

Figure S1 Expression heatmap of 306 differentially expressed genes were drawn using TCGA-LUAD. TCGA, The Cancer Genome Atlas; LUAD, lung adenocarcinoma.

Table S2 Results of GO enrichment analysis containing logFC for SLC2A1 related differential genes.

Ontology	ID	Description	setSize	enrichmentScore	NES	P value	p.adjust	qvalues	rank	leading_edge
CC	GO:0005576	Extracellular region	125	-0.292583838	-2.377642871	0.001490313	0.016661795	0.011692488	72	tags=36%, list=24%, signal=47%
CC	GO:0005615	Extracellular space	104	-0.338404417	-2.637076986	0.001517451	0.016661795	0.011692488	72	tags=40%, list=24%, signal=47%
MF	GO:0005488	Binding	276	0.358355609	2.222655997	0.002659574	0.016661795	0.011692488	140	tags=49%, list=46%, signal=273%
CC	GO:0005622	Intracellular anatomical structure	246	0.249840001	1.929538949	0.002898551	0.016661795	0.011692488	132	tags=48%, list=43%, signal=139%
CC	GO:0043228	Non-membrane-bounded organelle	110	0.351254306	3.064729333	0.002923977	0.016661795	0.011692488	178	tags=81%, list=58%, signal=53%
CC	GO:0043232	Intracellular non-membrane-bounded organelle	110	0.351254306	3.064729333	0.002923977	0.016661795	0.011692488	178	tags=81%, list=58%, signal=53%
BP	GO:0050794	Regulation of cellular process	195	0.2390881	2.136088519	0.002941176	0.016661795	0.011692488	140	tags=54%, list=46%, signal=81%
MF	GO:0005515	Protein binding	245	0.341020358	2.636977273	0.00295858	0.016661795	0.011692488	169	tags=62%, list=55%, signal=140%
CC	GO:0005634	Nucleus	121	0.29956241	2.708553234	0.00297619	0.016661795	0.011692488	177	tags=77%, list=58%, signal=54%
BP	GO:0016043	Cellular component organization	134	0.349091002	3.14216494	0.003215434	0.016661795	0.011692488	169	tags=75%, list=55%, signal=60%
BP	GO:0071840	Cellular component organization or biogenesis	134	0.349091002	3.14216494	0.003215434	0.016661795	0.011692488	169	tags=75%, list=55%, signal=60%
CC	GO:0005737	Cytoplasm	216	0.214867889	1.854808664	0.008928571	0.042410714	0.029761905	112	tags=43%, list=37%, signal=92%

Table S3 Results of KEGG enrichment analysis containing logFC for SLC2A1 related differential genes.

ID	Description	setSize	enrichmentScore	NES	P value	p.adjust	qvalues	rank	leading_edge
hsa04110	Cell cycle	16	0.506896552	2.266032203	0.001429971	0.005719886	0.003010466	159	tags=100%, list=52%, signal=51%
hsa04114	Oocyte meiosis	11	0.484745763	1.830681737	0.009039901	0.018079801	0.009515685	163	tags=100%, list=53%, signal=48%

Table S4 Results of GSEA enrichment analysis containing logFC for SLC2A1 related differential genes

ID	Description	setSize	enrichmentScore	NES	P value	p.adjust	qvalues	rank	leading_edge
HALLMARK_G2M_CHECKPOINT	HALLMARK_G2M_CHECKPOINT	35	0.551469393	3.387921132	4.00E-08	3.20E-07	4.21E-08	149	tags=97%, list=49%, signal=56%
HALLMARK_E2F_TARGETS	HALLMARK_E2F_TARGETS	30	0.448623465	2.541945996	7.17E-05	2.87E-04	3.77E-05	101	tags=70%, list=33%, signal=52%
HALLMARK_MITOTIC_SPINDLE	HALLMARK_MITOTIC_SPINDLE	22	0.485915493	2.466256924	1.86E-04	4.95E-04	6.52E-05	168	tags=100%, list=55%, signal=49%
HALLMARK_GLYCOLYSIS	HALLMARK_GLYCOLYSIS	18	0.493055556	2.332225144	9.62E-04	0.001923517	2.53E-04	164	tags=100%, list=54%, signal=49%
HALLMARK_MTORC1_SIGNALING	HALLMARK_MTORC1_SIGNALING	10	0.537546645	1.948032945	0.009670248	0.015472396	0.002035842	123	tags=90%, list=40%, signal=56%
HALLMARK_SPERMATOGENESIS	HALLMARK_SPERMATOGENESIS	10	0.525471687	1.904274105	0.012270596	0.016360794	0.002152736	118	tags=90%, list=39%, signal=57%
HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION	15	0.422654174	1.854485291	0.016337481	0.018671406	0.002456764	162	tags=93%, list=53%, signal=46%

