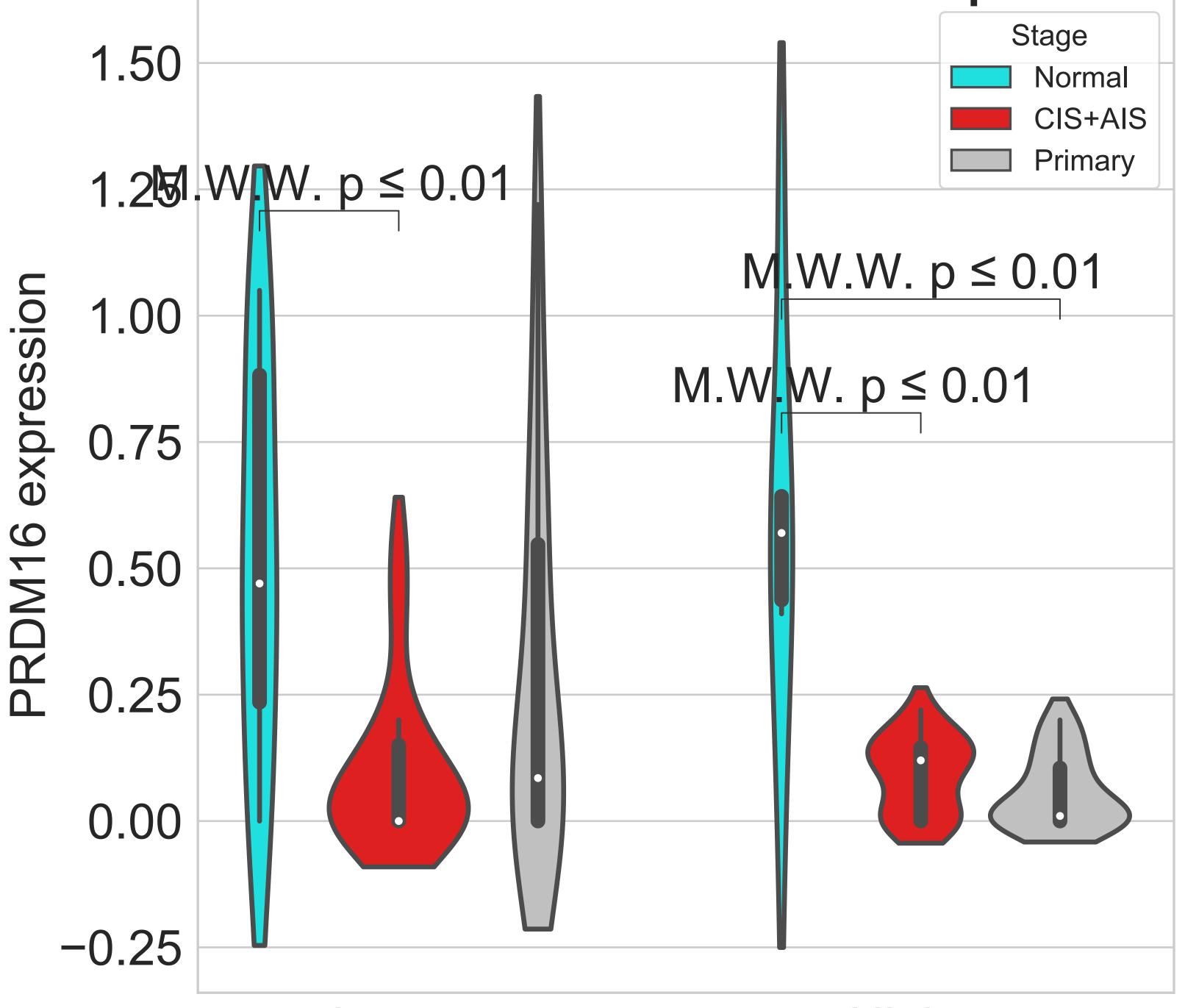
PRDM16: Kruskal-Wallis p=0.002



Lower Higher Mutation Shared Count (SYN) per TMB