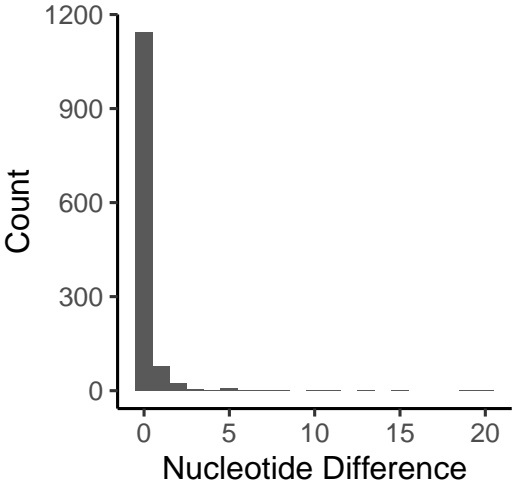


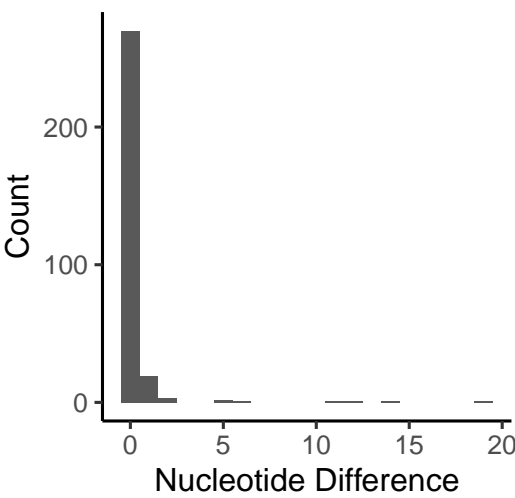
IGHV1-2*02

1277 sequences assigned
1143 (89.5%) exact matches, in which:
1130 unique CDR3
7 unique J



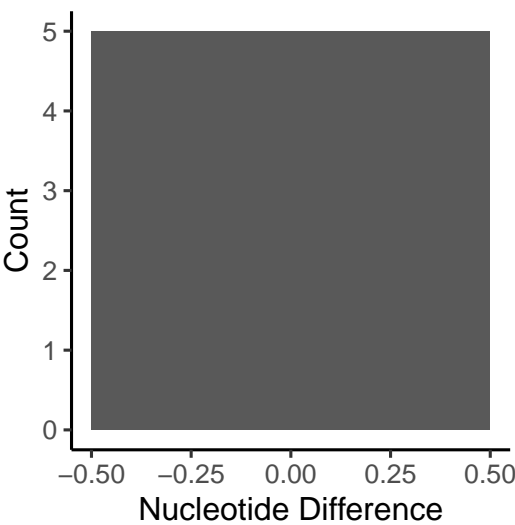
IGHV1-18*01

299 sequences assigned
270 (90.3%) exact matches, in which:
267 unique CDR3
6 unique J



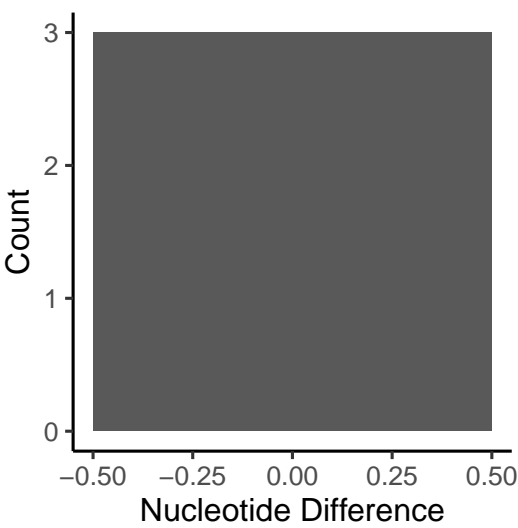
IGHV1-45*02

6 sequences assigned
5 (83.3%) exact matches, in which:
5 unique CDR3
3 unique J



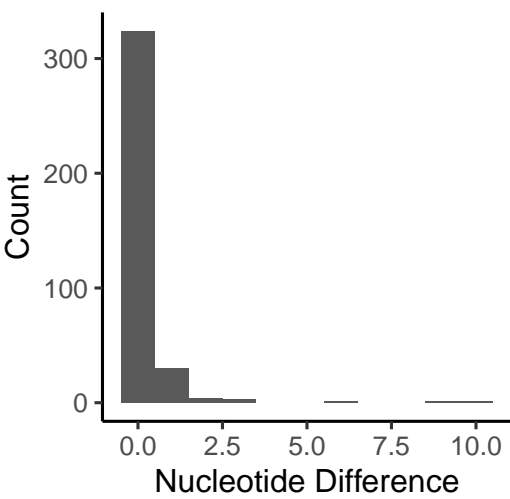
IGHV1-3*02

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



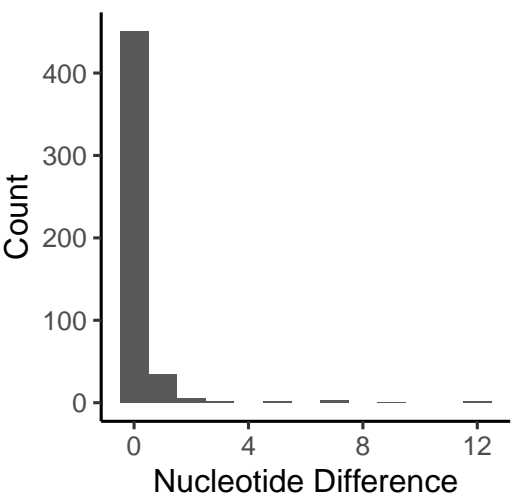
IGHV1-18*04

364 sequences assigned
324 (89%) exact matches, in which:
322 unique CDR3
6 unique J



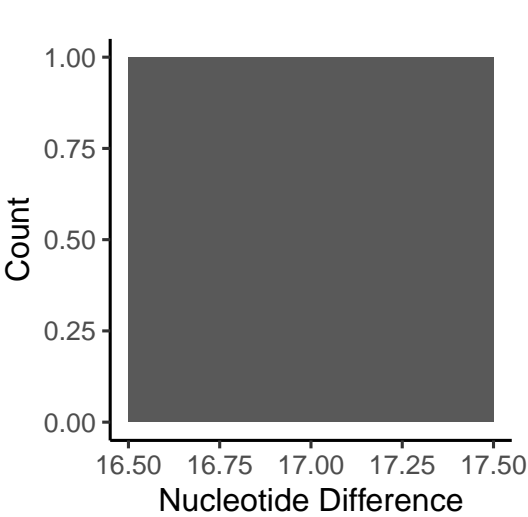
IGHV1-46*01

501 sequences assigned
451 (90%) exact matches, in which:
441 unique CDR3
7 unique J



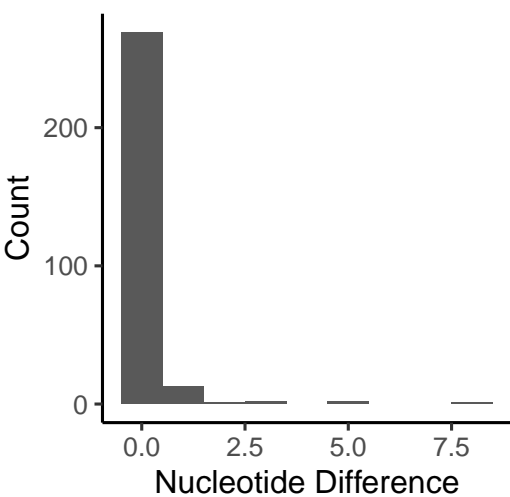
IGHV1-3*03

1 sequences assigned
No exact matches.



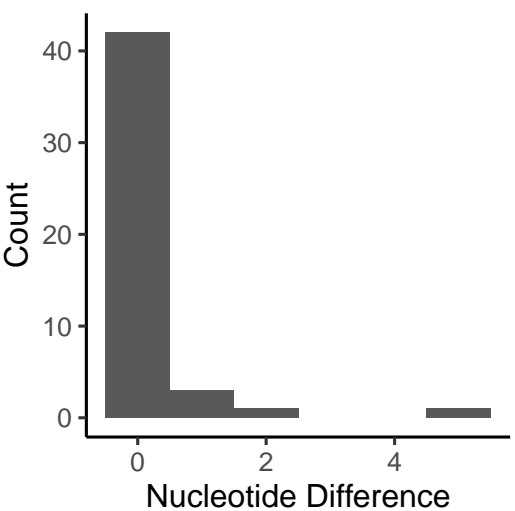
IGHV1-24*01

288 sequences assigned
269 (93.4%) exact matches, in which:
268 unique CDR3
7 unique J



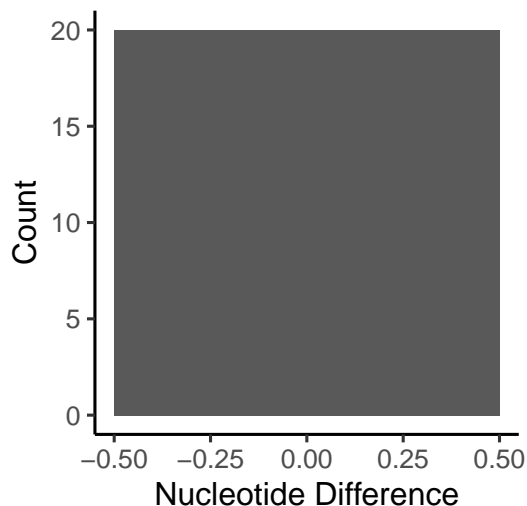
IGHV1-58*01

47 sequences assigned
42 (89.4%) exact matches, in which:
42 unique CDR3
4 unique J



