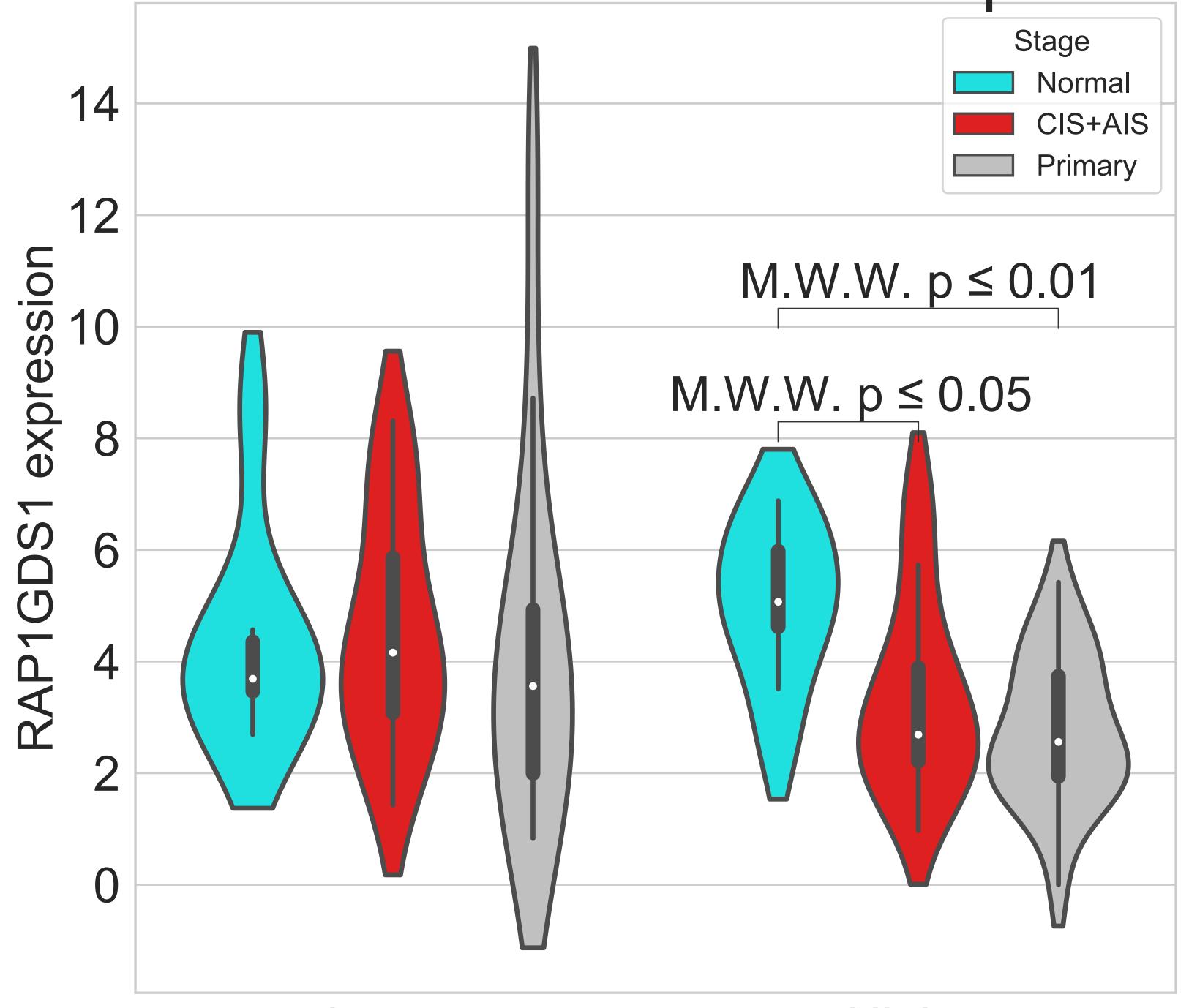
RAP1GDS1: Kruskal-Wallis p=0.014



Lower Higher Mutation Shared Count (SYN) per TMB