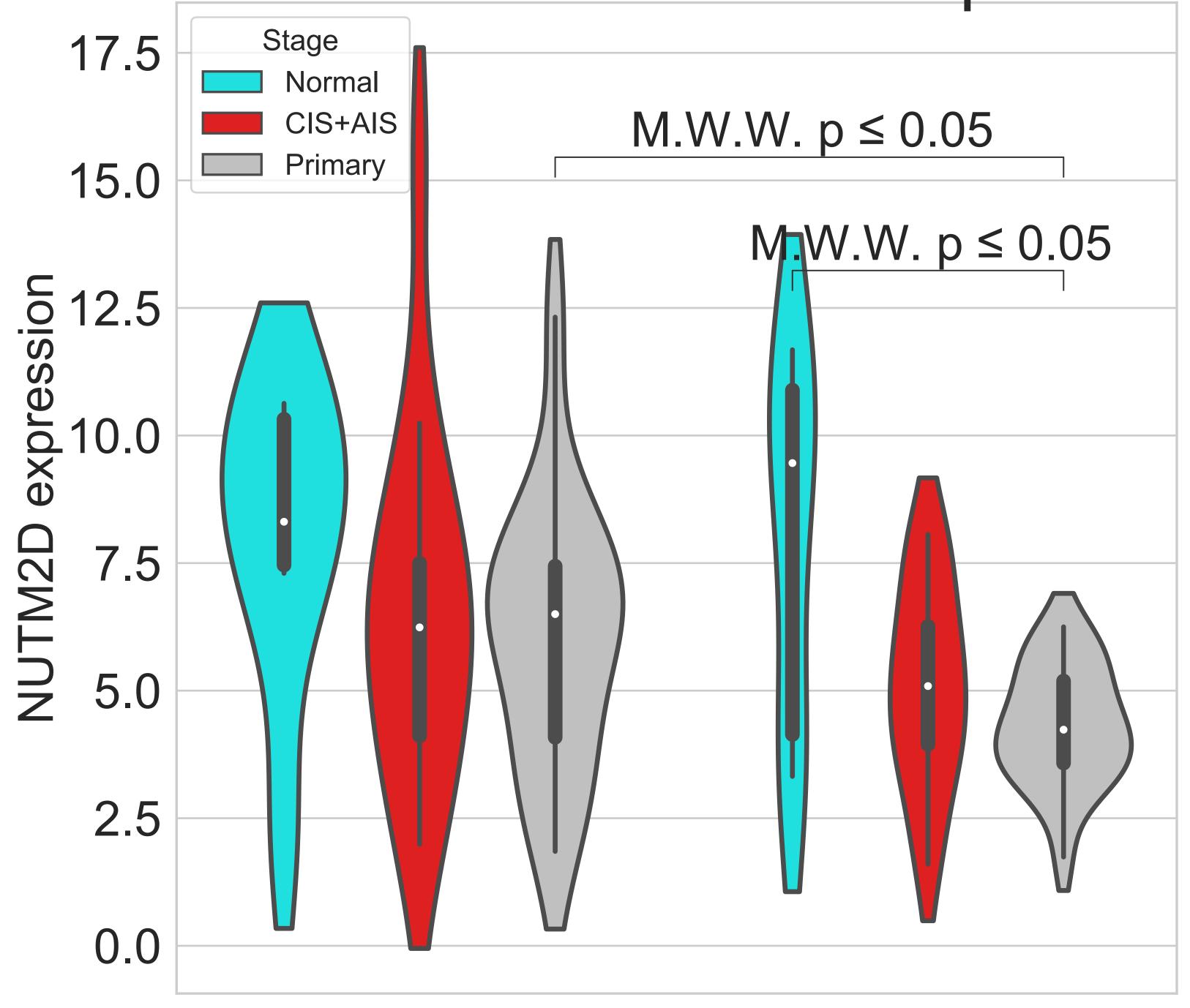
NUTM2D: Kruskal-Wallis p=0.008



Lower Higher Mutation Shared Count per TMB