

Clinical and molecular correlates of tumor aneuploidy in metastatic non-small cell lung cancer

Liam F. Spurr^{1,2} and Sean P. Pitroda^{2,3*}

¹*Pritzker School of Medicine, The University of Chicago, Chicago, IL*

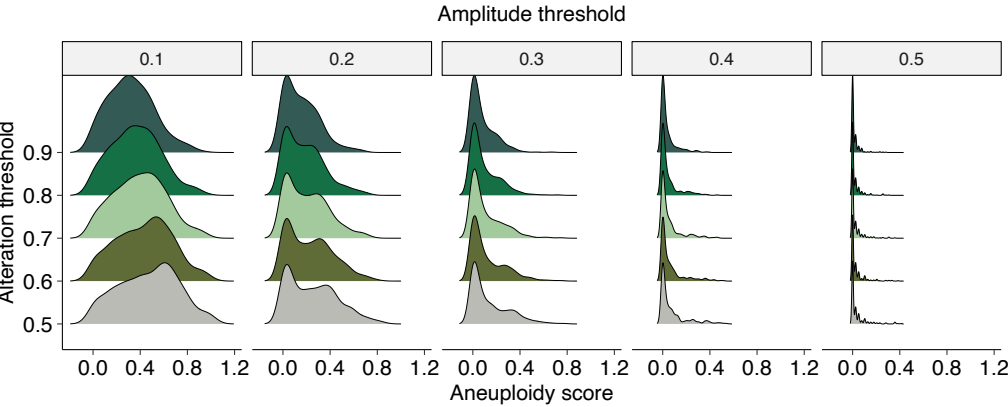
²*Department of Radiation and Cellular Oncology, The University of Chicago, Chicago, IL*

³*Ludwig Center for Metastasis Research, The University of Chicago, Chicago, IL*

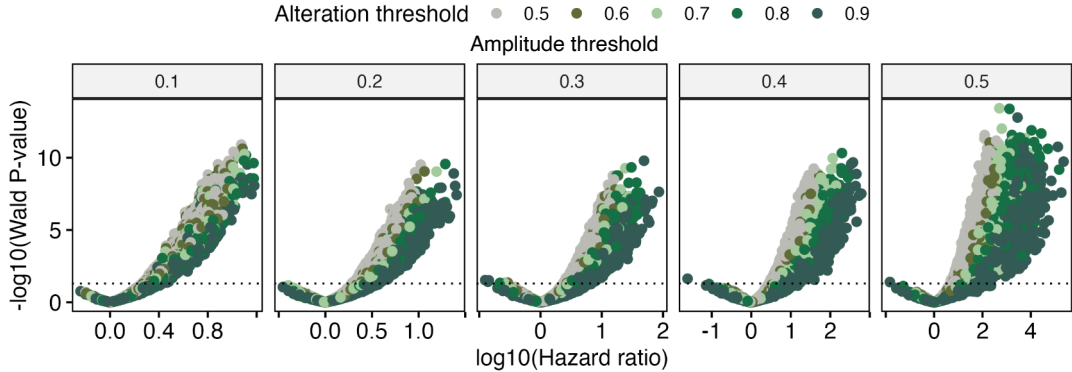
**To whom correspondence should be addressed*

Supplementary Figure 1: (a) Density plots of aneuploidy scores (AS) at different alteration thresholds (the fraction of an arm which must be altered to constitute an arm-level copy number aberration) and different amplitude thresholds (the magnitude of \log_2 copy ratio required to constitute a copy-number segment as altered). **(b)** Scatter plot of hazard ratios and corresponding Wald P -values from multivariable Cox proportional hazards models with tumor mutational burden (TMB) at different alteration and amplitude thresholds across 10,000 bootstrap samples. The dotted line delineates $P=0.05$ ($n=306$ samples). **(c)** Histogram of segment \log_2 copy ratios across 309 samples. Vertical lines identify the selected -0.1 and 0.1 deletion and amplification thresholds. The horizontal dotted line indicates the half-maximum height of the distribution.

