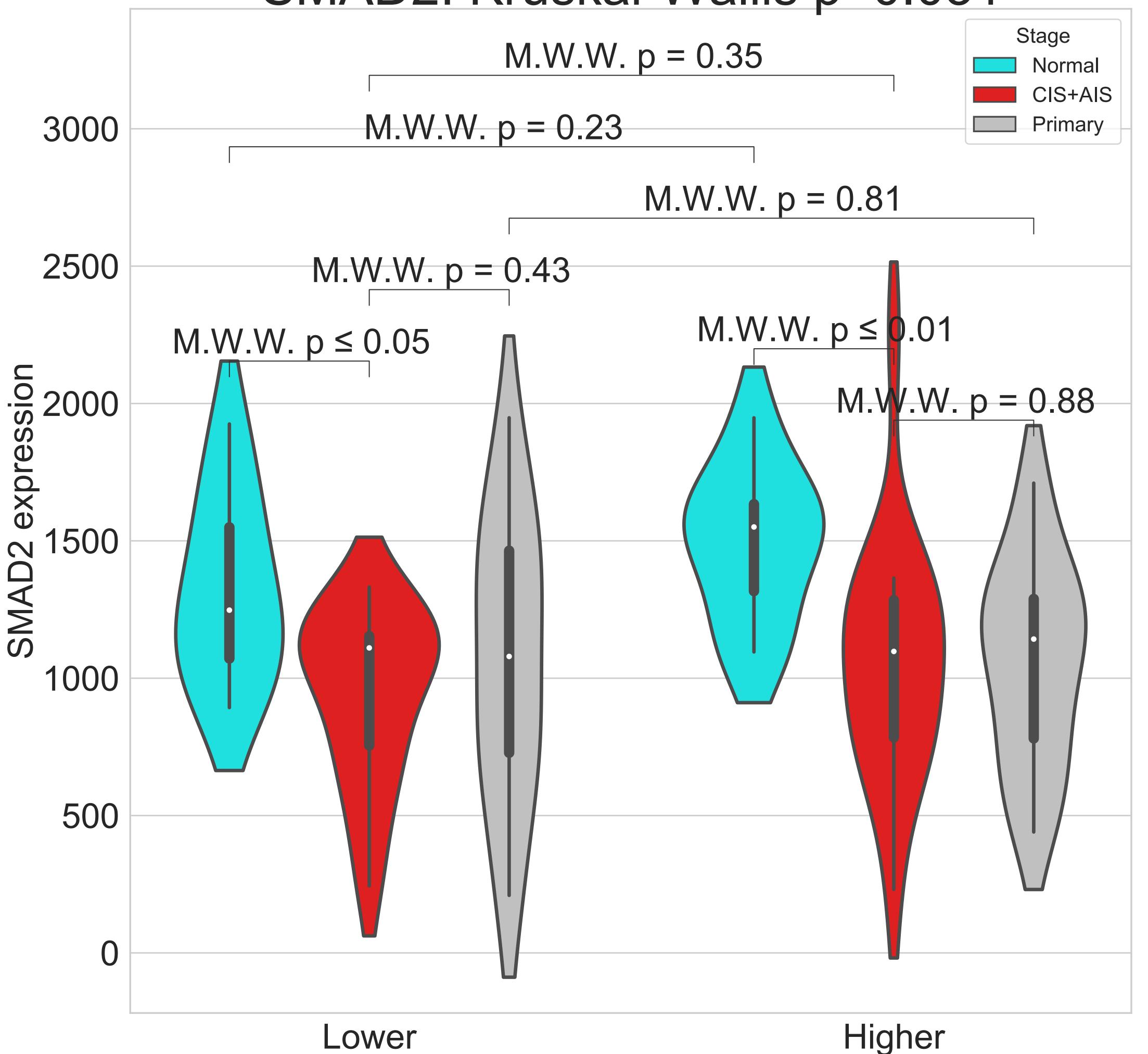
SMAD2: Kruskal-Wallis p=0.031



Mutation Shared Count (SYN)