

Mutation position distribution of NHEJ

Sequences: % Total (% NHEJ, no.)

4.5% (31.8% , 11052)

3.6% (25.5% , 8841)

2.7% (19.1% , 6631)

1.8% (12.7% , 4420)

0.9% (6.4% , 2210)

0.0% (0.0% , 0)

0 40 80 120 160 200 240

Reference amplicon position (bp)

- Insertions
- Deletions
- Substitutions
- - - Predicted cleavage position
- sgRNA

