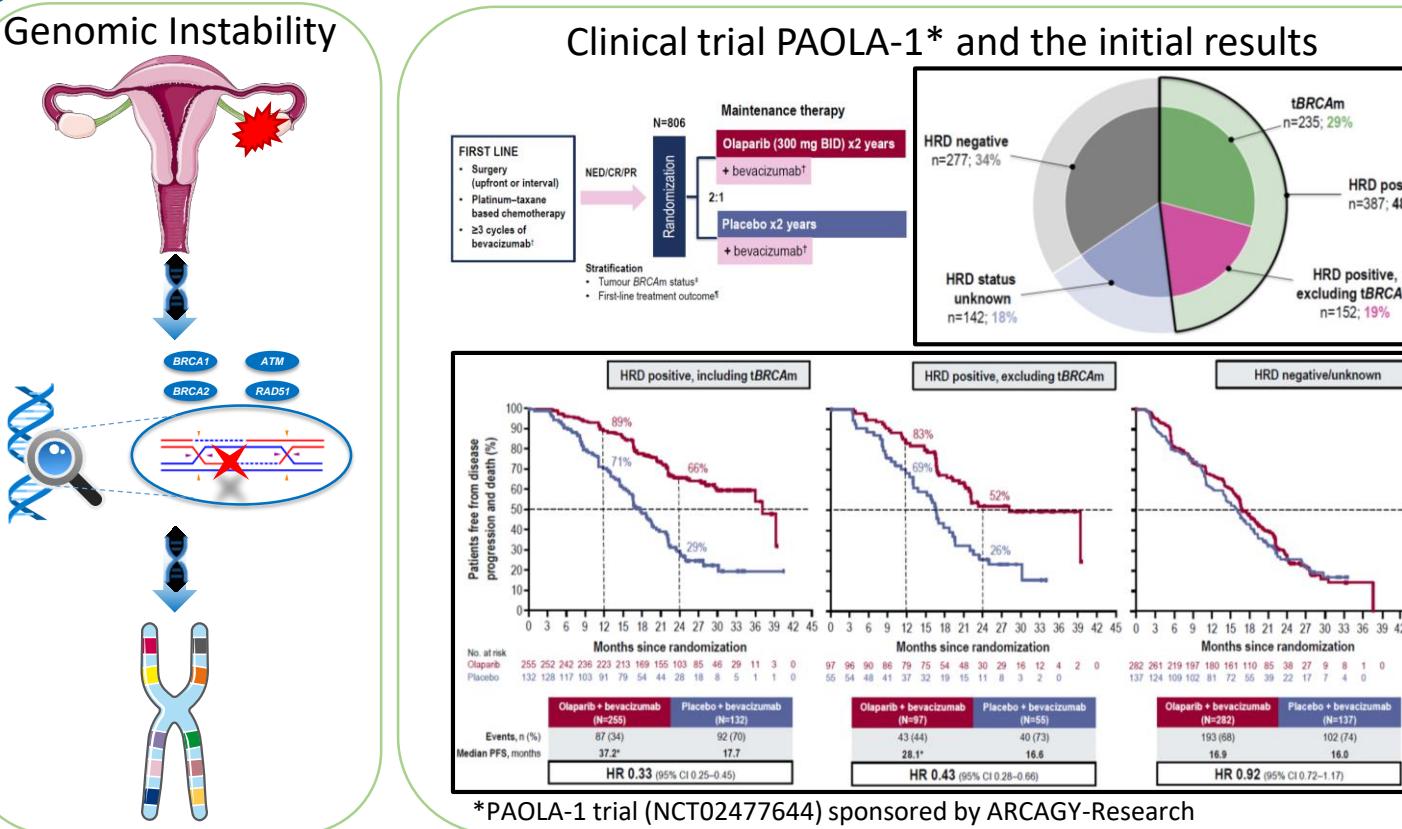


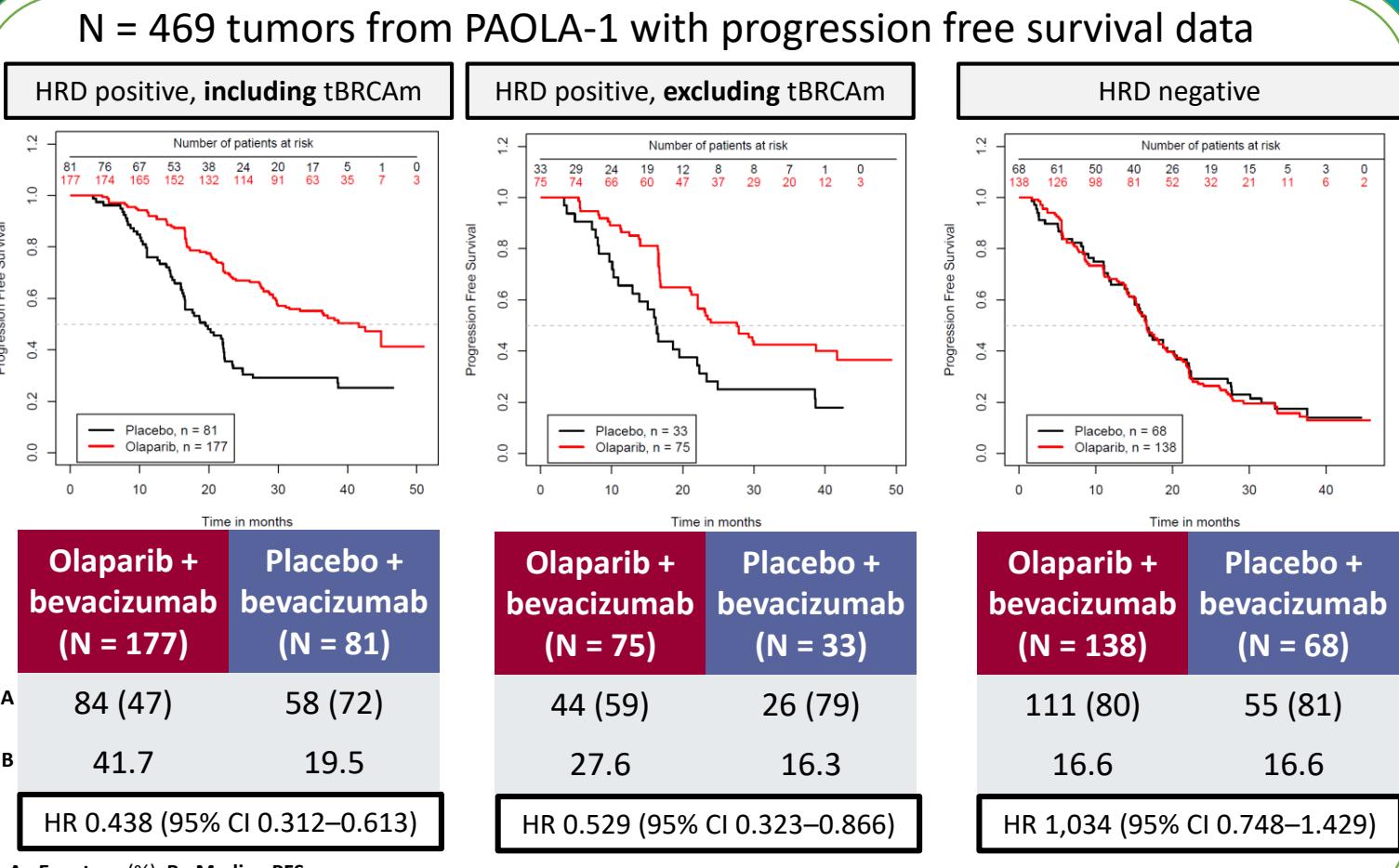
# Development of a genomic instability score for ovarian cancers from a limited panel of genes.

