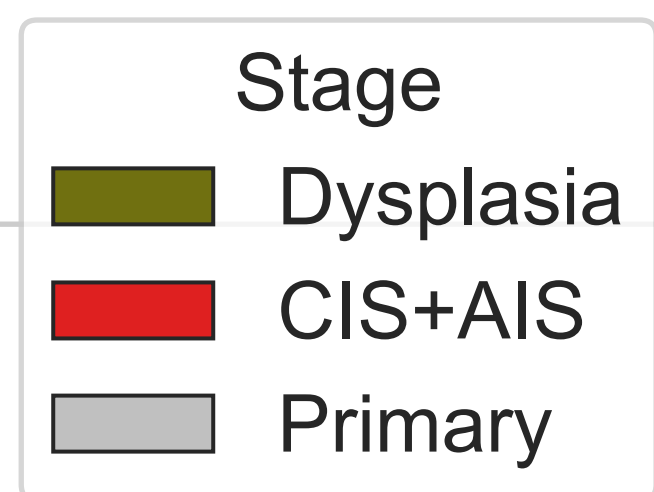


Kruskal-Wallis p=0.000

Number of somatic CNV segment (count)



100
80
60
40
20
0

**

*

Lower Higher
Mutation Shared Count (SYN)

