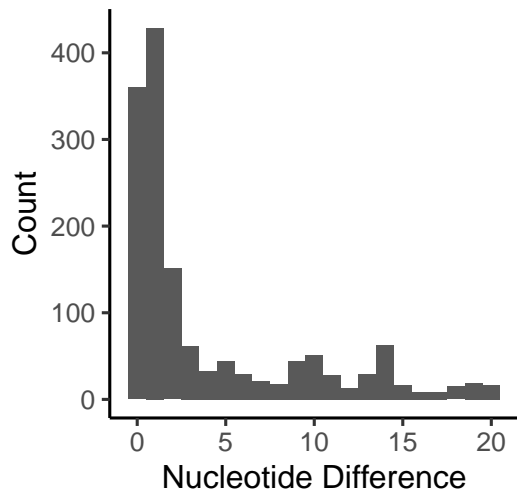


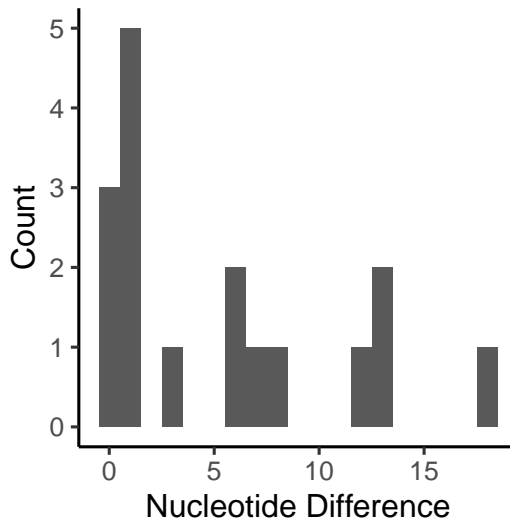
IGHV1-2*04

1536 sequences assigned
360 (23.4%) exact matches, in which:
288 unique CDR3
6 unique J



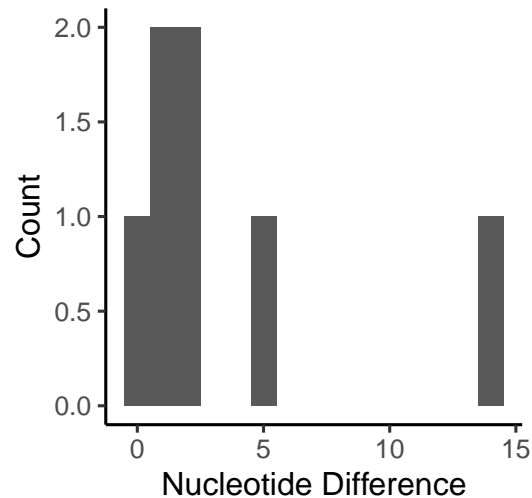
IGHV1-8*01

19 sequences assigned
3 (15.8%) exact matches, in which:
3 unique CDR3
2 unique J



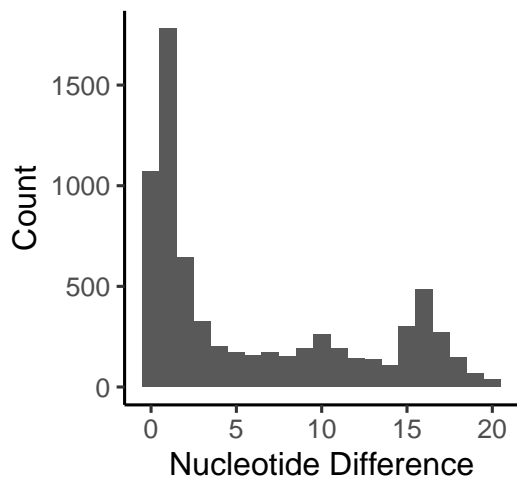
IGHV1-45*02

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



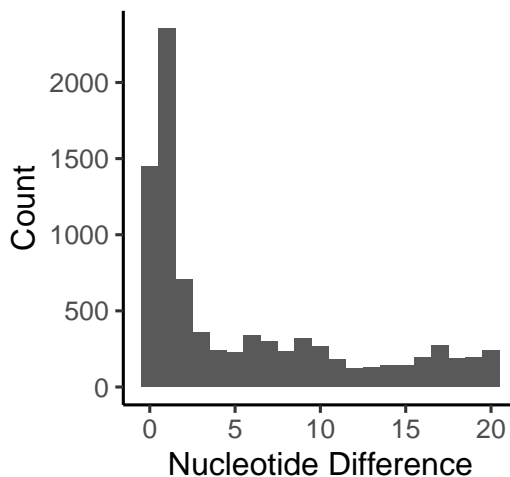
IGHV1-2*06

8312 sequences assigned
1073 (12.9%) exact matches, in which:
799 unique CDR3
6 unique J



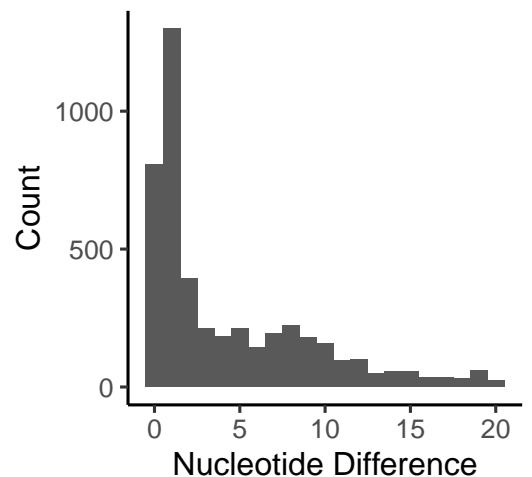
IGHV1-18*01

10514 sequences assigned
1450 (13.8%) exact matches, in which:
1112 unique CDR3
6 unique J



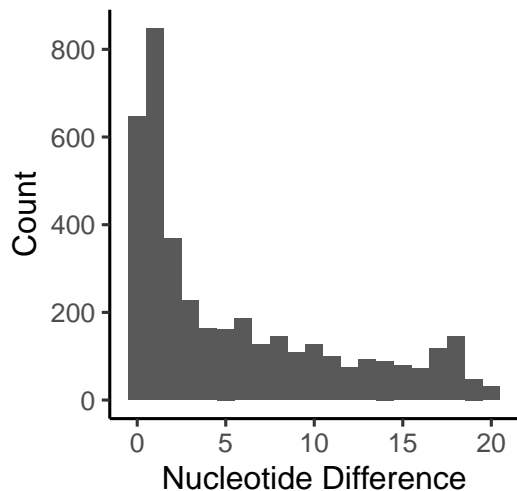
IGHV1-46*01

4802 sequences assigned
808 (16.8%) exact matches, in which:
603 unique CDR3
6 unique J



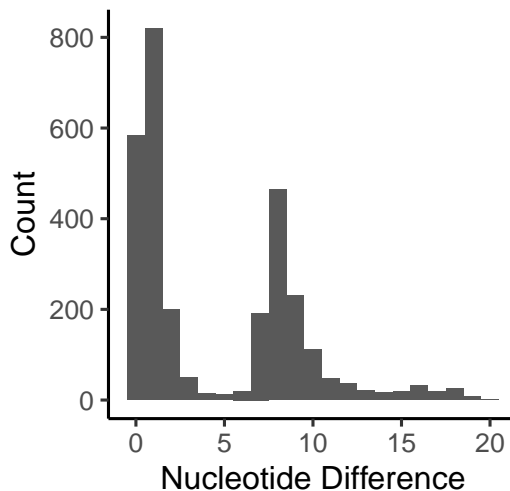
IGHV1-3*01_05

5216 sequences assigned
646 (12.4%) exact matches, in which:
513 unique CDR3
6 unique J



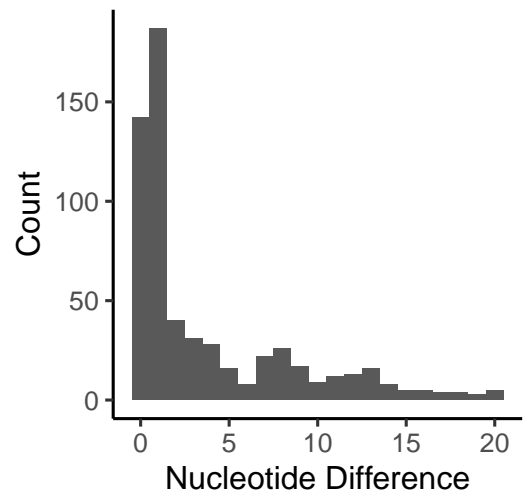
IGHV1-24*01

3071 sequences assigned
583 (19%) exact matches, in which:
435 unique CDR3
6 unique J



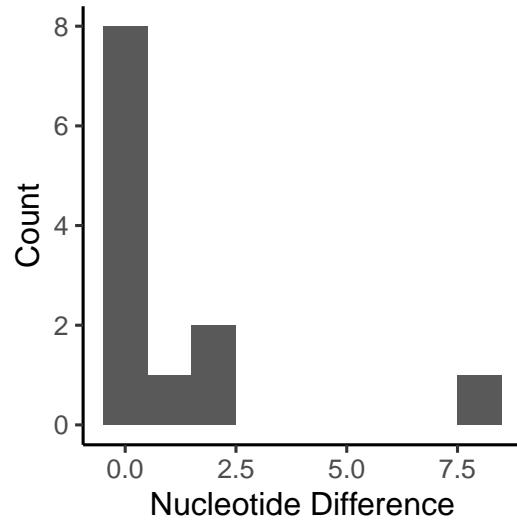
IGHV1-58*01_03

623 sequences assigned
142 (22.8%) exact matches, in which:
110 unique CDR3
6 unique J



