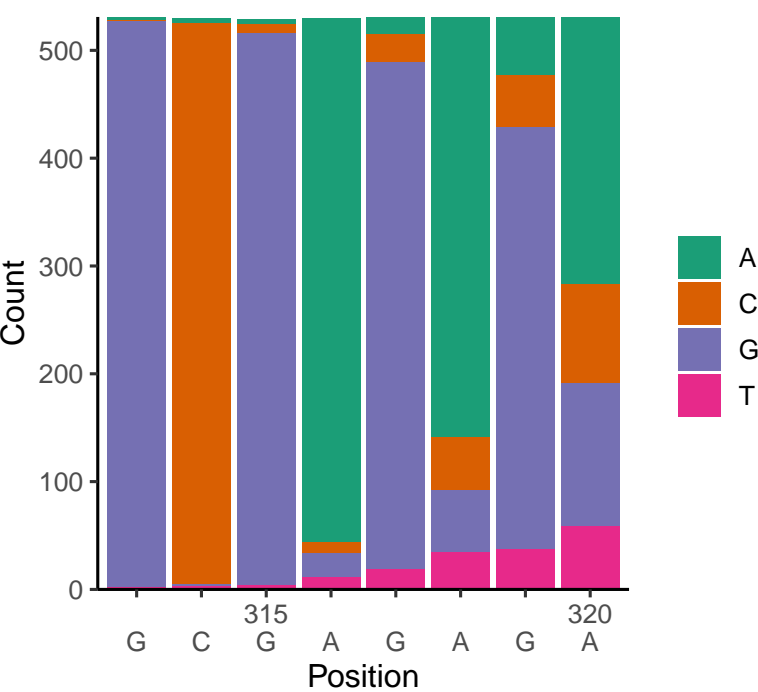
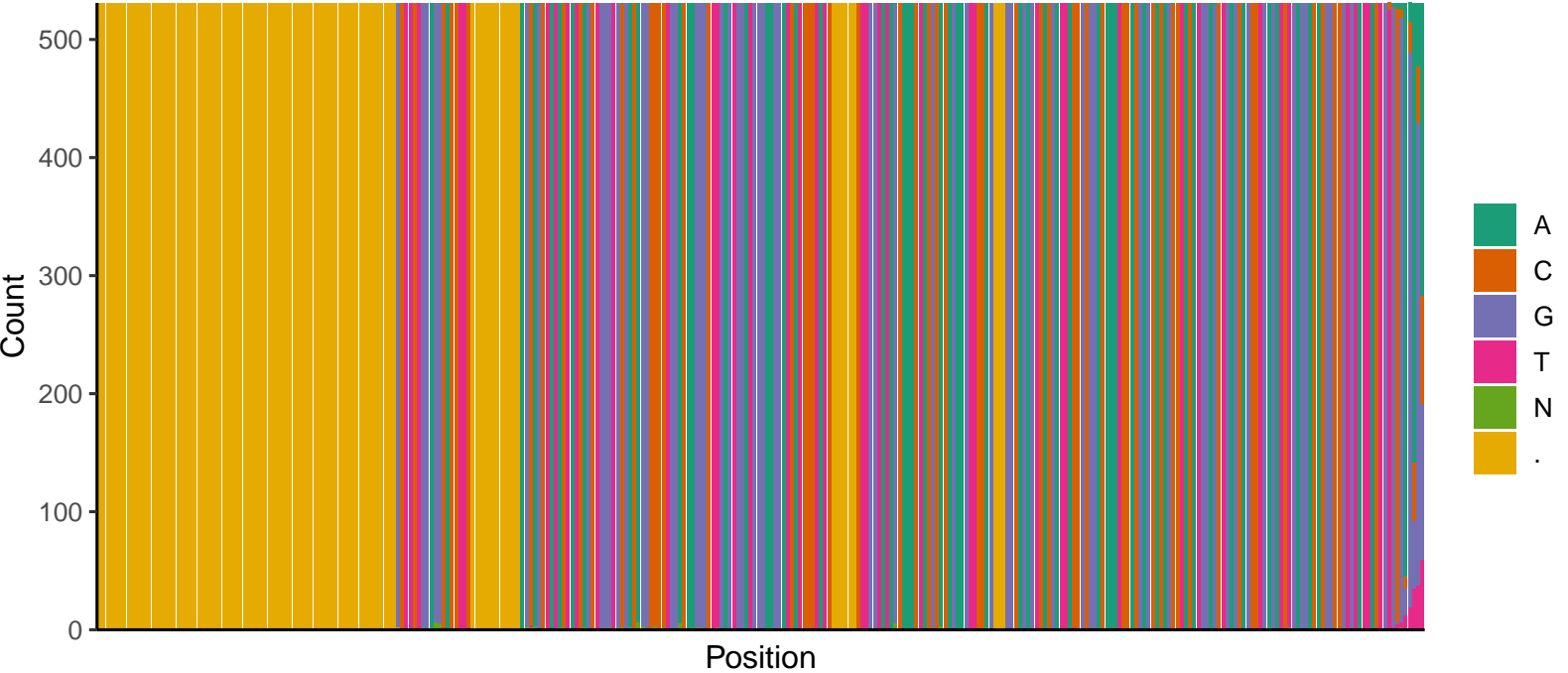


