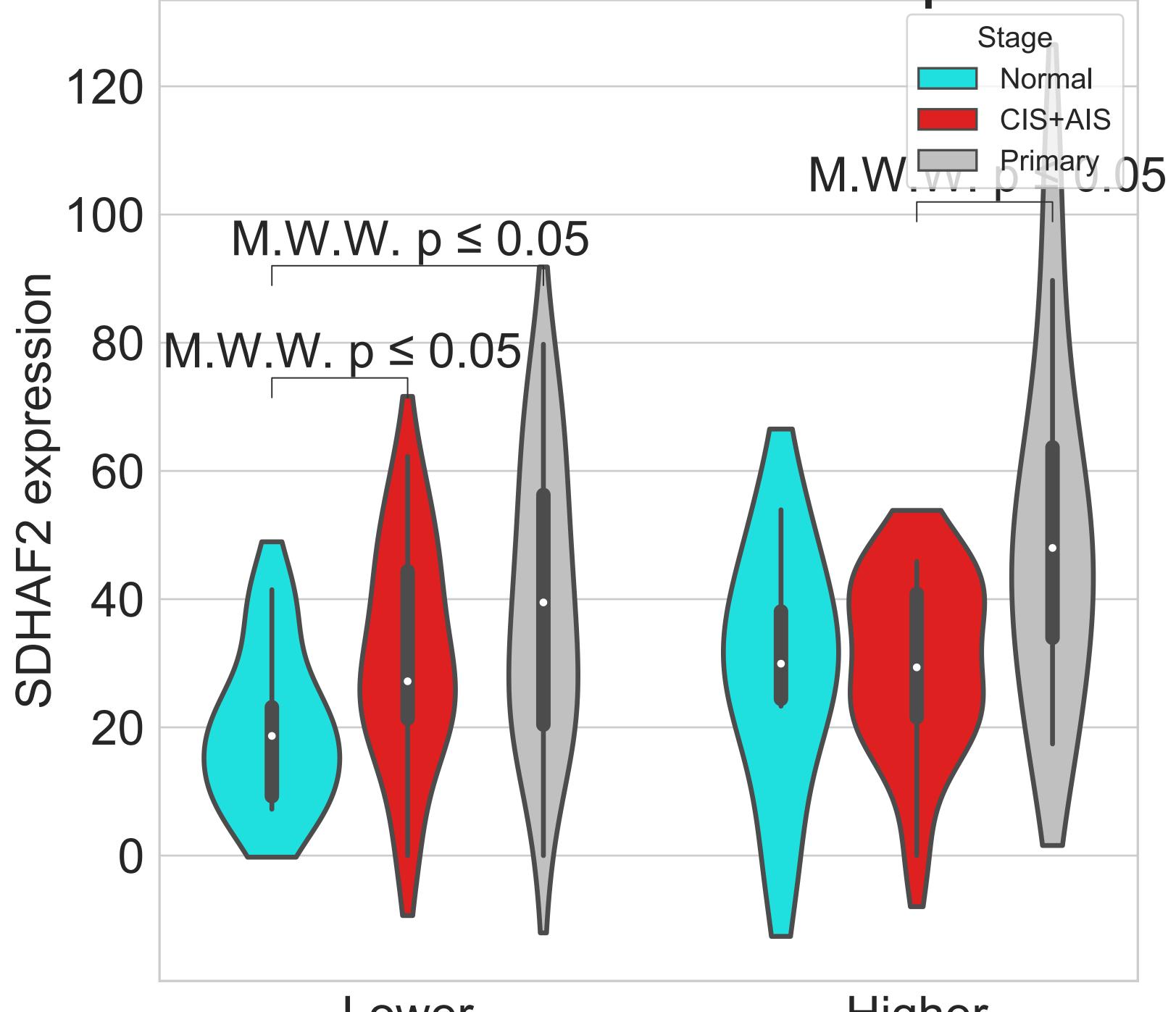
SDHAF2: Kruskal-Wallis p=0.020



Lower Higher Mutation Shared Count per TMB