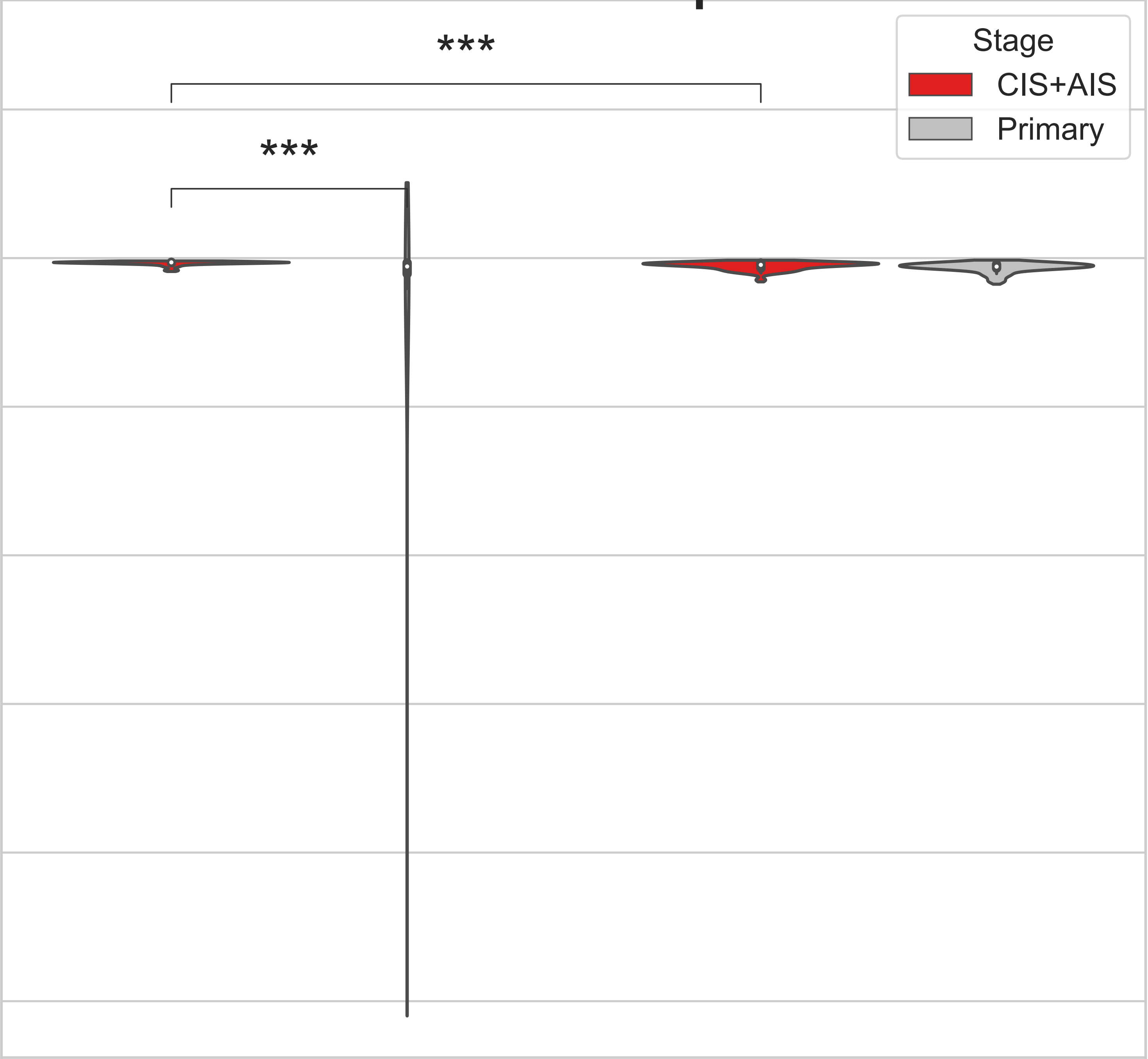


Kruskal-Wallis p=0.000

Number of somatic CNV segment (count)



Lower Higher
Mutation Shared Proportion (SYN)