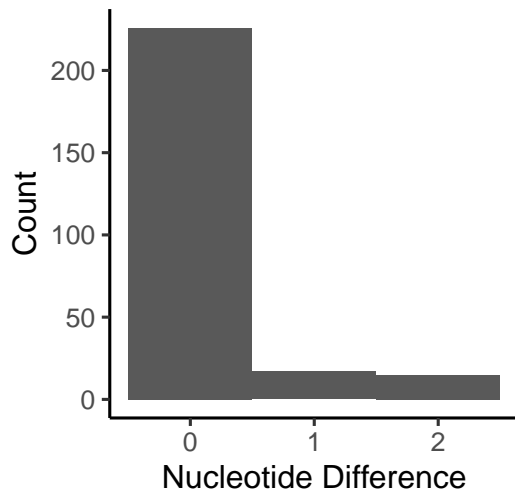


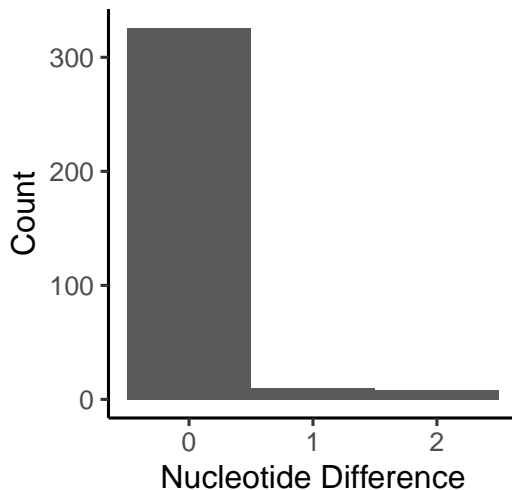
IGHV1-2*04

258 sequences assigned
226 (87.6%) exact matches, in which:
226 unique CDR3
5 unique J



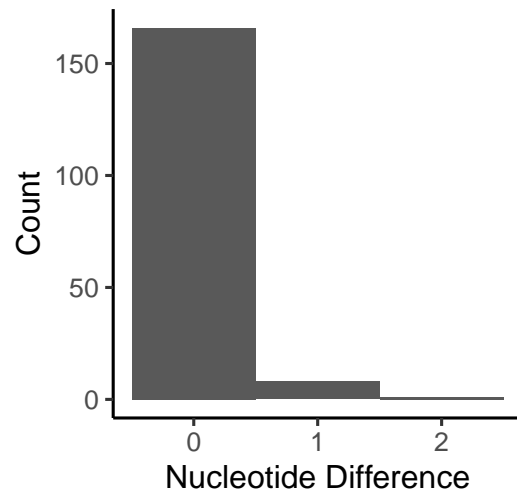
IGHV1-18*01

344 sequences assigned
326 (94.8%) exact matches, in which:
325 unique CDR3
6 unique J



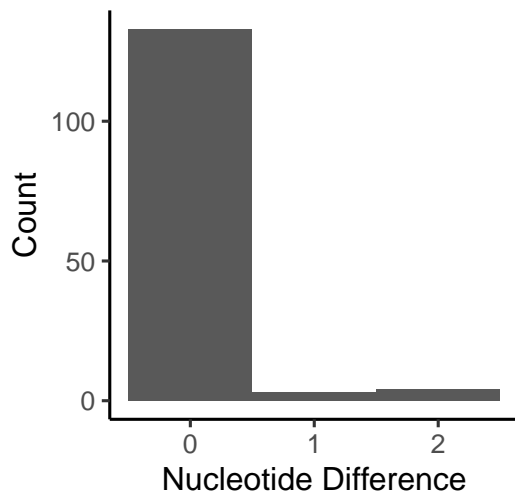
IGHV1-46*01

175 sequences assigned
166 (94.9%) exact matches, in which:
166 unique CDR3
5 unique J



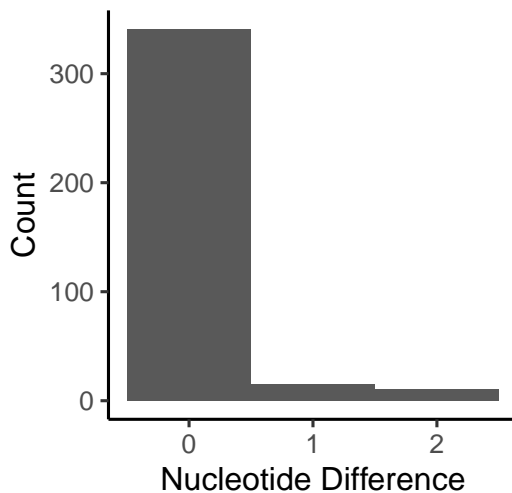
IGHV1-3*01_05

140 sequences assigned
133 (95%) exact matches, in which:
133 unique CDR3
6 unique J



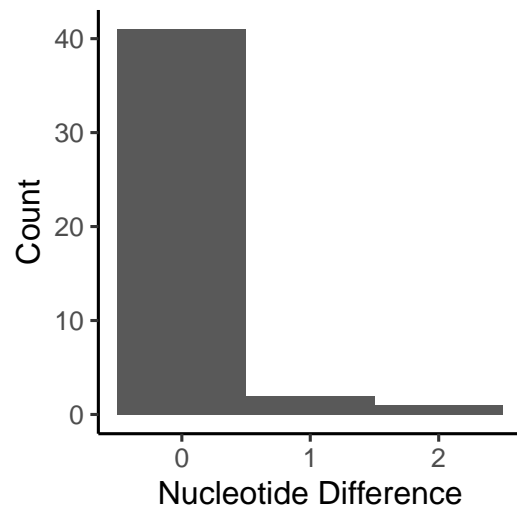
IGHV1-18*04

367 sequences assigned
341 (92.9%) exact matches, in which:
340 unique CDR3
6 unique J



