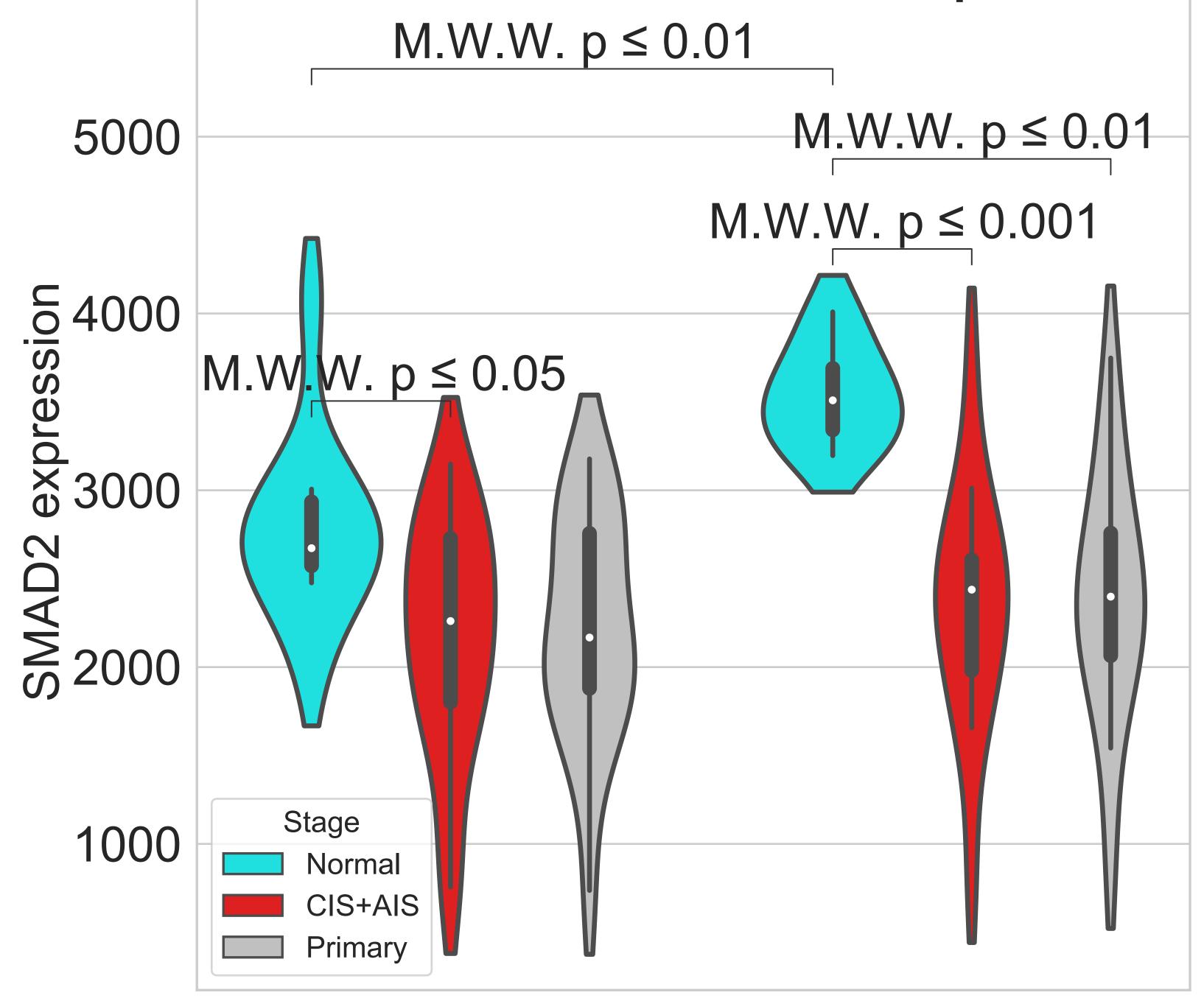
SMAD2: Kruskal-Wallis p=0.002



Lower Higher Mutation Shared Proportion (Union & SYN)