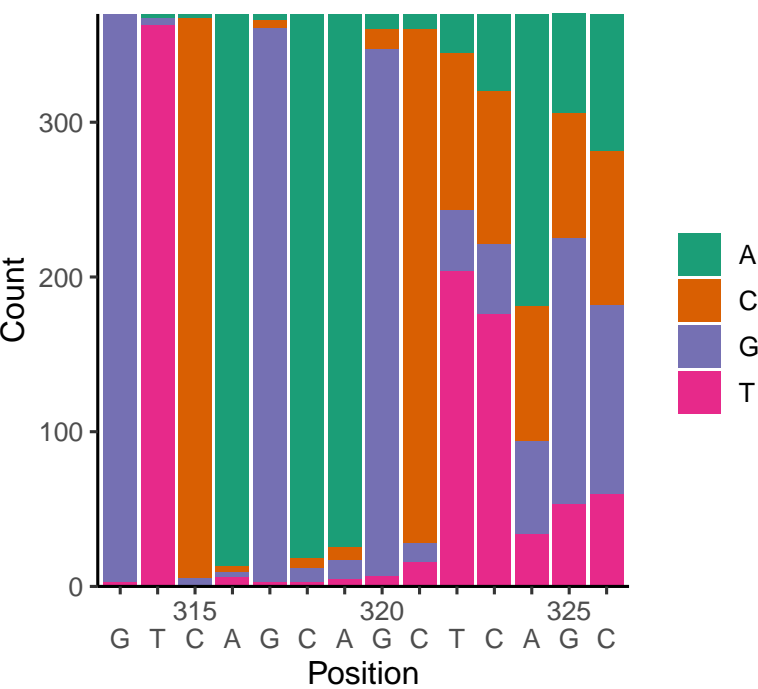
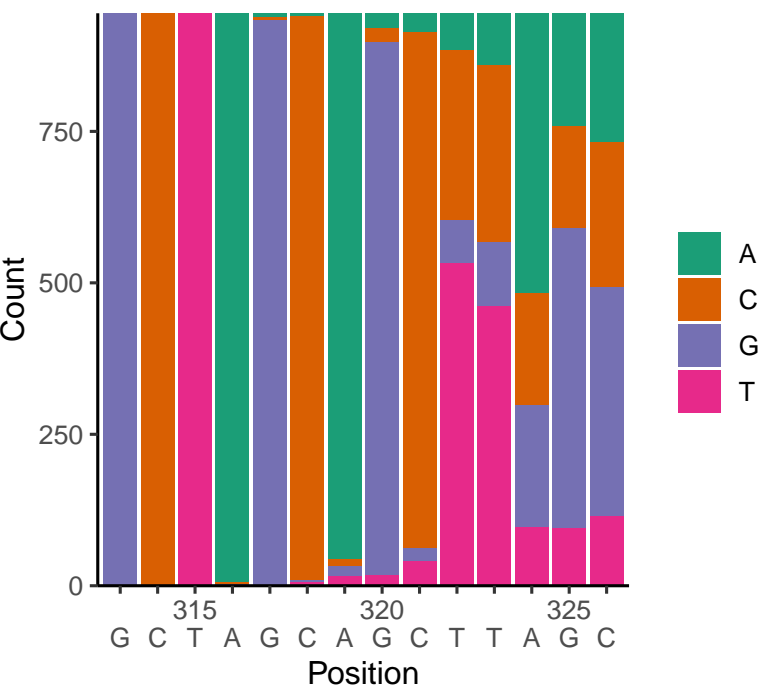