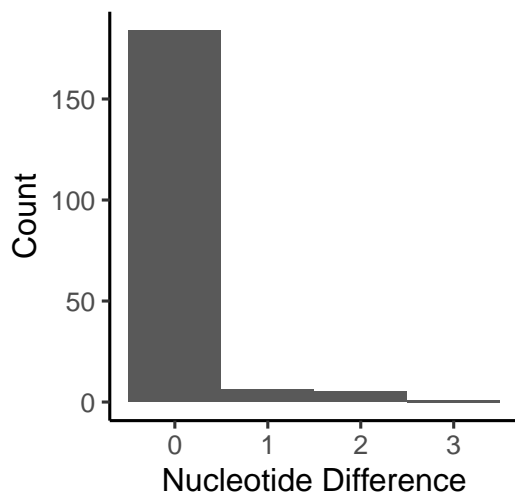
IGHV1-58*01_03

44 sequences assigned
41 (93.2%) exact matches, in which:
41 unique CDR3
4 unique J



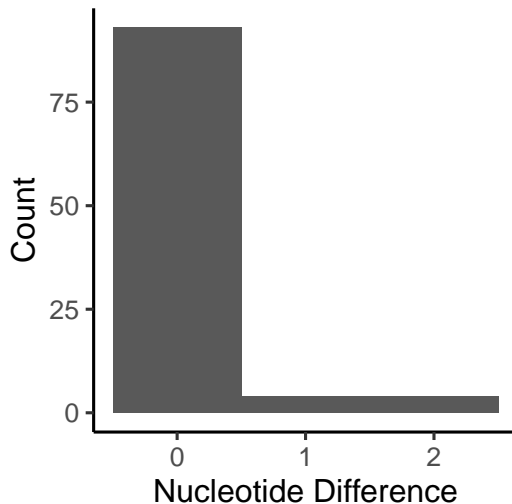
IGHV1-8*01

196 sequences assigned
184 (93.9%) exact matches, in which:
184 unique CDR3
6 unique J



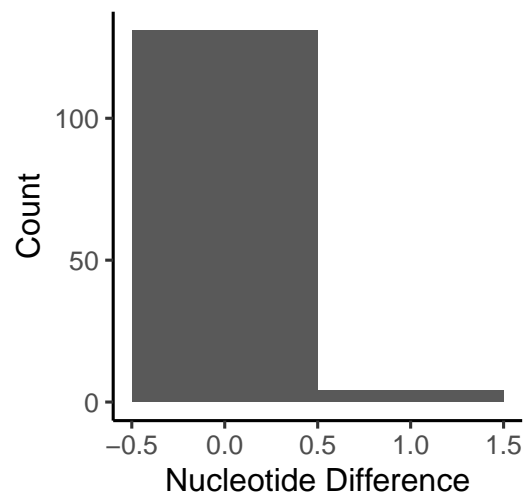
IGHV1-24*01

101 sequences assigned
93 (92.1%) exact matches, in which:
93 unique CDR3
6 unique J



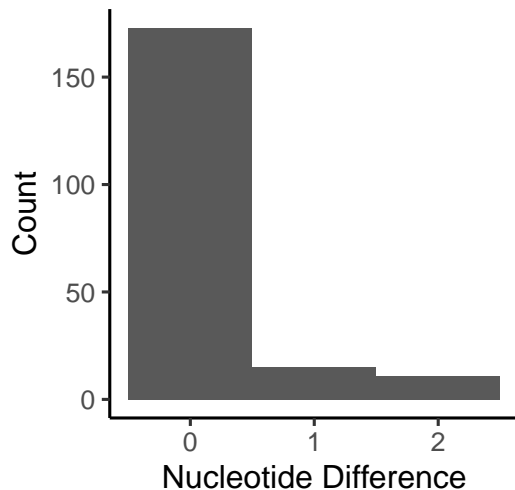
IGHV1-69*06_14

135 sequences assigned
131 (97%) exact matches, in which:
131 unique CDR3
5 unique J



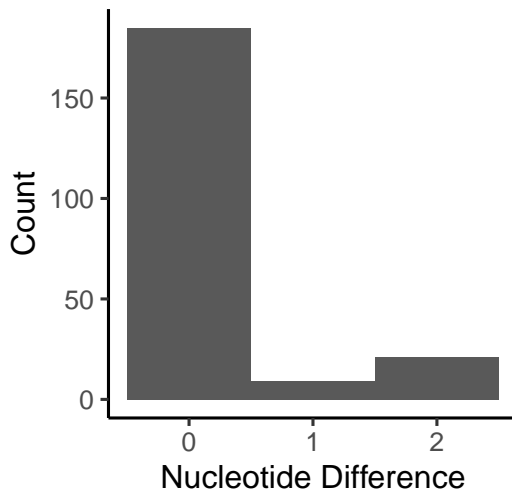
IGHV2-5*02

199 sequences assigned
173 (86.9%) exact matches, in which:
173 unique CDR3
6 unique J



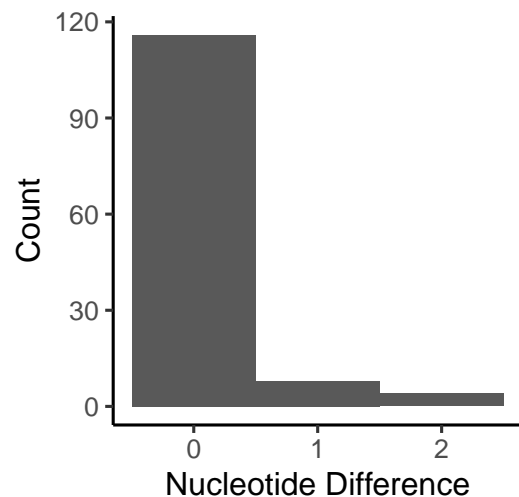
IGHV3-7*01

215 sequences assigned
185 (86%) exact matches, in which:
185 unique CDR3
6 unique J



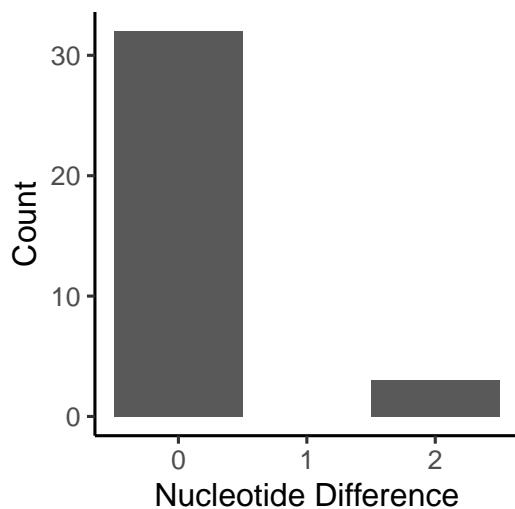
IGHV3-11*01

128 sequences assigned
116 (90.6%) exact matches, in which:
115 unique CDR3
5 unique J



