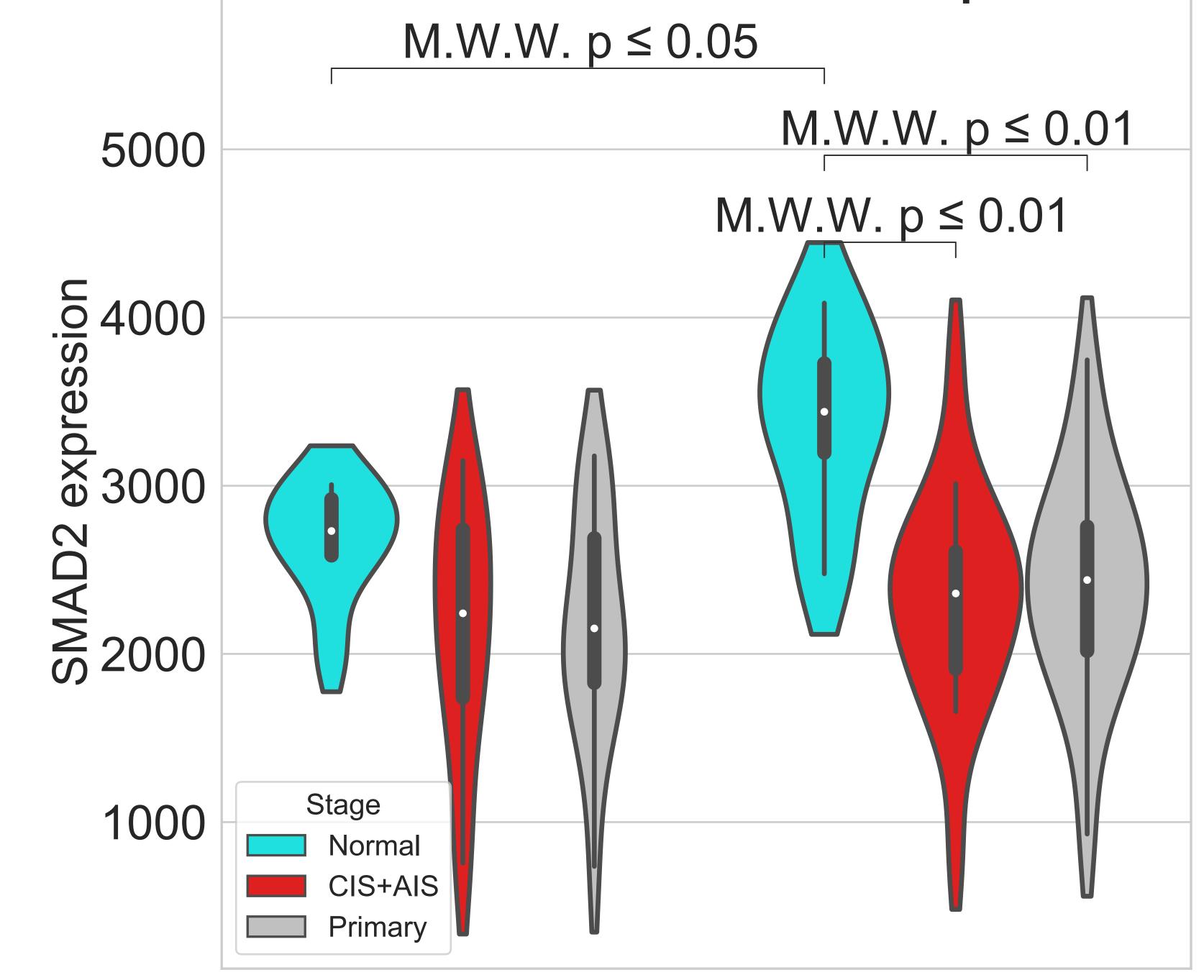
SMAD2: Kruskal-Wallis p=0.002



Lower Higher Mutation Shared Count per TMB