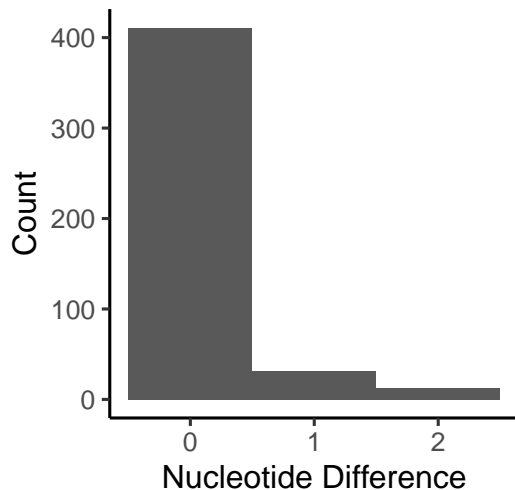


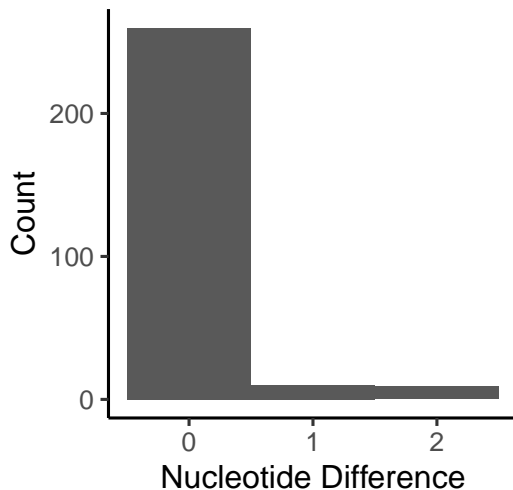
IGHV1–2*02

455 sequences assigned
411 (90.3%) exact matches, in which:
409 unique CDR3
6 unique J



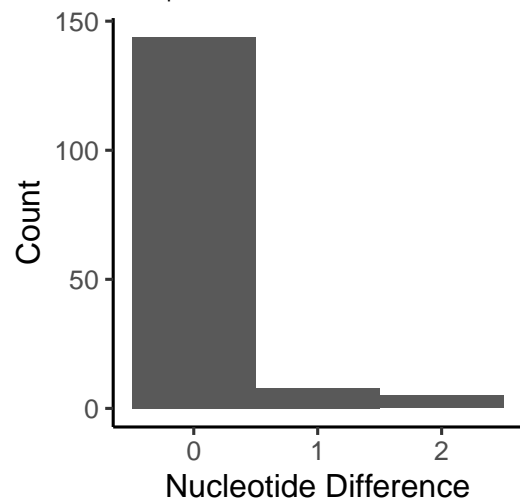
IGHV1–8*01

279 sequences assigned
260 (93.2%) exact matches, in which:
259 unique CDR3
6 unique J



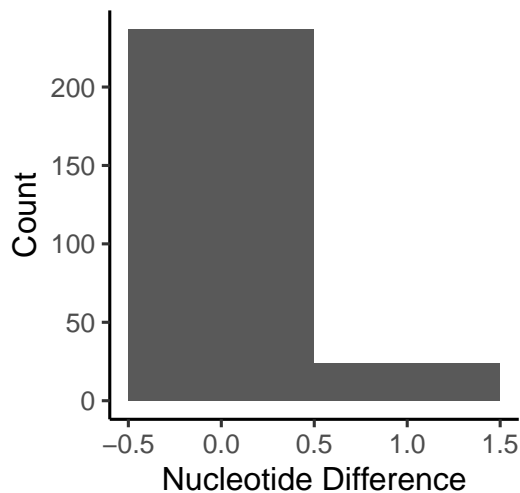
IGHV1–46*01

157 sequences assigned
144 (91.7%) exact matches, in which:
144 unique CDR3
5 unique J



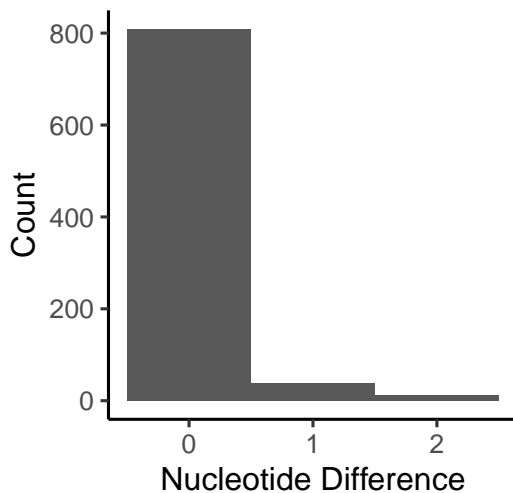
IGHV1–2*06

261 sequences assigned
237 (90.8%) exact matches, in which:
233 unique CDR3
6 unique J



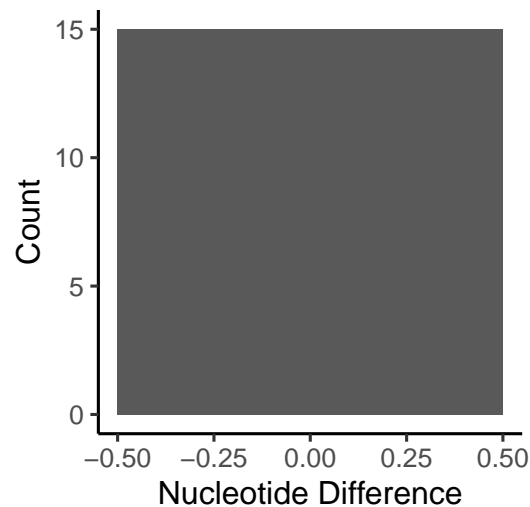
IGHV1–18*01

858 sequences assigned
809 (94.3%) exact matches, in which:
809 unique CDR3
6 unique J



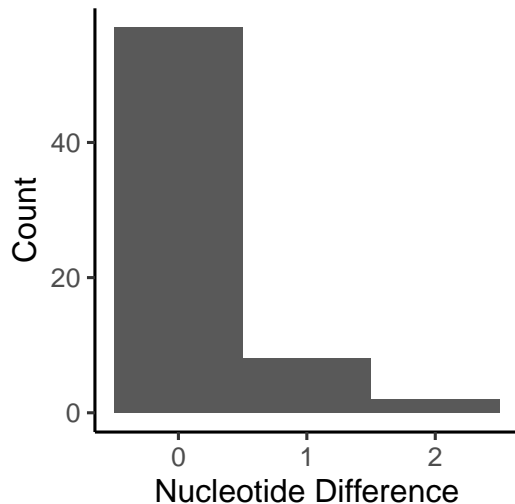
IGHV1–58*02

15 sequences assigned
15 (100%) exact matches, in which:
15 unique CDR3
5 unique J



