

Table S1 Post-operative abnormal coagulation functions modeling cohort summary

Biochemical indicator	Normal range	Normal before surgery	
		Normal after surgery)	Abnormal after surgery
White blood cell ($10^9/L$)	4.0-10.0	218	76
Thrombocyte ($10^9/L$)	100-400	4	306
Hemoglobin (g/L)	120-160	53	210
Neutrophil (10^9 g/L)	1.8-8.0	246	59
Lymphocyte ($10^9/L$)	0.90-5.20	173	139
Monocyte	0.16-1.0	46	268
PT ($10^9/L$)	11.0-14.5	67	240
INR	<1.2	27	287
FIB (g/L)	2.0-4.0	26	240
APTT (s)	28-42.8	28	268
D-dimer (ng/mL FEU)	68-494	168	98

PT, prothrombin time; APTT, activated-partial-thromboplastin-time; INR, international normalized ratio; FIB, fibrinogen.

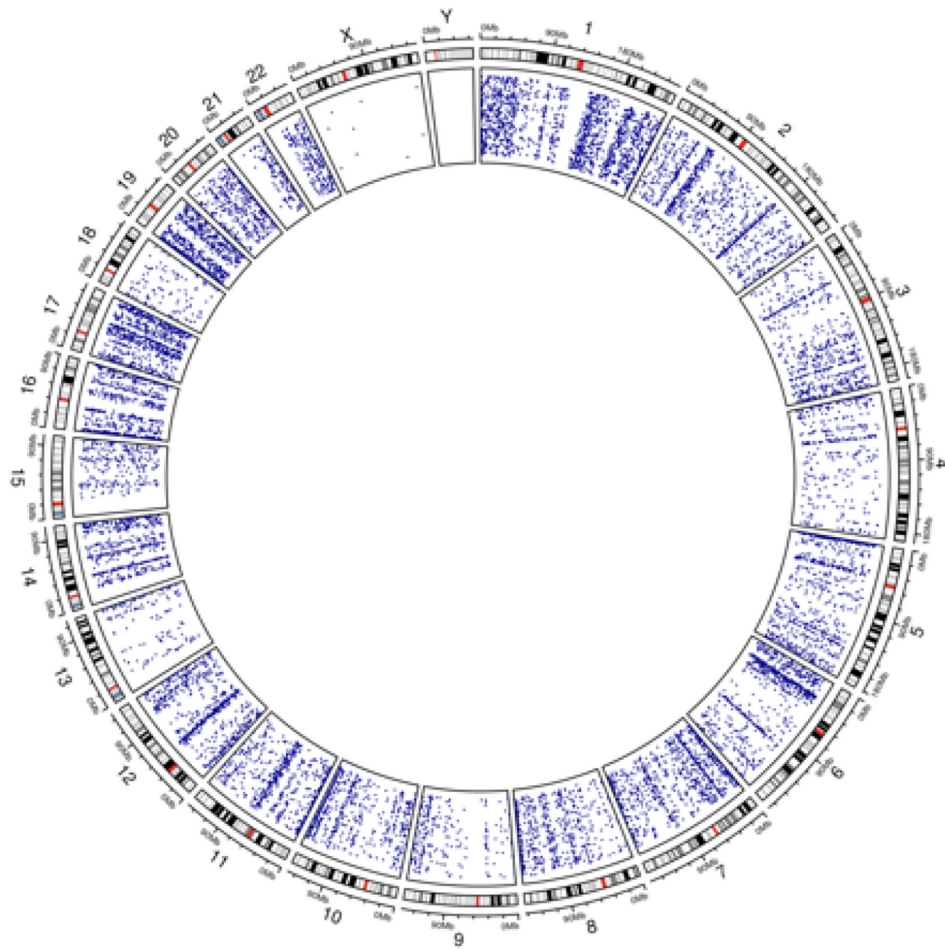


Figure S1 Targeted sequencing enrichment panel probes location.

