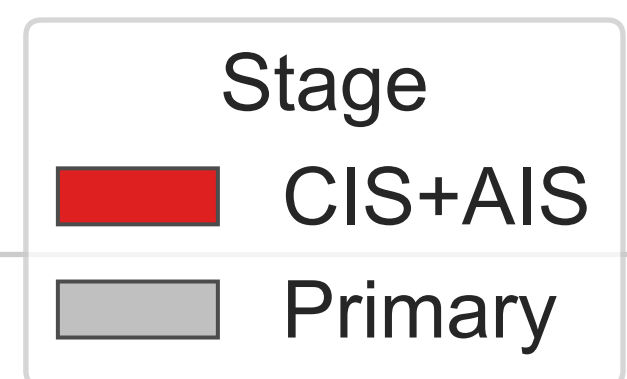


Kruskal-Wallis p=0.000

1e9

Size of somatic CNV region (bp)



**

Lower Higher
Mutation Shared Count per TMB

