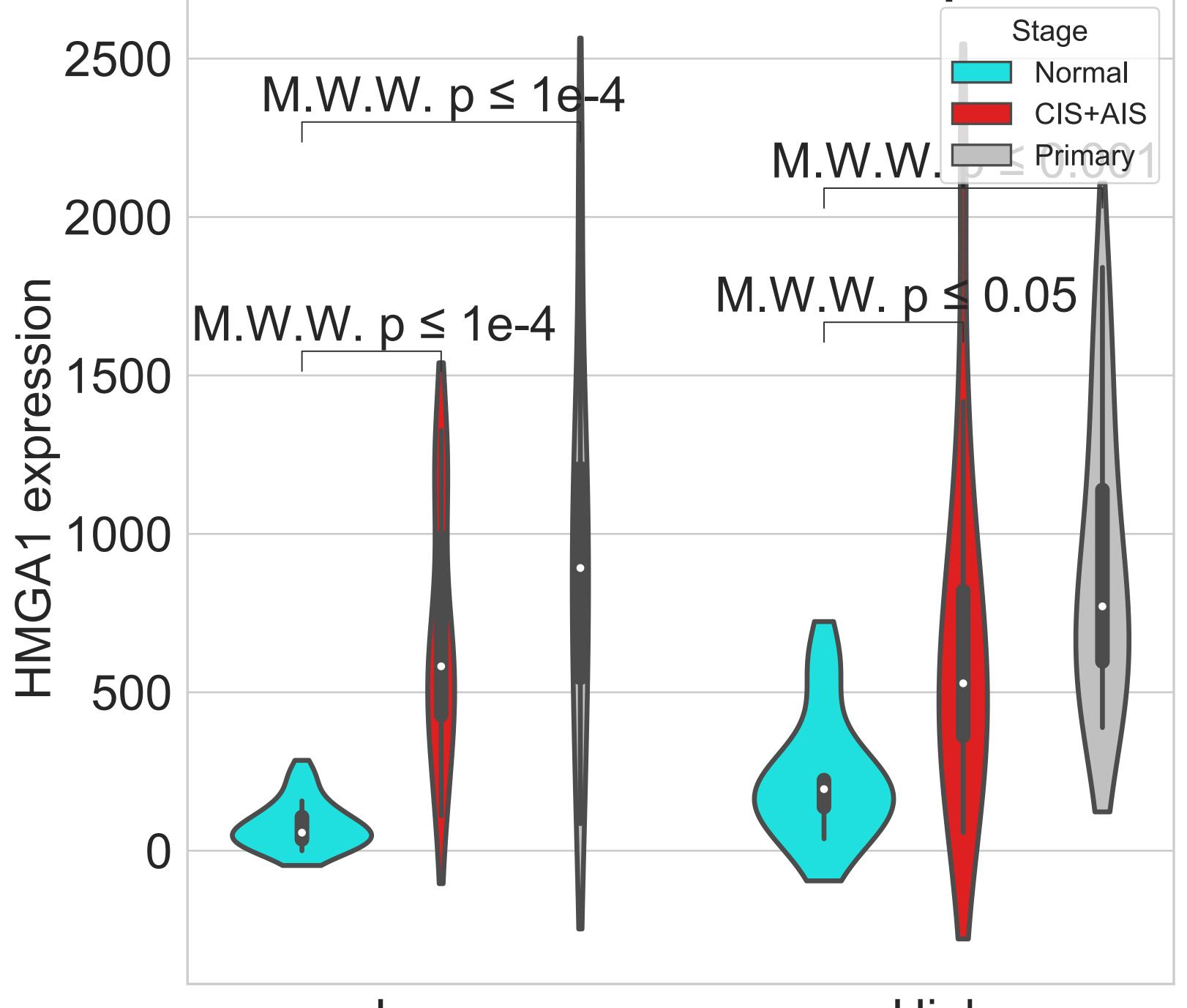
HMGA1: Kruskal-Wallis p=0.000



Lower Higher Mutation Shared Count per TMB