In-frame mutation
(3730 reads)

71.4%
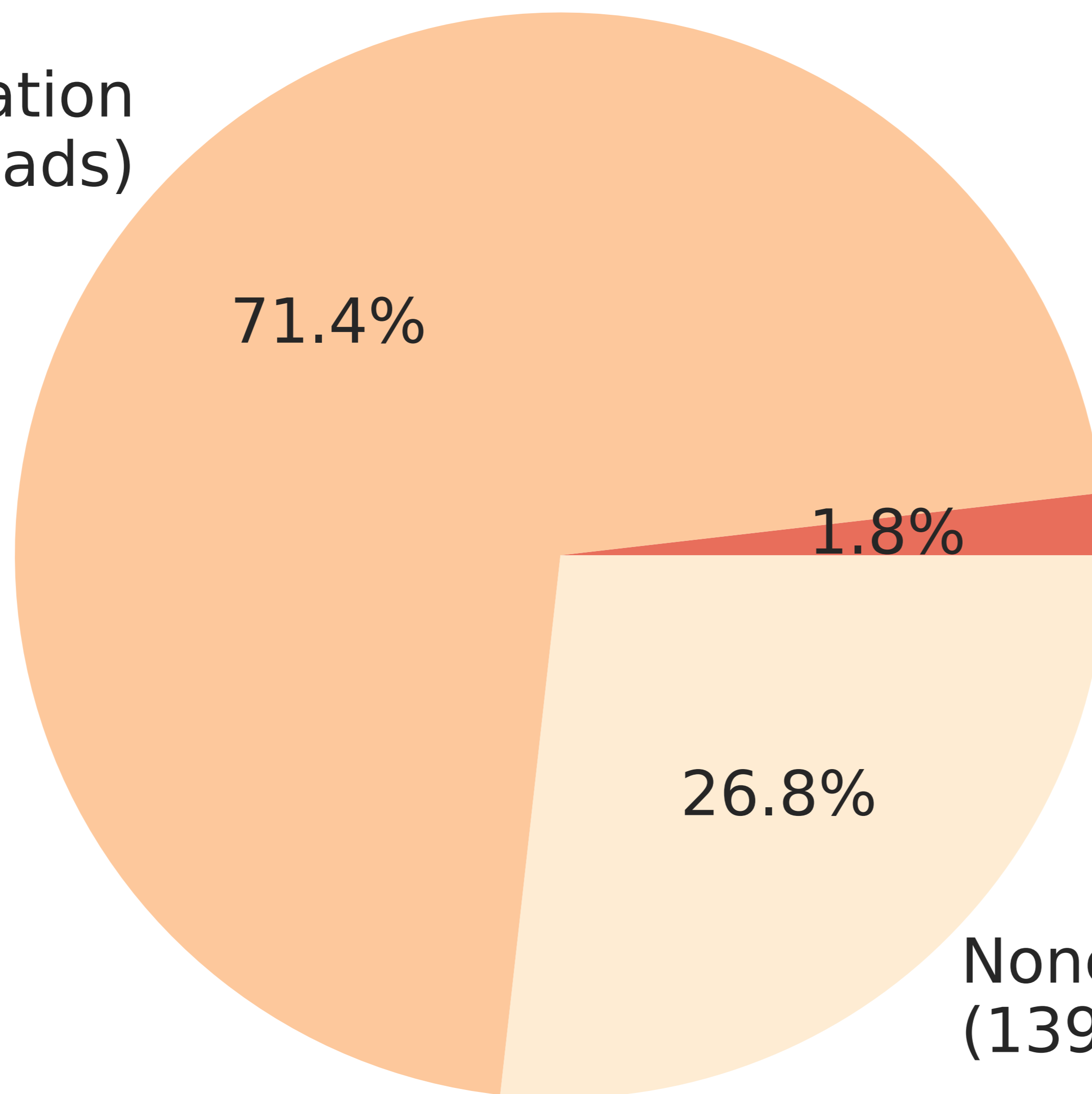
Frameshift mutation
(96 reads)

1.8%

26.8%

Noncoding mutation
(1398 reads)

Reference sequence

Coding sequence/s

Predicted cleavage position

sgRNA