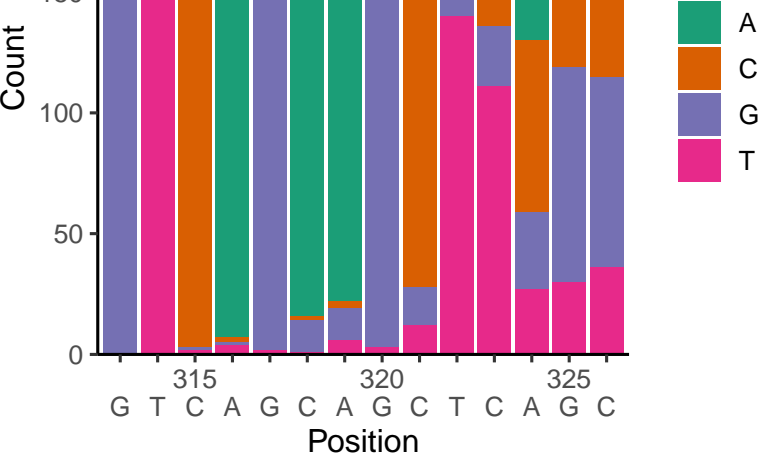


Gene TRBV7-1*ap01_G291C_T296C_C314T



Gene TRBV7-1*ap01_G291C_T296C_C314T



TRBV7-1*ap01_G291C_T296C_C314T- Final 3 nucleotides as a triplet

Count

20

15

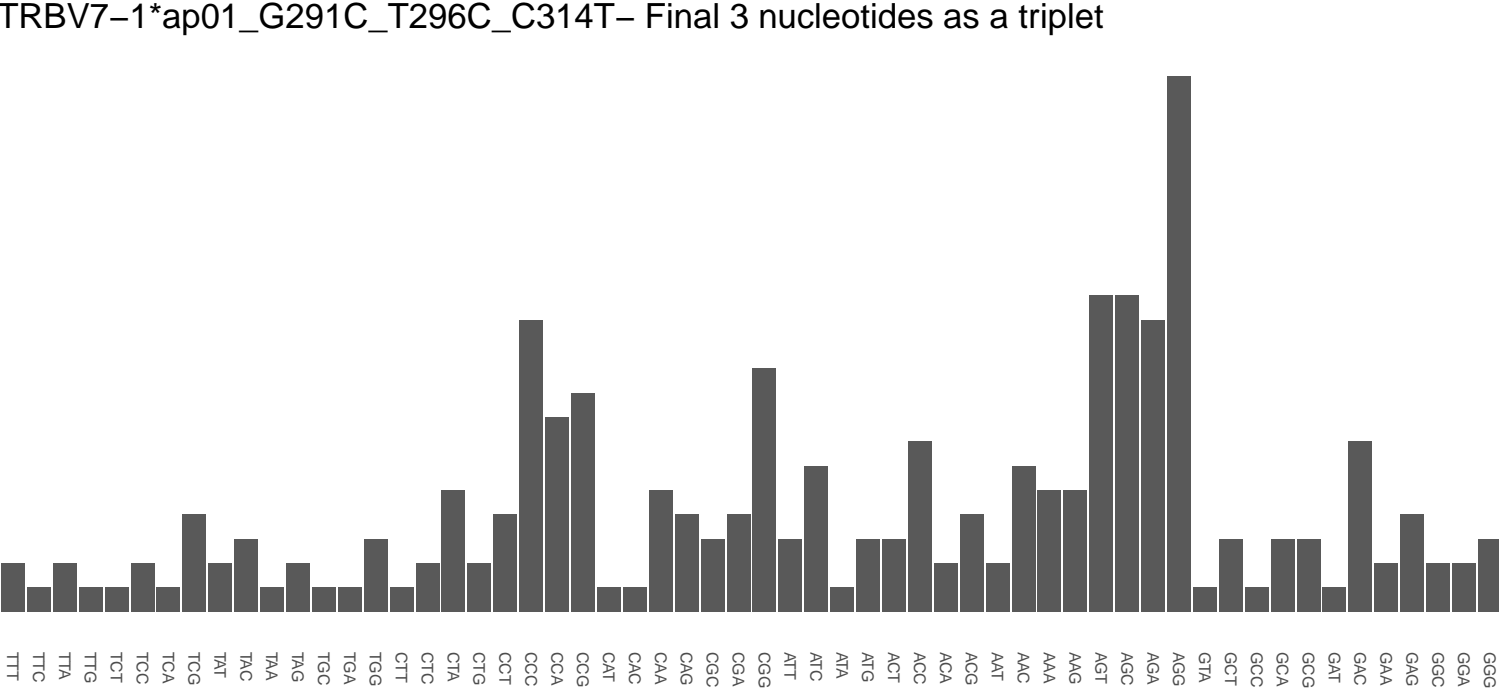
10

5

0

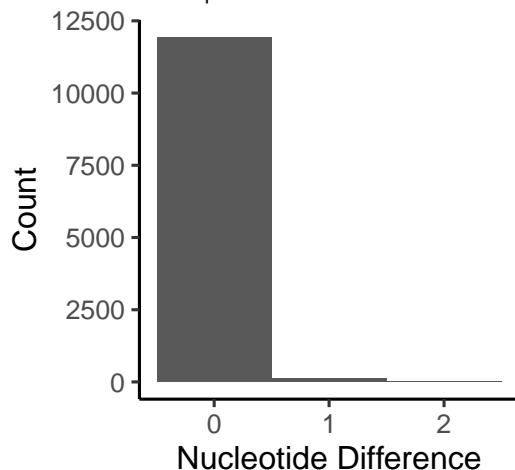
Triplet

TTT TTC TTA TTG TCT TCC TCA TCG TAT TAC TAA TAG TGC TGA TGG CTT CTC CTA CTG CCT CCC CCA CCG CAT CAC CAA CAG CGC CGA CGG ATT ATC ATA ATG ACT ACC ACA ACG AAT AAC AAA AAG AGT AGC AGA AGG GTA GCT GCC GCA GCG GAT GAC GAA GAG GGC GGA GGG



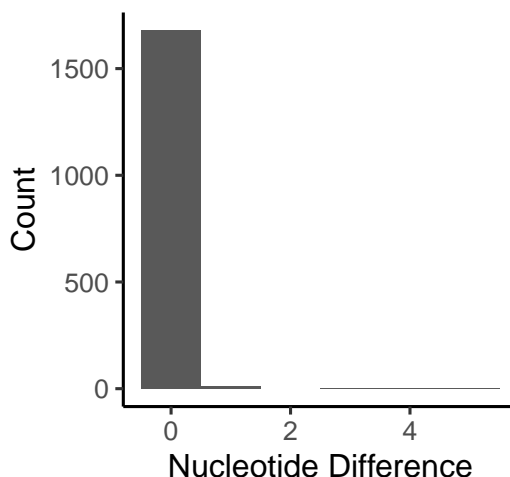
TRBV20-1*ap01

12073 sequences assigned
11935 (98.9%) exact matches, in which:
11722 unique CDR3
13 unique J



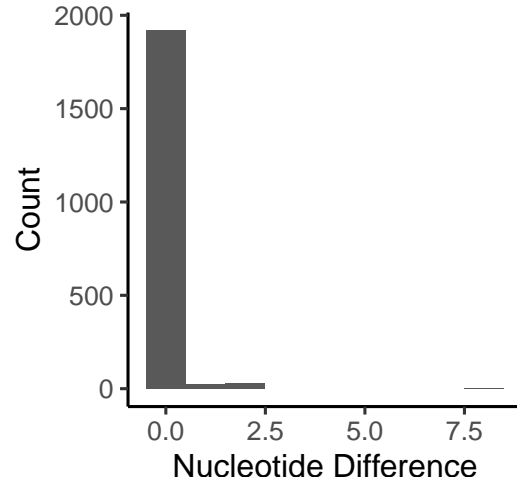
TRBV10-2*ap01

1697 sequences assigned
1679 (98.9%) exact matches, in which:
1630 unique CDR3
13 unique J