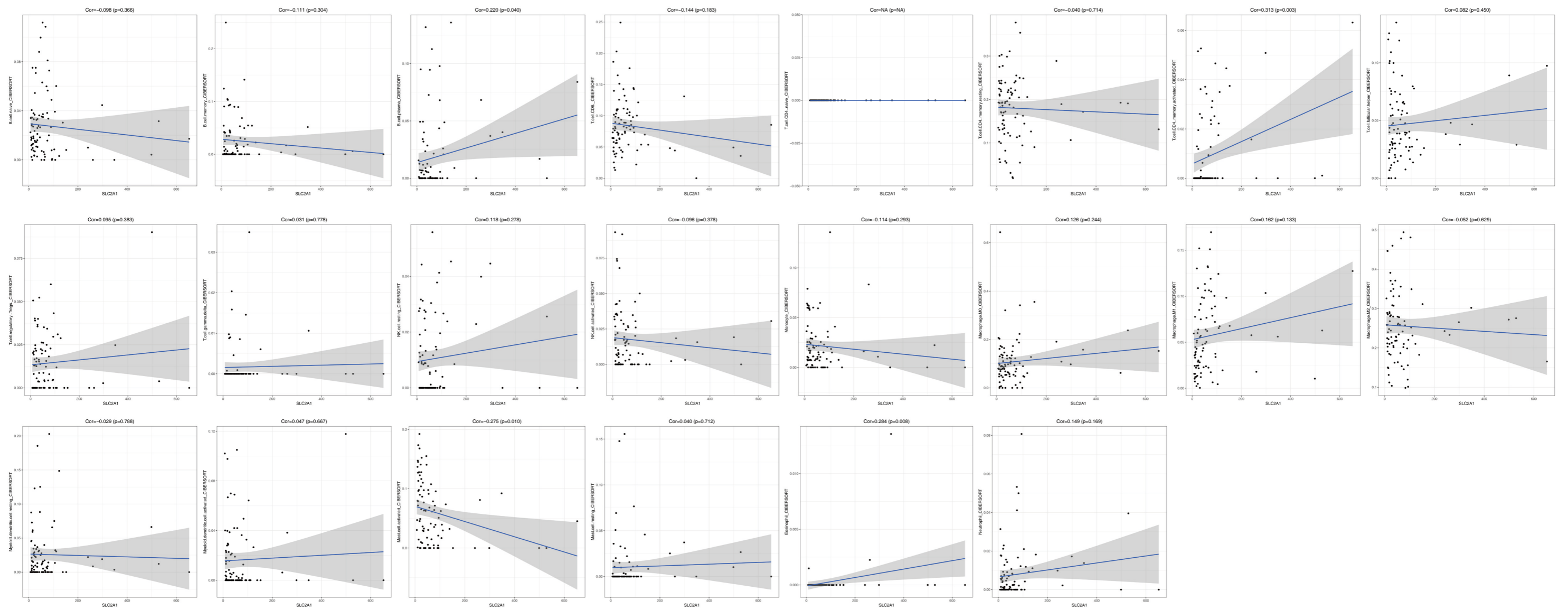


Figure S2 Results of the correlation analysis between SLC2A1 and 22 tumor immune infiltration cells by CIBERSORT using GSE40419.