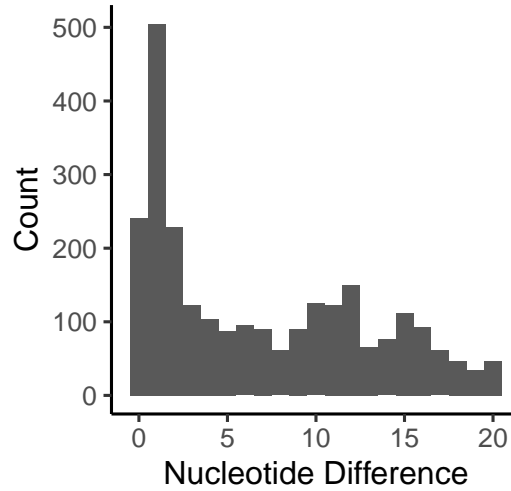
IGHV1-69-2*01

19 sequences assigned
8 (42.1%) exact matches, in which:
7 unique CDR3
3 unique J



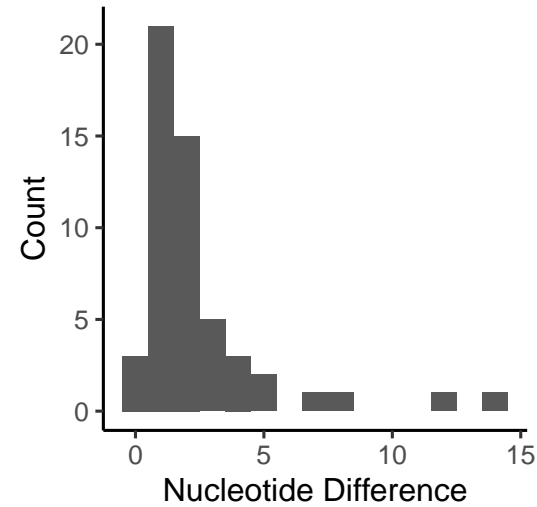
IGHV2-5*02

3282 sequences assigned
241 (7.3%) exact matches, in which:
180 unique CDR3
5 unique J



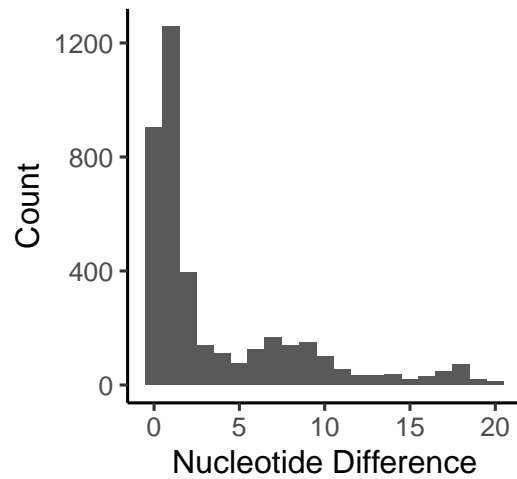
IGHV2-70*12

56 sequences assigned
3 (5.4%) exact matches, in which:
2 unique CDR3
2 unique J



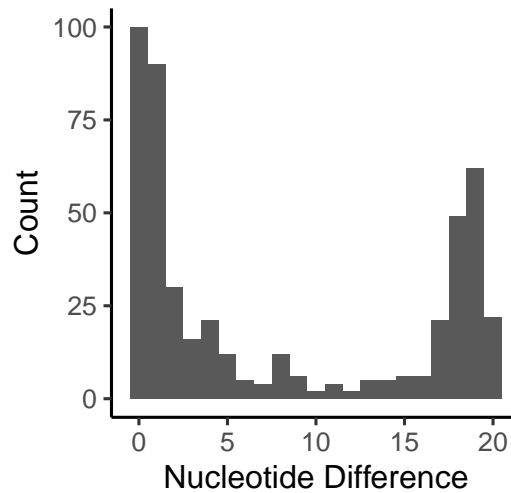
IGHV1-69*06_14

4162 sequences assigned
903 (21.7%) exact matches, in which:
728 unique CDR3
6 unique J



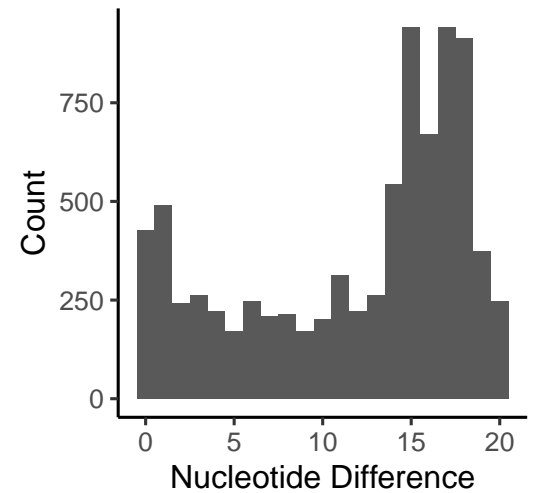
IGHV2-26*01

506 sequences assigned
100 (19.8%) exact matches, in which:
83 unique CDR3
5 unique J



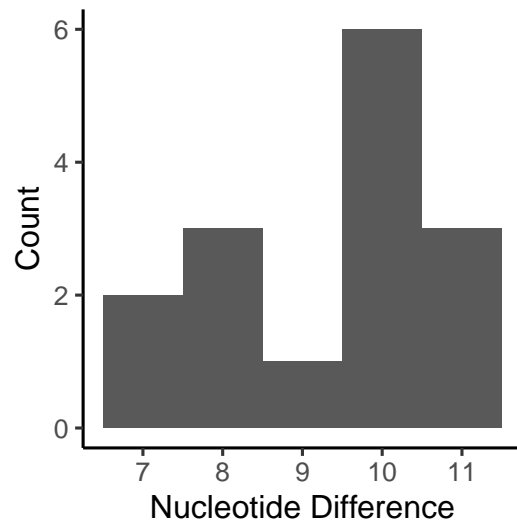
IGHV3-7*04

9740 sequences assigned
426 (4.4%) exact matches, in which:
288 unique CDR3
6 unique J



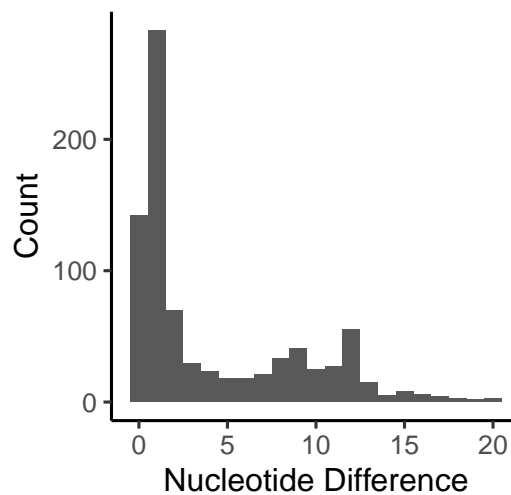
IGHV1-NL1*01

15 sequences assigned
No exact matches.



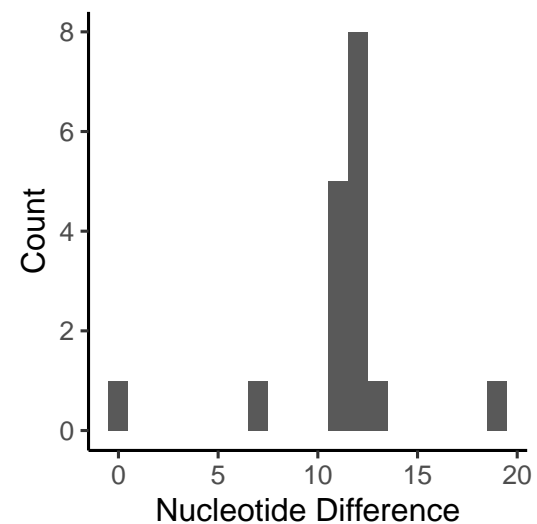
IGHV2-70*01

918 sequences assigned
142 (15.5%) exact matches, in which:
87 unique CDR3
4 unique J