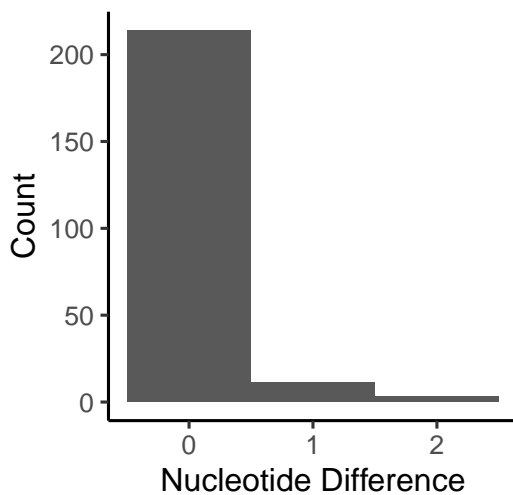
IGHV1–3*01_05

67 sequences assigned
57 (85.1%) exact matches, in which:
57 unique CDR3
6 unique J



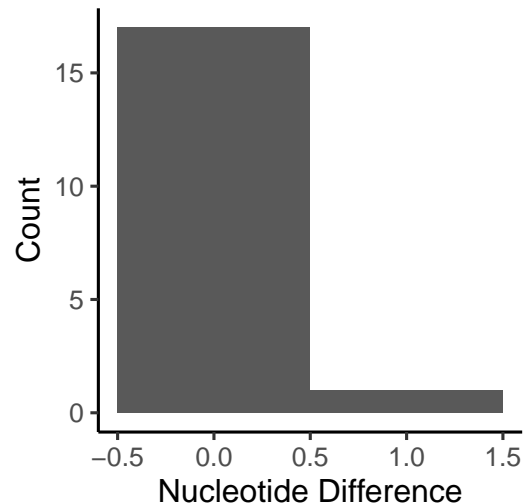
IGHV1–24*01

228 sequences assigned
214 (93.9%) exact matches, in which:
214 unique CDR3
6 unique J



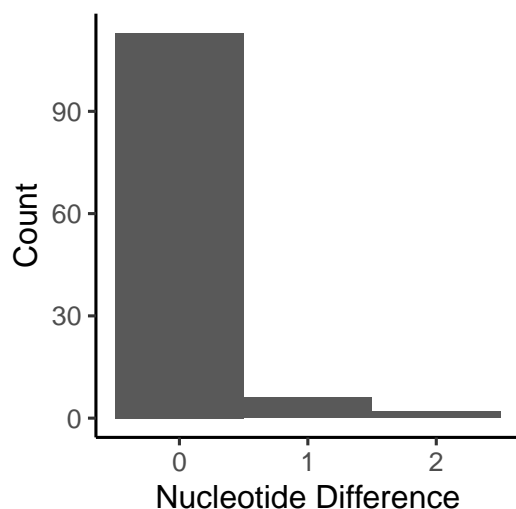
IGHV1–58*01_03

18 sequences assigned
17 (94.4%) exact matches, in which:
17 unique CDR3
4 unique J



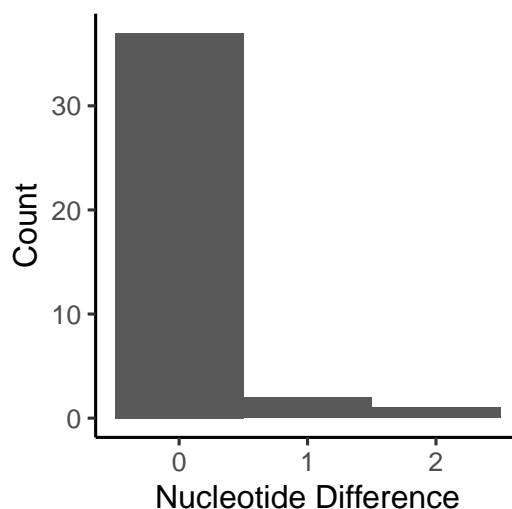
IGHV1-69*04_09

121 sequences assigned
113 (93.4%) exact matches, in which:
113 unique CDR3
6 unique J



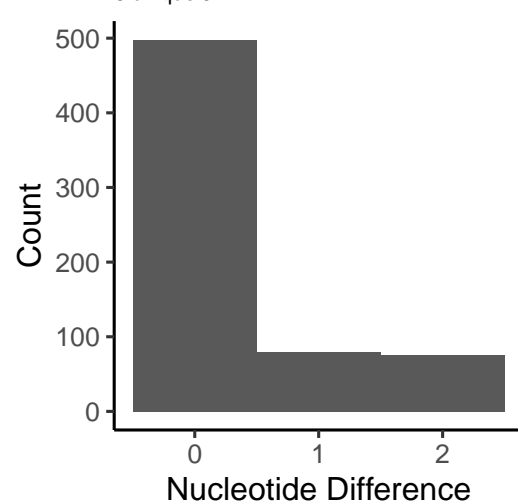
IGHV2-26*01

40 sequences assigned
37 (92.5%) exact matches, in which:
37 unique CDR3
6 unique J



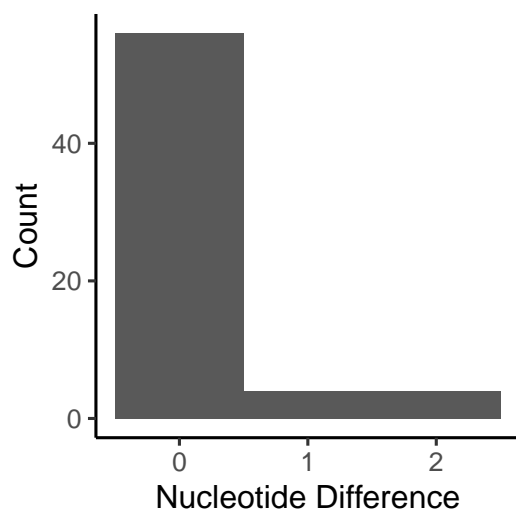
IGHV3-7*01

654 sequences assigned
498 (76.1%) exact matches, in which:
431 unique CDR3
6 unique J



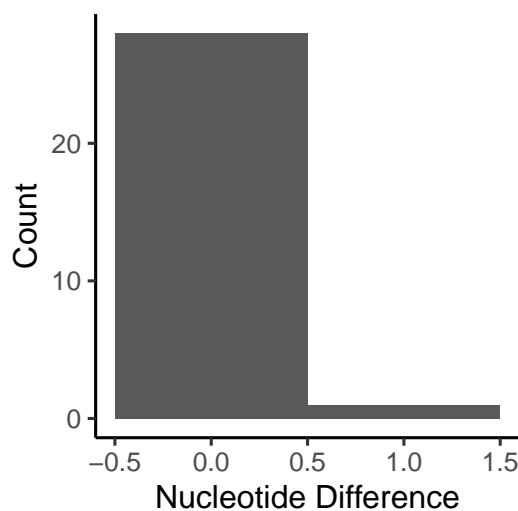
IGHV2-5*01

64 sequences assigned
56 (87.5%) exact matches, in which:
56 unique CDR3
6 unique J