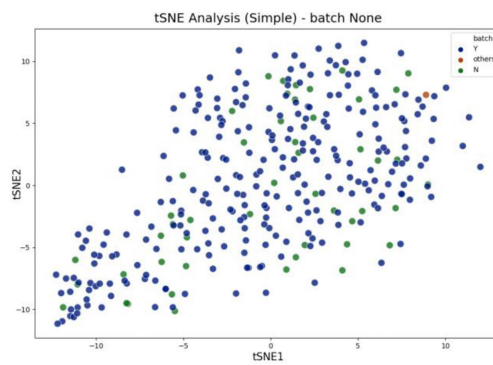
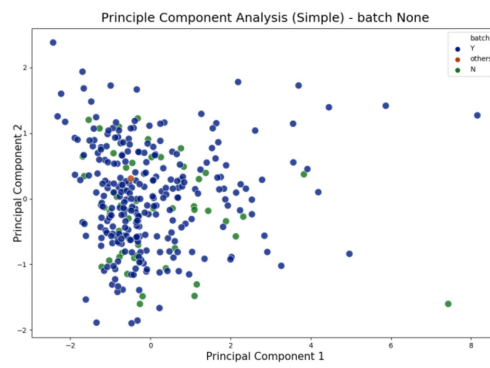


Figure S2 Correlation analysis between anesthetic reagent dosage and degree of overall methylation changes.

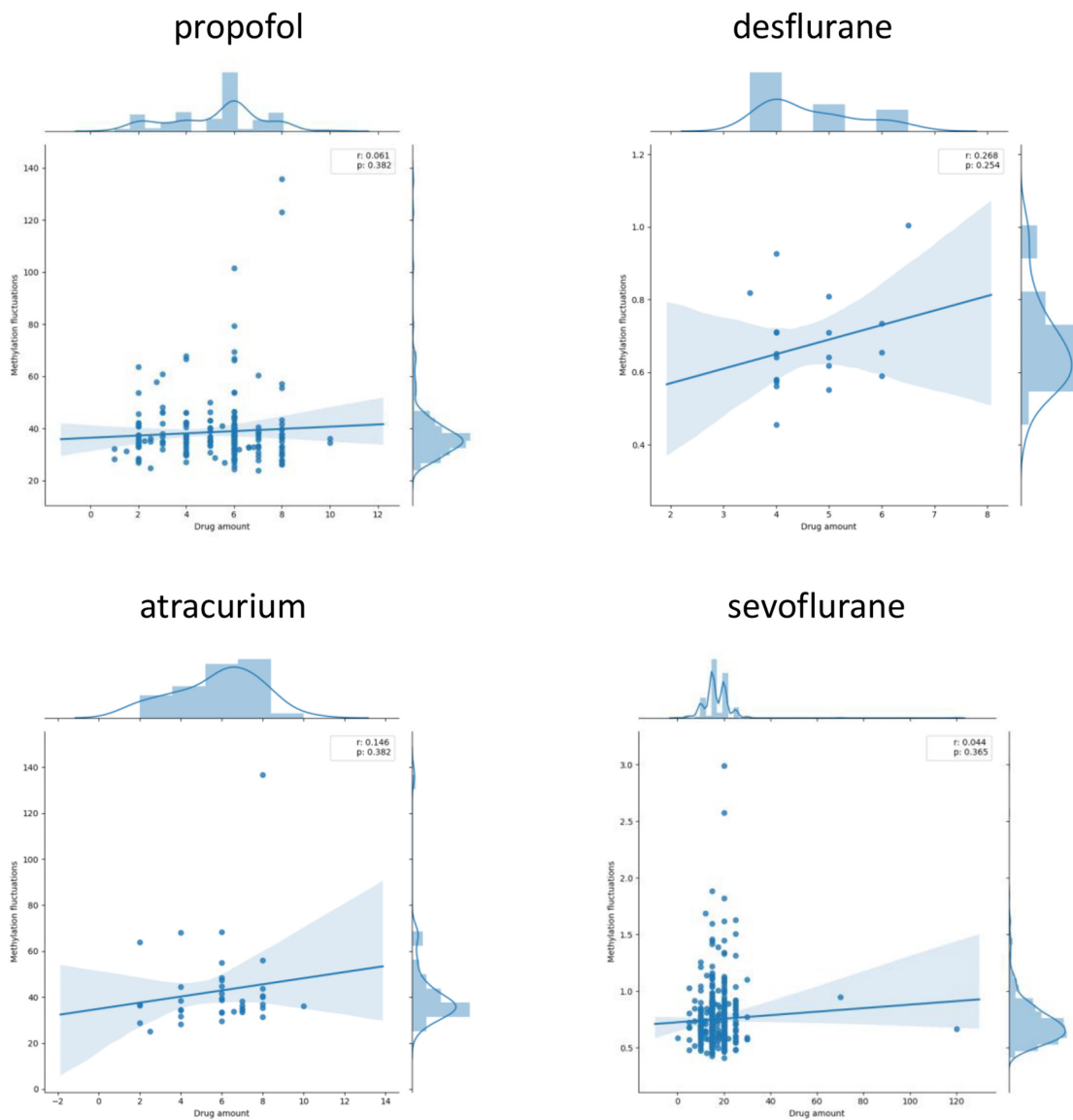


Figure S3 PCA analysis of methylation changes using different intubation methods.

