

Supplementary Materials: Early Assessment of Chemotherapy Response in Advanced Non-Small Cell Lung Cancer with Circulating Tumor DNA

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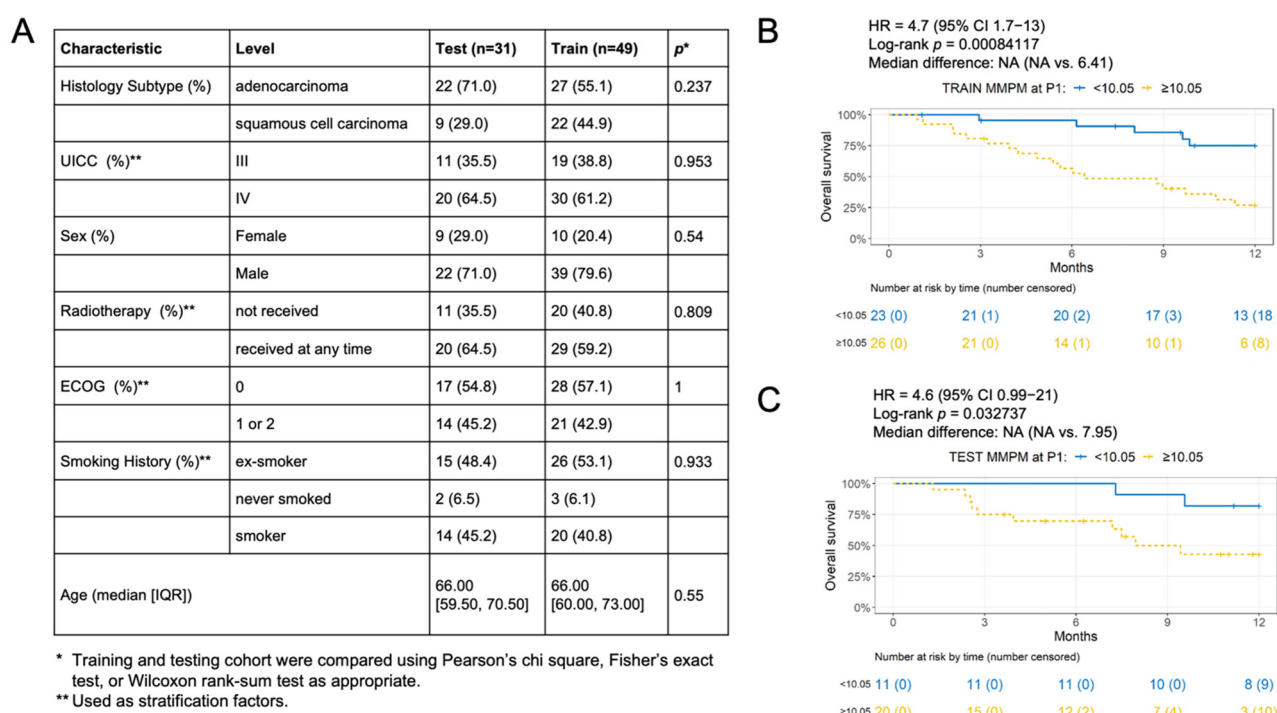


Figure S1. Association between overall survival and ctDNA level after one chemotherapy cycle. (A) Comparison of baseline characteristics between test and training cohorts. Overall survival for >10 vs. ≤10 mean mutant molecules per milliliter (MMPM) in the first available plasma after one cycle of chemotherapy in the training (B) and test (C) sets.

