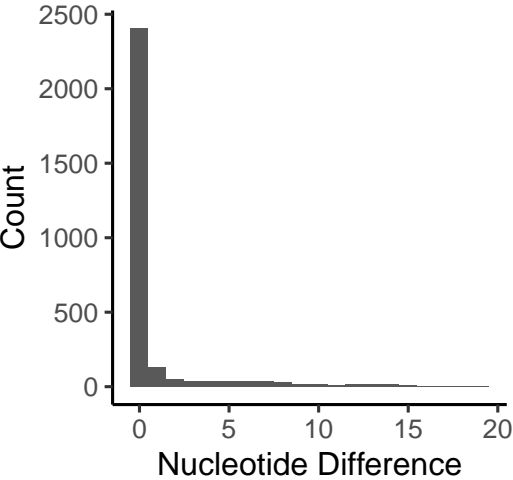


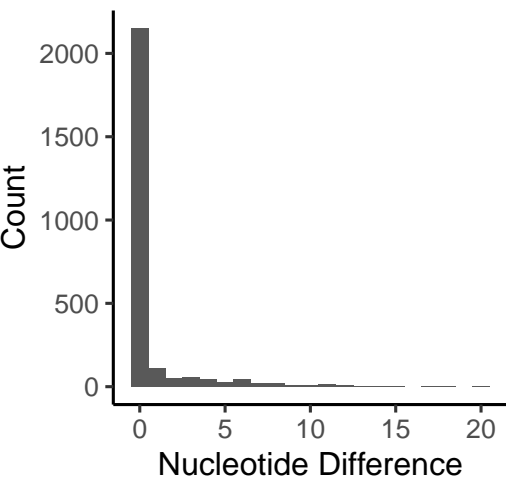
IGHV1-2*02

2932 sequences assigned
2405 (82%) exact matches, in which:
2398 unique CDR3
6 unique J



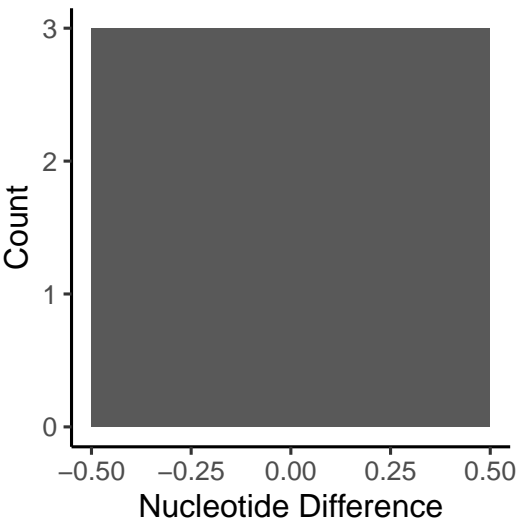
IGHV1-8*01

2598 sequences assigned
2150 (82.8%) exact matches, in which:
2145 unique CDR3
6 unique J



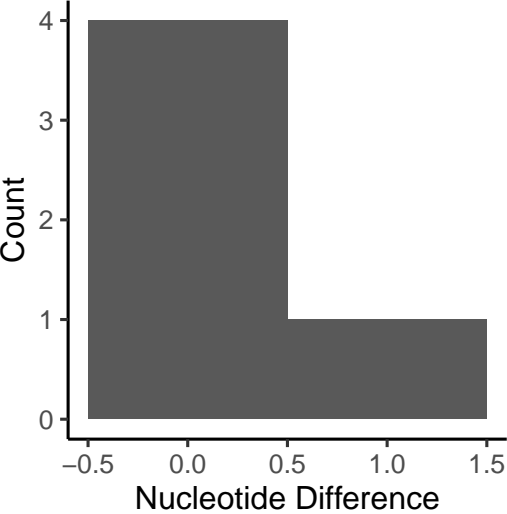
IGHV1-45*02

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



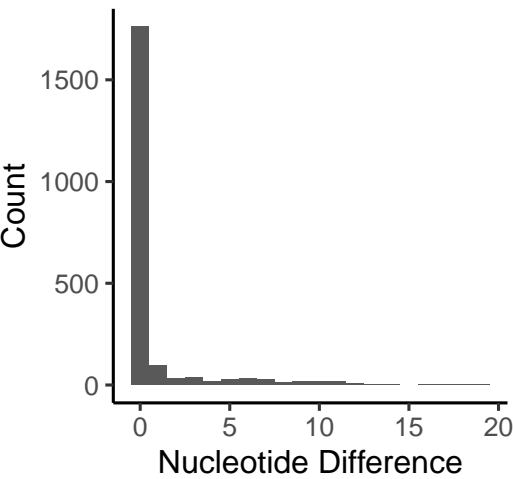
IGHV1-3*02

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



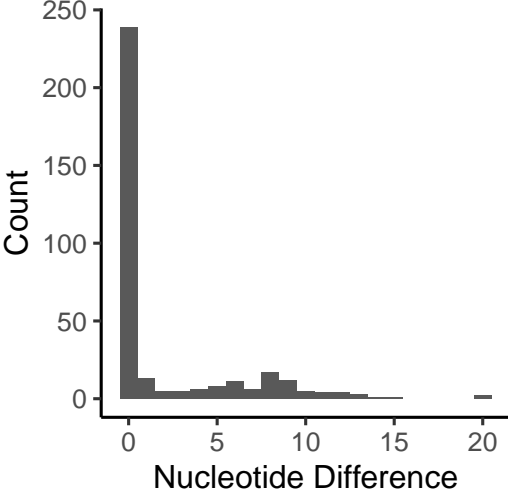
IGHV1-18*01

2122 sequences assigned
1761 (83%) exact matches, in which:
1755 unique CDR3
6 unique J



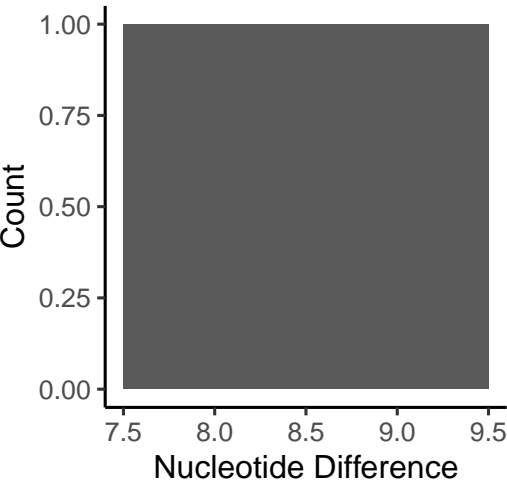
IGHV1-46*01

342 sequences assigned
239 (69.9%) exact matches, in which:
239 unique CDR3
6 unique J



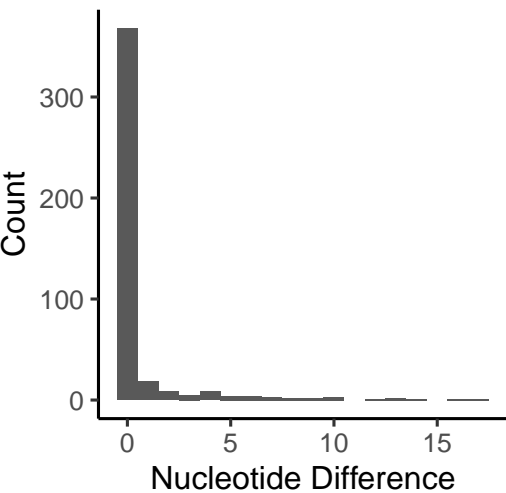
IGHV1-3*01_05

2 sequences assigned
No exact matches.



