Figures and figure supplements

Tumor copy number alteration burden is a pan-cancer prognostic factor associated with recurrence and death

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Figure 1. Tumor copy number landscape of conservatively treated primary prostate cancer, compared to other primary prostate cancer cohorts. (a) Heat map of copy number alterations in conservative treatment CNA cohort, as well as TCGA, MSKCC, and IMPACT primary prostate cancer cohorts. (b) Frequency distribution of CNA burden, as log of percentage of genome copy number altered, for the conservative treatment prostate cancer cohort and three other primary prostate cancer cohorts.

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Figure 2. Tumor copy number alteration burden is associated with death from prostate cancer in conservatively treated patients. (a) Cumulative Incidence of death from disease (dashed lines) and death from other causes (solid lines) for patients with high (≥ median) and non-high CNA burden. (b) Risk of death from prostate cancer within 5 years of diagnosis for different CNA burden levels. (c) Hazard ratio of death from prostate cancer for different CNA burden levels, adjusted for various factors.
Figure 2 continued

lines) based in cases with high CNA burden (red lines, CNA Burden greater than or equal to the median CNA burden of this cohort, 1.48) or non-high CNA burden (black lines, CNA Burden < median). (b) Risk for death from prostate cancer within 5 years of diagnosis. Univariate risk for 5 year prostate cancer-specific death, calculated by locally weighted Kaplan–Meier estimates (solid black line) with 95% confidence interval (dashed black lines) overlaid on the distribution of CNA burden (gray). (c) Association of tumor CNA burden with available cancer outcomes in the conservative treatment primary prostate cancer TAPG1 cohort, TCGA primary cancer cohorts, and the MSK-IMPACT clinical sequencing prostate and pan-cancer cohorts of primary and metastatic tumors. Forest plot of hazard ratio (per 5% CNA burden) with 95% confidence interval shown for cancer-specific mortality (dark blue), overall mortality (light blue), and cancer recurrence (green). Supplementary Tables and Figures.

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Figure 2—figure supplement 1. Kaplan-Meier plot of biochemical recurrence in TCGA primary prostate cohort. The highest quartile tumor CNA burden (above 75 percentile CNA burden, green) is compared to lower three quartiles (blue) with risk table showing the number of patients present at each time point.

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**Figure 2—figure supplement 2.** Tumor CNA burden in multiple cancers is associated with disease free survival and overall survival. Kaplan-Meier plot of disease free survival (left) and overall survival (right) of TCGA cohorts of (a) endometrial cancer and (b) colorectal cancer. The highest quartile CNA (above 75 percentile CNA burden, green) is compared to lower three quartiles (blue).

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Figure 2—figure supplement 3. Correlation between CNA burden from IMPACT targeted sequencing assay and whole exome sequencing (WES) of same samples, pan-cancer. The relationship between CNA burden determined by IMPACT targeted sequencing and WES in a subset of pan-cancer IMPACT cohort samples analyzed by both approaches (n = 1005) is shown (rho = 0.88, p-value=0).
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Figure 2—figure supplement 4. Tumor CNA burden in primary prostate cancer is prognostic for overall survival when assayed by clinically approved sequencing panel. Kaplan-Meier plot of overall survival of IMPACT primary prostate cancer cohort by CNA burden quartile in (a) primary and (b) metastatic tumors. The highest quartile CNA (above 75 percentile CNA burden, green) is compared to lower three quartiles (blue).

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**Figure 2—figure supplement 5.** Forest Plot of Hazard Ratios (individual and pooled) for meta-analysis assessing the association between tumor CNA burden and overall survival in (a) primary cancer and (b) patients with metastatic cancer in the pan-cancer IMPACT cohort.

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