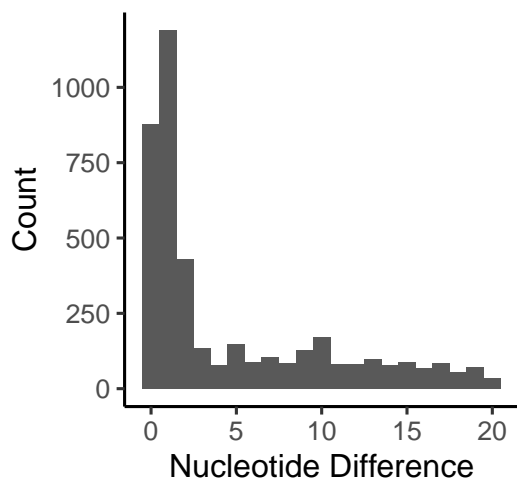


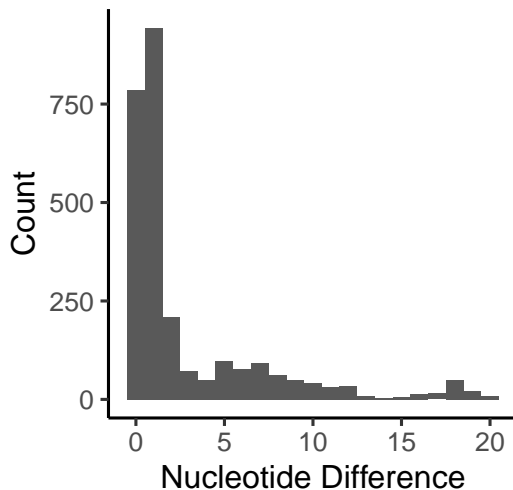
IGHV1-2*02

4319 sequences assigned
879 (20.4%) exact matches, in which:
693 unique CDR3
6 unique J



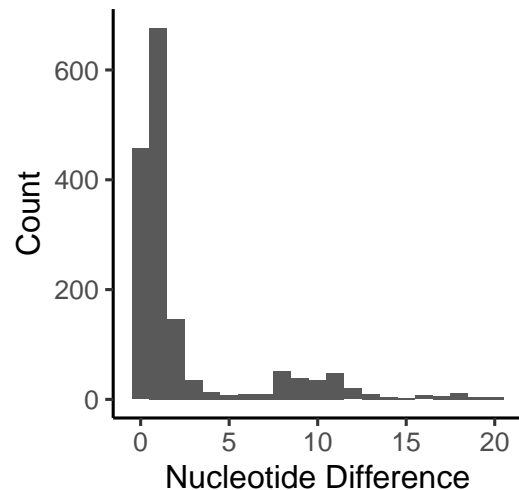
IGHV1-8*01

2779 sequences assigned
785 (28.2%) exact matches, in which:
644 unique CDR3
6 unique J



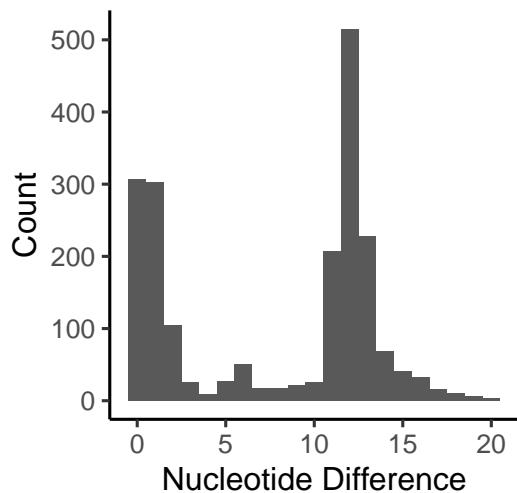
IGHV1-24*01

1605 sequences assigned
457 (28.5%) exact matches, in which:
373 unique CDR3
6 unique J



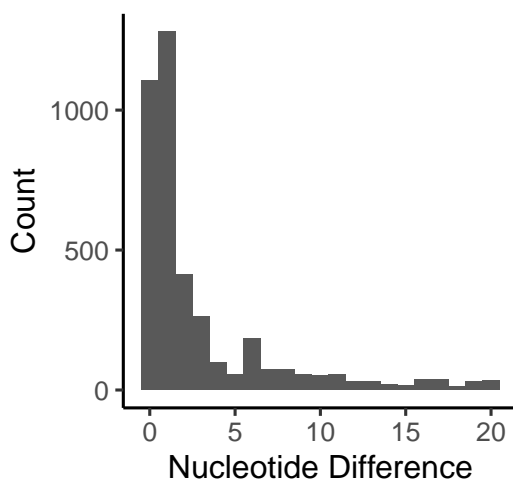
IGHV1-2*04

2041 sequences assigned
307 (15%) exact matches, in which:
254 unique CDR3
6 unique J



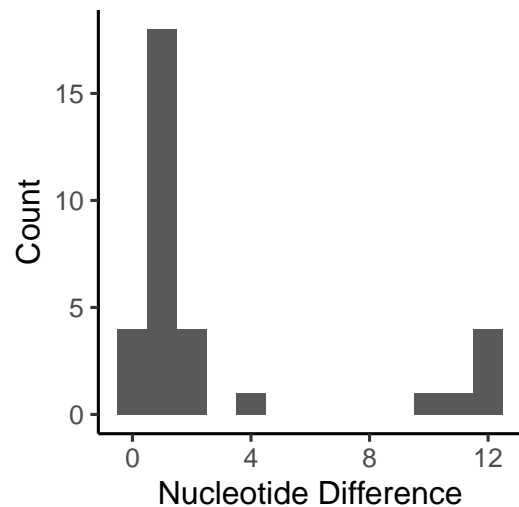
IGHV1-18*01

4178 sequences assigned
1107 (26.5%) exact matches, in which:
888 unique CDR3
6 unique J



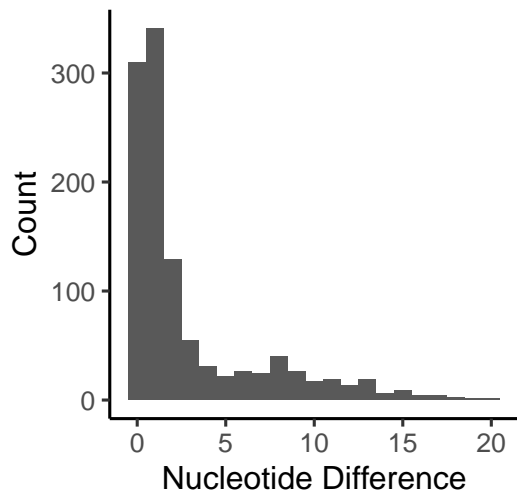
IGHV1-45*02

33 sequences assigned
4 (12.1%) exact matches, in which:
4 unique CDR3
2 unique J



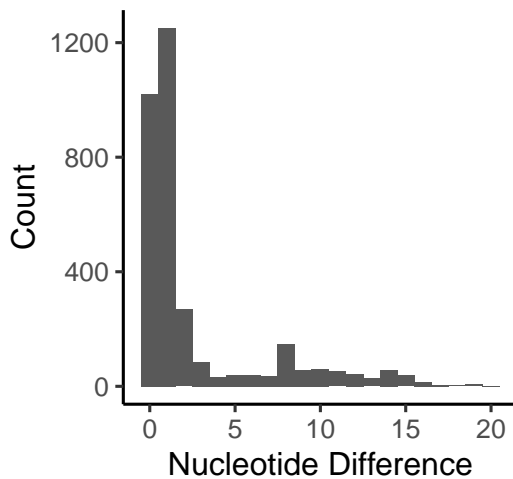
IGHV1-3*01_05

1125 sequences assigned
310 (27.6%) exact matches, in which:
250 unique CDR3
5 unique J



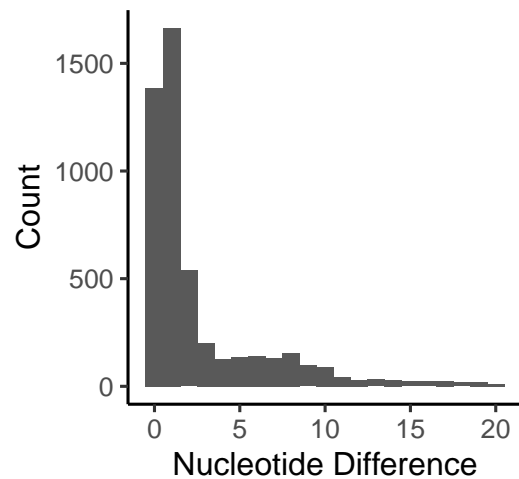
IGHV1-18*04

3561 sequences assigned
1021 (28.7%) exact matches, in which:
825 unique CDR3
6 unique J



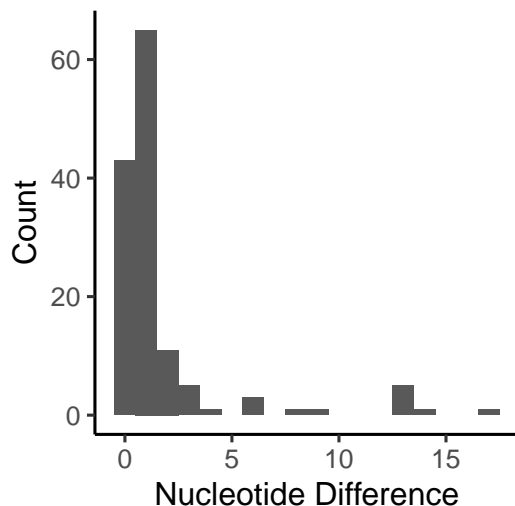
IGHV1-46*01

5161 sequences assigned
1386 (26.9%) exact matches, in which:
1125 unique CDR3
6 unique J



