

Table S1 The characteristics of samples included in SHFK cohort

Sample	Pathological type	Stage	Line of therapy	Response	Group of response
1	Squamous cell carcinoma	IIIB	Second	PR	DCB
2	Adenocarcinoma	IVB	Second	SD	NDB
3	Adenocarcinoma	IVB	Second	SD	NDB
4	Squamous cell carcinoma	IVA	Second	SD	DCB
5	Adenocarcinoma	IVA	Second	SD	DCB
6	Squamous cell carcinoma	IVA	Second	PR	DCB
7	Adenocarcinoma	IVB	Second	PR	DCB
8	Squamous cell carcinoma	IVA	Second	PR	DCB
9	Squamous cell carcinoma	IVB	Second	PR	DCB
10	Squamous cell carcinoma	IVB	Second	PR	DCB
11	Squamous cell carcinoma	IVA	Second	PD	NDB
12	Squamous cell carcinoma	IV	Second	SD	DCB
13	Squamous cell carcinoma	IVA	Second	PR	DCB
14	Large cell carcinoma	IVB	Second	PR	DCB
15	Squamous cell carcinoma	IVB	Second	PR	DCB
16	Squamous cell carcinoma	IVB	Second	PD	NDB

SHFK, Shanghai Fei Ke; PR, partial response; DCB, durable clinical benefit; SD, stable disease; NDB, non-durable clinical benefit; PD, progress disease.

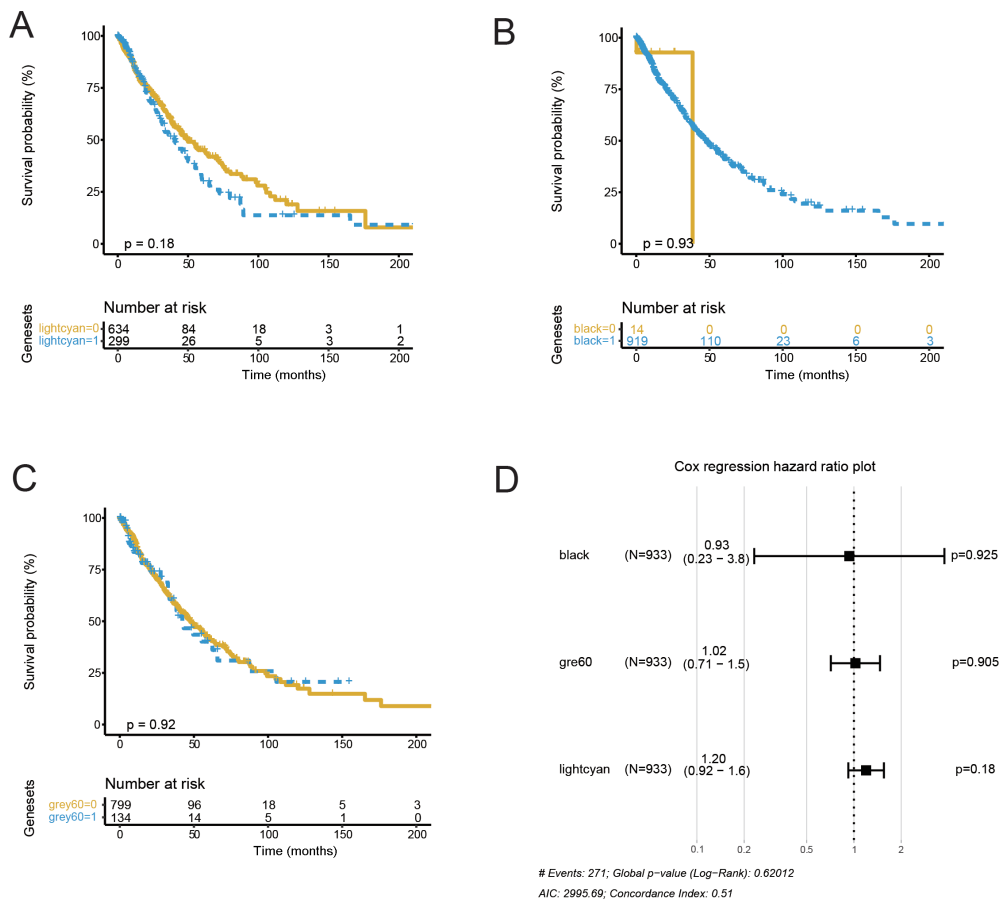


Figure S1 Three gene modules were not related to survival and prognosis. (A-C) Overall survival plot for the expression of rna_lightcyan, rna_black and rna_grey60 in TCGA-NSCLC cohort (LUAD plus LUSC). Lightcyan/black/grey60 =1 indicated positive expression of the genesets, while lightcyan/black/grey60 =0 indicated negative expression of the genesets. (D) Cox regression results of three genesets in survival model. None of the genesets were statistically significant in the model. TCGA, The Cancer Genome Atlas; NSCLC, non-small cell lung cancer; LUAD, lung adenocarcinoma; LUSC, lung squamous cell carcinoma.