

Mutation position distribution: RICTOR

Sequences: % Total (% RICTOR, no.)

12.2% (65.0% , 9215)

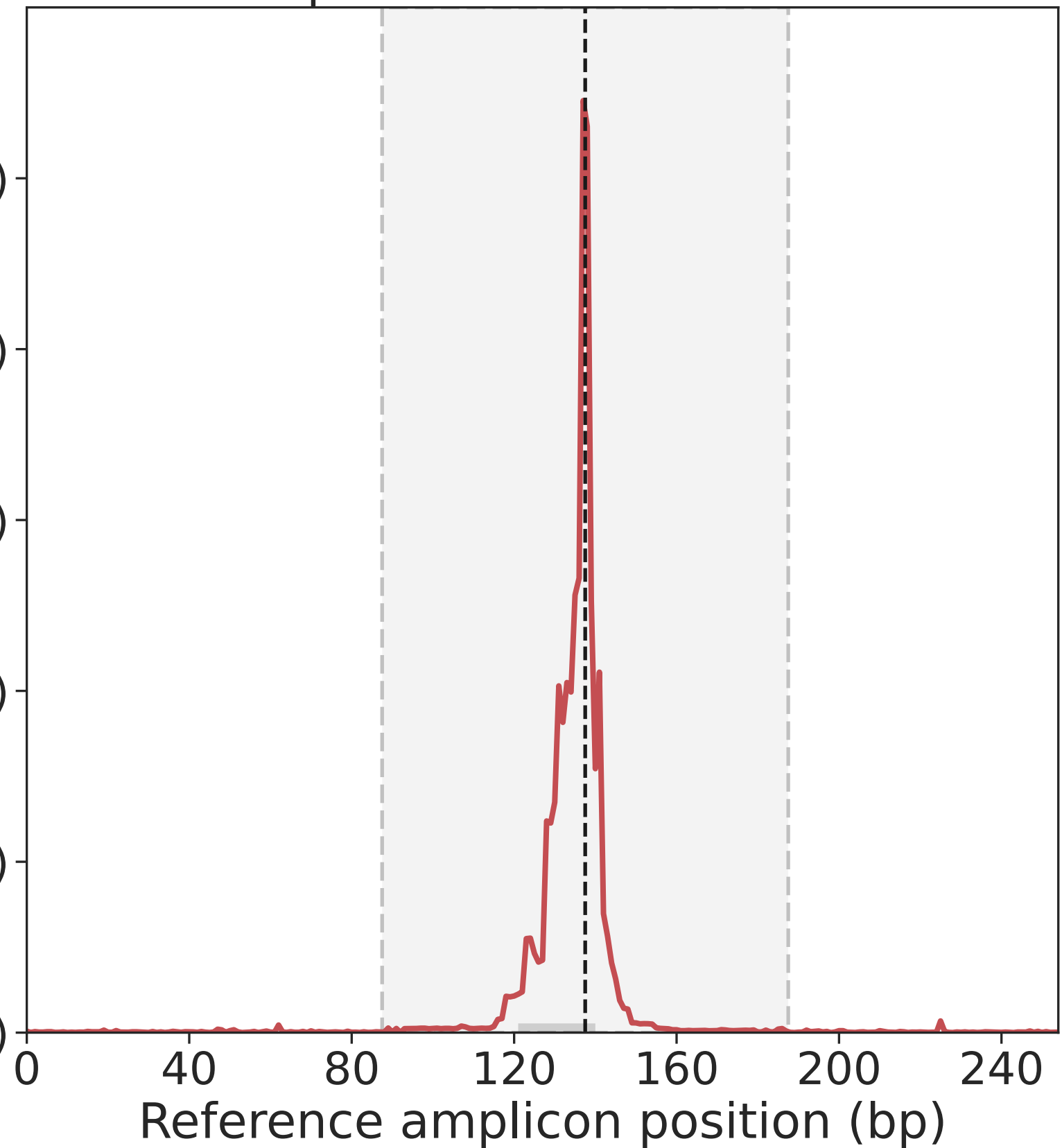
9.8% (52.0% , 7372)

7.3% (39.0% , 5529)

4.9% (26.0% , 3686)

2.4% (13.0% , 1843)

0.0% (0.0% , 0)



- Quantification window
- Combined Insertions/Deletions/Substitutions: RICTOR
- Predicted cleavage position
- sgRNA