Gene TRBV7-1*ap01_T296C_C314T



Gene TRBV7-7*ap01_C315T



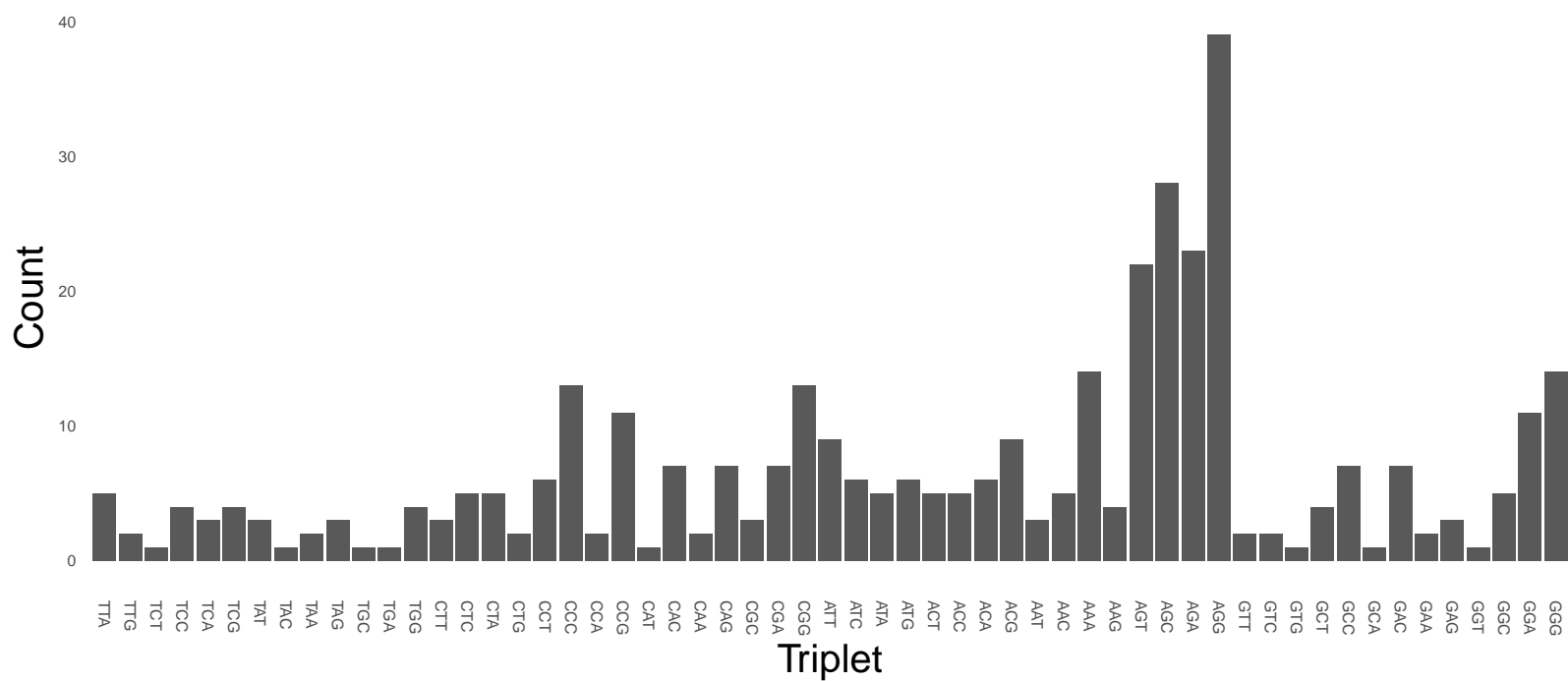
Gene TRBV7-1*ap01_T296C_C314T



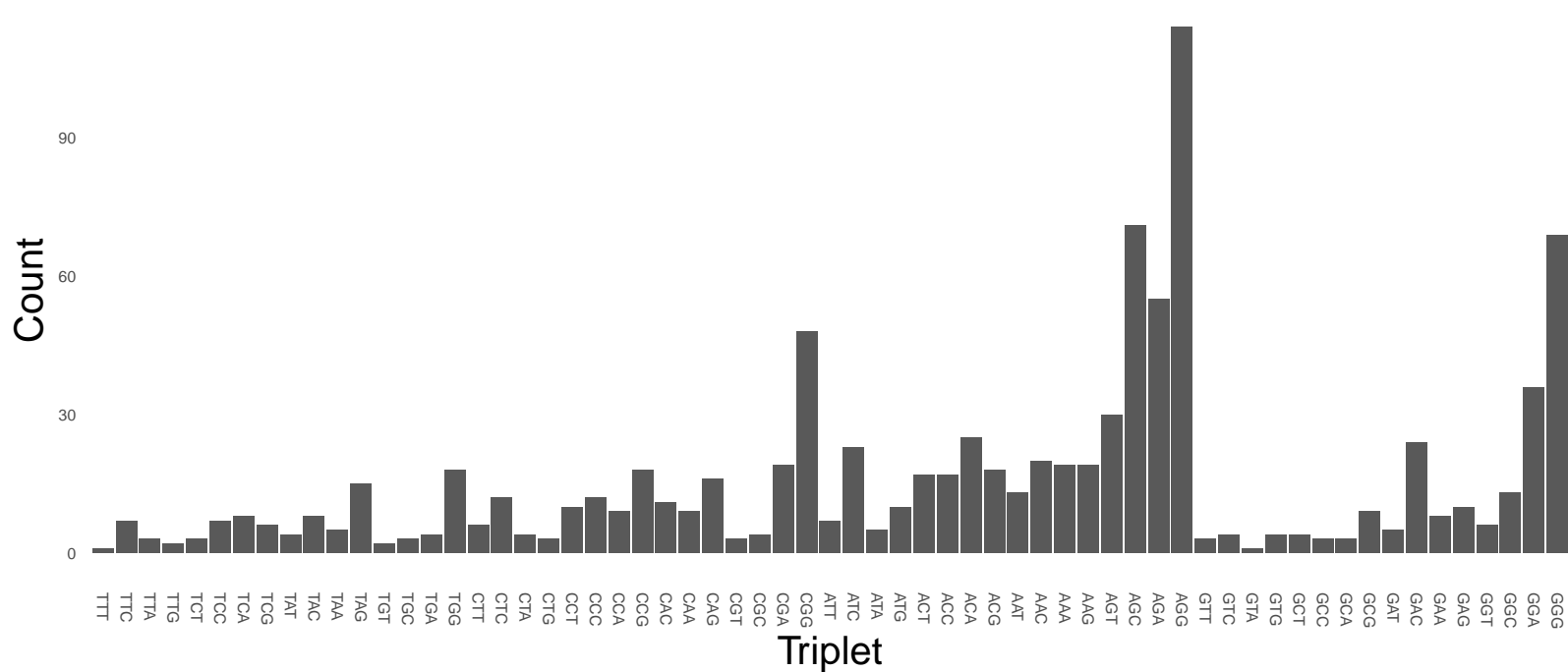
Gene TRBV7-7*ap01_C315T



TRBV7-1*ap01_T296C_C314T- Final 3 nucleotides as a triplet

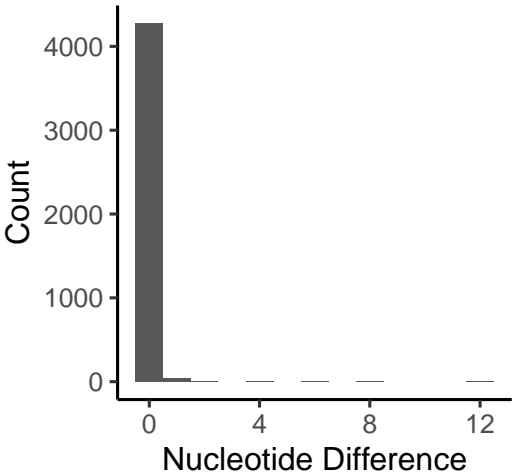


TRBV7-7*ap01_C315T- Final 3 nucleotides as a triplet



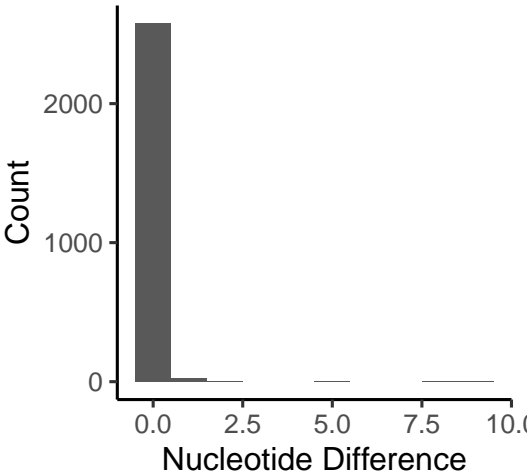
TRBV10-1*ap01

4325 sequences assigned
4274 (98.8%) exact matches, in which:
4166 unique CDR3
13 unique J



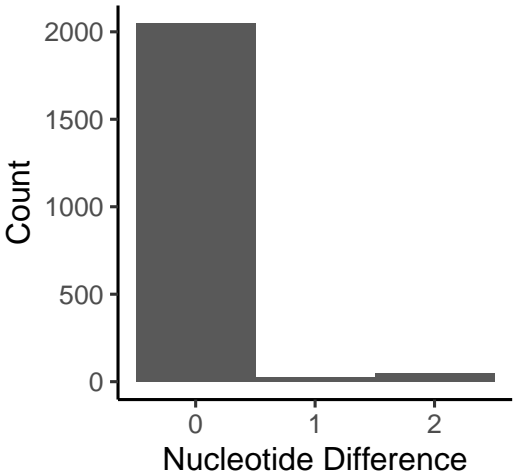
TRBV10-2*ap01

2609 sequences assigned
2577 (98.8%) exact matches, in which:
2527 unique CDR3
13 unique J



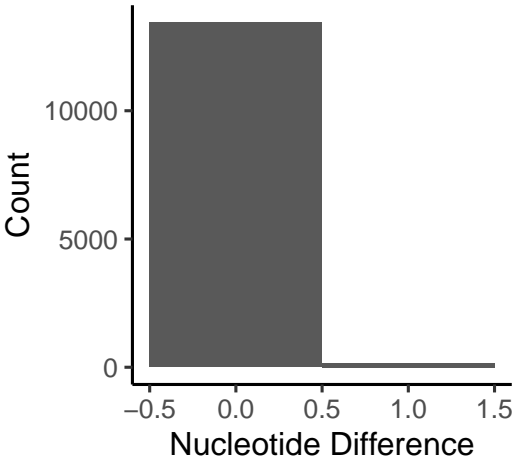
TRBV13*ap01

2122 sequences assigned
2048 (96.5%) exact matches, in which:
1993 unique CDR3
13 unique J



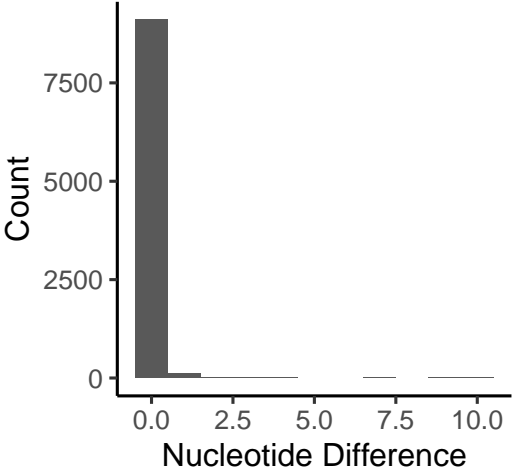
TRBV20-1*ap01

13603 sequences assigned
13442 (98.8%) exact matches, in which:
13251 unique CDR3
13 unique J



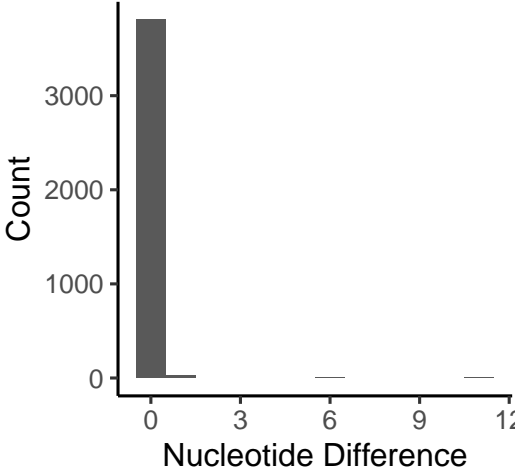
TRBV10-3*ap01

9219 sequences assigned
9105 (98.8%) exact matches, in which:
8937 unique CDR3
13 unique J



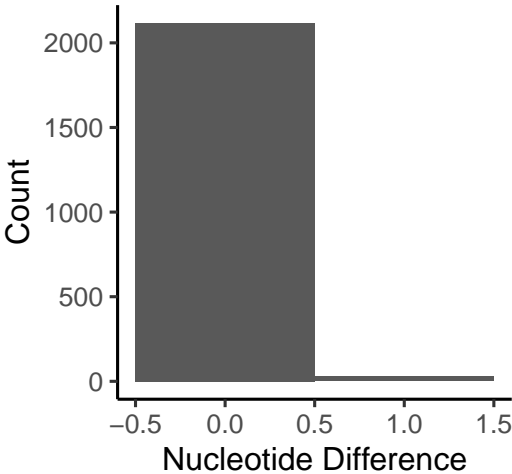
TRBV14*ap01

3834 sequences assigned
3807 (99.3%) exact matches, in which:
3758 unique CDR3
13 unique J



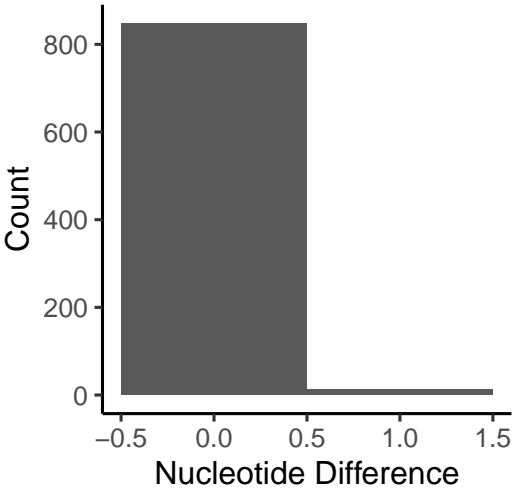
TRBV20-1*ap02

2146 sequences assigned
2117 (98.6%) exact matches, in which:
2090 unique CDR3
13 unique J