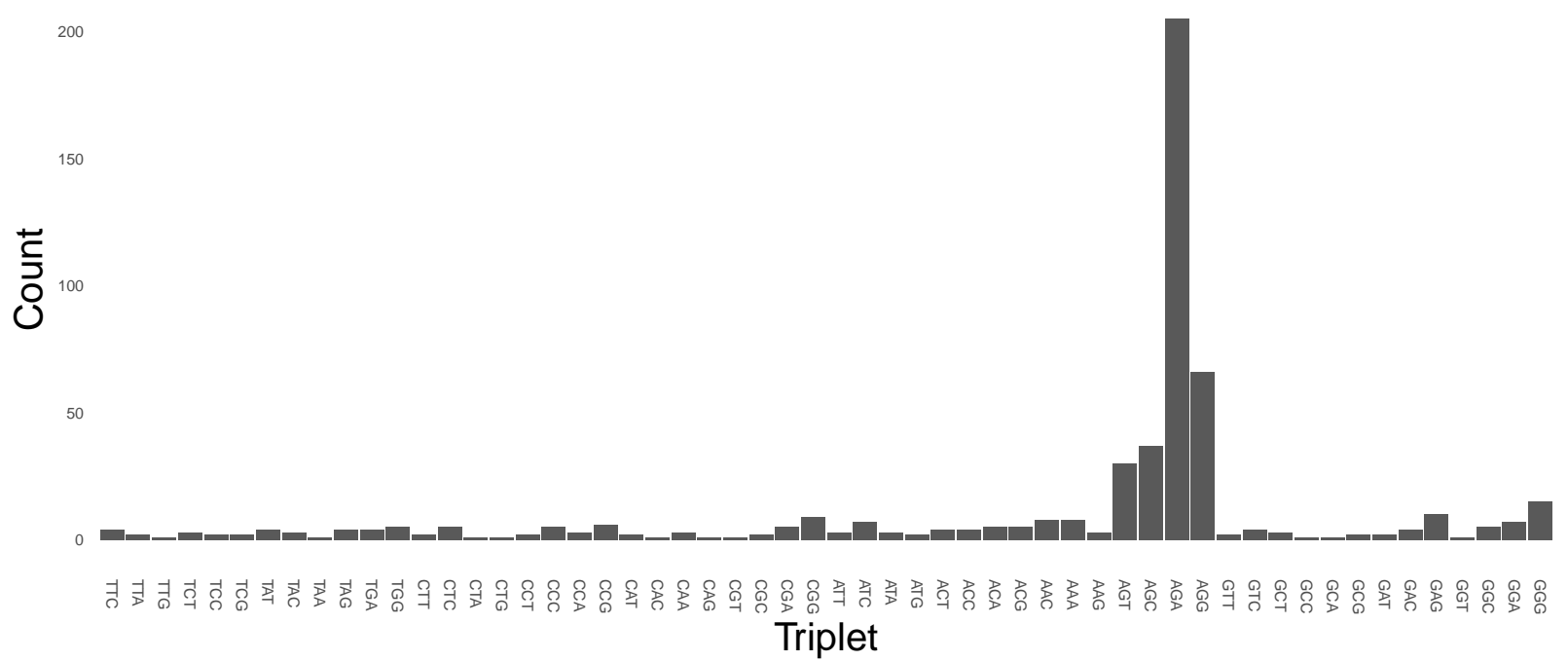
Gene IGHV1-69*04_09_G112A



Gene IGHV1-69*04_09_G112A

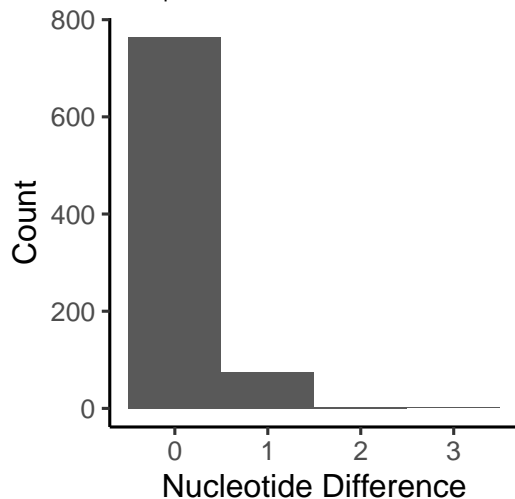


IGHV1-69*04_09_G112A- Final 3 nucleotides as a triplet



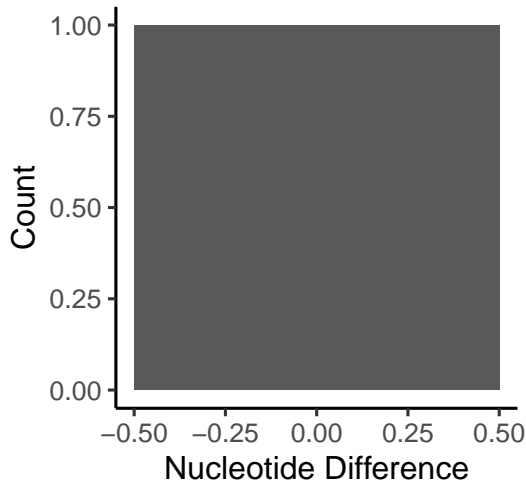
IGHV1-2*06

845 sequences assigned
765 (90.5%) exact matches, in which:
763 unique CDR3
6 unique J



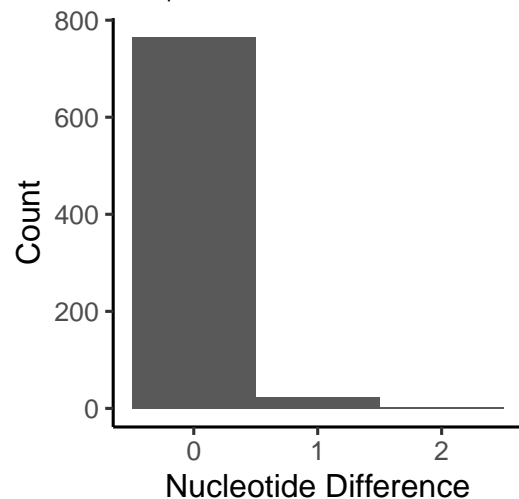
IGHV1-8*03

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



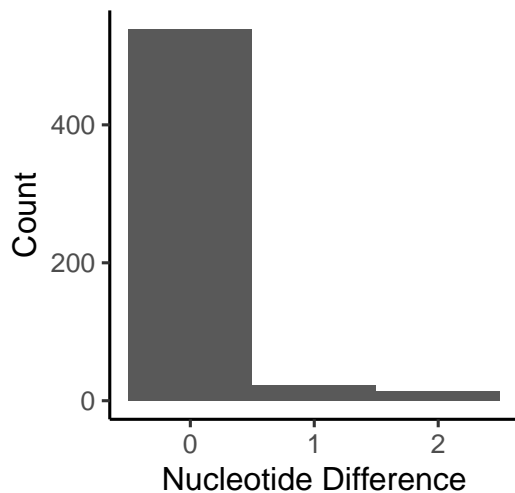
IGHV1-24*01

792 sequences assigned
766 (96.7%) exact matches, in which:
764 unique CDR3
7 unique J



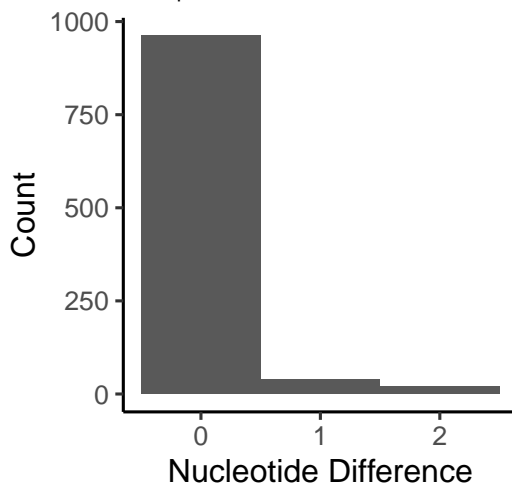
IGHV1-3*01_05

576 sequences assigned
539 (93.6%) exact matches, in which:
539 unique CDR3
7 unique J



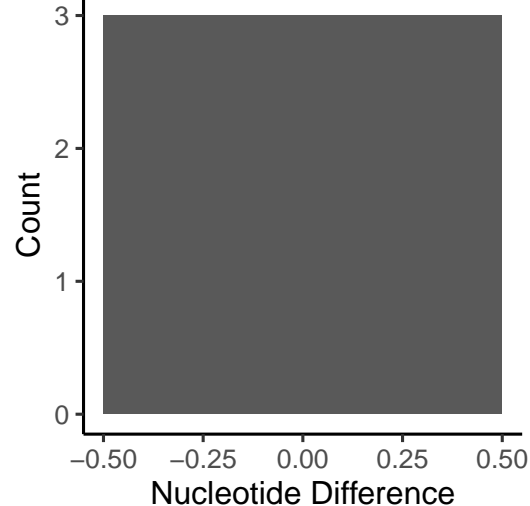
IGHV1-18*01

1021 sequences assigned
962 (94.2%) exact matches, in which:
961 unique CDR3
7 unique J



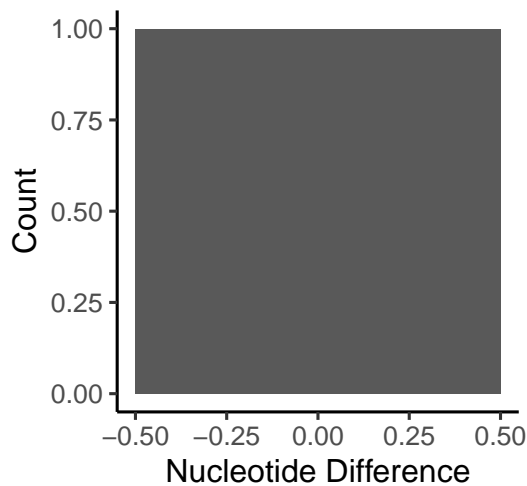
IGHV1-45*02

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



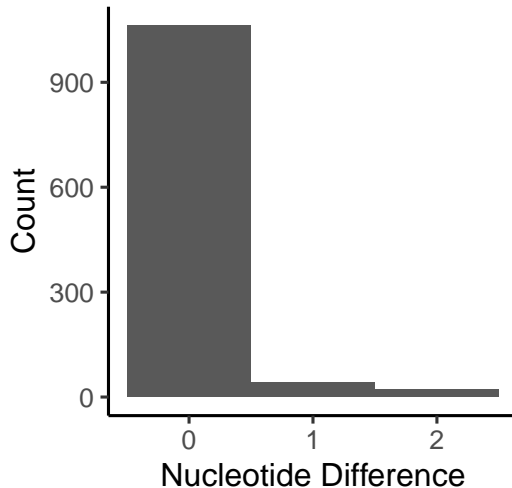
IGHV1-8*01

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



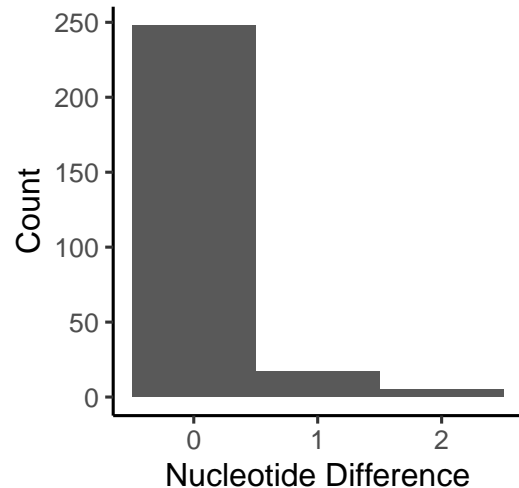
IGHV1-18*04

1126 sequences assigned
1063 (94.4%) exact matches, in which:
1060 unique CDR3
7 unique J