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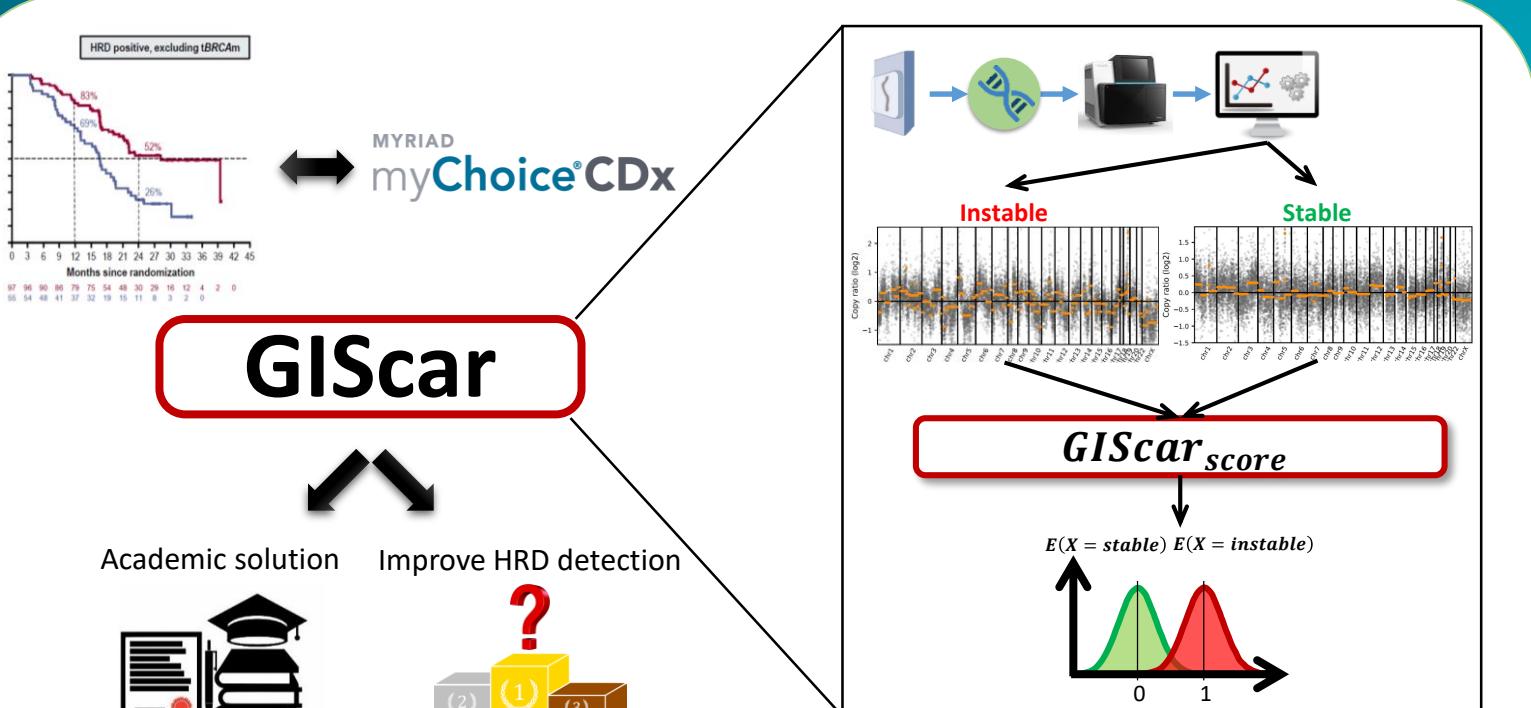
## Introduction



