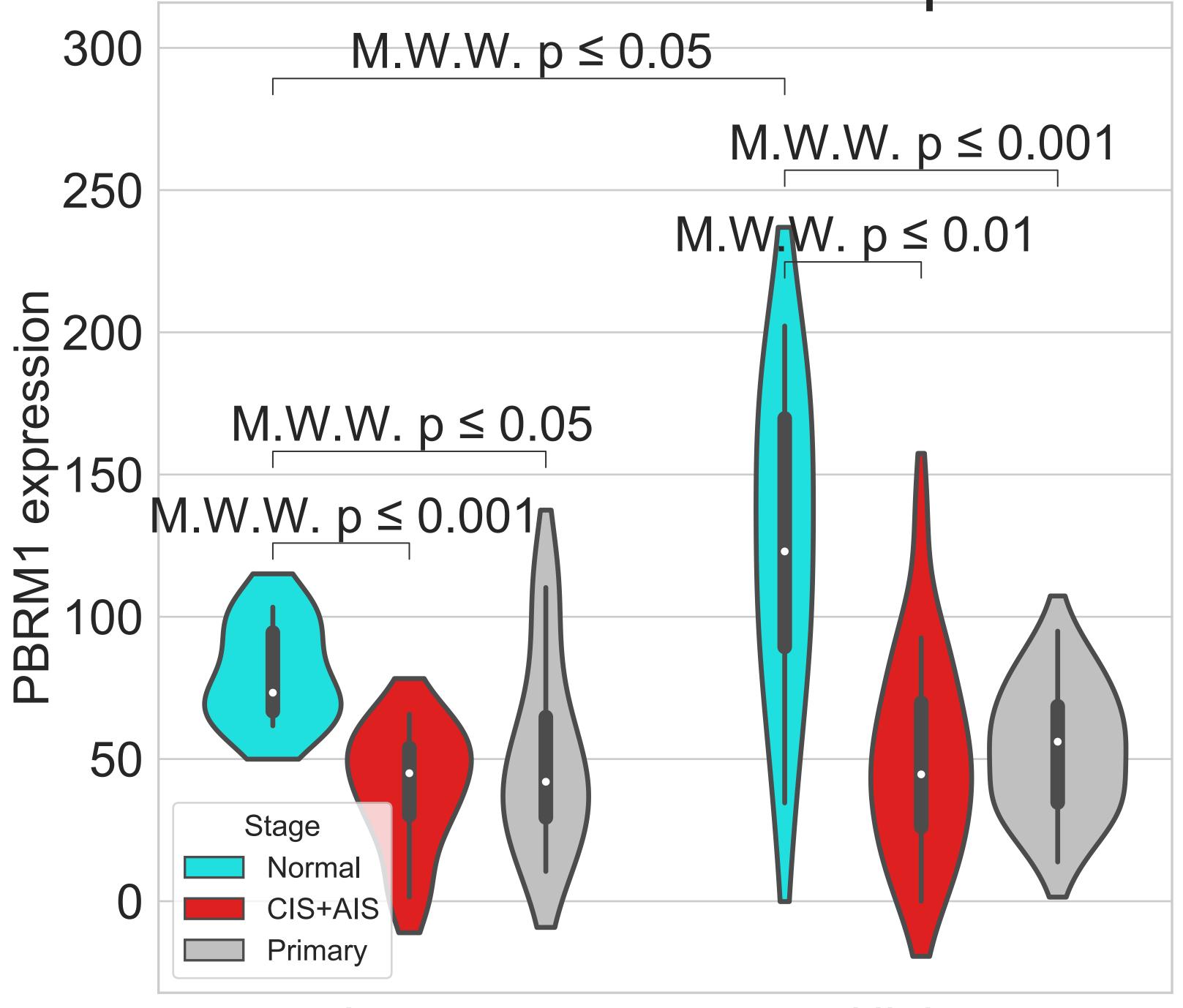
PBRM1: Kruskal-Wallis p=0.000



Lower Higher Mutation Shared Count (SYN) per TMB