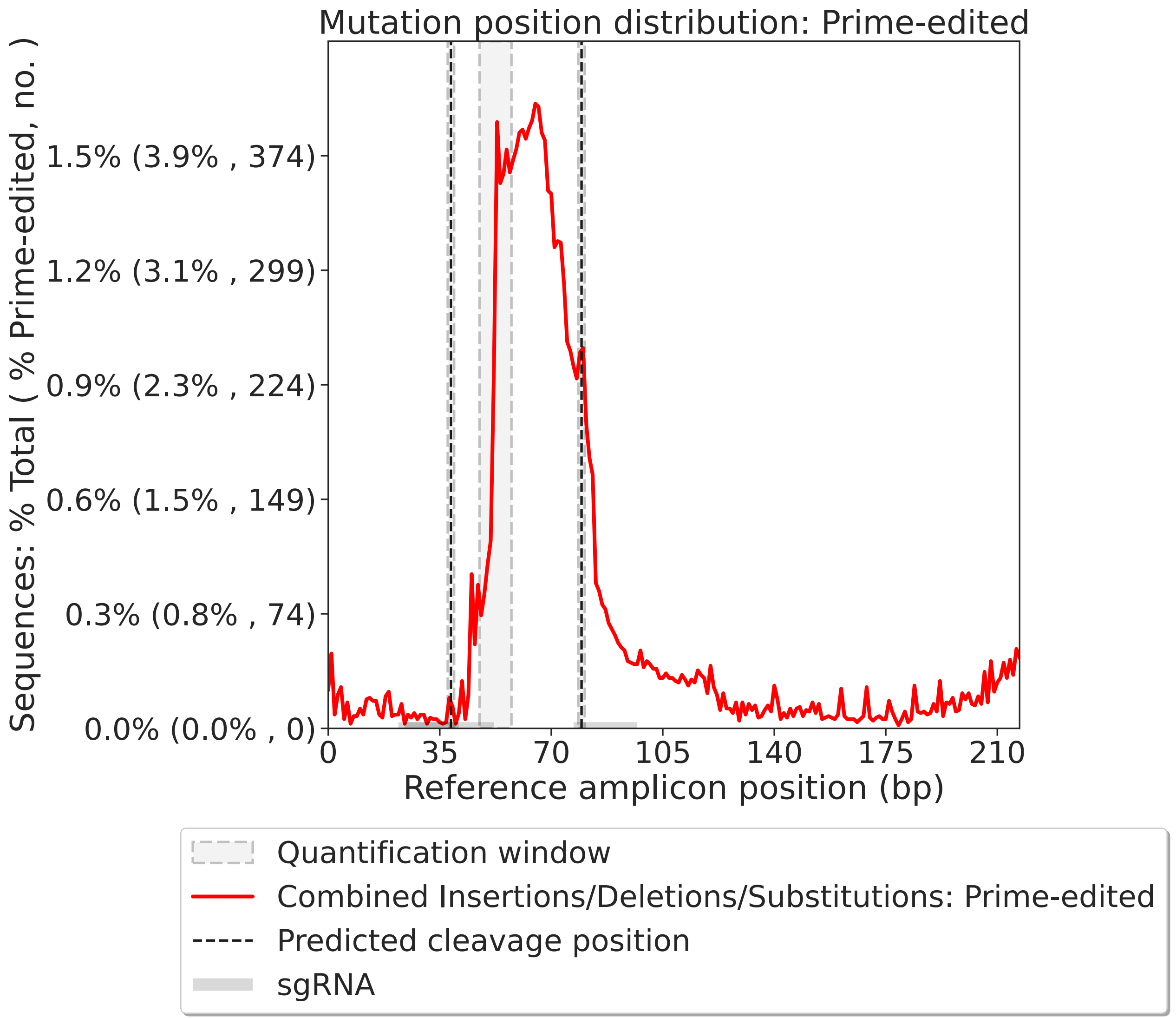
Mutation position distribution: Prime-edited
Sequences: % Total ( % Prime-edited, no. )
1.5% (3.9% , 374)
1.2% (3.1% , 299)
0.9% (2.3% , 224)
0.6% (1.5% , 149)
0.3% (0.8% , 74)
0.0% (0.0% , 0)
0
35
70
105
140
175
210
Reference amplicon position (bp)
Quantification window
Combined Insertions/Deletions/Substitutions: Prime-edited
Predicted cleavage position
sgRNA