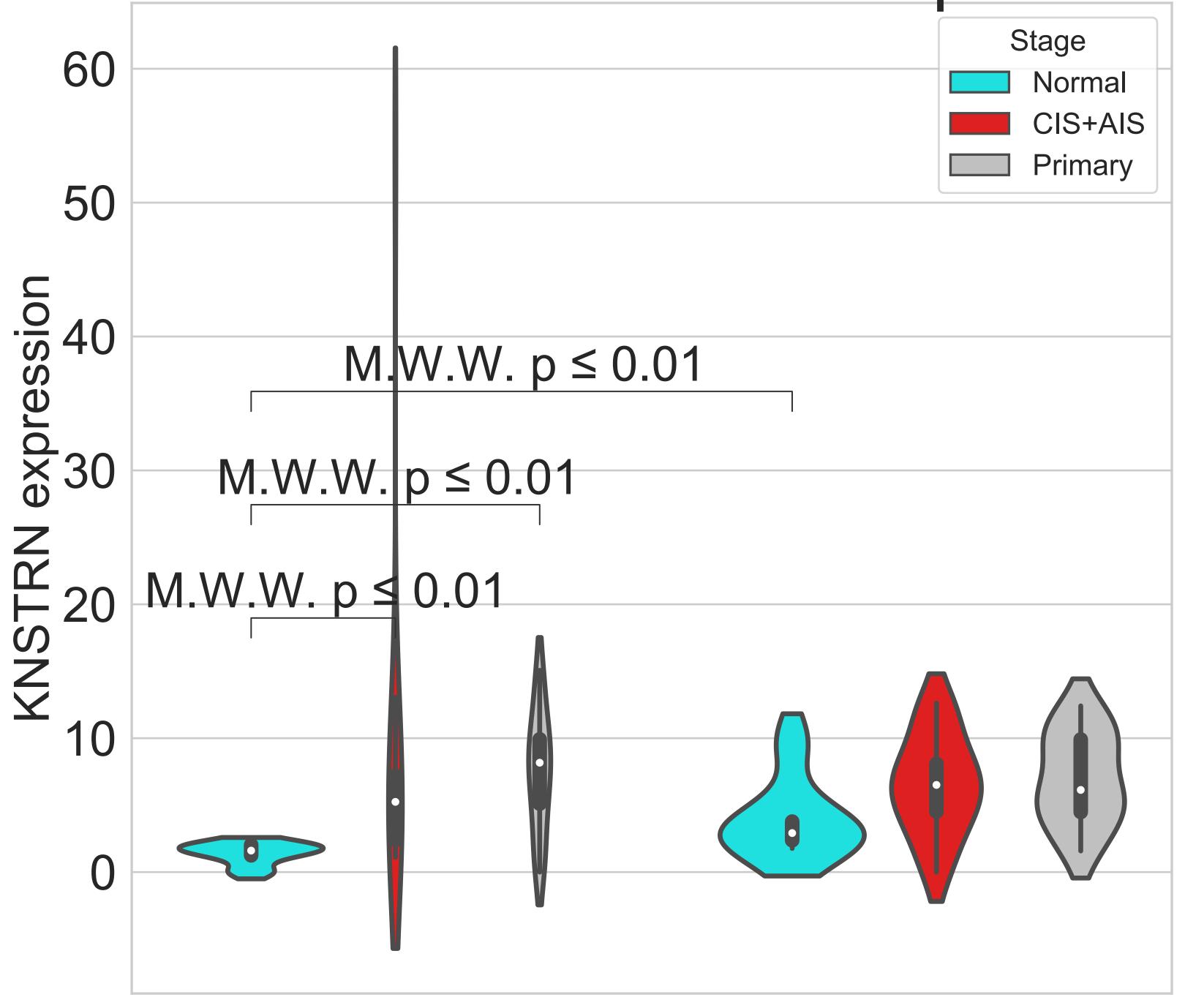
KNSTRN: Kruskal-Wallis p=0.002



Lower
Mutation Shared Count per TMB