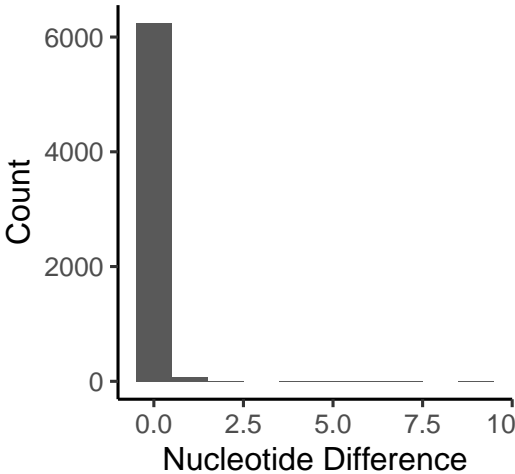
TRBV1*ap01

860 sequences assigned
848 (98.6%) exact matches, in which:
826 unique CDR3
13 unique J



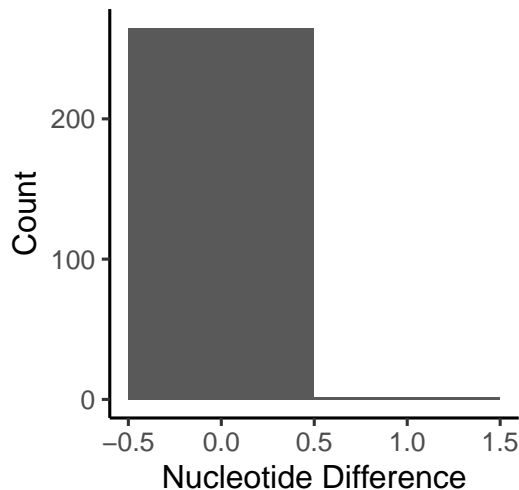
TRBV15*ap02

6326 sequences assigned
6244 (98.7%) exact matches, in which:
6120 unique CDR3
13 unique J



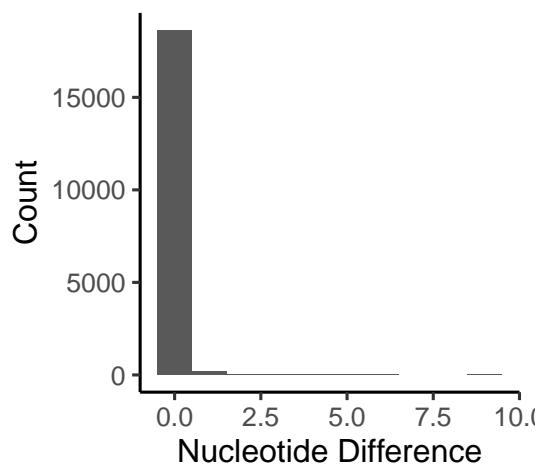
TRBV16*ap01

267 sequences assigned
265 (99.3%) exact matches, in which:
262 unique CDR3
13 unique J



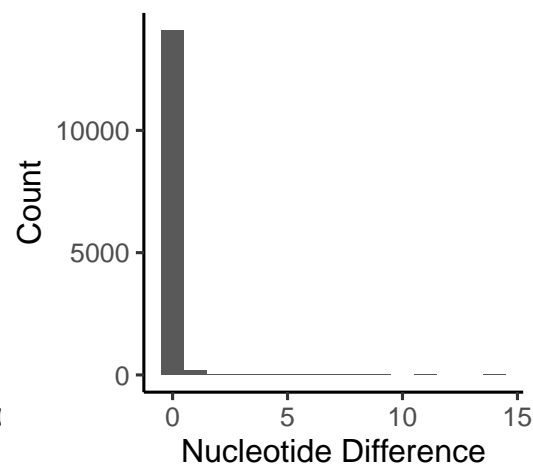
TRBV19*ap01

18816 sequences assigned
18631 (99%) exact matches, in which:
18437 unique CDR3
13 unique J



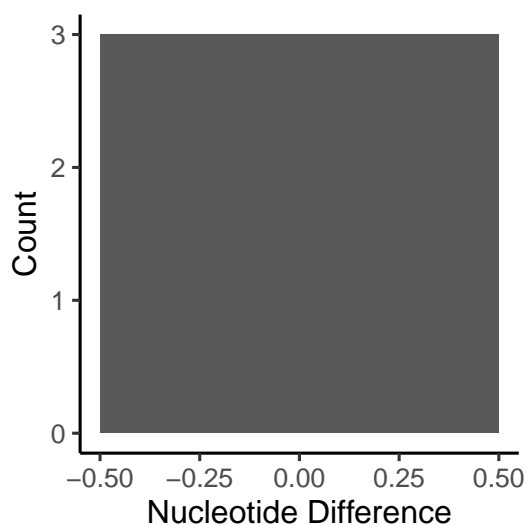
TRBV27*ap01

14319 sequences assigned
14100 (98.5%) exact matches, in which:
13755 unique CDR3
13 unique J



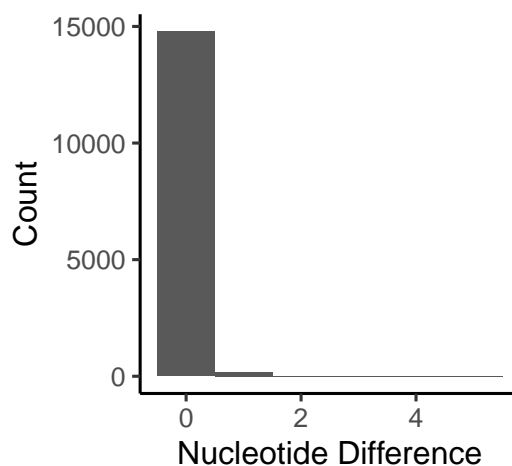
TRBV17*ap01

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



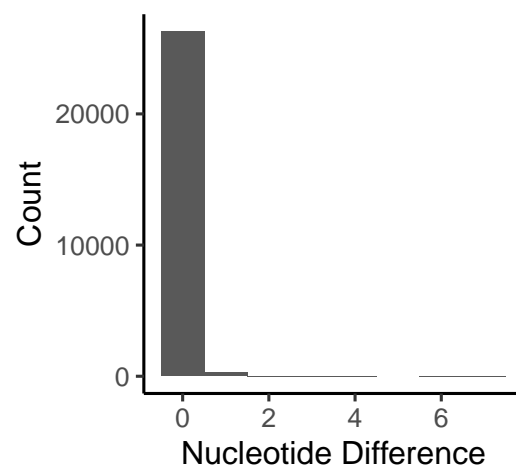
TRBV2*ap01

14979 sequences assigned
14784 (98.7%) exact matches, in which:
14483 unique CDR3
13 unique J



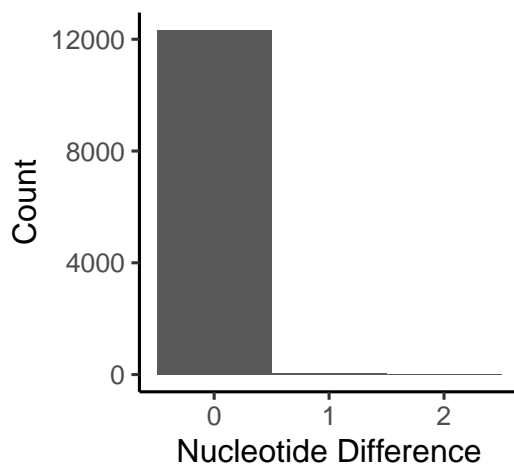
TRBV28*ap01

26565 sequences assigned
26285 (98.9%) exact matches, in which:
25844 unique CDR3
13 unique J



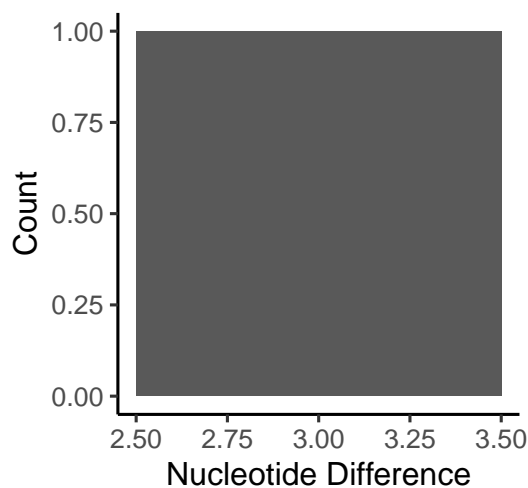
TRBV18*ap01

12404 sequences assigned
12338 (99.5%) exact matches, in which:
12188 unique CDR3
13 unique J



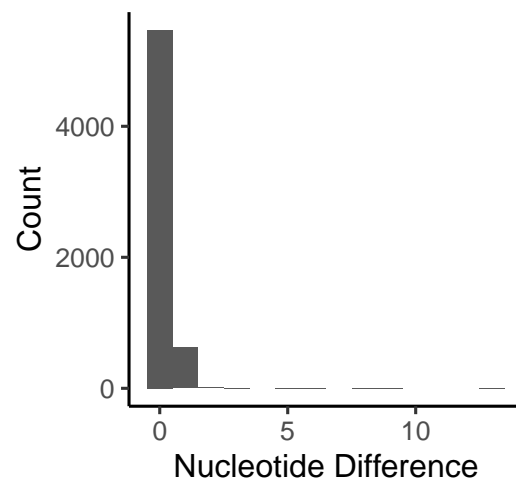
TRBV26*ap01

1 sequences assigned
No exact matches.



