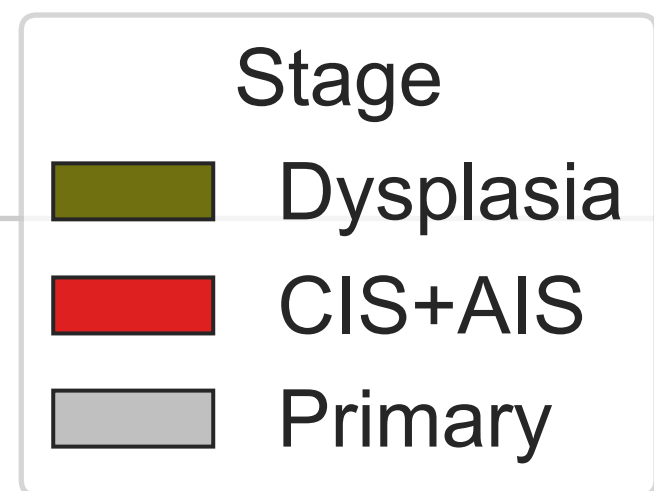


Kruskal-Wallis p=0.000

Number of somatic CNV segment (count)



100
80
60
40
20
0

*

*

Lower

Higher

Mutation Shared Count

