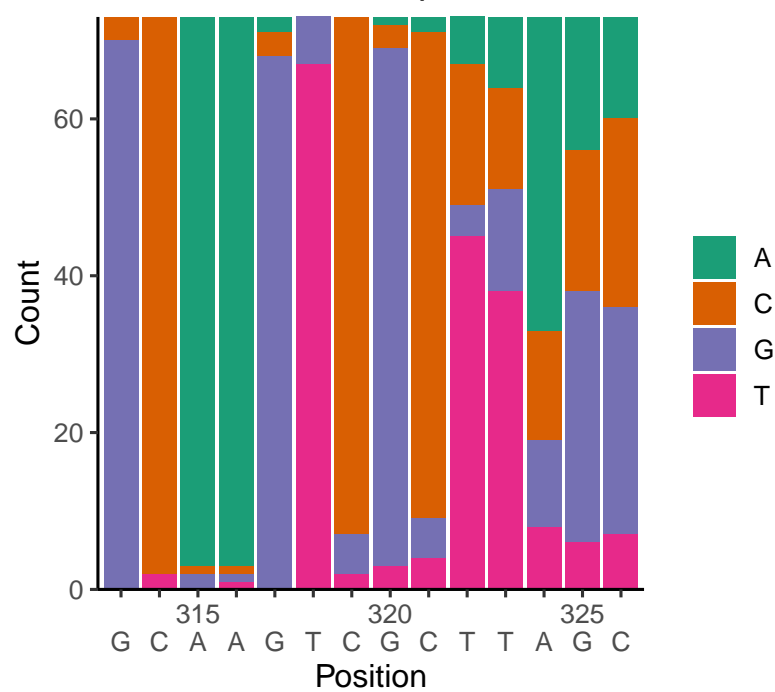
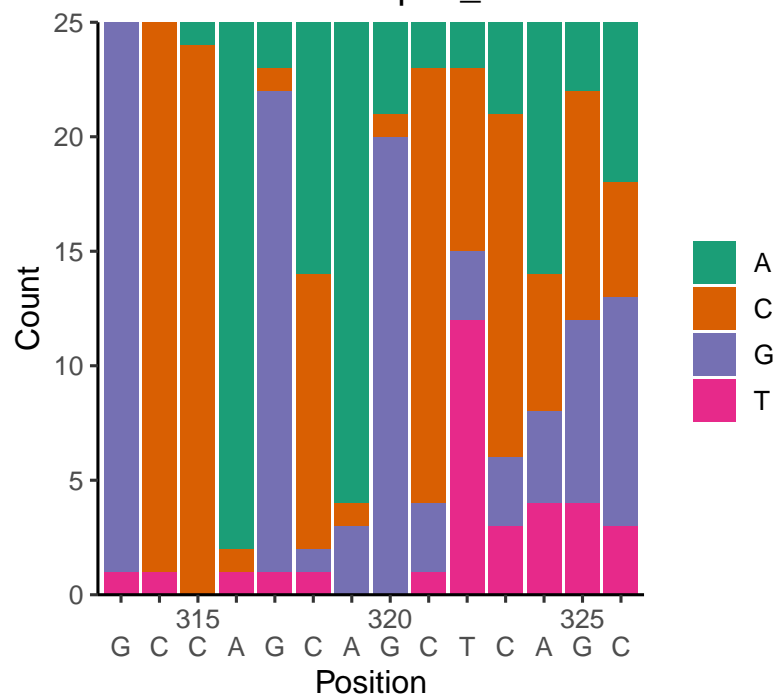