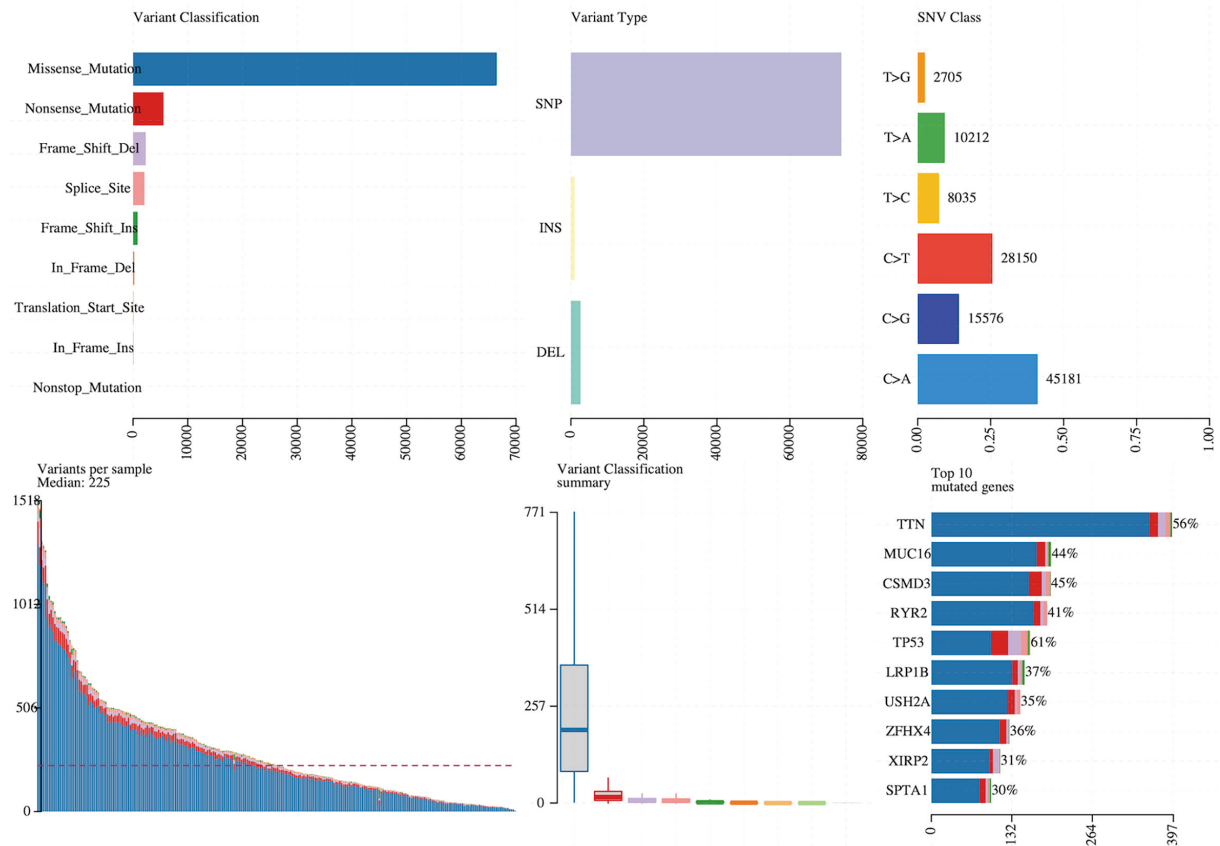
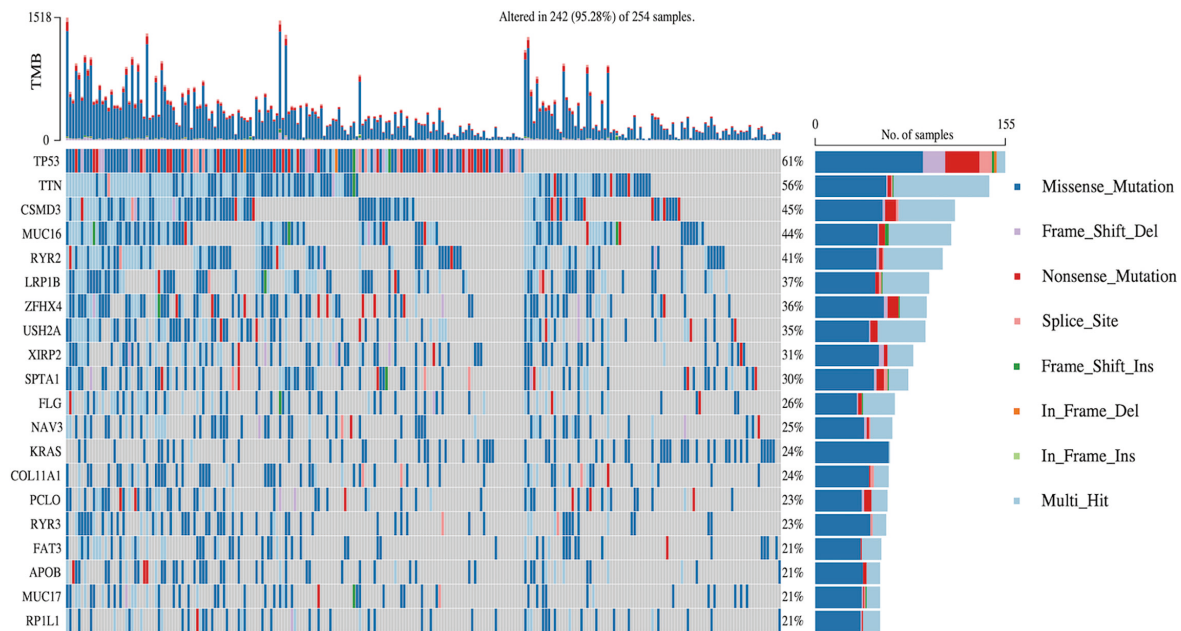


