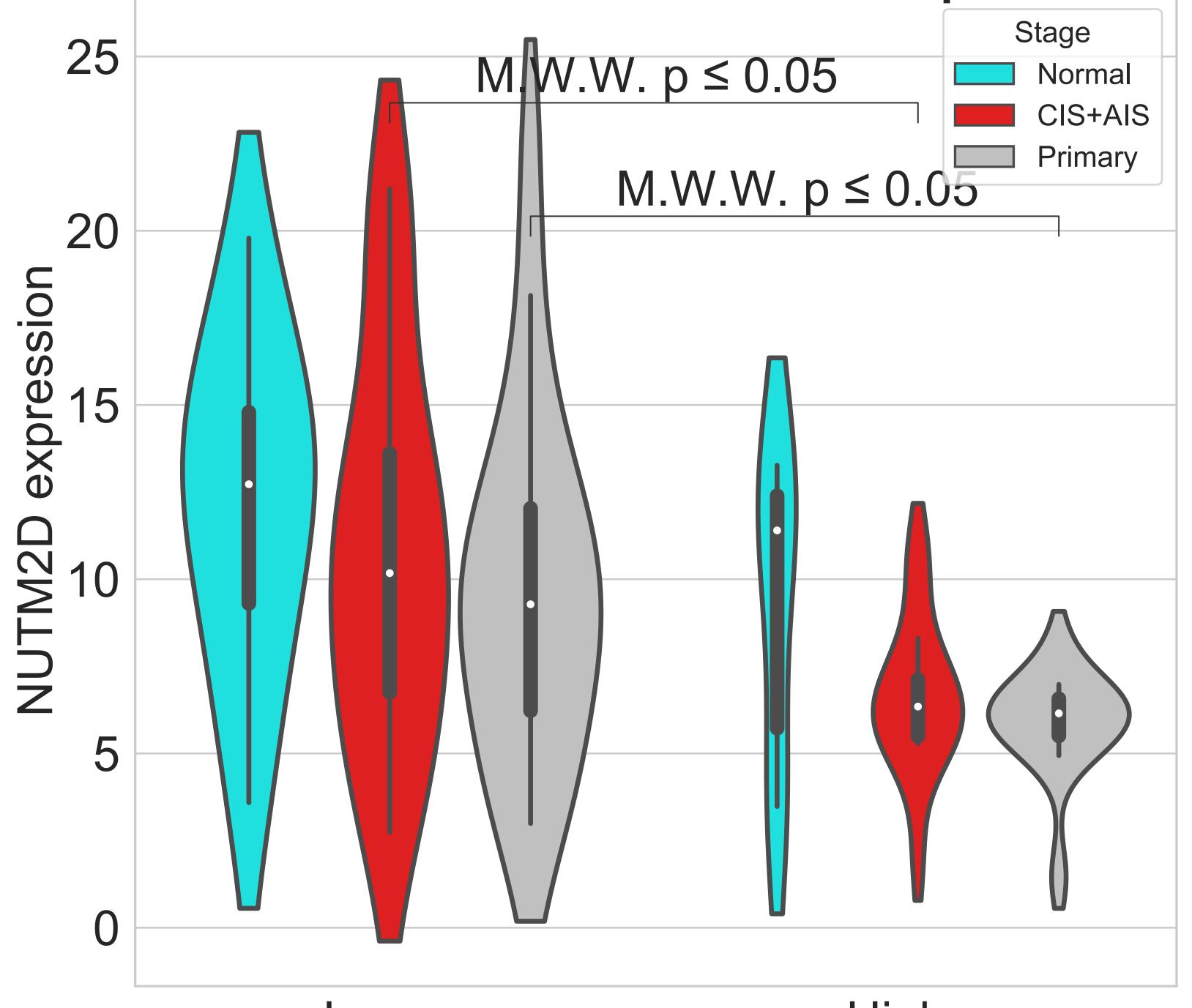
NUTM2D: Kruskal-Wallis p=0.004



Lower Higher Mutation Shared Count per TMB