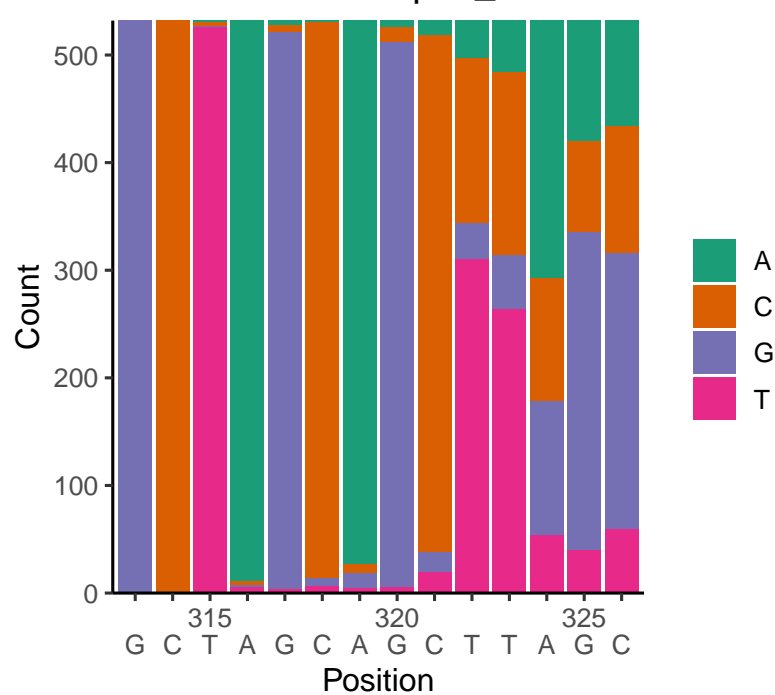
Gene TRBV12-2*ap01_G301A



Gene TRBV7-1*ap01_T296C



Gene TRBV7-7*ap01_C315T



Gene TRBV12-2*ap01_G301A



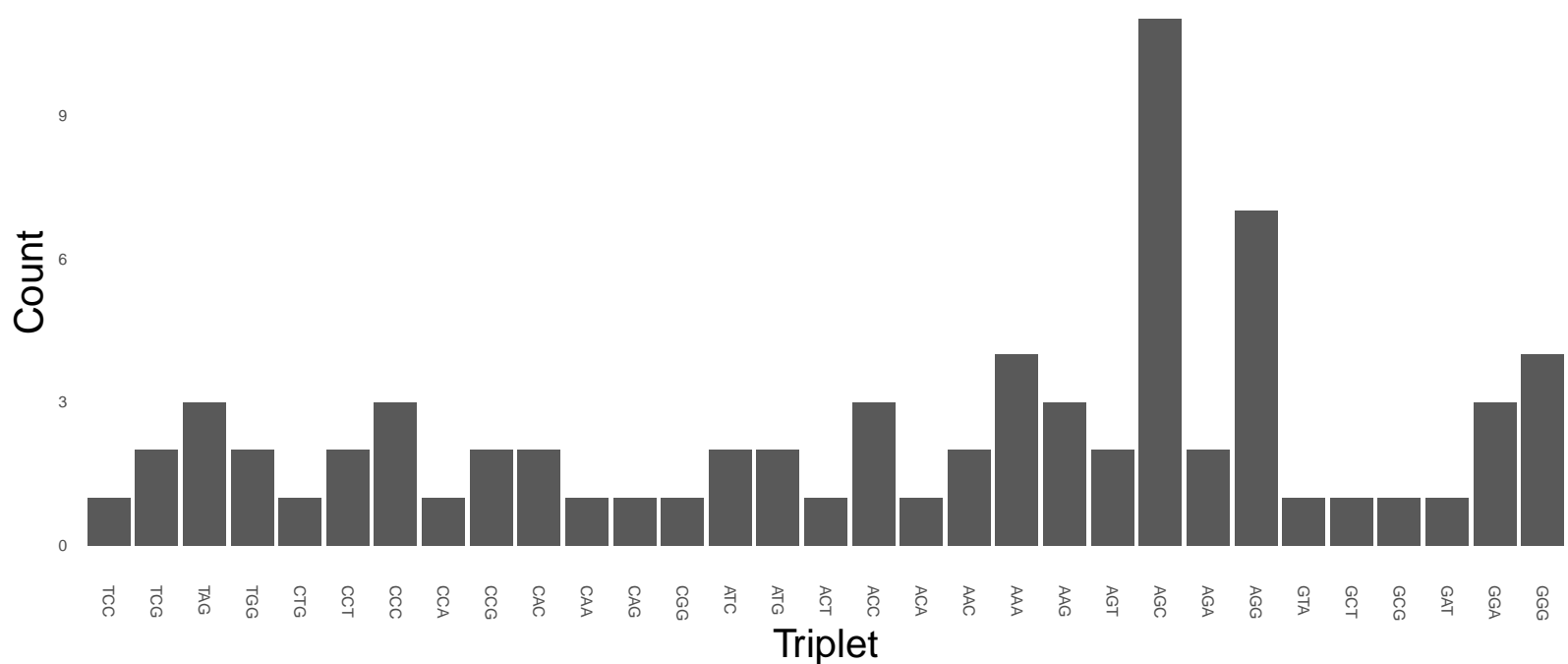
Gene TRBV7-1*ap01_T296C



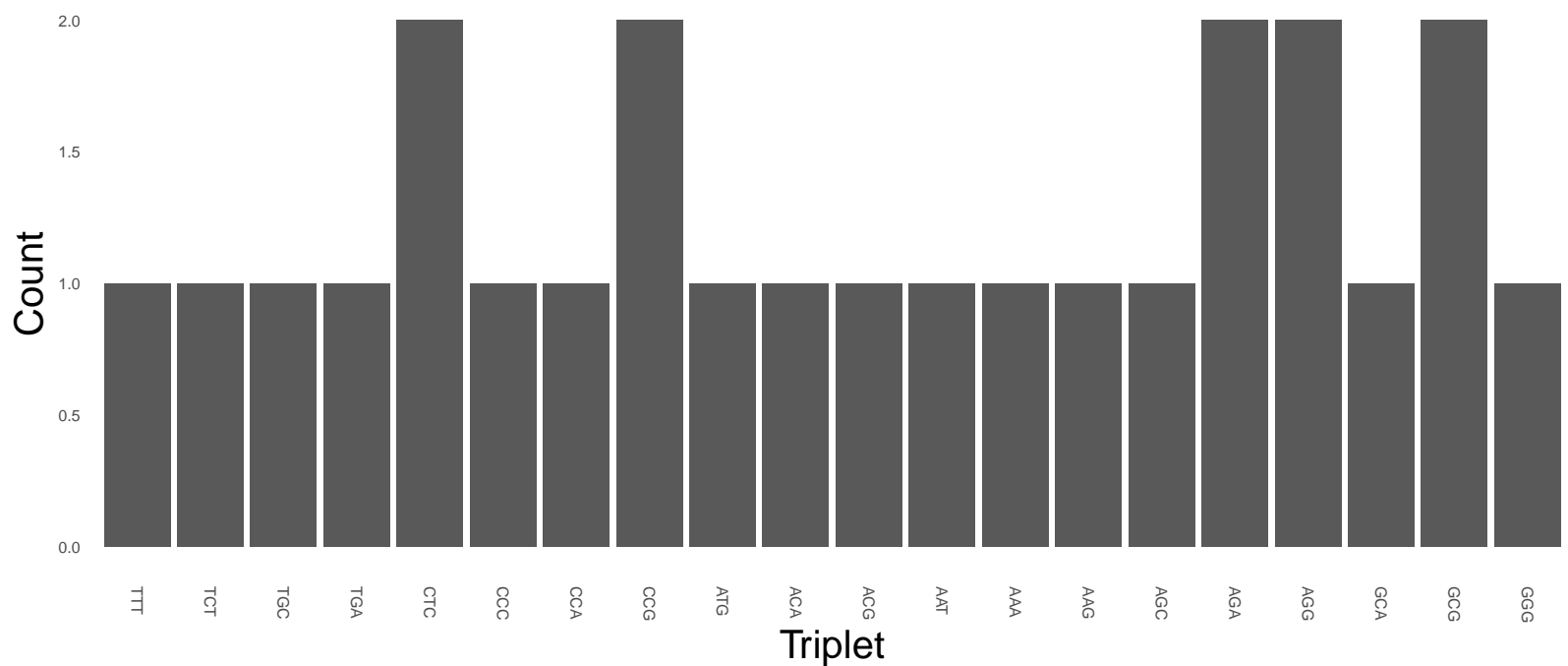
Gene TRBV7-7*ap01_C315T



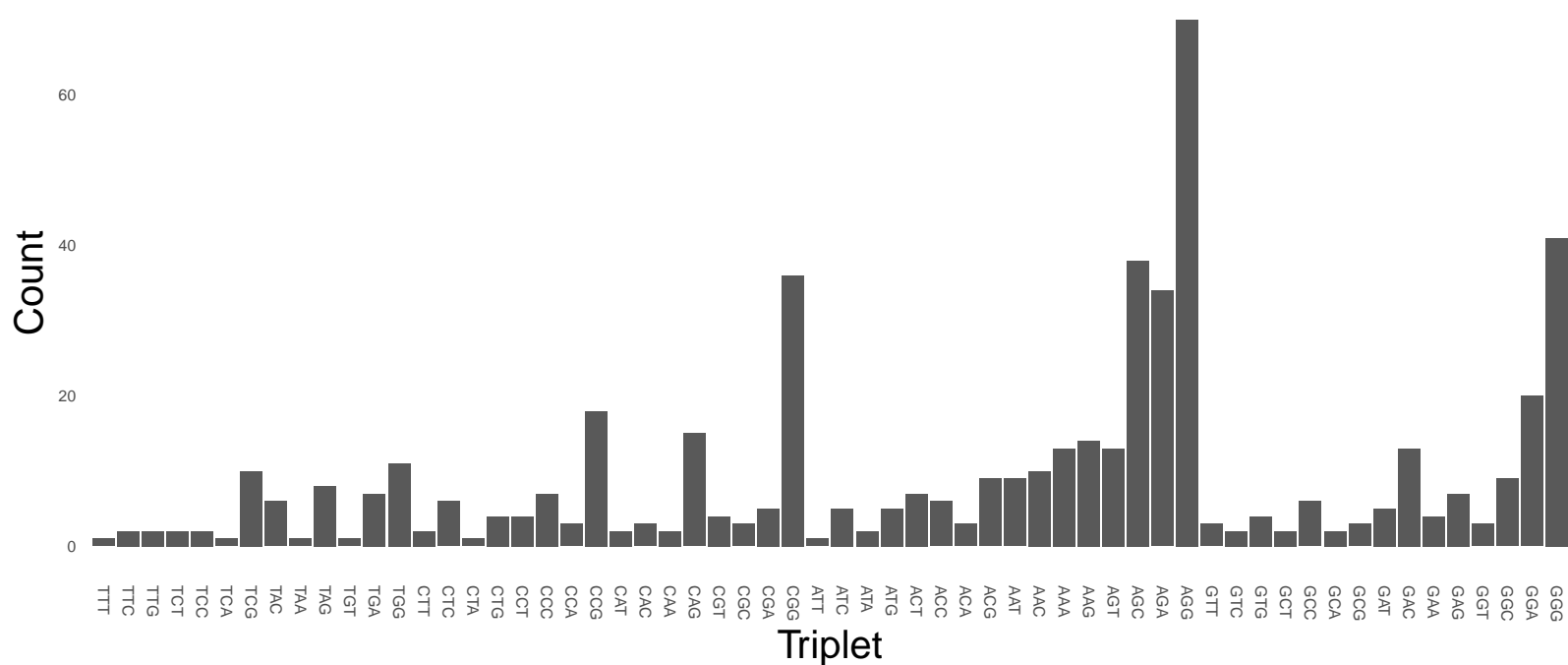
TRBV12-2*ap01_G301A- Final 3 nucleotides as a triplet



TRBV7-1*ap01_T296C- Final 3 nucleotides as a triplet

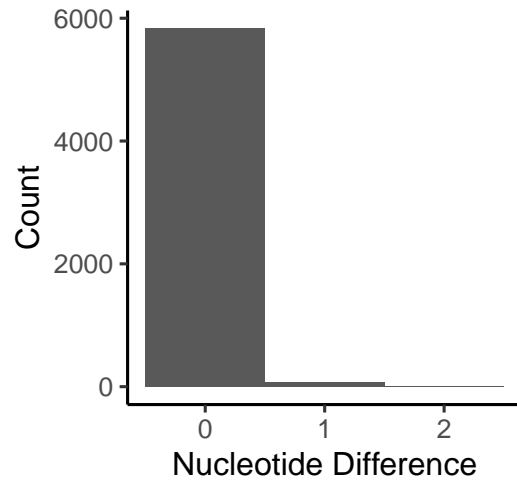


TRBV7-7*ap01_C315T- Final 3 nucleotides as a triplet



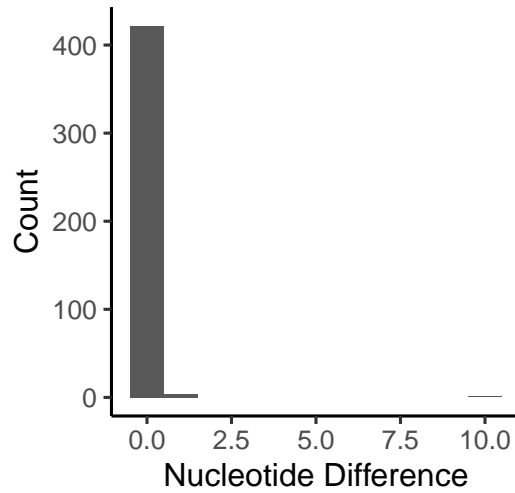
TRBV20-1*ap01

5905 sequences assigned
5834 (98.8%) exact matches, in which:
5734 unique CDR3
13 unique J



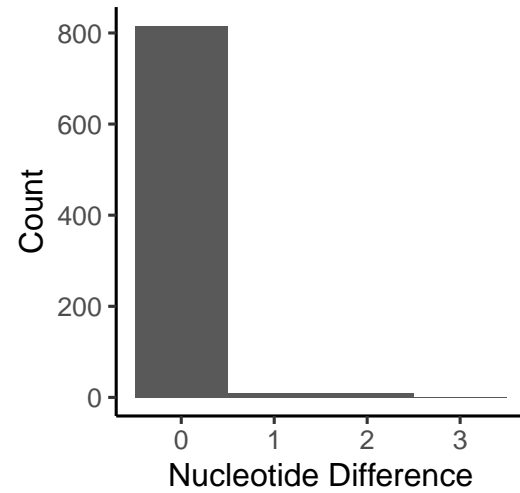
TRBV10-2*ap01

427 sequences assigned
422 (98.8%) exact matches, in which:
418 unique CDR3
13 unique J



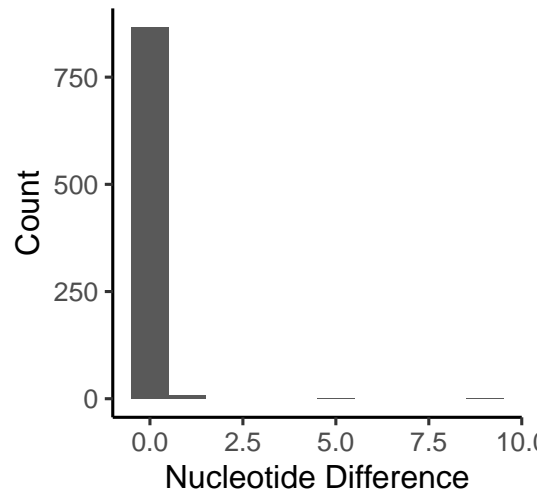
TRBV13*ap01

835 sequences assigned
816 (97.7%) exact matches, in which:
809 unique CDR3
13 unique J



