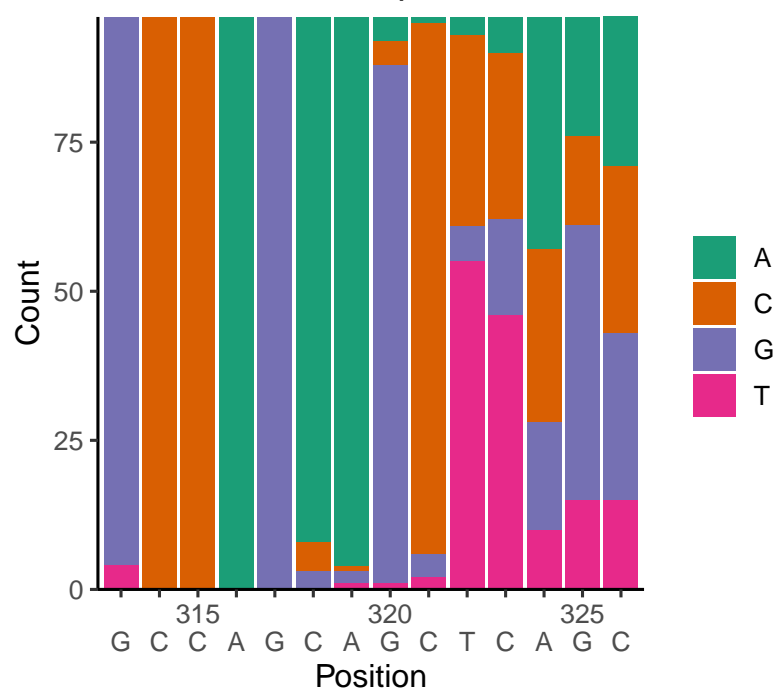
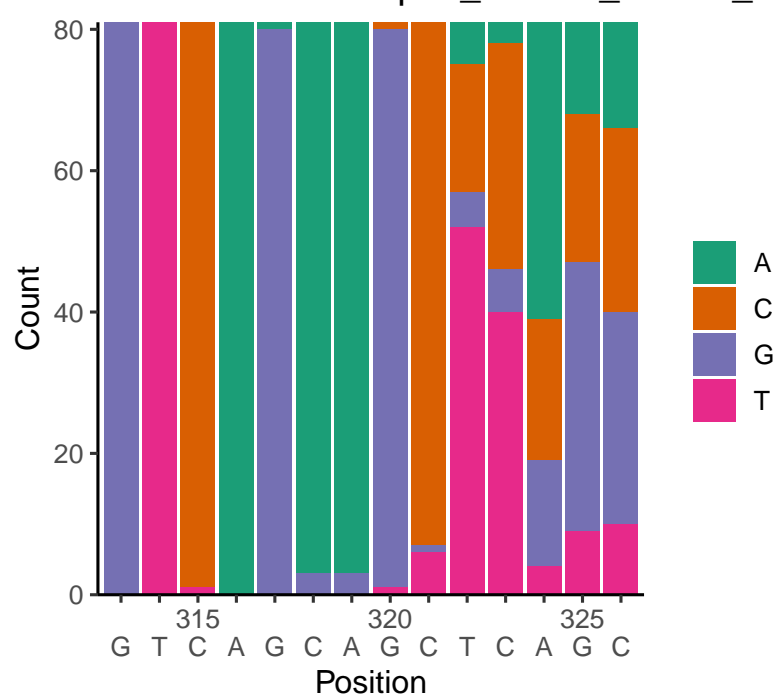


