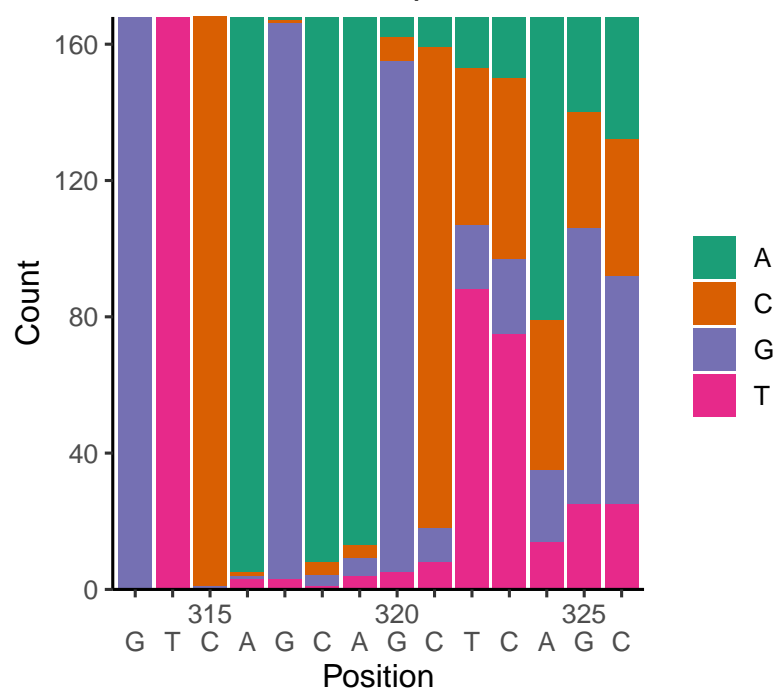
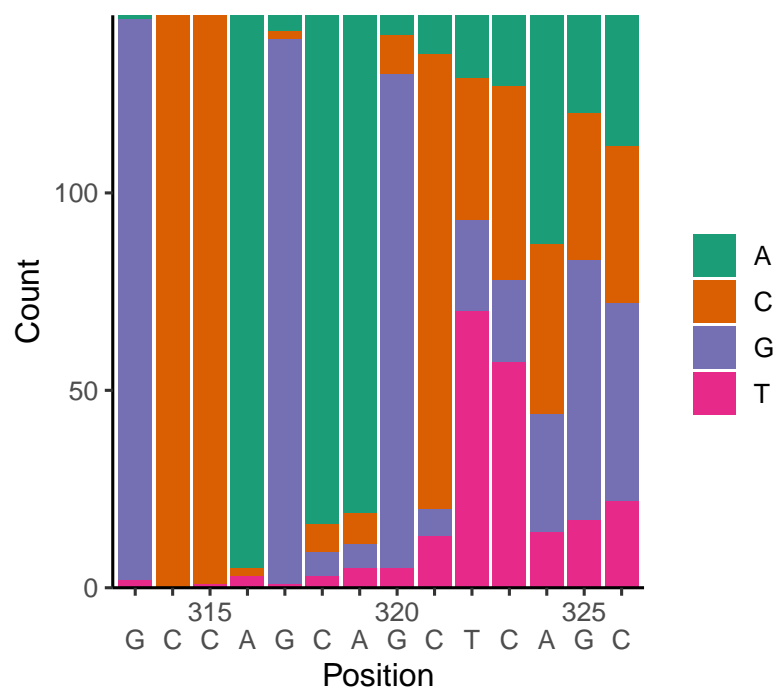


