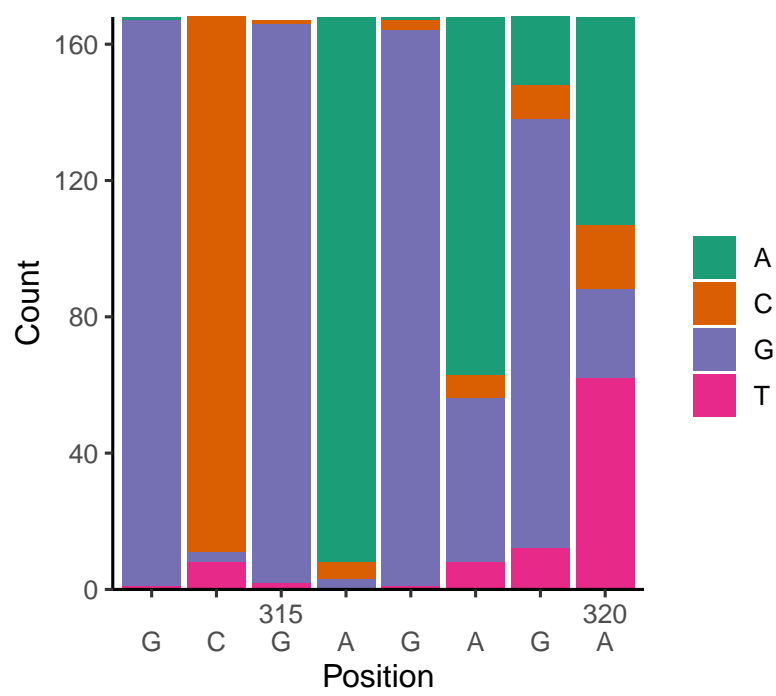
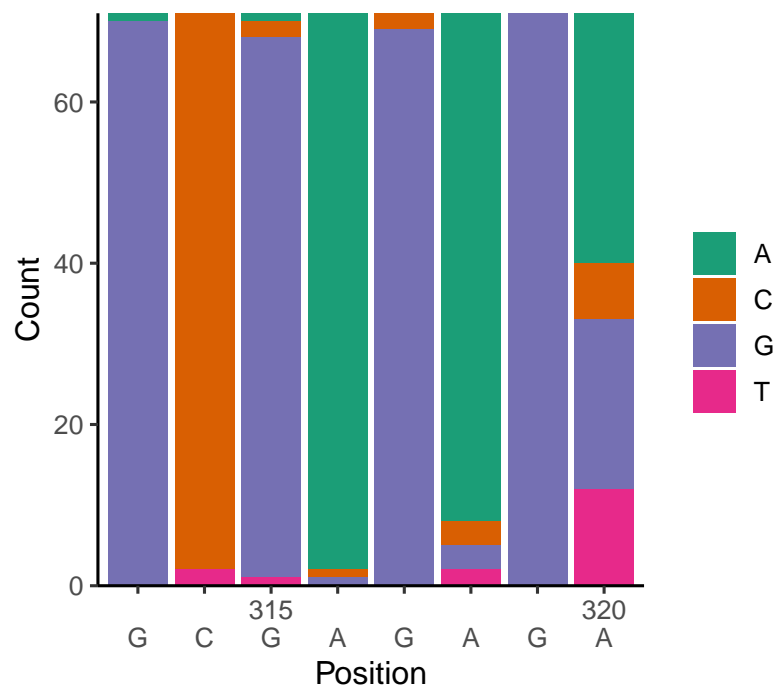


