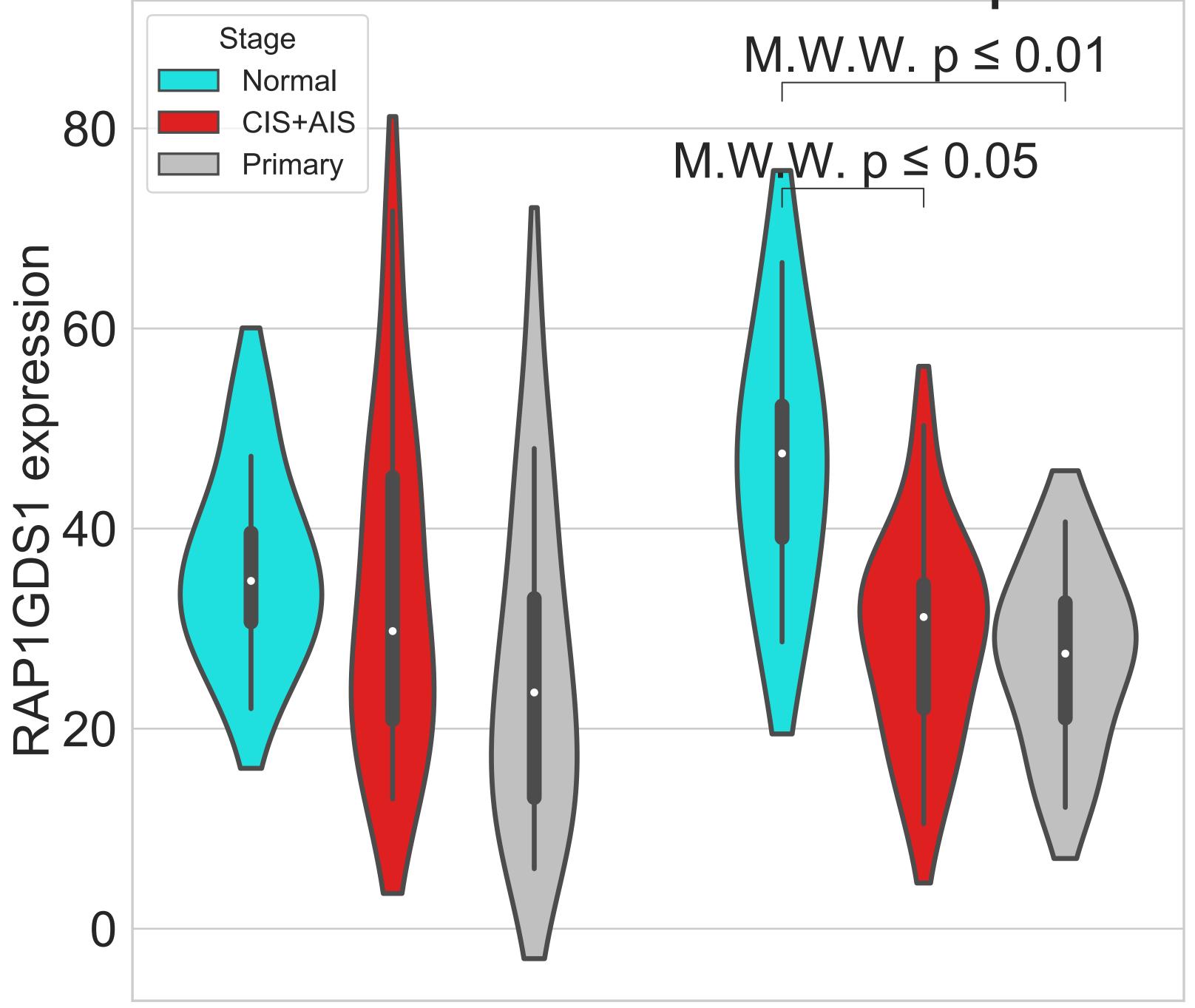
RAP1GDS1: Kruskal-Wallis p=0.032



Lower
Mutation Shared Count (SYN) per TMB