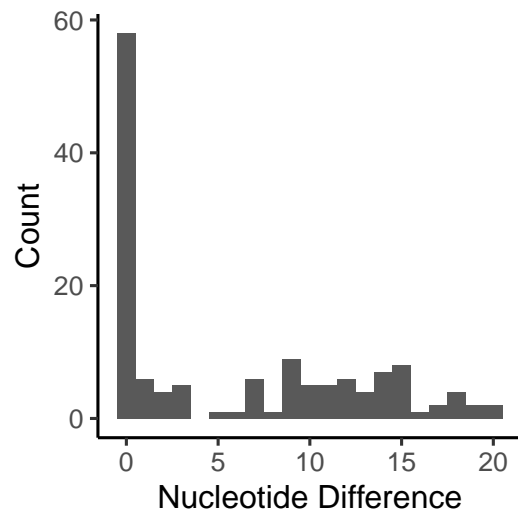
IGHV4-28*01_07

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



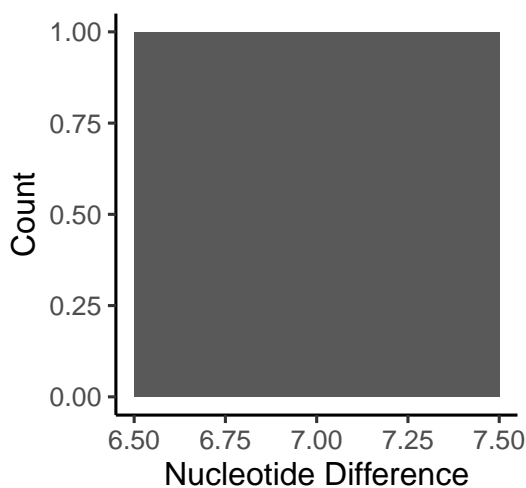
IGHV3-43D*03

146 sequences assigned
58 (39.7%) exact matches, in which:
55 unique CDR3
5 unique J



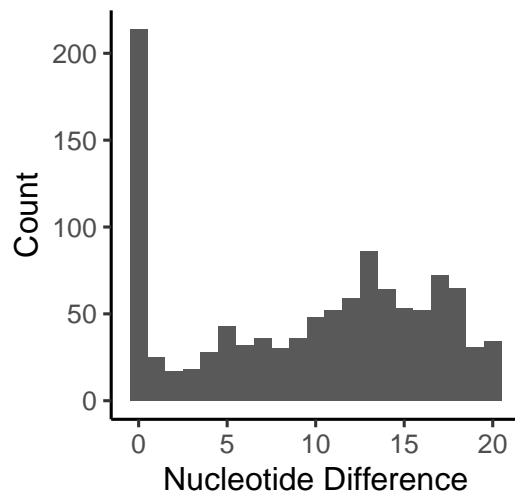
IGHV3-NL1*01

3 sequences assigned
No exact matches.



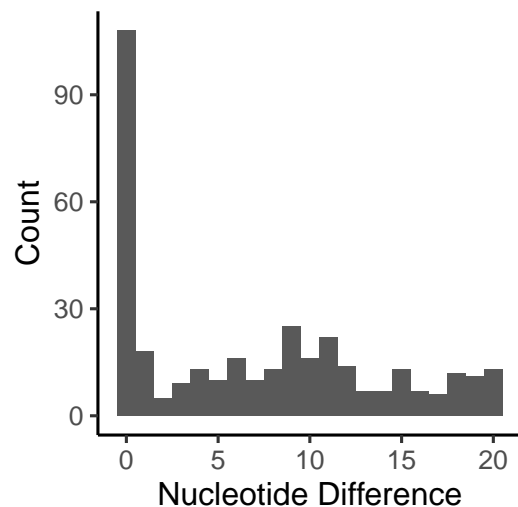
IGHV4-30-4*01

1189 sequences assigned
214 (18%) exact matches, in which:
212 unique CDR3
6 unique J



