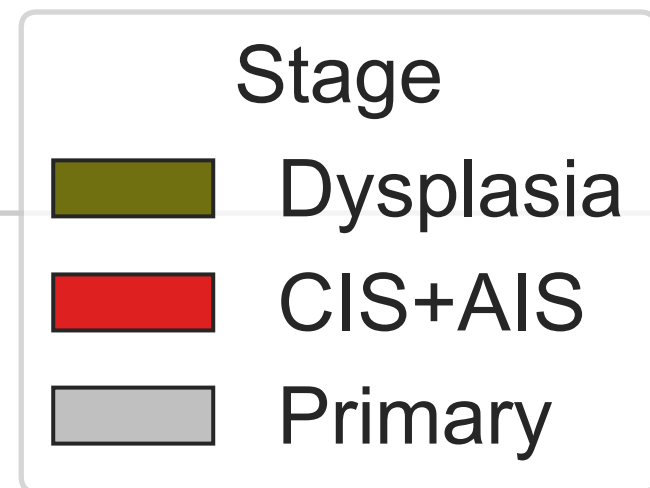


# Kruskal-Wallis p=0.000

Number of somatic CNV segment (count)



Lower Higher  
Mutation Shared Proportion (Union & SYN)