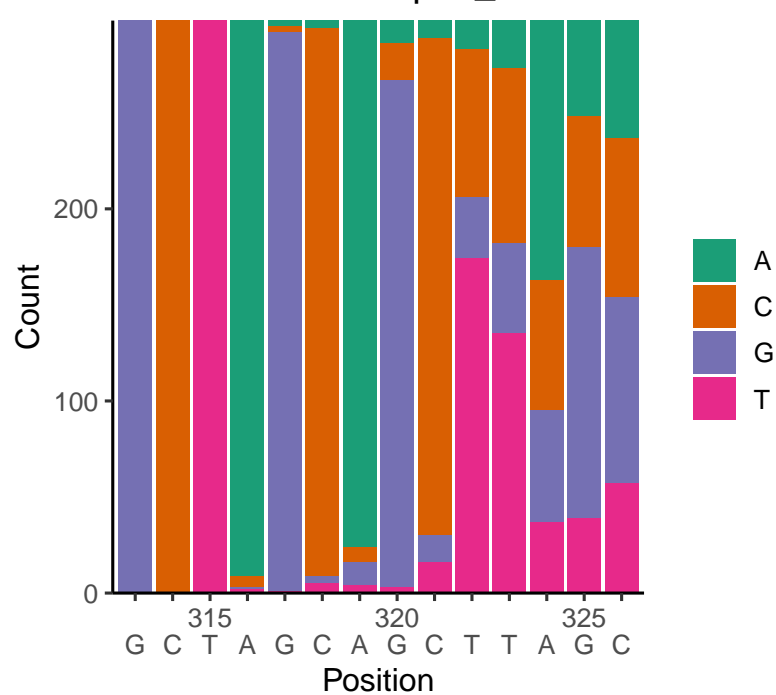
Gene TRBV7-1*ap01_G291C_T296C



Gene TRBV7-1*ap01_G291C_T296C_C314T



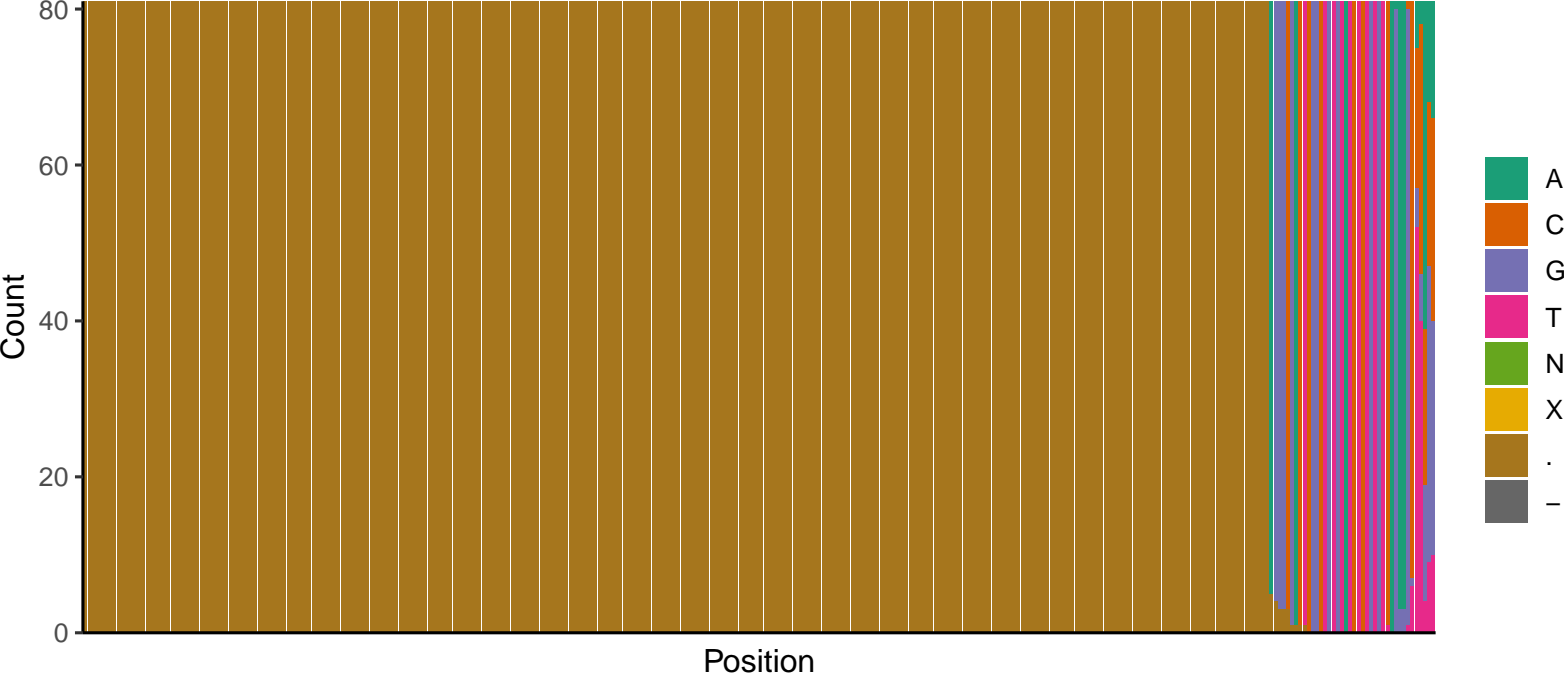
Gene TRBV7-7*ap01_C315T



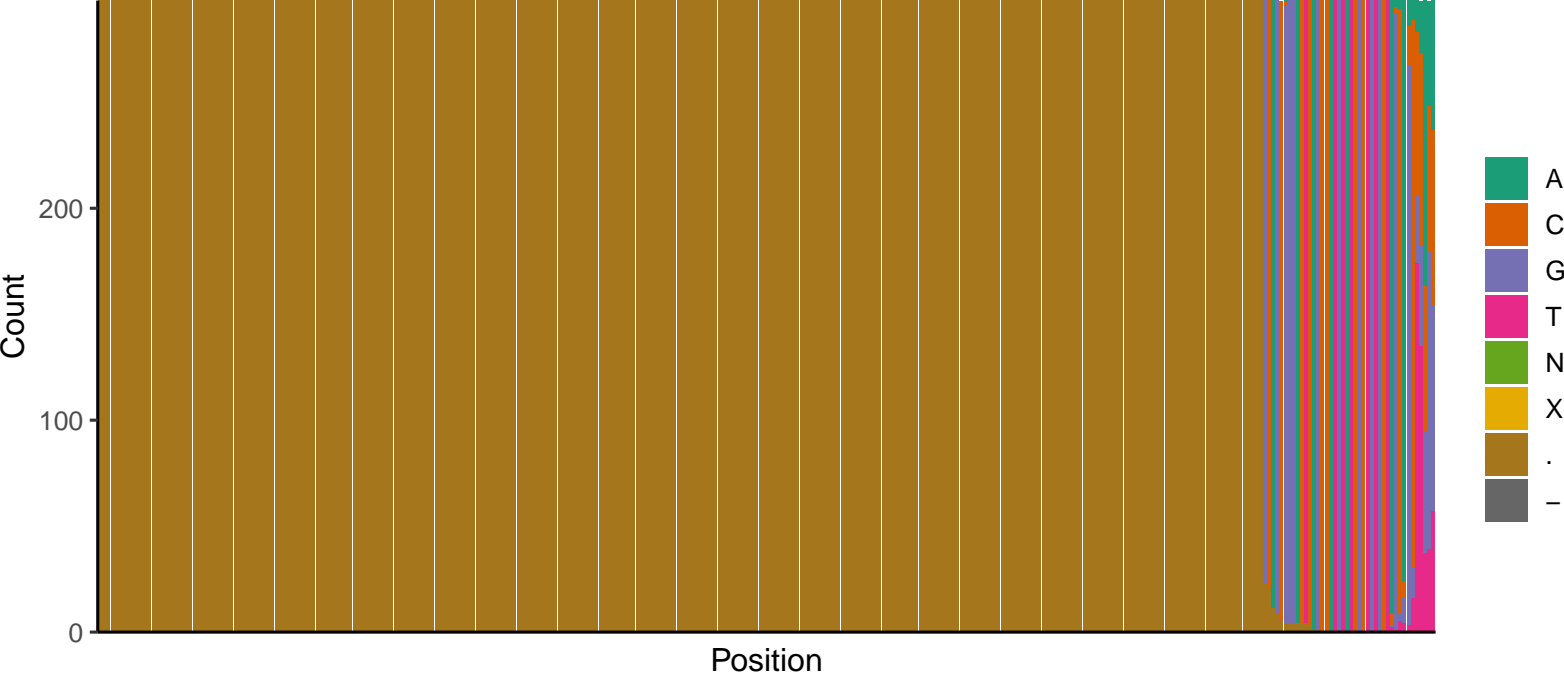
Gene TRBV7-1*ap01_G291C_T296C



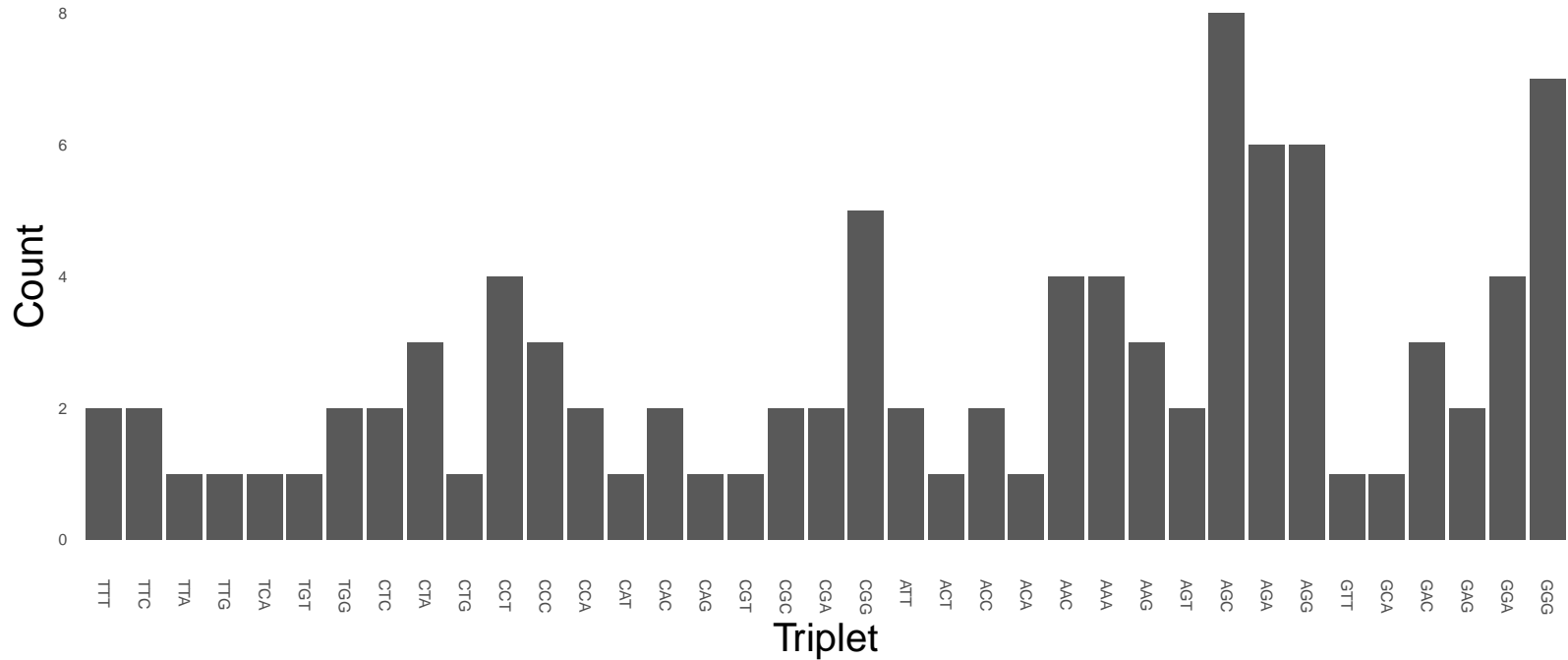
Gene TRBV7-1*ap01_G291C_T296C_C314T



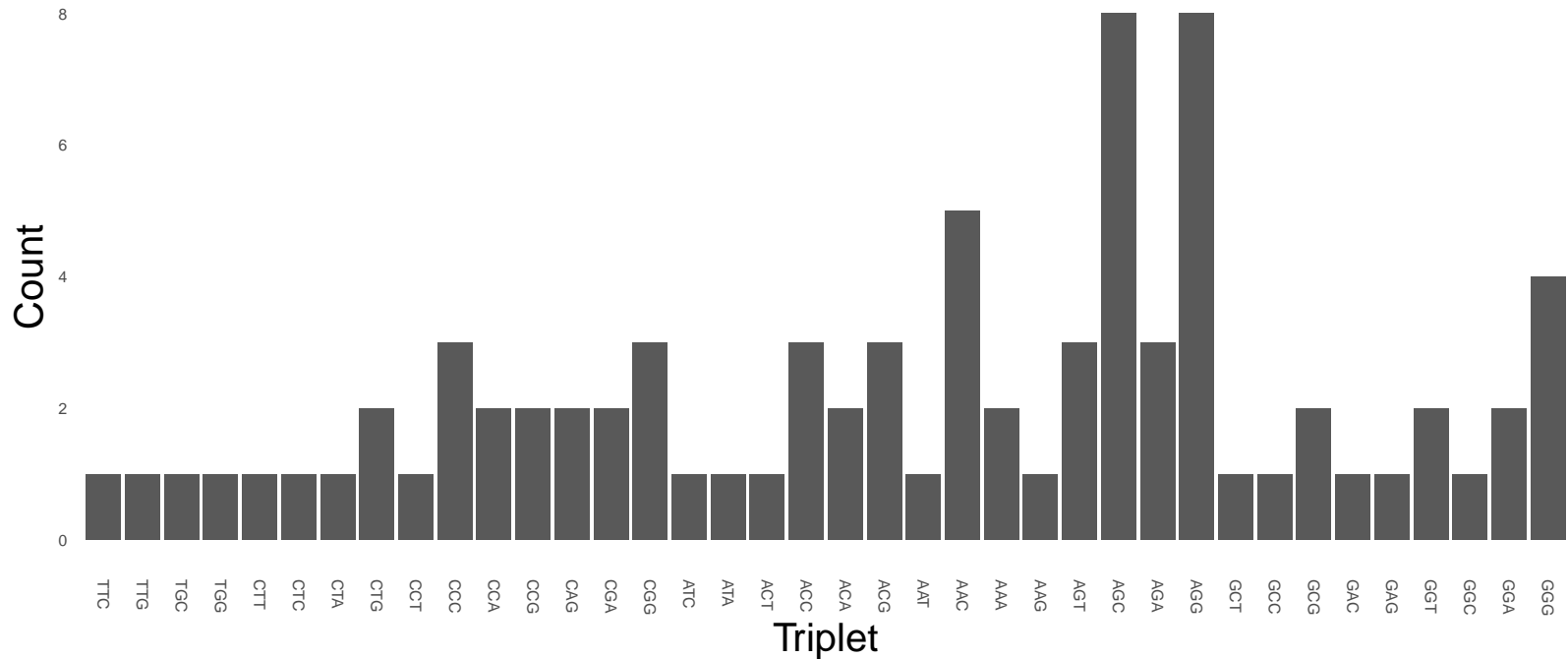
Gene TRBV7-7*ap01_C315T



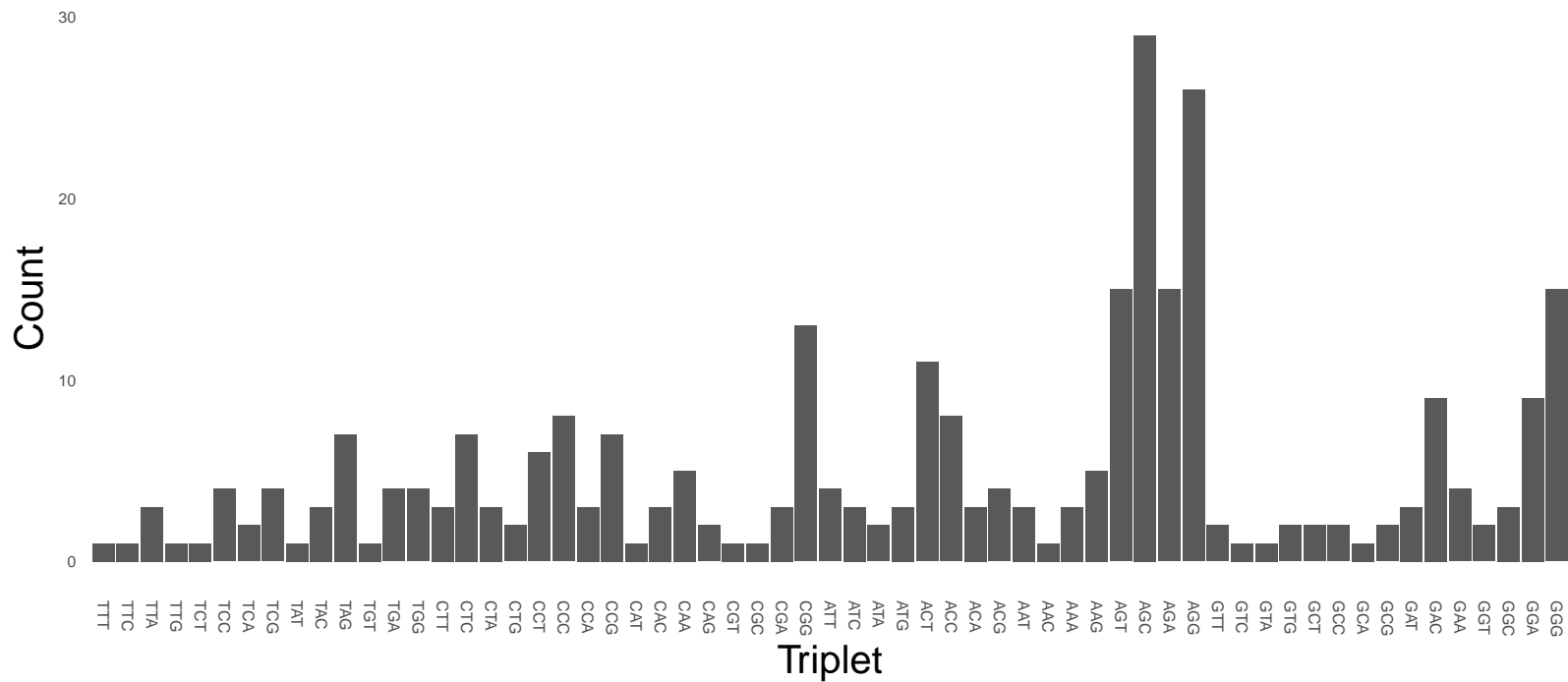
TRBV7-1*ap01_G291C_T296C- Final 3 nucleotides as a triplet