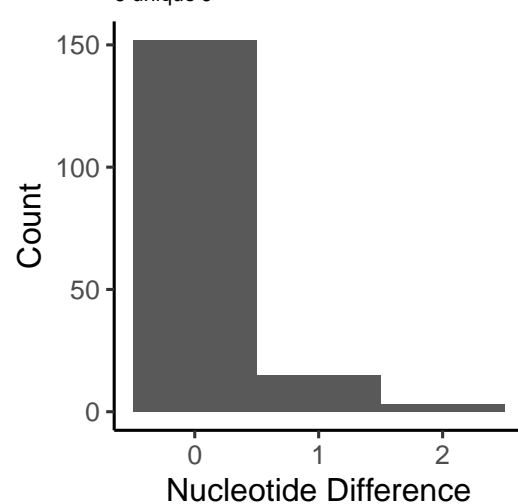
IGHV2-70*01

29 sequences assigned
28 (96.6%) exact matches, in which:
28 unique CDR3
5 unique J



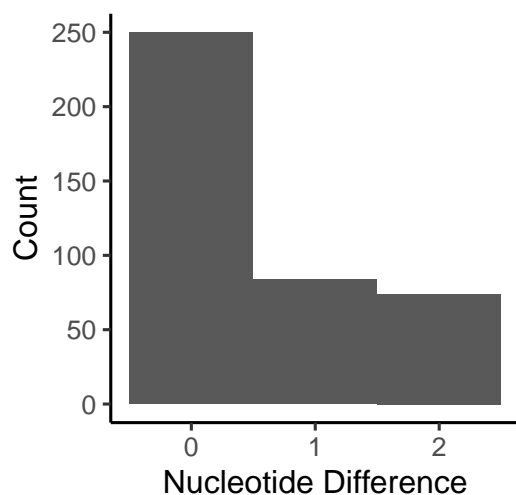
IGHV3-9*01

170 sequences assigned
152 (89.4%) exact matches, in which:
144 unique CDR3
6 unique J



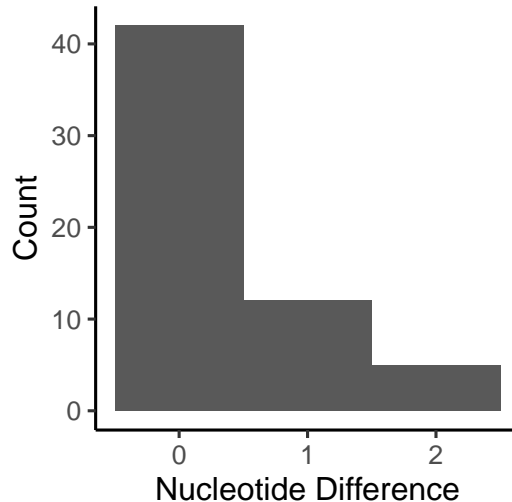
IGHV2-5*02

408 sequences assigned
250 (61.3%) exact matches, in which:
224 unique CDR3
6 unique J



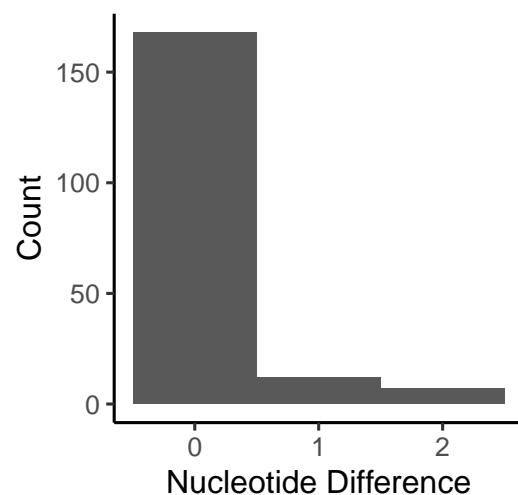
IGHV2-70*11_15

59 sequences assigned
42 (71.2%) exact matches, in which:
42 unique CDR3
5 unique J



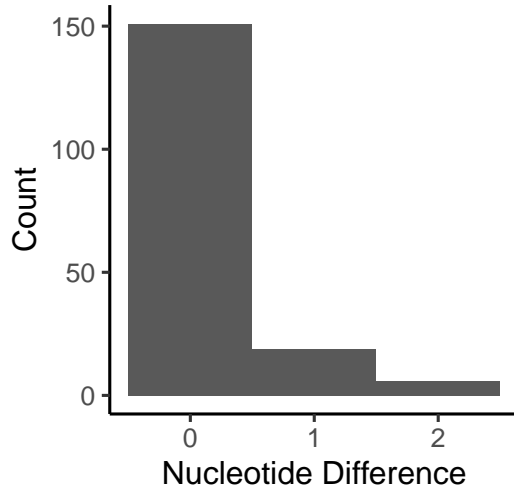
IGHV3-11*01

187 sequences assigned
168 (89.8%) exact matches, in which:
154 unique CDR3
6 unique J



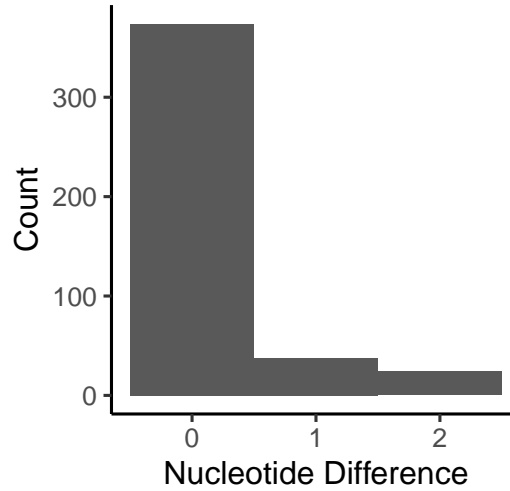
IGHV3-11*06

176 sequences assigned
151 (85.8%) exact matches, in which:
137 unique CDR3
6 unique J



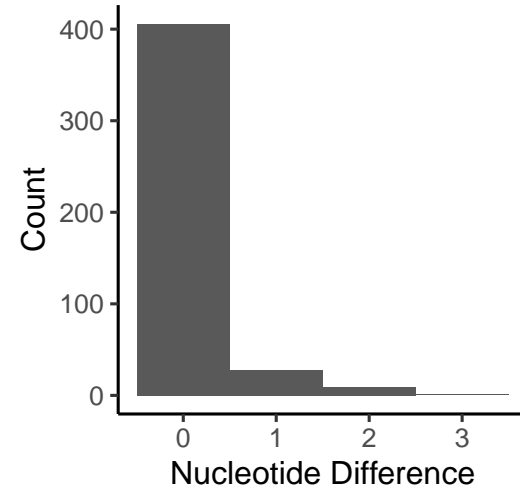
IGHV3-15*01_02

436 sequences assigned
374 (85.8%) exact matches, in which:
317 unique CDR3
6 unique J