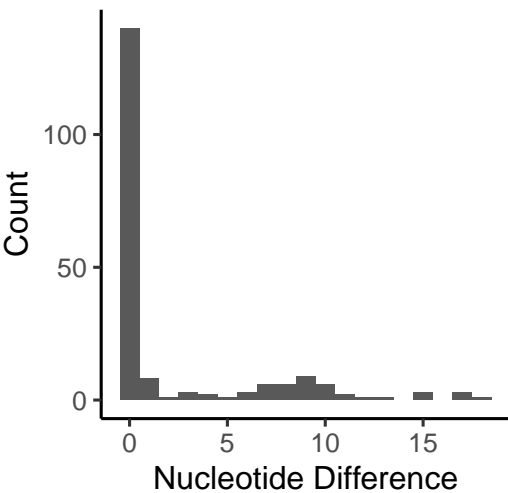
IGHV1-24*01

431 sequences assigned
368 (85.4%) exact matches, in which:
368 unique CDR3
6 unique J



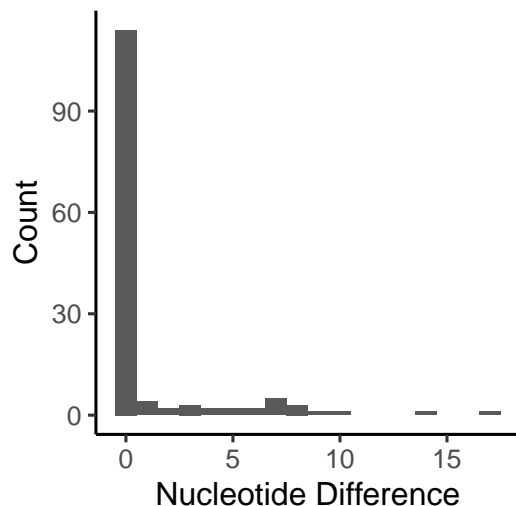
IGHV1-46*03

196 sequences assigned
140 (71.4%) exact matches, in which:
140 unique CDR3
6 unique J



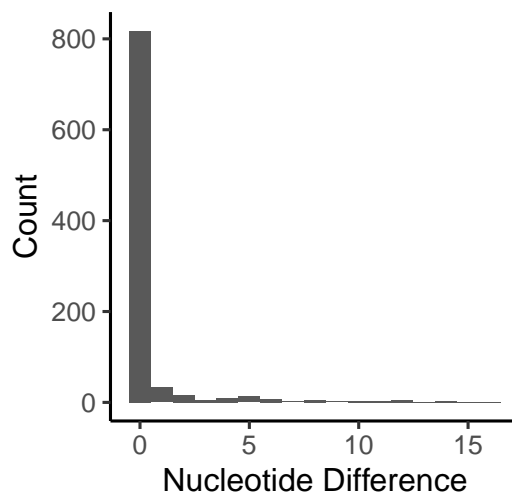
IGHV1-58*01_03

141 sequences assigned
114 (80.9%) exact matches, in which:
114 unique CDR3
5 unique J



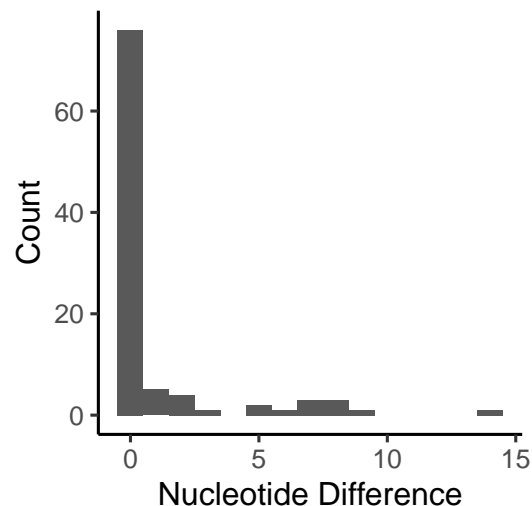
IGHV1-69*06_14

930 sequences assigned
818 (88%) exact matches, in which:
818 unique CDR3
6 unique J



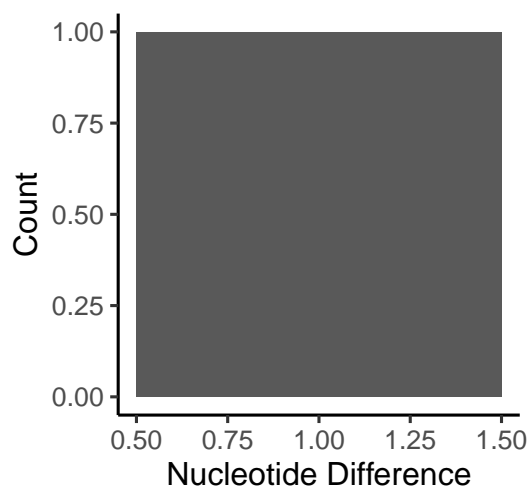
IGHV2-26*01

97 sequences assigned
76 (78.4%) exact matches, in which:
76 unique CDR3
5 unique J



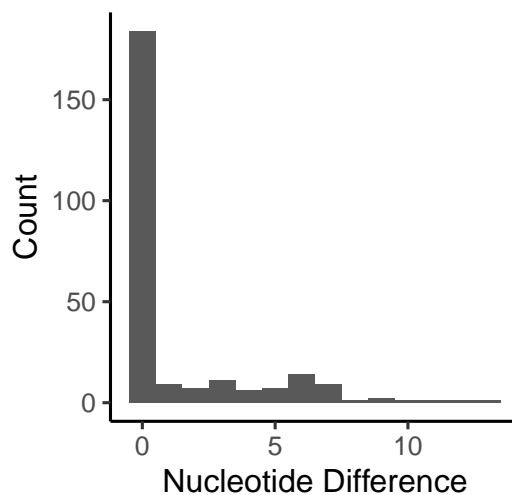
IGHV1-68*01

1 sequences assigned
No exact matches.