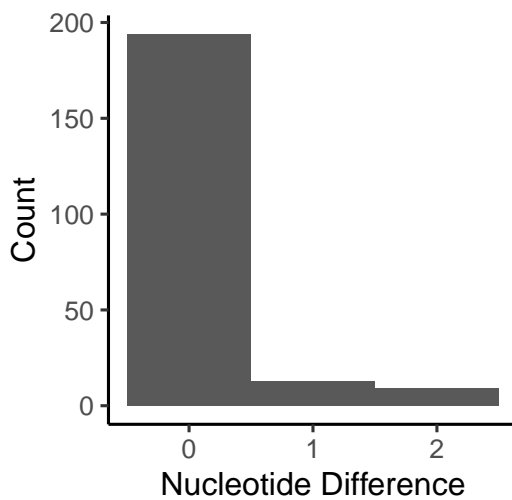
IGHV2-26*01

35 sequences assigned
32 (91.4%) exact matches, in which:
32 unique CDR3
5 unique J



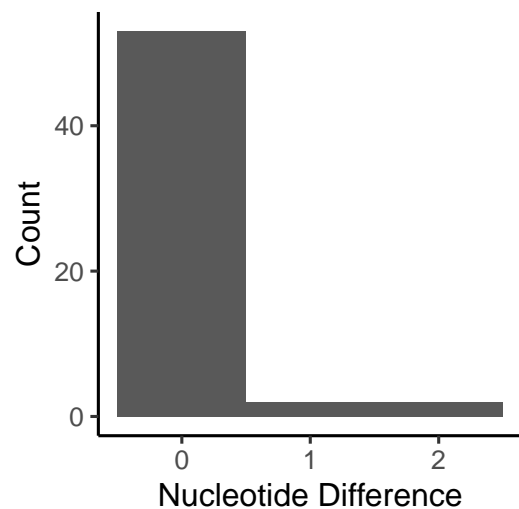
IGHV3-7*03

216 sequences assigned
194 (89.8%) exact matches, in which:
194 unique CDR3
5 unique J



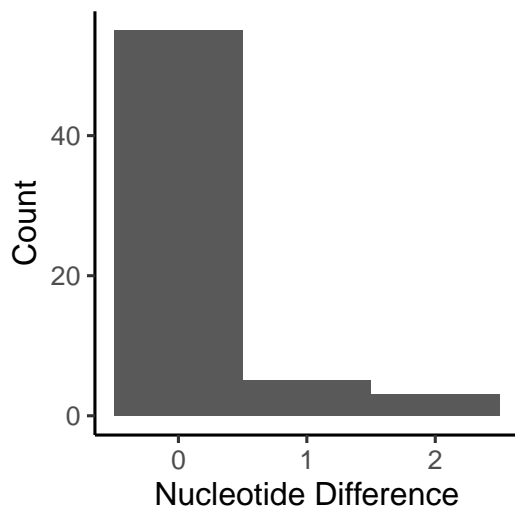
IGHV3-11*06

57 sequences assigned
53 (93%) exact matches, in which:
53 unique CDR3
4 unique J



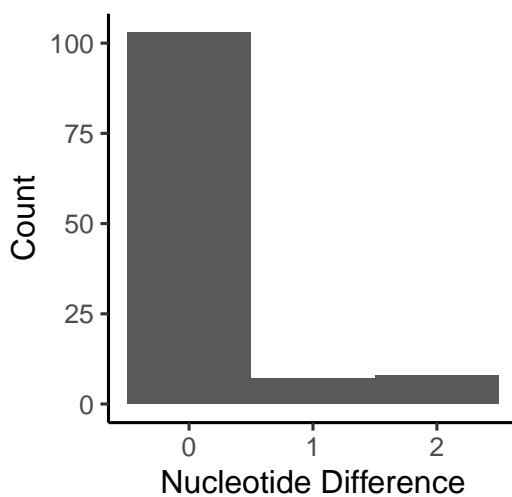
IGHV2-70*01

63 sequences assigned
55 (87.3%) exact matches, in which:
55 unique CDR3
5 unique J



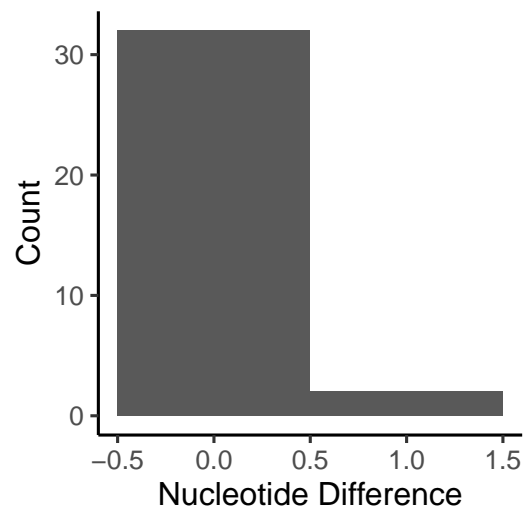
IGHV3-9*01

118 sequences assigned
103 (87.3%) exact matches, in which:
103 unique CDR3
5 unique J



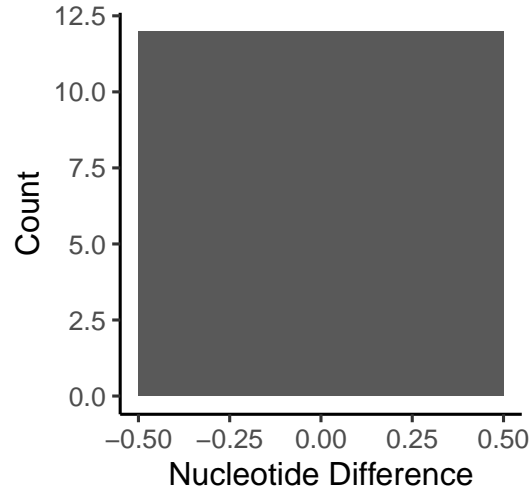
IGHV3-13*01

34 sequences assigned
32 (94.1%) exact matches, in which:
32 unique CDR3
5 unique J