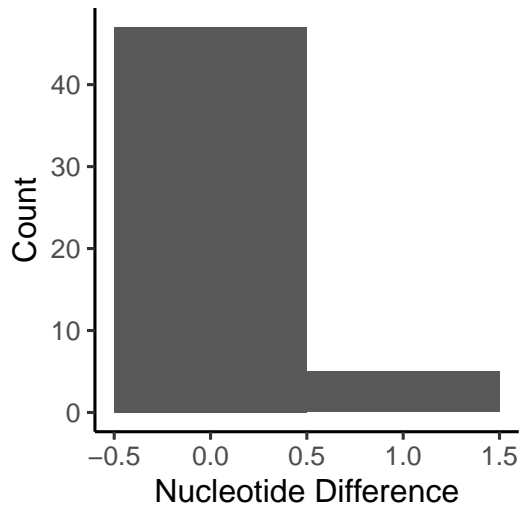
IGHV3-30-3*01

444 sequences assigned
406 (91.4%) exact matches, in which:
390 unique CDR3
6 unique J



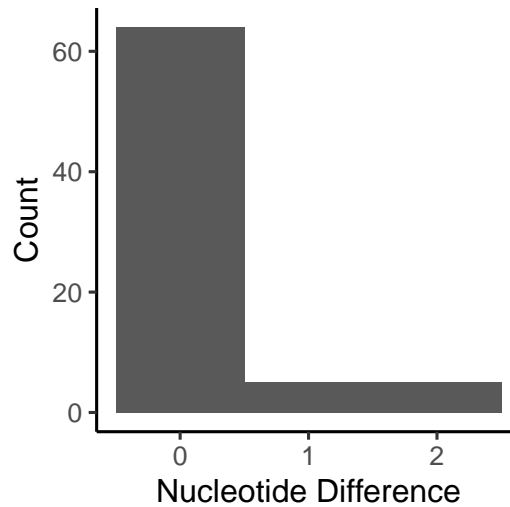
IGHV3-13*01

52 sequences assigned
47 (90.4%) exact matches, in which:
43 unique CDR3
5 unique J



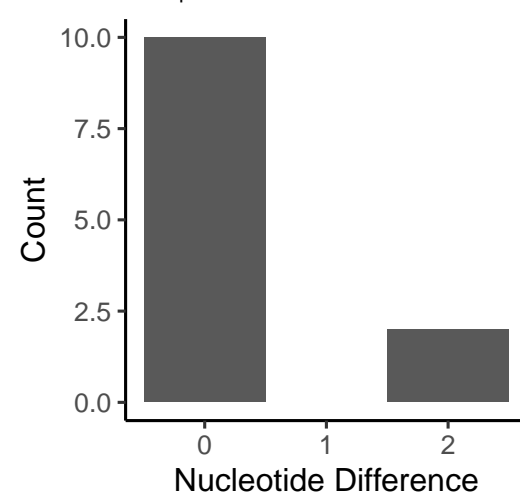
IGHV3-20*01_02

74 sequences assigned
64 (86.5%) exact matches, in which:
61 unique CDR3
5 unique J



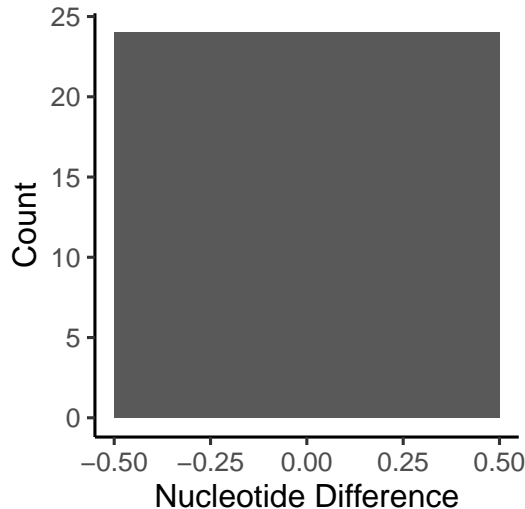
IGHV3-30*03

12 sequences assigned
10 (83.3%) exact matches, in which:
9 unique CDR3
3 unique J



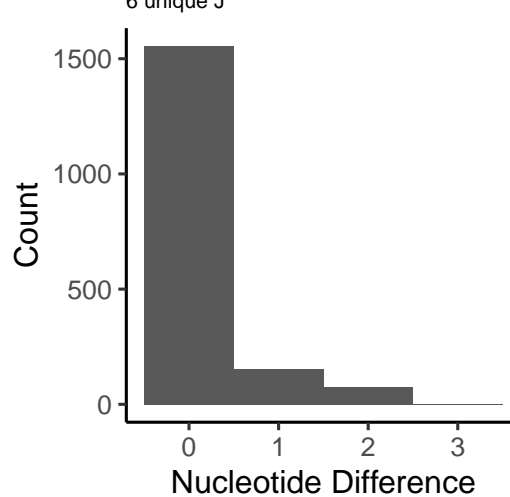
IGHV3-13*05

24 sequences assigned
24 (100%) exact matches, in which:
24 unique CDR3
5 unique J



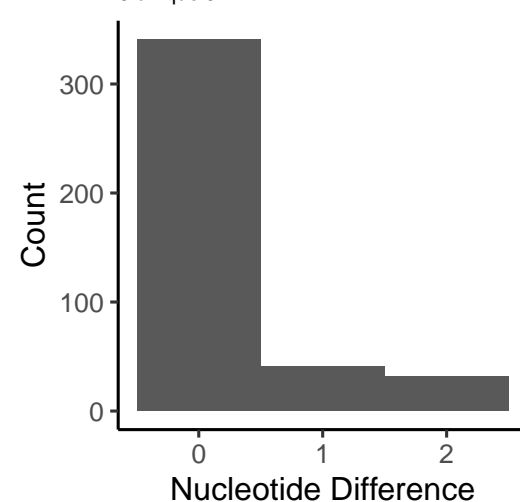
IGHV3-21*01_02

1784 sequences assigned
1555 (87.2%) exact matches, in which:
1279 unique CDR3
6 unique J



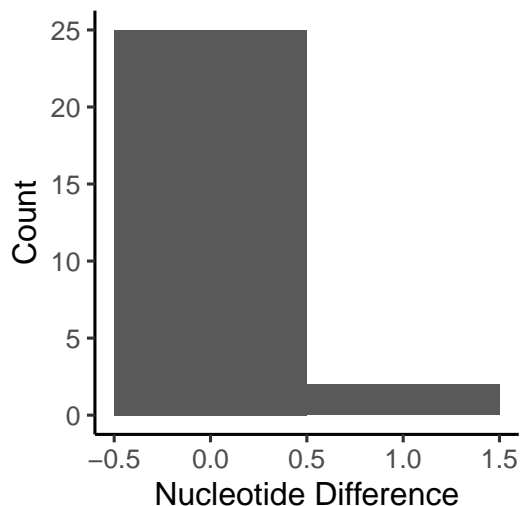
IGHV3-33*01

414 sequences assigned
341 (82.4%) exact matches, in which:
309 unique CDR3
6 unique J