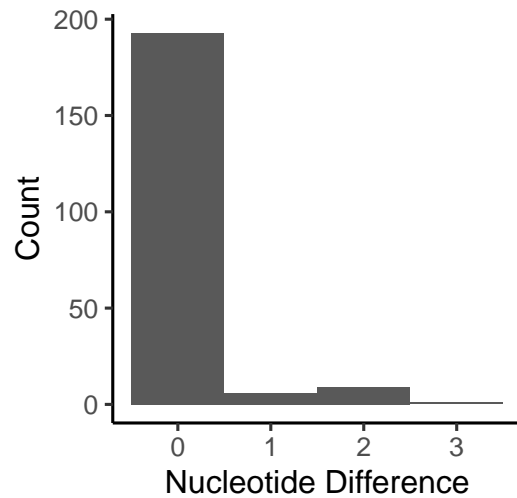
IGHV1-46*01

270 sequences assigned
248 (91.9%) exact matches, in which:
248 unique CDR3
7 unique J



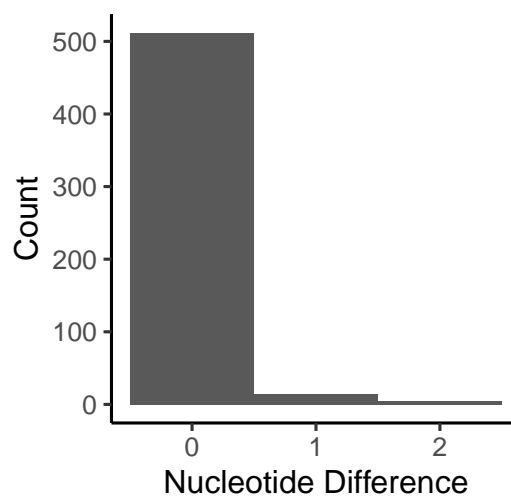
IGHV1-46*03

209 sequences assigned
193 (92.3%) exact matches, in which:
193 unique CDR3
6 unique J



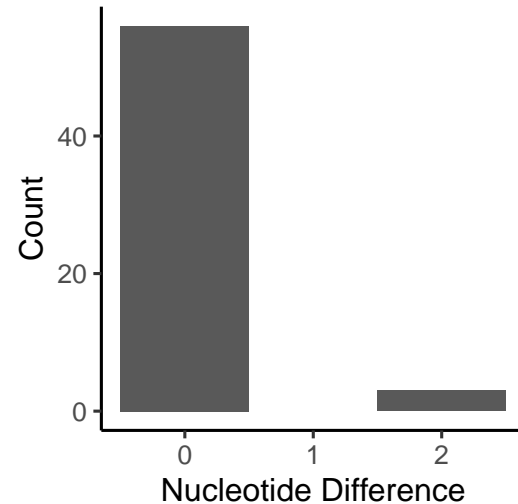
IGHV1-69*04_09_G112A

531 sequences assigned
512 (96.4%) exact matches, in which:
512 unique CDR3
6 unique J



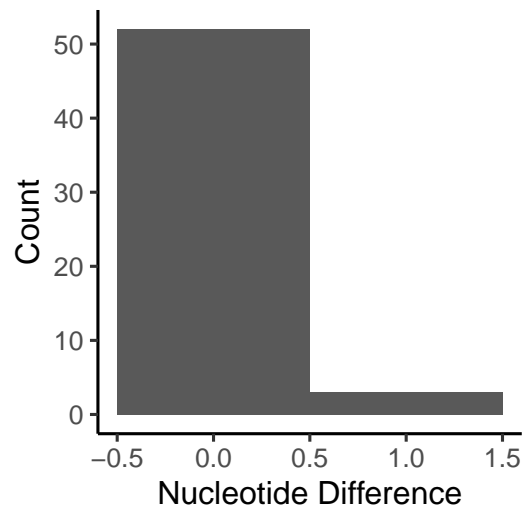
IGHV2-26*01

59 sequences assigned
56 (94.9%) exact matches, in which:
56 unique CDR3
7 unique J



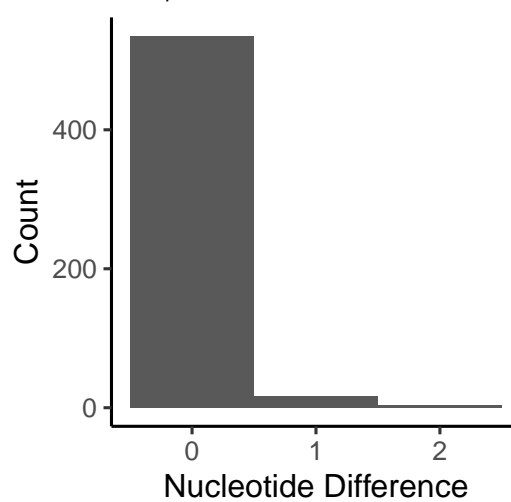
IGHV1-58*02

55 sequences assigned
52 (94.5%) exact matches, in which:
52 unique CDR3
6 unique J



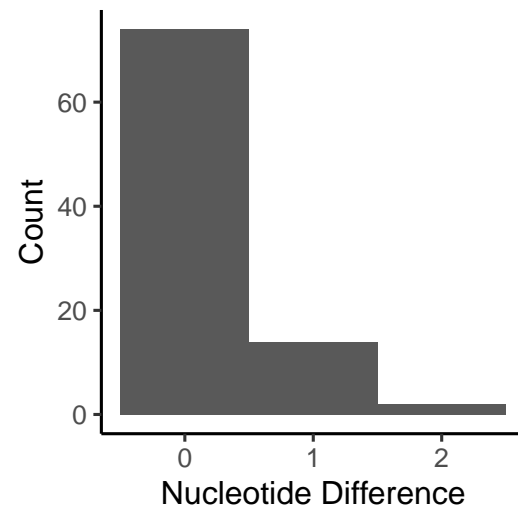
IGHV1-69*06_14

555 sequences assigned
535 (96.4%) exact matches, in which:
535 unique CDR3
7 unique J



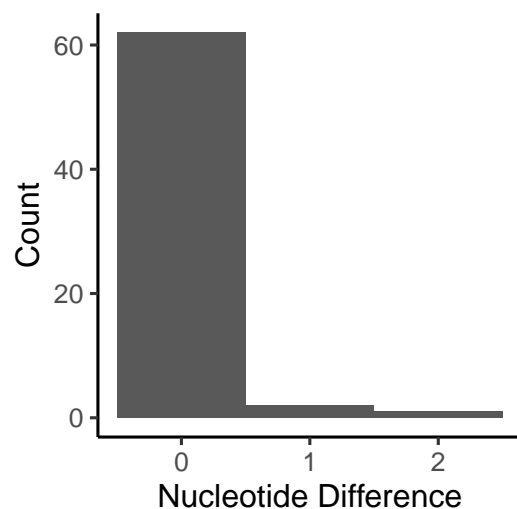
IGHV2-70*01

90 sequences assigned
74 (82.2%) exact matches, in which:
69 unique CDR3
5 unique J



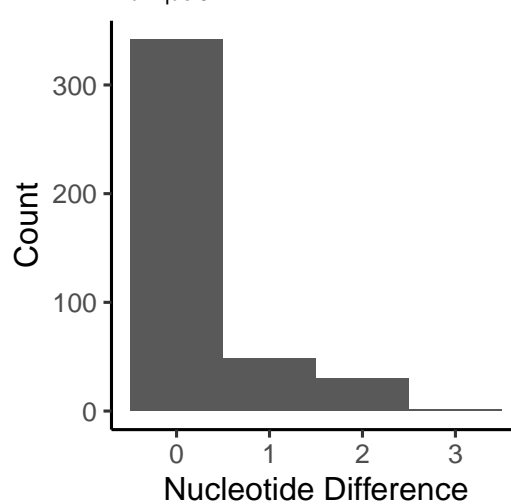
IGHV1-58*01_03

65 sequences assigned
62 (95.4%) exact matches, in which:
62 unique CDR3
6 unique J



