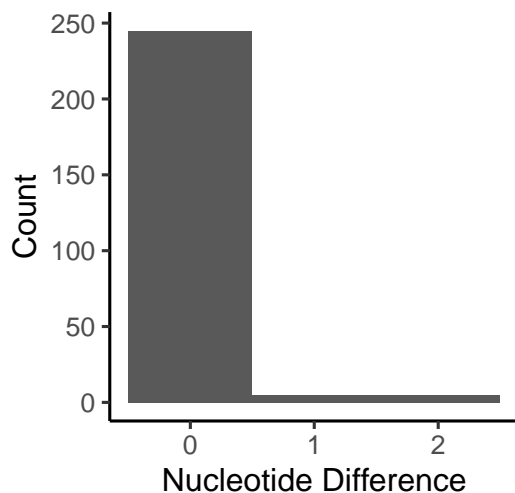


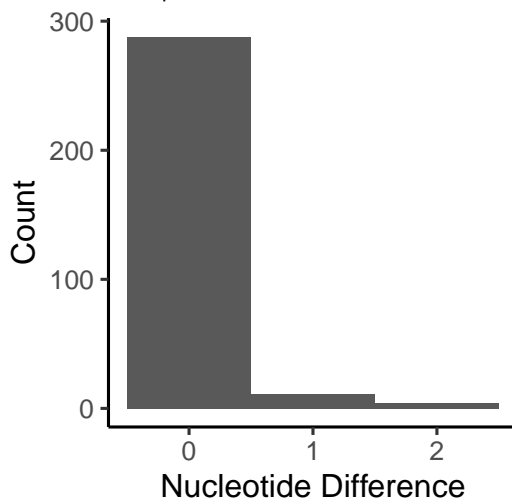
IGHV1–2*04

255 sequences assigned
245 (96.1%) exact matches, in which:
245 unique CDR3
5 unique J



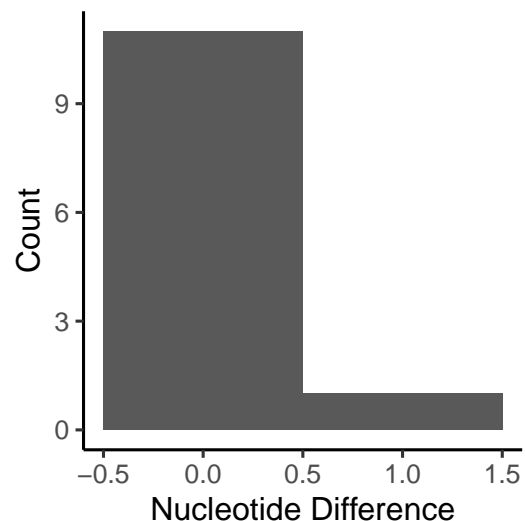
IGHV1–24*01

303 sequences assigned
288 (95%) exact matches, in which:
288 unique CDR3
6 unique J



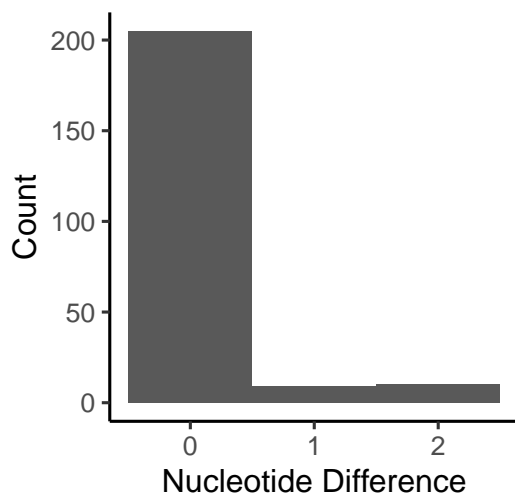
IGHV1–58*02

12 sequences assigned
11 (91.7%) exact matches, in which:
11 unique CDR3
3 unique J



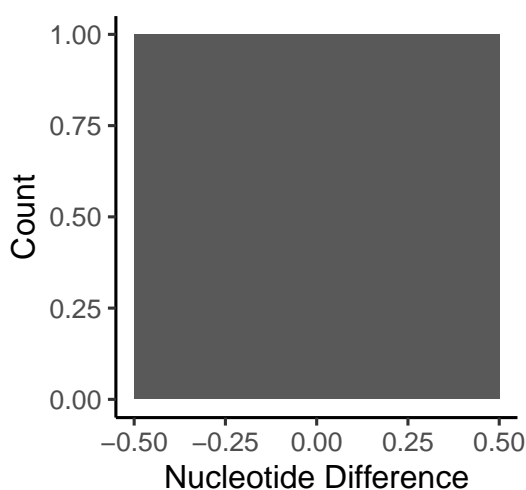
IGHV1–3*01_05

224 sequences assigned
205 (91.5%) exact matches, in which:
205 unique CDR3
6 unique J



