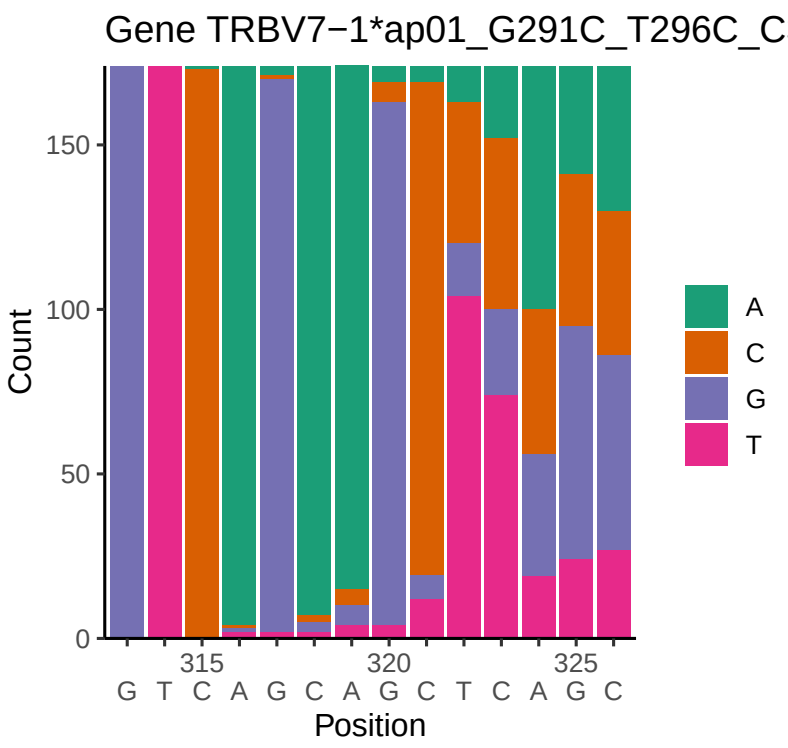
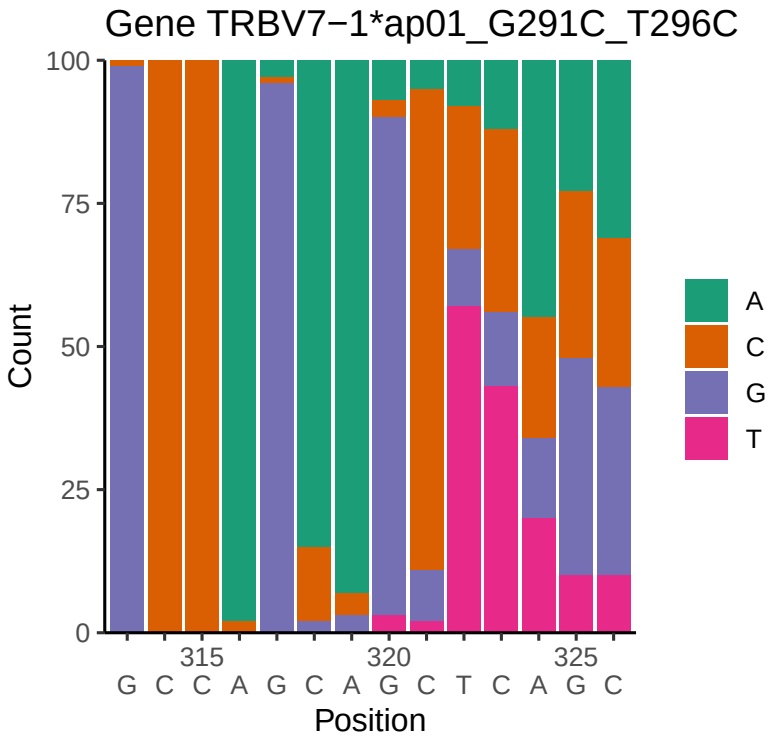

Gene TRBV7−1*ap01_G291C_T296C_C314T
Count
150
100
50
0
315
320
325
G T C A G C A G C T C A G C
Position
A
C
G
T


Gene TRBV7−1*ap01_G291C_T296C
Count
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50
25
0
315
320
325
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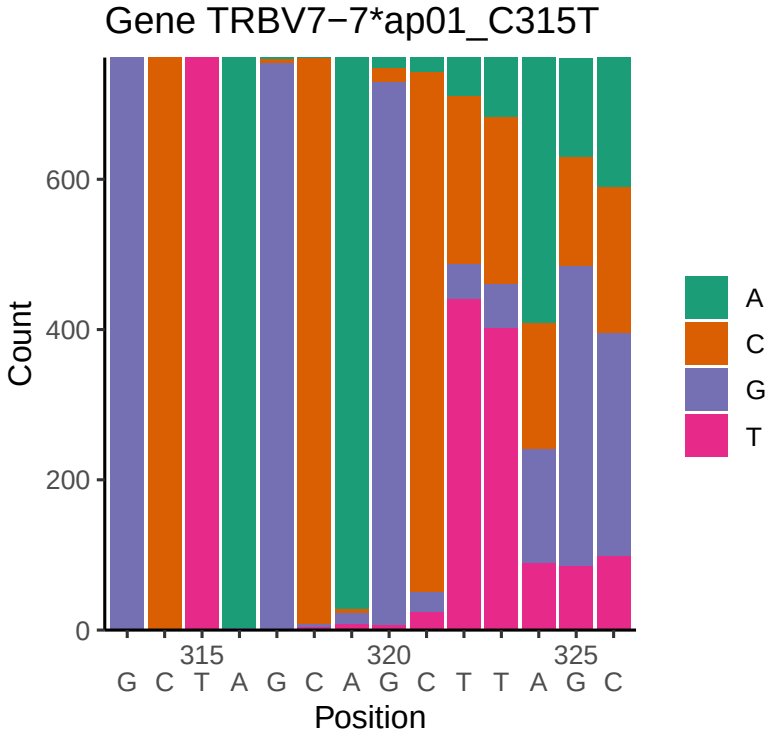
Position
A
C
G
T


