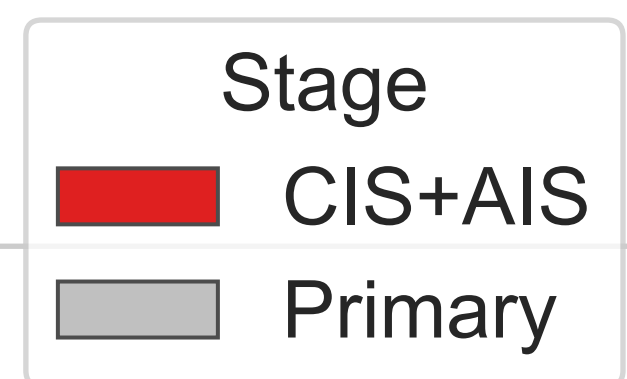


Kruskal-Wallis p=0.000

1e9

Size of somatic CNV region (bp)



**

Lower

Higher

Mutation Shared Count

