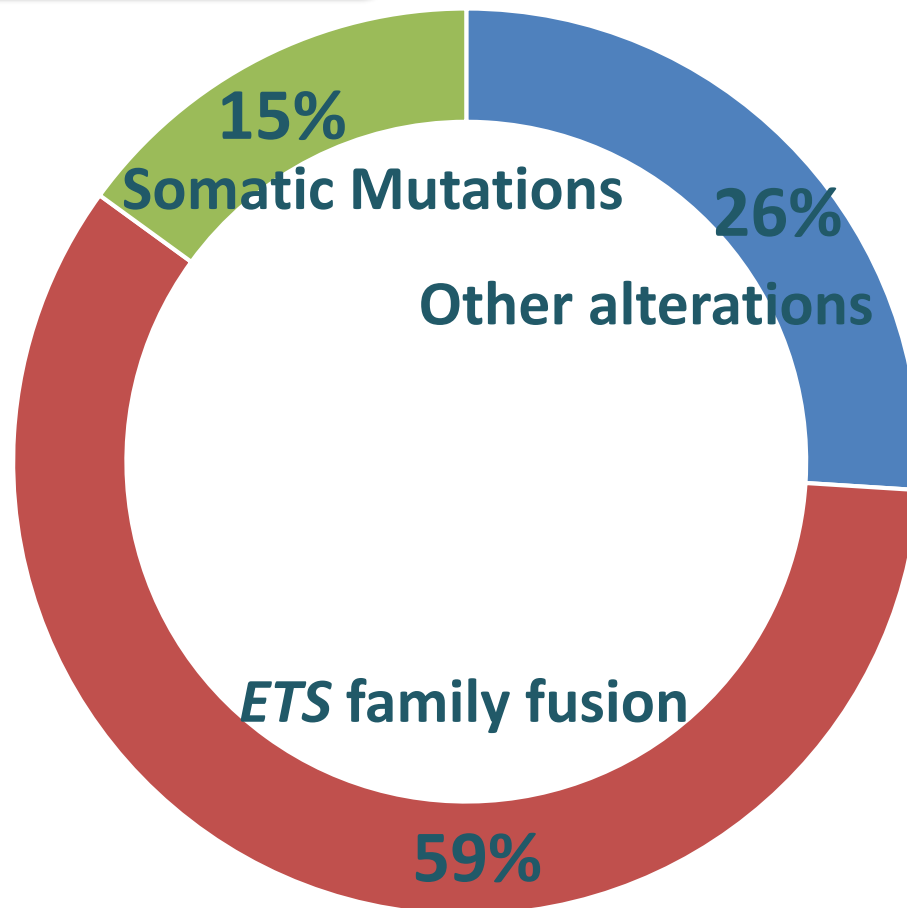


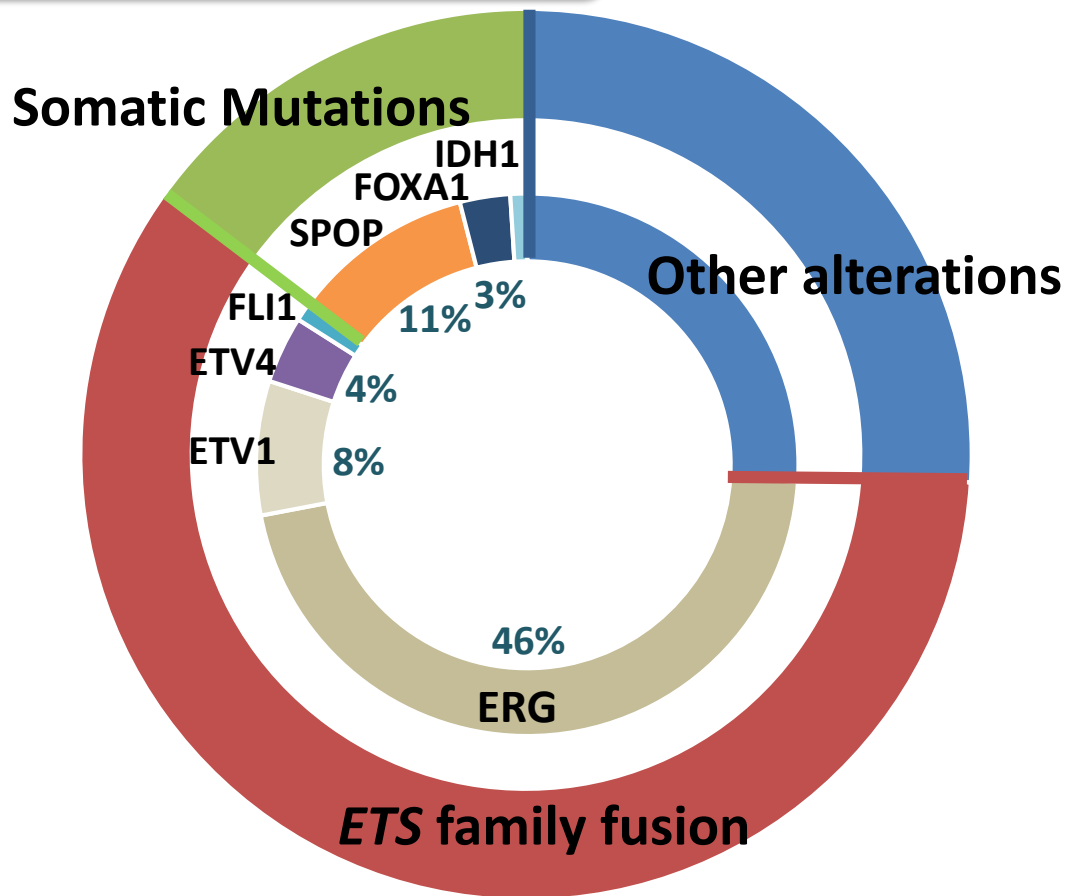
***SPOP* and *FOXA1* alterations in prostate cancer. Relationship with *ERG* overexpression and grade group classification**

