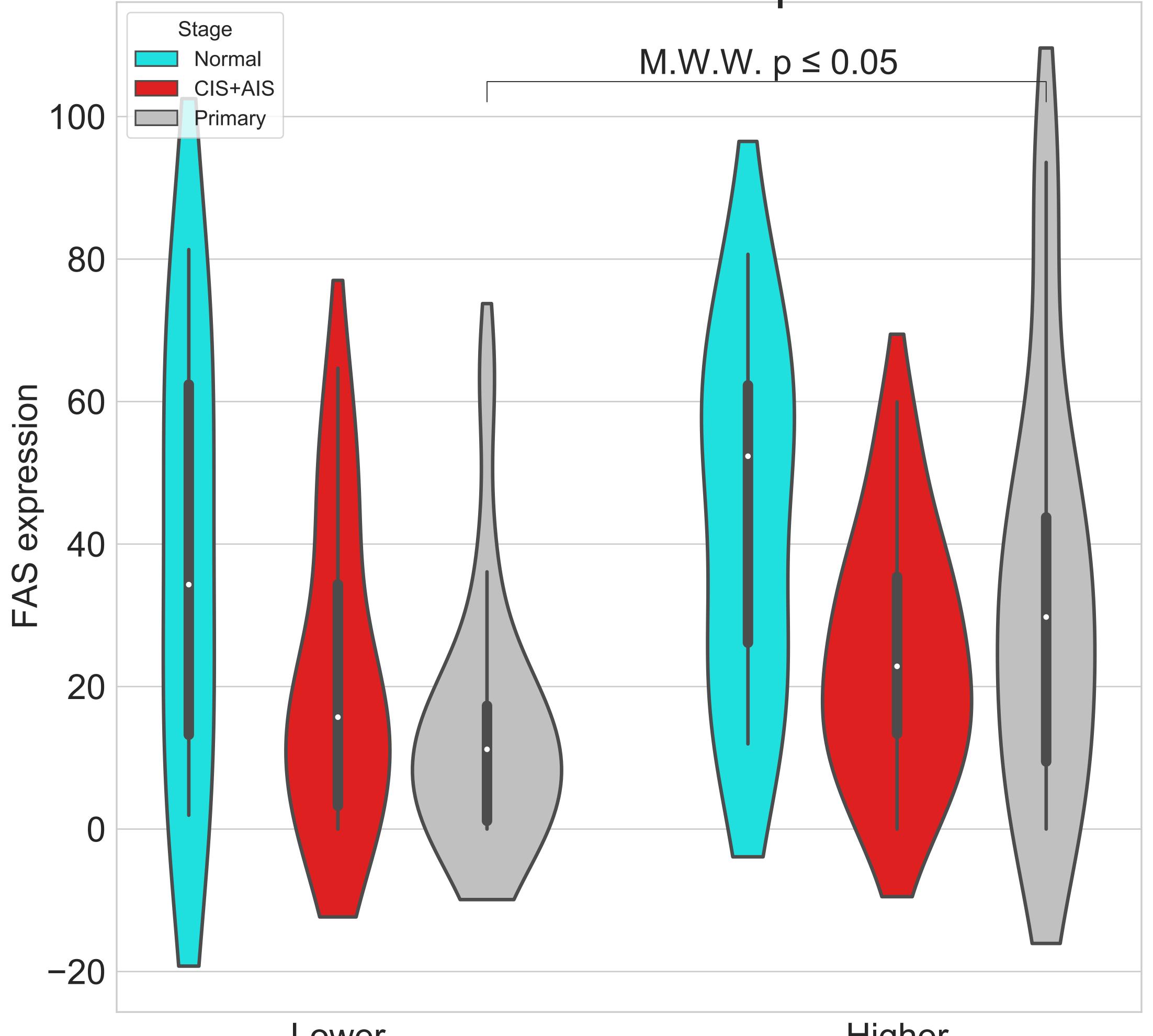
FAS: Kruskal-Wallis p=0.032



Lower
Mutation Shared Count per TMB