Abstract 8543

Identifying biomarkers associated with disease-free survival in early-stage lung cancer

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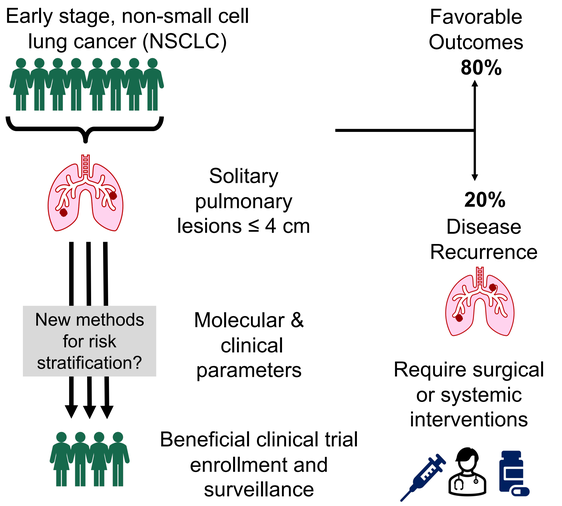
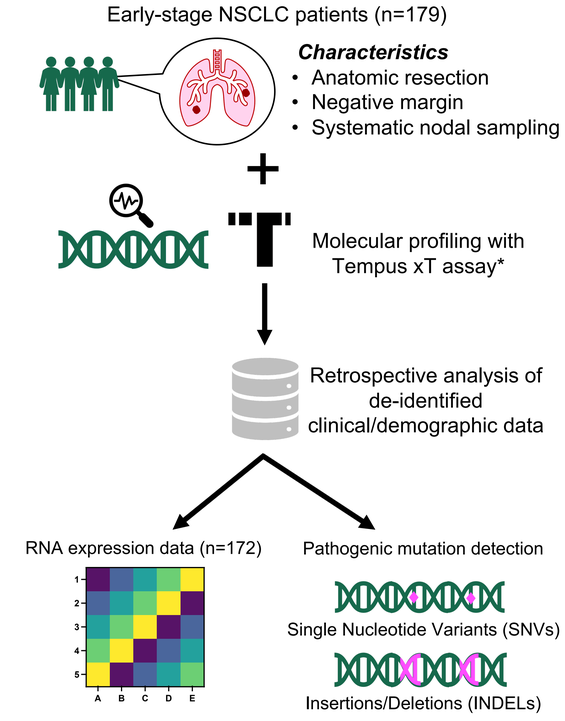
INTRODUCTION



METHODS



*Tempus xT solid tumor assay - DNA-seq of 595-648 genes at 500x coverage; whole-exome capture RNA-seq

Bivariate Cox-proportional Hazards models assessed association of individual variables with recurrence-free survival (time from surgery until recurrence/death).

SUMMARY

- **Increased expression of *NTRK1* and *CD274 (PD-L1)*, decreased expression of *ERBB2* (*HER2*), and high neoantigen tumor burden are associated with an increased risk for disease recurrence following surgery, suggesting mechanistic implications for heightened tumor aggressiveness and/or metastatic potential.**
- Future work will validate our findings in a broader set of early-stage NSCLC patients, with the goal of better identifying patients at a high risk of recurrence who would benefit from increased surveillance or systemic therapy.

RESULTS

Patient Characteristic	Total N = 179
Age	
Median (IQR)[1]	69 (63, 74)
Range	49, 85
Gender	**n (%)**
Female	111 (62%)
Male	68 (38%)
Race	**n (%)**
Caucasian	148 (83%)
Black/African American	22 (12%)
Asian	5 (2.8%)
Other	4 (2.2%)
Ethnicity	**n (%)**
Non-Hispanic/Latino	176 (98%)
Hispanic/Latino	3 (1.7%)
Smoking pack years	
Median (IQR)[1]	30 (10, 50)
Range	0, 200
Unknown	1
Recurrence/death event	**n (%)**
Yes	36 (20%)
No	143 (80%)
Pathologic stage at diagnosis	**n (%)**
IA1	19 (11%)
IA2	89 (50%)
IA3	58 (32%)
IB	13 (7.3%)
Histology	**n (%)**
Adenocarcinoma	136 (76%)
Squamous cell carcinoma	43 (24%)
Tumor size (greatest dimension)	
Median (IQR)	1.80 (1.5, 2.5)
Range	0.3, 3.9

[1]*IQR: Interquartile range*

Table 1. Demographic and clinical information for all patients included in this study.

The most common somatically mutated genes in our cohort were *TP53* (33% of tumors) and *KRAS* (16% of tumors), consistent with previous studies

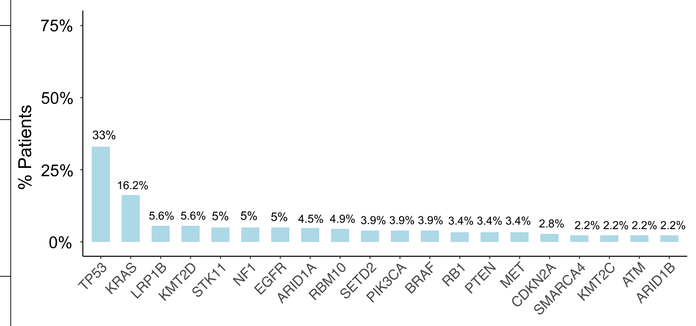


Figure 1. Percentage of patients with a pathogenic or likely pathogenic somatic mutation found in the top 20 commonly mutated genes in our cohort.

Increasing log_{10}-RNA expression for *NTRK1* and *CD274* (*PD-L1*) and decreasing log_{10}-RNA expression for *EGFR* and *ERBB2* (*HER2*) were associated with increased risk of recurrence/death

Gene	HR[2]	95% CI[3]	p-value
NTRK1	5.95	1.16, 30.4	0.027
CD274 (PD-L1)	7.88	1.61, 38.6	0.013
EGFR	0.24	0.05, 1.21	0.071
ERBB2 (HER2)	0.20	0.04, 0.97	0.042

[2]*HR: Hazard ratio.* [3]*CI: Confidence interval*

Table 2. HR, CI, and p-value information for genes whose log_{10}-RNA expression was associated with recurrence/death events. Of note, EGFR expression was not statistically significant but trended towards an association. Total N=172, recurrence/death event N=34. p-values computed through bivariate Cox-proportional Hazards models.

Patients with a high neoantigen tumor burden displayed more rapid time to recurrence compared to patients with a low neoantigen tumor burden

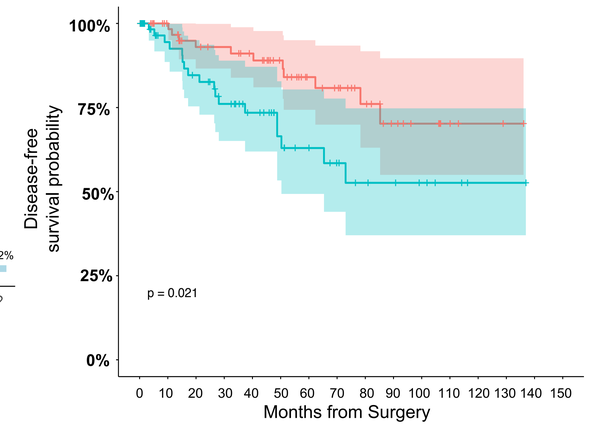


Figure 2. Kaplan-Meier curve comparing disease-free survival for patients with low vs. high neoantigen tumor burden. Patients were arbitrarily dichotomized at the median (1.6). p-value was computed by the log-rank test. N=148 patients with neoantigen tumor burden score available.

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