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

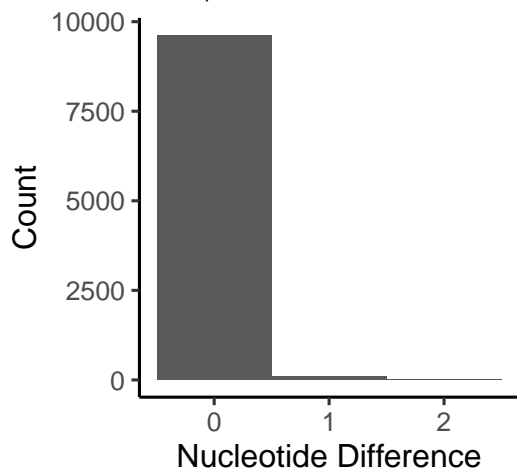


TRBV7-7*ap01_C315T- Final 3 nucleotides as a triplet



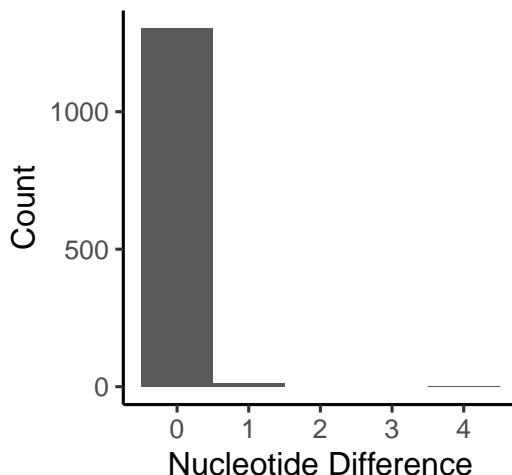
TRBV20-1*ap01

9731 sequences assigned
9624 (98.9%) exact matches, in which:
9468 unique CDR3
15 unique J



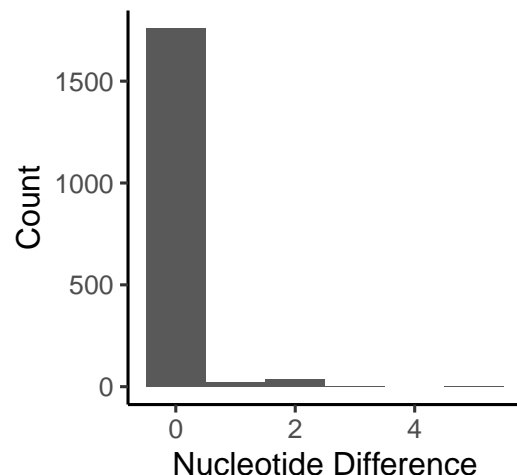
TRBV10-2*ap01

1316 sequences assigned
1303 (99%) exact matches, in which:
1270 unique CDR3
14 unique J



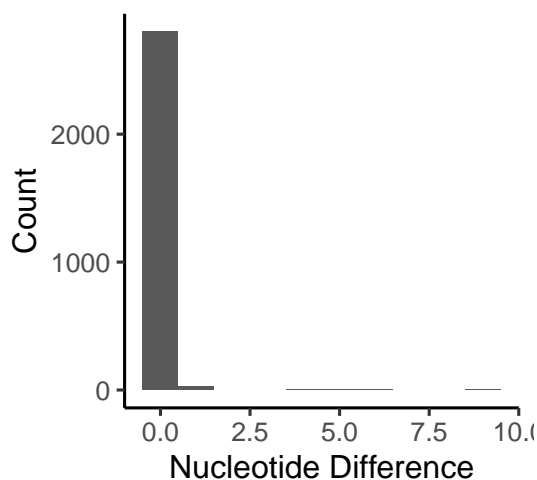
TRBV13*ap01

1820 sequences assigned
1759 (96.6%) exact matches, in which:
1734 unique CDR3
14 unique J



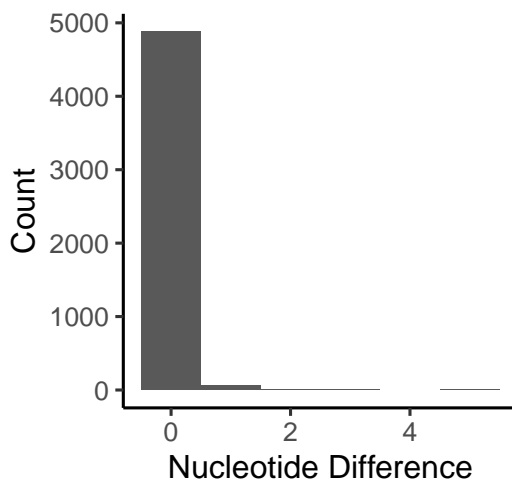
TRBV10-1*ap01

2836 sequences assigned
2801 (98.8%) exact matches, in which:
2729 unique CDR3
14 unique J



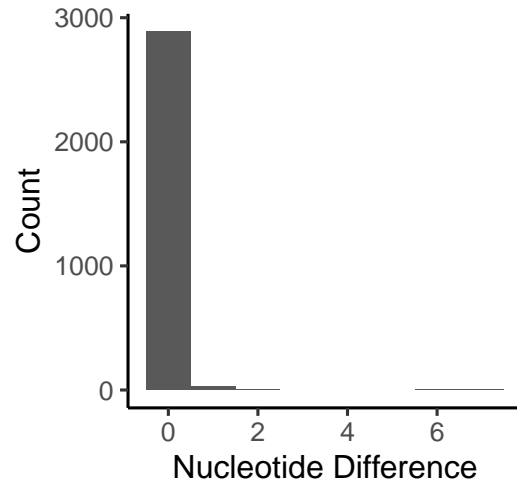
TRBV10-3*ap01

4939 sequences assigned
4879 (98.8%) exact matches, in which:
4779 unique CDR3
14 unique J



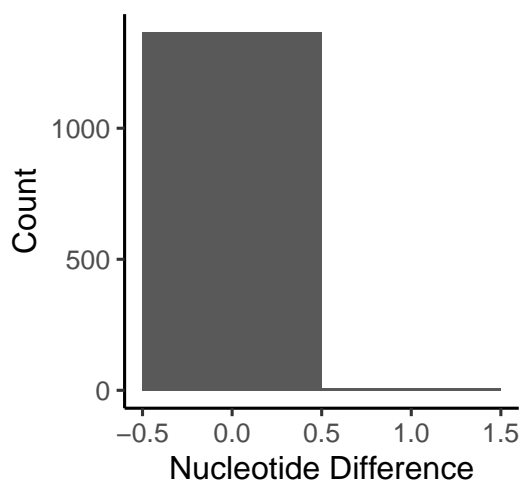
TRBV14*ap01

2921 sequences assigned
2887 (98.8%) exact matches, in which:
2850 unique CDR3
14 unique J



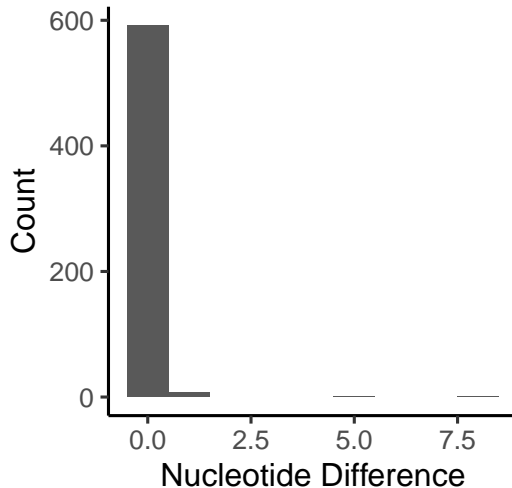
TRBV20-1*ap02

1375 sequences assigned
1367 (99.4%) exact matches, in which:
1348 unique CDR3
14 unique J



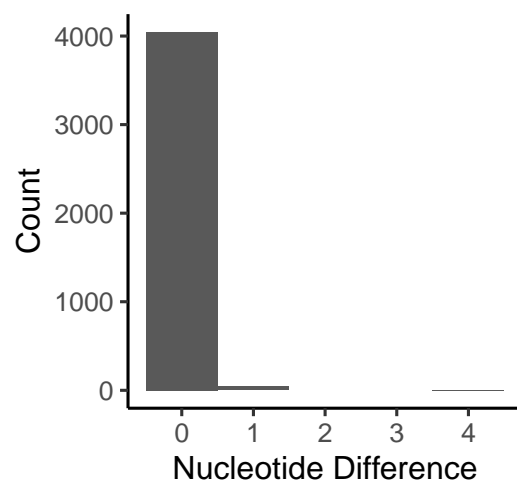
TRBV1*ap01

601 sequences assigned
592 (98.5%) exact matches, in which:
579 unique CDR3
14 unique J



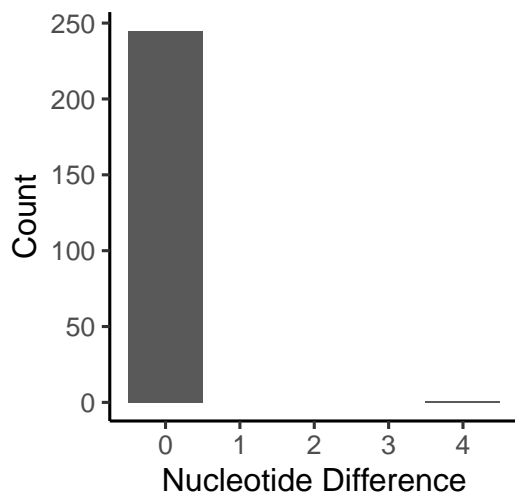
TRBV15*ap02

4088 sequences assigned
4045 (98.9%) exact matches, in which:
3950 unique CDR3
14 unique J



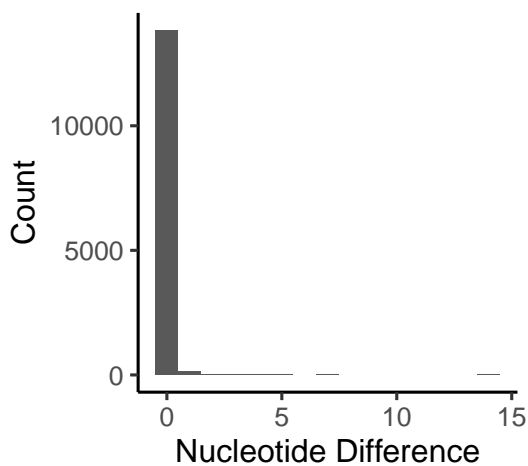
TRBV16*ap01

246 sequences assigned
245 (99.6%) exact matches, in which:
243 unique CDR3
14 unique J



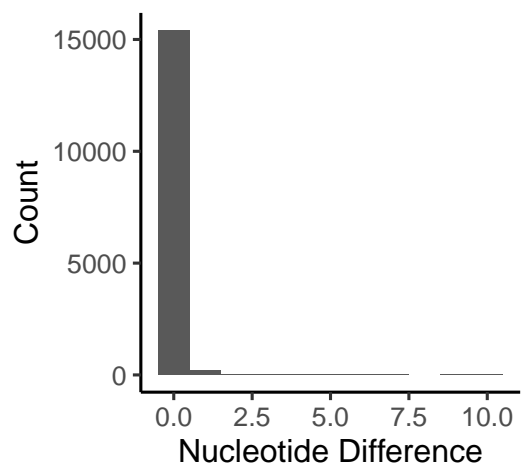
TRBV19*ap01

13984 sequences assigned
13838 (99%) exact matches, in which:
13698 unique CDR3
14 unique J