Gene TRBV7−7*ap01_C315T
Count
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400
200
0
315
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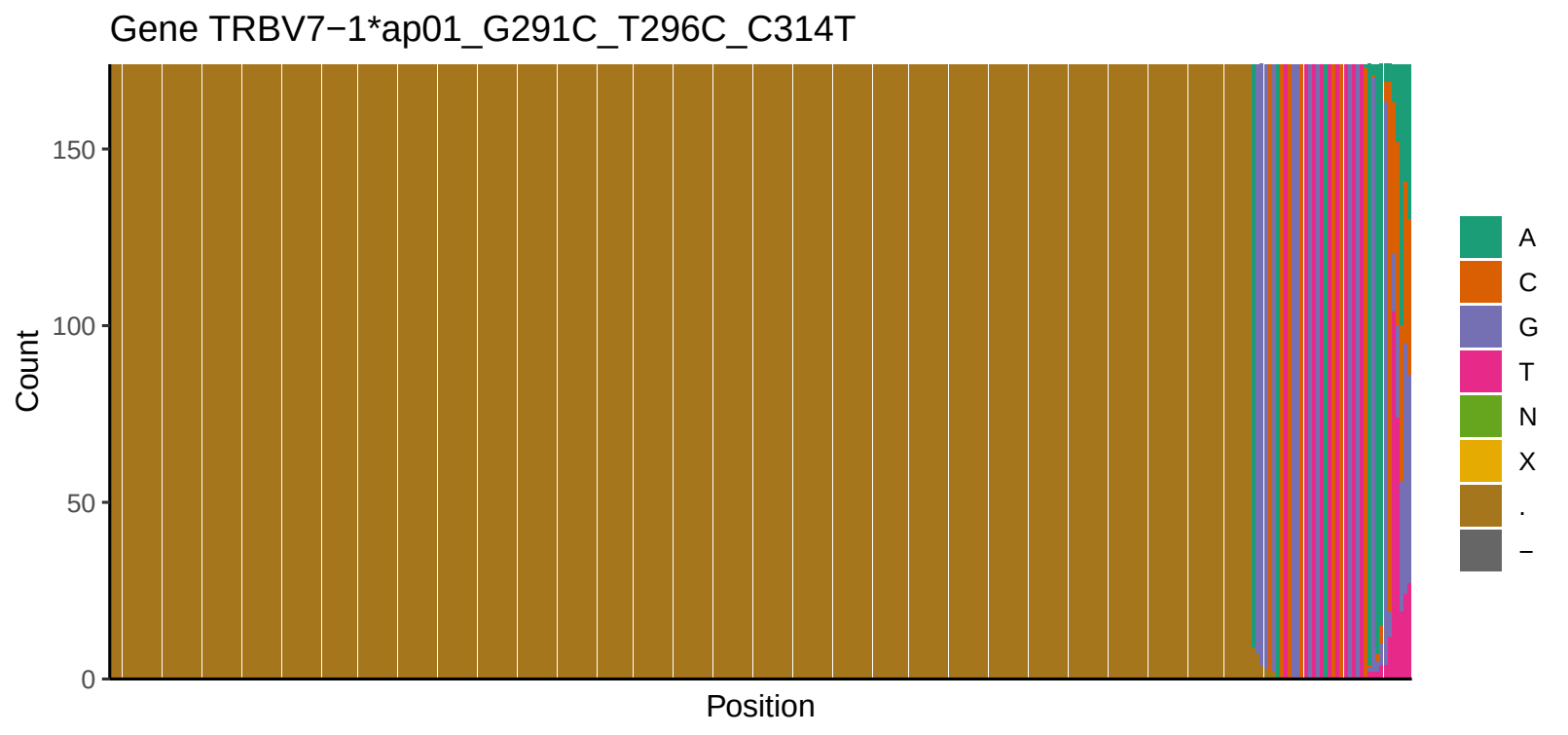
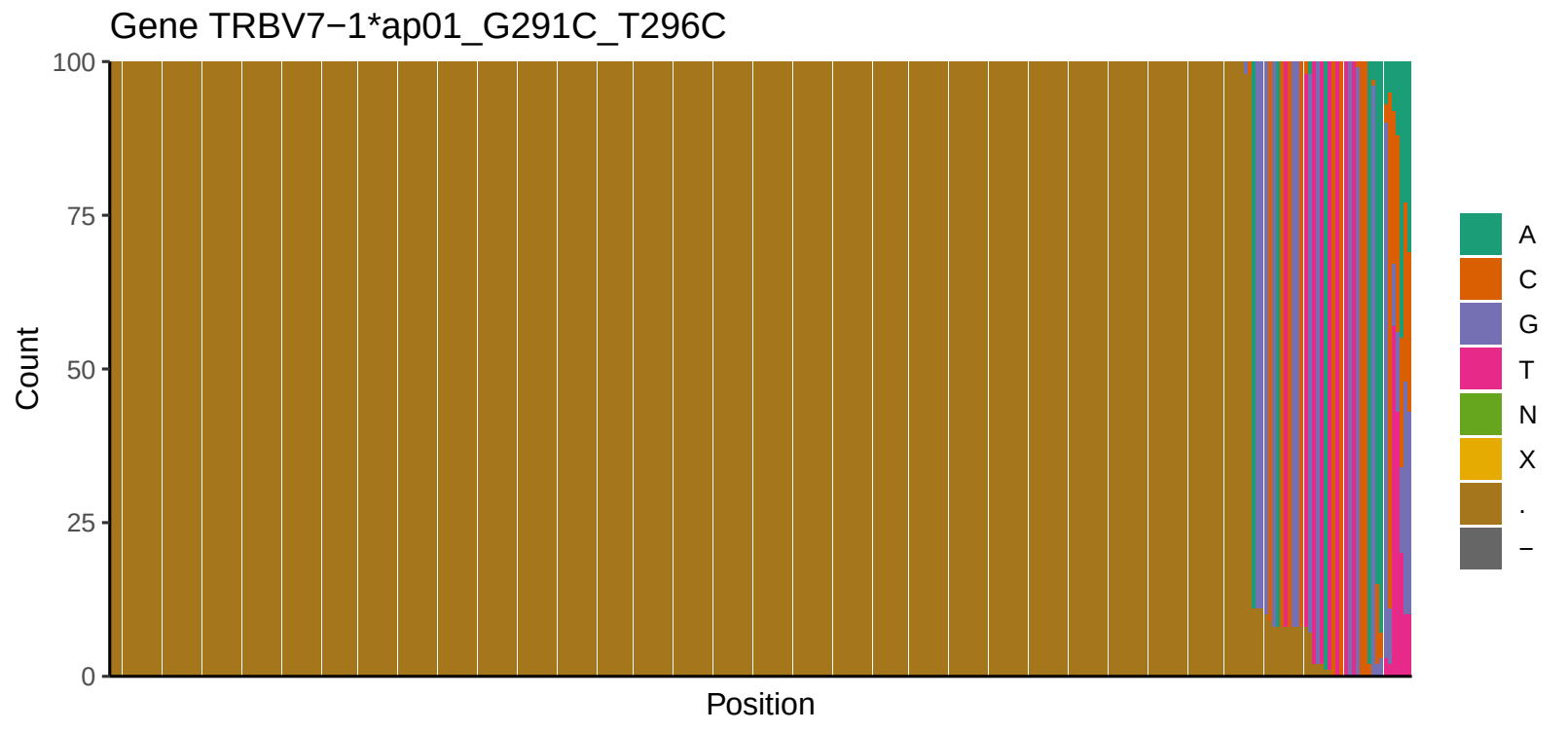
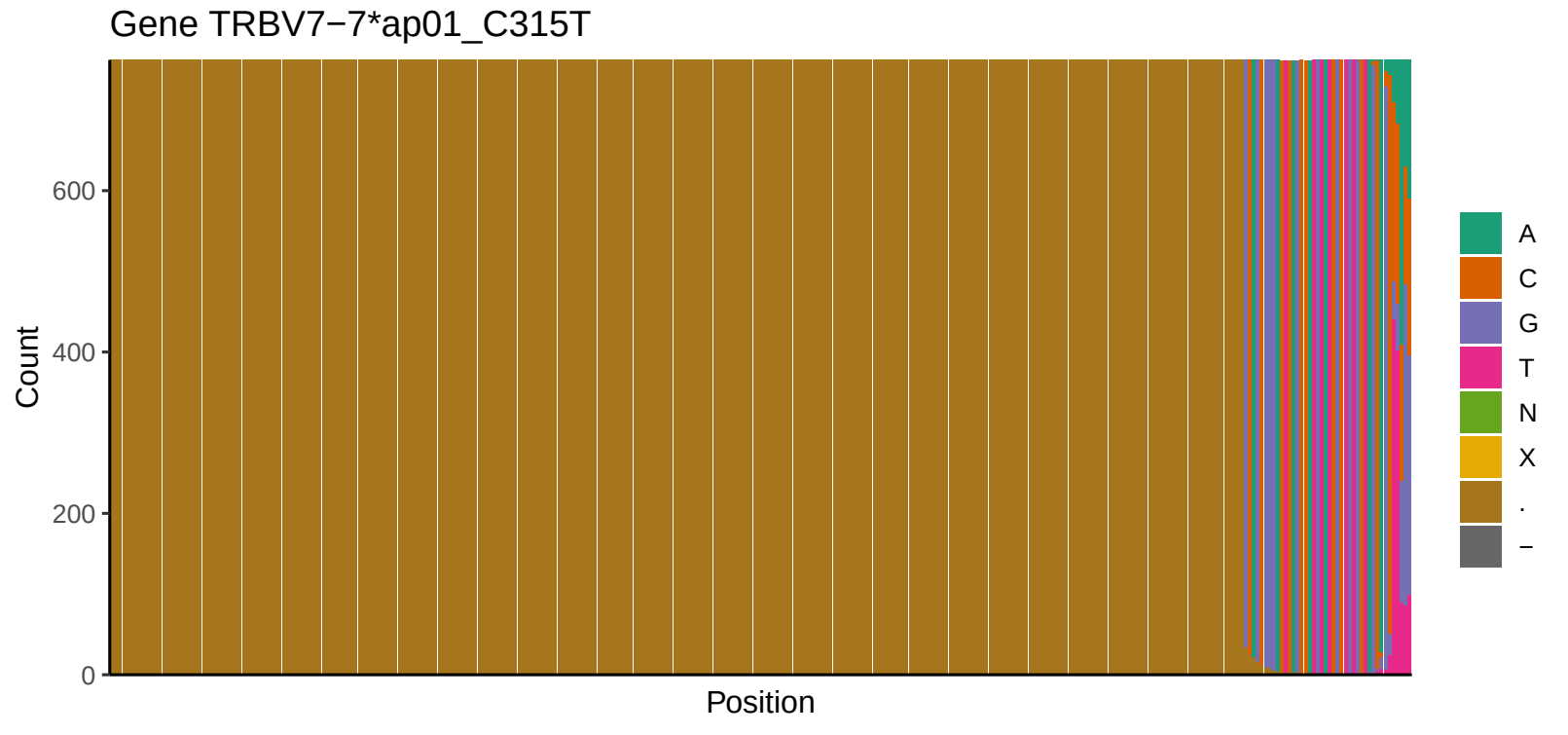
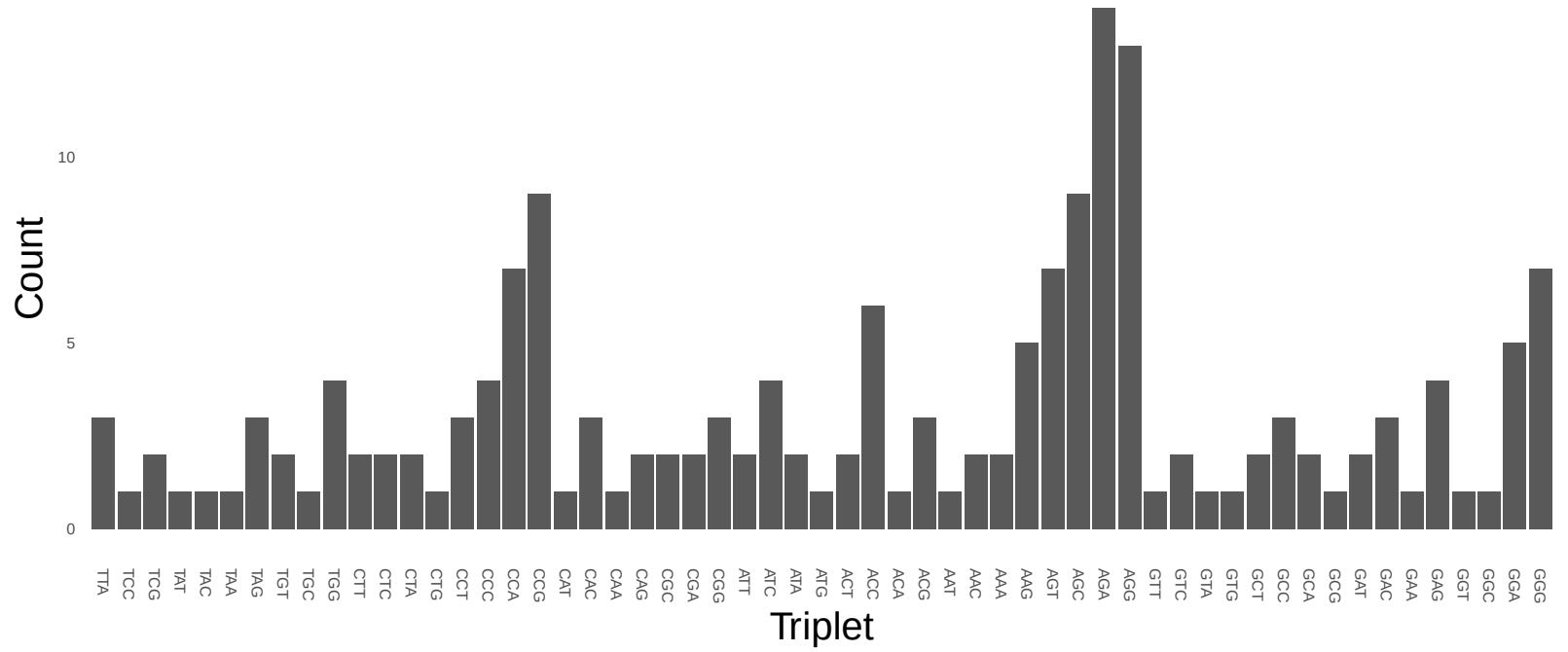
G C T A G C A G C T T A G C
Position
A
C
G
T


