

Systematic evaluation of collagen family gene transcripts: Implications for prognostic stratification in lung cancer patients

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Supplementary Data

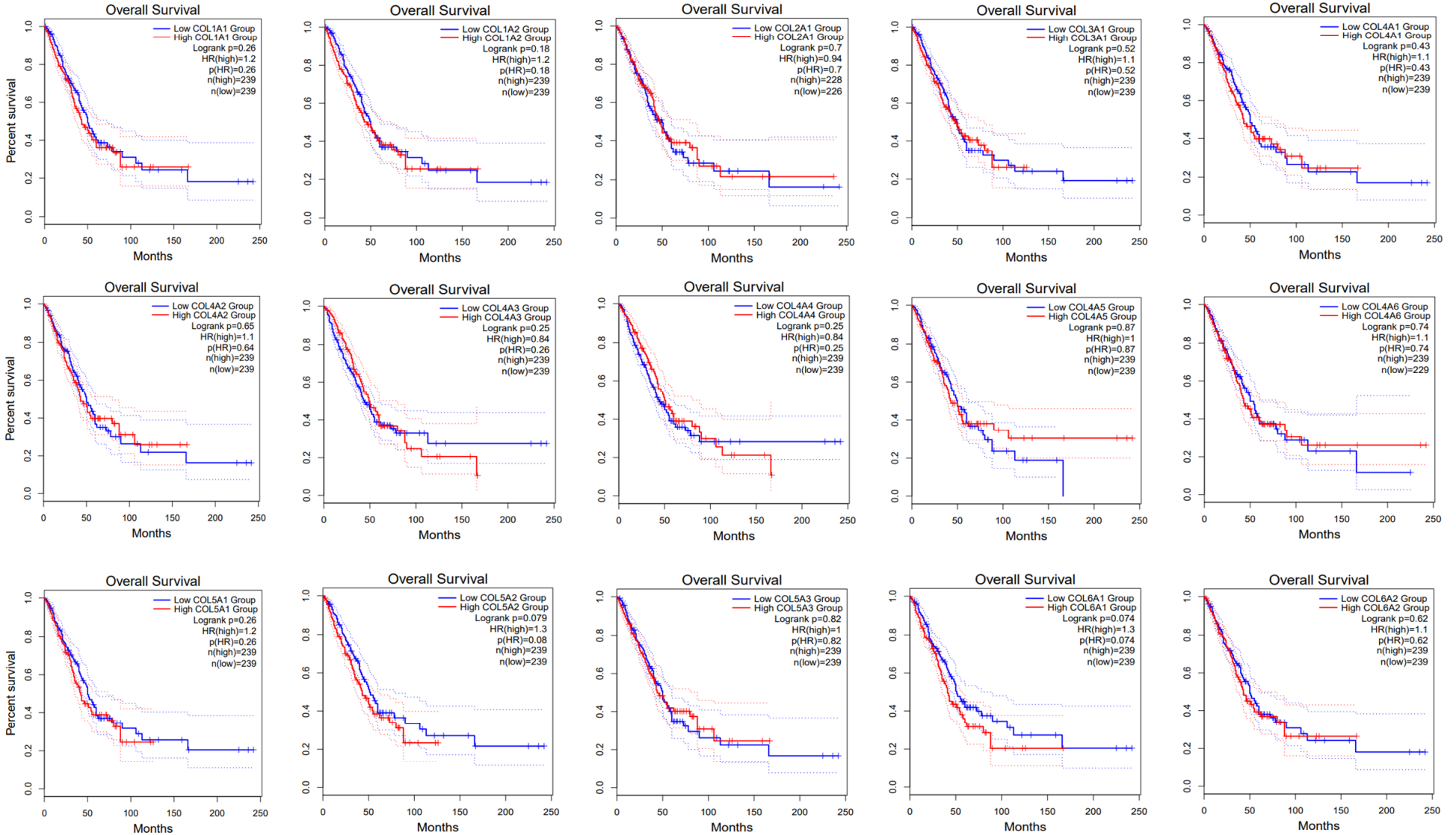
Suppl. Table S1 — Demographic and clinical data of the LUAD and LUSC patients

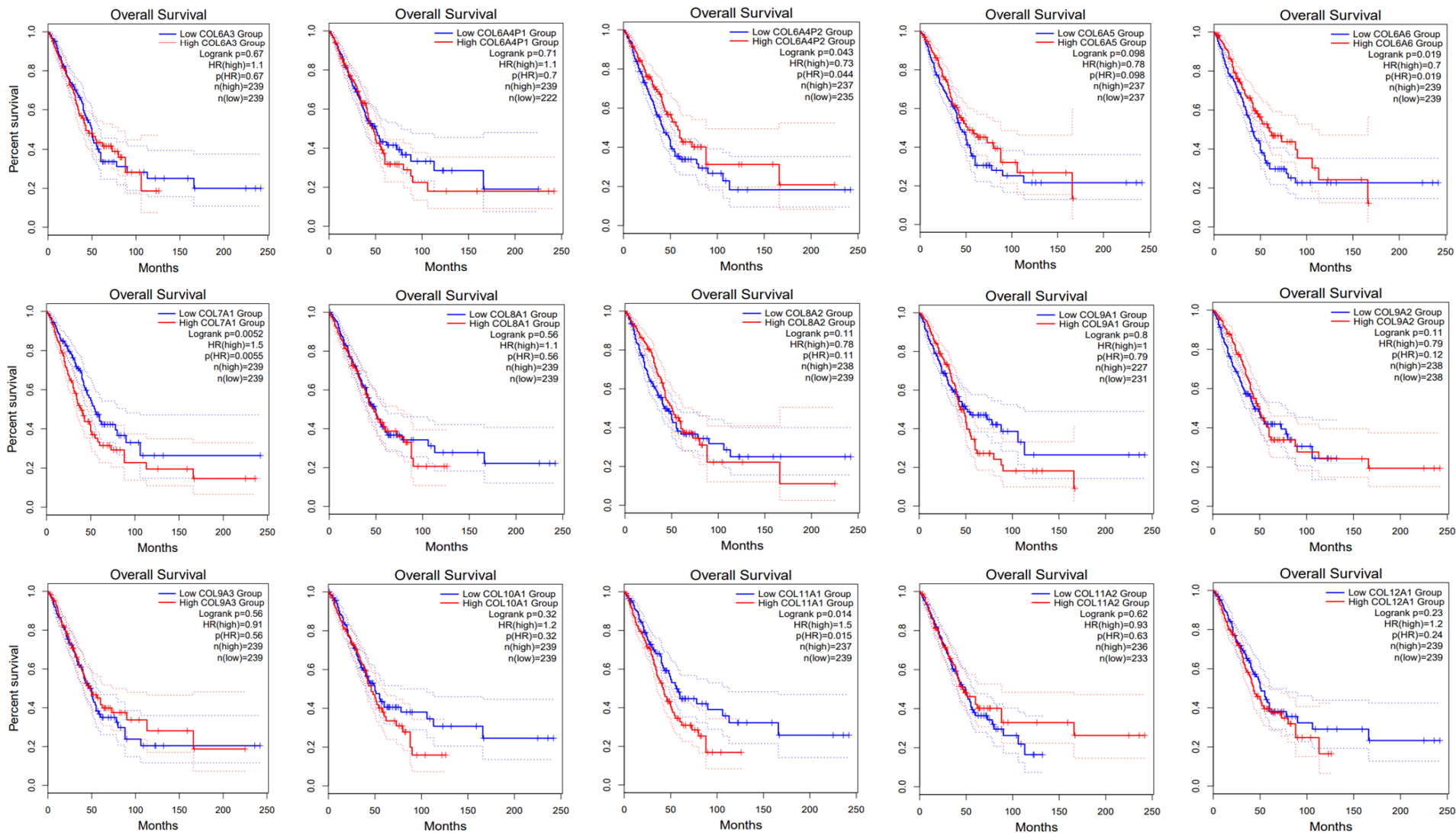
Characteristic	LUAD patients	Patient data n:483 (%)
Gender		
Male		221 (45.7%)
Female		262 (54.2%)
Diagnosis median age, years		60.5 (range, 33-88)
Overall Survival Status		
Surviving		301 (62.3%)
Death		182 (37.6%)
Primary Diagnosis		
Adenocarcinoma, NOS		328 (67.9%)
Adenocarcinoma with mixed subtypes		108 (22.3%)
Bronchiolo-alveolar carcinoma, non-mucinous		19 (3.9%)
Bronchiolo-alveolar adenocarcinoma, NOS		3 (0.6%)
Papillary adenocarcinoma, NOS		22 (4.5%)
Micropapillary carcinoma, NOS		3 (0.6%)
Tissue or organ of origin		
Upper lobe, lung		282 (58.3%)
Middle lobe, lung		21 (4.3%)
Lower lobe, lung		160 (33.1%)
Overlapping lesion of lung		4 (0.8%)
Lung, NOS		14 (2.8%)
Main bronchus		2 (0.41%)
AJCC Pathologic_M		
M0		330 (68.3%)
MX		125 (25.8%)
M1		24 (4.9%)
ND		4 (0.8%)
AJCC Pathologic_N		
N0		311 (64.3%)
NX		11 (2.2%)
N1		89 (18.4%)
N2		69 (14.2%)
N3		2 (0.41%)
ND		1 (0.2%)
AJCC Pathologic_stage		
Stage IA		125 (25.8%)
Stage IB		131 (27.1%)
Stage IIA		46 (9.5%)
Stage IIB		64 (13.2%)
Stage IIIA		67 (13.8%)
Stage IIIB		11 (2.2%)
Stage IV		25 (5.1%)
ND		14 (2.8%)
AJCC Pathologic_T		
TX		3 (0.6%)

