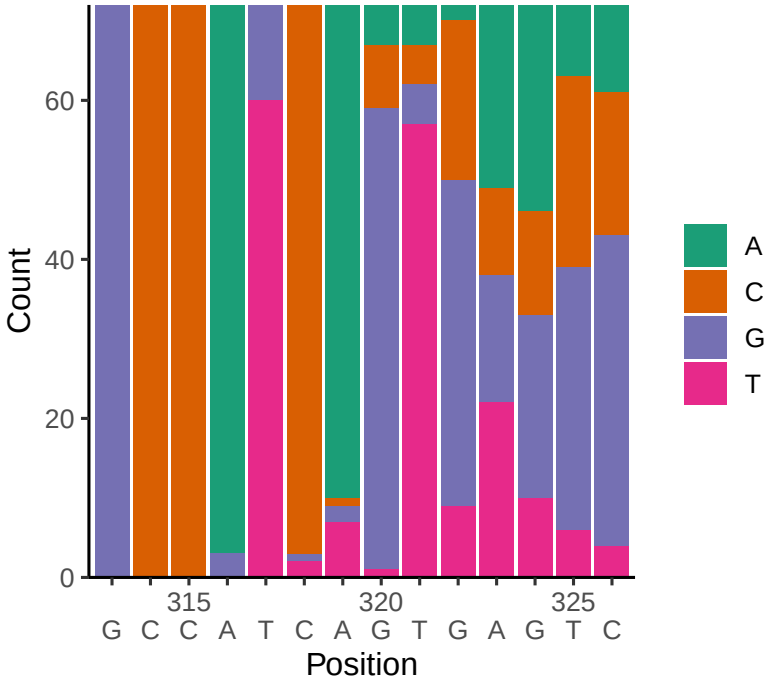
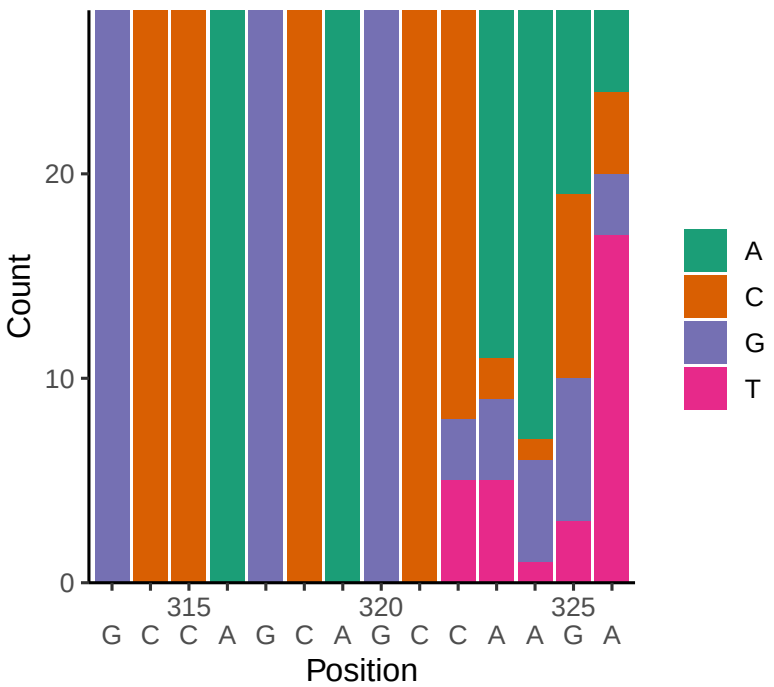
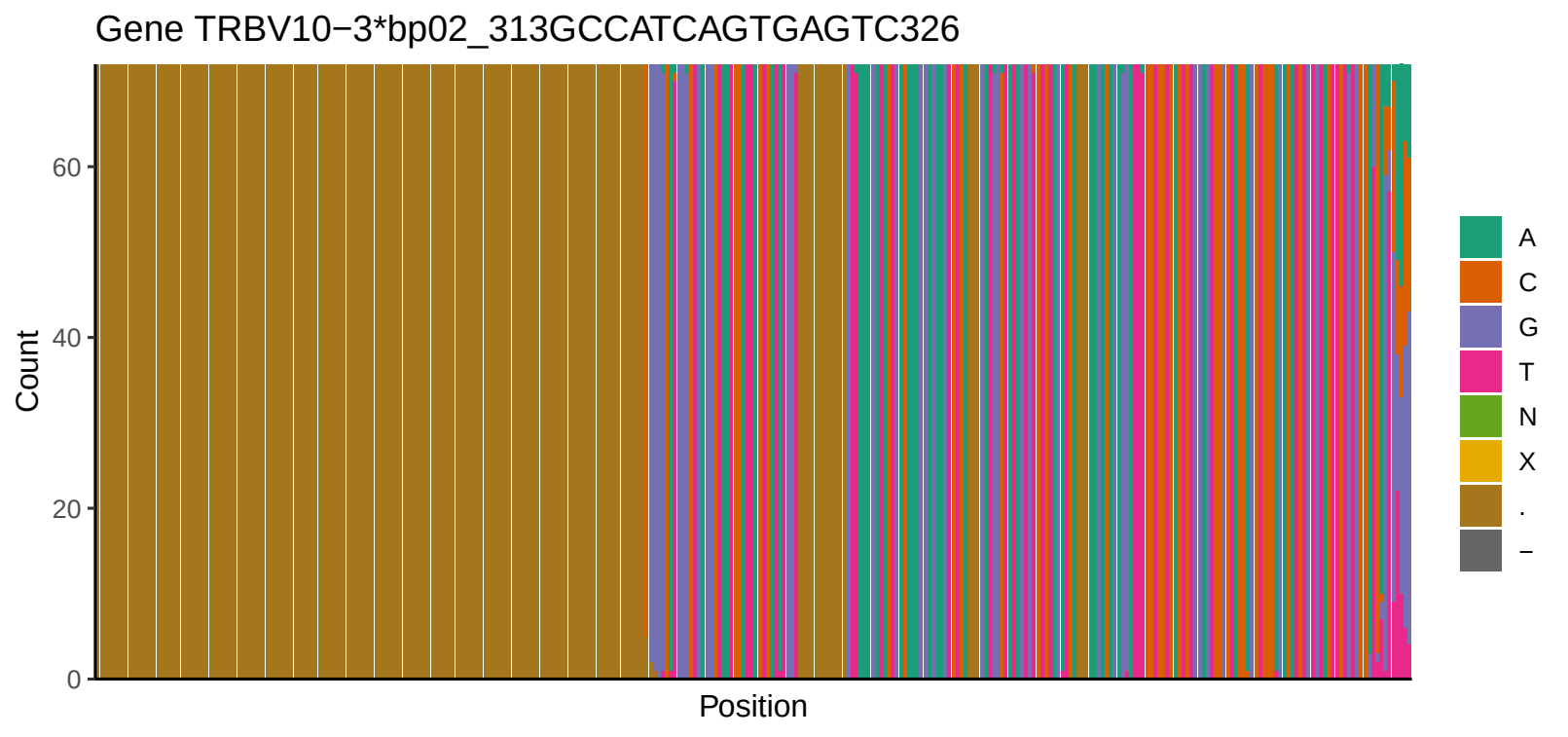
Gene TRBV10−3*bp02_313GCCATCAGTGAGTC326

