

Integrative analysis of 1q23.3 copy number gain in metastatic urothelial carcinoma - Supplemental Information - Chromosomal Instability

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1 Fraction Genome Altered

Hurst et al. [1] defined with “Fraction Genome Altered” (FGA) a measure of chromosomal instability of samples. Specifically, the authors defined FGA as the fraction of clones either gained or lost. By analyzing all segments in both cohorts, we found a percentage of FGA of approximately 24%, slightly lower than the 29% Hurst et al. found for invasive UC ($pT \geq 2$). The boxplot in Supplemental Figure S6 shows the distributions of FGA for all loci in the Spanish and DFCI cohorts. FGA was not associated with OS after recurrence/start of treatment (Spanish cohort: $P = 0.31$; DFCI cohort: $P = 0.72$), initial pathologic stage ($pT \geq 2$; Spanish cohort: $P = 0.68$; DFCI cohort: $P = 0.36$) or type of tissue (primary vs. metastasis in the DFCI cohort; $P = 0.71$).

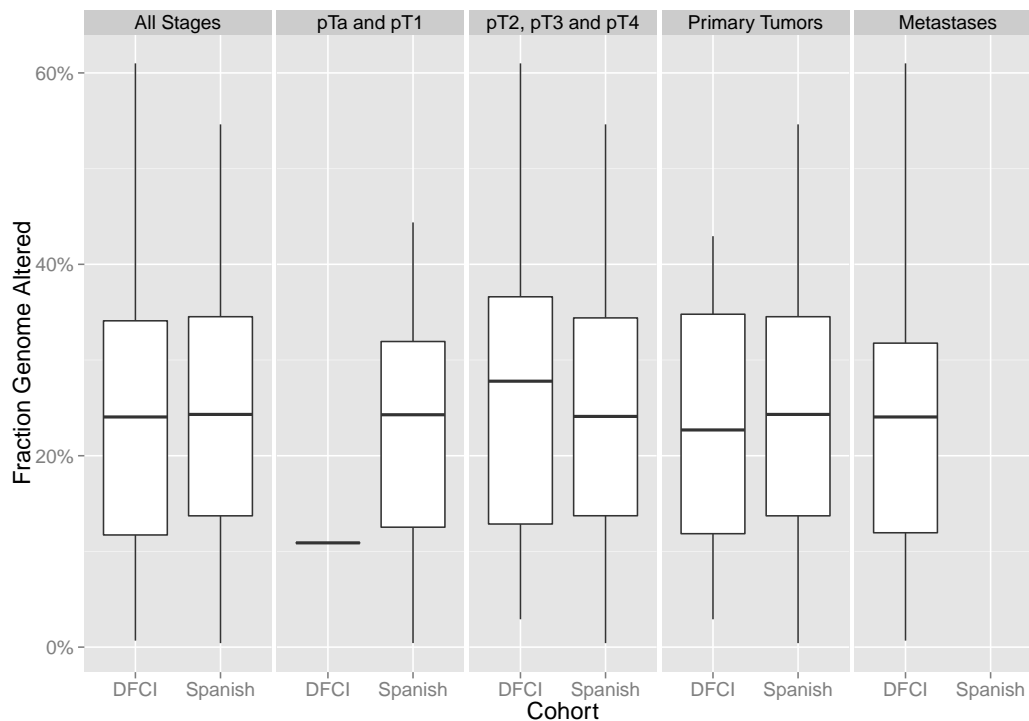


Figure S6: Fraction of genome altered (FGA, [1]) in both cohorts. For the DFCI cohort, only one sample was non-invasive ($pT < 2$) at time of surgery.

References

- [1] C D Hurst, F M Platt, C F Taylor, and M A Knowles. Novel tumor subgroups of urothelial carcinoma of the bladder defined by integrated genomic analysis. *Clin Cancer Res*, 18(21):5865–5877, Nov 2012.