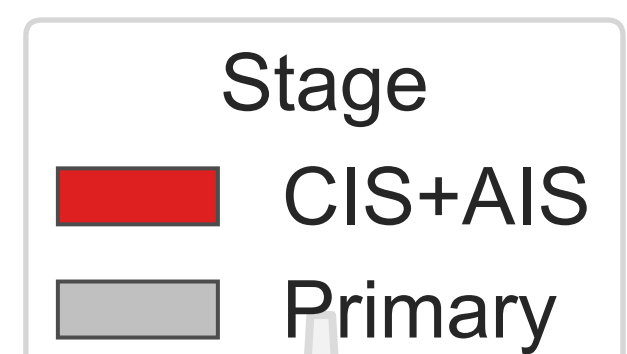


Kruskal-Wallis p=0.000

1e9

Size of somatic CNV region (bp)

2.0  
1.5  
1.0  
0.5  
0.0



\*\*\*

\*\*\*\*

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Lower

Higher

Mutation Shared Proportion

