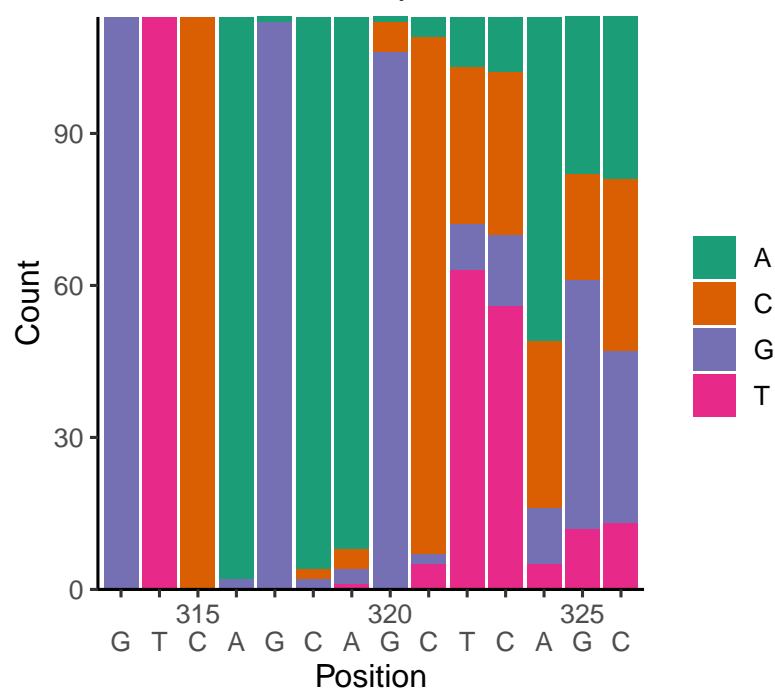
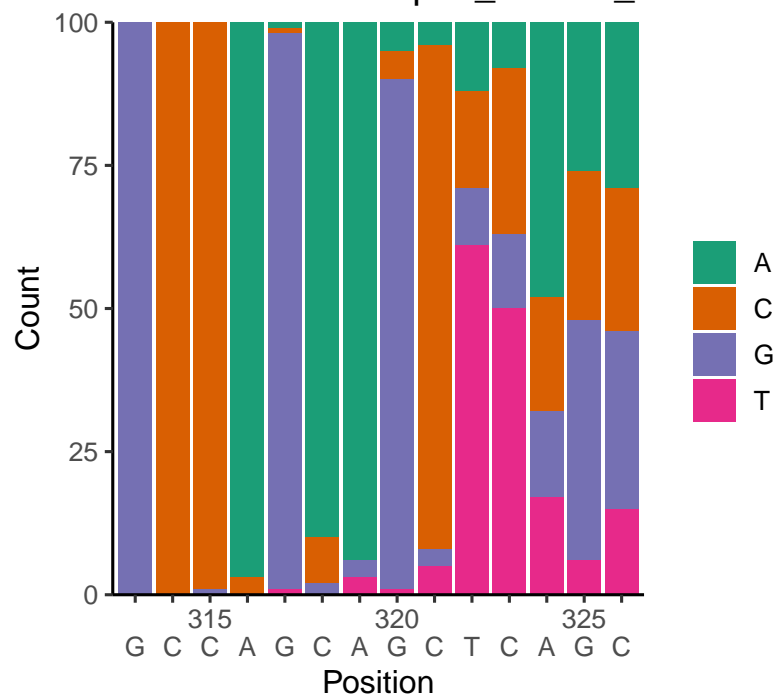