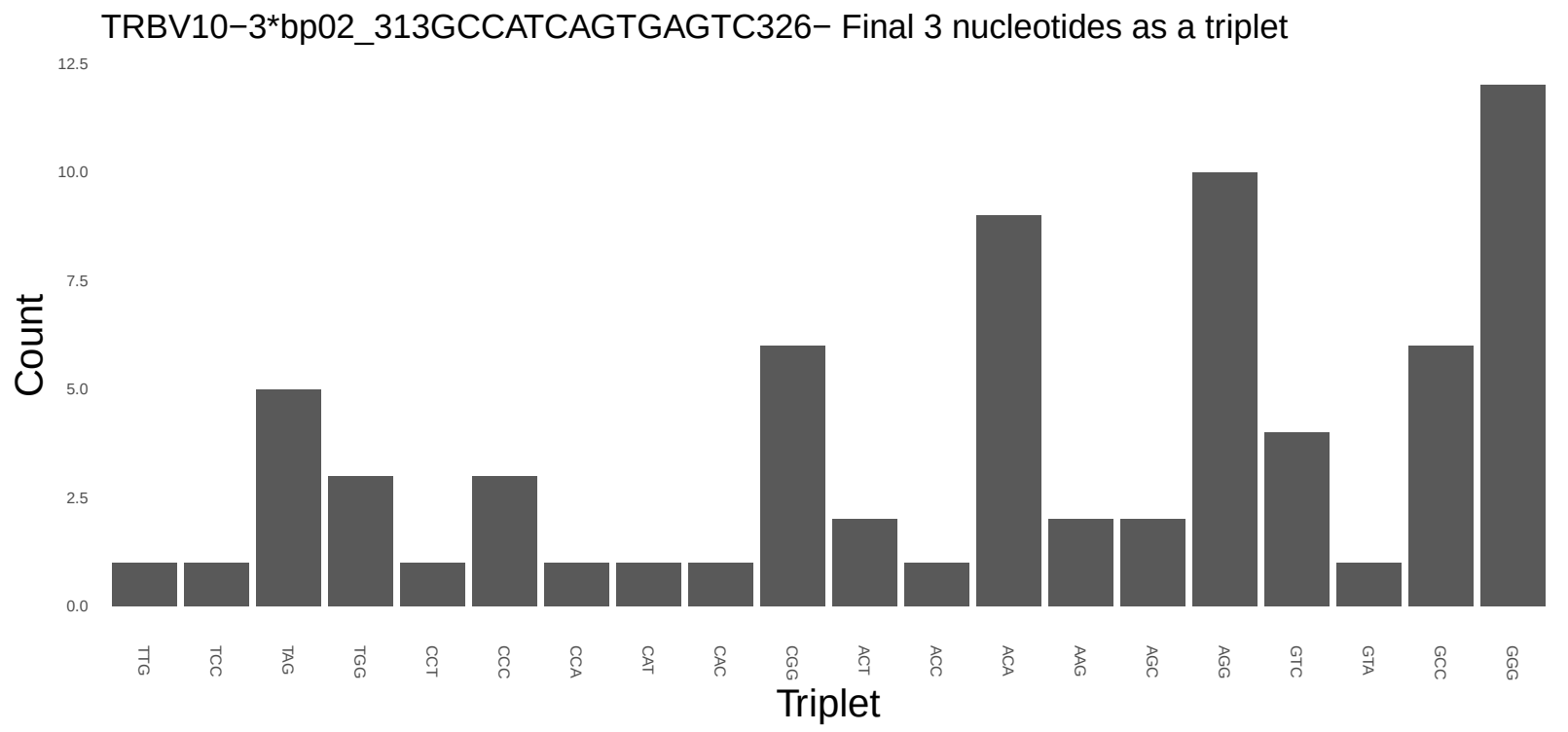


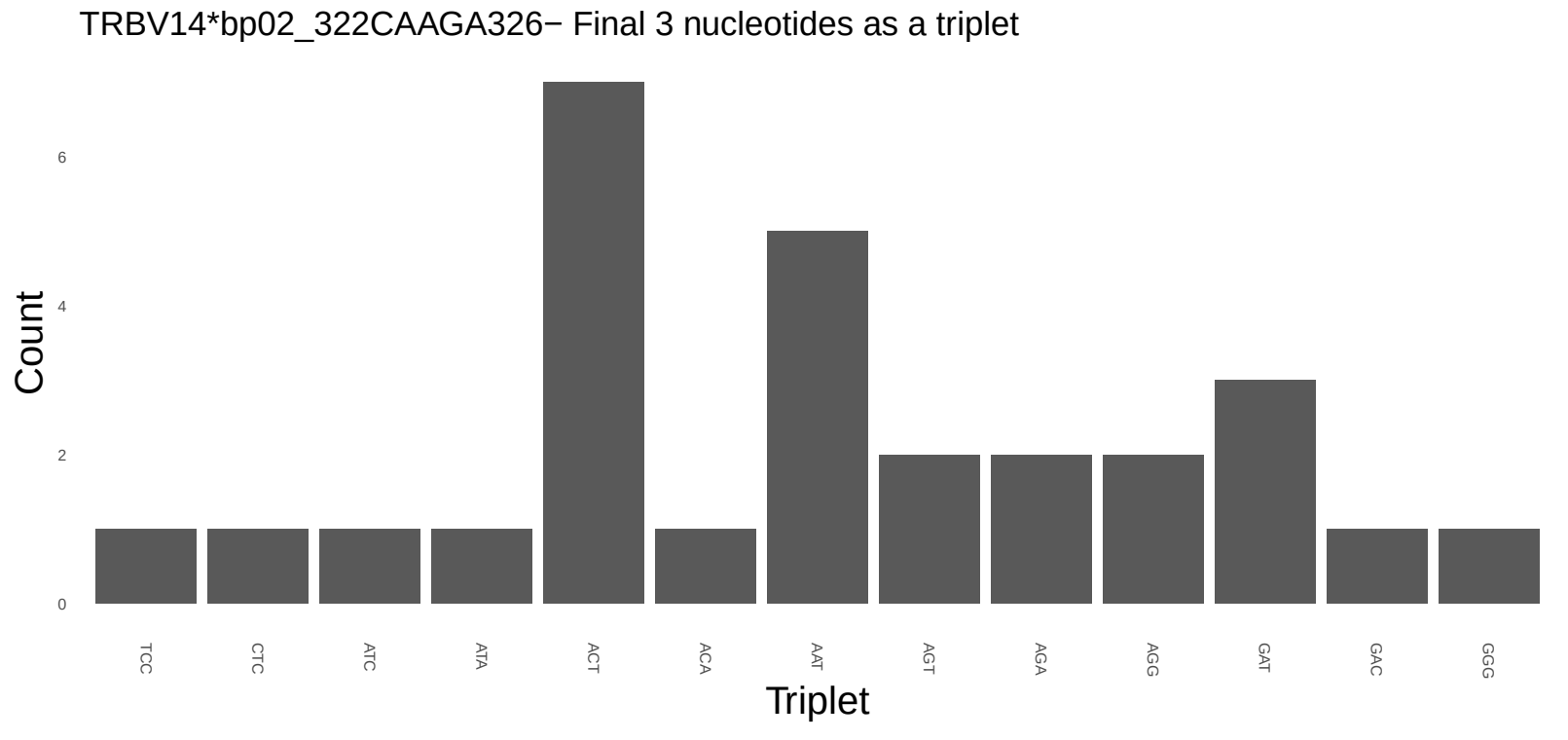
Gene TRBV14*bp02_322CAAGA326




Gene TRBV10−3*bp02_313GCCATCAGTGAGTC326
Count
0
20
40
60
Position
A
C
G
T
N
X
.
–

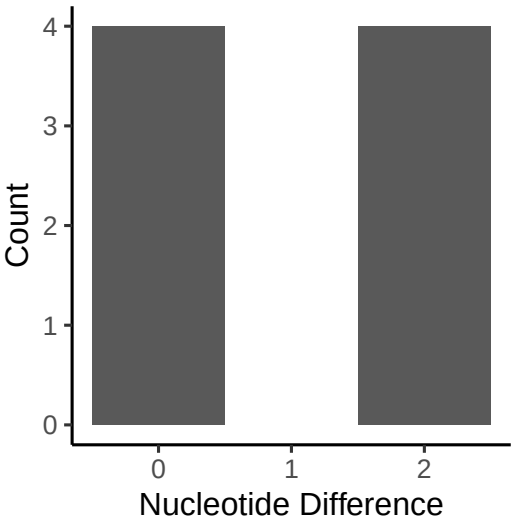
Gene TRBV14*bp02_322CAAGA326
Count
0
10
20
Position
A
C
G
T
N
X
.
–


TRBV10−3*bp02_313GCCATCAGTGAGTC326− Final 3 nucleotides as a triplet
Count
12.5
10.0
7.5
5.0
2.5
0.0
TTG
TCC
TAG
TGG
CCT
CCC
CCA
CAT
CAC
CGG
ACT
ACC
ACA
AAG
AGC
AGG
GTC
GTA
GCC
GGG
Triplet


TRBV14*bp02_322CAAGA326− Final 3 nucleotides as a triplet
Count
6
4
2
0
TCC
CTC
ATC
ATA
ACT
ACA
AAT
AGT
AGA
AGG
GAT
GAC
GGG
Triplet

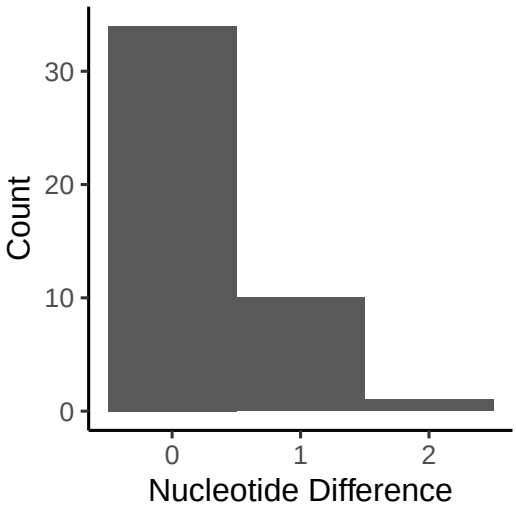
TRBV10−1*bp01

8 sequences assigned
4 (50%) exact matches, in which:
3 unique CDR3
3 unique J



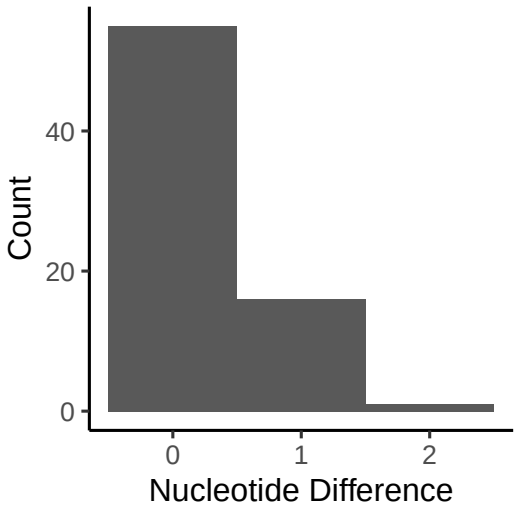
TRBV20−1*bp03

45 sequences assigned
34 (75.6%) exact matches, in which:
24 unique CDR3
10 unique J