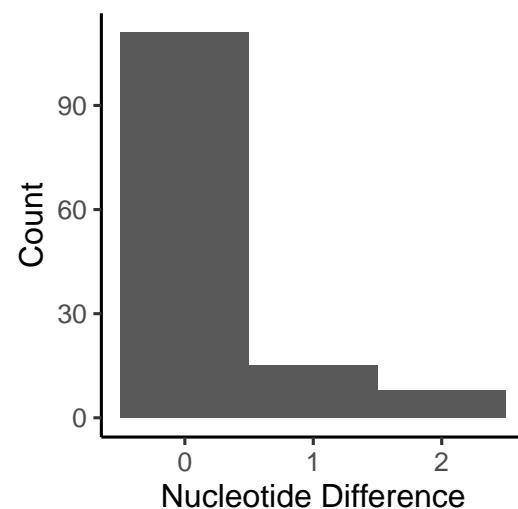
IGHV2-5*02

421 sequences assigned
342 (81.2%) exact matches, in which:
341 unique CDR3
7 unique J



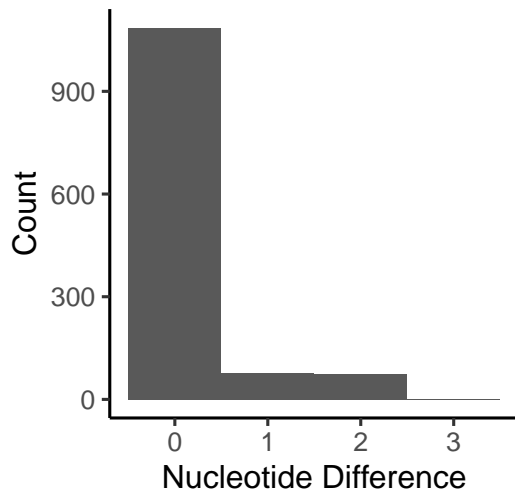
IGHV2-70*11_15

134 sequences assigned
111 (82.8%) exact matches, in which:
111 unique CDR3
6 unique J



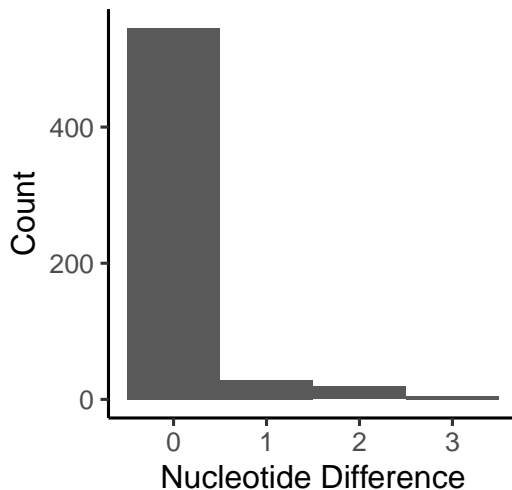
IGHV3-7*03

1241 sequences assigned
1086 (87.5%) exact matches, in which:
1066 unique CDR3
7 unique J



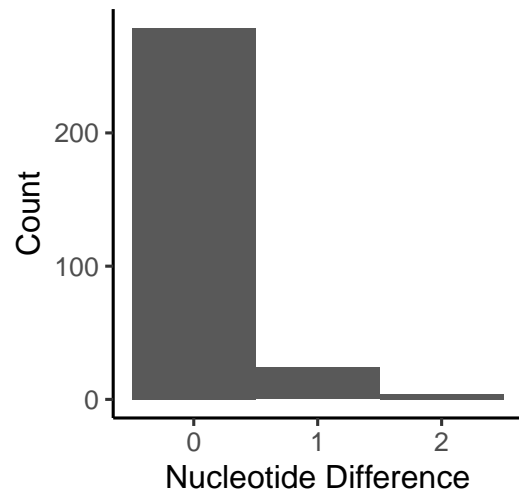
IGHV3-15*01_02

599 sequences assigned
546 (91.2%) exact matches, in which:
540 unique CDR3
7 unique J



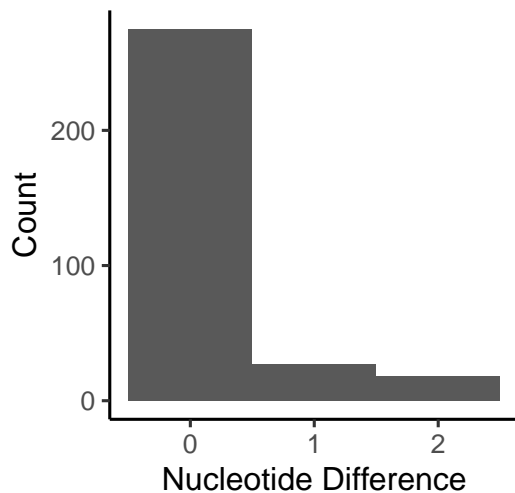
IGHV3-33*01

307 sequences assigned
279 (90.9%) exact matches, in which:
275 unique CDR3
7 unique J



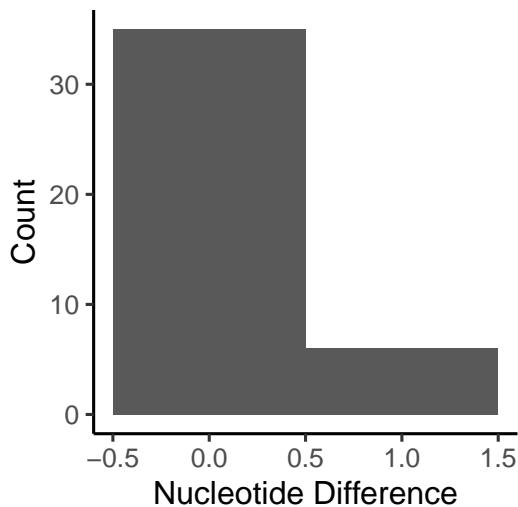
IGHV3-11*06

320 sequences assigned
275 (85.9%) exact matches, in which:
273 unique CDR3
7 unique J



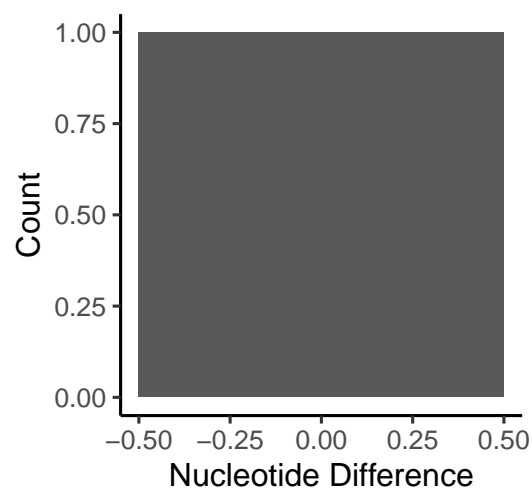
IGHV3-20*01_02

41 sequences assigned
35 (85.4%) exact matches, in which:
35 unique CDR3
5 unique J



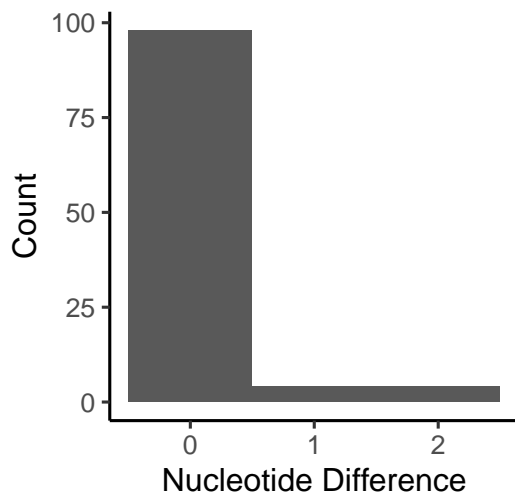
IGHV3-38-3*01

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



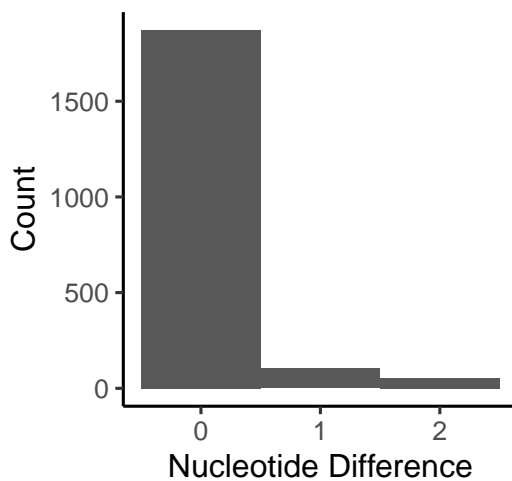
IGHV3-13*05

106 sequences assigned
98 (92.5%) exact matches, in which:
97 unique CDR3
6 unique J



