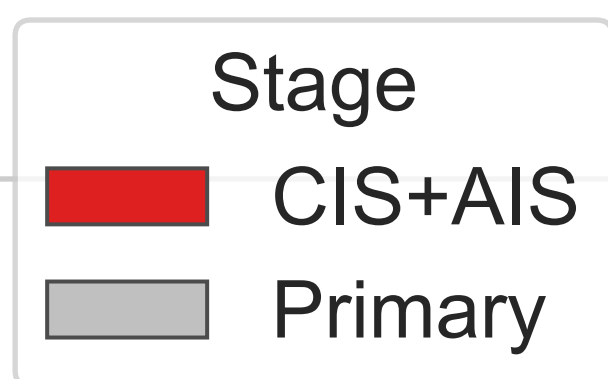


Kruskal-Wallis p=0.000

1e9

Size of somatic CNV region (bp)



**

Lower Higher

Mutation Shared Count (SYN)

