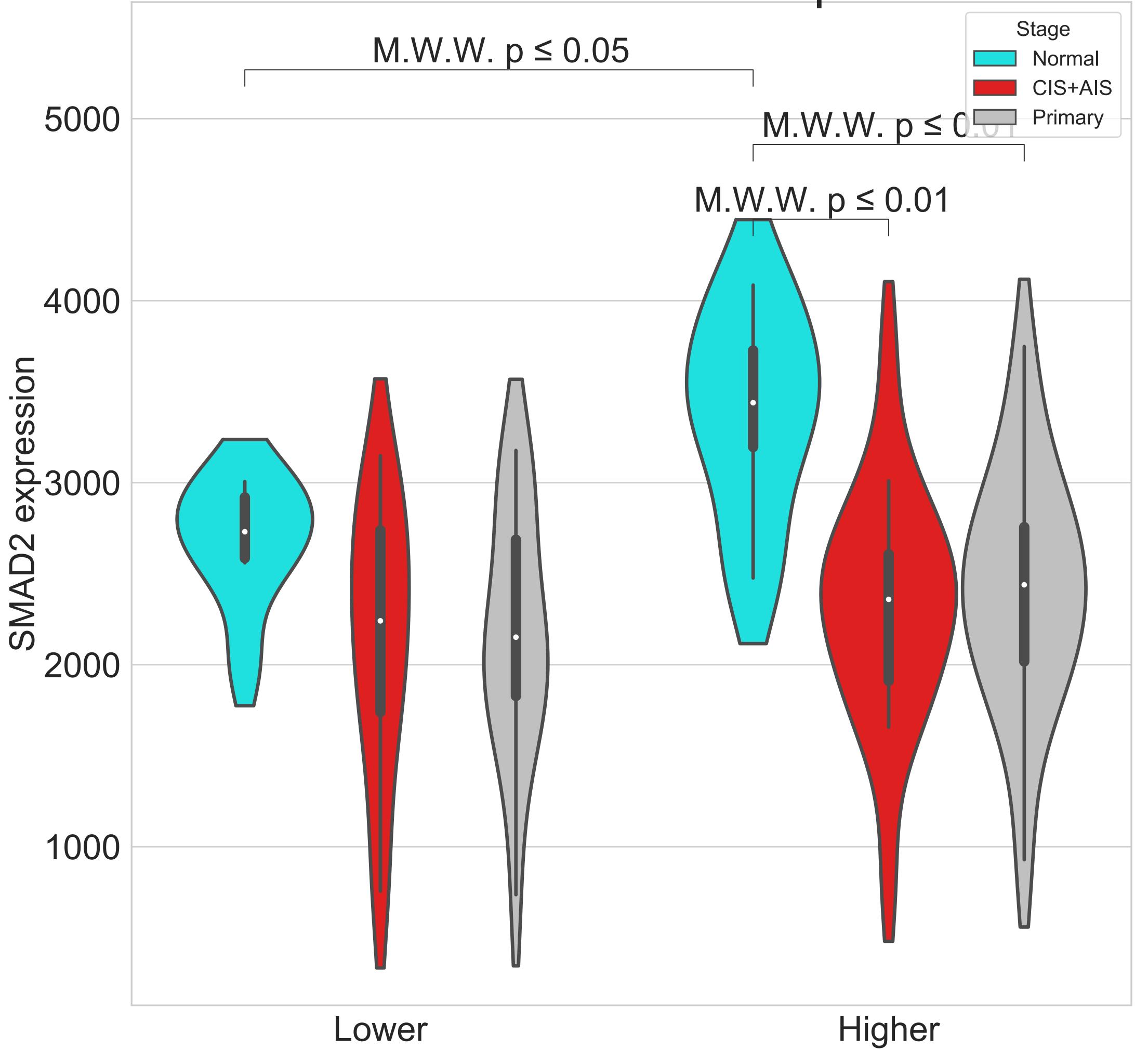
SMAD2: Kruskal-Wallis p=0.002



Mutation Shared Count per TMB