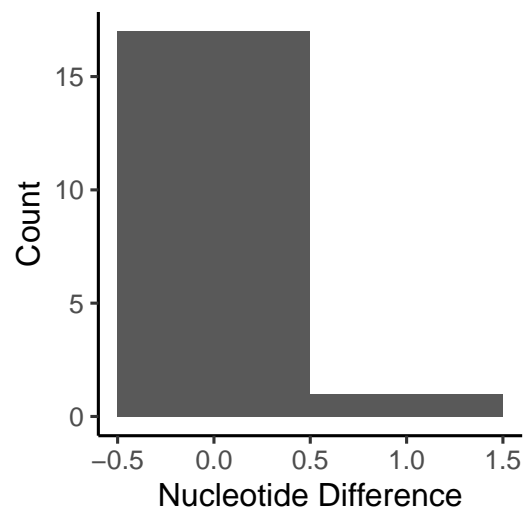
IGHV1–45*02

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



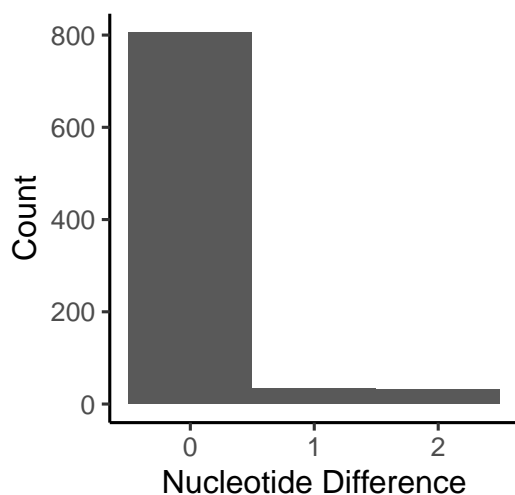
IGHV1–58*01_03

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



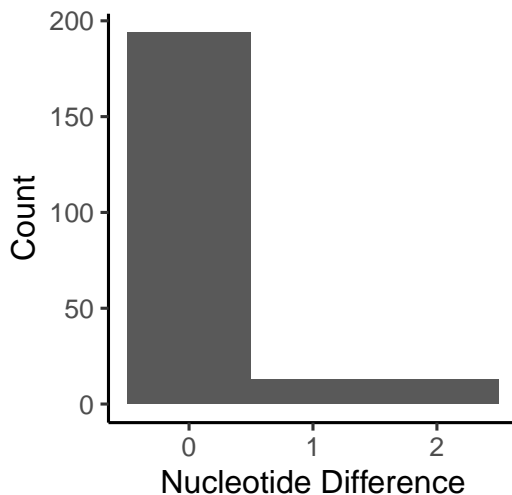
IGHV1–18*04

871 sequences assigned
806 (92.5%) exact matches, in which:
805 unique CDR3
6 unique J



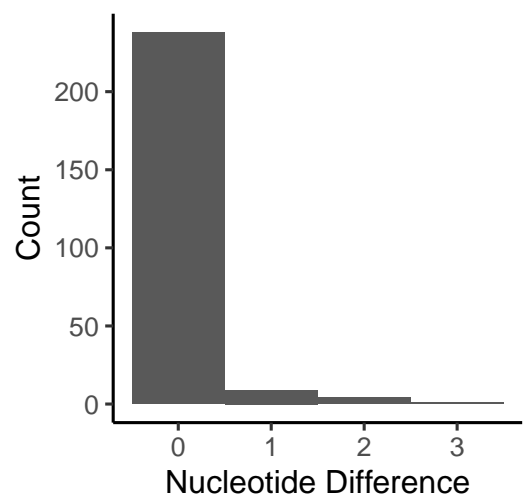
IGHV1–46*01

220 sequences assigned
194 (88.2%) exact matches, in which:
194 unique CDR3
6 unique J



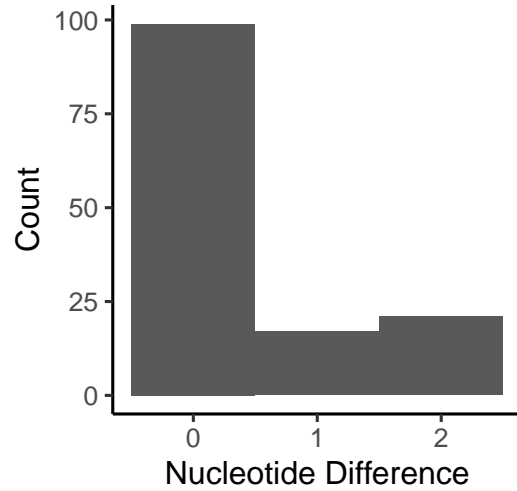
IGHV1–69*04_09

252 sequences assigned
238 (94.4%) exact matches, in which:
238 unique CDR3
6 unique J



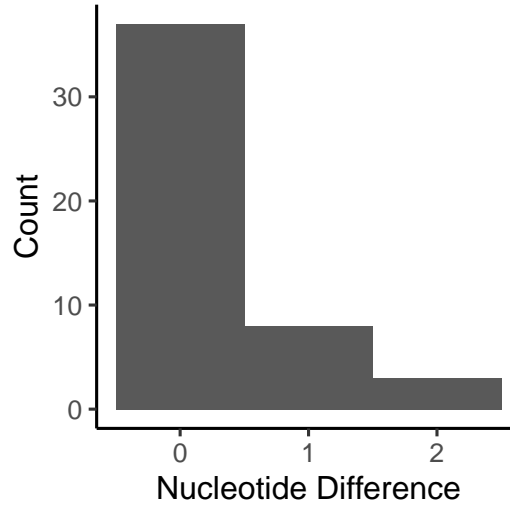
IGHV2-5*02

137 sequences assigned
99 (72.3%) exact matches, in which:
97 unique CDR3
6 unique J



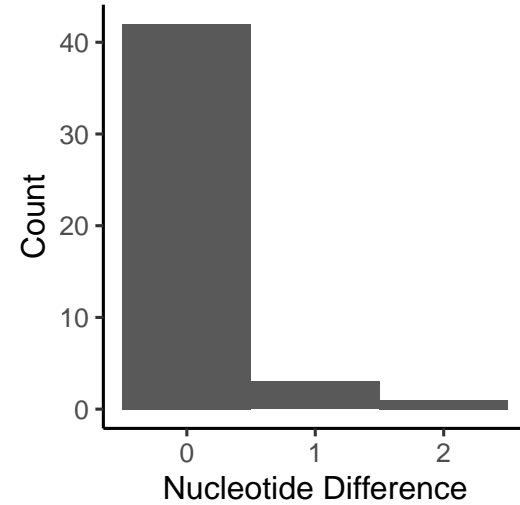
IGHV2-70*11_15

48 sequences assigned
37 (77.1%) exact matches, in which:
37 unique CDR3
4 unique J



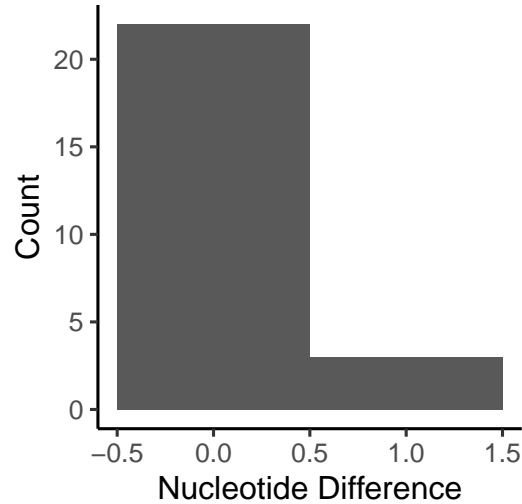
IGHV3-13*05

46 sequences assigned
42 (91.3%) exact matches, in which:
40 unique CDR3
5 unique J