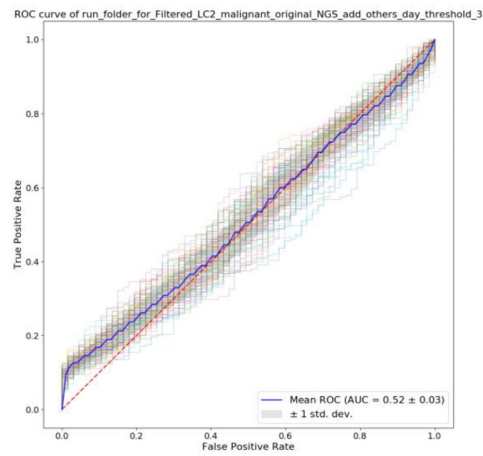
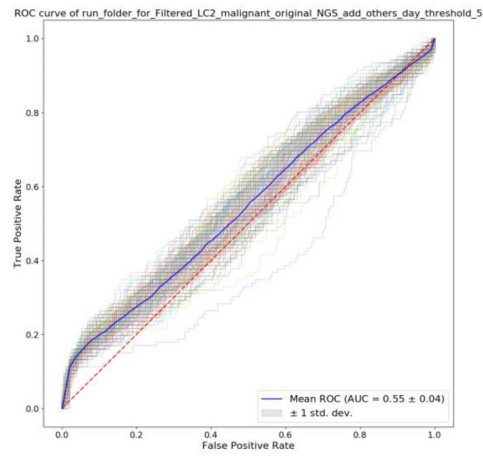


Figure S4 Predicting patients' in-patient length after surgery using GA-induced DMRs.