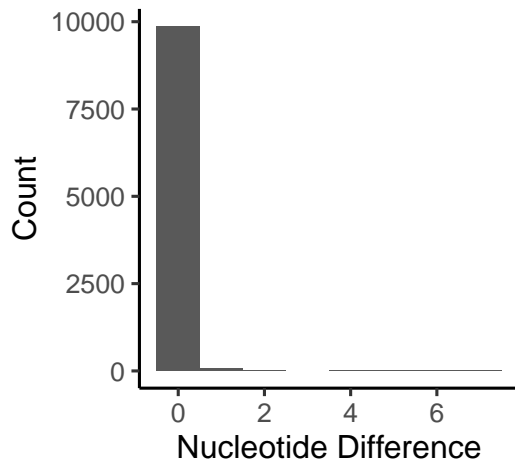
TRBV30*ap01

6119 sequences assigned
5469 (89.4%) exact matches, in which:
5402 unique CDR3
13 unique J



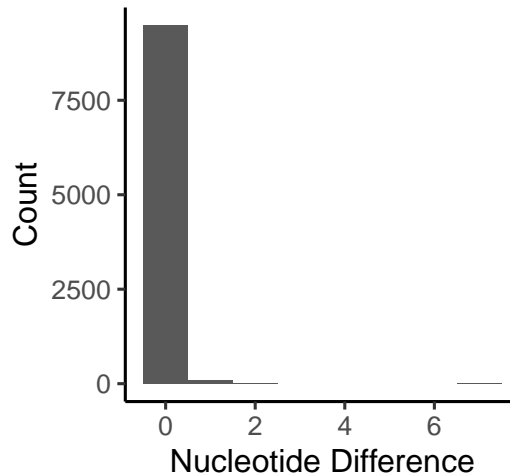
TRBV9*ap01

9968 sequences assigned
9873 (99%) exact matches, in which:
9705 unique CDR3
13 unique J



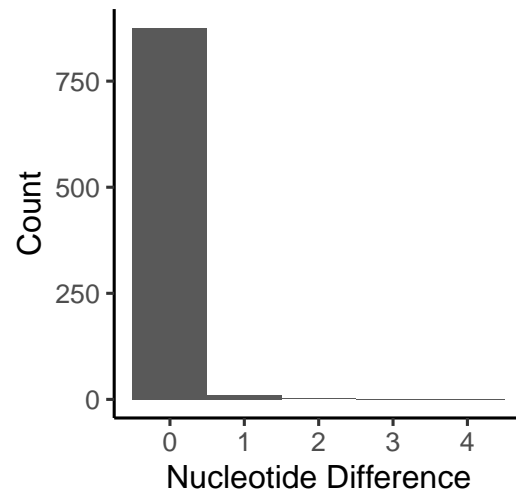
TRBV11-2*ap01

9580 sequences assigned
9482 (99%) exact matches, in which:
9278 unique CDR3
13 unique J



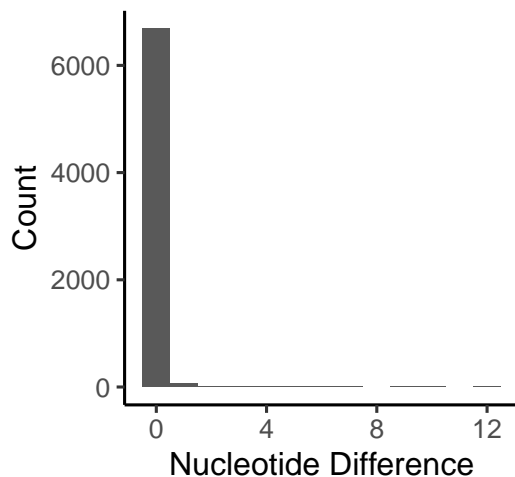
TRBV12-2*ap01

890 sequences assigned
876 (98.4%) exact matches, in which:
863 unique CDR3
13 unique J



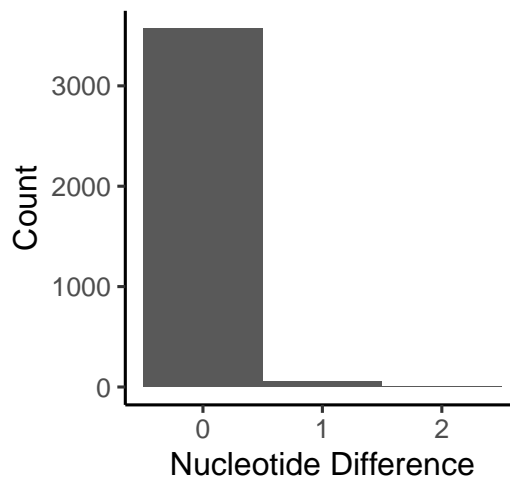
TRBV21-1*ap01

6787 sequences assigned
6684 (98.5%) exact matches, in which:
6594 unique CDR3
13 unique J



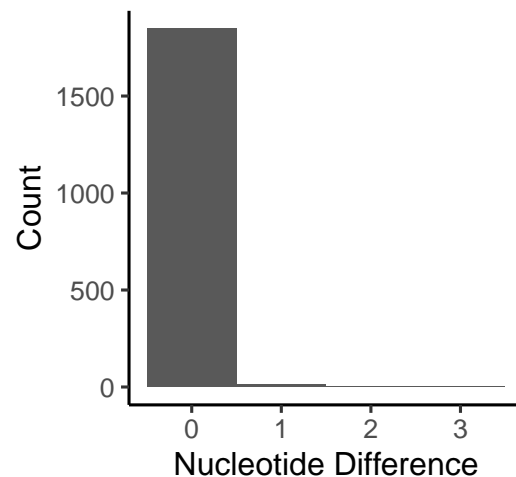
TRBV11-3*ap01

3622 sequences assigned
3569 (98.5%) exact matches, in which:
3504 unique CDR3
13 unique J



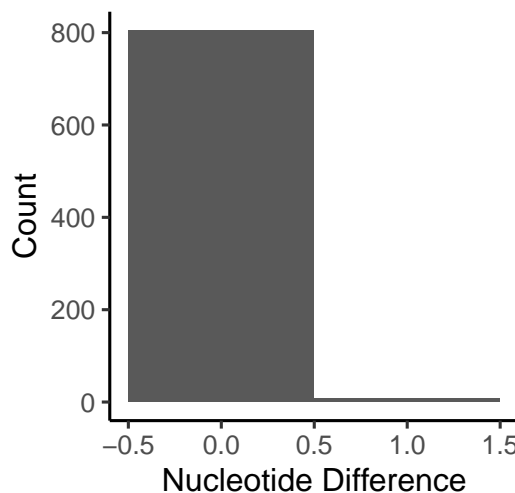
TRBV12-5*ap01

1864 sequences assigned
1847 (99.1%) exact matches, in which:
1816 unique CDR3
13 unique J



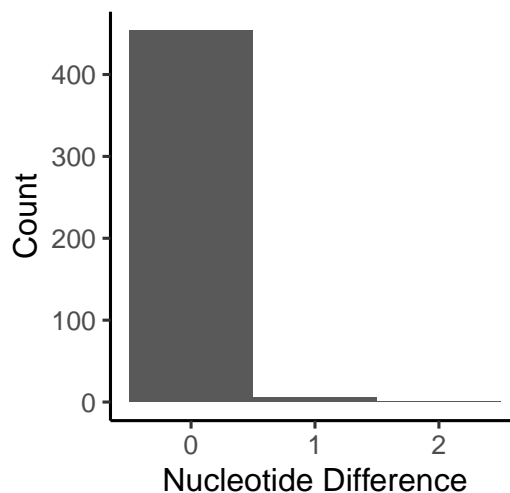
TRBV11-1*ap01

813 sequences assigned
805 (99%) exact matches, in which:
788 unique CDR3
13 unique J



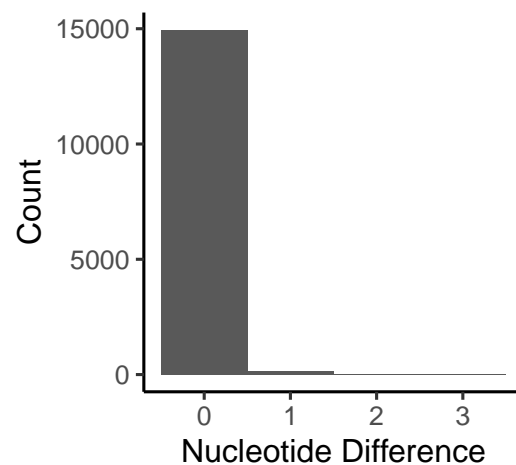
TRBV12-1*ap01

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



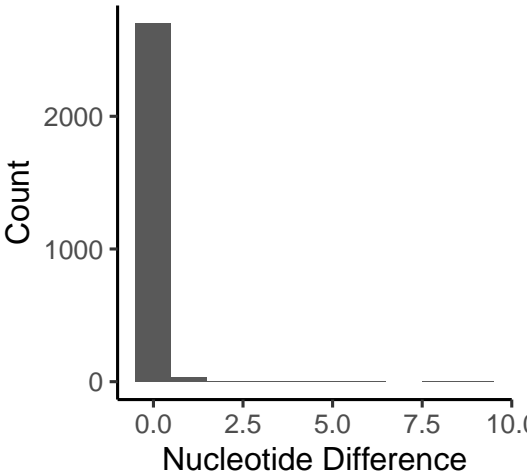
TRBV12-34*ap01

15118 sequences assigned
14954 (98.9%) exact matches, in which:
14655 unique CDR3
13 unique J