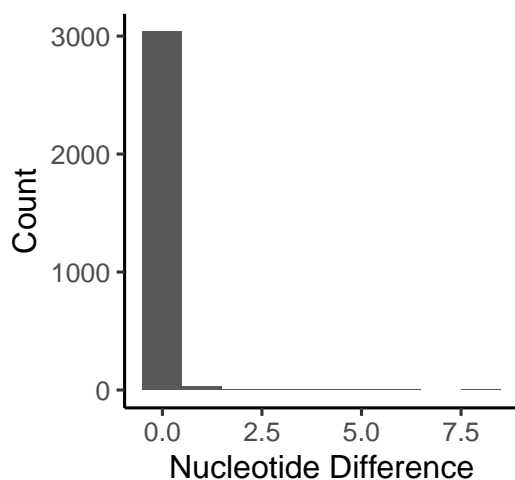
TRBV13*ap01

1972 sequences assigned
1919 (97.3%) exact matches, in which:
1883 unique CDR3
13 unique J



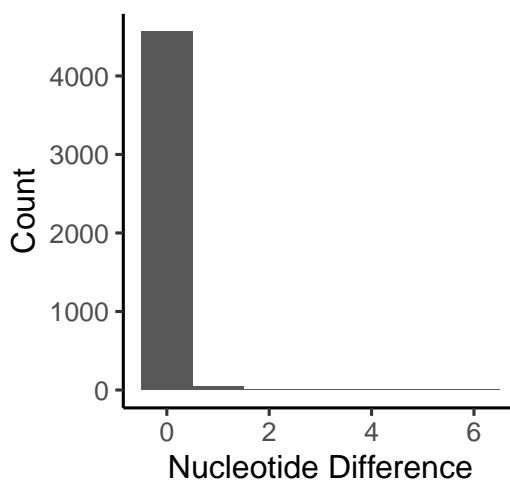
TRBV10-1*ap01

3081 sequences assigned
3037 (98.6%) exact matches, in which:
2960 unique CDR3
13 unique J



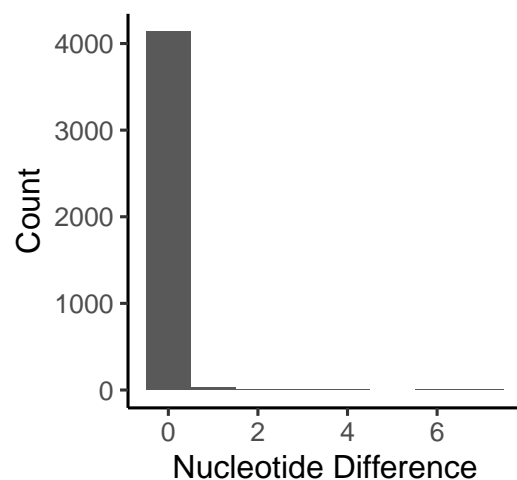
TRBV10-3*ap01

4621 sequences assigned
4563 (98.7%) exact matches, in which:
4466 unique CDR3
13 unique J



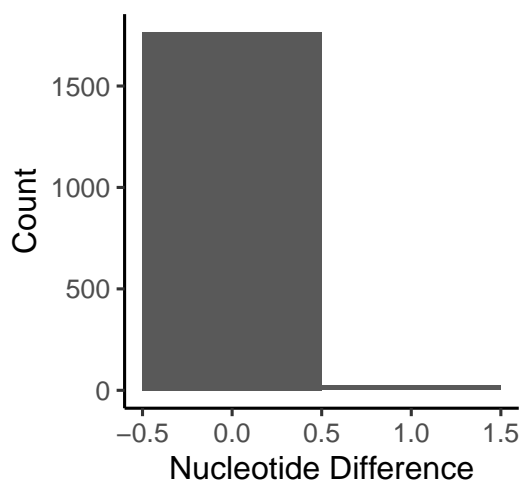
TRBV14*ap01

4170 sequences assigned
4136 (99.2%) exact matches, in which:
4062 unique CDR3
13 unique J



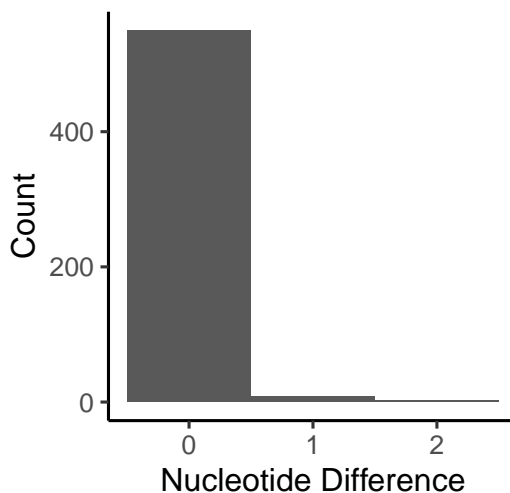
TRBV20-1*ap02

1790 sequences assigned
1766 (98.7%) exact matches, in which:
1734 unique CDR3
13 unique J



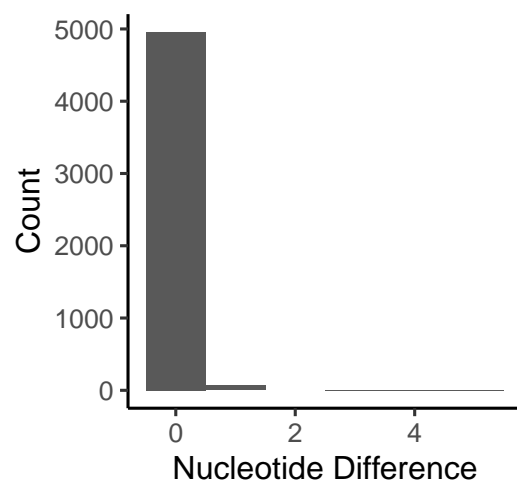
TRBV1*ap01

560 sequences assigned
550 (98.2%) exact matches, in which:
532 unique CDR3
13 unique J



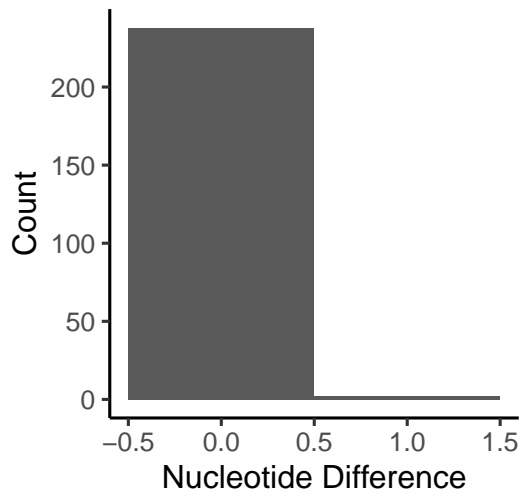
TRBV15*ap02

5026 sequences assigned
4957 (98.6%) exact matches, in which:
4841 unique CDR3
13 unique J



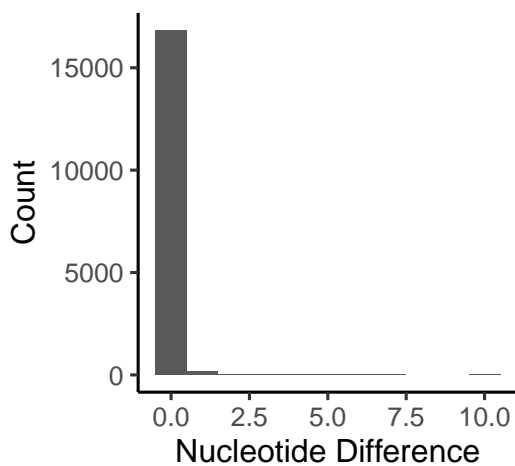
TRBV16*ap01

240 sequences assigned
238 (99.2%) exact matches, in which:
237 unique CDR3
13 unique J



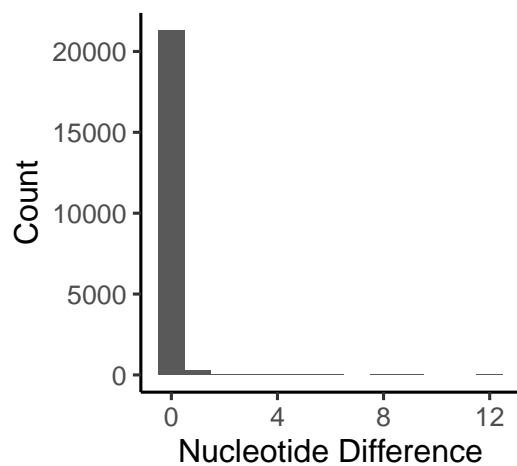
TRBV19*ap01

17014 sequences assigned
16836 (99%) exact matches, in which:
16660 unique CDR3
13 unique J