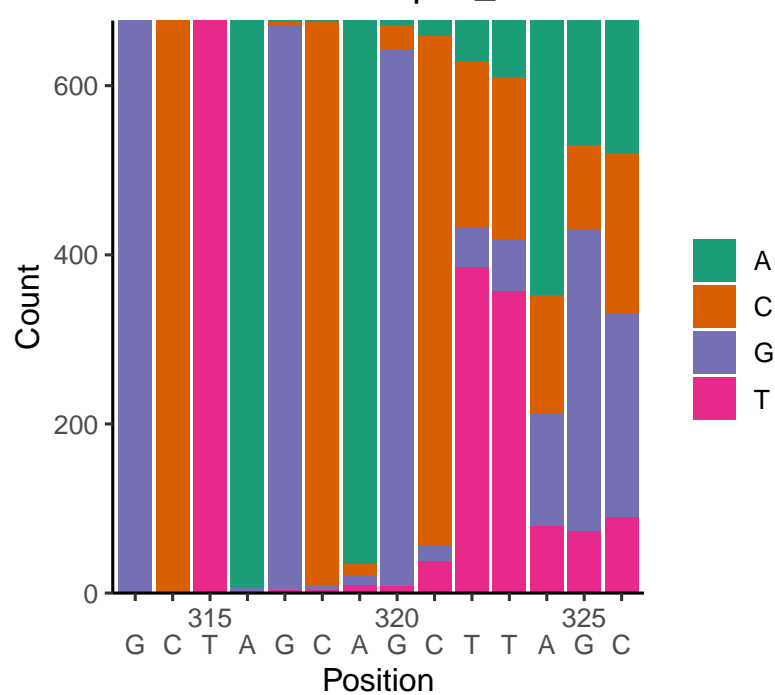
Gene TRBV7-1*ap01_G291C_T296C_C314T



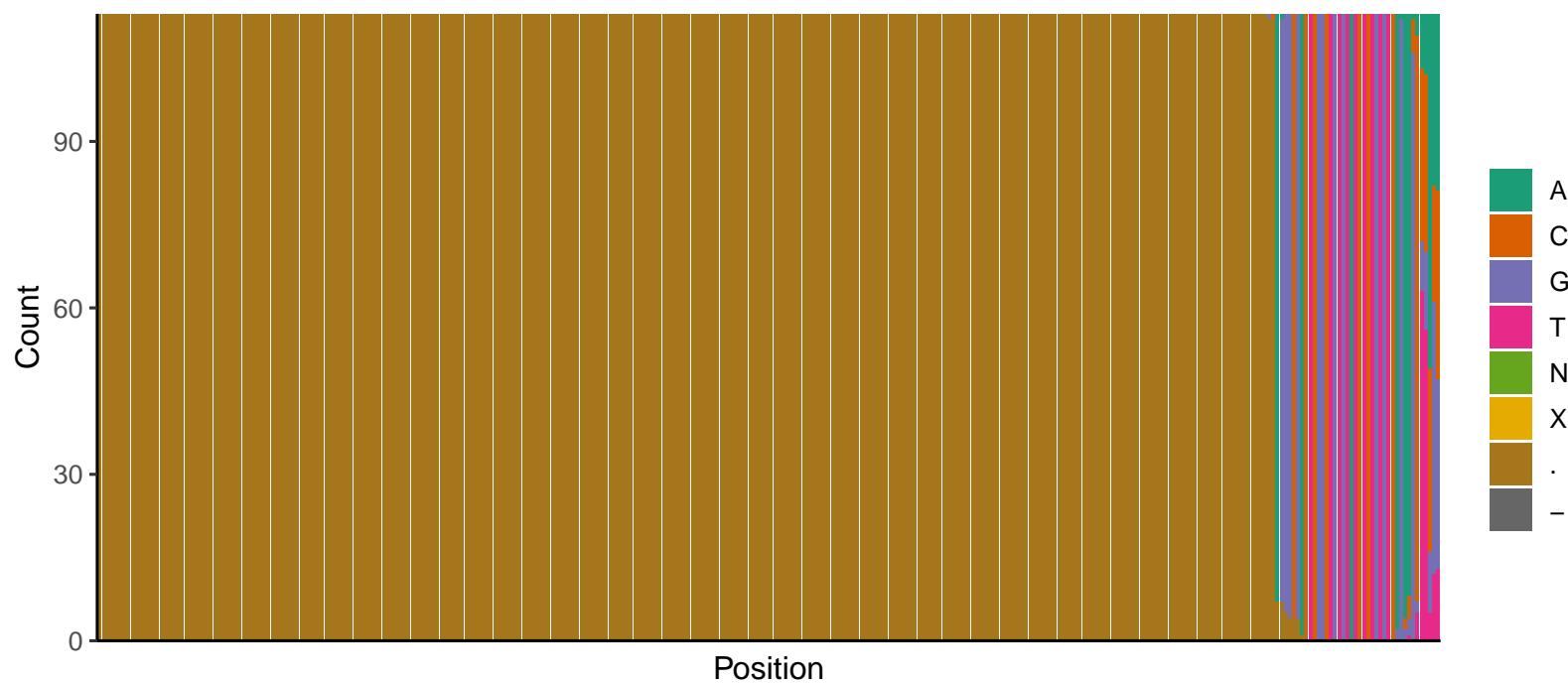
Gene TRBV7-1*ap01_G291C_T296C



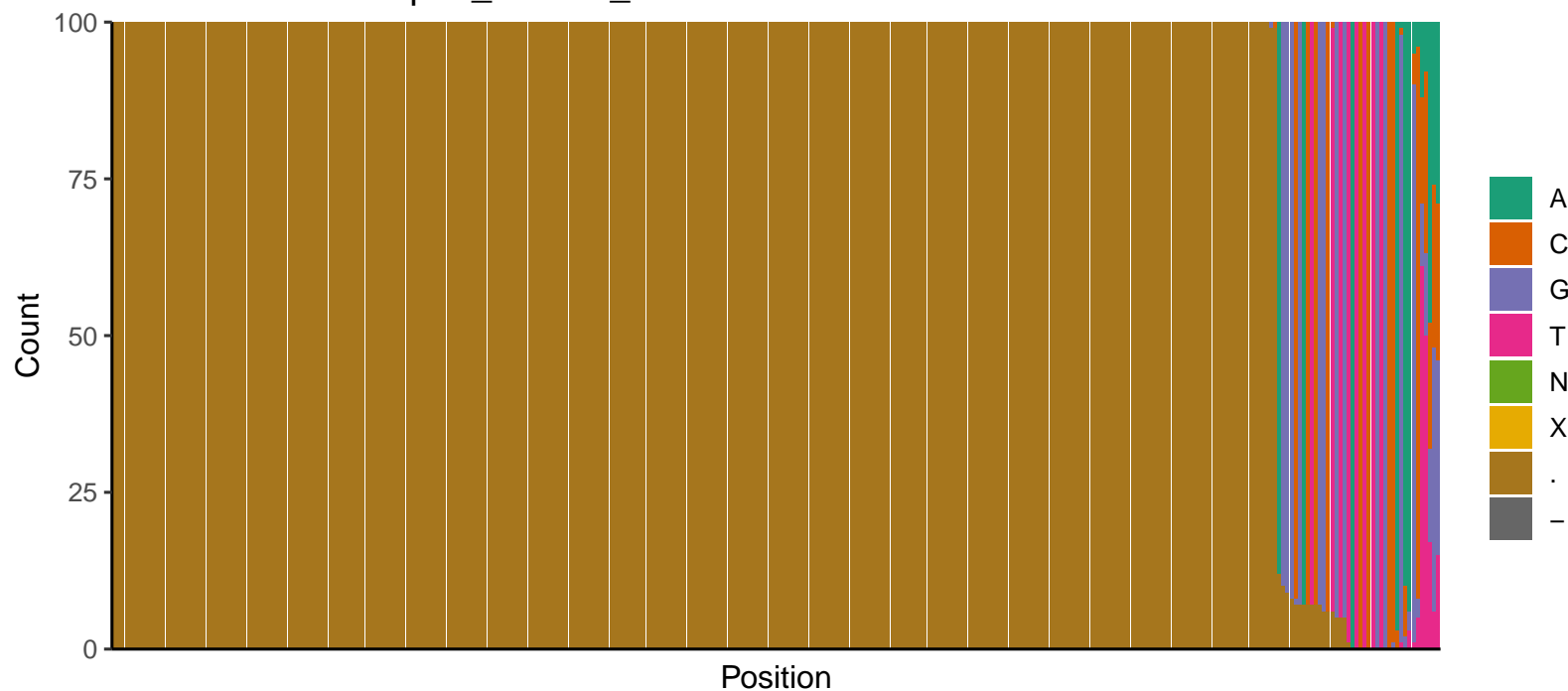
Gene TRBV7-7*ap01_C315T



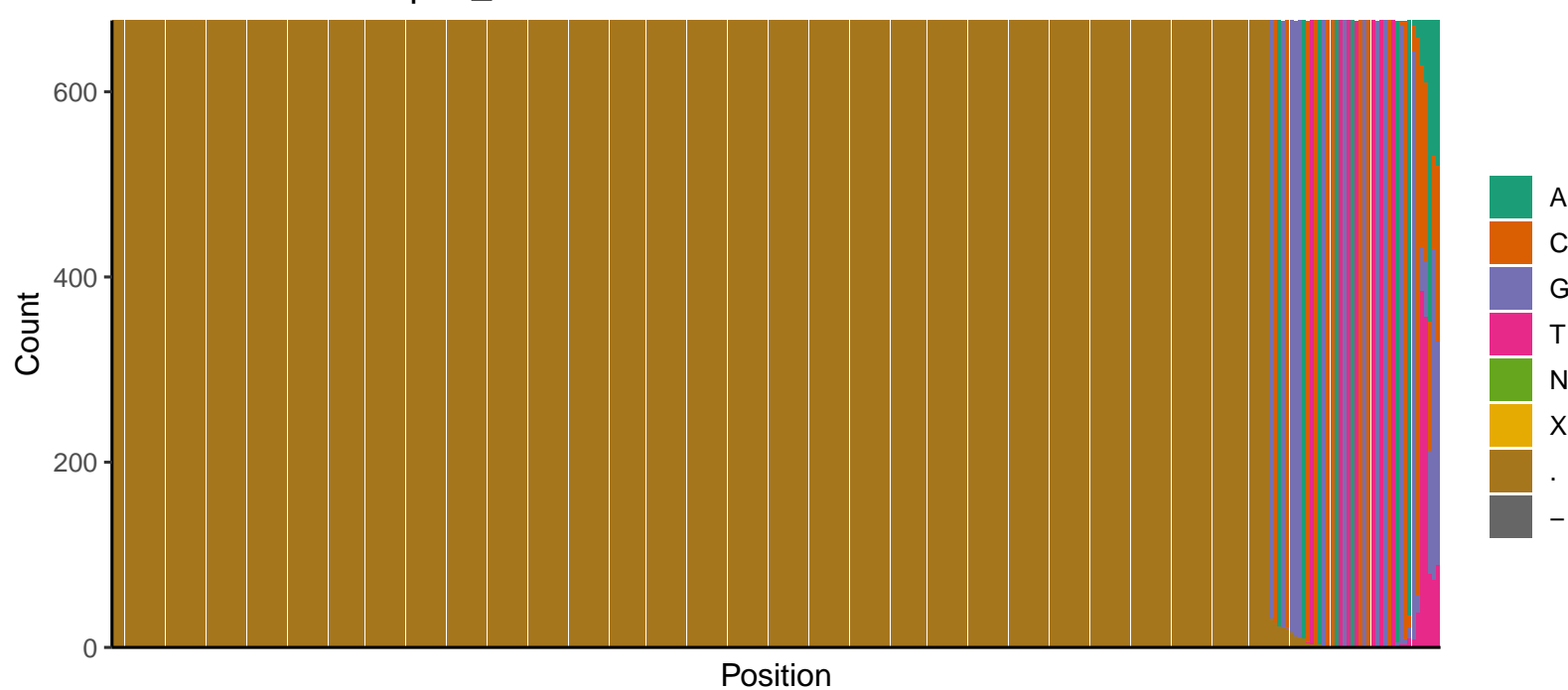
Gene TRBV7-1*ap01_G291C_T296C_C314T



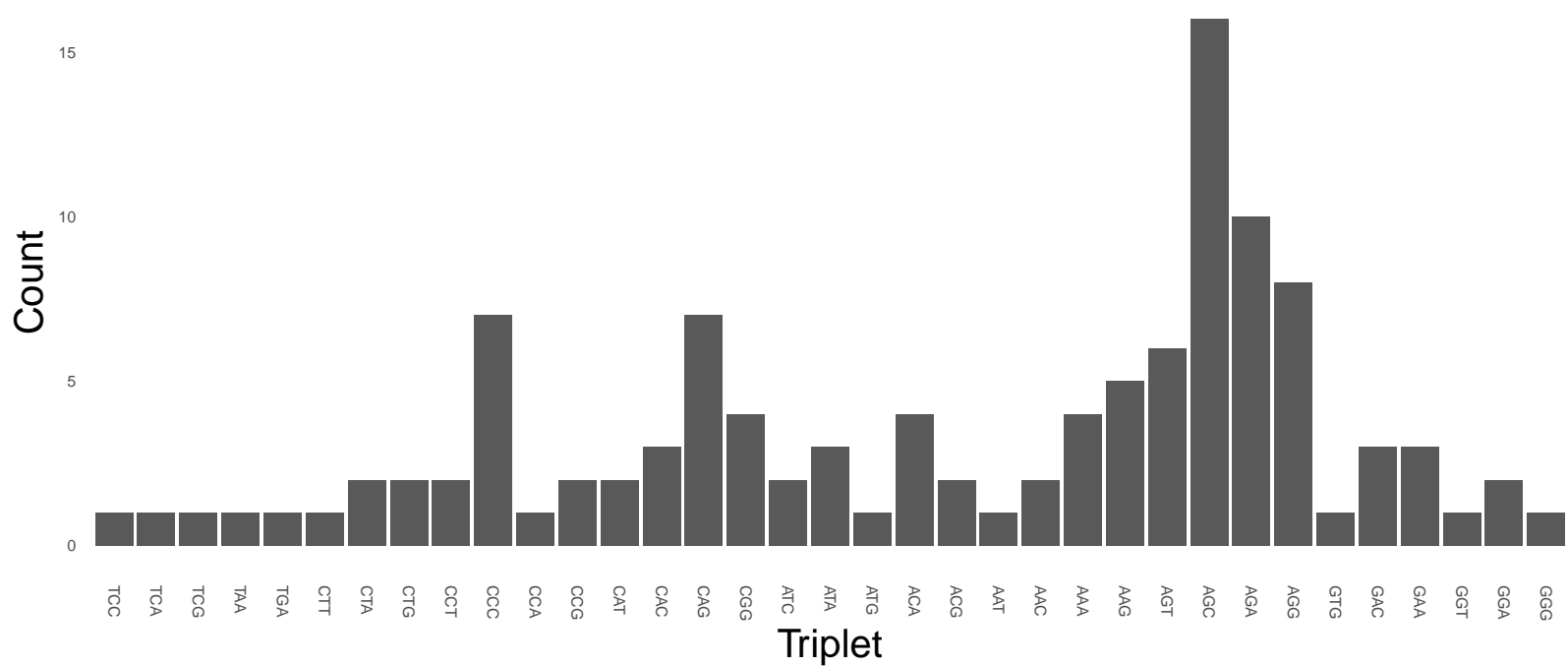
Gene TRBV7-1*ap01_G291C_T296C



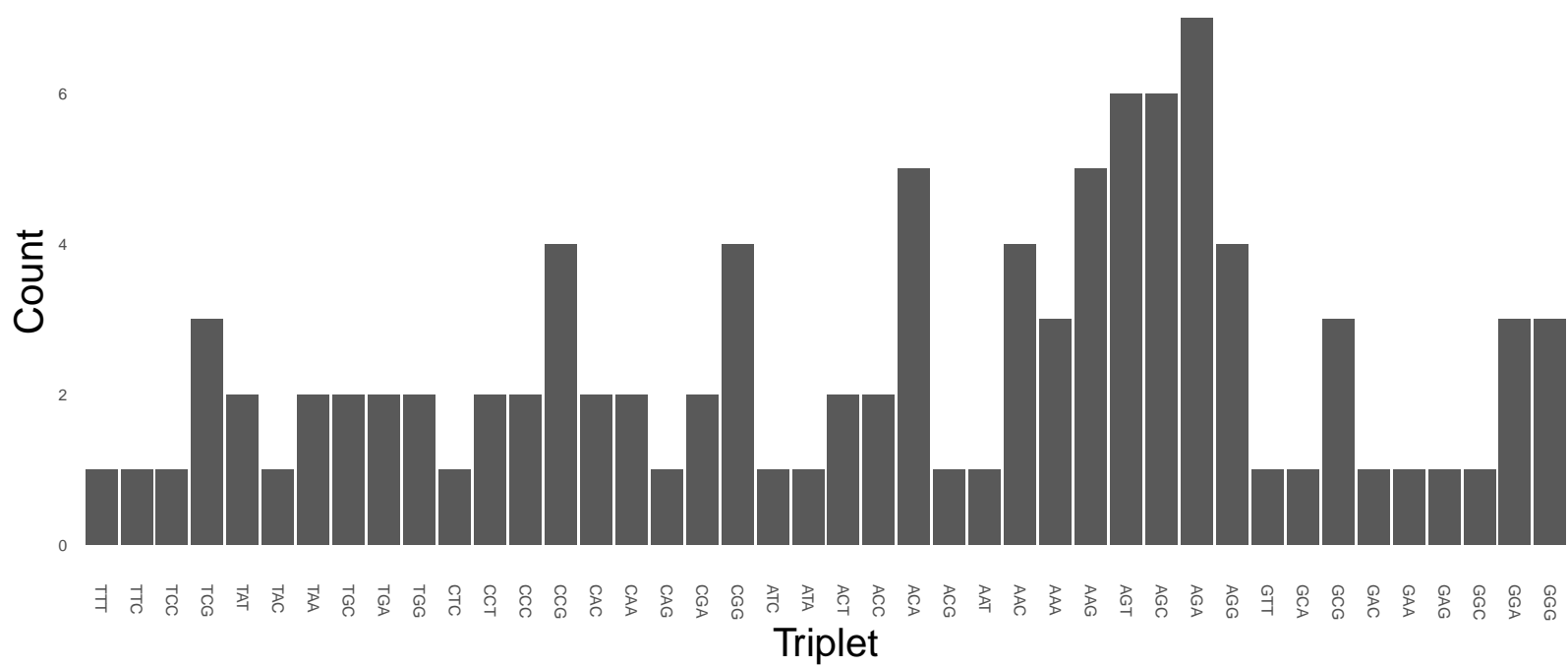
Gene TRBV7-7*ap01_C315T



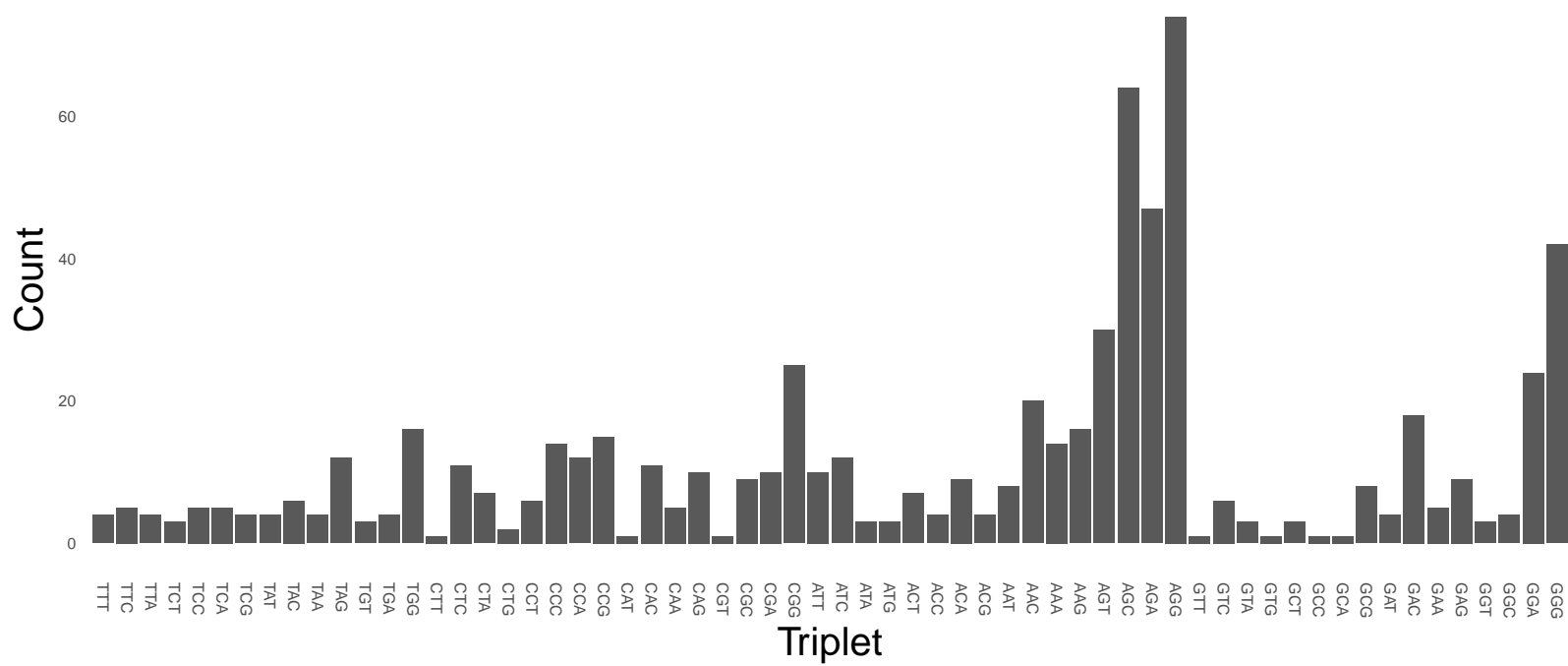
TRBV7-1*ap01_G291C_T296C_C314T- Final 3 nucleotides as a triplet



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

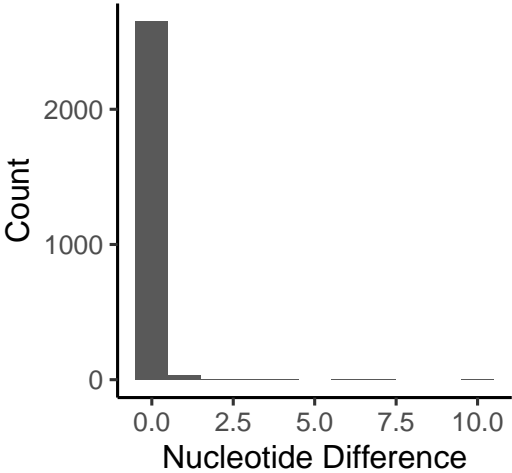


TRBV7-7*ap01_C315T- Final 3 nucleotides as a triplet



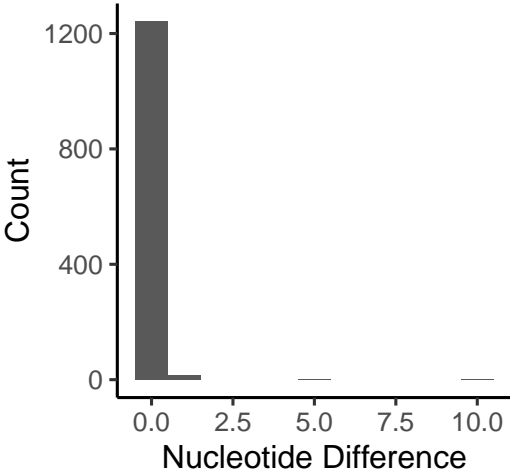
TRBV10-1*ap01

2687 sequences assigned
2650 (98.6%) exact matches, in which:
2551 unique CDR3
14 unique J



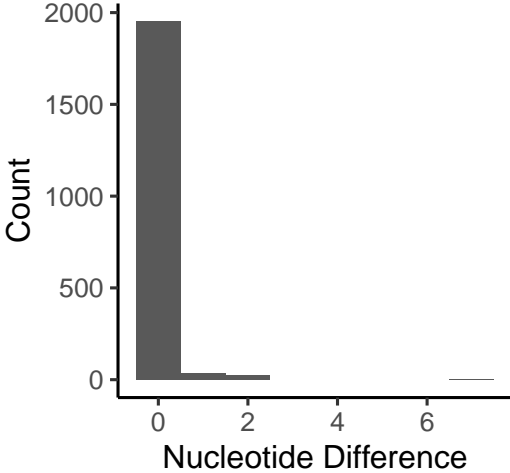
TRBV10-2*ap01

1260 sequences assigned
1242 (98.6%) exact matches, in which:
1202 unique CDR3
14 unique J