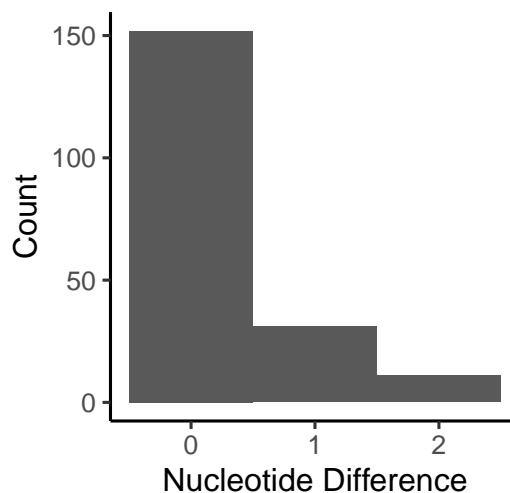
IGHV3-43*01

27 sequences assigned
25 (92.6%) exact matches, in which:
24 unique CDR3
5 unique J



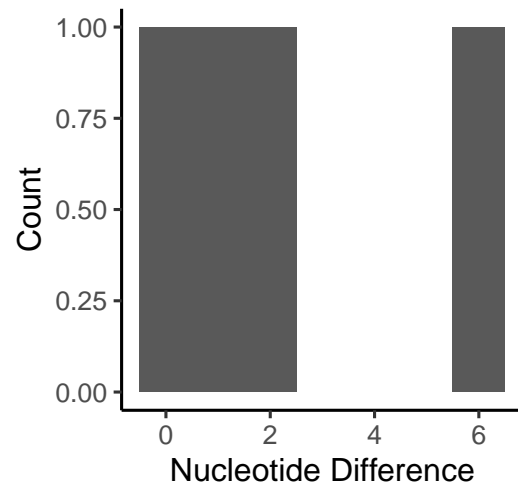
IGHV3-48*03

194 sequences assigned
152 (78.4%) exact matches, in which:
141 unique CDR3
6 unique J



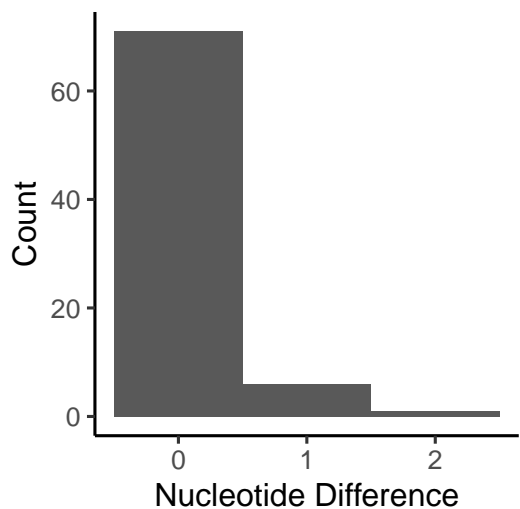
IGHV3-52*01_03

4 sequences assigned
1 (25%) exact matches, in which:
1 unique CDR3
1 unique J



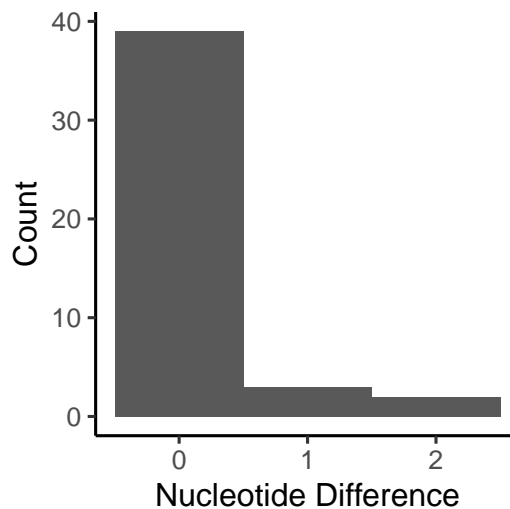
IGHV3-43*02

78 sequences assigned
71 (91%) exact matches, in which:
69 unique CDR3
4 unique J



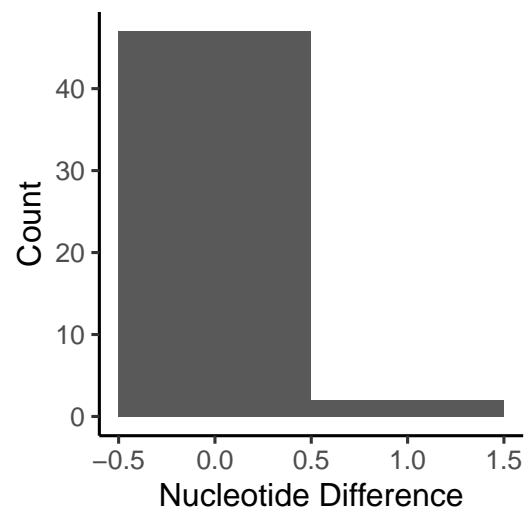
IGHV3-49*04

44 sequences assigned
39 (88.6%) exact matches, in which:
37 unique CDR3
4 unique J



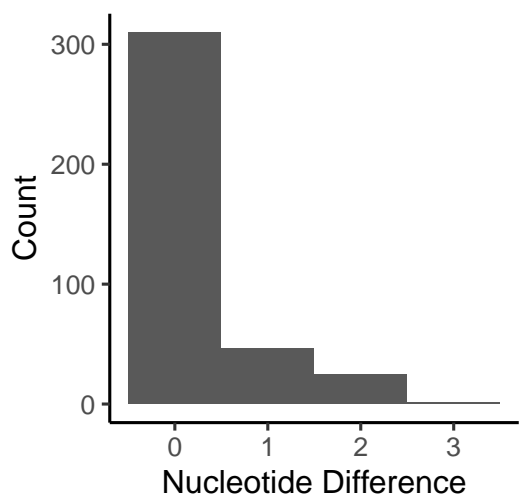
IGHV3-53*04

49 sequences assigned
47 (95.9%) exact matches, in which:
46 unique CDR3
5 unique J



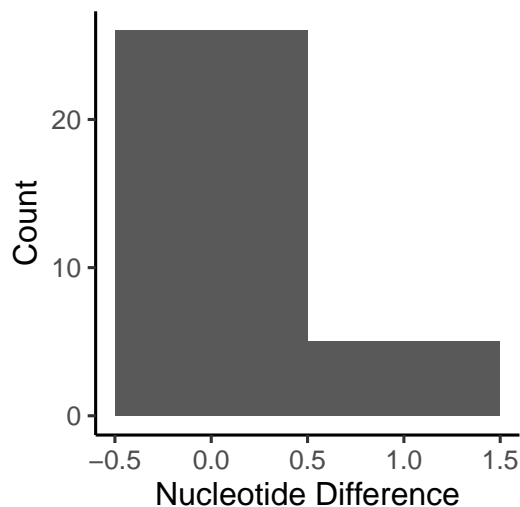
IGHV3-48*02

382 sequences assigned
310 (81.2%) exact matches, in which:
264 unique CDR3
6 unique J