Gene TRBV7−1*ap01_G291C_T296C_C314T
Count
150
100
50
0
Position
A
C
G
T
N
X
.
–

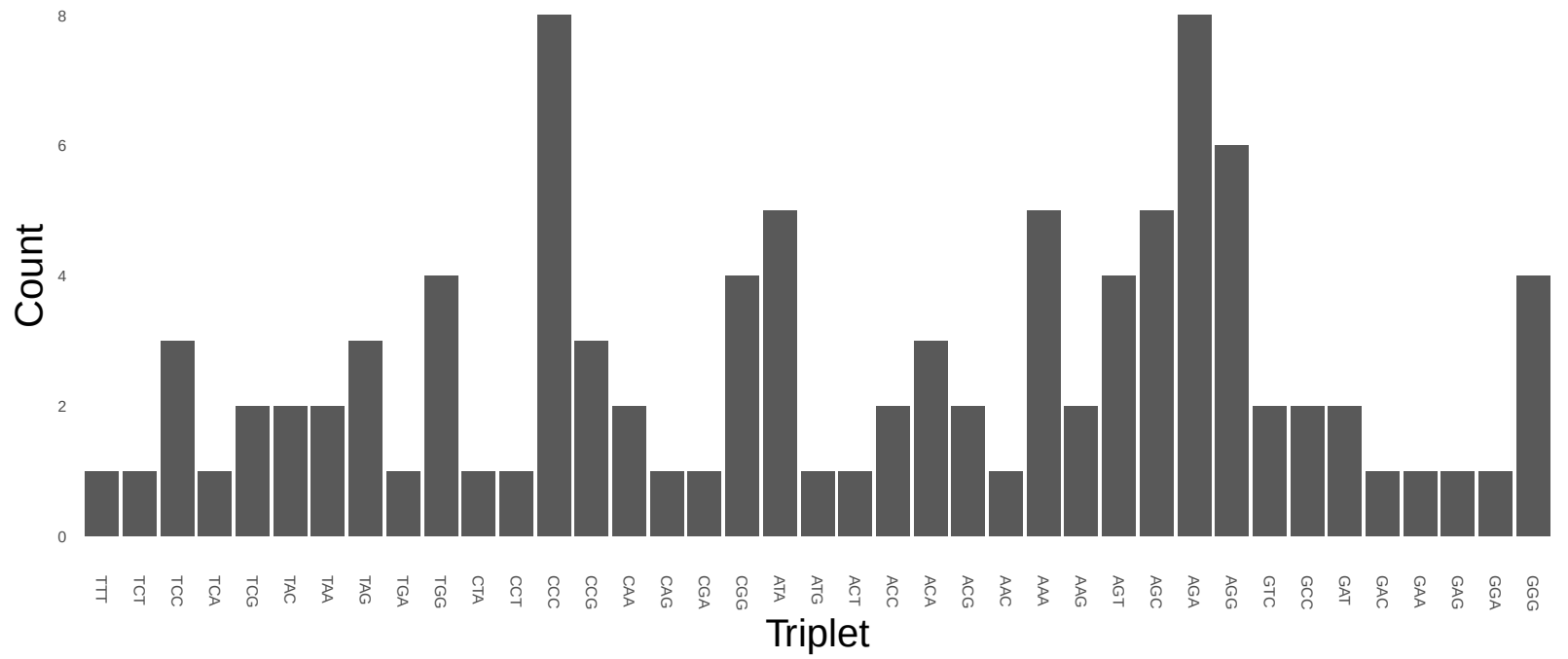

Gene TRBV7−1*ap01_G291C_T296C
Count
100
75
50
25
0
Position
A
C
G
T
N
X
.
–


Gene TRBV7−7*ap01_C315T
Count
600
400
200
0
Position
A
C
G
T
N
X
.
–

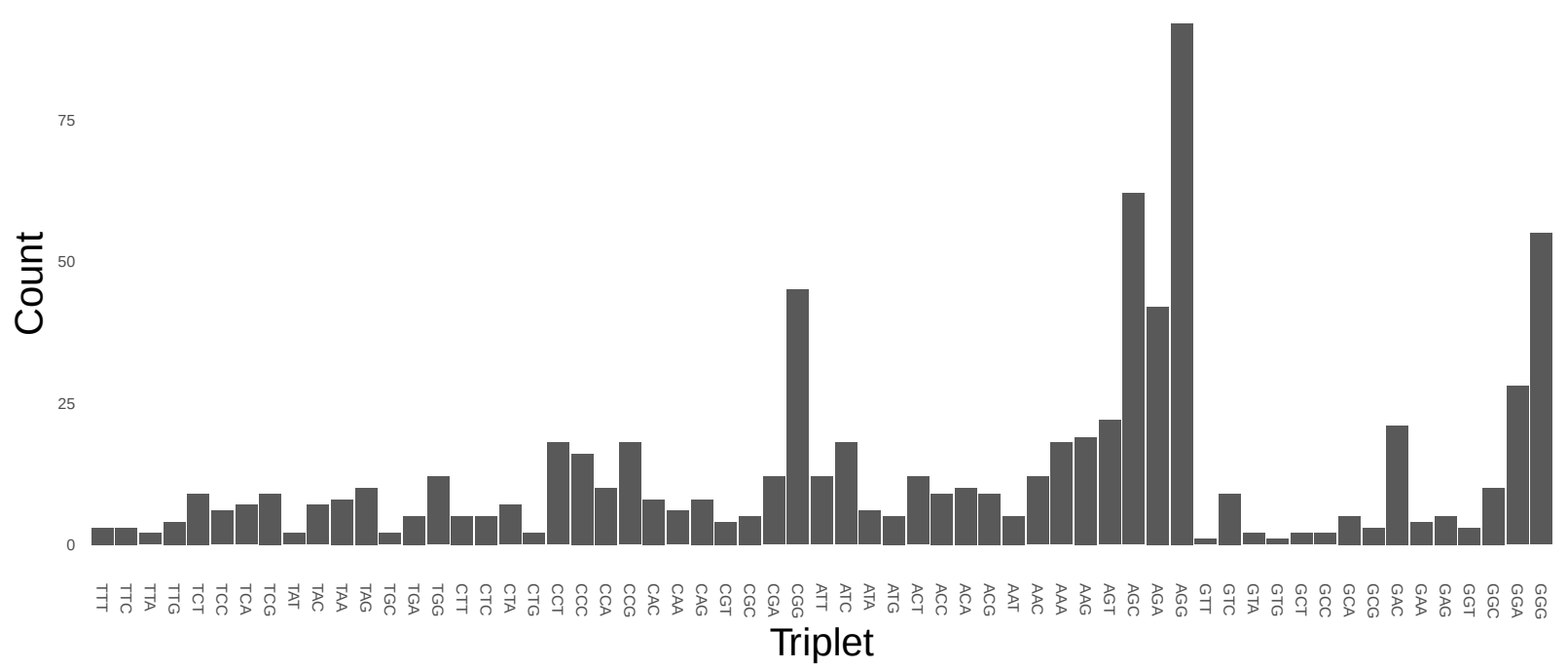
TRBV7−1*ap01_G291C_T296C_C314T− Final 3 nucleotides as a triplet



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

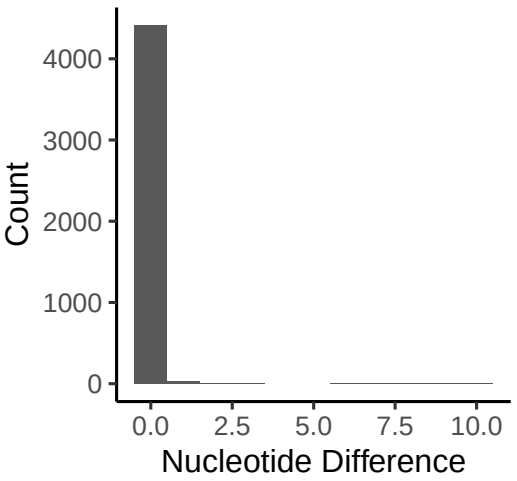


TRBV7−7*ap01_C315T− Final 3 nucleotides as a triplet



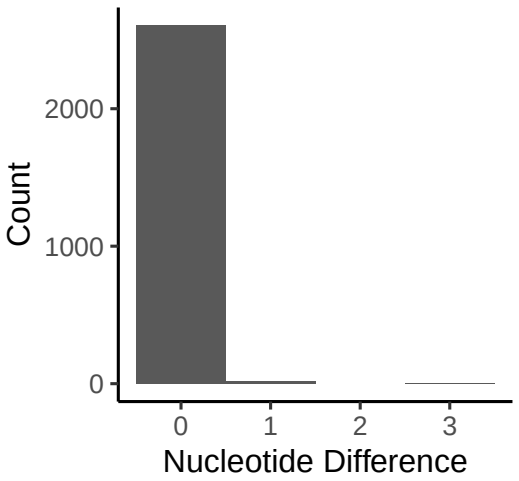
TRBV10−1*ap01

4446 sequences assigned
4411 (99.2%) exact matches, in which:
4334 unique CDR3
13 unique J



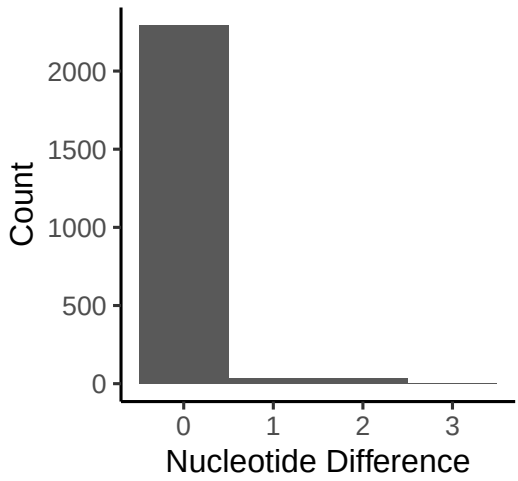
TRBV10−2*ap01

2625 sequences assigned
2606 (99.3%) exact matches, in which:
2577 unique CDR3
13 unique J



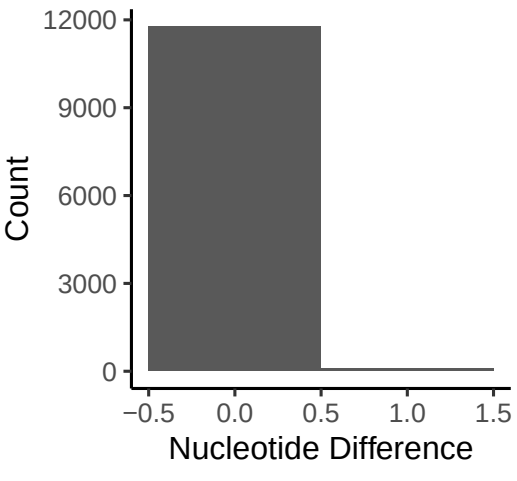
TRBV13*ap01

2364 sequences assigned
2292 (97%) exact matches, in which:
2257 unique CDR3
13 unique J



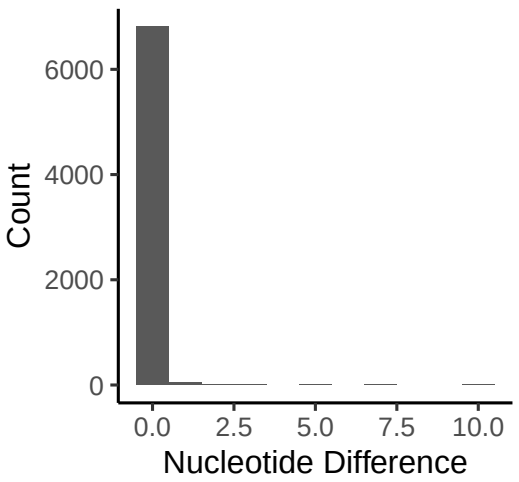
TRBV20−1*ap01

11876 sequences assigned
11774 (99.1%) exact matches, in which:
11678 unique CDR3
13 unique J



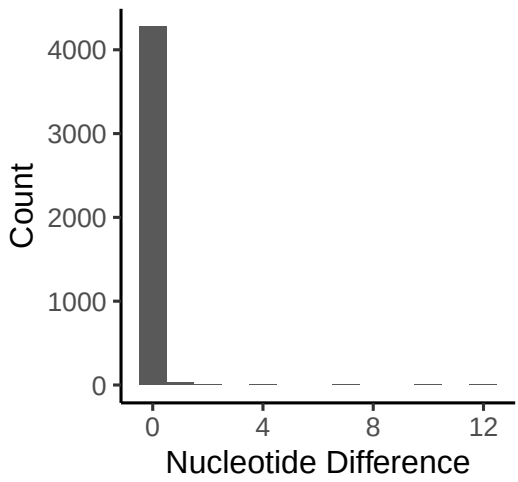
TRBV10−3*ap01

6872 sequences assigned
6810 (99.1%) exact matches, in which:
6729 unique CDR3
13 unique J



