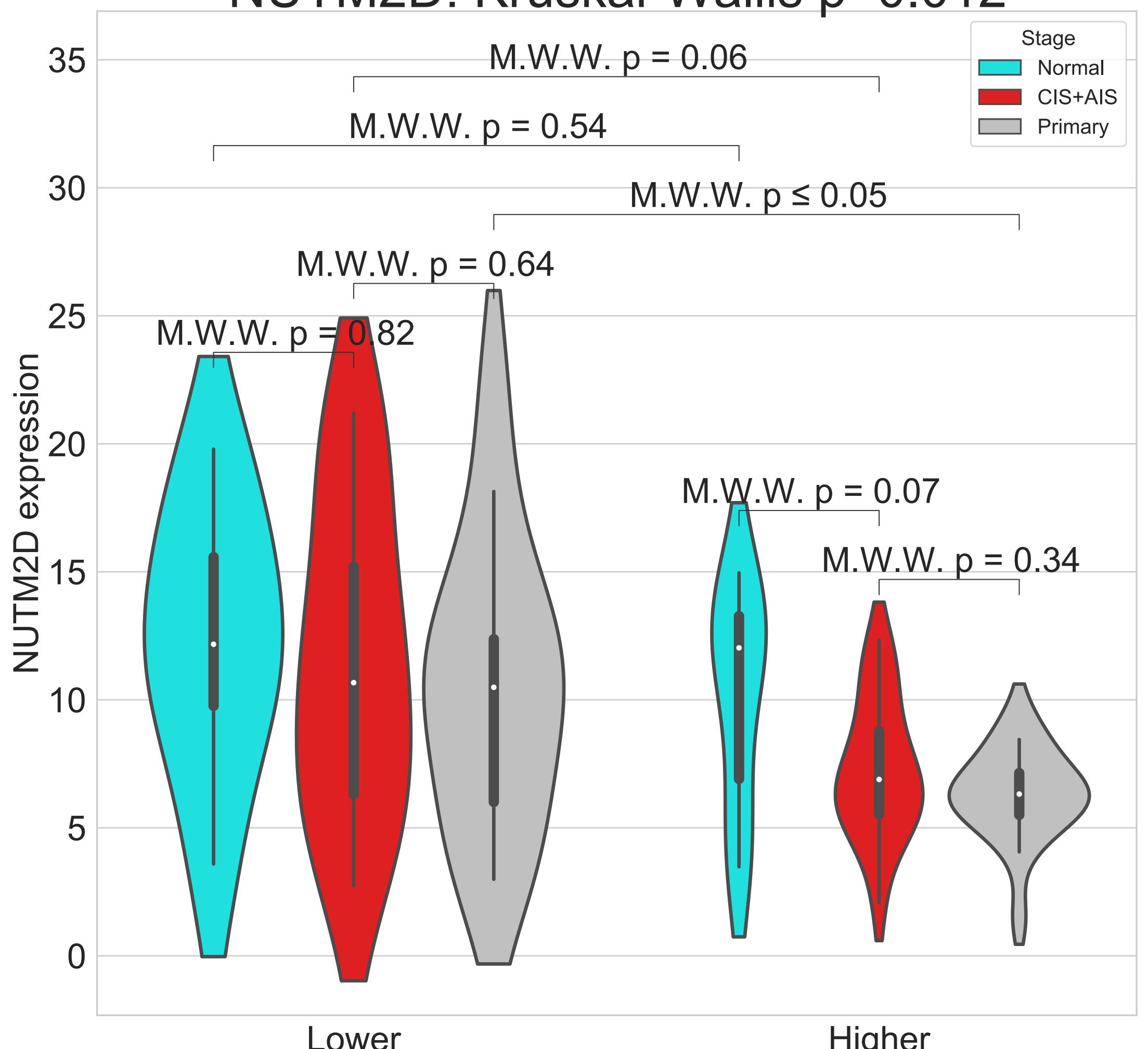
NUTM2D: Kruskal-Wallis p=0.012



Lower
Mutation Shared Count (SYN) per TMB