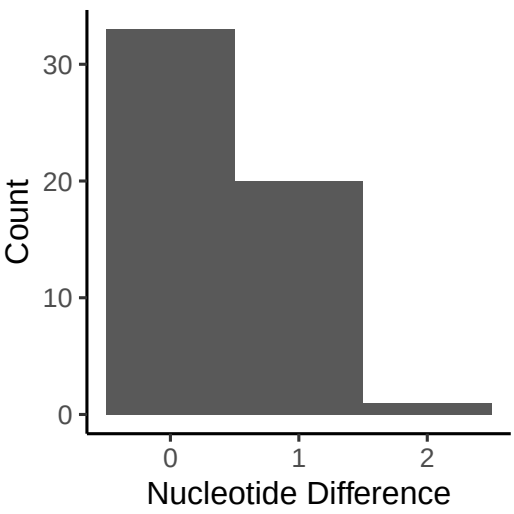
TRBV10−3*bp02_313GCC

72 sequences assigned
55 (76.4%) exact matches, in which:
34 unique CDR3
8 unique J



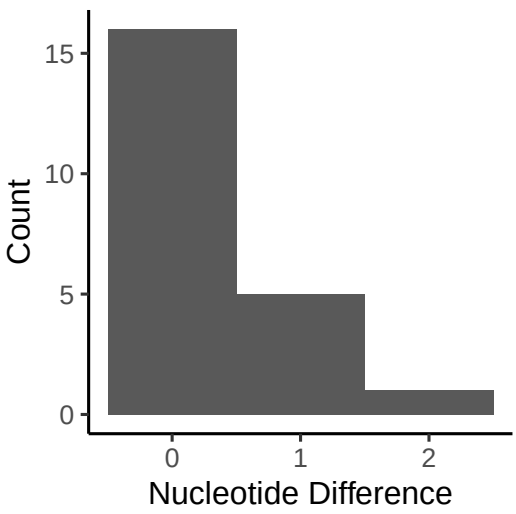
TRBV20−1*bp01

54 sequences assigned
33 (61.1%) exact matches, in which:
26 unique CDR3
9 unique J



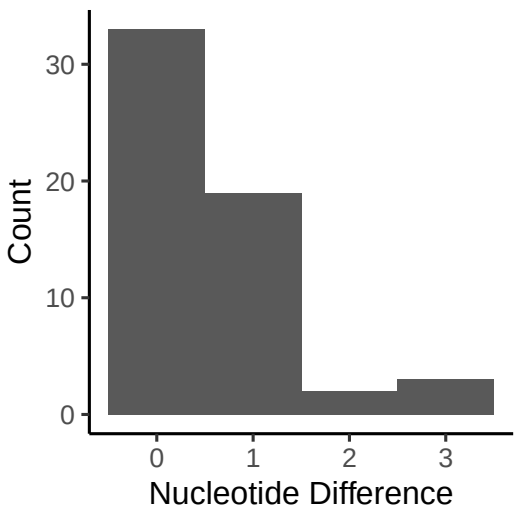
TRBV10−2*bp01

22 sequences assigned
16 (72.7%) exact matches, in which:
10 unique CDR3
7 unique J



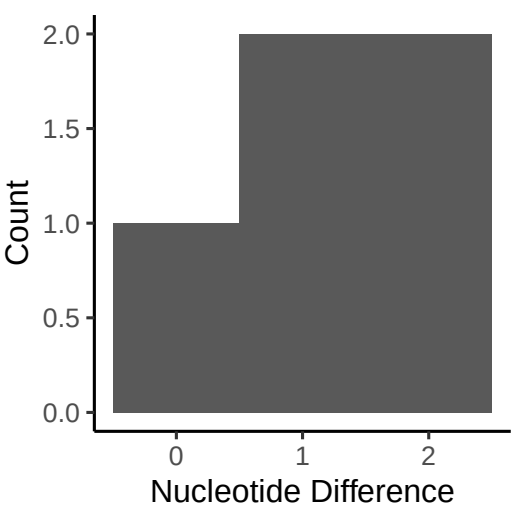
TRBV13*bp01

57 sequences assigned
33 (57.9%) exact matches, in which:
26 unique CDR3
7 unique J



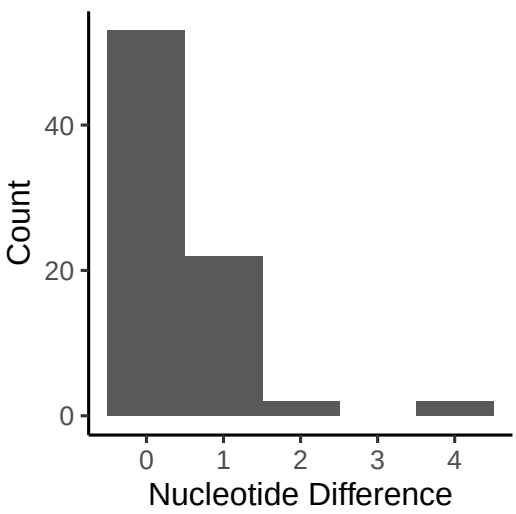
TRBV10−1*bp02

5 sequences assigned
1 (20%) exact matches, in which:
1 unique CDR3
1 unique J



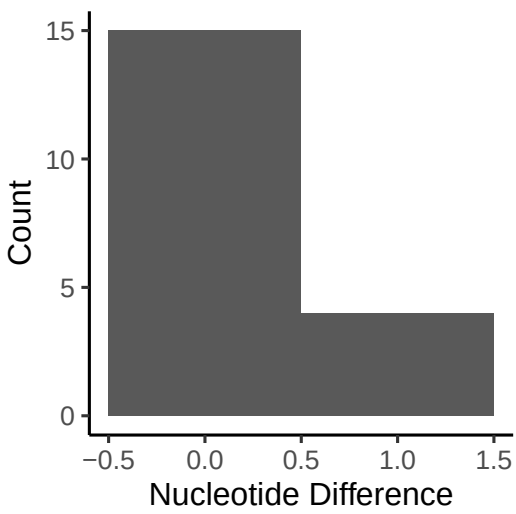
TRBV10−3*bp01

79 sequences assigned
53 (67.1%) exact matches, in which:
33 unique CDR3
7 unique J



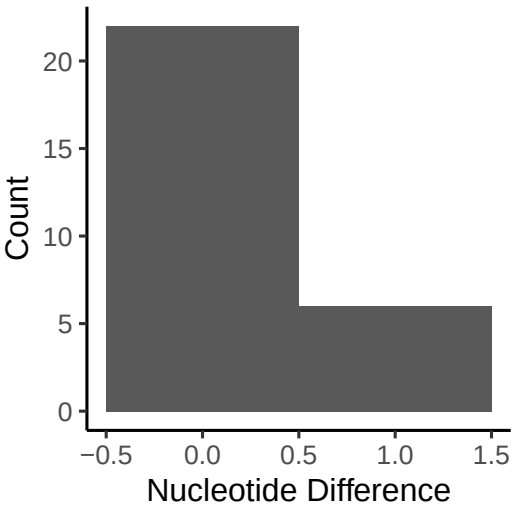
TRBV14*bp01

19 sequences assigned
15 (78.9%) exact matches, in which:
12 unique CDR3
5 unique J



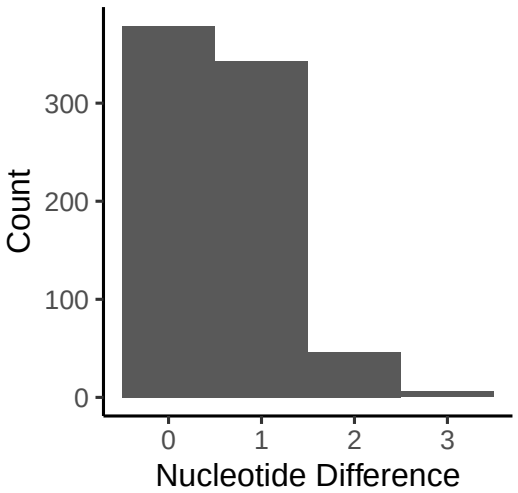
TRBV14*bp02_322CAAG/

28 sequences assigned
22 (78.6%) exact matches, in which:
15 unique CDR3
6 unique J



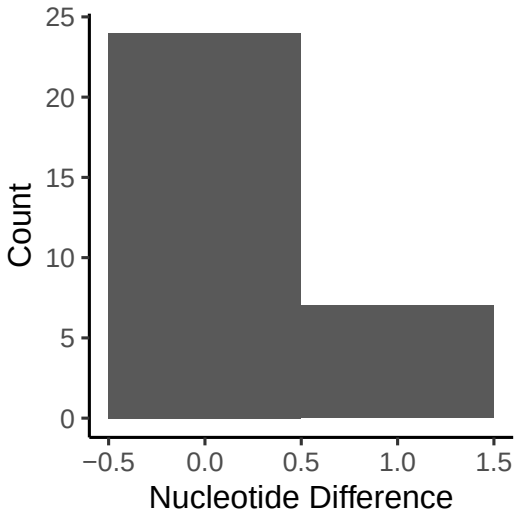
TRBV19*bp01

774 sequences assigned
379 (49%) exact matches, in which:
187 unique CDR3
12 unique J



