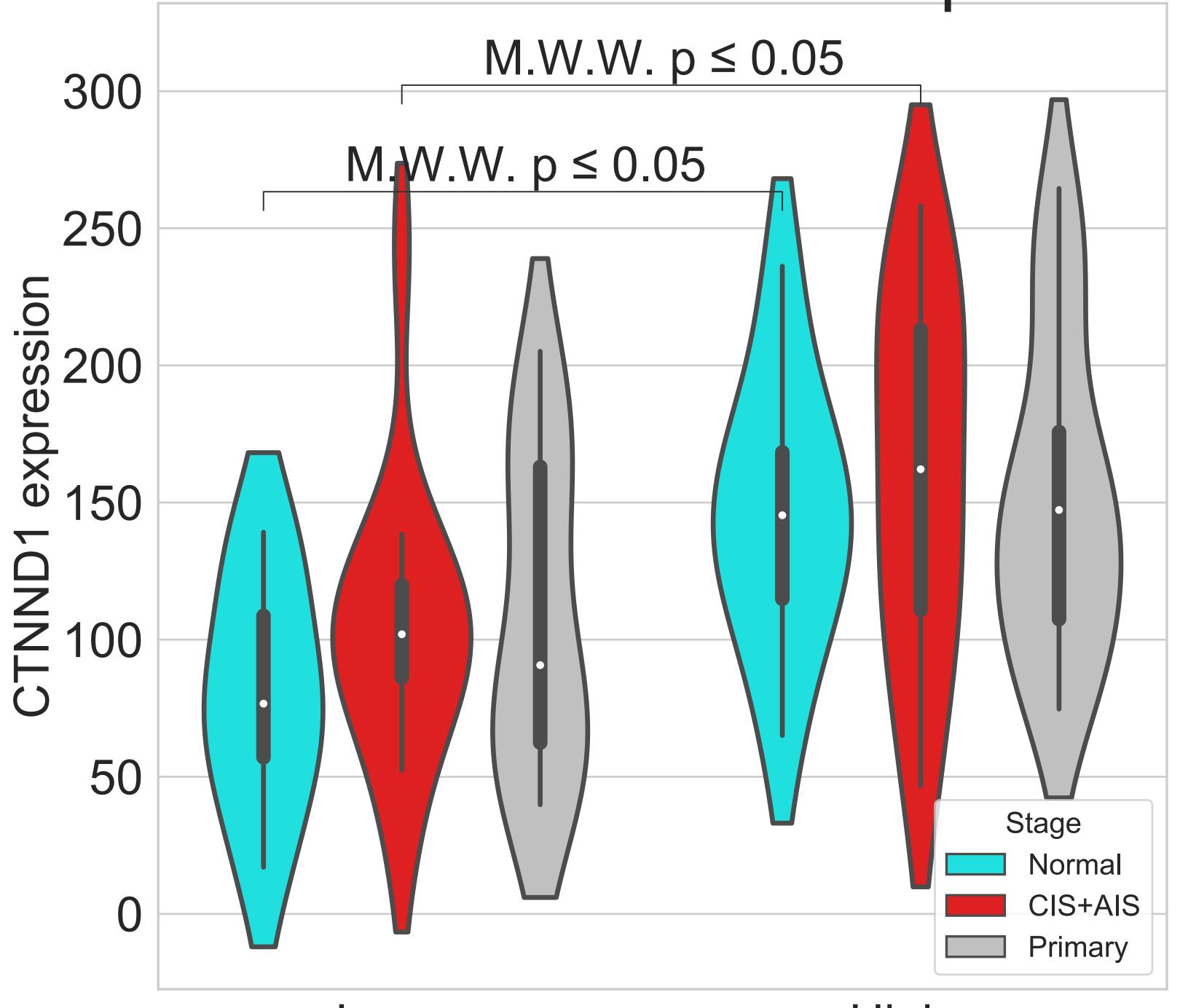
CTNND1: Kruskal-Wallis p=0.007



Lower Higher Mutation Shared Count per TMB