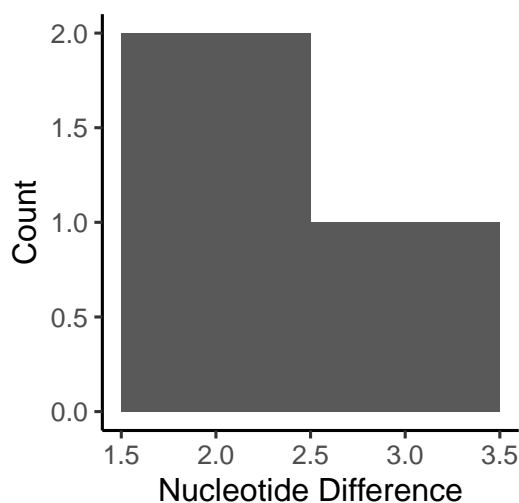
TRBV27*ap01

21626 sequences assigned
21317 (98.6%) exact matches, in which:
20803 unique CDR3
13 unique J



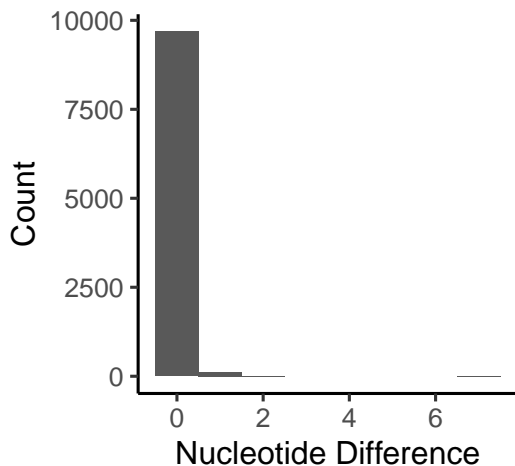
TRBV17*ap01

3 sequences assigned
No exact matches.



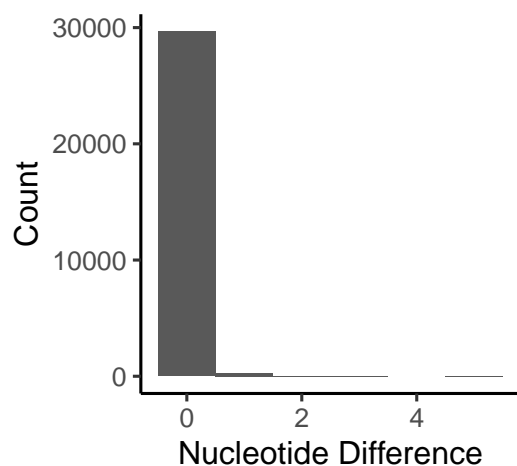
TRBV2*ap01

9805 sequences assigned
9687 (98.8%) exact matches, in which:
9495 unique CDR3
13 unique J



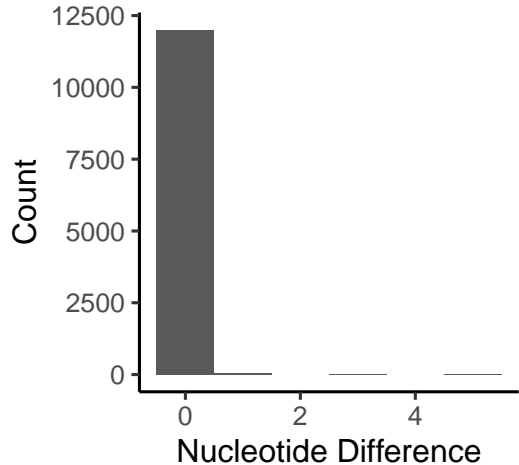
TRBV28*ap01

29979 sequences assigned
29667 (99%) exact matches, in which:
29132 unique CDR3
13 unique J



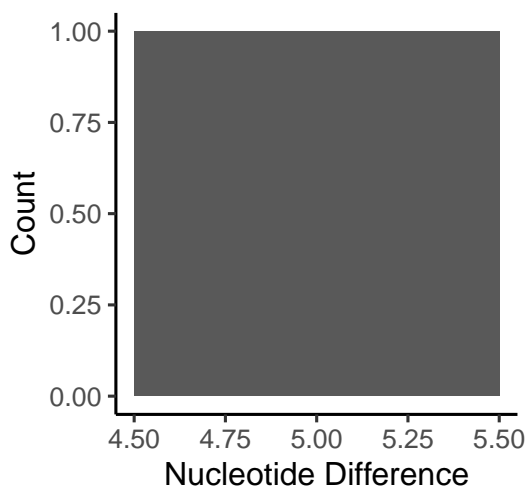
TRBV18*ap01

12066 sequences assigned
12004 (99.5%) exact matches, in which:
11868 unique CDR3
13 unique J



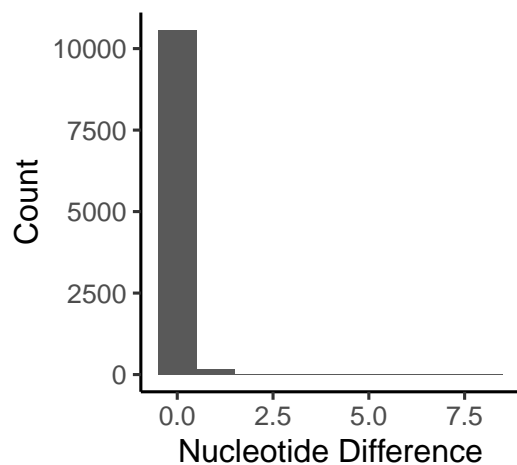
TRBV26*ap01

1 sequences assigned
No exact matches.



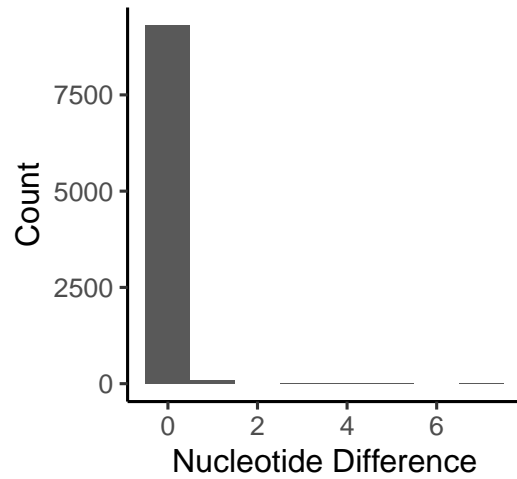
TRBV30*ap01

10748 sequences assigned
10577 (98.4%) exact matches, in which:
10420 unique CDR3
13 unique J



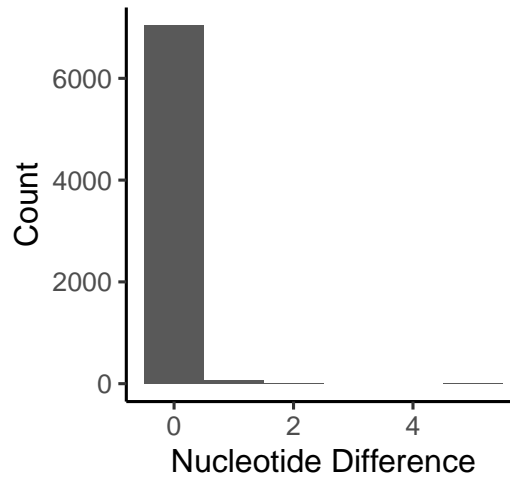
TRBV9*ap01

9413 sequences assigned
9304 (98.8%) exact matches, in which:
9141 unique CDR3
13 unique J



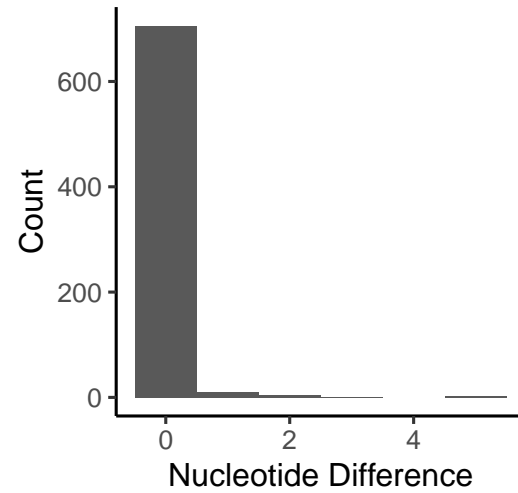
TRBV11-2*ap01

7111 sequences assigned
7040 (99%) exact matches, in which:
6879 unique CDR3
13 unique J