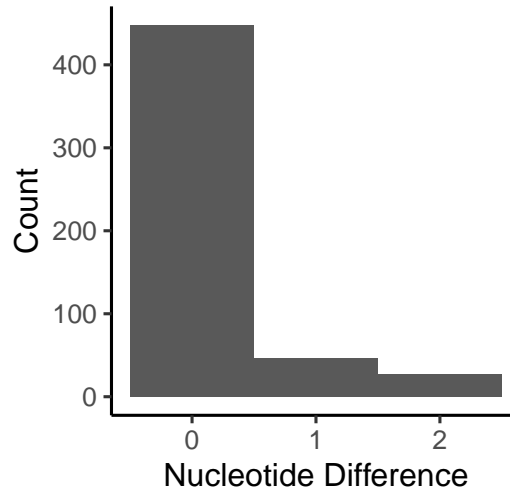
IGHV2-26*01

25 sequences assigned
22 (88%) exact matches, in which:
22 unique CDR3
5 unique J



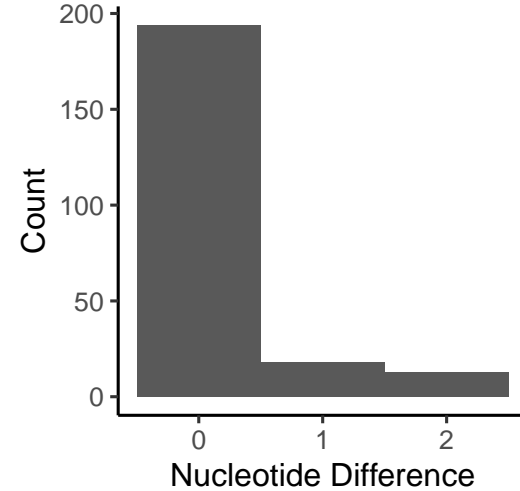
IGHV3-7*03

521 sequences assigned
448 (86%) exact matches, in which:
443 unique CDR3
6 unique J



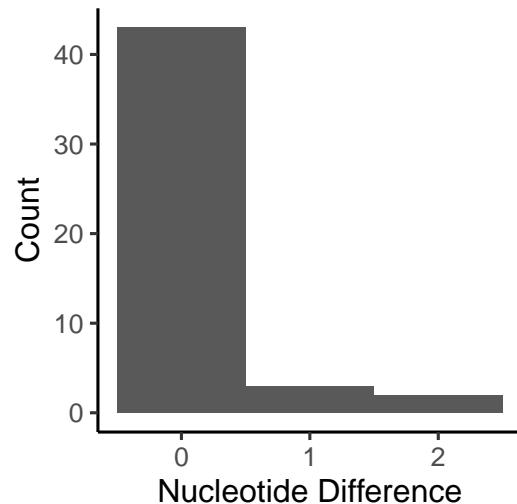
IGHV3-15*01_02

225 sequences assigned
194 (86.2%) exact matches, in which:
190 unique CDR3
6 unique J



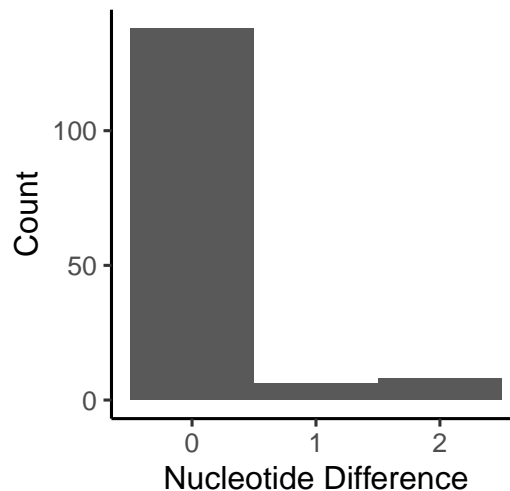
IGHV2-70*01

48 sequences assigned
43 (89.6%) exact matches, in which:
43 unique CDR3
6 unique J



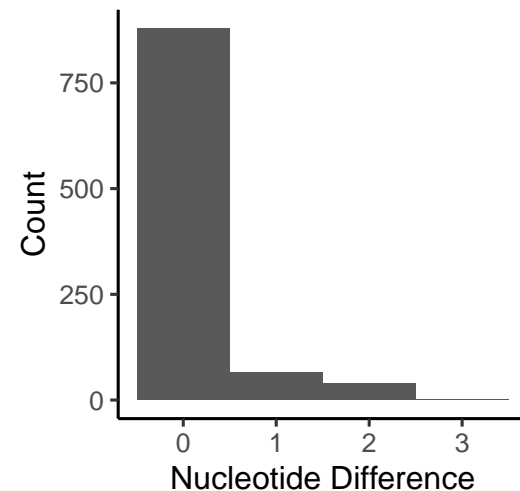
IGHV3-11*06

152 sequences assigned
138 (90.8%) exact matches, in which:
138 unique CDR3
6 unique J



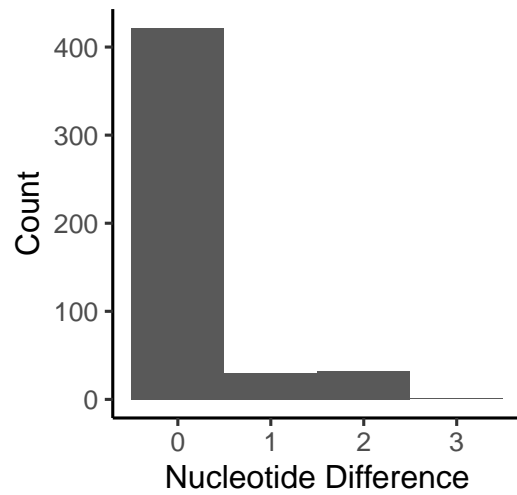
IGHV3-21*01_02

985 sequences assigned
879 (89.2%) exact matches, in which:
864 unique CDR3
6 unique J



