ARRAY-COMPARATIVE GENOMIC HYBRIDIZATION AS A NOVEL HIGH-THROUGHPUT APPROACH IN BLADDER CANCER TREATMENT

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INTRODUCTION

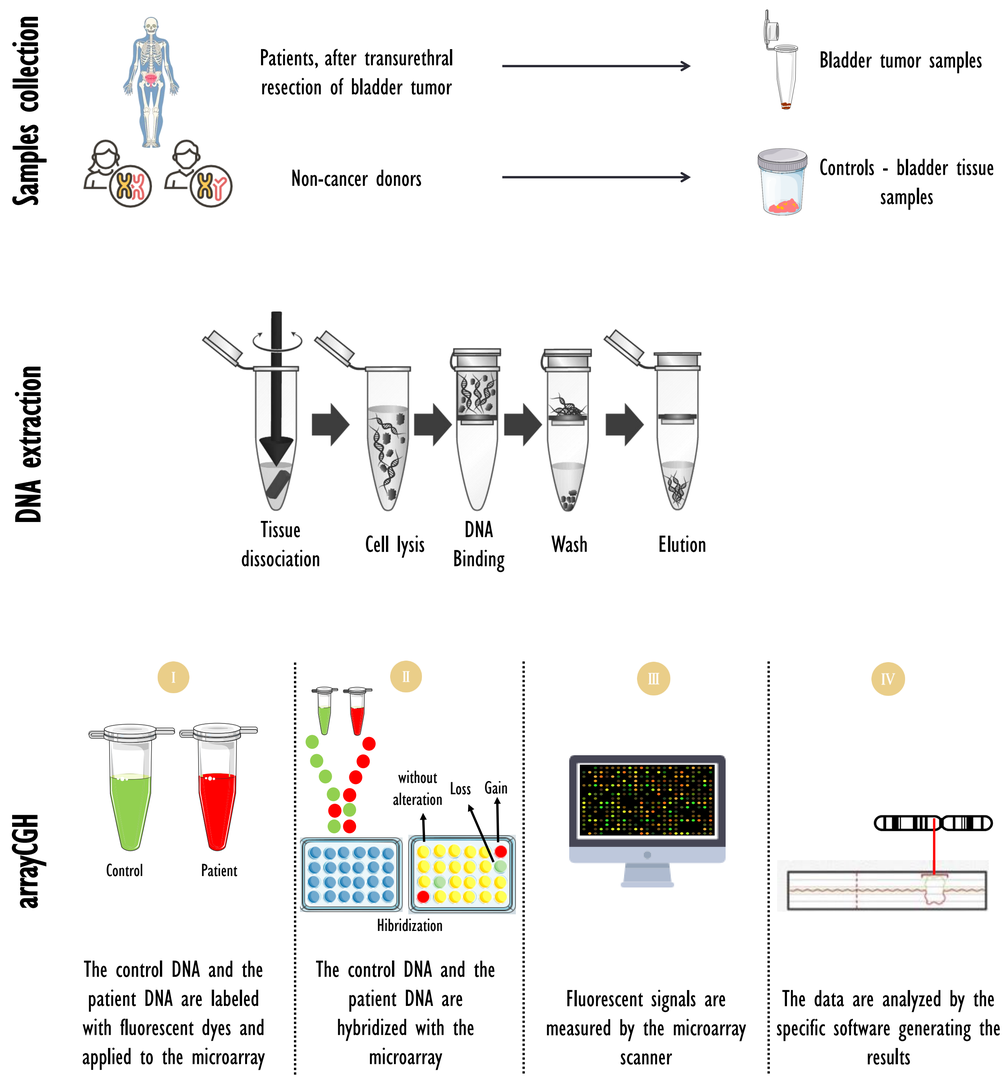
Bladder cancer (BC) is the second most common genitourinary malignancy with high recurrence rates. BC is the sixth tumor with the highest incidence and the eighth one with the highest mortality.