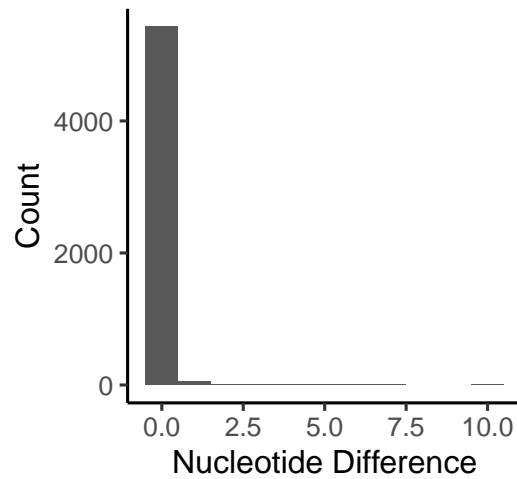
TRBV12-2*ap01

725 sequences assigned
706 (97.4%) exact matches, in which:
690 unique CDR3
13 unique J



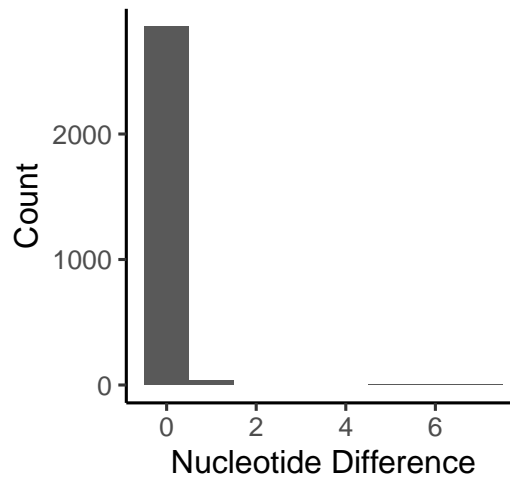
TRBV21-1*ap01

5504 sequences assigned
5427 (98.6%) exact matches, in which:
5348 unique CDR3
13 unique J



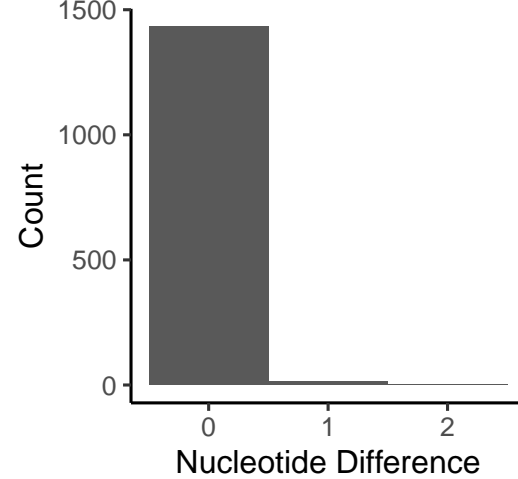
TRBV11-3*ap01

2891 sequences assigned
2855 (98.8%) exact matches, in which:
2809 unique CDR3
13 unique J



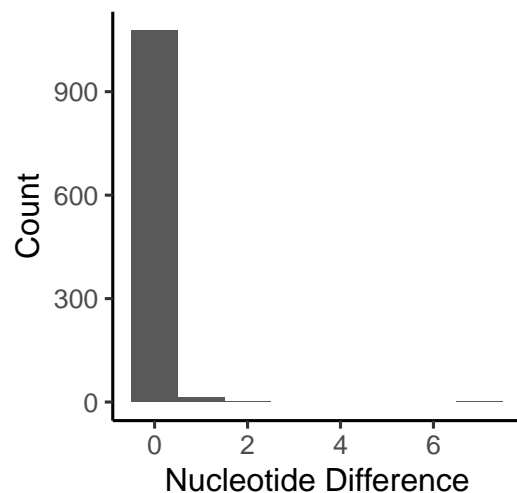
TRBV12-5*ap01

1450 sequences assigned
1432 (98.8%) exact matches, in which:
1405 unique CDR3
13 unique J



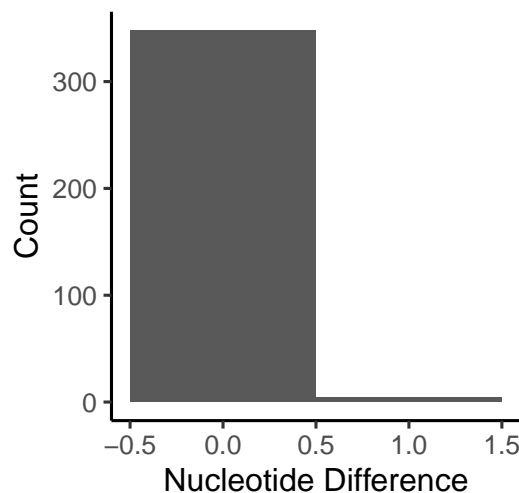
TRBV11-1*ap01

1094 sequences assigned
1078 (98.5%) exact matches, in which:
1056 unique CDR3
13 unique J



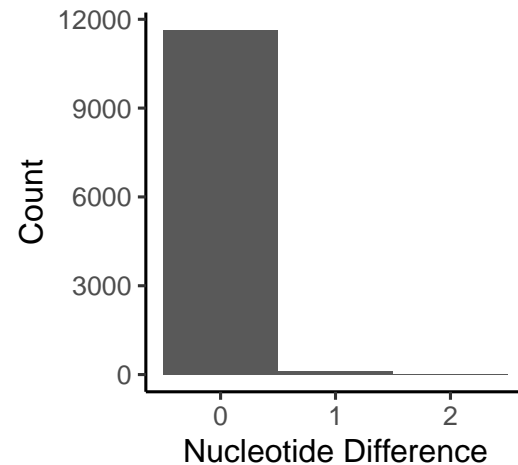
TRBV12-1*ap01

352 sequences assigned
348 (98.9%) exact matches, in which:
342 unique CDR3
13 unique J



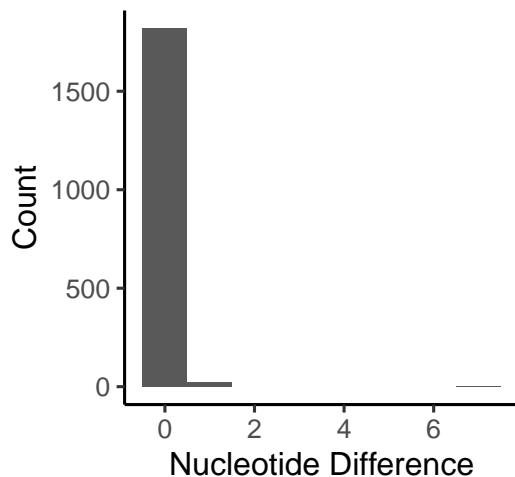
TRBV12-34*ap01

11771 sequences assigned
11645 (98.9%) exact matches, in which:
11432 unique CDR3
13 unique J



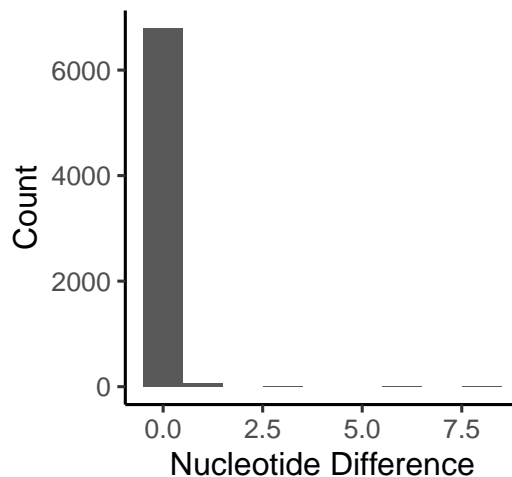
TRBV23-1*ap01

1842 sequences assigned
1819 (98.8%) exact matches, in which:
1786 unique CDR3
13 unique J



