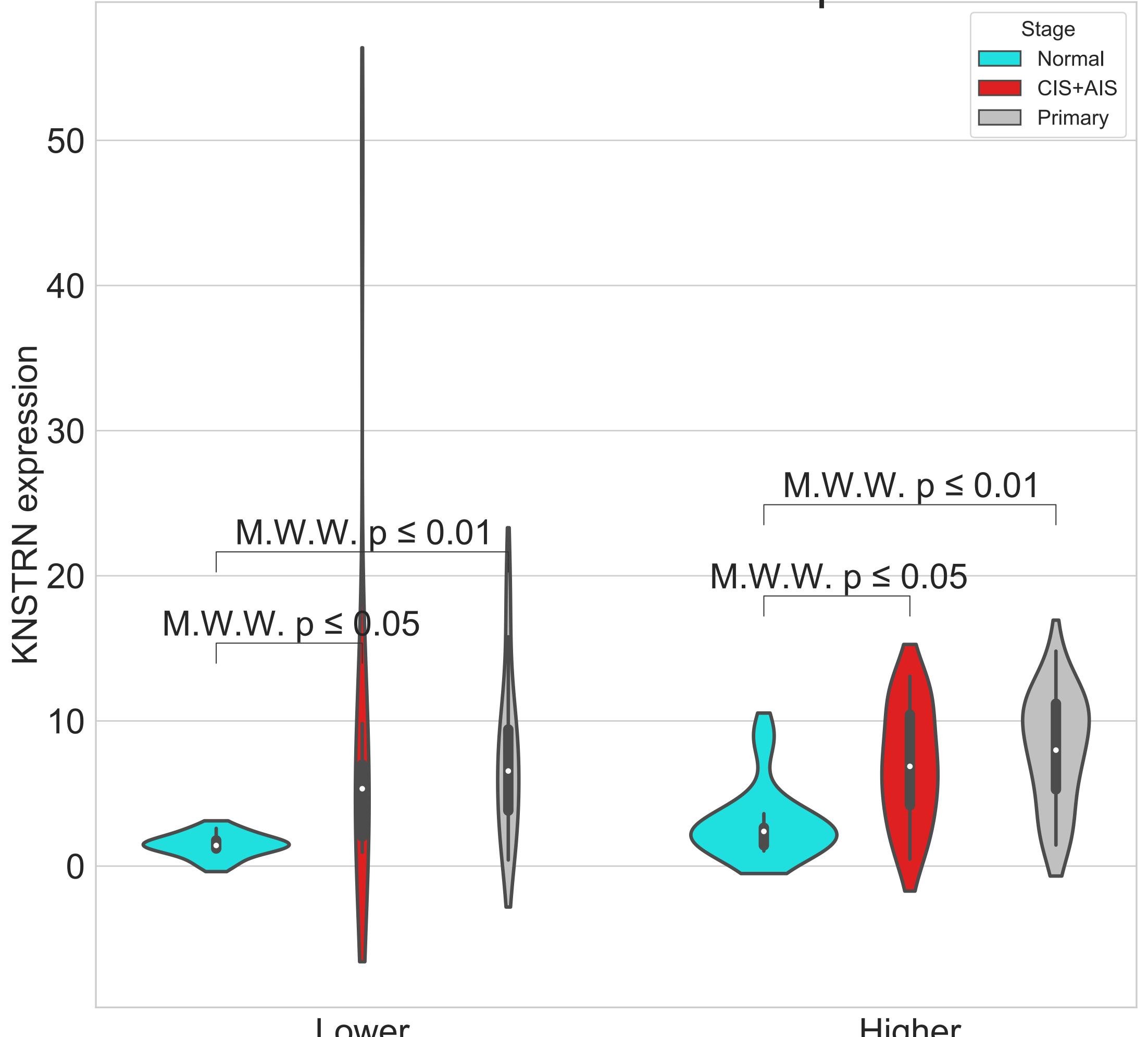
KNSTRN: Kruskal-Wallis p=0.001



Higher Lower Mutation Shared Count (SYN) per TMB