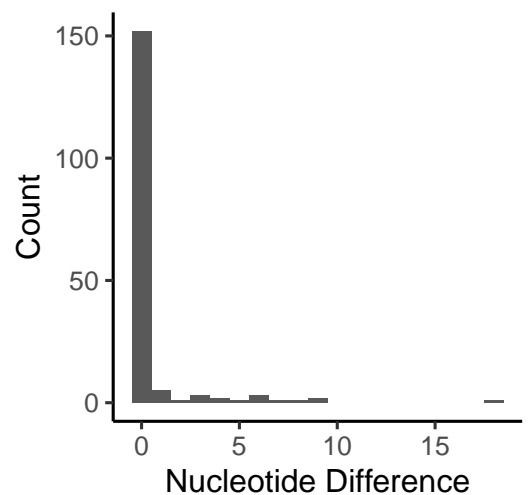
IGHV2-5*01

254 sequences assigned
184 (72.4%) exact matches, in which:
184 unique CDR3
6 unique J



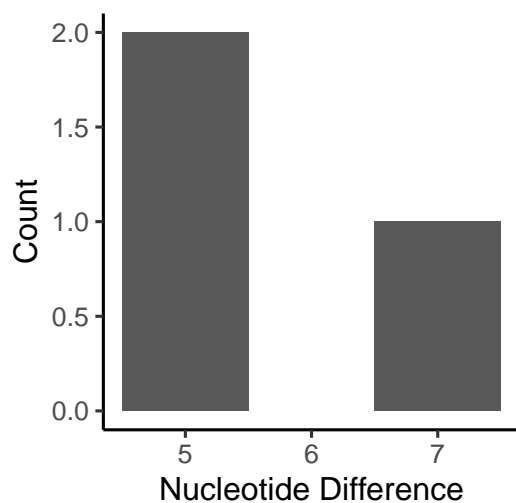
IGHV2-70*01

172 sequences assigned
152 (88.4%) exact matches, in which:
150 unique CDR3
5 unique J



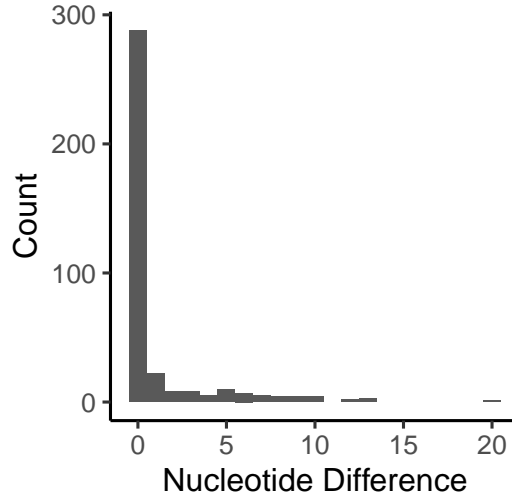
IGHV1-69-2*01

3 sequences assigned
No exact matches.



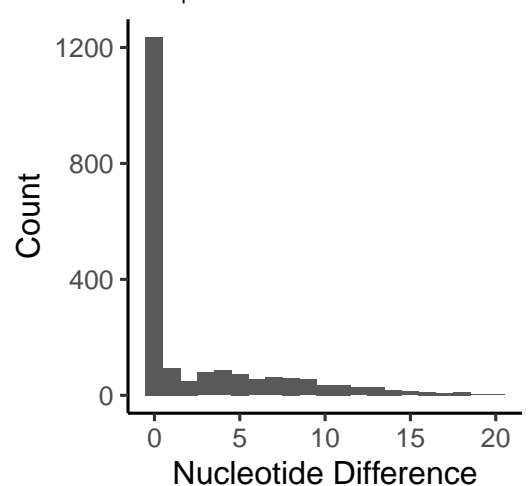
IGHV2-5*02

373 sequences assigned
288 (77.2%) exact matches, in which:
286 unique CDR3
6 unique J



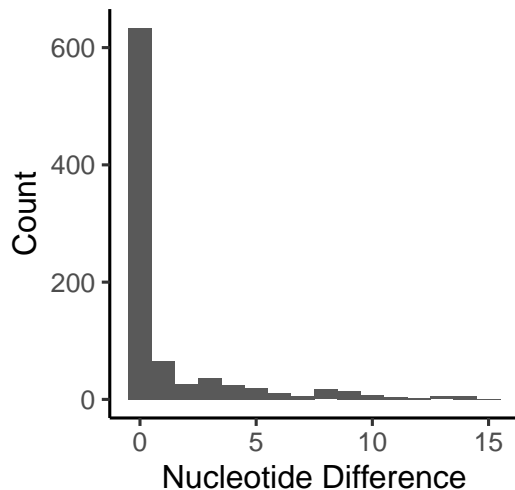
IGHV3-7*01

2050 sequences assigned
1236 (60.3%) exact matches, in which:
1187 unique CDR3
6 unique J



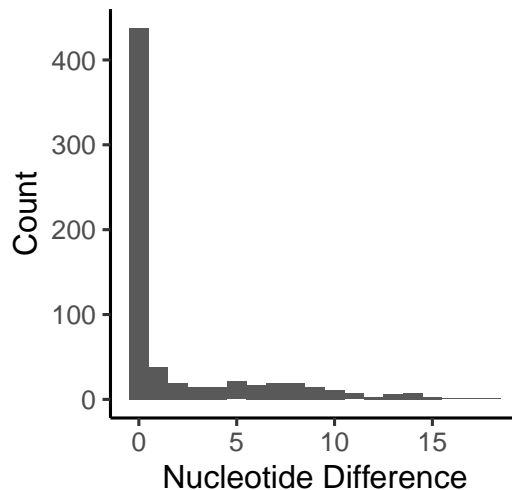
IGHV3-9*01

880 sequences assigned
634 (72%) exact matches, in which:
618 unique CDR3
6 unique J



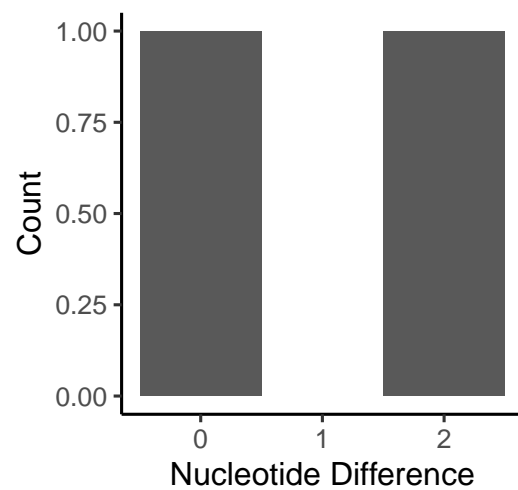
IGHV3-15*01_02

658 sequences assigned
438 (66.6%) exact matches, in which:
428 unique CDR3
6 unique J



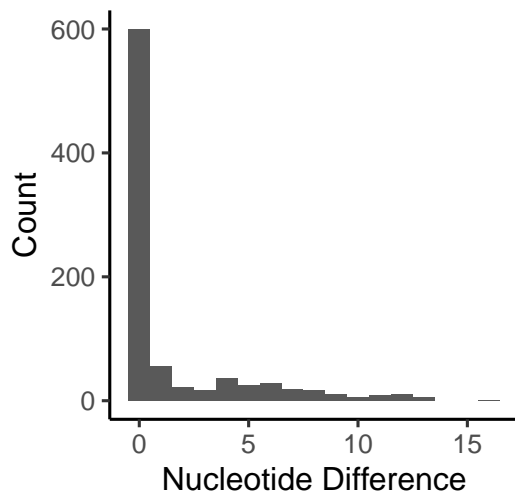
IGHV3-30-3*01

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



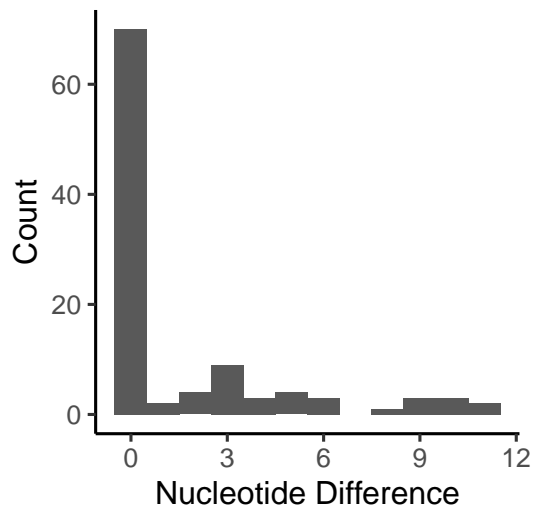
IGHV3-11*01

860 sequences assigned
600 (69.8%) exact matches, in which:
590 unique CDR3
6 unique J



