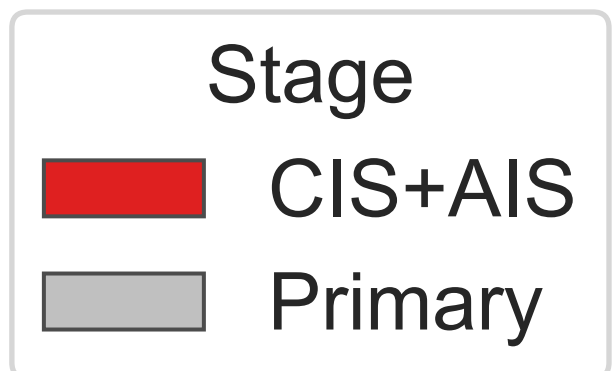


Kruskal-Wallis p=0.000

1e9

Size of somatic CNV region (bp)



M.W.W.  $p \leq 0.001$

M.W.W.  $p \leq 1e-4$

M.W.W.  $p \leq 0.05$

Lower Higher  
Mutation Shared Count per TMB