Figure S3 Waterfall plot of somatic mutations in patients with SLC2A1 overexpression in TCGA-LUAD. TCGA, The Cancer Genome Atlas; LUAD, lung adenocarcinoma.

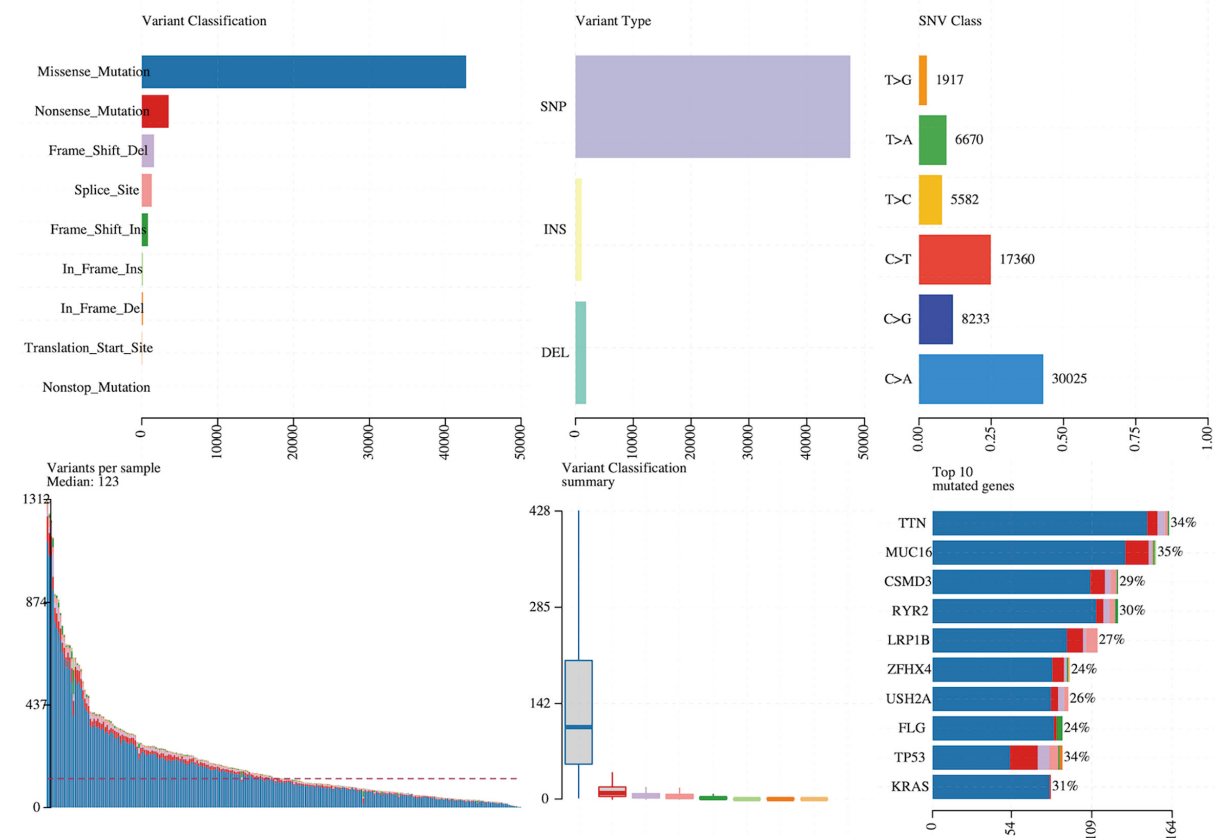
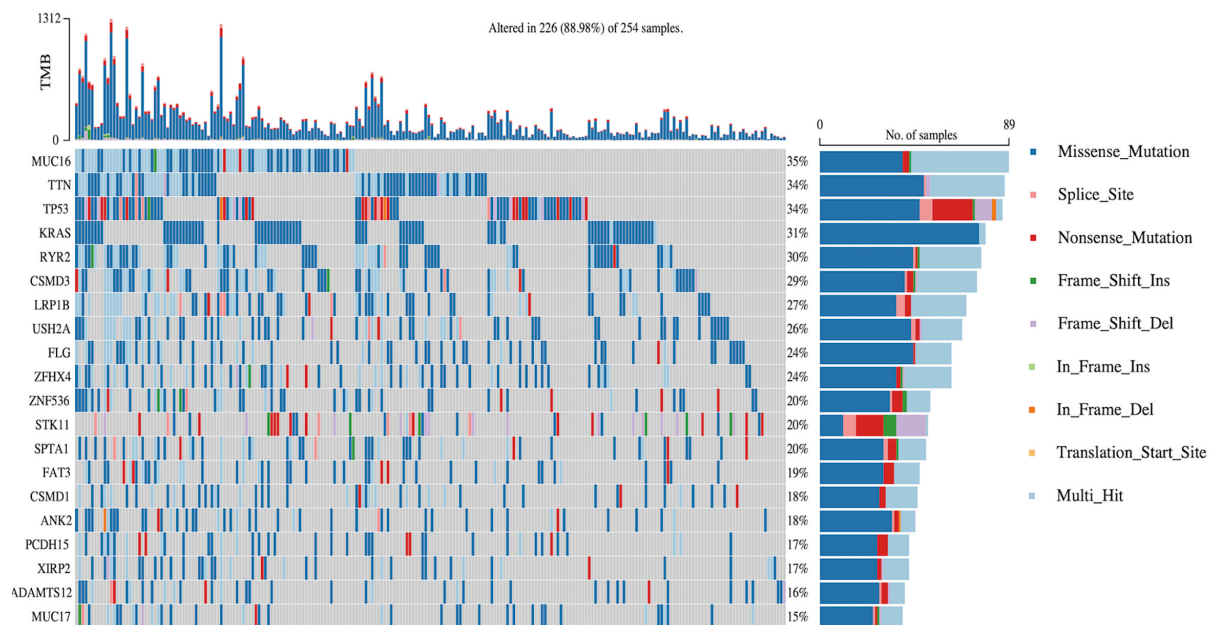