**Silvia Hernández-Llodrà, CEXS – Universitat Pompeu Fabra
Urological Cancer Research Group – FIMIM, Parc de Salut-Mar
Barcelona**

Prostate cancer: Two pathways

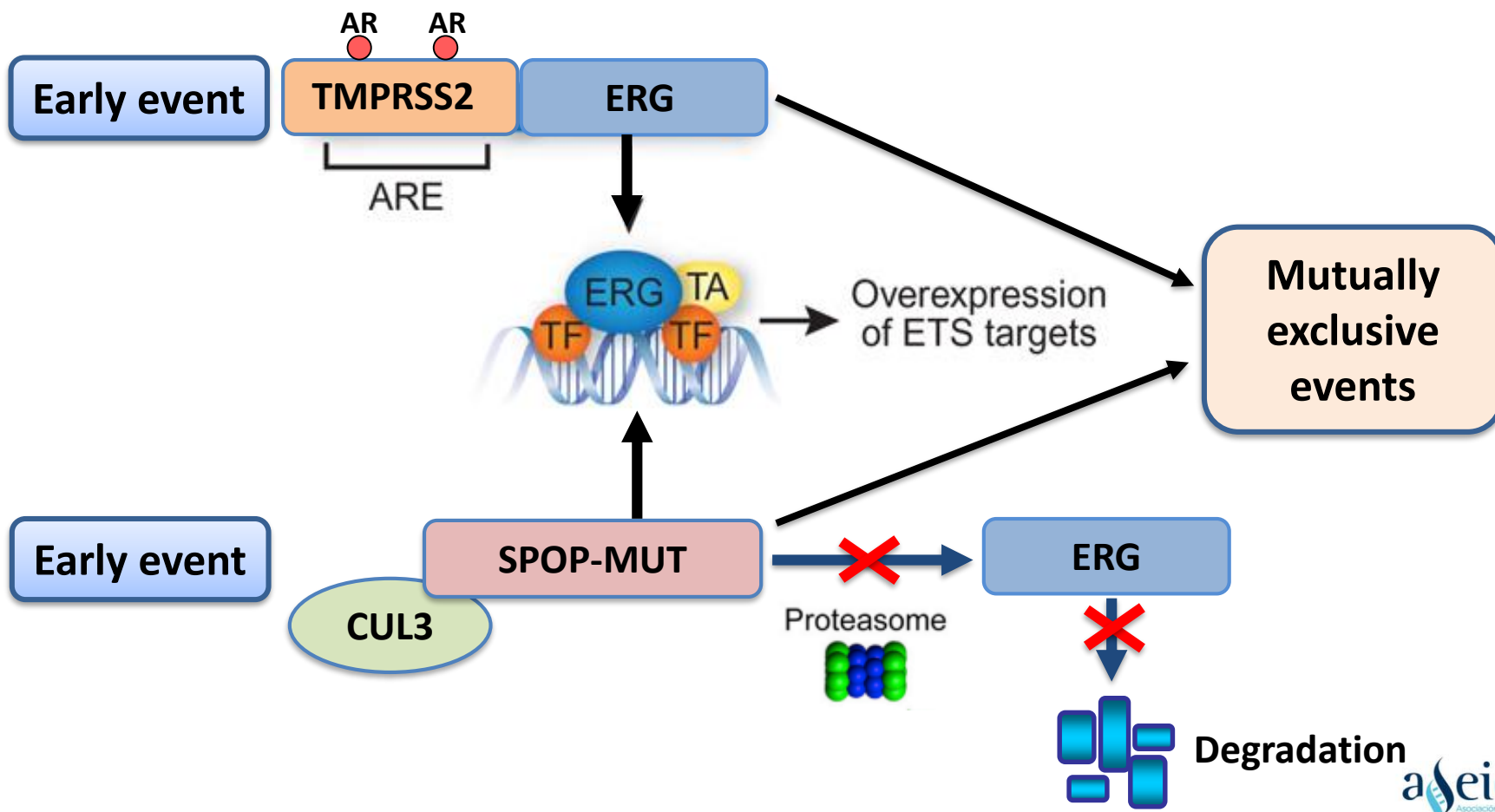


The Cancer Genome Atlas (TCGA) 2015



■ OTHER ALTERATIONS ■ ETS FUSIONS ■ MUTATIONS

Prostate cancer: *ERG* rearrangements or *SPOP* mutations



Objectives

To analyze the prevalence of *SPOP*, *FOXA1* and *IDH1* alterations in PrCa, and to determine the relationship of these alterations with *ERG* status, and with the different clinical and pathological variables.

