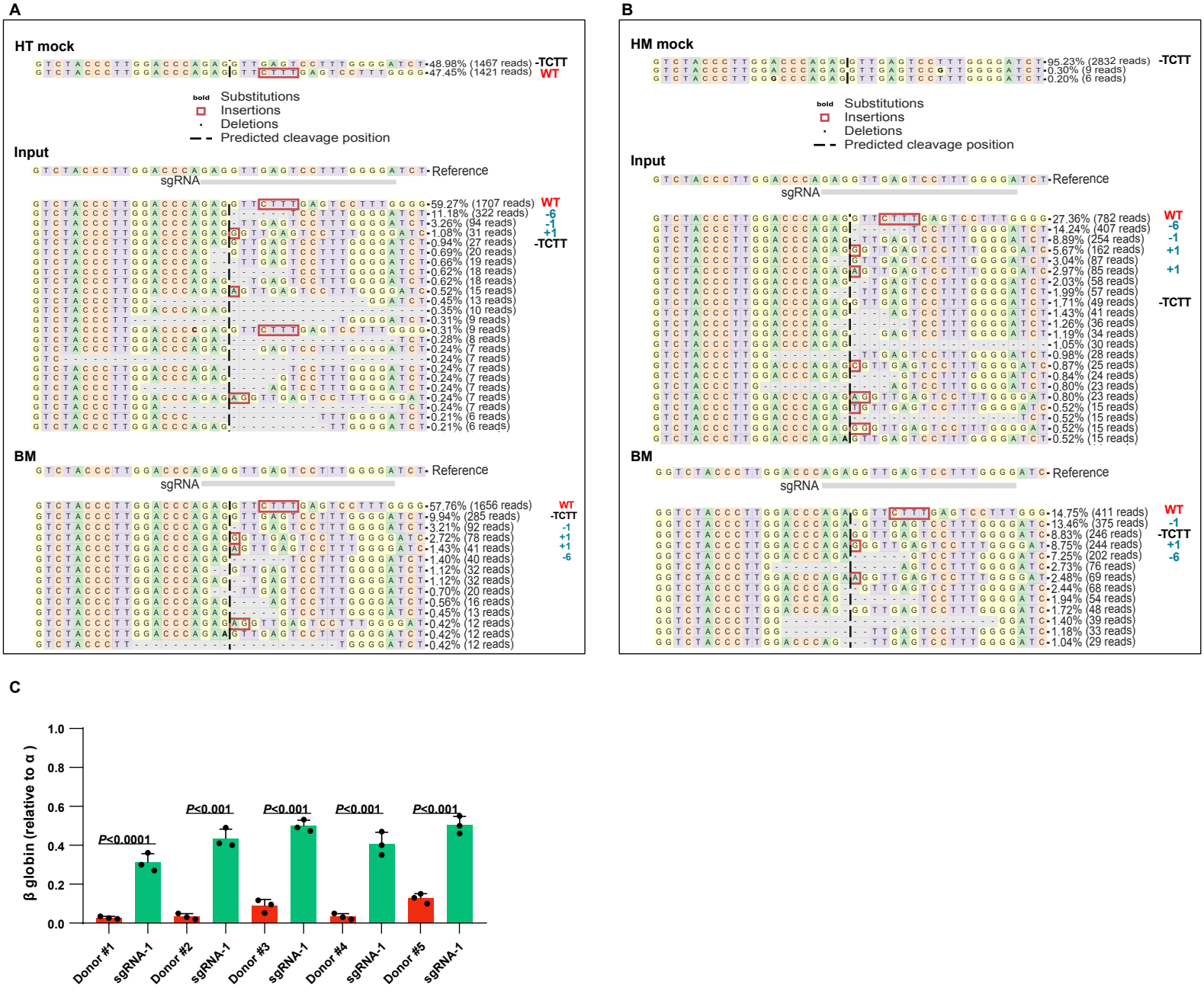
A
HT mock
-48.98% (1467 reads) -TCTT
-47.45% (1421 reads) WT
bold Substitutions
Insertions
Deletions
Predicted cleavage position
Input
Reference
sgRNA
-59.27% (1707 reads) WT
-11.18% (322 reads) -6
-3.26% (94 reads) -1
-1.08% (31 reads) +1
-0.94% (27 reads) -TCTT
-0.69% (20 reads)
-0.66% (19 reads)
-0.62% (18 reads)
-0.62% (18 reads)
-0.52% (15 reads)
-0.45% (13 reads)
-0.35% (10 reads)
-0.31% (9 reads)
-0.31% (9 reads)
-0.28% (8 reads)
-0.24% (7 reads)
-0.24% (7 reads)
-0.24% (7 reads)
-0.24% (7 reads)
-0.24% (7 reads)
-0.24% (7 reads)
-0.24% (7 reads)
-0.21% (6 reads)
-0.21% (6 reads)
BM
Reference
sgRNA
-57.76% (1656 reads) WT
-9.94% (285 reads) -TCTT
-3.21% (92 reads) -1
-2.72% (78 reads) +1
-1.43% (41 reads) +1
-1.40% (40 reads) -6
-1.12% (32 reads)
-1.12% (32 reads)
-0.70% (20 reads)
-0.56% (16 reads)
-0.45% (13 reads)
-0.42% (12 reads)
-0.42% (12 reads)
B
HM mock
-95.23% (2832 reads) -TCTT
-0.30% (9 reads)
-0.20% (6 reads)
bold Substitutions
Insertions
Deletions
Predicted cleavage position
Input
Reference
sgRNA
-27.36% (782 reads) WT
-14.24% (407 reads) -6
-8.89% (254 reads) -1
-5.67% (162 reads) +1
-3.04% (87 reads)
-2.97% (85 reads) +1
-2.03% (58 reads)
-1.99% (57 reads)
-1.71% (49 reads) -TCTT
-1.43% (41 reads)
-1.26% (36 reads)
-1.19% (34 reads)
-1.05% (30 reads)
-0.98% (28 reads)
-0.87% (25 reads)
-0.84% (24 reads)
-0.80% (23 reads)
-0.80% (23 reads)
-0.52% (15 reads)
-0.52% (15 reads)
-0.52% (15 reads)
-0.52% (15 reads)
BM
Reference
sgRNA
-14.75% (411 reads) WT
-13.46% (375 reads) -1
-8.83% (246 reads) -TCTT
-8.75% (244 reads) +1
-7.25% (202 reads) -6
-2.73% (76 reads)
-2.48% (69 reads)
-2.44% (68 reads)
-1.94% (54 reads)
-1.72% (48 reads)
-1.40% (39 reads)
-1.18% (33 reads)
-1.04% (29 reads)
C
β globin (relative to α)
1.0
0.8
0.6
0.4
0.2
0.0
P<0.0001
P<0.001
P<0.001
P<0.001
P<0.001
Donor #1
sgRNA-1
Donor #2
sgRNA-1
Donor #3
sgRNA-1
Donor #4
sgRNA-1
Donor #5
sgRNA-1