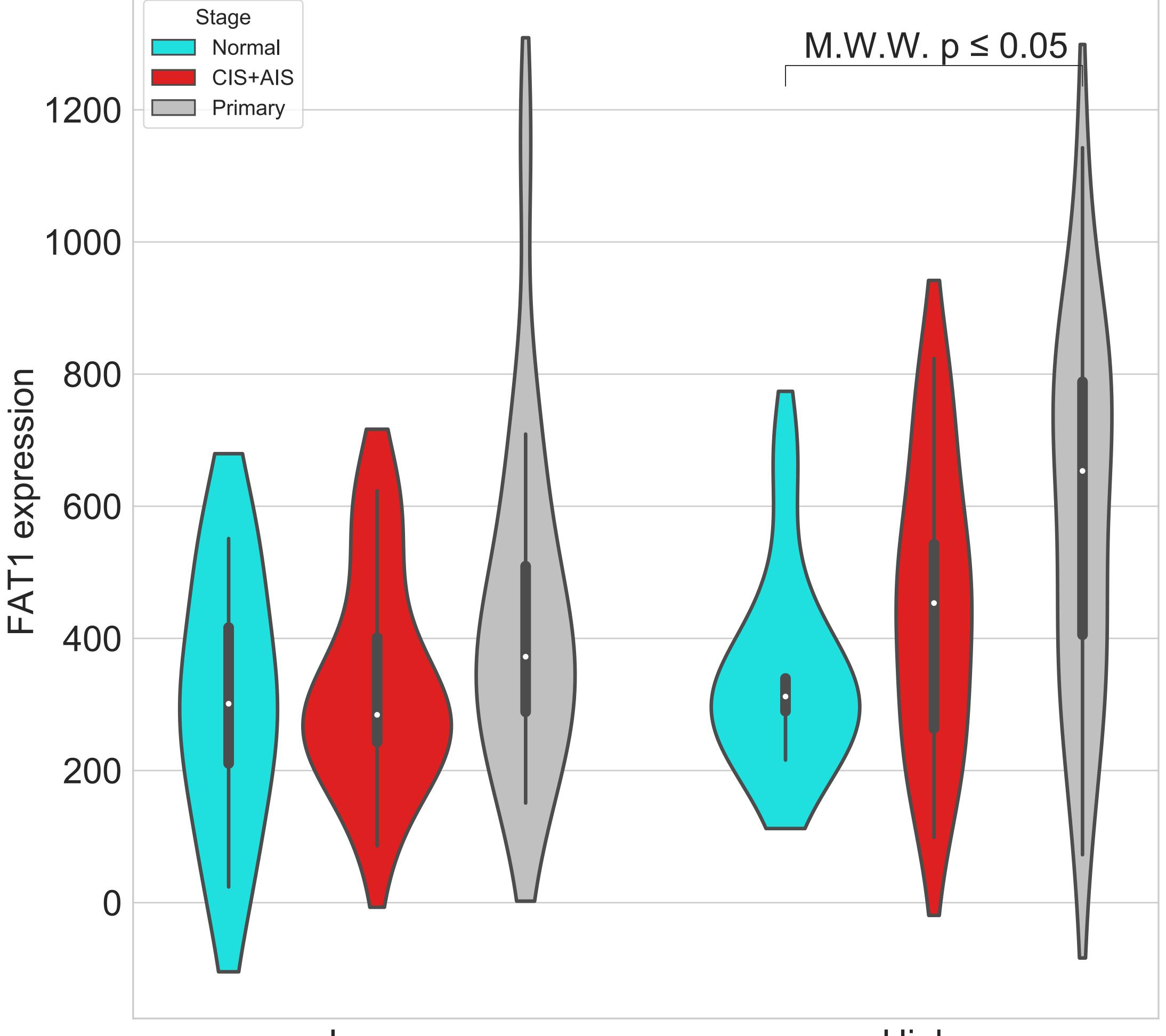
FAT1: Kruskal-Wallis p=0.032



Higher Lower Mutation Shared Count per TMB