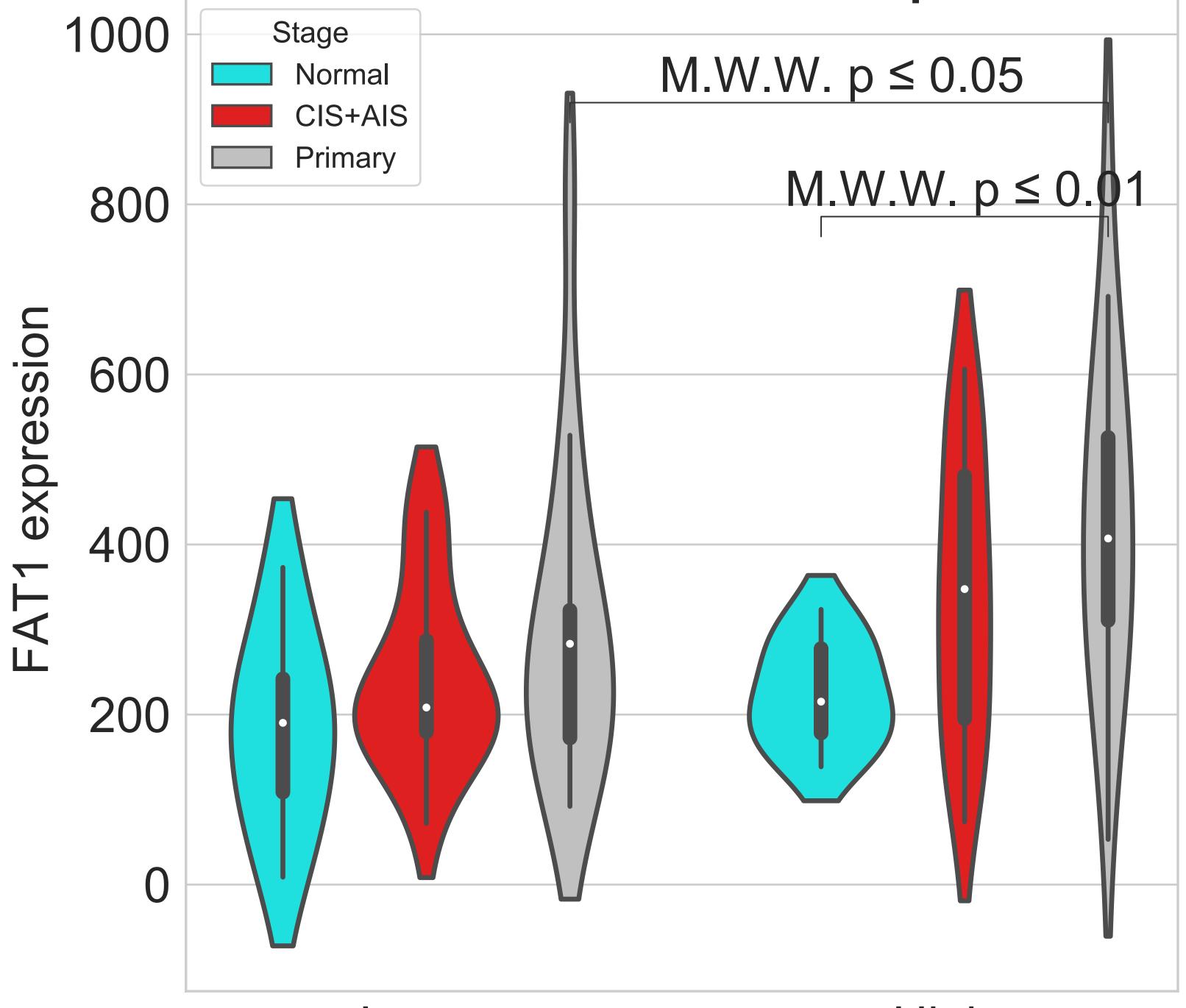
FAT1: Kruskal-Wallis p=0.008



Lower
Mutation Shared Count per TMB