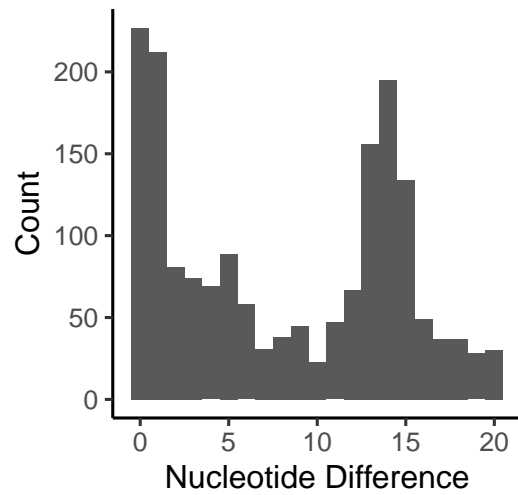
IGHV3-9*01

17 sequences assigned
1 (5.9%) exact matches, in which:
1 unique CDR3
1 unique J



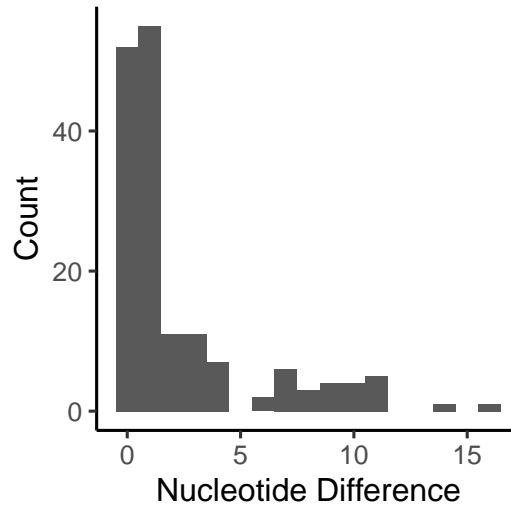
IGHV3-11*06

2317 sequences assigned
227 (9.8%) exact matches, in which:
173 unique CDR3
5 unique J



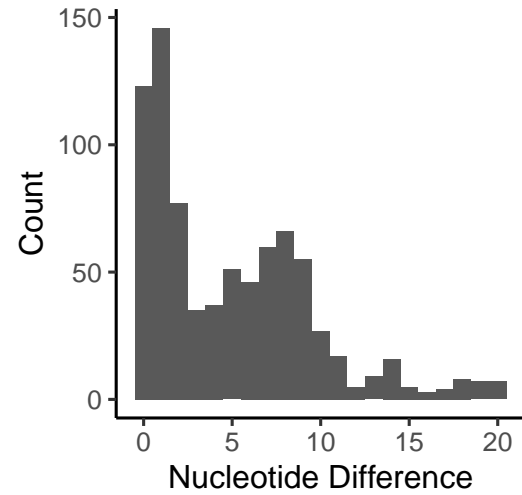
IGHV3-13*05

200 sequences assigned
52 (26%) exact matches, in which:
34 unique CDR3
4 unique J



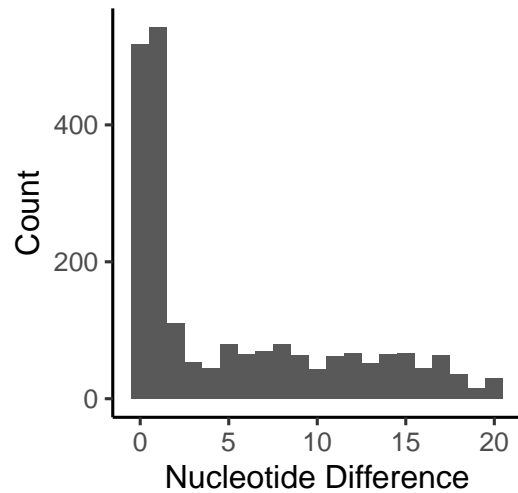
IGHV3-20*03_04

839 sequences assigned
123 (14.7%) exact matches, in which:
76 unique CDR3
5 unique J



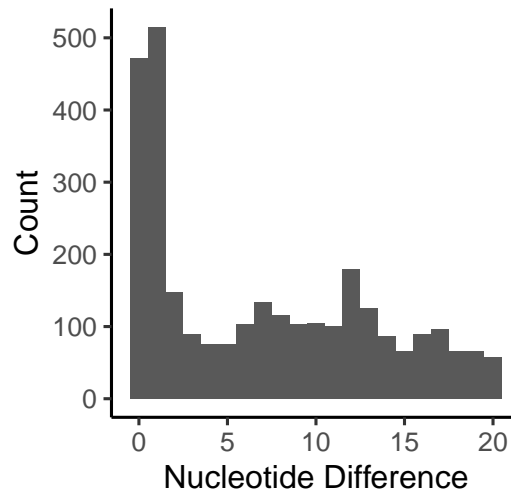
IGHV3-11*03_05

3200 sequences assigned
518 (16.2%) exact matches, in which:
312 unique CDR3
6 unique J



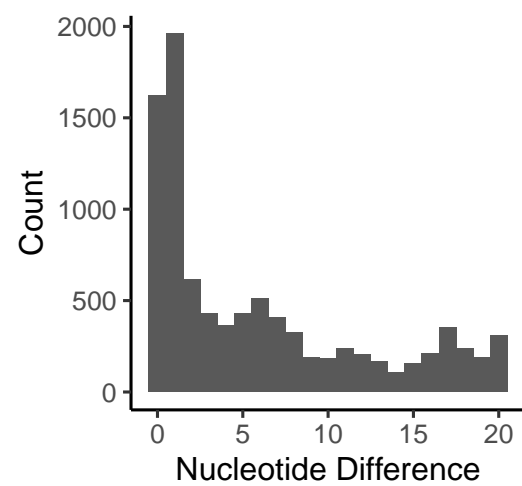
IGHV3-15*01_02

3858 sequences assigned
472 (12.2%) exact matches, in which:
268 unique CDR3
6 unique J



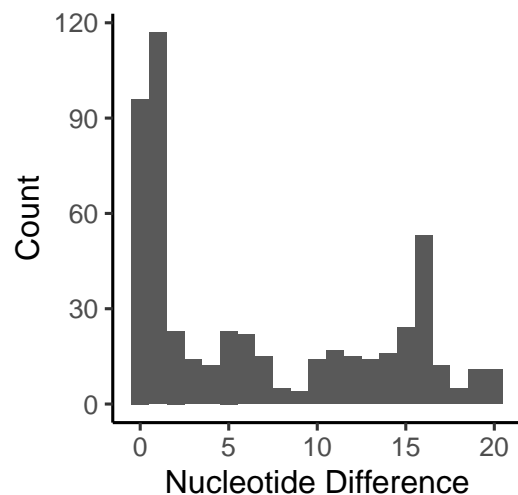
IGHV3-21*01_02

12235 sequences assigned
1620 (13.2%) exact matches, in which:
978 unique CDR3
6 unique J



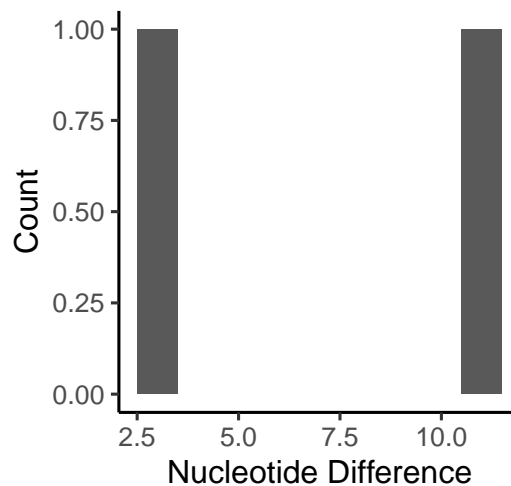
IGHV3-13*04

764 sequences assigned
96 (12.6%) exact matches, in which:
61 unique CDR3
5 unique J



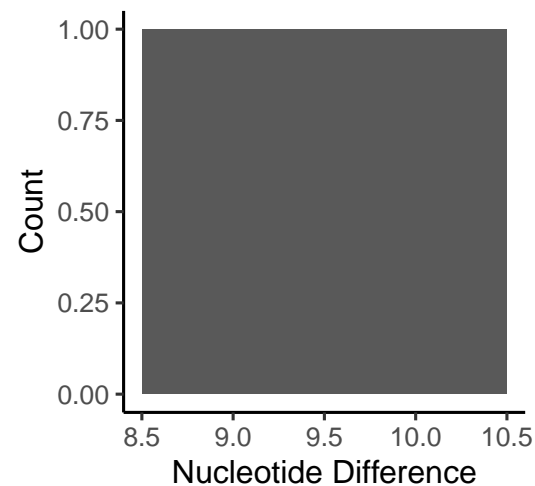
IGHV3-19*01

2 sequences assigned
No exact matches.



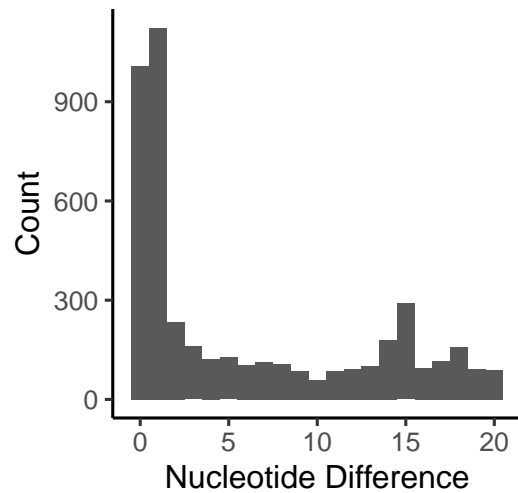
IGHV3-22*01_02

12 sequences assigned
No exact matches.