Gene IGHV4-38-2*02_A70G



Gene IGHV4-39*02_C258G



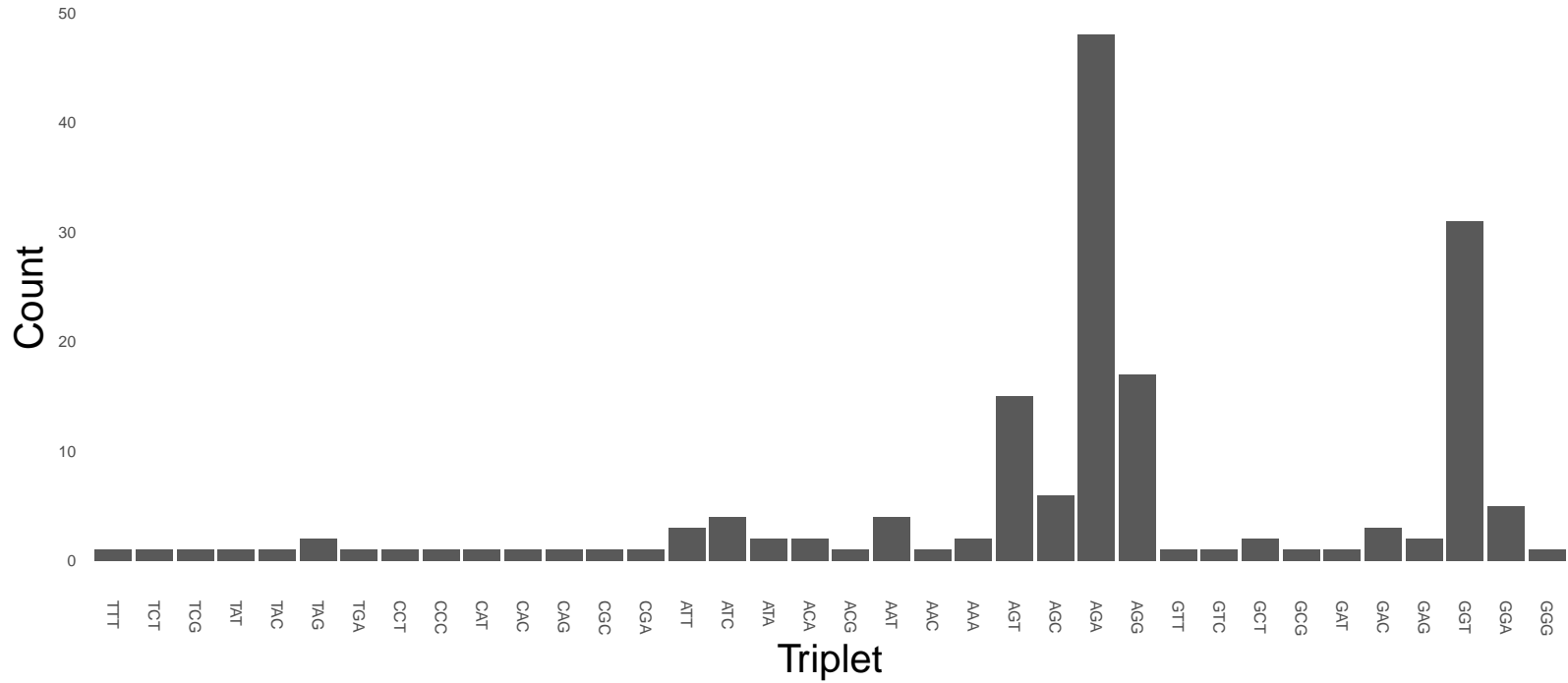
Gene IGHV4-38-2*02_A70G



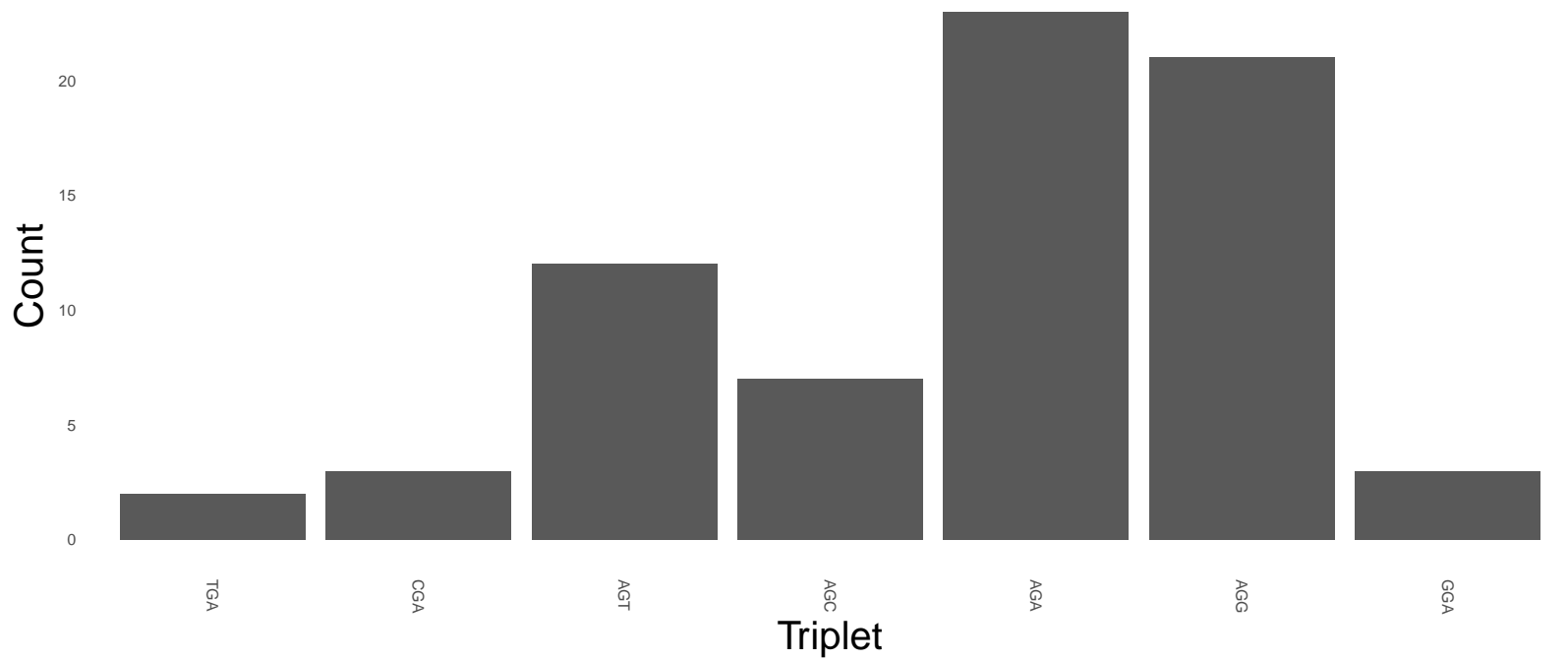
Gene IGHV4-39*02_C258G



IGHV4-38-2*02_A70G- Final 3 nucleotides as a triplet

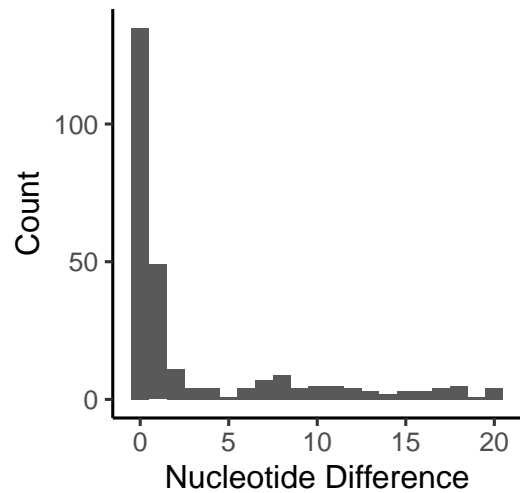


IGHV4-39*02_C258G- Final 3 nucleotides as a triplet



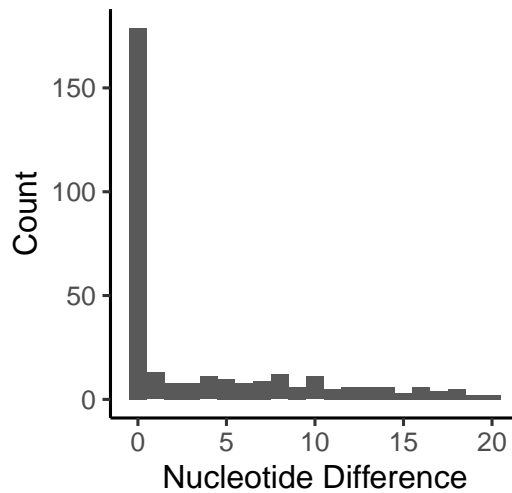
IGHV1-2*02

296 sequences assigned
135 (45.6%) exact matches, in which:
135 unique CDR3
6 unique J



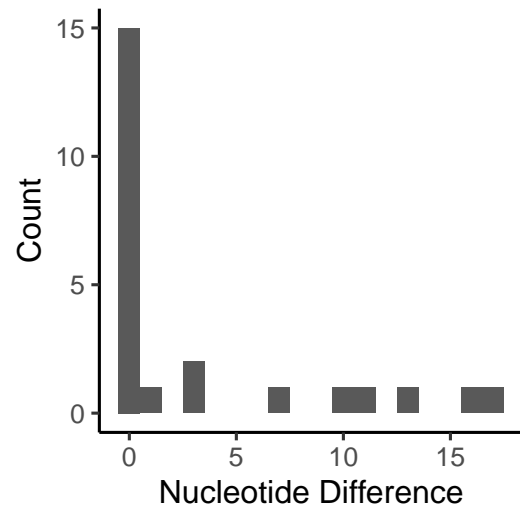
IGHV1-18*01

351 sequences assigned
179 (51%) exact matches, in which:
178 unique CDR3
5 unique J



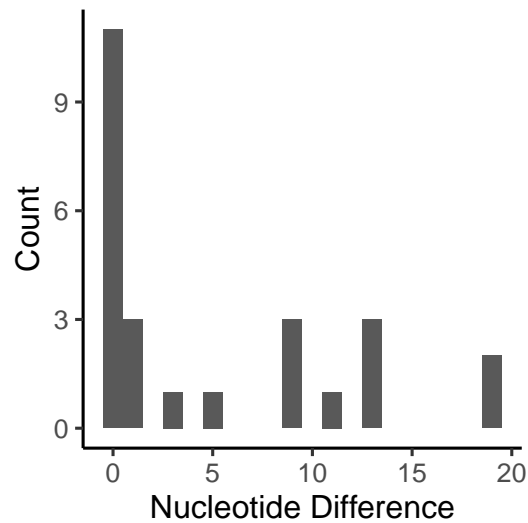
IGHV1-46*03

24 sequences assigned
15 (62.5%) exact matches, in which:
15 unique CDR3
4 unique J



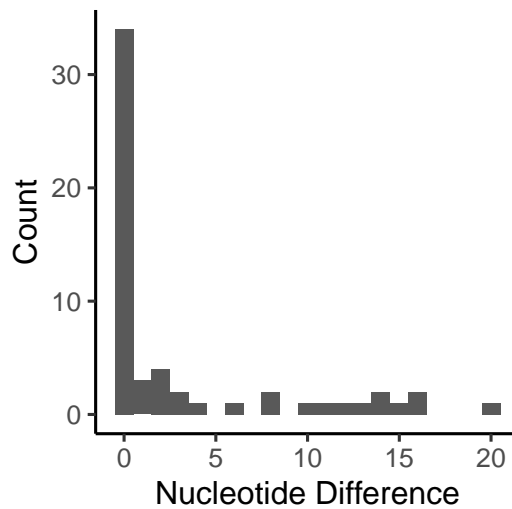
IGHV1-3*01_05

28 sequences assigned
11 (39.3%) exact matches, in which:
11 unique CDR3
4 unique J



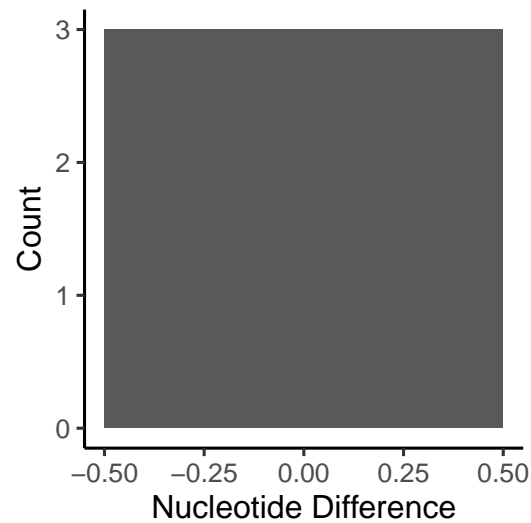
IGHV1-24*01

59 sequences assigned
34 (57.6%) exact matches, in which:
34 unique CDR3
5 unique J



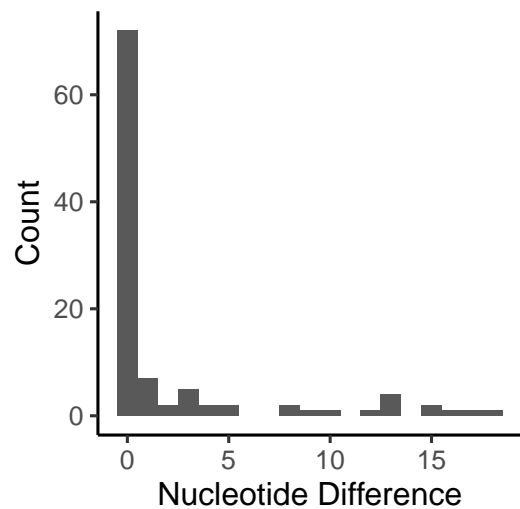
IGHV1-58*02

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



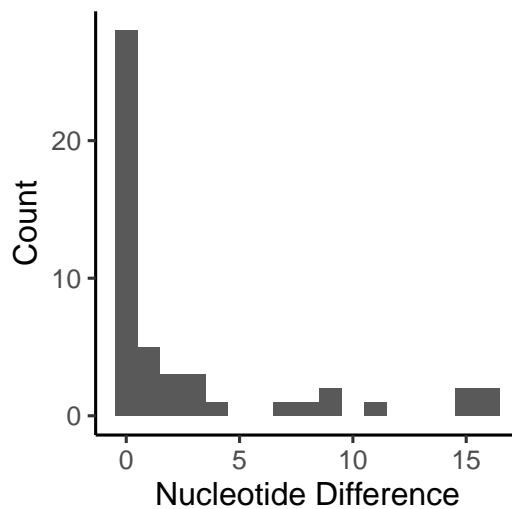
IGHV1-8*01

110 sequences assigned
72 (65.5%) exact matches, in which:
72 unique CDR3
5 unique J