APTT - cg02032606

INR - cg25471923

Neutrophil - cg22157239

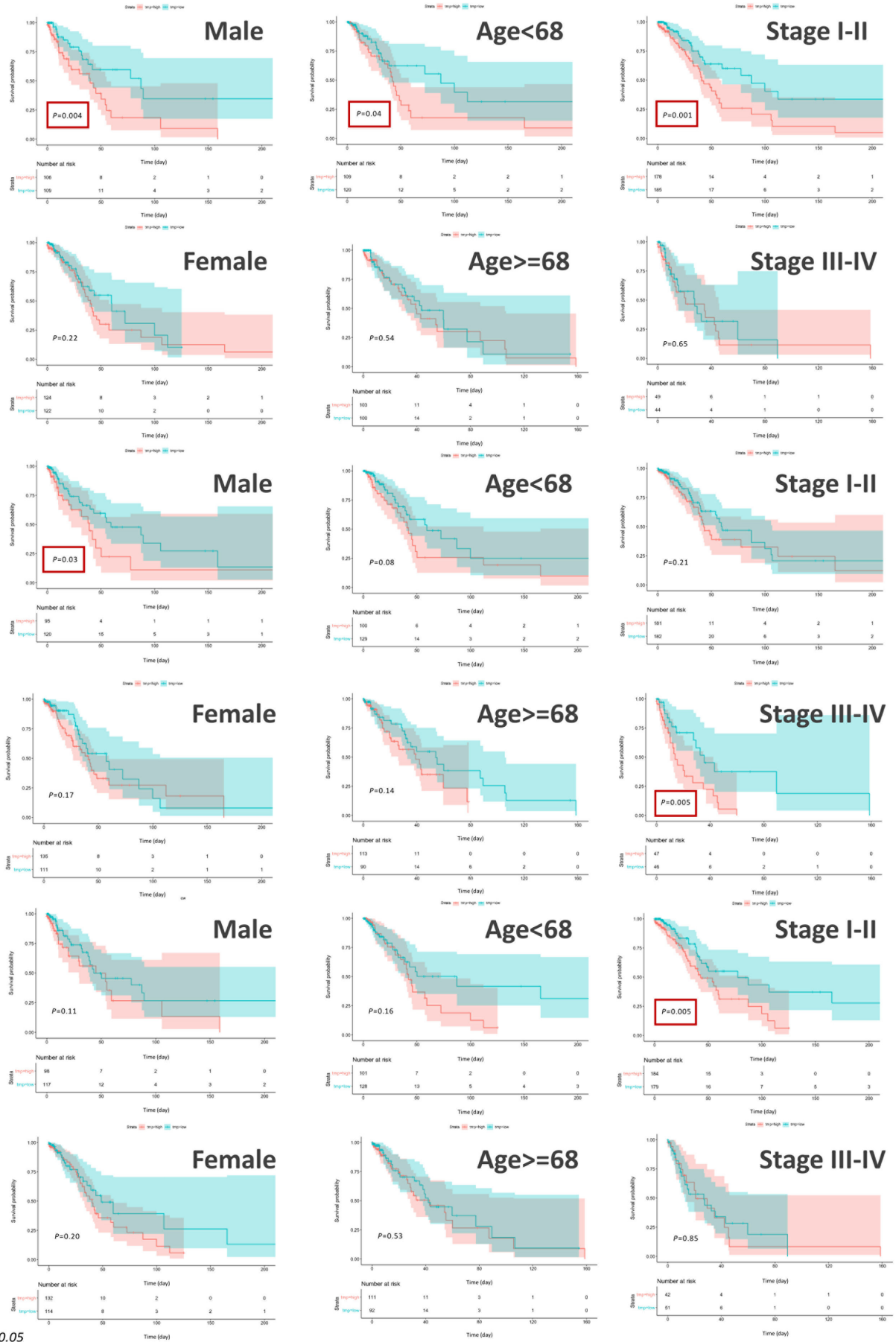
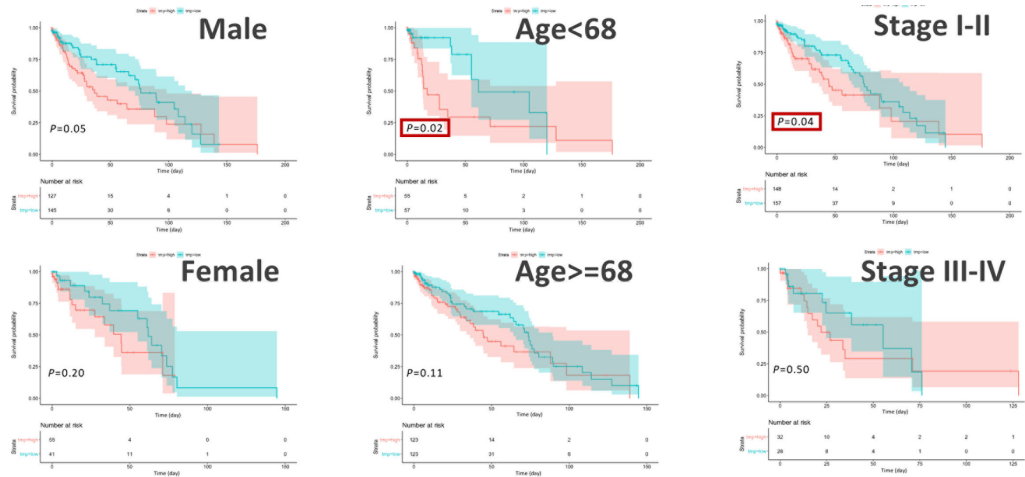
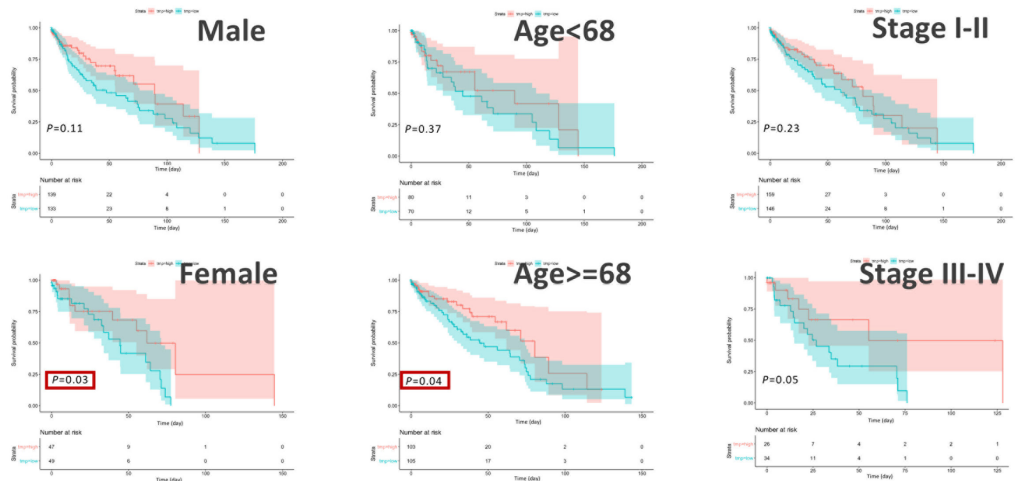


