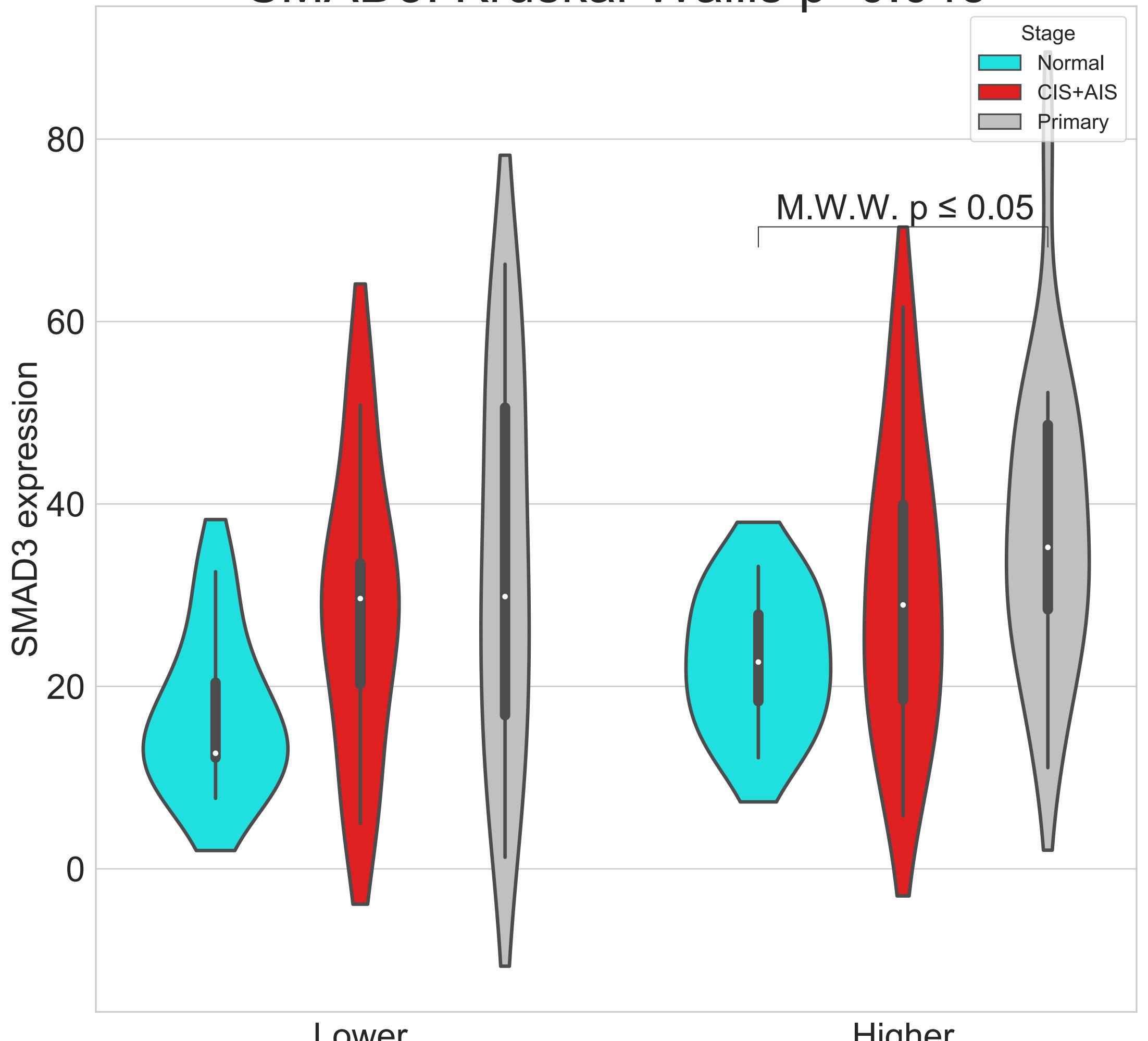
SMAD3: Kruskal-Wallis p=0.045



Lower
Mutation Shared Count per TMB