Frameshift mutation
(4264 reads)

75.1%
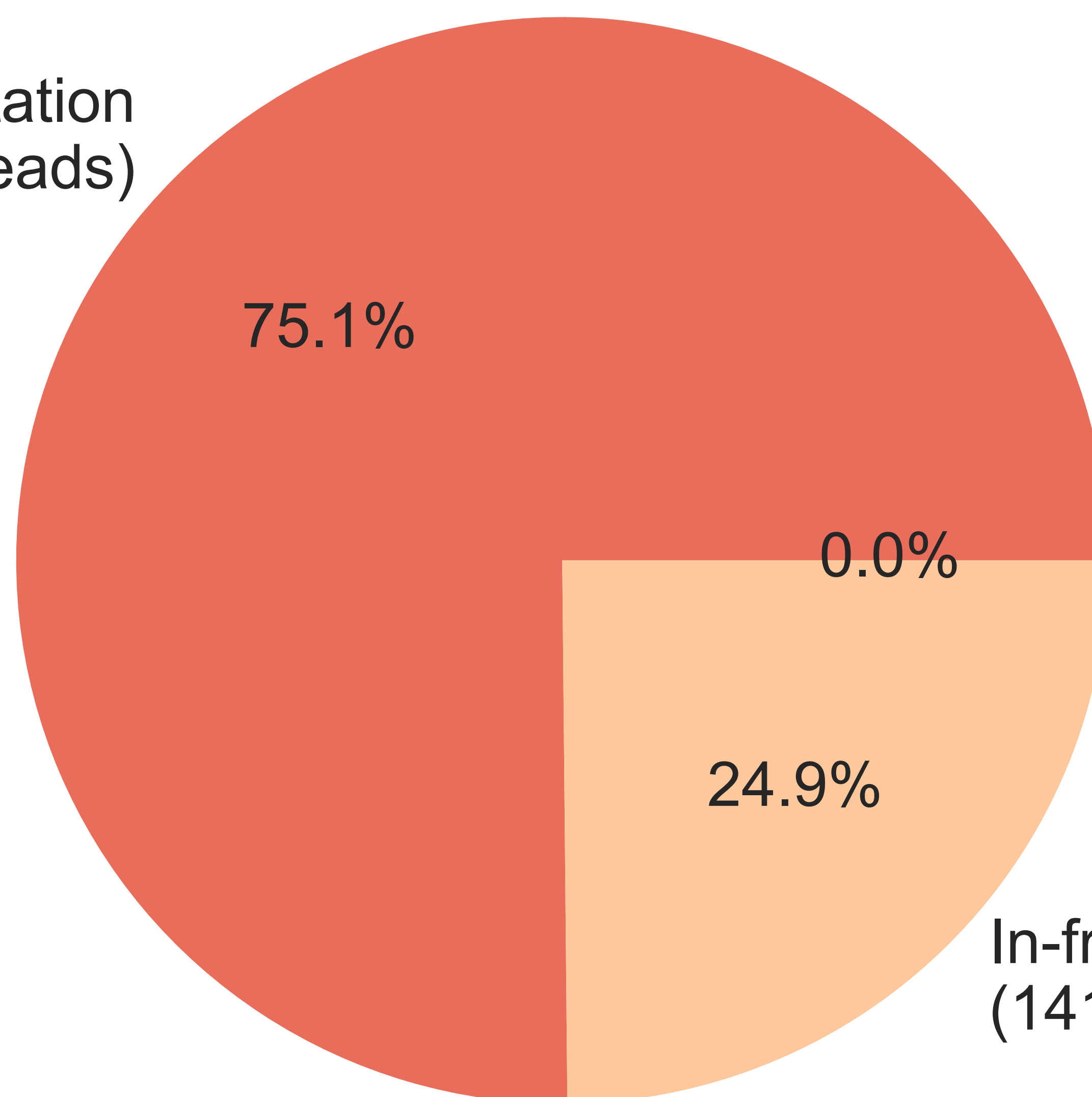
Noncoding mutation
(0 reads)

0.0%

24.9%

In-frame mutation
(1410 reads)

Reference sequence

Coding sequence/s

Predicted cleavage position

sgRNA