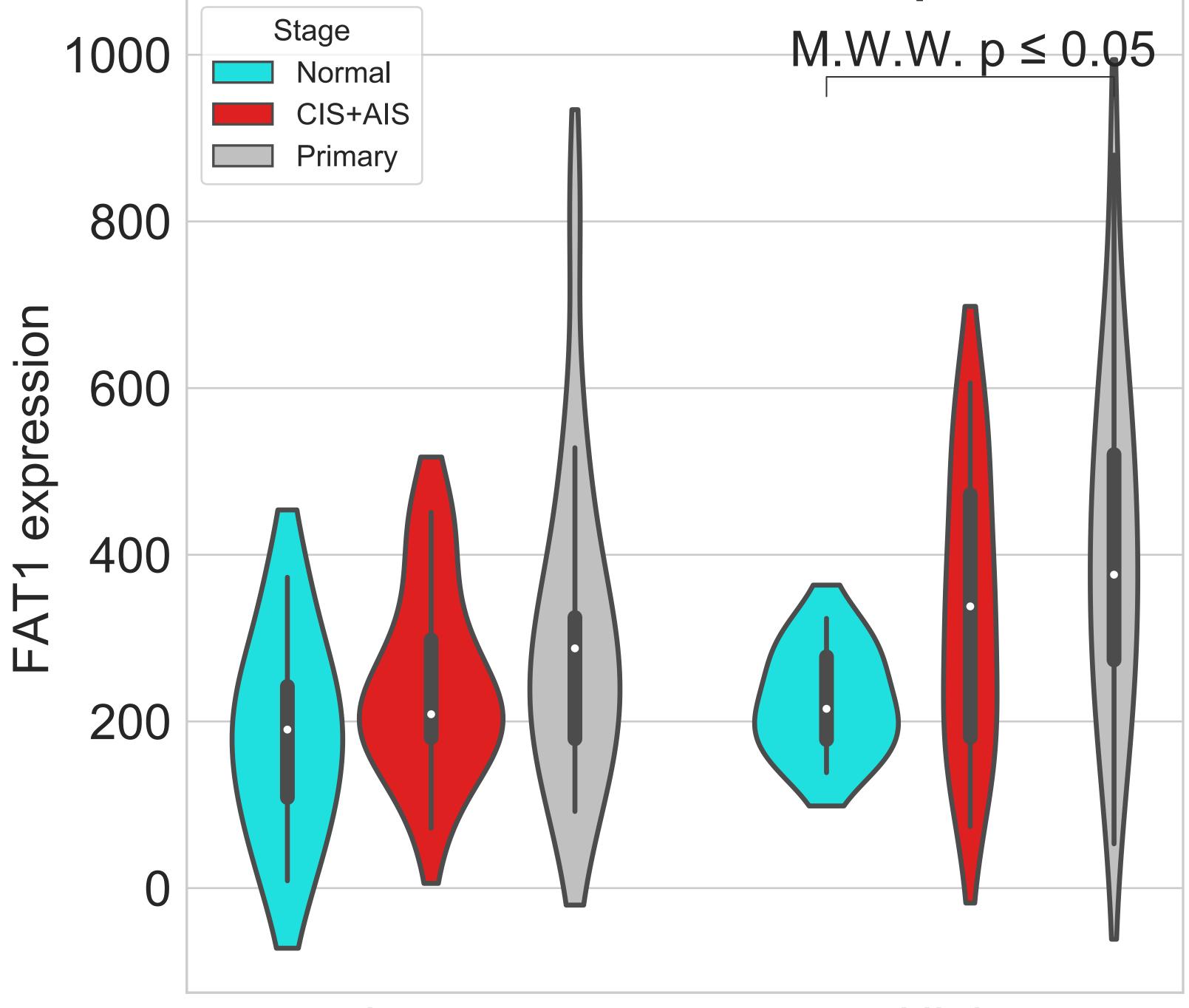
FAT1: Kruskal-Wallis p=0.025



Lower
Mutation Shared Count (SYN) per TMB