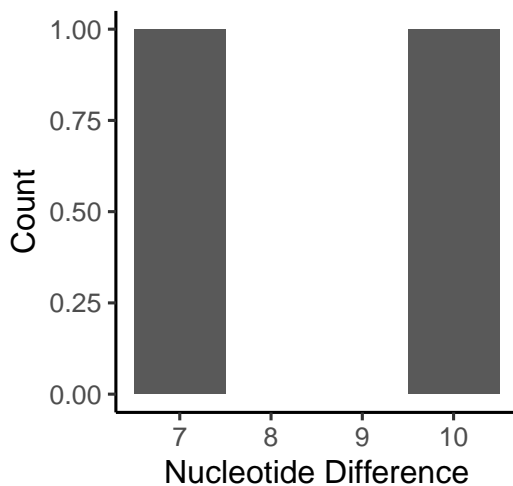
IGHV3-64D*06

596 sequences assigned
108 (18.1%) exact matches, in which:
107 unique CDR3
6 unique J



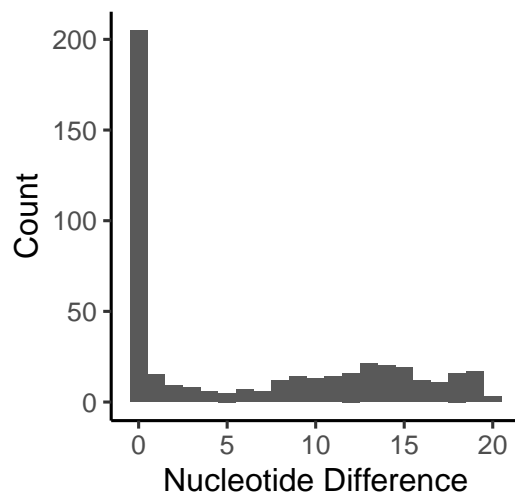
IGHV4-28*03

2 sequences assigned
No exact matches.



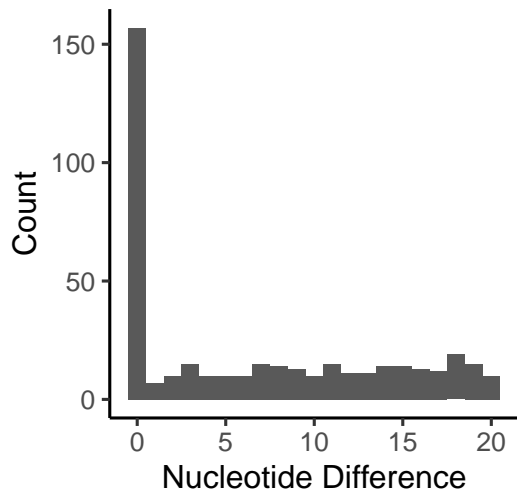
IGHV4-30-2*01

532 sequences assigned
205 (38.5%) exact matches, in which:
201 unique CDR3
6 unique J



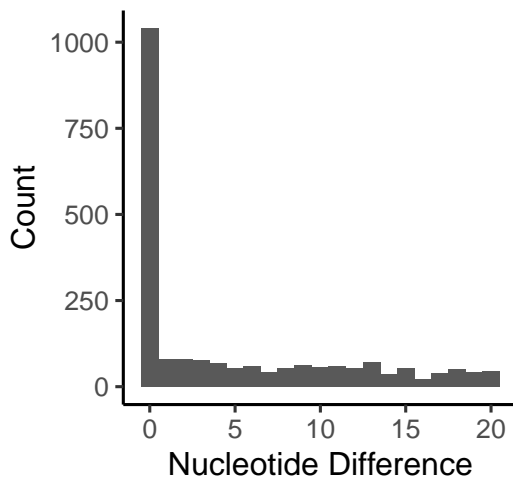
IGHV4-31*03_04

507 sequences assigned
157 (31%) exact matches, in which:
155 unique CDR3
6 unique J