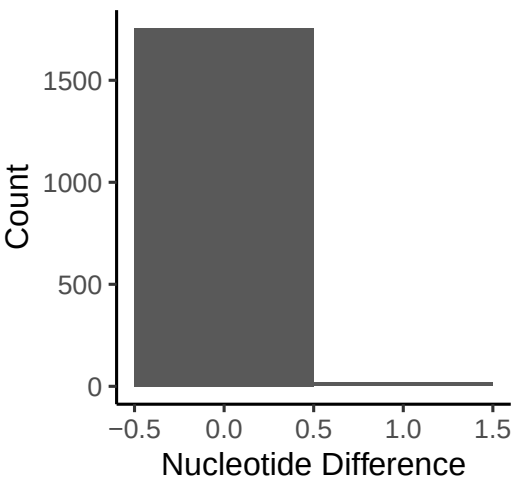
TRBV14*ap01

4309 sequences assigned
4275 (99.2%) exact matches, in which:
4240 unique CDR3
13 unique J



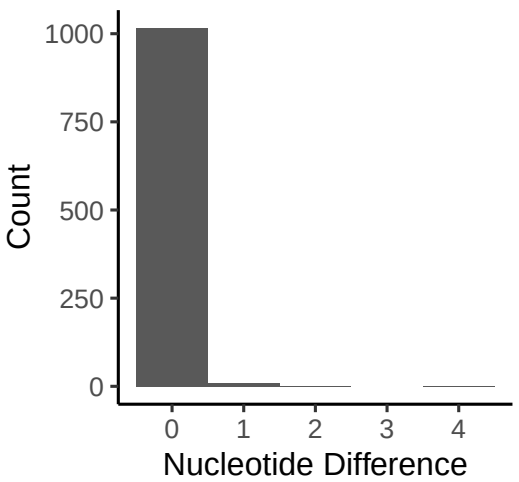
TRBV20−1*ap02

1774 sequences assigned
1756 (99%) exact matches, in which:
1744 unique CDR3
13 unique J



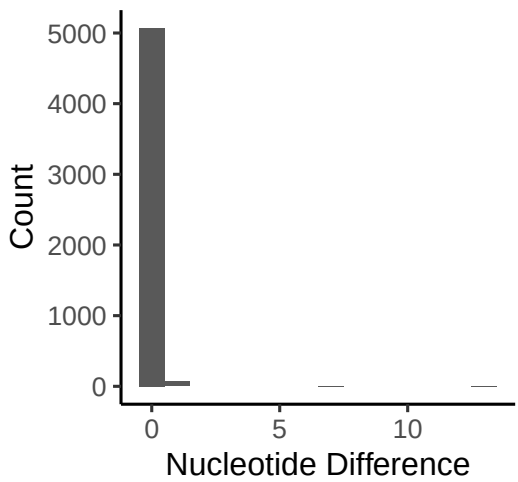
TRBV1*ap01

1028 sequences assigned
1016 (98.8%) exact matches, in which:
996 unique CDR3
13 unique J



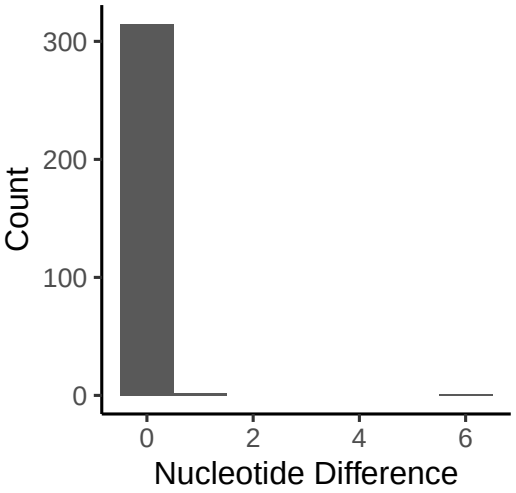
TRBV15*ap02

5144 sequences assigned
5070 (98.6%) exact matches, in which:
5005 unique CDR3
13 unique J



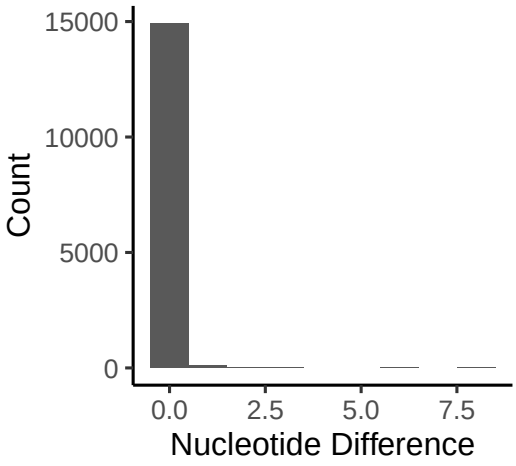
TRBV16*ap01

318 sequences assigned
315 (99.1%) exact matches, in which:
315 unique CDR3
12 unique J



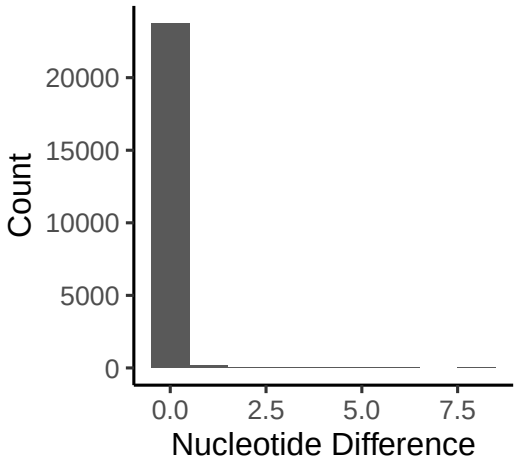
TRBV2*ap01

15067 sequences assigned
14931 (99.1%) exact matches, in which:
14731 unique CDR3
14 unique J



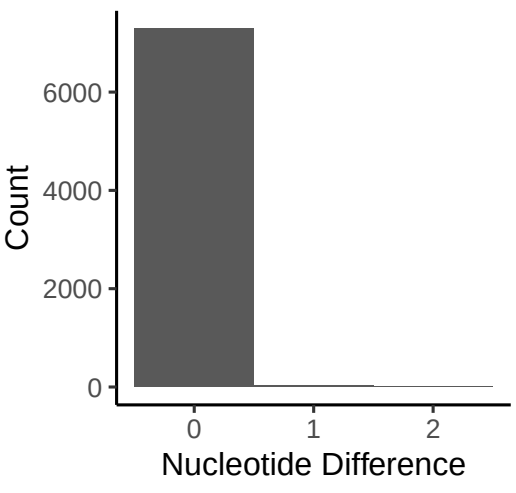
TRBV28*ap01

23949 sequences assigned
23757 (99.2%) exact matches, in which:
23591 unique CDR3
13 unique J



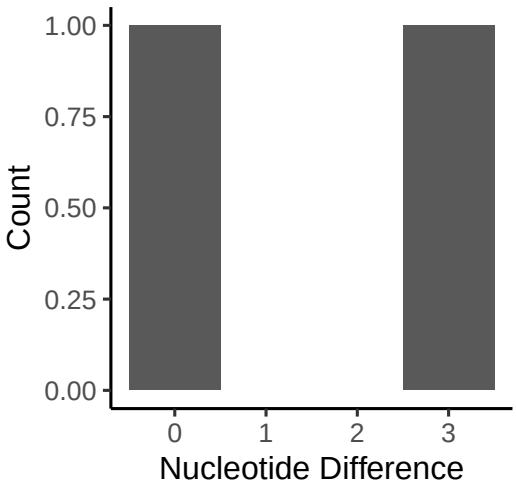
TRBV18*ap01

7313 sequences assigned
7289 (99.7%) exact matches, in which:
7253 unique CDR3
13 unique J



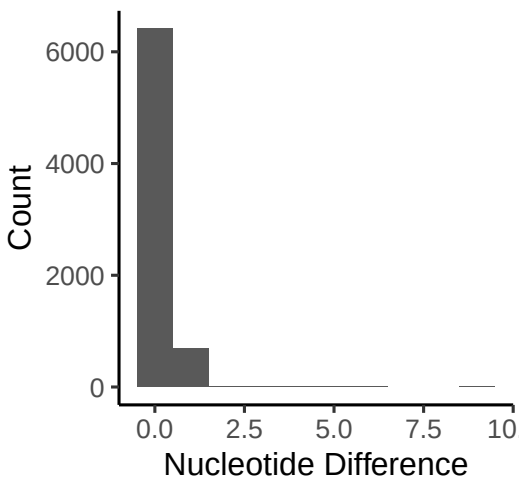
TRBV26*ap01

2 sequences assigned
1 (50%) exact matches, in which:
1 unique CDR3
1 unique J



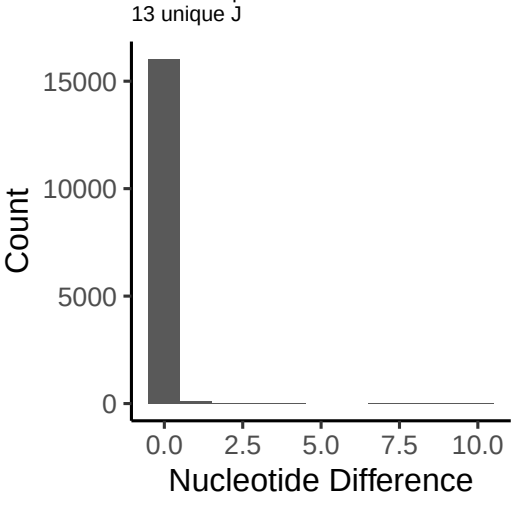
TRBV30*ap01

7135 sequences assigned
6413 (89.9%) exact matches, in which:
6276 unique CDR3
13 unique J



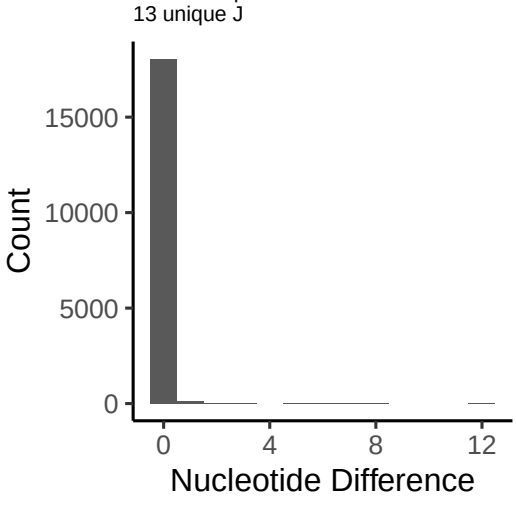
TRBV19*ap01

16187 sequences assigned
16042 (99.1%) exact matches, in which:
15968 unique CDR3
13 unique J



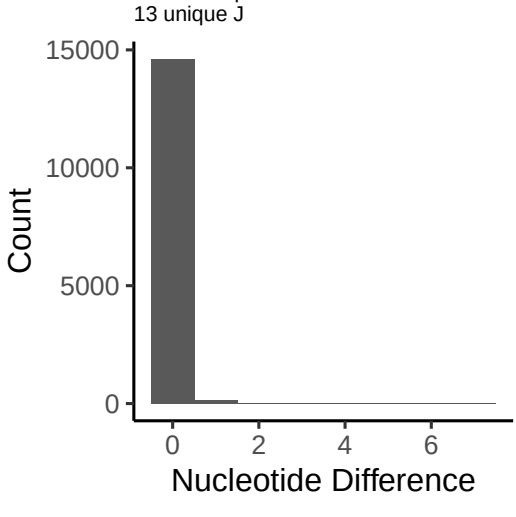
TRBV27*ap01

18223 sequences assigned
18056 (99.1%) exact matches, in which:
17863 unique CDR3
13 unique J