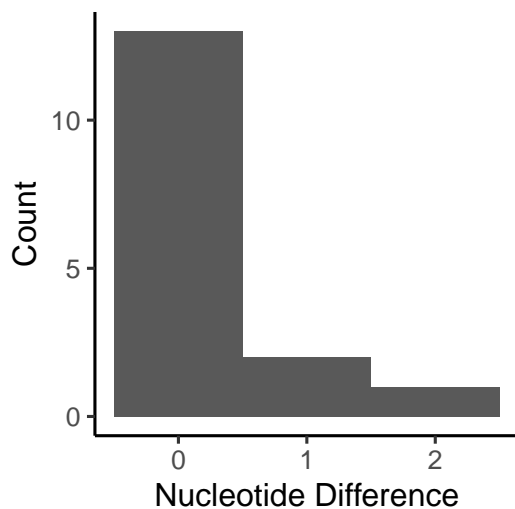
TRBV27*ap01

15624 sequences assigned
15417 (98.7%) exact matches, in which:
15026 unique CDR3
14 unique J



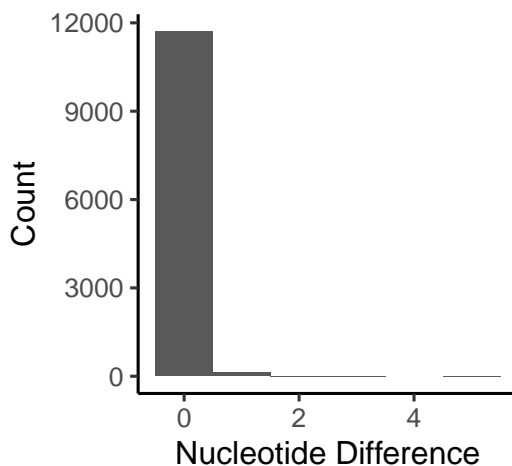
TRBV17*ap01

16 sequences assigned
13 (81.2%) exact matches, in which:
13 unique CDR3
7 unique J



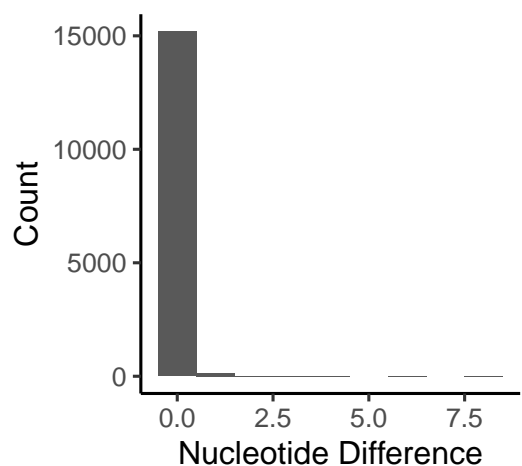
TRBV2*ap01

11848 sequences assigned
11707 (98.8%) exact matches, in which:
11490 unique CDR3
14 unique J



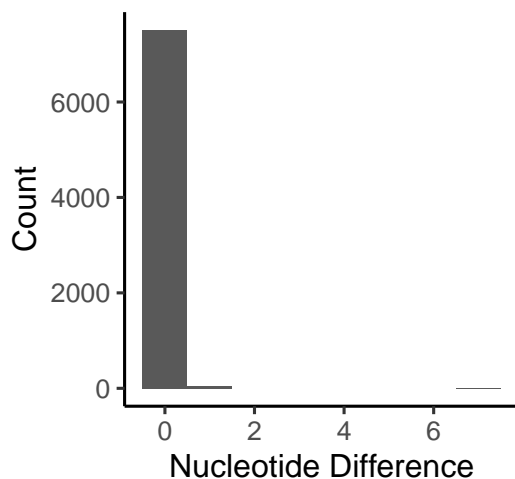
TRBV28*ap01

15333 sequences assigned
15192 (99.1%) exact matches, in which:
14834 unique CDR3
14 unique J



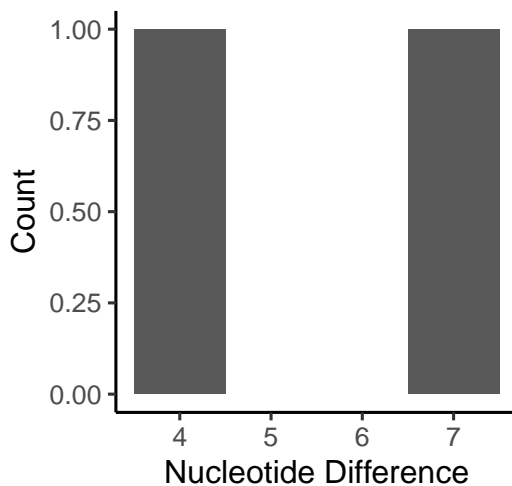
TRBV18*ap01

7557 sequences assigned
7508 (99.4%) exact matches, in which:
7404 unique CDR3
14 unique J



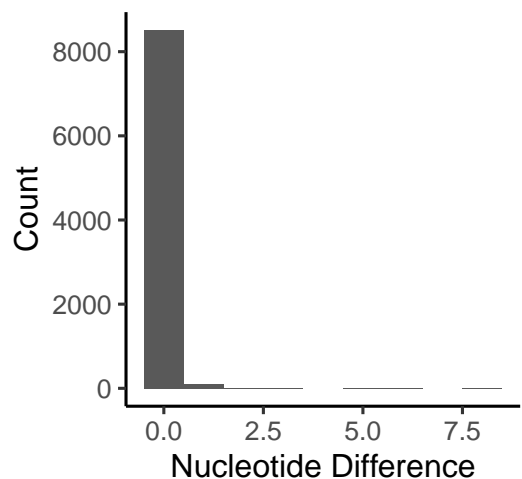
TRBV26*ap01

2 sequences assigned
No exact matches.



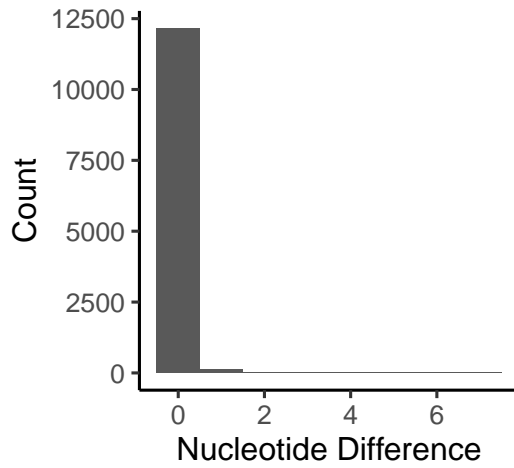
TRBV30*ap01

8637 sequences assigned
8514 (98.6%) exact matches, in which:
8414 unique CDR3
14 unique J



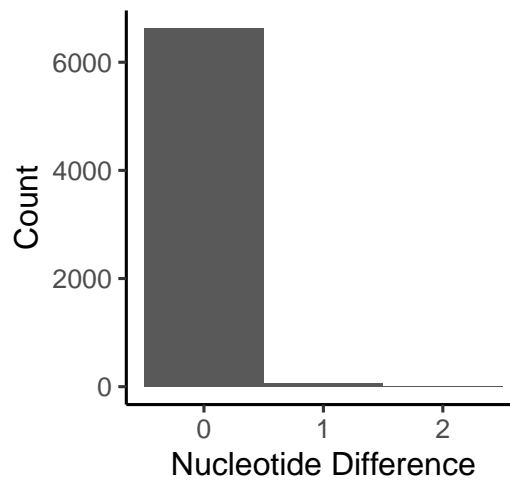
TRBV9*ap01

12293 sequences assigned
12164 (99%) exact matches, in which:
11960 unique CDR3
14 unique J



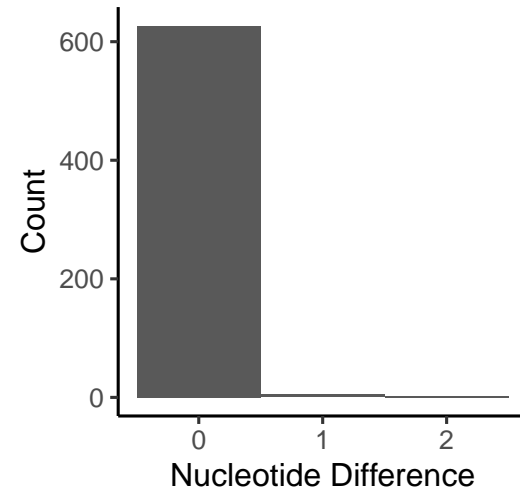
TRBV11-2*ap01

6698 sequences assigned
6626 (98.9%) exact matches, in which:
6496 unique CDR3
14 unique J



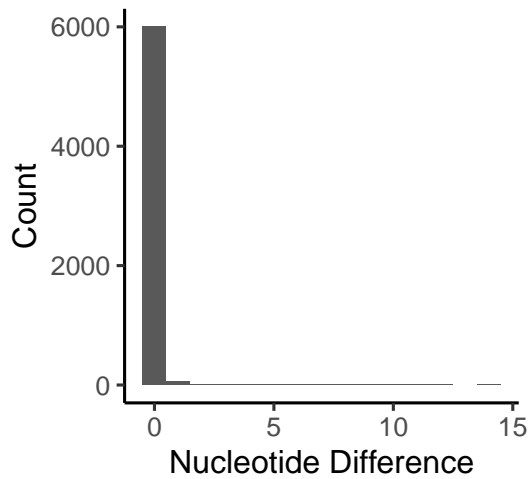
TRBV12-2*ap01

635 sequences assigned
627 (98.7%) exact matches, in which:
613 unique CDR3
14 unique J



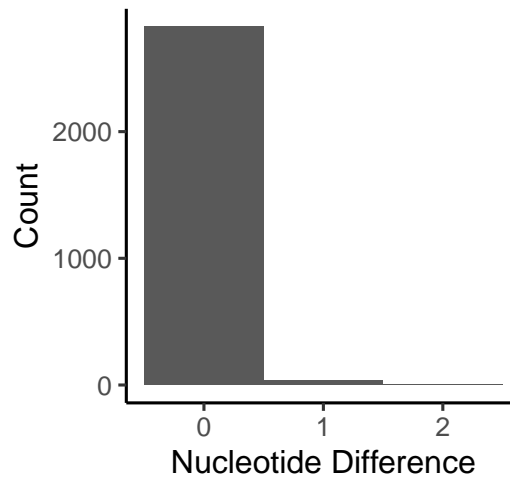
TRBV21-1*ap01

6100 sequences assigned
6002 (98.4%) exact matches, in which:
5893 unique CDR3
14 unique J



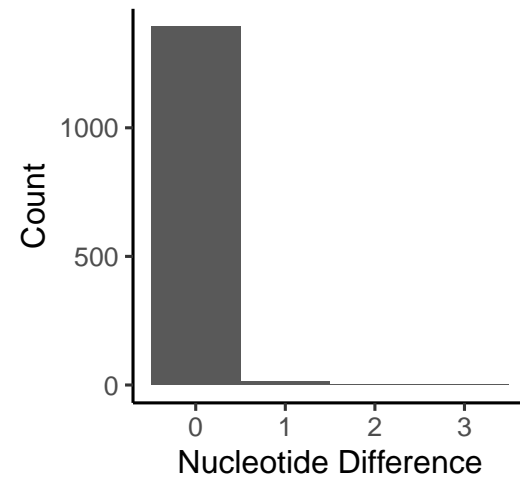
TRBV11-3*ap01

2863 sequences assigned
2828 (98.8%) exact matches, in which:
2781 unique CDR3
14 unique J