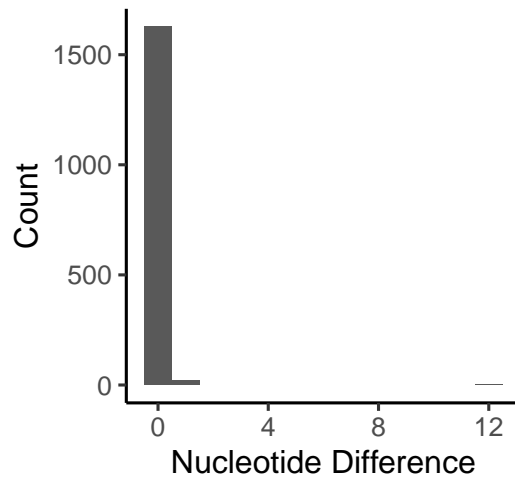
TRBV10-1*ap01

877 sequences assigned
867 (98.9%) exact matches, in which:
863 unique CDR3
13 unique J



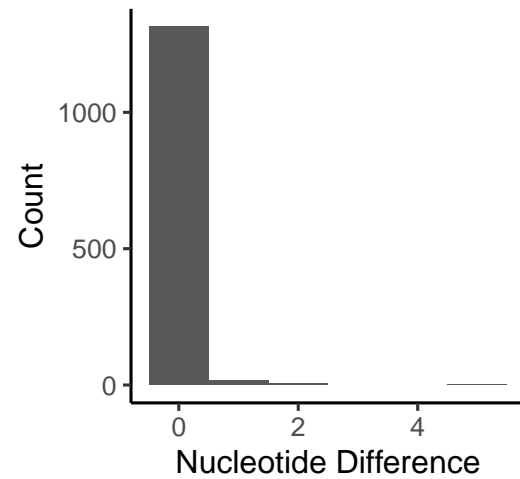
TRBV10-3*ap01

1650 sequences assigned
1627 (98.6%) exact matches, in which:
1613 unique CDR3
13 unique J



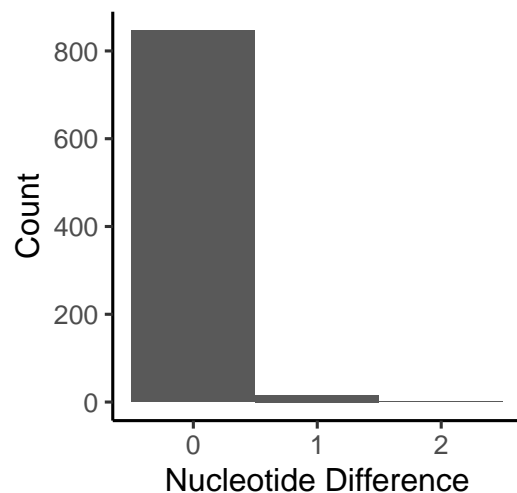
TRBV14*ap01

1336 sequences assigned
1314 (98.4%) exact matches, in which:
1299 unique CDR3
13 unique J



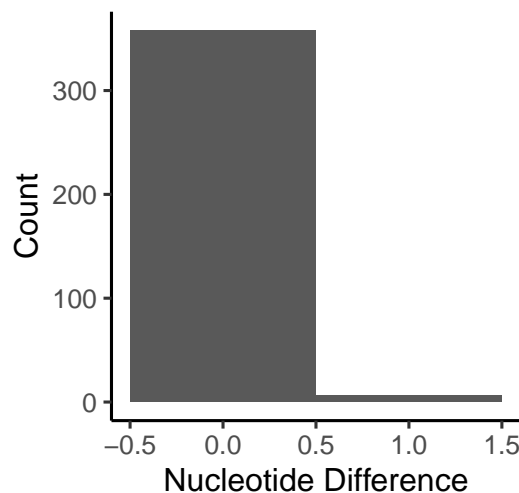
TRBV20-1*ap02

864 sequences assigned
847 (98%) exact matches, in which:
823 unique CDR3
13 unique J



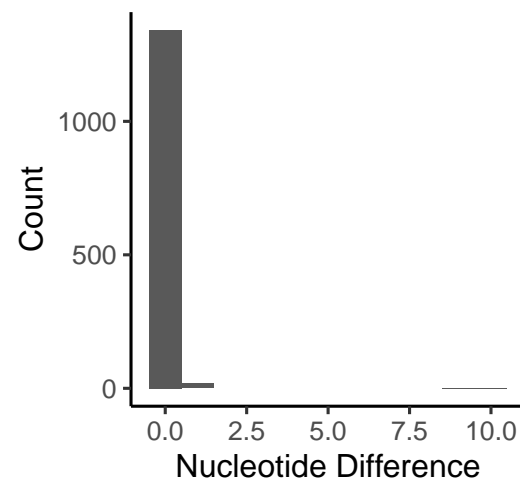
TRBV1*ap01

364 sequences assigned
358 (98.4%) exact matches, in which:
353 unique CDR3
13 unique J



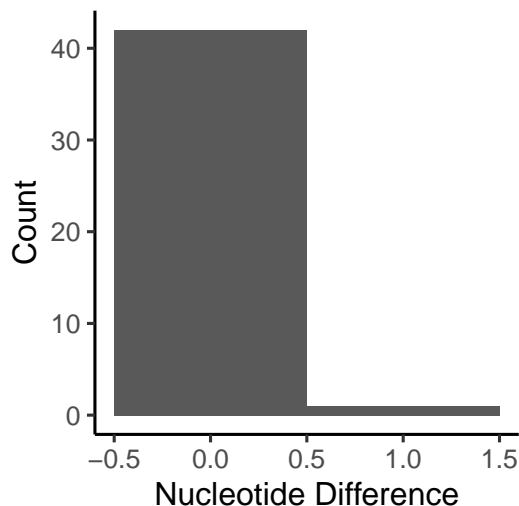
TRBV15*ap02

1363 sequences assigned
1342 (98.5%) exact matches, in which:
1335 unique CDR3
13 unique J



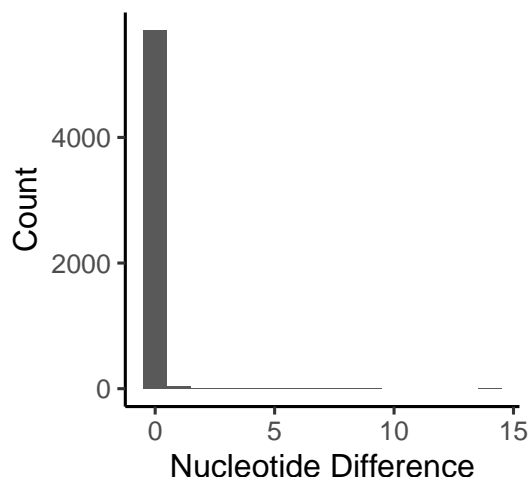
TRBV16*ap01

43 sequences assigned
42 (97.7%) exact matches, in which:
42 unique CDR3
11 unique J



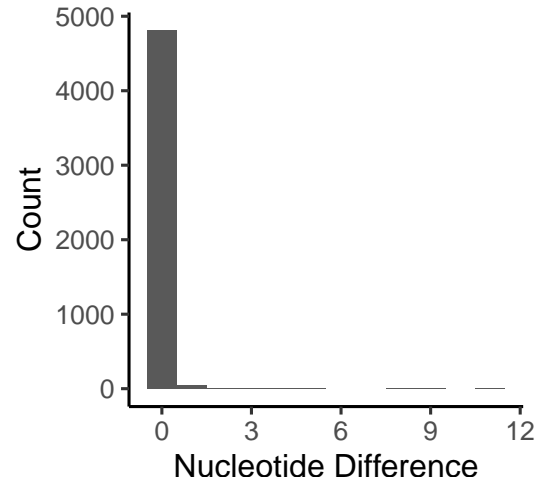
TRBV19*ap01

5760 sequences assigned
5704 (99%) exact matches, in which:
5667 unique CDR3
13 unique J



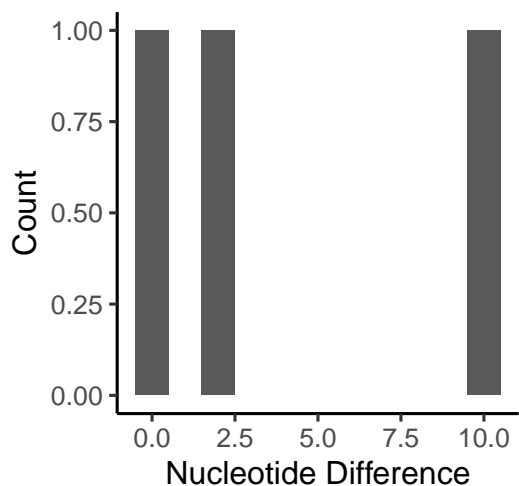
TRBV27*ap01

4865 sequences assigned
4810 (98.9%) exact matches, in which:
4789 unique CDR3
13 unique J



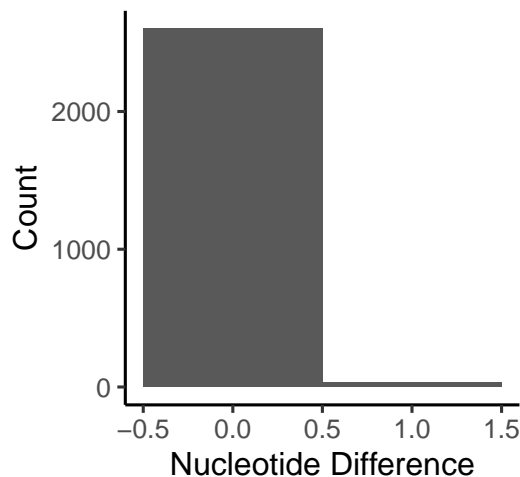
TRBV17*ap01

3 sequences assigned
1 (33.3%) exact matches, in which:
1 unique CDR3
1 unique J



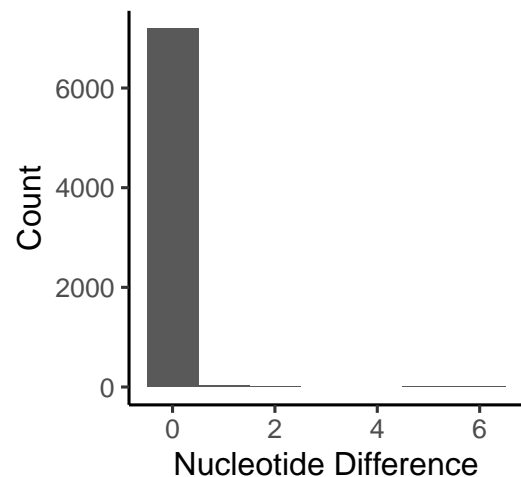
TRBV2*ap01

2632 sequences assigned
2601 (98.8%) exact matches, in which:
2584 unique CDR3
13 unique J