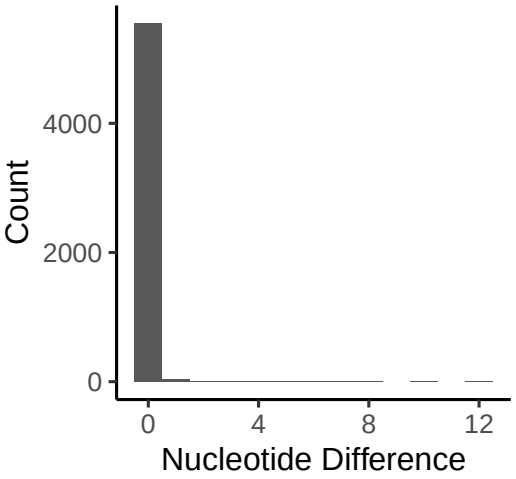
TRBV9*ap01

14779 sequences assigned
14623 (98.9%) exact matches, in which:
14519 unique CDR3
13 unique J



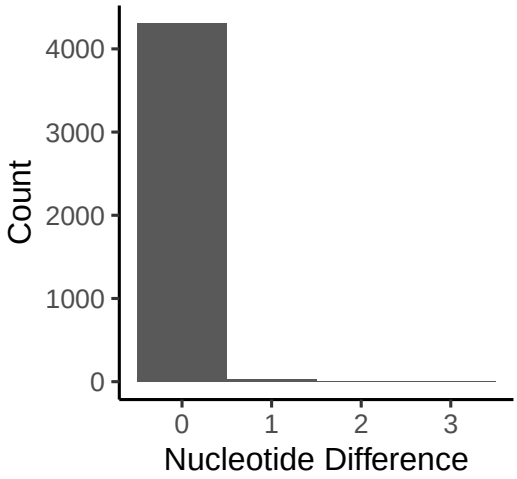
TRBV21−1*ap01

5606 sequences assigned
5547 (98.9%) exact matches, in which:
5527 unique CDR3
13 unique J



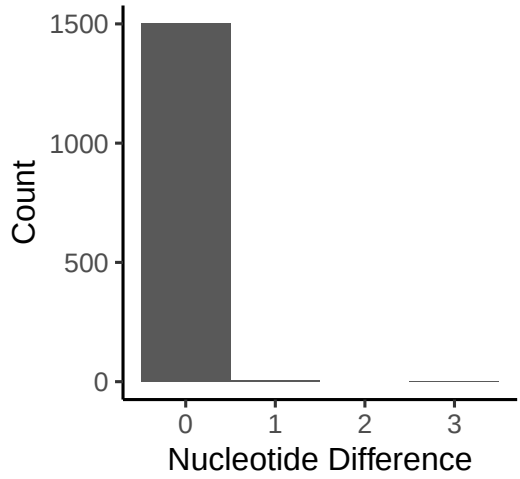
TRBV11−3*ap01

4336 sequences assigned
4306 (99.3%) exact matches, in which:
4283 unique CDR3
13 unique J



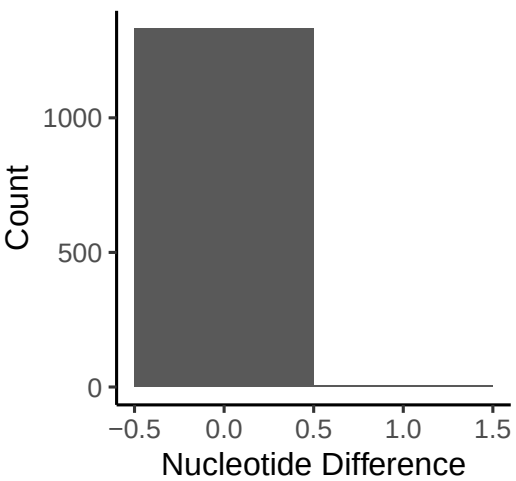
TRBV12−5*ap01

1510 sequences assigned
1502 (99.5%) exact matches, in which:
1487 unique CDR3
13 unique J



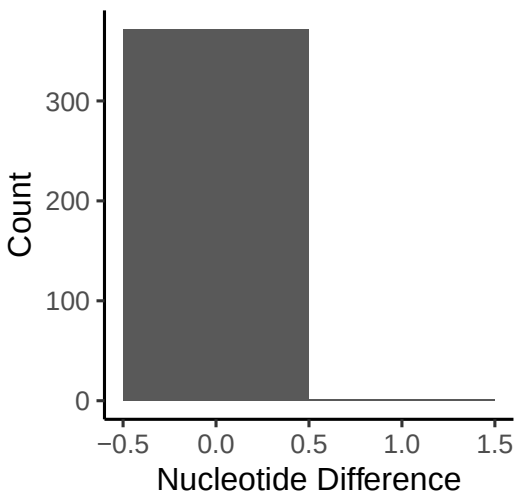
TRBV11−1*ap01

1338 sequences assigned
1331 (99.5%) exact matches, in which:
1320 unique CDR3
13 unique J



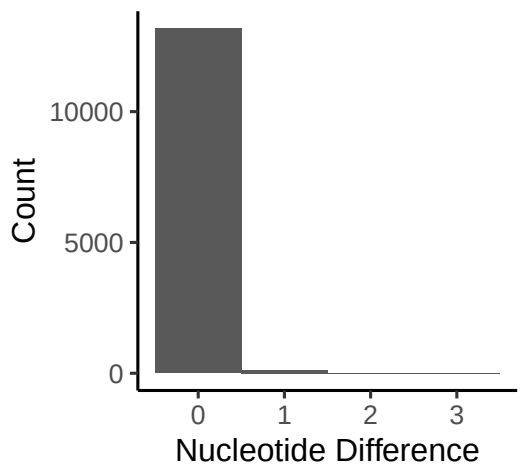
TRBV12−1*ap01

374 sequences assigned
372 (99.5%) exact matches, in which:
371 unique CDR3
13 unique J



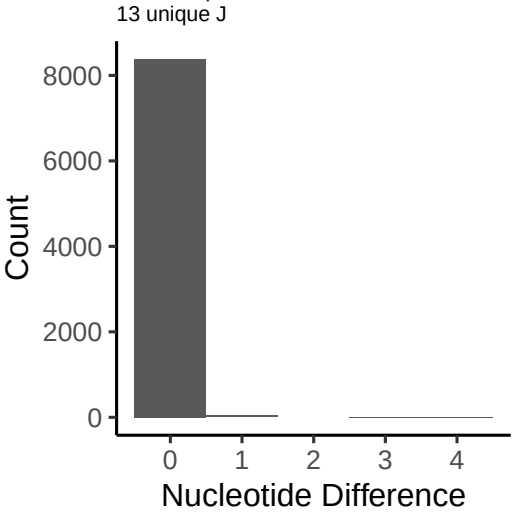
TRBV12−34*ap01

13313 sequences assigned
13178 (99%) exact matches, in which:
13036 unique CDR3
13 unique J



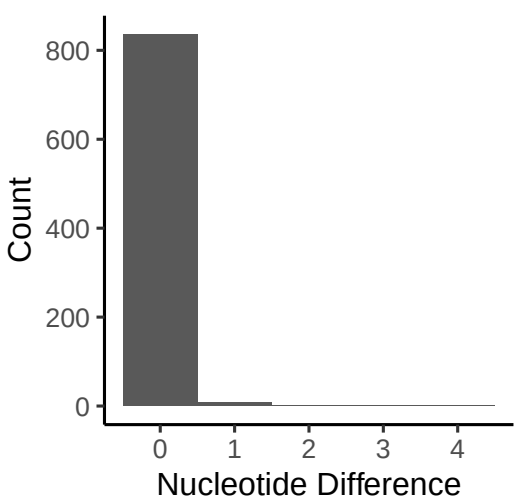
TRBV11−2*ap01

8425 sequences assigned
8383 (99.5%) exact matches, in which:
8333 unique CDR3
13 unique J



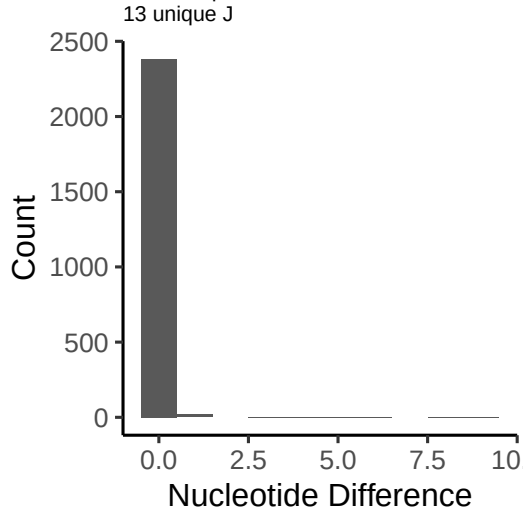
TRBV12−2*ap01

849 sequences assigned
836 (98.5%) exact matches, in which:
826 unique CDR3
13 unique J



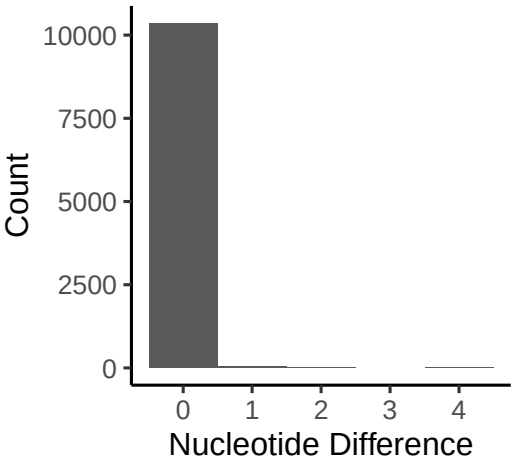
TRBV23−1*ap01

2406 sequences assigned
2382 (99%) exact matches, in which:
2368 unique CDR3
13 unique J



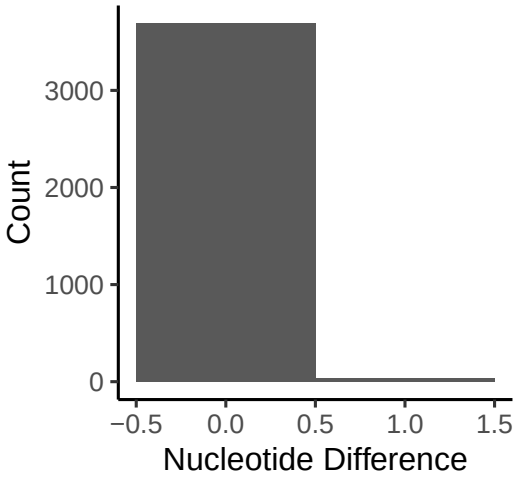
TRBV3−12*ap01

10417 sequences assigned
10359 (99.4%) exact matches, in which:
10303 unique CDR3
13 unique J