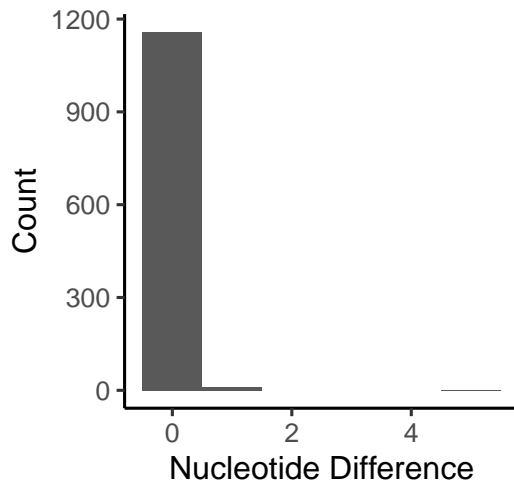
TRBV12-5*ap01

1410 sequences assigned
1393 (98.8%) exact matches, in which:
1356 unique CDR3
14 unique J



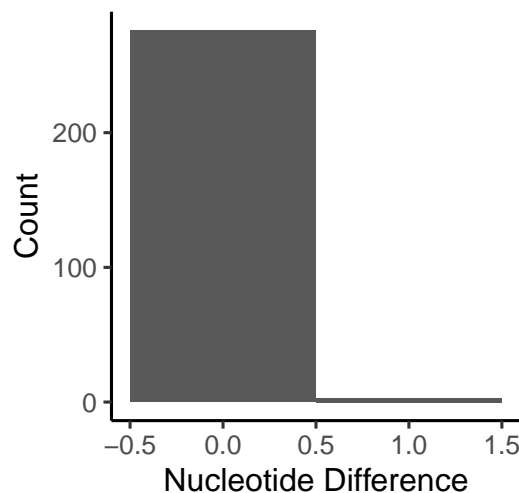
TRBV11-1*ap01

1170 sequences assigned
1158 (99%) exact matches, in which:
1140 unique CDR3
14 unique J



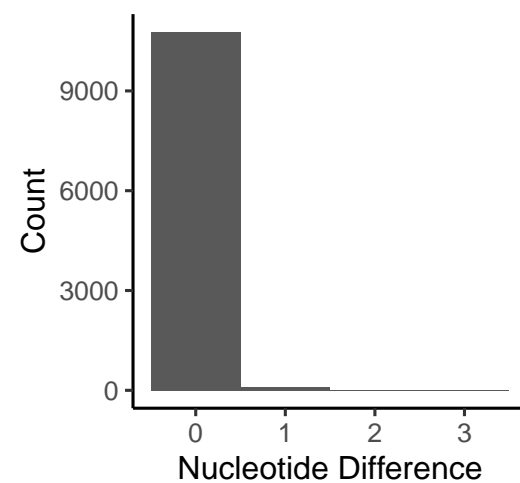
TRBV12-1*ap01

279 sequences assigned
276 (98.9%) exact matches, in which:
267 unique CDR3
14 unique J



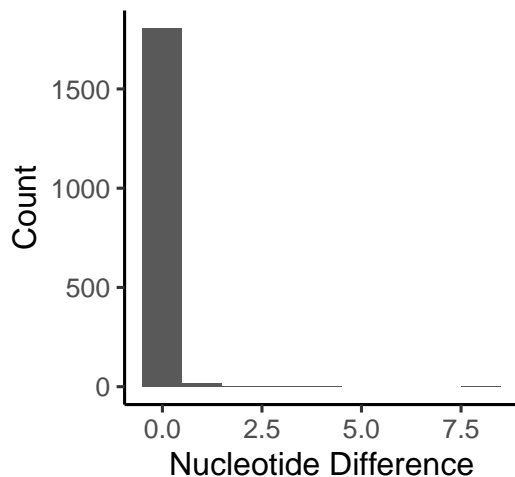
TRBV12-34*ap01

10872 sequences assigned
10769 (99.1%) exact matches, in which:
10601 unique CDR3
14 unique J



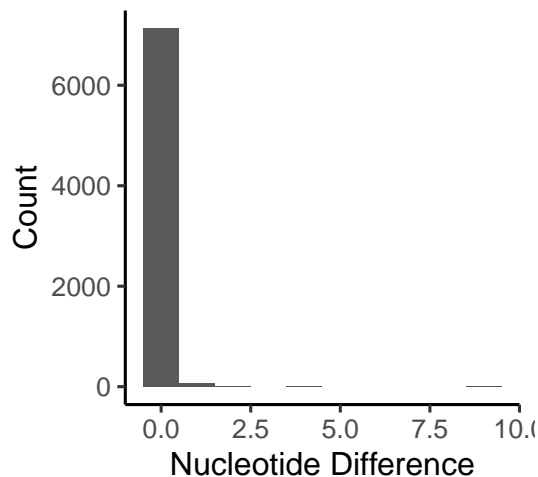
TRBV23-1*ap01

1834 sequences assigned
1805 (98.4%) exact matches, in which:
1771 unique CDR3
14 unique J



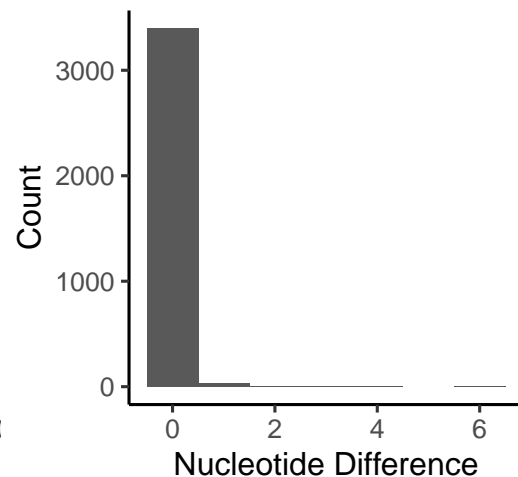
TRBV4-1*ap01

7211 sequences assigned
7132 (98.9%) exact matches, in which:
6996 unique CDR3
14 unique J



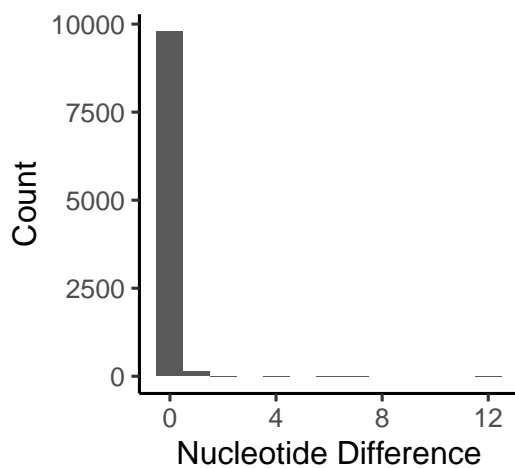
TRBV25-1*ap01

3440 sequences assigned
3397 (98.8%) exact matches, in which:
3337 unique CDR3
14 unique J



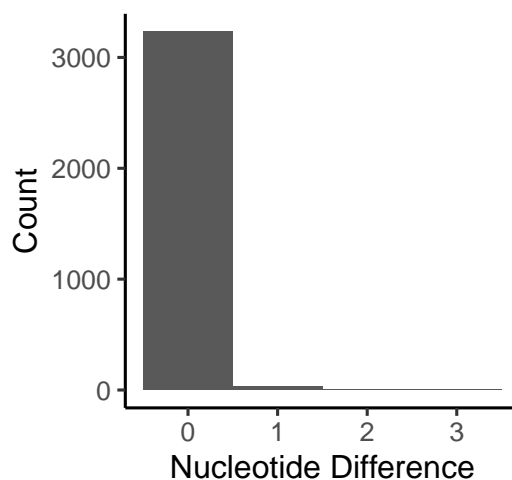
TRBV3-12*ap01

9928 sequences assigned
9791 (98.6%) exact matches, in which:
9620 unique CDR3
14 unique J



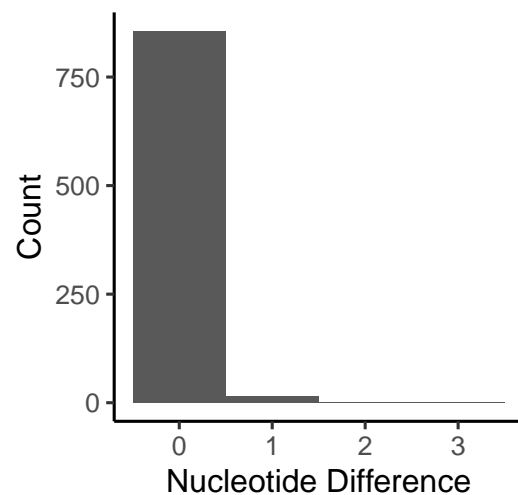
TRBV4-2*ap01

3265 sequences assigned
3232 (99%) exact matches, in which:
3186 unique CDR3
14 unique J



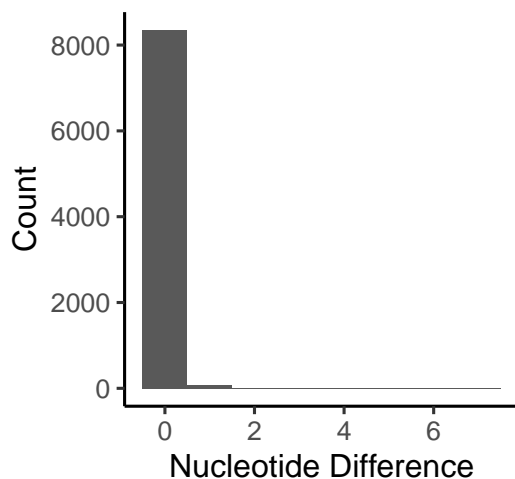
TRBV5-3*ap01

873 sequences assigned
856 (98.1%) exact matches, in which:
830 unique CDR3
14 unique J



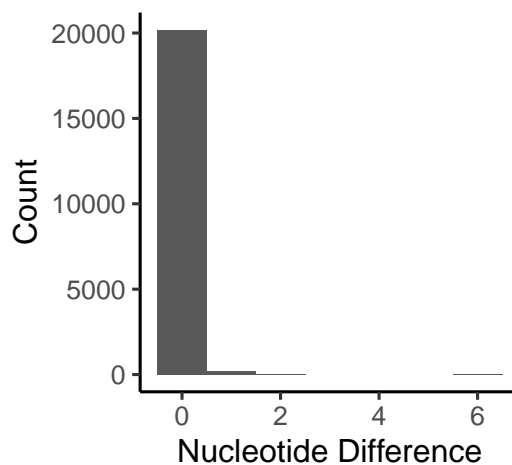
TRBV24-1*ap01

8444 sequences assigned
8350 (98.9%) exact matches, in which:
8233 unique CDR3
14 unique J



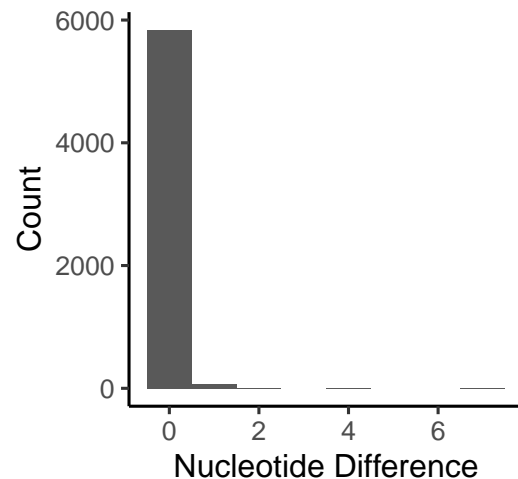
TRBV5-1*ap01

20410 sequences assigned
20189 (98.9%) exact matches, in which:
19783 unique CDR3
14 unique J



