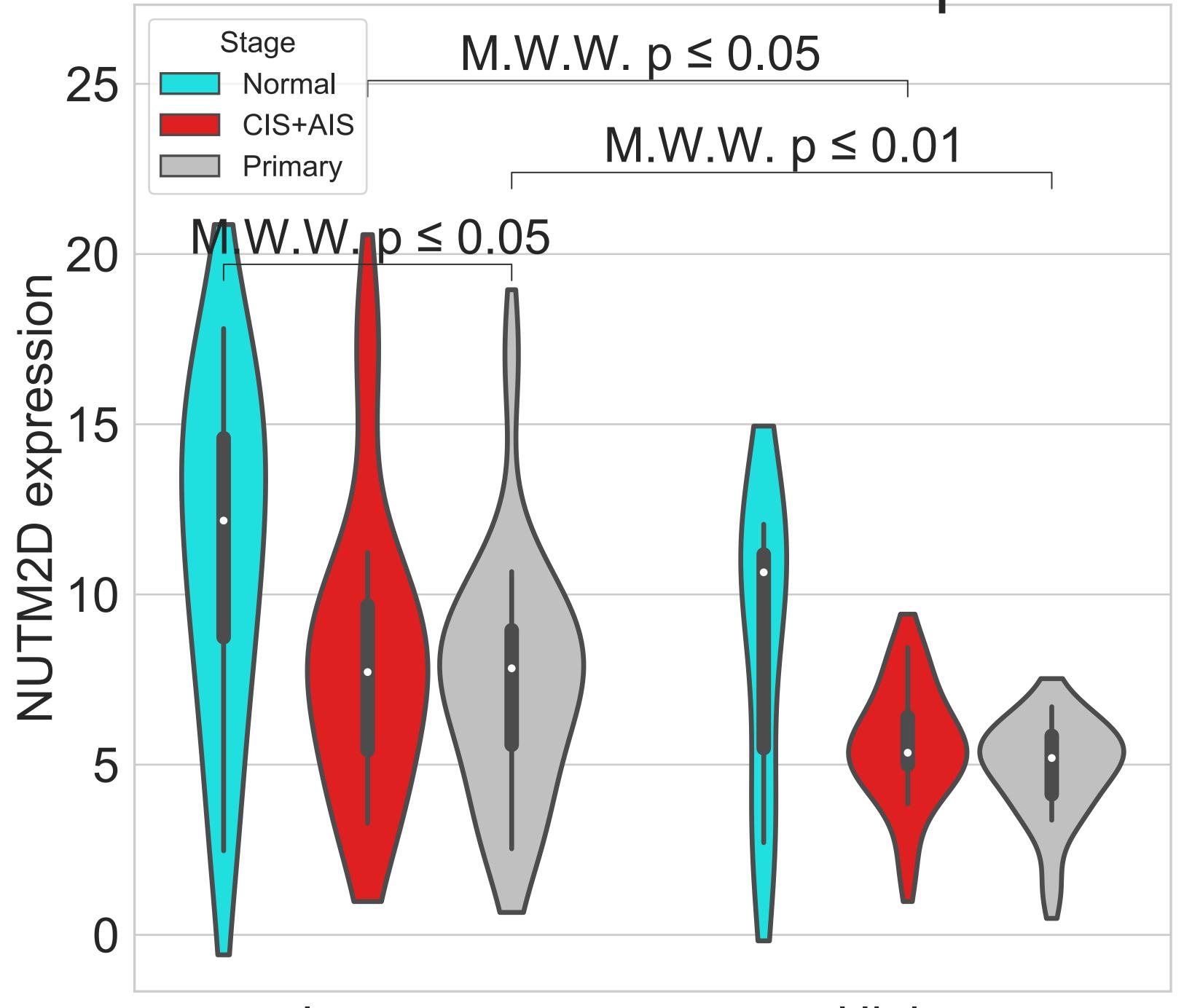
NUTM2D: Kruskal-Wallis p=0.002



Lower
Mutation Shared Count per TMB