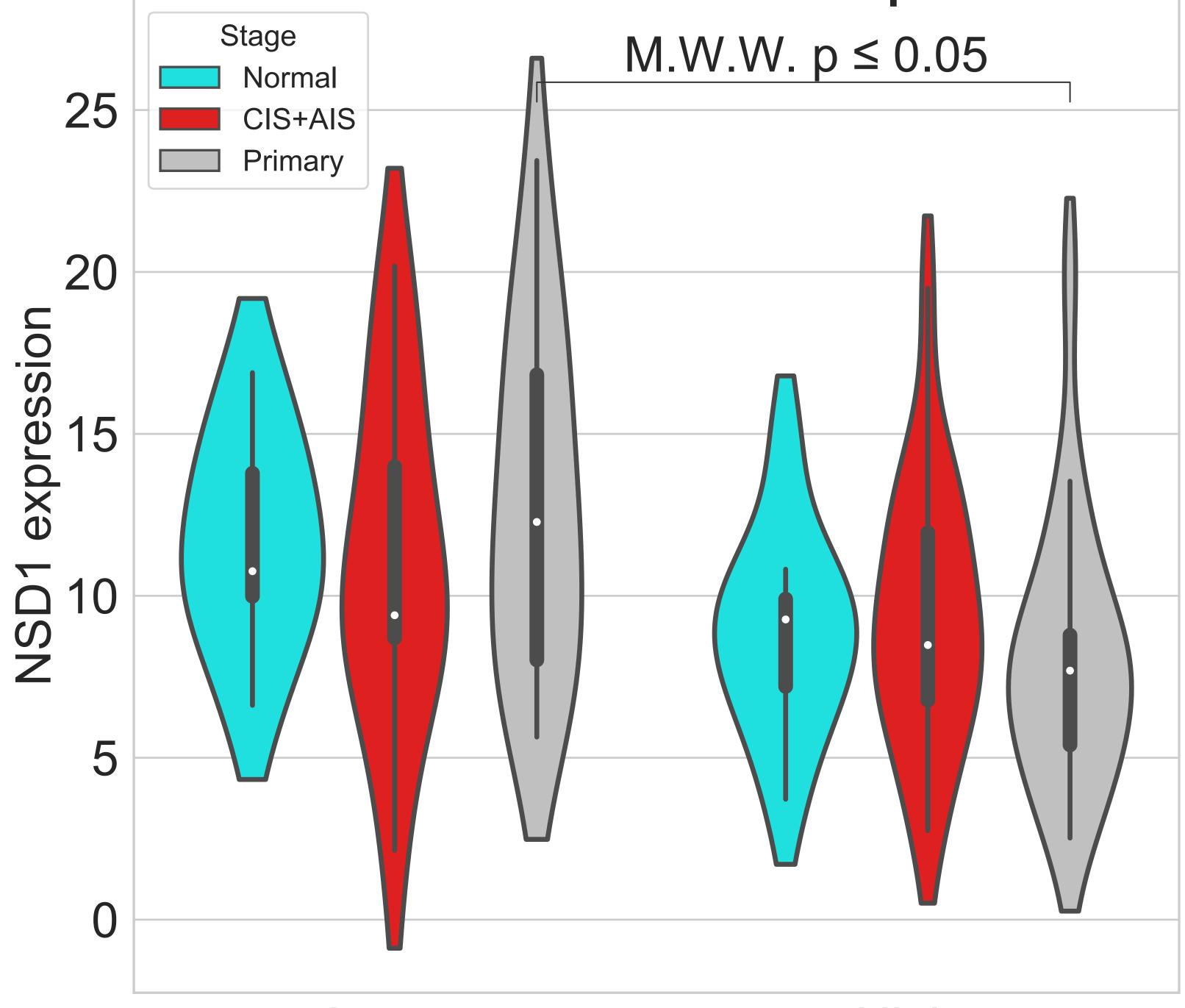
NSD1: Kruskal-Wallis p=0.043



Lower Higher Mutation Shared Count (SYN) per TMB