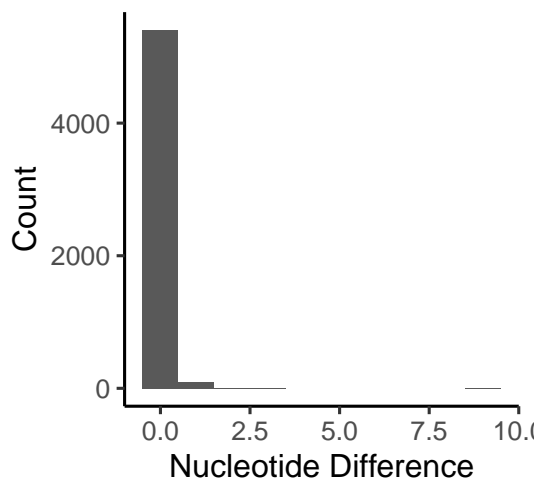
TRBV28*ap01

7233 sequences assigned
7190 (99.4%) exact matches, in which:
7147 unique CDR3
13 unique J



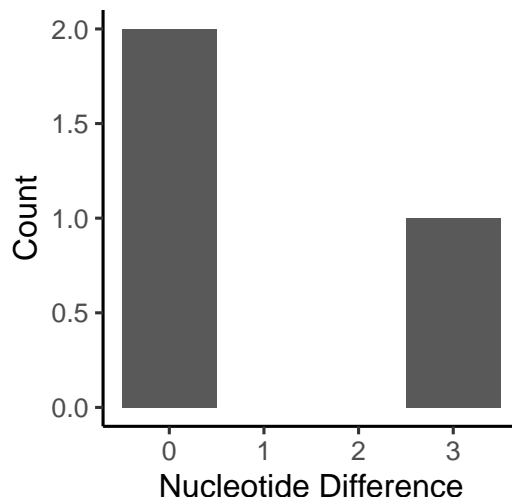
TRBV18*ap01

5501 sequences assigned
5404 (98.2%) exact matches, in which:
5323 unique CDR3
13 unique J



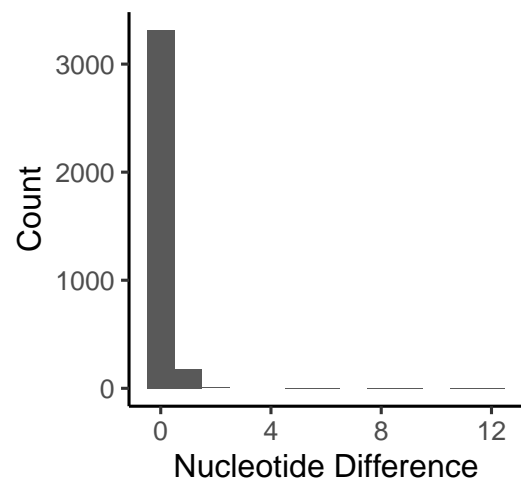
TRBV26*ap01

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



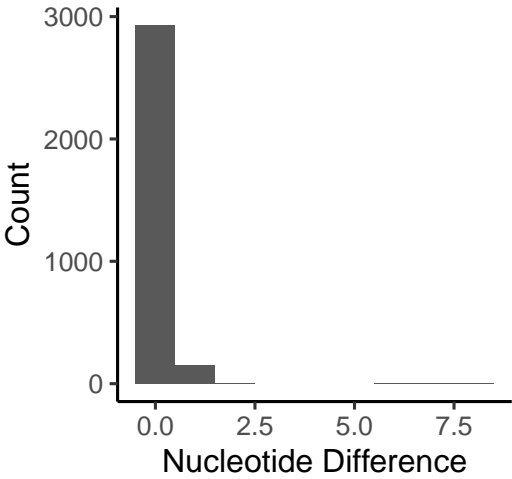
TRBV30*ap01

3509 sequences assigned
3315 (94.5%) exact matches, in which:
3176 unique CDR3
13 unique J



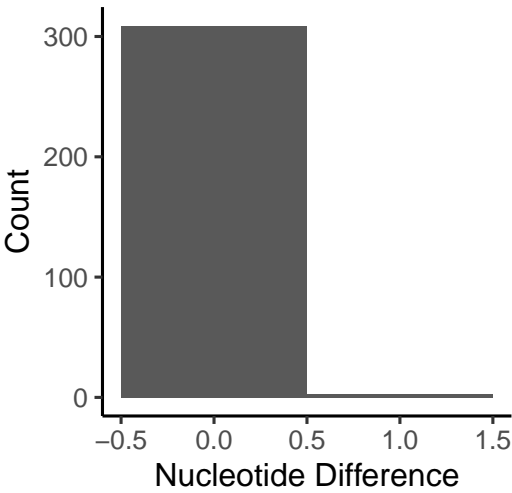
TRBV30*ap02

3088 sequences assigned
2928 (94.8%) exact matches, in which:
2775 unique CDR3
13 unique J



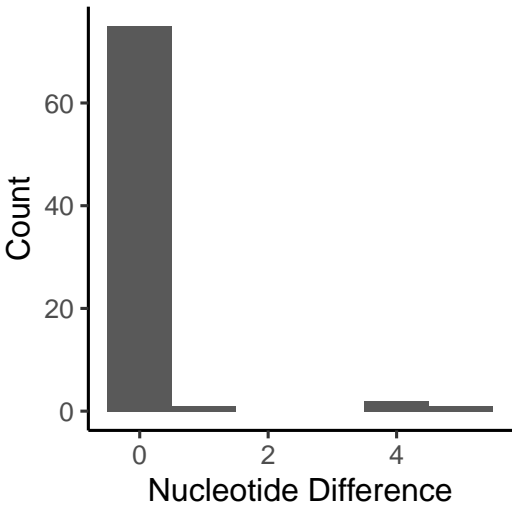
TRBV11-1*ap01

312 sequences assigned
309 (99%) exact matches, in which:
308 unique CDR3
13 unique J



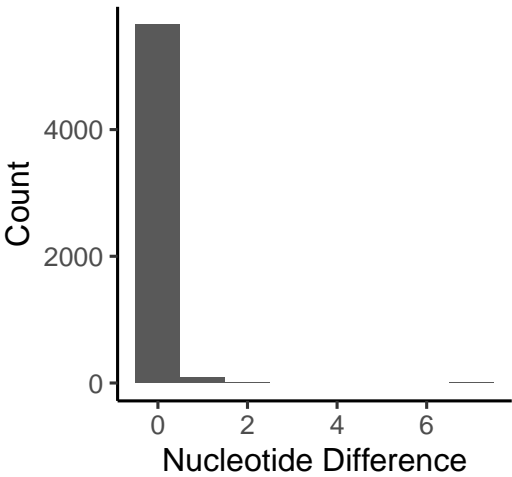
TRBV12-1*ap01

79 sequences assigned
75 (94.9%) exact matches, in which:
75 unique CDR3
13 unique J



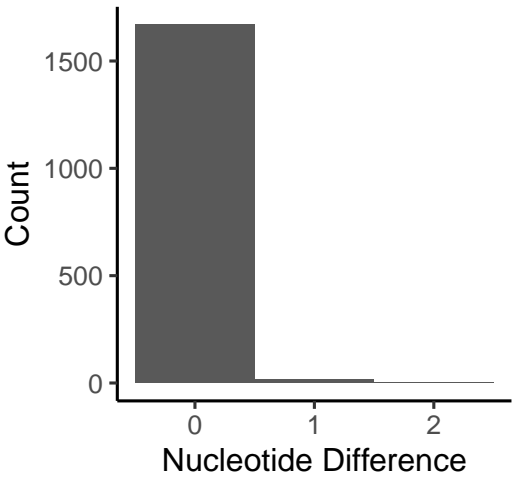
TRBV9*ap01

5747 sequences assigned
5655 (98.4%) exact matches, in which:
5607 unique CDR3
13 unique J



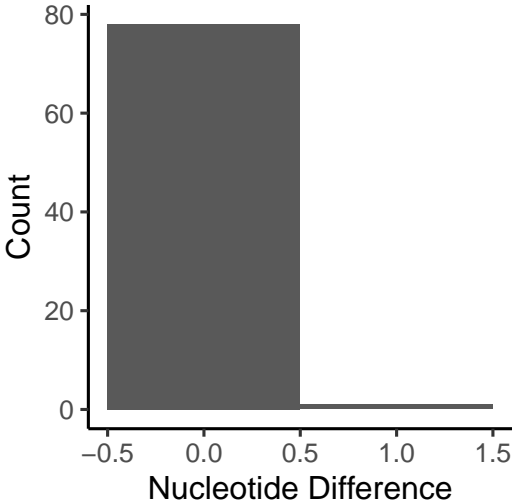
TRBV11-2*ap01

1688 sequences assigned
1669 (98.9%) exact matches, in which:
1662 unique CDR3
13 unique J



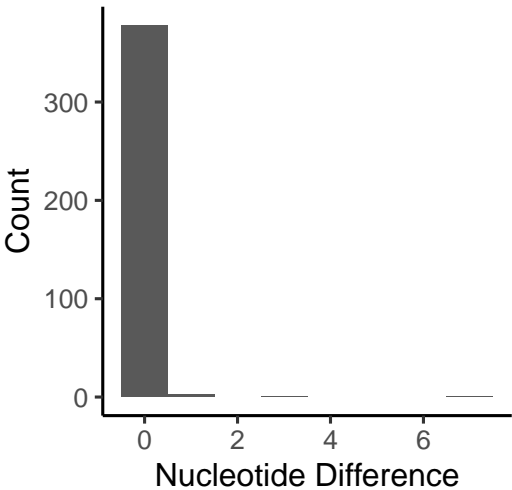
TRBV12-2*ap01

79 sequences assigned
78 (98.7%) exact matches, in which:
76 unique CDR3
13 unique J