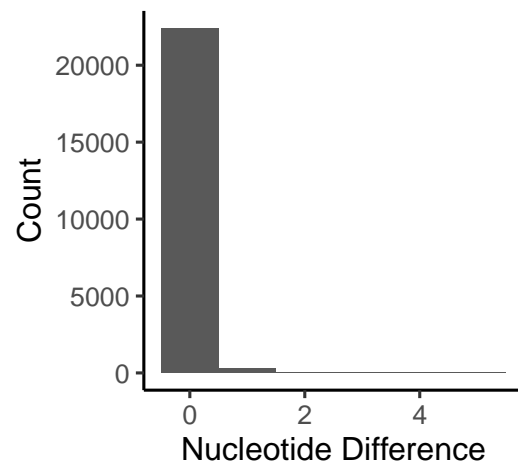
TRBV4-1*ap01

6852 sequences assigned
6790 (99.1%) exact matches, in which:
6621 unique CDR3
13 unique J



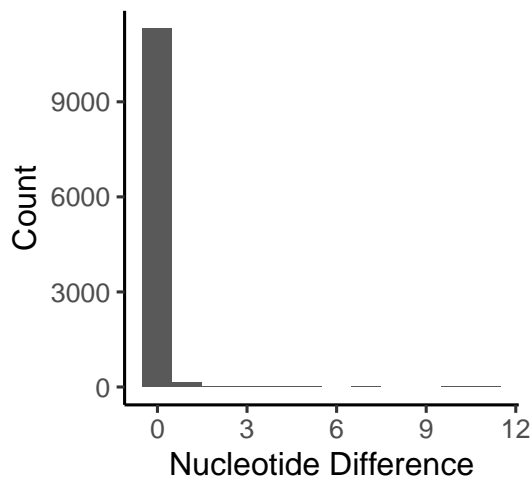
TRBV5-1*ap01

22676 sequences assigned
22409 (98.8%) exact matches, in which:
21878 unique CDR3
13 unique J



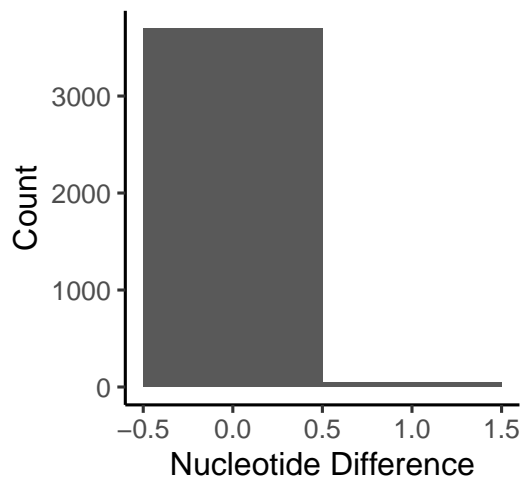
TRBV3-12*ap01

11464 sequences assigned
11306 (98.6%) exact matches, in which:
11071 unique CDR3
13 unique J



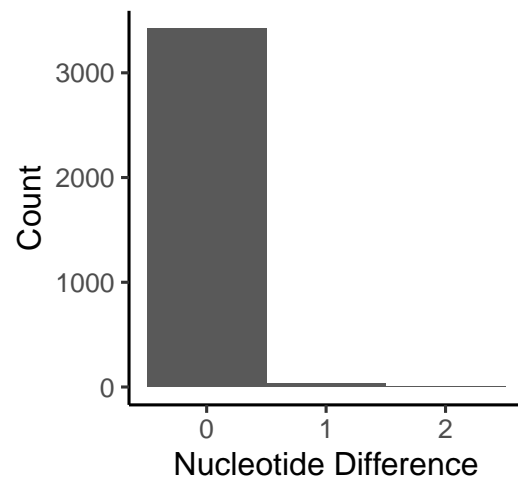
TRBV4-2*ap01

3745 sequences assigned
3694 (98.6%) exact matches, in which:
3626 unique CDR3
13 unique J



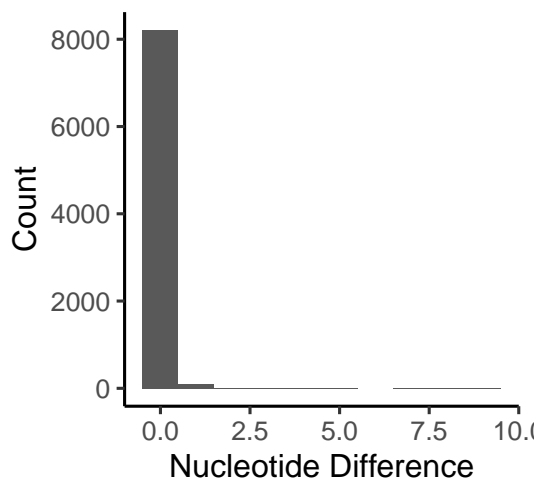
TRBV25-1*ap01

3455 sequences assigned
3421 (99%) exact matches, in which:
3368 unique CDR3
13 unique J



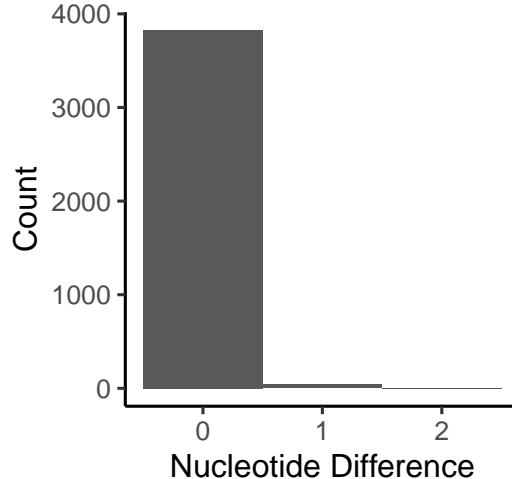
TRBV24-1*ap01

8327 sequences assigned
8211 (98.6%) exact matches, in which:
8077 unique CDR3
13 unique J



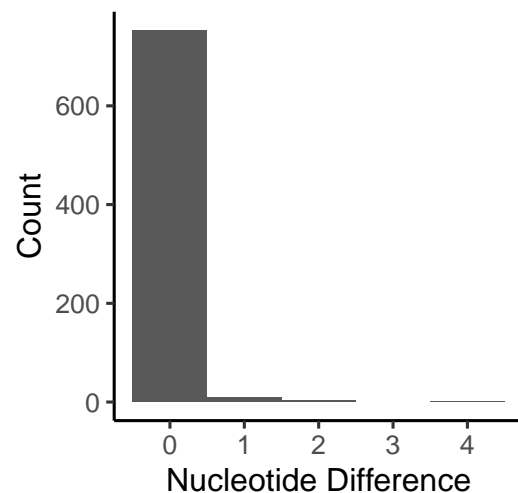
TRBV4-3*ap01

3870 sequences assigned
3827 (98.9%) exact matches, in which:
3747 unique CDR3
13 unique J



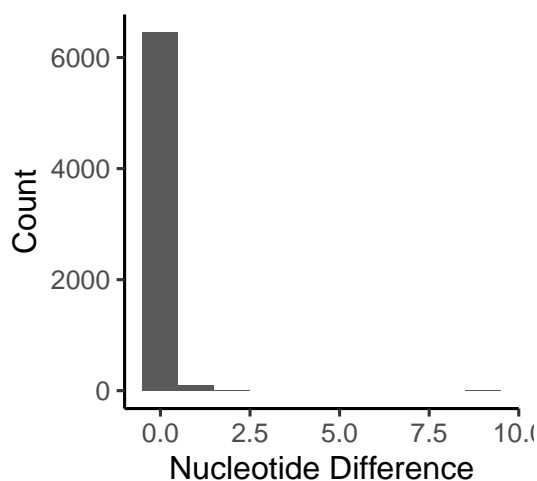
TRBV5-3*ap01

767 sequences assigned
753 (98.2%) exact matches, in which:
742 unique CDR3
13 unique J



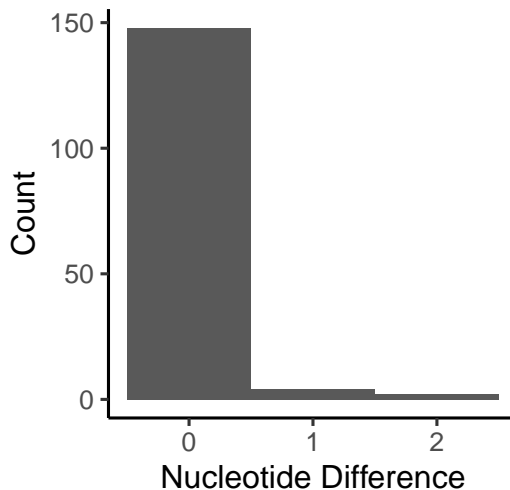
TRBV5-4*ap01

6547 sequences assigned
6453 (98.6%) exact matches, in which:
6306 unique CDR3
13 unique J