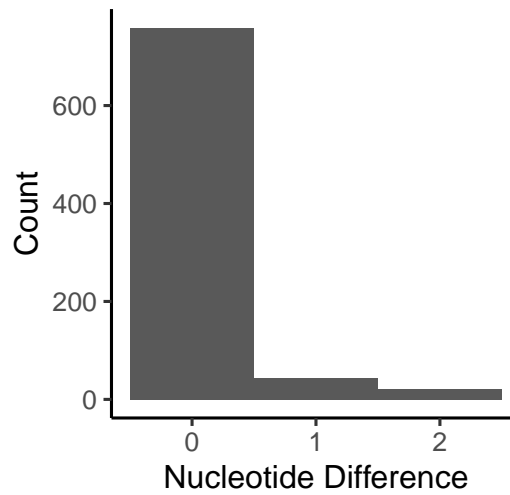
IGHV3-13*05

12 sequences assigned
12 (100%) exact matches, in which:
12 unique CDR3
4 unique J



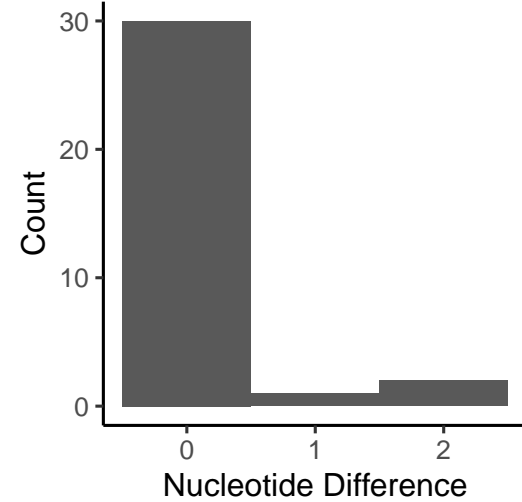
IGHV3-21*01_02

824 sequences assigned
759 (92.1%) exact matches, in which:
755 unique CDR3
6 unique J



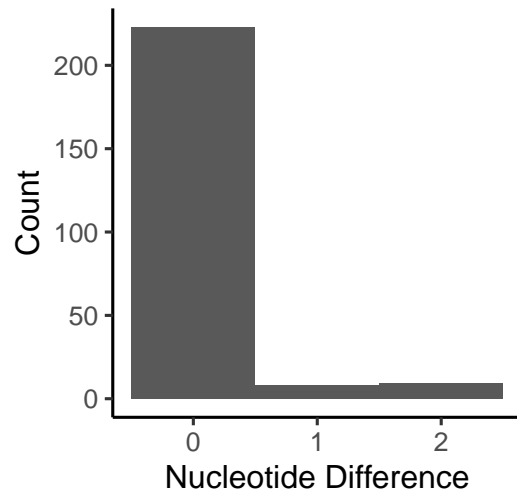
IGHV3-43*01

33 sequences assigned
30 (90.9%) exact matches, in which:
30 unique CDR3
4 unique J



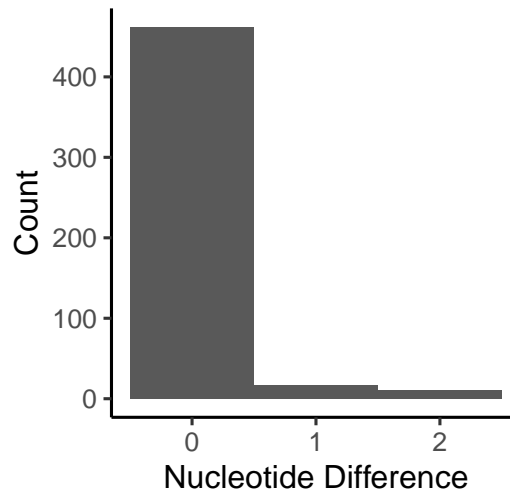
IGHV3-15*01_02

240 sequences assigned
223 (92.9%) exact matches, in which:
223 unique CDR3
6 unique J



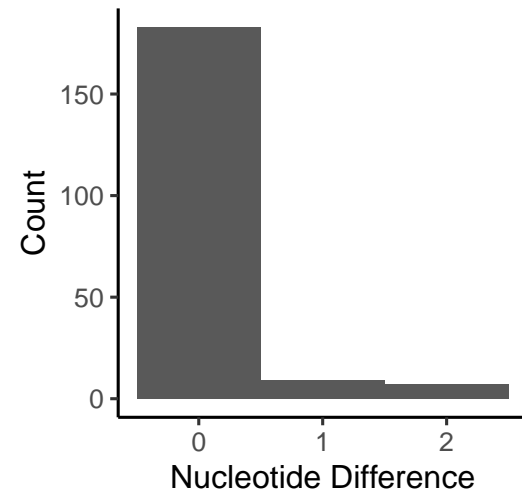
IGHV3-30-3*01

490 sequences assigned
462 (94.3%) exact matches, in which:
462 unique CDR3
6 unique J



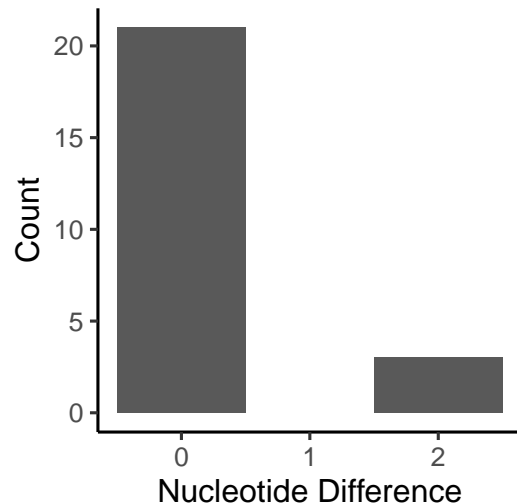
IGHV3-48*02

199 sequences assigned
183 (92%) exact matches, in which:
182 unique CDR3
6 unique J



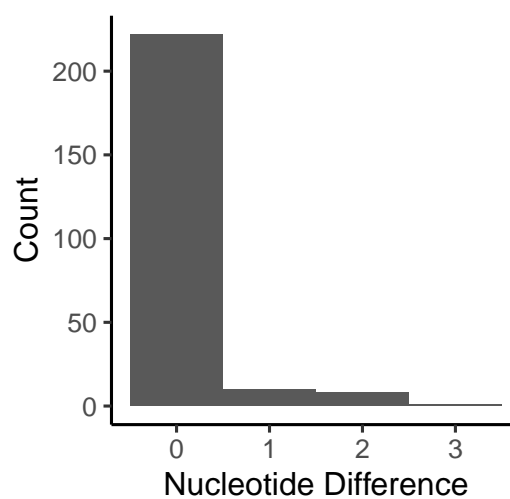
IGHV3-20*01_02

24 sequences assigned
21 (87.5%) exact matches, in which:
21 unique CDR3
5 unique J