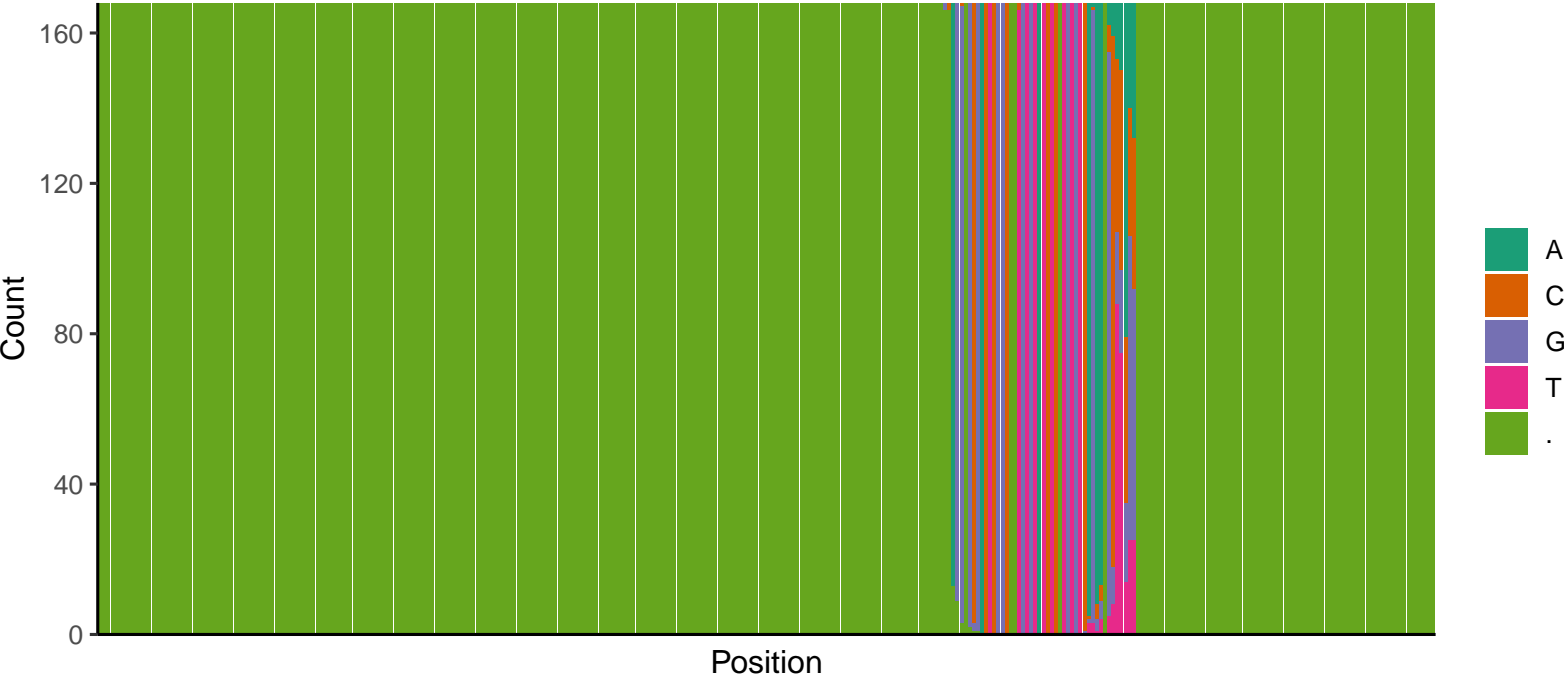
Gene TRBV7-1*ap01_G291C_T296C_C314T



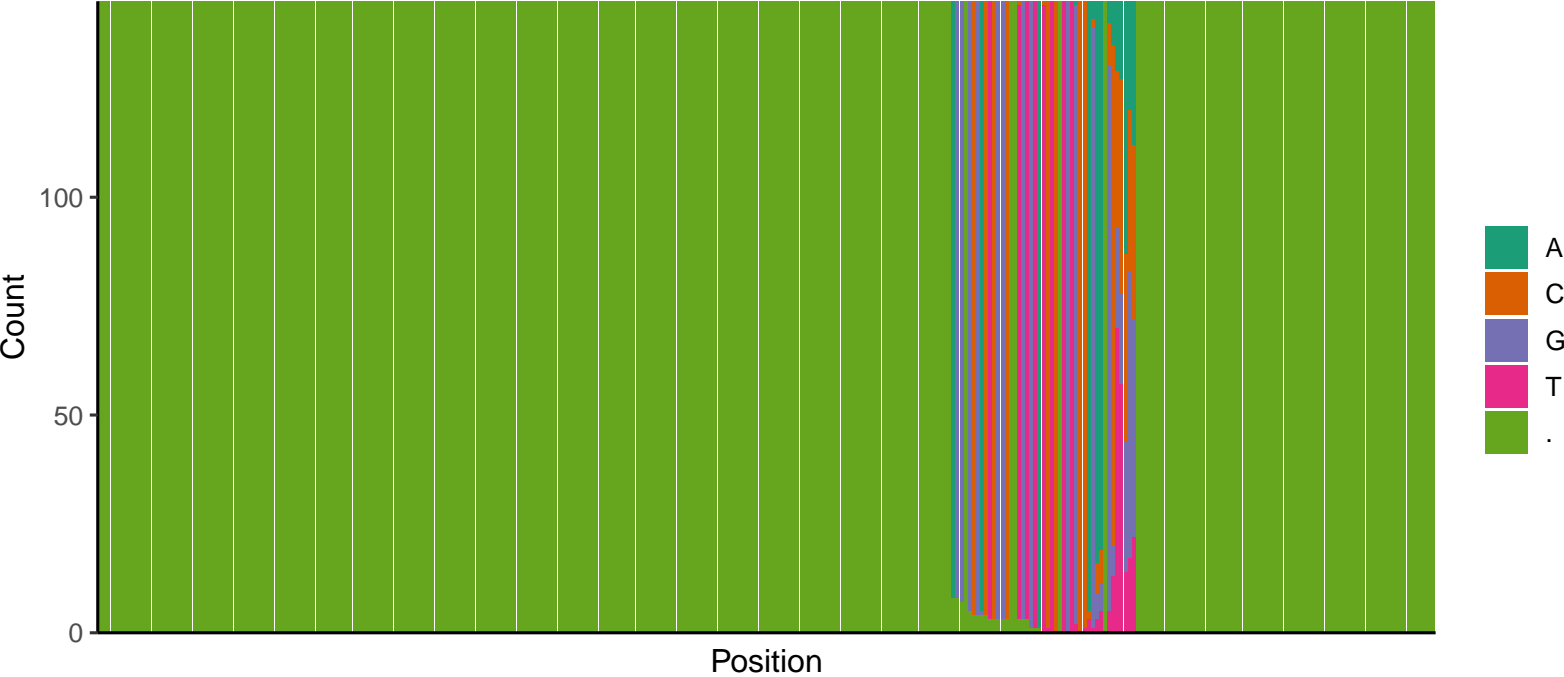
Gene TRBV7-1*ap01_G291C_T296C



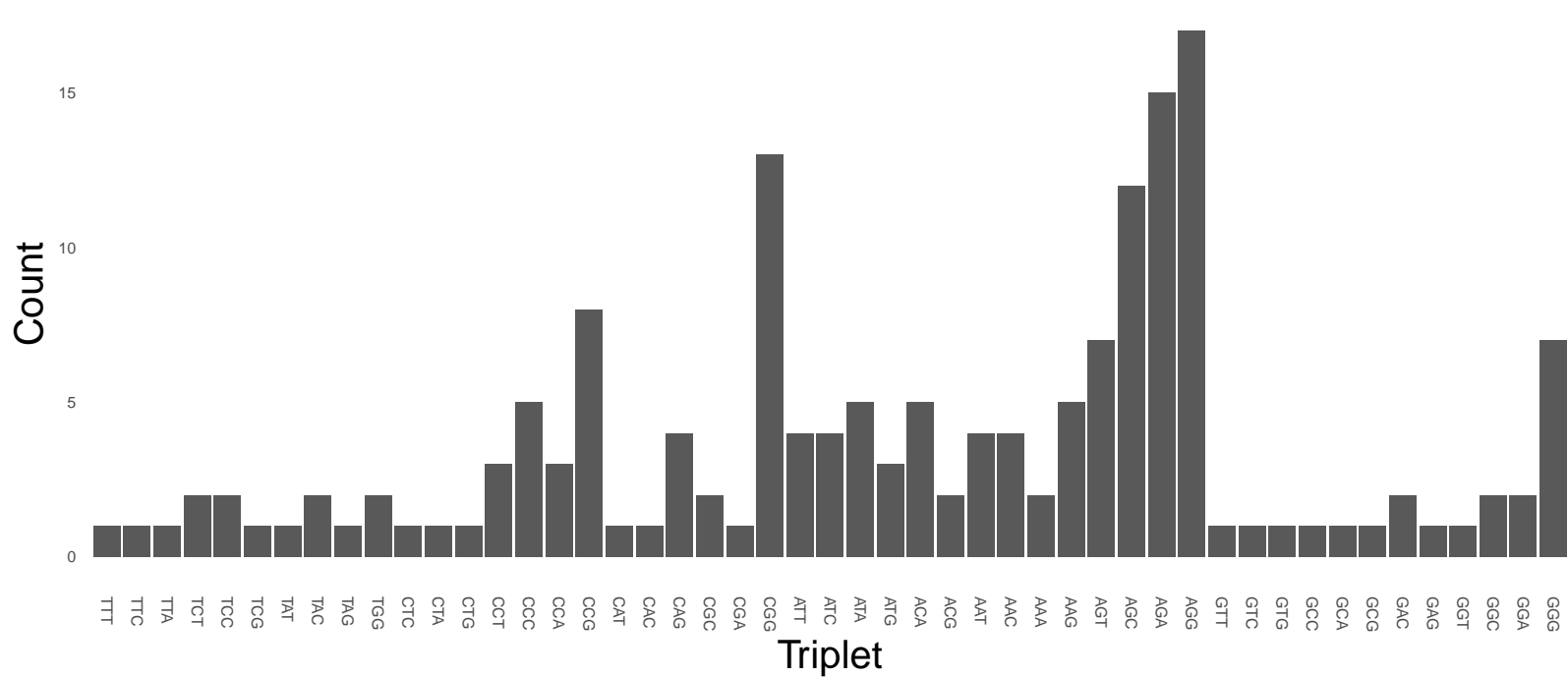
Gene TRBV7-1*ap01_G291C_T296C_C314T



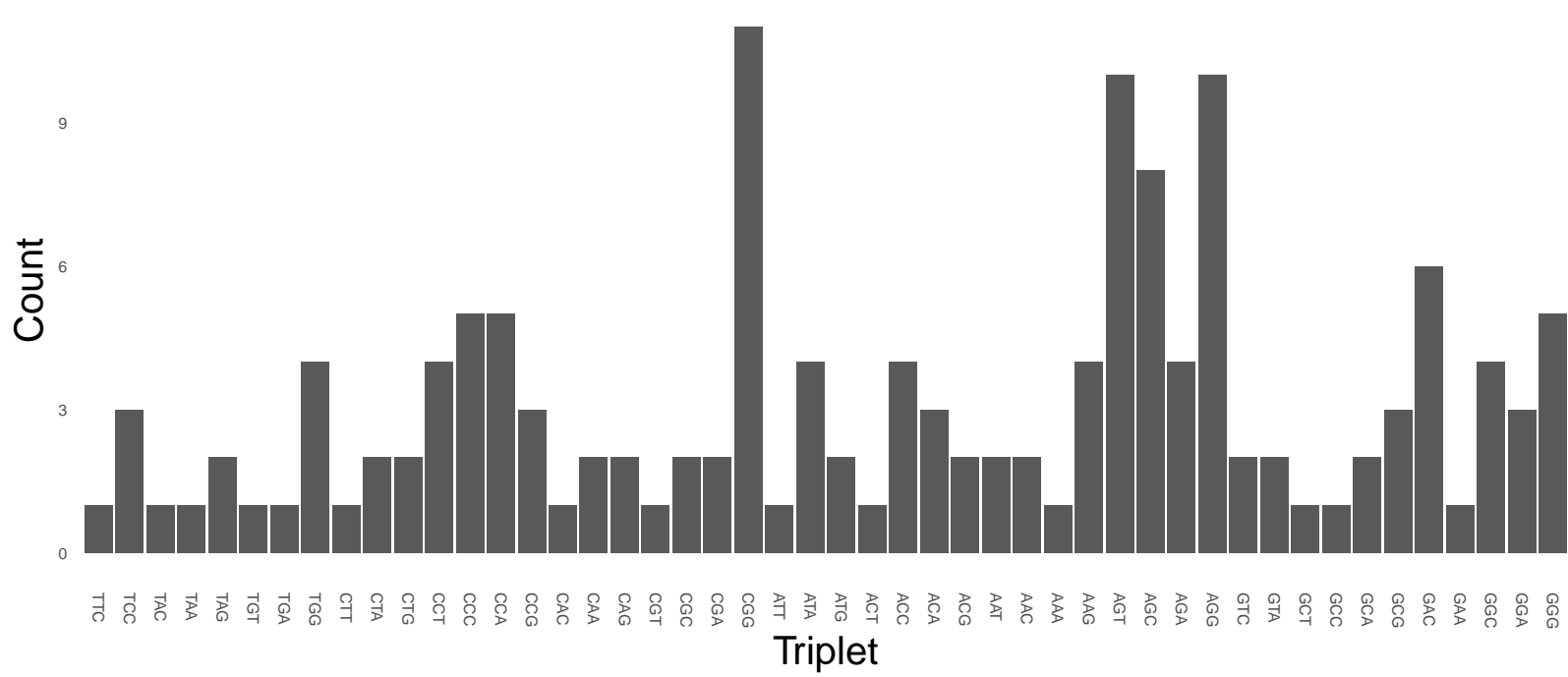
Gene TRBV7-1*ap01_G291C_T296C



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

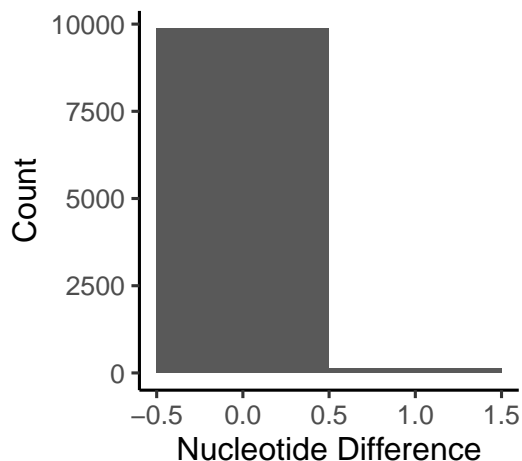


TRBV7-1*ap01_G291C_T296C- Final 3 nucleotides as a triplet



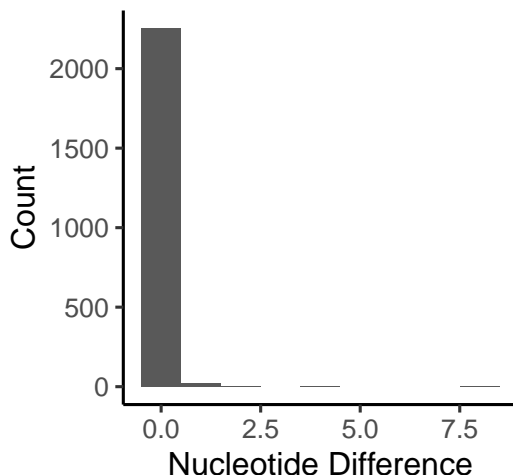
TRBV20-1*ap01

10024 sequences assigned
9884 (98.6%) exact matches, in which:
9702 unique CDR3
13 unique J