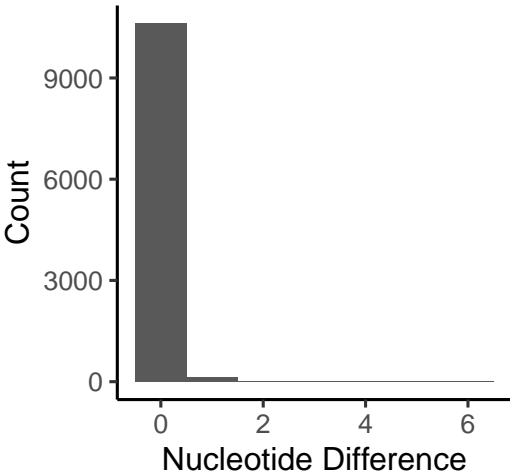
TRBV23-1*ap01

2741 sequences assigned
2700 (98.5%) exact matches, in which:
2661 unique CDR3
13 unique J



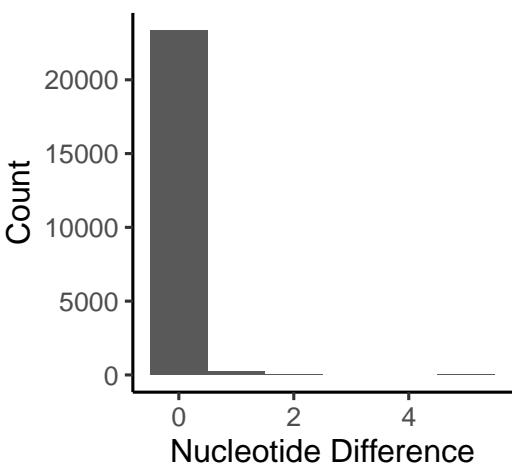
TRBV24-1*ap01

10779 sequences assigned
10617 (98.5%) exact matches, in which:
10439 unique CDR3
13 unique J



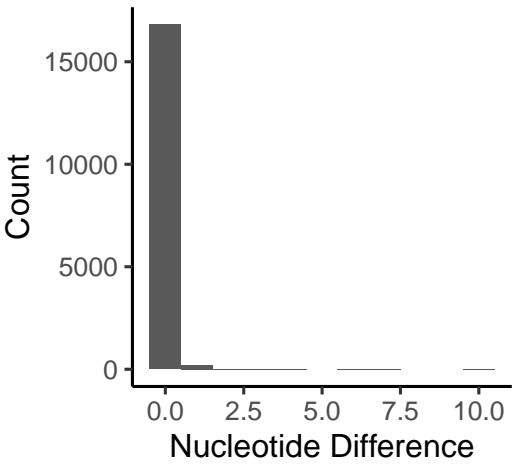
TRBV5-1*ap01

23613 sequences assigned
23363 (98.9%) exact matches, in which:
22833 unique CDR3
13 unique J



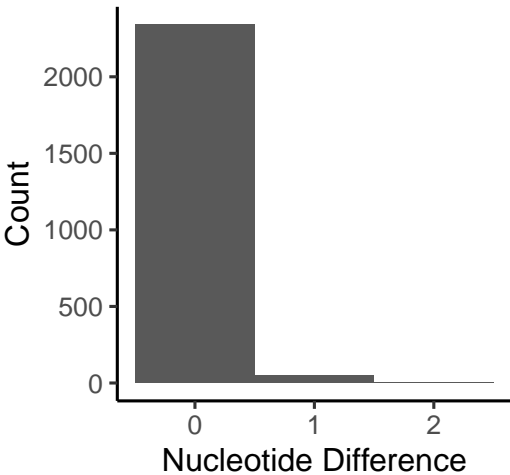
TRBV3-12*ap01

17044 sequences assigned
16819 (98.7%) exact matches, in which:
16477 unique CDR3
13 unique J



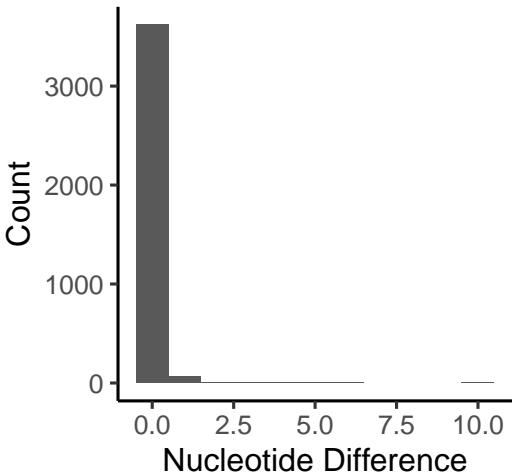
TRBV4-2*ap01

2390 sequences assigned
2340 (97.9%) exact matches, in which:
2276 unique CDR3
13 unique J



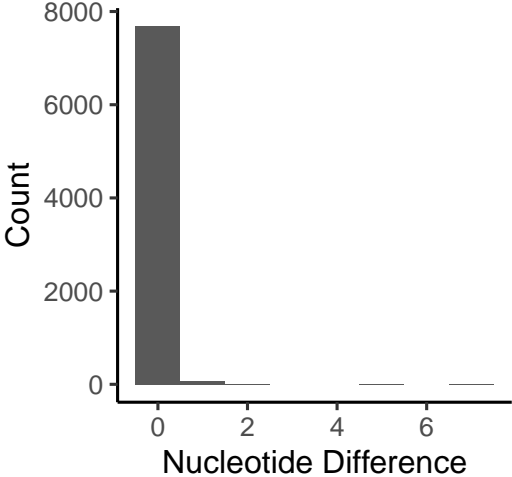
TRBV25-1*ap01

3691 sequences assigned
3620 (98.1%) exact matches, in which:
3546 unique CDR3
13 unique J



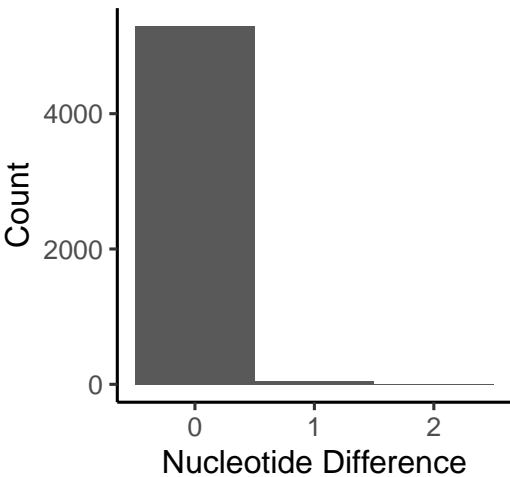
TRBV4-1*ap01

7762 sequences assigned
7688 (99%) exact matches, in which:
7537 unique CDR3
13 unique J



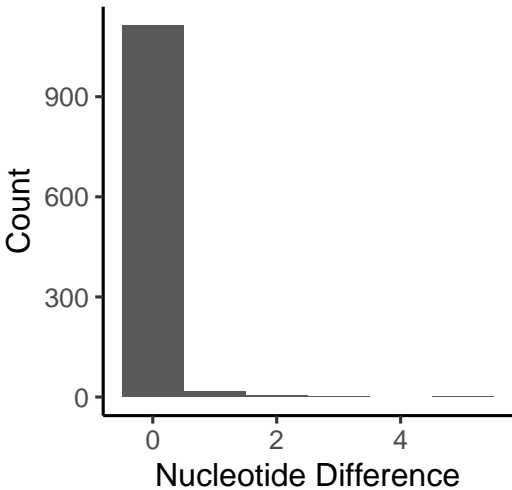
TRBV4-3*ap01

5349 sequences assigned
5295 (99%) exact matches, in which:
5209 unique CDR3
13 unique J



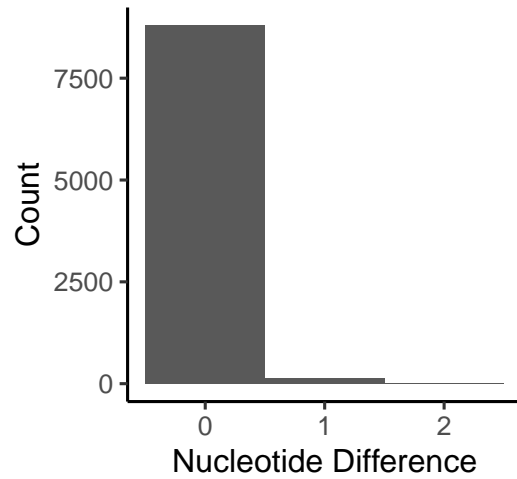
TRBV5-3*ap01

1138 sequences assigned
1114 (97.9%) exact matches, in which:
1097 unique CDR3
13 unique J