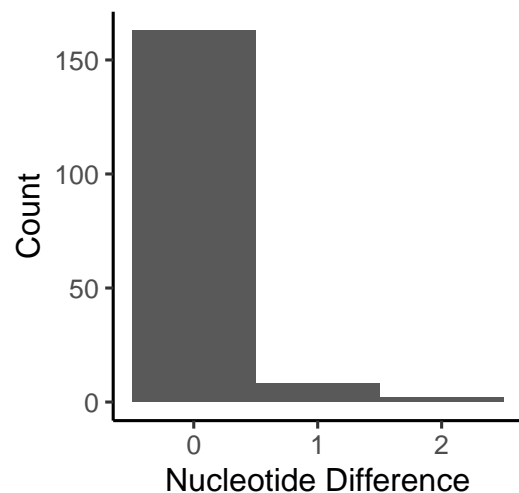
IGHV3-21*01_02

2030 sequences assigned
1872 (92.2%) exact matches, in which:
1839 unique CDR3
7 unique J



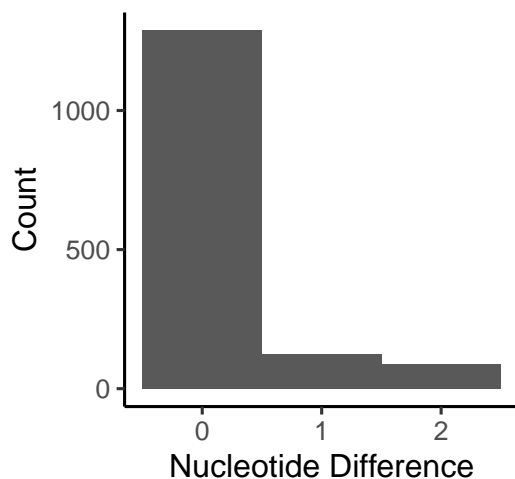
IGHV3-43*01

173 sequences assigned
163 (94.2%) exact matches, in which:
162 unique CDR3
7 unique J



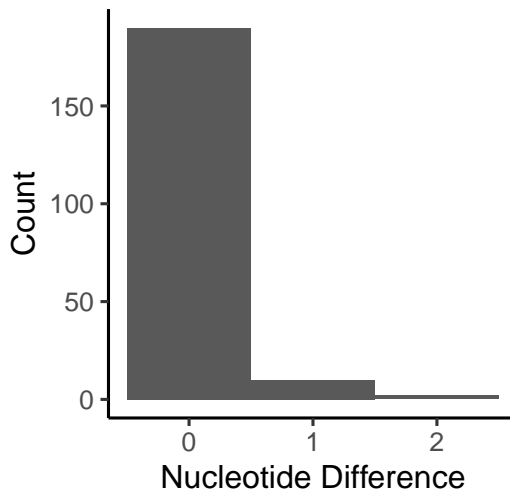
IGHV3-48*02

1498 sequences assigned
1288 (86%) exact matches, in which:
1270 unique CDR3
7 unique J



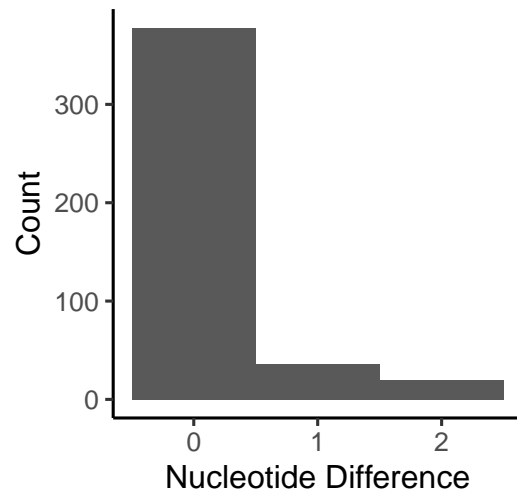
IGHV3-53*04

202 sequences assigned
190 (94.1%) exact matches, in which:
187 unique CDR3
6 unique J



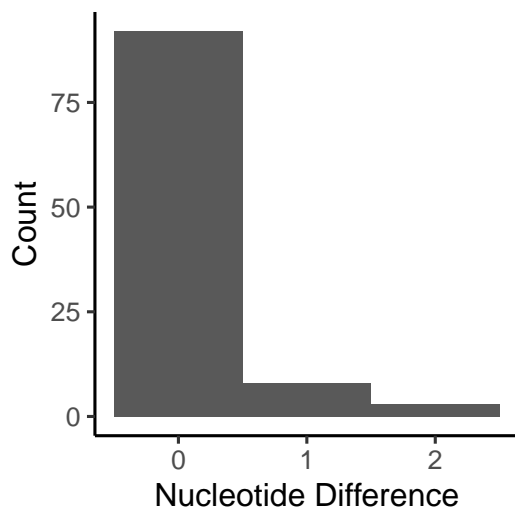
IGHV3-66*01

434 sequences assigned
378 (87.1%) exact matches, in which:
373 unique CDR3
7 unique J



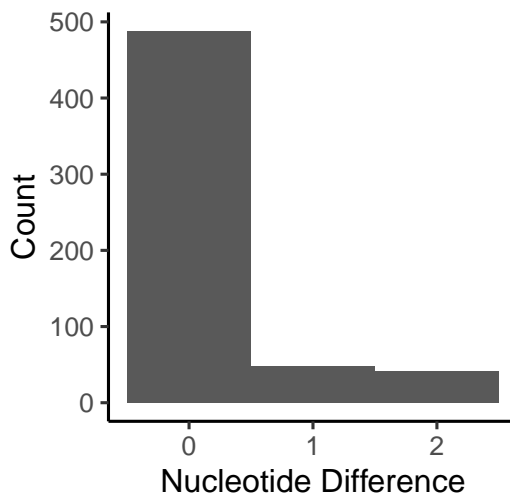
IGHV3-49*04

103 sequences assigned
92 (89.3%) exact matches, in which:
92 unique CDR3
6 unique J



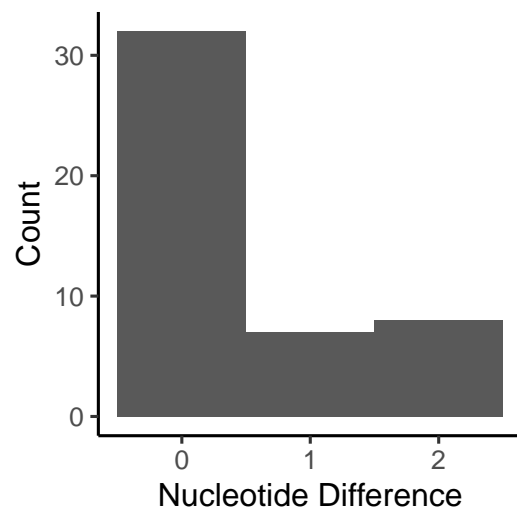
IGHV3-53*01_02

578 sequences assigned
488 (84.4%) exact matches, in which:
480 unique CDR3
7 unique J



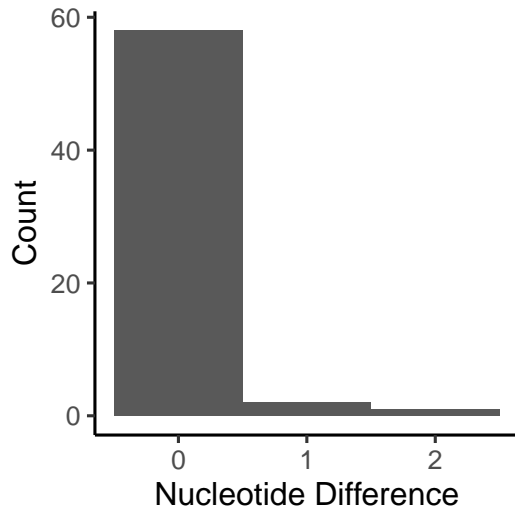
IGHV3-72*01

47 sequences assigned
32 (68.1%) exact matches, in which:
32 unique CDR3
4 unique J