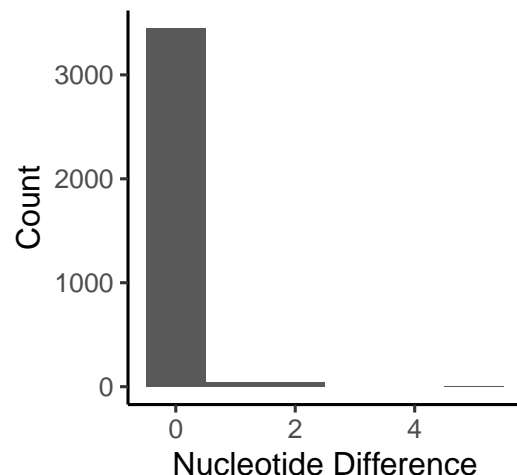
TRBV10-2*ap01

2276 sequences assigned
2253 (99%) exact matches, in which:
2211 unique CDR3
13 unique J



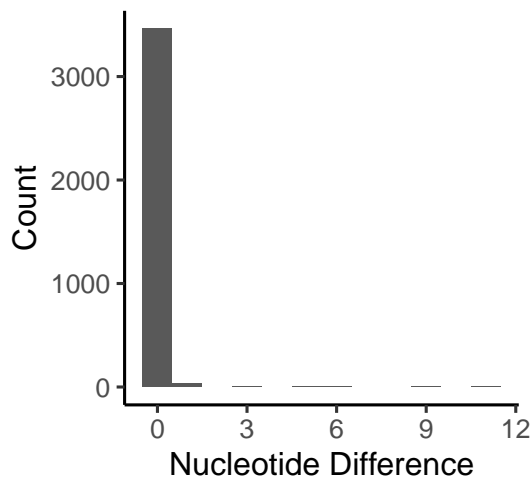
TRBV13*ap01

3538 sequences assigned
3447 (97.4%) exact matches, in which:
3319 unique CDR3
13 unique J



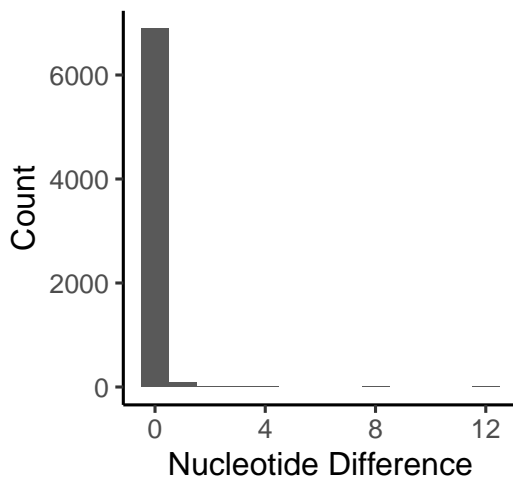
TRBV10-1*ap01

3508 sequences assigned
3462 (98.7%) exact matches, in which:
3361 unique CDR3
13 unique J



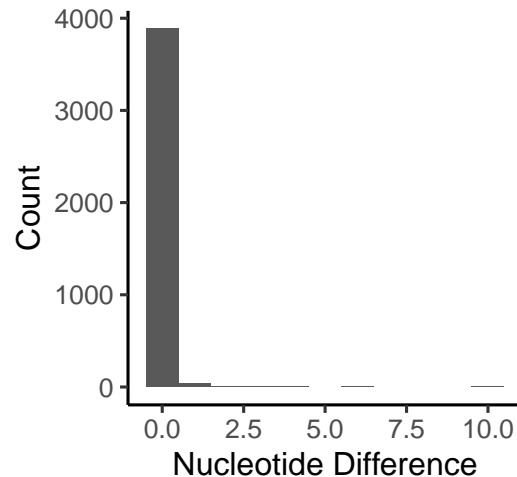
TRBV10-3*ap01

6984 sequences assigned
6890 (98.7%) exact matches, in which:
6741 unique CDR3
13 unique J



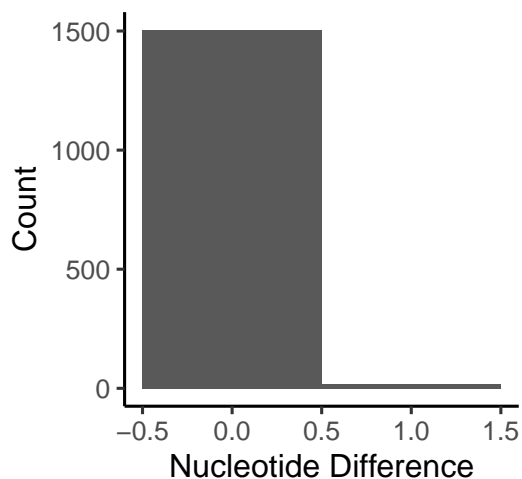
TRBV14*ap01

3938 sequences assigned
3886 (98.7%) exact matches, in which:
3814 unique CDR3
13 unique J



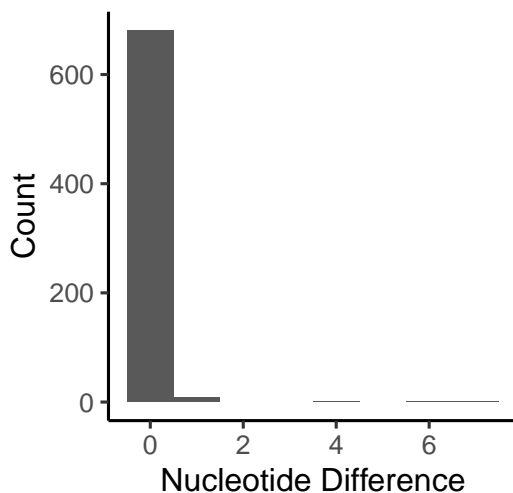
TRBV20-1*ap02

1521 sequences assigned
1504 (98.9%) exact matches, in which:
1473 unique CDR3
13 unique J



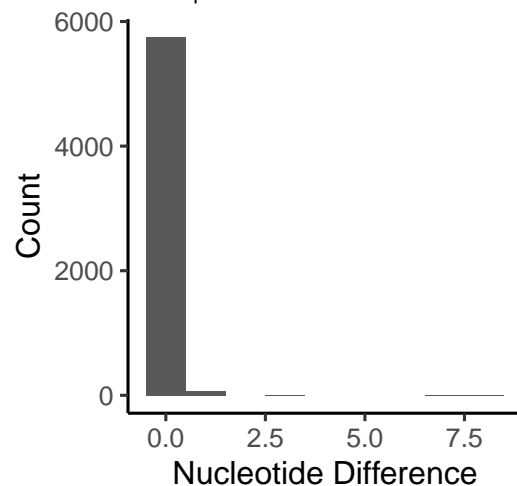
TRBV1*ap01

693 sequences assigned
681 (98.3%) exact matches, in which:
658 unique CDR3
13 unique J



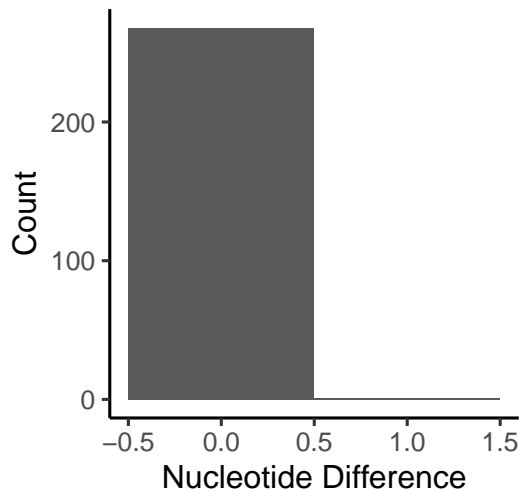
TRBV15*ap02

5824 sequences assigned
5751 (98.7%) exact matches, in which:
5613 unique CDR3
13 unique J



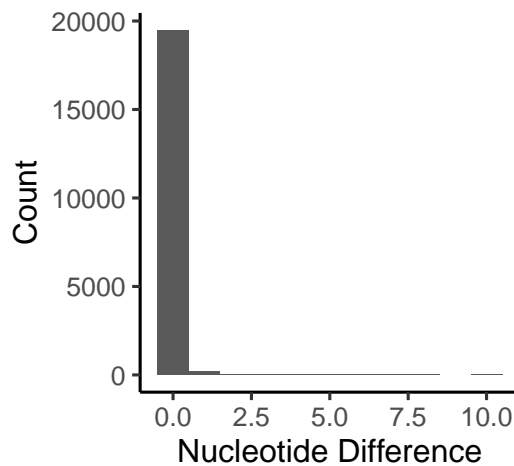
TRBV16*ap01

269 sequences assigned
268 (99.6%) exact matches, in which:
267 unique CDR3
13 unique J



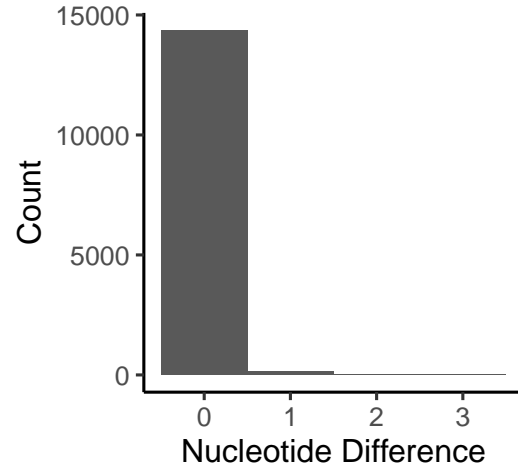
TRBV19*ap01

19714 sequences assigned
19484 (98.8%) exact matches, in which:
19272 unique CDR3
14 unique J



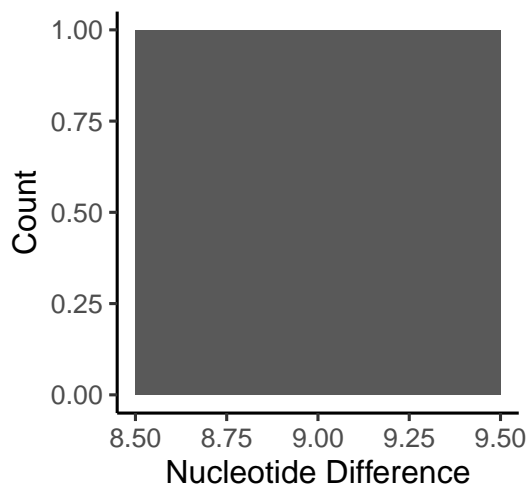
TRBV28*ap01

14517 sequences assigned
14367 (99%) exact matches, in which:
14135 unique CDR3
13 unique J



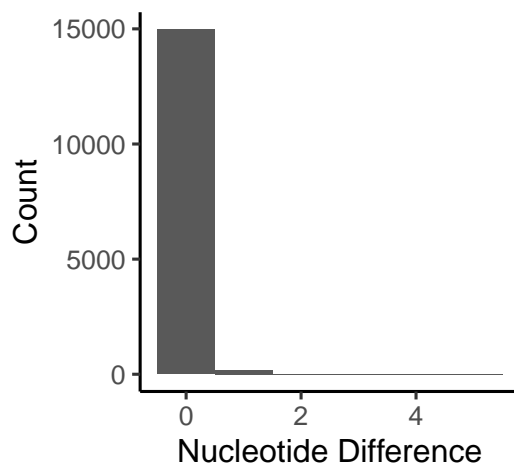
TRBV17*ap01

1 sequences assigned
No exact matches.