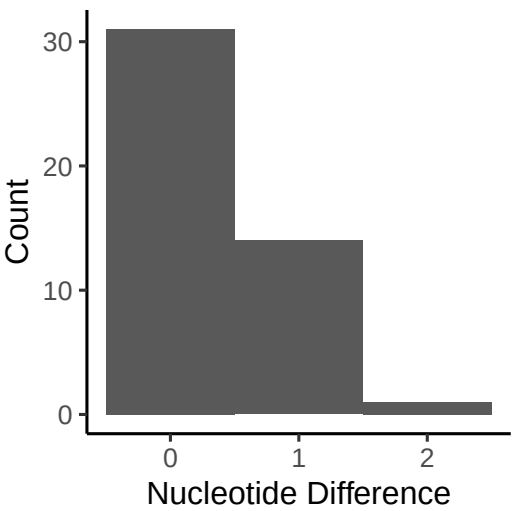
TRBV28*bp01

31 sequences assigned
24 (77.4%) exact matches, in which:
23 unique CDR3
8 unique J



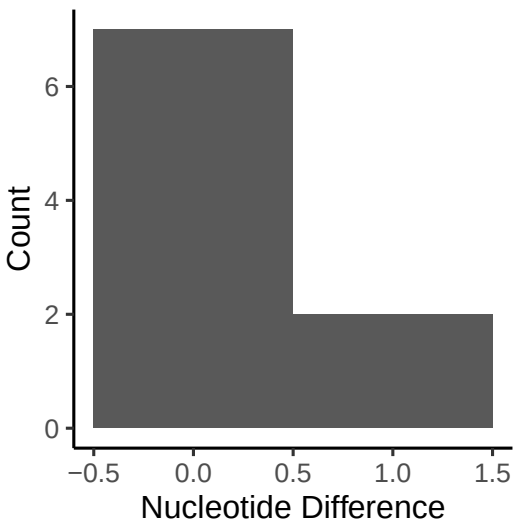
TRBV15*bp02

46 sequences assigned
31 (67.4%) exact matches, in which:
16 unique CDR3
7 unique J



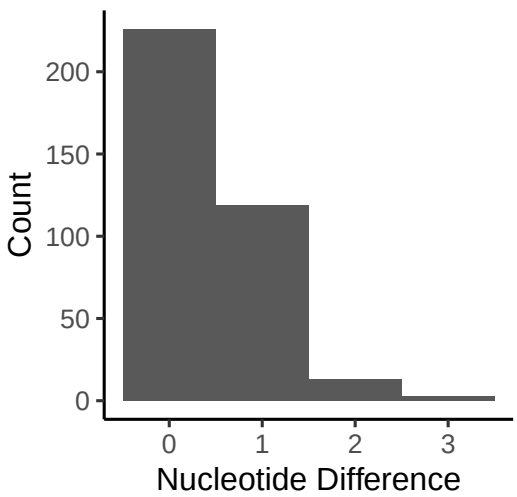
TRBV2*bp01

9 sequences assigned
7 (77.8%) exact matches, in which:
6 unique CDR3
3 unique J



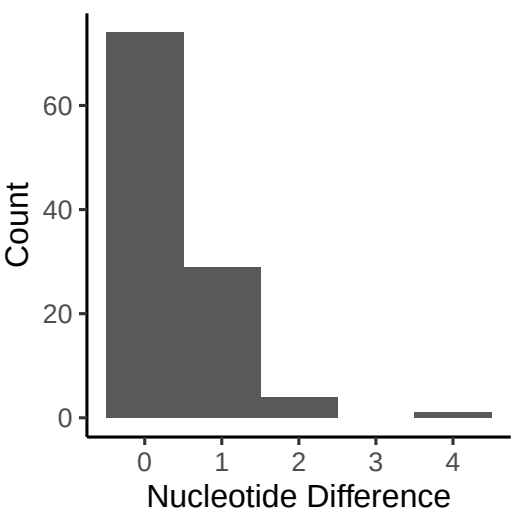
TRBV30*bp01

361 sequences assigned
226 (62.6%) exact matches, in which:
95 unique CDR3
11 unique J



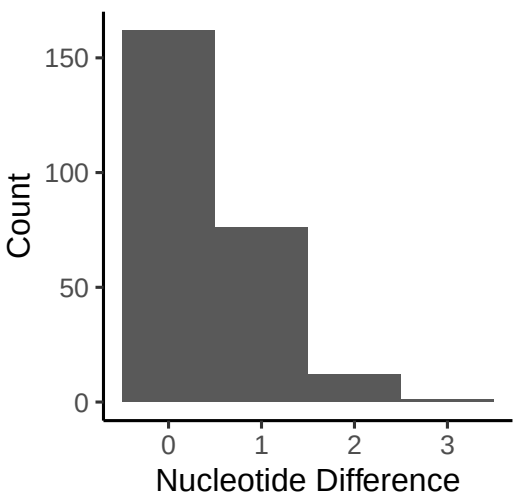
TRBV18*bp01

108 sequences assigned
74 (68.5%) exact matches, in which:
37 unique CDR3
10 unique J



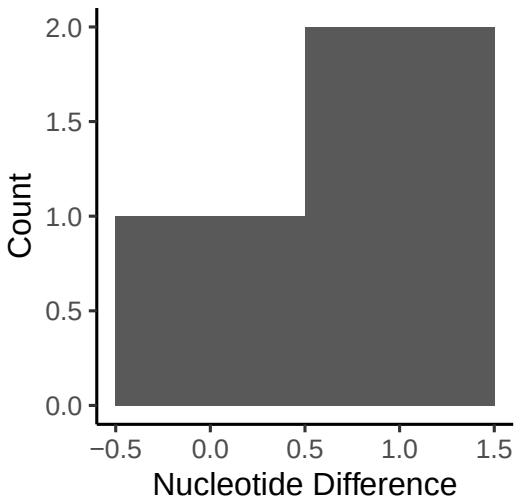
TRBV27*bp01

251 sequences assigned
162 (64.5%) exact matches, in which:
122 unique CDR3
12 unique J



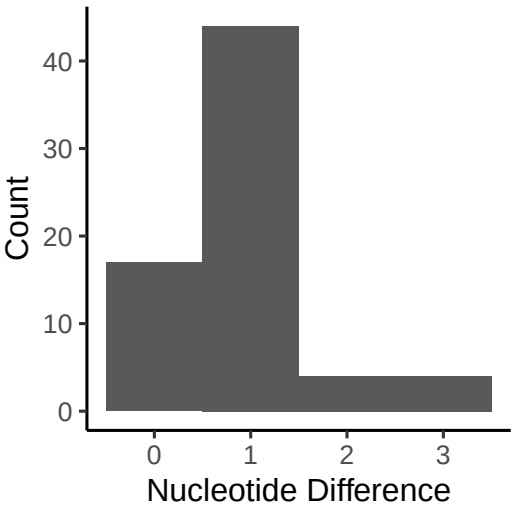
TRBV9*bp01

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



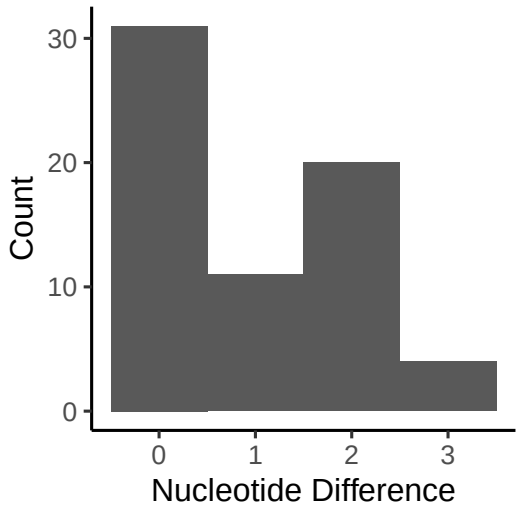
TRBV11−1*bp01

69 sequences assigned
17 (24.6%) exact matches, in which:
8 unique CDR3
4 unique J



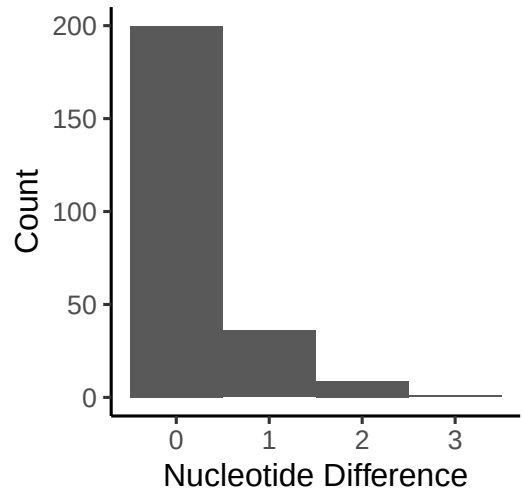
TRBV11−2*bp01

66 sequences assigned
31 (47%) exact matches, in which:
24 unique CDR3
9 unique J



