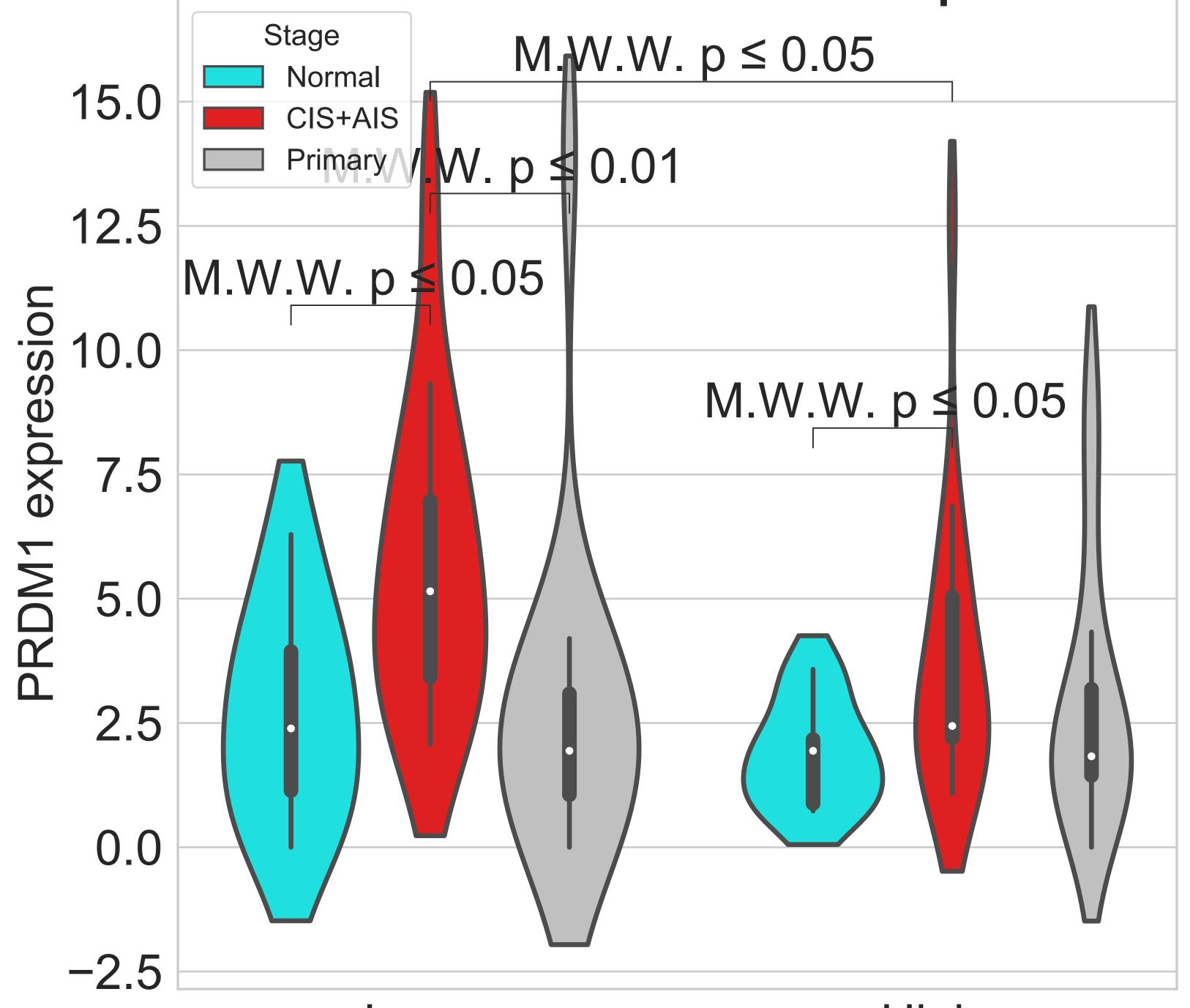
PRDM1: Kruskal-Wallis p=0.003



Lower Higher Mutation Shared Count per TMB