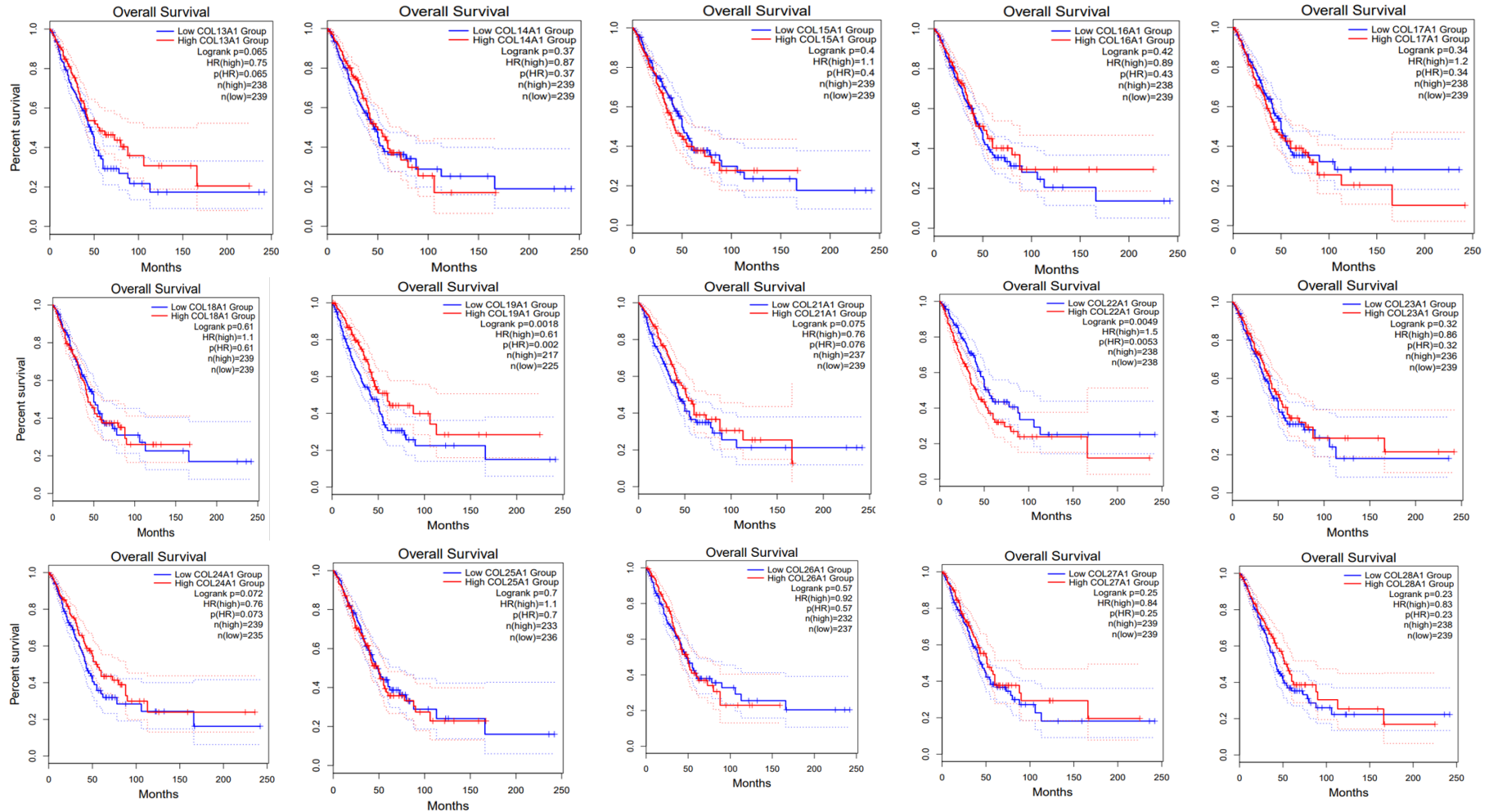
T1	162 (33.5%)
T2	258 (53.4%)
T3	41 (8.4%)
T4	19 (3.9%)
LUSC patients [Patient data n:*489 (%)]	
Gender	
Male	361
Female	128
Diagnosis median age, years	64.5 (range, 39-90)
Overall Survival Status	
Surviving	276
Death	213
Primary Diagnosis	
Squamous cell carcinoma, NOS	455
Squamous cell carcinoma, keratinizing, NOS	12
Squamous cell carcinoma, large cell, nonkeratinizing, NOS	3
Squamous cell carcinoma, small cell, nonkeratinizing	1
Basaloid squamous cell carcinoma	14
Papillary squamous cell carcinoma	4
Tissue or organ of origin	
Upper lobe, lung	255
Middle lobe, lung	15
Lower lobe, lung	169
Overlapping lesion of lung	8
Lung, NOS	35
Main bronchus	7
AJCC Pathologic_M	
M0	401
MX	77
M1	7
ND	4
AJCC Pathologic_N	
N0	312
NX	6
N1	128
N2	38
N3	5
AJCC Pathologic_stage	
Stage I	3
Stage IA	87
Stage IB	148
Stage II	3
Stage IIA	64
Stage IIB	91
Stage III	3
Stage IIIA	60
Stage IIIB	19
Stage IV	7
ND	4
AJCC Pathologic_T	
T1	48
T1a	24
T1b	39
T2	167
T1Ia	84
T1Ib	34
T3	69
T4	24