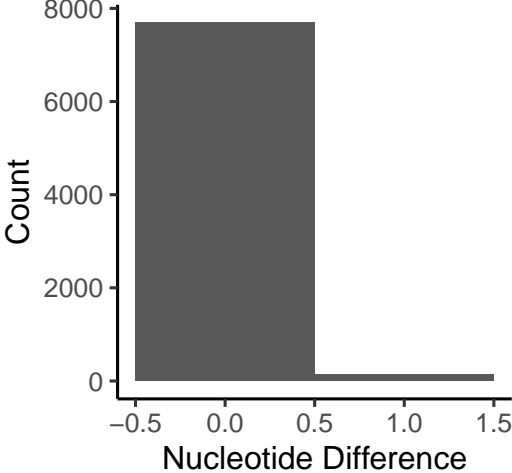
TRBV13*ap01

2014 sequences assigned
1952 (96.9%) exact matches, in which:
1878 unique CDR3
14 unique J



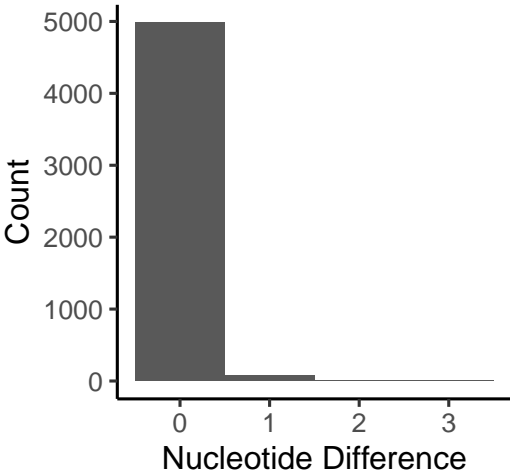
TRBV20-1*ap01

7823 sequences assigned
7692 (98.3%) exact matches, in which:
7535 unique CDR3
14 unique J



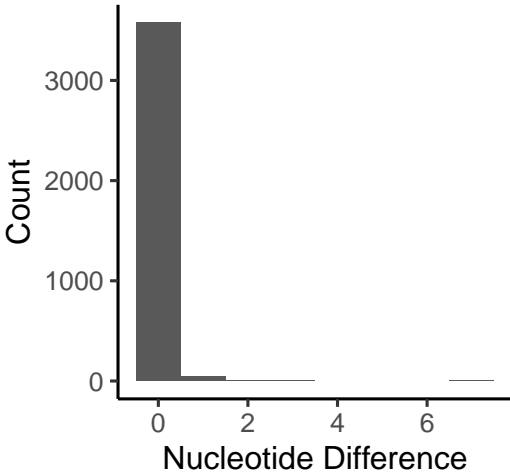
TRBV10-3*ap01

5065 sequences assigned
4982 (98.4%) exact matches, in which:
4818 unique CDR3
14 unique J



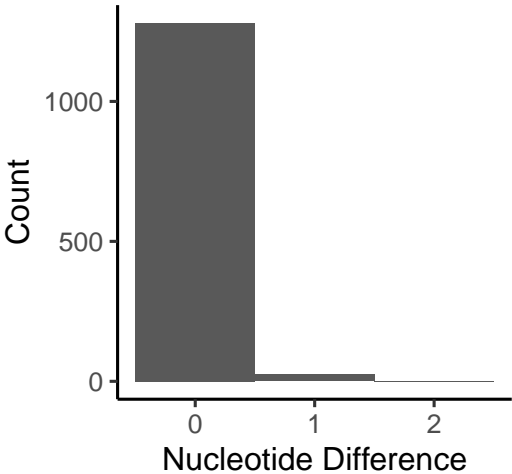
TRBV14*ap01

3628 sequences assigned
3576 (98.6%) exact matches, in which:
3502 unique CDR3
14 unique J



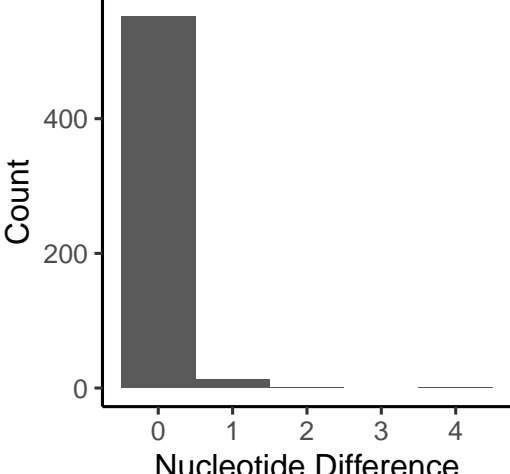
TRBV20-1*ap02

1306 sequences assigned
1280 (98%) exact matches, in which:
1254 unique CDR3
14 unique J



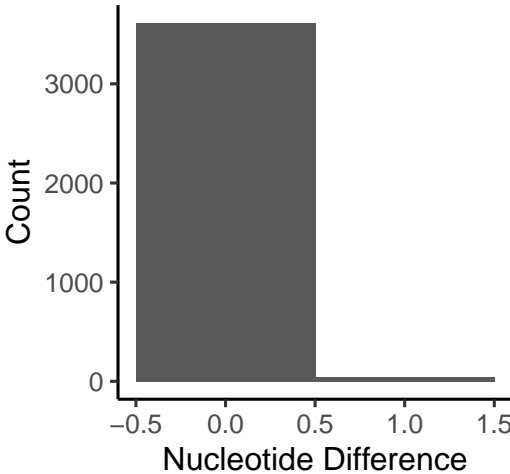
TRBV1*ap01

566 sequences assigned
552 (97.5%) exact matches, in which:
521 unique CDR3
14 unique J



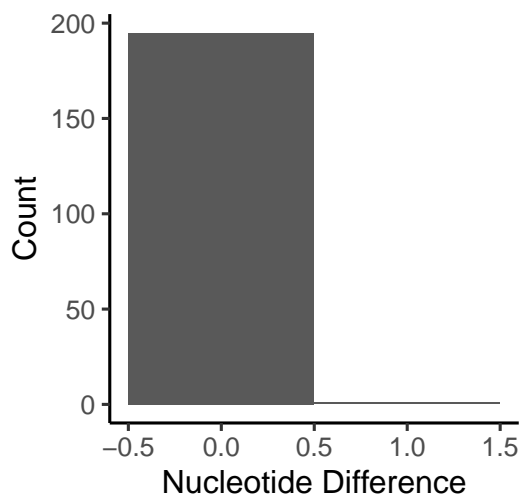
TRBV15*ap02

3655 sequences assigned
3613 (98.9%) exact matches, in which:
3519 unique CDR3
14 unique J