## Clinical Validation



## GIScar Genomic Instability Scar



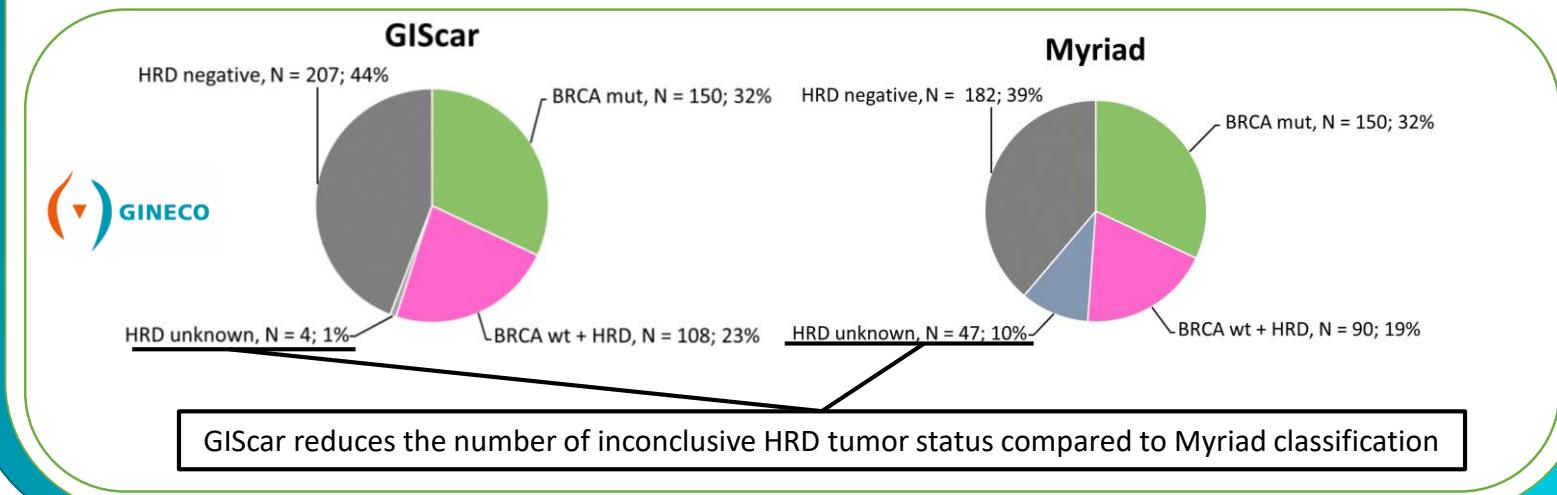
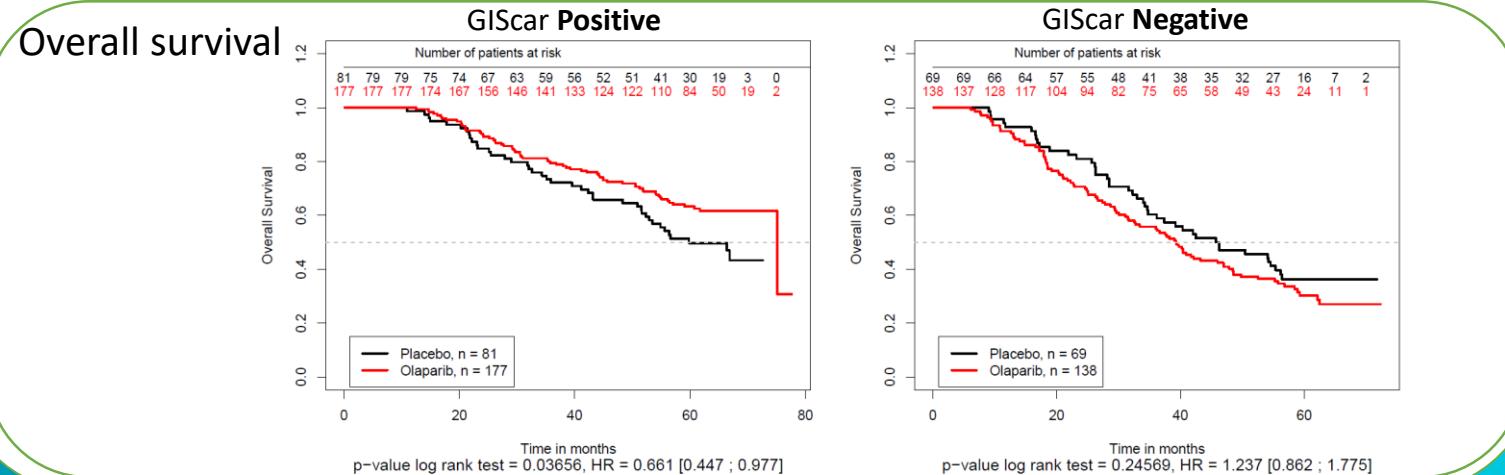