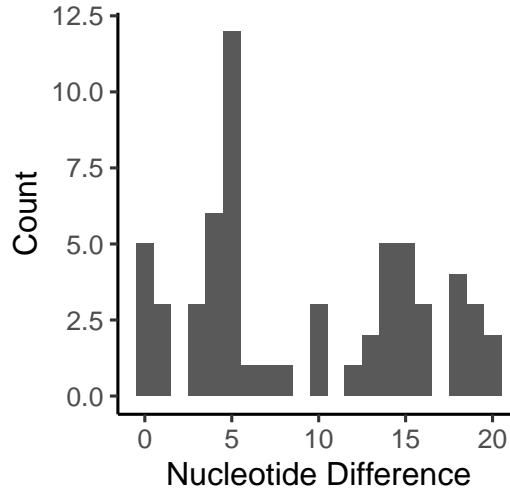
IGHV3-30*01

5754 sequences assigned
1007 (17.5%) exact matches, in which:
642 unique CDR3
6 unique J



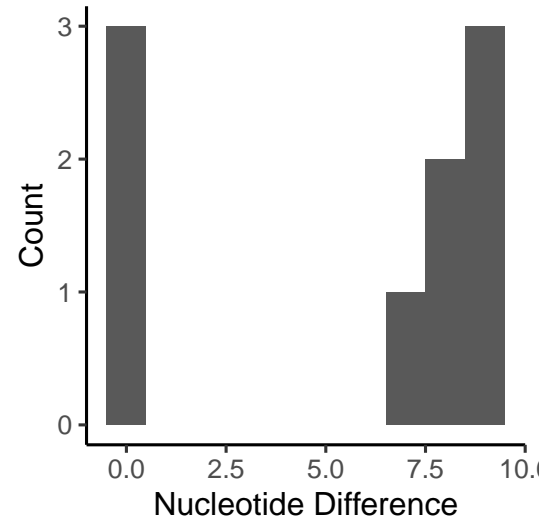
IGHV3-30-3*03

389 sequences assigned
5 (1.3%) exact matches, in which:
5 unique CDR3
2 unique J



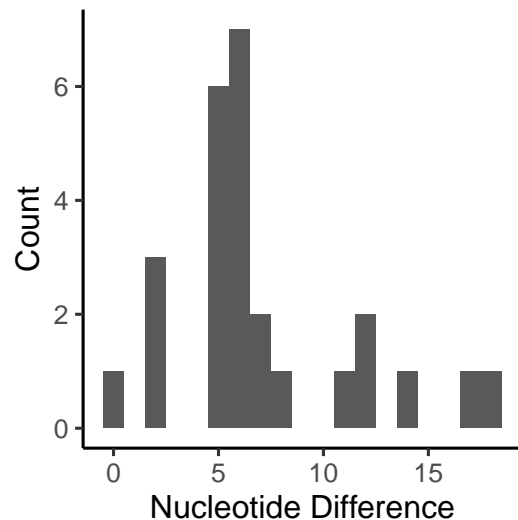
IGHV3-35*01

9 sequences assigned
3 (33.3%) exact matches, in which:
3 unique CDR3
3 unique J



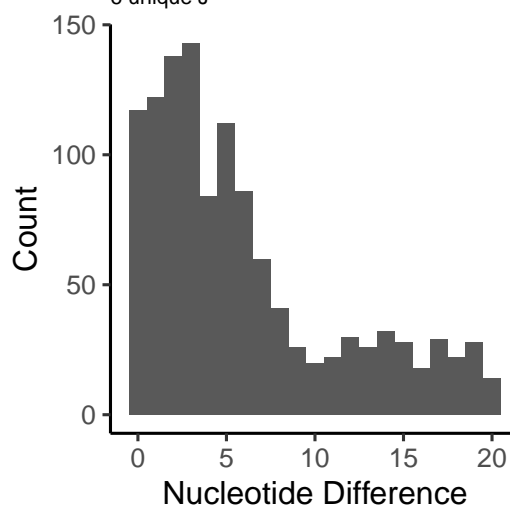
IGHV3-30-3*01

47 sequences assigned
1 (2.1%) exact matches, in which:
1 unique CDR3
1 unique J



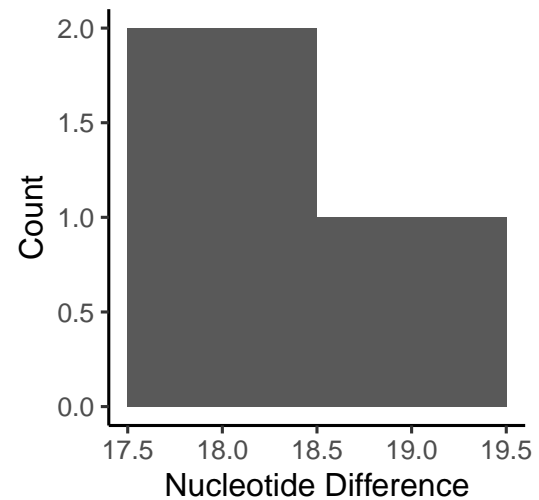
IGHV3-30*07

1364 sequences assigned
117 (8.6%) exact matches, in which:
106 unique CDR3
6 unique J



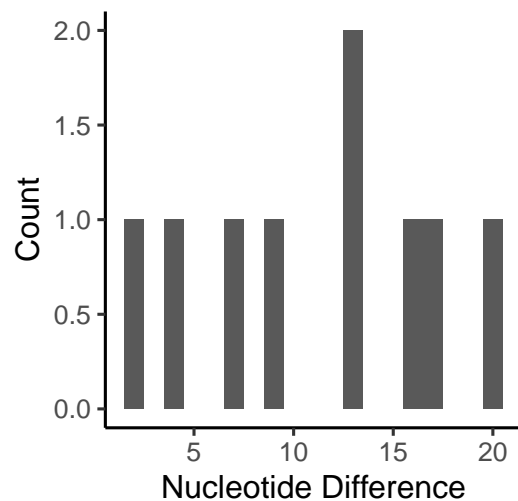
IGHV3-43*01

14 sequences assigned
No exact matches.



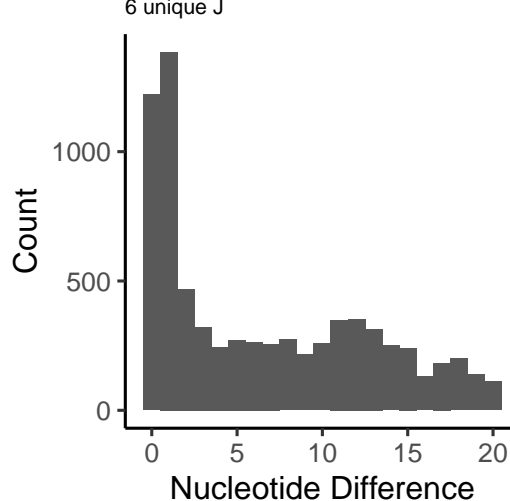
IGHV3-30-5*02

12 sequences assigned
No exact matches.



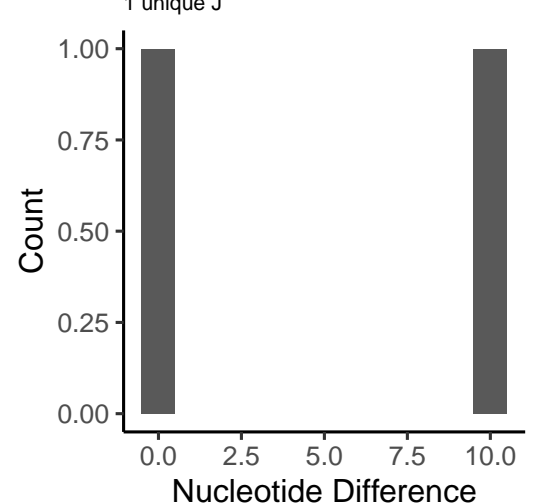
IGHV3-33*01

10305 sequences assigned
1221 (11.8%) exact matches, in which:
796 unique CDR3
6 unique J



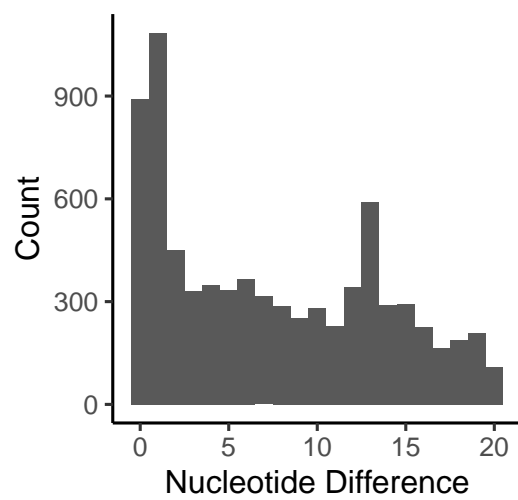
IGHV3-47*01

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



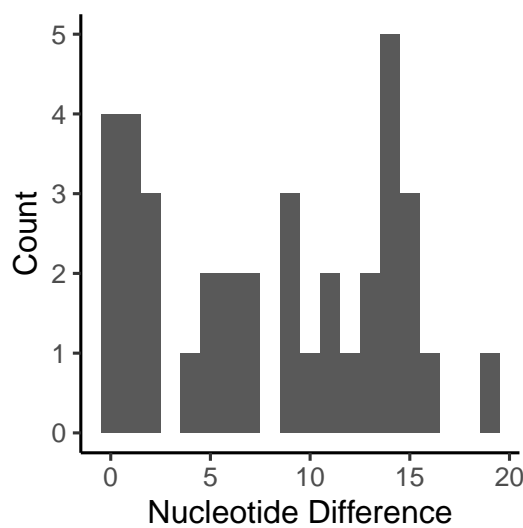
IGHV3-48*03

9609 sequences assigned
891 (9.3%) exact matches, in which:
550 unique CDR3
6 unique J



