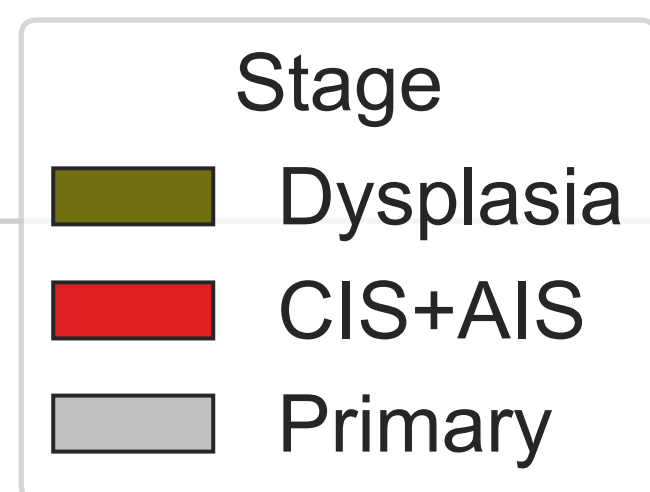


Kruskal-Wallis $p=0.000$

Number of somatic CNV segment (count)



Lower Higher
Mutation Shared Proportion (Union & SYN)

