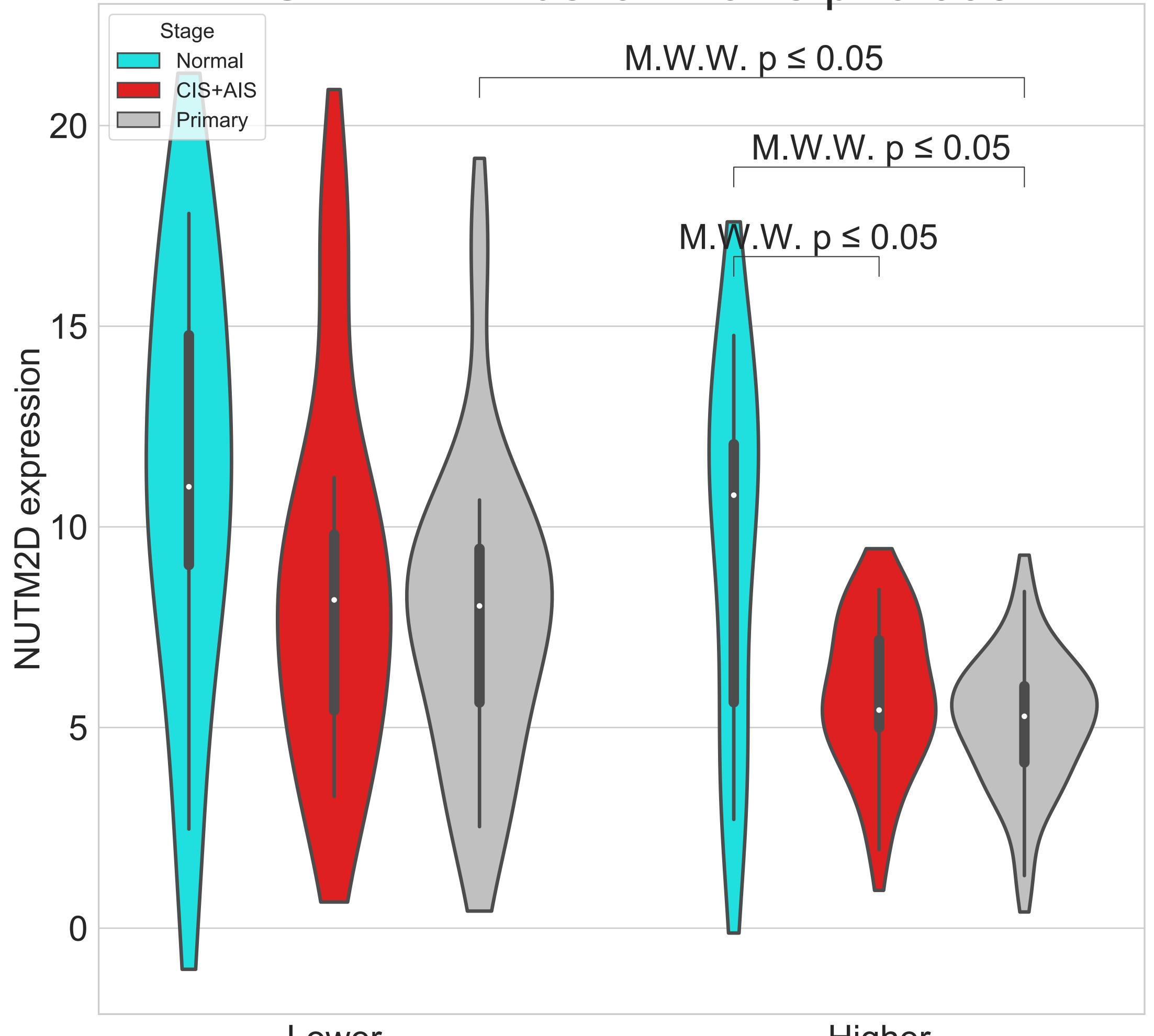
NUTM2D: Kruskal-Wallis p=0.003



Lower
Mutation Shared Count per TMB