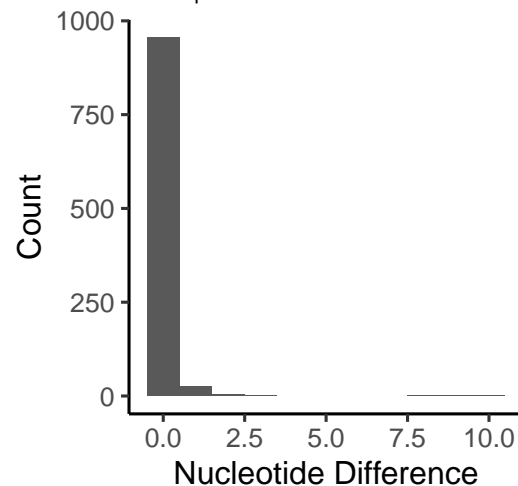
TRBV2*ap01

15186 sequences assigned
14974 (98.6%) exact matches, in which:
14581 unique CDR3
13 unique J



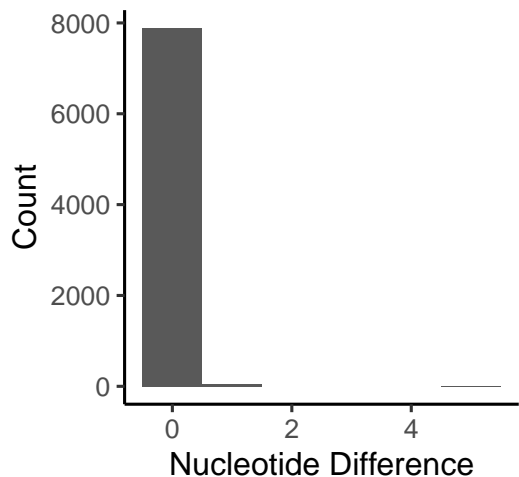
TRBV30*ap02

987 sequences assigned
955 (96.8%) exact matches, in which:
941 unique CDR3
13 unique J



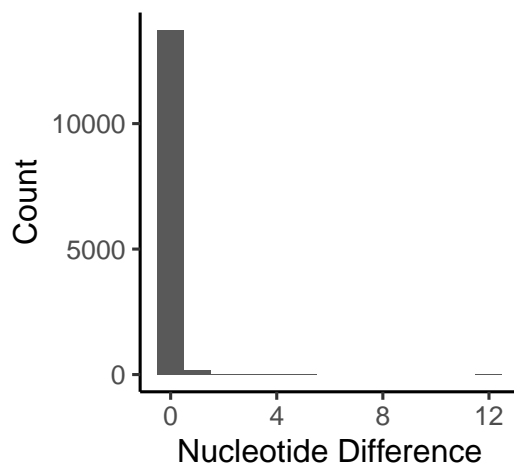
TRBV18*ap01

7940 sequences assigned
7887 (99.3%) exact matches, in which:
7782 unique CDR3
13 unique J



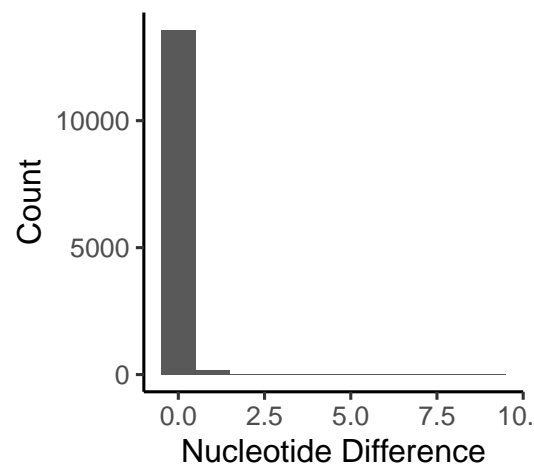
TRBV27*ap01

13956 sequences assigned
13738 (98.4%) exact matches, in which:
13374 unique CDR3
13 unique J



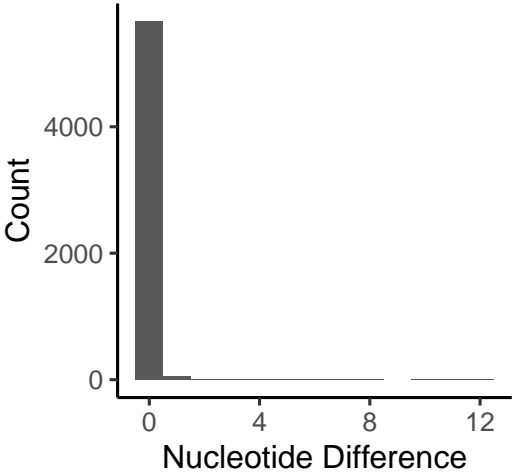
TRBV9*ap01

13758 sequences assigned
13580 (98.7%) exact matches, in which:
13275 unique CDR3
13 unique J



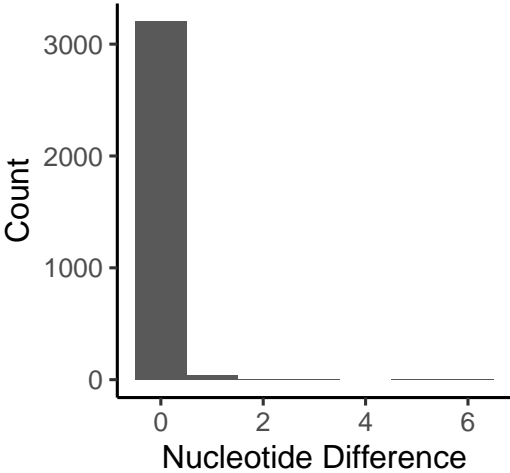
TRBV21-1*ap01

5751 sequences assigned
5666 (98.5%) exact matches, in which:
5583 unique CDR3
14 unique J



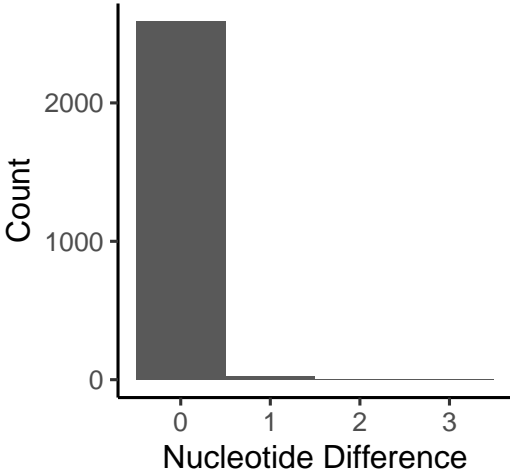
TRBV11-3*ap01

3246 sequences assigned
3203 (98.7%) exact matches, in which:
3165 unique CDR3
13 unique J



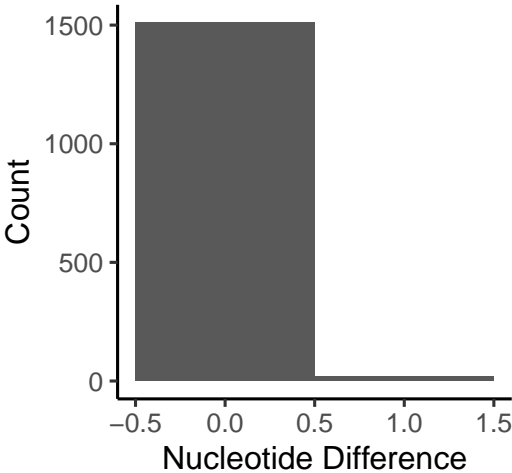
TRBV12-5*ap01

2620 sequences assigned
2589 (98.8%) exact matches, in which:
2531 unique CDR3
13 unique J



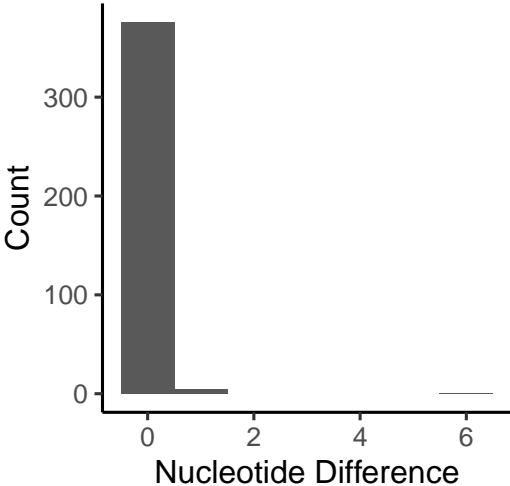
TRBV11-1*ap01

1527 sequences assigned
1510 (98.9%) exact matches, in which:
1486 unique CDR3
13 unique J