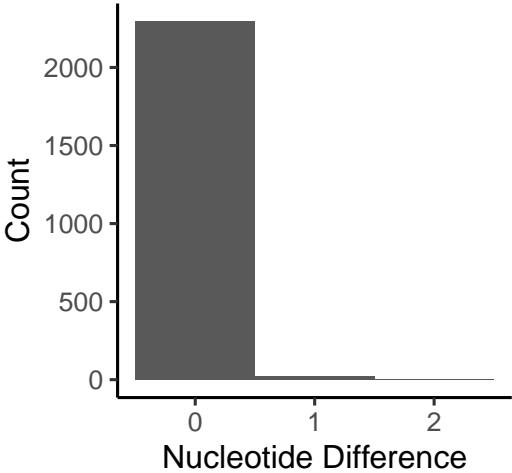
TRBV5-4*ap01

5915 sequences assigned
5837 (98.7%) exact matches, in which:
5726 unique CDR3
14 unique J



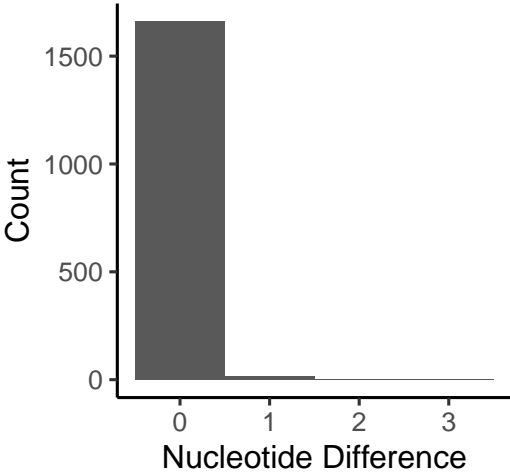
TRBV5-5*ap01

2319 sequences assigned
2295 (99%) exact matches, in which:
2266 unique CDR3
14 unique J



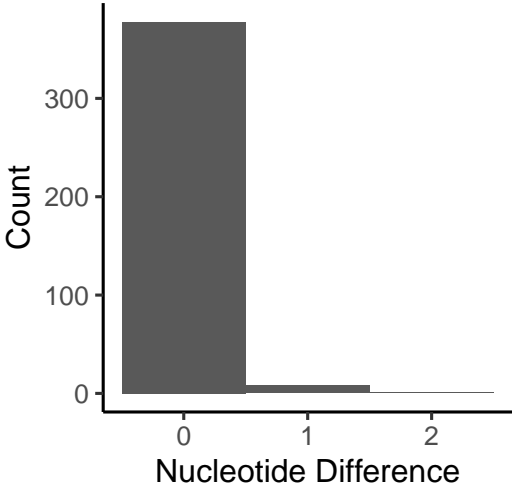
TRBV5-8*ap01

1683 sequences assigned
1661 (98.7%) exact matches, in which:
1631 unique CDR3
14 unique J



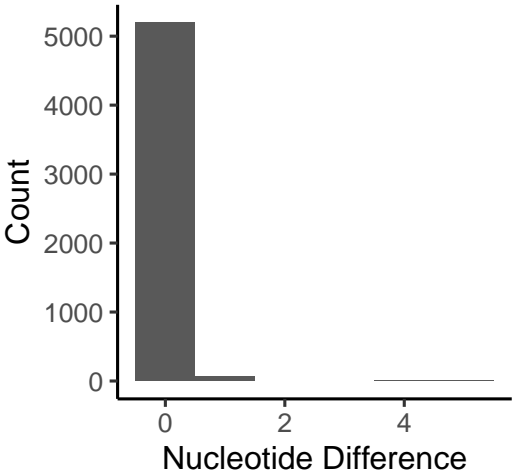
TRBV6-7*ap01

387 sequences assigned
378 (97.7%) exact matches, in which:
368 unique CDR3
14 unique J



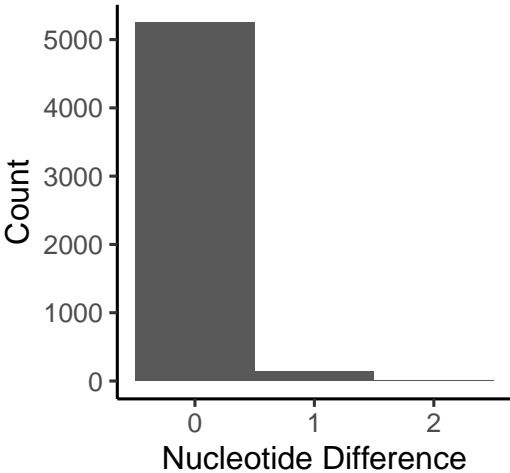
TRBV5-6*ap01

5265 sequences assigned
5195 (98.7%) exact matches, in which:
5065 unique CDR3
14 unique J



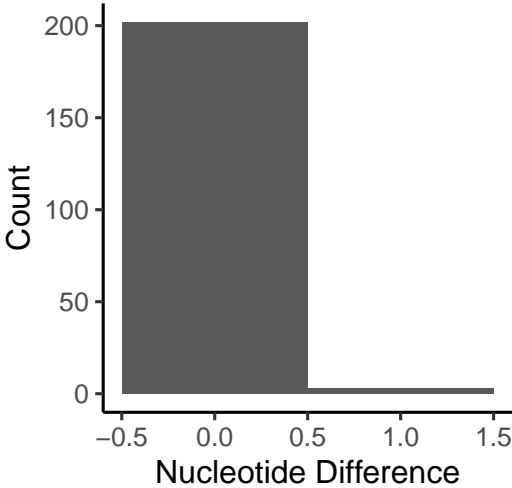
TRBV6-1*ap01

5385 sequences assigned
5247 (97.4%) exact matches, in which:
5126 unique CDR3
14 unique J



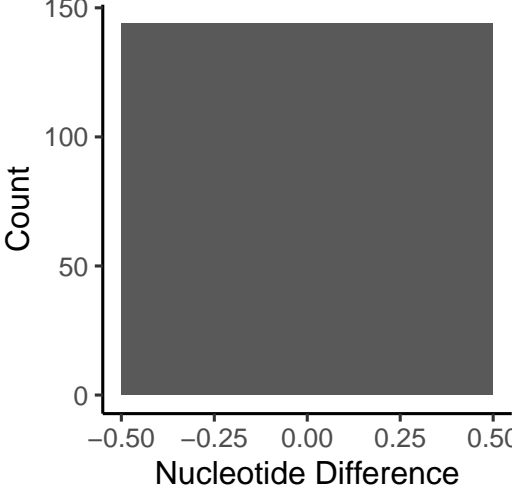
TRBV6-8*ap01

205 sequences assigned
202 (98.5%) exact matches, in which:
193 unique CDR3
14 unique J



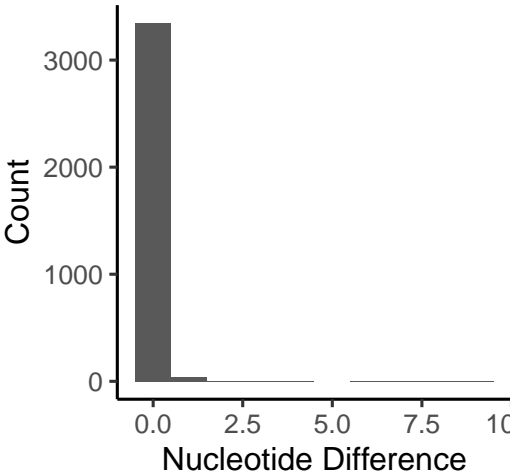
TRBV5-7*ap01

144 sequences assigned
144 (100%) exact matches, in which:
143 unique CDR3
13 unique J



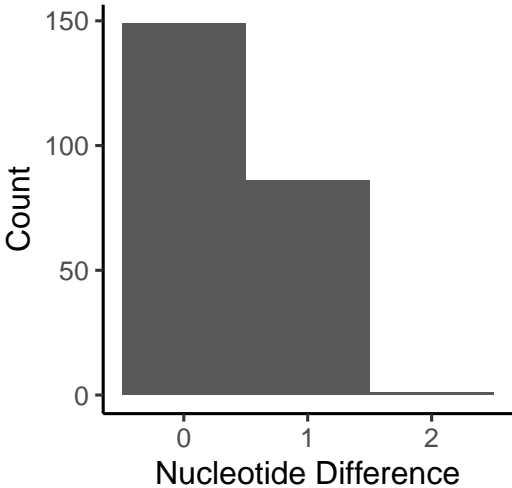
TRBV6-4*ap01

3398 sequences assigned
3346 (98.5%) exact matches, in which:
3286 unique CDR3
14 unique J



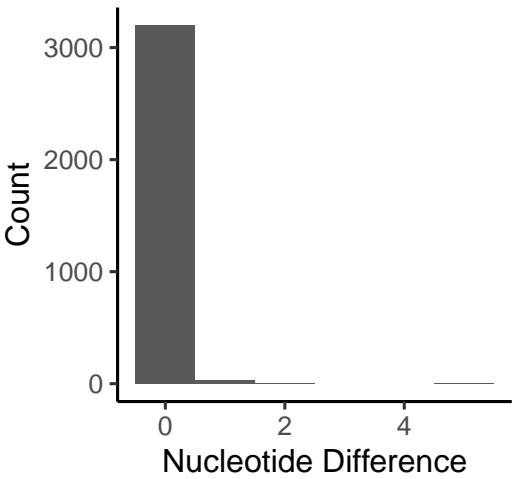
TRBV6-9*ap01

236 sequences assigned
149 (63.1%) exact matches, in which:
146 unique CDR3
14 unique J



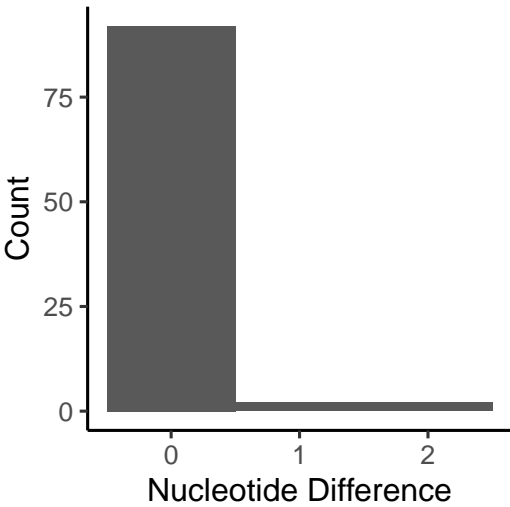
TRBV6-23*ap01

3233 sequences assigned
3198 (98.9%) exact matches, in which:
3122 unique CDR3
14 unique J