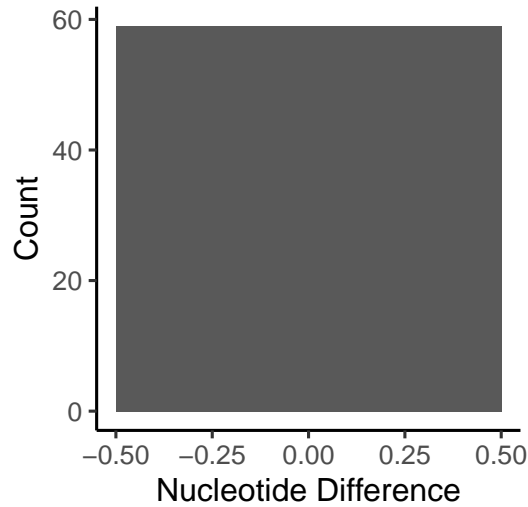
IGHV3-30-3*01

485 sequences assigned
422 (87%) exact matches, in which:
419 unique CDR3
6 unique J



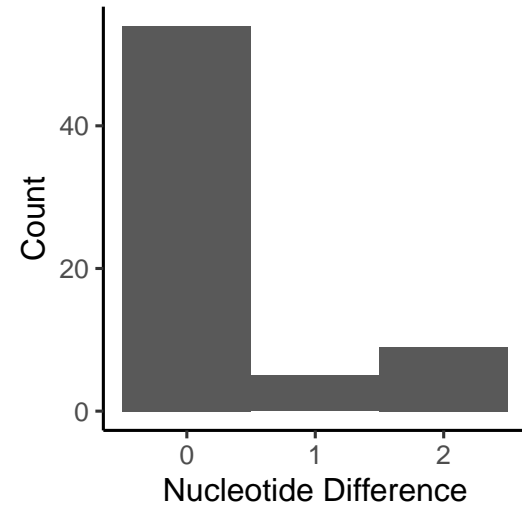
IGHV3-43*01

59 sequences assigned
59 (100%) exact matches, in which:
59 unique CDR3
5 unique J



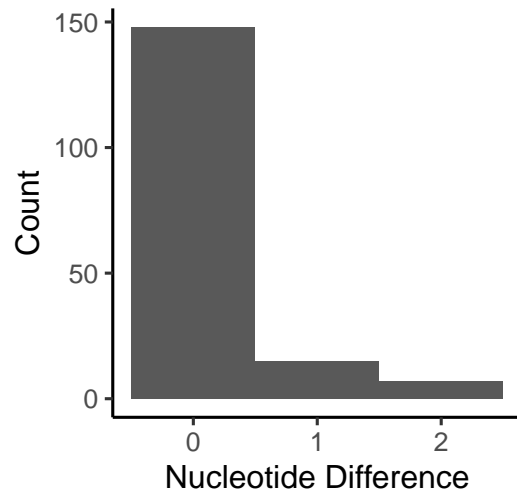
IGHV3-49*03_05

68 sequences assigned
54 (79.4%) exact matches, in which:
54 unique CDR3
5 unique J



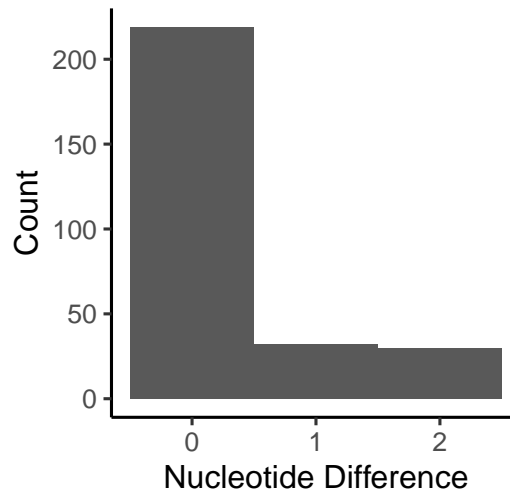
IGHV3-33*01

170 sequences assigned
148 (87.1%) exact matches, in which:
145 unique CDR3
6 unique J



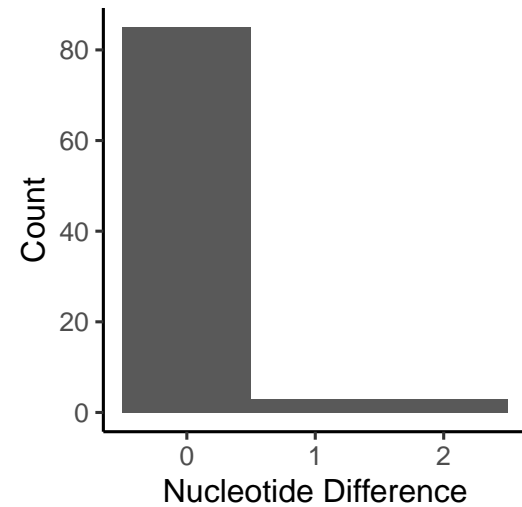
IGHV3-48*02

281 sequences assigned
219 (77.9%) exact matches, in which:
216 unique CDR3
6 unique J



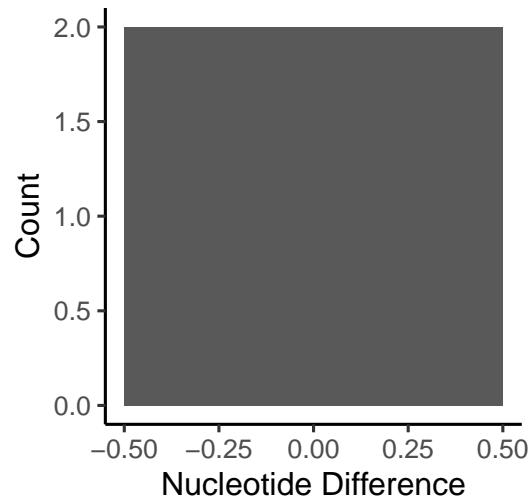
IGHV3-53*04

91 sequences assigned
85 (93.4%) exact matches, in which:
83 unique CDR3
6 unique J



