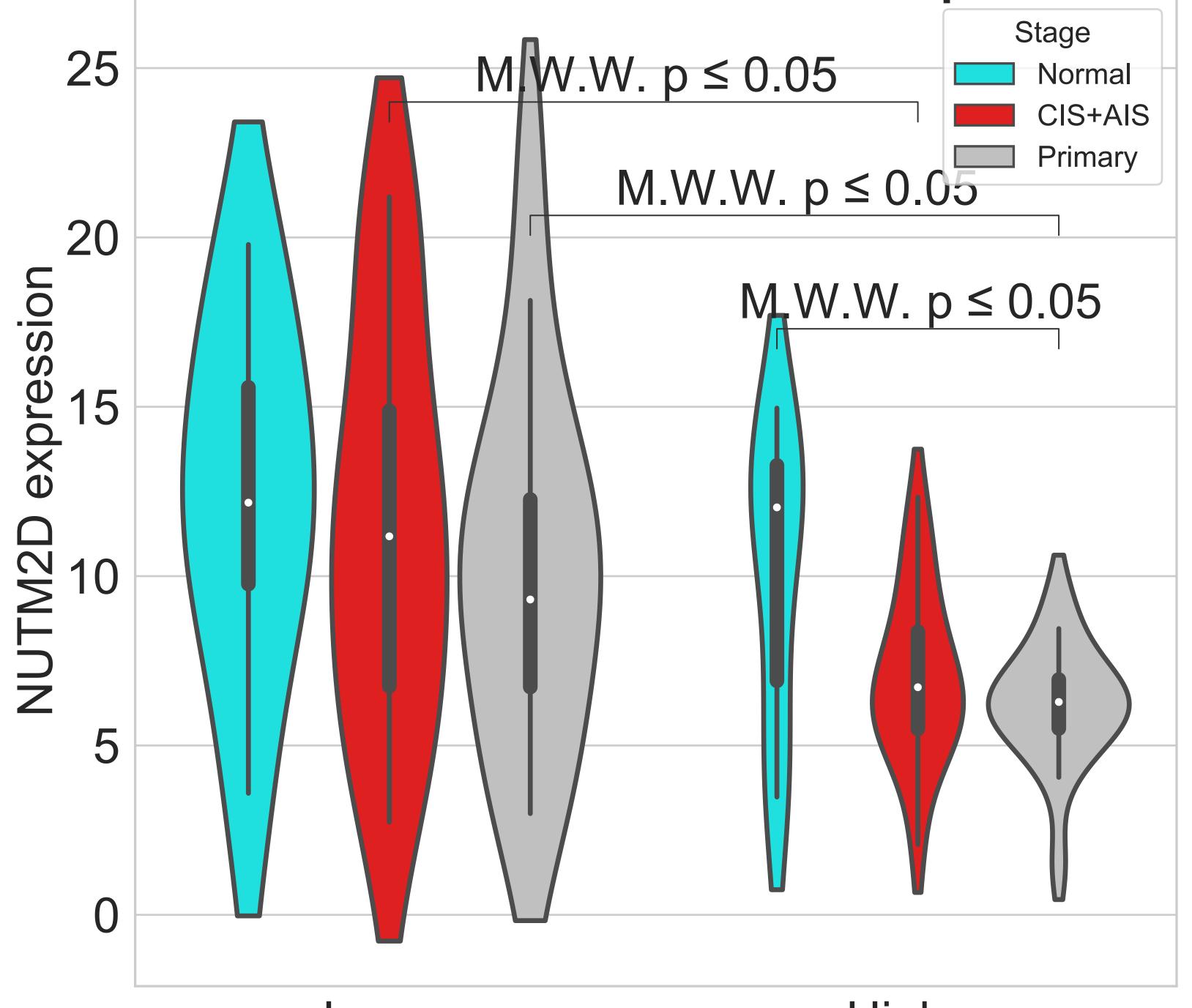
NUTM2D: Kruskal-Wallis p=0.006



Lower Higher Mutation Shared Count per TMB