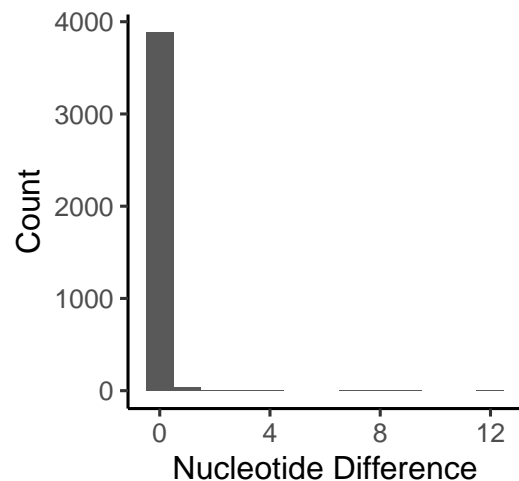
TRBV5-7*ap01

154 sequences assigned
148 (96.1%) exact matches, in which:
144 unique CDR3
13 unique J



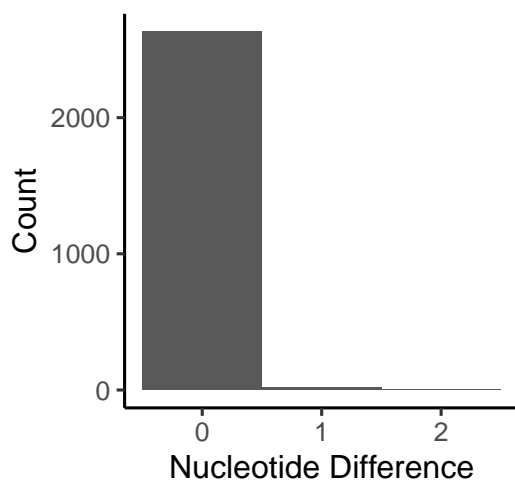
TRBV6-4*ap01

3938 sequences assigned
3884 (98.6%) exact matches, in which:
3828 unique CDR3
13 unique J



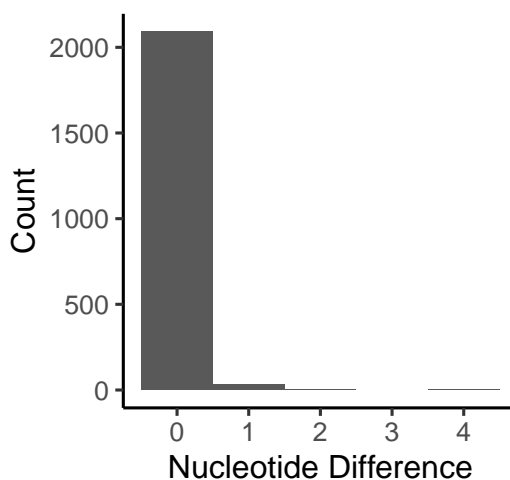
TRBV5-5*ap01

2653 sequences assigned
2631 (99.2%) exact matches, in which:
2608 unique CDR3
13 unique J



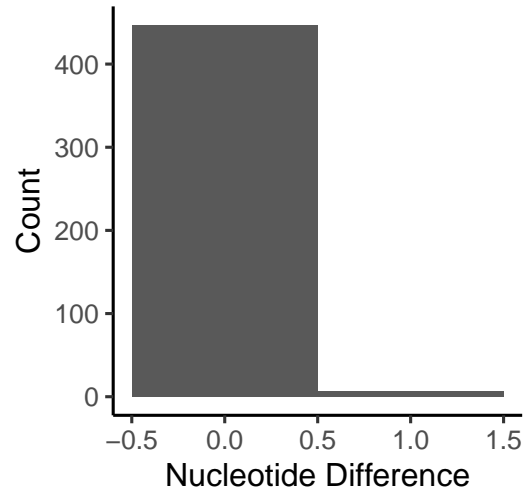
TRBV5-8*ap01

2125 sequences assigned
2091 (98.4%) exact matches, in which:
2046 unique CDR3
13 unique J



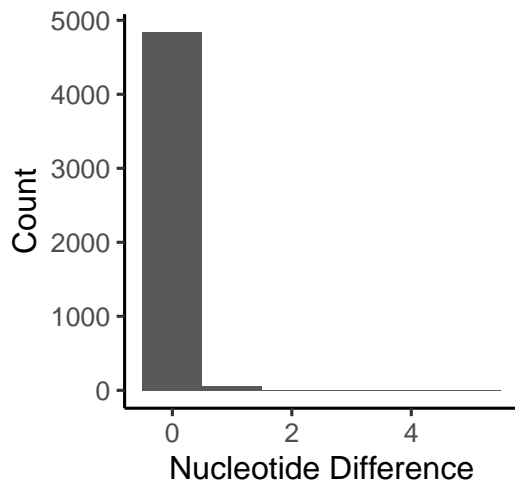
TRBV6-7*ap01

454 sequences assigned
447 (98.5%) exact matches, in which:
434 unique CDR3
13 unique J



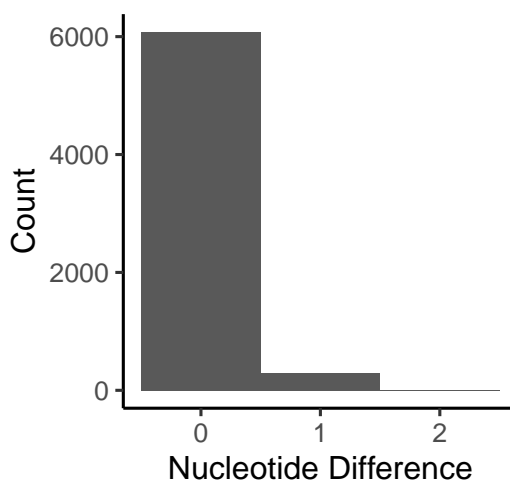
TRBV5-6*ap01

4906 sequences assigned
4841 (98.7%) exact matches, in which:
4690 unique CDR3
13 unique J



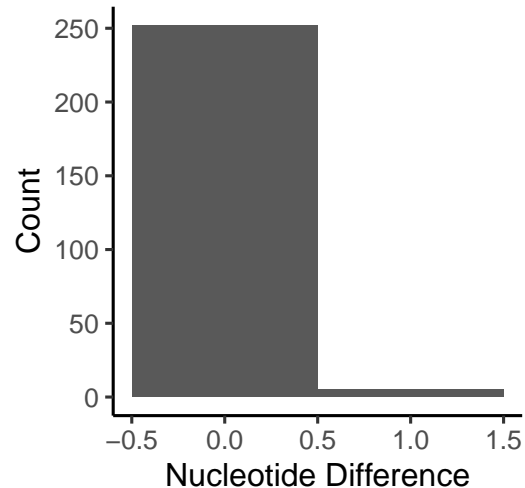
TRBV6-1*ap01

6381 sequences assigned
6078 (95.3%) exact matches, in which:
5949 unique CDR3
13 unique J



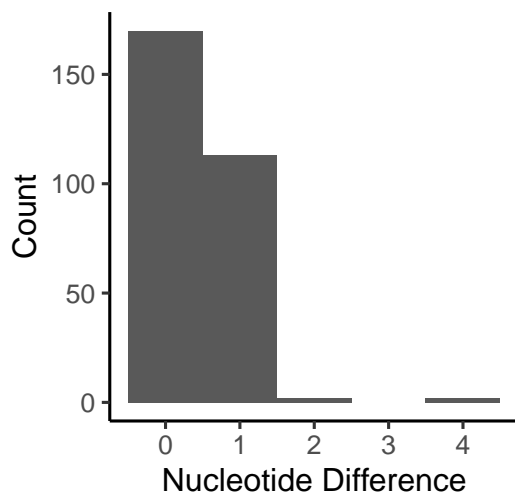
TRBV6-8*ap01

257 sequences assigned
252 (98.1%) exact matches, in which:
247 unique CDR3
13 unique J