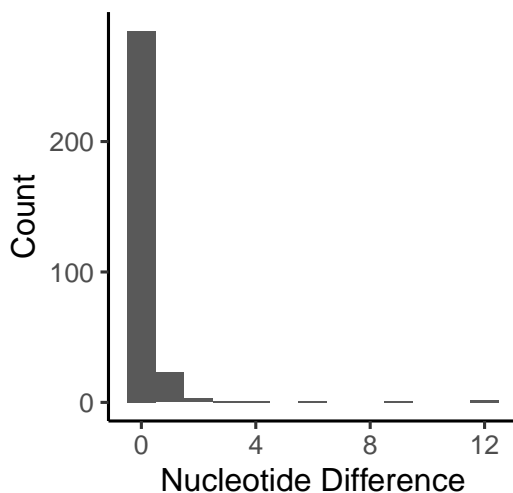
IGHV1-58*02

20 sequences assigned
20 (100%) exact matches, in which:
20 unique CDR3
5 unique J



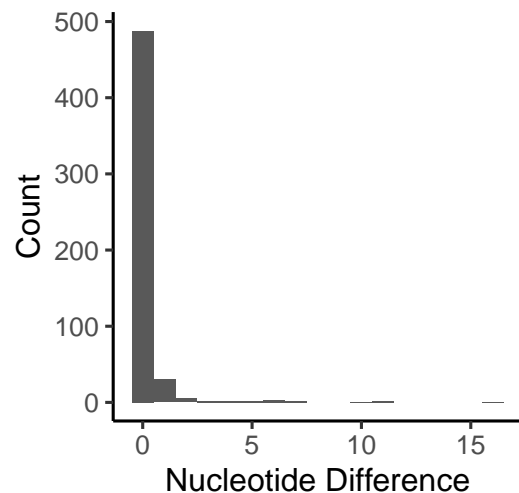
IGHV1-69*04

317 sequences assigned
285 (89.9%) exact matches, in which:
284 unique CDR3
7 unique J



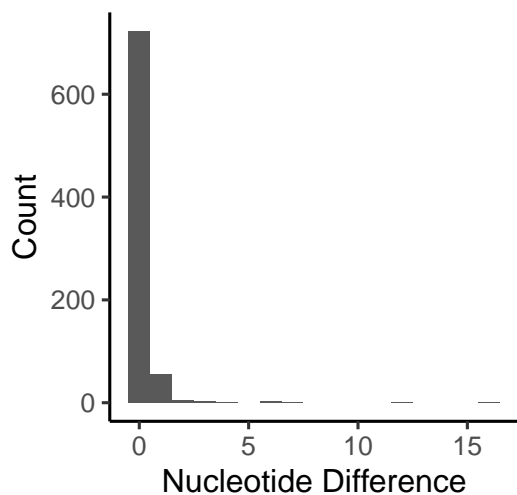
IGHV2-5*02

538 sequences assigned
488 (90.7%) exact matches, in which:
485 unique CDR3
6 unique J



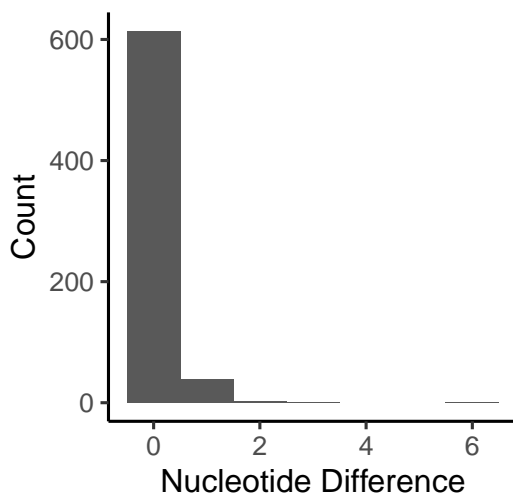
IGHV1-69*01

791 sequences assigned
723 (91.4%) exact matches, in which:
715 unique CDR3
6 unique J



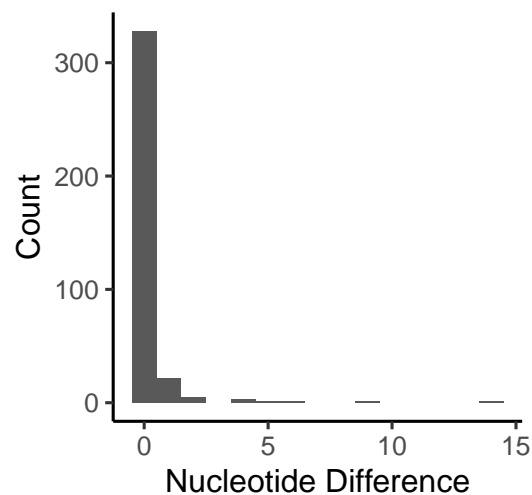
IGHV1-69*06

658 sequences assigned
614 (93.3%) exact matches, in which:
606 unique CDR3
6 unique J



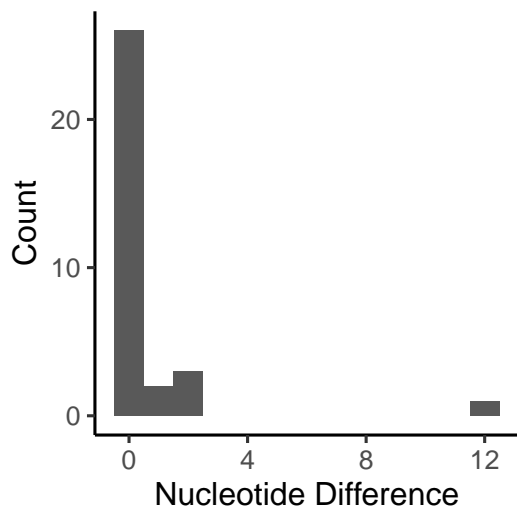
IGHV2-26*01

362 sequences assigned
328 (90.6%) exact matches, in which:
327 unique CDR3
7 unique J



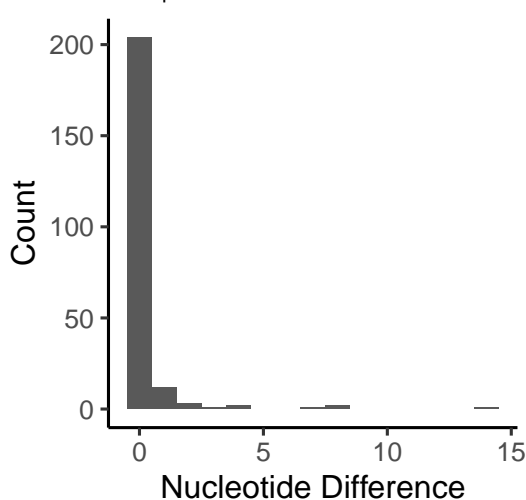
IGHV1-69-2*01

32 sequences assigned
26 (81.2%) exact matches, in which:
26 unique CDR3
4 unique J



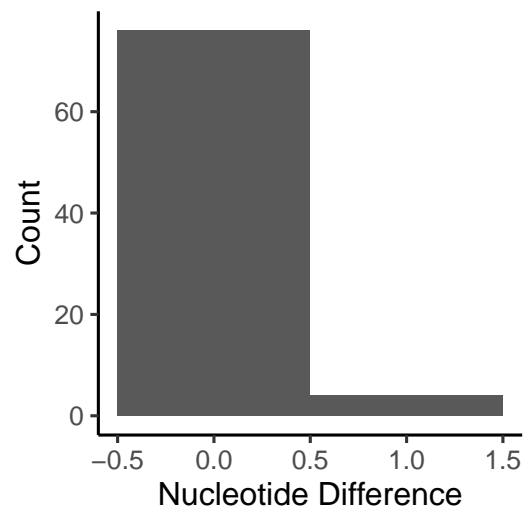
IGHV2-5*01

226 sequences assigned
204 (90.3%) exact matches, in which:
203 unique CDR3
6 unique J



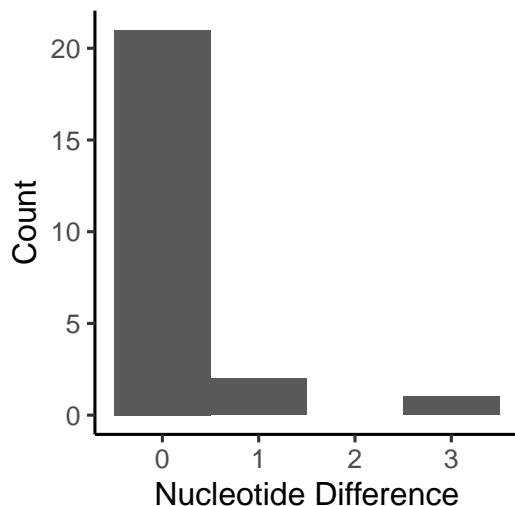
IGHV2-70*01

80 sequences assigned
76 (95%) exact matches, in which:
75 unique CDR3
5 unique J



