Mutation position distribution: Reference

Sequences: % Total (% Reference, no.)

1.1% (2.0% , 285)

0.9% (1.6% , 228)

0.7% (1.2% , 171)

0.5% (0.8% , 114)

0.2% (0.4% , 57)

0.0% (0.0% , 0)

0 35 70 105 140 175 210

Reference amplicon position (bp)

Quantification window

Combined Insertions/Deletions/Substitutions: Reference

----- Predicted cleavage position

sgRNA