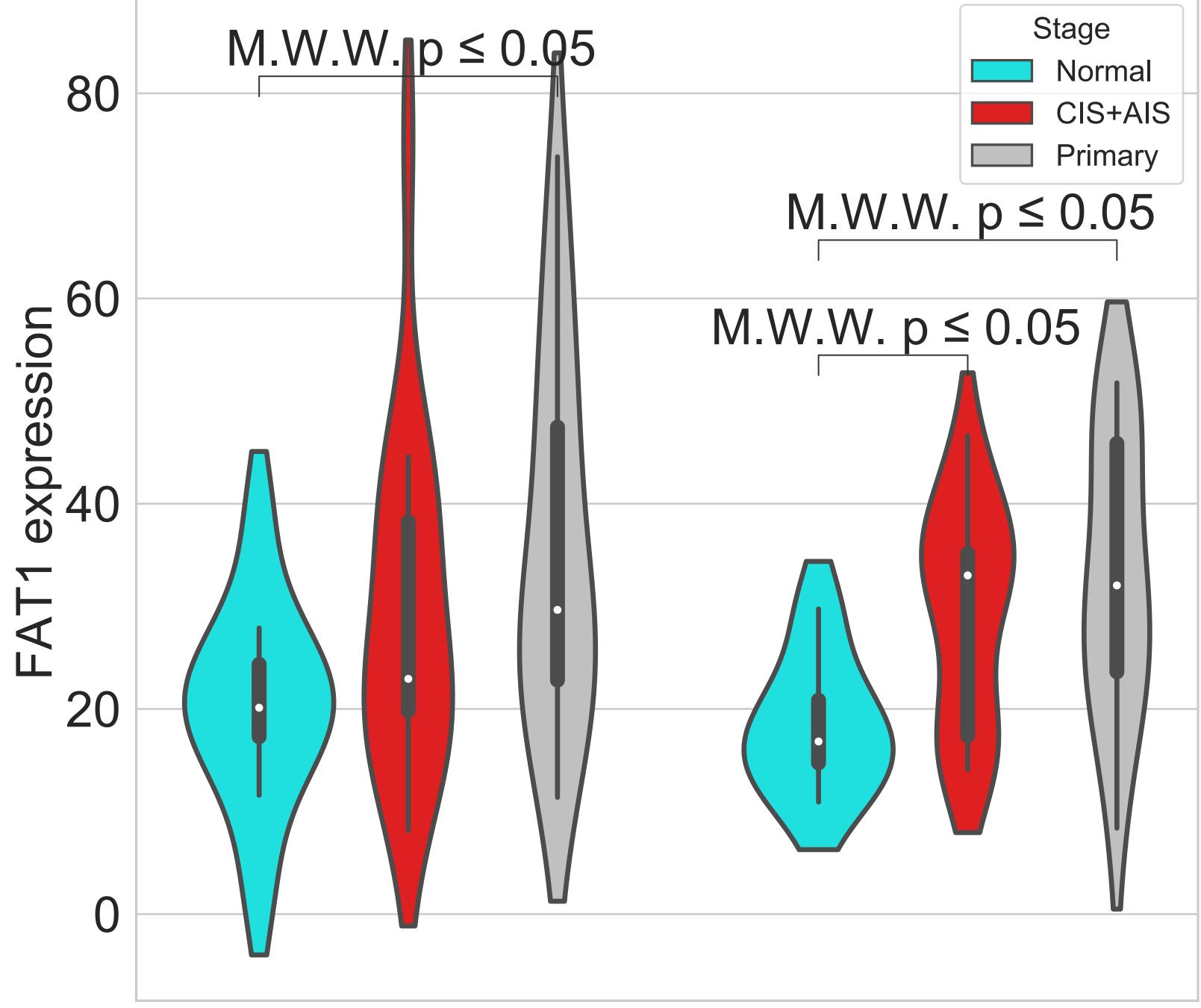
FAT1: Kruskal-Wallis p=0.034



Lower Higher Mutation Shared Proportion (SYN)