Supplementary tables

Table S1. Clinical characteristics of LS-SCLC patients with tumor tissue biopsies

Characteristics	n=203
Age, mean (SD)	59.0 (8.83)
Age group, No. (%)	
<60	107 (52.7%)
≥60	96 (47.3%)
Sex, No. (%)	
Male	143 (70.4%)
Female	60 (29.6%)
Smoking, No. (%)	
Current/former smoker	90 (44.3%)
Non-smoker	113 (55.7%)

SD, standard deviation.

Table S2. Clinical characteristics of the external LS-SCLC cohort

Characteristics	n=218
Age, mean (SD)	65.5 (8.67)
Age group, No. (%)	
<60	27 (12.4)
≥60	96 (44.0)
Unknown	95 (43.6)
Sex, No. (%)	
Male	150 (68.8)
Female	68 (31.2)
Smoking, No. (%)	
Current/former smoker	117 (53.7)
Non-smoker	25 (11.5)
Unknown	76 (34.9)
Stage, No. (%)	
I	65 (29.8)
II	16 (7.3)
III	91 (41.7)
Unknown	46 (21.1)
TMB, mean (SD)	5.20 (6.89)

SD, standard deviation; TMB, tumor mutation burden (mutations/Mb).

Table S3. Clinical characteristics of LS-SCLC ctDNA dCRT cohorts

Characteristics	Training (n=45)	Test (n=29)	No shrinkage data (n=7)	*p*
Age, mean (SD)	58.0 (9.09)	57.6 (7.31)	60.9 (6.49)	0.647
Age group, No. (%)				0.794
<60	25 (55.6)	17 (58.6)	3 (42.9)	
≥60	20 (44.4)	12 (41.4)	4 (57.1)	
Sex, No. (%)				0.928
Male	36 (80.0)	23 (79.3)	6 (85.7)	

Female	9 (20.0)	6 (20.7)	1 (14.3)	
Smoking, No. (%)				0.149
Current/former smoker	31 (68.9)	18 (62.1)	7 (100.0)	
Non-smoker	14 (31.1)	11 (37.9)	0 (0.0)	
Stage, No. (%)				>0.99
I/II	6 (13.3)	3 (10.3)	1 (14.3)	
III	39 (86.7)	26 (89.7)	6 (85.7)	
PCI, No. (%)				0.062
Yes	32 (71.1)	22 (75.9)	2 (28.6)	
No	13 (28.9)	7 (24.1)	5 (71.4)	

SD, standard deviation; PCI, prophylactic cranial irradiation.

Table S4. Clinical characteristics of LS-SCLC ctDNA IO cohort

Characteristics	**n=86**
Age, mean (SD)	59.3 (7.95)
Age group, No. (%)	
<60	36 (41.9)
≥60	50 (58.1)
Sex, No. (%)	
Male	63 (73.3)
Female	23 (26.7)
Smoking, No. (%)	
Current/former smoker	53 (61.6)
Non-smoker	33 (38.4)
Stage, No. (%)	
I/II	9 (10.5)
III	77 (89.5)
PCI, No. (%)	
Yes	73 (84.9)
No	13 (15.1)

SD, standard deviation; PCI, prophylactic cranial irradiation.