Material and Methods

Tumor samples and patients

Parc de Salut MAR-MarBiobank

Frozen prostate tumors = 111
non-tumor prostate samples = 3

WHO-ISUP (2016)

GG1= 28

GG2= 34

GG3= 21

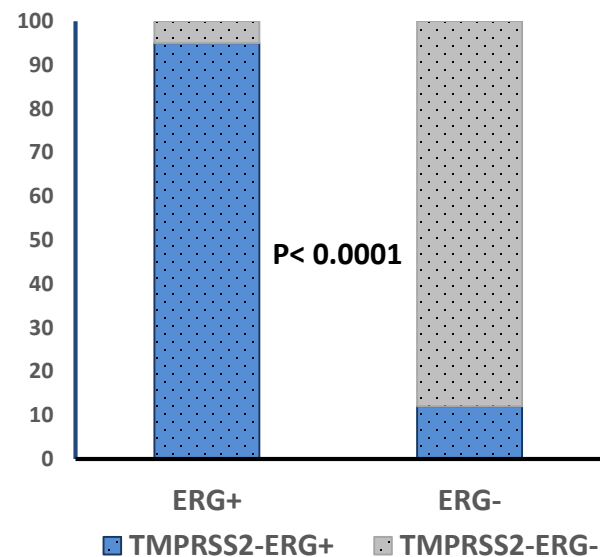
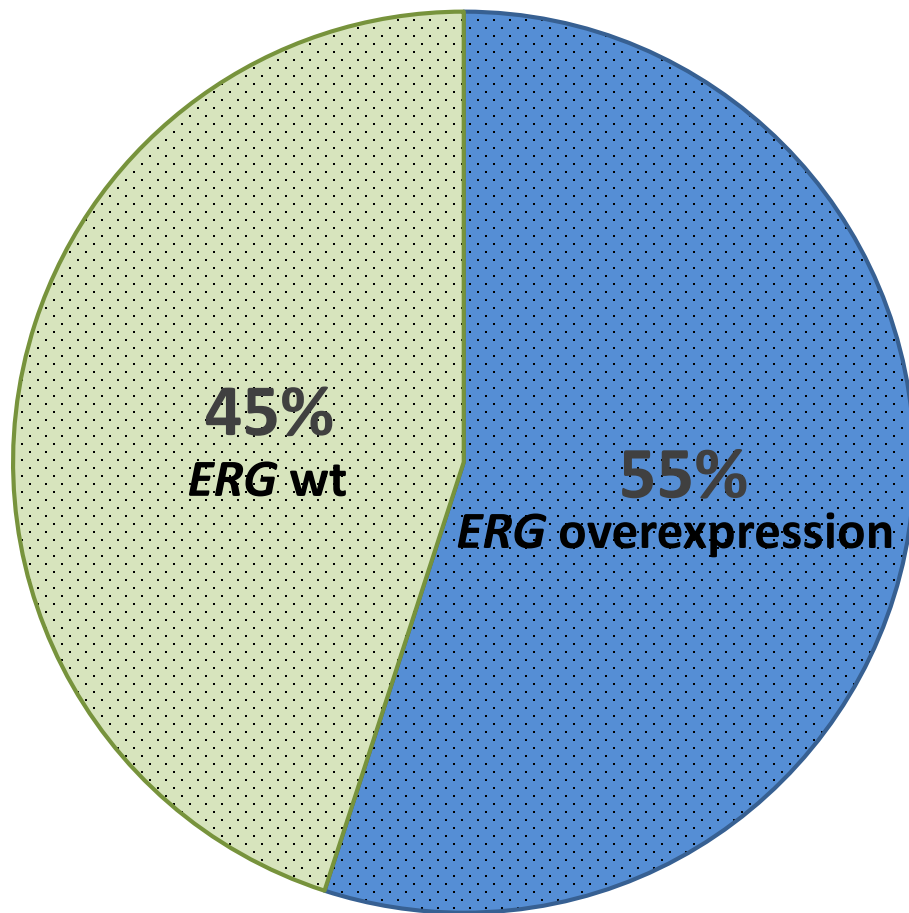
GG4= 17

