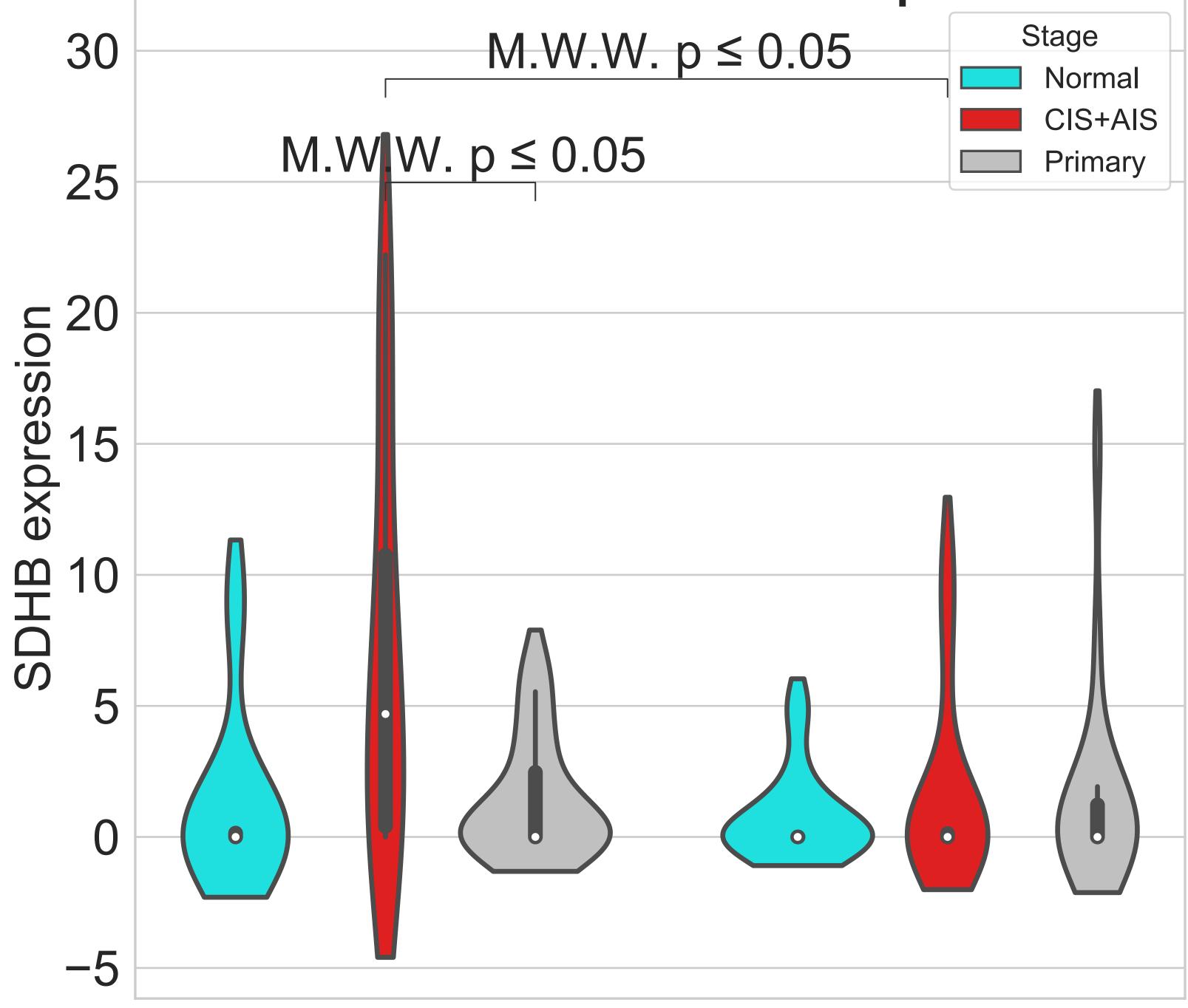
SDHB: Kruskal-Wallis p=0.031



Lower Higher Mutation Shared Count per TMB