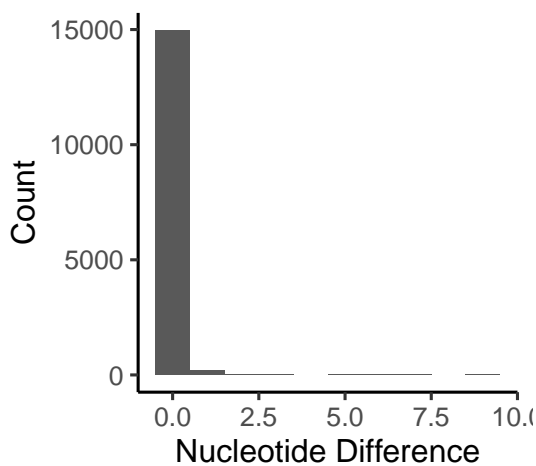
TRBV16*ap01

196 sequences assigned
195 (99.5%) exact matches, in which:
192 unique CDR3
14 unique J



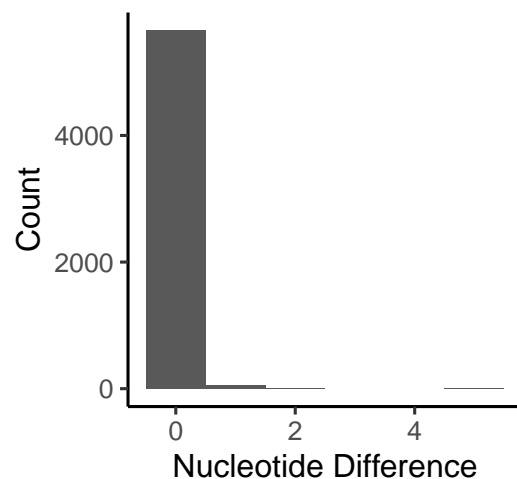
TRBV19*ap01

15200 sequences assigned
14974 (98.5%) exact matches, in which:
14766 unique CDR3
14 unique J



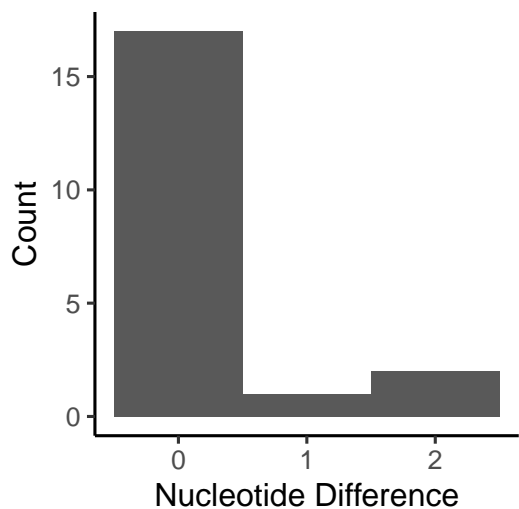
TRBV28*ap01

5722 sequences assigned
5659 (98.9%) exact matches, in which:
5577 unique CDR3
14 unique J



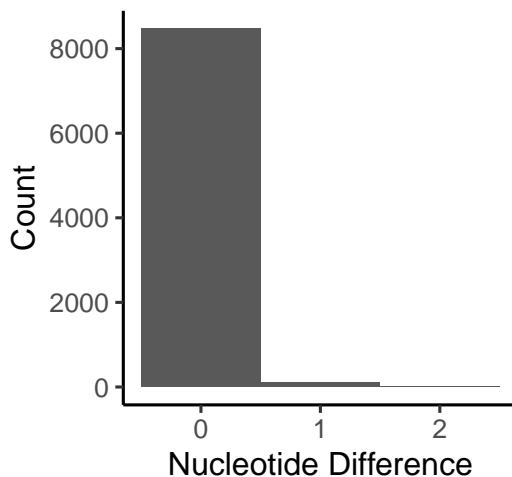
TRBV17*ap01

20 sequences assigned
17 (85%) exact matches, in which:
17 unique CDR3
8 unique J



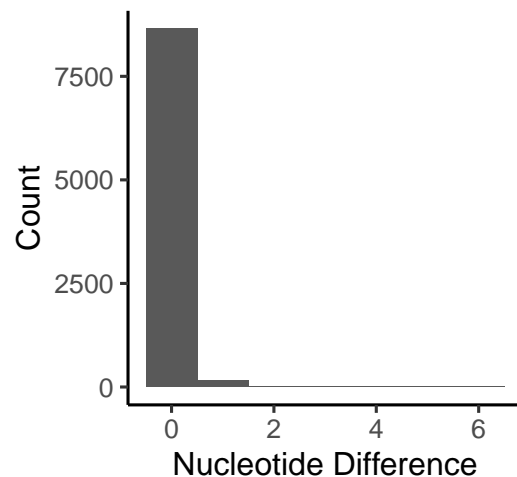
TRBV2*ap01

8590 sequences assigned
8470 (98.6%) exact matches, in which:
8250 unique CDR3
14 unique J



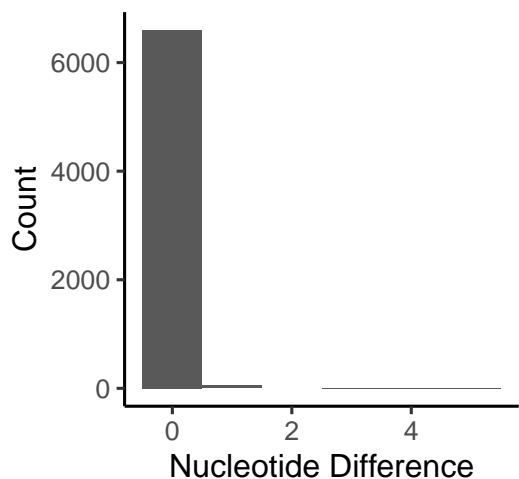
TRBV30*ap02

8814 sequences assigned
8649 (98.1%) exact matches, in which:
8464 unique CDR3
14 unique J



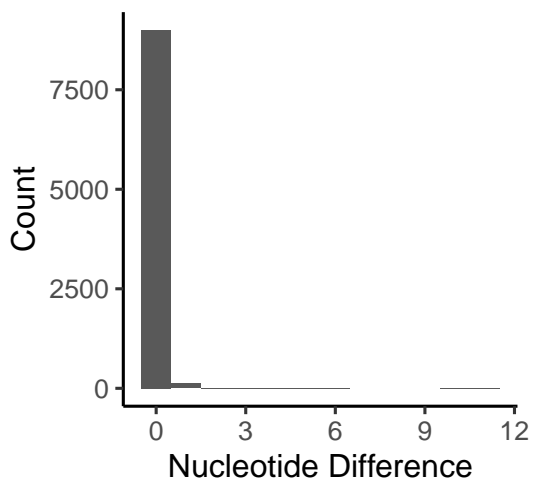
TRBV18*ap01

6654 sequences assigned
6600 (99.2%) exact matches, in which:
6515 unique CDR3
14 unique J



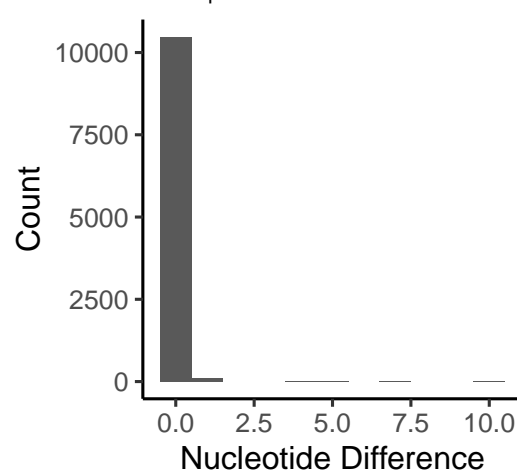
TRBV27*ap01

9136 sequences assigned
9000 (98.5%) exact matches, in which:
8849 unique CDR3
14 unique J



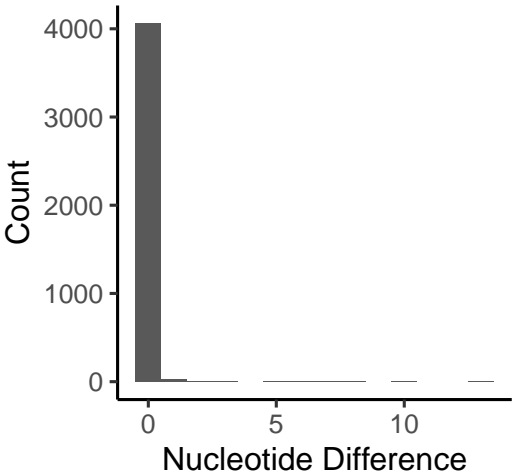
TRBV9*ap01

10591 sequences assigned
10478 (98.9%) exact matches, in which:
10302 unique CDR3
14 unique J



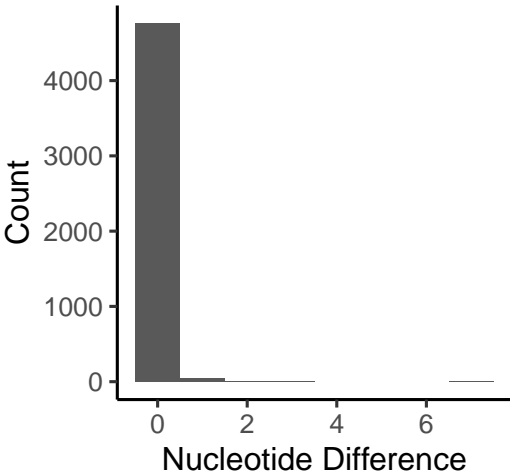
TRBV21-1*ap01

4118 sequences assigned
4061 (98.6%) exact matches, in which:
4017 unique CDR3
14 unique J



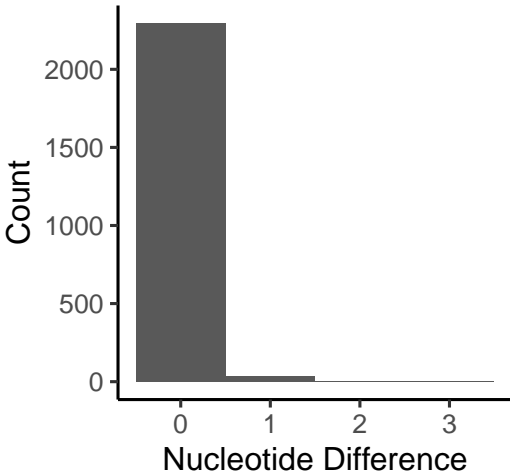
TRBV11-3*ap01

4815 sequences assigned
4760 (98.9%) exact matches, in which:
4693 unique CDR3
14 unique J



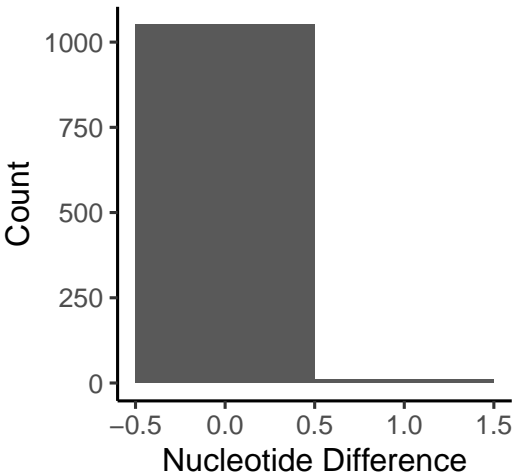
TRBV12-5*ap01

2332 sequences assigned
2294 (98.4%) exact matches, in which:
2246 unique CDR3
14 unique J