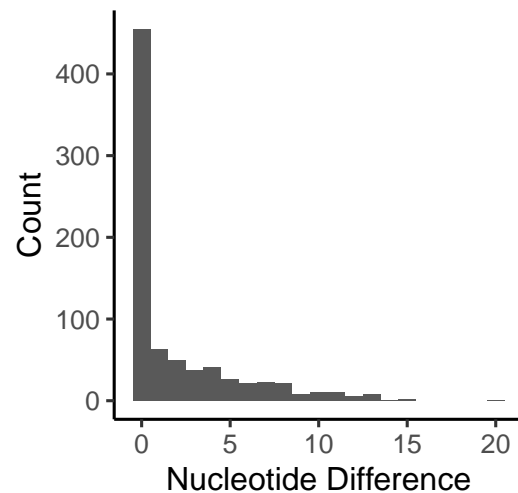
IGHV3-20*01_02

104 sequences assigned
70 (67.3%) exact matches, in which:
67 unique CDR3
6 unique J



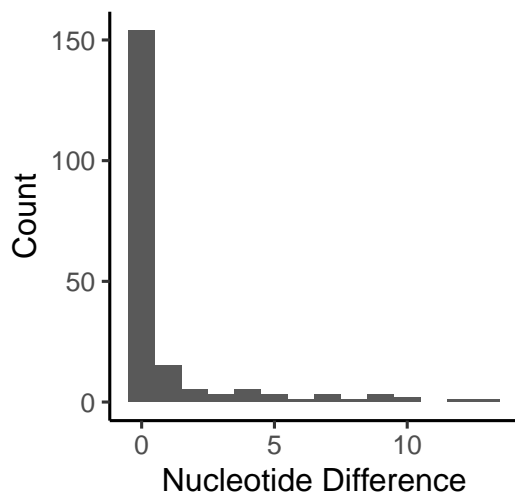
IGHV3-30*03

787 sequences assigned
455 (57.8%) exact matches, in which:
440 unique CDR3
6 unique J



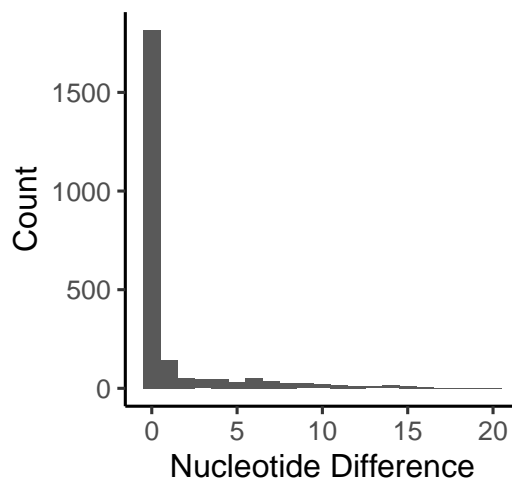
IGHV3-13*01

197 sequences assigned
154 (78.2%) exact matches, in which:
149 unique CDR3
5 unique J



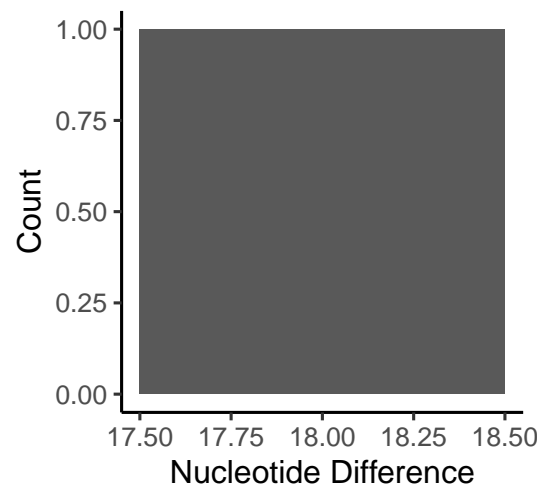
IGHV3-21*01_02

2377 sequences assigned
1816 (76.4%) exact matches, in which:
1782 unique CDR3
6 unique J



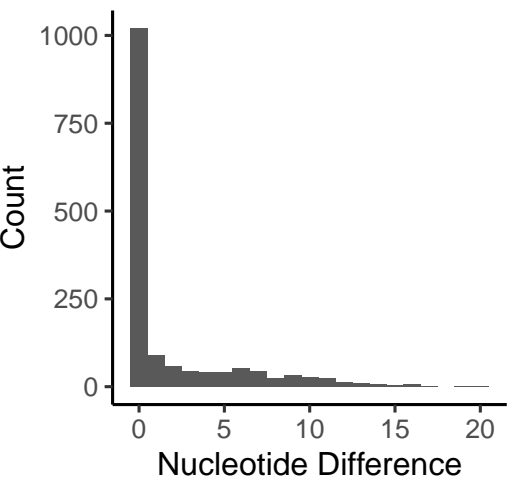
IGHV3-30-3*03

1 sequences assigned
No exact matches.



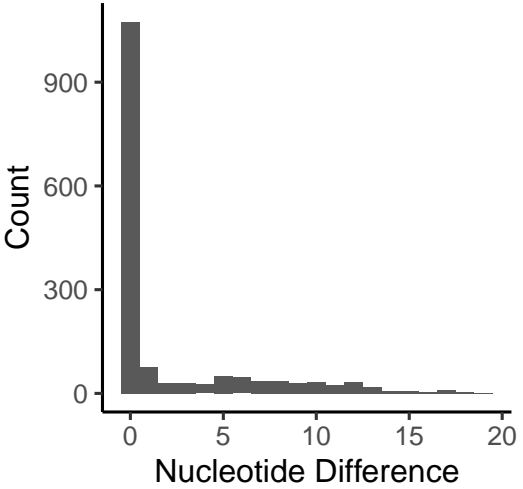
IGHV3-33*01

1551 sequences assigned
1020 (65.8%) exact matches, in which:
999 unique CDR3
6 unique J