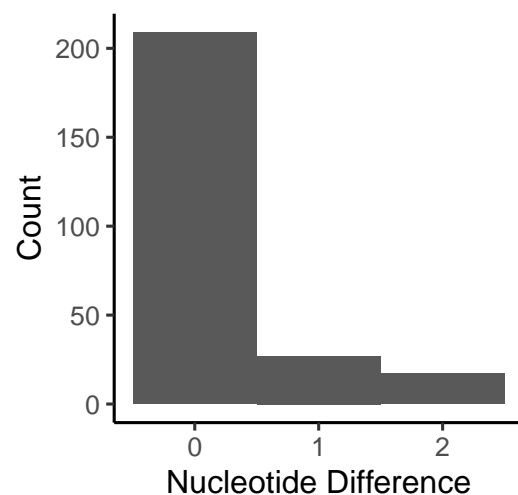
IGHV3-49*03_05

31 sequences assigned
26 (83.9%) exact matches, in which:
25 unique CDR3
5 unique J



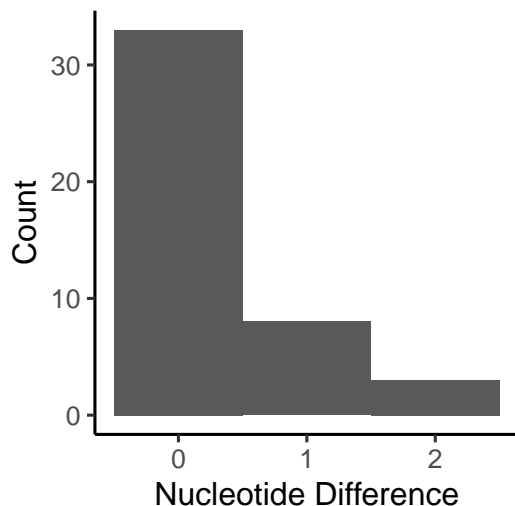
IGHV3-53*01_02

253 sequences assigned
209 (82.6%) exact matches, in which:
188 unique CDR3
6 unique J



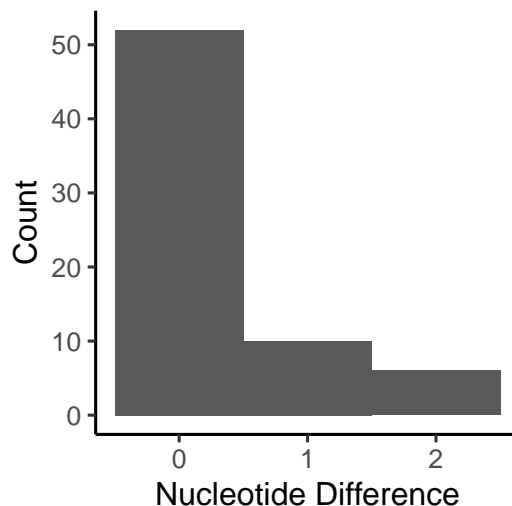
IGHV3-64*01

44 sequences assigned
33 (75%) exact matches, in which:
31 unique CDR3
5 unique J



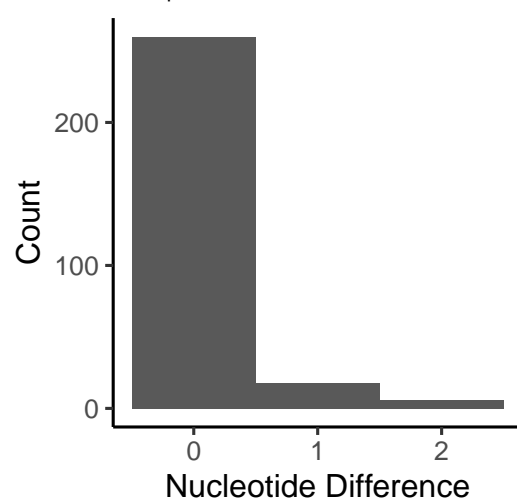
IGHV3-73*01_02

68 sequences assigned
52 (76.5%) exact matches, in which:
38 unique CDR3
4 unique J



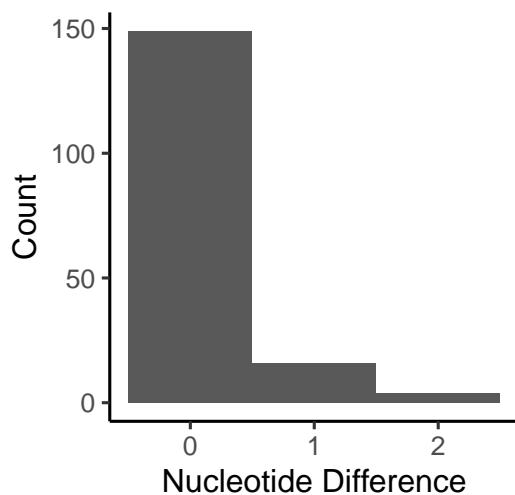
IGHV4-4*07

284 sequences assigned
260 (91.5%) exact matches, in which:
253 unique CDR3
6 unique J



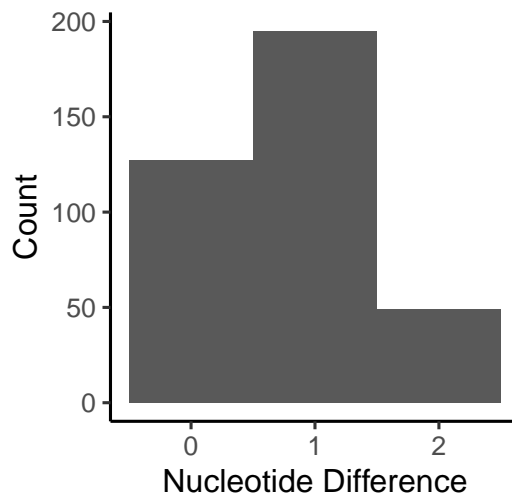
IGHV3-66*01

169 sequences assigned
149 (88.2%) exact matches, in which:
137 unique CDR3
5 unique J



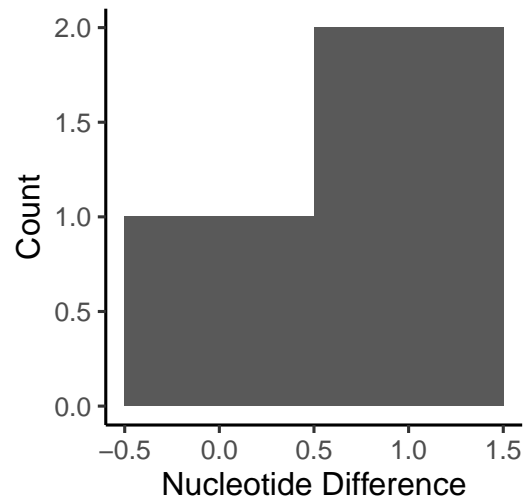
IGHV3-74*01_02

371 sequences assigned
127 (34.2%) exact matches, in which:
107 unique CDR3
6 unique J