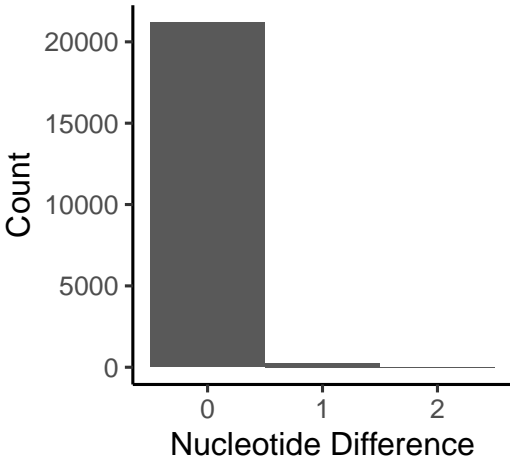
TRBV12-1*ap01

382 sequences assigned
376 (98.4%) exact matches, in which:
369 unique CDR3
13 unique J



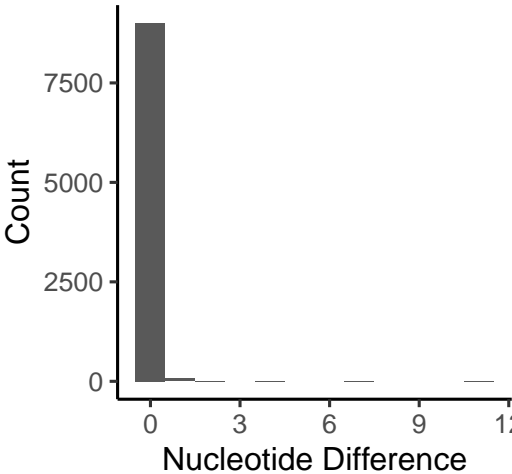
TRBV12-34*ap01

21447 sequences assigned
21190 (98.8%) exact matches, in which:
20745 unique CDR3
13 unique J



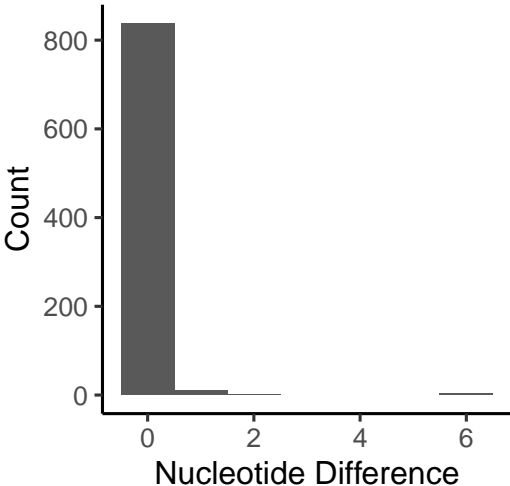
TRBV11-2*ap01

9087 sequences assigned
9005 (99.1%) exact matches, in which:
8888 unique CDR3
13 unique J



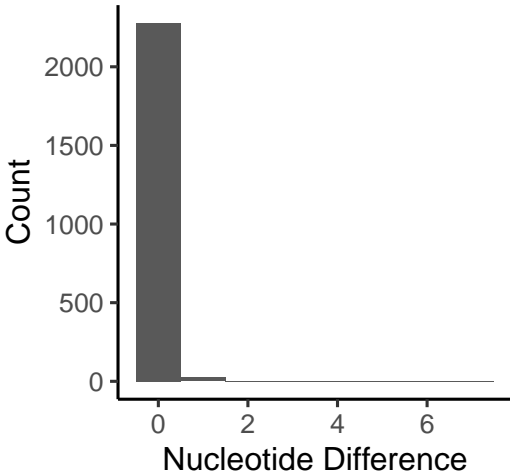
TRBV12-2*ap01

853 sequences assigned
838 (98.2%) exact matches, in which:
820 unique CDR3
13 unique J



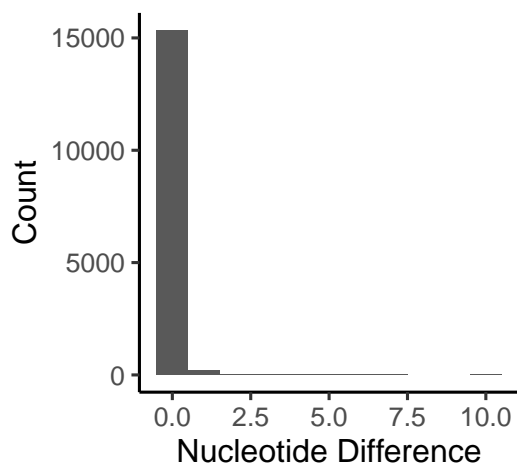
TRBV23-1*ap01

2311 sequences assigned
2278 (98.6%) exact matches, in which:
2235 unique CDR3
13 unique J



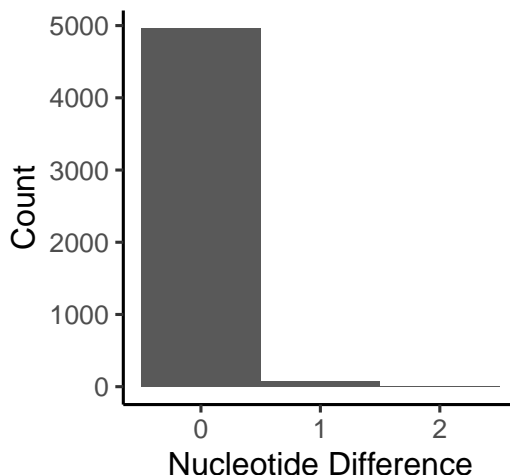
TRBV3-12*ap01

15569 sequences assigned
15346 (98.6%) exact matches, in which:
14980 unique CDR3
13 unique J



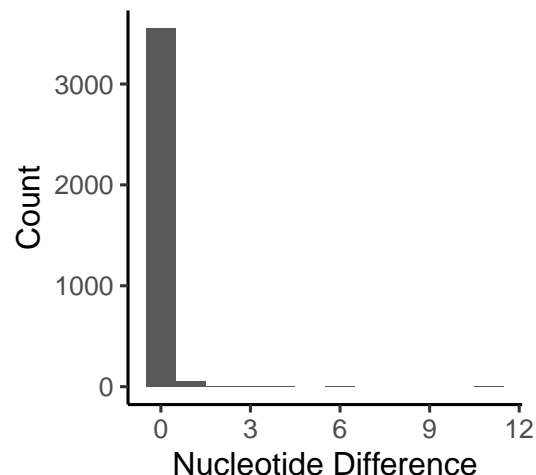
TRBV4-2*ap01

5039 sequences assigned
4961 (98.5%) exact matches, in which:
4824 unique CDR3
13 unique J



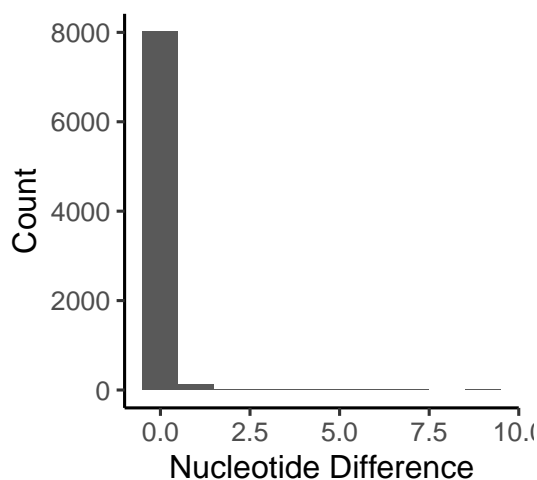
TRBV25-1*ap01

3610 sequences assigned
3551 (98.4%) exact matches, in which:
3448 unique CDR3
13 unique J



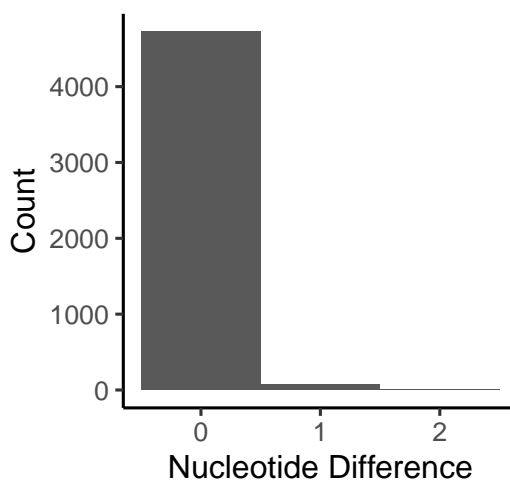
TRBV24-1*ap01

8162 sequences assigned
8014 (98.2%) exact matches, in which:
7829 unique CDR3
13 unique J



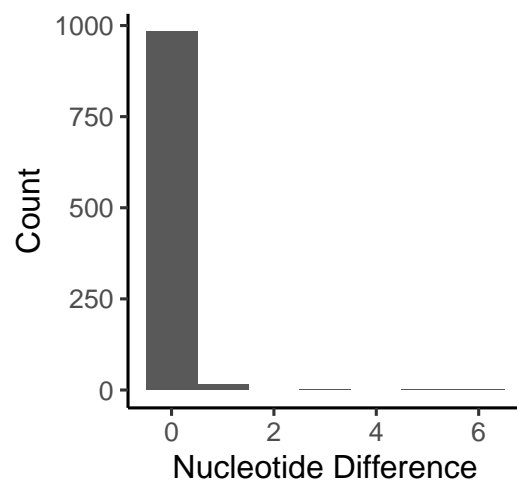
TRBV4-3*ap01

4793 sequences assigned
4724 (98.6%) exact matches, in which:
4608 unique CDR3
13 unique J