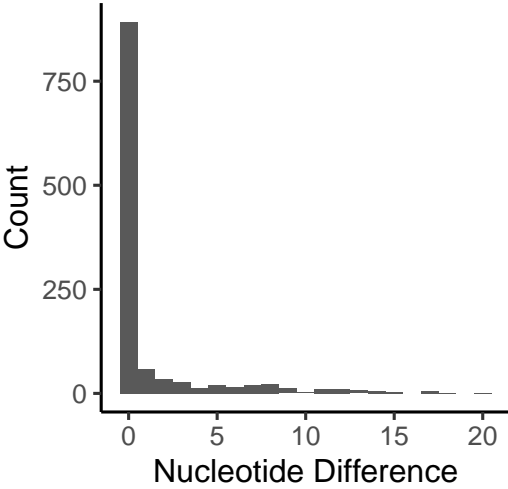
IGHV3-48*02

1579 sequences assigned
1075 (68.1%) exact matches, in which:
1048 unique CDR3
6 unique J



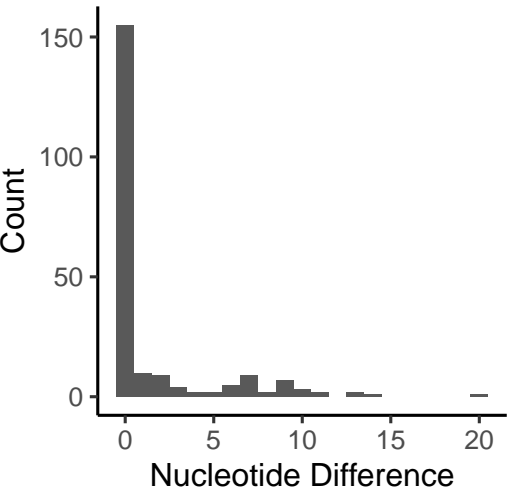
IGHV3-53*01_02

1165 sequences assigned
893 (76.7%) exact matches, in which:
881 unique CDR3
6 unique J



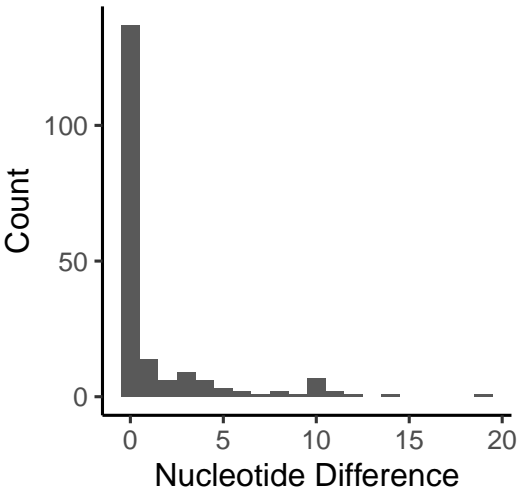
IGHV3-43*01

214 sequences assigned
155 (72.4%) exact matches, in which:
154 unique CDR3
6 unique J



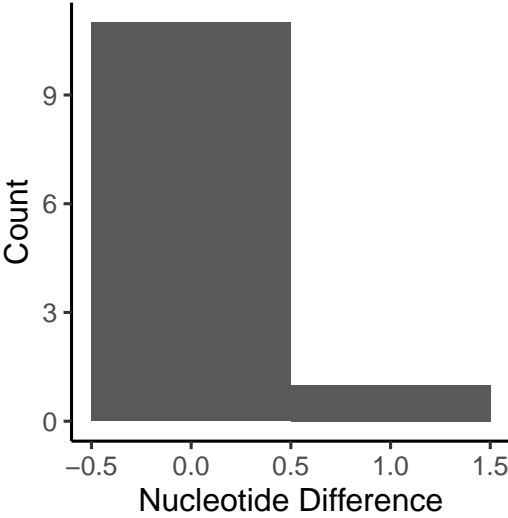
IGHV3-49*03_05

195 sequences assigned
137 (70.3%) exact matches, in which:
135 unique CDR3
6 unique J



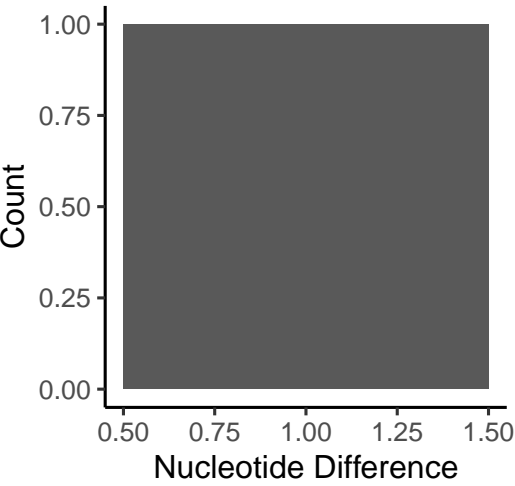
IGHV3-64*02_07

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



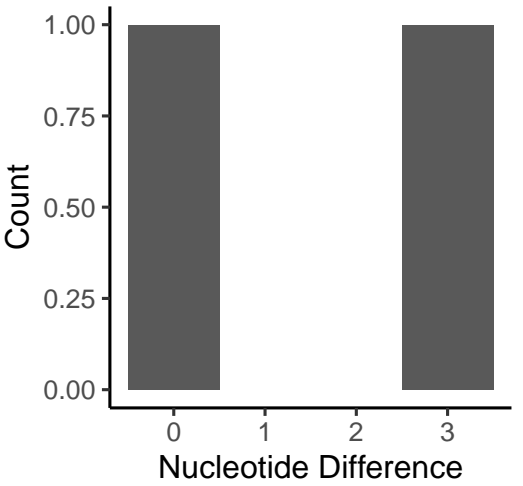
IGHV3-47*02

1 sequences assigned
No exact matches.



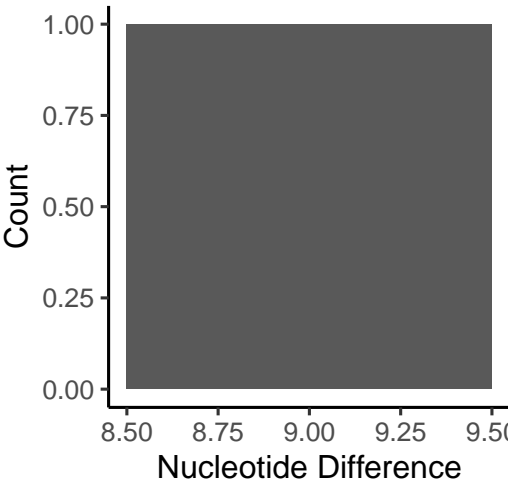
IGHV3-52*01_03

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



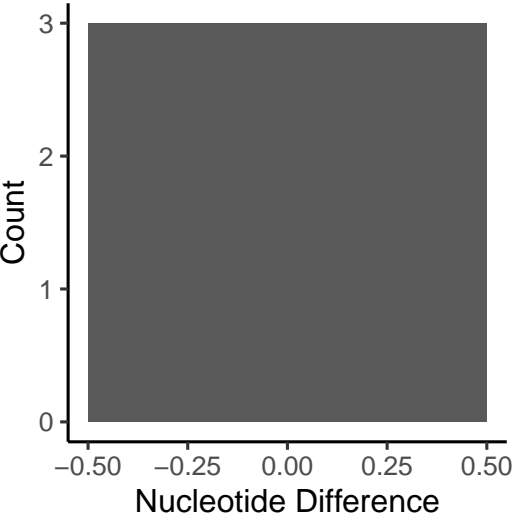
IGHV3-66*01

2 sequences assigned
No exact matches.



