



**Figure S1** Identification of the genomic instability-associated lncRNA. (A) Patients were ranked in decreasing order of the cumulative number of somatic mutations. The top 25% of patients (n=91) were defined as the GU group, and the last 25% (n=90) were defined as the GS group. Forty lncRNA (top 20 increasing and top 20 decreasing lncRNA) are presented in heatmap. (B) Eight genomic instability-associated lncRNA identified by univariate Cox regression method. lncRNA, long non-coding RNA; GU, genomically unstable; GS, genomically stable.

**Table S1** Clinical baseline of training and testing cohorts

Covariates	Type	Total cohort, n (%)	Training cohort, n (%)	Testing cohort, n (%)	P value
Age	≤65	153 (45.4)	70 (41.42)	83 (49.4)	0.156
	>65	181 (53.71)	98 (57.99)	83 (49.4)	
	Unknown	3 (0.89)	1 (0.59)	2 (1.19)	
Gender	Female	119 (35.31)	60 (35.5)	59 (35.12)	1
	Male	218 (64.69)	109 (64.5)	109 (64.88)	
Grade	G1–2	129 (38.28)	64 (37.87)	65 (38.69)	1
	G3	199 (59.05)	98 (57.99)	101 (60.12)	
	Unknow	9 (2.67)	7 (4.14)	2 (1.19)	
Stage	Stage I–II	152 (45.1)	68 (40.24)	84 (50.00)	0.1298
	Stage III–IV	171 (50.74)	92 (54.44)	79 (47.02)	
	Unknown	14 (4.15)	9 (5.33)	5 (2.98)	
T	T1–2	89 (26.41)	41 (24.26)	48 (28.57)	0.4377
	T3–4	244 (72.4)	126 (74.56)	118 (70.24)	
	Unknown	4 (1.19)	2 (1.18)	2 (1.19)	
M	M0	303 (89.91)	149 (88.17)	154 (91.67)	0.2761
	M1	22 (6.53)	14 (8.28)	8 (4.76)	
	Unknown	12 (3.56)	6 (3.55)	6 (3.57)	
N	N0	99 (29.38)	49 (28.99)	50 (29.76)	1
	N1–3	227 (67.36)	114 (67.46)	113 (67.26)	
	Unknown	11 (3.26)	6 (3.55)	5 (2.98)	

T, tumor; N, node; M, metastasis.