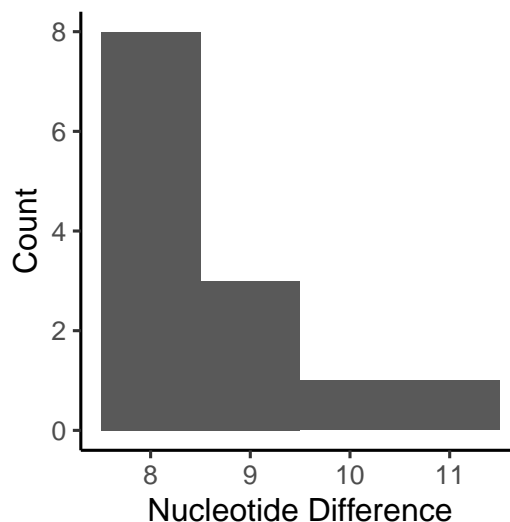
IGHV1–58*02

137 sequences assigned
43 (31.4%) exact matches, in which:
38 unique CDR3
5 unique J



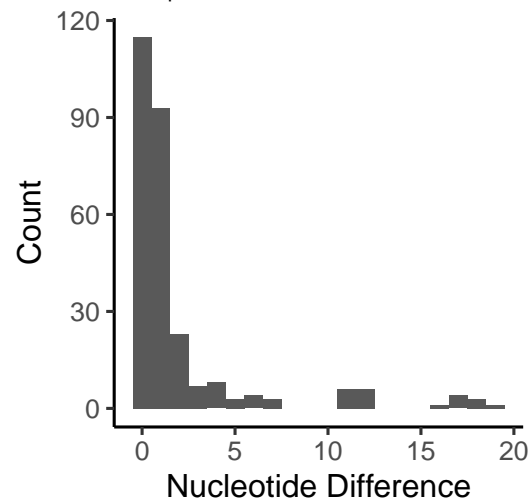
IGHV1–NL1*01

13 sequences assigned
No exact matches.



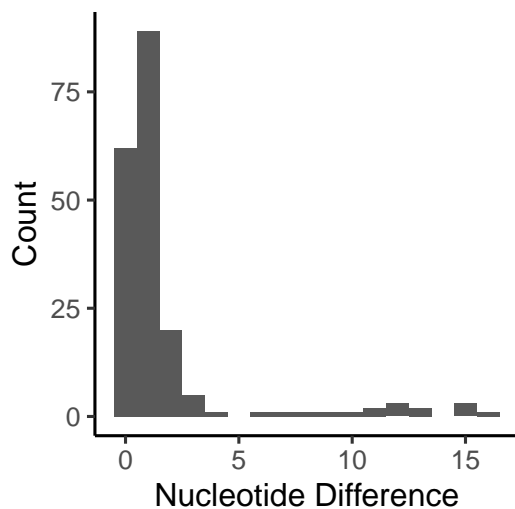
IGHV2–26*01

278 sequences assigned
115 (41.4%) exact matches, in which:
98 unique CDR3
5 unique J



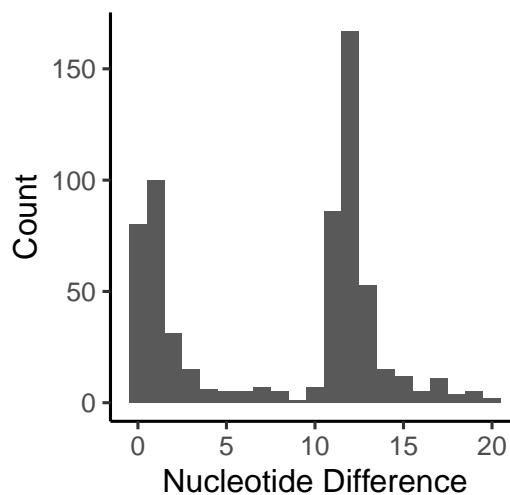
IGHV1–58*01_03

193 sequences assigned
62 (32.1%) exact matches, in which:
46 unique CDR3
5 unique J



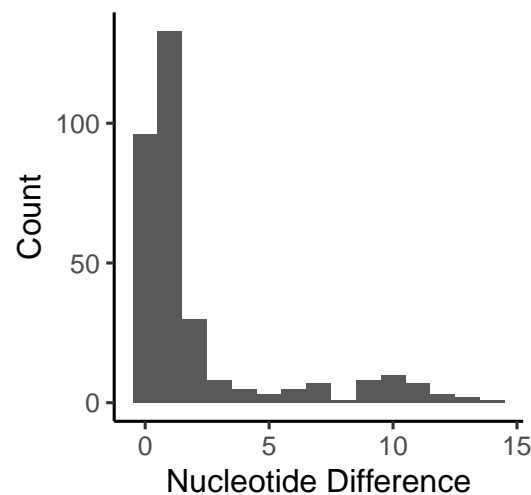
IGHV2–5*01

977 sequences assigned
80 (8.2%) exact matches, in which:
63 unique CDR3
6 unique J



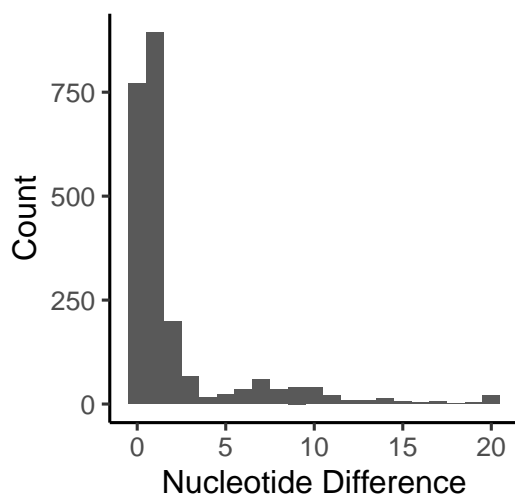
IGHV2–70*01

319 sequences assigned
96 (30.1%) exact matches, in which:
75 unique CDR3
5 unique J



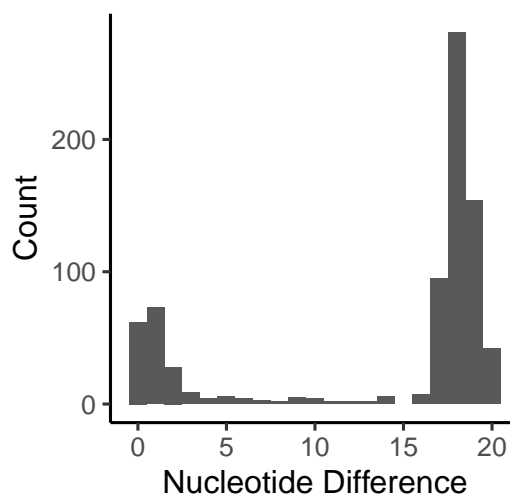
IGHV1–69*04_09

2336 sequences assigned
770 (33%) exact matches, in which:
667 unique CDR3
6 unique J



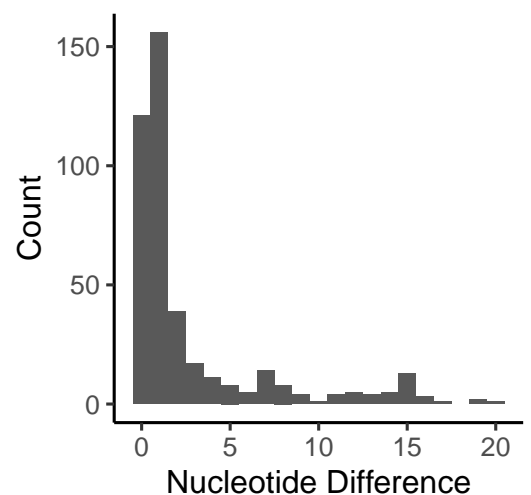
IGHV2–5*02

860 sequences assigned
62 (7.2%) exact matches, in which:
50 unique CDR3
5 unique J



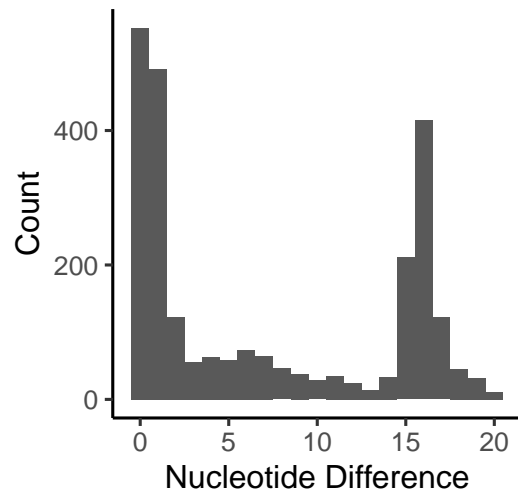
IGHV2–70*11_15

441 sequences assigned
121 (27.4%) exact matches, in which:
96 unique CDR3
5 unique J