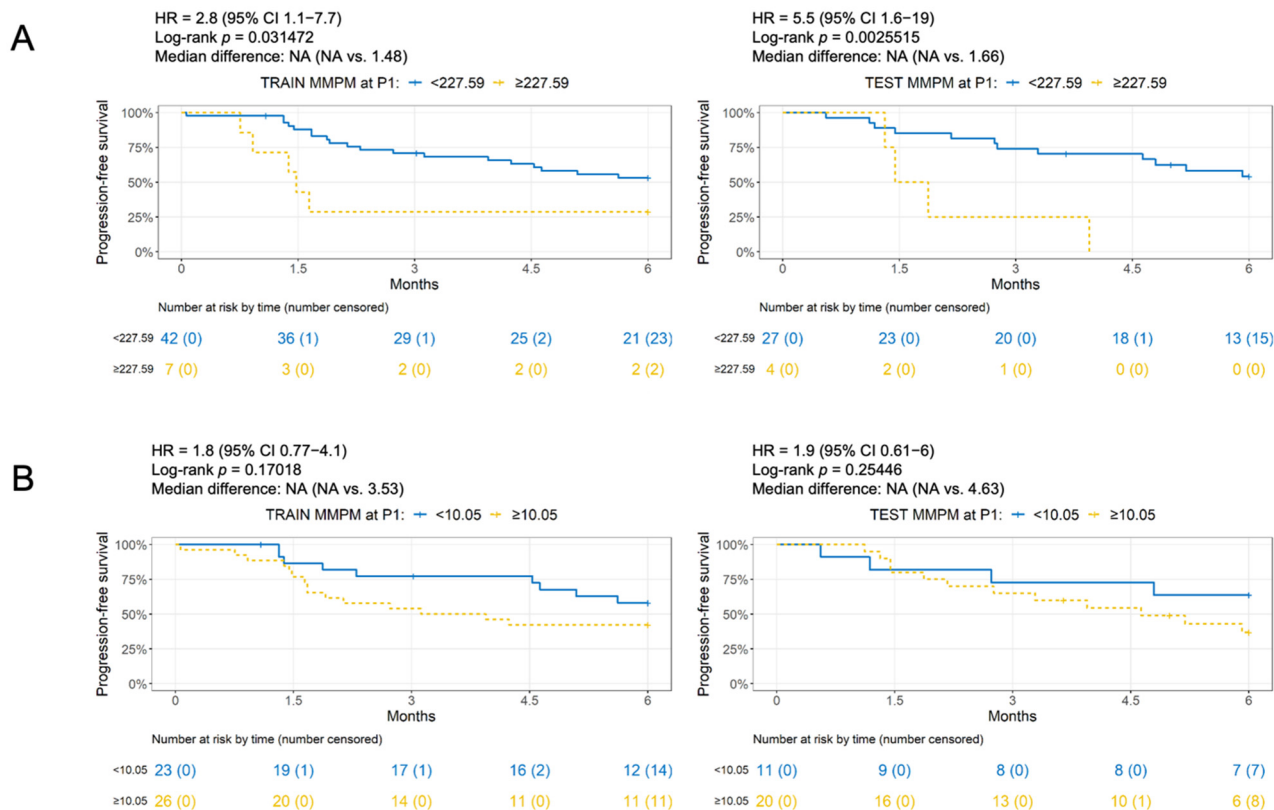


Figure S2. Association between progression-free survival and ctDNA level after one chemotherapy cycle. **(A)** Progression-free survival for >227 vs. ≤ 227 mean mutant molecules per milliliter (MMPM) in the first available plasma after one cycle of chemotherapy in the training (**left**) and test (**right**) cohorts. **(B)** Progression-free survival for >10 vs. ≤ 10 mean mutant molecules per milliliter (MMPM) in the first available plasma after one cycle of chemotherapy in the training (**left**) and test (**right**) cohorts.

Table S1. Summary of First Line Treatment Description.

First Line Treatment	Overall <i>n</i> (%)
Chemotherapy	92 (100)
Carboplatin or Cisplatin	91 (99)
Platinum-based Vinorelbine	49 (53)
Platinum-based Pemetrexed	27 (29)
Platinum-based Gemcitabine	6 (7)
Platinum-based Paclitaxel	3 (3)
Platinum-based Abraxane	2 (2)
Platinum-based Paclitaxel and Abraxane	2 (2)
Platinum-based Vinorelbine and Pemetrexed	1 (1)
Platinum-based Vinorelbine and Vincristine	1 (1)
Platinum-free Pemetrexed	1 (1)

Table S2. Most Frequently Mutated Genes in Baseline Plasma ($N = 92$).

