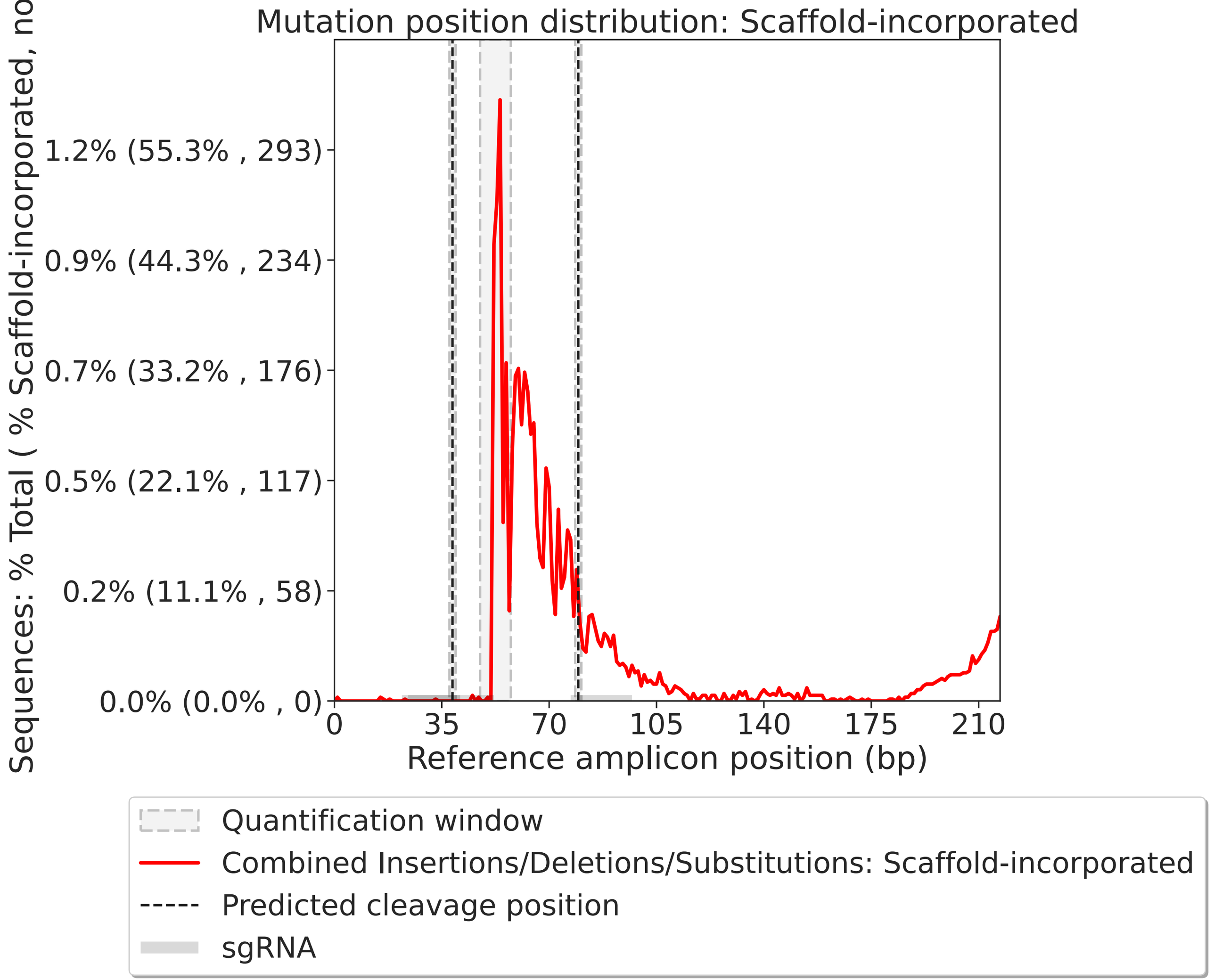
Mutation position distribution: Scaffold-incorporated
Sequences: % Total (% Scaffold-incorporated, no
1.2% (55.3% , 293)
0.9% (44.3% , 234)
0.7% (33.2% , 176)
0.5% (22.1% , 117)
0.2% (11.1% , 58)
0.0% (0.0% , 0)
0
35
70
105
140
175
210
Reference amplicon position (bp)
Quantification window
Combined Insertions/Deletions/Substitutions: Scaffold-incorporated
Predicted cleavage position
sgRNA