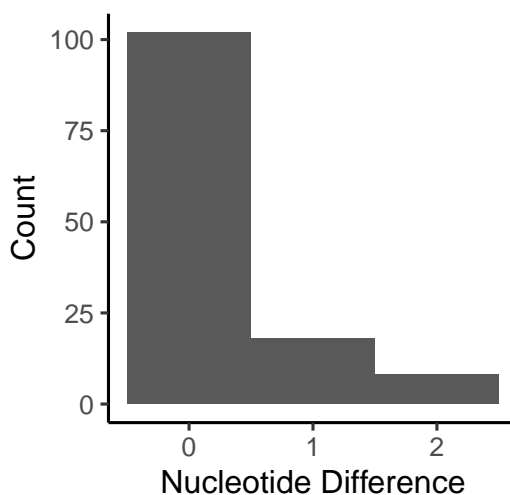
IGHV3-49*03_05

61 sequences assigned
58 (95.1%) exact matches, in which:
57 unique CDR3
6 unique J



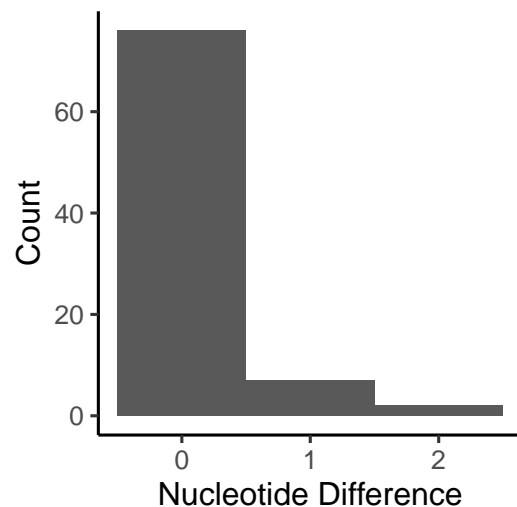
IGHV3-64*01

128 sequences assigned
102 (79.7%) exact matches, in which:
98 unique CDR3
6 unique J



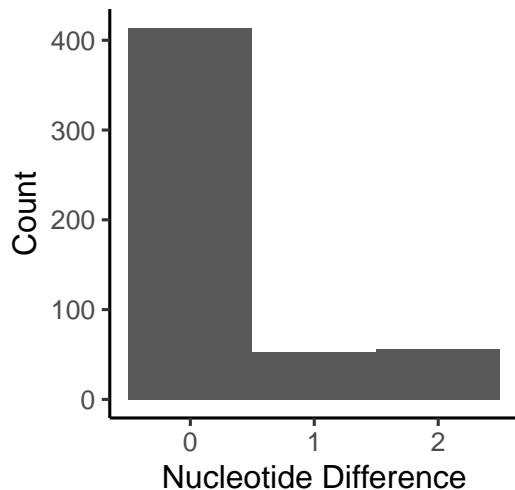
IGHV3-73*01_02

85 sequences assigned
76 (89.4%) exact matches, in which:
76 unique CDR3
6 unique J



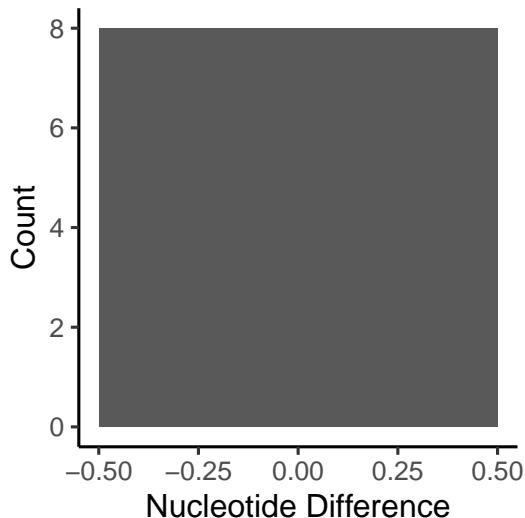
IGHV3-74*01_02

523 sequences assigned
414 (79.2%) exact matches, in which:
407 unique CDR3
7 unique J



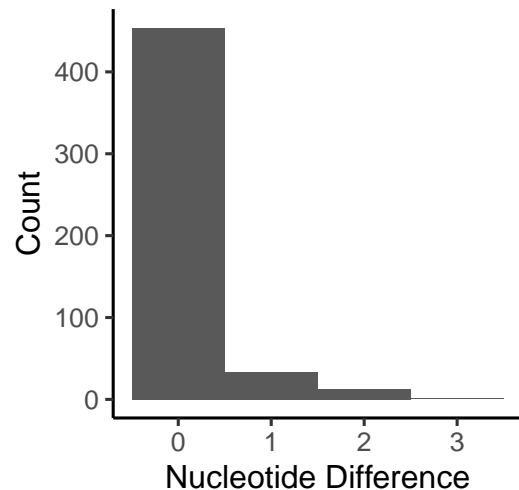
IGHV4-28*01_07

8 sequences assigned
8 (100%) exact matches, in which:
8 unique CDR3
4 unique J



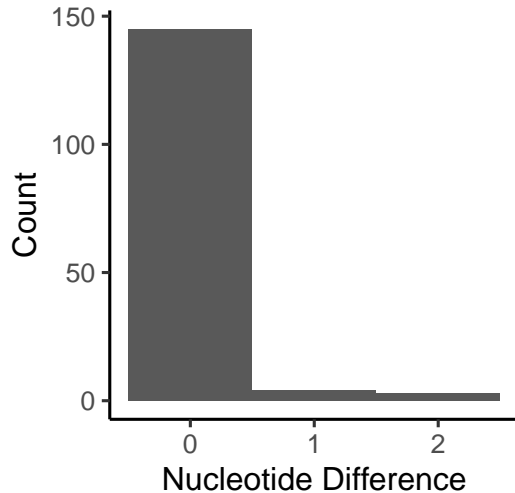
IGHV4-31*03_04

501 sequences assigned
454 (90.6%) exact matches, in which:
454 unique CDR3
6 unique J



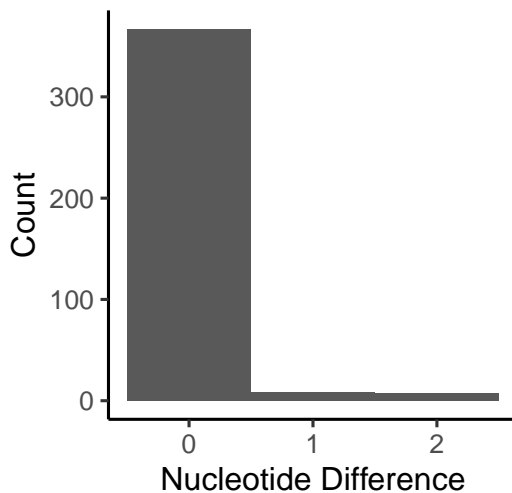
IGHV3-43D*03

152 sequences assigned
145 (95.4%) exact matches, in which:
141 unique CDR3
7 unique J



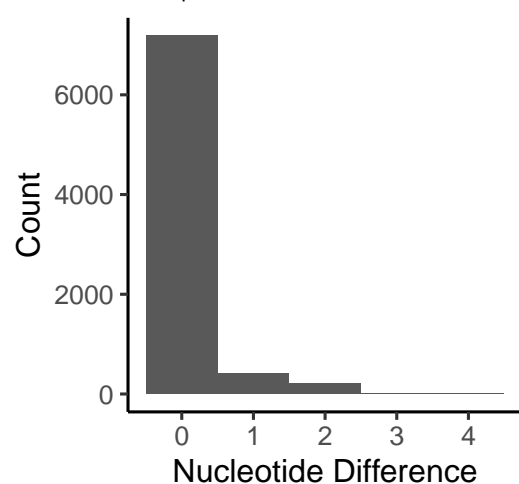
IGHV4-30-2*01

382 sequences assigned
367 (96.1%) exact matches, in which:
365 unique CDR3
6 unique J



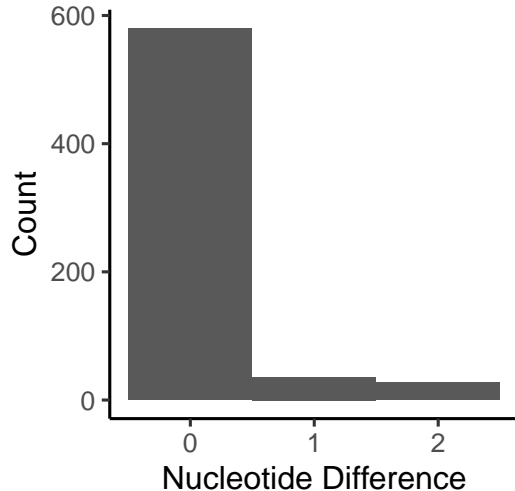
IGHV4-34*01_02

7817 sequences assigned
7185 (91.9%) exact matches, in which:
7100 unique CDR3
7 unique J