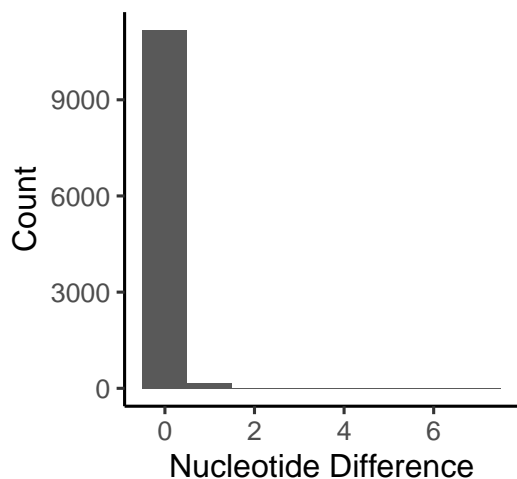
TRBV5-3*ap01

1002 sequences assigned
983 (98.1%) exact matches, in which:
958 unique CDR3
13 unique J



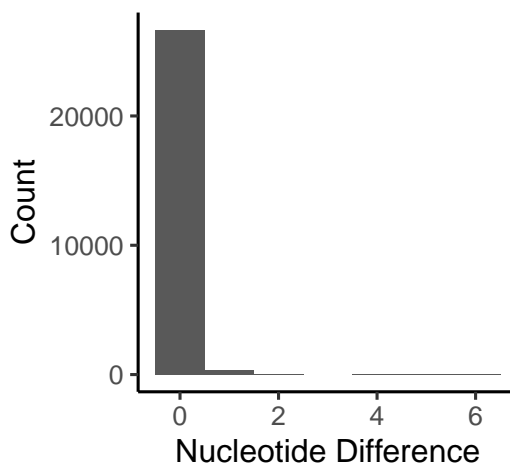
TRBV4-1*ap01

11346 sequences assigned
11175 (98.5%) exact matches, in which:
10885 unique CDR3
13 unique J



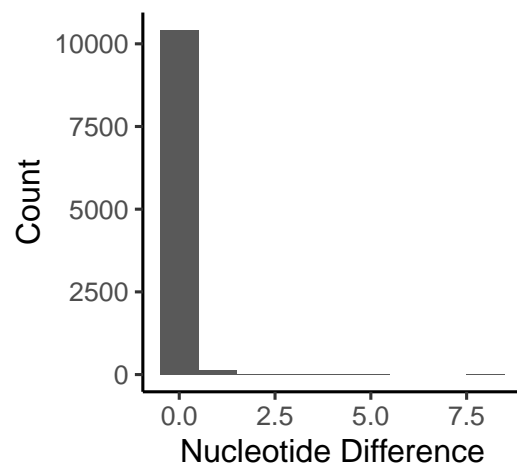
TRBV5-1*ap01

27043 sequences assigned
26663 (98.6%) exact matches, in which:
25925 unique CDR3
13 unique J



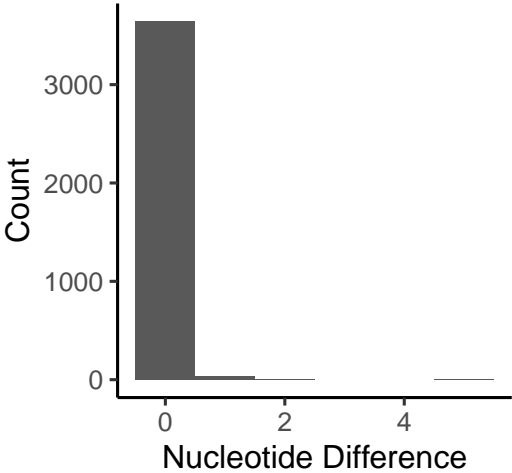
TRBV5-4*ap01

10574 sequences assigned
10424 (98.6%) exact matches, in which:
10166 unique CDR3
13 unique J



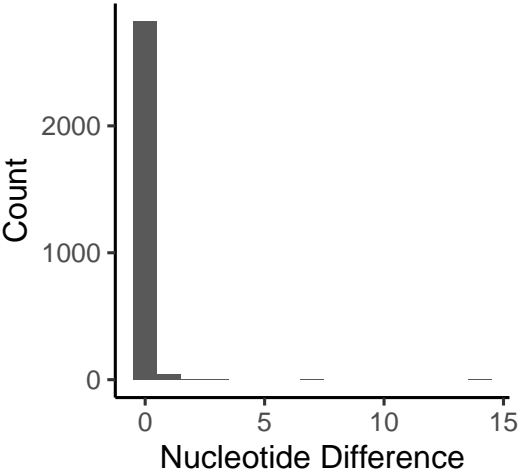
TRBV5-5*ap01

3680 sequences assigned
3643 (99%) exact matches, in which:
3599 unique CDR3
13 unique J



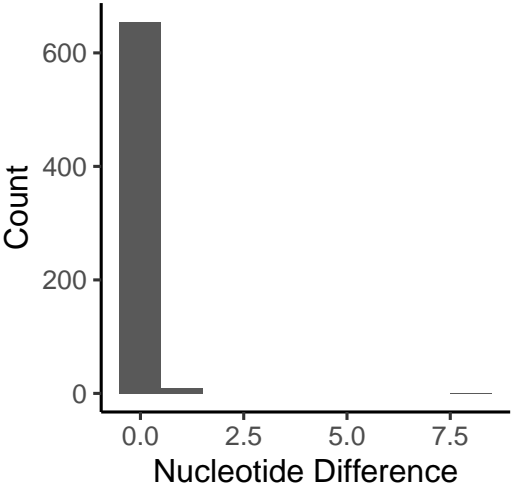
TRBV5-8*ap01

2875 sequences assigned
2823 (98.2%) exact matches, in which:
2781 unique CDR3
13 unique J



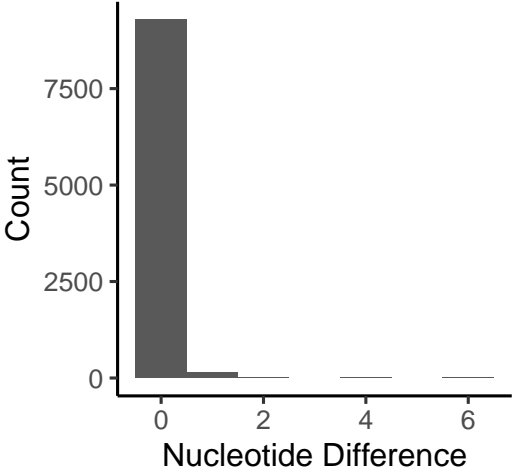
TRBV6-7*ap01

666 sequences assigned
655 (98.3%) exact matches, in which:
641 unique CDR3
13 unique J



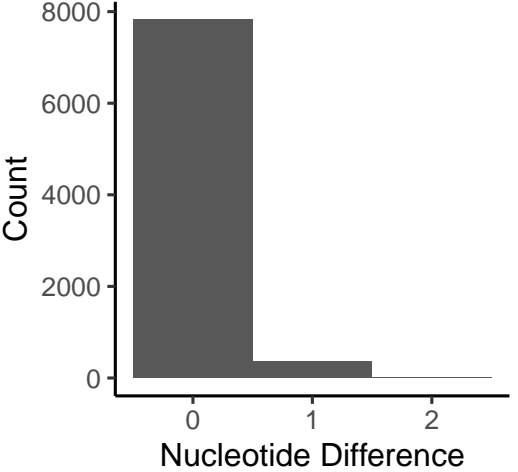
TRBV5-6*ap01

9426 sequences assigned
9285 (98.5%) exact matches, in which:
8951 unique CDR3
13 unique J



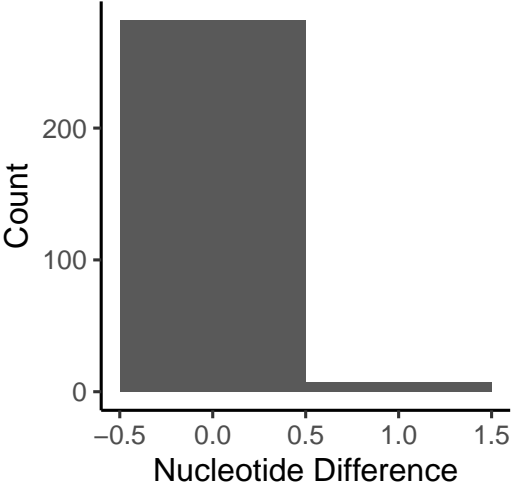
TRBV6-1*ap01

8196 sequences assigned
7823 (95.4%) exact matches, in which:
7604 unique CDR3
13 unique J



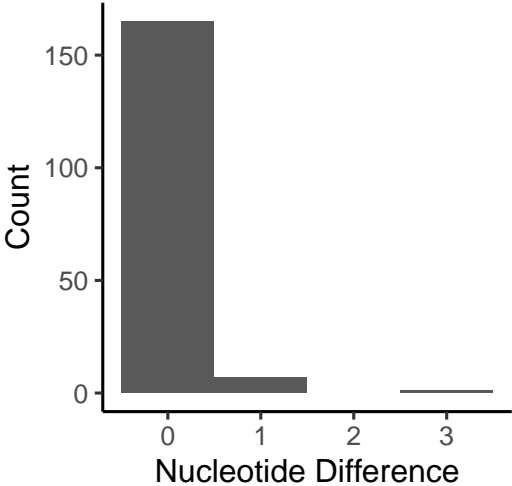
TRBV6-8*ap01

289 sequences assigned
282 (97.6%) exact matches, in which:
276 unique CDR3
13 unique J



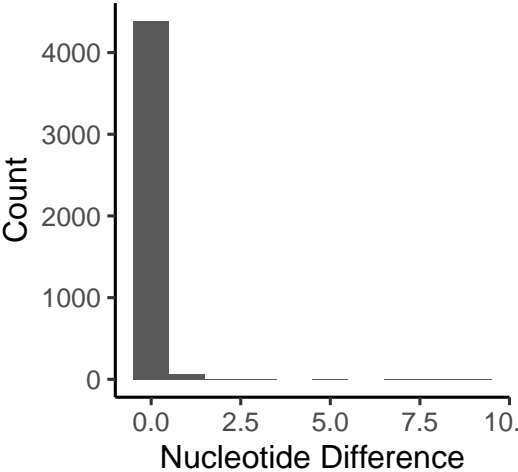
TRBV5-7*ap01

173 sequences assigned
165 (95.4%) exact matches, in which:
162 unique CDR3
13 unique J