Gene	N (%)
<i>TP53</i>	52 (57)
<i>NPAP1</i>	29 (32)
<i>KRAS</i>	27 (29)
<i>EGFR</i>	18 (20)
<i>KIT</i>	17 (18)
<i>APC</i>	16 (17)
<i>BRCA2</i>	16 (17)
<i>FAM135B</i>	16 (17)
<i>POM121L12</i>	15 (16)
<i>SLC8A1</i>	15 (16)
<i>USP29</i>	15 (16)
<i>CSMD3</i>	14 (15)
<i>FBXL7</i>	14 (15)
<i>CHRM2</i>	13 (14)
<i>KIAA1211</i>	13 (14)
<i>LRRC7</i>	13 (14)
<i>MET</i>	13 (14)
<i>ALK</i>	12 (13)
<i>BRCA1</i>	12 (13)
<i>ERBB2</i>	12 (13)
<i>KEAP1</i>	12 (13)
<i>LRRTM1</i>	12 (13)
<i>LRRTM4</i>	12 (13)
<i>BRINP2</i>	11 (12)
<i>DDI1</i>	11 (12)
<i>KPRP</i>	11 (12)
<i>SLITRK5</i>	11 (12)
<i>ZNF521</i>	11 (12)
<i>BCHE</i>	10 (11)
<i>BRAF</i>	10 (11)
<i>BRINP3</i>	10 (11)
<i>MKRN3</i>	10 (11)
<i>NLRP3</i>	10 (11)
<i>PDGFRA</i>	10 (11)
<i>RET</i>	10 (11)
<i>SLITRK4</i>	10 (11)

Note: Genes are only counted once per subject regardless of specific mutation. Mutations include both synonymous and nonsynonymous single nucleotide variants, insertions and deletions.

Table S3. Hazard Ratios and Confidence Intervals for Potential Adjustment Variables.

Analysis for Full Population ($n = 92$)		PFS		OS	
Variable	HR (95% CI)	logrank p^*	HR (95% CI)	logrank p^*	
Histology Subtype		0.17		0.24	
Squamous cell carcinoma	0.65 (0.35–1.20)		0.67 (0.34–1.32)		
Adenocarcinoma	Reference		Reference		
Age	1.00 (0.97–1.03)	0.91	1.02 (0.98–1.06)	0.33	
Sex		0.14		0.30	
Male	0.62 (0.33–1.17)		0.70 (0.35–1.38)		
Female	Reference		Reference		
Smoking History		0.58		0.090	
Never Smoked	1.41 (0.33–6.00)		1.99 (0.45–8.74)		
Smoker	1.36 (0.75–2.47)		2.05 (1.05–3.98)		

Ex-Smoker	Reference	Reference	
ECOG			0.0053
1 or 2	1.12 (0.62–2.04)	2.43(1.28–4.62)	
0	Reference	Reference	
UICC			0.0061
IV	2.40 (1.26–4.59)	1.67 (0.84–3.32)	
III	Reference	Reference	
Radiotherapy (any time)			0.088
Received	0.72 (0.40–1.30)	0.58 (0.30–1.09)	
Not received	Reference	Reference	
Radiotherapy (within 365 days)			0.14
Received	0.77 (0.43–1.39)	0.62 (0.33–1.17)	
Not received	Reference	Reference	
Radiotherapy (within 182 days)			0.41
Received	0.73 (0.40–1.30)	0.76 (0.40–1.45)	
Not received	Reference	Reference	

Note: Abbreviations: PFS, progression free survival; OS, overall survival. *Global *p*-values presented for categorical variables with more than 2 levels. Unadjusted Cox proportional hazards models were performed for each potential adjustment variable. *p*-values in bold are below the 0.1 threshold used to select variables for inclusion in multivariate Cox proportional hazards models.