In-frame mutation
(7118 reads)

68.0%
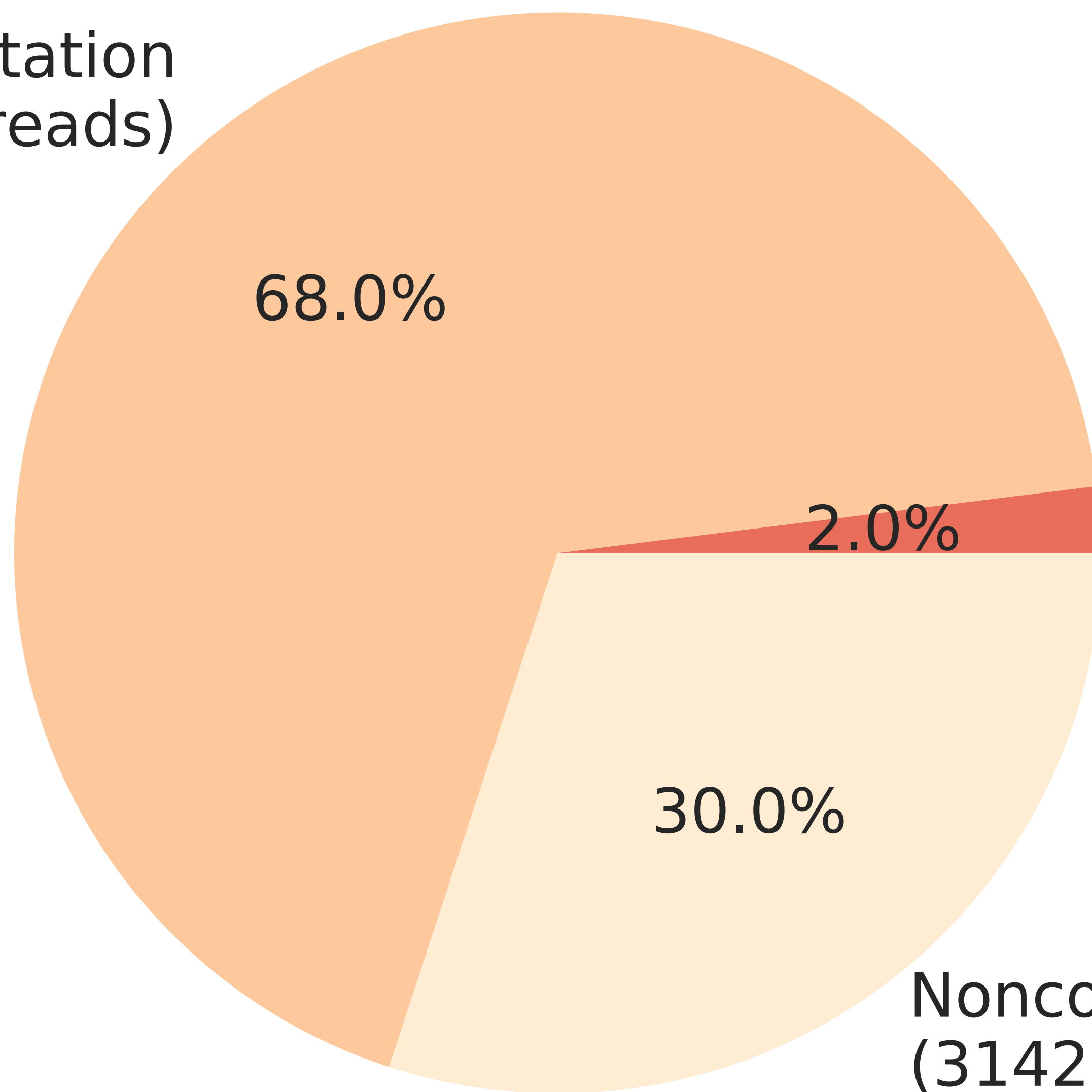
Frameshift mutation
(207 reads)

2.0%

30.0%

Noncoding mutation
(3142 reads)

—— Reference sequence
—— Coding sequence/s
----- Predicted cleavage position
—— sgRNA