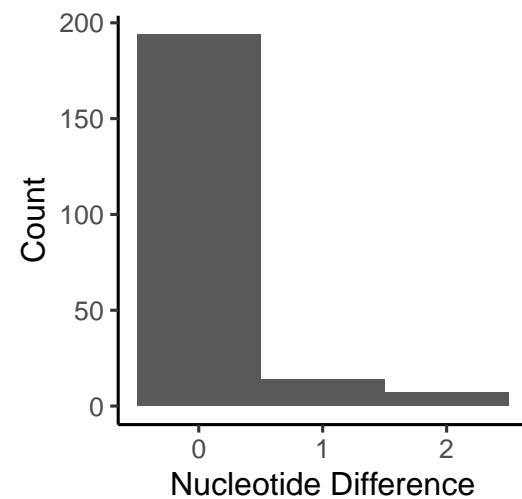
IGHV3-33*01

241 sequences assigned
222 (92.1%) exact matches, in which:
222 unique CDR3
6 unique J



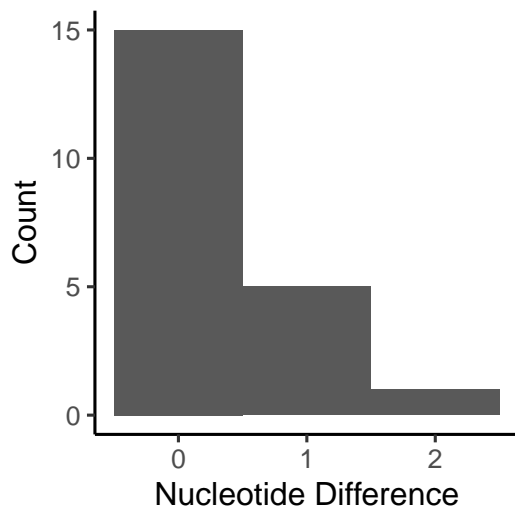
IGHV3-48*03

215 sequences assigned
194 (90.2%) exact matches, in which:
192 unique CDR3
6 unique J



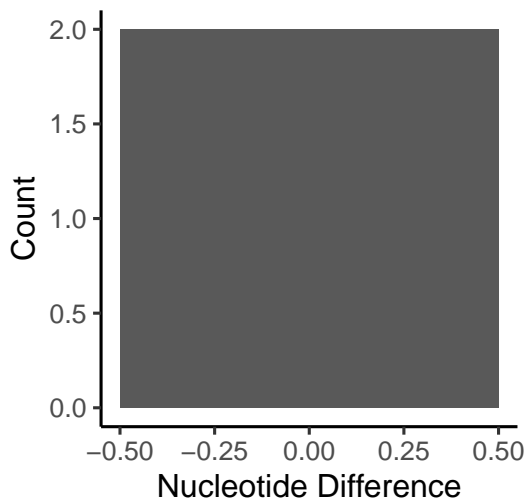
IGHV3-49*04

21 sequences assigned
15 (71.4%) exact matches, in which:
15 unique CDR3
4 unique J



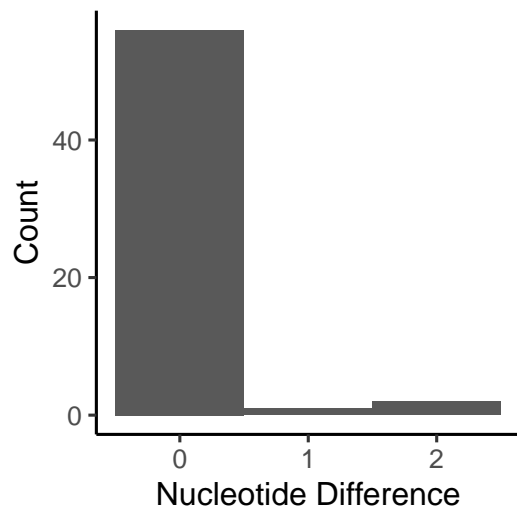
IGHV3-64*02_07

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



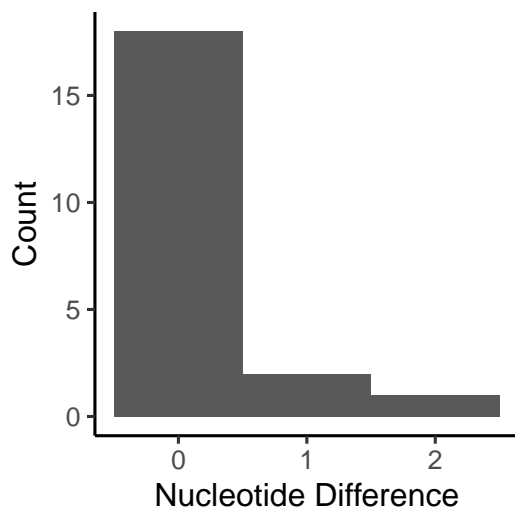
IGHV3-73*01_02

59 sequences assigned
56 (94.9%) exact matches, in which:
56 unique CDR3
5 unique J



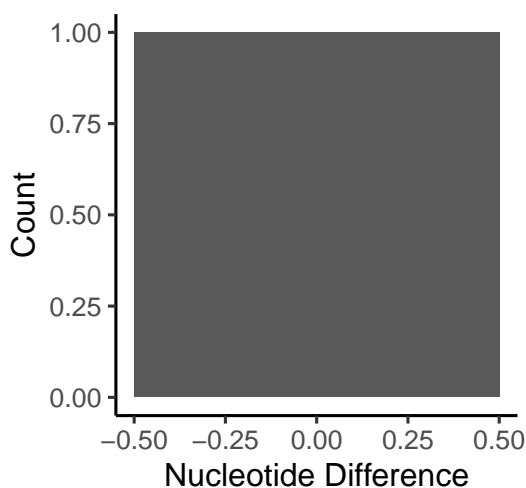
IGHV3-49*03_05

21 sequences assigned
18 (85.7%) exact matches, in which:
18 unique CDR3
4 unique J



