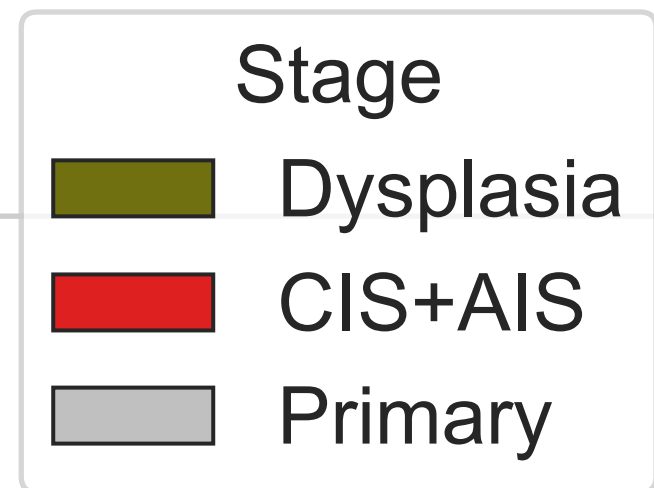


Kruskal-Wallis p=0.000

Number of somatic CNV segment (count)



**

*

100

80

60

40

20

0

*

Lower

Higher

Mutation Shared Count (SYN)

