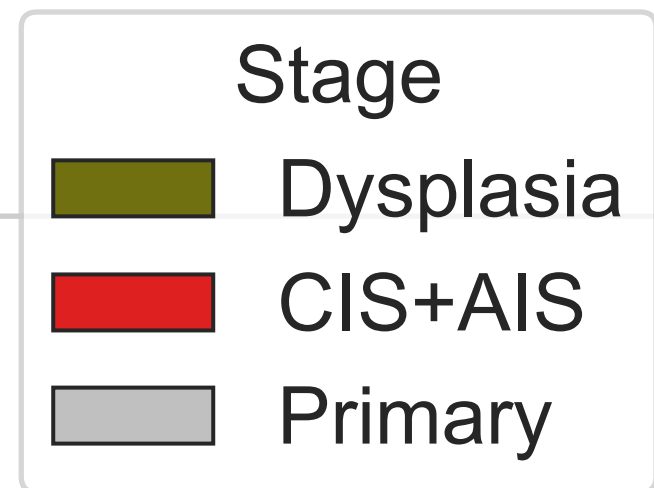


# Kruskal-Wallis $p=0.000$

Number of somatic CNV segment (count)



M.W.W.  $p \leq 0.01$

M.W.W.  $p \leq 0.05$

M.W.W.  $p \leq 0.05$

M.W.W.  $p \leq 0.001$

M.W.W.  $p \leq 0.001$

Lower Higher  
Mutation Shared Count (SYN)