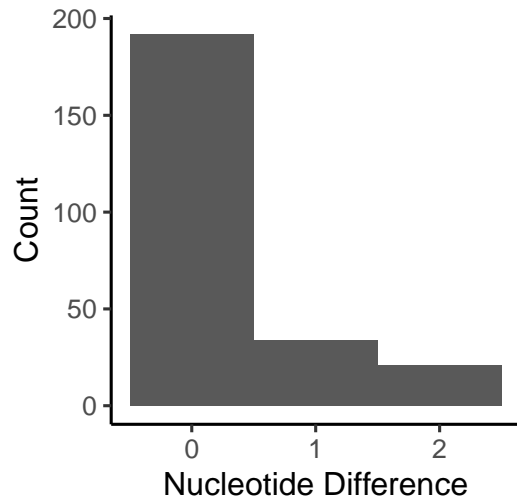
IGHV3-69-1*02

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



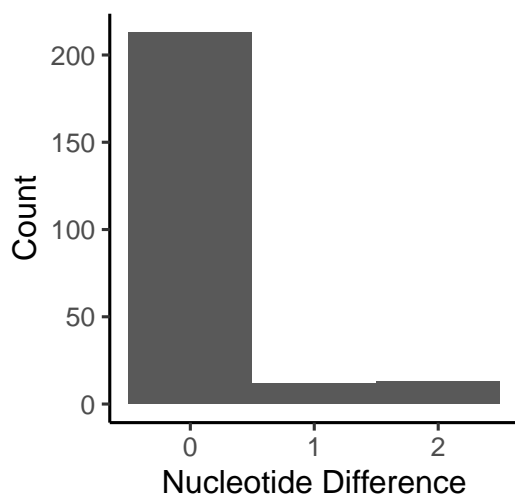
IGHV3-74*01_02

247 sequences assigned
192 (77.7%) exact matches, in which:
189 unique CDR3
6 unique J



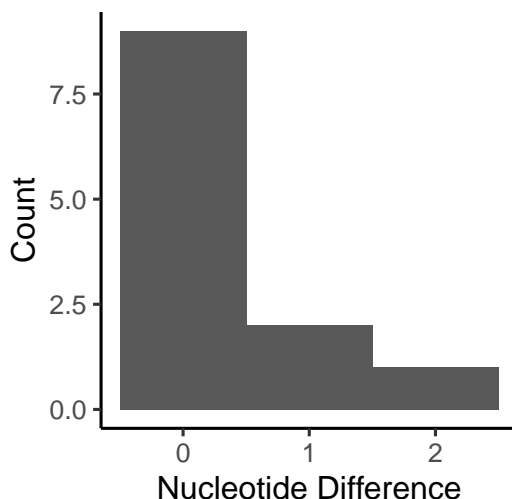
IGHV3-53*01_02

238 sequences assigned
213 (89.5%) exact matches, in which:
213 unique CDR3
6 unique J



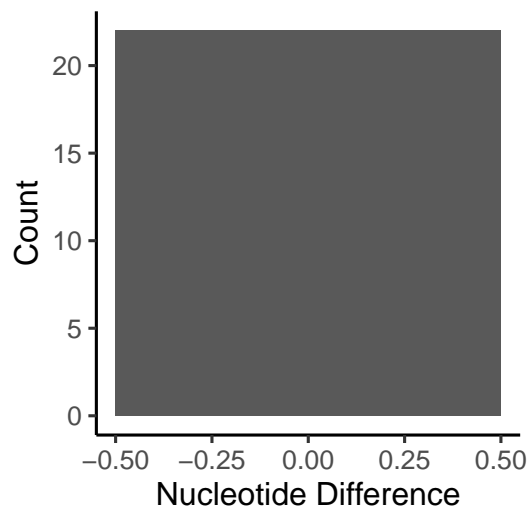
IGHV3-72*01

12 sequences assigned
9 (75%) exact matches, in which:
9 unique CDR3
3 unique J



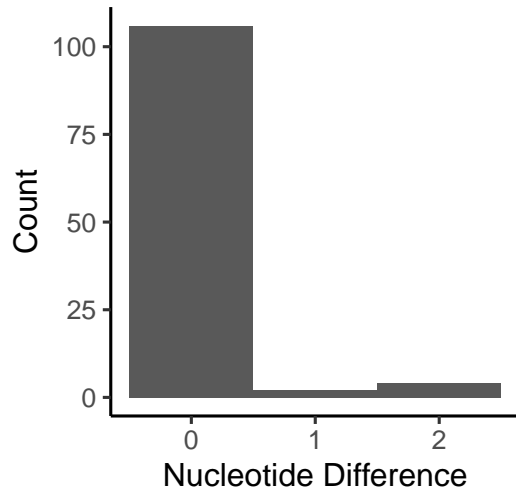
IGHV3-43D*04

22 sequences assigned
22 (100%) exact matches, in which:
22 unique CDR3
4 unique J



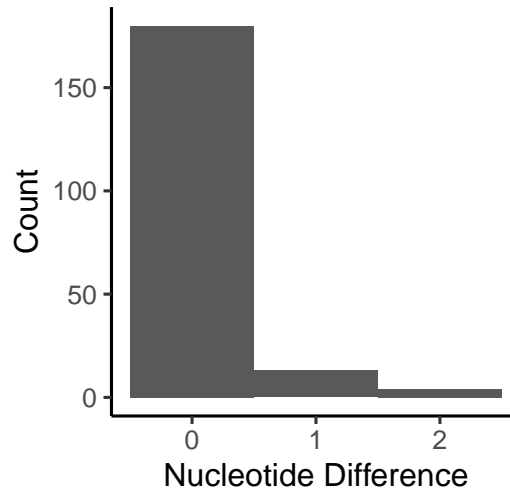
IGHV3–64D*06

112 sequences assigned
106 (94.6%) exact matches, in which:
106 unique CDR3
6 unique J