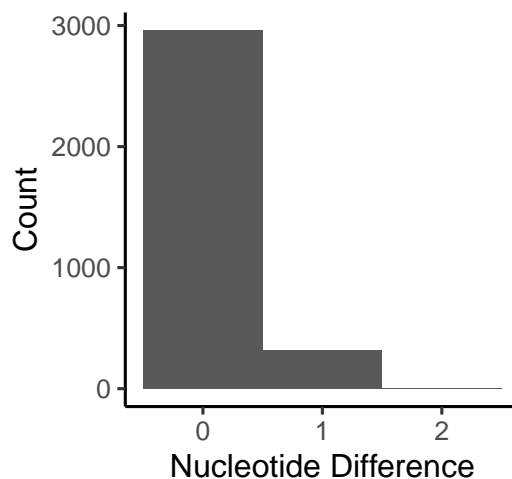
TRBV6–9*ap01

287 sequences assigned
170 (59.2%) exact matches, in which:
169 unique CDR3
13 unique J



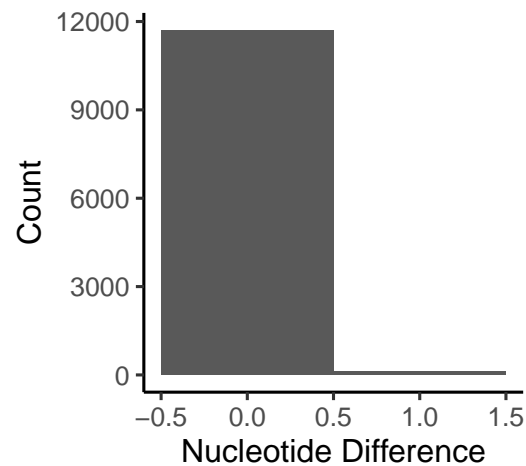
TRBV6–56*ap02

3286 sequences assigned
2960 (90.1%) exact matches, in which:
2902 unique CDR3
13 unique J



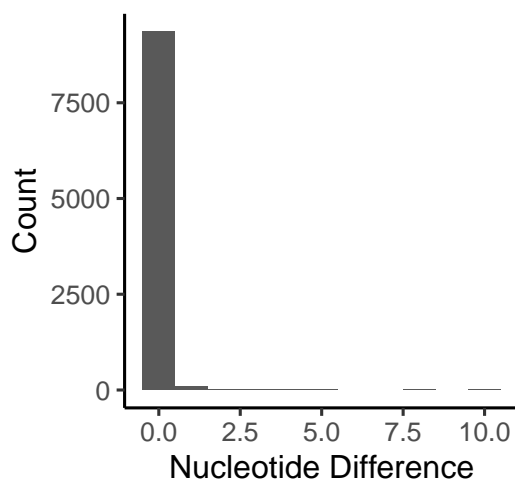
TRBV7–2*ap01

11818 sequences assigned
11707 (99.1%) exact matches, in which:
11492 unique CDR3
13 unique J



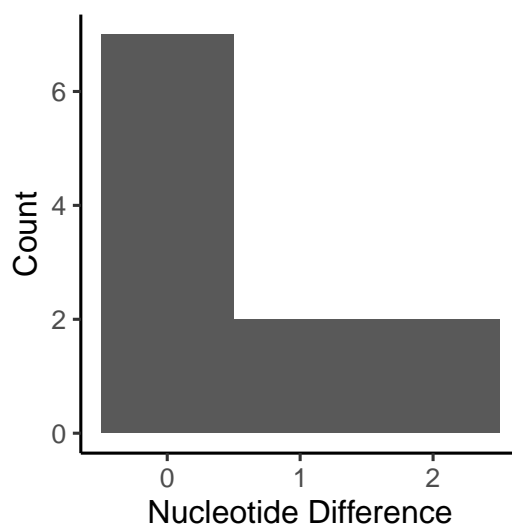
TRBV6–23*ap01

9451 sequences assigned
9355 (99%) exact matches, in which:
9109 unique CDR3
13 unique J



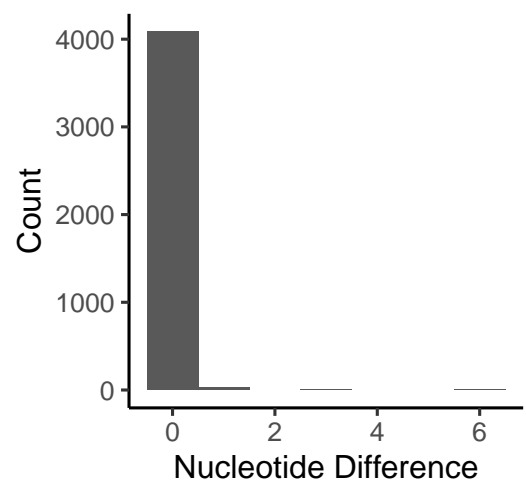
TRBV7–1*ap01

11 sequences assigned
7 (63.6%) exact matches, in which:
7 unique CDR3
5 unique J



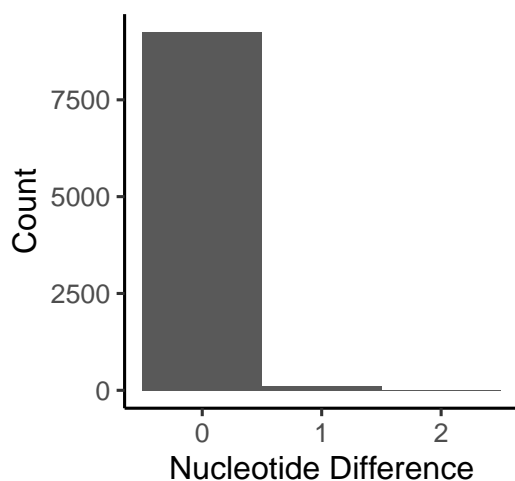
TRBV7–3*ap01

4112 sequences assigned
4085 (99.3%) exact matches, in which:
4019 unique CDR3
13 unique J



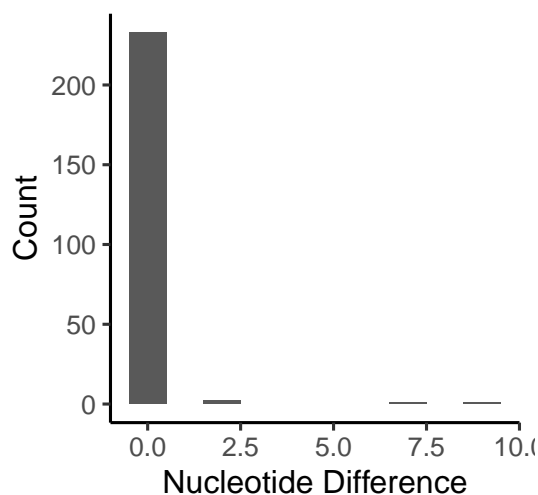
TRBV6–56*ap01

9365 sequences assigned
9249 (98.8%) exact matches, in which:
9061 unique CDR3
13 unique J



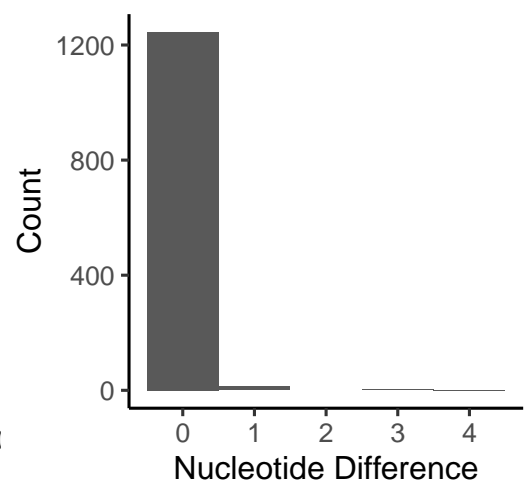
TRBV7–1*ap01_G291C_

237 sequences assigned
233 (98.3%) exact matches, in which:
228 unique CDR3
13 unique J



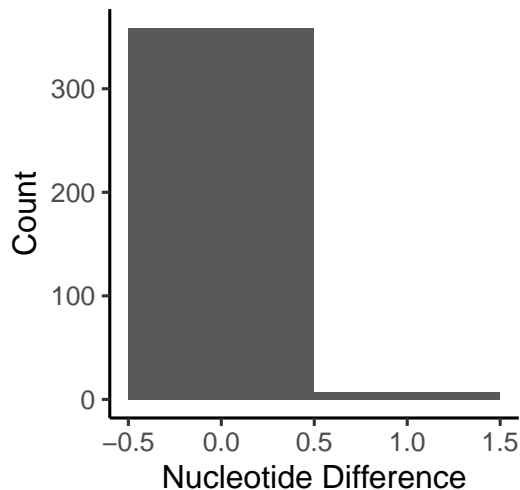
TRBV7–3*ap03

1263 sequences assigned
1245 (98.6%) exact matches, in which:
1216 unique CDR3
13 unique J



