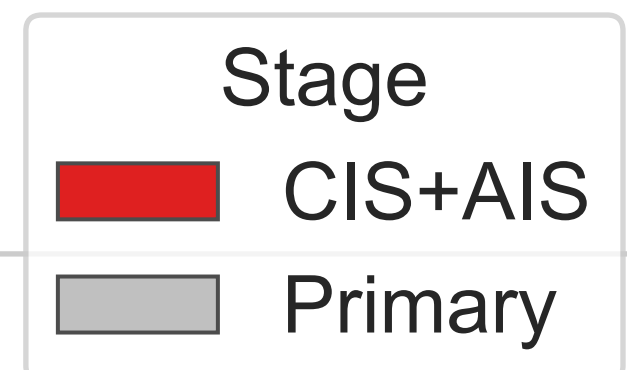


Kruskal-Wallis p=0.000

1e9

Size of somatic CNV region (bp)

3.0
2.5
2.0
1.5
1.0
0.5
0.0



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*

*

Lower Higher
Mutation Shared Count (SYN)