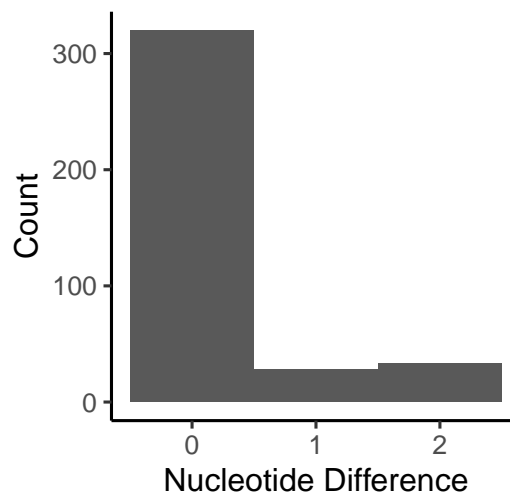
IGHV3-38-3*01

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



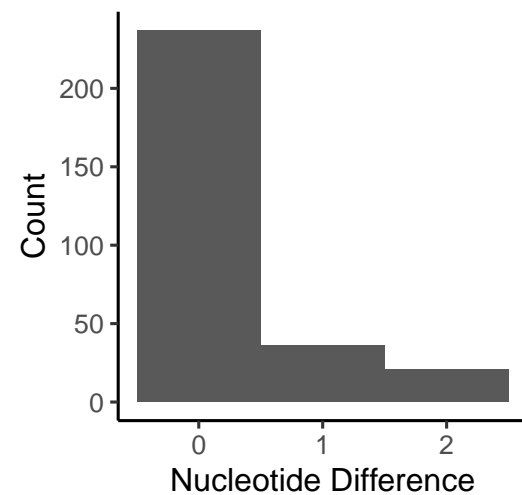
IGHV3-48*04

381 sequences assigned
320 (84%) exact matches, in which:
315 unique CDR3
6 unique J



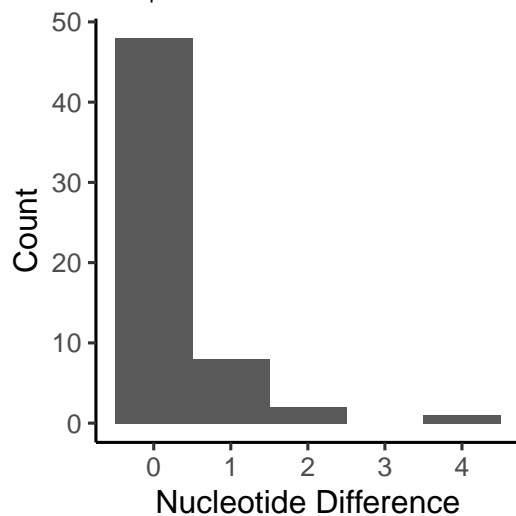
IGHV3-53*01_02

294 sequences assigned
237 (80.6%) exact matches, in which:
233 unique CDR3
6 unique J



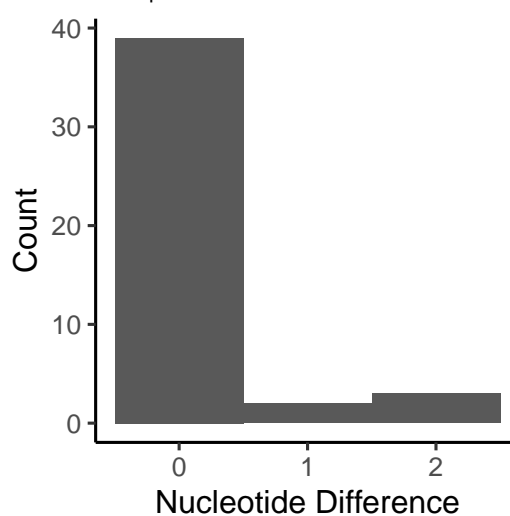
IGHV3-64*01

59 sequences assigned
48 (81.4%) exact matches, in which:
47 unique CDR3
5 unique J



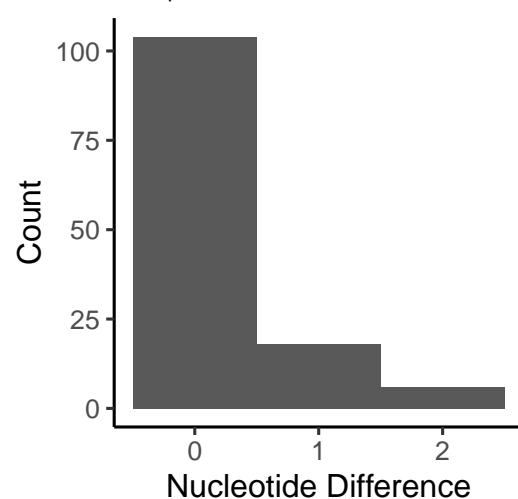
IGHV3-73*01_02

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



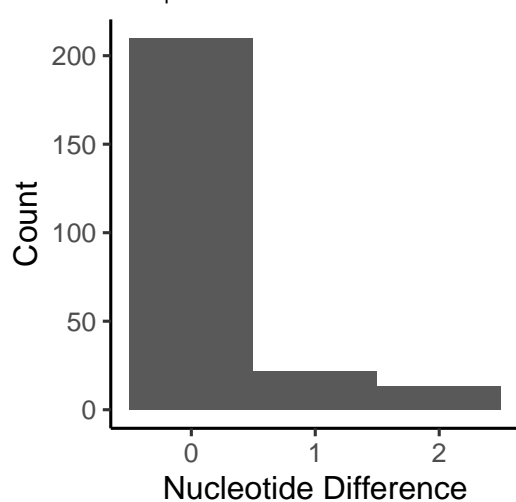
IGHV3-64D*06

128 sequences assigned
104 (81.2%) exact matches, in which:
103 unique CDR3
6 unique J