Figure S5 Prognosis prediction in LUAD using GA-induced DMR methylation, stratified by gender, age, and disease stage.

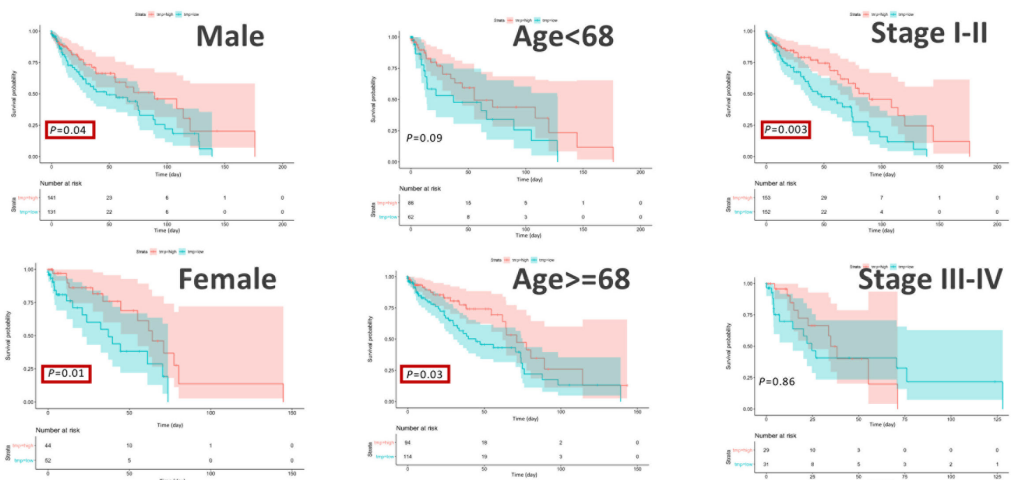
APTT-
cg02032606



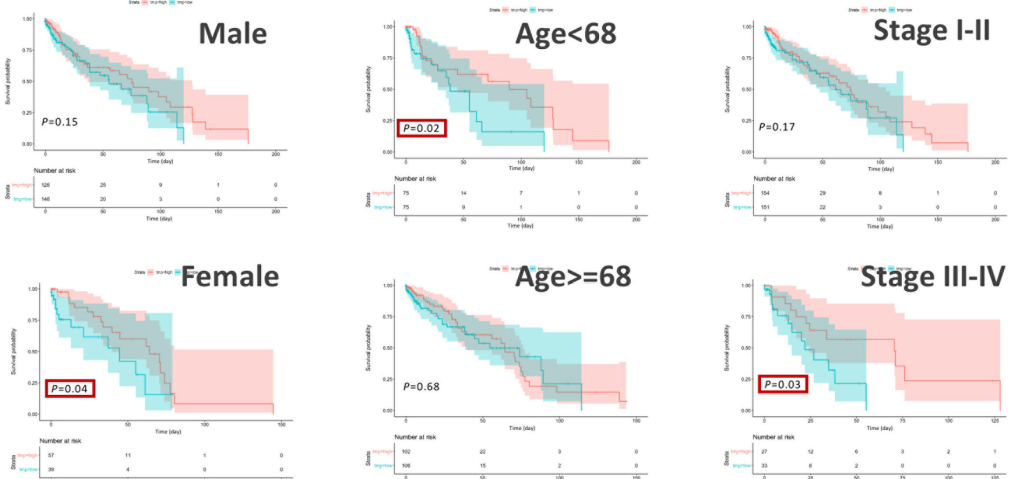
APTT-
cg10438649



D-dimer-cg05024121



Neutrophil-cg06598461



*red square, P<0.05

Figure S6 Prognosis prediction in LUSC using GA-induced DMR methylation, stratified by gender, age, and disease stage.