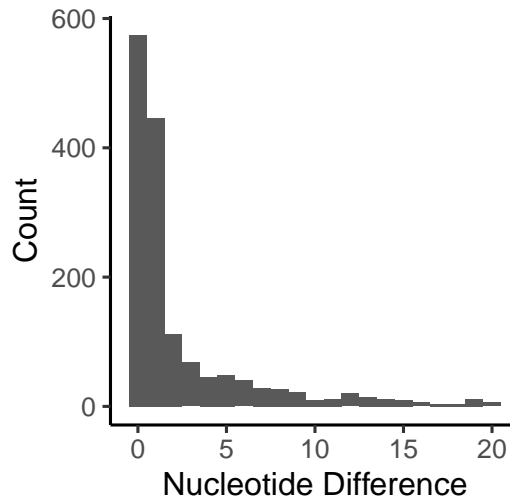
IGHV3-7*01

2644 sequences assigned
553 (20.9%) exact matches, in which:
350 unique CDR3
6 unique J



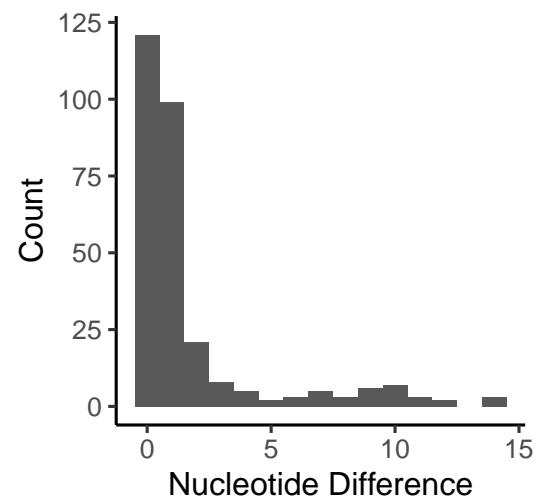
IGHV3-11*01

1540 sequences assigned
575 (37.3%) exact matches, in which:
353 unique CDR3
6 unique J



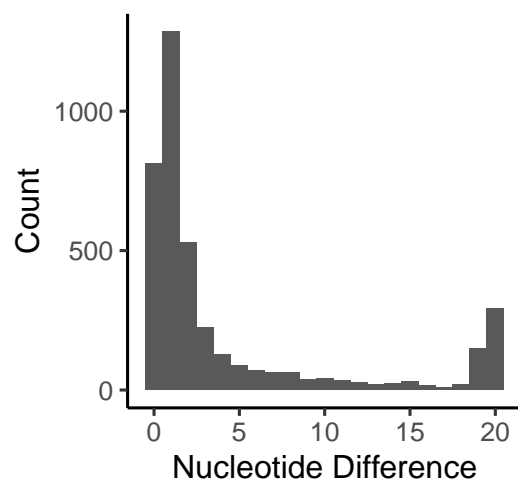
IGHV3-13*01

309 sequences assigned
121 (39.2%) exact matches, in which:
71 unique CDR3
5 unique J



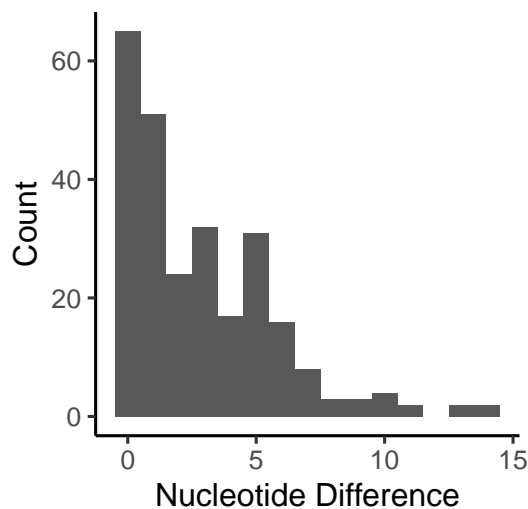
IGHV3-7*03

5162 sequences assigned
811 (15.7%) exact matches, in which:
446 unique CDR3
6 unique J



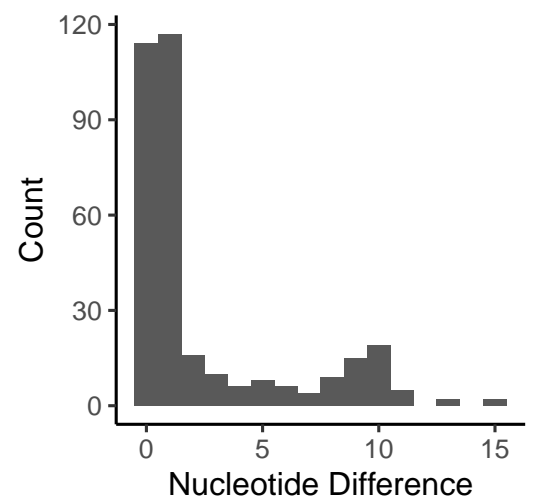
IGHV3-11*06

261 sequences assigned
65 (24.9%) exact matches, in which:
64 unique CDR3
6 unique J



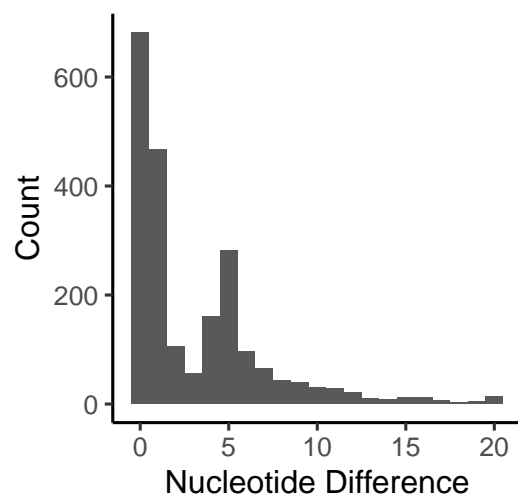
IGHV3-13*04

333 sequences assigned
114 (34.2%) exact matches, in which:
68 unique CDR3
6 unique J



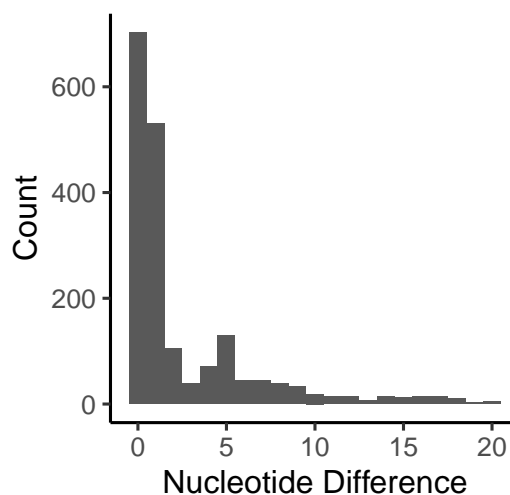
IGHV3-9*01

2227 sequences assigned
682 (30.6%) exact matches, in which:
407 unique CDR3
6 unique J



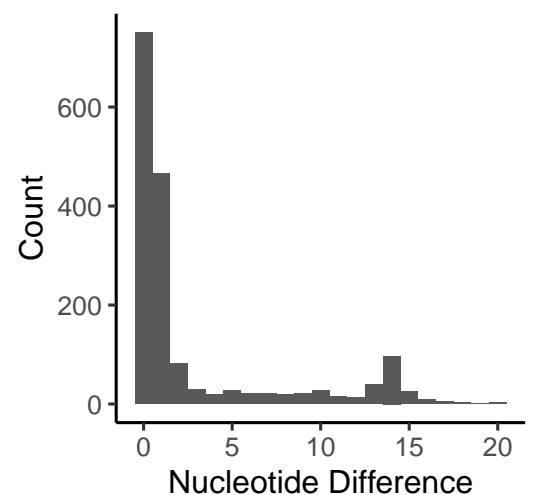
IGHV3-11*03_05

1891 sequences assigned
703 (37.2%) exact matches, in which:
412 unique CDR3
6 unique J



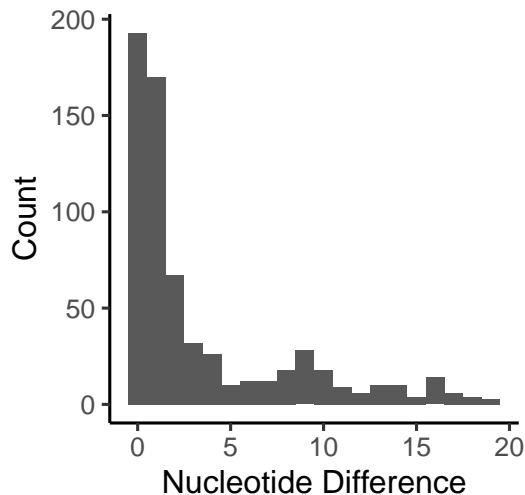
IGHV3-15*01_02

2591 sequences assigned
751 (29%) exact matches, in which:
418 unique CDR3
6 unique J



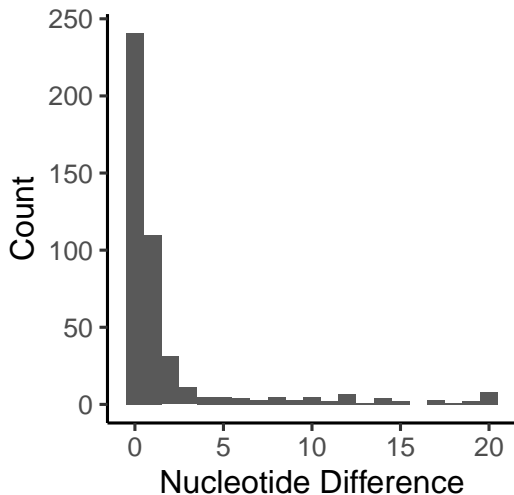
IGHV3-20*03_04

682 sequences assigned
193 (28.3%) exact matches, in which:
101 unique CDR3
5 unique J