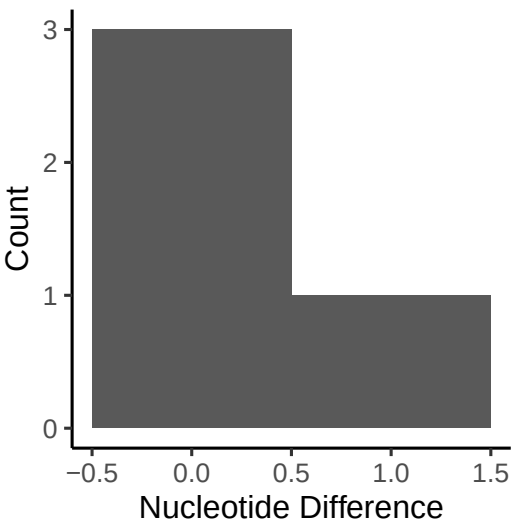
TRBV12−34*bp01

246 sequences assigned
200 (81.3%) exact matches, in which:
110 unique CDR3
13 unique J



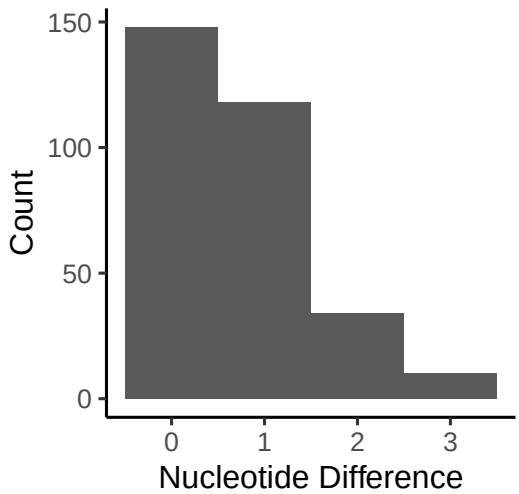
TRBV21−1*bp01

4 sequences assigned
3 (75%) exact matches, in which:
2 unique CDR3
2 unique J



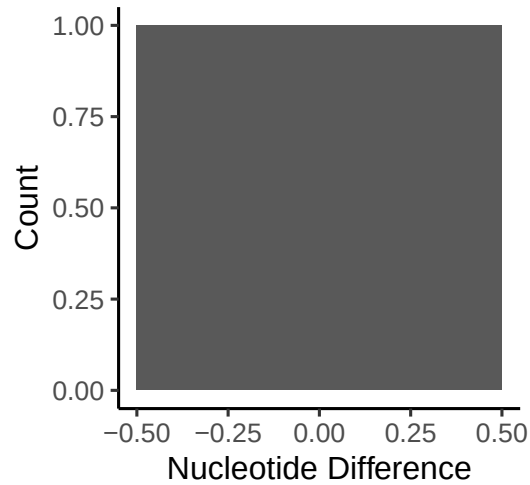
TRBV11−3*bp01

310 sequences assigned
148 (47.7%) exact matches, in which:
94 unique CDR3
12 unique J



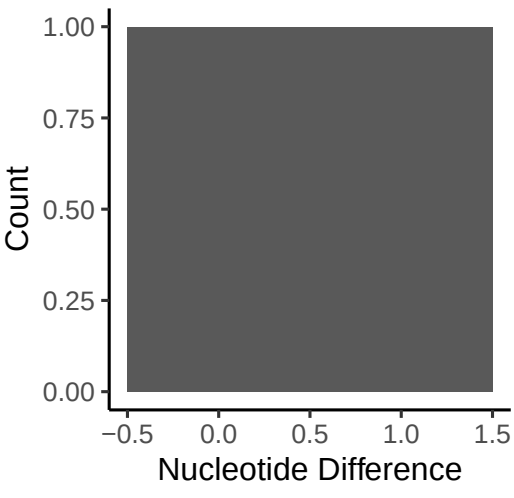
TRBV3−2*bp02

1 sequences assigned
1 (100%) exact matches, in which:
1 unique CDR3
1 unique J



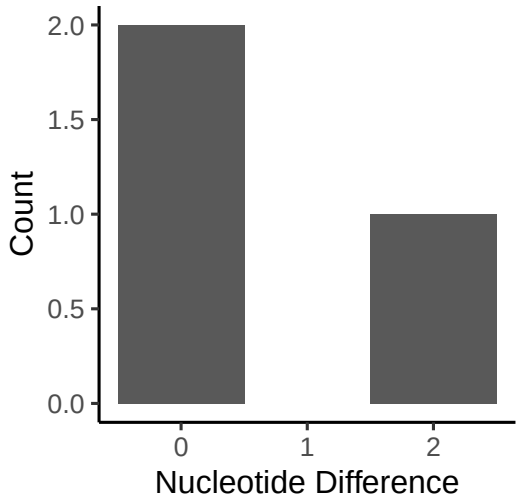
TRBV21−1*bp02

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



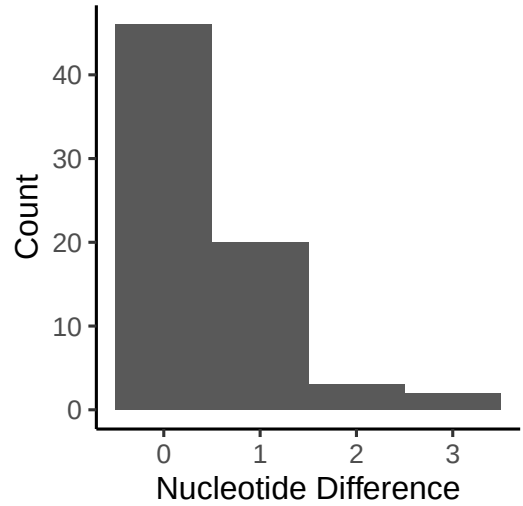
TRBV12−5*bp01

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



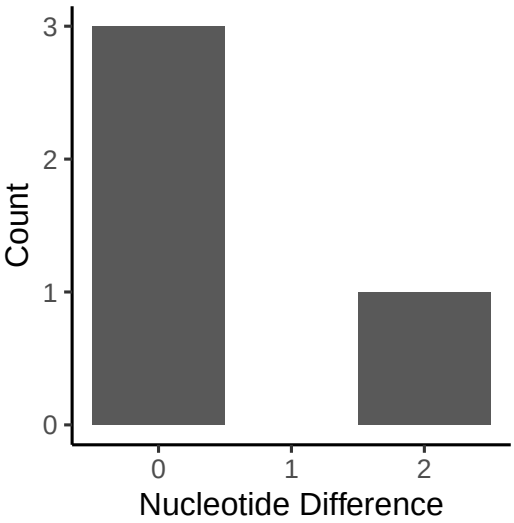
TRBV24−1*bp01

71 sequences assigned
46 (64.8%) exact matches, in which:
30 unique CDR3
6 unique J



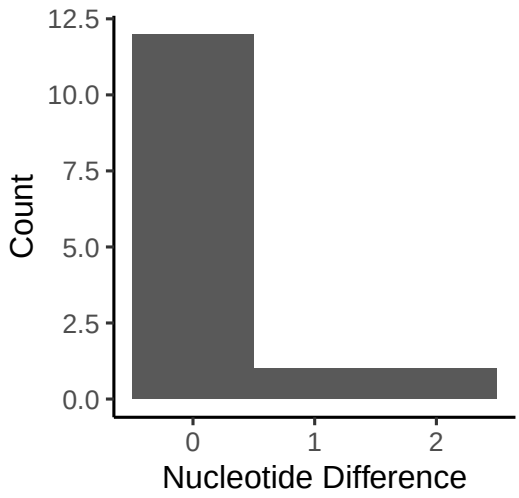
TRBV4−1*bp01

4 sequences assigned
3 (75%) exact matches, in which:
2 unique CDR3
2 unique J



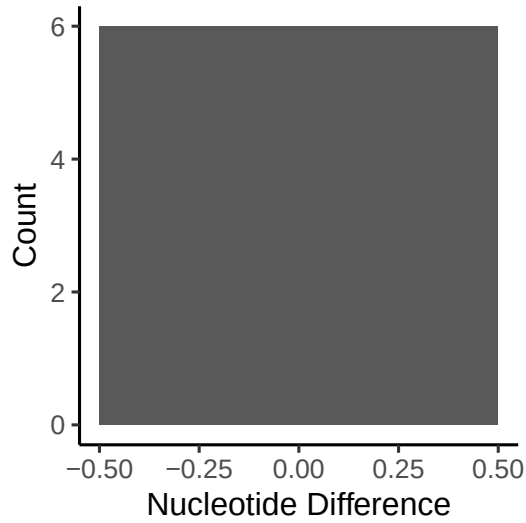
TRBV4−3*bp01

14 sequences assigned
12 (85.7%) exact matches, in which:
8 unique CDR3
6 unique J