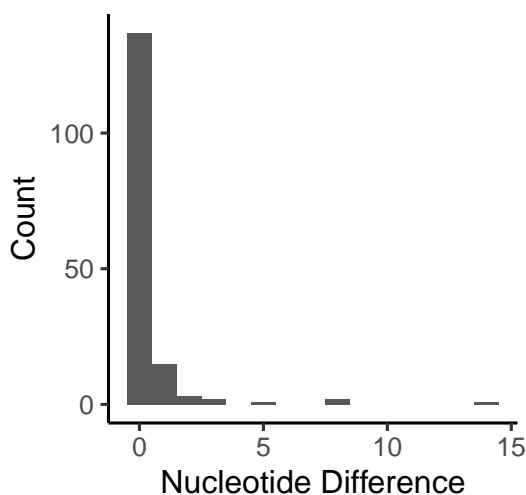
IGHV2-70*04

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



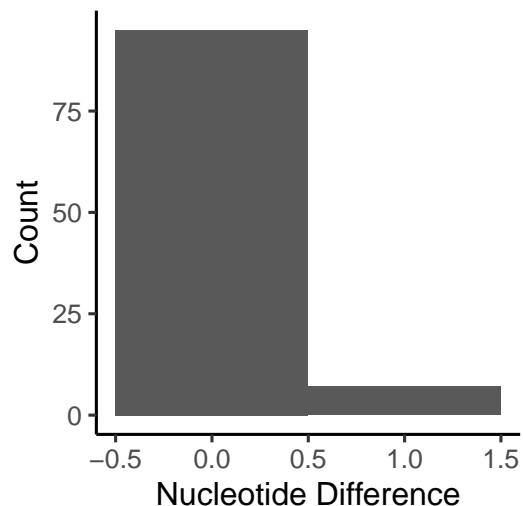
IGHV3-7*05

161 sequences assigned
137 (85.1%) exact matches, in which:
135 unique CDR3
5 unique J



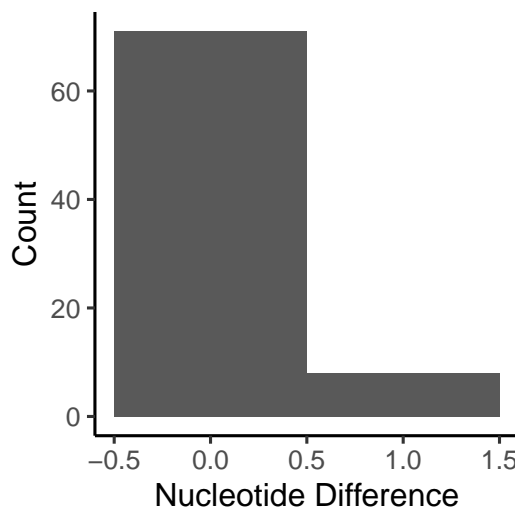
IGHV3-13*04

102 sequences assigned
95 (93.1%) exact matches, in which:
94 unique CDR3
6 unique J



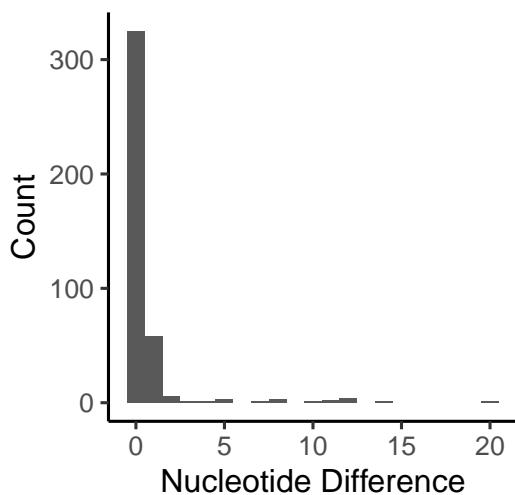
IGHV2-70*15

79 sequences assigned
71 (89.9%) exact matches, in which:
71 unique CDR3
6 unique J



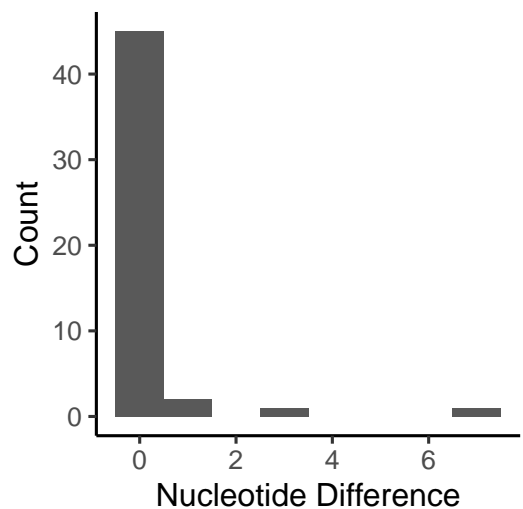
IGHV3-11*05

407 sequences assigned
325 (79.9%) exact matches, in which:
317 unique CDR3
6 unique J



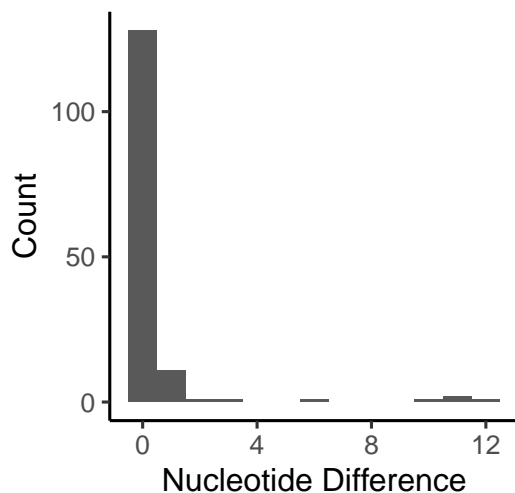
IGHV3-13*05

49 sequences assigned
45 (91.8%) exact matches, in which:
43 unique CDR3
5 unique J



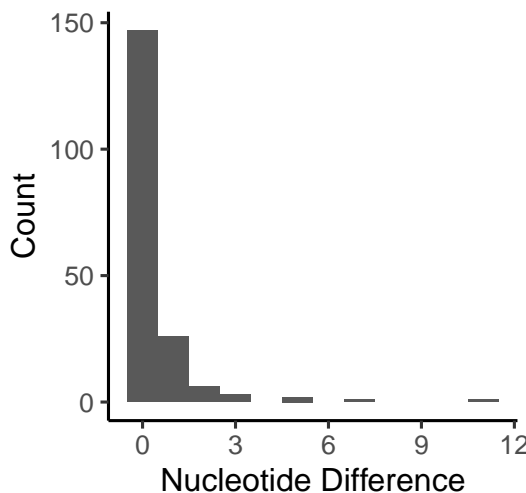
IGHV3-7*04

146 sequences assigned
128 (87.7%) exact matches, in which:
128 unique CDR3
6 unique J



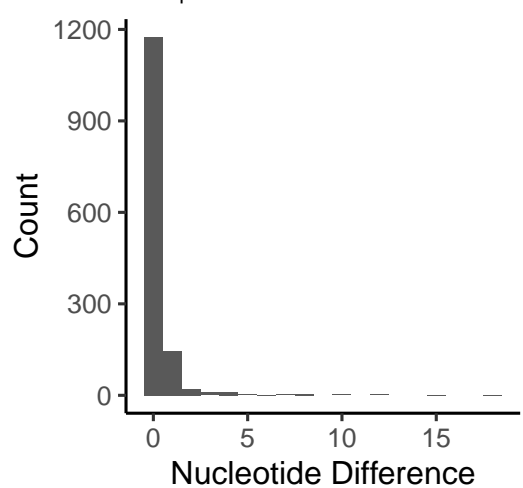
IGHV3-11*06

186 sequences assigned
147 (79%) exact matches, in which:
146 unique CDR3
6 unique J



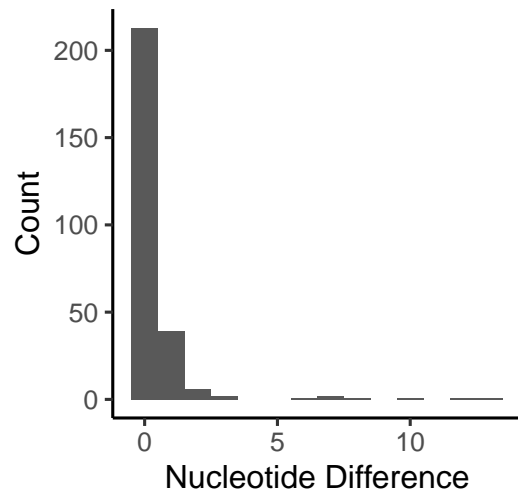
IGHV3-15*01

1383 sequences assigned
1175 (85%) exact matches, in which:
1154 unique CDR3
7 unique J