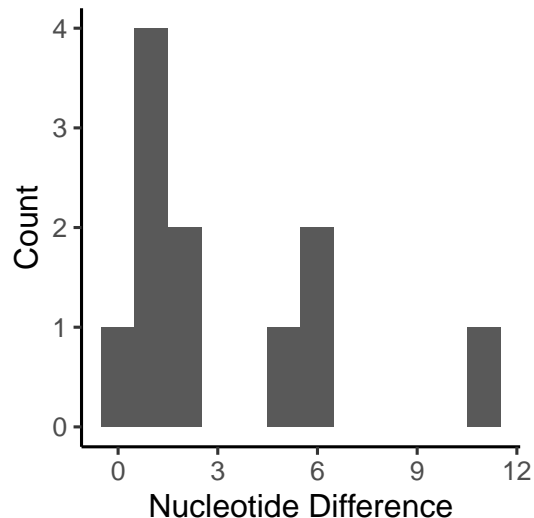
IGHV3-30*03

941 sequences assigned
241 (25.6%) exact matches, in which:
225 unique CDR3
6 unique J



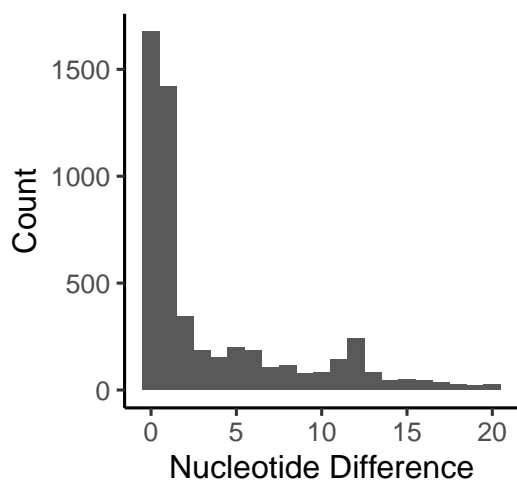
IGHV3-38-3*01

11 sequences assigned
1 (9.1%) exact matches, in which:
1 unique CDR3
1 unique J



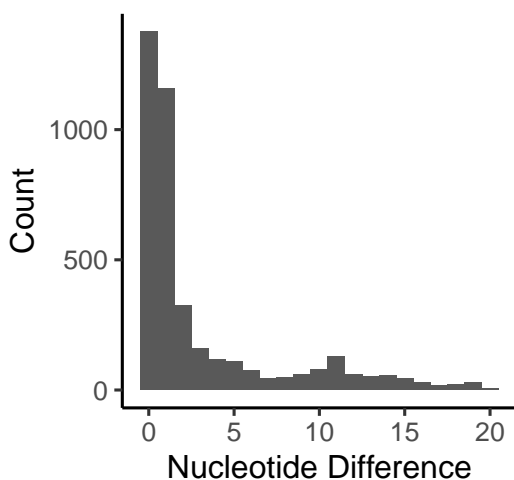
IGHV3-21*01_02

5502 sequences assigned
1676 (30.5%) exact matches, in which:
958 unique CDR3
6 unique J



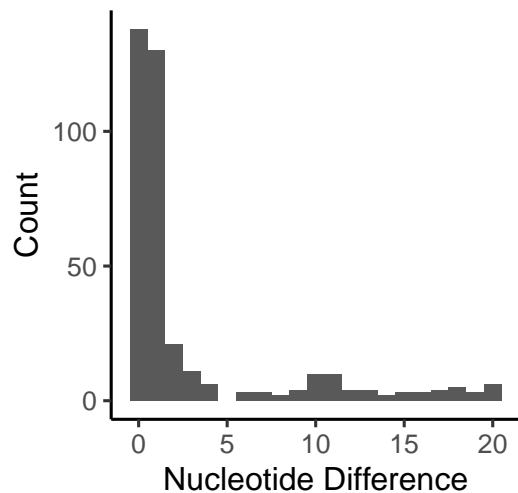
IGHV3-33*01

4056 sequences assigned
1376 (33.9%) exact matches, in which:
828 unique CDR3
6 unique J



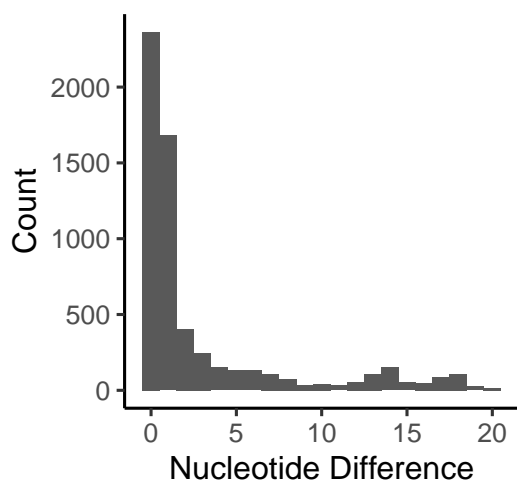
IGHV3-43*01

389 sequences assigned
138 (35.5%) exact matches, in which:
73 unique CDR3
5 unique J



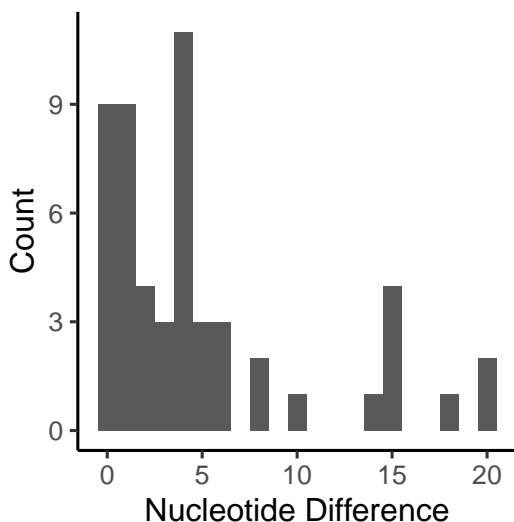
IGHV3-30-3*01

6240 sequences assigned
2363 (37.9%) exact matches, in which:
1407 unique CDR3
6 unique J



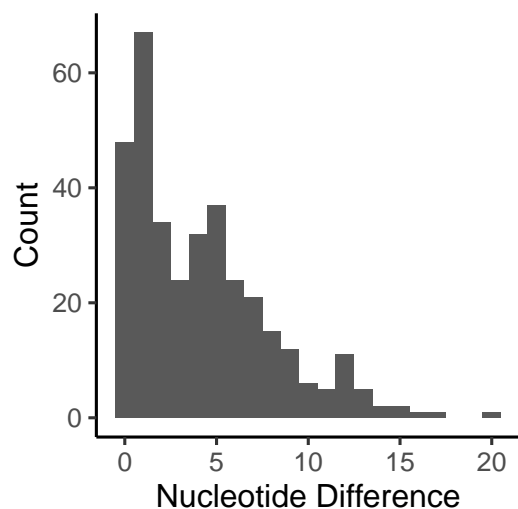
IGHV3-33*05

54 sequences assigned
9 (16.7%) exact matches, in which:
9 unique CDR3
2 unique J



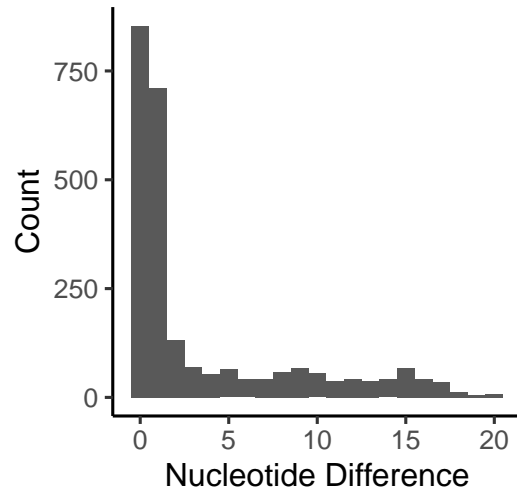
IGHV3-48*01

351 sequences assigned
48 (13.7%) exact matches, in which:
47 unique CDR3
4 unique J



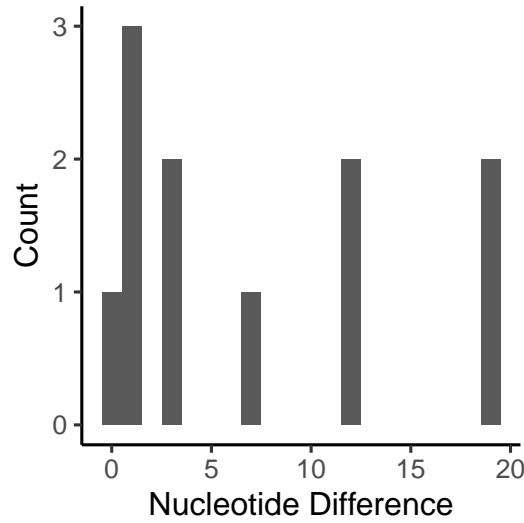
IGHV3-48*02

2598 sequences assigned
854 (32.9%) exact matches, in which:
462 unique CDR3
6 unique J