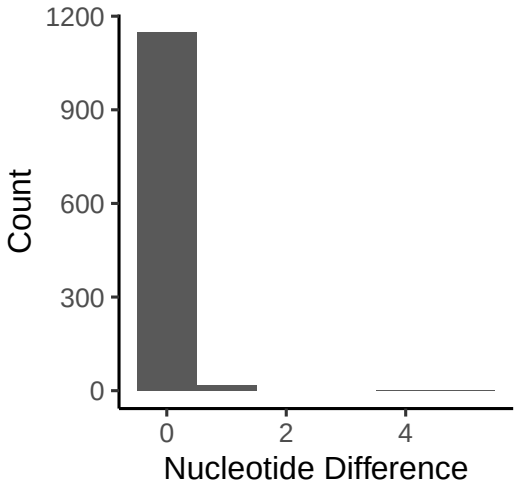
TRBV4−2*ap01

3728 sequences assigned
3690 (99%) exact matches, in which:
3643 unique CDR3
13 unique J



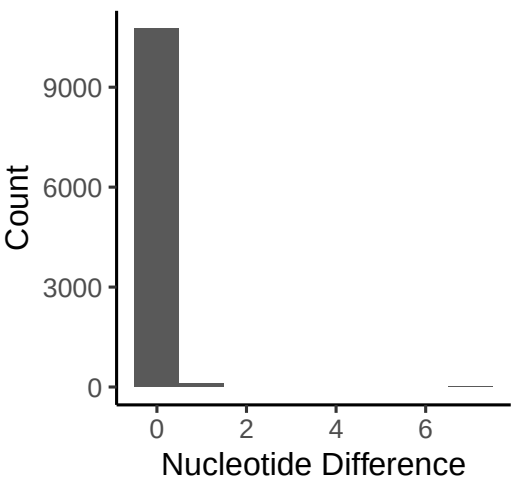
TRBV5−3*ap01

1168 sequences assigned
1148 (98.3%) exact matches, in which:
1136 unique CDR3
13 unique J



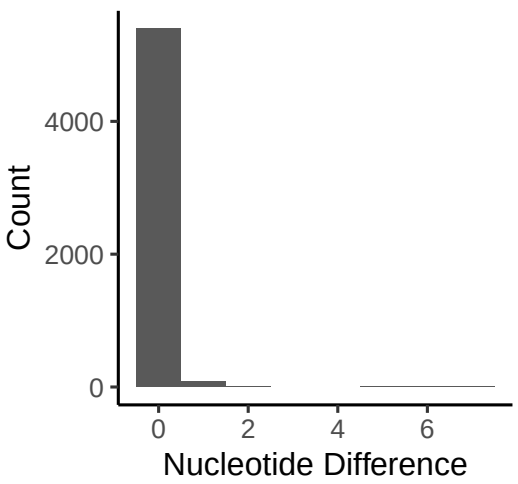
TRBV4−1*ap01

10848 sequences assigned
10756 (99.2%) exact matches, in which:
10606 unique CDR3
13 unique J



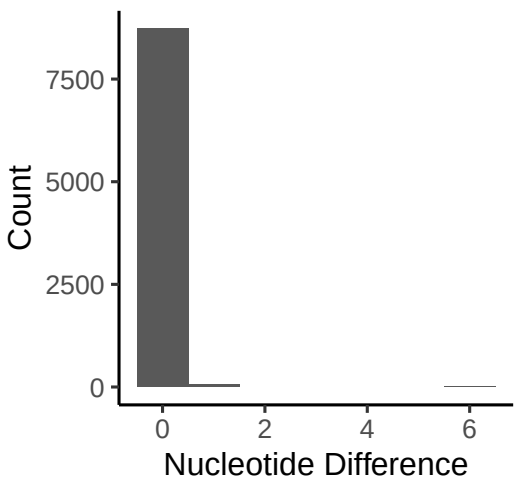
TRBV25−1*ap01

5478 sequences assigned
5395 (98.5%) exact matches, in which:
5269 unique CDR3
13 unique J



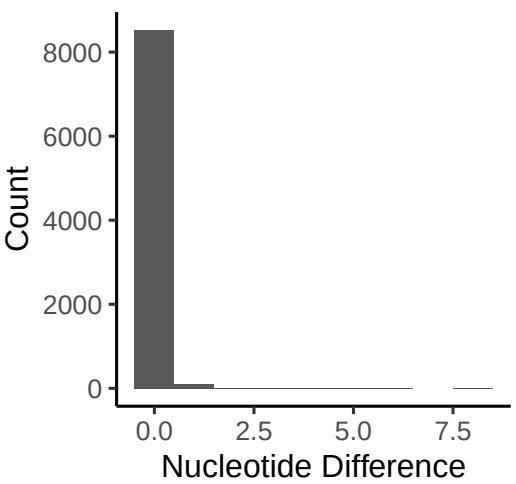
TRBV5−4*ap01

8793 sequences assigned
8726 (99.2%) exact matches, in which:
8623 unique CDR3
13 unique J



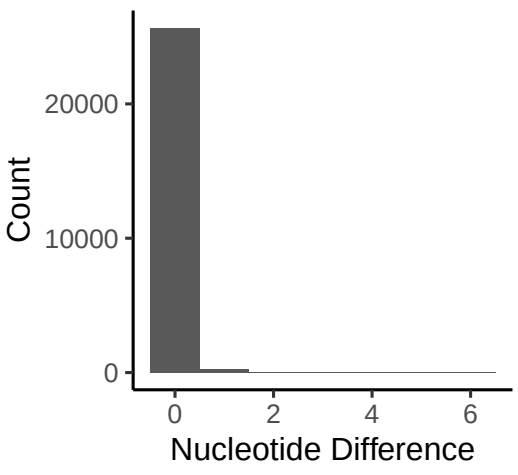
TRBV24−1*ap01

8644 sequences assigned
8525 (98.6%) exact matches, in which:
8428 unique CDR3
13 unique J



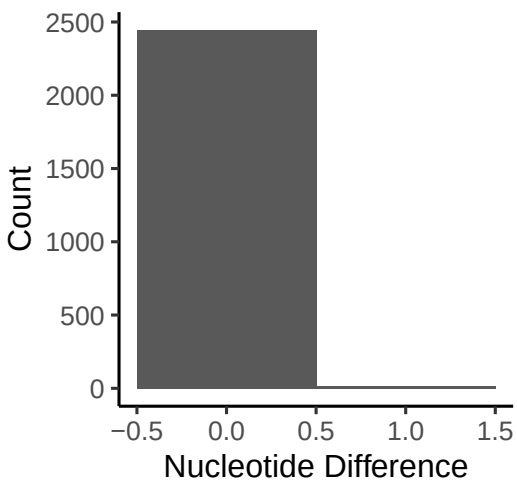
TRBV5−1*ap01

25941 sequences assigned
25666 (98.9%) exact matches, in which:
25301 unique CDR3
13 unique J



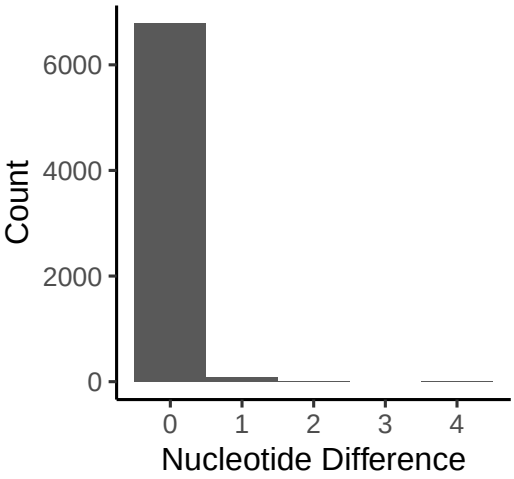
TRBV5−5*ap01

2460 sequences assigned
2445 (99.4%) exact matches, in which:
2434 unique CDR3
13 unique J



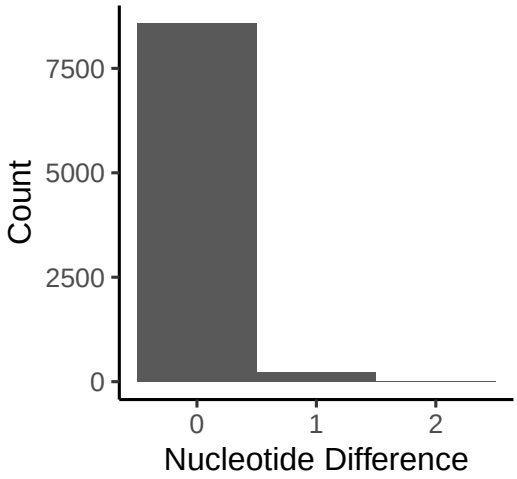
TRBV5−6*ap01

6874 sequences assigned
6784 (98.7%) exact matches, in which:
6656 unique CDR3
13 unique J



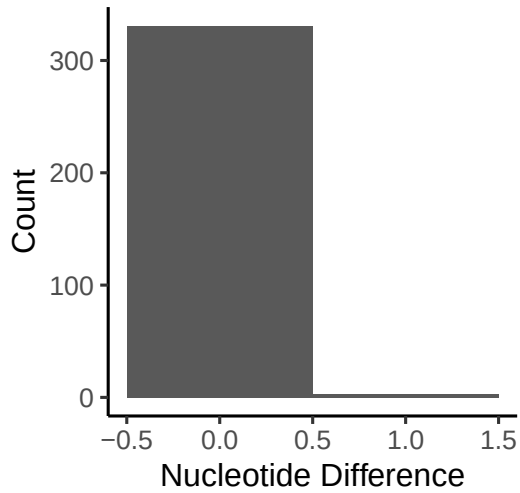
TRBV6−1*ap01

8796 sequences assigned
8576 (97.5%) exact matches, in which:
8420 unique CDR3
14 unique J



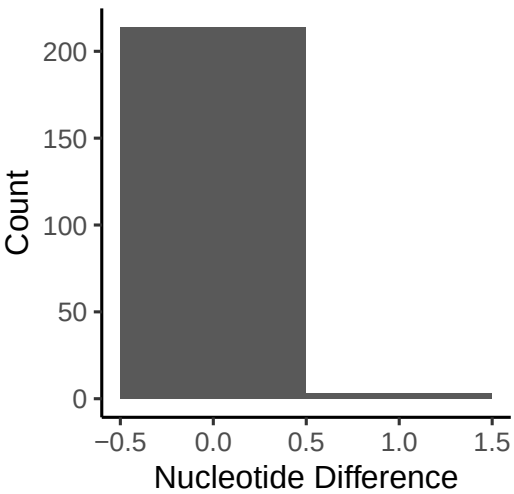
TRBV6−8*ap01

334 sequences assigned
331 (99.1%) exact matches, in which:
322 unique CDR3
13 unique J



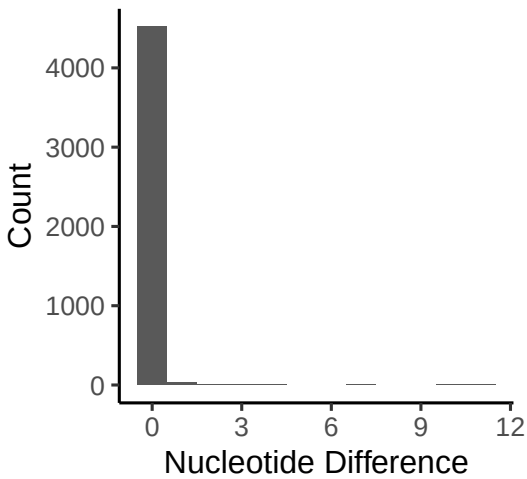
TRBV5−7*ap01

217 sequences assigned
214 (98.6%) exact matches, in which:
205 unique CDR3
13 unique J



