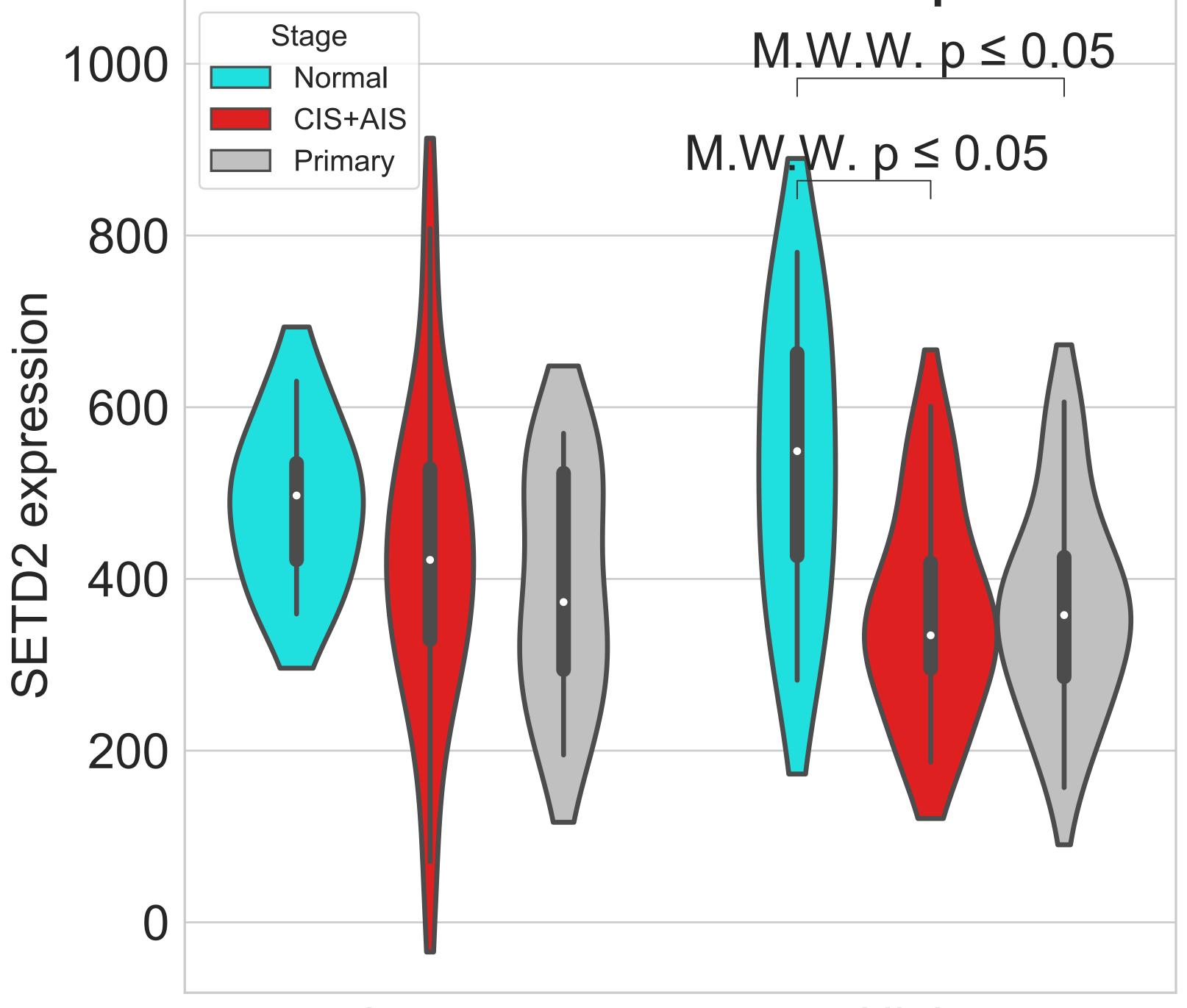
SETD2: Kruskal-Wallis p=0.036



Lower Higher Mutation Shared Count (SYN) per TMB