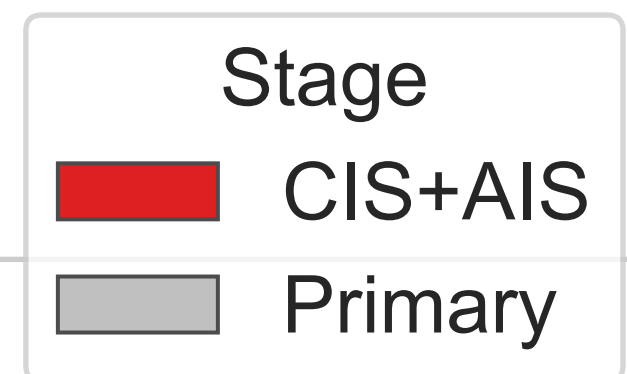


Kruskal-Wallis p=0.000

1e9

Size of somatic CNV region (bp)



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Lower Higher  
Mutation Shared Count per TMB

