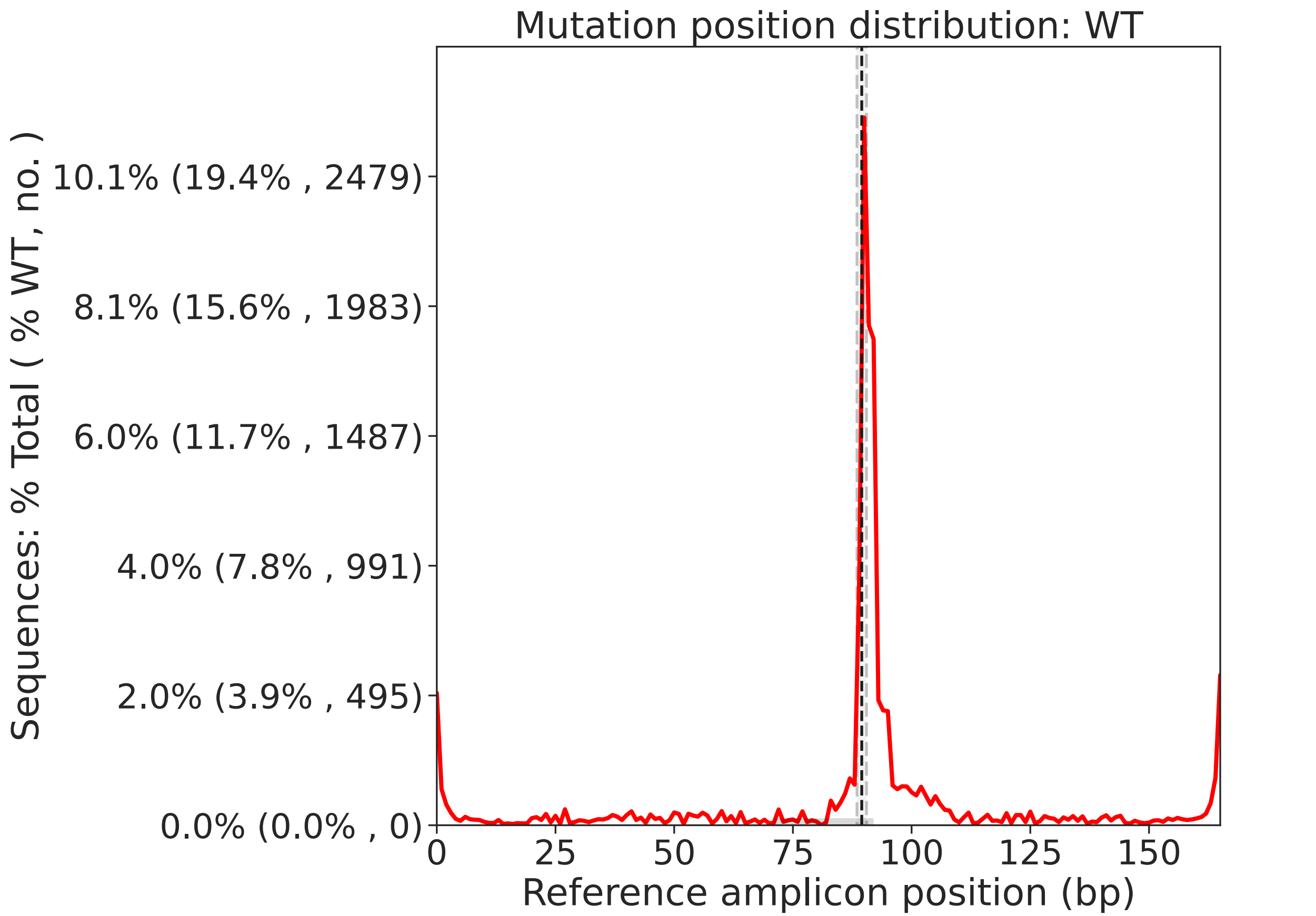
Mutation position distribution: WT
Sequences: % Total ( % WT, no. )
10.1% (19.4% , 2479)
8.1% (15.6% , 1983)
6.0% (11.7% , 1487)
4.0% (7.8% , 991)
2.0% (3.9% , 495)
0.0% (0.0% , 0)
0
25
50
75
100
125
150
Reference amplicon position (bp)
Quantification window
Combined Insertions/Deletions/Substitutions: WT
Predicted cleavage position
sgRNA