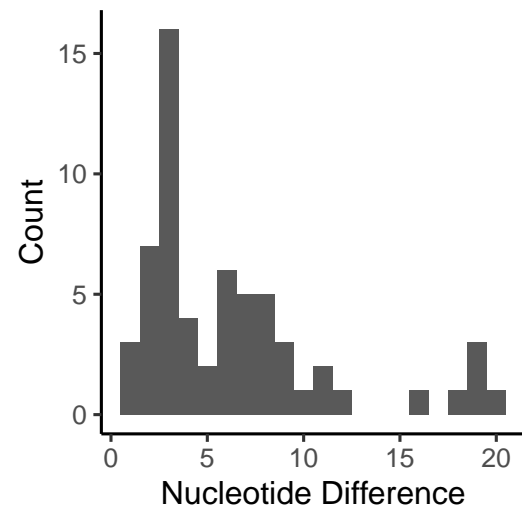
IGHV3-53*05

14 sequences assigned
1 (7.1%) exact matches, in which:
1 unique CDR3
1 unique J



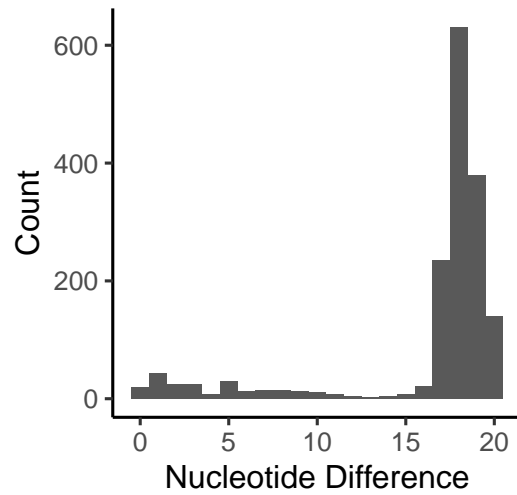
IGHV3-64*04

82 sequences assigned
No exact matches.



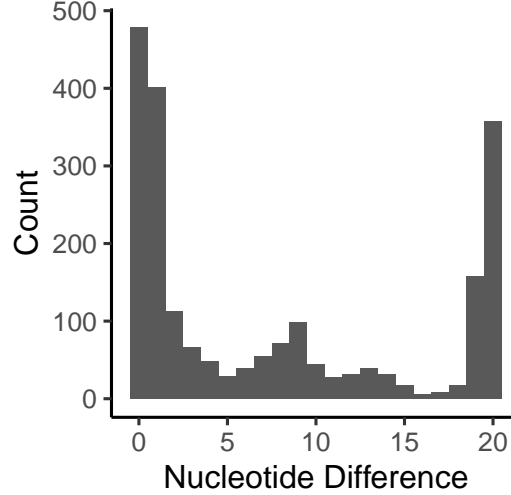
IGHV3-48*04

1790 sequences assigned
19 (1.1%) exact matches, in which:
19 unique CDR3
4 unique J



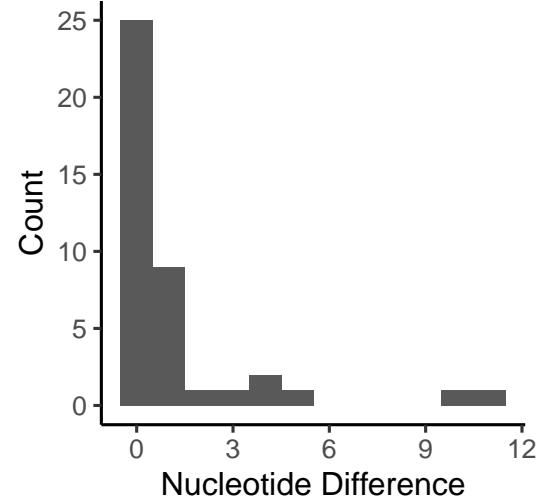
IGHV3-53*01_02

2704 sequences assigned
479 (17.7%) exact matches, in which:
295 unique CDR3
6 unique J



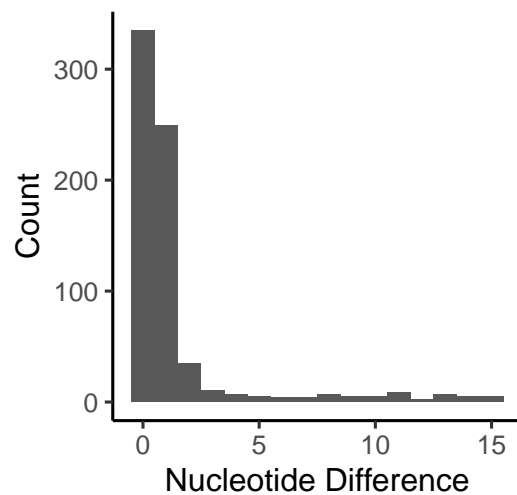
IGHV3-64*02_07

41 sequences assigned
25 (61%) exact matches, in which:
14 unique CDR3
3 unique J



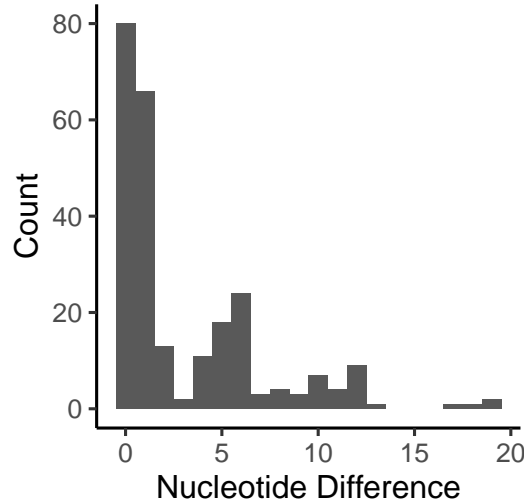
IGHV3-49*03_05

695 sequences assigned
335 (48.2%) exact matches, in which:
194 unique CDR3
6 unique J



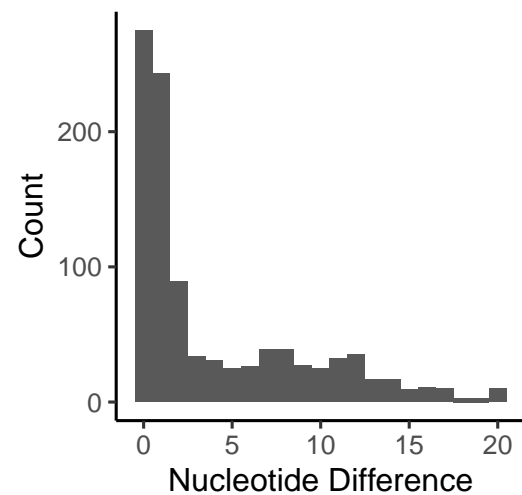
IGHV3-64*01

251 sequences assigned
80 (31.9%) exact matches, in which:
52 unique CDR3
5 unique J



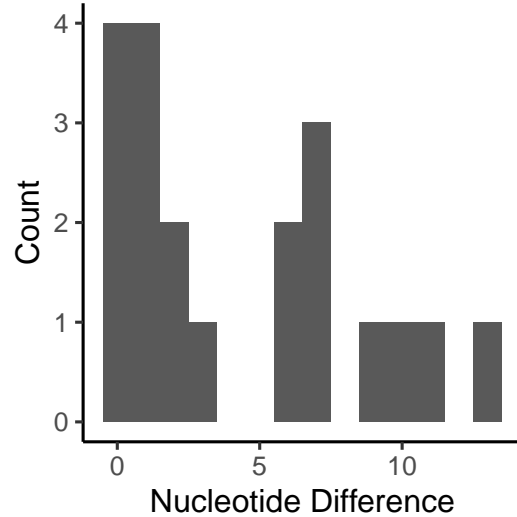
IGHV3-66*01

1007 sequences assigned
275 (27.3%) exact matches, in which:
165 unique CDR3
5 unique J



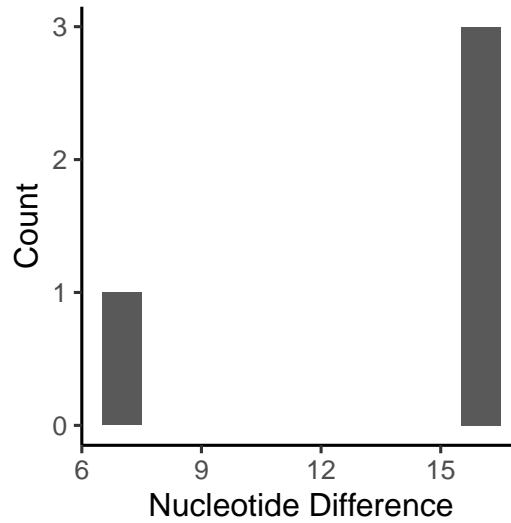
IGHV3-66*03

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



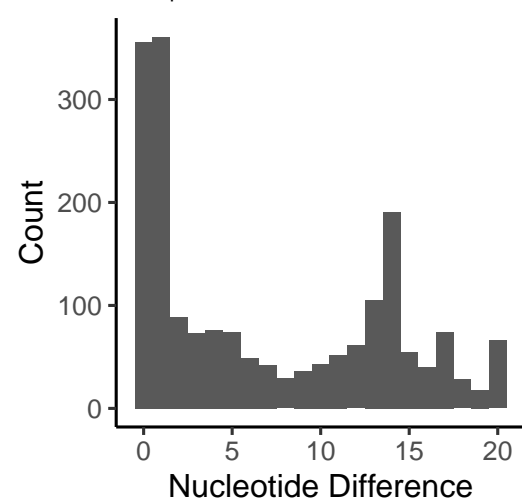
IGHV3-71*01_04

4 sequences assigned
No exact matches.



