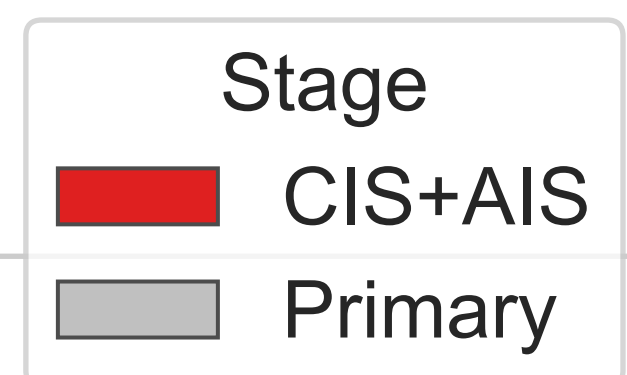


Kruskal-Wallis p=0.000

1e9

Size of somatic CNV region (bp)

3.0
2.5
2.0
1.5
1.0
0.5
0.0



**

*

Lower

Higher

Mutation Shared Count