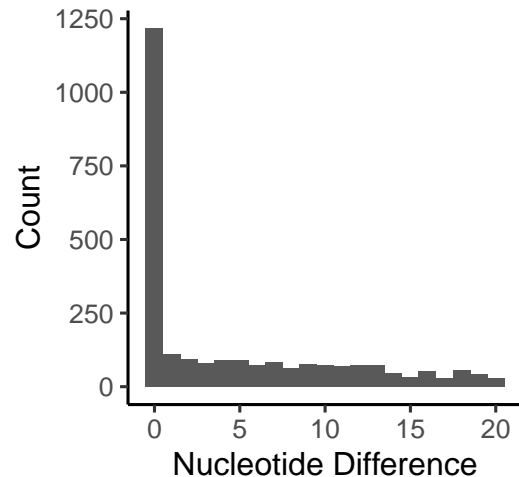
IGHV4-39*07

2550 sequences assigned
1040 (40.8%) exact matches, in which:
1024 unique CDR3
6 unique J



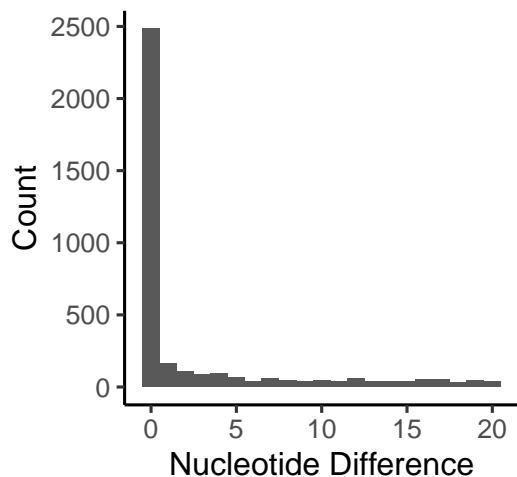
IGHV4-59*01_07

2884 sequences assigned
1217 (42.2%) exact matches, in which:
1195 unique CDR3
6 unique J



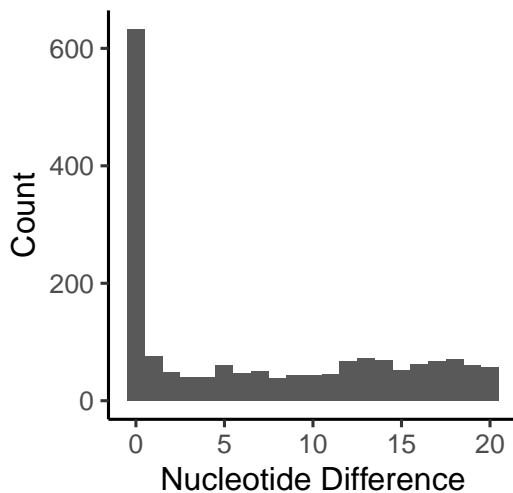
IGHV4-34*01_02

4122 sequences assigned
2484 (60.3%) exact matches, in which:
2444 unique CDR3
6 unique J



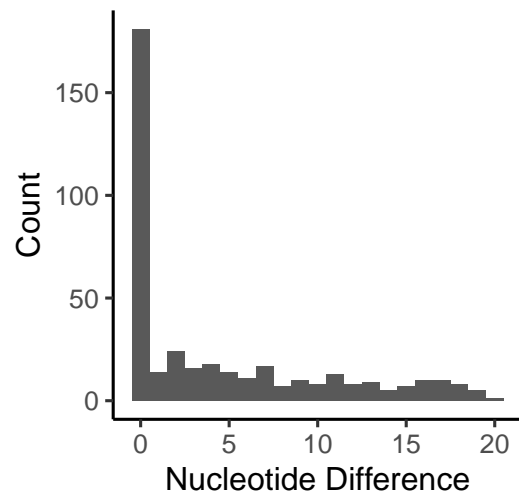
IGHV4-39*01_05

2195 sequences assigned
633 (28.8%) exact matches, in which:
619 unique CDR3
6 unique J