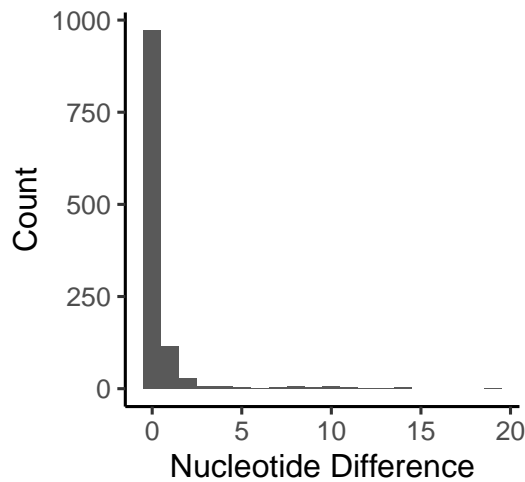
IGHV3-20*04

267 sequences assigned
213 (79.8%) exact matches, in which:
210 unique CDR3
6 unique J



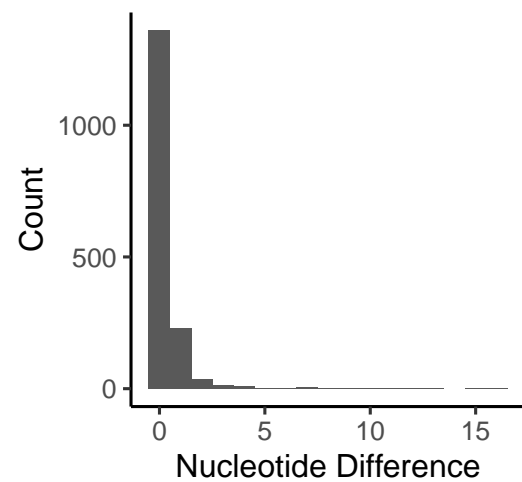
IGHV3-23*04

1169 sequences assigned
972 (83.1%) exact matches, in which:
953 unique CDR3
6 unique J



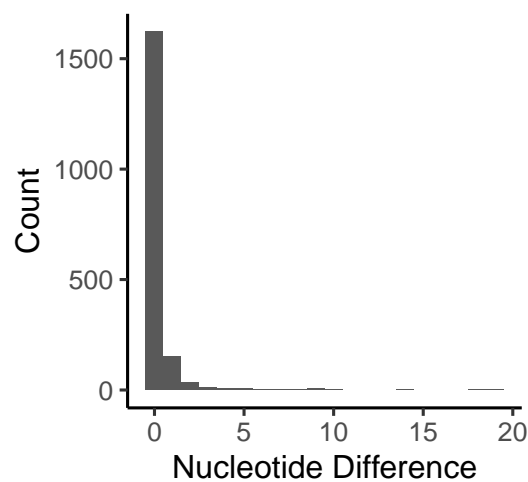
IGHV3-33*01

1672 sequences assigned
1360 (81.3%) exact matches, in which:
1319 unique CDR3
7 unique J



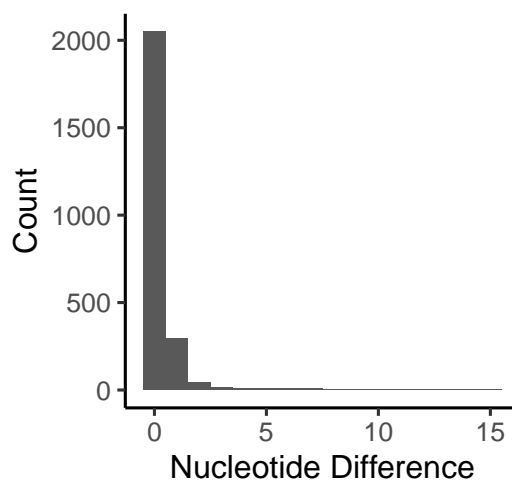
IGHV3-21*01

1857 sequences assigned
1622 (87.3%) exact matches, in which:
1573 unique CDR3
7 unique J



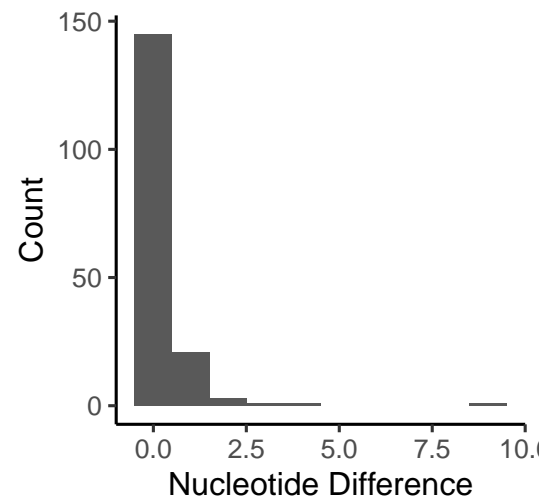
IGHV3-30-3*01

2453 sequences assigned
2049 (83.5%) exact matches, in which:
1995 unique CDR3
7 unique J



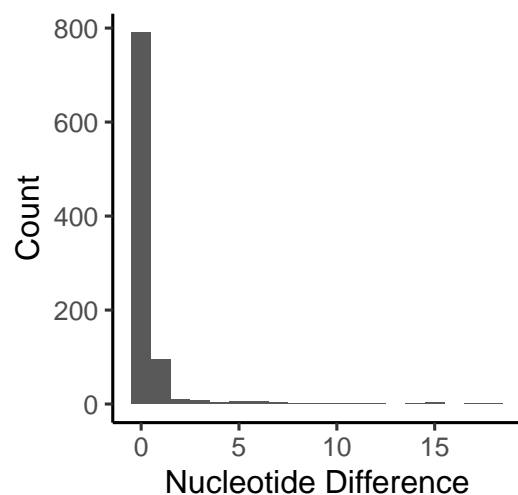
IGHV3-43*01

172 sequences assigned
145 (84.3%) exact matches, in which:
142 unique CDR3
7 unique J



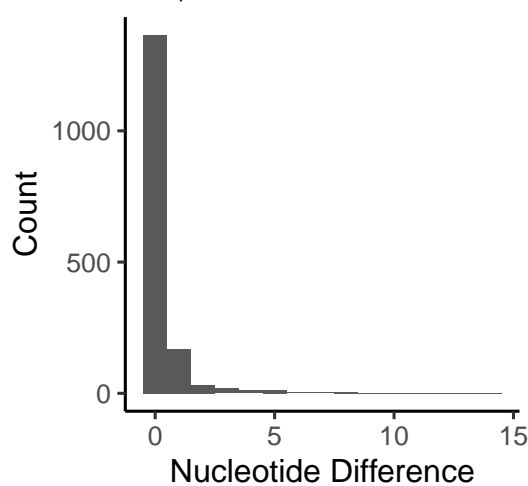
IGHV3-23*01

937 sequences assigned
791 (84.4%) exact matches, in which:
768 unique CDR3
6 unique J



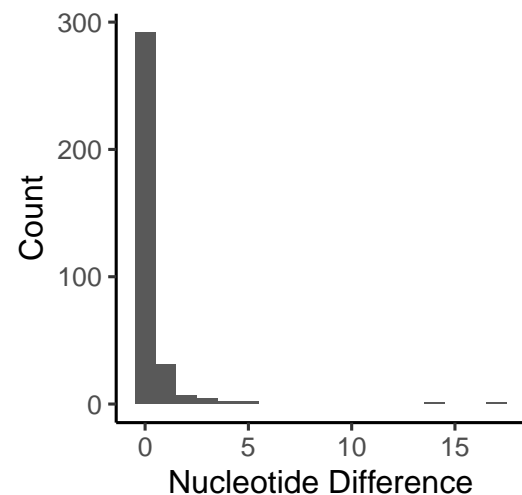
IGHV3-30*18

1629 sequences assigned
1365 (83.8%) exact matches, in which:
1346 unique CDR3
7 unique J



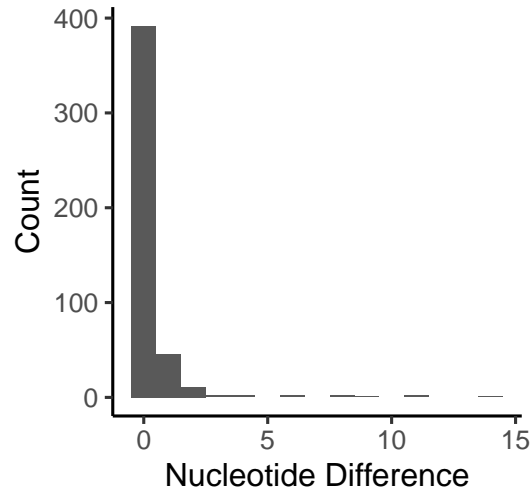
IGHV3-48*01

340 sequences assigned
292 (85.9%) exact matches, in which:
286 unique CDR3
6 unique J



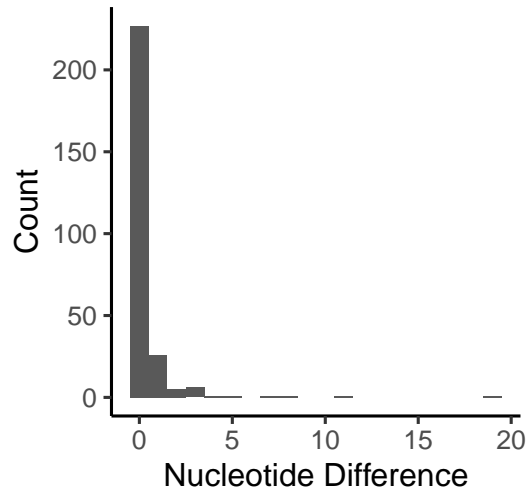
IGHV3-48*02

461 sequences assigned
392 (85%) exact matches, in which:
378 unique CDR3
6 unique J