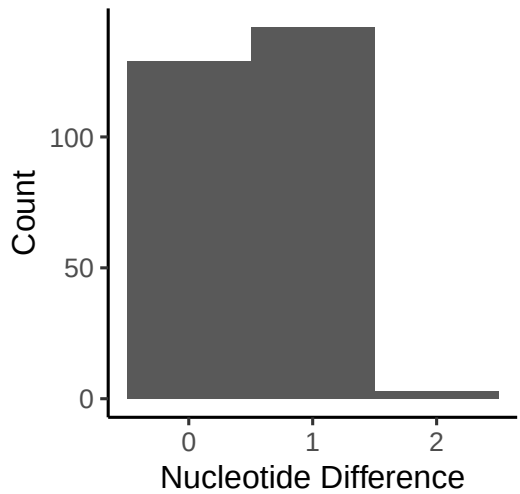
TRBV6−4*ap01

4559 sequences assigned
4519 (99.1%) exact matches, in which:
4477 unique CDR3
13 unique J



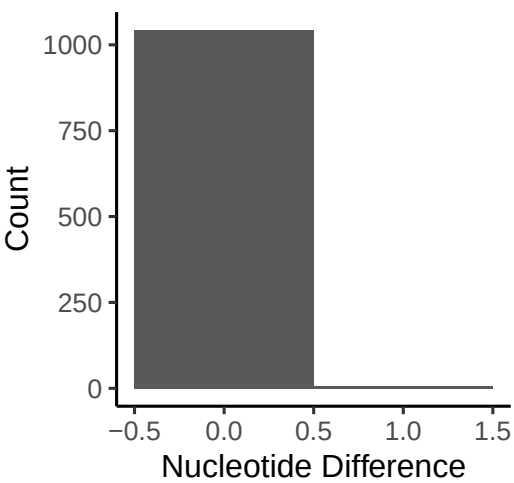
TRBV6−9*ap01

274 sequences assigned
129 (47.1%) exact matches, in which:
127 unique CDR3
12 unique J



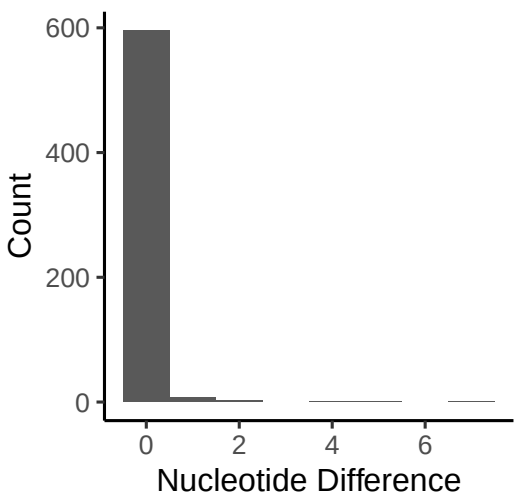
TRBV5−8*ap01

1050 sequences assigned
1043 (99.3%) exact matches, in which:
1033 unique CDR3
13 unique J



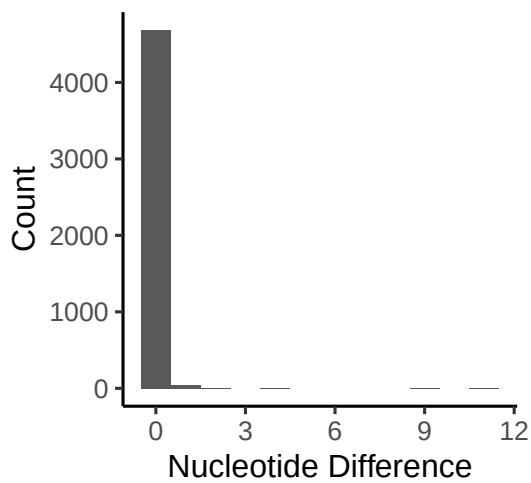
TRBV6−7*ap01

609 sequences assigned
596 (97.9%) exact matches, in which:
586 unique CDR3
13 unique J



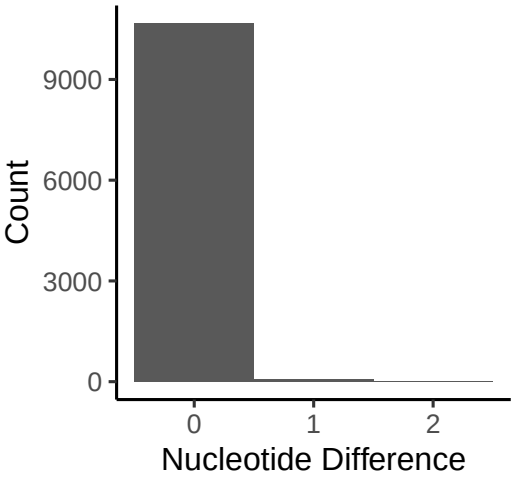
TRBV6−23*ap01

4733 sequences assigned
4685 (99%) exact matches, in which:
4552 unique CDR3
13 unique J



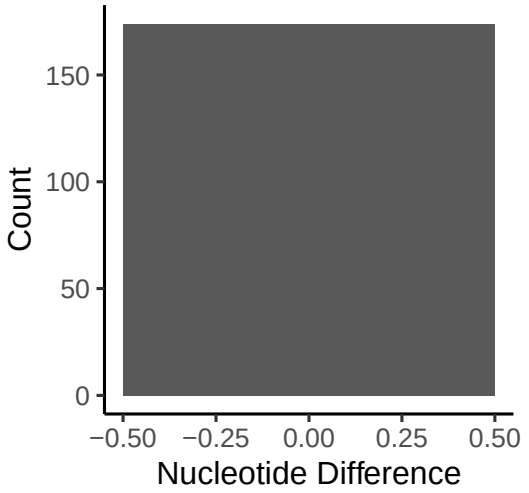
TRBV6−56*ap01

10756 sequences assigned
10669 (99.2%) exact matches, in which:
10459 unique CDR3
13 unique J



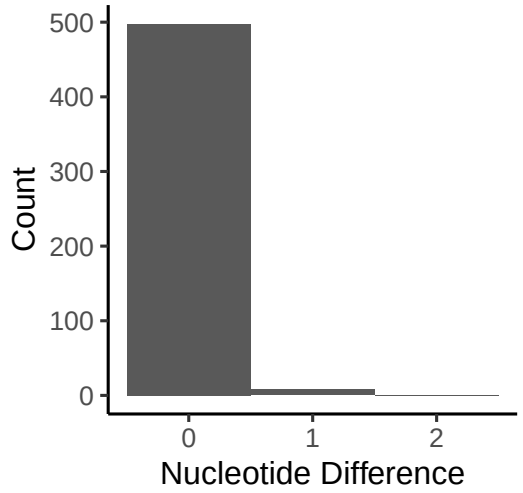
TRBV7−1*ap01_G291C_

174 sequences assigned
174 (100%) exact matches, in which:
174 unique CDR3
12 unique J



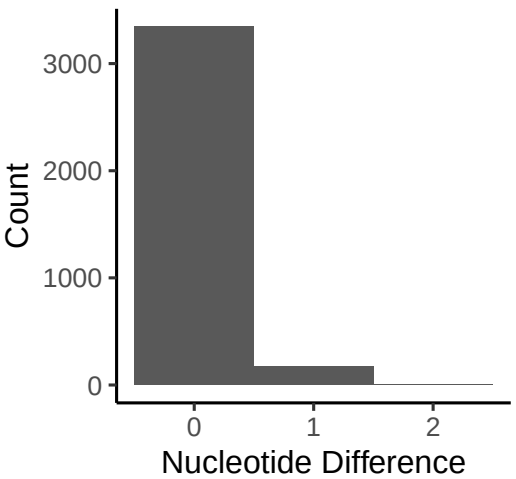
TRBV7−4*ap01

507 sequences assigned
498 (98.2%) exact matches, in which:
494 unique CDR3
13 unique J



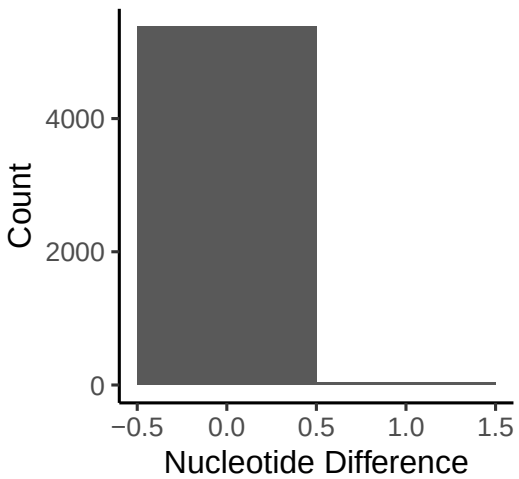
TRBV6−56*ap02

3517 sequences assigned
3344 (95.1%) exact matches, in which:
3268 unique CDR3
13 unique J



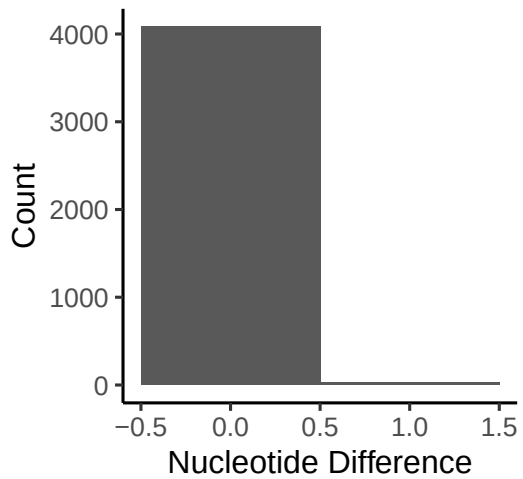
TRBV7−2*ap01

5414 sequences assigned
5379 (99.4%) exact matches, in which:
5323 unique CDR3
13 unique J



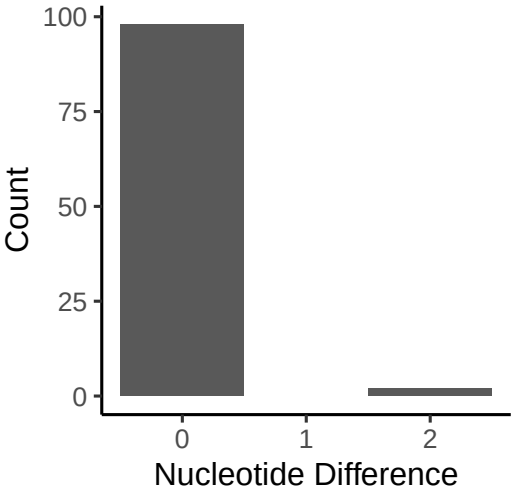
TRBV7−6*ap01

4113 sequences assigned
4083 (99.3%) exact matches, in which:
4042 unique CDR3
13 unique J