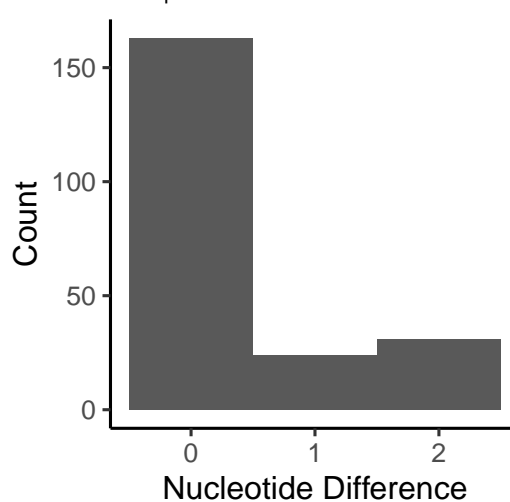
IGHV3-66*01

245 sequences assigned
210 (85.7%) exact matches, in which:
208 unique CDR3
6 unique J



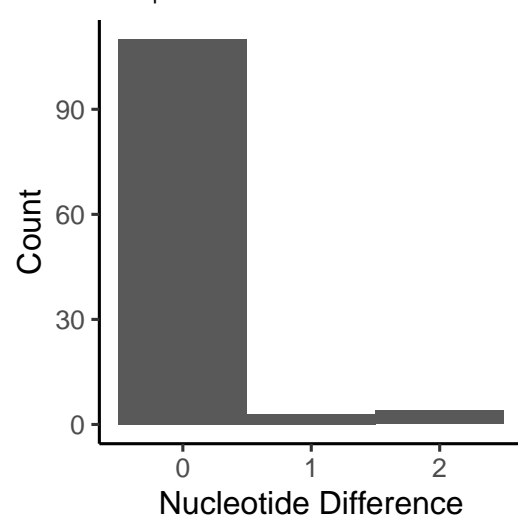
IGHV3-74*01_02

218 sequences assigned
163 (74.8%) exact matches, in which:
159 unique CDR3
6 unique J



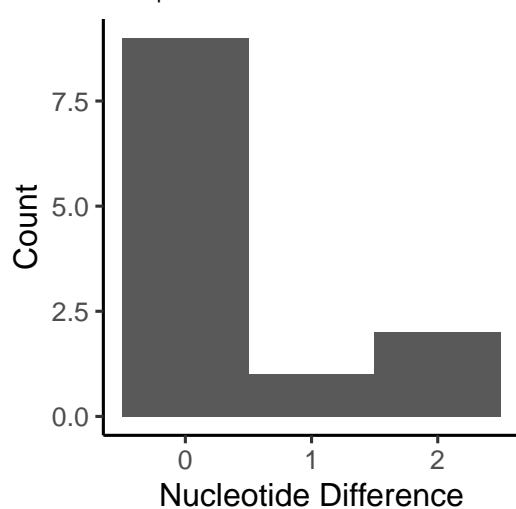
IGHV3-64D*09

117 sequences assigned
110 (94%) exact matches, in which:
110 unique CDR3
5 unique J



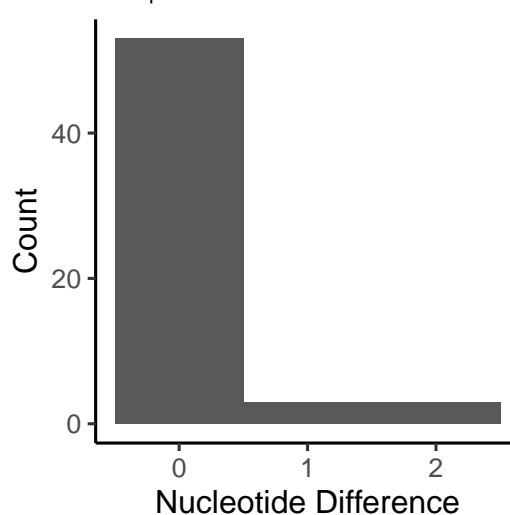
IGHV3-72*01

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



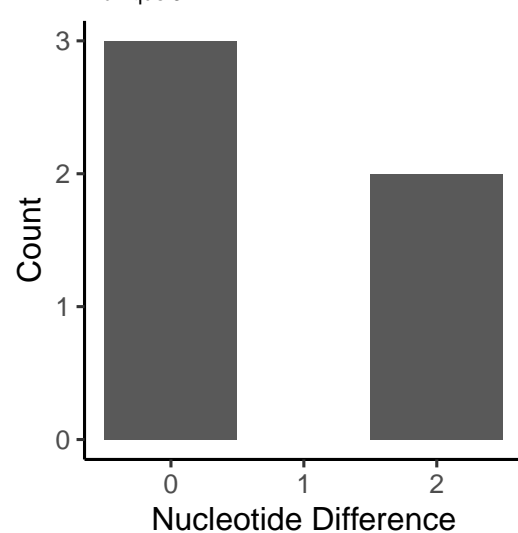
IGHV3-43D*03

59 sequences assigned
53 (89.8%) exact matches, in which:
53 unique CDR3
5 unique J



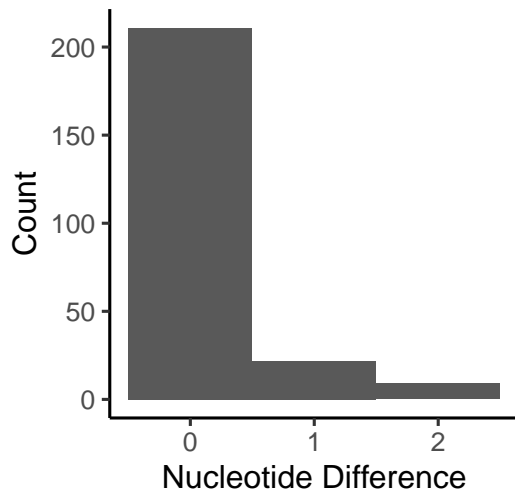
IGHV4-28*01_07

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



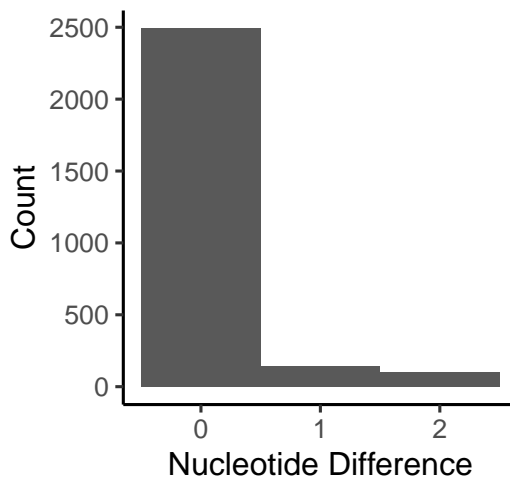
IGHV4-30-4*01

242 sequences assigned
211 (87.2%) exact matches, in which:
209 unique CDR3
6 unique J