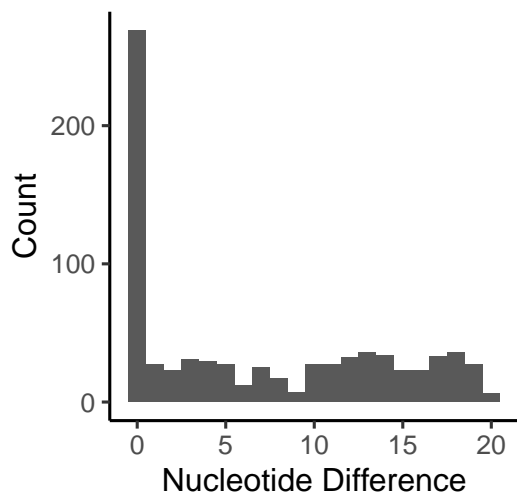
IGHV4-61*01

469 sequences assigned
181 (38.6%) exact matches, in which:
177 unique CDR3
6 unique J



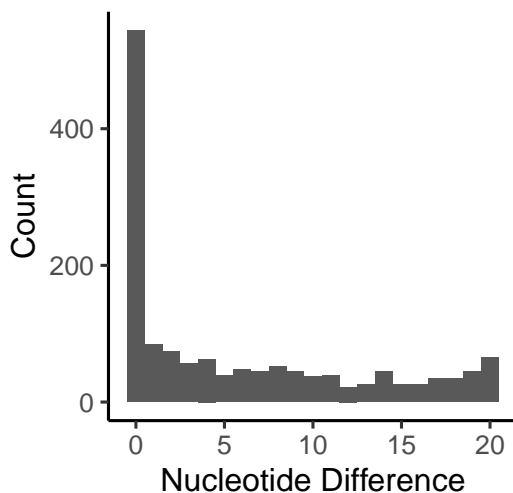
IGHV4-38-2*02

911 sequences assigned
269 (29.5%) exact matches, in which:
266 unique CDR3
6 unique J



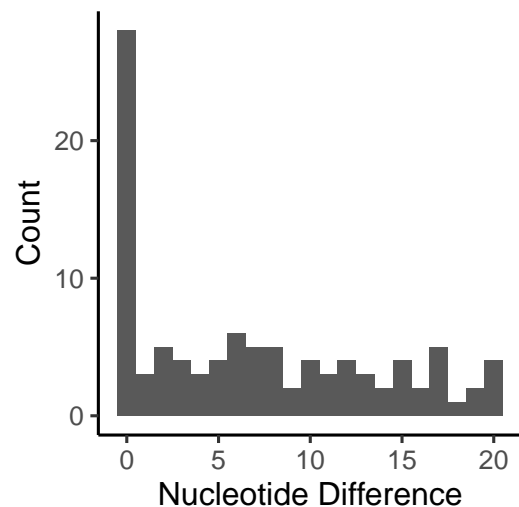
IGHV4-59*08

1915 sequences assigned
544 (28.4%) exact matches, in which:
526 unique CDR3
6 unique J



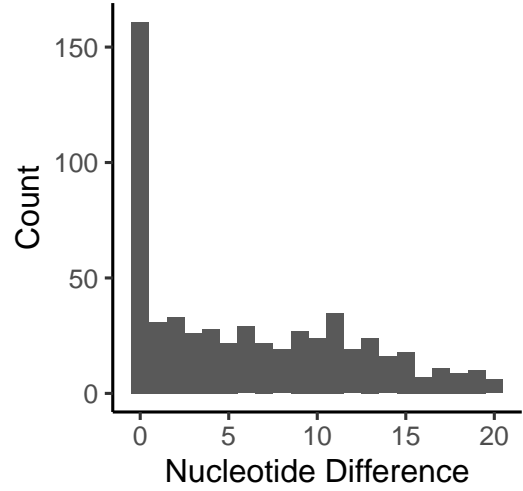
IGHV5-10-1*01_03

113 sequences assigned
28 (24.8%) exact matches, in which:
28 unique CDR3
5 unique J