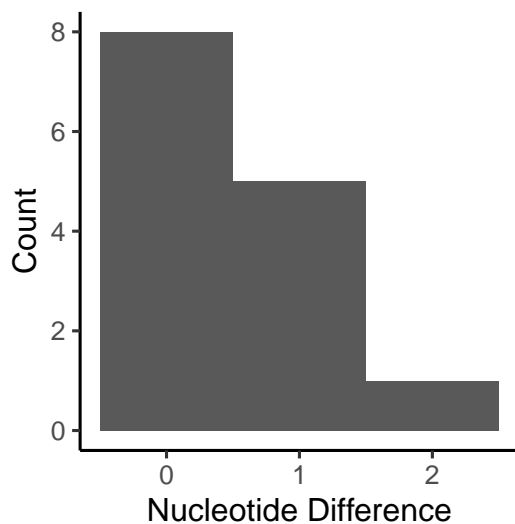
IGHV4-28*01_07

3 sequences assigned
1 (33.3%) exact matches, in which:
1 unique CDR3
1 unique J



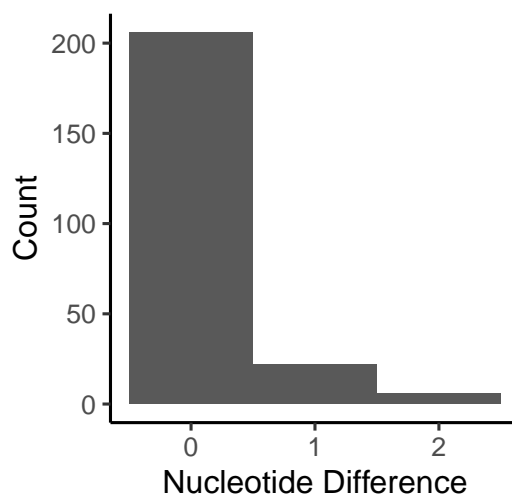
IGHV3-72*01

14 sequences assigned
8 (57.1%) exact matches, in which:
7 unique CDR3
3 unique J



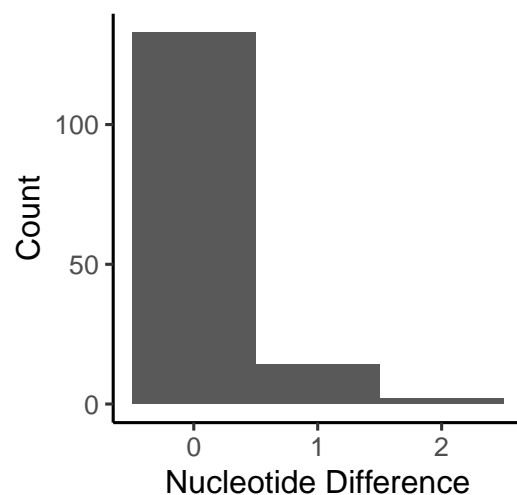
IGHV3-64D*06

234 sequences assigned
206 (88%) exact matches, in which:
199 unique CDR3
6 unique J



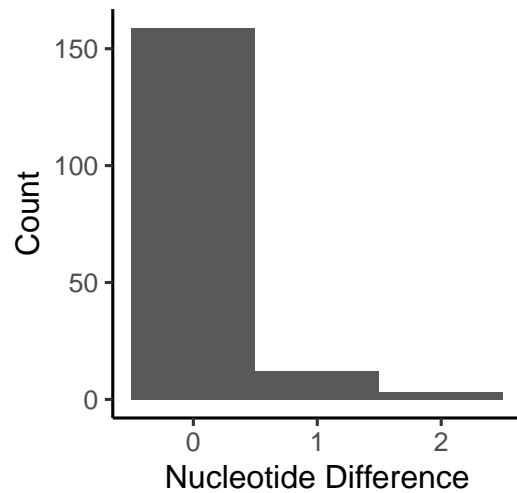
IGHV4-30-2*01

149 sequences assigned
133 (89.3%) exact matches, in which:
132 unique CDR3
6 unique J



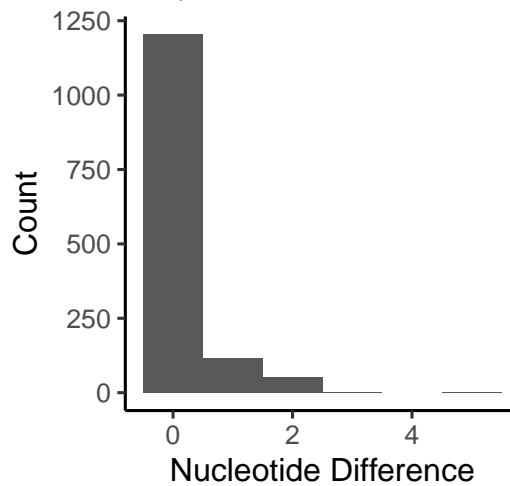
IGHV4-30-4*01

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



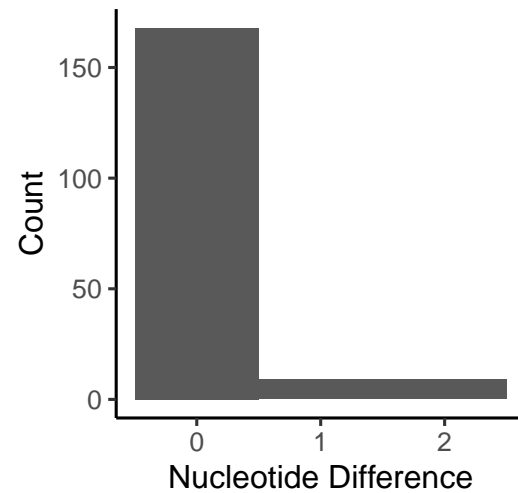
IGHV4-39*01_05

1375 sequences assigned
1204 (87.6%) exact matches, in which:
1134 unique CDR3
6 unique J



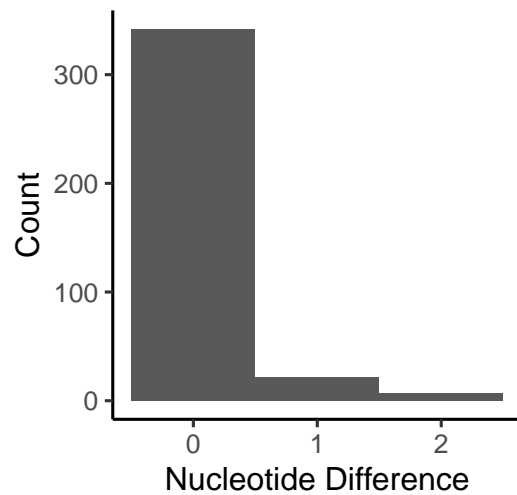
IGHV4-61*01

186 sequences assigned
168 (90.3%) exact matches, in which:
160 unique CDR3
6 unique J