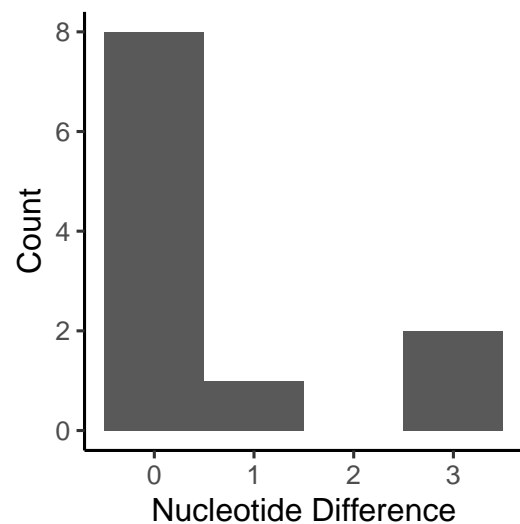
IGHV1-46*01

50 sequences assigned
28 (56%) exact matches, in which:
28 unique CDR3
5 unique J



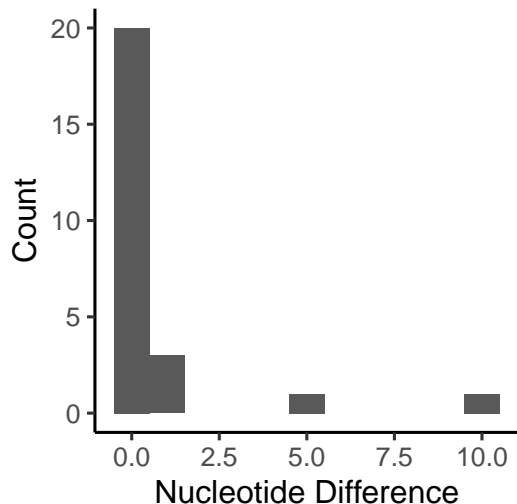
IGHV1-58*01_03

12 sequences assigned
8 (66.7%) exact matches, in which:
8 unique CDR3
5 unique J



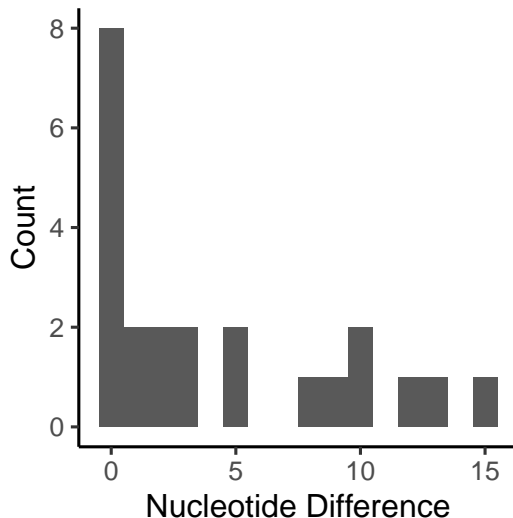
IGHV1-69*02

27 sequences assigned
20 (74.1%) exact matches, in which:
20 unique CDR3
5 unique J



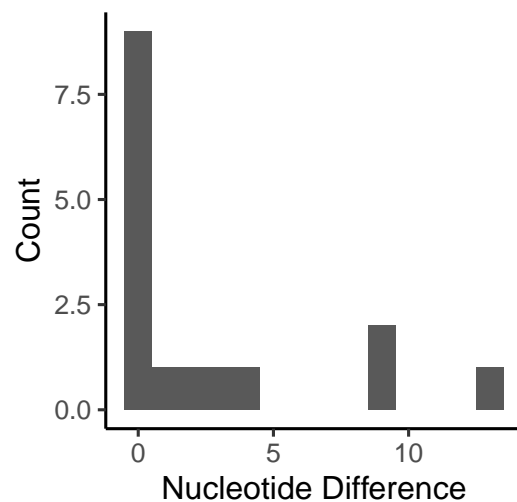
IGHV2-5*02

28 sequences assigned
8 (28.6%) exact matches, in which:
8 unique CDR3
4 unique J



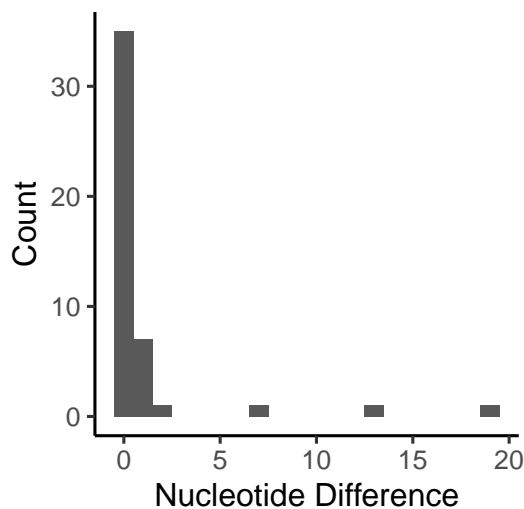
IGHV2-70*11_15

16 sequences assigned
9 (56.2%) exact matches, in which:
9 unique CDR3
4 unique J



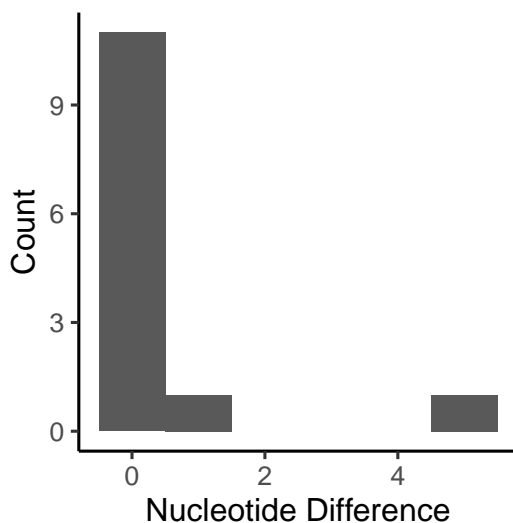
IGHV1-69*06_14

54 sequences assigned
35 (64.8%) exact matches, in which:
35 unique CDR3
5 unique J



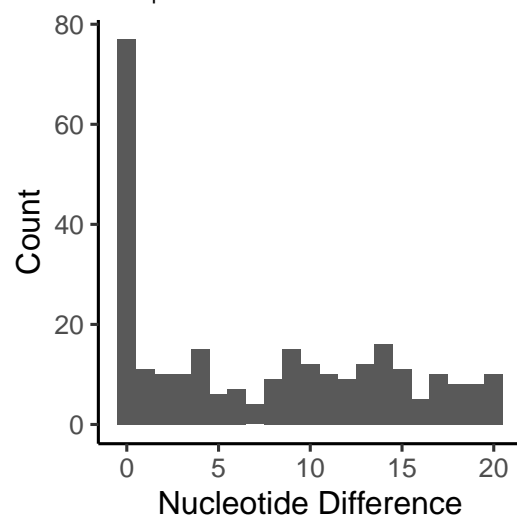
IGHV2-26*01

13 sequences assigned
11 (84.6%) exact matches, in which:
11 unique CDR3
4 unique J



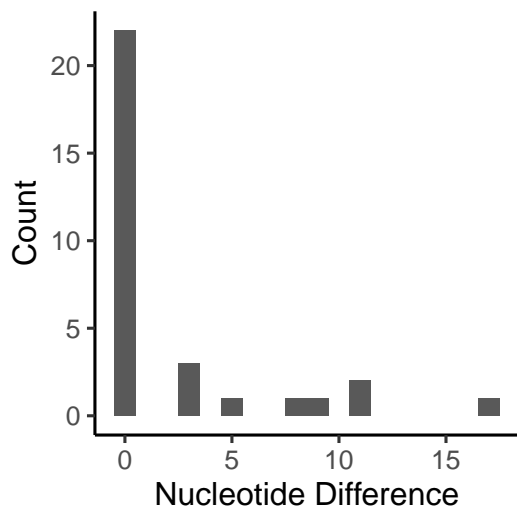
IGHV3-7*01

307 sequences assigned
77 (25.1%) exact matches, in which:
77 unique CDR3
5 unique J



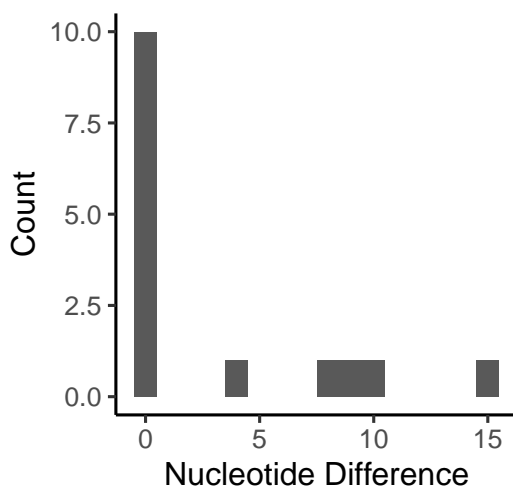
IGHV2-5*01

31 sequences assigned
22 (71%) exact matches, in which:
22 unique CDR3
4 unique J



