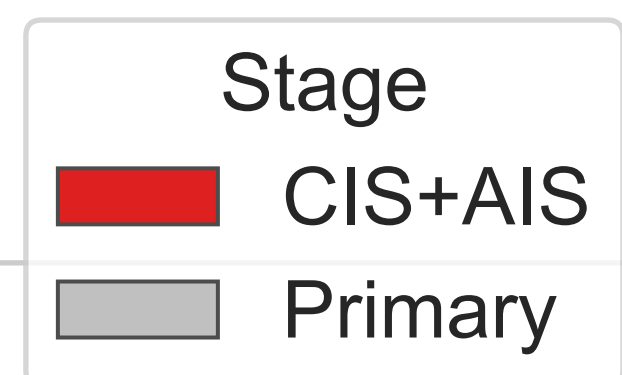


Kruskal-Wallis p=0.000

1e9

Size of somatic CNV region (bp)



*

Lower Higher
Mutation Shared Count (SYN) per TMB