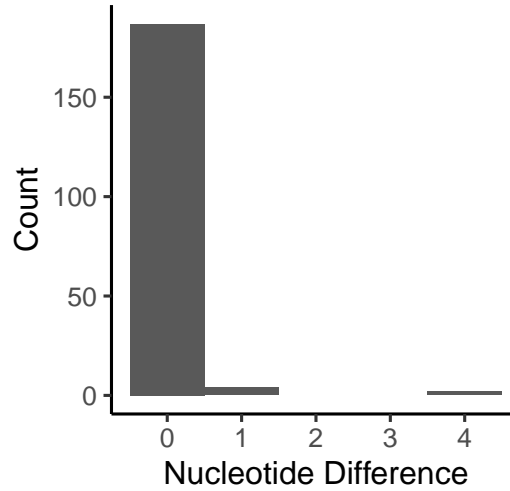
TRBV5-4*ap01

8920 sequences assigned
8796 (98.6%) exact matches, in which:
8632 unique CDR3
13 unique J



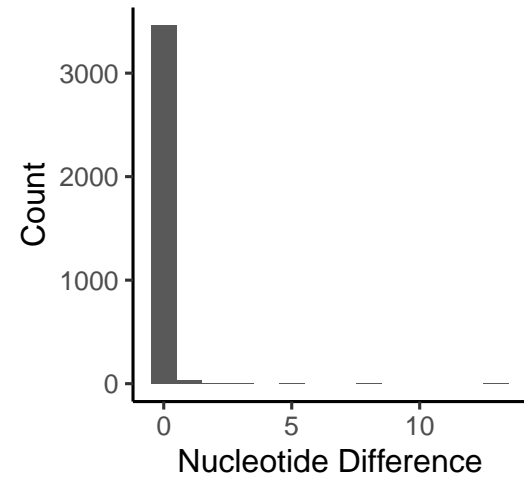
TRBV5-7*ap01

193 sequences assigned
187 (96.9%) exact matches, in which:
183 unique CDR3
12 unique J



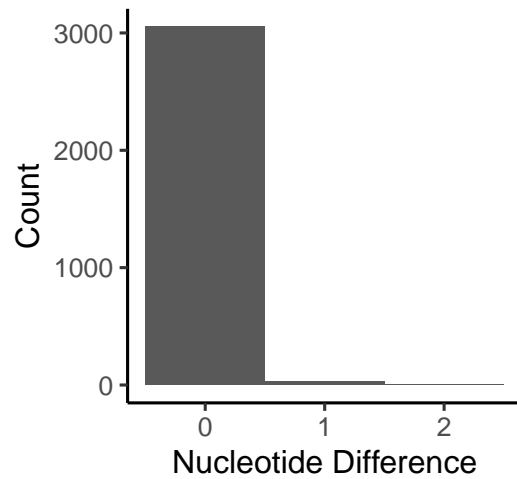
TRBV6-4*ap01

3513 sequences assigned
3461 (98.5%) exact matches, in which:
3399 unique CDR3
13 unique J



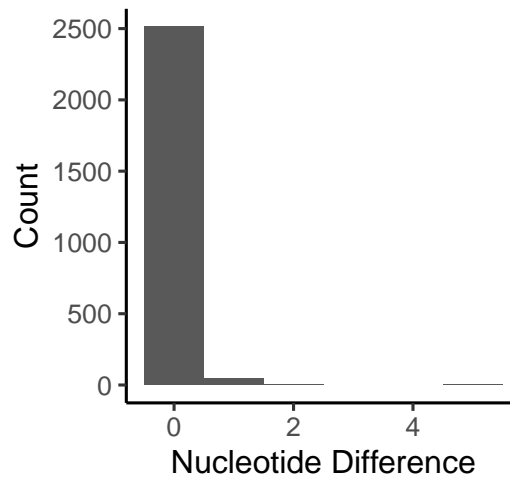
TRBV5-5*ap01

3082 sequences assigned
3053 (99.1%) exact matches, in which:
3028 unique CDR3
13 unique J



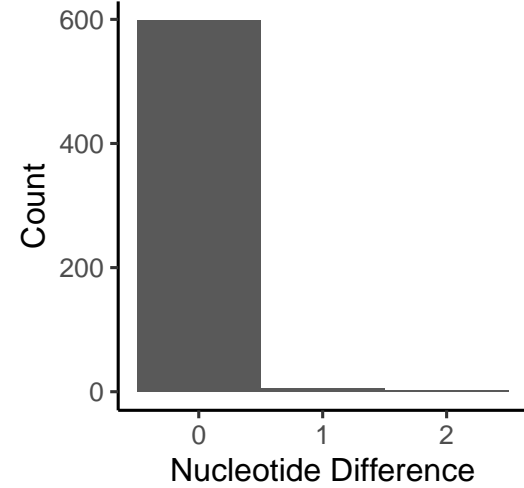
TRBV5-8*ap01

2560 sequences assigned
2513 (98.2%) exact matches, in which:
2471 unique CDR3
13 unique J



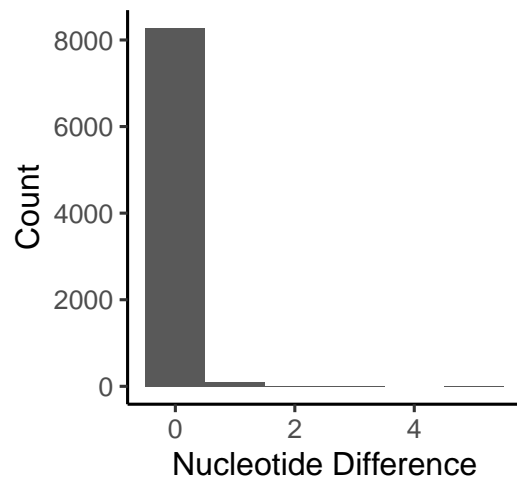
TRBV6-7*ap01

607 sequences assigned
599 (98.7%) exact matches, in which:
579 unique CDR3
13 unique J



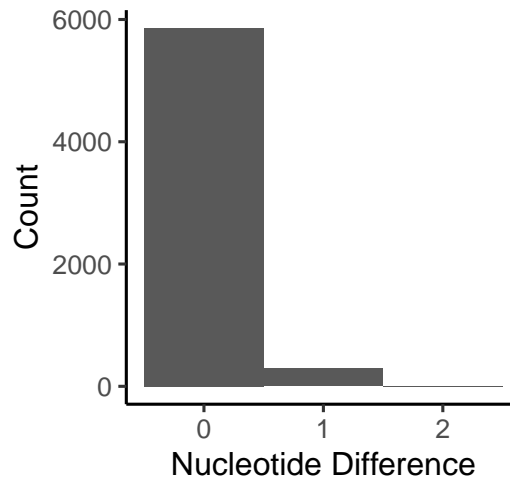
TRBV5-6*ap01

8383 sequences assigned
8275 (98.7%) exact matches, in which:
8075 unique CDR3
13 unique J



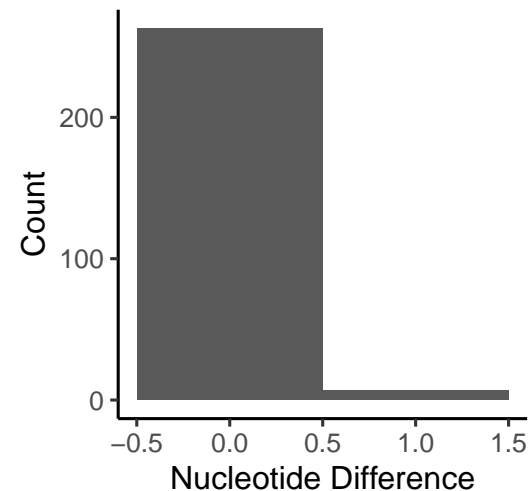
TRBV6-1*ap01

6153 sequences assigned
5860 (95.2%) exact matches, in which:
5723 unique CDR3
13 unique J



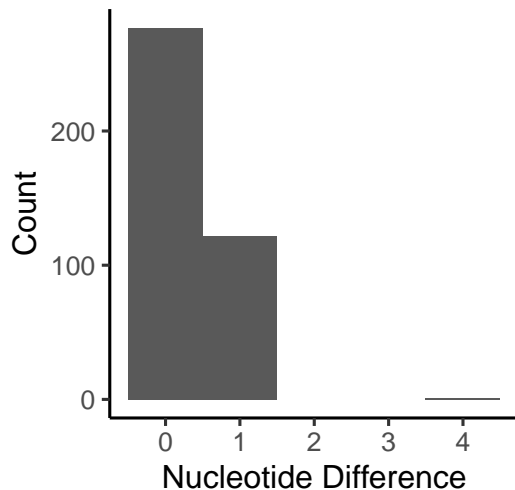
TRBV6-8*ap01

270 sequences assigned
263 (97.4%) exact matches, in which:
259 unique CDR3
13 unique J