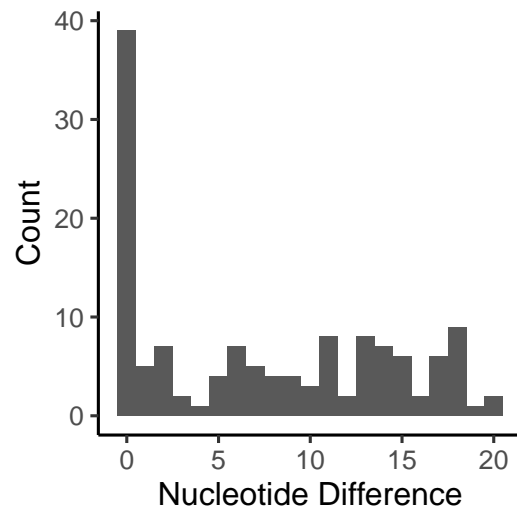
IGHV2-70*01

15 sequences assigned
10 (66.7%) exact matches, in which:
10 unique CDR3
4 unique J



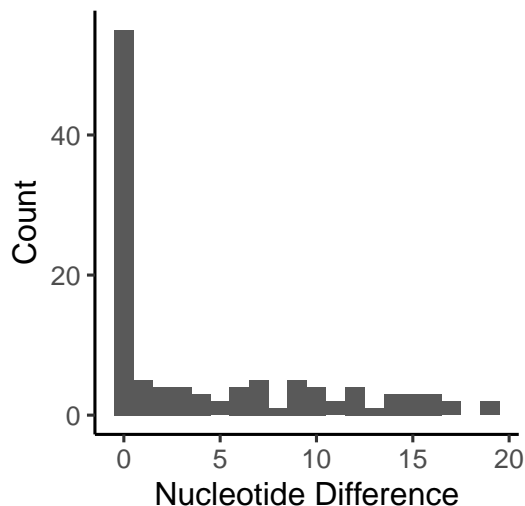
IGHV3-7*03

147 sequences assigned
39 (26.5%) exact matches, in which:
39 unique CDR3
5 unique J



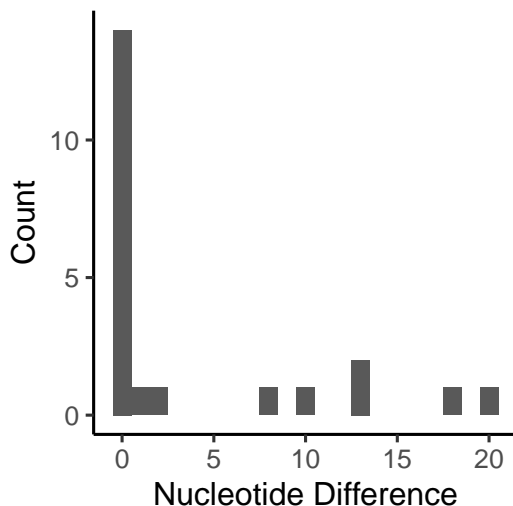
IGHV3-9*01

116 sequences assigned
55 (47.4%) exact matches, in which:
54 unique CDR3
6 unique J



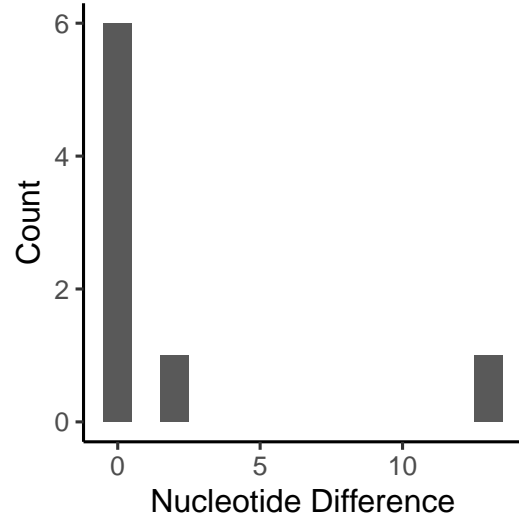
IGHV3-13*01

24 sequences assigned
14 (58.3%) exact matches, in which:
14 unique CDR3
4 unique J



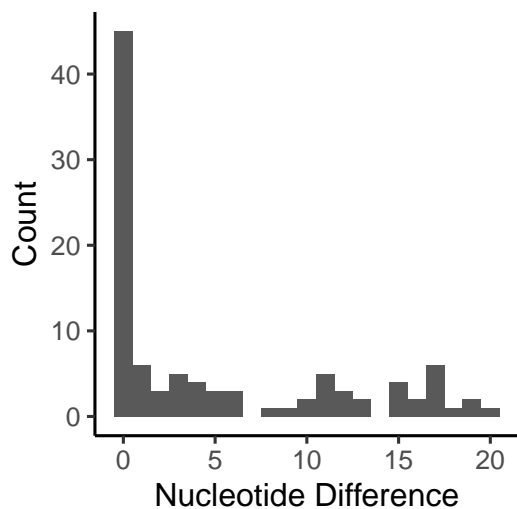
IGHV3-20*01_02

10 sequences assigned
6 (60%) exact matches, in which:
6 unique CDR3
3 unique J



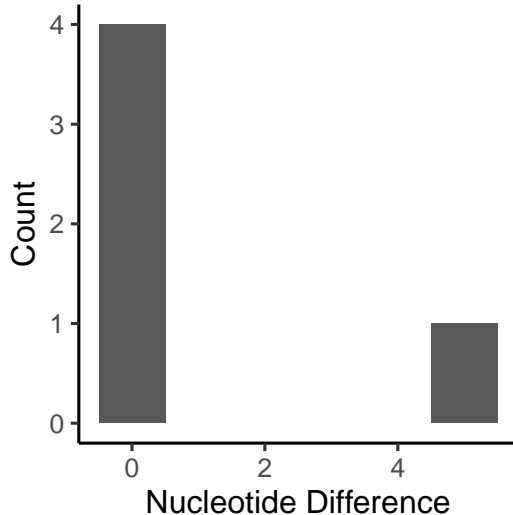
IGHV3-11*01

110 sequences assigned
45 (40.9%) exact matches, in which:
44 unique CDR3
5 unique J



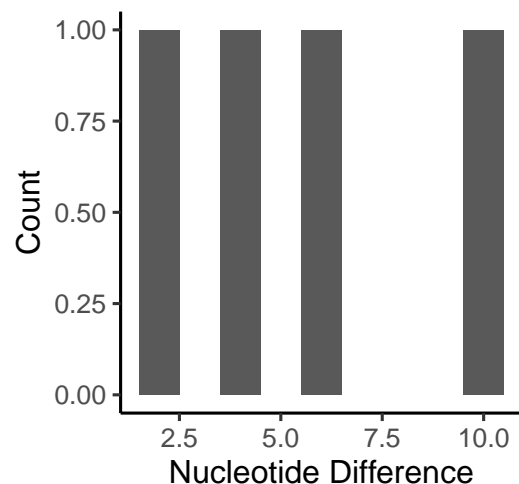
IGHV3-13*05

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



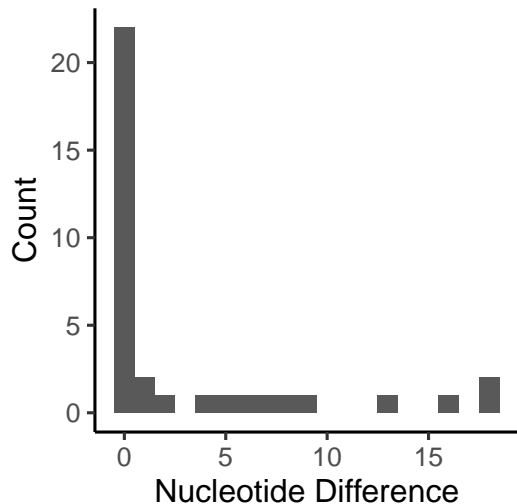
IGHV3-20*03_04

4 sequences assigned
No exact matches.



