SMAD2: Kruskal-Wallis p=0.024 Stage M.W. p = 0.76Normal CIS+AIS M.W.W. p ≤ 0.05 Primary 3000 M.W.W. p = 0.84M.W.W. p ≤ 0.01 2500 M.W.W. p = 0.54M.W.W. p = 0.75M.W.W. p = 0.101000 500 Higher Lower

Mutation Shared Count (SYN) per TMB