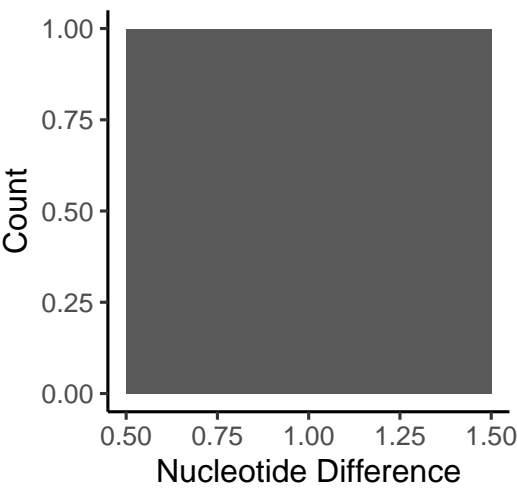
IGHV3-66*03

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



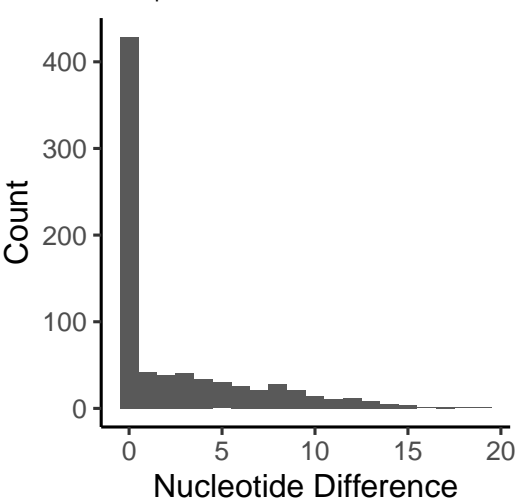
IGHV3-71*01_04

1 sequences assigned
No exact matches.



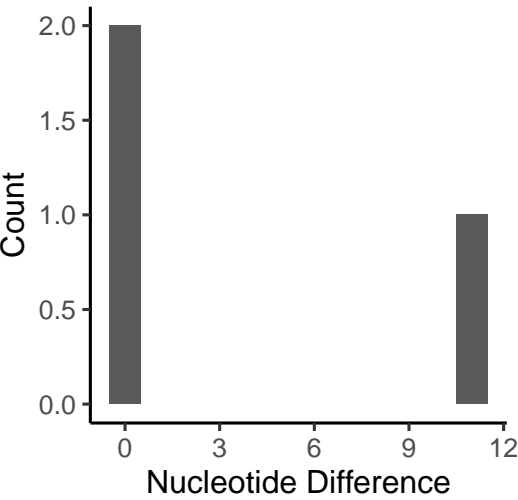
IGHV3-74*01_02

773 sequences assigned
429 (55.5%) exact matches, in which:
401 unique CDR3
6 unique J



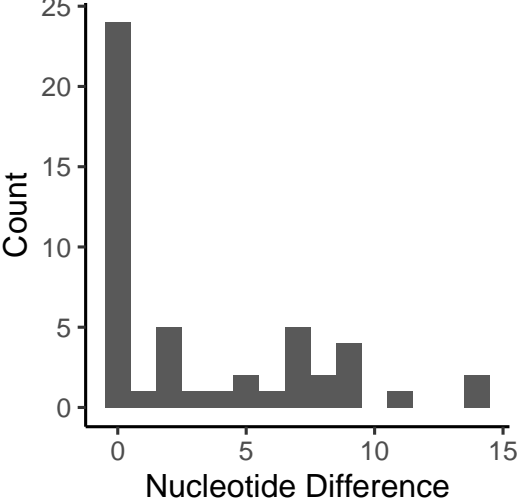
IGHV3-69-1*01

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



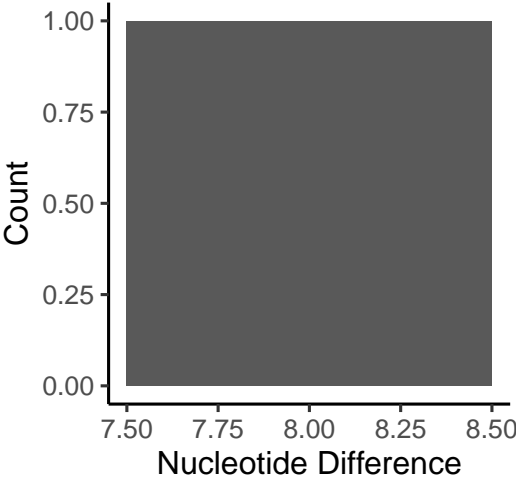
IGHV3-72*01

49 sequences assigned
24 (49%) exact matches, in which:
23 unique CDR3
4 unique J



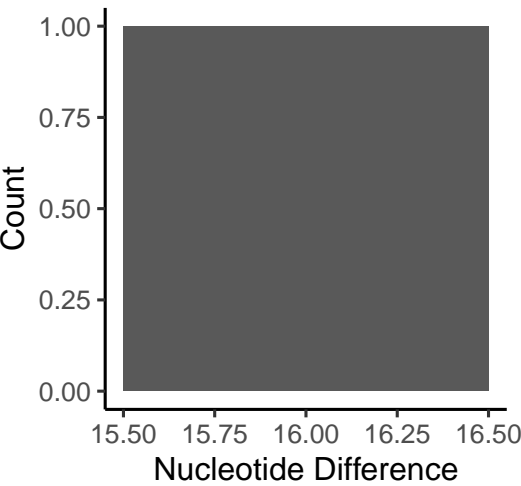
IGHV3-64D*09

2 sequences assigned
No exact matches.



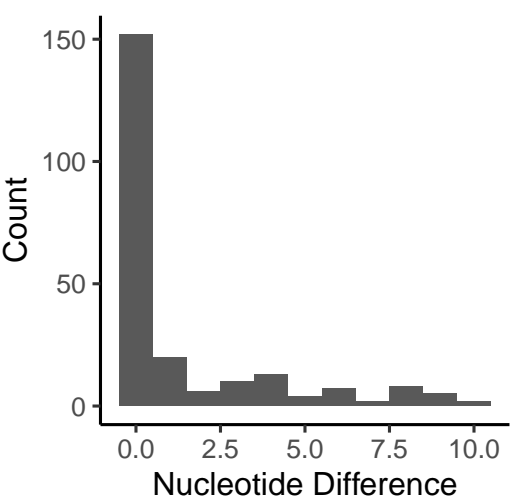
IGHV3-69-1*02

1 sequences assigned
No exact matches.