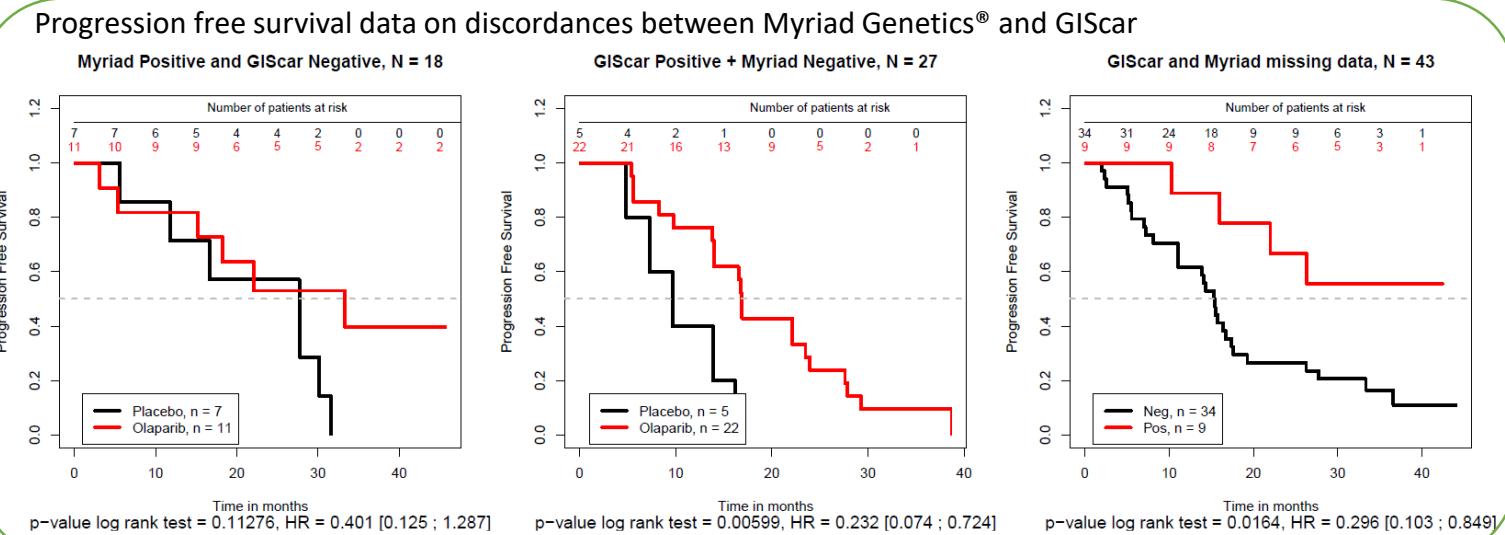
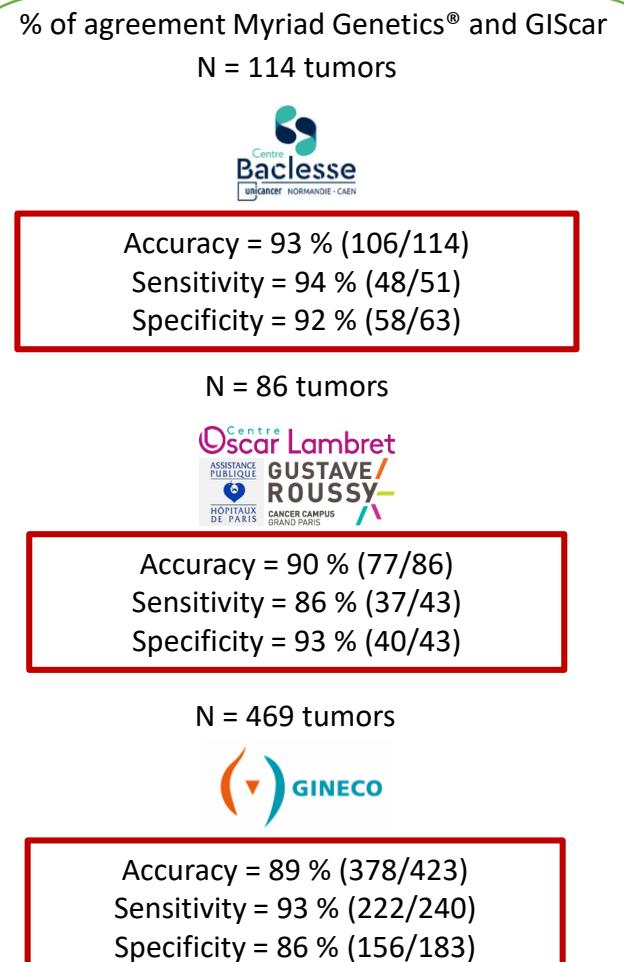
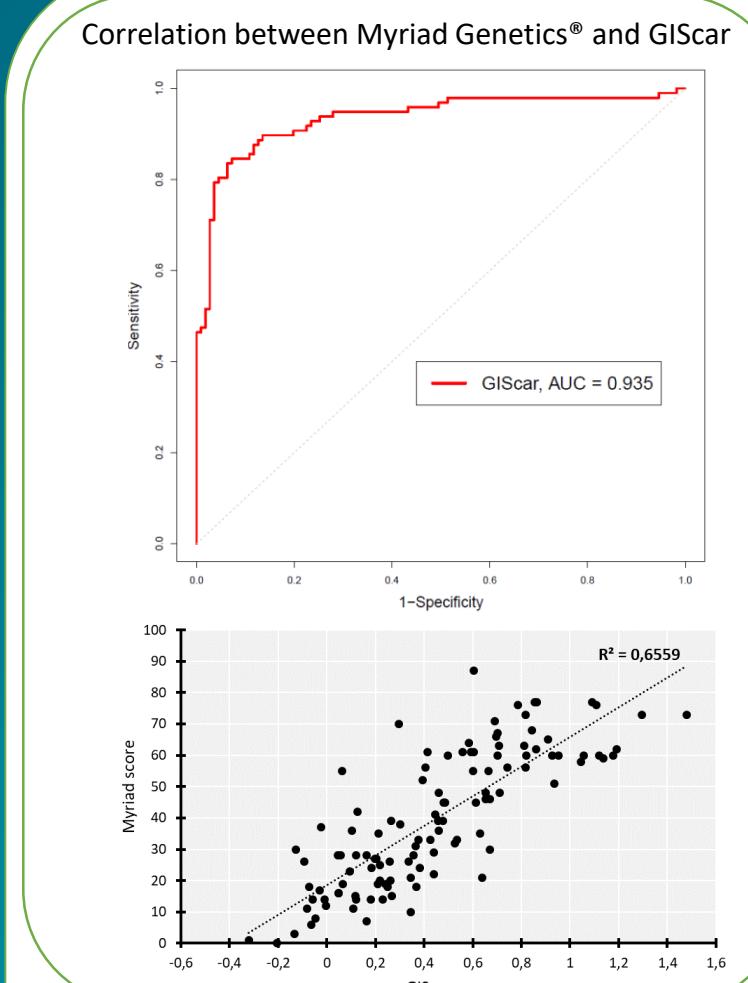
## Tumor collections