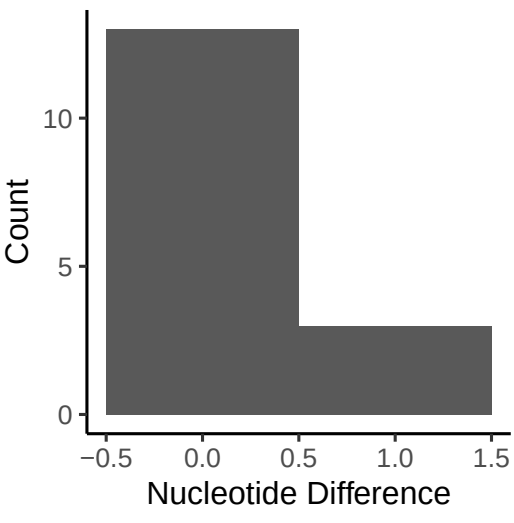
TRBV5−3*bp01

6 sequences assigned
6 (100%) exact matches, in which:
3 unique CDR3
3 unique J



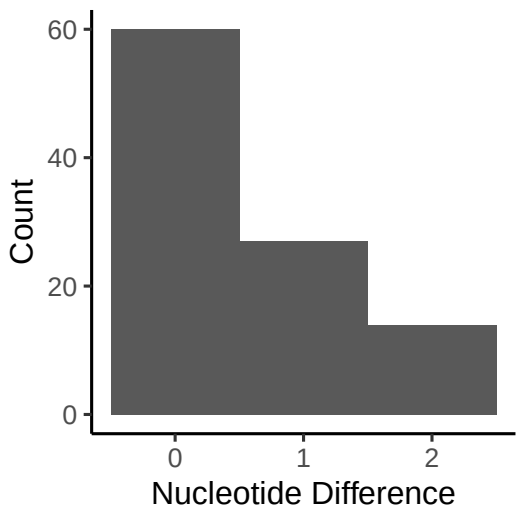
TRBV24−1*bp02

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



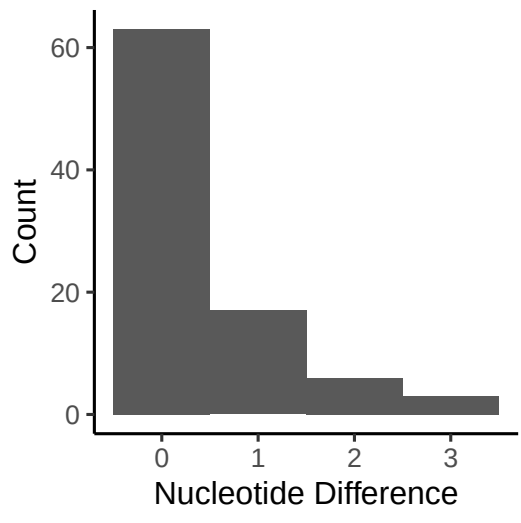
TRBV5−1*bp01

101 sequences assigned
60 (59.4%) exact matches, in which:
39 unique CDR3
9 unique J



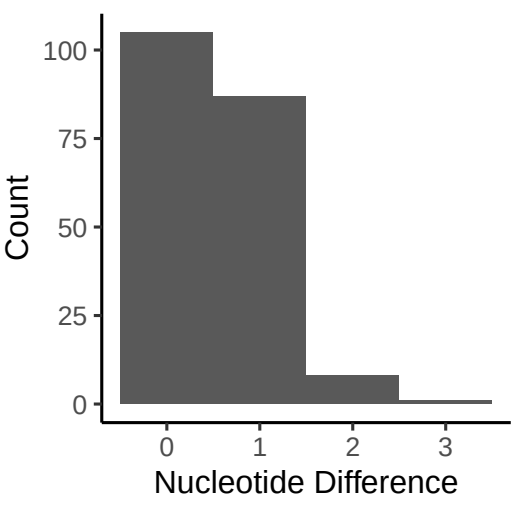
TRBV5−4*bp01

89 sequences assigned
63 (70.8%) exact matches, in which:
42 unique CDR3
9 unique J



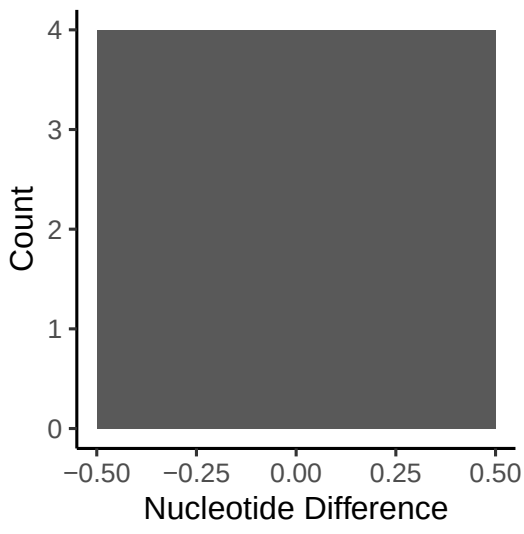
TRBV4−2*bp01

201 sequences assigned
105 (52.2%) exact matches, in which:
65 unique CDR3
8 unique J



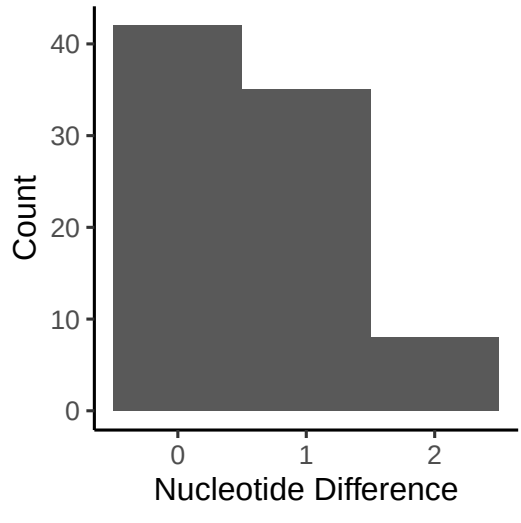
TRBV25−1*bp01

4 sequences assigned
4 (100%) exact matches, in which:
3 unique CDR3
3 unique J



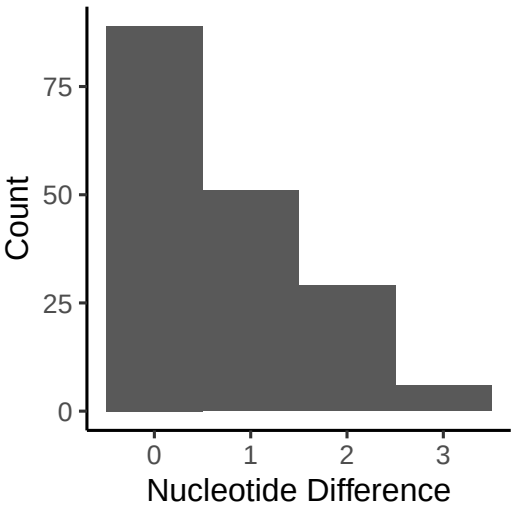
TRBV5−5*bp01

85 sequences assigned
42 (49.4%) exact matches, in which:
24 unique CDR3
7 unique J



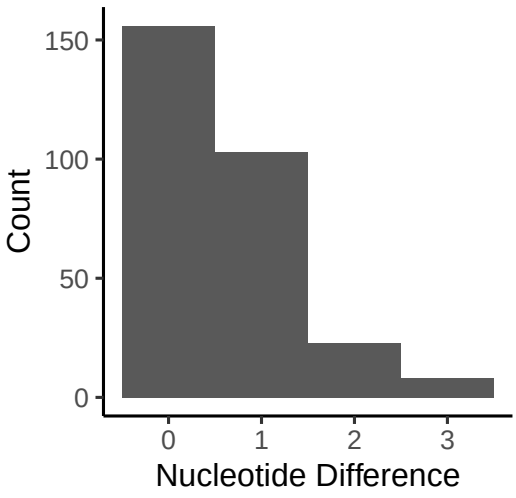
TRBV5−6*bp01

175 sequences assigned
89 (50.9%) exact matches, in which:
49 unique CDR3
12 unique J



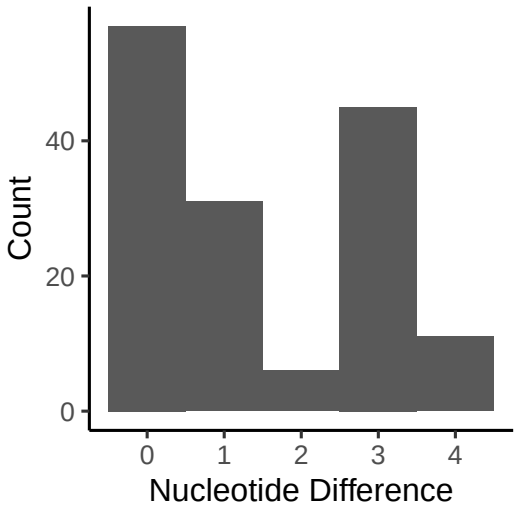
TRBV6−1*bp01

290 sequences assigned
156 (53.8%) exact matches, in which:
110 unique CDR3
11 unique J



