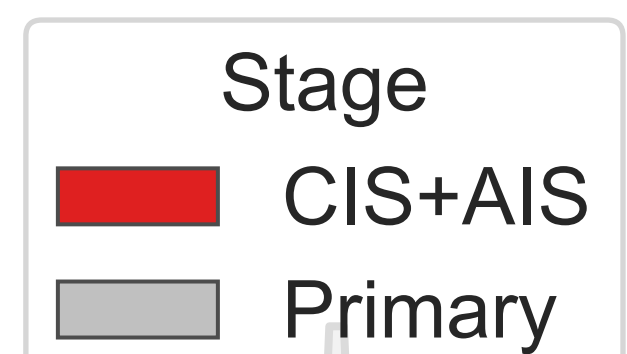


Kruskal-Wallis p=0.000

1e9

Size of somatic CNV region (bp)

2.0
1.5
1.0
0.5
0.0



Lower Higher
Mutation Shared Count per TMB