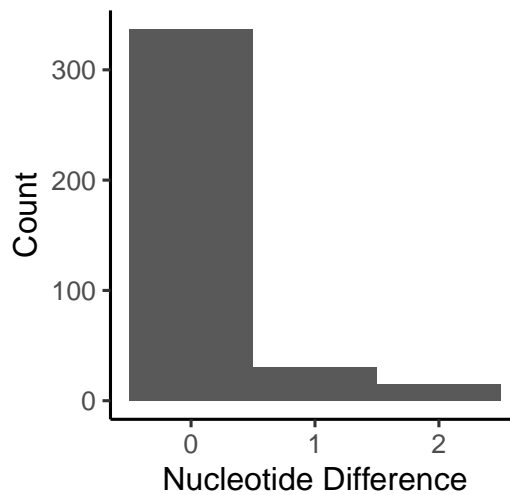
IGHV4-31*03_04

371 sequences assigned
342 (92.2%) exact matches, in which:
332 unique CDR3
6 unique J



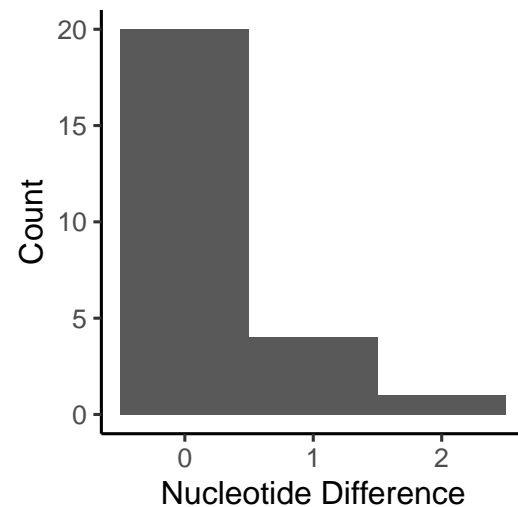
IGHV4-59*08

382 sequences assigned
337 (88.2%) exact matches, in which:
331 unique CDR3
6 unique J



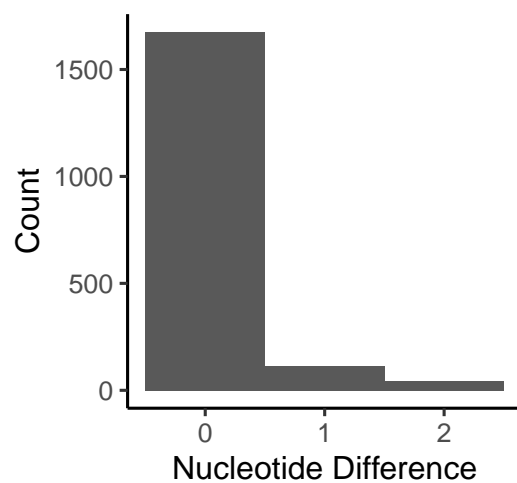
IGHV5-10-1*01_03

25 sequences assigned
20 (80%) exact matches, in which:
20 unique CDR3
4 unique J



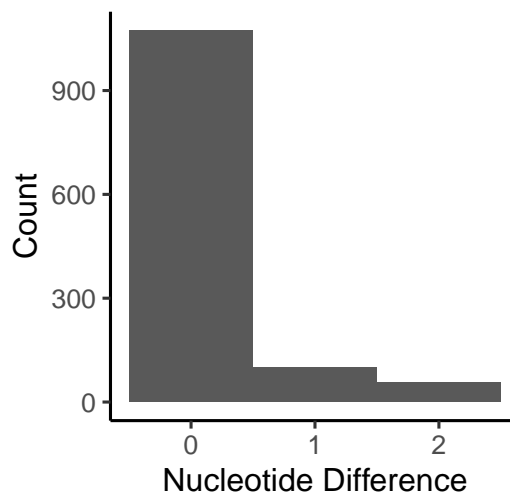
IGHV4-34*01_02

1831 sequences assigned
1675 (91.5%) exact matches, in which:
1650 unique CDR3
6 unique J



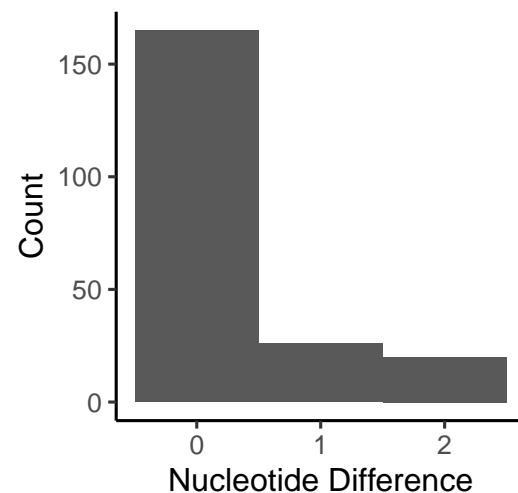
IGHV4-59*01_07

1232 sequences assigned
1074 (87.2%) exact matches, in which:
1042 unique CDR3
6 unique J



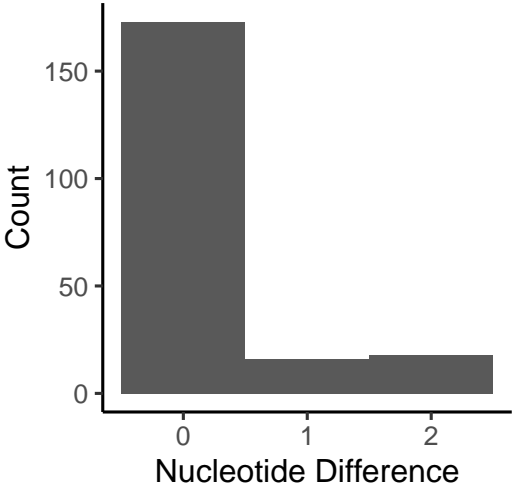
IGHV5-51*01_03

211 sequences assigned
165 (78.2%) exact matches, in which:
163 unique CDR3
6 unique J



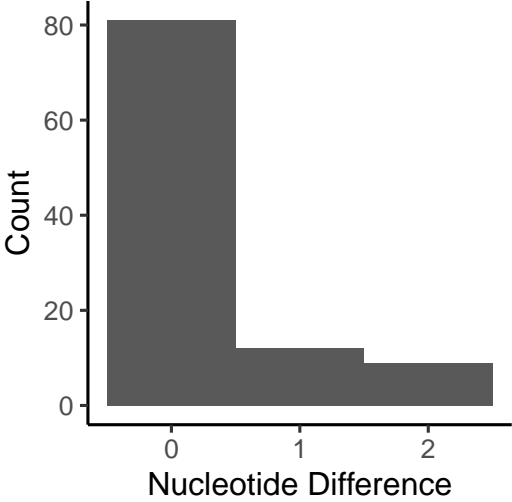
IGHV6-1*01_02

207 sequences assigned
173 (83.6%) exact matches, in which:
172 unique CDR3
6 unique J



IGHV7-4-1*02

102 sequences assigned
81 (79.4%) exact matches, in which:
80 unique CDR3
5 unique J



Allele Usage



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_G88AIGHV5–51*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_G88AIGHV5–51*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)IGHV4–39*02_C258GIGHV5–51*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.

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_G88AIGHV5–51*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_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.