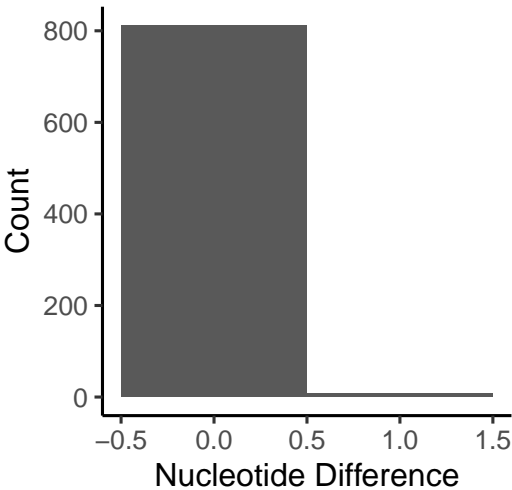
TRBV21-1*ap01

383 sequences assigned
378 (98.7%) exact matches, in which:
375 unique CDR3
13 unique J



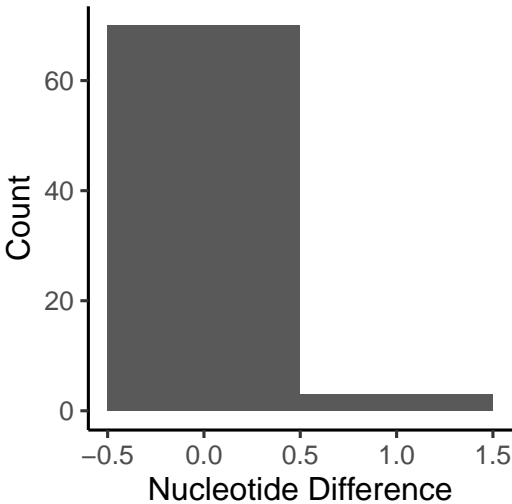
TRBV11-3*ap01

819 sequences assigned
812 (99.1%) exact matches, in which:
809 unique CDR3
13 unique J



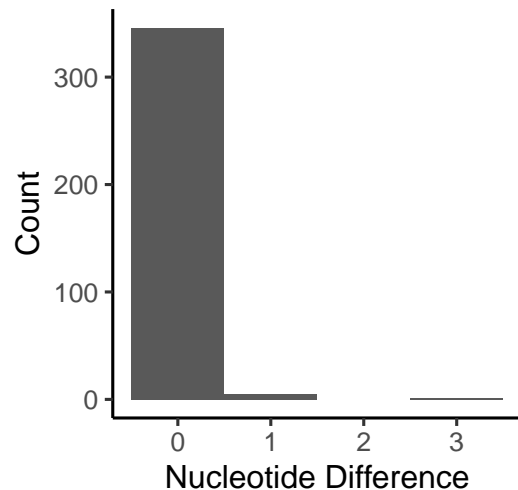
TRBV12-2*ap01_G301A

73 sequences assigned
70 (95.9%) exact matches, in which:
66 unique CDR3
11 unique J



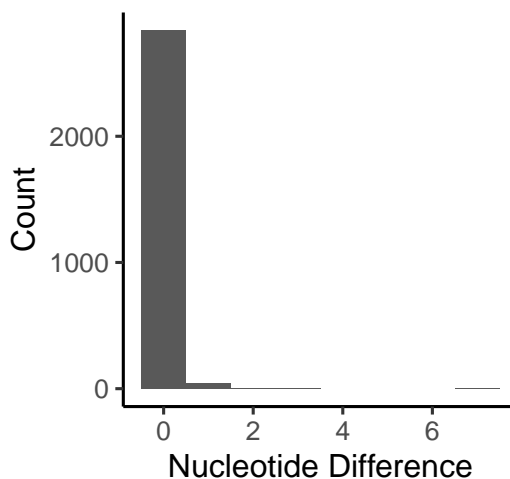
TRBV12–5*ap01

352 sequences assigned
346 (98.3%) exact matches, in which:
341 unique CDR3
13 unique J



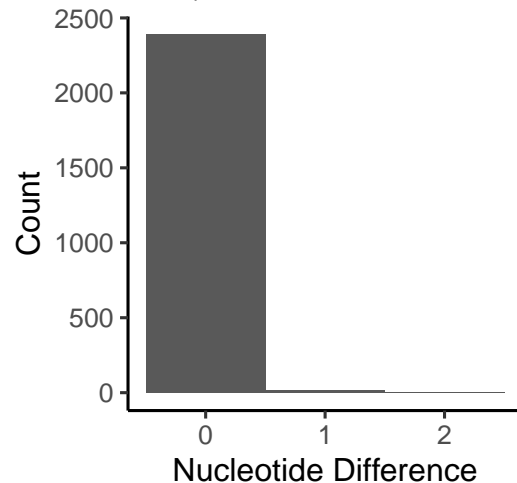
TRBV3–12*ap01

2884 sequences assigned
2839 (98.4%) exact matches, in which:
2827 unique CDR3
13 unique J



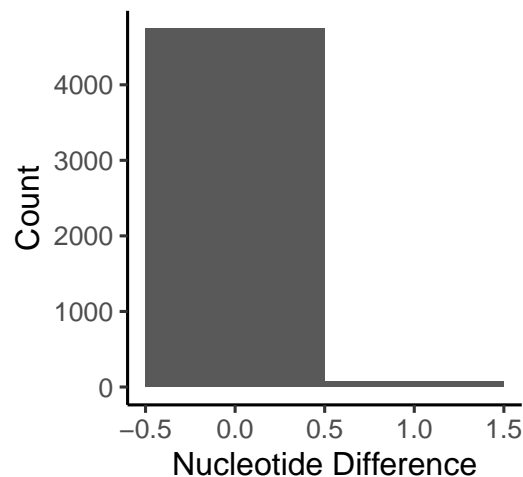
TRBV4–2*ap01

2405 sequences assigned
2390 (99.4%) exact matches, in which:
2359 unique CDR3
13 unique J



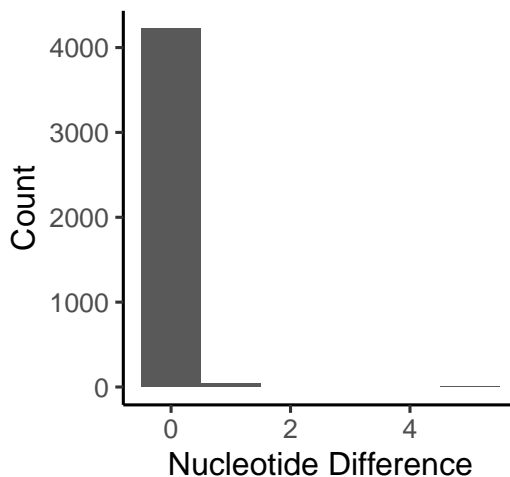
TRBV12–34*ap01

4818 sequences assigned
4742 (98.4%) exact matches, in which:
4710 unique CDR3
13 unique J



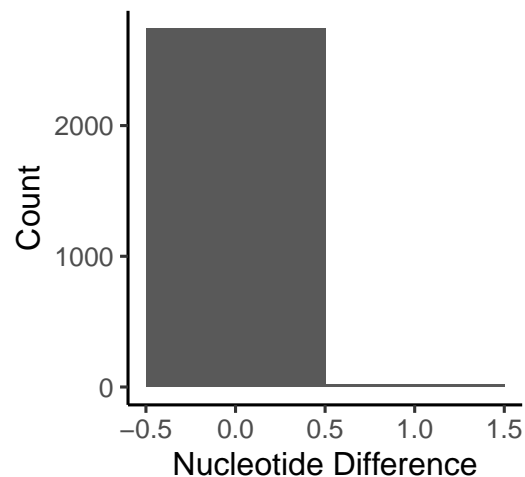
TRBV4–1*ap01

4268 sequences assigned
4222 (98.9%) exact matches, in which:
4149 unique CDR3
13 unique J



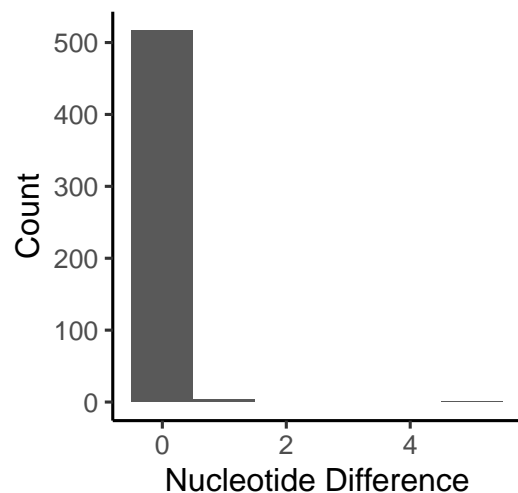
TRBV4–3*ap01

2761 sequences assigned
2741 (99.3%) exact matches, in which:
2698 unique CDR3
13 unique J



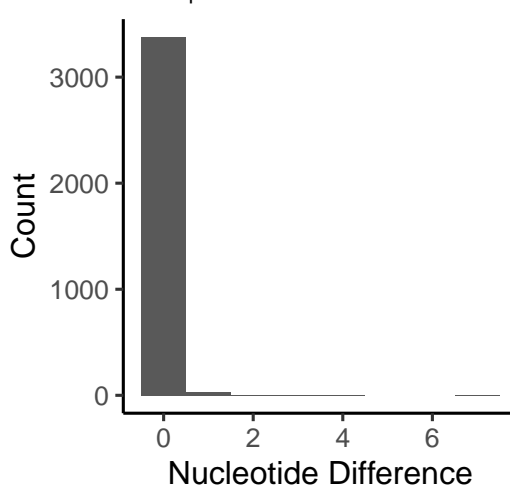
TRBV23–1*ap01

521 sequences assigned
517 (99.2%) exact matches, in which:
515 unique CDR3
13 unique J