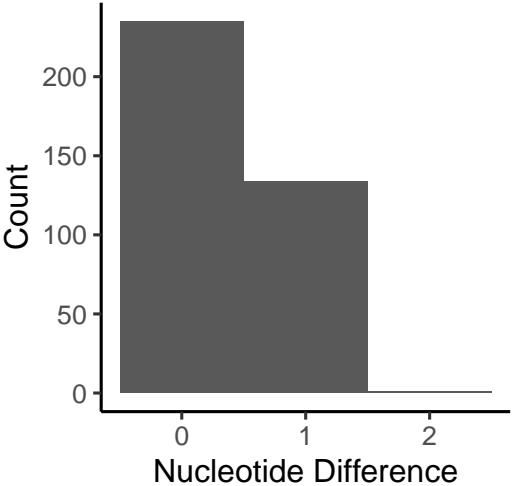
TRBV6-4*ap01

4466 sequences assigned
4386 (98.2%) exact matches, in which:
4308 unique CDR3
13 unique J



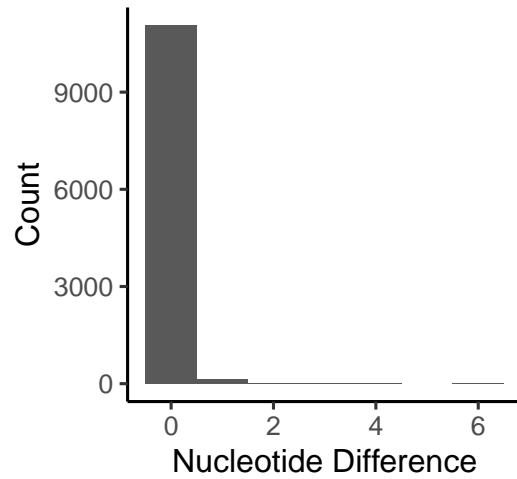
TRBV6-9*ap01

370 sequences assigned
235 (63.5%) exact matches, in which:
230 unique CDR3
13 unique J



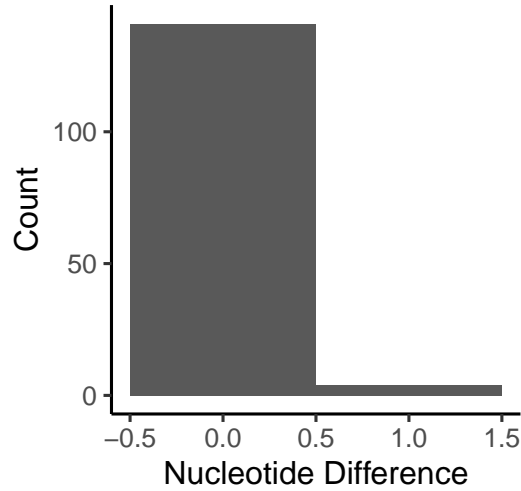
TRBV6-23*ap01

11210 sequences assigned
11060 (98.7%) exact matches, in which:
10728 unique CDR3
13 unique J



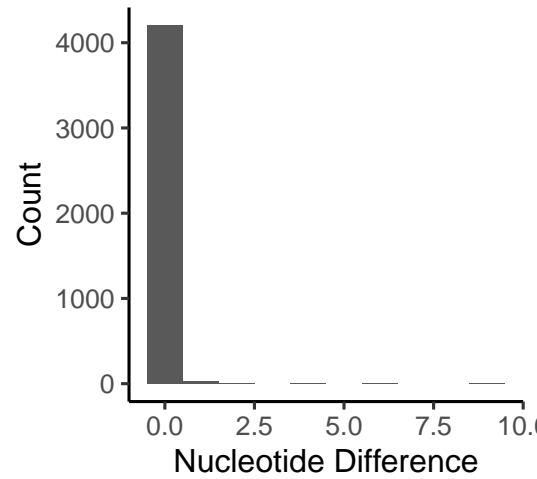
TRBV7-1*ap01_G291C_

145 sequences assigned
141 (97.2%) exact matches, in which:
141 unique CDR3
13 unique J



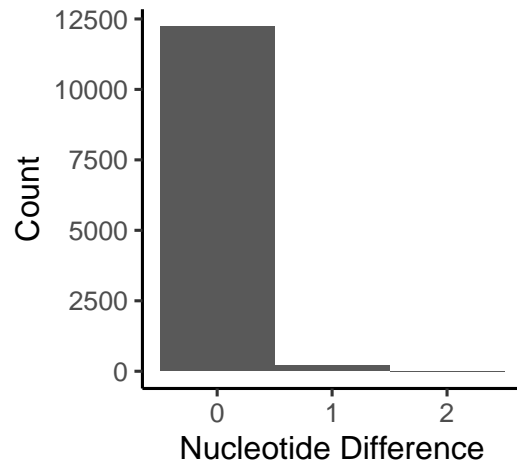
TRBV7-3*ap01

4240 sequences assigned
4203 (99.1%) exact matches, in which:
4135 unique CDR3
13 unique J



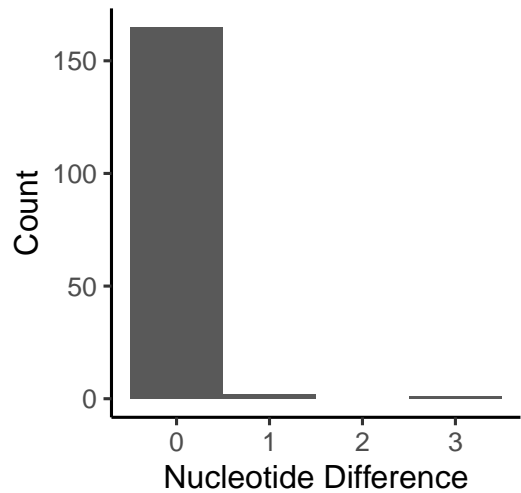
TRBV6-56*ap01

12437 sequences assigned
12233 (98.4%) exact matches, in which:
11871 unique CDR3
13 unique J



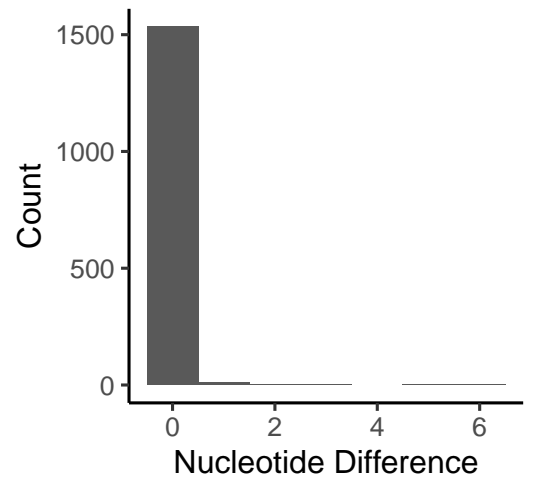
TRBV7-1*ap01_G291C_

168 sequences assigned
165 (98.2%) exact matches, in which:
165 unique CDR3
13 unique J



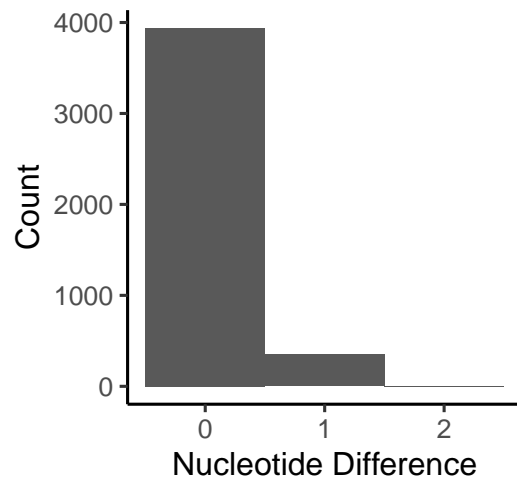
TRBV7-3*ap03

1553 sequences assigned
1534 (98.8%) exact matches, in which:
1504 unique CDR3
13 unique J



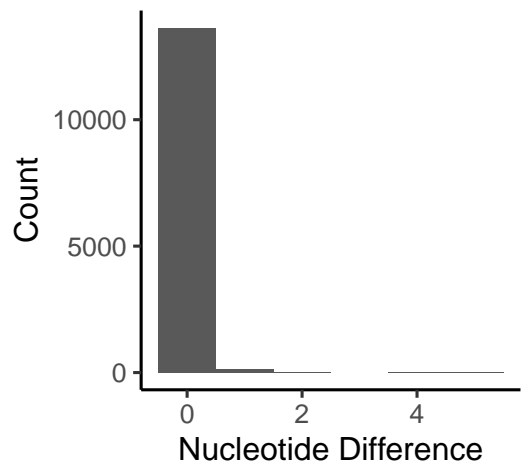
TRBV6-56*ap02

4294 sequences assigned
3939 (91.7%) exact matches, in which:
3834 unique CDR3
13 unique J



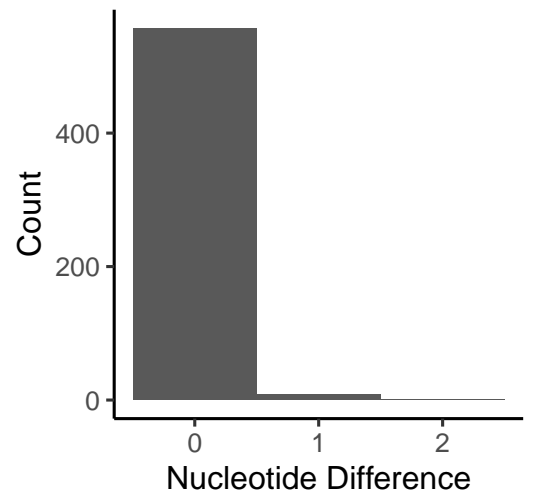
TRBV7-2*ap01

13761 sequences assigned
13634 (99.1%) exact matches, in which:
13409 unique CDR3
13 unique J