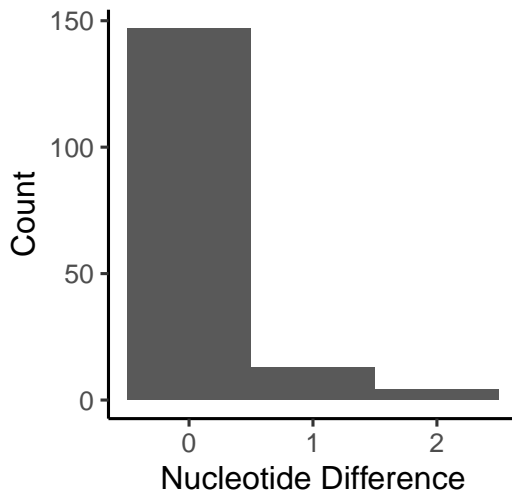
IGHV3-64D*06

643 sequences assigned
580 (90.2%) exact matches, in which:
575 unique CDR3
7 unique J



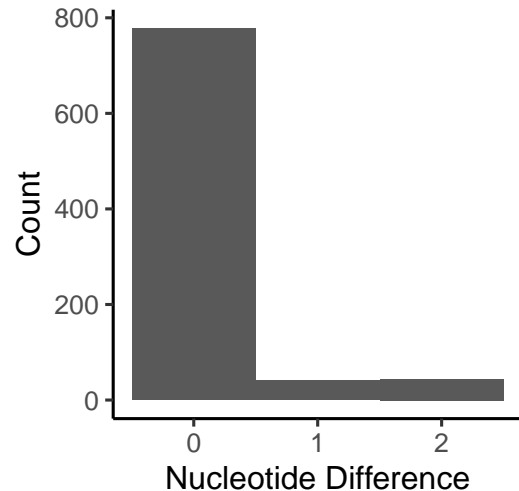
IGHV4-30-4*07

164 sequences assigned
147 (89.6%) exact matches, in which:
145 unique CDR3
6 unique J



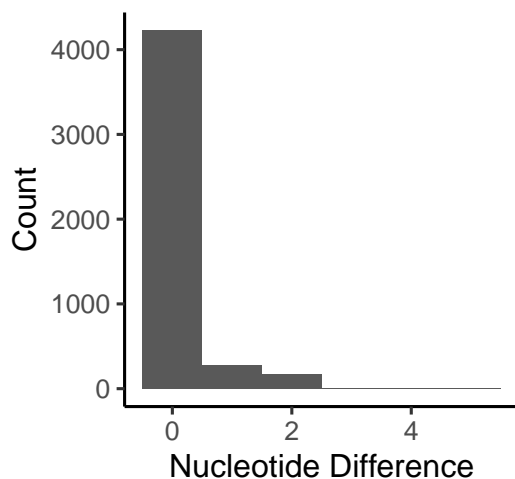
IGHV4-38-2*02

862 sequences assigned
778 (90.3%) exact matches, in which:
769 unique CDR3
6 unique J



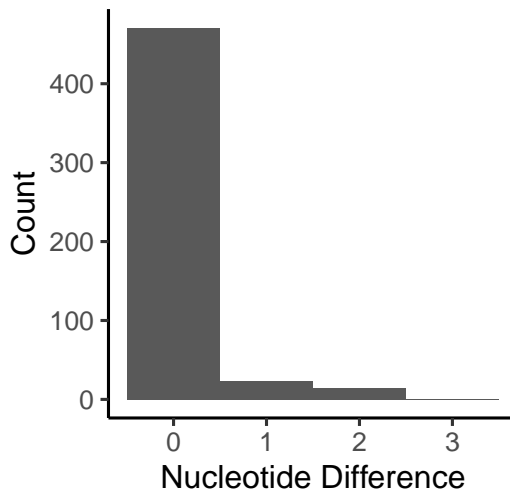
IGHV4-39*01_05

4682 sequences assigned
4227 (90.3%) exact matches, in which:
4174 unique CDR3
7 unique J



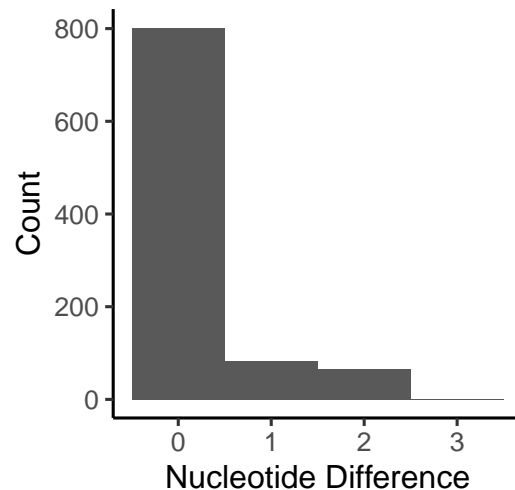
IGHV4-61*01

509 sequences assigned
471 (92.5%) exact matches, in which:
469 unique CDR3
6 unique J



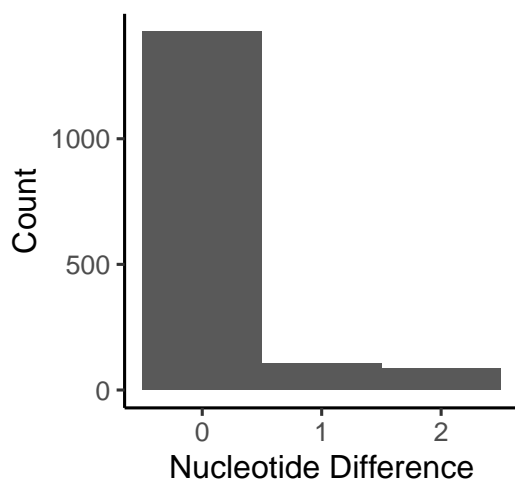
IGHV6-1*01_02

952 sequences assigned
802 (84.2%) exact matches, in which:
798 unique CDR3
7 unique J



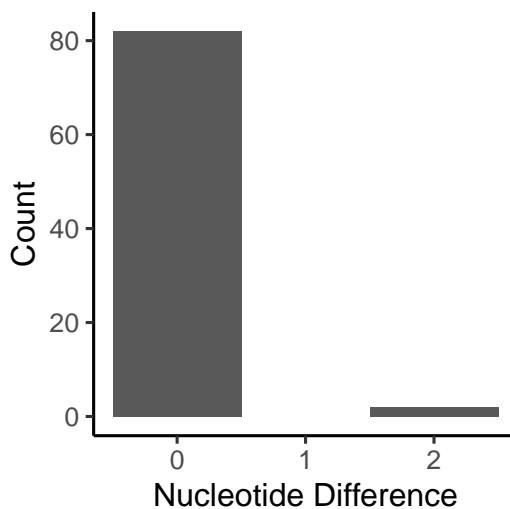
IGHV4-59*08

1618 sequences assigned
1426 (88.1%) exact matches, in which:
1415 unique CDR3
7 unique J



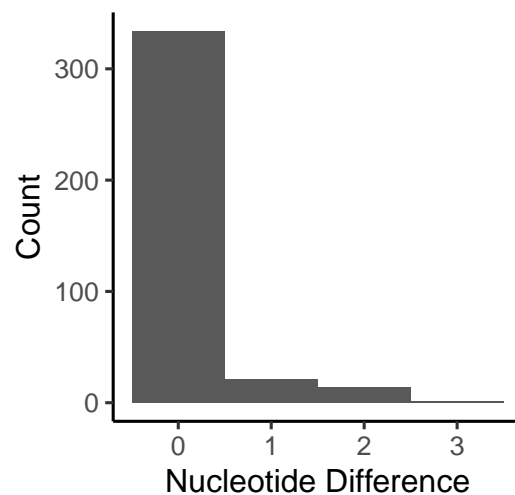
IGHV5-10-1*01_03

84 sequences assigned
82 (97.6%) exact matches, in which:
82 unique CDR3
7 unique J