BC is the **9th** most common cancer worldwide

Despite their high incidence and prevalence, there has been little progress in diagnosis, prognosis and therapy. Since the prognostic tools currently available have limitations and acquired changes in specific genes are thought to be significant in the development of bladder tumours, we needed to improve the research in this field of genetic changes associated with the BC.

AIM: Characterization of the genomic profile of bladder cancer using the array-Comparative Genomic Hybridization (aCGH) technique.

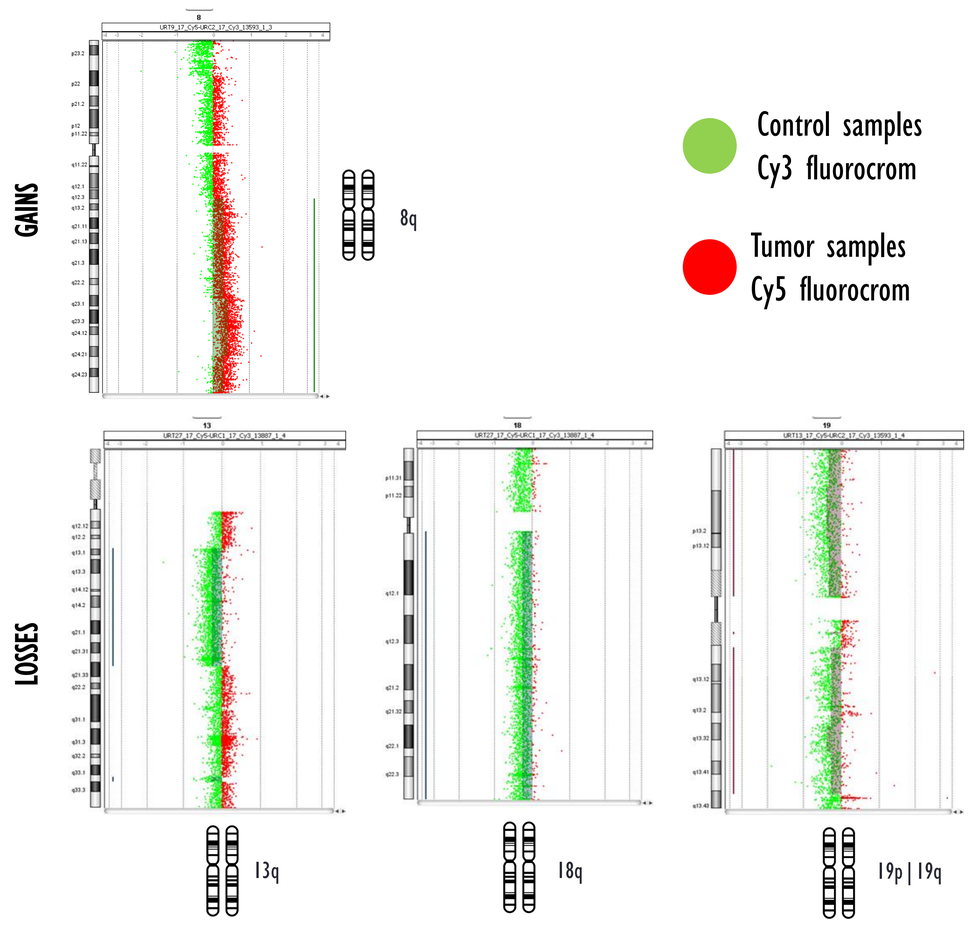
MATERIAL AND METHODS



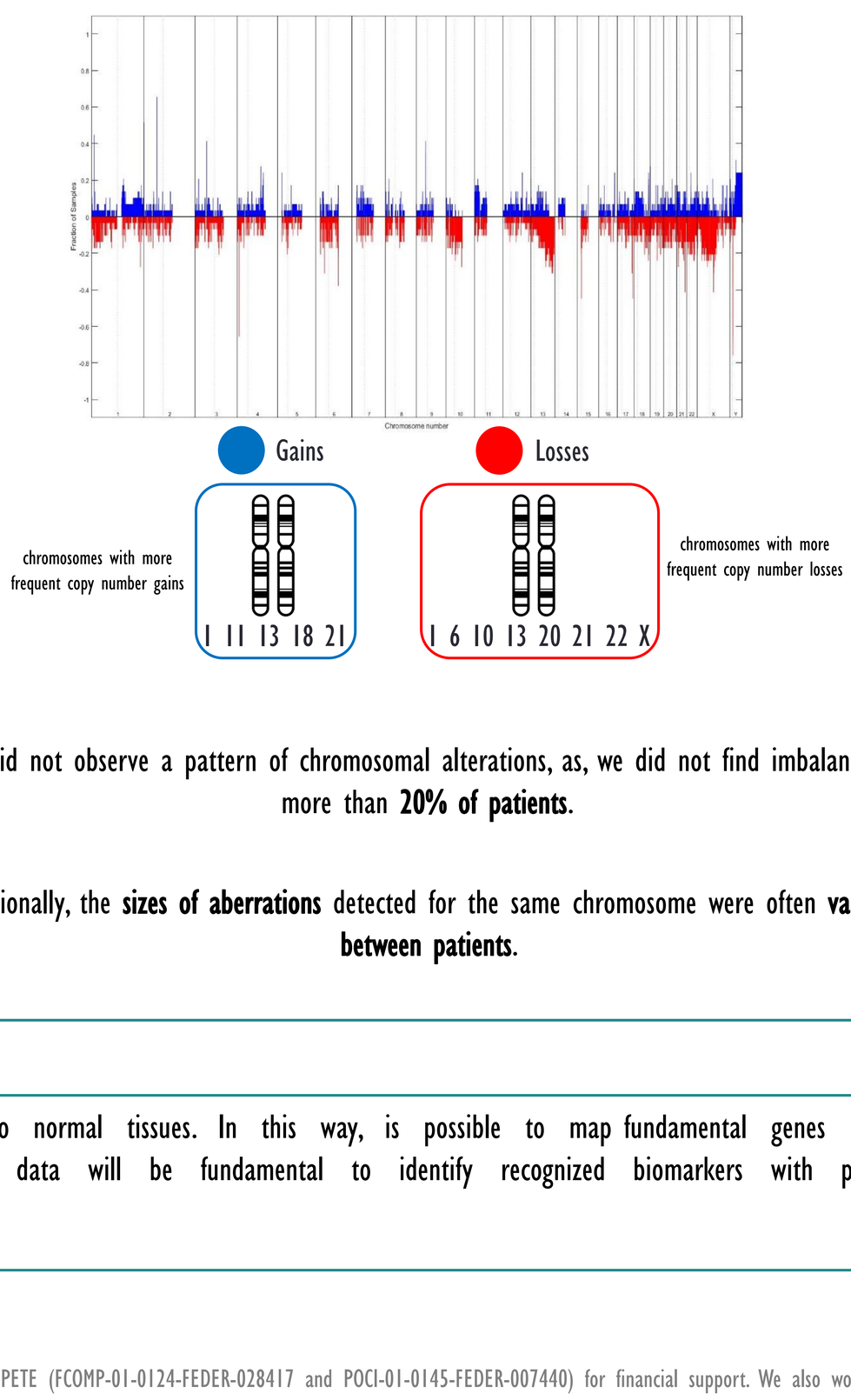
Histopathological information from the patients was analyzed and clinical data registered.

RESULTS

(A) Genomic changes identified in one of the patients of the present study:



(B) Ideogram representative of all genomic changes identified:



We did not observe a pattern of chromosomal alterations, as, we did not find imbalances in more than **20% of patients**.

Additionally, the **sizes of aberrations** detected for the same chromosome were often **variable between patients**.

CONCLUSIONS

This approach allowed us to identify altered chromosomal regions in bladder cancer comparing to normal tissues. In this way, is possible to map fundamental genes related to disease initiation and progression. The correlation between molecular and clinical-pathological data will be fundamental to identify recognized biomarkers with possible diagnostic and prognostic interest.

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