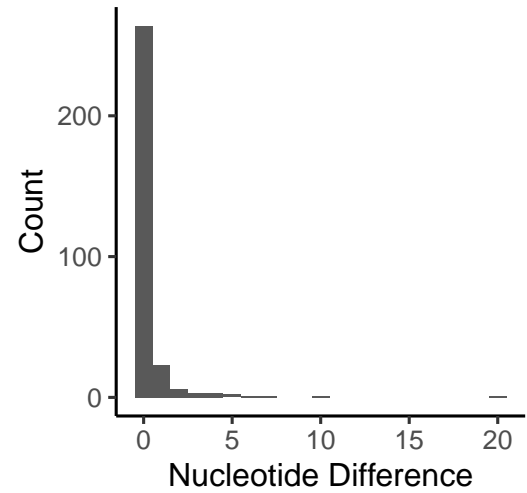
IGHV3-53*01

272 sequences assigned
227 (83.5%) exact matches, in which:
224 unique CDR3
6 unique J



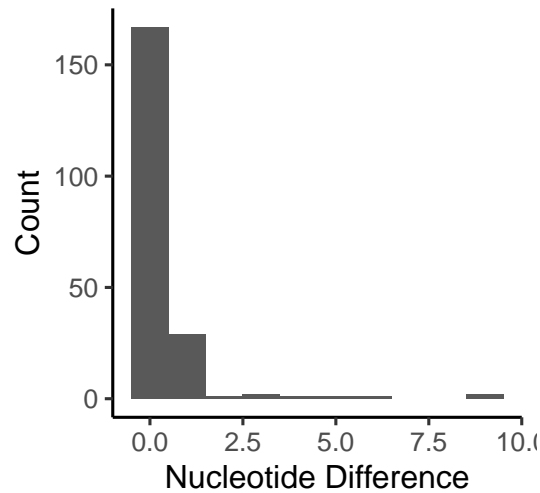
IGHV3-66*01

305 sequences assigned
264 (86.6%) exact matches, in which:
258 unique CDR3
7 unique J



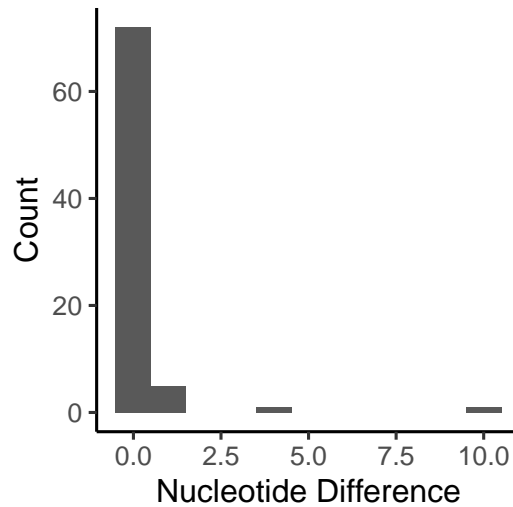
IGHV3-49*03

204 sequences assigned
167 (81.9%) exact matches, in which:
160 unique CDR3
5 unique J



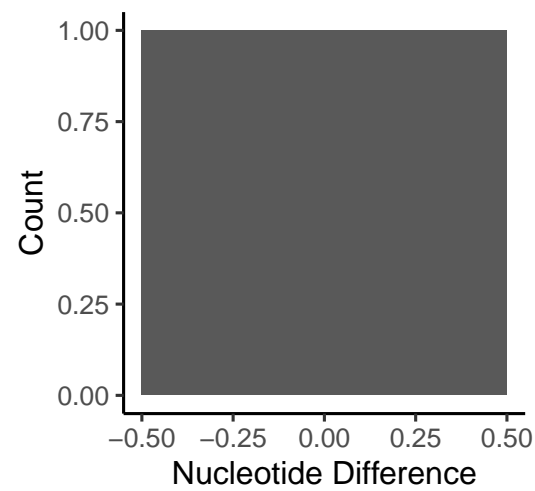
IGHV3-53*02

79 sequences assigned
72 (91.1%) exact matches, in which:
70 unique CDR3
5 unique J



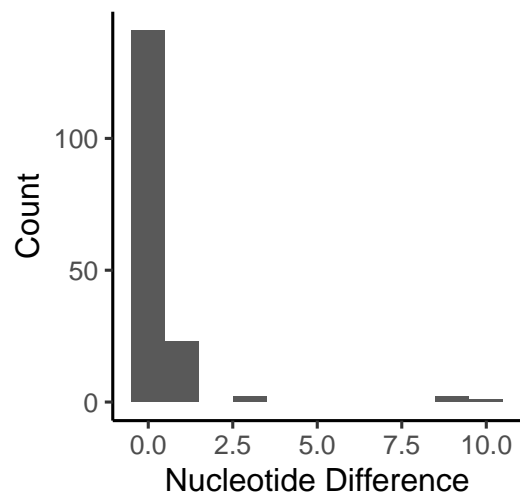
IGHV3-69-1*01

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



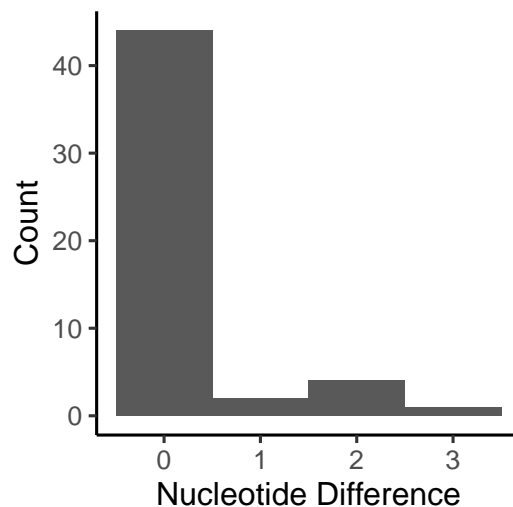
IGHV3-49*05

169 sequences assigned
141 (83.4%) exact matches, in which:
140 unique CDR3
4 unique J



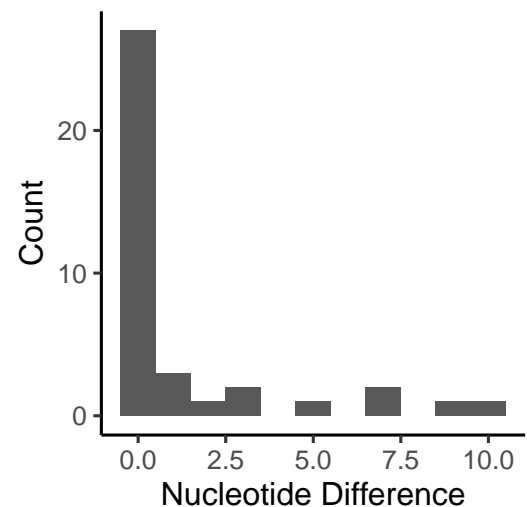
IGHV3-64*01

51 sequences assigned
44 (86.3%) exact matches, in which:
44 unique CDR3
5 unique J



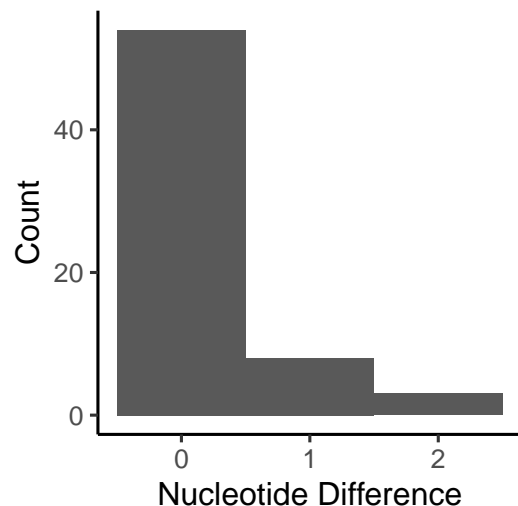
IGHV3-72*01

38 sequences assigned
27 (71.1%) exact matches, in which:
27 unique CDR3
5 unique J



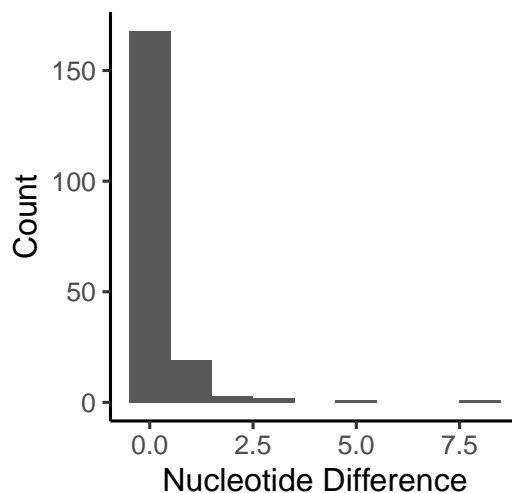
IGHV3-73*01

65 sequences assigned
54 (83.1%) exact matches, in which:
52 unique CDR3
6 unique J