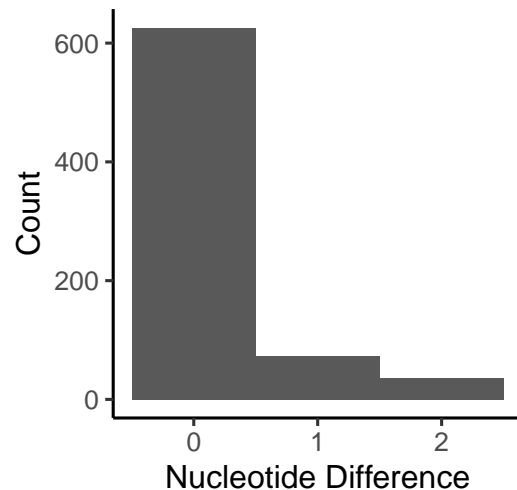
IGHV4-34*01_02

2737 sequences assigned
2492 (91%) exact matches, in which:
2453 unique CDR3
6 unique J



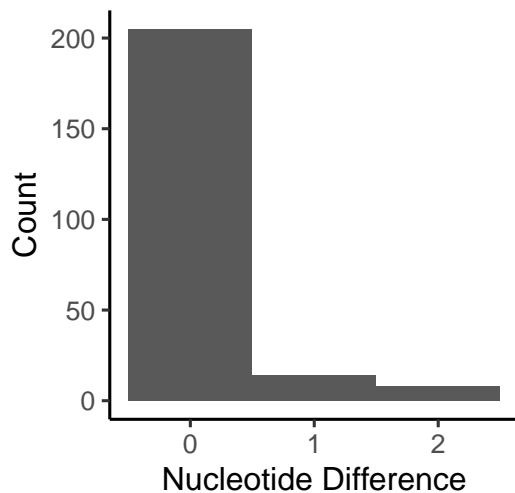
IGHV4-39*01_05

735 sequences assigned
626 (85.2%) exact matches, in which:
616 unique CDR3
6 unique J



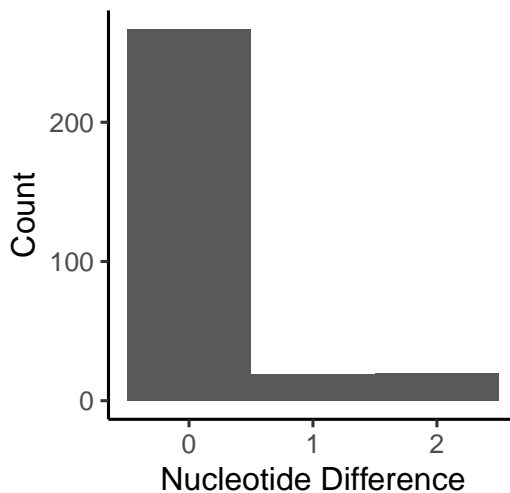
IGHV4-30-2*01

227 sequences assigned
205 (90.3%) exact matches, in which:
201 unique CDR3
6 unique J



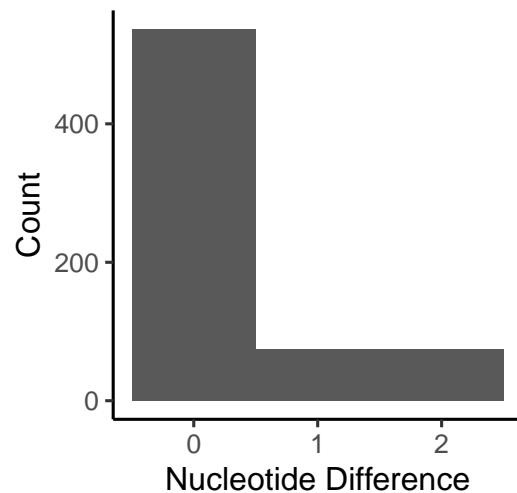
IGHV4-38-2*02

306 sequences assigned
267 (87.3%) exact matches, in which:
266 unique CDR3
6 unique J



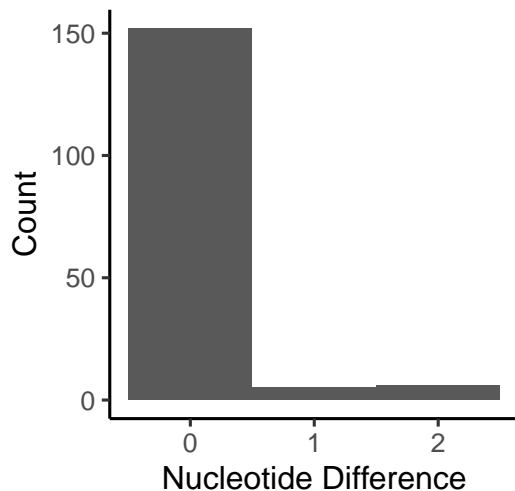
IGHV4-59*08

686 sequences assigned
537 (78.3%) exact matches, in which:
526 unique CDR3
6 unique J



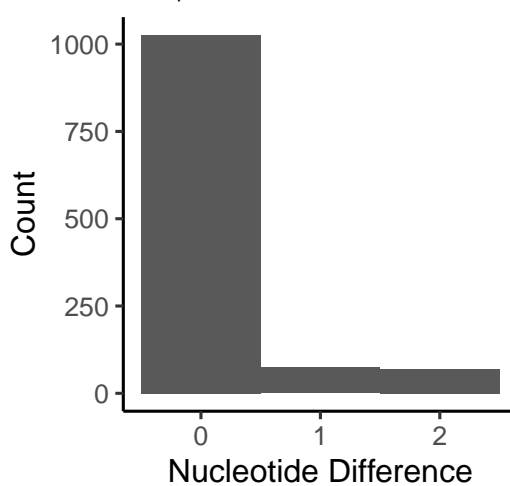
IGHV4-31*03_04

163 sequences assigned
152 (93.3%) exact matches, in which:
152 unique CDR3
6 unique J



