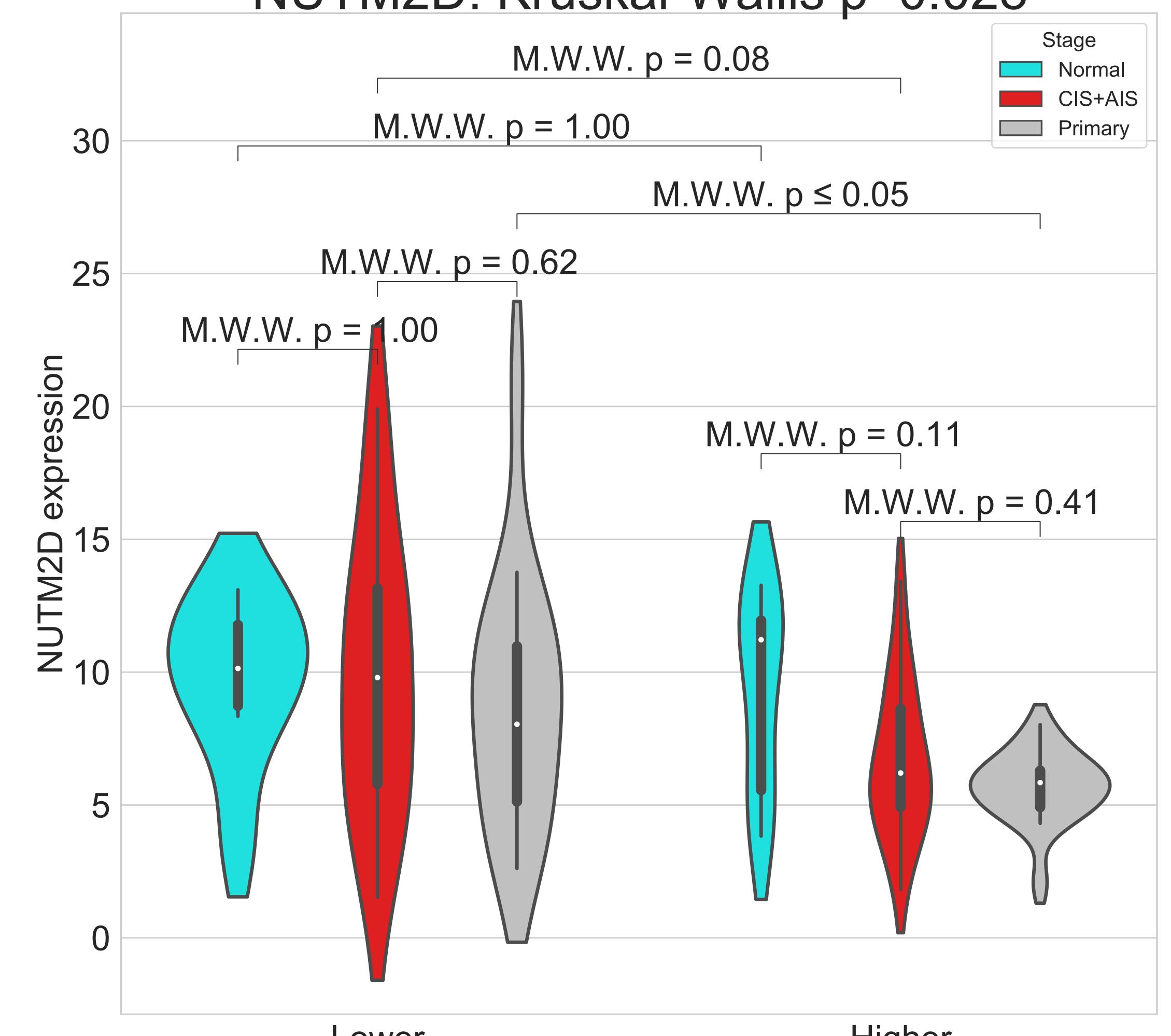
NUTM2D: Kruskal-Wallis p=0.028



Lower
Mutation Shared Count per TMB