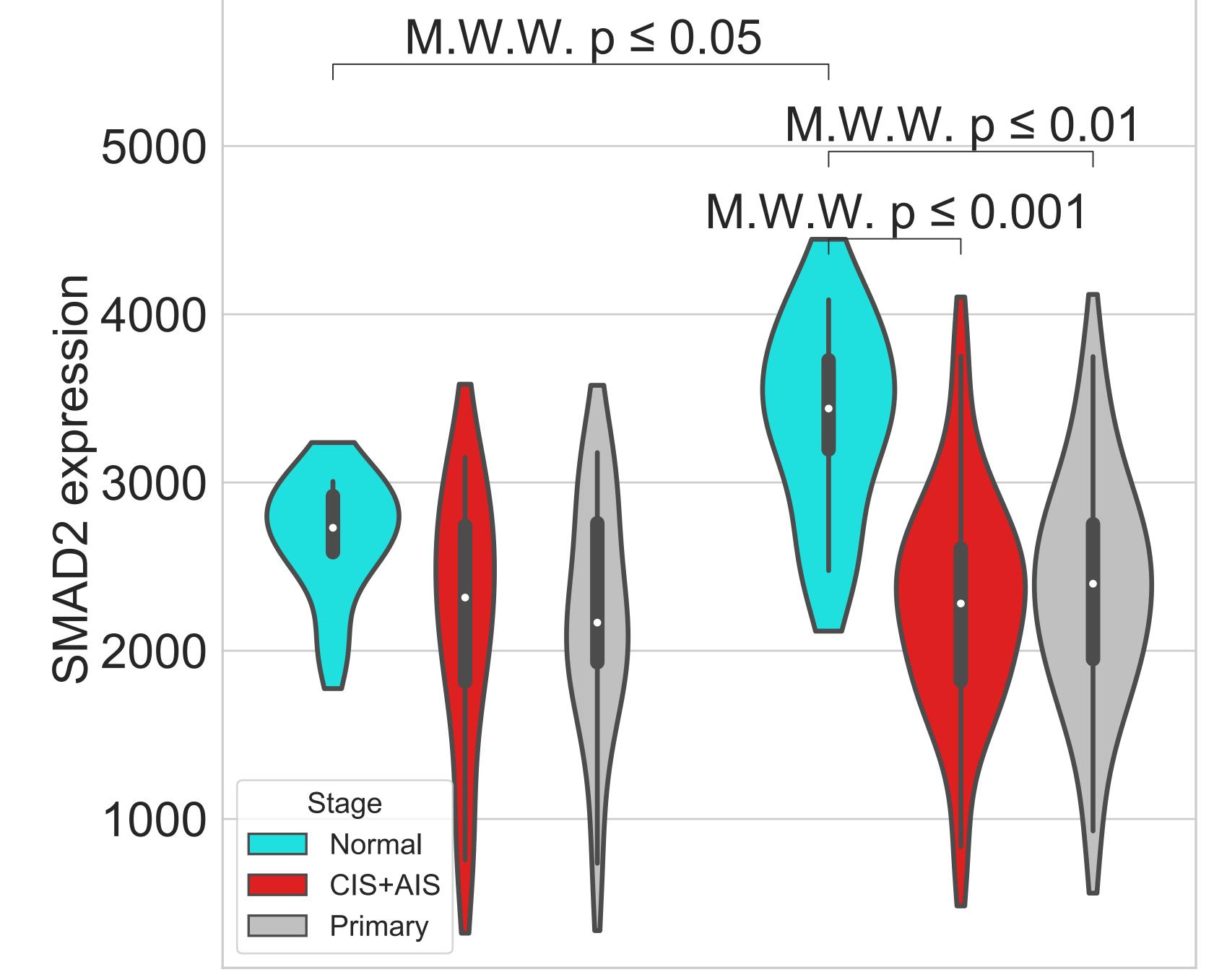
SMAD2: Kruskal-Wallis p=0.003



Lower Higher Mutation Shared Proportion (SYN)