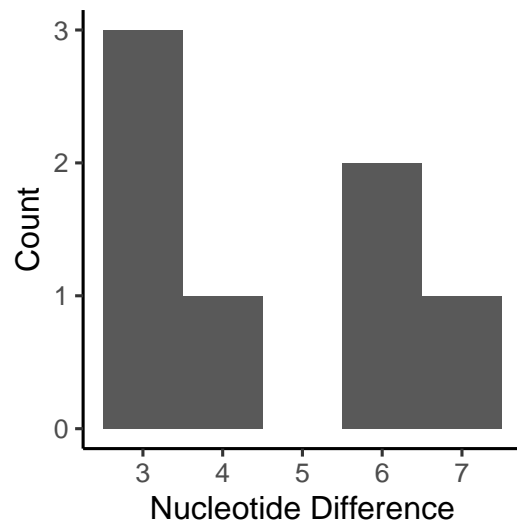
IGHV3-74*01_02

2223 sequences assigned
356 (16%) exact matches, in which:
212 unique CDR3
6 unique J



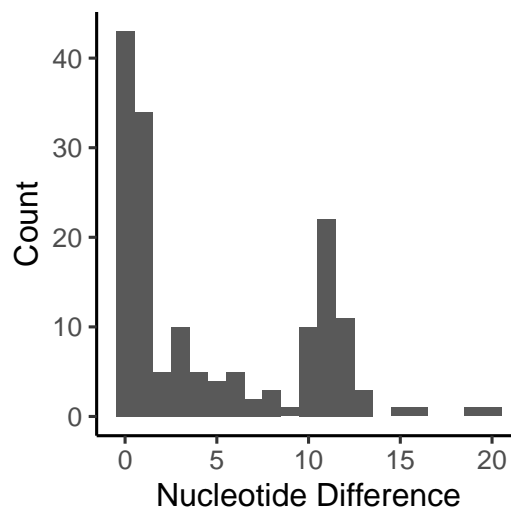
IGHV3-69-1*01

8 sequences assigned
No exact matches.



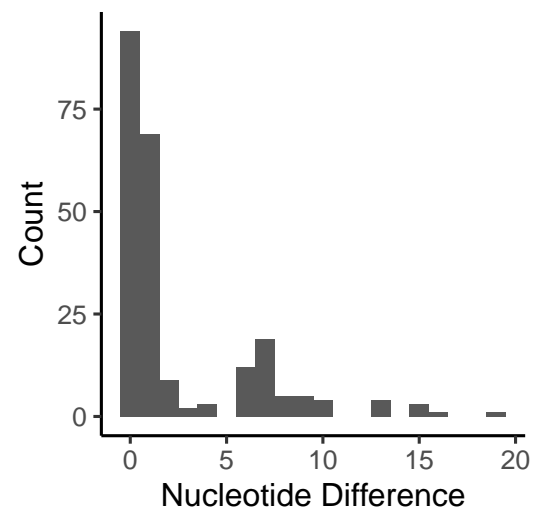
IGHV3-72*01

176 sequences assigned
43 (24.4%) exact matches, in which:
26 unique CDR3
3 unique J



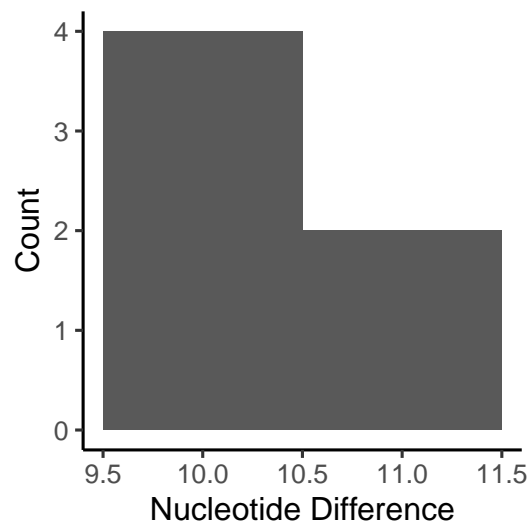
IGHV3-43D*03

231 sequences assigned
94 (40.7%) exact matches, in which:
52 unique CDR3
4 unique J



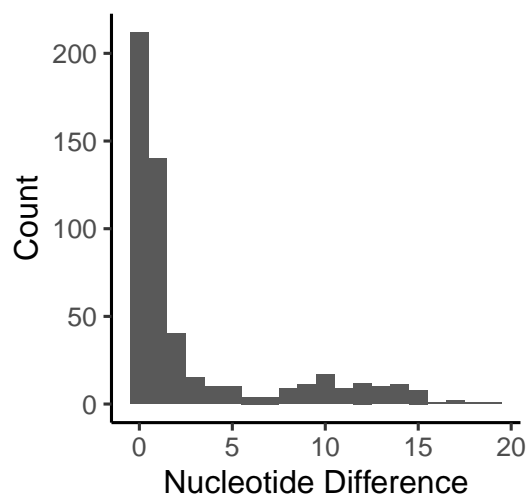
IGHV3-69-1*02

6 sequences assigned
No exact matches.



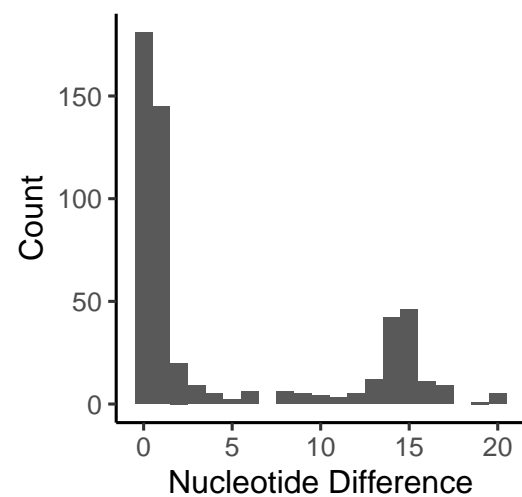
IGHV3-73*01_02

528 sequences assigned
212 (40.2%) exact matches, in which:
119 unique CDR3
5 unique J



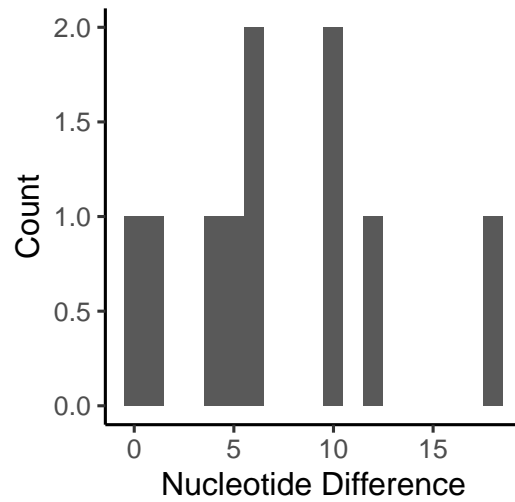
IGHV3-64D*06

773 sequences assigned
181 (23.4%) exact matches, in which:
99 unique CDR3
5 unique J



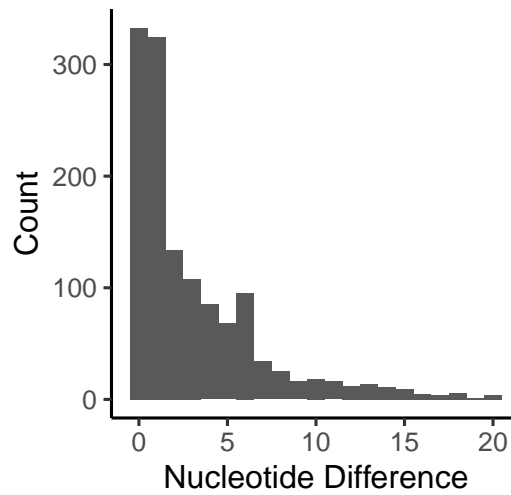
IGHV3–NL1*01

10 sequences assigned
1 (10%) exact matches, in which:
1 unique CDR3
1 unique J



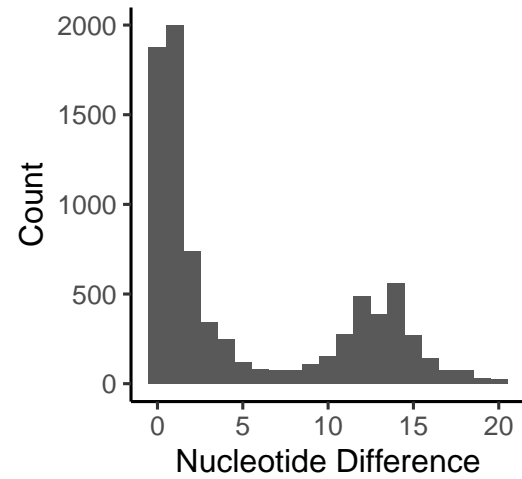
IGHV4–30–4*01

1414 sequences assigned
333 (23.6%) exact matches, in which:
272 unique CDR3
6 unique J