GG5= 11

Methods

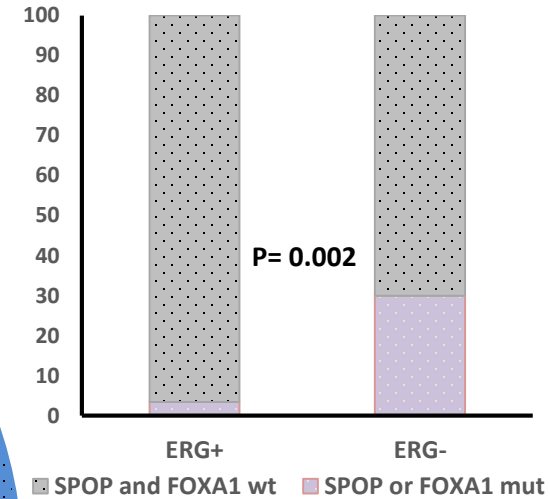
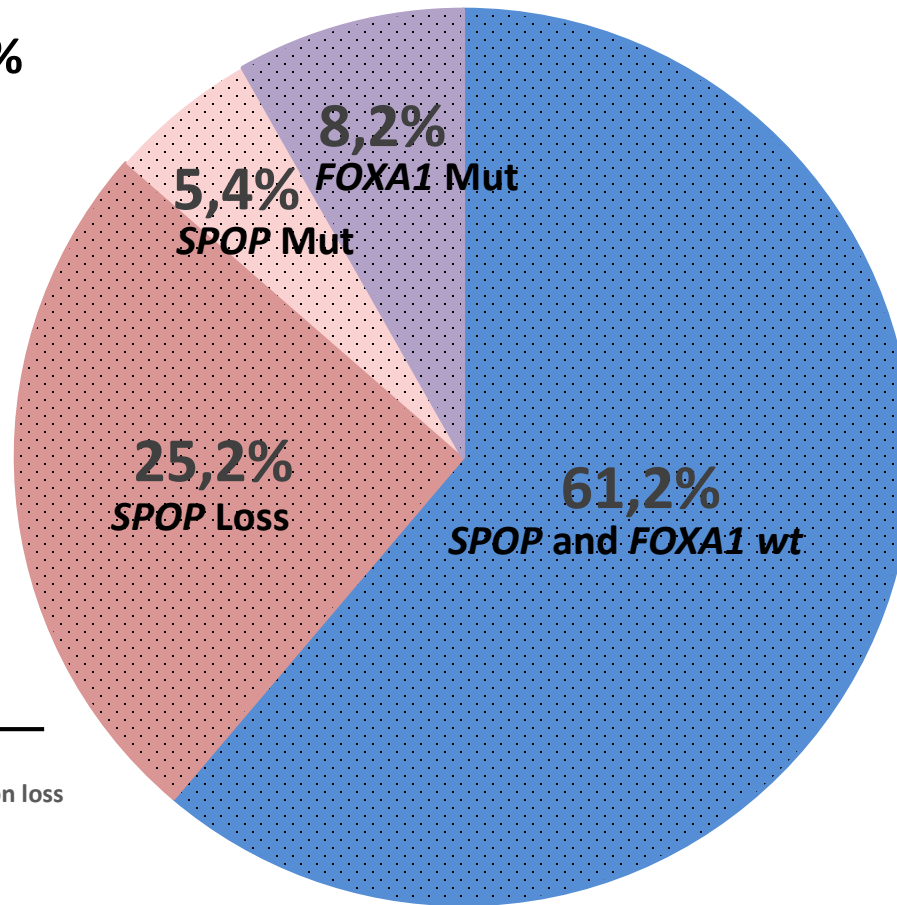
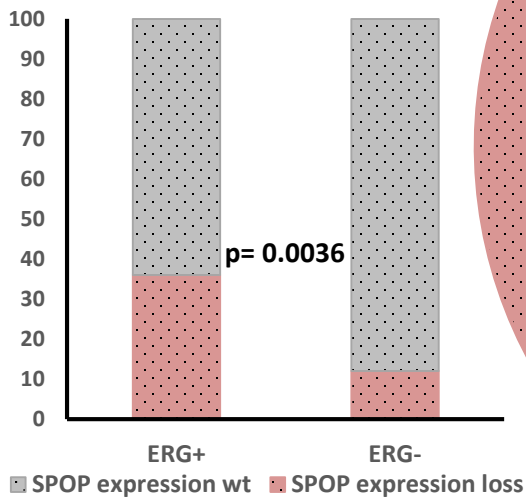
- RNA extraction and RT
- *TMPRSS2-ERG*, *ERG*, *SPOP* qPCR (TaqMan[®] Gene Expression Assays)
- *GADPH* as internal control
- *SPOP*, *FOXA1* and *IDH1* mutational analysis
- Kaplan-Meier test