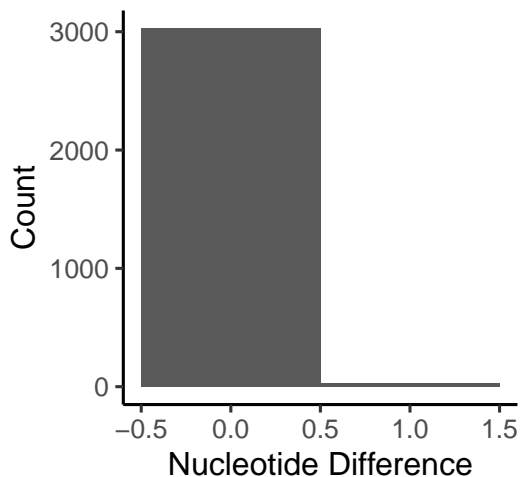
TRBV7-4*ap01

366 sequences assigned
359 (98.1%) exact matches, in which:
352 unique CDR3
13 unique J



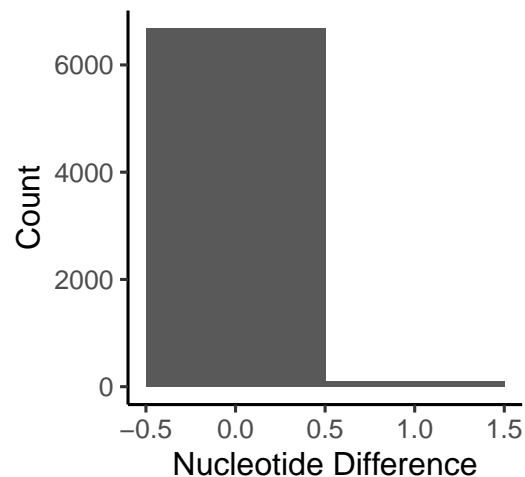
TRBV7-8*ap01

3058 sequences assigned
3028 (99%) exact matches, in which:
2952 unique CDR3
13 unique J



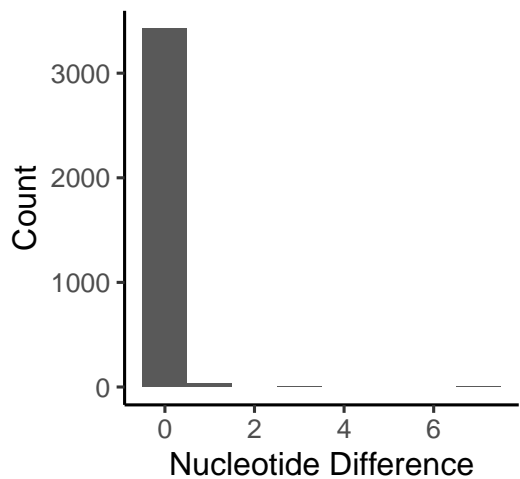
TRBV29-1*ap01

6775 sequences assigned
6681 (98.6%) exact matches, in which:
6541 unique CDR3
13 unique J



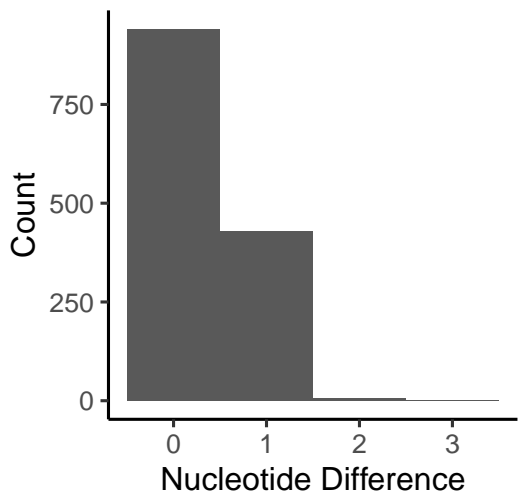
TRBV7-6*ap01

3459 sequences assigned
3425 (99%) exact matches, in which:
3350 unique CDR3
13 unique J



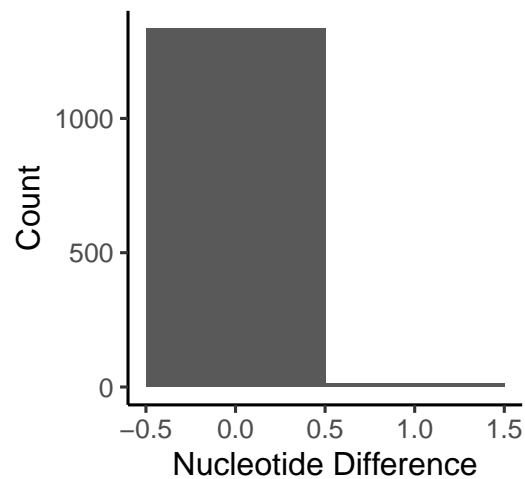
TRBV7-8*ap03

1378 sequences assigned
941 (68.3%) exact matches, in which:
914 unique CDR3
13 unique J



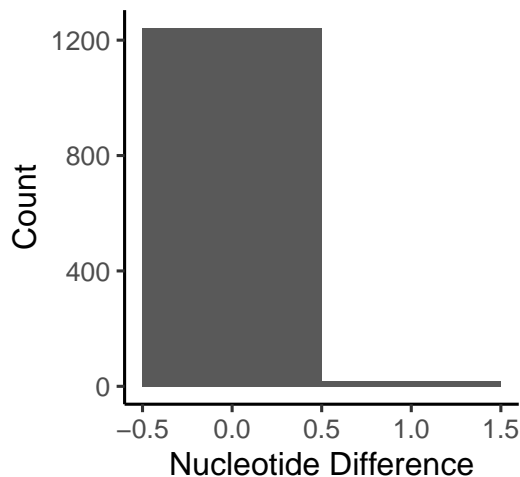
TRBV29-1*ap02

1347 sequences assigned
1334 (99%) exact matches, in which:
1303 unique CDR3
13 unique J



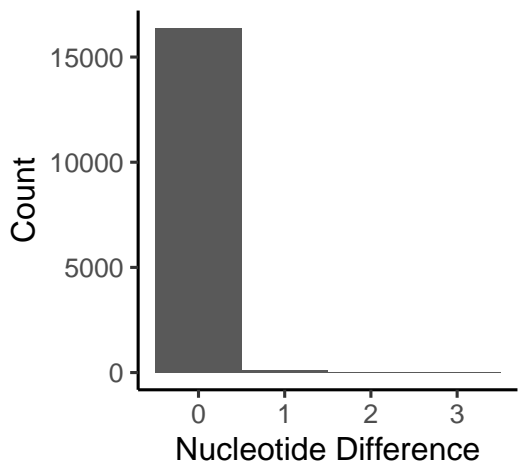
TRBV7-7*ap01

1261 sequences assigned
1242 (98.5%) exact matches, in which:
1217 unique CDR3
13 unique J

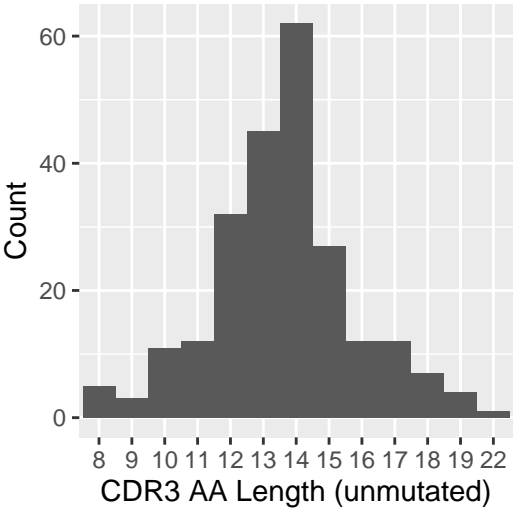


TRBV7-9*ap01

16528 sequences assigned
16391 (99.2%) exact matches, in which:
16159 unique CDR3
13 unique J



TRBV7-1*ap01_G291C_T296C_C314T





Warning – no inferred sequences found.

Warning – no inferred sequences found.