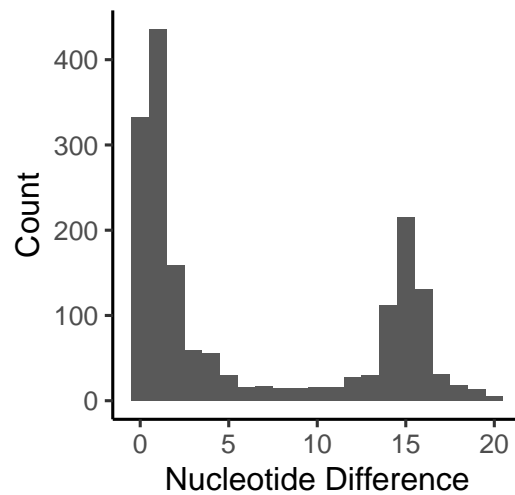
IGHV4–34*01_02

9027 sequences assigned
1878 (20.8%) exact matches, in which:
1298 unique CDR3
6 unique J



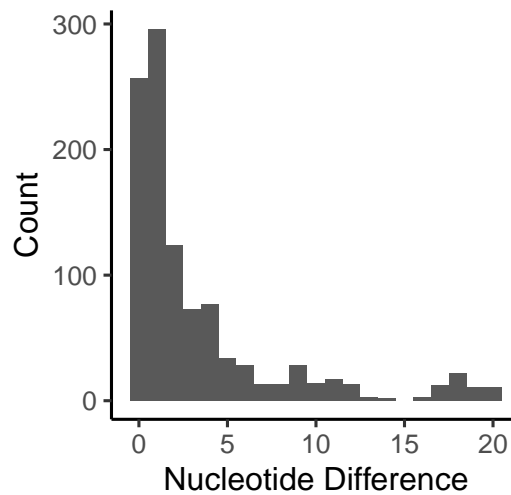
IGHV4–4*07

2313 sequences assigned
333 (14.4%) exact matches, in which:
274 unique CDR3
5 unique J



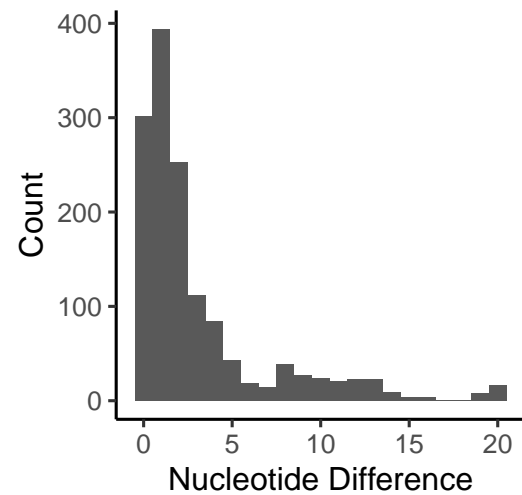
IGHV4–30–2*01

1183 sequences assigned
257 (21.7%) exact matches, in which:
190 unique CDR3
6 unique J



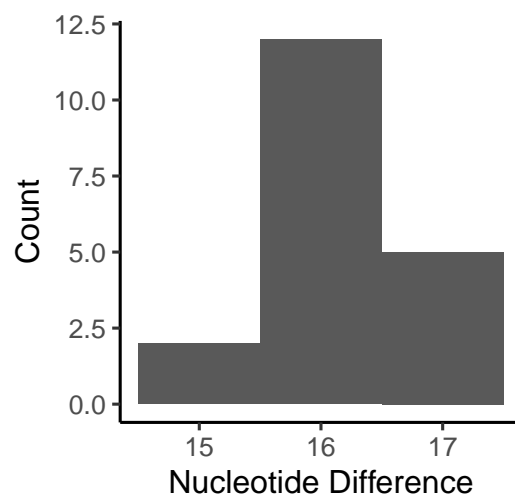
IGHV4–38–2*02

1576 sequences assigned
302 (19.2%) exact matches, in which:
257 unique CDR3
6 unique J



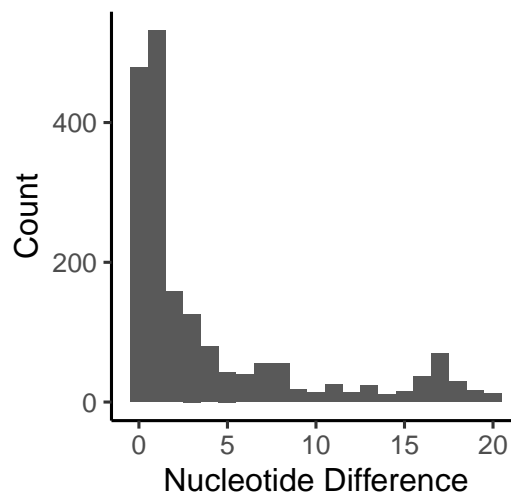
IGHV4–28*02_05

19 sequences assigned
No exact matches.



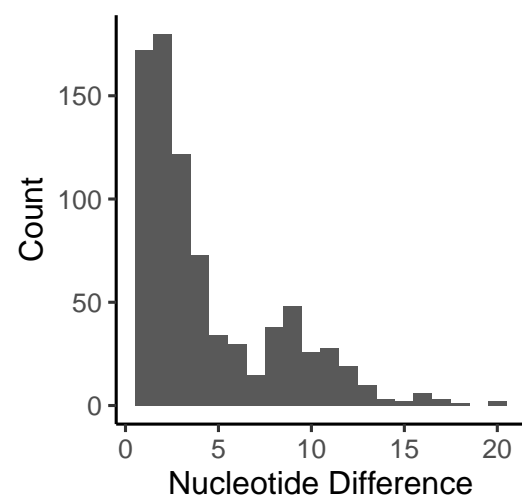
IGHV4–31*03_04

2134 sequences assigned
479 (22.4%) exact matches, in which:
398 unique CDR3
6 unique J



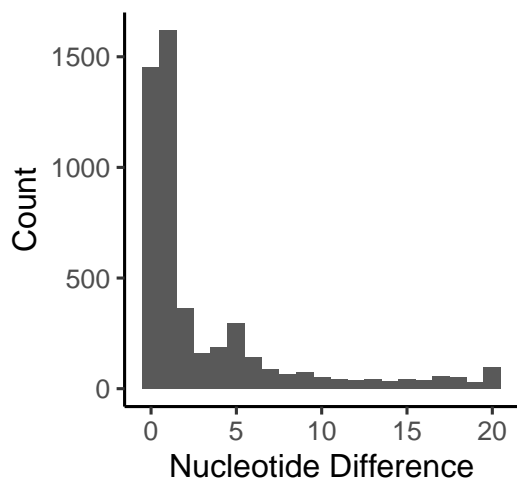
IGHV4–39*07

820 sequences assigned
No exact matches.



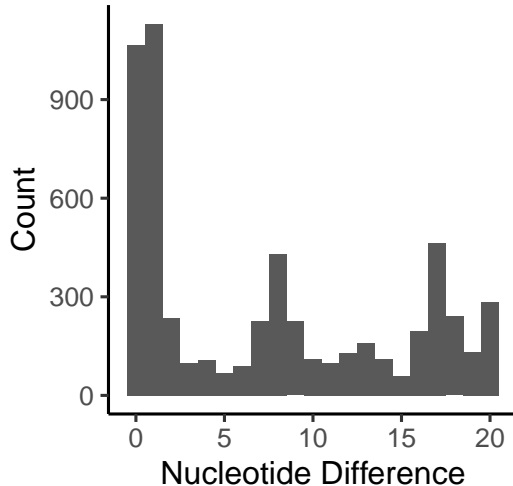
IGHV4-39*01_05

6862 sequences assigned
1451 (21.1%) exact matches, in which:
1161 unique CDR3
6 unique J



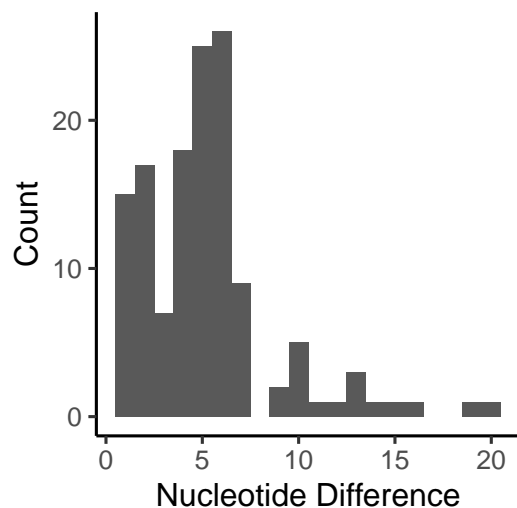
IGHV4-59*01_07

10528 sequences assigned
1066 (10.1%) exact matches, in which:
858 unique CDR3
6 unique J



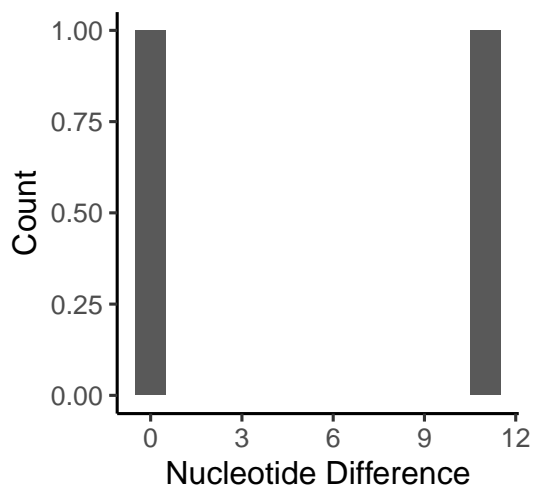
IGHV4-61*08

141 sequences assigned
No exact matches.