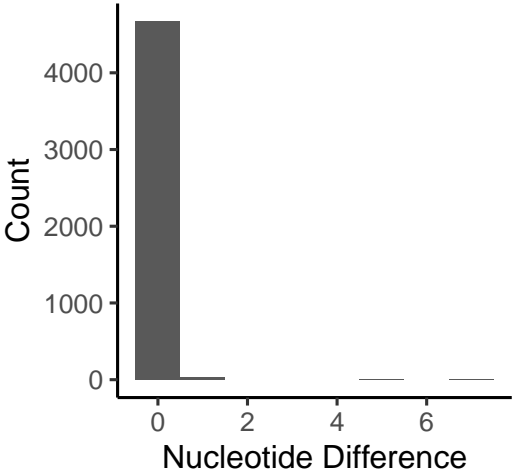
TRBV7-4*ap01

567 sequences assigned
557 (98.2%) exact matches, in which:
543 unique CDR3
13 unique J



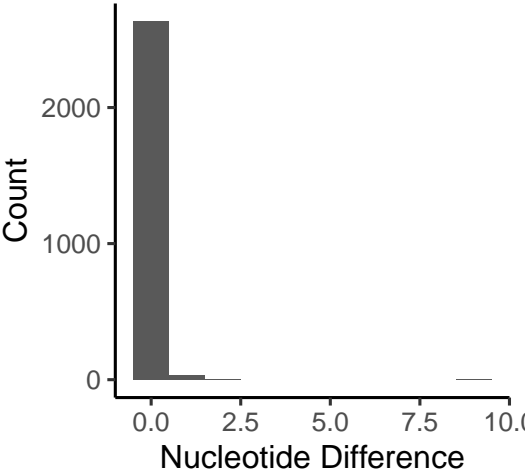
TRBV7-6*ap01

4710 sequences assigned
4670 (99.2%) exact matches, in which:
4555 unique CDR3
13 unique J



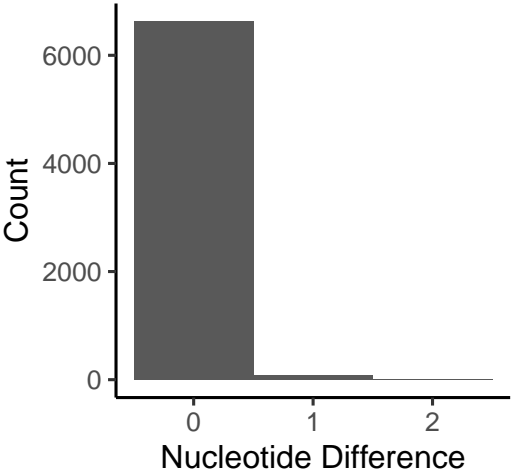
TRBV7-8*ap02

2671 sequences assigned
2633 (98.6%) exact matches, in which:
2587 unique CDR3
13 unique J



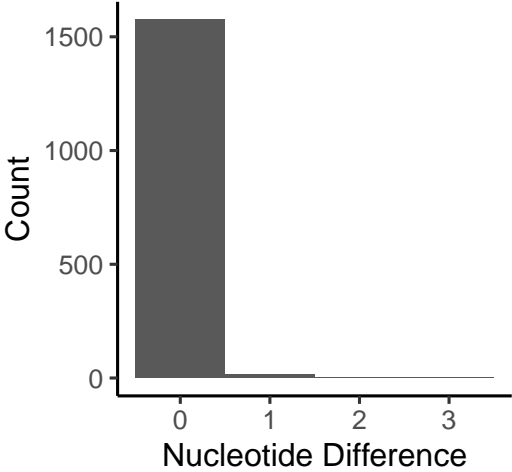
TRBV29-1*ap01

6722 sequences assigned
6627 (98.6%) exact matches, in which:
6436 unique CDR3
13 unique J



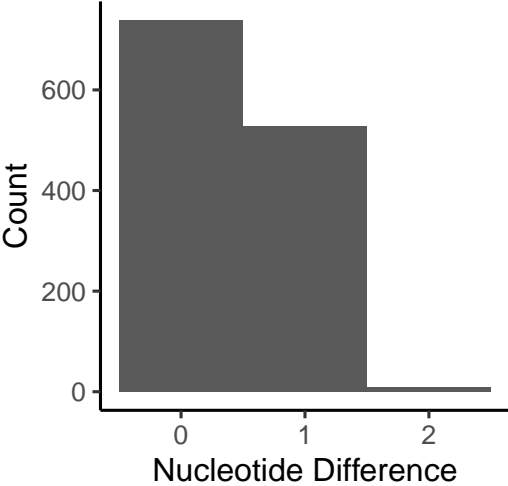
TRBV7-7*ap01

1591 sequences assigned
1575 (99%) exact matches, in which:
1546 unique CDR3
13 unique J



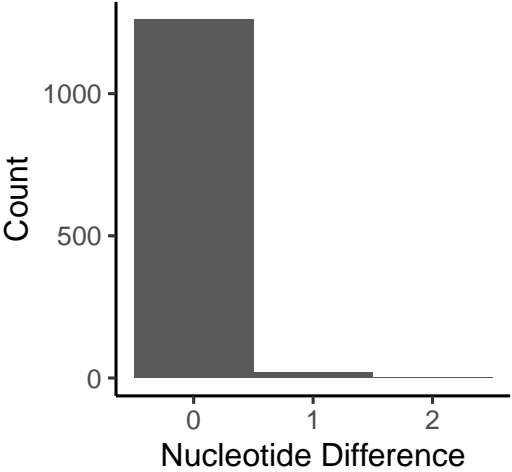
TRBV7-8*ap03

1275 sequences assigned
739 (58%) exact matches, in which:
712 unique CDR3
13 unique J



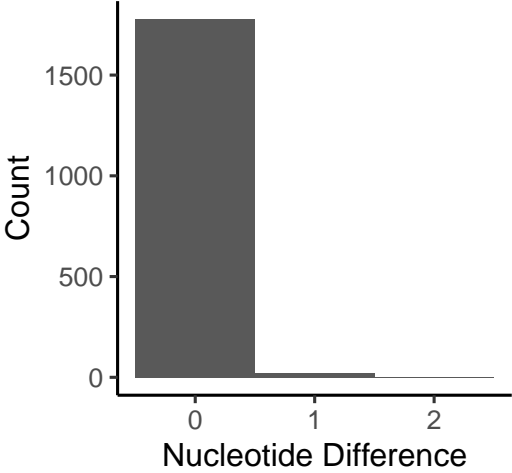
TRBV29-1*ap02

1282 sequences assigned
1260 (98.3%) exact matches, in which:
1229 unique CDR3
13 unique J



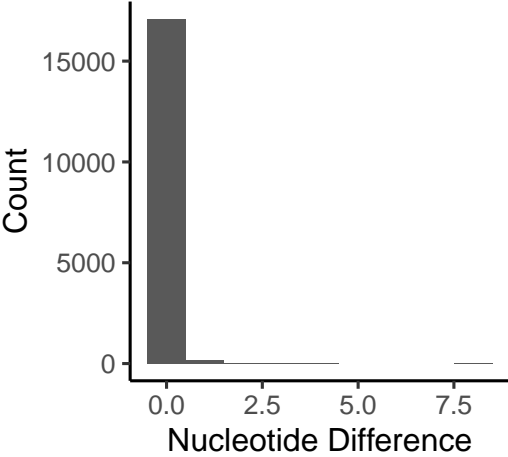
TRBV7-8*ap01

1799 sequences assigned
1778 (98.8%) exact matches, in which:
1721 unique CDR3
13 unique J

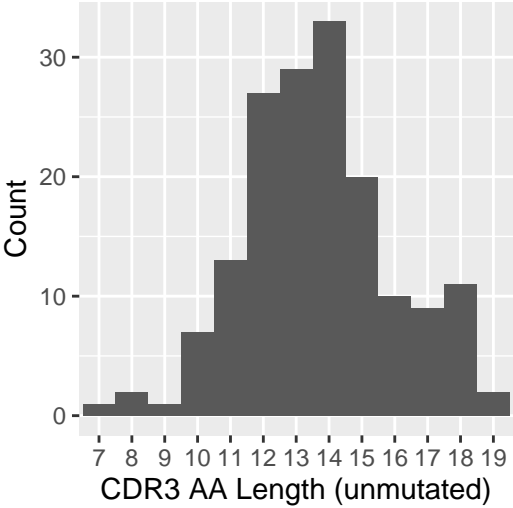


TRBV7-9*ap01

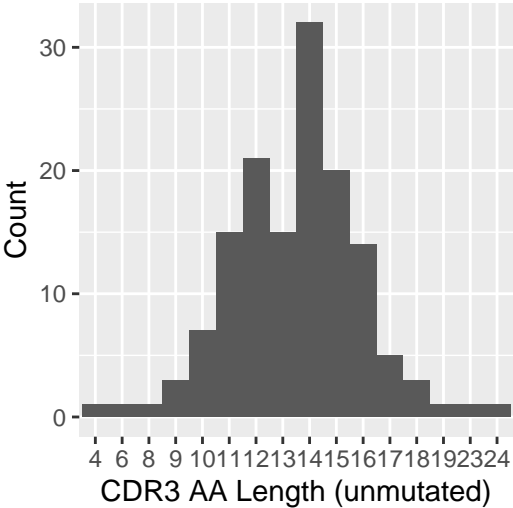
17271 sequences assigned
17099 (99%) exact matches, in which:
16795 unique CDR3
13 unique J



TRBV7-1*ap01_G291C_T296C_C314T



TRBV7-1*ap01_G291C_T296C





Warning – no inferred sequences found.