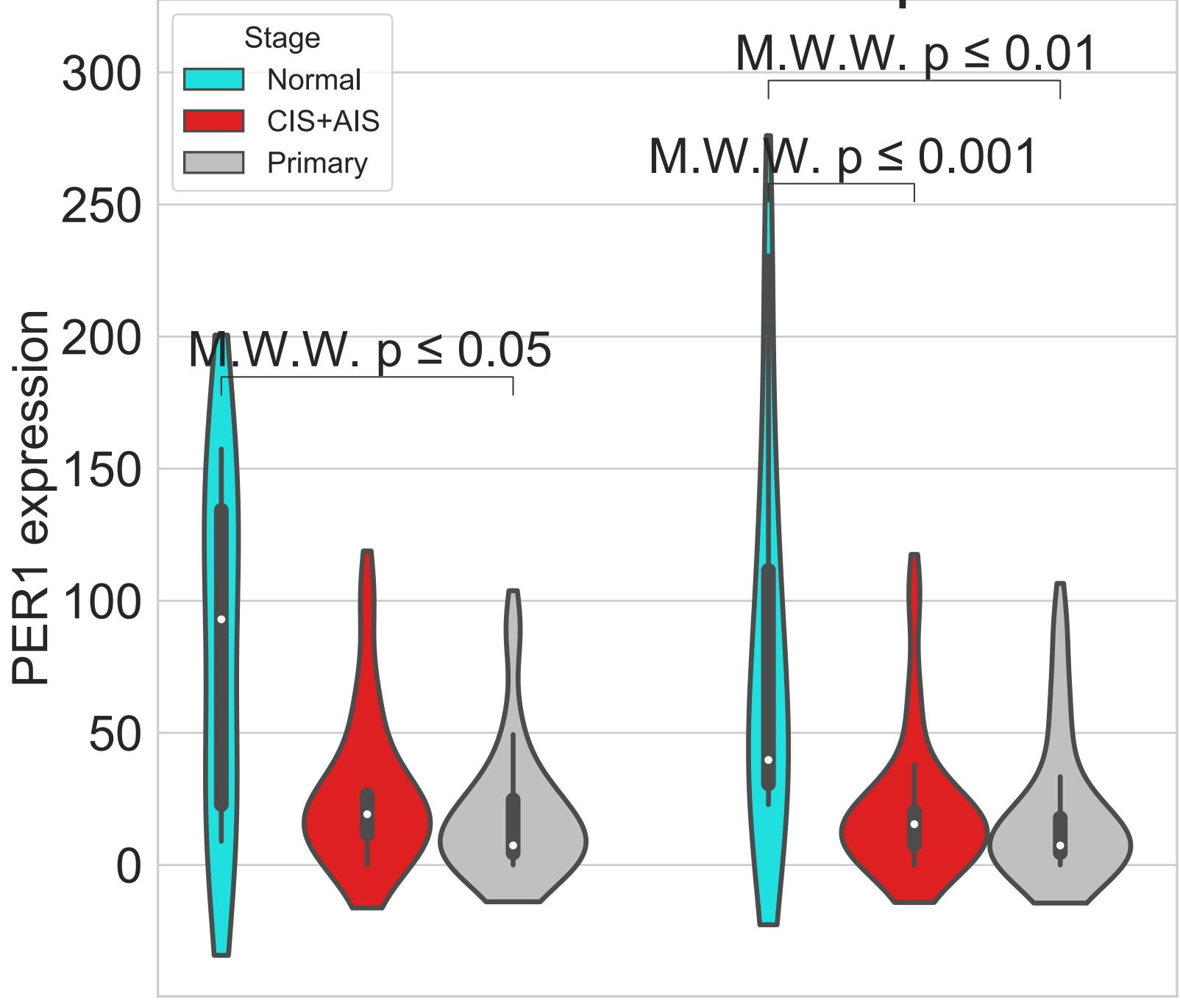
PER1: Kruskal-Wallis p=0.001



Lower Higher Mutation Shared Count per TMB