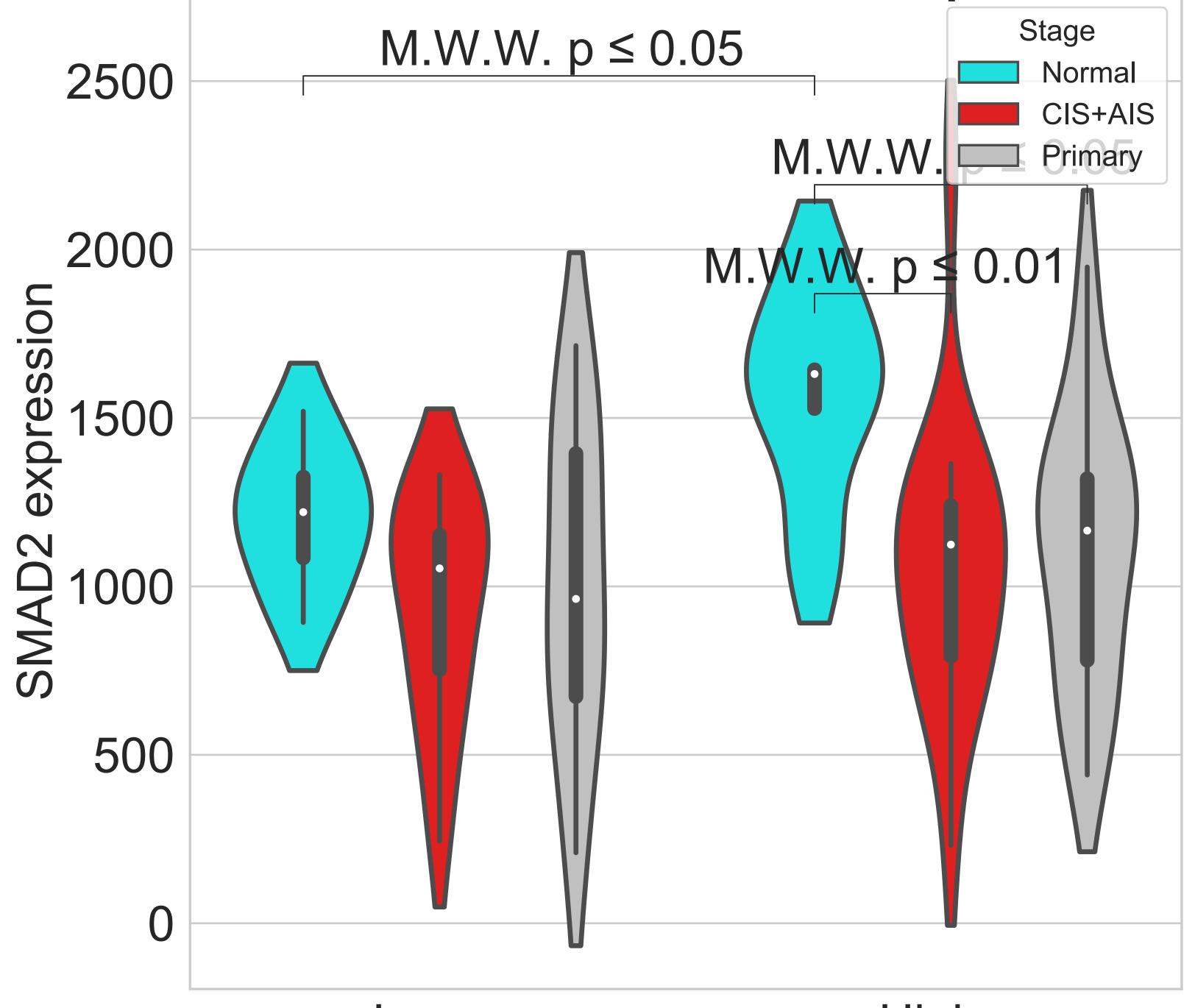
SMAD2: Kruskal-Wallis p=0.019



Lower Higher Mutation Shared Count per TMB