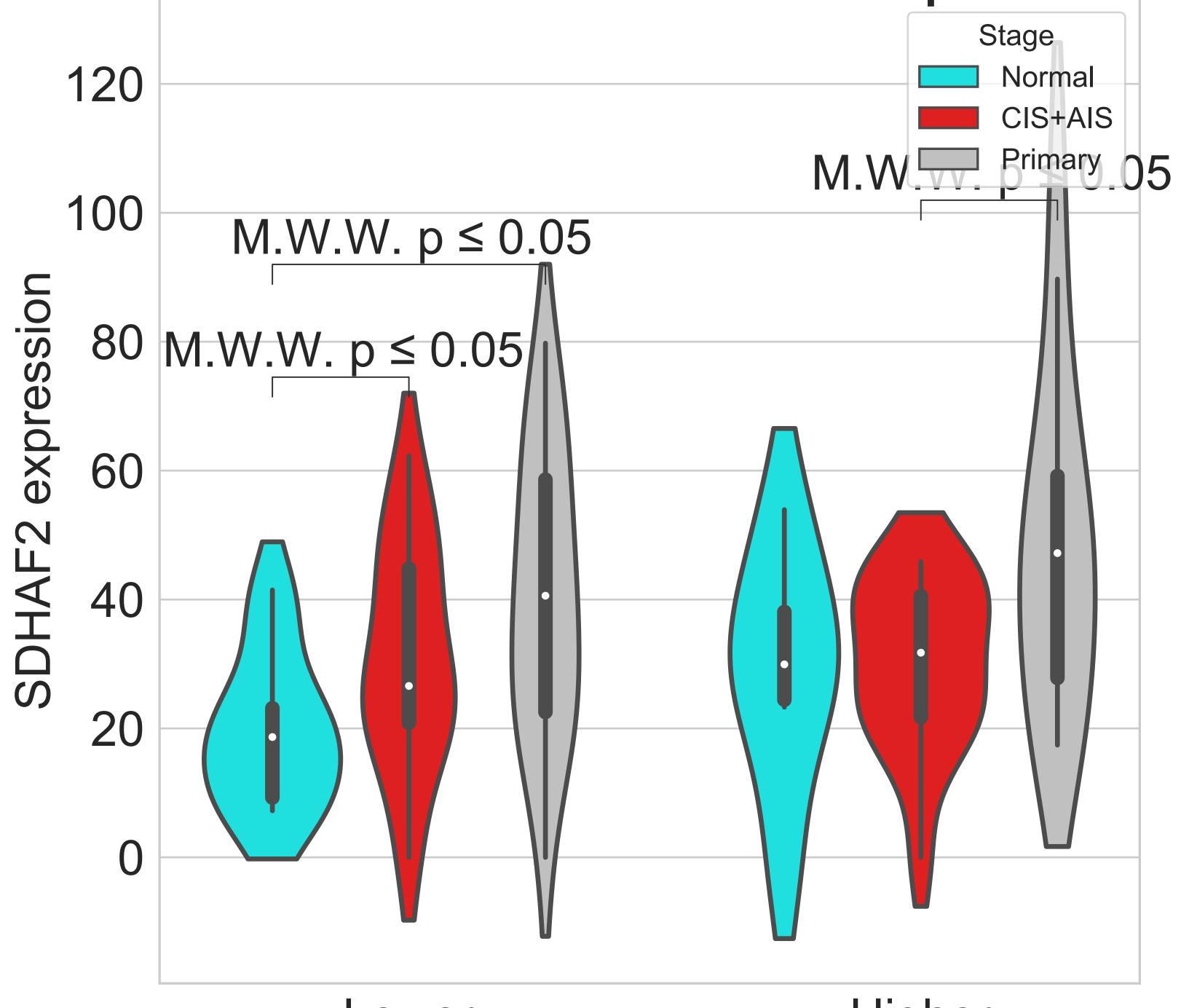
SDHAF2: Kruskal-Wallis p=0.028



Lower Higher Mutation Shared Count (SYN) per TMB