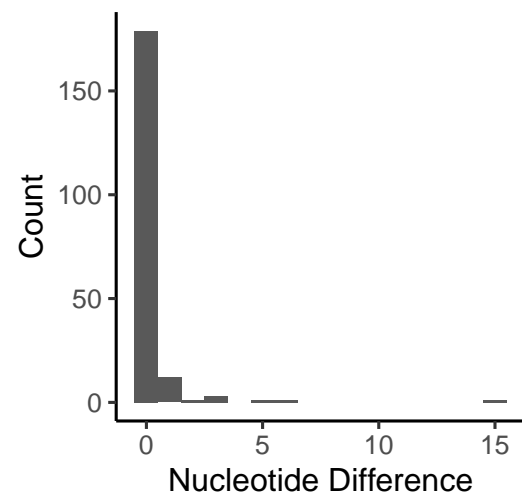
IGHV3-64D*06

194 sequences assigned
168 (86.6%) exact matches, in which:
161 unique CDR3
6 unique J



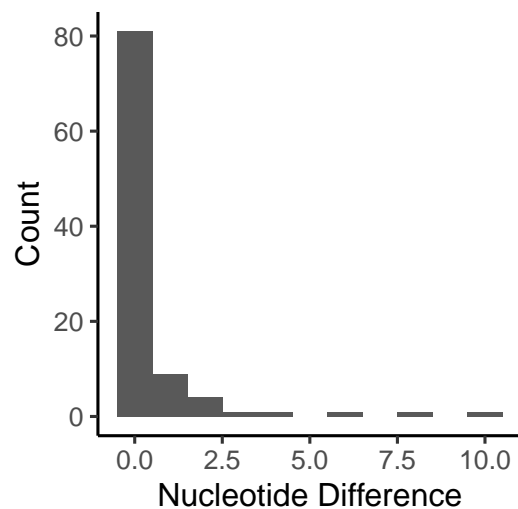
IGHV4-4*07

198 sequences assigned
179 (90.4%) exact matches, in which:
176 unique CDR3
6 unique J



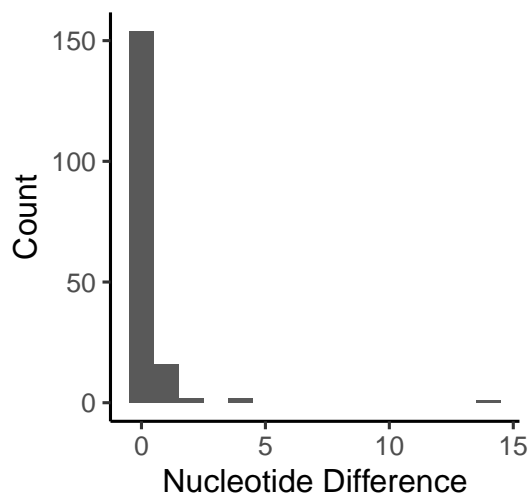
IGHV3-73*02

99 sequences assigned
81 (81.8%) exact matches, in which:
78 unique CDR3
5 unique J



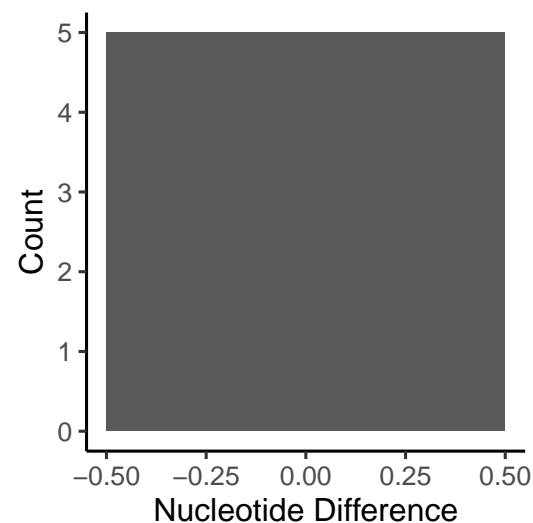
IGHV3-64D*08

176 sequences assigned
154 (87.5%) exact matches, in which:
150 unique CDR3
6 unique J



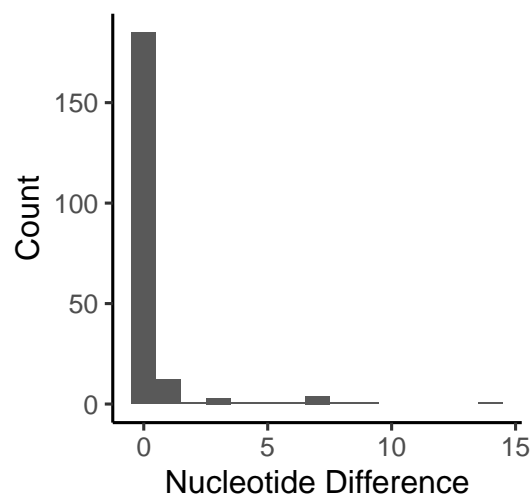
IGHV4-28*01

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



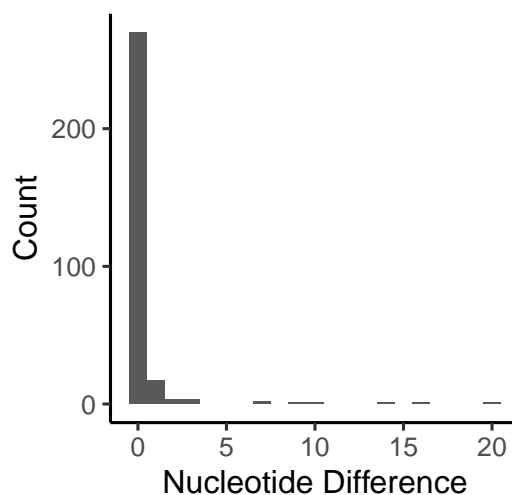
IGHV3-74*01

211 sequences assigned
185 (87.7%) exact matches, in which:
183 unique CDR3
7 unique J



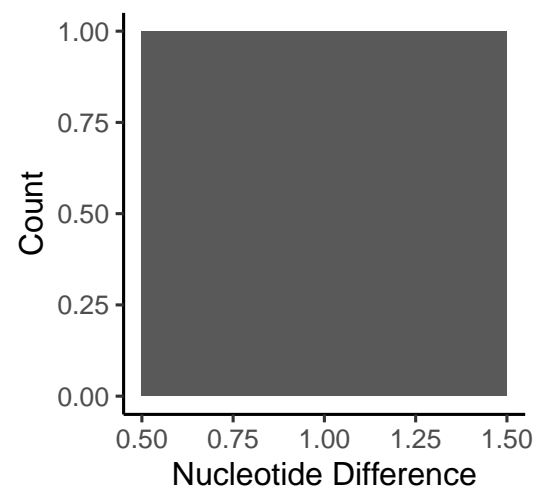
IGHV4-4*02

300 sequences assigned
270 (90%) exact matches, in which:
266 unique CDR3
6 unique J



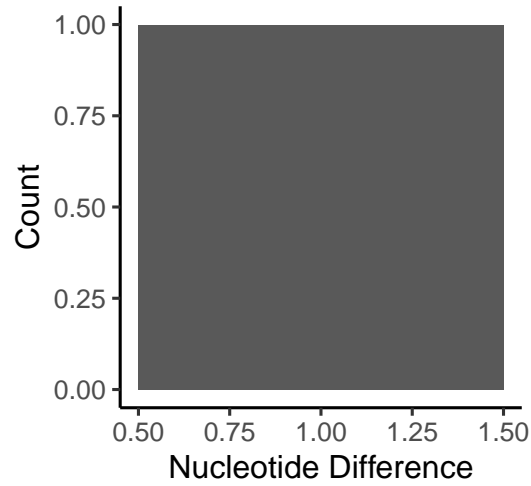
IGHV4-28*03

1 sequences assigned
No exact matches.



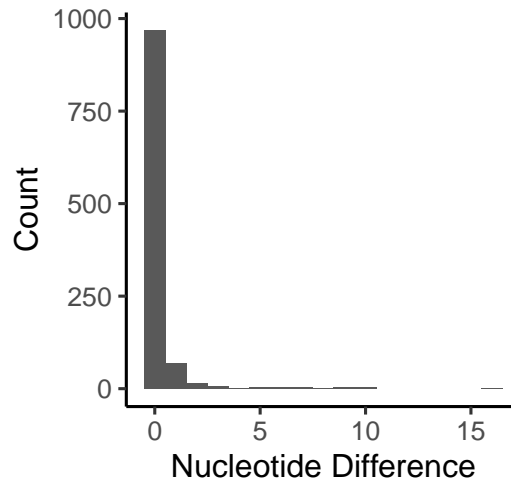
IGHV4-28*04

1 sequences assigned
No exact matches.