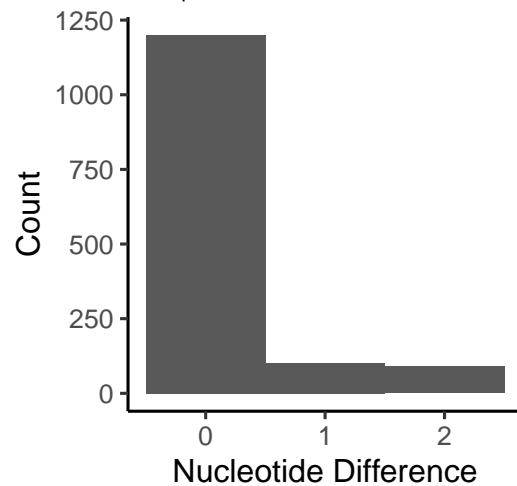
IGHV4-39*07

1170 sequences assigned
1026 (87.7%) exact matches, in which:
1019 unique CDR3
6 unique J



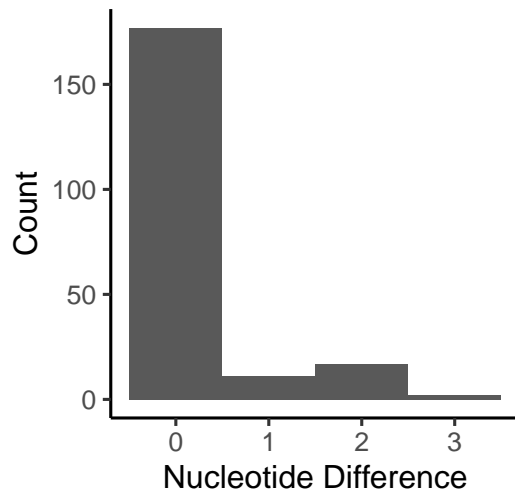
IGHV4-59*01_07

1392 sequences assigned
1200 (86.2%) exact matches, in which:
1184 unique CDR3
6 unique J



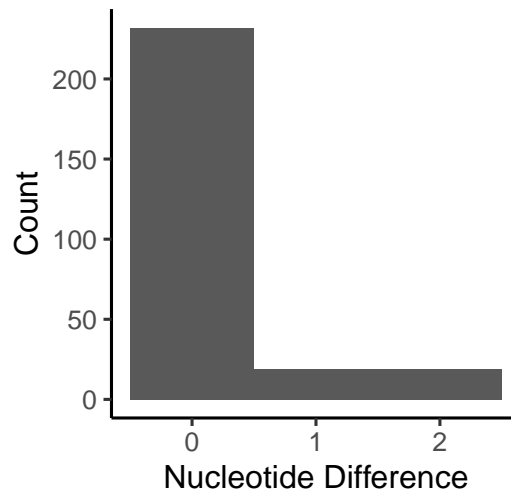
IGHV4–61*01

207 sequences assigned
177 (85.5%) exact matches, in which:
174 unique CDR3
6 unique J



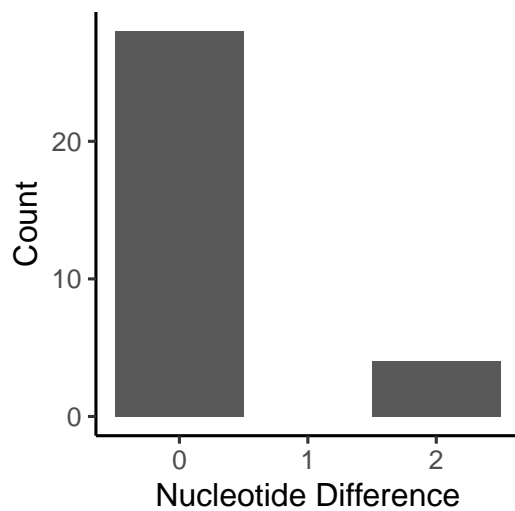
IGHV6–1*01_02

270 sequences assigned
232 (85.9%) exact matches, in which:
231 unique CDR3
6 unique J



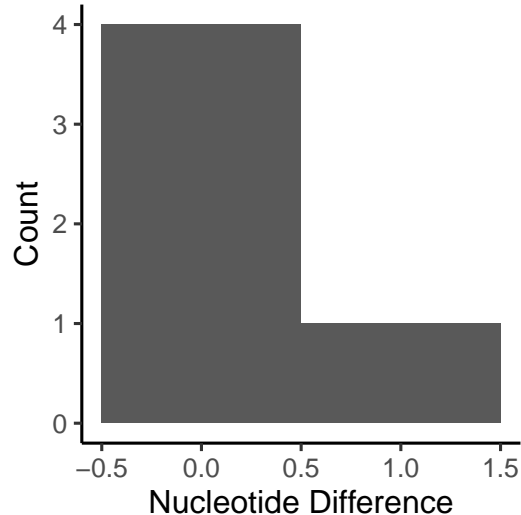
IGHV5–10–1*01_03

32 sequences assigned
28 (87.5%) exact matches, in which:
28 unique CDR3
5 unique J



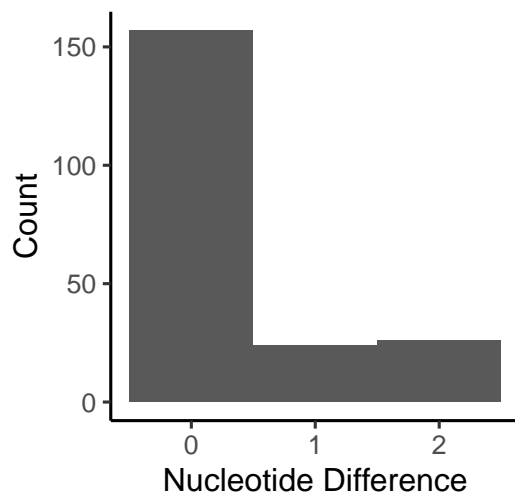
IGHV7–4–1*01

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



IGHV5–51*01_03

207 sequences assigned
157 (75.8%) exact matches, in which:
157 unique CDR3
6 unique J





Novel sequence(s) IGHV1-59*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.

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.