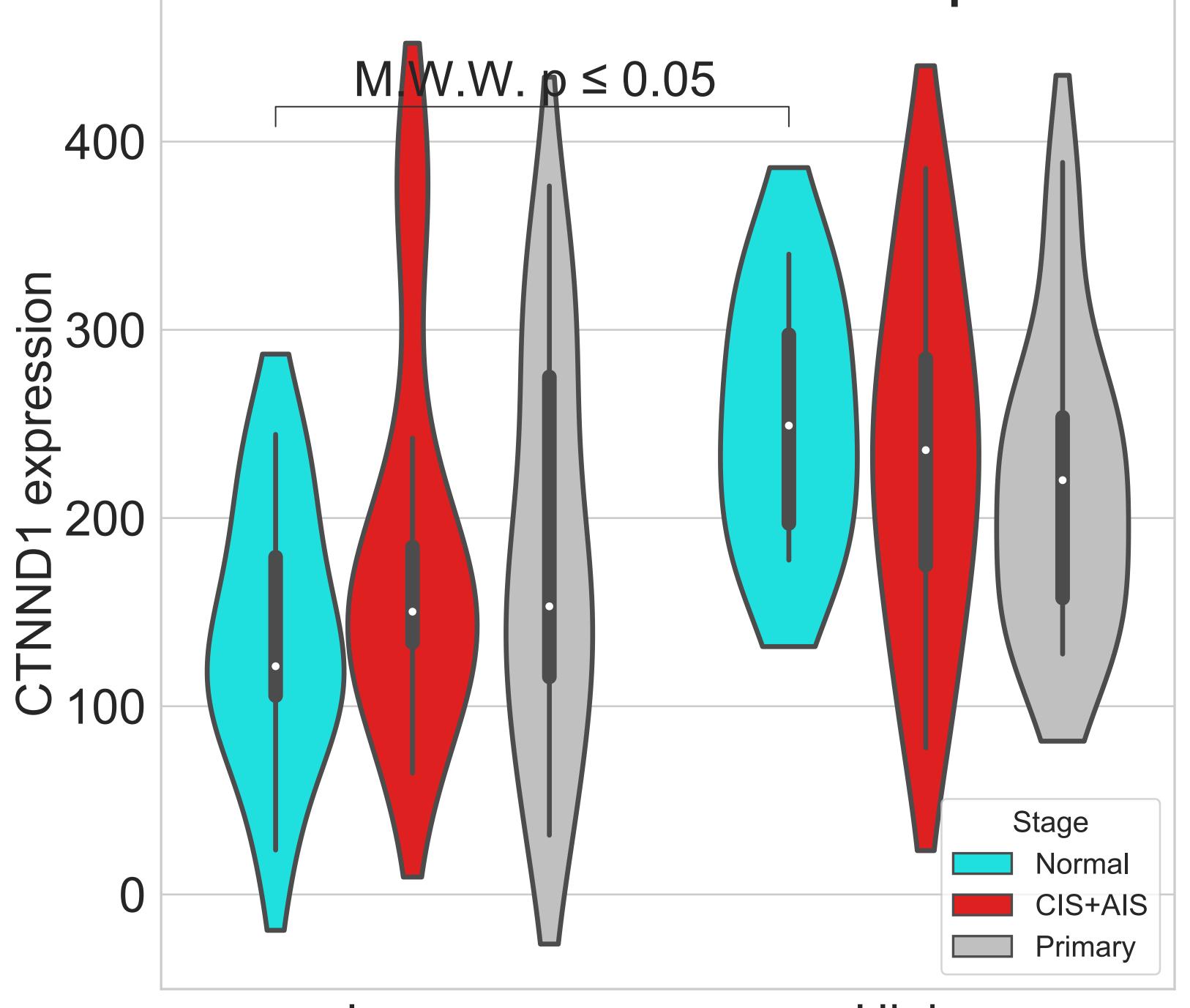
CTNND1: Kruskal-Wallis p=0.048



Lower Higher Mutation Shared Count per TMB