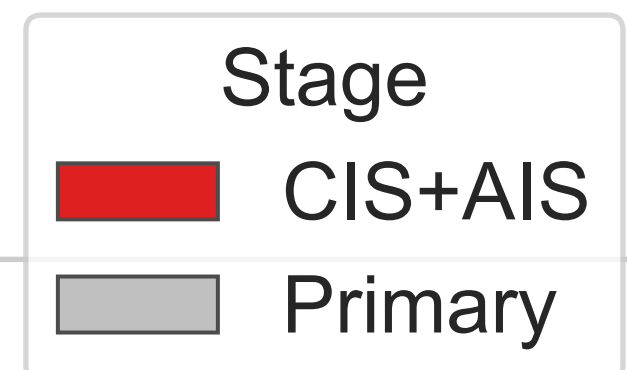


Kruskal-Wallis p=0.000

1e9

Size of somatic CNV region (bp)

3.0  
2.5  
2.0  
1.5  
1.0  
0.5  
0.0



\*\*\*\*

\*\*

Lower

Higher

Mutation Shared Proportion

