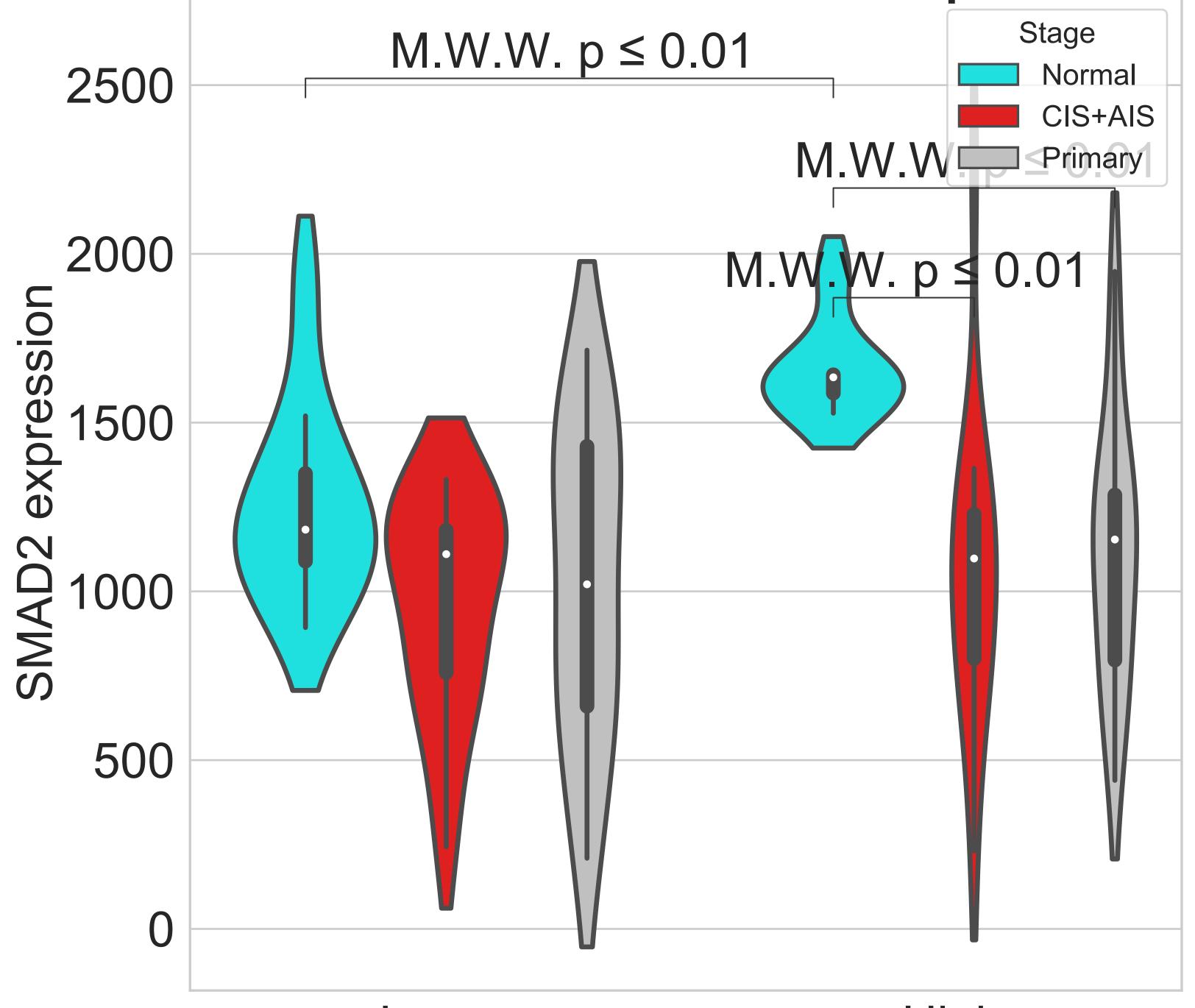
SMAD2: Kruskal-Wallis p=0.010



Lower
Mutation Shared Count (SYN) per TMB