[ND: Not defined; NOS: Not otherwise specified.

*Survival analysis were performed with available 486 LUSC patient data from 489 LUSC patients given above which GEPIA extracts from TGCA database]

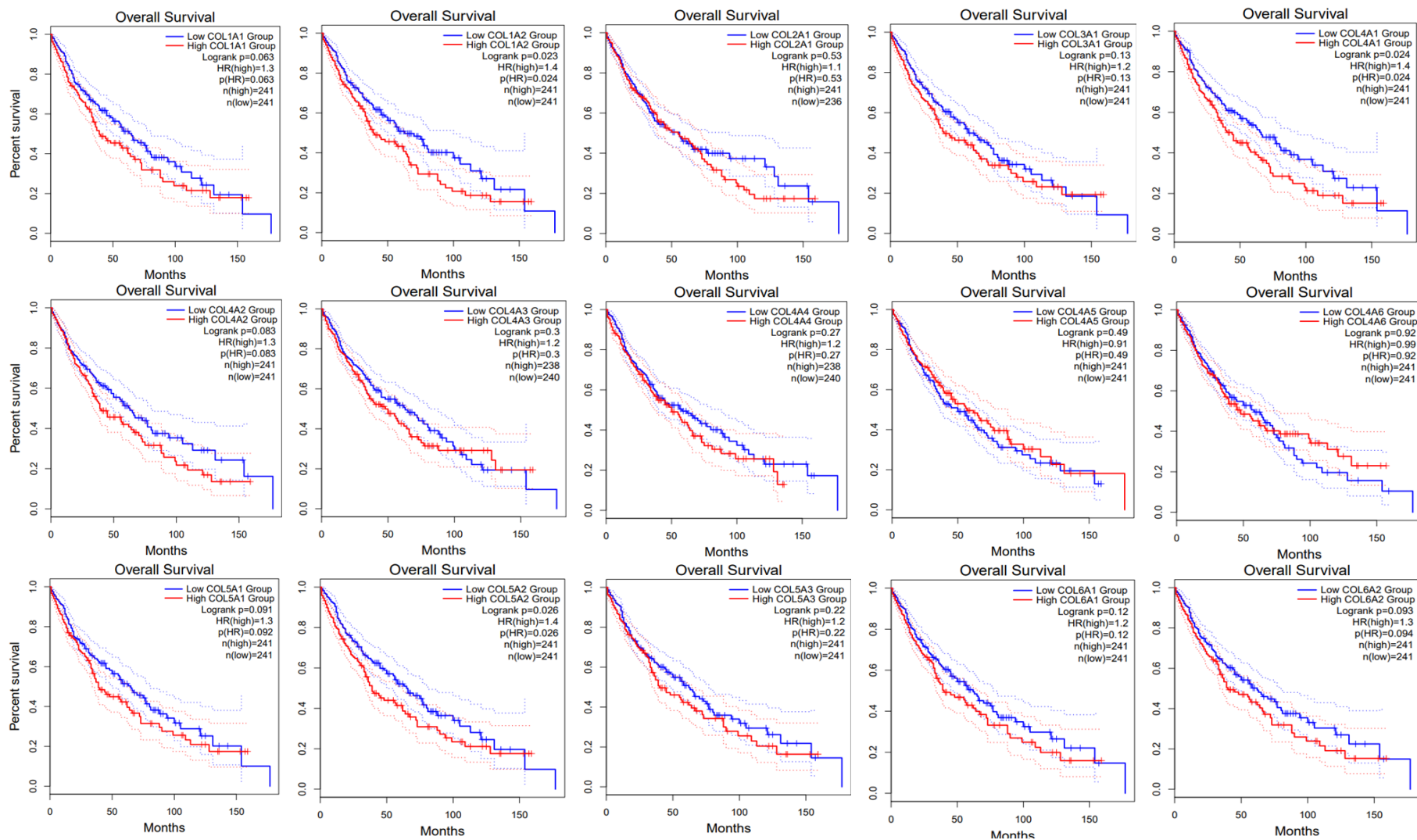


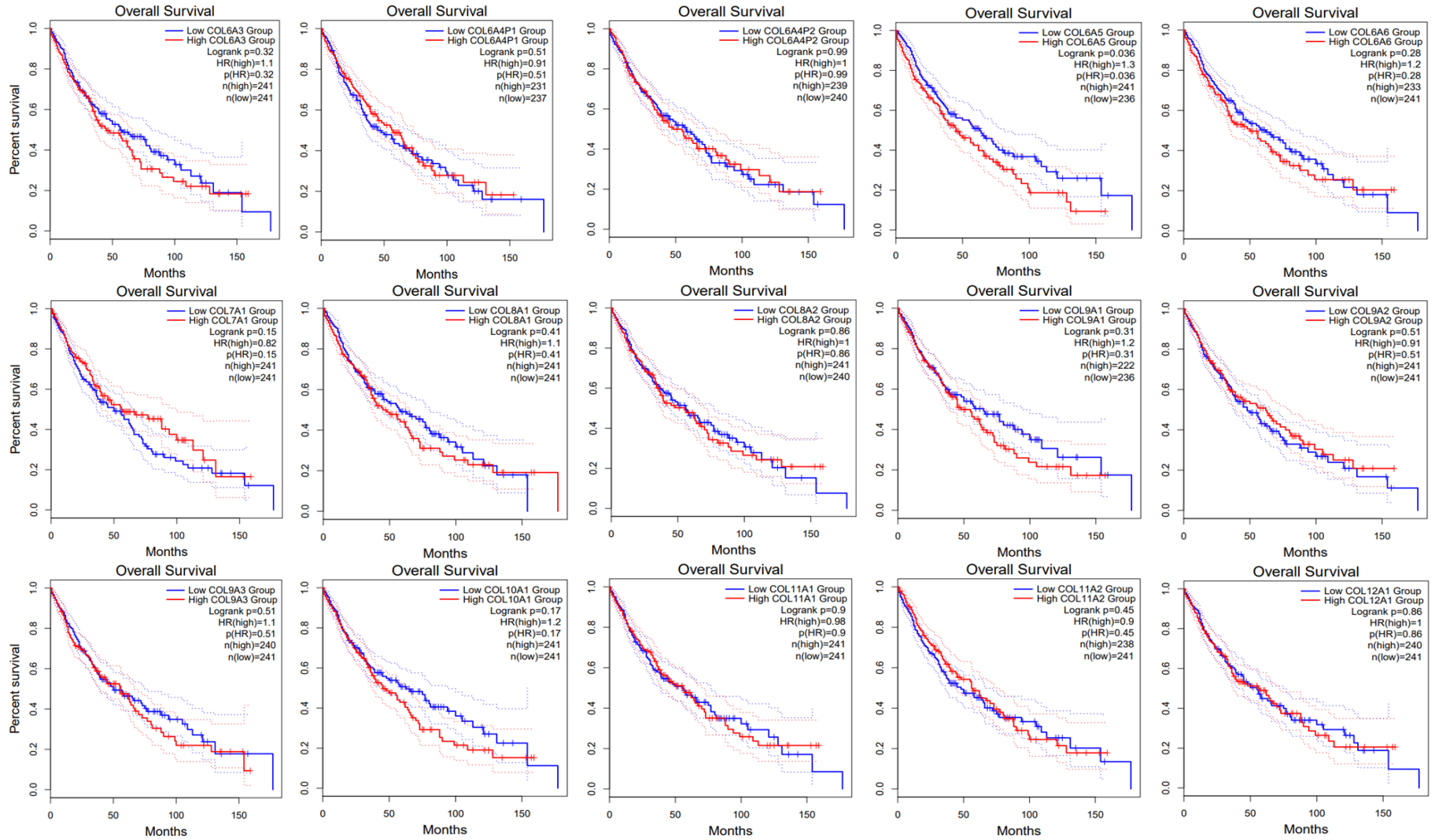


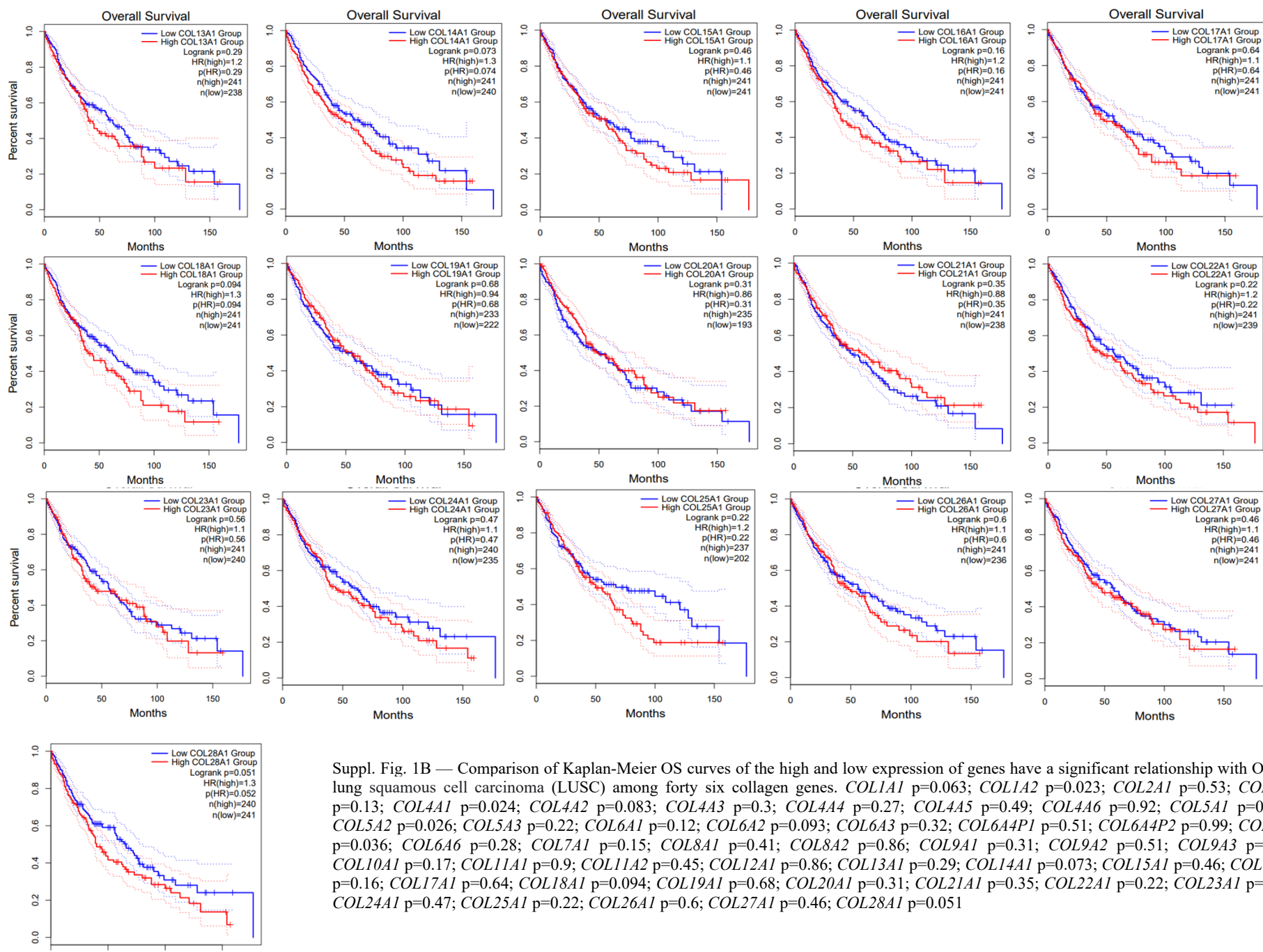


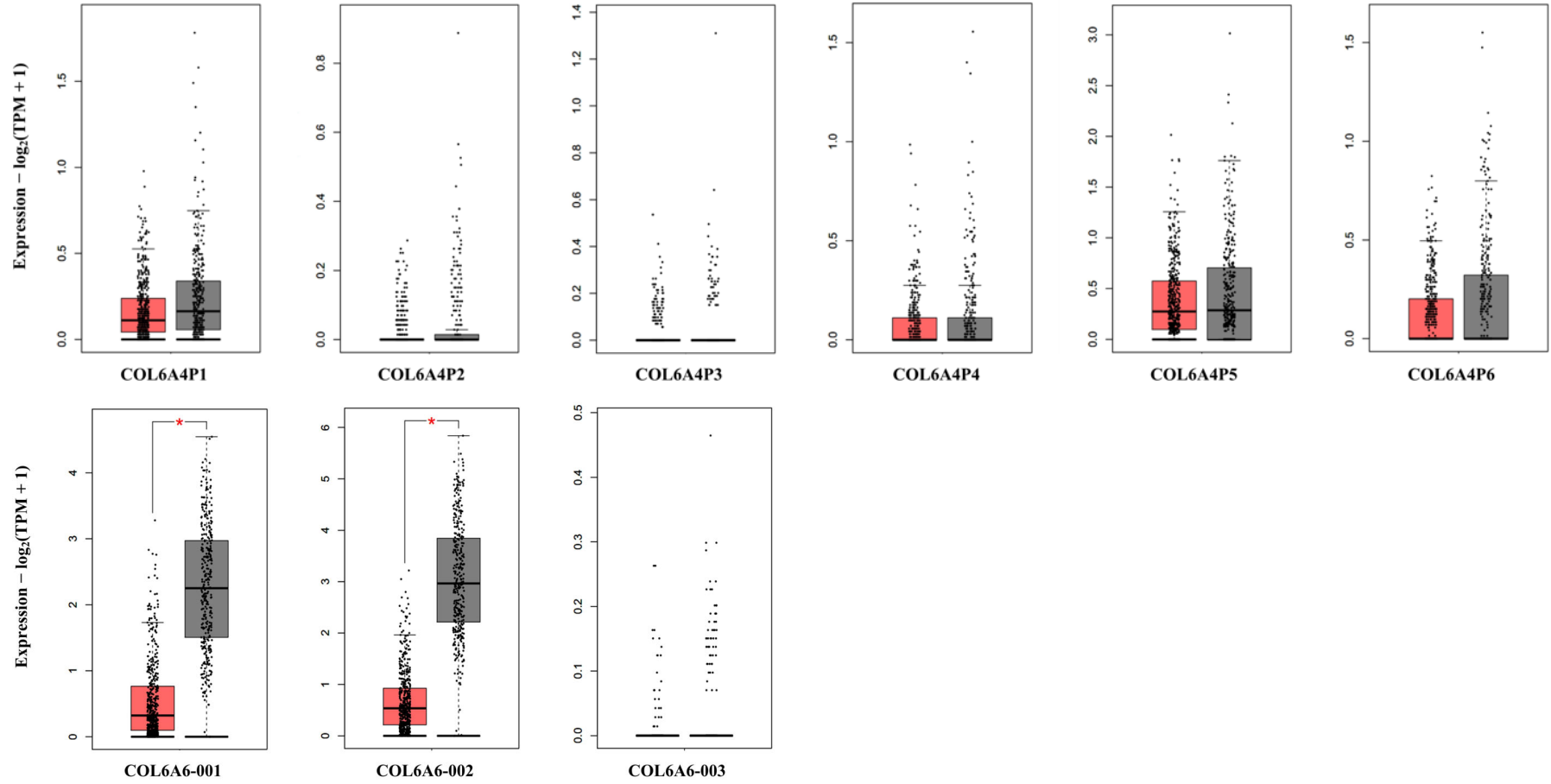
Suppl. Fig. 1A — Comparison of Kaplan-Meier curves of the high and low expression of genes have a significant relationship with OS for lung adenocarcinoma (LUAD) among forty five collagen genes*. *COL1A1* p=0.26; *COL1A2* p=0.18; *COL2A1* p=0.7; *COL3A1* p=0.52; *COL4A1* p=0.43; *COL4A2* p=0.65; *COL4A3* p=0.25; *COL4A4* p=0.25; *COL4A5* p=0.87; *COL4A6* p=0.74; *COL5A1* p=0.26; *COL5A2* p=0.079; *COL5A3* p=0.82; *COL6A1* p=0.074; *COL6A2* p=0.62; *COL6A3* p=0.67; *COL6A4P1* p=0.71; *COL6A4P2* p=0.043; *COL6A5* p=0.098; *COL6A6* p=0.019; *COL7A1* p=0.0052; *COL8A1* p=0.56; *COL8A2* p=0.11; *COL9A1* p=0.8; *COL9A2* p=0.11; *COL9A3* p=0.56; *COL10A1* p=0.32; *COL11A1* p=0.014; *COL11A2* p=0.62; *COL12A1* p=0.23; *COL13A1* p=0.065; *COL14A1* p=0.37; *COL15A1* p=0.4; *COL16A1* p=0.42; *COL17A1* p=0.34; *COL18A1* p=0.61; *COL19A1* p=0.0018; *COL21A1* p=0.075; *COL22A1* p=0.0049; *COL23A1* p=0.32; *COL24A1* p=0.072; *COL25A1* p=0.7; *COL26A1* p=0.57; *COL27A1* p=0.25; *COL28A1* p=0.23

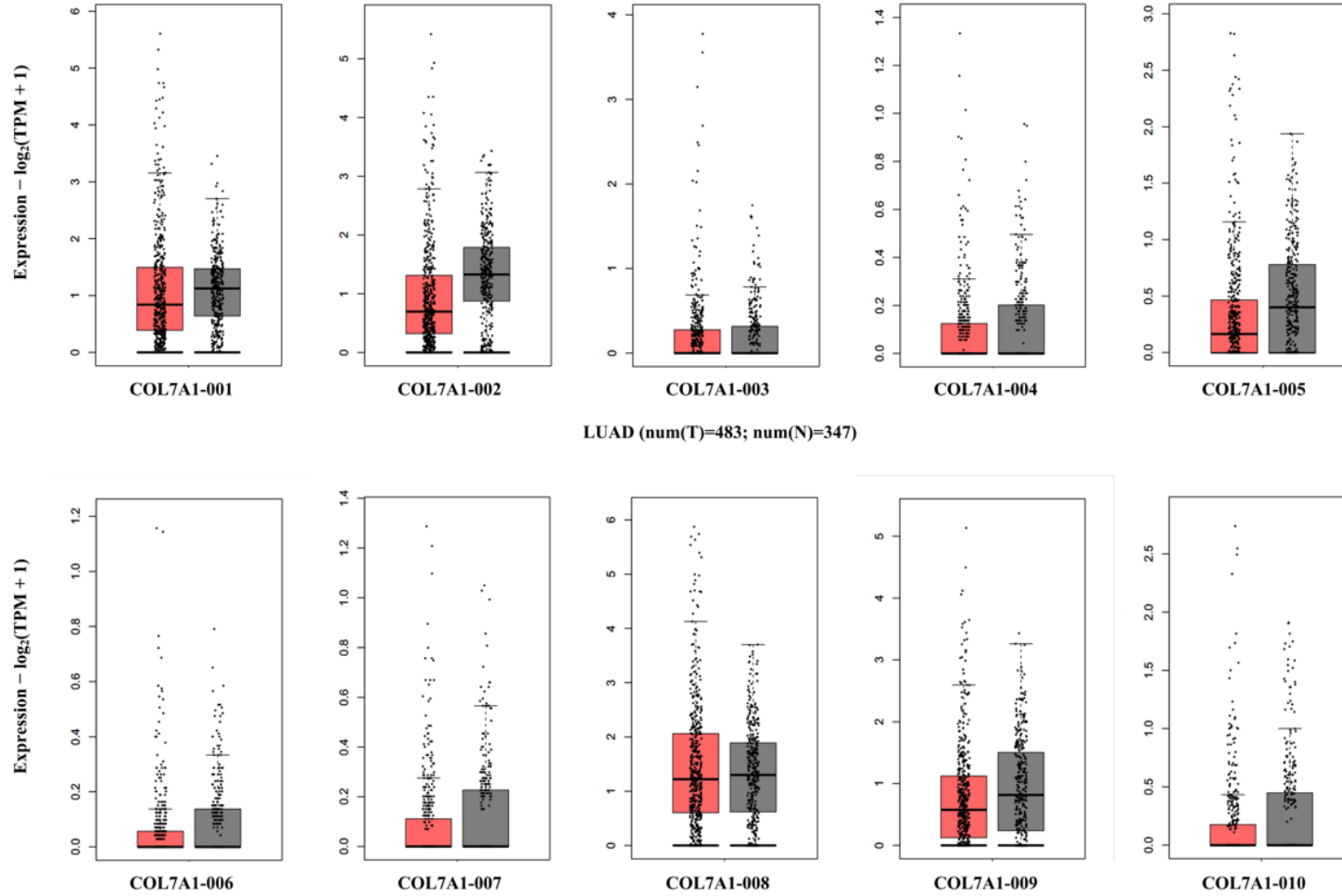
[*Since *COL20A1* gene isn't significant in terms of survival, GEPIA2 does not form a graph. Therefore, it is not included in the analysis]

