In-frame mutation
(6566 reads)

65.3%
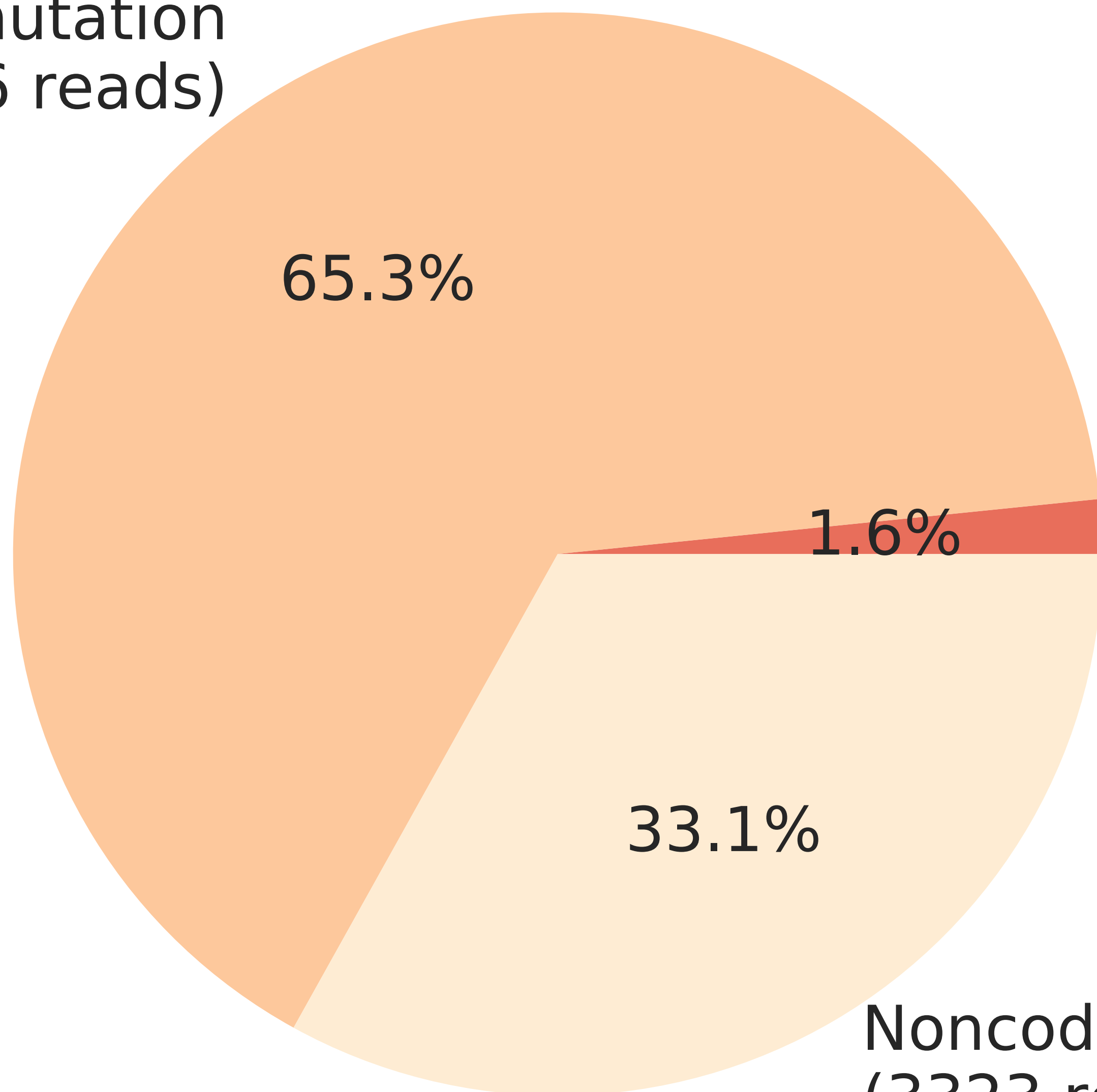
Frameshift mutation
(163 reads)

1.6%

33.1%

Noncoding mutation
(3323 reads)

Reference sequence

Coding sequence/s

Predicted cleavage position

sgRNA