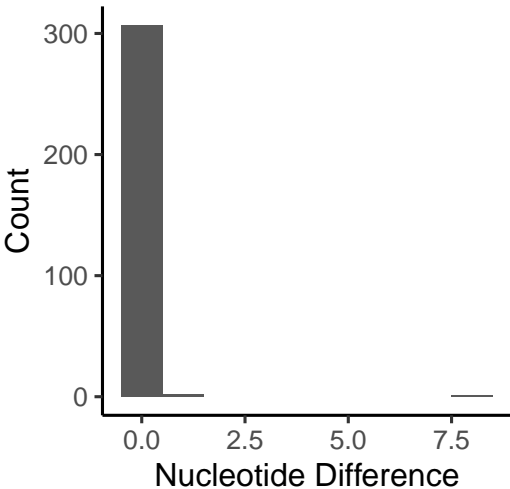
TRBV11-1*ap01

1060 sequences assigned
1051 (99.2%) exact matches, in which:
1024 unique CDR3
14 unique J



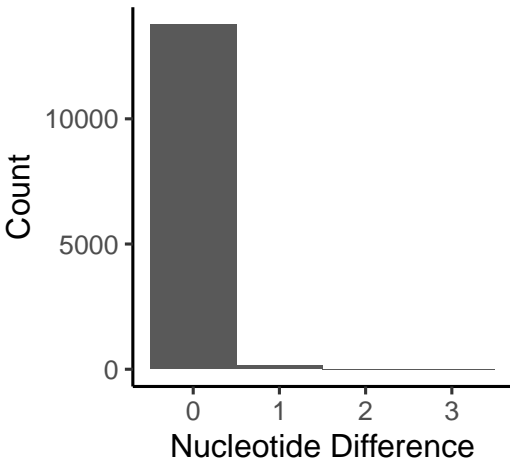
TRBV12-1*ap01

310 sequences assigned
307 (99%) exact matches, in which:
296 unique CDR3
14 unique J



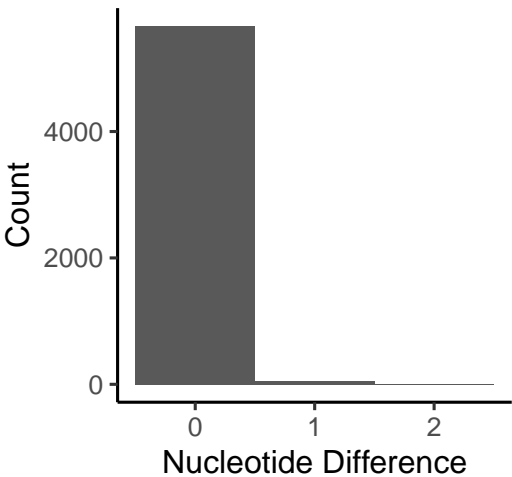
TRBV12-34*ap01

13927 sequences assigned
13767 (98.9%) exact matches, in which:
13495 unique CDR3
14 unique J



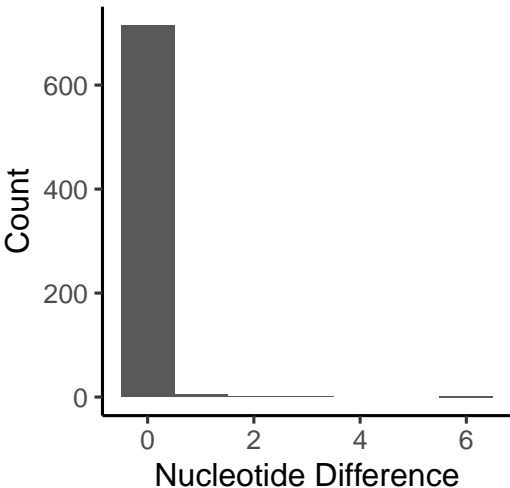
TRBV11-2*ap01

5719 sequences assigned
5669 (99.1%) exact matches, in which:
5546 unique CDR3
14 unique J



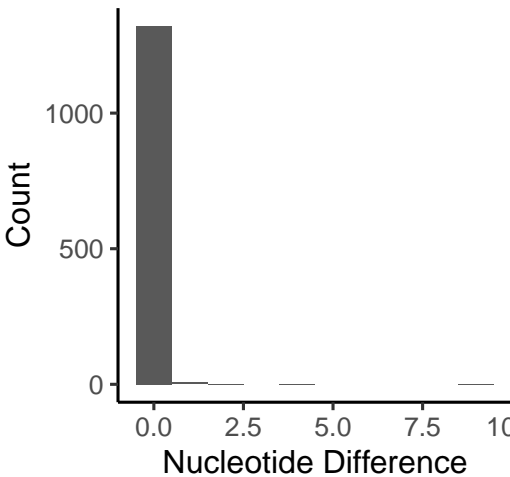
TRBV12-2*ap01

724 sequences assigned
715 (98.8%) exact matches, in which:
690 unique CDR3
14 unique J



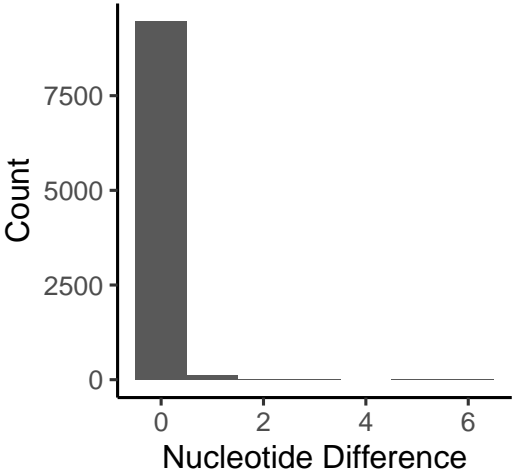
TRBV23-1*ap01

1331 sequences assigned
1321 (99.2%) exact matches, in which:
1306 unique CDR3
14 unique J



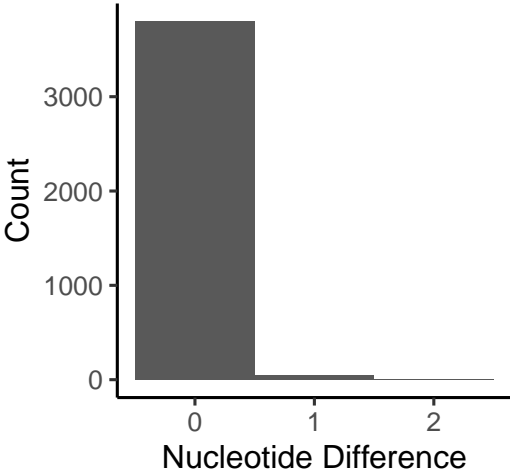
TRBV3-12*ap01

9601 sequences assigned
9461 (98.5%) exact matches, in which:
9242 unique CDR3
14 unique J



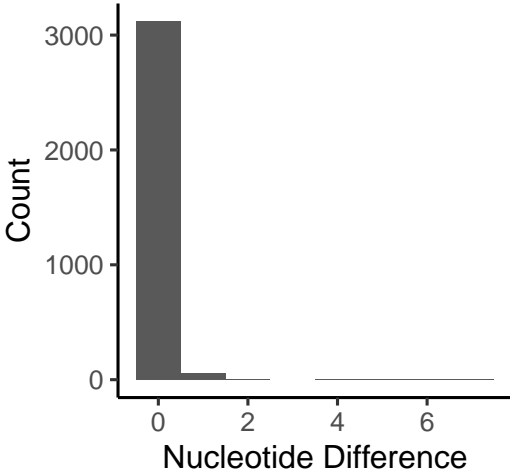
TRBV4-2*ap01

3852 sequences assigned
3798 (98.6%) exact matches, in which:
3718 unique CDR3
14 unique J



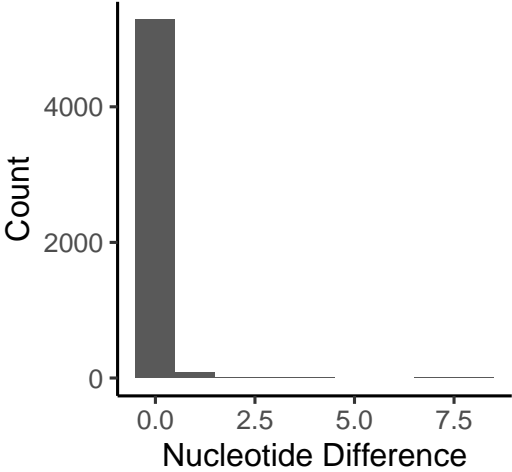
TRBV25-1*ap01

3184 sequences assigned
3119 (98%) exact matches, in which:
3044 unique CDR3
14 unique J



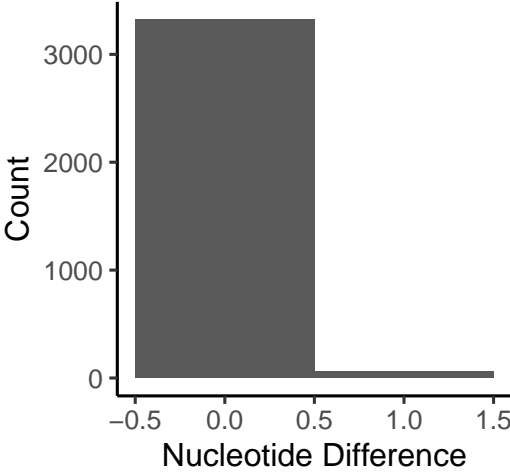
TRBV24-1*ap01

5365 sequences assigned
5284 (98.5%) exact matches, in which:
5174 unique CDR3
14 unique J



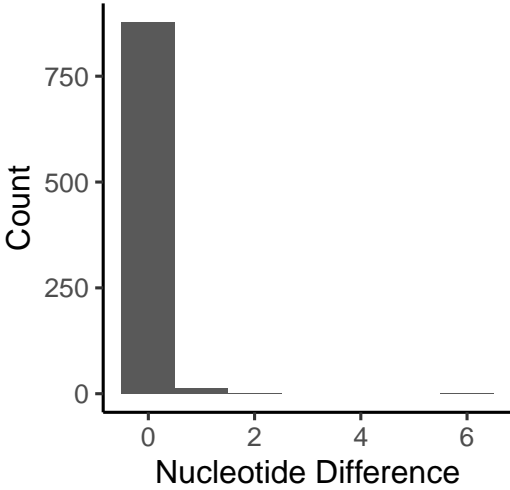
TRBV4-3*ap01

3378 sequences assigned
3321 (98.3%) exact matches, in which:
3280 unique CDR3
14 unique J



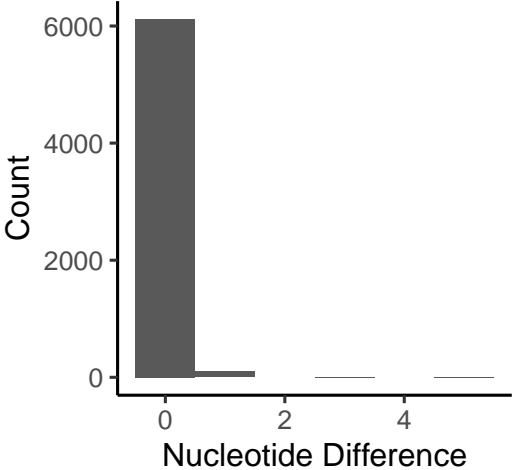
TRBV5-3*ap01

892 sequences assigned
878 (98.4%) exact matches, in which:
850 unique CDR3
14 unique J