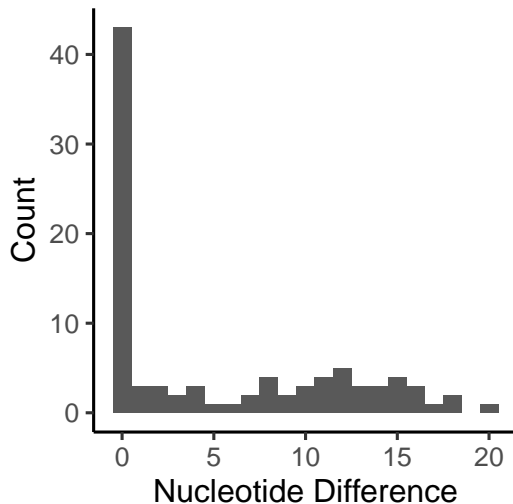
IGHV3-11*06

38 sequences assigned
22 (57.9%) exact matches, in which:
22 unique CDR3
4 unique J



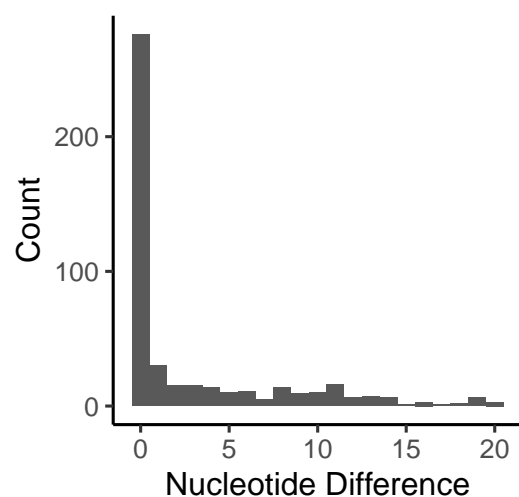
IGHV3-15*01_02

98 sequences assigned
43 (43.9%) exact matches, in which:
43 unique CDR3
4 unique J



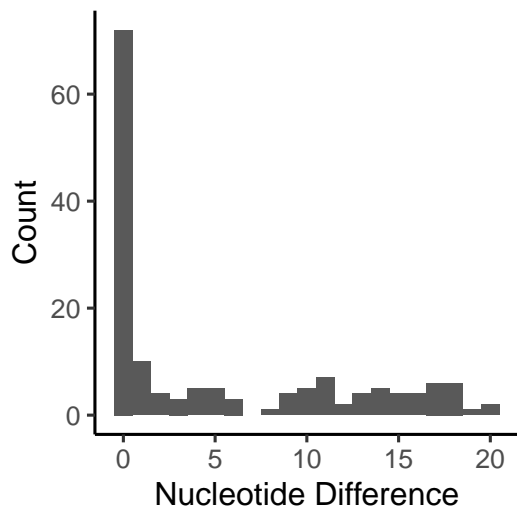
IGHV3-21*01_02

483 sequences assigned
276 (57.1%) exact matches, in which:
275 unique CDR3
6 unique J



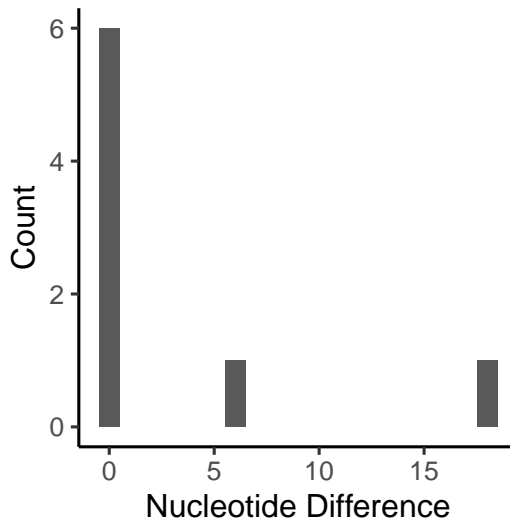
IGHV3-30-3*01

167 sequences assigned
72 (43.1%) exact matches, in which:
72 unique CDR3
5 unique J



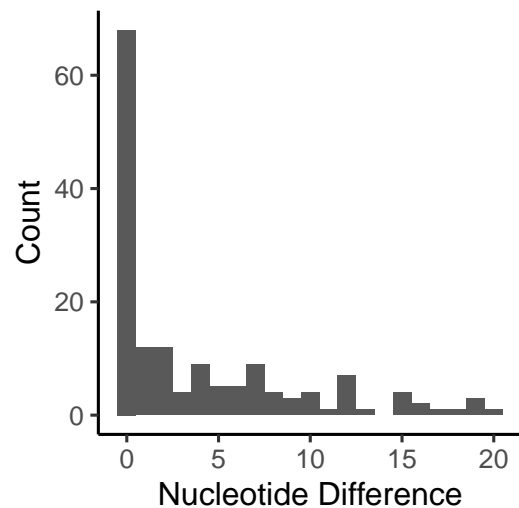
IGHV3-43*02

8 sequences assigned
6 (75%) exact matches, in which:
6 unique CDR3
2 unique J



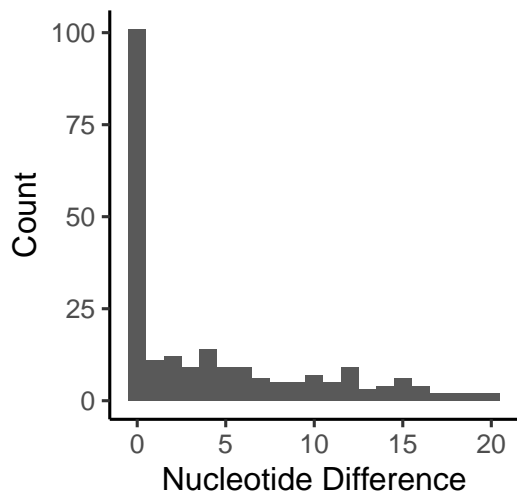
IGHV3-48*03

171 sequences assigned
68 (39.8%) exact matches, in which:
68 unique CDR3
6 unique J



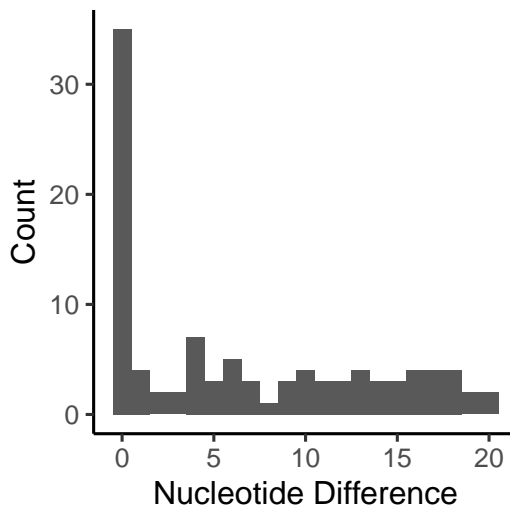
IGHV3-33*01

249 sequences assigned
101 (40.6%) exact matches, in which:
101 unique CDR3
4 unique J



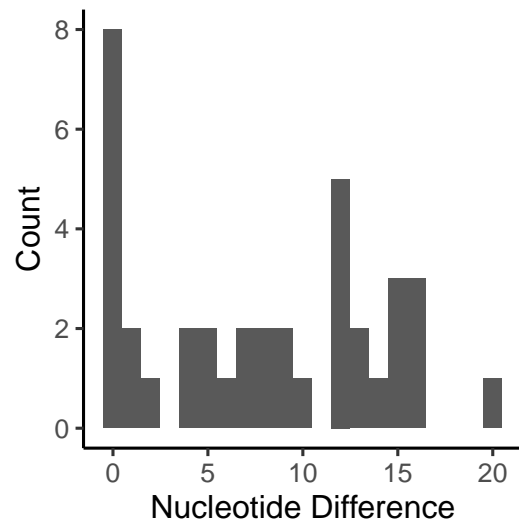
IGHV3-48*01

121 sequences assigned
35 (28.9%) exact matches, in which:
32 unique CDR3
6 unique J



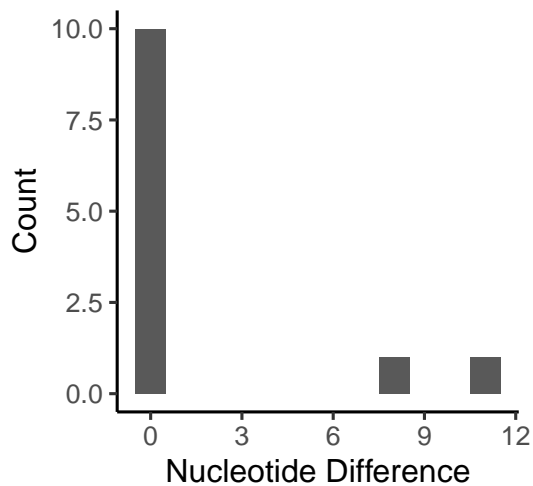
IGHV3-49*04

43 sequences assigned
8 (18.6%) exact matches, in which:
8 unique CDR3
2 unique J



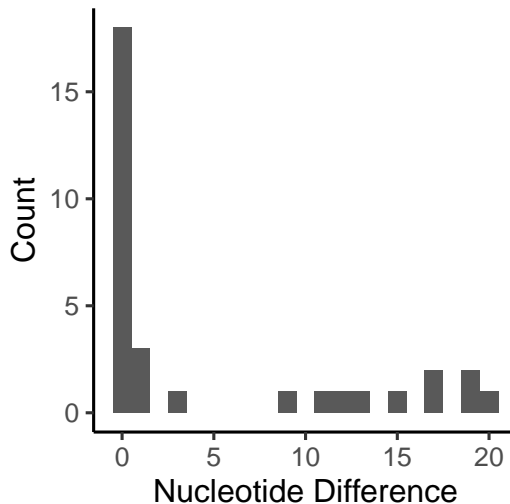
IGHV3-43*01

16 sequences assigned
10 (62.5%) exact matches, in which:
10 unique CDR3
3 unique J



