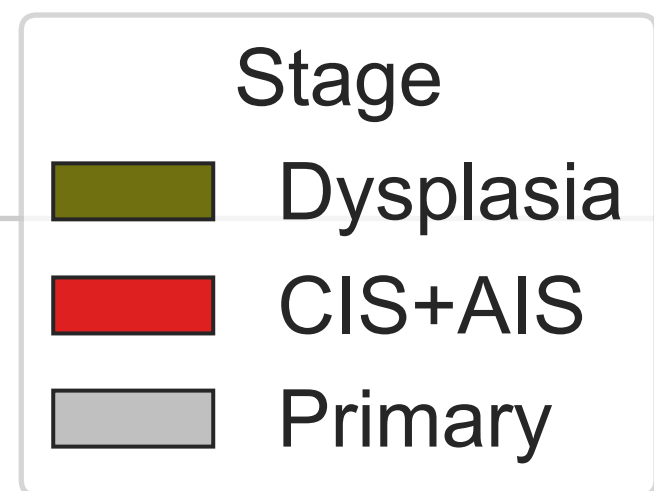


Kruskal-Wallis p=0.000

Number of somatic CNV segment (count)



100  
80  
60  
40  
20  
0

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\*

\*\*\*

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Lower

Higher

Mutation Shared Count