***TMPRSS2-ERG* and *ERG* overexpression in prostate cancer**

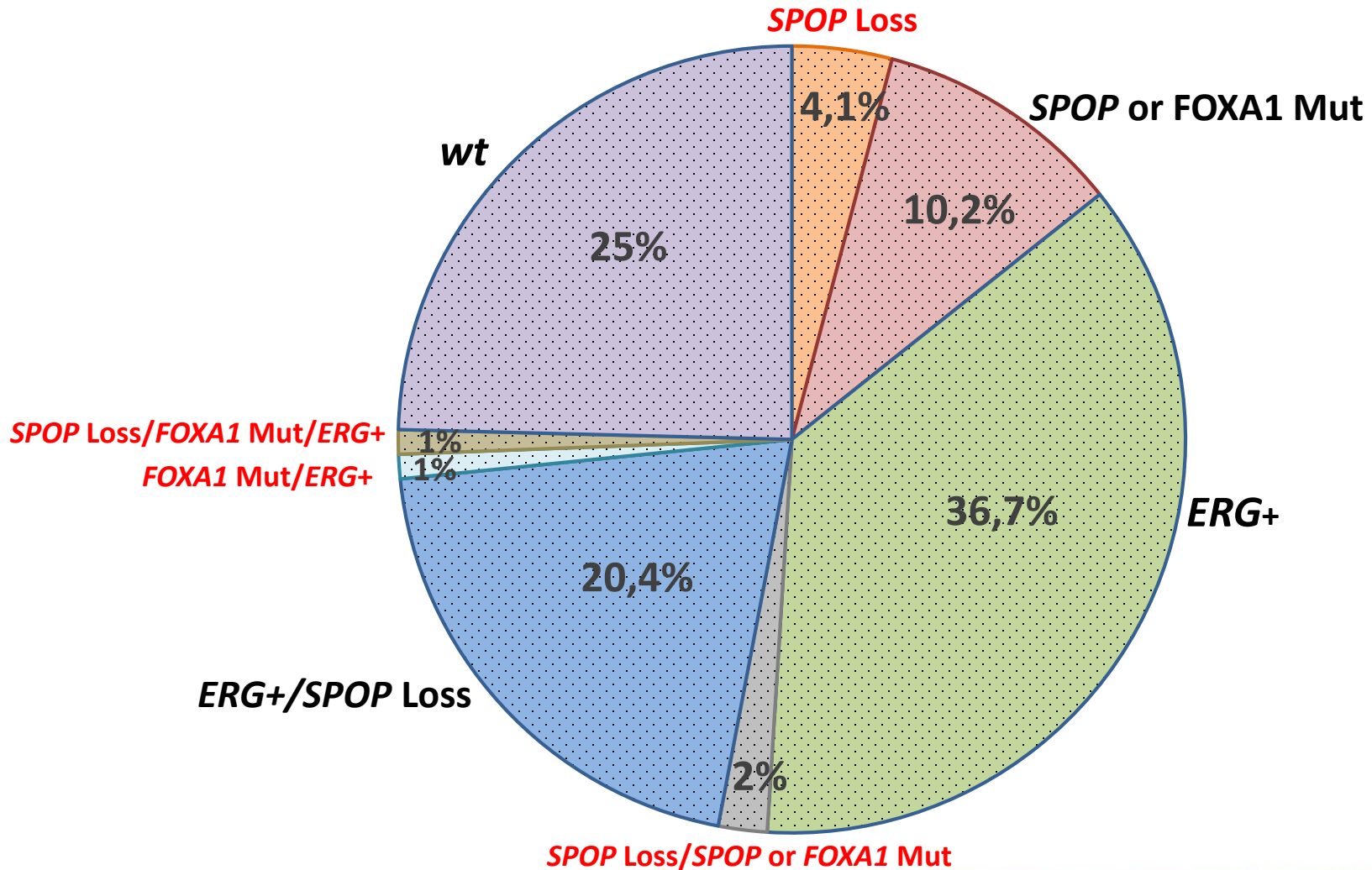


SPOP and FOXA1 alterations in prostate cancer

IDH1 mut 0%

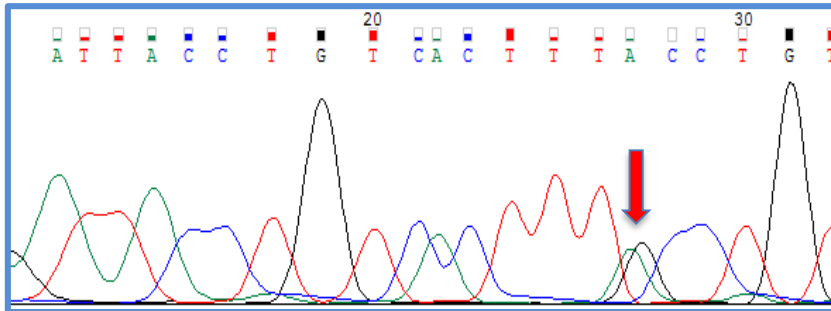


Different combinations of *SPOP*, *FOXA1* and *ERG* alterations in prostate cancer