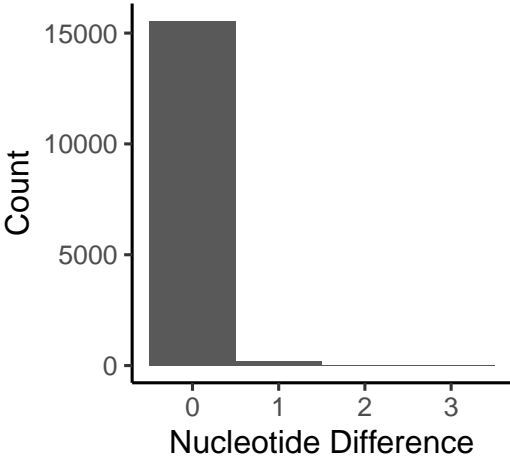
TRBV4-1*ap01

6223 sequences assigned
6119 (98.3%) exact matches, in which:
5955 unique CDR3
14 unique J



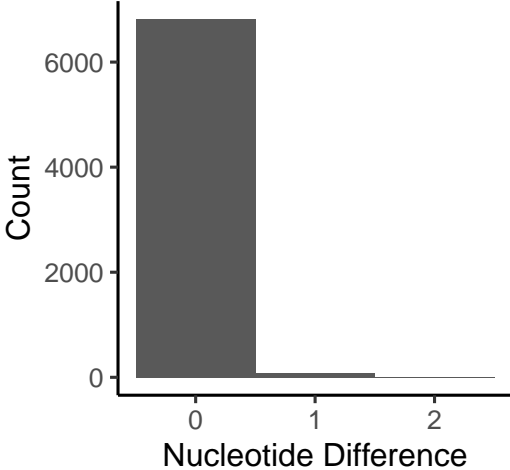
TRBV5-1*ap01

15780 sequences assigned
15555 (98.6%) exact matches, in which:
15111 unique CDR3
14 unique J



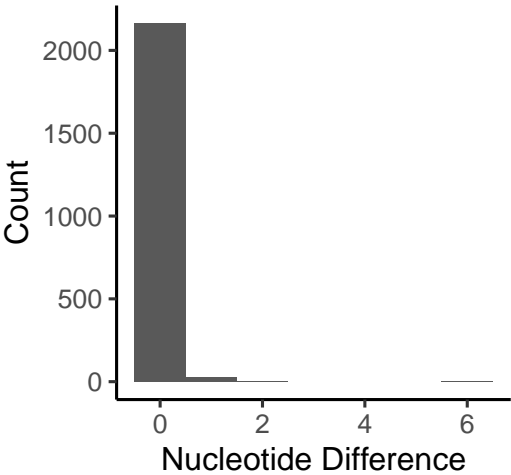
TRBV5-4*ap01

6897 sequences assigned
6819 (98.9%) exact matches, in which:
6639 unique CDR3
14 unique J



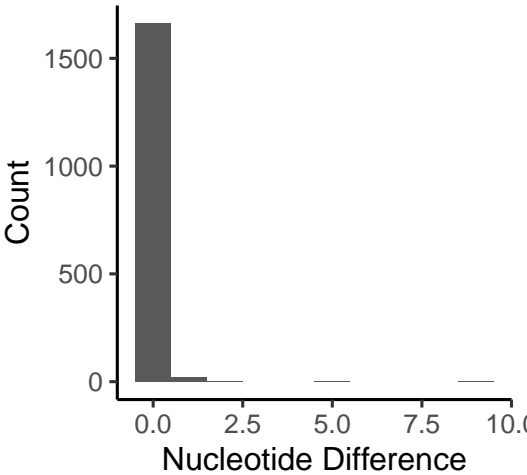
TRBV5-5*ap01

2193 sequences assigned
2163 (98.6%) exact matches, in which:
2136 unique CDR3
14 unique J



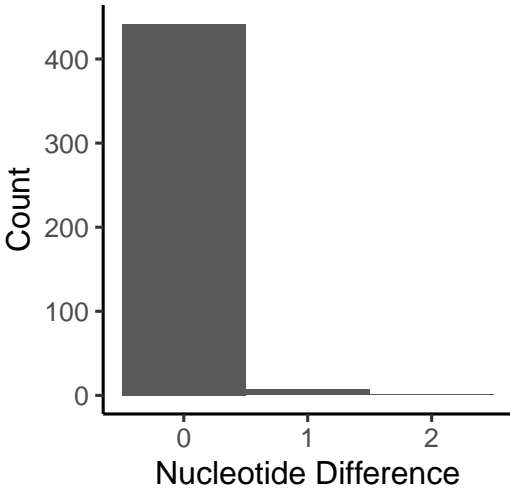
TRBV5-8*ap01

1689 sequences assigned
1662 (98.4%) exact matches, in which:
1636 unique CDR3
14 unique J



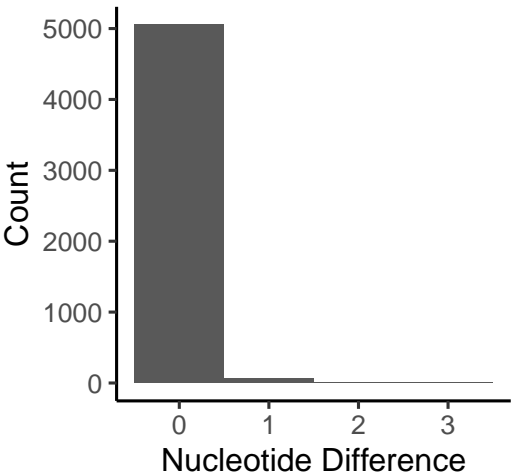
TRBV6-7*ap01

450 sequences assigned
442 (98.2%) exact matches, in which:
426 unique CDR3
14 unique J



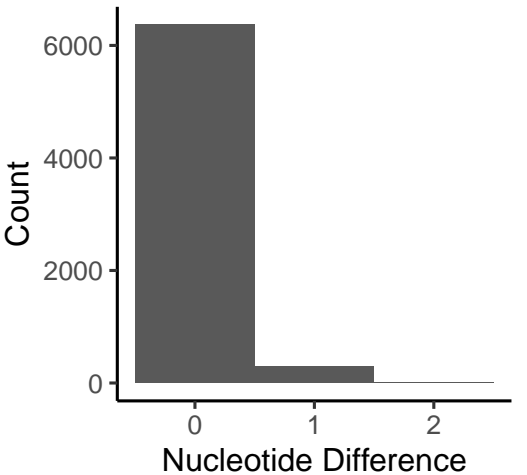
TRBV5-6*ap01

5127 sequences assigned
5054 (98.6%) exact matches, in which:
4865 unique CDR3
14 unique J



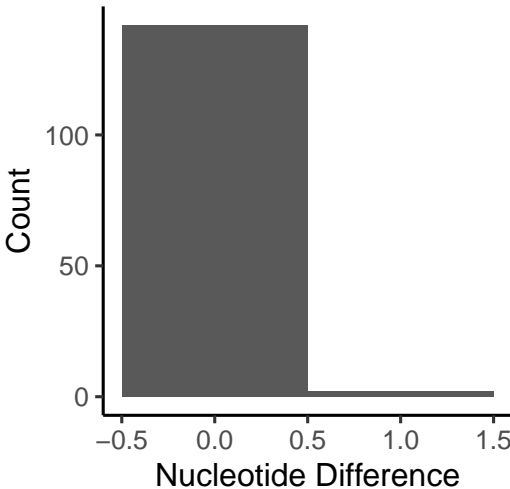
TRBV6-1*ap01

6659 sequences assigned
6368 (95.6%) exact matches, in which:
6138 unique CDR3
14 unique J



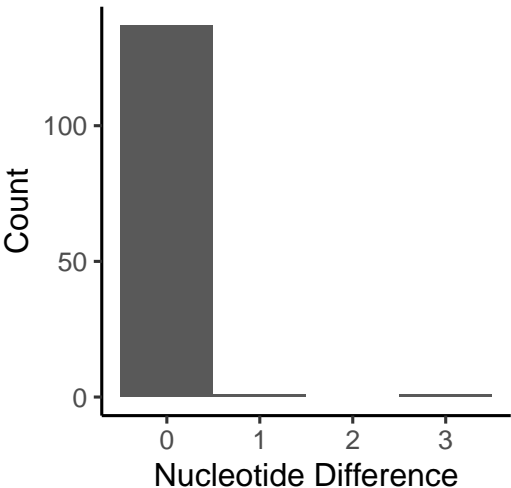
TRBV6-8*ap01

144 sequences assigned
142 (98.6%) exact matches, in which:
140 unique CDR3
14 unique J



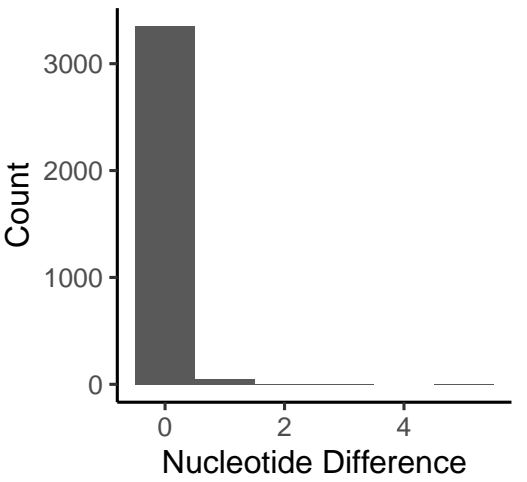
TRBV5-7*ap01

139 sequences assigned
137 (98.6%) exact matches, in which:
132 unique CDR3
14 unique J



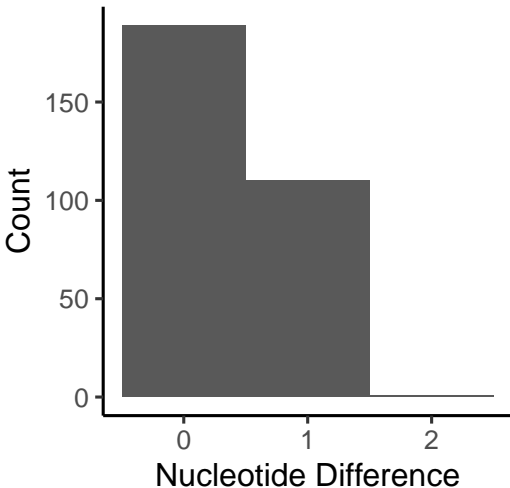
TRBV6-4*ap01

3405 sequences assigned
3352 (98.4%) exact matches, in which:
3285 unique CDR3
14 unique J



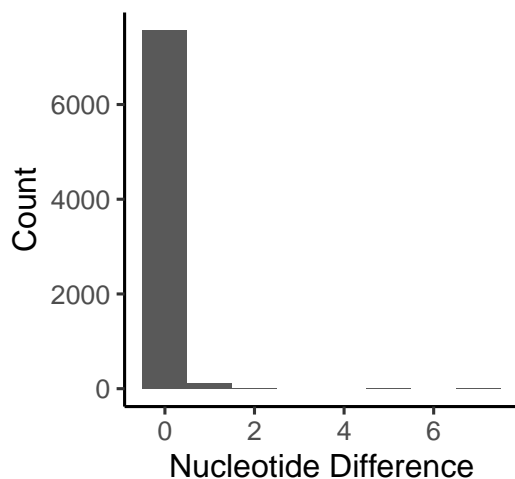
TRBV6-9*ap01

300 sequences assigned
189 (63%) exact matches, in which:
180 unique CDR3
14 unique J



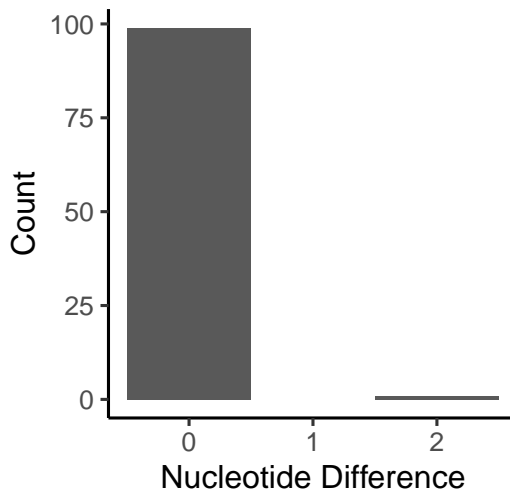
TRBV6-23*ap01

7686 sequences assigned
7565 (98.4%) exact matches, in which:
7297 unique CDR3
14 unique J



