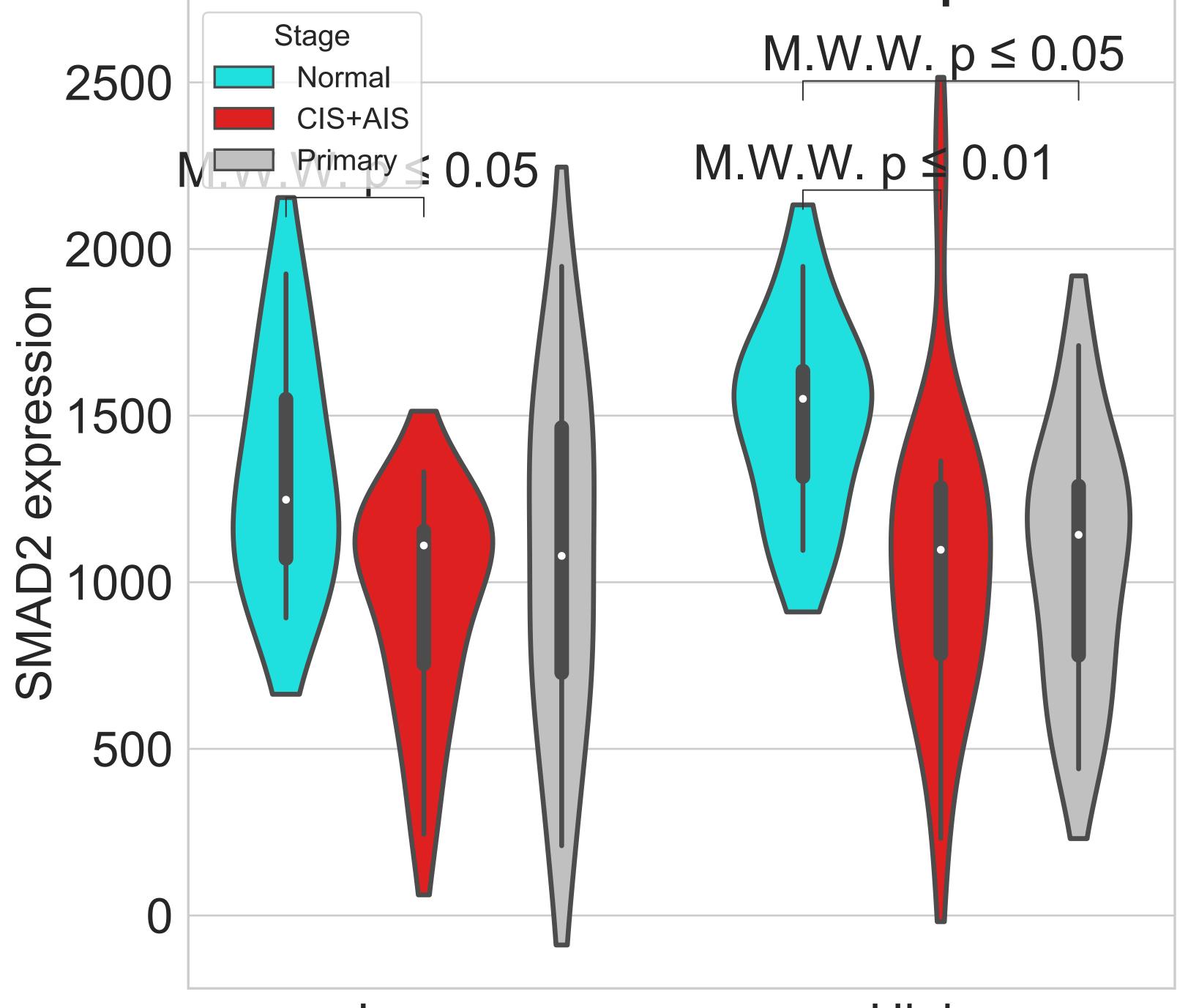
SMAD2: Kruskal-Wallis p=0.031



Lower
Mutation Shared Count (SYN)