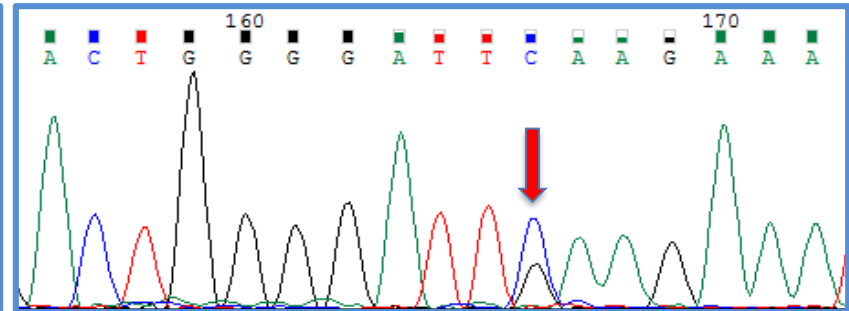


SPOP and FOXA1 mutations examples

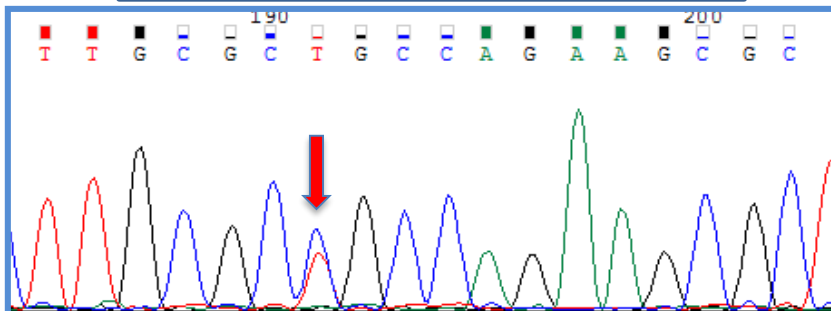
#Case 181
SPOP (A>G) Y87C



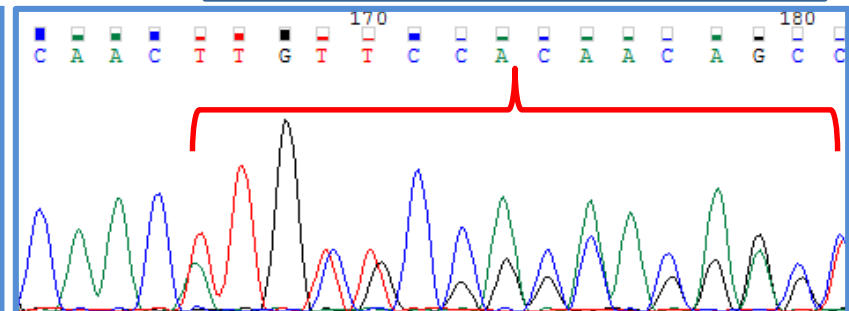
#Case 183
SPOP (C>G) F133L



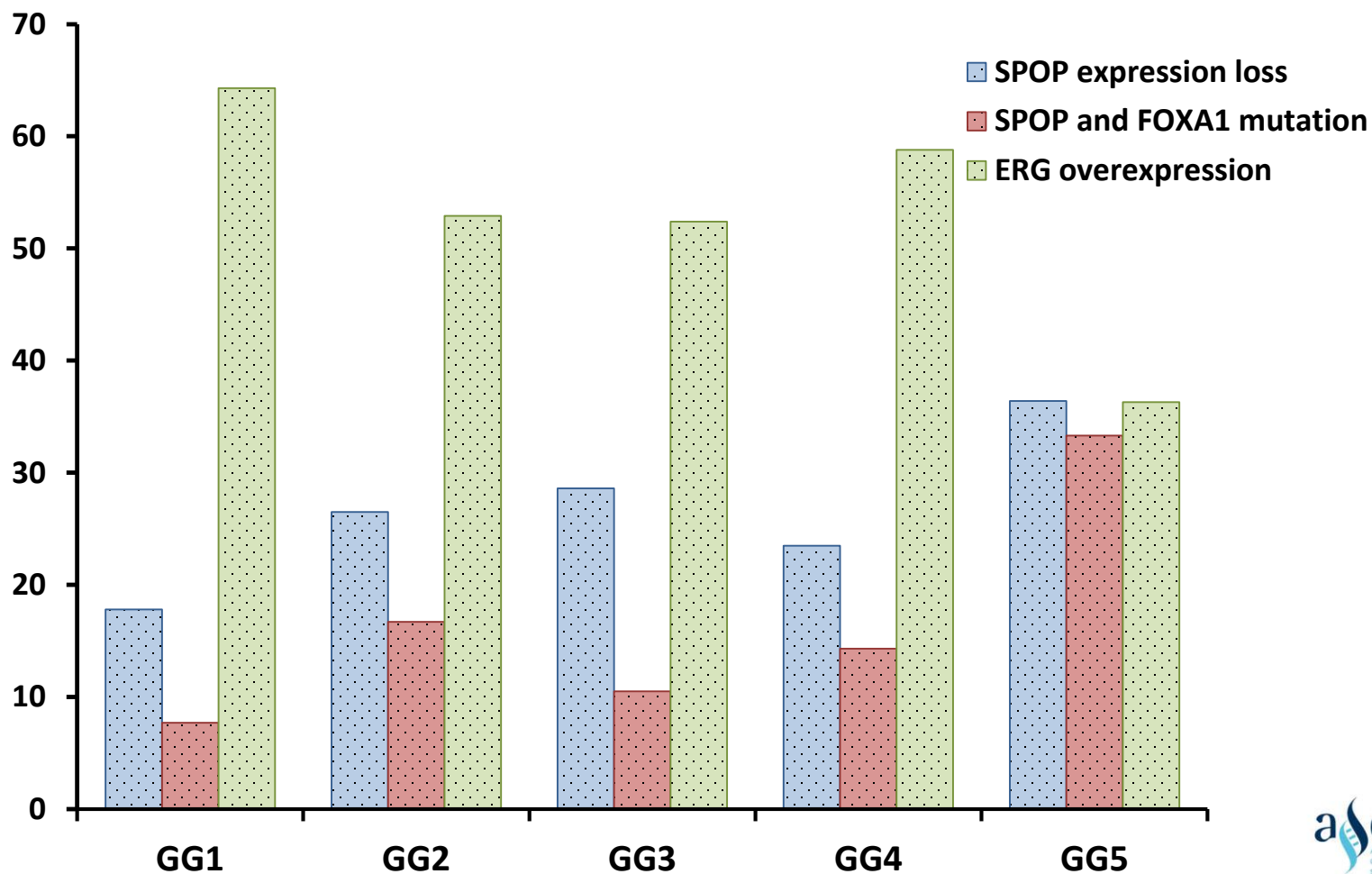
#Case 192
FOXA1 (C>T) R262C



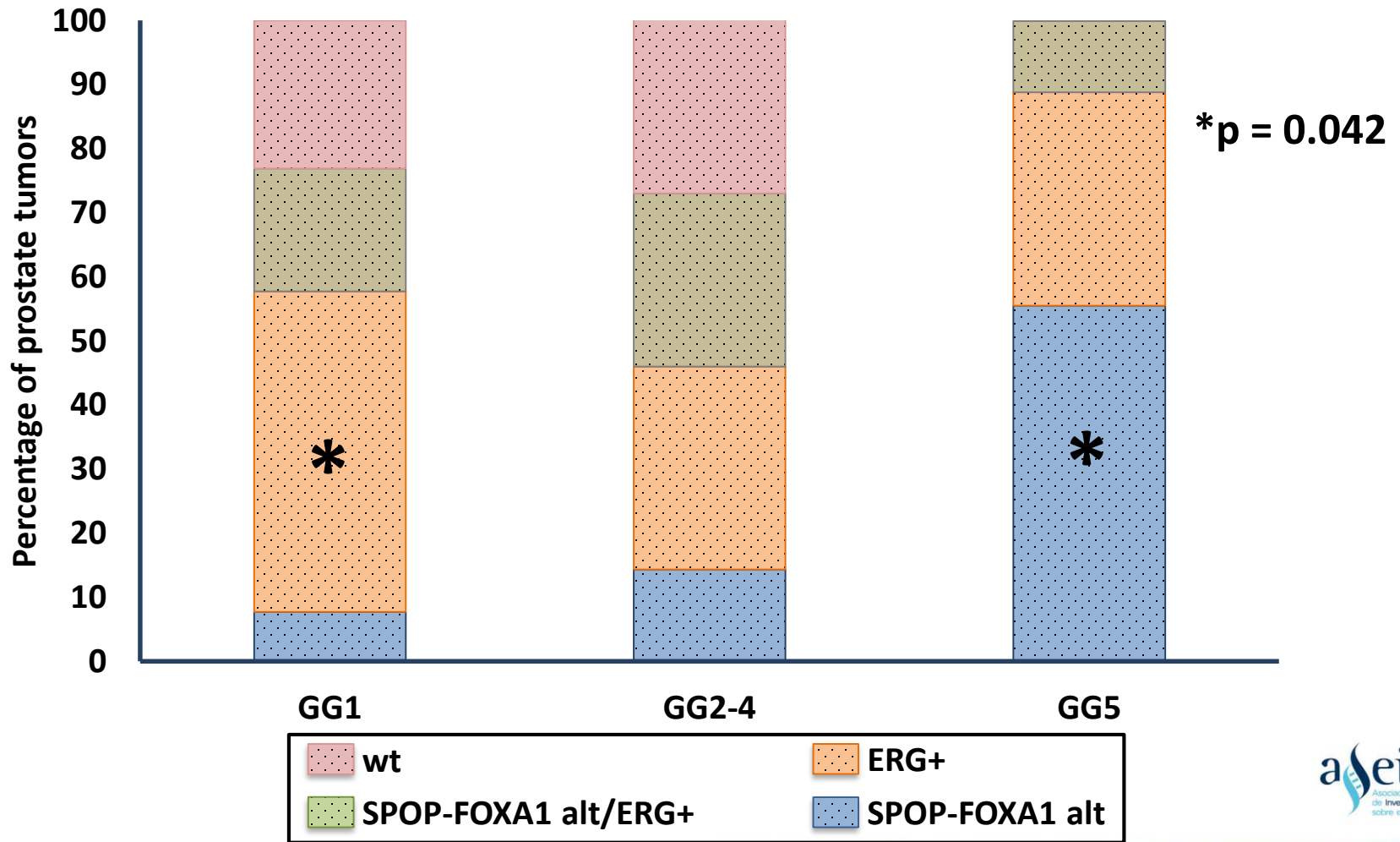
#Case 12
FOXA1 (ins/del) M253_R261



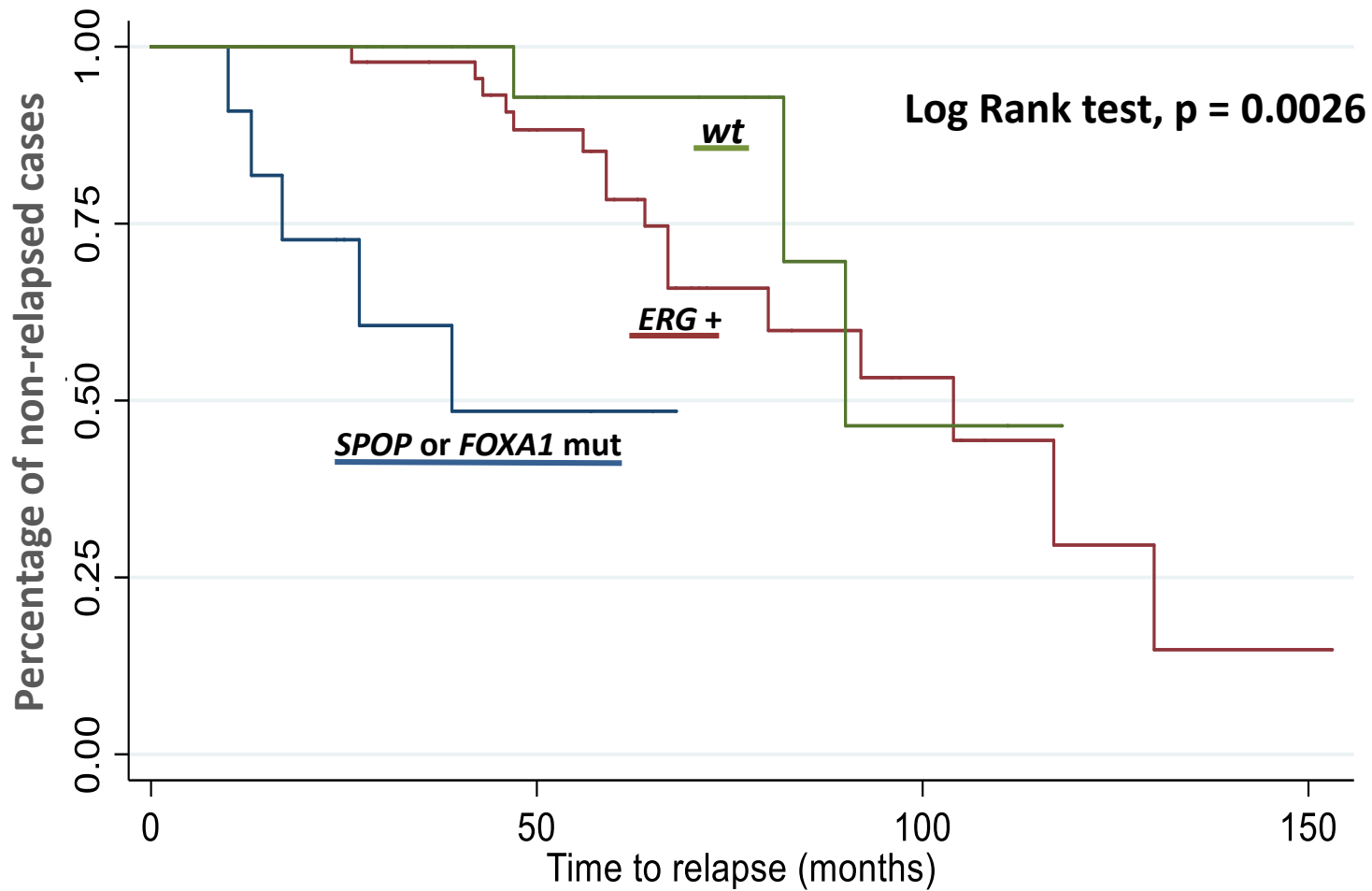
Distribution of *SPOP* and *FOXA1* alterations and *ERG* overexpression according to GG



Distribution of the different combinations of alterations according to the GG



***SPOP or FOXA1* mutations and biochemical (PSA) recurrence**



Conclusions

SPOP expression loss characterizes a significant number of PrCa, and is statistically associated with *ERG* overexpression.

SPOP and *FOXA1* mutations show an inverse statistical correlation with *ERG* overexpression

SPOP and *FOXA1* mutations are present in a significant percentage of *ERG wt* tumors but in a very low percentage of *ERG* overexpressing tumors

SPOP and *FOXA1* alterations (expression loss and mutations) are associated with GG5 tumors, but *ERG* overexpression is associated with GG1 PrCa.

SPOP and *FOXA1* mutations are strongly associated with a shorter time of PSA recurrence in PrCa.

Acknowledgements

Department of Pathology, Parc de Salut-Mar

Marta Lorenzo

Laura Segalés

Núria Juanpere

Josep Lloreta

Department of Urology, Parc de Salut-Mar

Lluís Fumadó

Lluís Cecchini