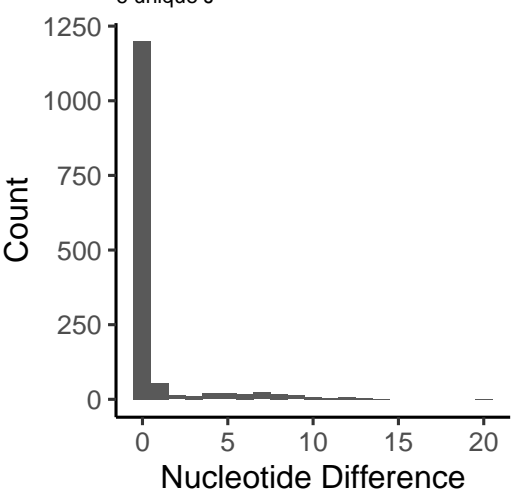
IGHV3-73*01_02

229 sequences assigned
152 (66.4%) exact matches, in which:
136 unique CDR3
6 unique J



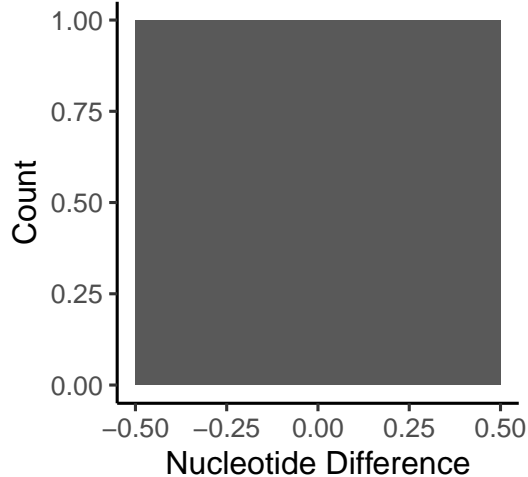
IGHV4-4*07

1415 sequences assigned
1200 (84.8%) exact matches, in which:
1169 unique CDR3
6 unique J



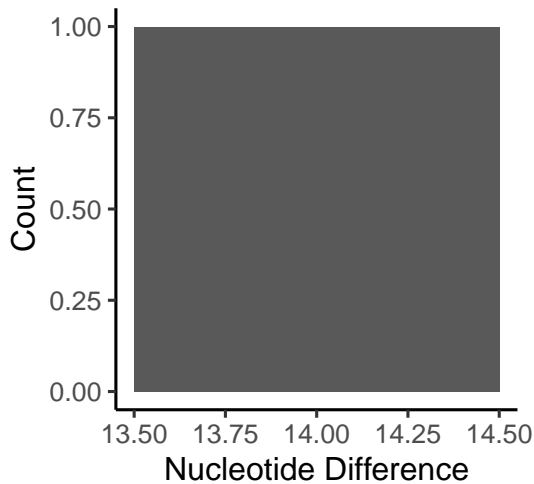
IGHV4-28*03

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



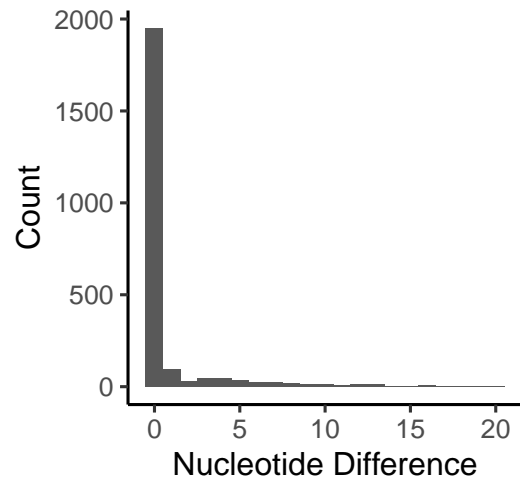
IGHV4-30-2*01

2 sequences assigned
No exact matches.



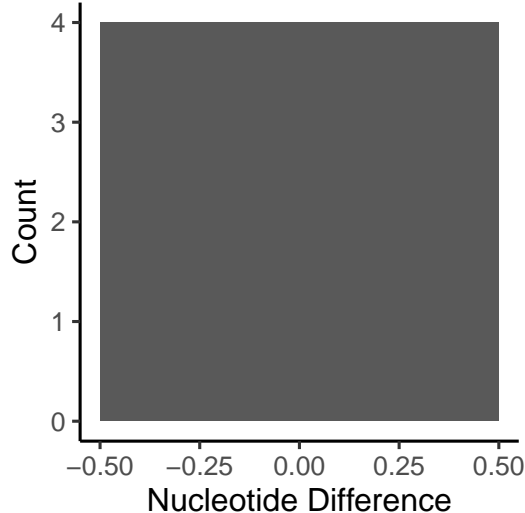
IGHV4-39*01_05

2363 sequences assigned
1949 (82.5%) exact matches, in which:
1915 unique CDR3
6 unique J



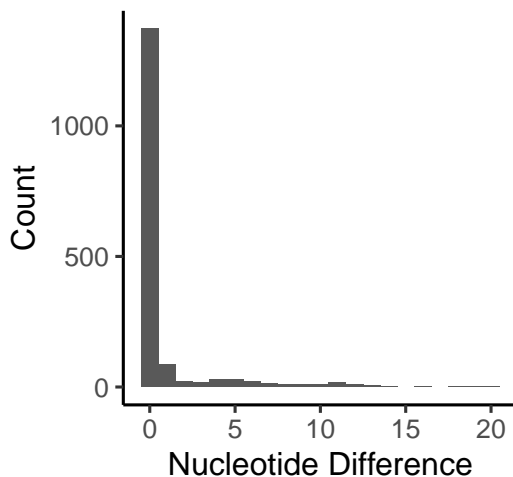
IGHV4-28*01_07

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



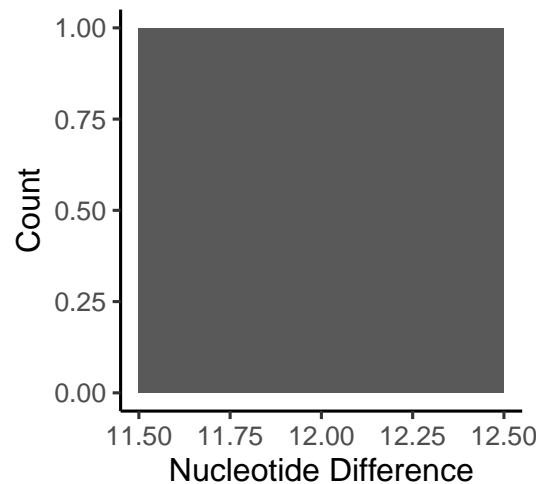
IGHV4-31*03_04

1656 sequences assigned
1372 (82.9%) exact matches, in which:
1351 unique CDR3
6 unique J



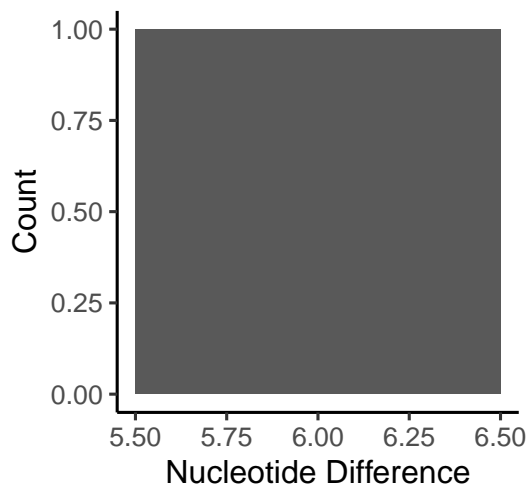
IGHV4-55*09

1 sequences assigned
No exact matches.