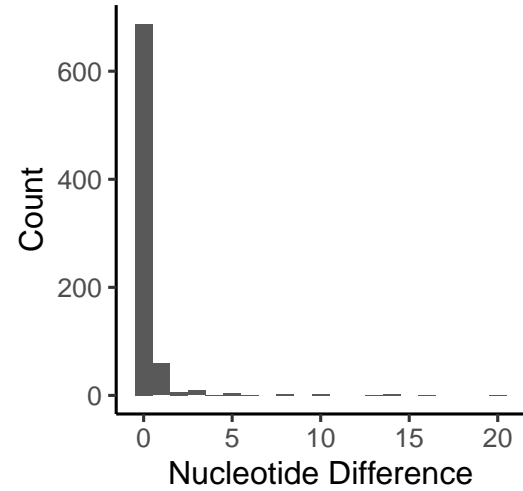
IGHV4-31*03

1078 sequences assigned
968 (89.8%) exact matches, in which:
961 unique CDR3
7 unique J



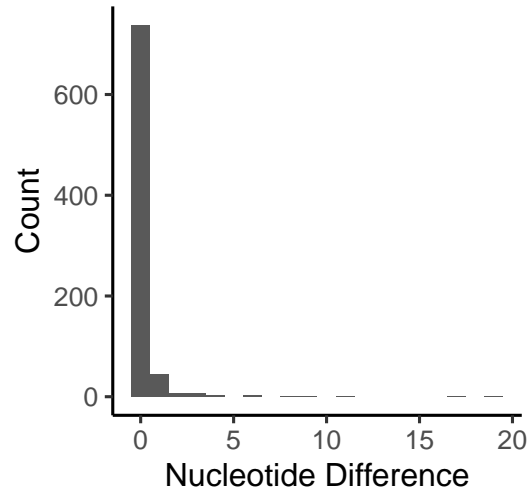
IGHV4-59*01

780 sequences assigned
688 (88.2%) exact matches, in which:
684 unique CDR3
7 unique J



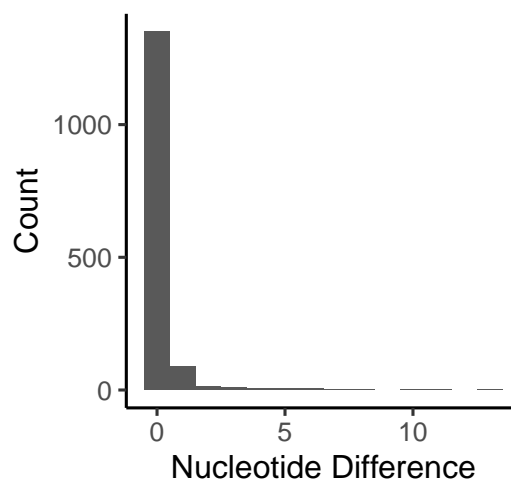
IGHV4-30-4*01

808 sequences assigned
738 (91.3%) exact matches, in which:
731 unique CDR3
7 unique J



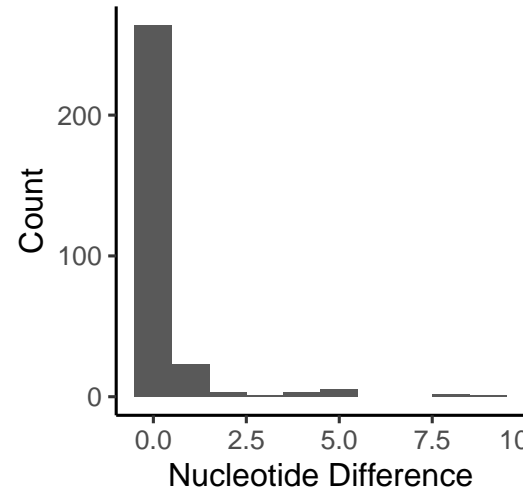
IGHV4-34*01

1482 sequences assigned
1350 (91.1%) exact matches, in which:
1327 unique CDR3
7 unique J



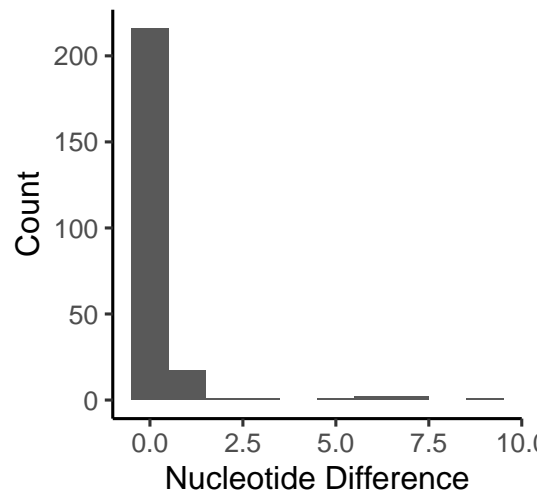
IGHV4-59*08

302 sequences assigned
264 (87.4%) exact matches, in which:
261 unique CDR3
6 unique J



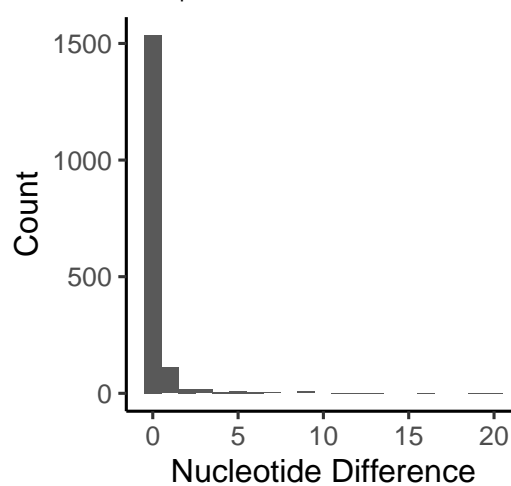
IGHV4-30-2*01

241 sequences assigned
216 (89.6%) exact matches, in which:
212 unique CDR3
6 unique J



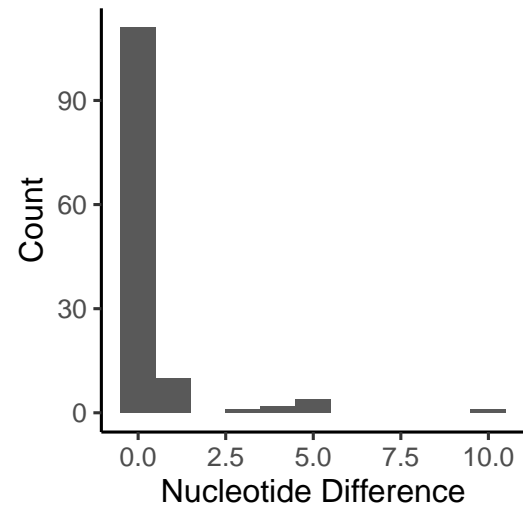
IGHV4-39*01

1720 sequences assigned
1536 (89.3%) exact matches, in which:
1510 unique CDR3
7 unique J



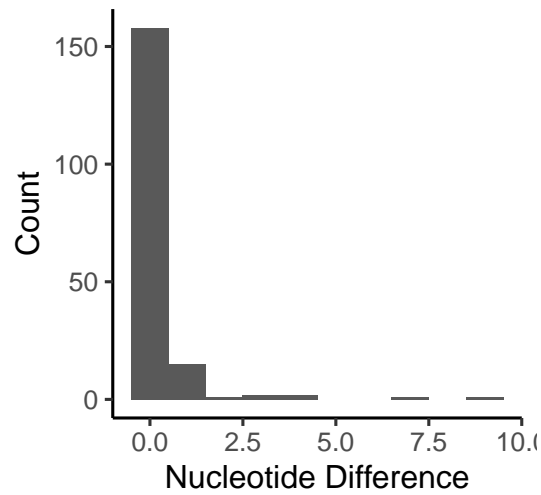
IGHV4-61*01

129 sequences assigned
111 (86%) exact matches, in which:
109 unique CDR3
7 unique J



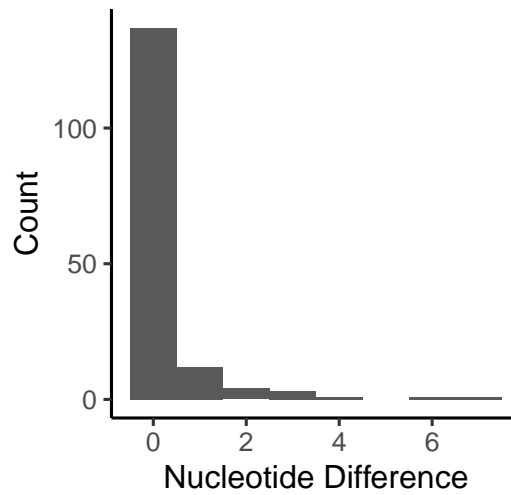
IGHV5-10-1*01

180 sequences assigned
158 (87.8%) exact matches, in which:
155 unique CDR3
6 unique J



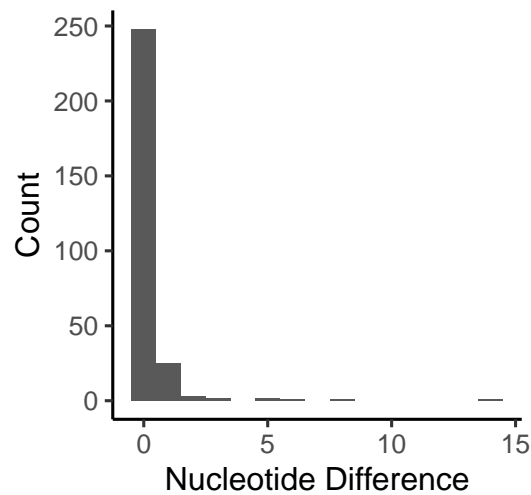
IGHV5-51*03

159 sequences assigned
137 (86.2%) exact matches, in which:
135 unique CDR3
6 unique J