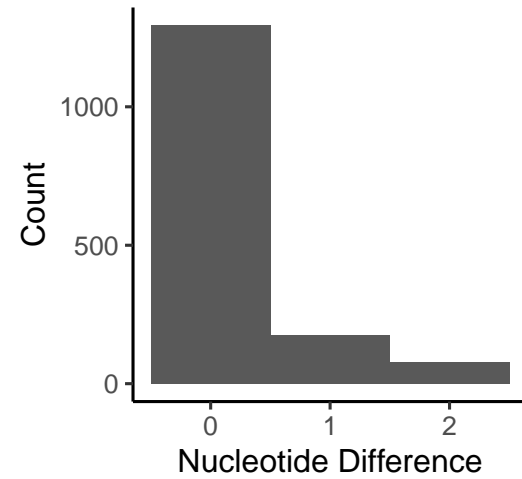
IGHV4–30–2*01

197 sequences assigned
180 (91.4%) exact matches, in which:
180 unique CDR3
6 unique J



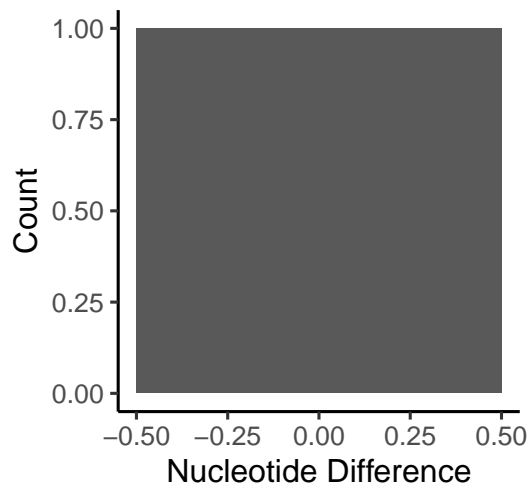
IGHV4–34*01_02

1546 sequences assigned
1294 (83.7%) exact matches, in which:
1285 unique CDR3
6 unique J



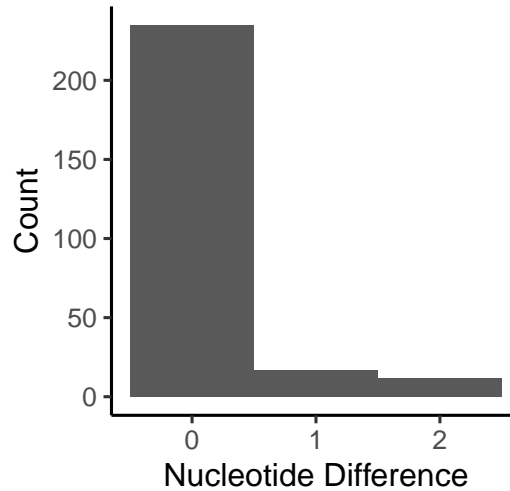
IGHV4–28*03

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



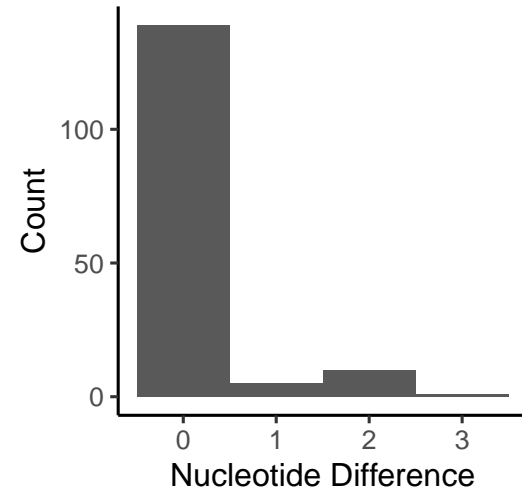
IGHV4–30–4*01

264 sequences assigned
235 (89%) exact matches, in which:
234 unique CDR3
5 unique J



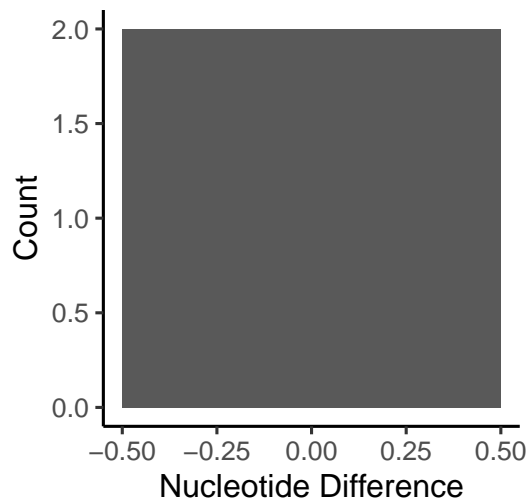
IGHV4–38–2*01

155 sequences assigned
139 (89.7%) exact matches, in which:
139 unique CDR3
5 unique J



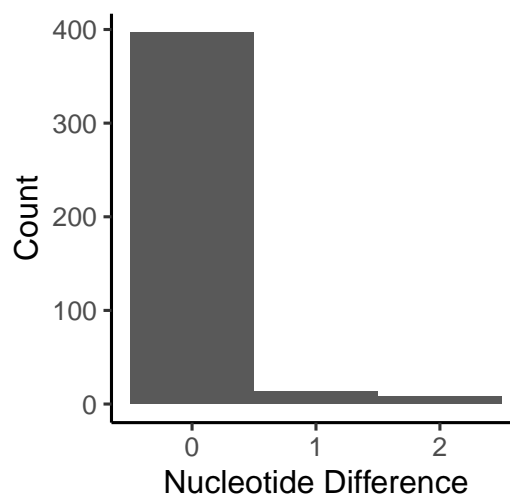
IGHV4–28*01_07

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



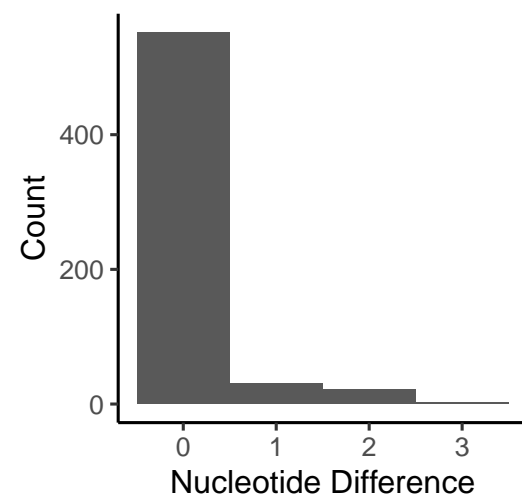
IGHV4–31*03_04

418 sequences assigned
397 (95%) exact matches, in which:
396 unique CDR3
6 unique J