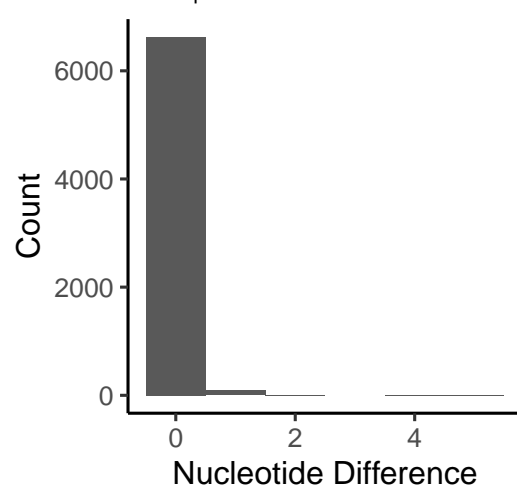
TRBV24–1*ap01

3413 sequences assigned
3378 (99%) exact matches, in which:
3344 unique CDR3
13 unique J



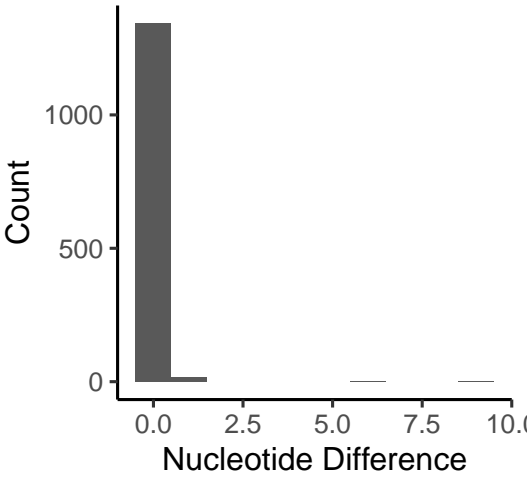
TRBV5–1*ap01

6718 sequences assigned
6624 (98.6%) exact matches, in which:
6524 unique CDR3
13 unique J



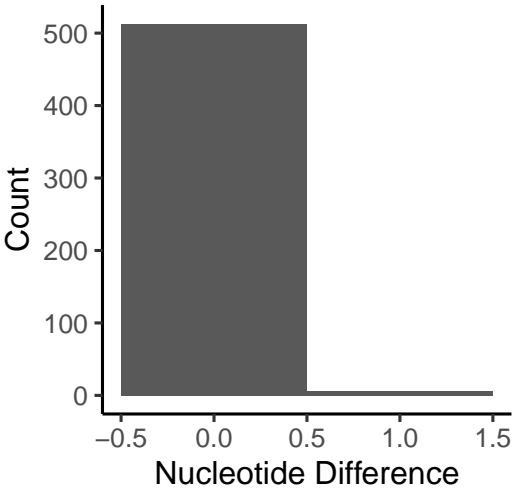
TRBV25-1*ap01

1362 sequences assigned
1343 (98.6%) exact matches, in which:
1326 unique CDR3
13 unique J



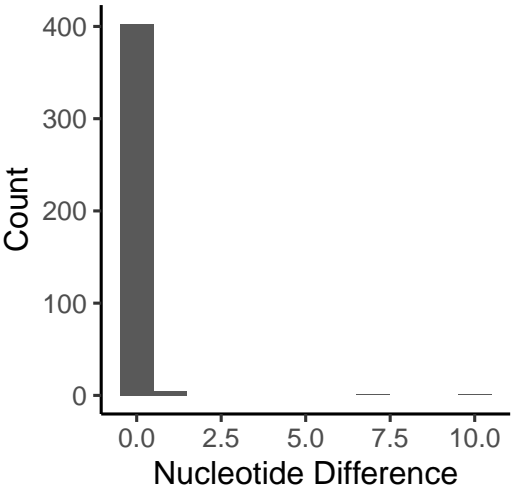
TRBV5-5*ap01

519 sequences assigned
513 (98.8%) exact matches, in which:
510 unique CDR3
13 unique J



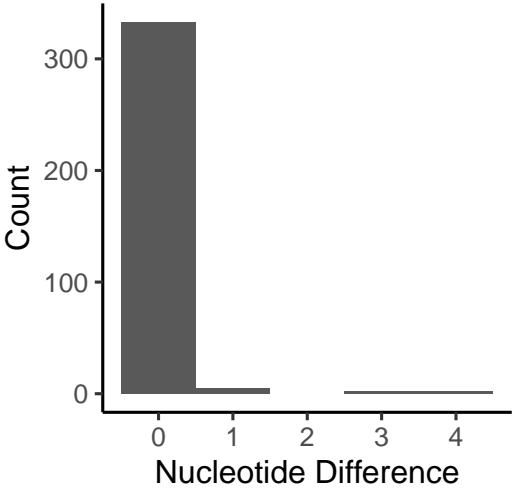
TRBV5-8*ap01

410 sequences assigned
403 (98.3%) exact matches, in which:
399 unique CDR3
13 unique J



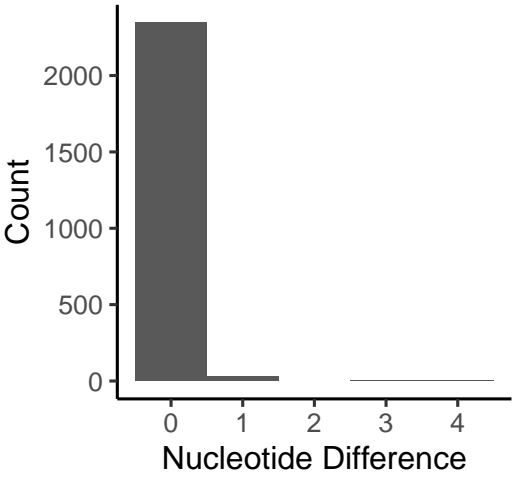
TRBV5-3*ap01

342 sequences assigned
333 (97.4%) exact matches, in which:
329 unique CDR3
13 unique J



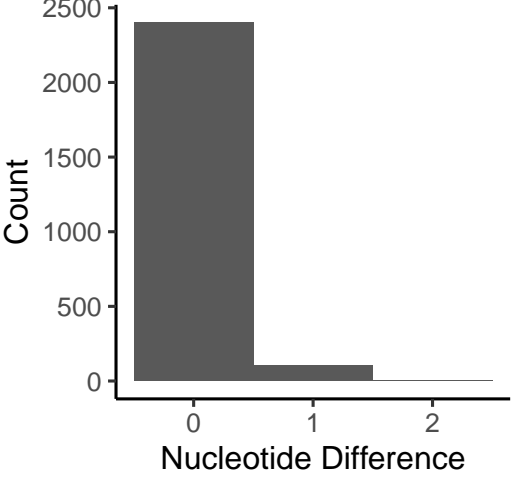
TRBV5-6*ap01

2376 sequences assigned
2346 (98.7%) exact matches, in which:
2316 unique CDR3
13 unique J



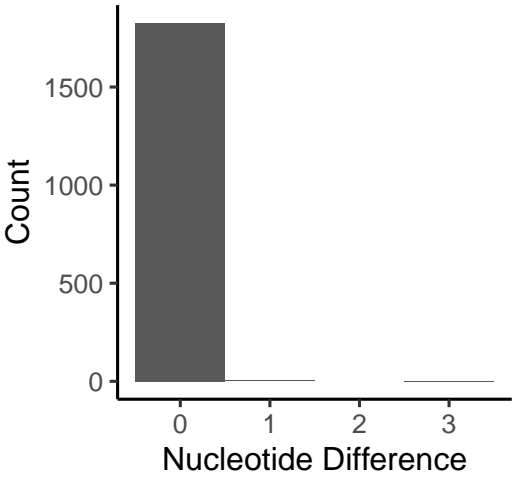
TRBV6-1*ap01

2506 sequences assigned
2400 (95.8%) exact matches, in which:
2374 unique CDR3
13 unique J



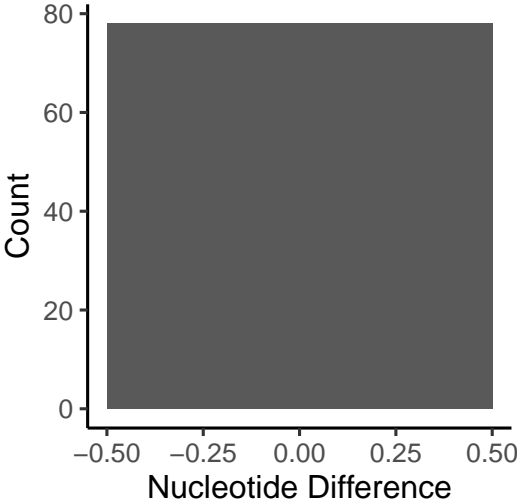
TRBV5-4*ap01

1833 sequences assigned
1826 (99.6%) exact matches, in which:
1817 unique CDR3
13 unique J



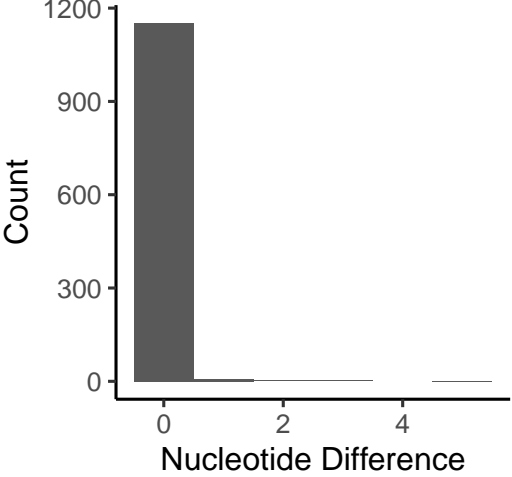
TRBV5-7*ap01

78 sequences assigned
78 (100%) exact matches, in which:
77 unique CDR3
11 unique J