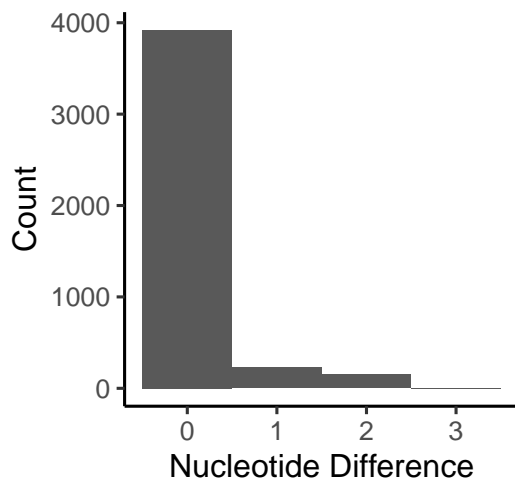
IGHV7-4-1*02

370 sequences assigned
334 (90.3%) exact matches, in which:
334 unique CDR3
7 unique J



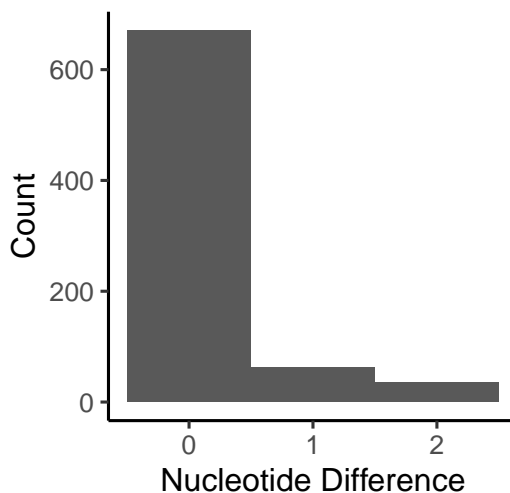
IGHV4-59*01_07

4300 sequences assigned
3920 (91.2%) exact matches, in which:
3877 unique CDR3
7 unique J

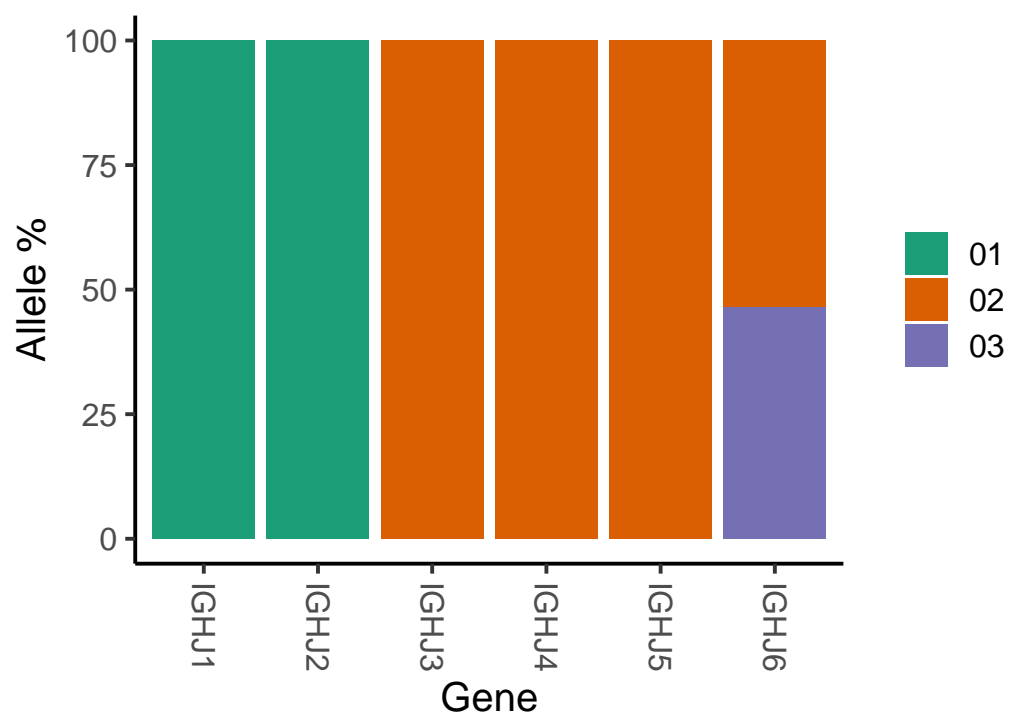


IGHV5-51*01_03

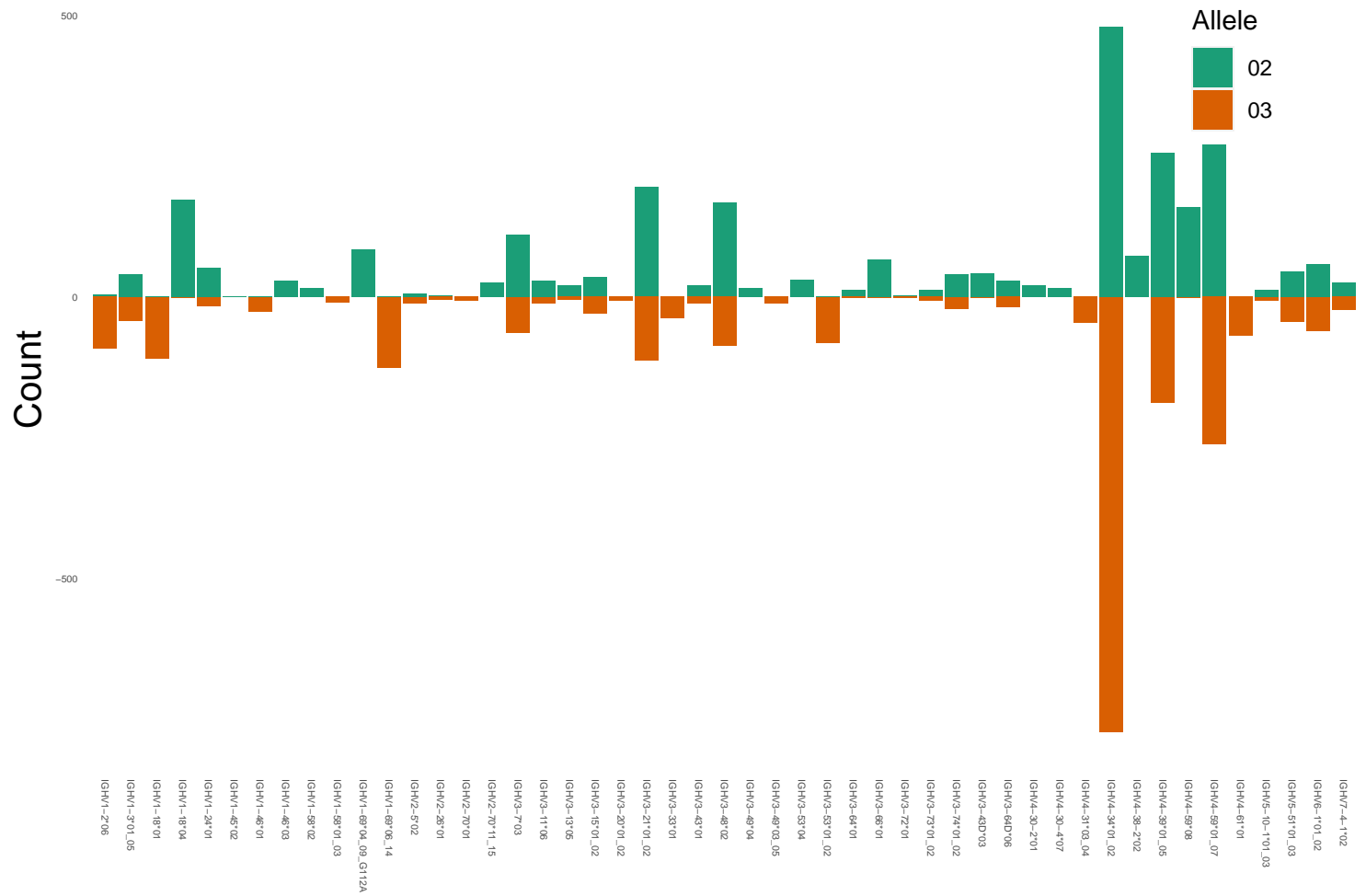
768 sequences assigned
671 (87.4%) exact matches, in which:
671 unique CDR3
7 unique J



Allele Usage



Sequence Count byIGHJ6 allele usage



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.

Warning – no inferred sequences found.