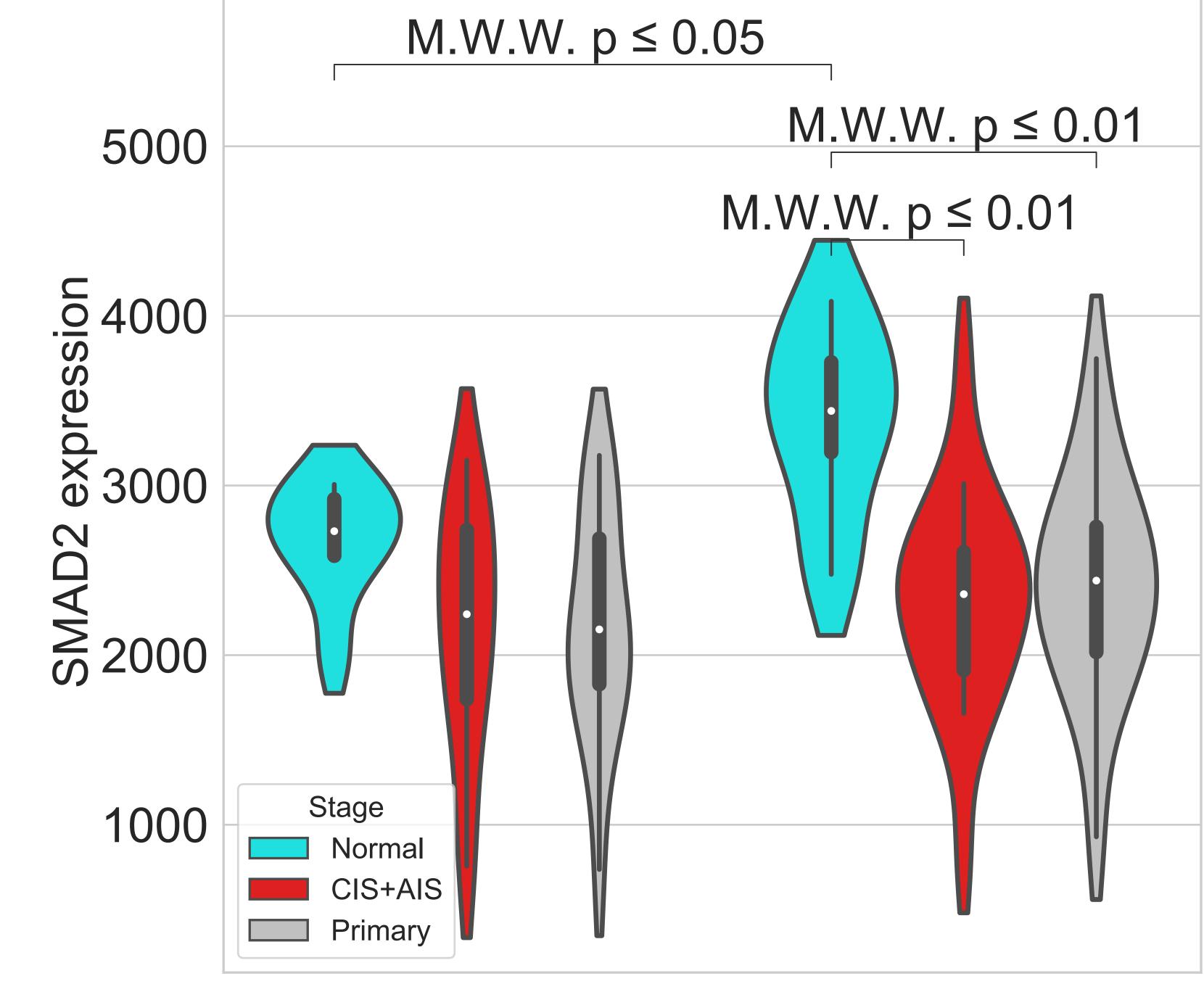
SMAD2: K.W. p=0.002 M.W.W. p ≤ 0.05



Lower Higher Mutation Shared Count per TMB