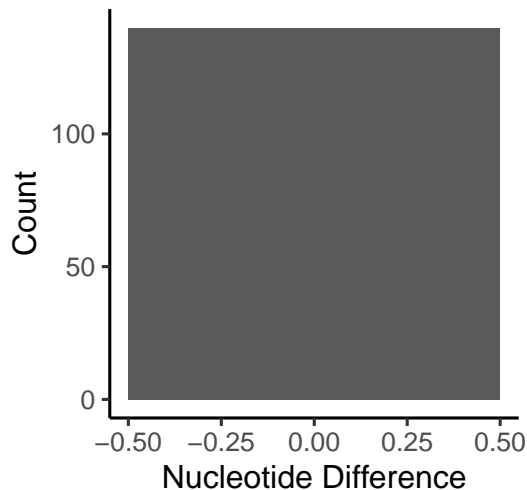
TRBV6-4*ap01

1167 sequences assigned
1152 (98.7%) exact matches, in which:
1143 unique CDR3
13 unique J



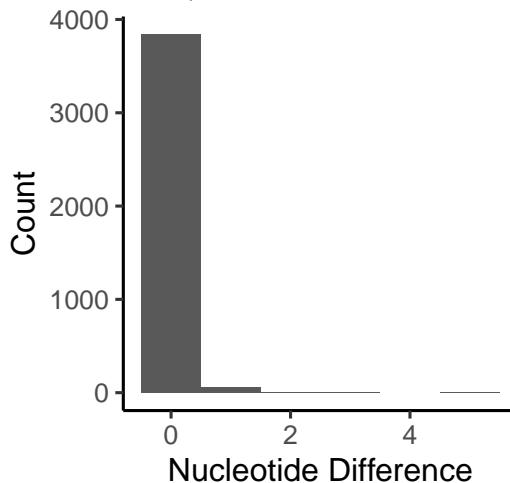
TRBV6-7*ap01

140 sequences assigned
140 (100%) exact matches, in which:
137 unique CDR3
11 unique J



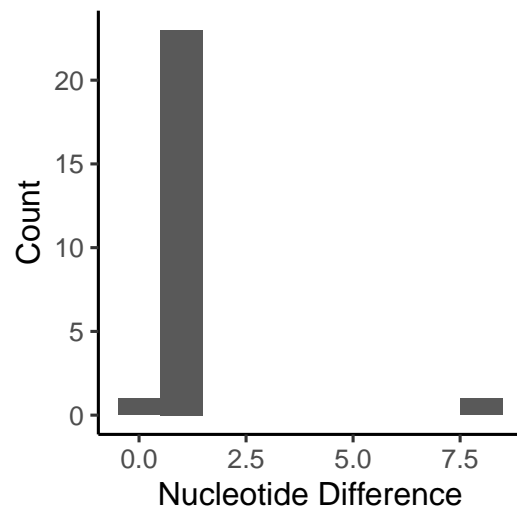
TRBV6-23*ap01

3904 sequences assigned
3840 (98.4%) exact matches, in which:
3808 unique CDR3
13 unique J



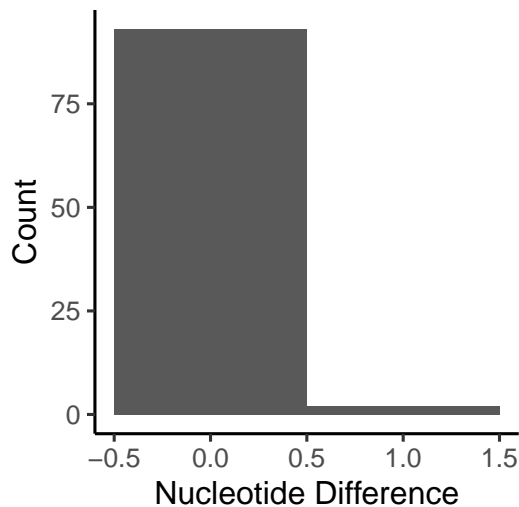
TRBV7-1*ap01_T296C

25 sequences assigned
1 (4%) exact matches, in which:
1 unique CDR3
1 unique J



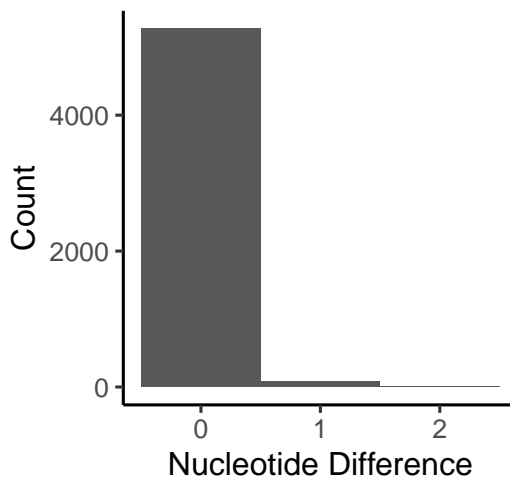
TRBV6-8*ap01

95 sequences assigned
93 (97.9%) exact matches, in which:
93 unique CDR3
13 unique J



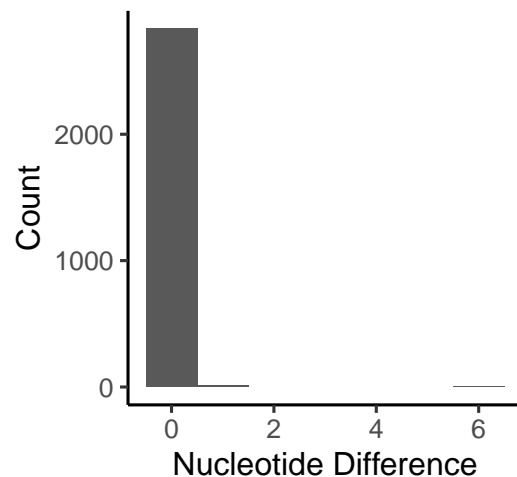
TRBV6-56*ap01

5351 sequences assigned
5272 (98.5%) exact matches, in which:
5198 unique CDR3
13 unique J



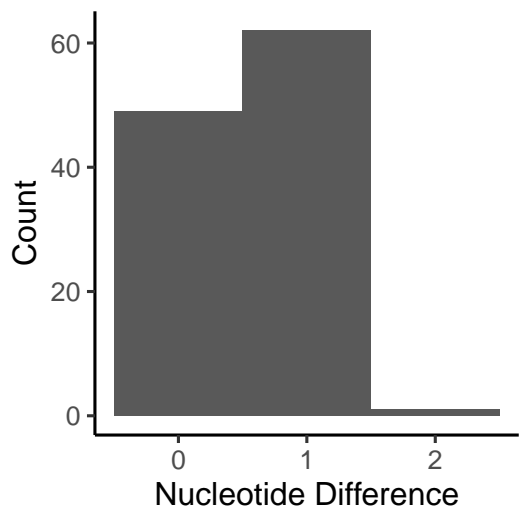
TRBV7-2*ap01

2847 sequences assigned
2835 (99.6%) exact matches, in which:
2816 unique CDR3
13 unique J



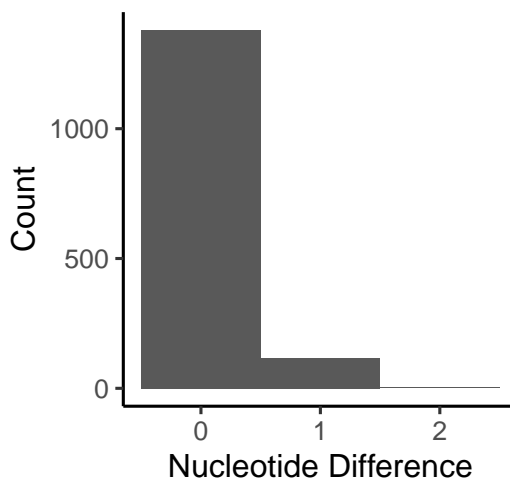
TRBV6-9*ap01

112 sequences assigned
49 (43.8%) exact matches, in which:
48 unique CDR3
11 unique J



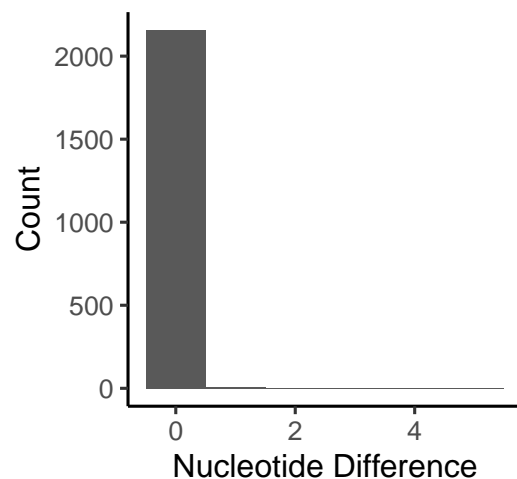
TRBV6-56*ap02

1500 sequences assigned
1380 (92%) exact matches, in which:
1364 unique CDR3
13 unique J



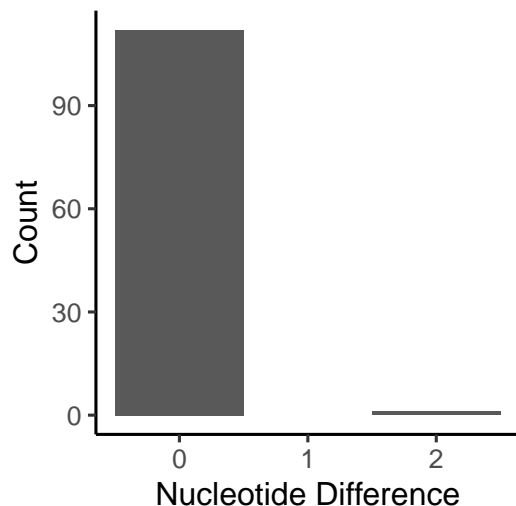
TRBV7-3*ap01

2171 sequences assigned
2157 (99.4%) exact matches, in which:
2139 unique CDR3
13 unique J