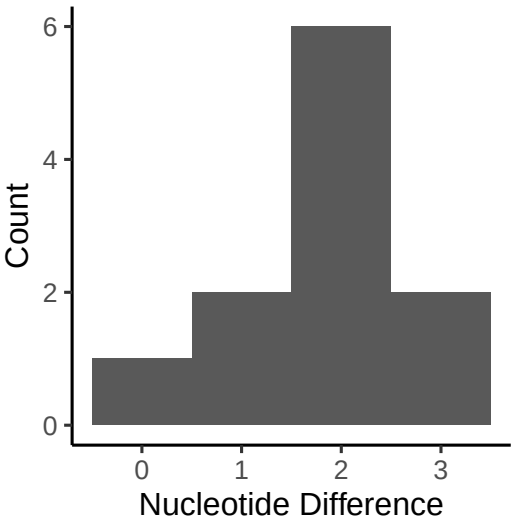
TRBV6−6*bp01

150 sequences assigned
57 (38%) exact matches, in which:
44 unique CDR3
10 unique J



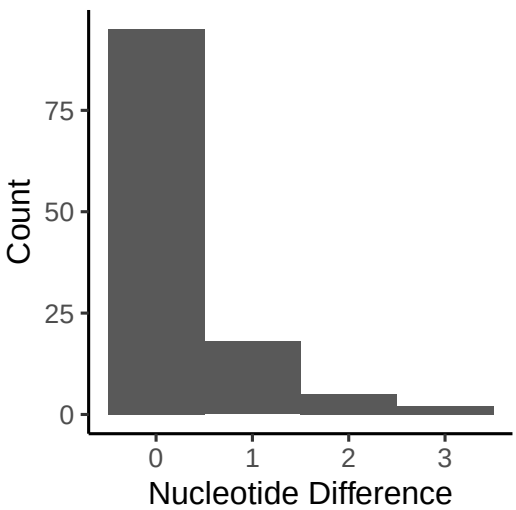
TRBV5−7*bp01

11 sequences assigned
1 (9.1%) exact matches, in which:
1 unique CDR3
1 unique J



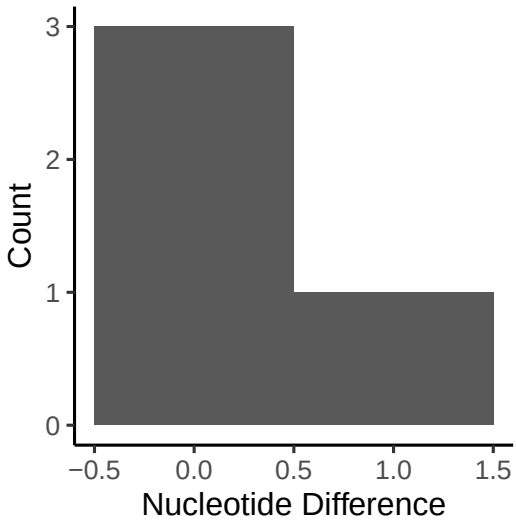
TRBV6−4*bp01

120 sequences assigned
95 (79.2%) exact matches, in which:
53 unique CDR3
9 unique J



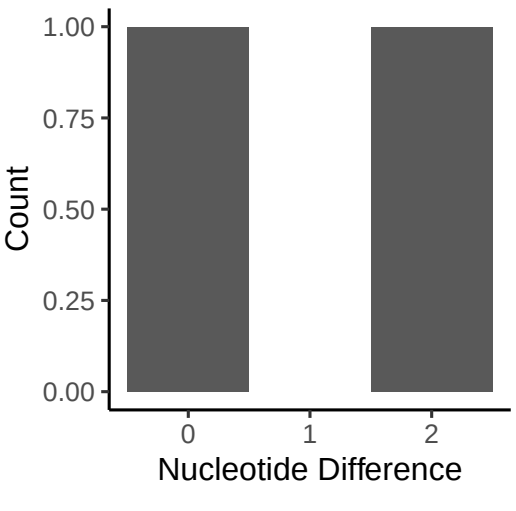
TRBV6−8*bp01

4 sequences assigned
3 (75%) exact matches, in which:
3 unique CDR3
3 unique J



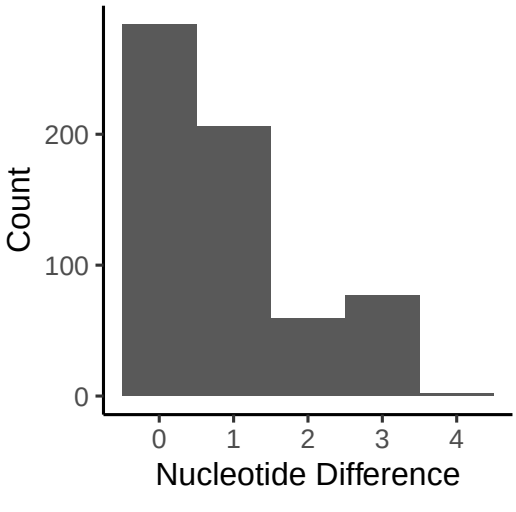
TRBV5−8*bp01

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



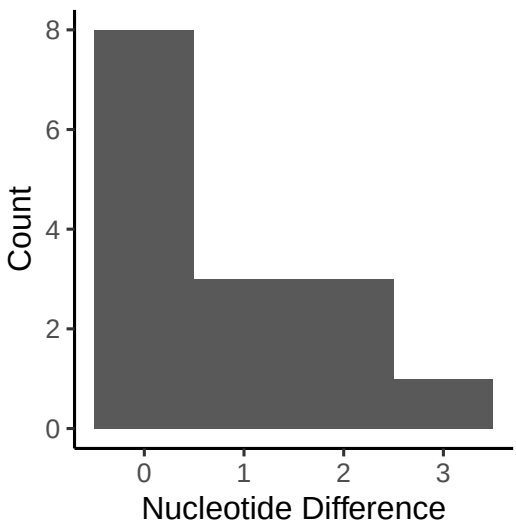
TRBV6−5*bp01

628 sequences assigned
284 (45.2%) exact matches, in which:
203 unique CDR3
13 unique J



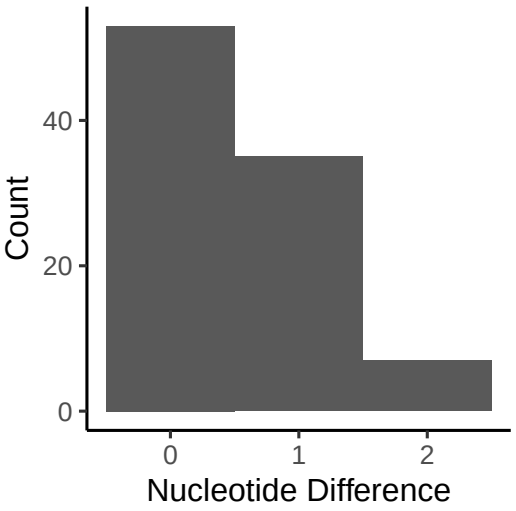
TRBV6−9*bp01

15 sequences assigned
8 (53.3%) exact matches, in which:
6 unique CDR3
4 unique J



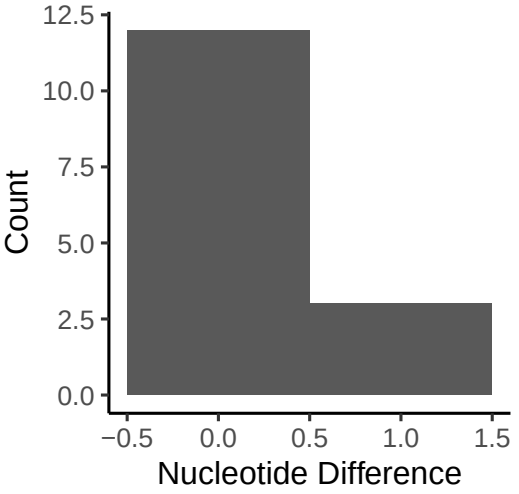
TRBV6−23*bp01

95 sequences assigned
53 (55.8%) exact matches, in which:
44 unique CDR3
11 unique J



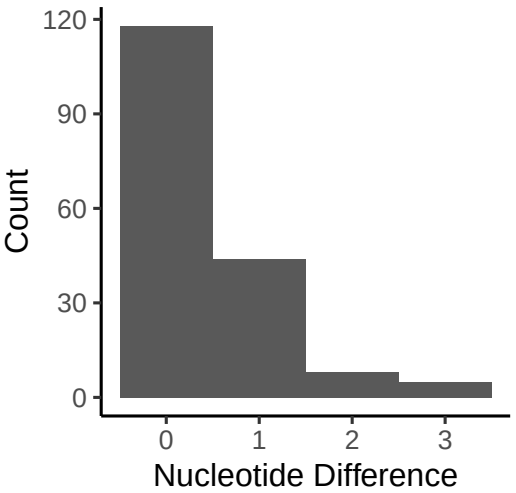
TRBV7−3*bp01

15 sequences assigned
12 (80%) exact matches, in which:
12 unique CDR3
5 unique J



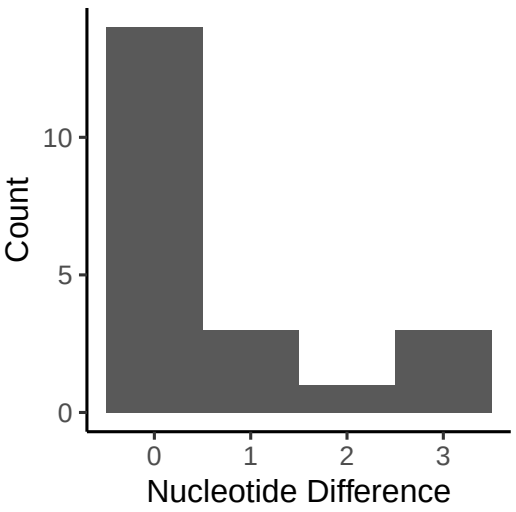
TRBV7−9*bp01

175 sequences assigned
118 (67.4%) exact matches, in which:
75 unique CDR3
9 unique J



