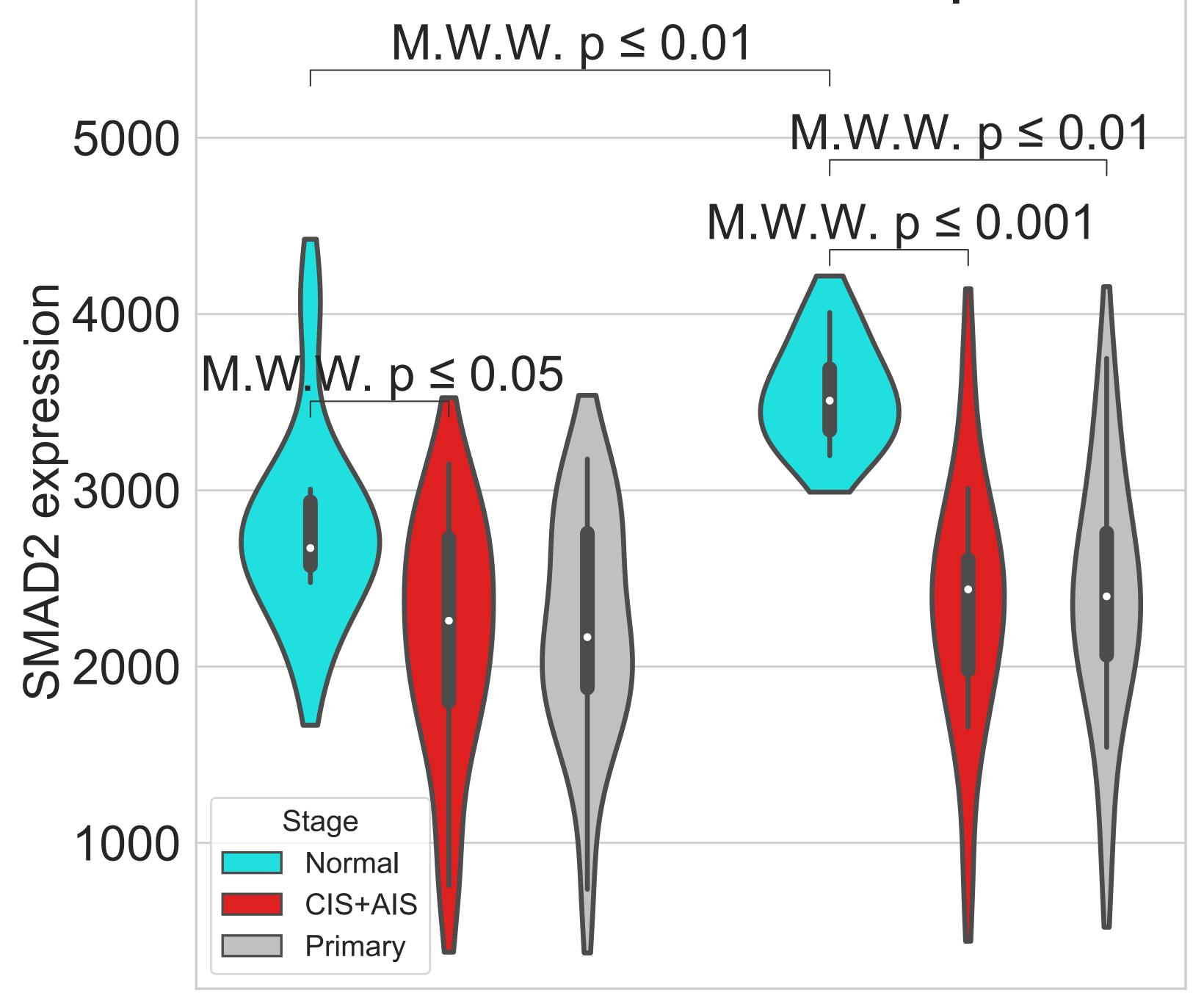
SMAD2: Kruskal-Wallis p=0.002



Lower
Mutation Shared Count (SYN) per TMB