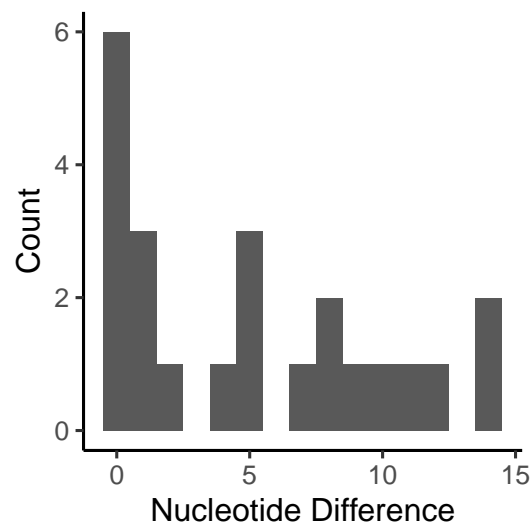
IGHV3-48*02

39 sequences assigned
18 (46.2%) exact matches, in which:
18 unique CDR3
4 unique J



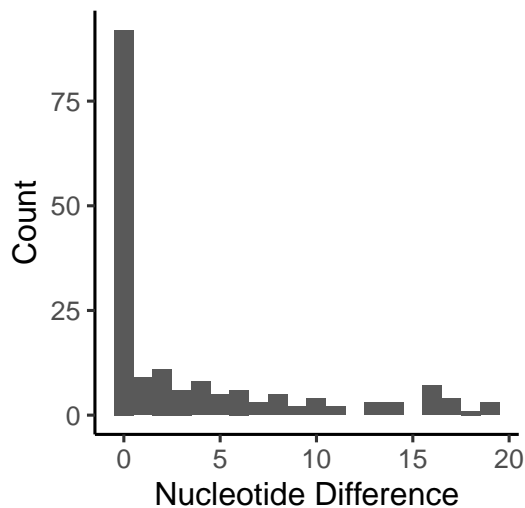
IGHV3-49*03_05

23 sequences assigned
6 (26.1%) exact matches, in which:
6 unique CDR3
4 unique J



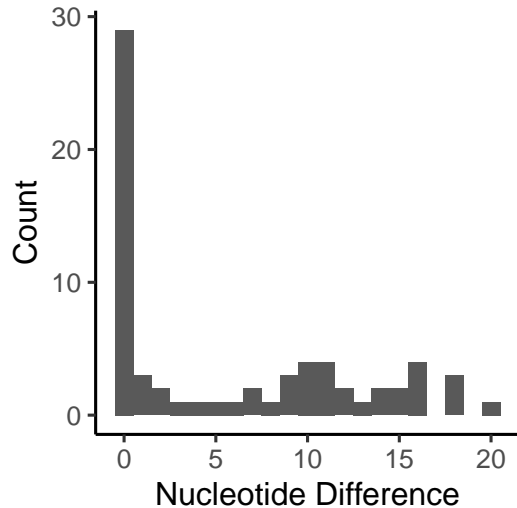
IGHV3-53*01_02

204 sequences assigned
92 (45.1%) exact matches, in which:
91 unique CDR3
6 unique J



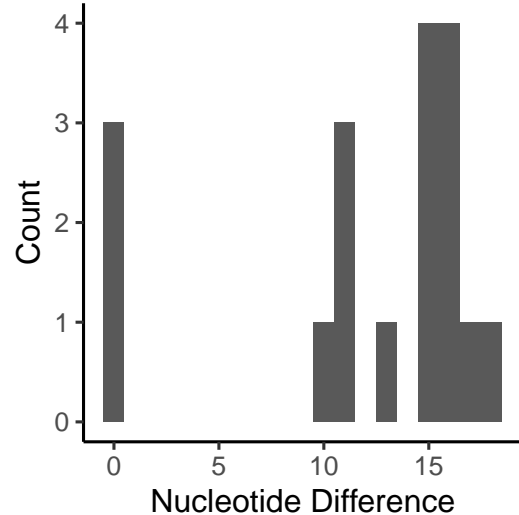
IGHV3-66*01

71 sequences assigned
29 (40.8%) exact matches, in which:
29 unique CDR3
4 unique J



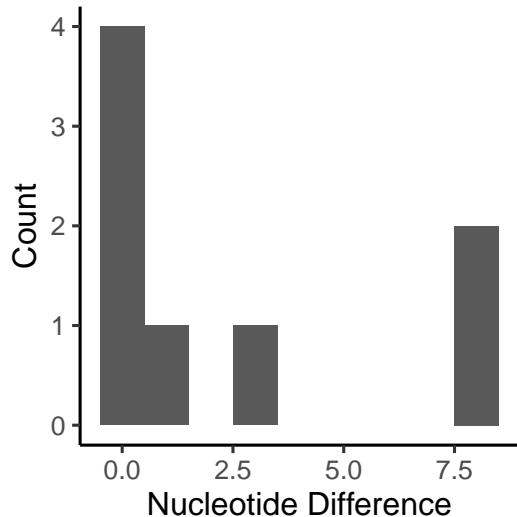
IGHV3-72*01

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



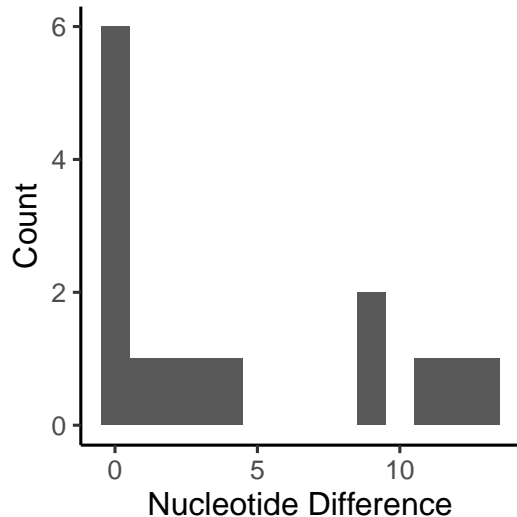
IGHV3-64*01

10 sequences assigned
4 (40%) exact matches, in which:
4 unique CDR3
2 unique J



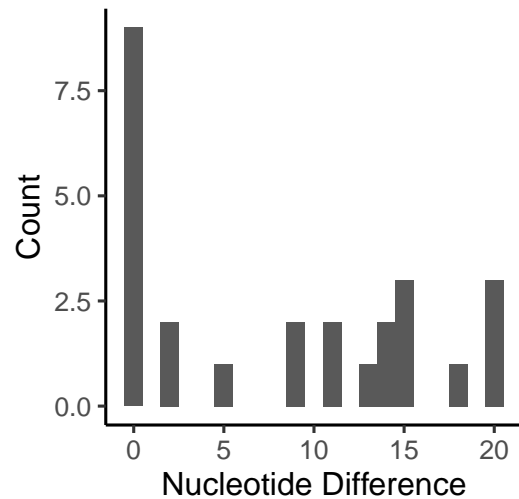
IGHV3-66*02

18 sequences assigned
6 (33.3%) exact matches, in which:
6 unique CDR3
2 unique J



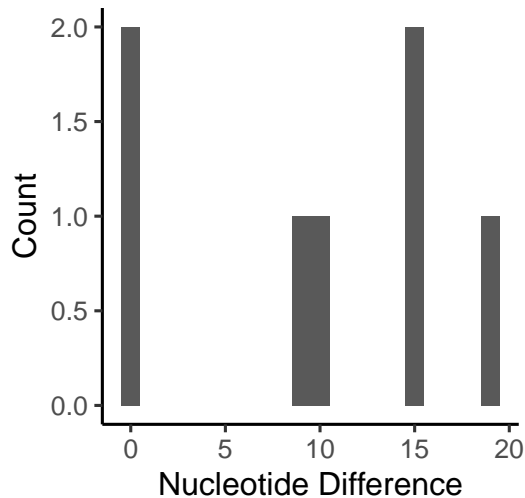
IGHV3-73*01_02

29 sequences assigned
9 (31%) exact matches, in which:
9 unique CDR3
3 unique J



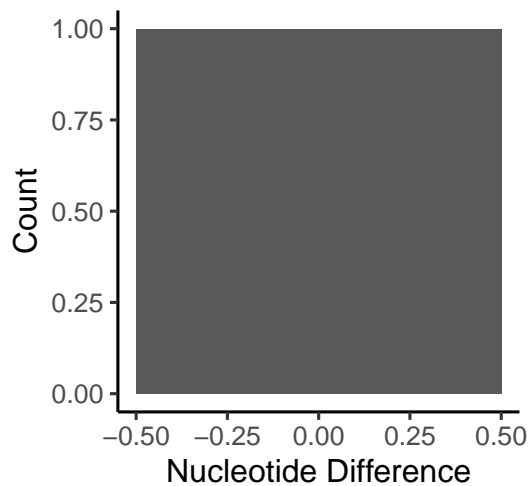
IGHV3-64*02_07

7 sequences assigned
2 (28.6%) exact matches, in which:
2 unique CDR3
2 unique J



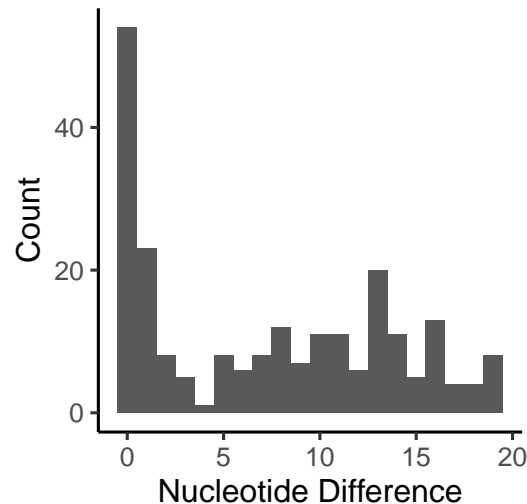
IGHV3-69-1*01

8 sequences assigned
1 (12.5%) exact matches, in which:
1 unique CDR3
1 unique J



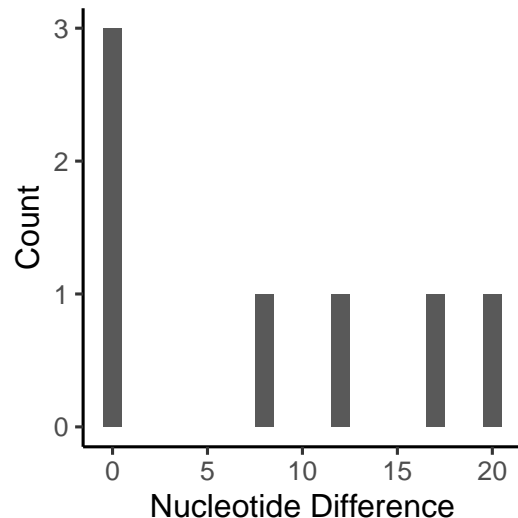
IGHV3-74*01_02

247 sequences assigned
54 (21.9%) exact matches, in which:
52 unique CDR3
6 unique J