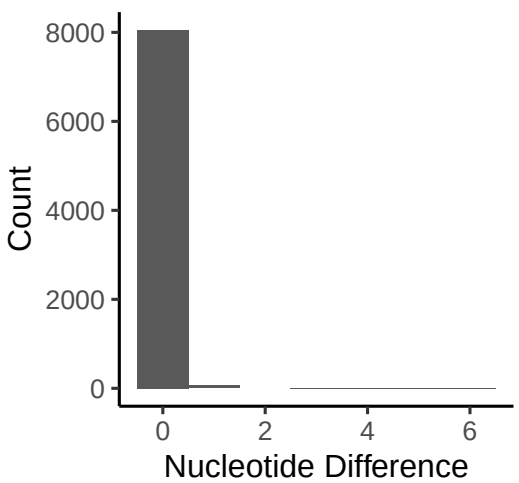
TRBV7−1*ap01_G291C_

100 sequences assigned
98 (98%) exact matches, in which:
97 unique CDR3
12 unique J



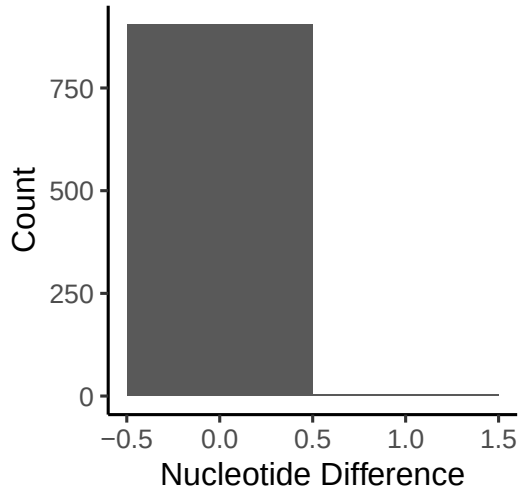
TRBV7−3*ap01

8126 sequences assigned
8052 (99.1%) exact matches, in which:
8000 unique CDR3
13 unique J



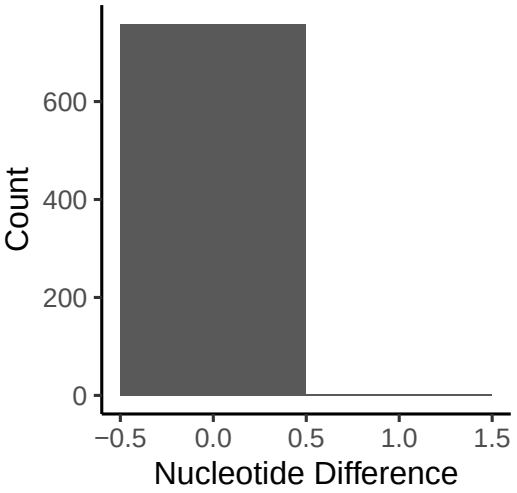
TRBV7−7*ap01

909 sequences assigned
905 (99.6%) exact matches, in which:
890 unique CDR3
13 unique J



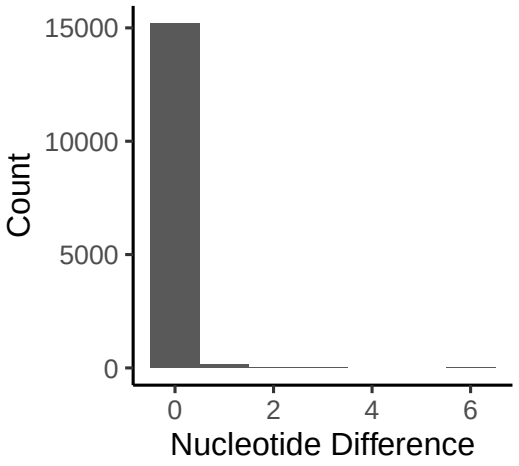
TRBV7−7*ap01_C315T

762 sequences assigned
759 (99.6%) exact matches, in which:
752 unique CDR3
13 unique J



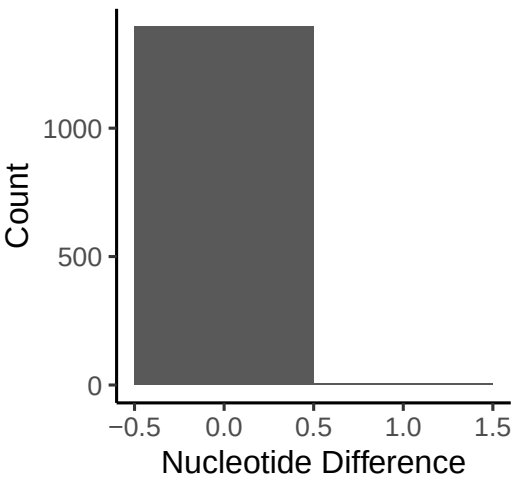
TRBV7−9*ap01

15349 sequences assigned
15209 (99.1%) exact matches, in which:
15048 unique CDR3
13 unique J



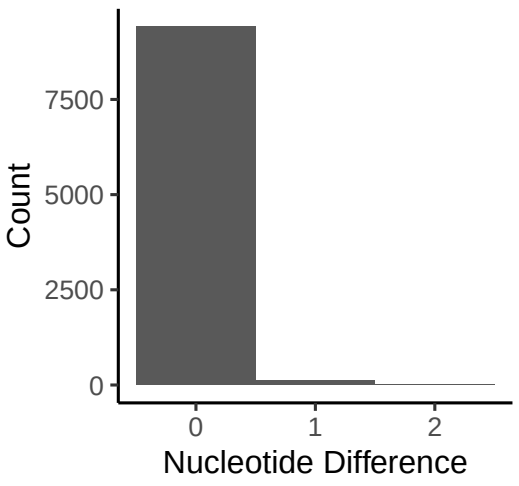
TRBV7−8*ap01

1402 sequences assigned
1395 (99.5%) exact matches, in which:
1376 unique CDR3
13 unique J



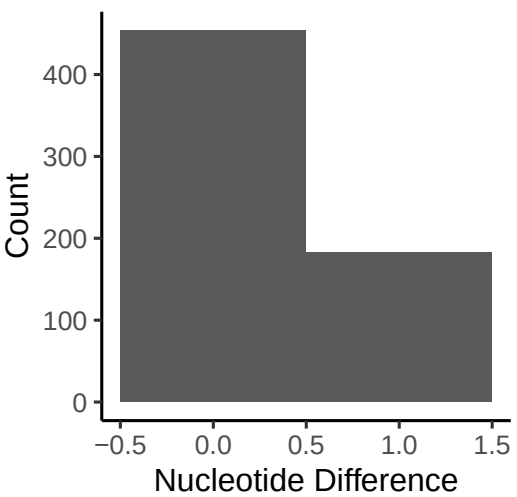
TRBV29−1*ap01

9542 sequences assigned
9410 (98.6%) exact matches, in which:
9195 unique CDR3
13 unique J



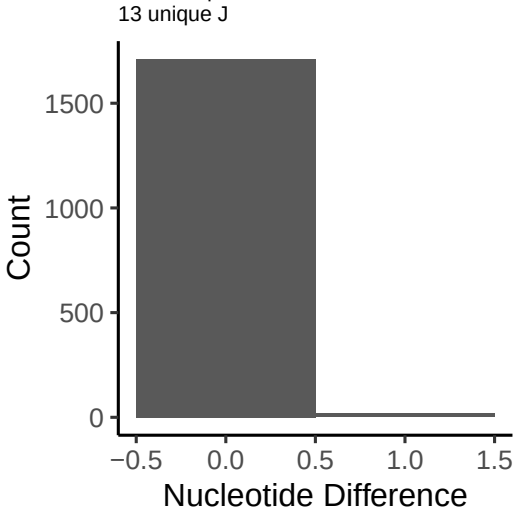
TRBV7−8*ap03

637 sequences assigned
454 (71.3%) exact matches, in which:
452 unique CDR3
13 unique J

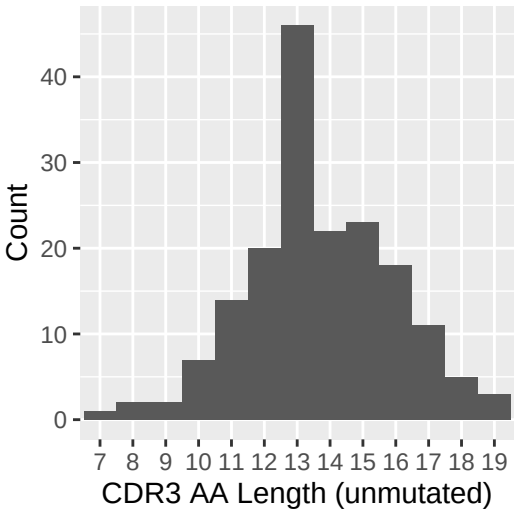


TRBV29−1*ap02

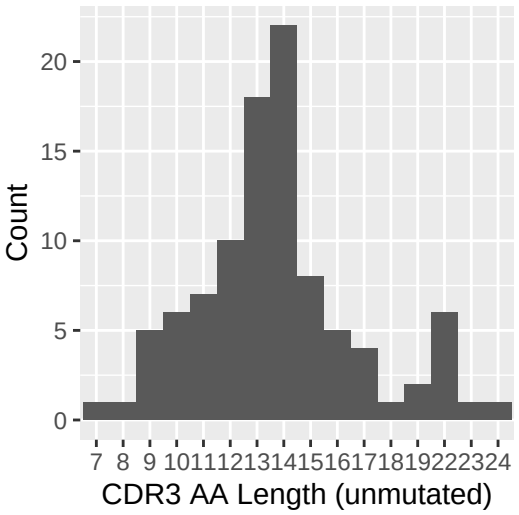
1730 sequences assigned
1711 (98.9%) exact matches, in which:
1661 unique CDR3
13 unique J



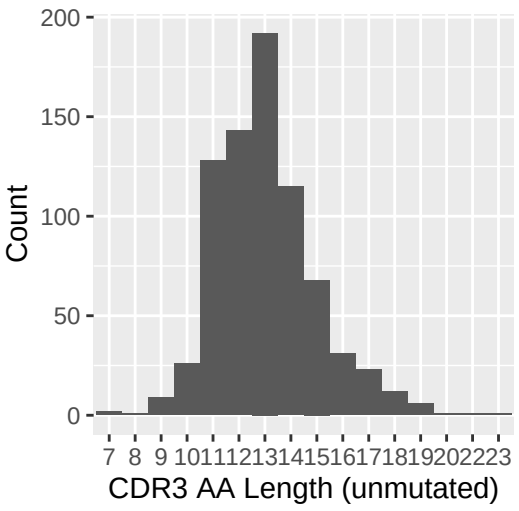
TRBV7−1*ap01_G291C_T296C_C314T



TRBV7−1*ap01_G291C_T296C



TRBV7−7*ap01_C315T



Allele Usage
Allele %
100
75
50
25
0
TRBJ1−1
TRBJ1−2
TRBJ1−3
TRBJ1−4
TRBJ1−5
TRBJ1−6
TRBJ2−1
TRBJ2−2
TRBJ2−3
TRBJ2−4
TRBJ2−5
TRBJ2−6
TRBJ2−7
TRBJ2−2P
Gene
01
02

Warning − no inferred sequences found.

Warning − no inferred sequences found.

Warning − no inferred sequences found.