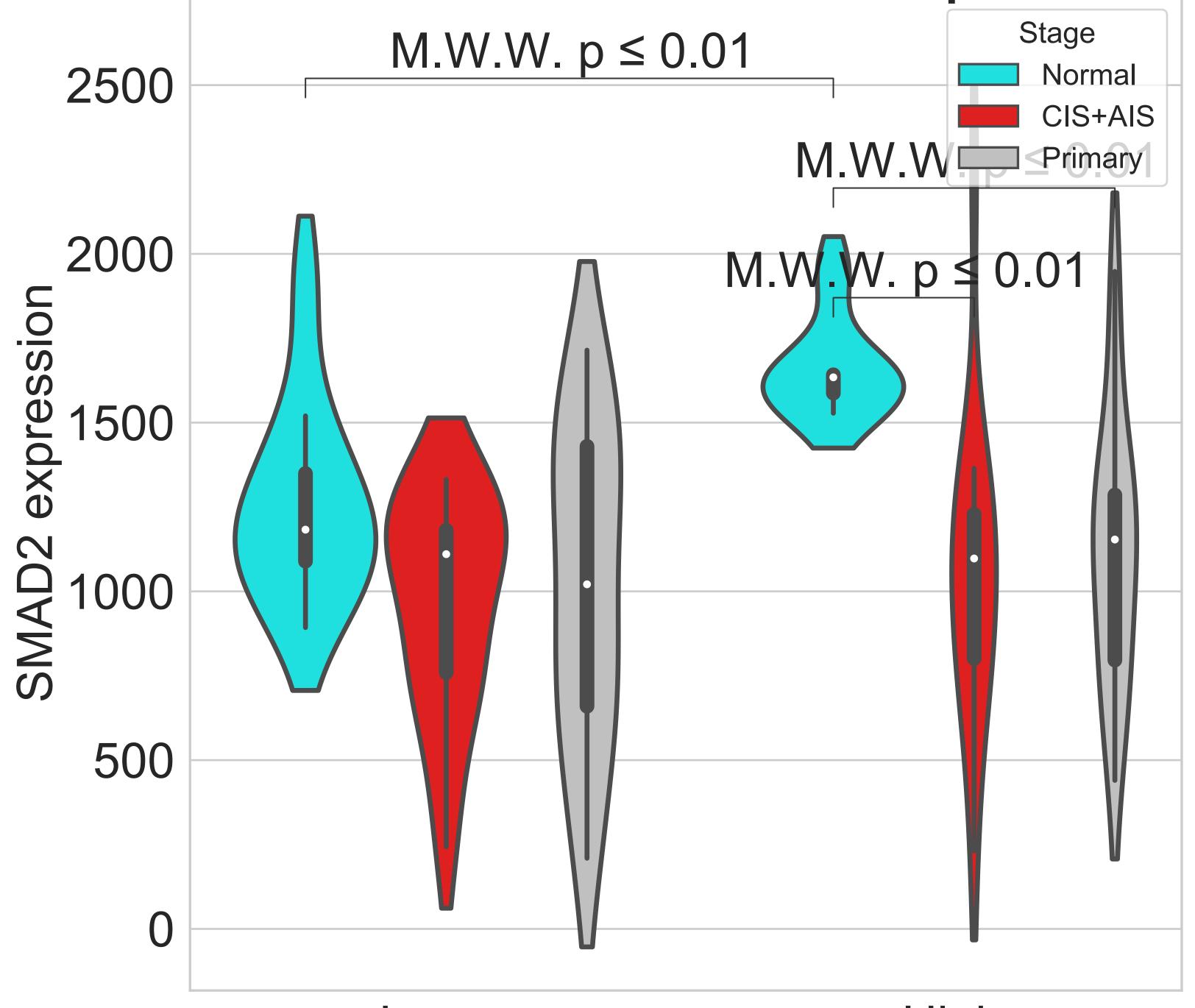
SMAD2: Kruskal-Wallis p=0.010



Lower Higher Mutation Shared Proportion (Union & SYN)