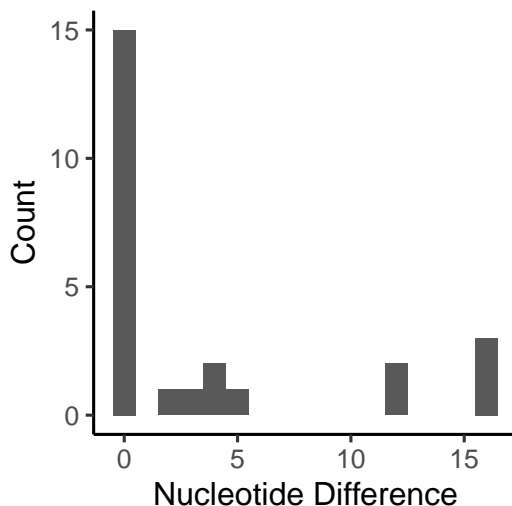
IGHV3-43D*04

7 sequences assigned
3 (42.9%) exact matches, in which:
3 unique CDR3
2 unique J



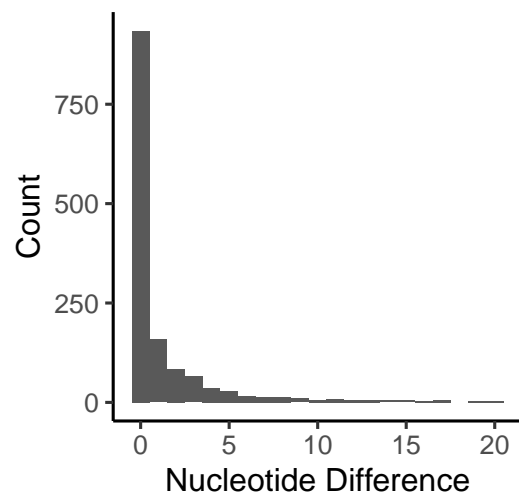
IGHV4-30-2*01

28 sequences assigned
15 (53.6%) exact matches, in which:
15 unique CDR3
4 unique J



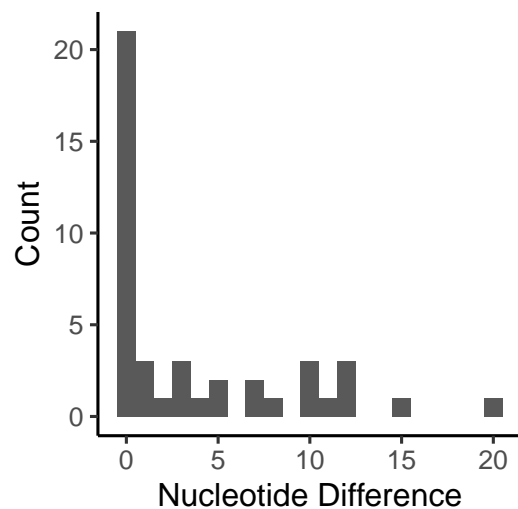
IGHV4-34*01_02

1448 sequences assigned
935 (64.6%) exact matches, in which:
929 unique CDR3
6 unique J



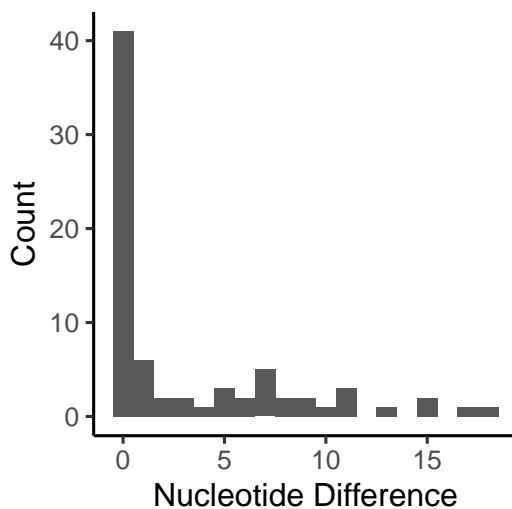
IGHV3-64D*06

48 sequences assigned
21 (43.8%) exact matches, in which:
21 unique CDR3
5 unique J



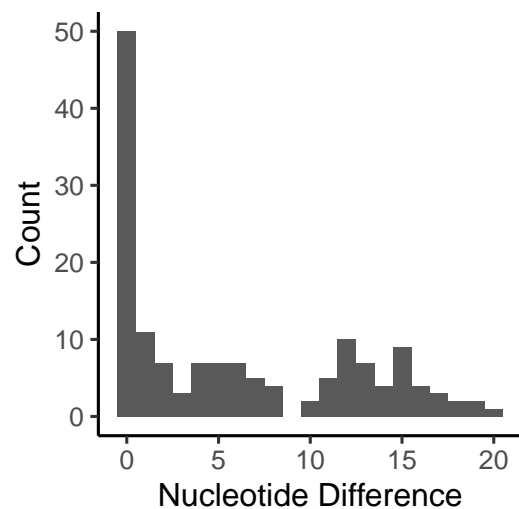
IGHV4-30-4*01

80 sequences assigned
41 (51.2%) exact matches, in which:
41 unique CDR3
5 unique J



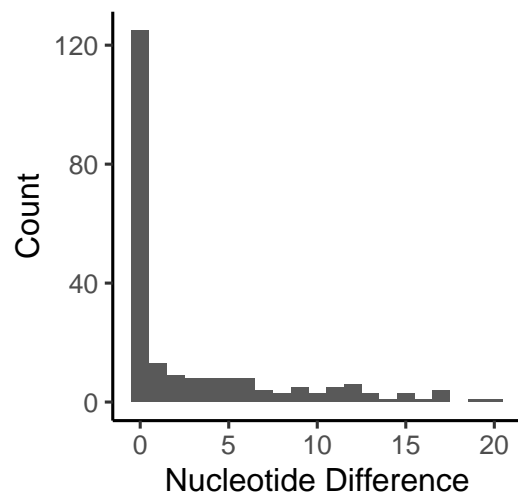
IGHV4-38-2*02_A70G

168 sequences assigned
50 (29.8%) exact matches, in which:
50 unique CDR3
5 unique J



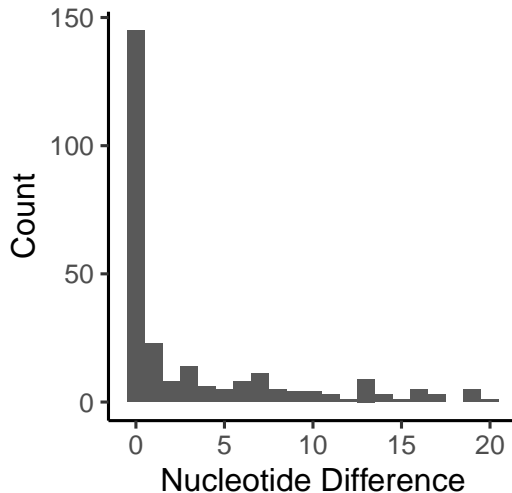
IGHV4-4*07

234 sequences assigned
125 (53.4%) exact matches, in which:
124 unique CDR3
6 unique J



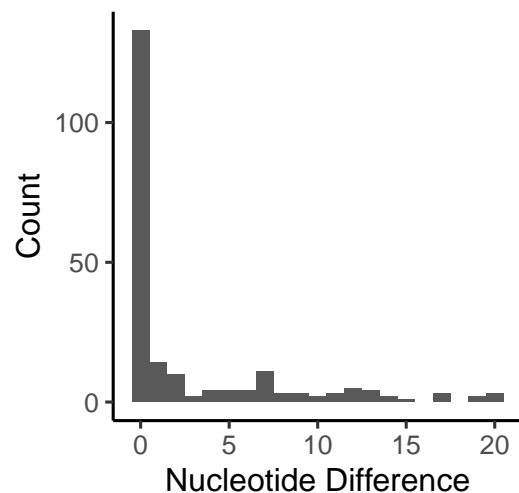
IGHV4-31*03_04

282 sequences assigned
145 (51.4%) exact matches, in which:
145 unique CDR3
6 unique J