Supplementary figure captions

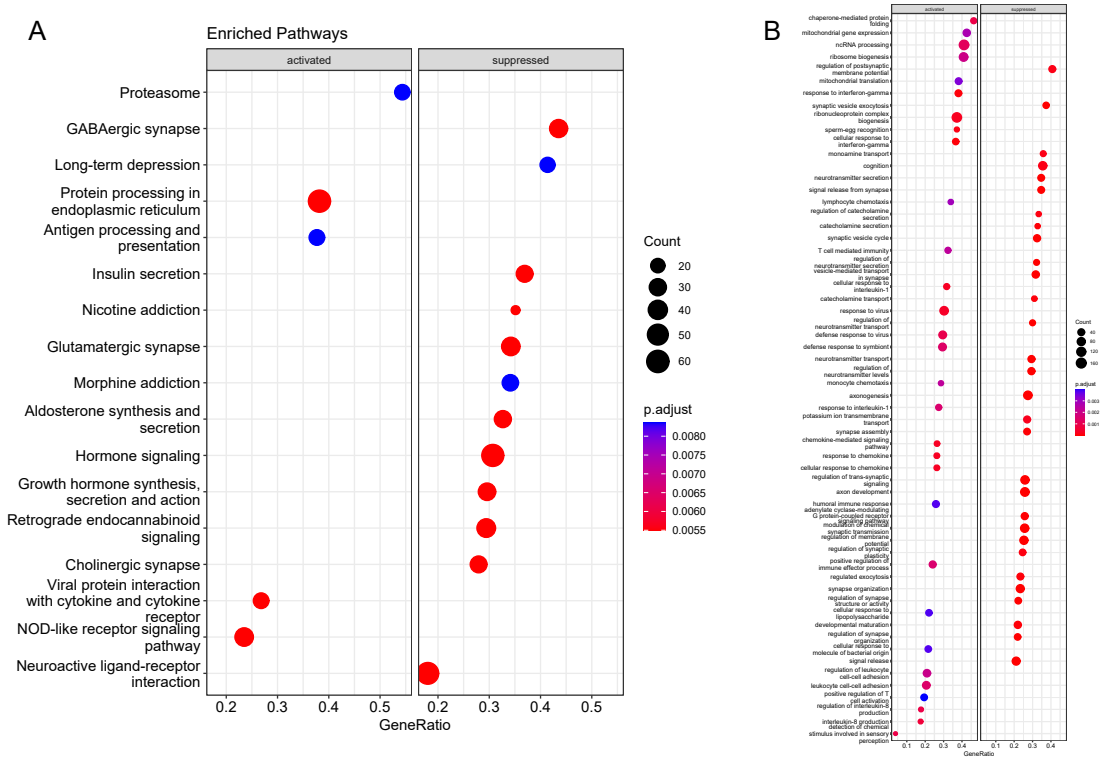


Figure S1. Full results of the transcriptional analysis

(A) The pathway enrichment results of the KEGG analysis. (B) The pathway enrichment results of the GO analysis.