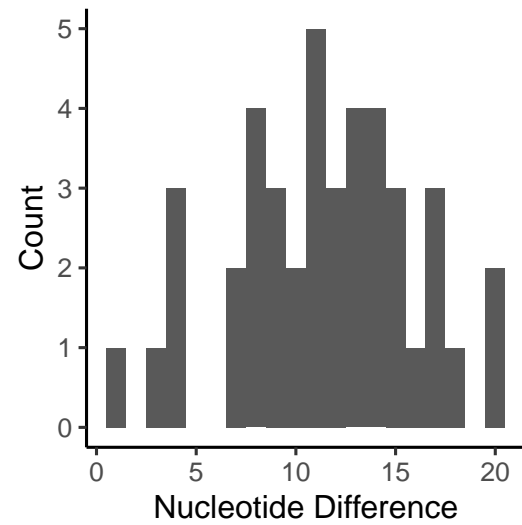
IGHV3-53*05

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



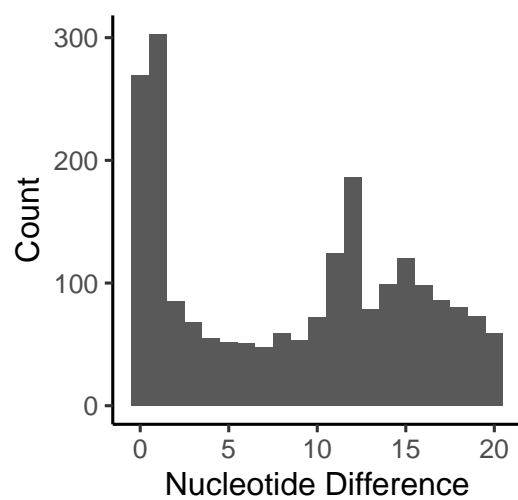
IGHV3-66*01

71 sequences assigned
No exact matches.



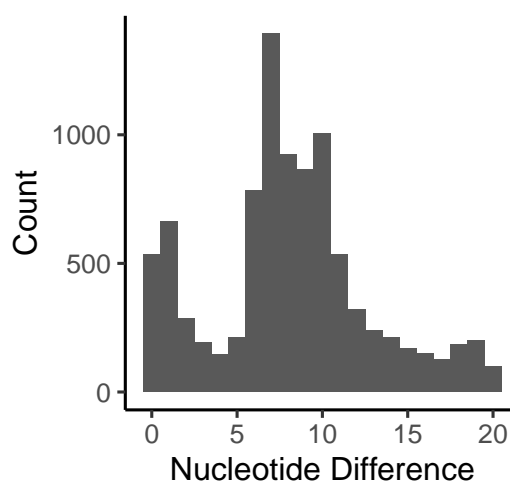
IGHV3-49*04

5135 sequences assigned
269 (5.2%) exact matches, in which:
158 unique CDR3
6 unique J



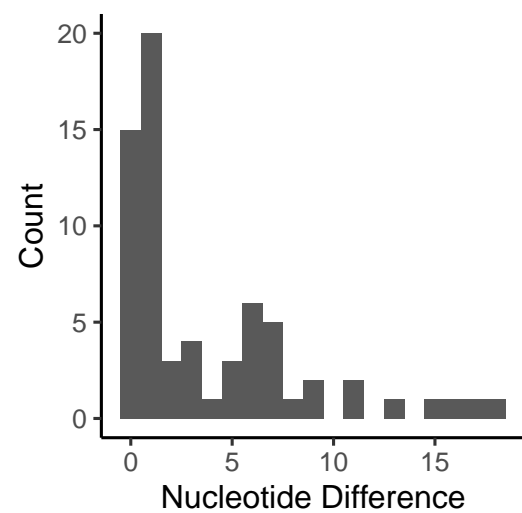
IGHV3-53*01_02

10092 sequences assigned
534 (5.3%) exact matches, in which:
356 unique CDR3
6 unique J



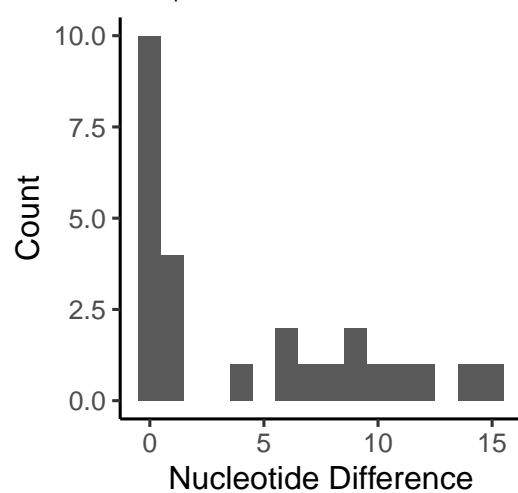
IGHV3-66*03

77 sequences assigned
15 (19.5%) exact matches, in which:
13 unique CDR3
3 unique J



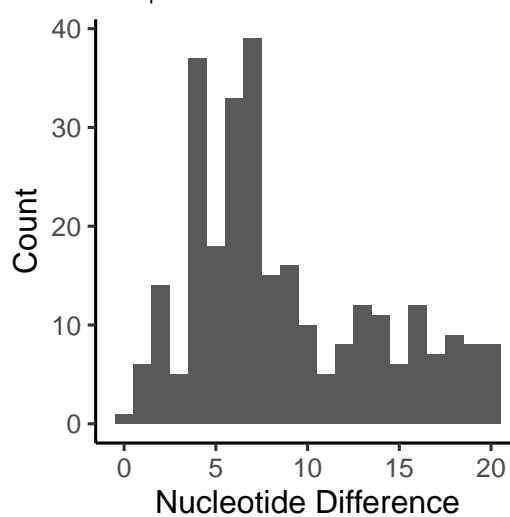
IGHV3-52*01_03

26 sequences assigned
10 (38.5%) exact matches, in which:
6 unique CDR3
4 unique J



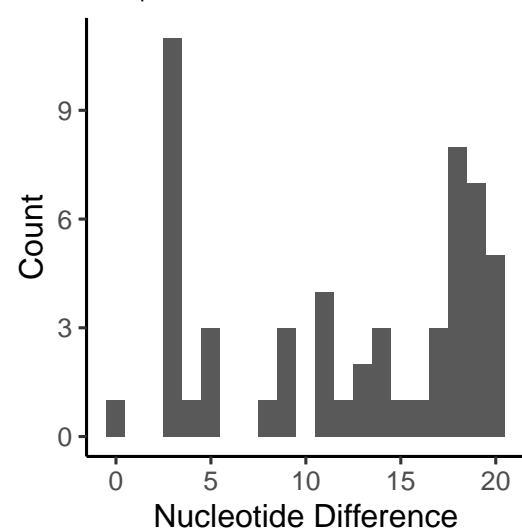
IGHV3-64*04

327 sequences assigned
1 (0.3%) exact matches, in which:
1 unique CDR3
1 unique J



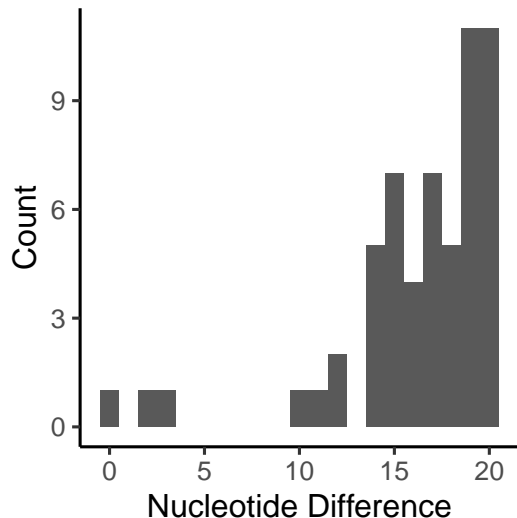
IGHV3-69-1*01

91 sequences assigned
1 (1.1%) exact matches, in which:
1 unique CDR3
1 unique J



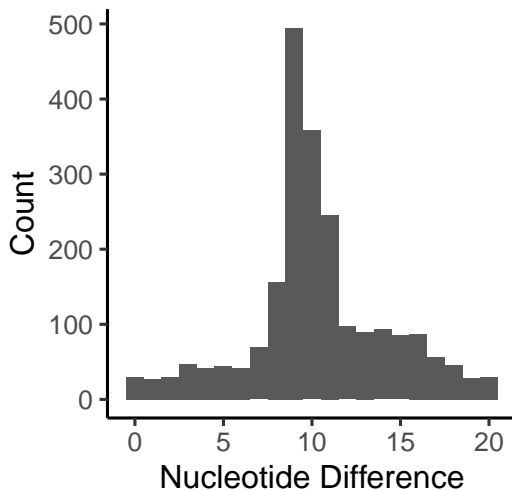
IGHV3-69-1*02

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



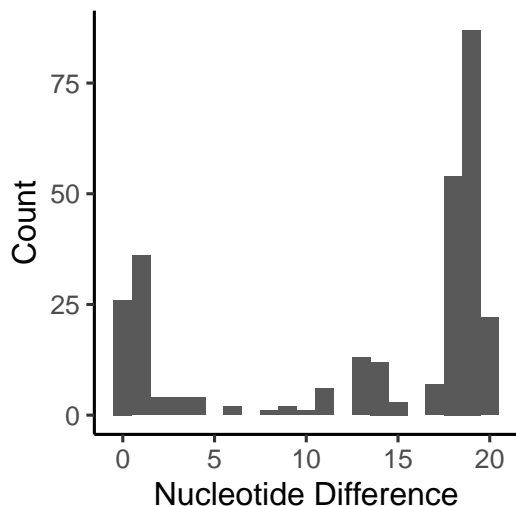
IGHV3-72*01

2730 sequences assigned
30 (1.1%) exact matches, in which:
22 unique CDR3
4 unique J