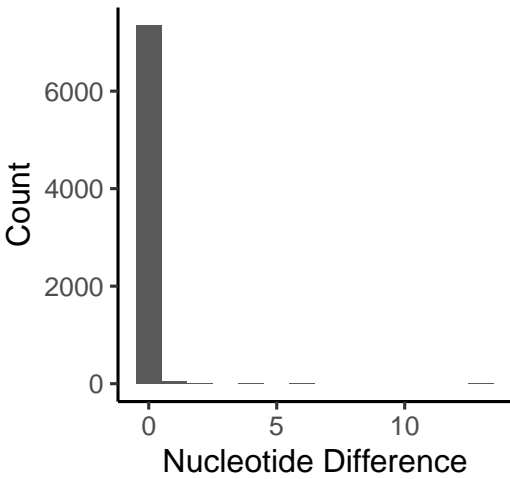
TRBV7-1*ap01_G291C_T

96 sequences assigned
92 (95.8%) exact matches, in which:
89 unique CDR3
11 unique J



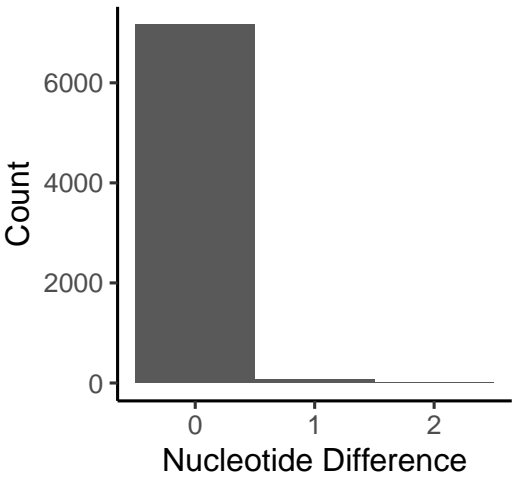
TRBV7-3*ap01

7422 sequences assigned
7348 (99%) exact matches, in which:
7222 unique CDR3
14 unique J



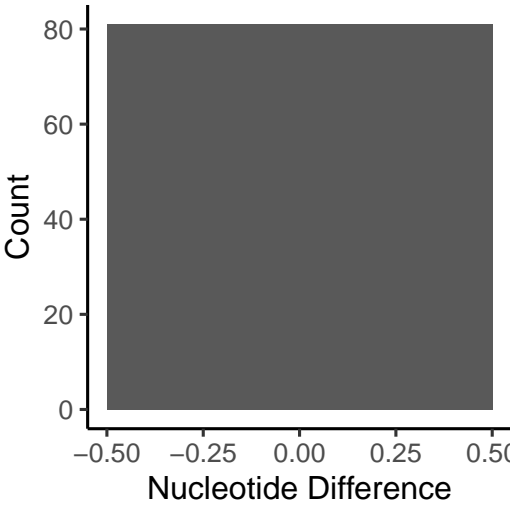
TRBV6-56*ap01

7231 sequences assigned
7161 (99%) exact matches, in which:
7018 unique CDR3
14 unique J



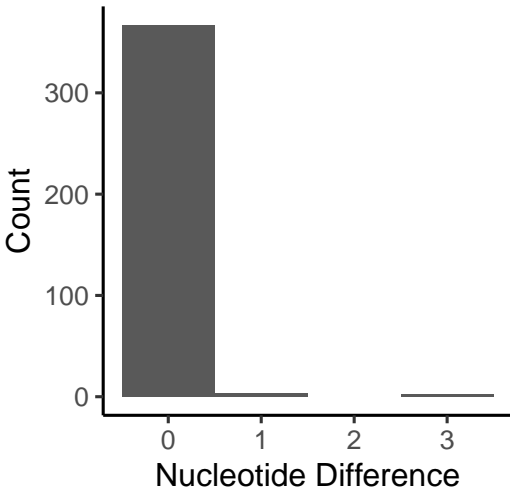
TRBV7-1*ap01_G291C_T

81 sequences assigned
81 (100%) exact matches, in which:
79 unique CDR3
13 unique J



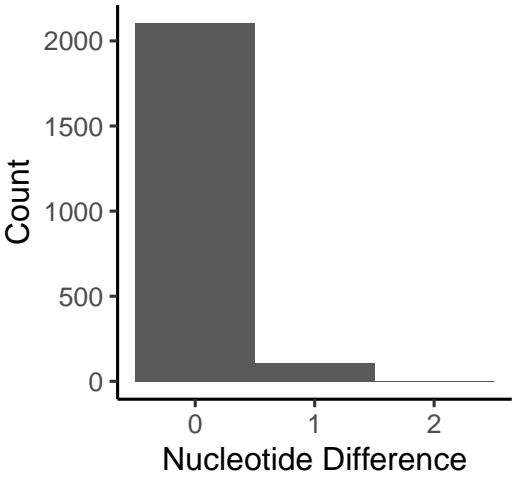
TRBV7-4*ap01

372 sequences assigned
367 (98.7%) exact matches, in which:
356 unique CDR3
14 unique J



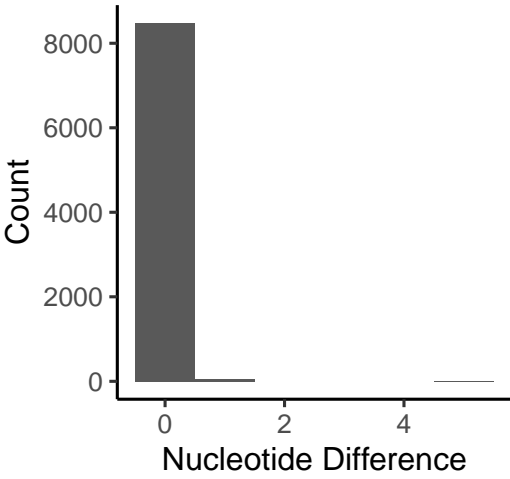
TRBV6-56*ap02

2213 sequences assigned
2105 (95.1%) exact matches, in which:
2059 unique CDR3
14 unique J



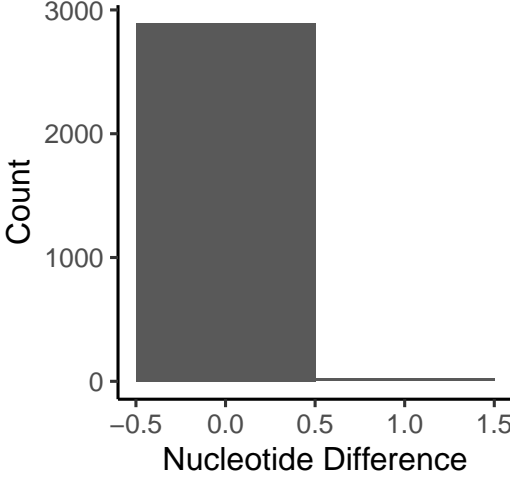
TRBV7-2*ap01

8540 sequences assigned
8478 (99.3%) exact matches, in which:
8325 unique CDR3
14 unique J



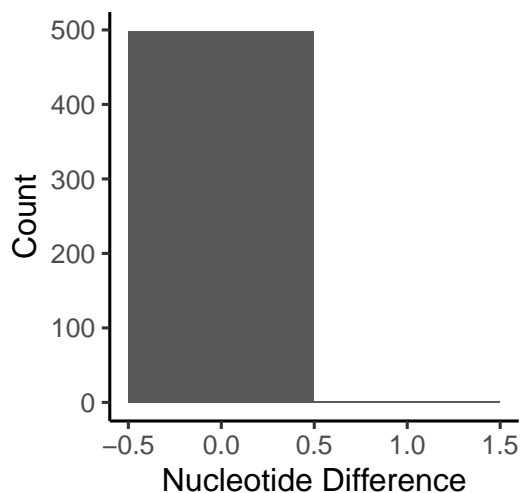
TRBV7-6*ap01

2916 sequences assigned
2894 (99.2%) exact matches, in which:
2841 unique CDR3
14 unique J



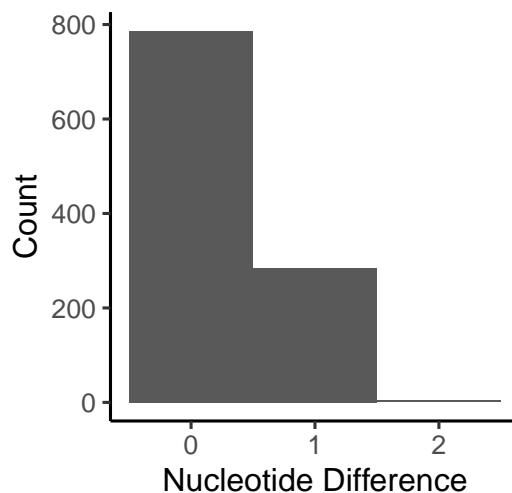
TRBV7-7*ap01

501 sequences assigned
499 (99.6%) exact matches, in which:
493 unique CDR3
13 unique J



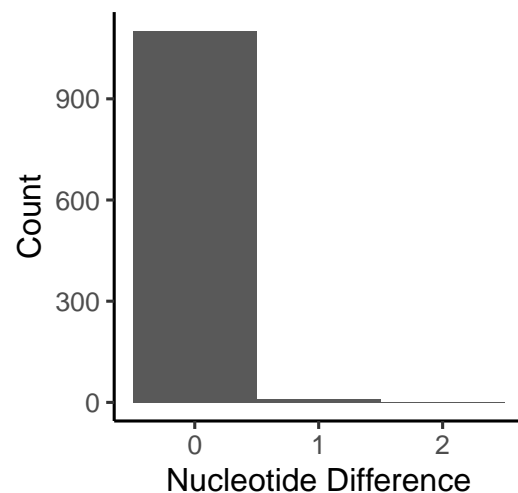
TRBV7-8*ap03

1075 sequences assigned
787 (73.2%) exact matches, in which:
768 unique CDR3
14 unique J



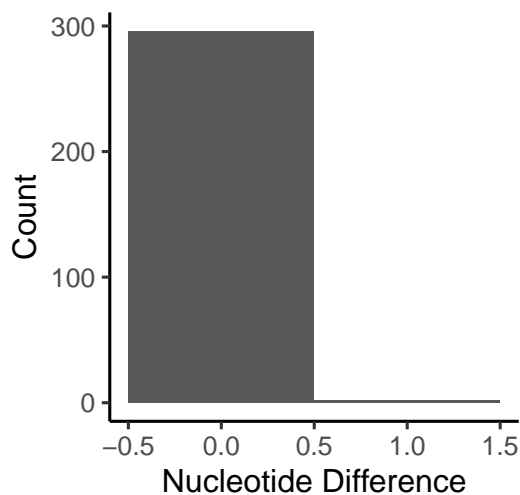
TRBV29-1*ap02

1114 sequences assigned
1102 (98.9%) exact matches, in which:
1091 unique CDR3
14 unique J



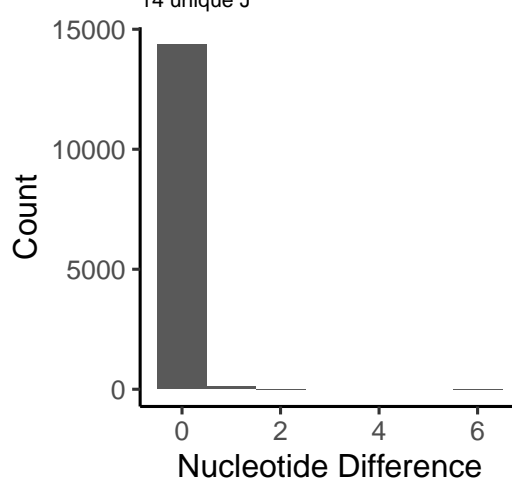
TRBV7-7*ap01_C315T

298 sequences assigned
296 (99.3%) exact matches, in which:
293 unique CDR3
13 unique J