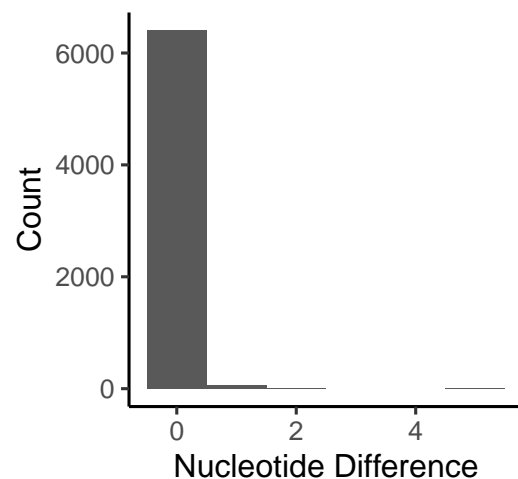
TRBV7-1*ap01_G291C_

100 sequences assigned
99 (99%) exact matches, in which:
97 unique CDR3
12 unique J



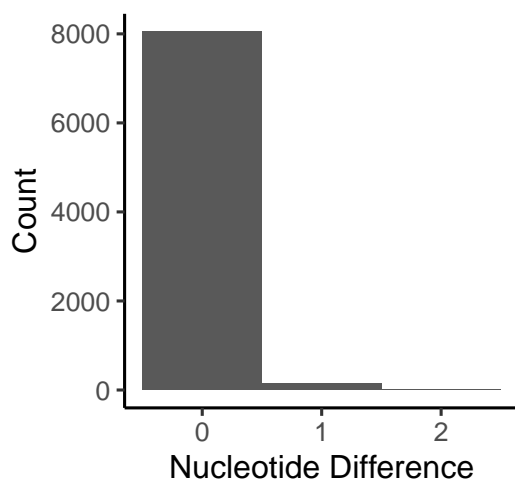
TRBV7-3*ap01

6473 sequences assigned
6404 (98.9%) exact matches, in which:
6265 unique CDR3
14 unique J



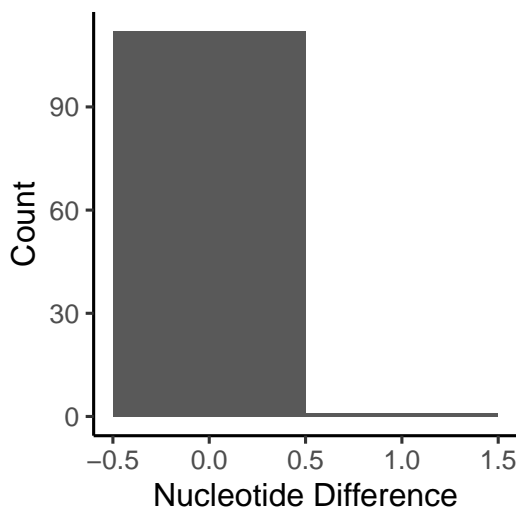
TRBV6-56*ap01

8187 sequences assigned
8048 (98.3%) exact matches, in which:
7790 unique CDR3
14 unique J



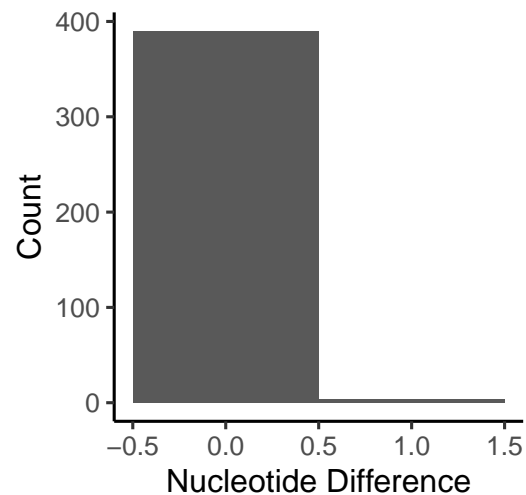
TRBV7-1*ap01_G291C_T

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



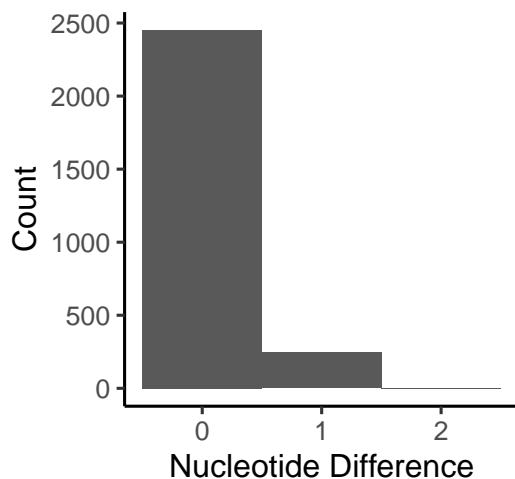
TRBV7-4*ap01

394 sequences assigned
390 (99%) exact matches, in which:
378 unique CDR3
14 unique J



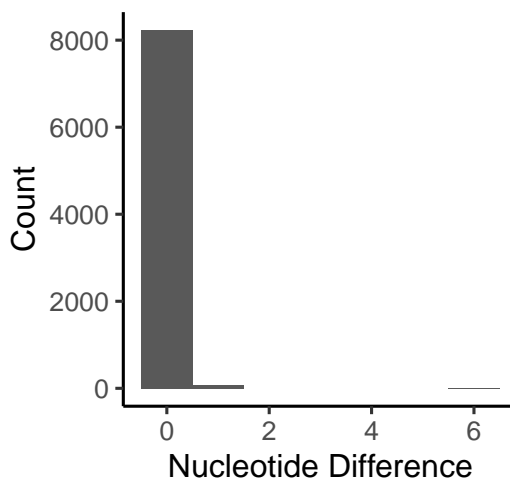
TRBV6-56*ap02

2698 sequences assigned
2452 (90.9%) exact matches, in which:
2376 unique CDR3
14 unique J



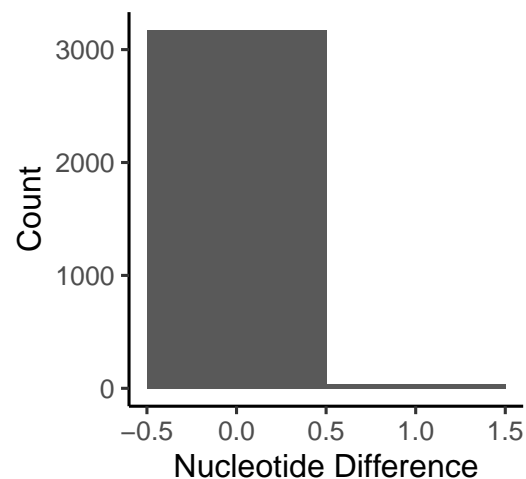
TRBV7-2*ap01

8308 sequences assigned
8232 (99.1%) exact matches, in which:
8104 unique CDR3
14 unique J



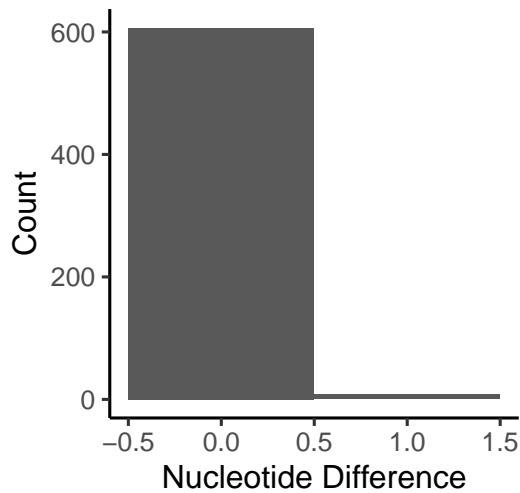
TRBV7-6*ap01

3212 sequences assigned
3173 (98.8%) exact matches, in which:
3114 unique CDR3
14 unique J



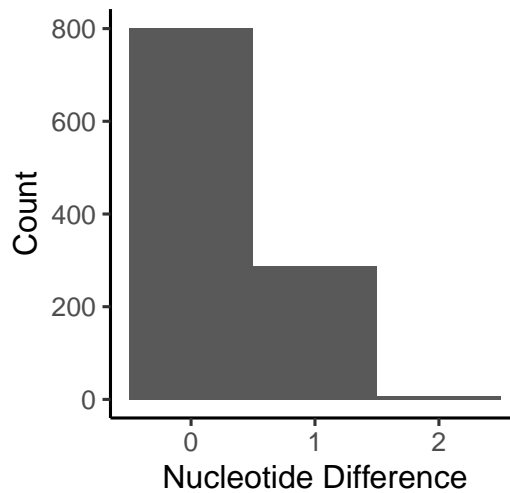
TRBV7-7*ap01

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



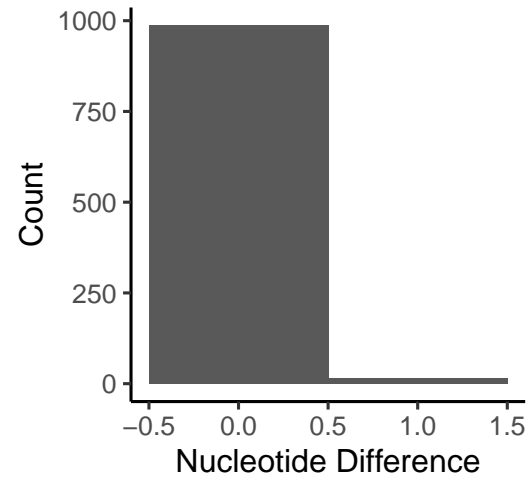
TRBV7-8*ap03

1096 sequences assigned
802 (73.2%) exact matches, in which:
789 unique CDR3
14 unique J



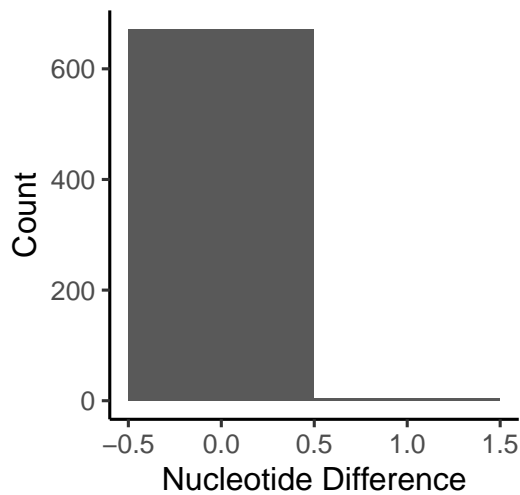
TRBV29-1*ap02

1002 sequences assigned
987 (98.5%) exact matches, in which:
960 unique CDR3
14 unique J



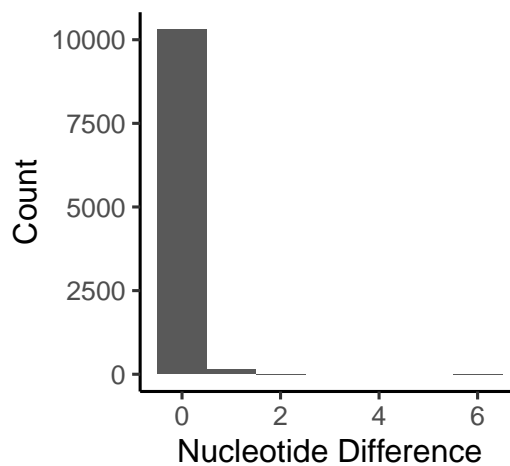
TRBV7-7*ap01_C315T

677 sequences assigned
672 (99.3%) exact matches, in which:
663 unique CDR3
13 unique J



