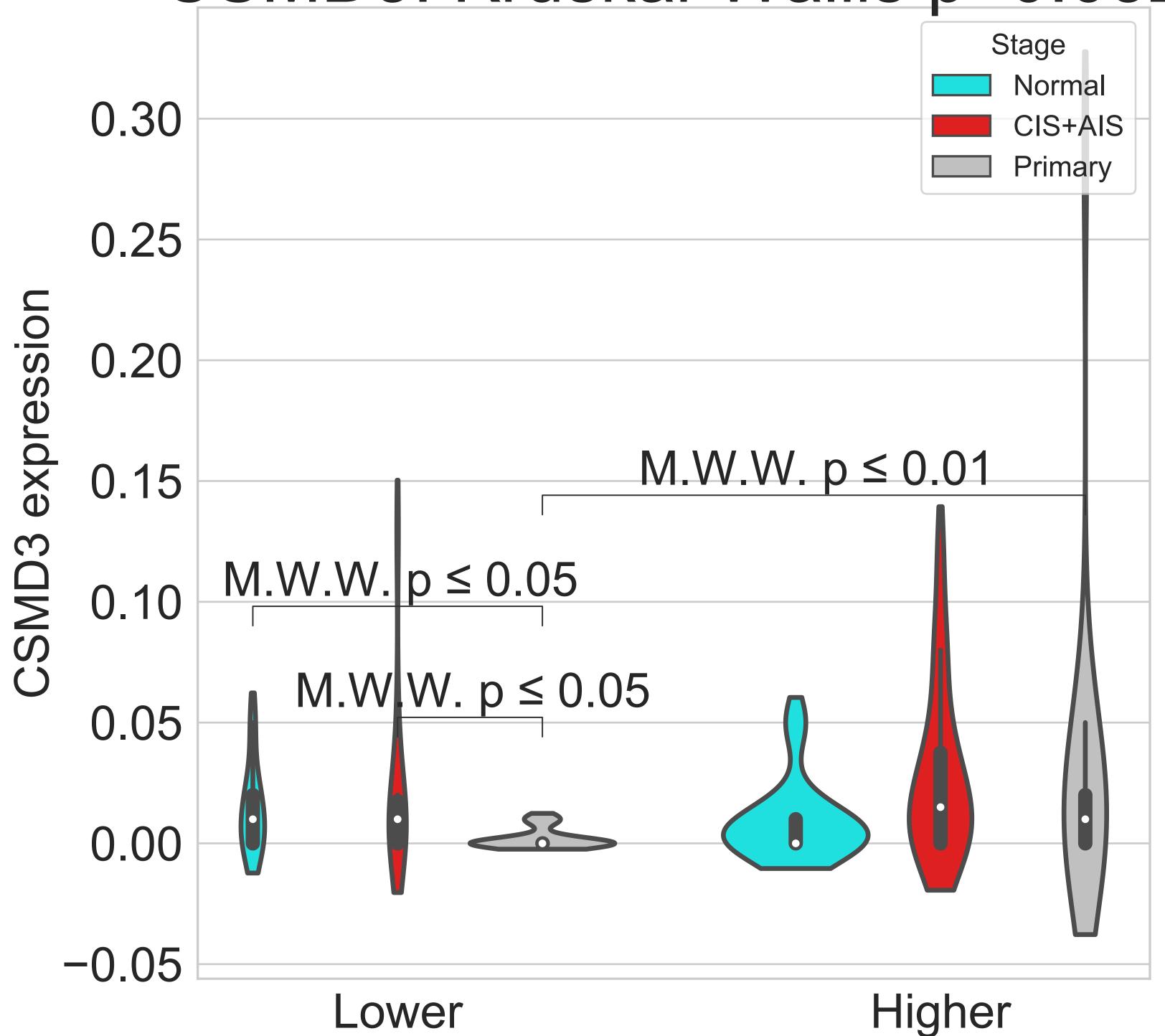
CSMD3: Kruskal-Wallis p=0.032



Mutation Shared Count per TMB