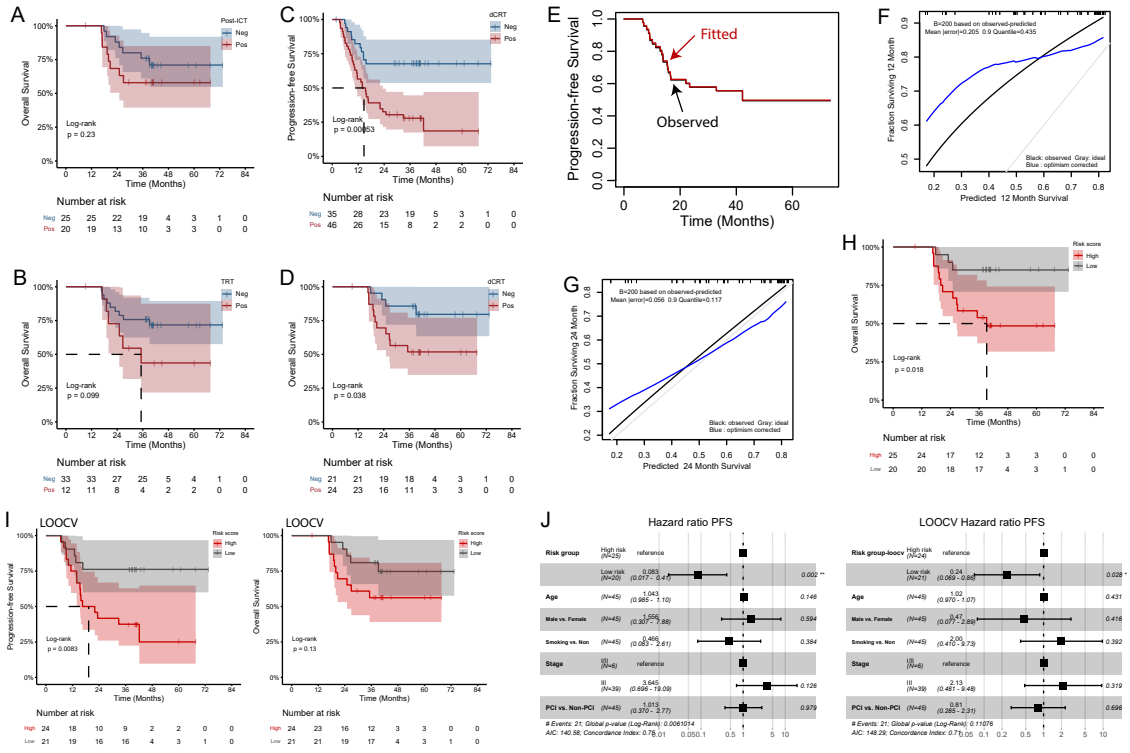


Figure S2. ct-DNA based survival prediction model developing and assessment

(A) (B) The associations of post-ICT and TRT ctDNA with OS in the training cohort. (C) (D) The associations of ctDNA detection during dCRT with PFS and OS in the training cohort. (E) The comparison observed survival curve and the fitted survival curve by the prediction model in the training cohort. (F) (G) The calibration plots for 12-mon and 24-mon PFS in the training cohort. (H) The comparison for OS between high-risk and low-risk patients in the training cohort. (I) The comparison for OS between high-risk and low-risk patients in LOOCV analysis. (J) The forest plots for multivariable Cox regression in the training cohort and LOOCV analysis.

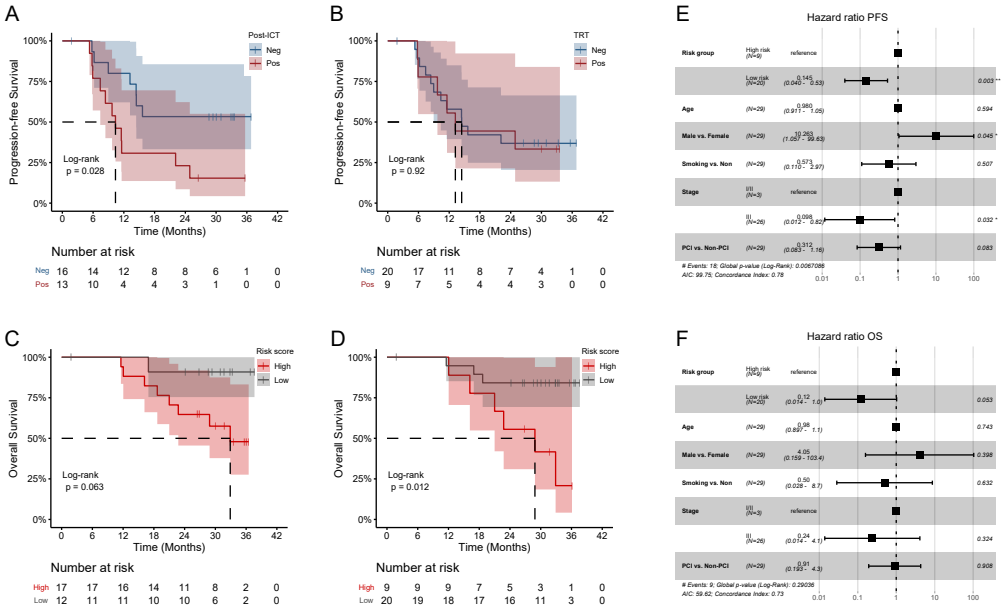


Figure S3. Performance assessment in the test cohort

(A) (B) The associations of post-ICT and TRT ctDNA with PFS in the test cohort. (C) (D) The comparison for OS between high-risk and low-risk patients classified using the 36-mon and 12-mon cutoffs. (E) (F) The forest plots for PFS and OS of multivariable Cox regression.