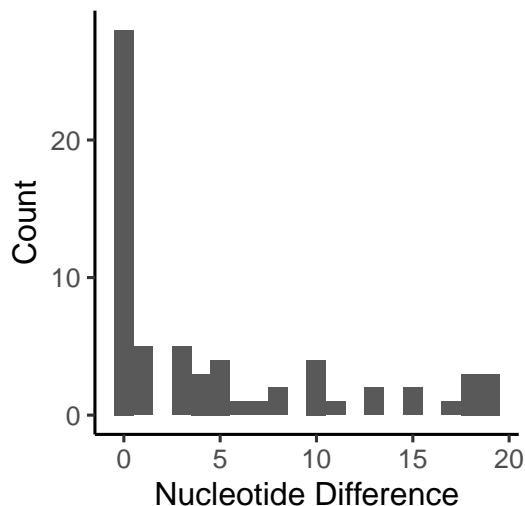
IGHV4-39*01_05

225 sequences assigned
133 (59.1%) exact matches, in which:
132 unique CDR3
6 unique J



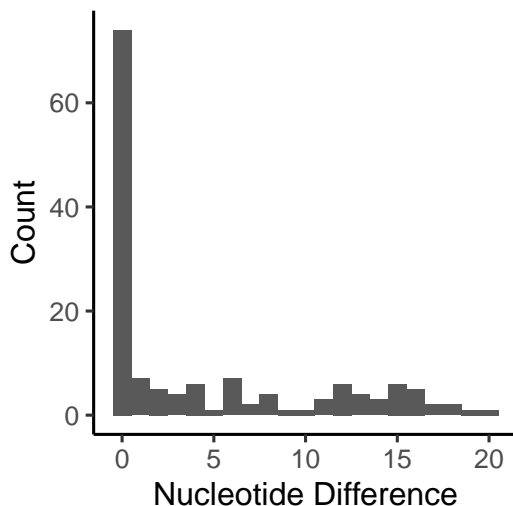
IGHV4-39*02_C258G

71 sequences assigned
28 (39.4%) exact matches, in which:
28 unique CDR3
4 unique J



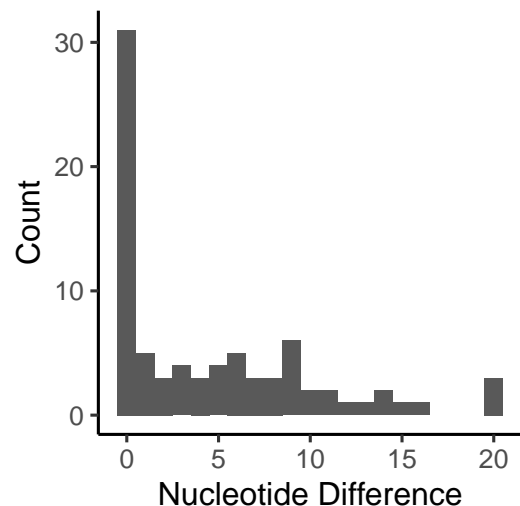
IGHV4-61*02

162 sequences assigned
74 (45.7%) exact matches, in which:
74 unique CDR3
5 unique J



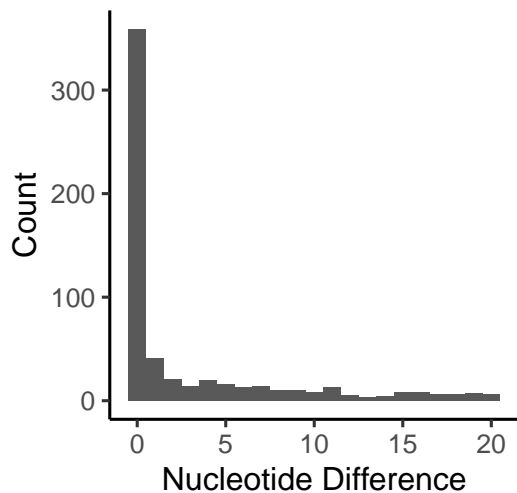
IGHV6-1*01_02

86 sequences assigned
31 (36%) exact matches, in which:
31 unique CDR3
4 unique J



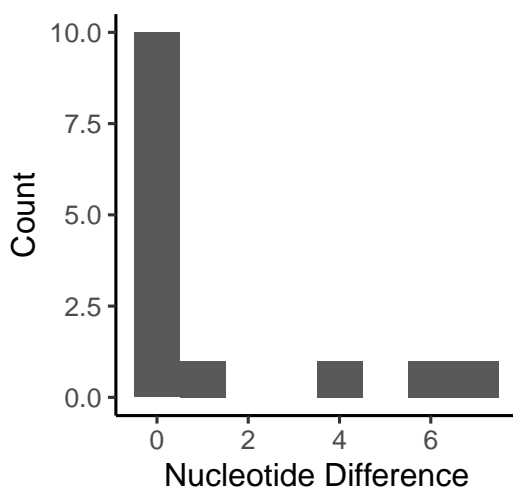
IGHV4-59*01_07

641 sequences assigned
359 (56%) exact matches, in which:
355 unique CDR3
6 unique J



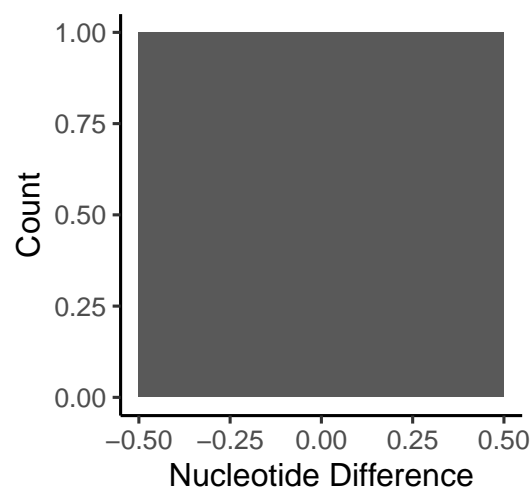
IGHV5-10-1*01_03

17 sequences assigned
10 (58.8%) exact matches, in which:
10 unique CDR3
3 unique J



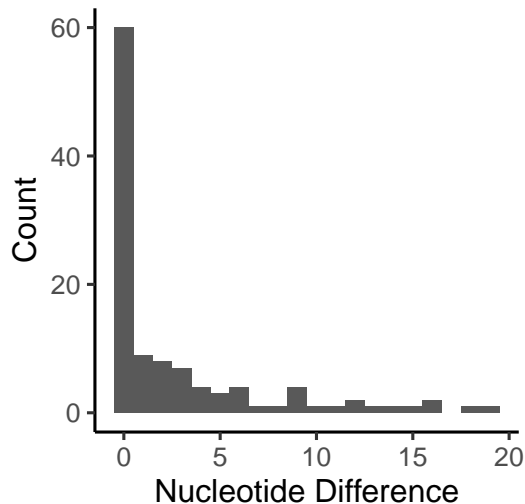
IGHV7-4-1*01

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



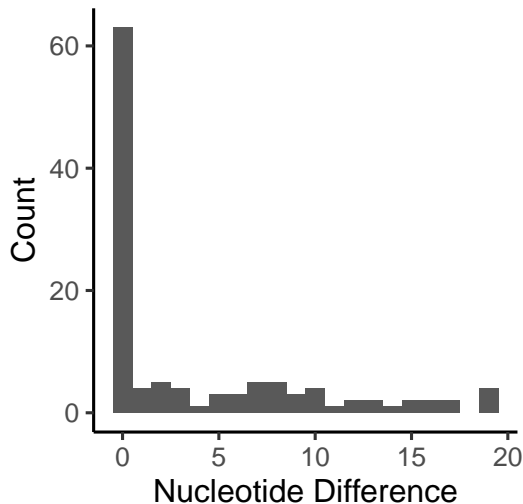
IGHV4-61*01

116 sequences assigned
60 (51.7%) exact matches, in which:
60 unique CDR3
6 unique J



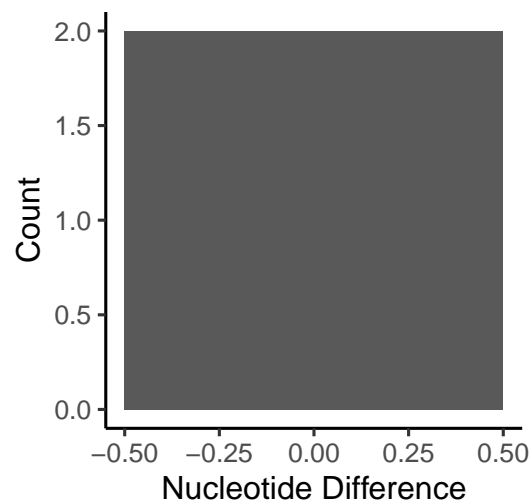
IGHV5-51*01_03

119 sequences assigned
63 (52.9%) exact matches, in which:
63 unique CDR3
4 unique J



IGHV7-4-1*02

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





Warning – no inferred sequences found.

Novel sequence(s) IGHV4–39*02_C258G 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.

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