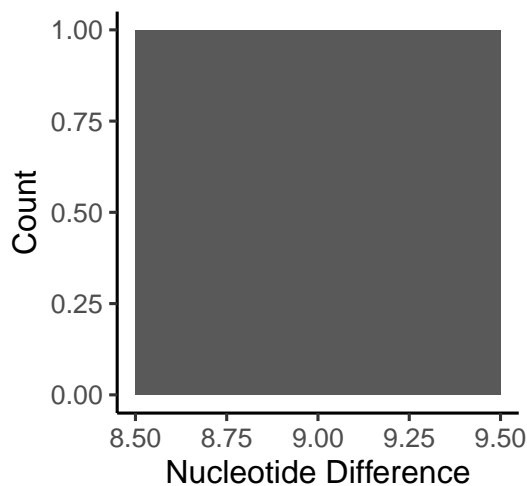
IGHV3-43D*04

332 sequences assigned
26 (7.8%) exact matches, in which:
15 unique CDR3
3 unique J



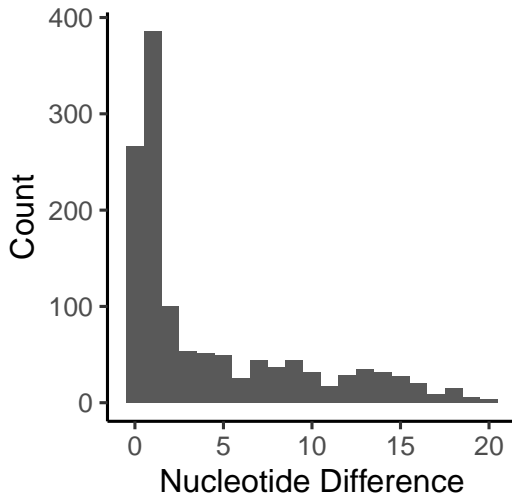
IGHV3-71*03

1 sequences assigned
No exact matches.



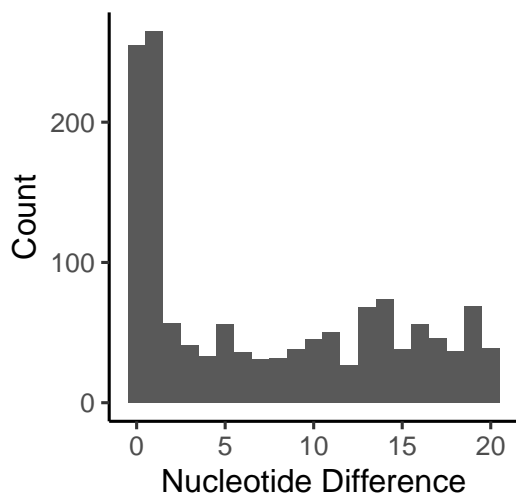
IGHV3-73*01_02

1456 sequences assigned
266 (18.3%) exact matches, in which:
151 unique CDR3
5 unique J



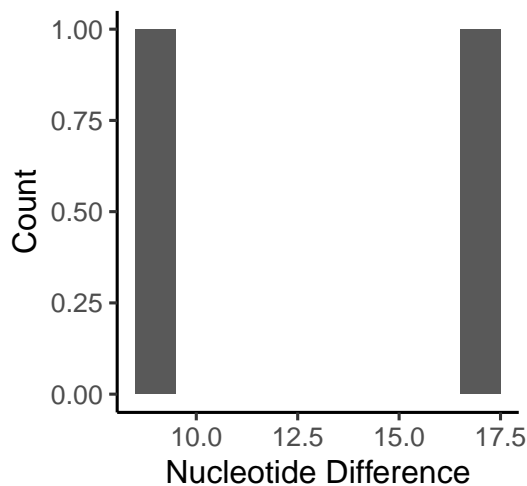
IGHV3-64D*06

2048 sequences assigned
255 (12.5%) exact matches, in which:
153 unique CDR3
6 unique J



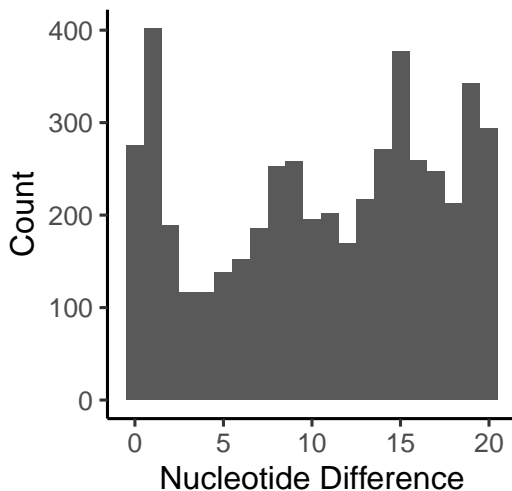
IGHV3-71*01_04

10 sequences assigned
No exact matches.



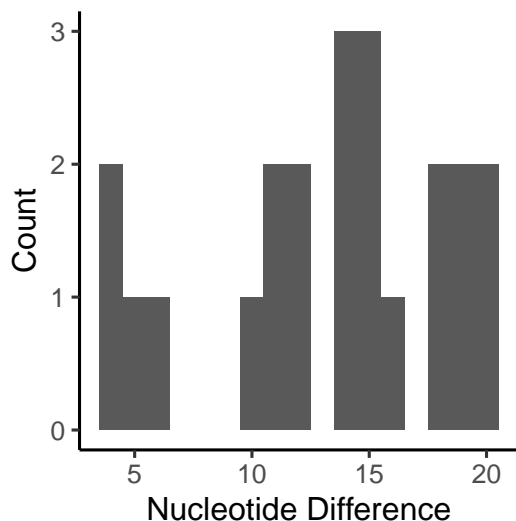
IGHV3-74*01_02

8505 sequences assigned
275 (3.2%) exact matches, in which:
185 unique CDR3
6 unique J



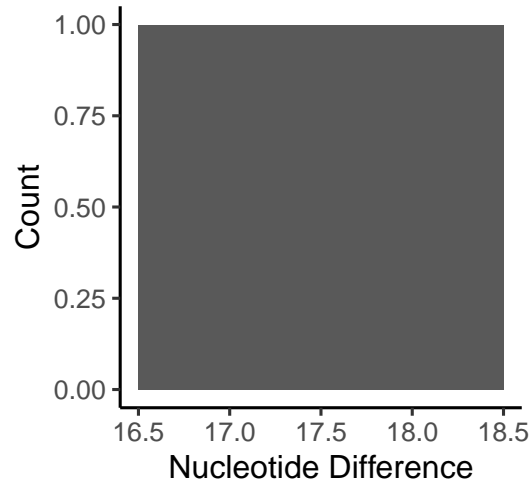
IGHV3-NL1*01

30 sequences assigned
No exact matches.



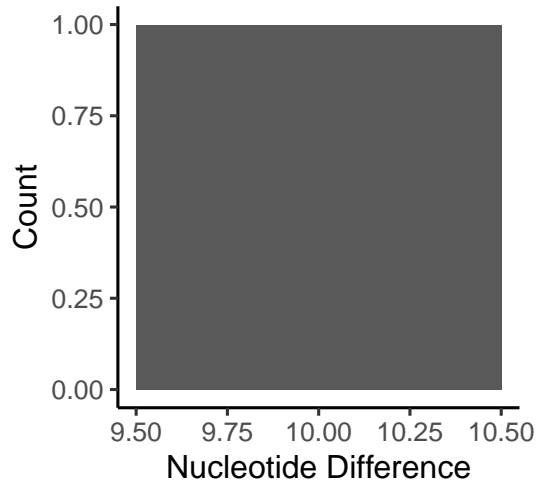
IGHV4-28*03

4 sequences assigned
No exact matches.



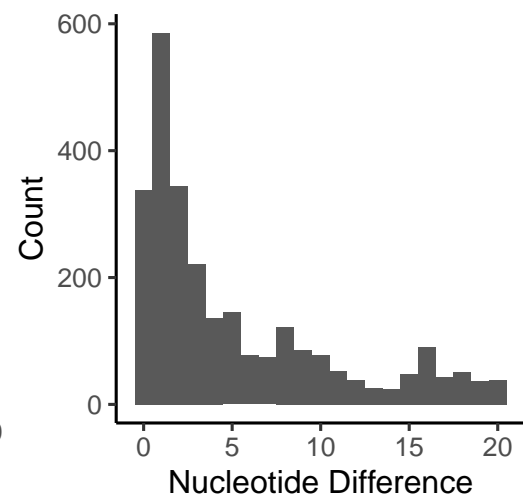
IGHV4-30-4*08

3 sequences assigned
No exact matches.