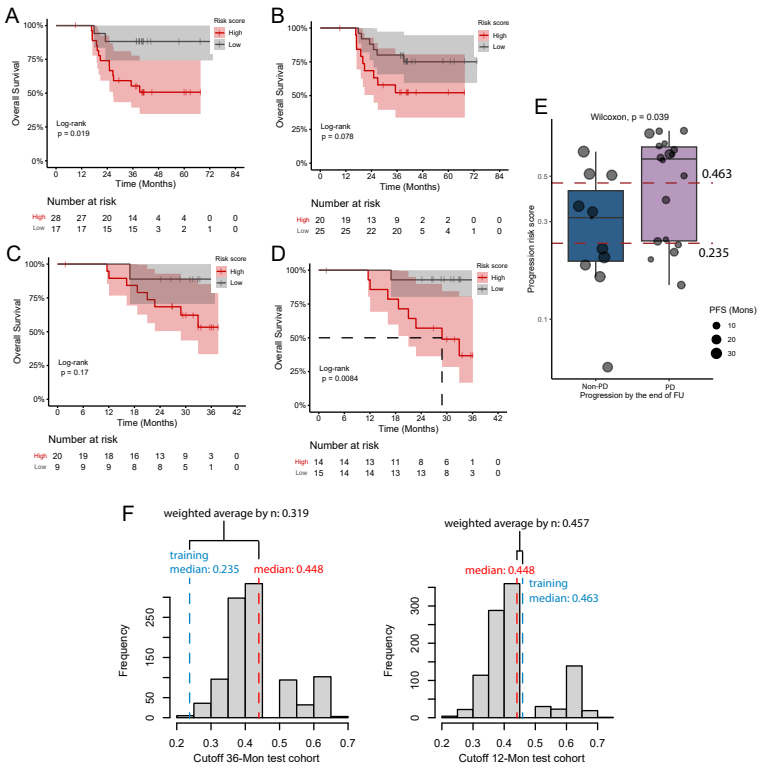
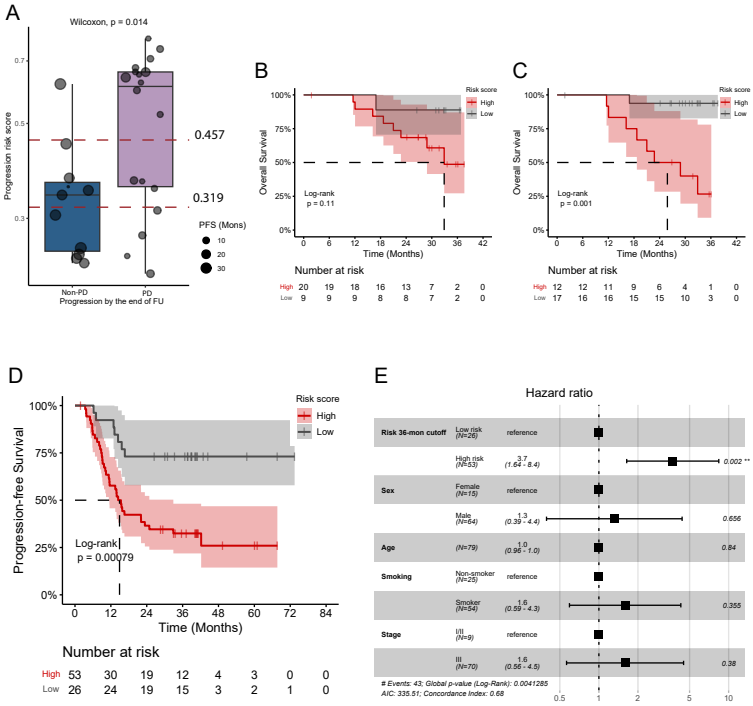


Figure S4. Bayesian algorithm development and cutoff updating methods

(A) (B) The comparison for OS between high-risk and low-risk patients classified using the 36-mon and 12-mon cutoffs in the training cohort. (C) (D) The comparison for OS between high-risk and low-risk patients classified using the 36-mon and 12-mon cutoffs in the test cohort. (E) The comparison of Bayesian risk scores between PD and non-PD patients. (F) Updated cutoffs were determined by weighted averages based on cohort size.



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36 **Figure S5. Bayesian algorithm with posteriors and performance**

37 (A) The comparison of predicted scores calculated using Bayesian algorithm with posteriors between PD and non-PD
38 patients in the test cohort. (B) The comparison of OS between high-risk and low-risk patients classified by the updated
39 36-mon cutoff in the test cohort. (C) The comparison of OS between high-risk and low-risk patients classified by the
40 updated 12-mon cutoff in the test cohort. (D) (E) The comparison of PFS between high-risk and low-risk patients
41 classified by the updated 36-mon cutoff in the ctDNA cohort.