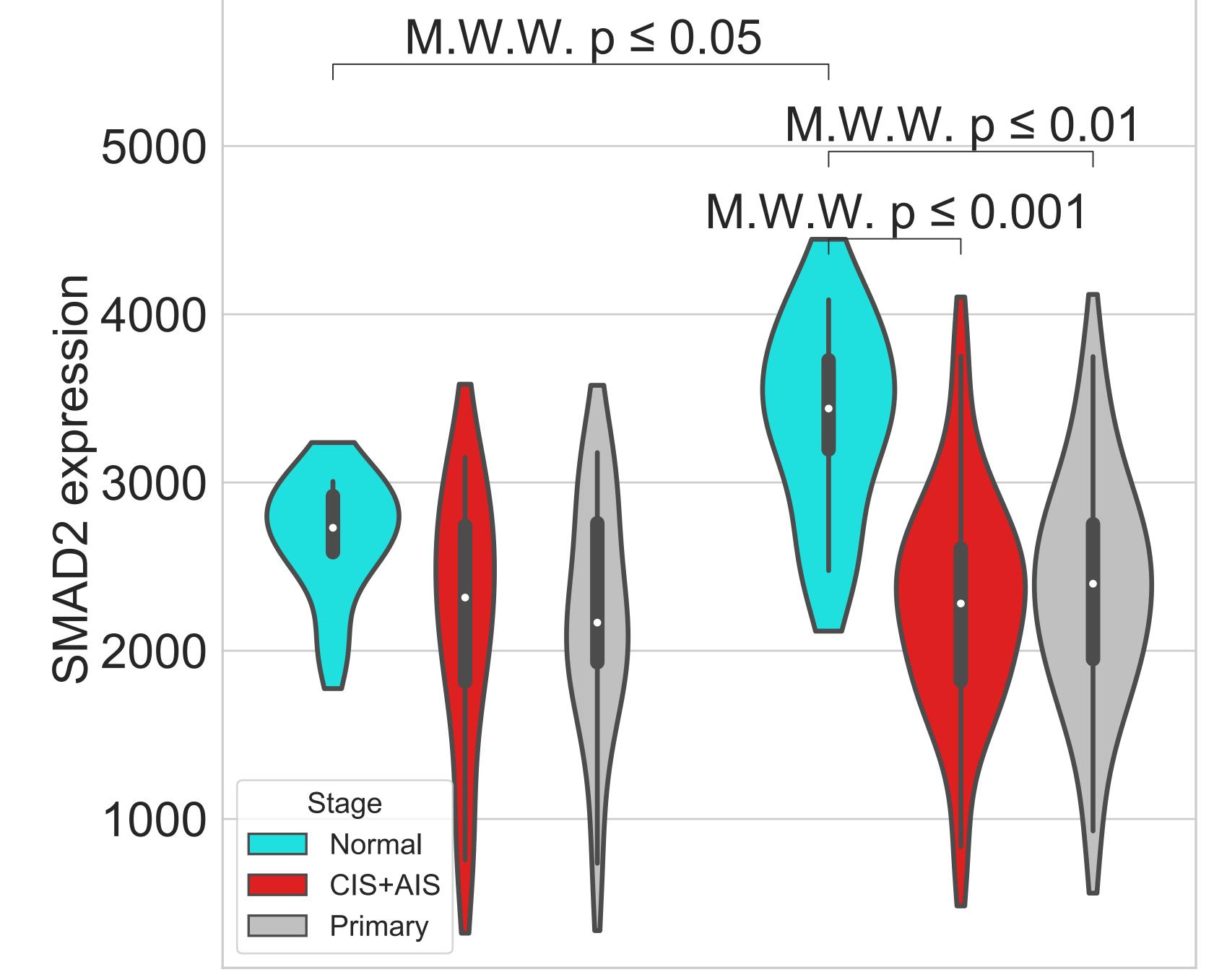
SMAD2: Kruskal-Wallis p=0.003



Lower Higher Mutation Shared Count (SYN) per TMB