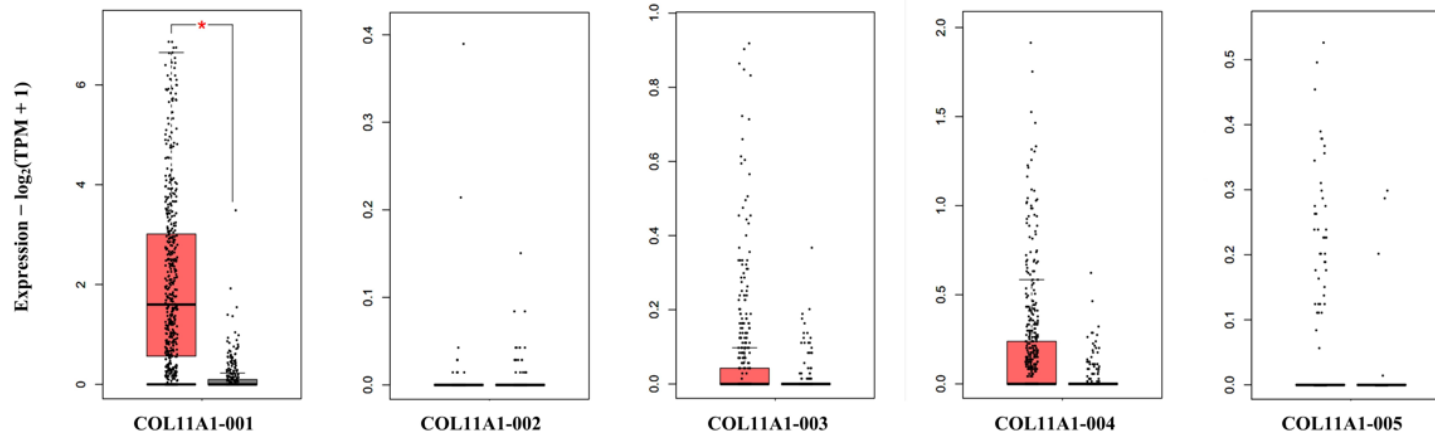




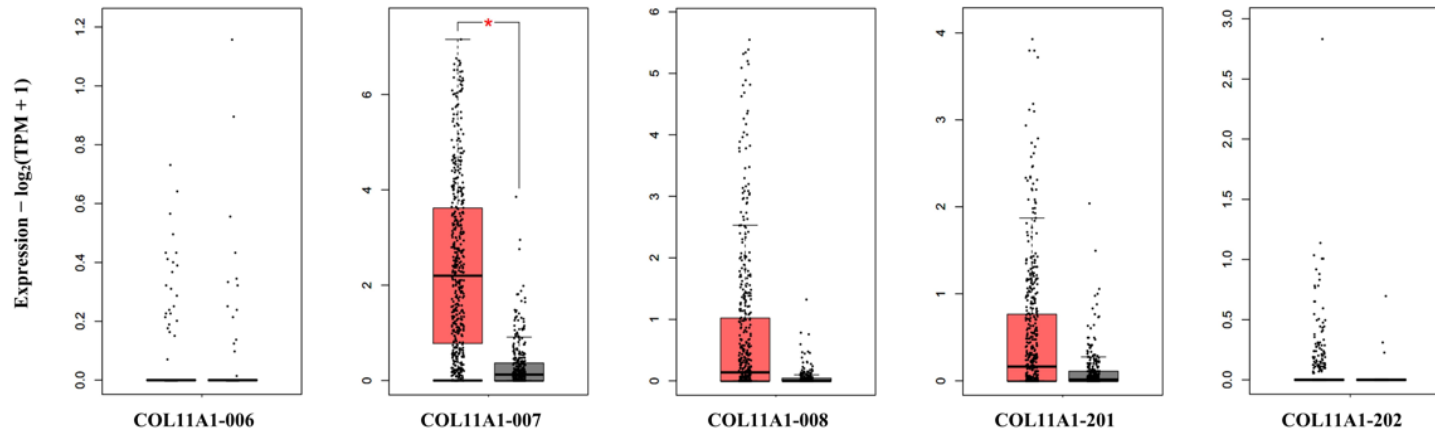


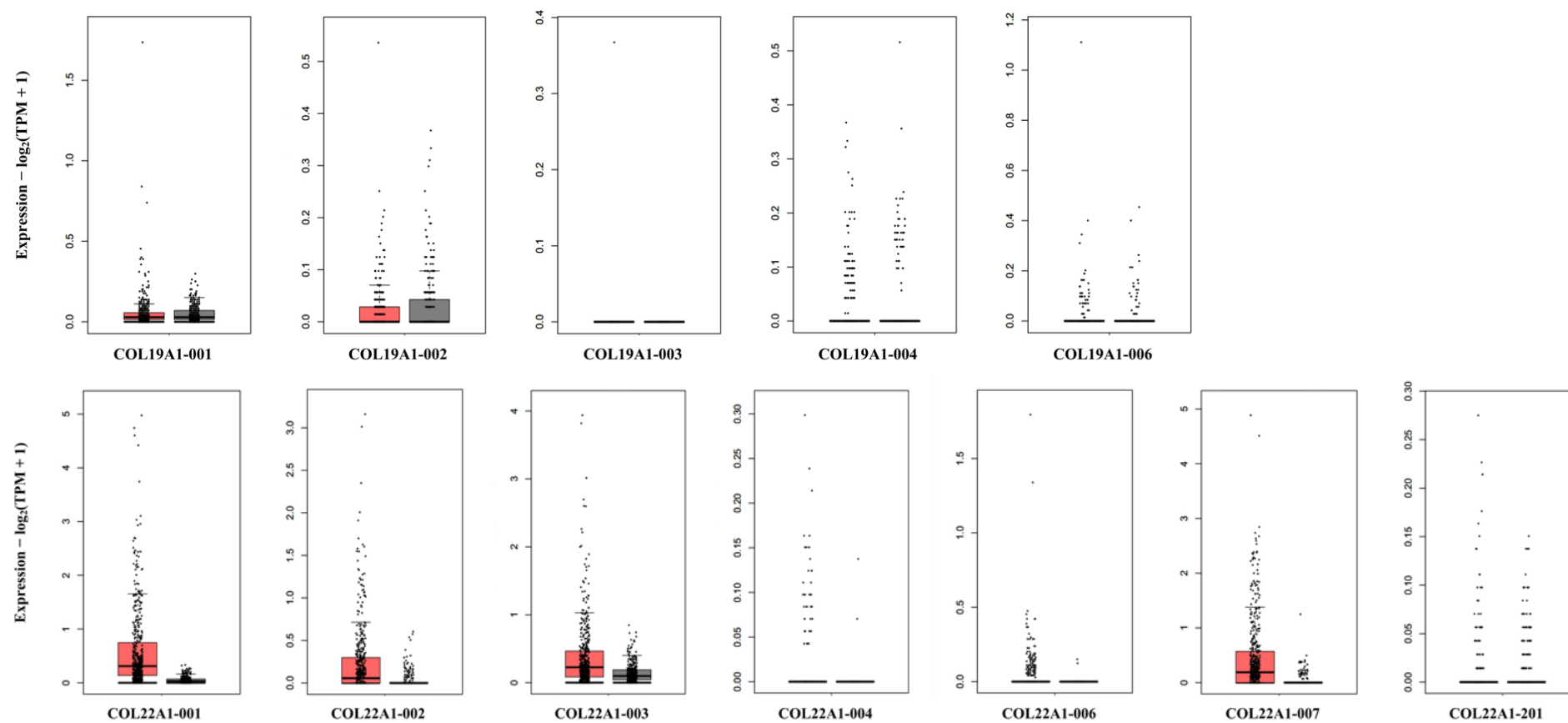




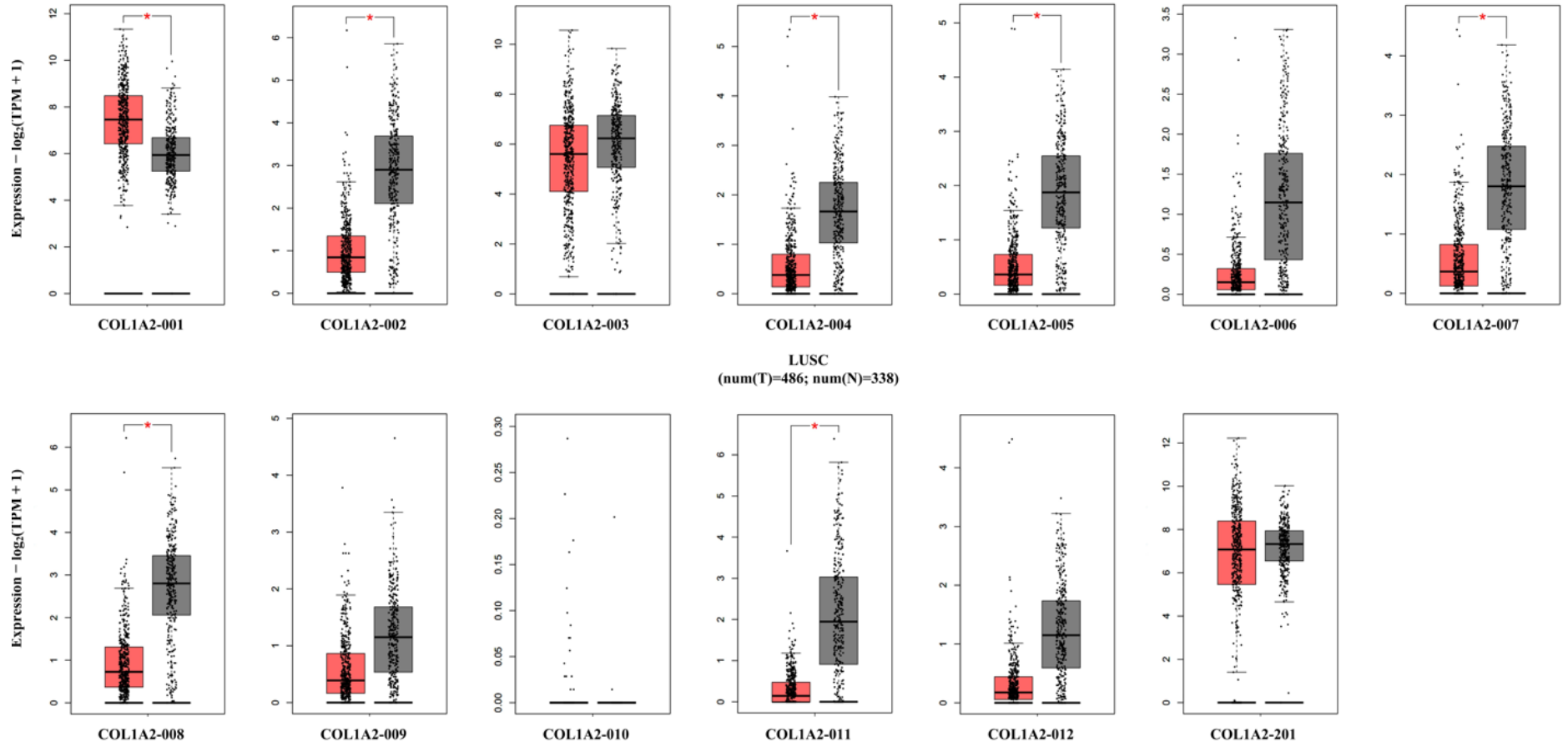


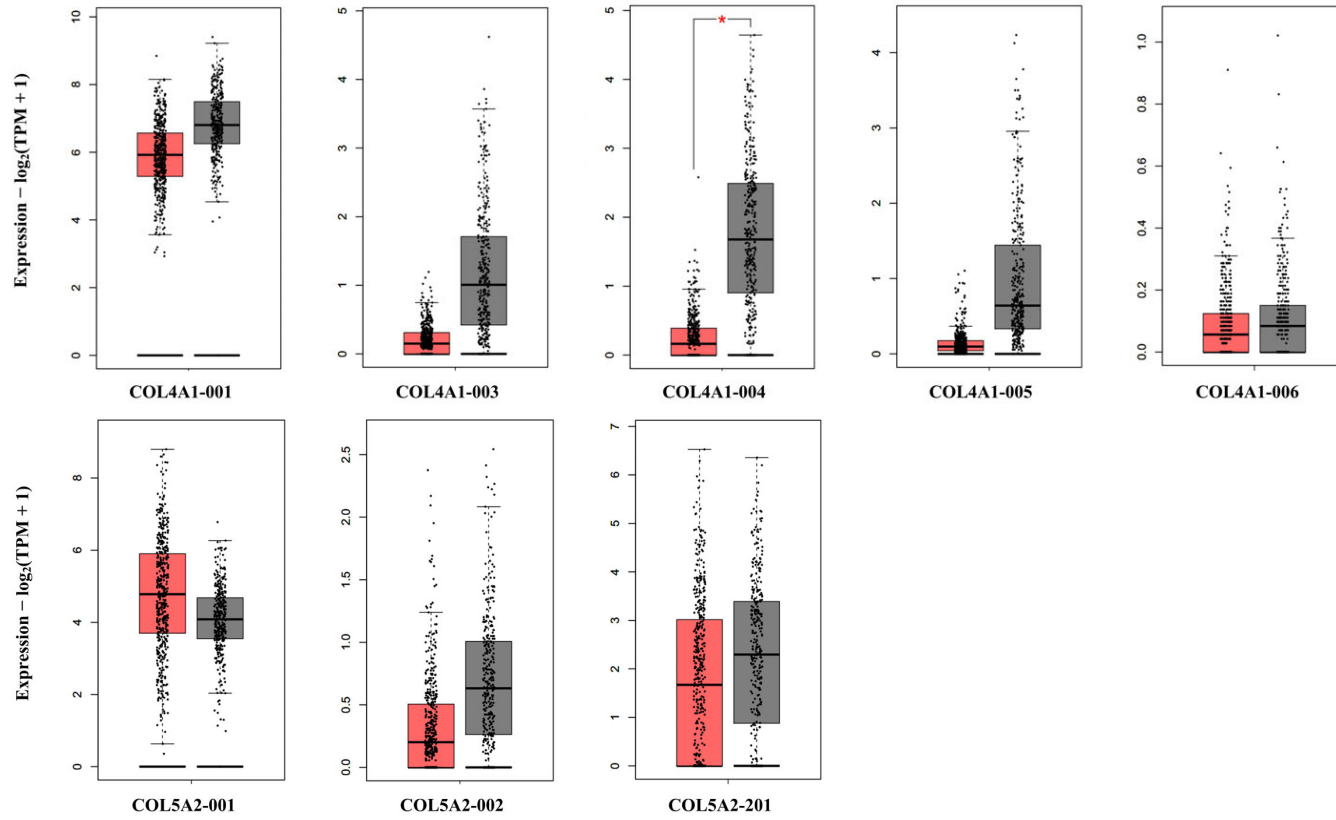
LUAD (num(T)=483; num(N)=347)

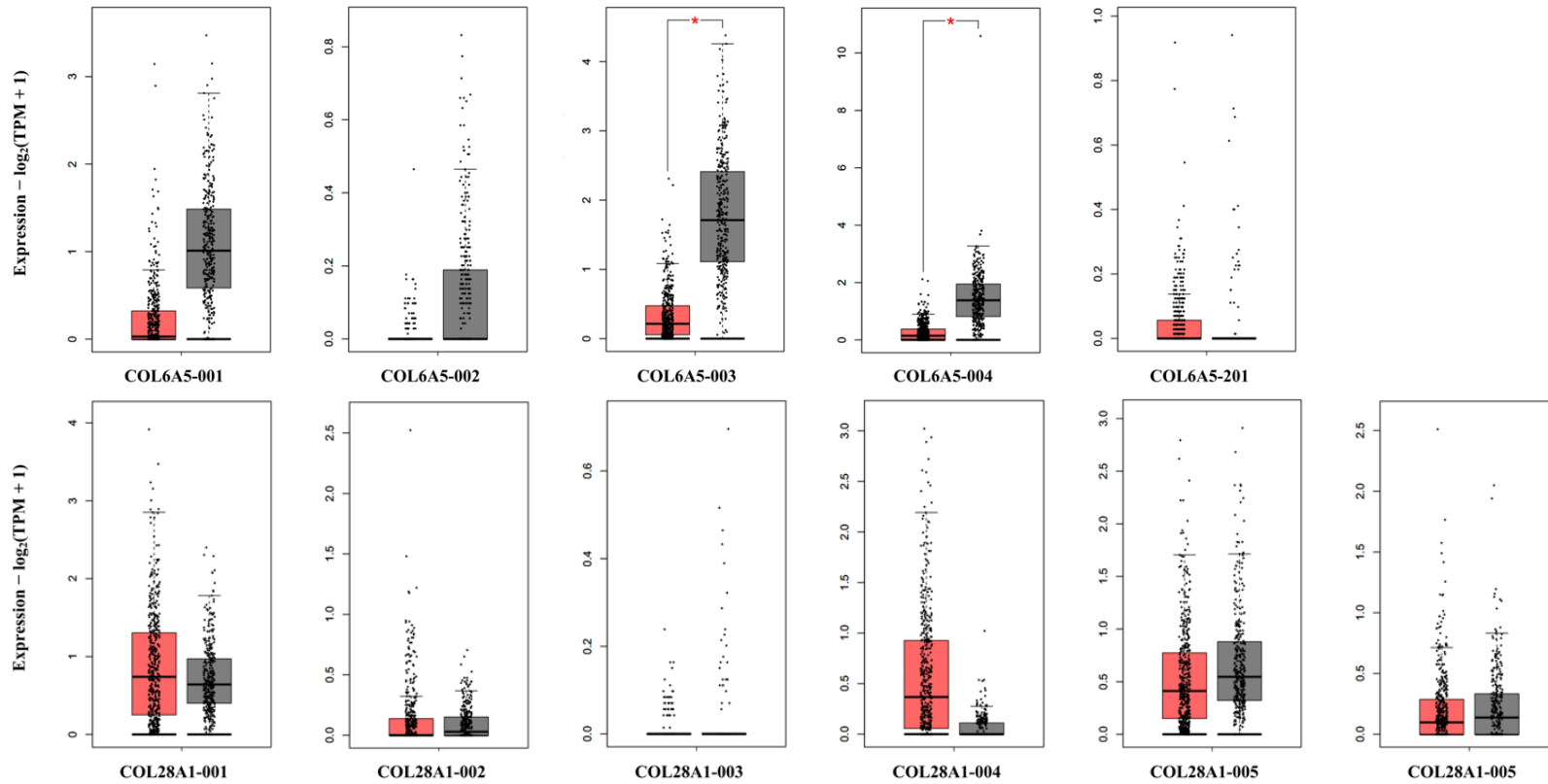




Suppl. Fig. 2A — Comparative analysis of the tissue-specific differential expression of *COL6A4P*, *COL6A6*, *COL7A1*, *COL11A1*, *COL19A1* and *COL22A1* transcripts in lung adenocarcinoma (LUAD)* using GEPIA2. [*Forty one box plots are based on 483 LUAD samples (marked in red) and 347 normal samples (marked in grey). (**P* < 0.05)]







Suppl. Fig. 2B — Comparative analysis of the tissue-specific differential expression of *COL1A2*, *COL5A2*, *COL6A5* and *COL28A1* transcripts in lung squamous cell carcinoma (LUSC)* using GEPIA2. [*Fourty one box plots are based on 486 LUSC samples (marked in red) and 338 normal samples (marked in grey). (* $P < 0.05$)]