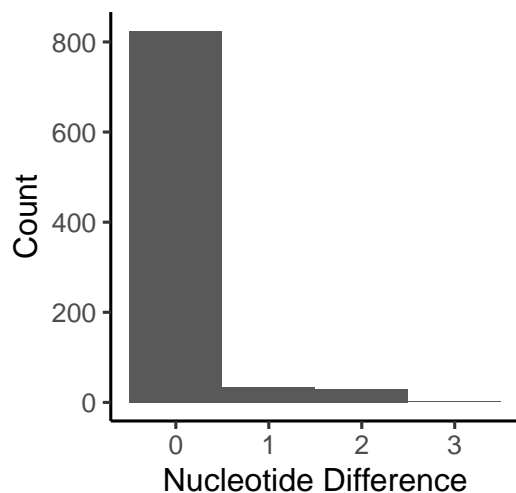
IGHV4–39*01_05

605 sequences assigned
552 (91.2%) exact matches, in which:
547 unique CDR3
6 unique J



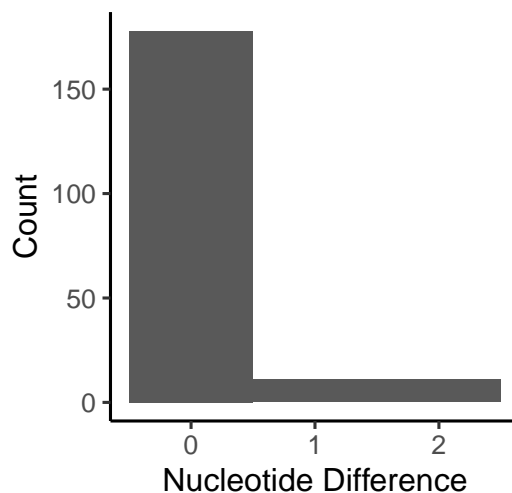
IGHV4–59*01_07

892 sequences assigned
825 (92.5%) exact matches, in which:
821 unique CDR3
6 unique J



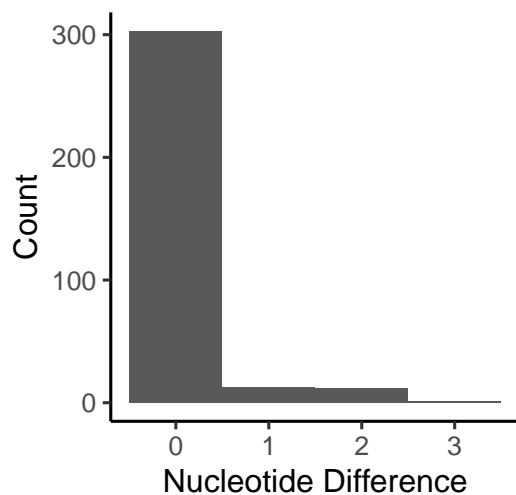
IGHV5–51*01_03

200 sequences assigned
178 (89%) exact matches, in which:
178 unique CDR3
6 unique J



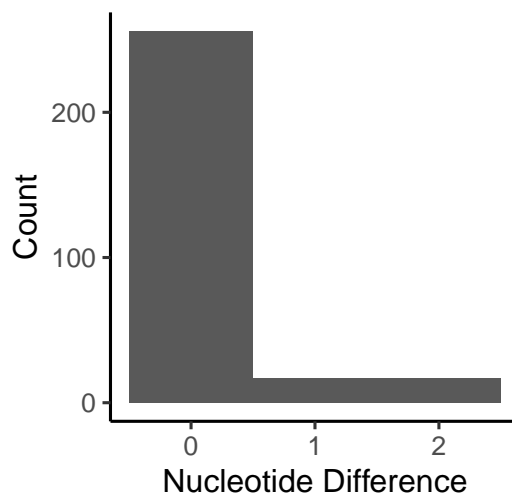
IGHV4–61*01

329 sequences assigned
303 (92.1%) exact matches, in which:
303 unique CDR3
6 unique J



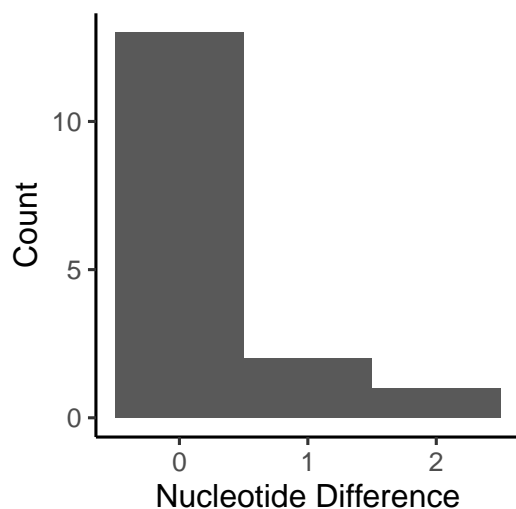
IGHV6–1*01_02

290 sequences assigned
256 (88.3%) exact matches, in which:
256 unique CDR3
6 unique J



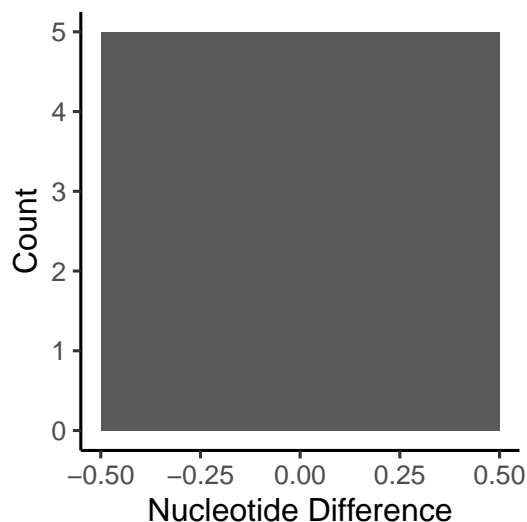
IGHV5–10–1*01_03

16 sequences assigned
13 (81.2%) exact matches, in which:
13 unique CDR3
4 unique J



IGHV7–4–1*01

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





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.

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.

Warning – no inferred sequences found.

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_G88AIGHV5-51*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)IGHV4-59*02_G88AIGHV5-51*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)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)IGHV3-11*06_T300C 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*11_C109T 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

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