Internal recruitment, N = 144 to adjust the model to Myriad results (30 missing data from Myriad)

External recruitment, N = 86 to assay the robustness of GIScar in other laboratories

Samples from PAOLA-1, N = 469 to validate the predictions of GIScar on Olaparib answer

## Technical validation



## Conclusions

- GIScar allows in one experiment the identification of BRCA variants and HRD score computation
- The tumor classification by GIScar is correlated to olaparib efficacy assessed by PFS
- We reduce by more than 90 % (4 versus 47) the number of inconclusive cases

## Acknowledgments

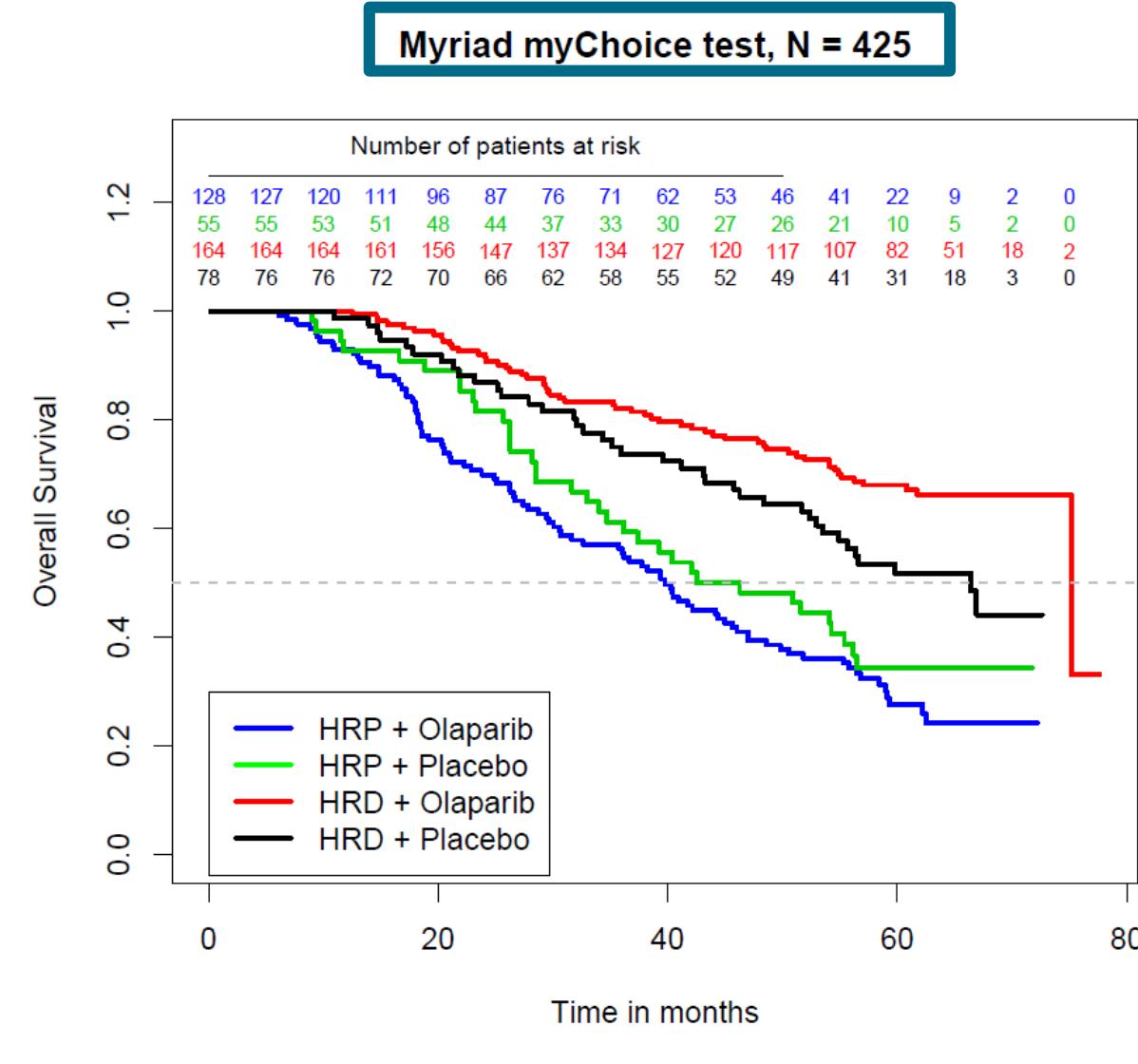
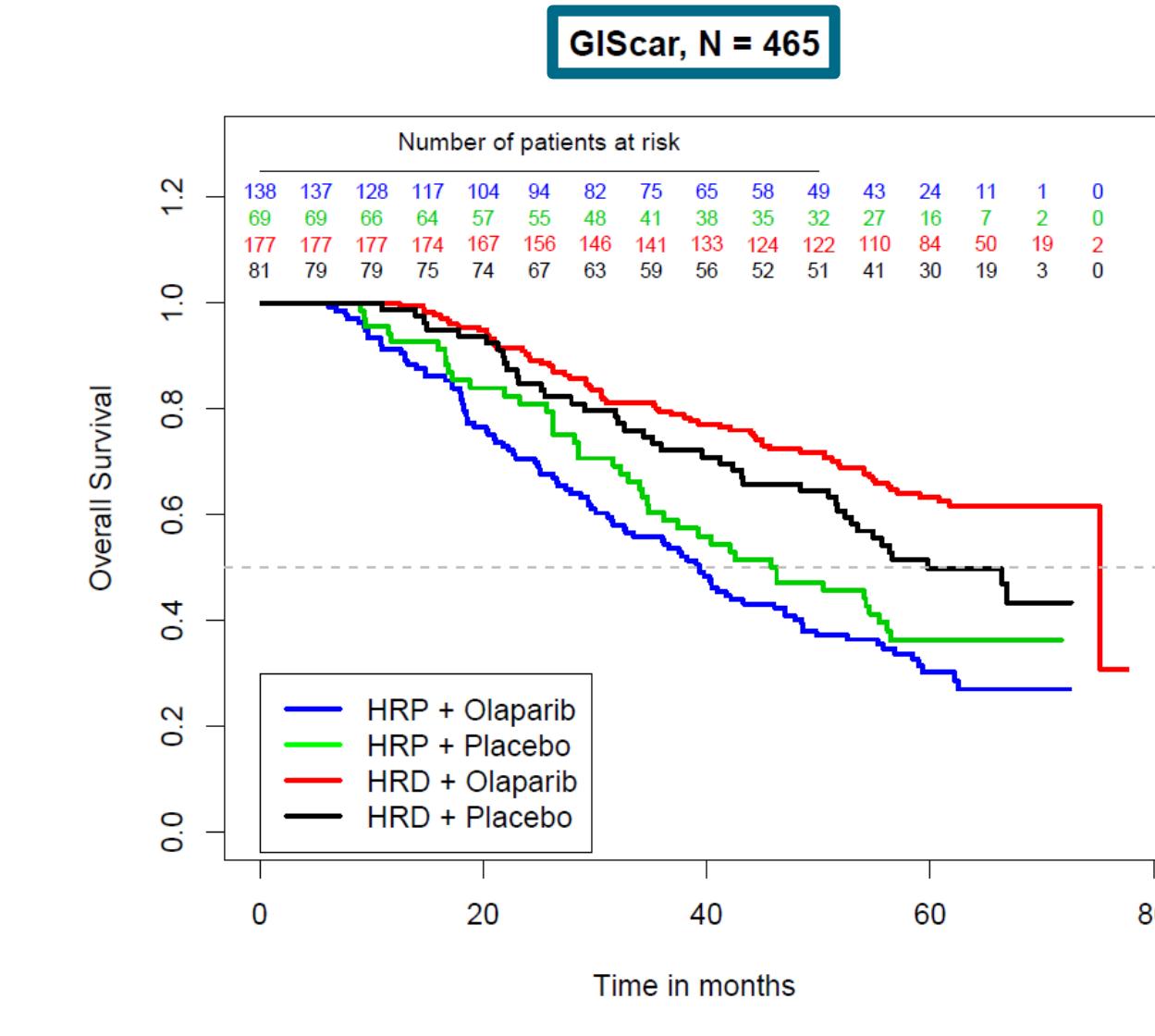
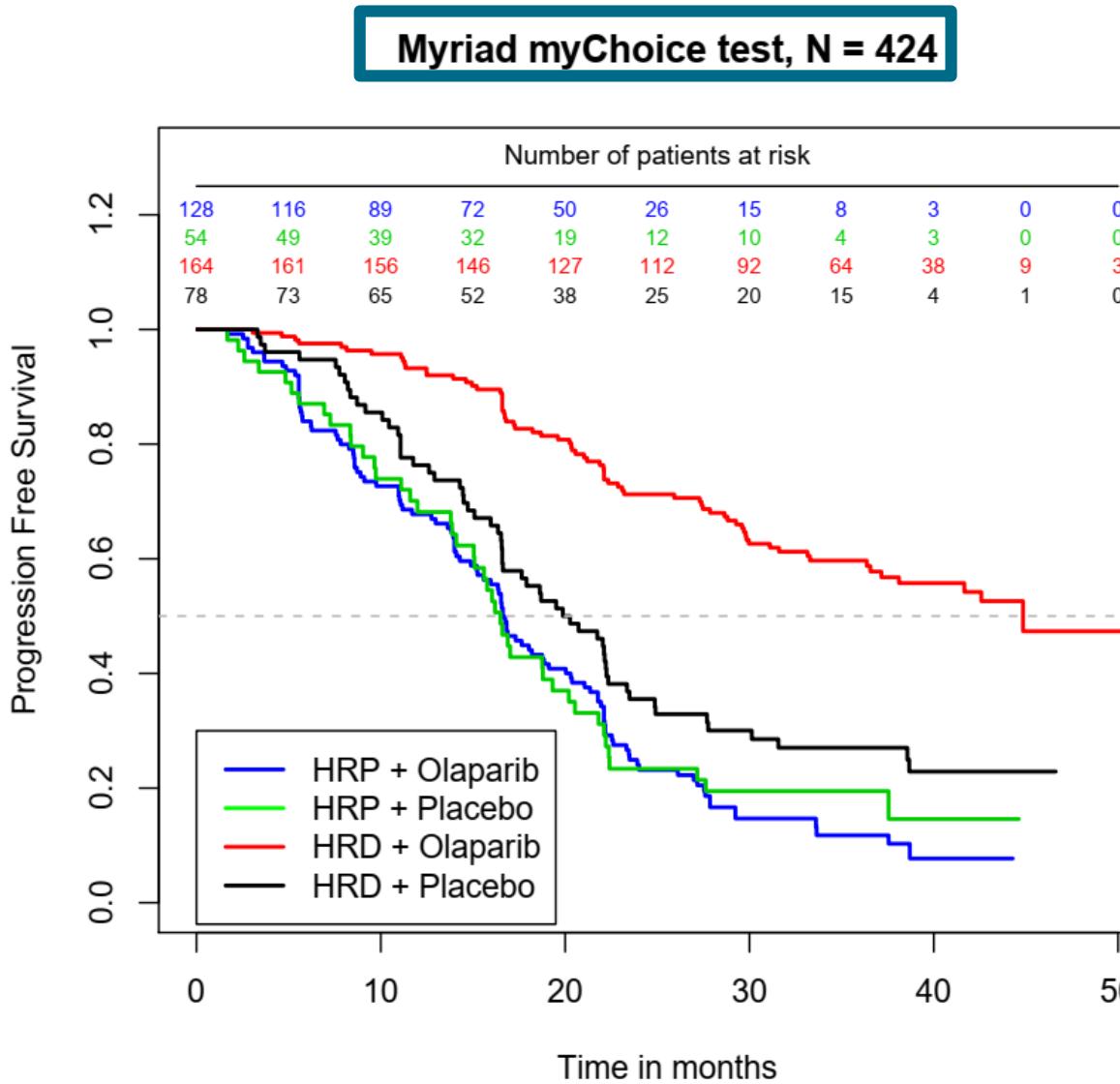
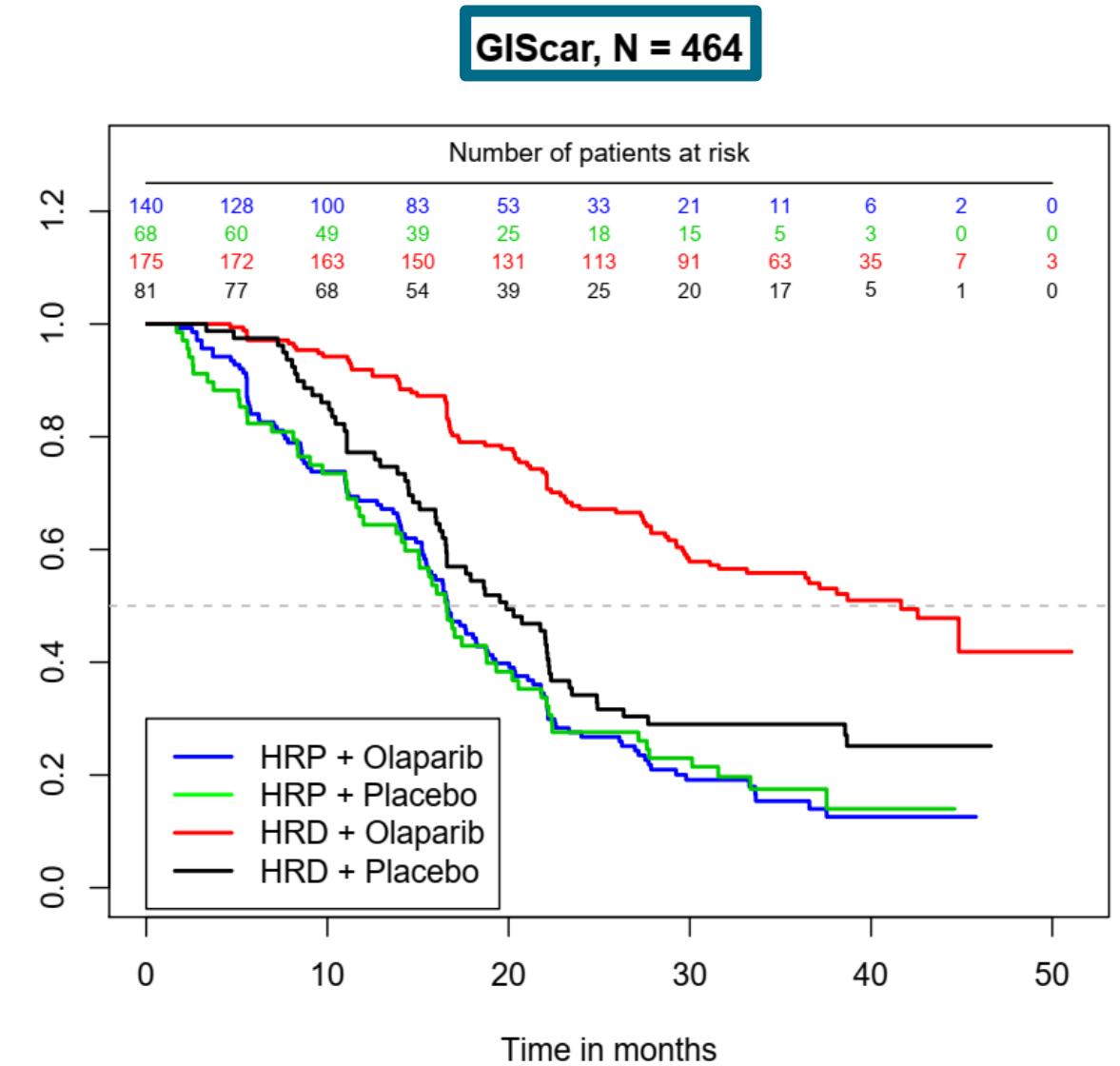
- Thanks to all the patients and their families, investigators, CRA and pathologists of each sites. Thanks to ARCAGY GINECO Central laboratory and Translational Research Team that allowed this research