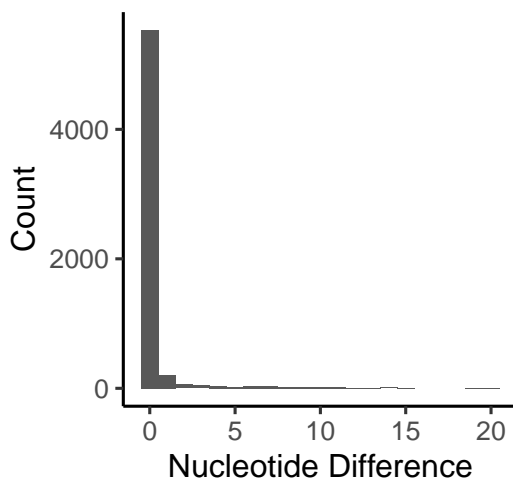
IGHV4-30-4*01

1 sequences assigned
No exact matches.



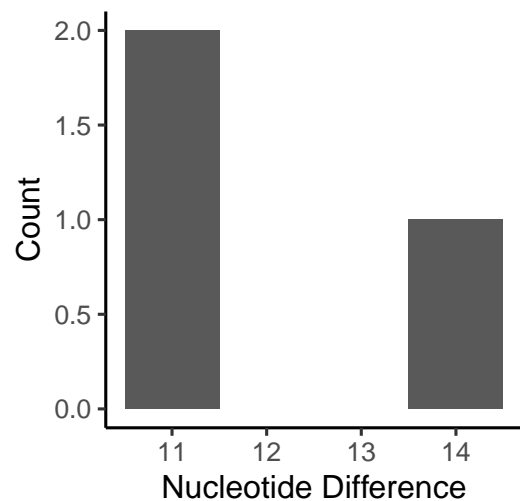
IGHV4-34*01_02

6079 sequences assigned
5534 (91%) exact matches, in which:
5483 unique CDR3
6 unique J



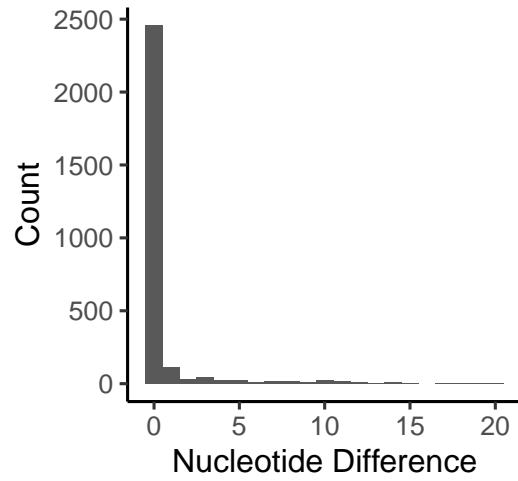
IGHV4-55*02_04_08

5 sequences assigned
No exact matches.



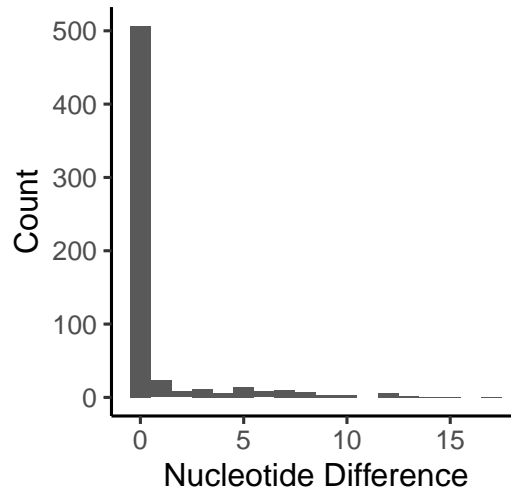
IGHV4-59*01_07

2820 sequences assigned
2457 (87.1%) exact matches, in which:
2429 unique CDR3
6 unique J



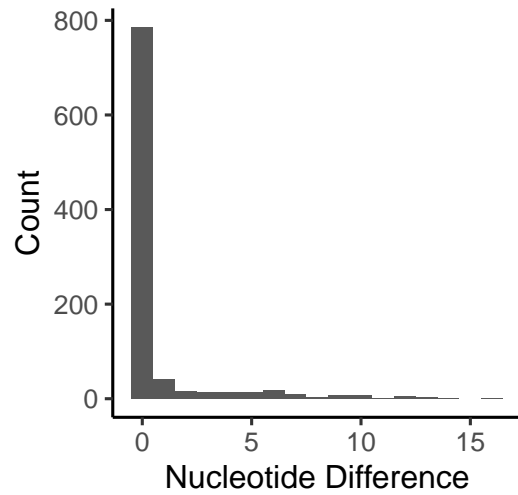
IGHV6-1*01_02

612 sequences assigned
507 (82.8%) exact matches, in which:
506 unique CDR3
6 unique J



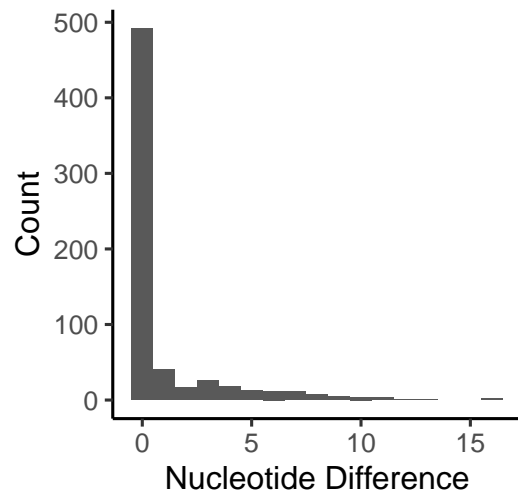
IGHV4-61*01

941 sequences assigned
786 (83.5%) exact matches, in which:
782 unique CDR3
6 unique J



IGHV5-51*01_03

653 sequences assigned
492 (75.3%) exact matches, in which:
489 unique CDR3
6 unique J





Warning - no inferred sequences found.

Novel sequence(s)IGHV4-59*02_G88AIGHV5-51*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_G88AIGHV5-51*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)IGHV4-39*02_C258GIGHV5-51*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_G88AIGHV5-51*07_A128G are not listed in the genotype and will be ignored.

Warning - no inferred sequences found.

Novel sequence(s)IGHV4-59*02_G88AIGHV5-51*07_A128G are not listed in the genotype and will be ignored.

Warning - no inferred sequences found.

Novel sequence(s)IGHV4-59*02_G88AIGHV5-51*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_G88AIGHV5-51*07_A128G are not listed in the genotype and will be ignored.

Warning - no inferred sequences found.

Novel sequence(s)IGHV4-59*02_G88AIGHV5-51*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_G88AIGHV5-51*07_A128G are not listed in the genotype and will be ignored.

Novel sequence(s)IGHV4-59*02_G88AIGHV5-51*07_A128G are not listed in the genotype and will be ignored.