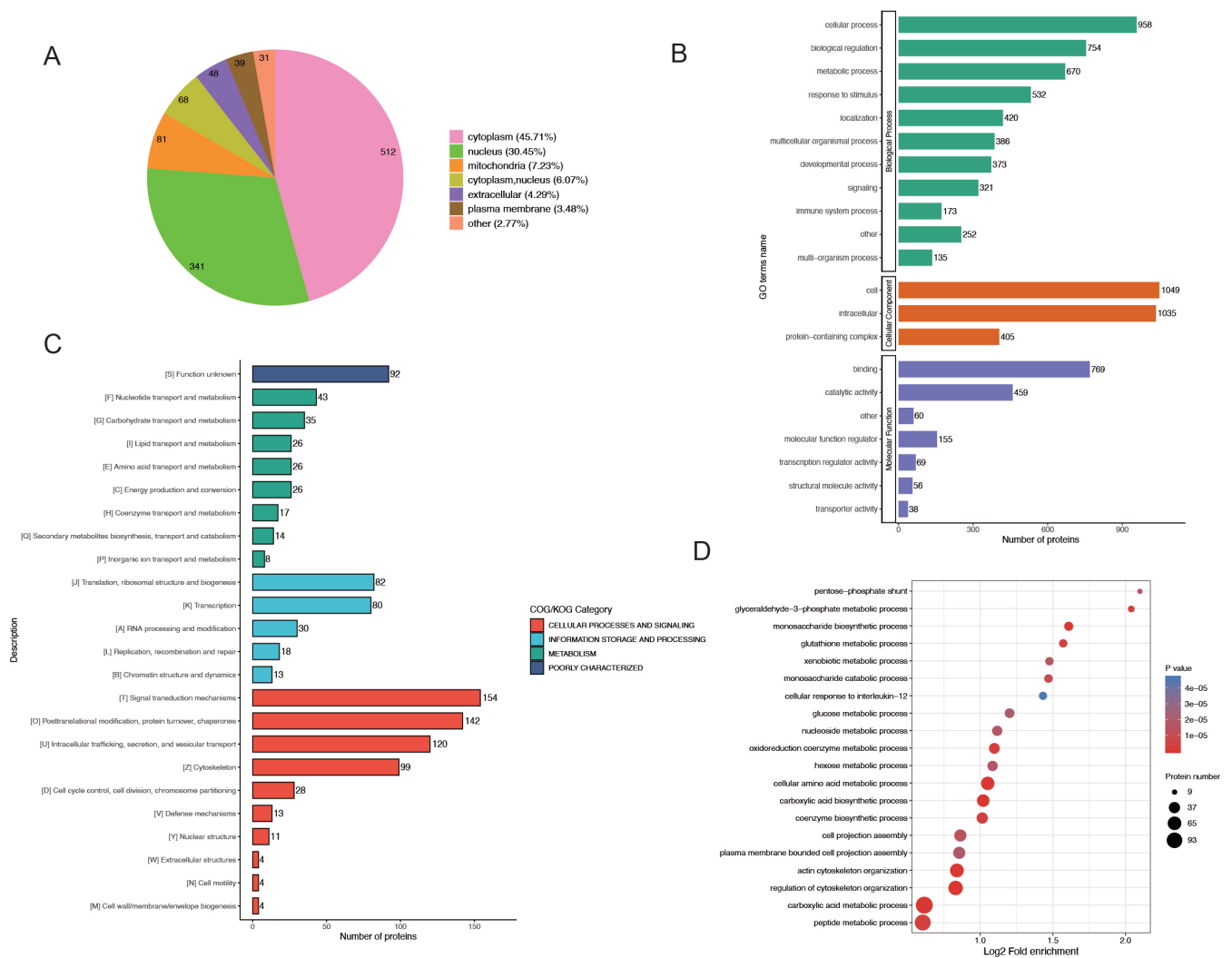


**Figure S1** Correlation between expression level of DE glycosyltransferases and prognosis in non-small cell lung cancer. (A) Kaplan-Meier analysis of overall survival according to GEO database, STT3A high expression in NSCLC patients correlates with worse survival rate ( $P=0.0055$ ). (B) In LUSC cohort, the expression level of STT3A is not correlated with prognosis ( $P=0.81$ ). (C-H) According to the survival analysis of TCGA database, the expression levels of STT3B, B4GALT5, DPM1, UGCG, C1GALT1C1 and ALG5 were not related to the survival of LUAD patients. (I) OGT expression was inversely related to poor prognosis whereas (J) STT3A expression positively correlated with poor prognosis ( $P=0.013$ ). DE, differentially expressed; GEO, Gene Expression Omnibus; NSCLC, non-small cell lung cancer; LUSC, lung squamous cell carcinoma; TCGA, The Cancer Genome Atlas; LUAD, lung adenocarcinoma.

**Table S1** Correlation between STT3A expression and clinicopathological variables in patients with lung adenocarcinoma

Variables	Number	STT3A expression		$\chi^2$	P value
		High	Low		
All patients	183	92	91		
Gender				1.975	0.1599
Male	102	56	46		
Female	81	36	45		
Age				2.013	0.1559
<60 years	73	32	41		
≥60 years	110	60	50		
Tumor size				0.9501	0.3297
≤3 cm	68	31	37		
>3 cm	115	61	54		
Tumor location				0.1312	0.7172
Left	72	35	37		
Right	111	57	54		
Pathological grade				0.9588	0.3275
I & II	117	62	55		
III	66	30	36		
Lymph node				2.886	0.0893
Negative	89	39	50		
Positive	94	53	41		
Metastasis				3.084	0.0791
Negative	180	92	88		
Positive	3	0	3		
TNM stage				0.3082	0.5822
I & II	113	55	58		
III & IV	70	37	33		



**Figure S2** GO/COG analysis of down-regulated protein after STT3A deletion in PC-9. (A) The number of down-regulated proteins in each cell component. (B) GO enrichment analysis found down-regulated protein in biological process, cellular component and molecular function, and (C) COG analysis confirmed down-regulated changes in cell cycle and cell signaling pathway. (D) The down-regulated changes of GO analysis in BP are mainly concentrated in glucose metabolic process, plasma membrane bounded assembly and mitochondrial metabolism. GO, Gene Ontology; COG, Cluster of Orthologous Groups; BP, biological process.