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## Survival data on PAOLA-1 data, N = 469

Progression Free survival

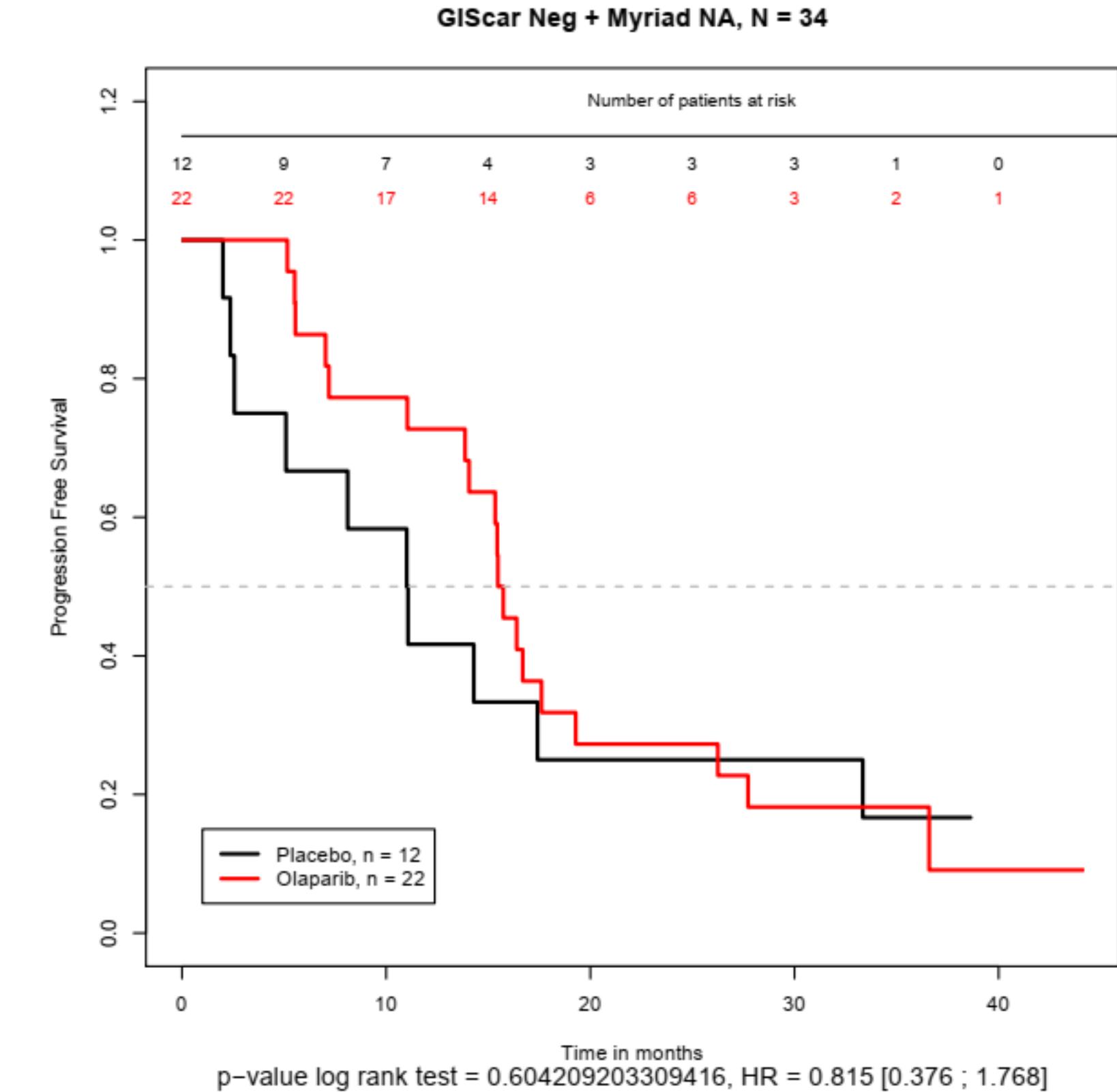
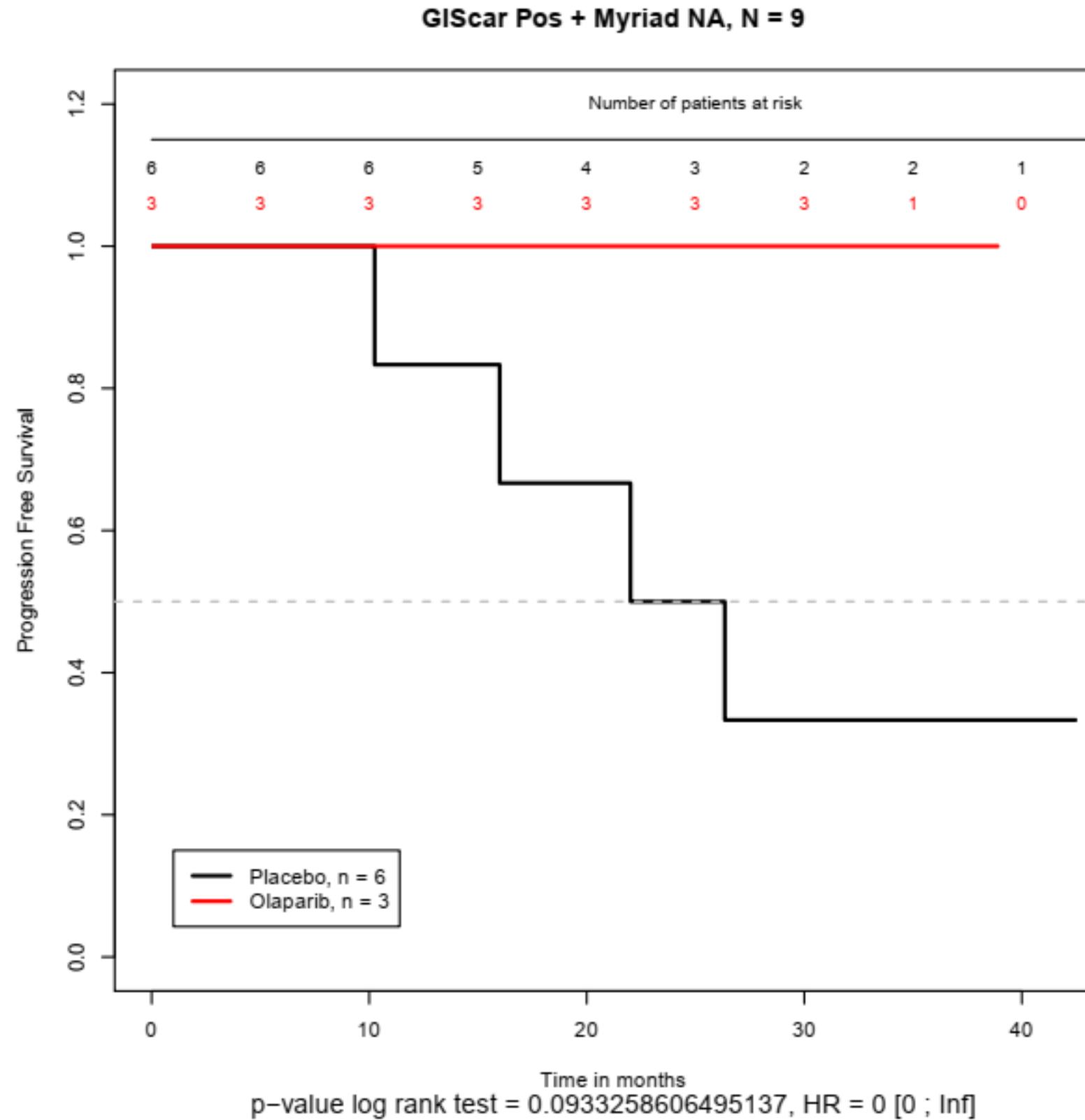
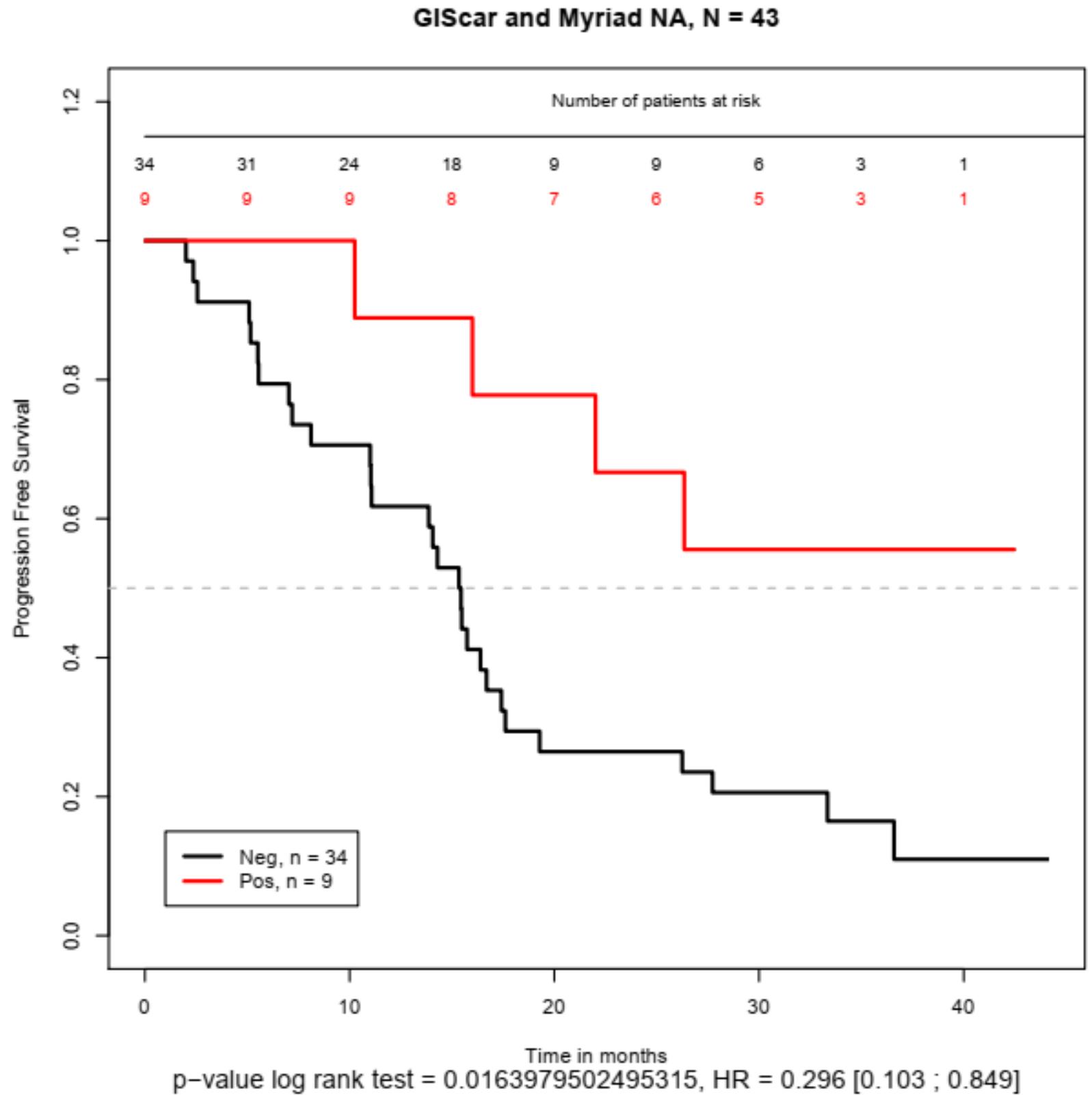