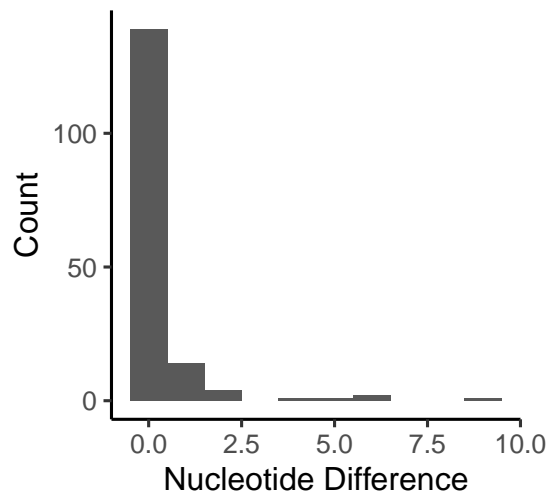
IGHV5-10-1*03

283 sequences assigned
248 (87.6%) exact matches, in which:
246 unique CDR3
6 unique J



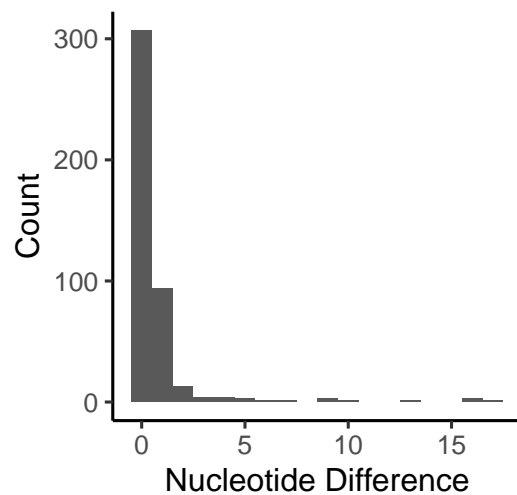
IGHV6-1*01

162 sequences assigned
139 (85.8%) exact matches, in which:
135 unique CDR3
7 unique J



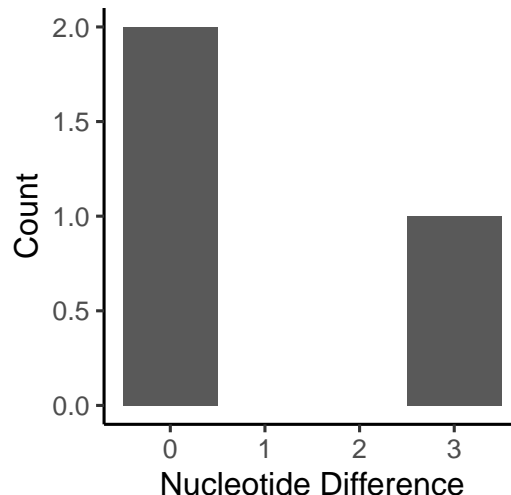
IGHV5-51*01

436 sequences assigned
307 (70.4%) exact matches, in which:
303 unique CDR3
7 unique J

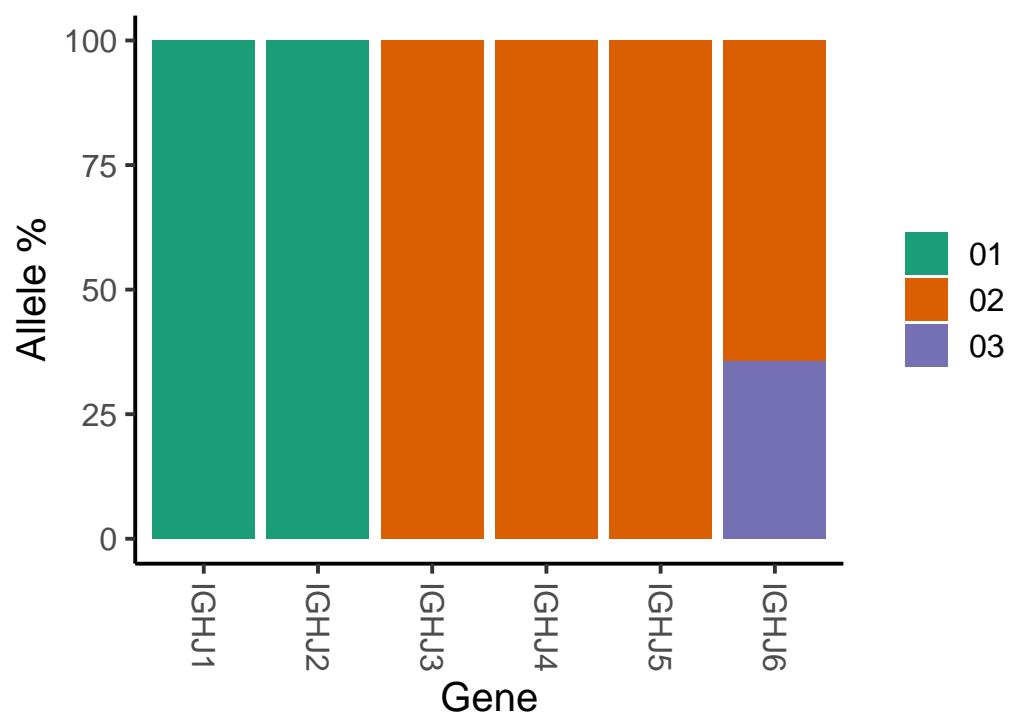


IGHV7-4-1*01

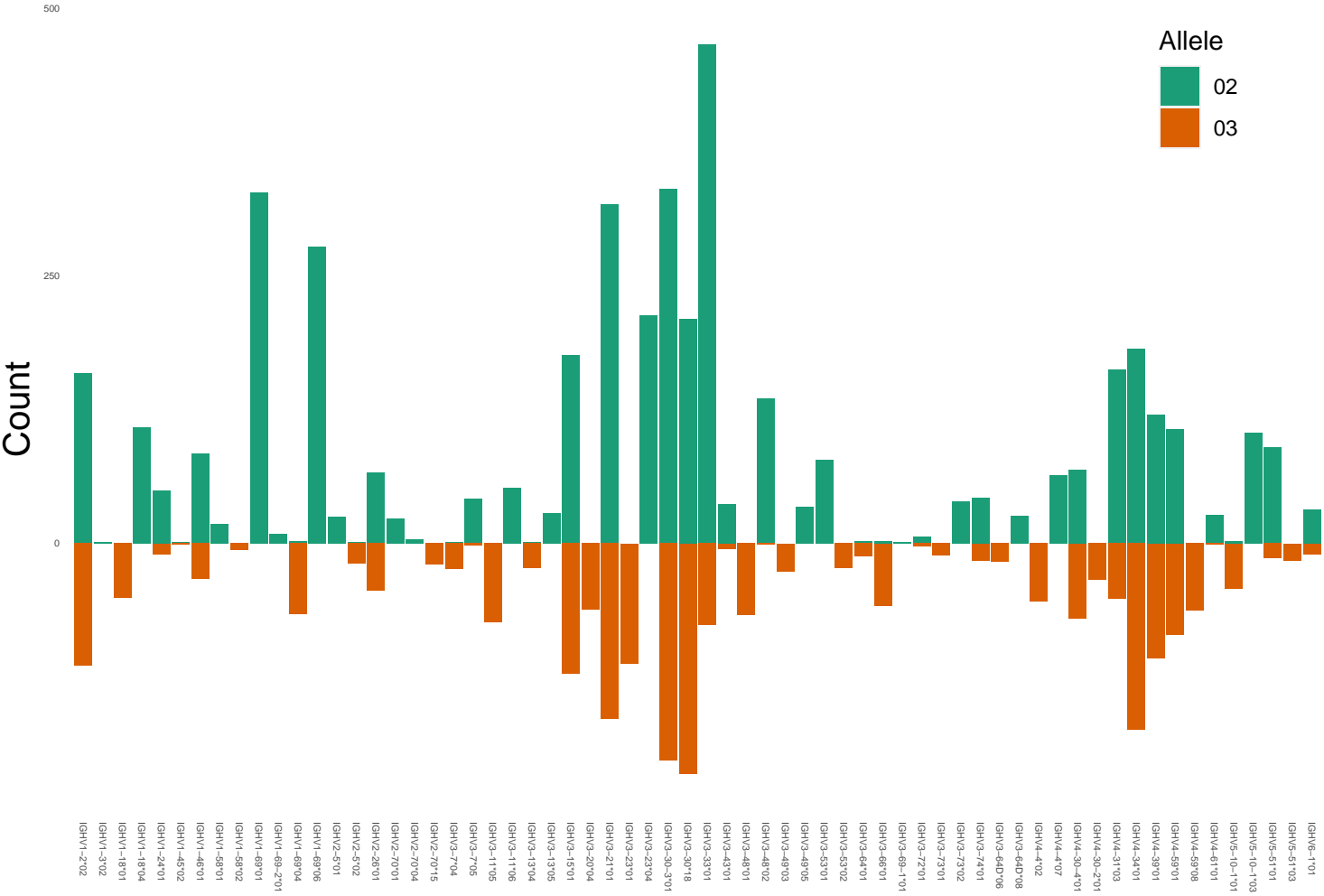
3 sequences assigned
2 (66.7%) exact matches, in which:
2 unique CDR3
1 unique J



Allele Usage



Sequence Count by IGHJ6 allele usage



Warning – no inferred sequences found.