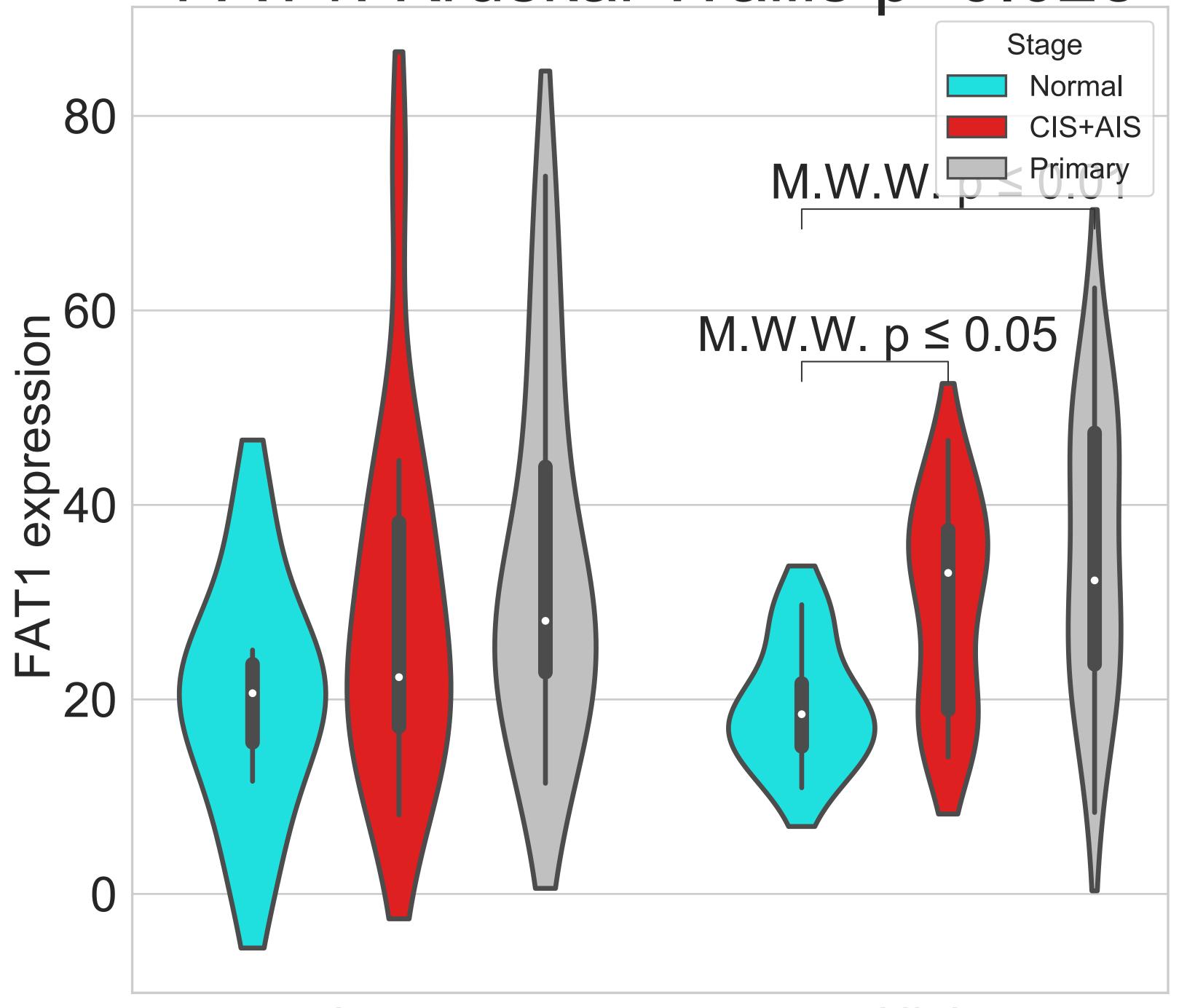
FAT1: Kruskal-Wallis p=0.028



Lower Higher Mutation Shared Proportion (SYN)