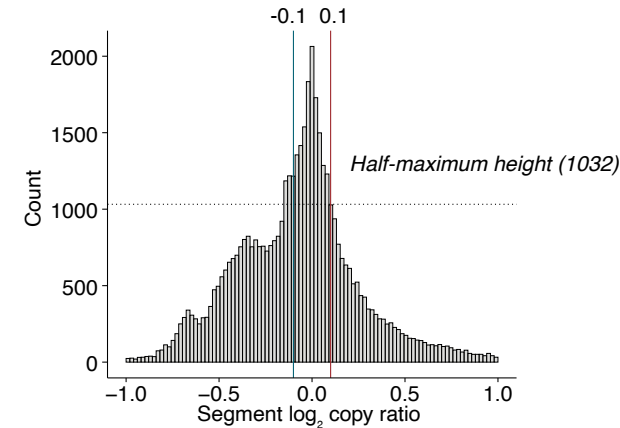
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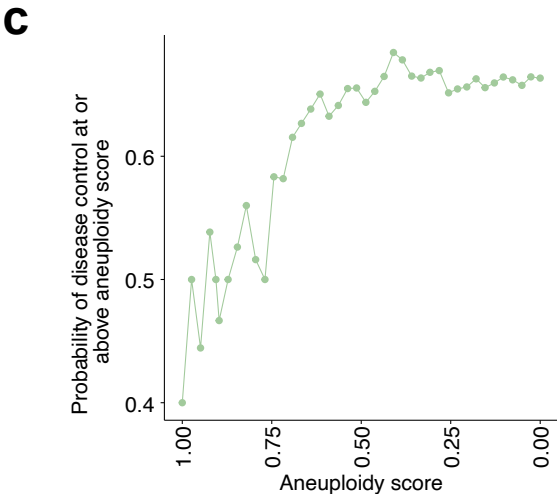
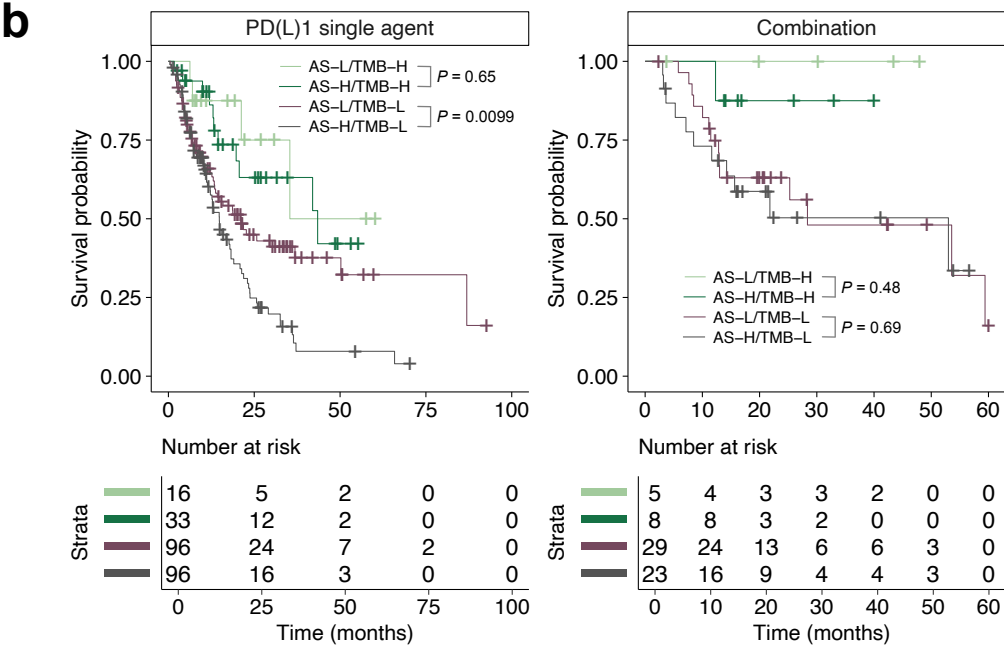
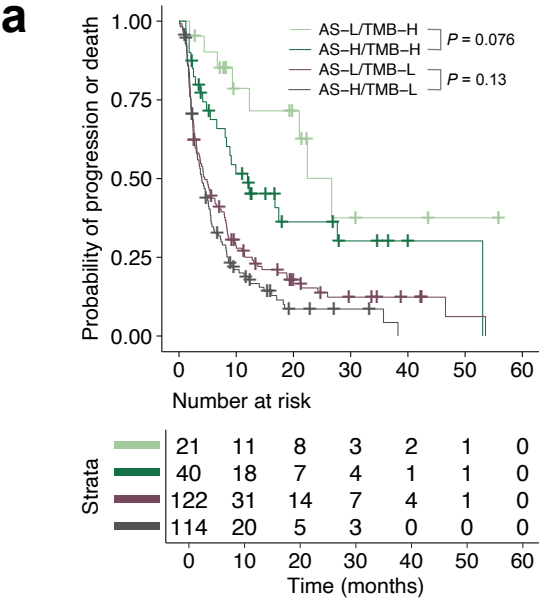
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c



Supplementary Figure 2: (a) Kaplan-Meier curves showing association of aneuploidy score (AS, binned at the median) and tumor mutational burden (TMB, binned at the 80th percentile) with progression-free survival in the SU2C-MARK cohort. Wald P-values for pairwise comparisons are shown. (H: high, L: low). **(b)** Kaplan-Meier curves of overall survival by molecular group stratified by treatment paradigm (single-agent anti-PD-(L)1 or combination anti-PD-(L)1/CTLA-4 agents with the exception of 1% of samples treated with chemotherapy and PD-(L)1 directed therapy). **(c)** Relationship between AS and probability of disease control (complete/partial response or stable disease) among tumors with AS at least as great as the x-axis value (n=306 samples).



Supplementary Figure 3: (a) Scatterplot with Spearman correlation between tumor mutational burden (TMB) and aneuploidy score (AS) (n=309 samples). Boxplots of AS by **(b)** tumor histology (n=309 patients) and **(c)** programmed cell-death ligand 1 (PD-L1) tumor proportion score (TPS, n=309 patients). Kruskal-Wallis test. (Adeno: adenocarcinoma, LC-NE: large cell neuroendocrine tumor). The top and bottom edges represent the first and third quartiles, respectively. The center line represents the median. Whiskers extend to the furthest data points before any outliers (within 1.5× the interquartile range).