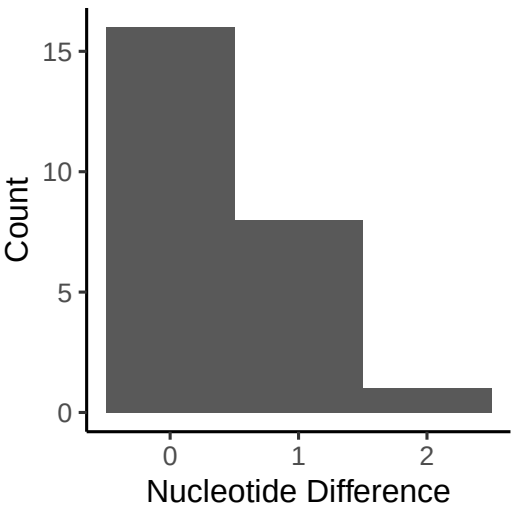
TRBV7−2*bp01

21 sequences assigned
14 (66.7%) exact matches, in which:
11 unique CDR3
7 unique J



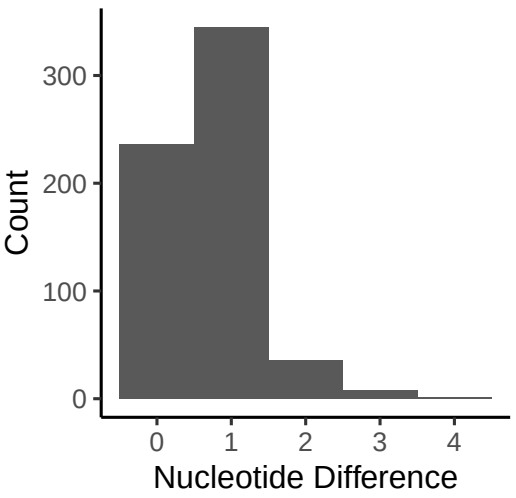
TRBV7−4*bp01

25 sequences assigned
16 (64%) exact matches, in which:
7 unique CDR3
3 unique J



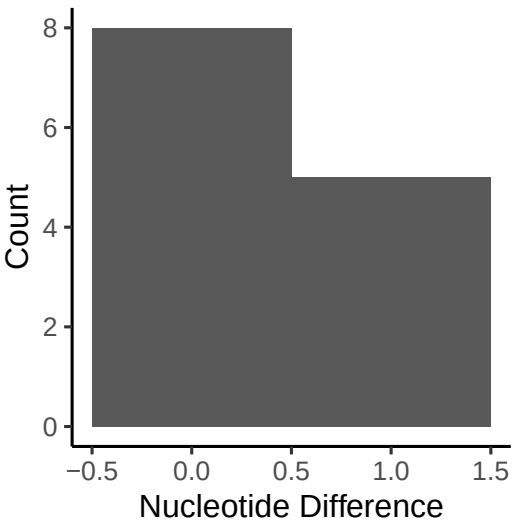
TRBV29−1*bp01

626 sequences assigned
236 (37.7%) exact matches, in which:
135 unique CDR3
10 unique J



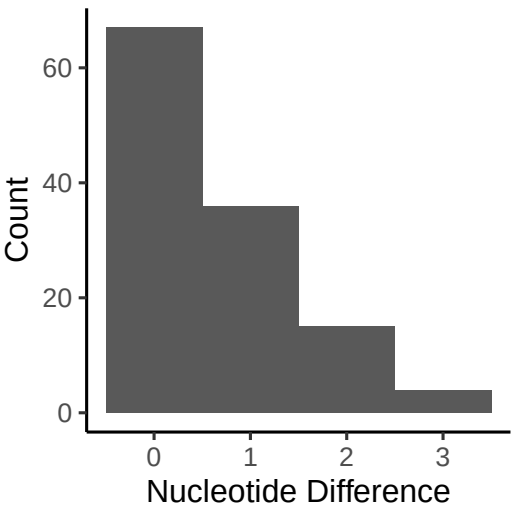
TRBV7−2*bp02

13 sequences assigned
8 (61.5%) exact matches, in which:
7 unique CDR3
5 unique J

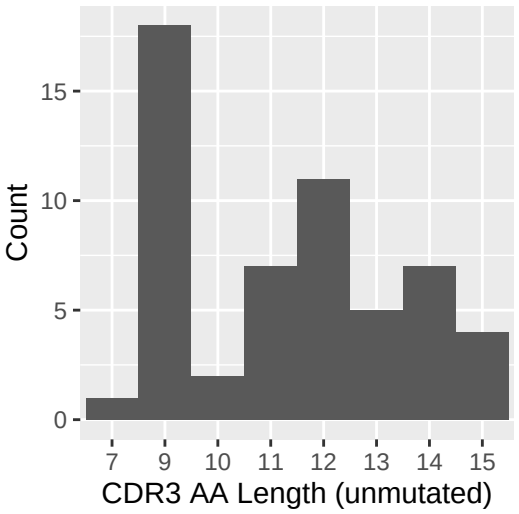


TRBV7−6*bp01

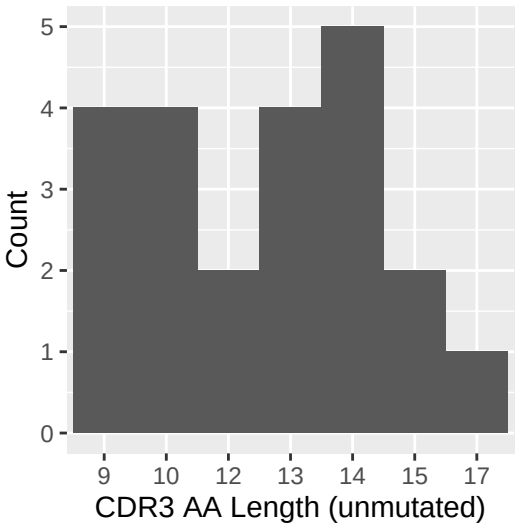
122 sequences assigned
67 (54.9%) exact matches, in which:
29 unique CDR3
8 unique J

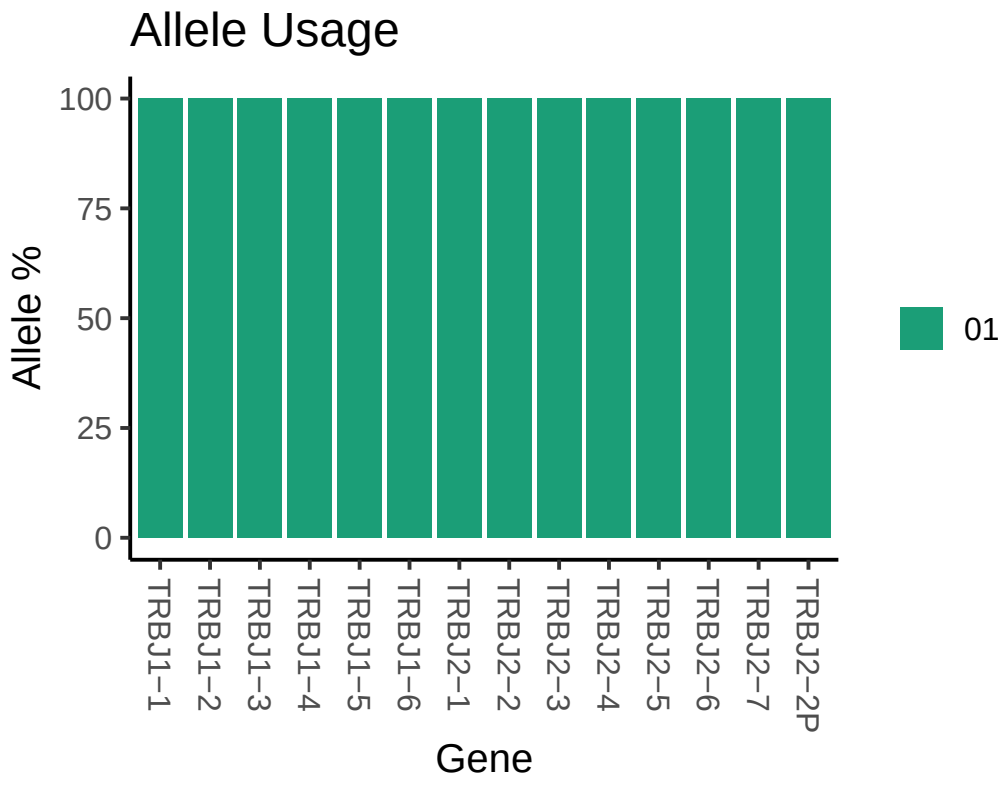


TRBV10−3*bp02_313GCCATCAGTGAGTC326



TRBV14*bp02_322CAAGA326




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

Warning − no inferred sequences found.

Warning − no inferred sequences found.

Warning − no inferred sequences found.