Abstract N° 935

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## GIScar on Myriad missing data (N = 43)

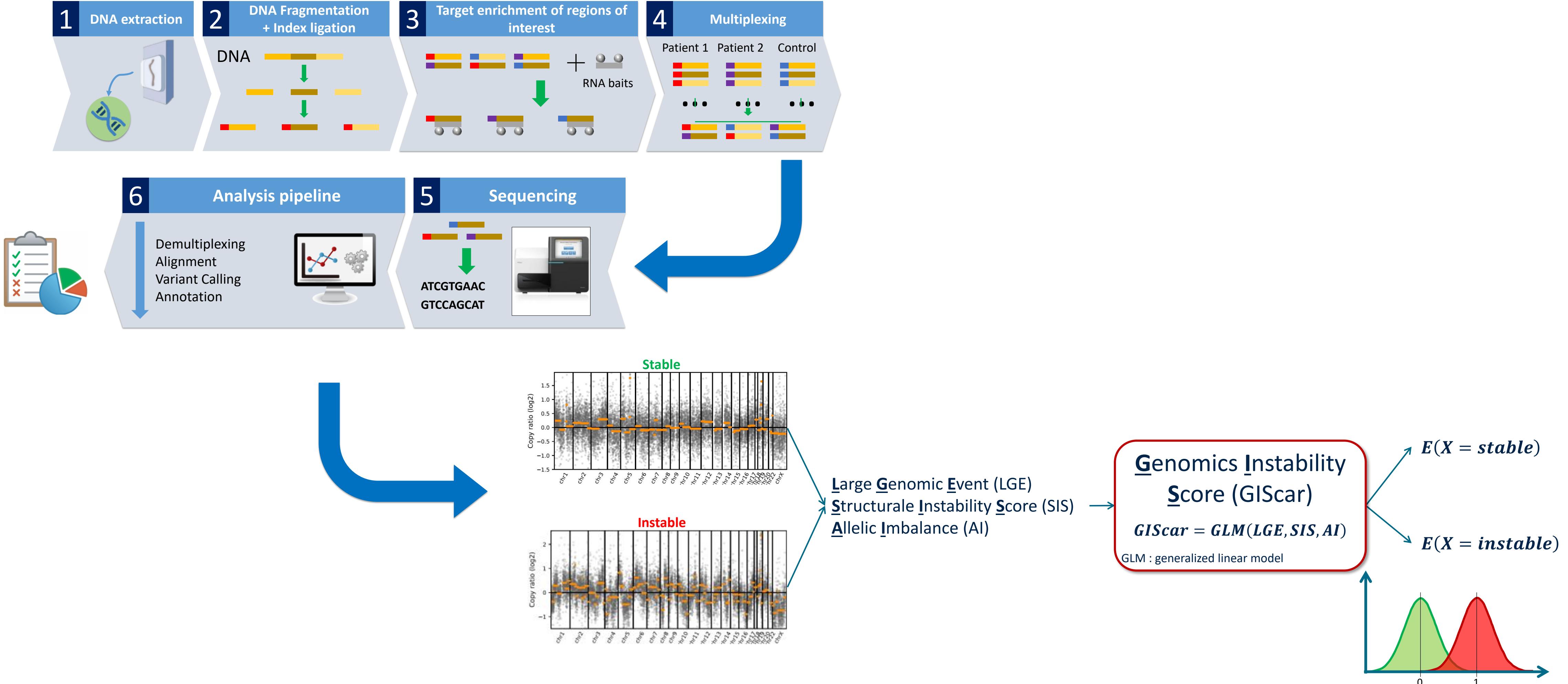


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## GIScar workflow



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Mercè GUZMAN-VENDRELL



## La Pitié

Florence Coulet

## ICO

Alain Morel