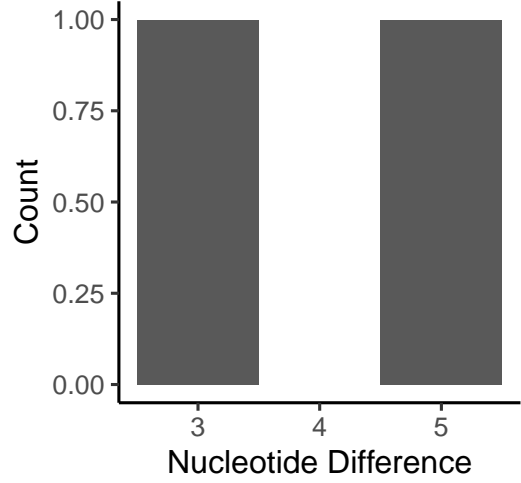
IGHV5–51*01_03

606 sequences assigned
161 (26.6%) exact matches, in which:
161 unique CDR3
6 unique J



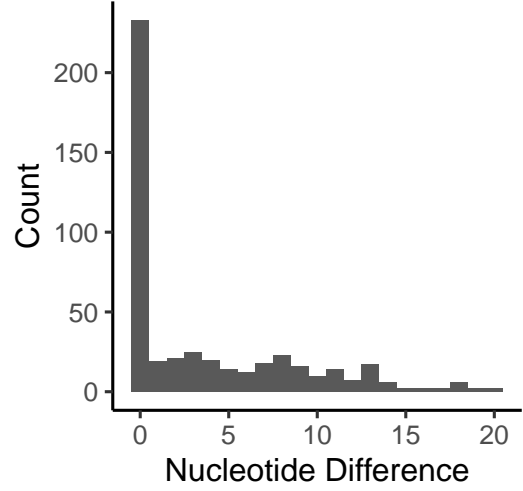
IGHV7–4–1*02

2 sequences assigned
No exact matches.



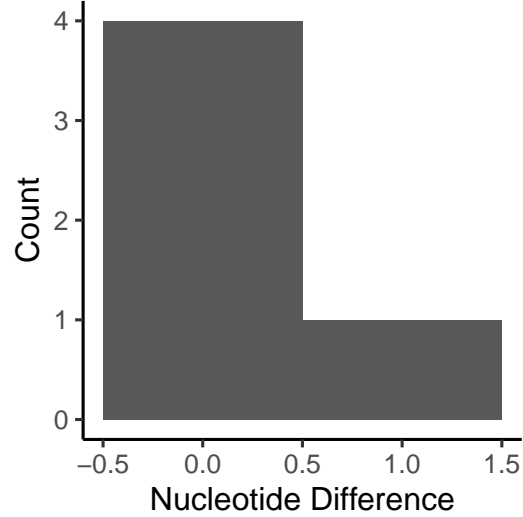
IGHV6–1*01_02

482 sequences assigned
233 (48.3%) exact matches, in which:
232 unique CDR3
6 unique J



IGHV7–4–1*01

5 sequences assigned
4 (80%) exact matches, in which:
4 unique CDR3
2 unique J





Warning - no inferred sequences found.

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 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 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 IGHV5-51*07_A128G 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.

Warning - no inferred sequences found.

Novel sequence(s) IGHV4-59*02_G88A 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 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.

Novel sequence(s) 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.

Novel sequence(s) IGHV1-69*04_09_G112A 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.

Warning - no inferred sequences found.

Novel sequence(s) 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 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) 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.

Warning - no inferred sequences found.

Warning - no inferred sequences found.

Warning - no inferred sequences found.

Novel sequence(s) IGHV4-59*02_G88A IGHV5-51*07_A128G are not listed in the genotype and will be ignored.

Warning - no inferred sequences found.

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