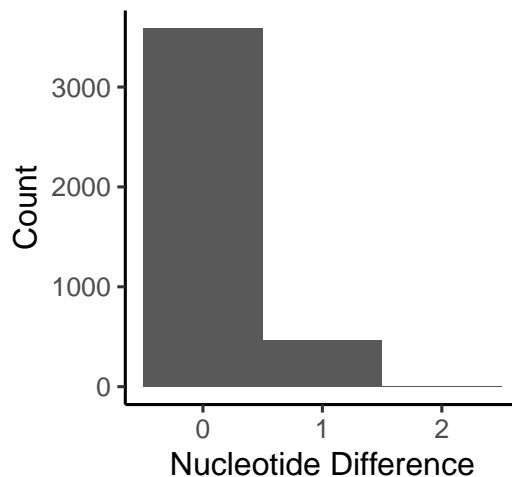
TRBV6-9*ap01

400 sequences assigned
277 (69.2%) exact matches, in which:
270 unique CDR3
13 unique J



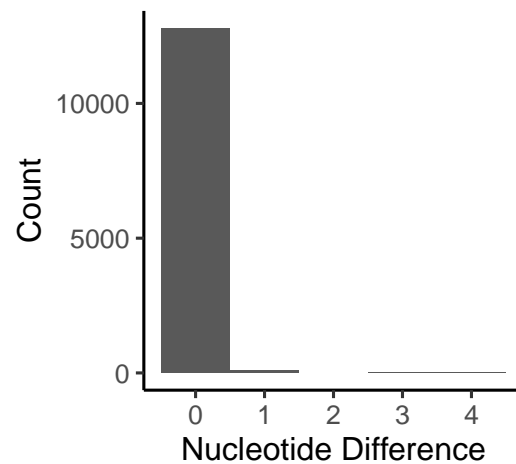
TRBV6-56*ap02

4057 sequences assigned
3587 (88.4%) exact matches, in which:
3503 unique CDR3
13 unique J



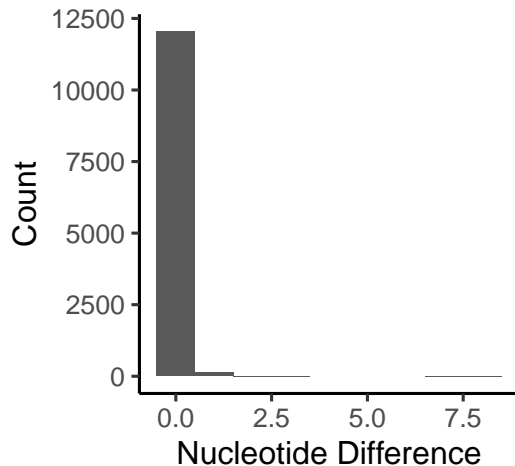
TRBV7-2*ap01

12899 sequences assigned
12793 (99.2%) exact matches, in which:
12595 unique CDR3
13 unique J



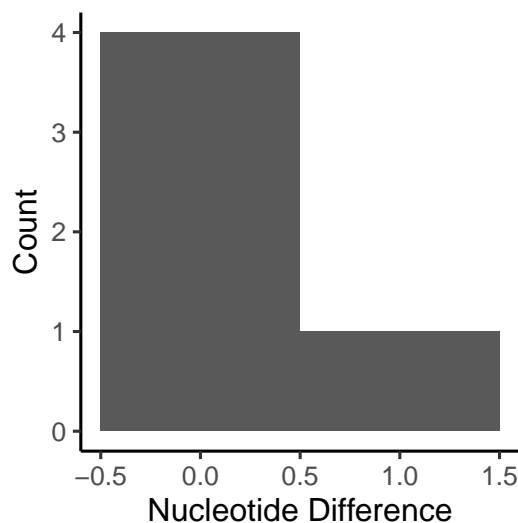
TRBV6-23*ap01

12189 sequences assigned
12045 (98.8%) exact matches, in which:
11793 unique CDR3
14 unique J



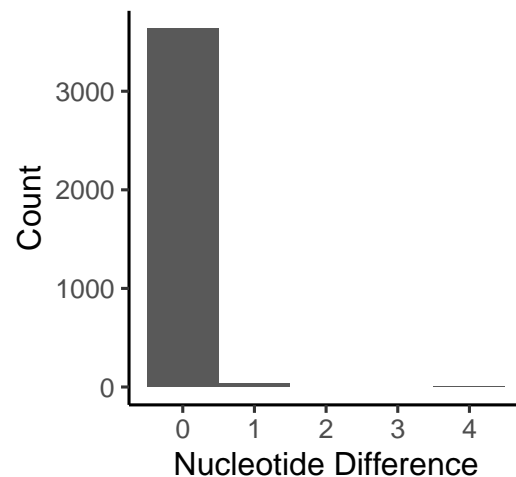
TRBV7-1*ap01

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



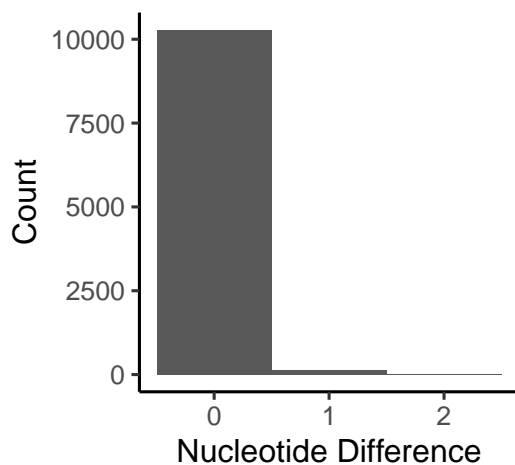
TRBV7-3*ap01

3675 sequences assigned
3634 (98.9%) exact matches, in which:
3594 unique CDR3
13 unique J



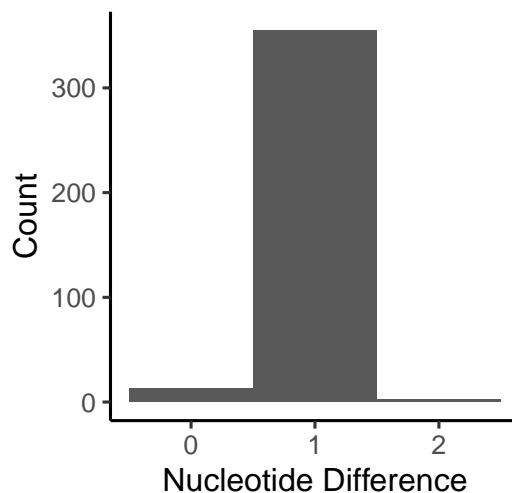
TRBV6-56*ap01

10409 sequences assigned
10282 (98.8%) exact matches, in which:
10017 unique CDR3
13 unique J



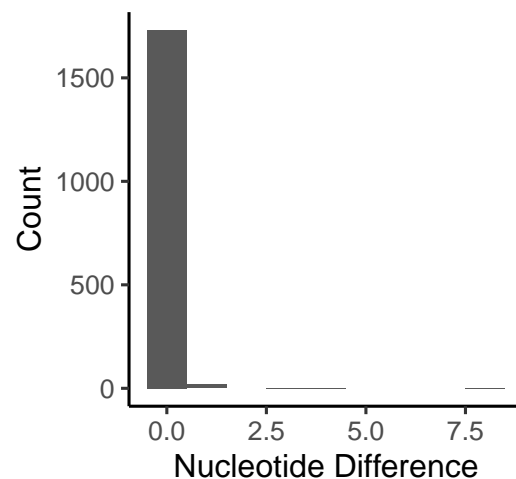
TRBV7-1*ap01_T296C_()

370 sequences assigned
13 (3.5%) exact matches, in which:
13 unique CDR3
7 unique J



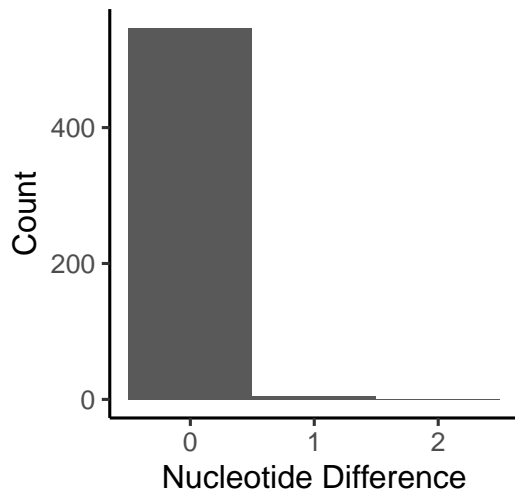
TRBV7-3*ap02

1753 sequences assigned
1731 (98.7%) exact matches, in which:
1708 unique CDR3
13 unique J



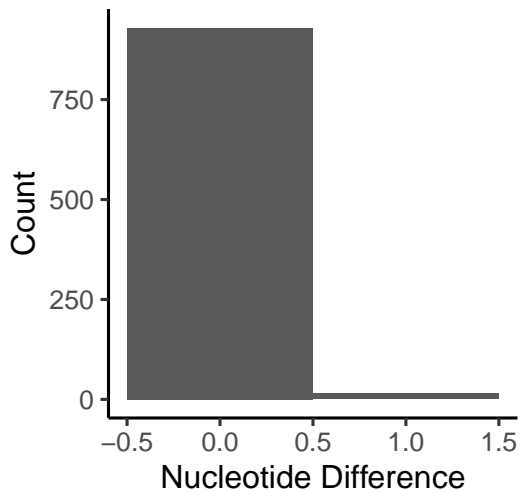
TRBV7-4*ap01

553 sequences assigned
547 (98.9%) exact matches, in which:
537 unique CDR3
13 unique J