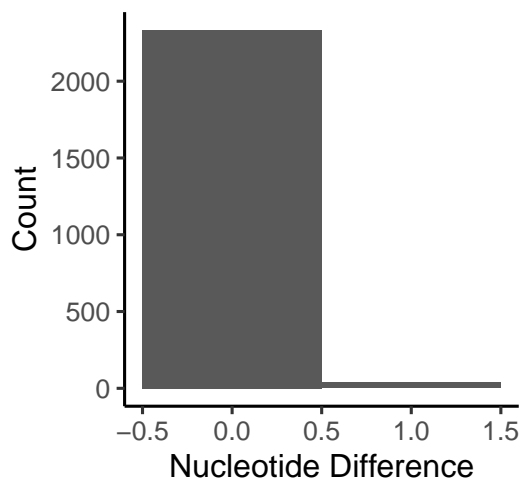
TRBV7-9*ap01

10443 sequences assigned
10306 (98.7%) exact matches, in which:
10070 unique CDR3
14 unique J



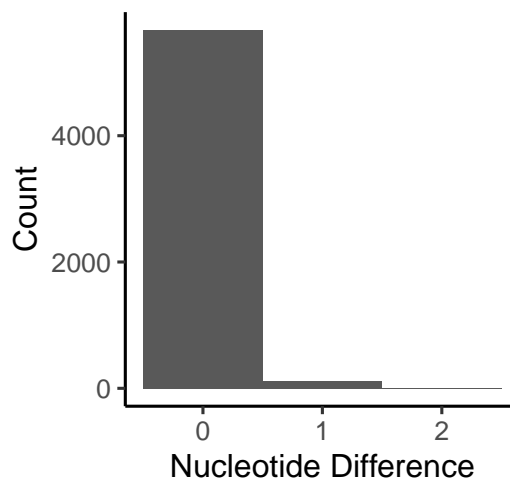
TRBV7-8*ap01

2372 sequences assigned
2333 (98.4%) exact matches, in which:
2289 unique CDR3
14 unique J

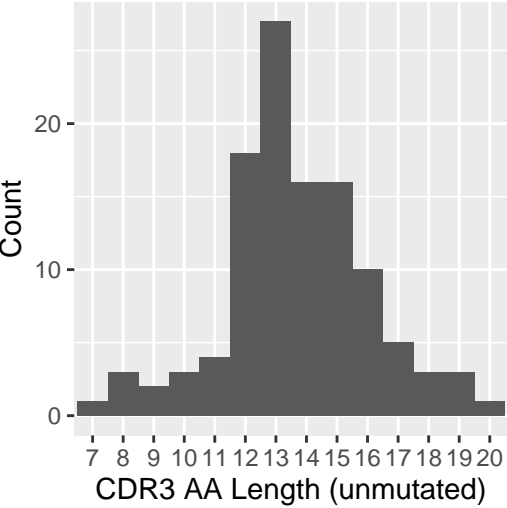


TRBV29-1*ap01

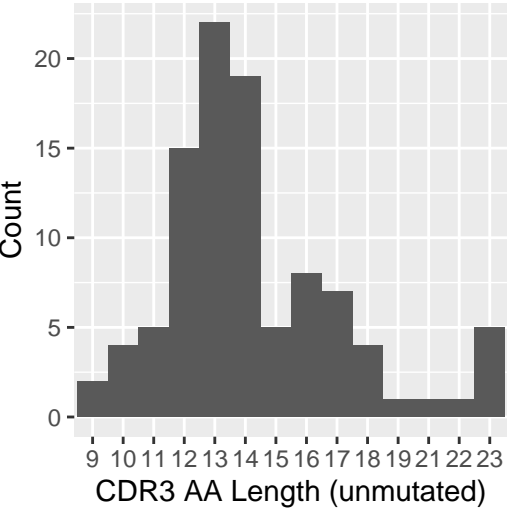
5787 sequences assigned
5673 (98%) exact matches, in which:
5502 unique CDR3
14 unique J



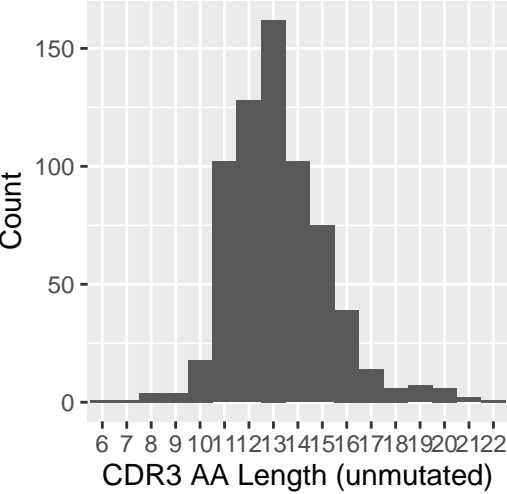
TRBV7-1*ap01_G291C_T296C_C314T

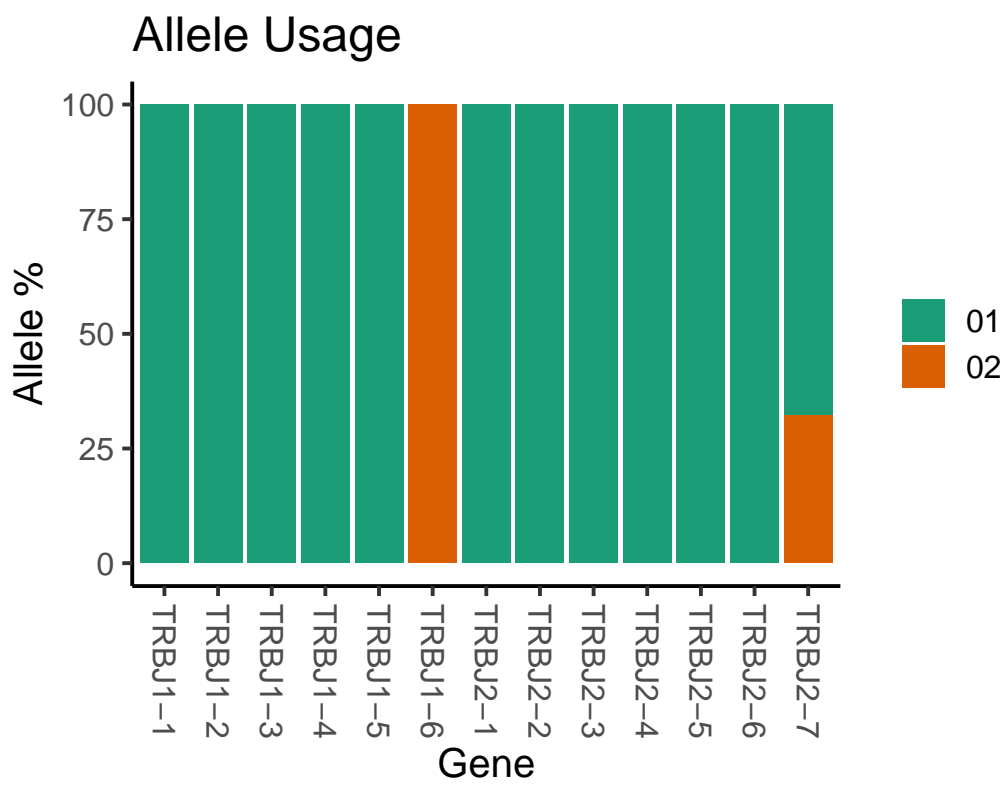


TRBV7-1*ap01_G291C_T296C

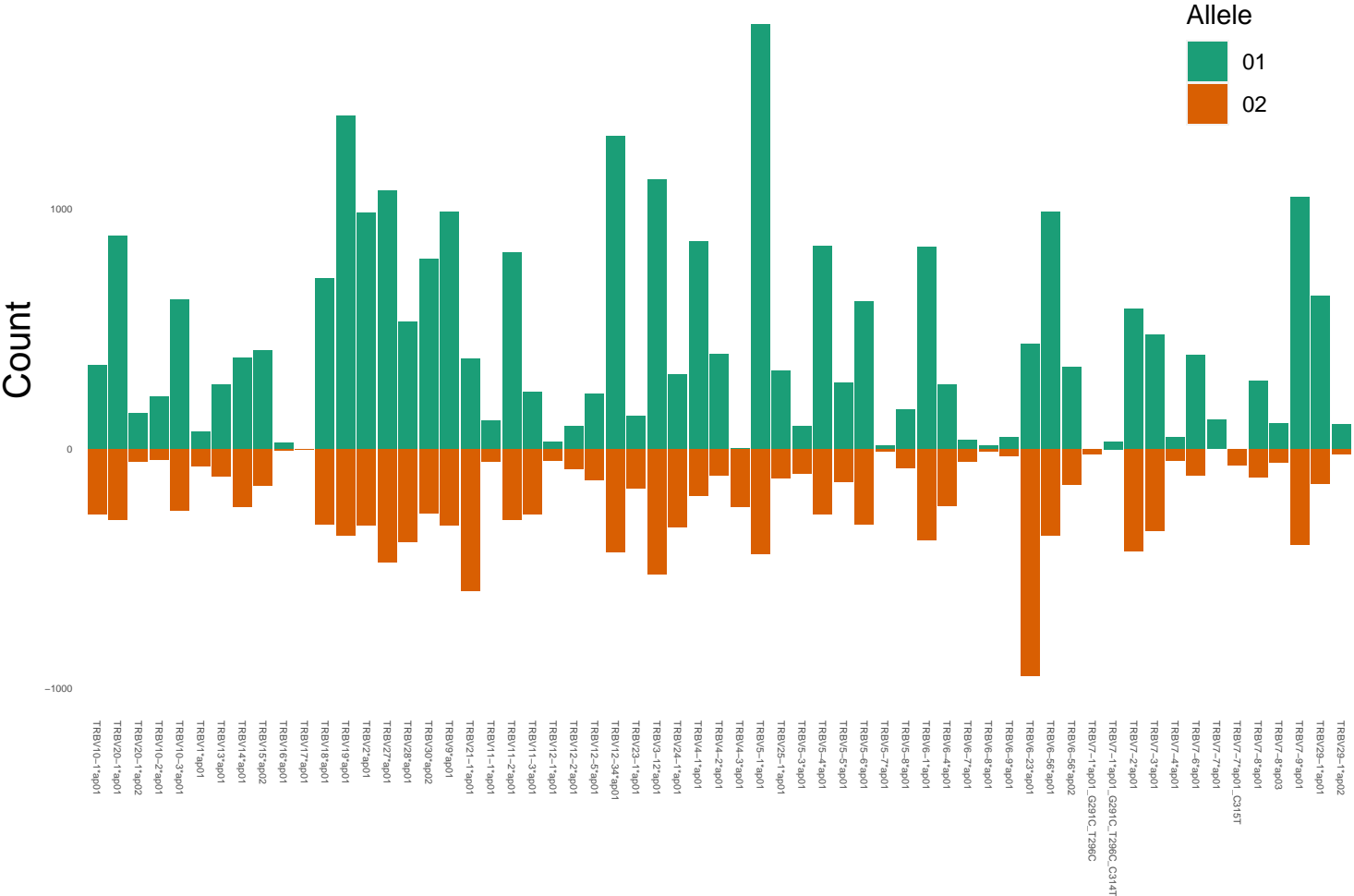


TRBV7-7*ap01_C315T





Sequence Count by TRBJ2–7 allele usage



[illegible]