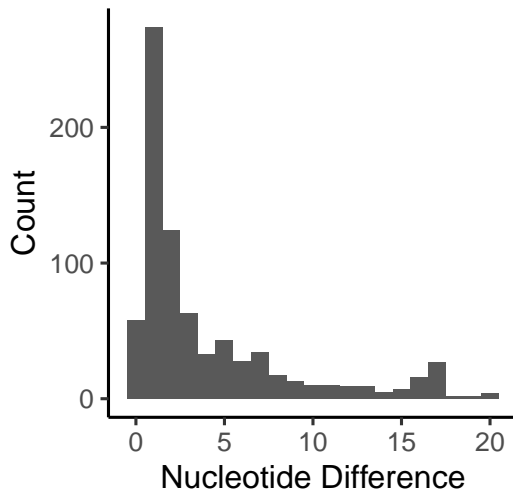
IGHV4-55*01_05

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



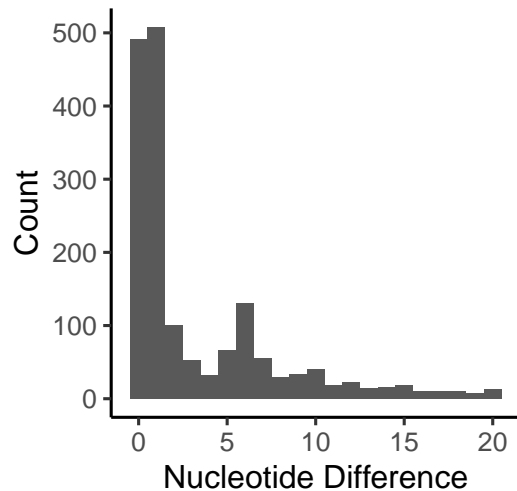
IGHV4-59*12

938 sequences assigned
58 (6.2%) exact matches, in which:
57 unique CDR3
5 unique J



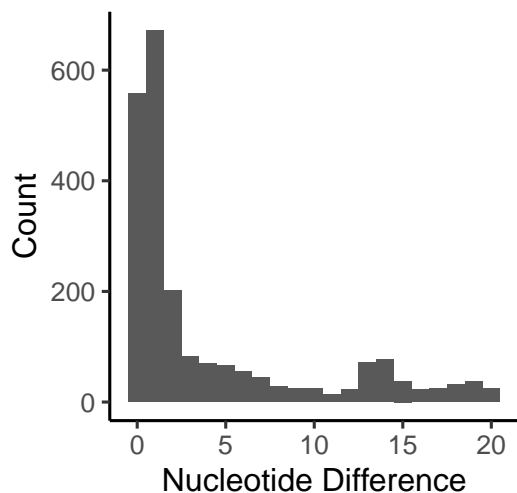
IGHV5-10-1*01_03

1965 sequences assigned
491 (25%) exact matches, in which:
305 unique CDR3
6 unique J



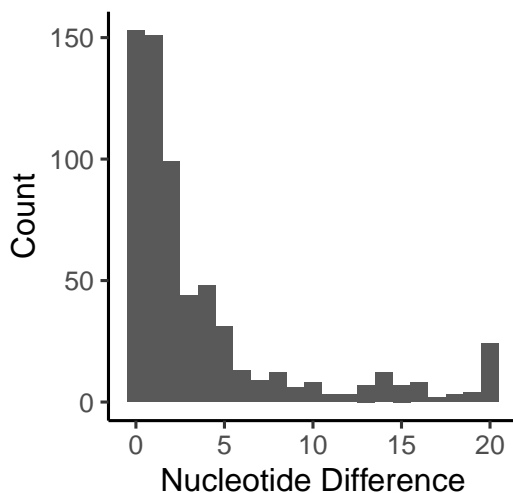
IGHV4-59*08

2434 sequences assigned
558 (22.9%) exact matches, in which:
447 unique CDR3
6 unique J



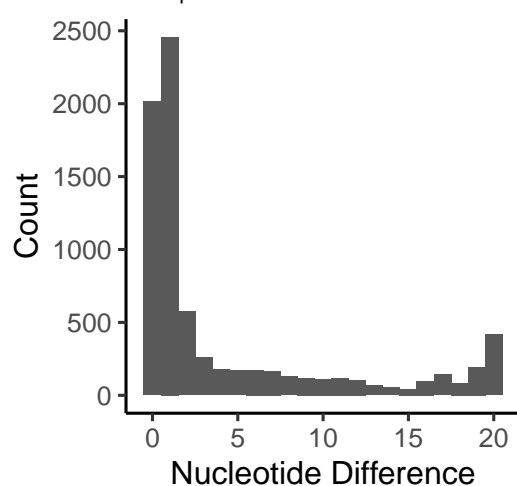
IGHV4-61*01

1703 sequences assigned
153 (9%) exact matches, in which:
129 unique CDR3
6 unique J



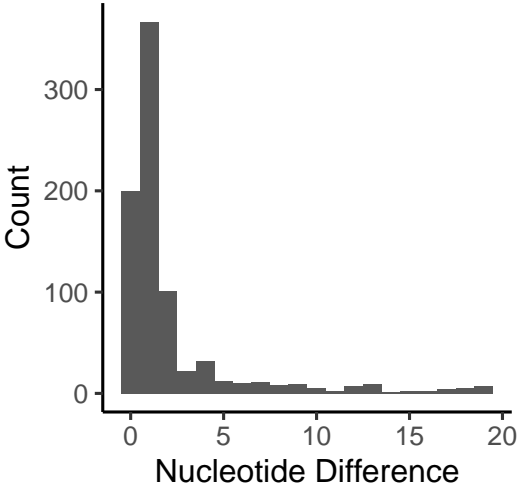
IGHV5-51*01_03

8249 sequences assigned
2015 (24.4%) exact matches, in which:
1083 unique CDR3
6 unique J



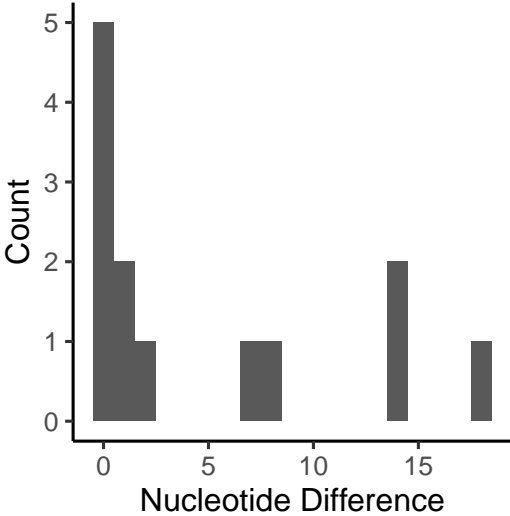
IGHV6-1*01_02

823 sequences assigned
200 (24.3%) exact matches, in which:
153 unique CDR3
6 unique J



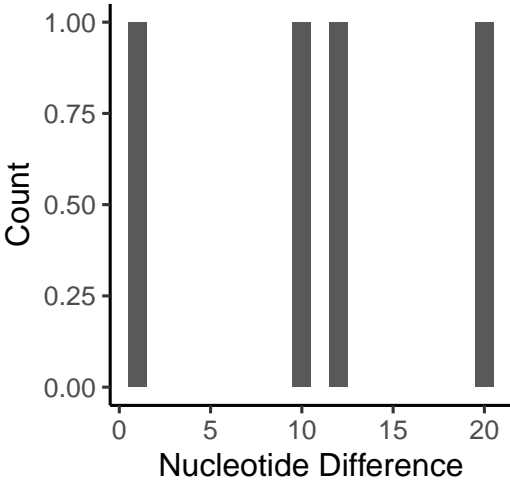
IGHV7-4-1*01

13 sequences assigned
5 (38.5%) exact matches, in which:
5 unique CDR3
1 unique J



IGHV7-4-1*02

4 sequences assigned
No exact matches.





Warning - no inferred sequences found.

Novel sequence(s) IGHV3-33*01_G75C IGHV4-59*02_G88A IGHV5-51*07_A128G are not listed in the genotype and will be ignored.

Novel sequence(s) IGHV3-33*01_G75C IGHV4-59*02_G88A IGHV5-51*07_A128G are not listed in the genotype and will be ignored.

Novel sequence(s) IGHV3-30*03_T288C 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) IGHV1-69*08_09_G112A IGHV4-59*02_G88A IGHV5-10-1*01_03_T258C IGHV5-51*07_A128G are not listed in the genotype and will be ignored.

Warning - no inferred sequences found.

Novel sequence(s) IGHV1-69*08_C191T IGHV3-48*03_T303G 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) IGHV3-30*03_T288C IGHV5-51*07_A128G are not listed in the genotype and will be ignored.

Warning: IGHV4-31*02, IGHV4-31*03_04 have identical germline sequences.

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

Novel sequence(s) IGHV1-69*04_09_G112A 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*08_C191T IGHV3-30*03_T288C IGHV3-30-3*02_G75C 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.