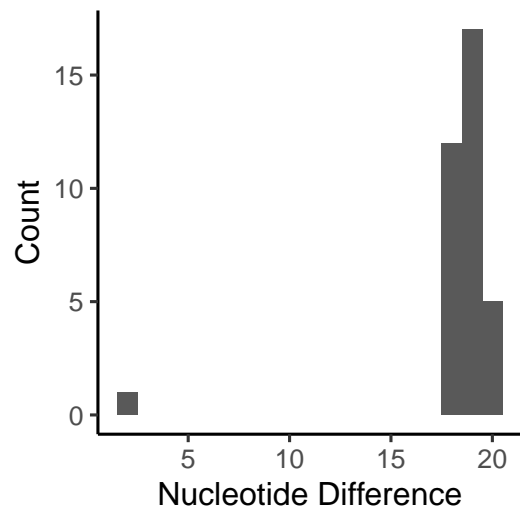
IGHV4-38-2*01

4419 sequences assigned
338 (7.6%) exact matches, in which:
265 unique CDR3
6 unique J



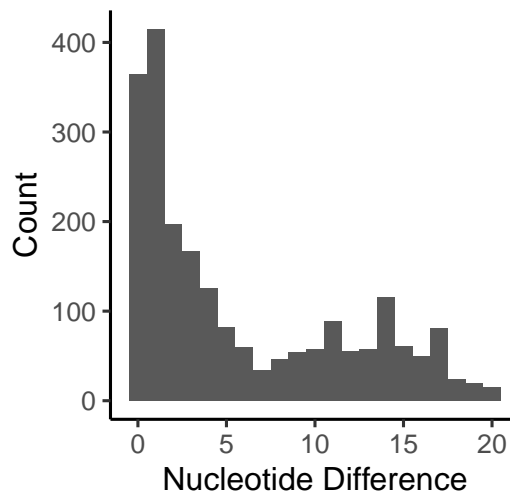
IGHV4-30-2*01

43 sequences assigned
No exact matches.



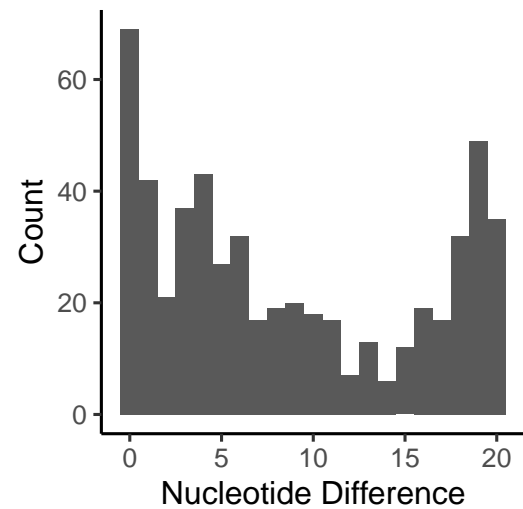
IGHV4-31*03_04

2520 sequences assigned
365 (14.5%) exact matches, in which:
294 unique CDR3
6 unique J



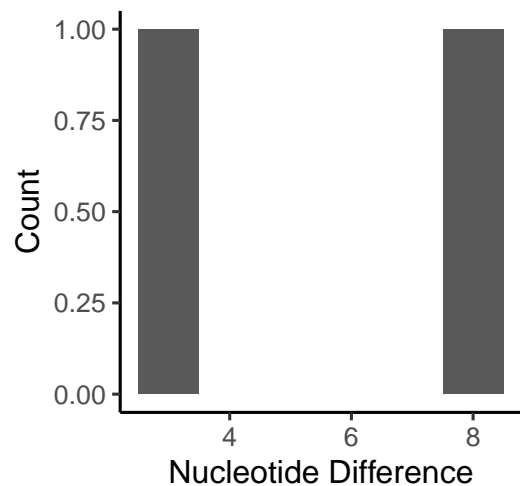
IGHV4-38-2*02

1605 sequences assigned
69 (4.3%) exact matches, in which:
52 unique CDR3
4 unique J



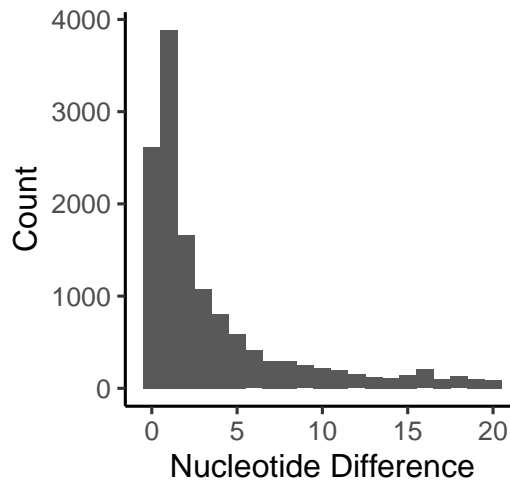
IGHV4-30-2*04

5 sequences assigned
No exact matches.



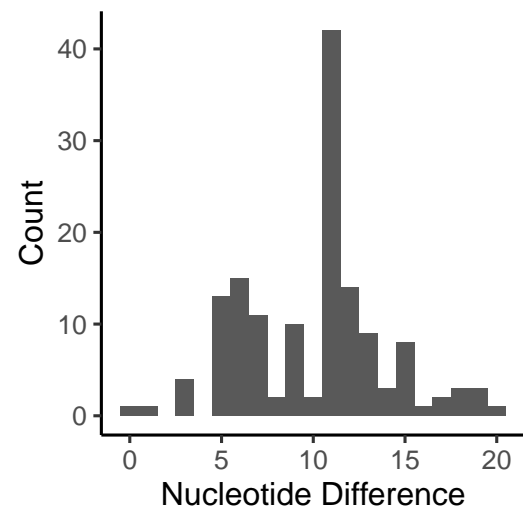
IGHV4-34*01_02

14838 sequences assigned
2615 (17.6%) exact matches, in which:
1798 unique CDR3
6 unique J



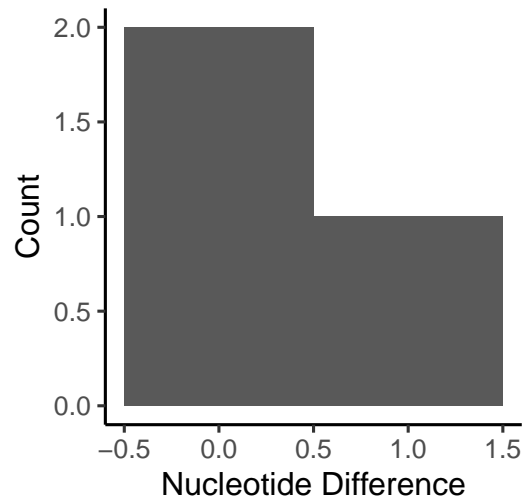
IGHV4-39*07

176 sequences assigned
1 (0.6%) exact matches, in which:
1 unique CDR3
0 unique J



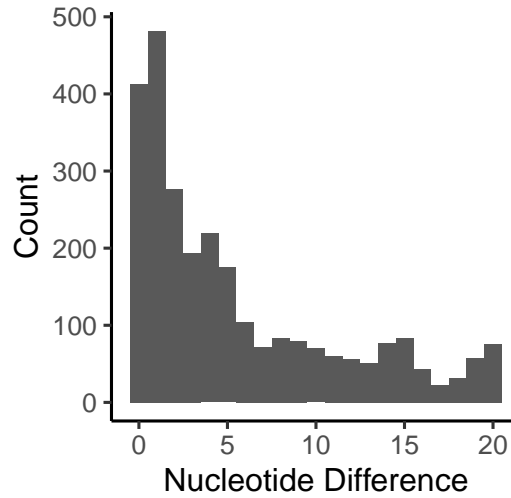
IGHV4-55*01_05

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



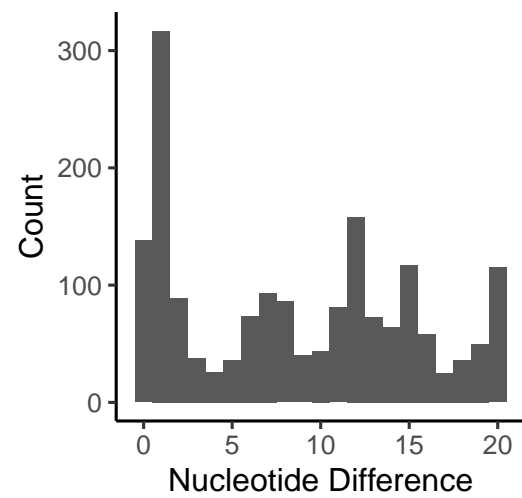
IGHV4-61*01

3560 sequences assigned
413 (11.6%) exact matches, in which:
343 unique CDR3
6 unique J