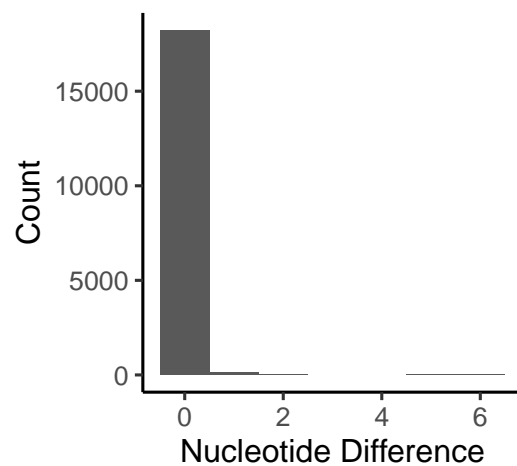
TRBV7-7*ap01_C315T

945 sequences assigned
930 (98.4%) exact matches, in which:
912 unique CDR3
13 unique J



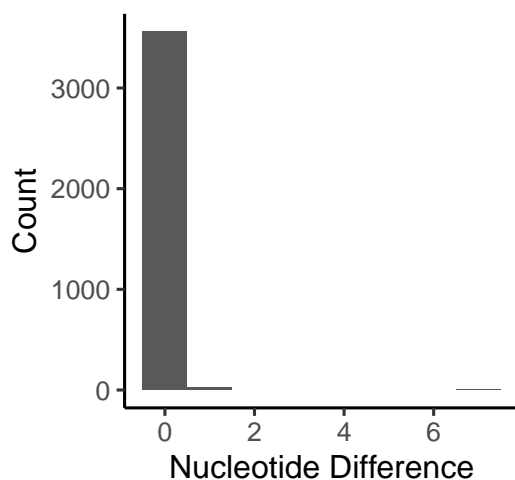
TRBV7-9*ap01

18378 sequences assigned
18228 (99.2%) exact matches, in which:
17977 unique CDR3
13 unique J



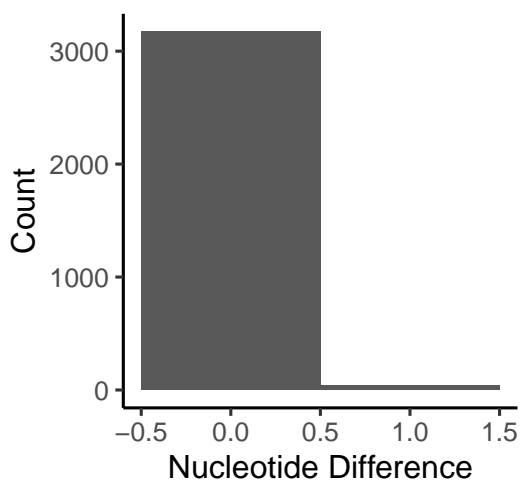
TRBV7-6*ap01

3588 sequences assigned
3559 (99.2%) exact matches, in which:
3486 unique CDR3
13 unique J



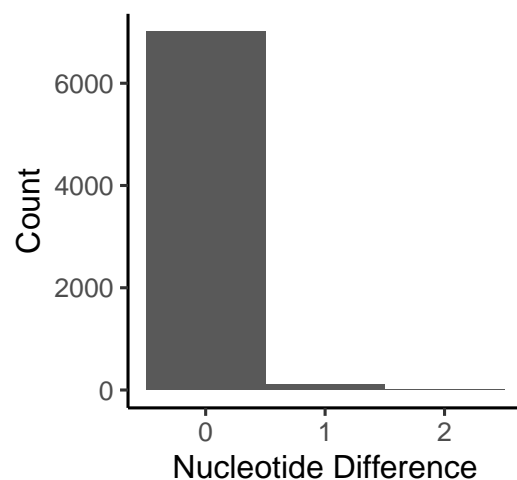
TRBV7-8*ap01

3211 sequences assigned
3172 (98.8%) exact matches, in which:
3105 unique CDR3
13 unique J



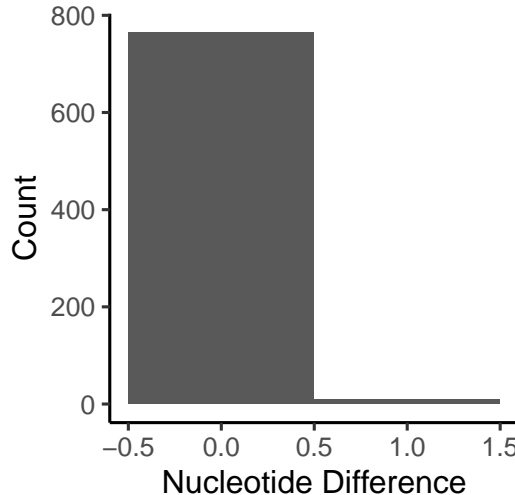
TRBV29-1*ap01

7107 sequences assigned
7008 (98.6%) exact matches, in which:
6888 unique CDR3
13 unique J



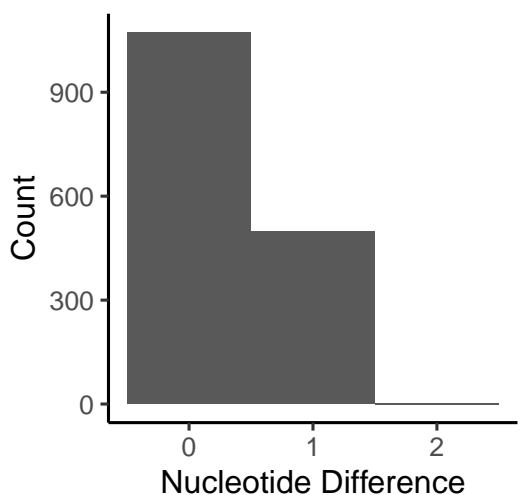
TRBV7-7*ap01

775 sequences assigned
765 (98.7%) exact matches, in which:
751 unique CDR3
13 unique J



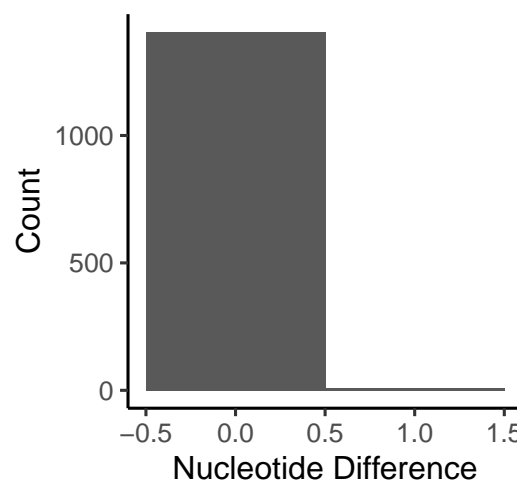
TRBV7-8*ap03

1574 sequences assigned
1073 (68.2%) exact matches, in which:
1051 unique CDR3
13 unique J

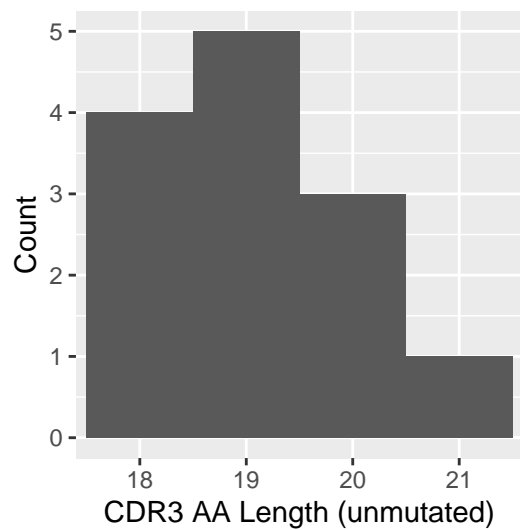


TRBV29-1*ap02

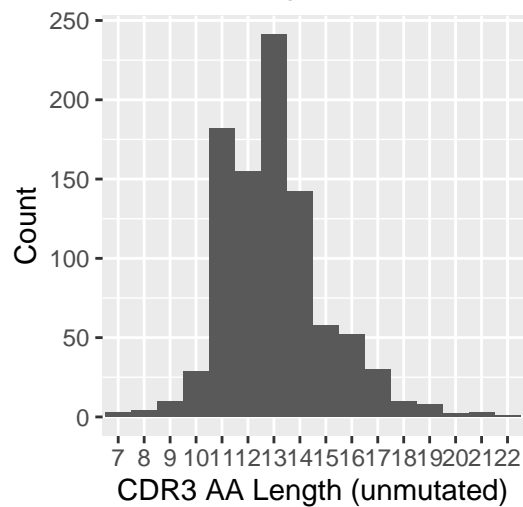
1416 sequences assigned
1406 (99.3%) exact matches, in which:
1378 unique CDR3
13 unique J



TRBV7-1*ap01_T296C_C314T



TRBV7-7*ap01_C315T





Warning – no inferred sequences found.