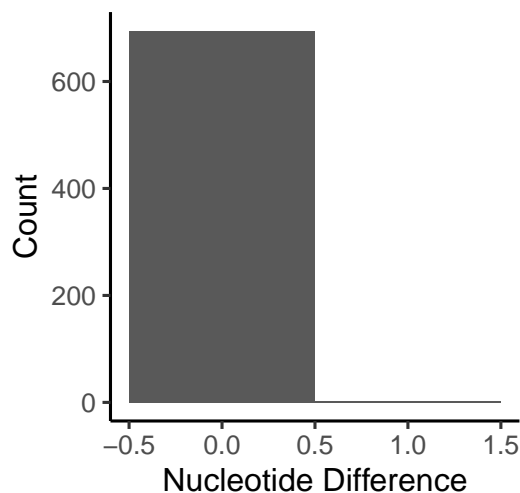
TRBV7-4*ap01

113 sequences assigned
112 (99.1%) exact matches, in which:
112 unique CDR3
12 unique J



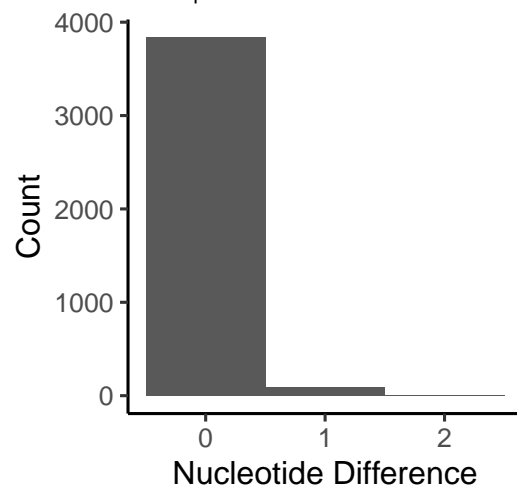
TRBV7-8*ap01

697 sequences assigned
695 (99.7%) exact matches, in which:
693 unique CDR3
13 unique J



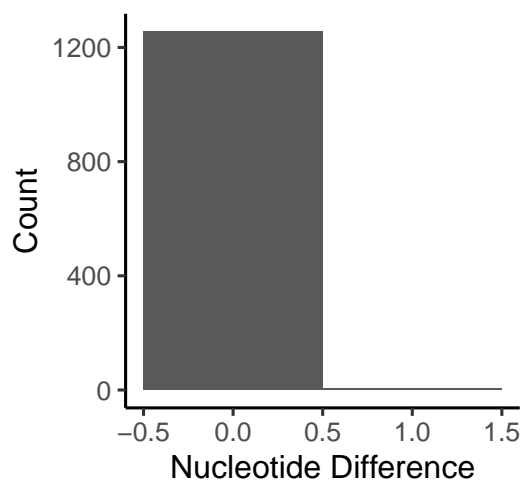
TRBV29-1*ap01

3932 sequences assigned
3837 (97.6%) exact matches, in which:
3692 unique CDR3
13 unique J



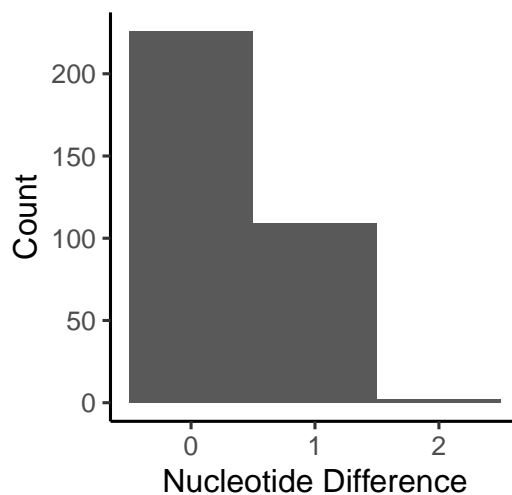
TRBV7-6*ap01

1260 sequences assigned
1255 (99.6%) exact matches, in which:
1242 unique CDR3
13 unique J



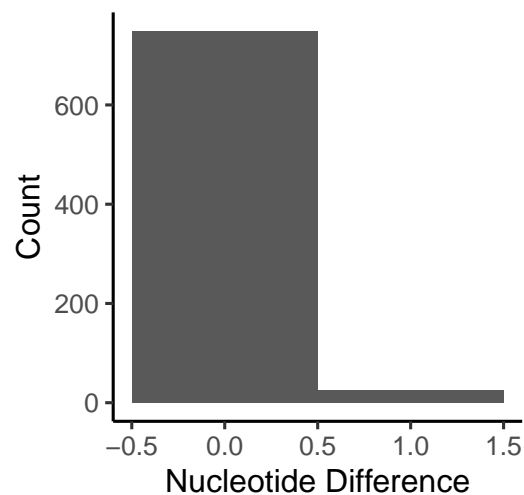
TRBV7-8*ap03

337 sequences assigned
226 (67.1%) exact matches, in which:
225 unique CDR3
13 unique J



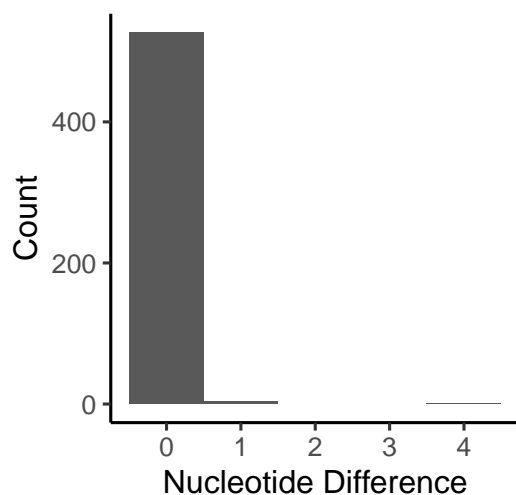
TRBV29-1*ap02

774 sequences assigned
749 (96.8%) exact matches, in which:
713 unique CDR3
13 unique J



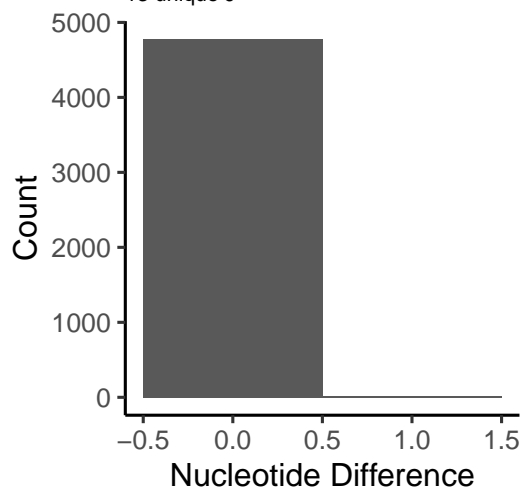
TRBV7-7*ap01_C315T

532 sequences assigned
527 (99.1%) exact matches, in which:
521 unique CDR3
13 unique J

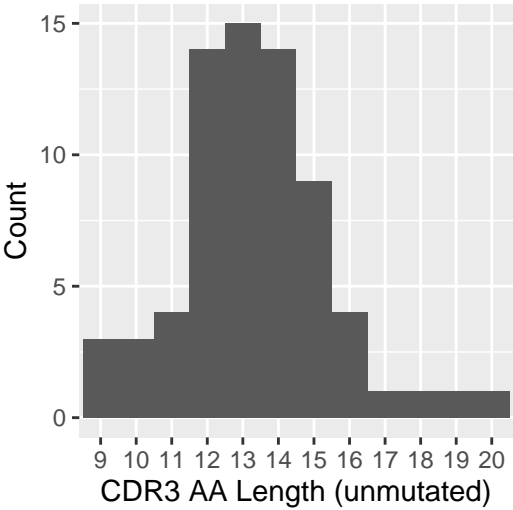


TRBV7-9*ap01

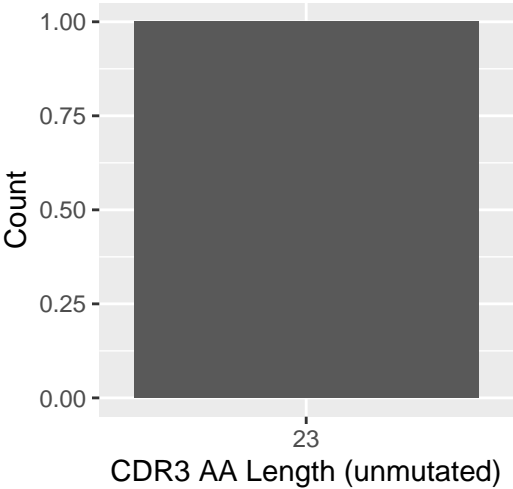
4798 sequences assigned
4778 (99.6%) exact matches, in which:
4741 unique CDR3
13 unique J



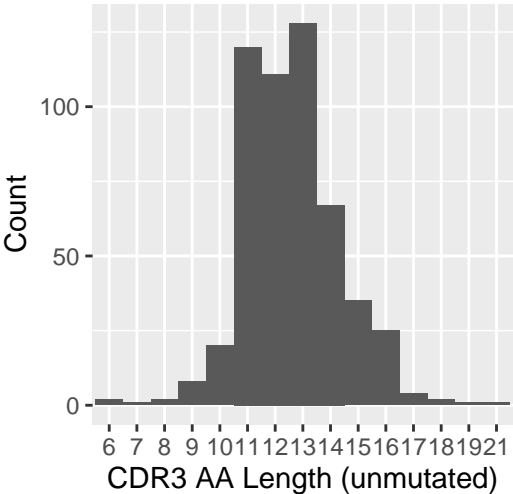
TRBV12-2*ap01_G301A



TRBV7-1*ap01_T296C



TRBV7-7*ap01_C315T





Warning – no inferred sequences found.