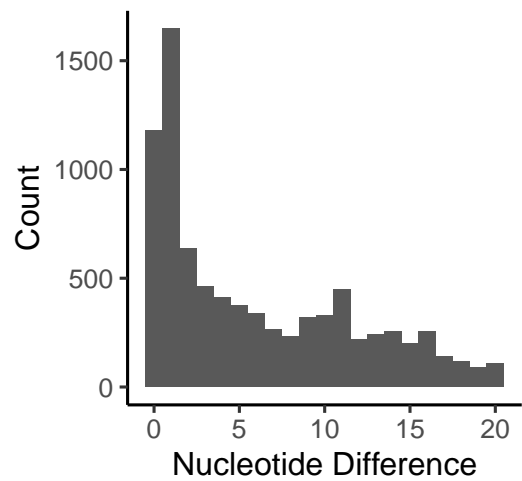
IGHV6-1*01_02

2666 sequences assigned
138 (5.2%) exact matches, in which:
103 unique CDR3
5 unique J



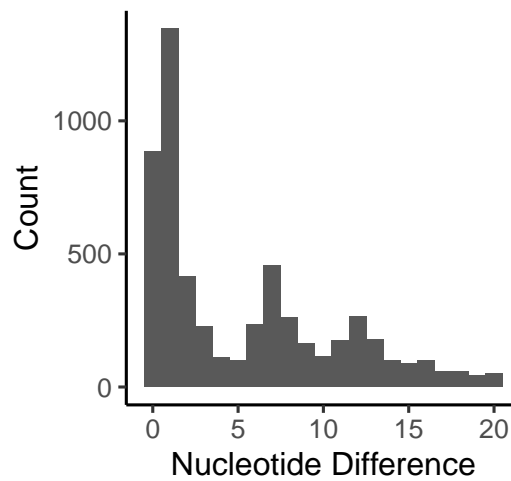
IGHV4-59*01_07

11048 sequences assigned
1178 (10.7%) exact matches, in which:
913 unique CDR3
6 unique J



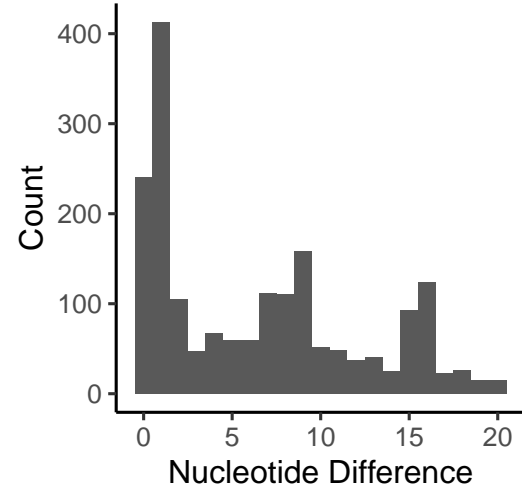
IGHV5-10-1*01_03

6743 sequences assigned
884 (13.1%) exact matches, in which:
529 unique CDR3
6 unique J



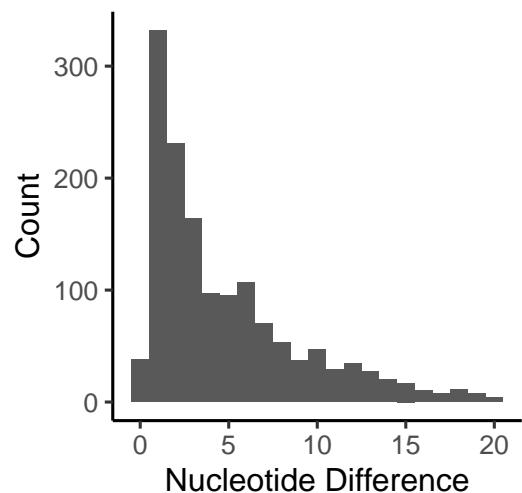
IGHV7-4-1*02

2607 sequences assigned
240 (9.2%) exact matches, in which:
170 unique CDR3
4 unique J



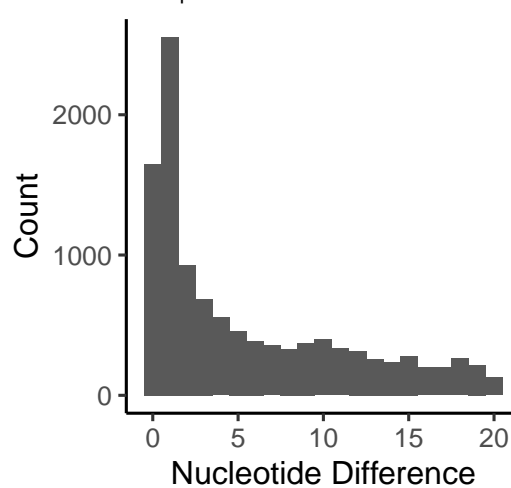
IGHV4-59*12

1545 sequences assigned
38 (2.5%) exact matches, in which:
37 unique CDR3
4 unique J



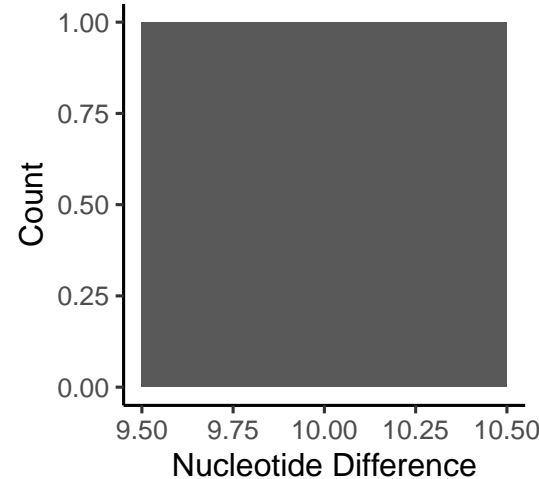
IGHV5-51*01_03

12571 sequences assigned
1649 (13.1%) exact matches, in which:
924 unique CDR3
6 unique J

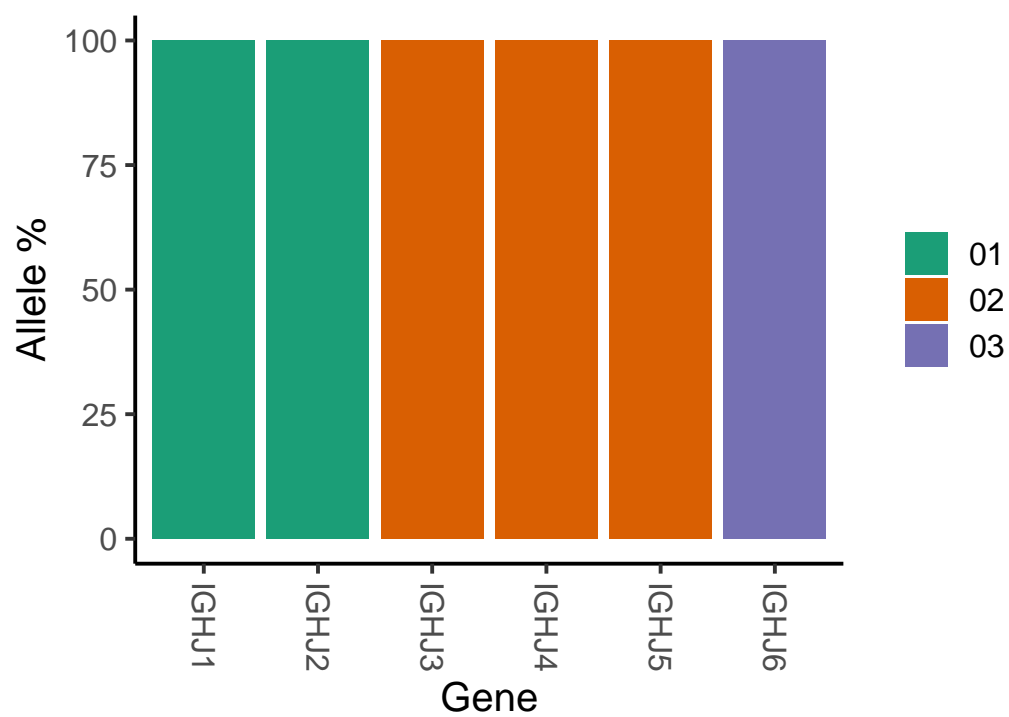


IGHV7-81*01

1 sequences assigned
No exact matches.



Allele Usage



Warning:IGHV4-51*02_IGHV4-51*02_G75C_IGHV4-59*02_G88A 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) 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.

Novel sequence(s) IGHV4-4*02_03_C300T 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) IGHV4-59*02_G88A are not listed in the genotype and will be ignored.

Novel sequence(s) IGHV1-69*08_C191T IGHV3-11*06_T300C IGHV3-30*03_T288C 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.

Warning – no inferred sequences found.

Novel sequence(s) IGHV3-30*03_T288C IGHV3-30-3*01_T288C 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) IGHV3-48*04_A193T_C198T_A200C_C201T_T210A 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) IGHV5-51*07_A128G are not listed in the genotype and will be ignored.

Novel sequence(s) IGHV3-33*01_C288T 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) IGHV3-33*01_T105C_A173T_T192G_C288T are not listed in the genotype and will be ignored.

Novel sequence(s) IGHV3-30*04_T288C IGHV3-33*01_G75C IGHV4-30-2*03_T288C IGHV4-59*02_G88A are not listed in the genotype and will be ignored.

Novel sequence(s) IGHV3-11*06_T300C 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) 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) IGHV5-51*07_A128G are not listed in the genotype and will be ignored.