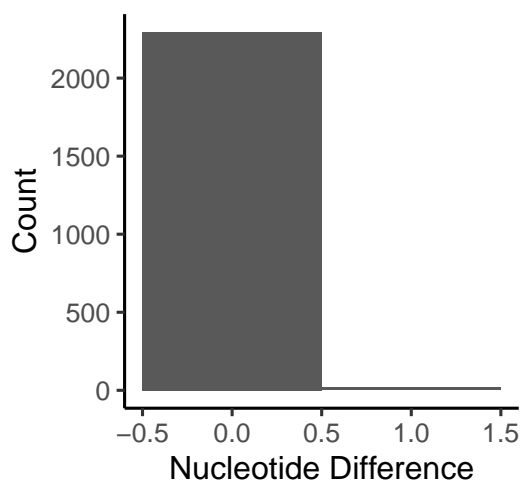
TRBV7-9*ap01

14475 sequences assigned
14366 (99.2%) exact matches, in which:
14181 unique CDR3
14 unique J



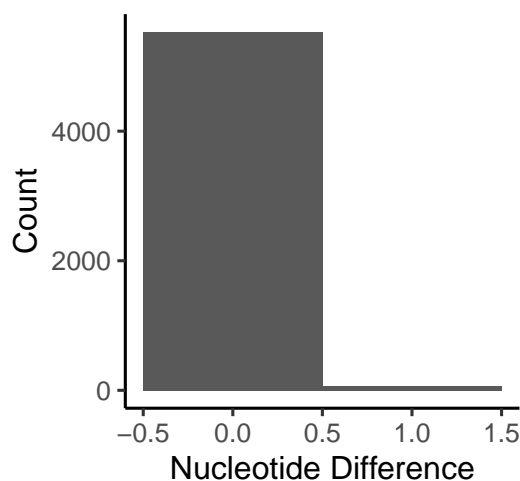
TRBV7-8*ap01

2312 sequences assigned
2295 (99.3%) exact matches, in which:
2244 unique CDR3
14 unique J

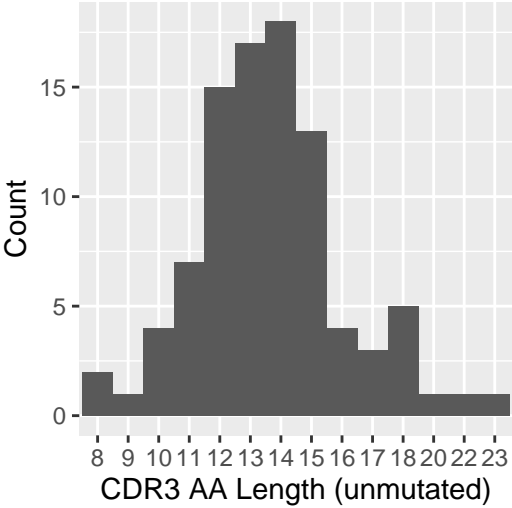


TRBV29-1*ap01

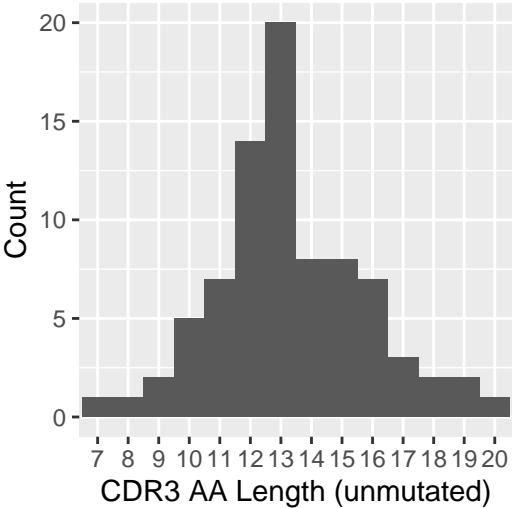
5596 sequences assigned
5530 (98.8%) exact matches, in which:
5453 unique CDR3
14 unique J



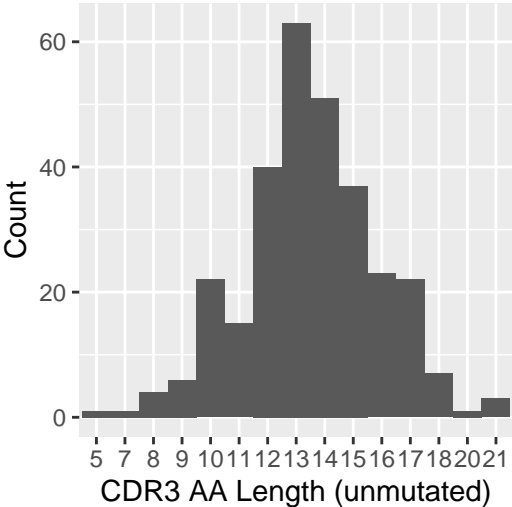
TRBV7-1*ap01_G291C_T296C

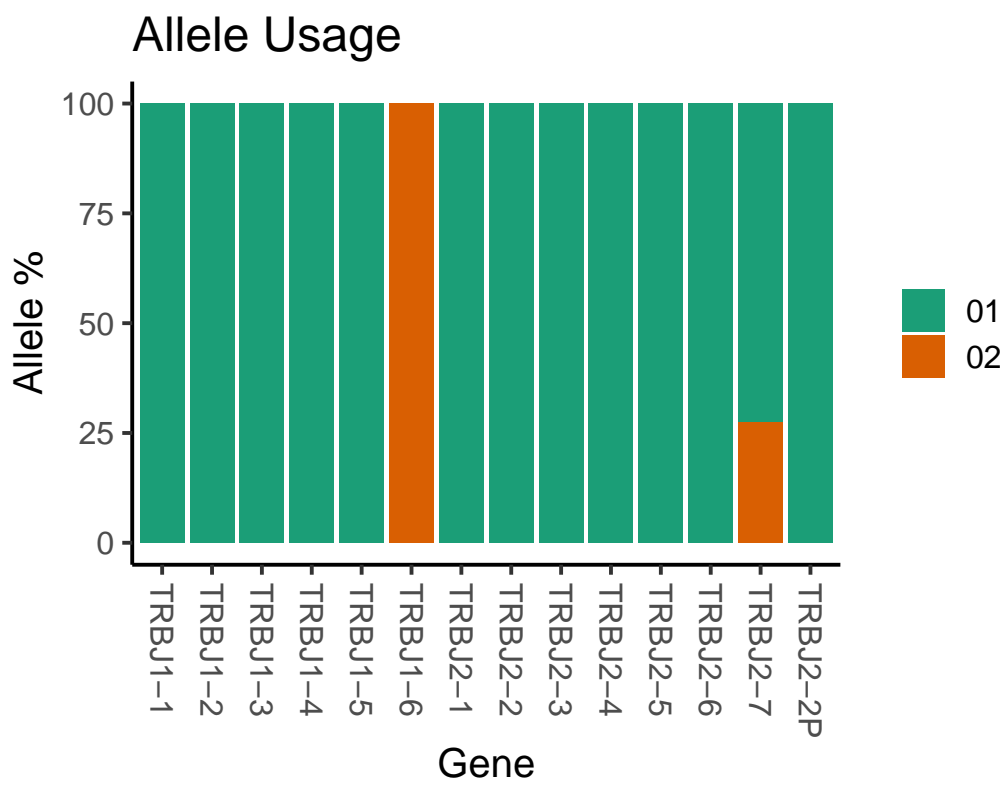


TRBV7-1*ap01_G291C_T296C_C314T

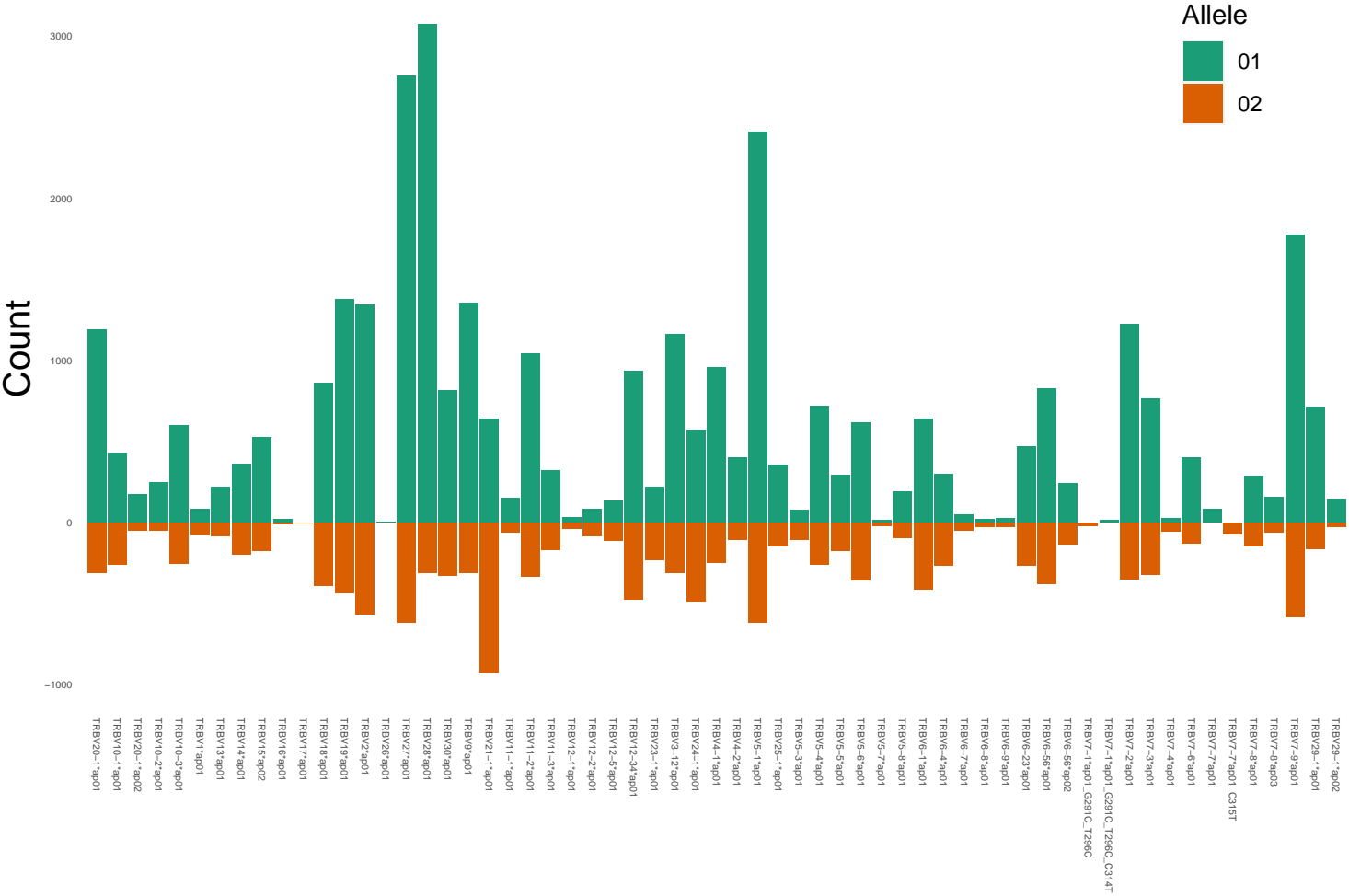


TRBV7-7*ap01_C315T





Sequence Count by TRBJ2-7 allele usage



[illegible]