Figure S4 Waterfall plot of somatic mutations in patients with SLC2A1 low expression in TCGA-LUAD. TCGA, The Cancer Genome Atlas; LUAD, lung adenocarcinoma.

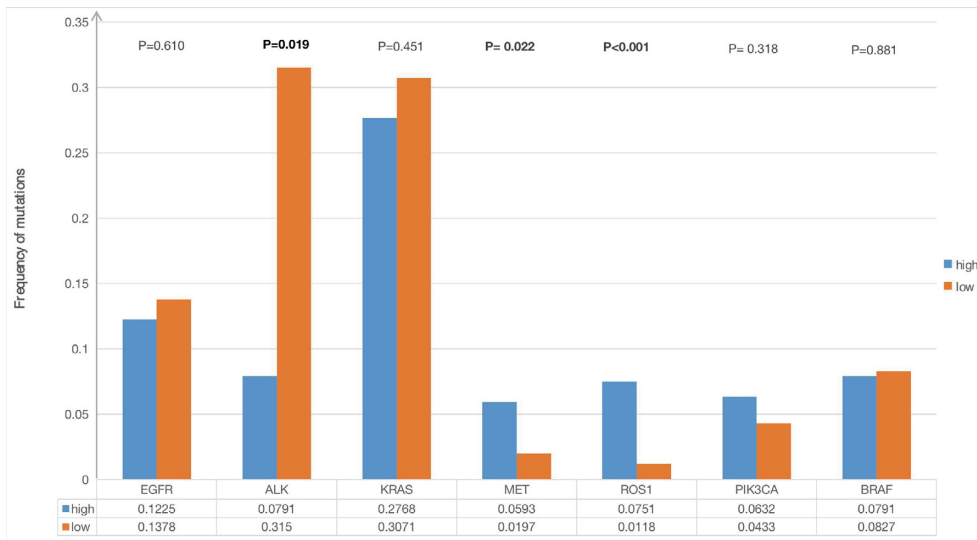


Figure S5 Mutation frequency of driver genes in SLC2A1 high and low expression groups.

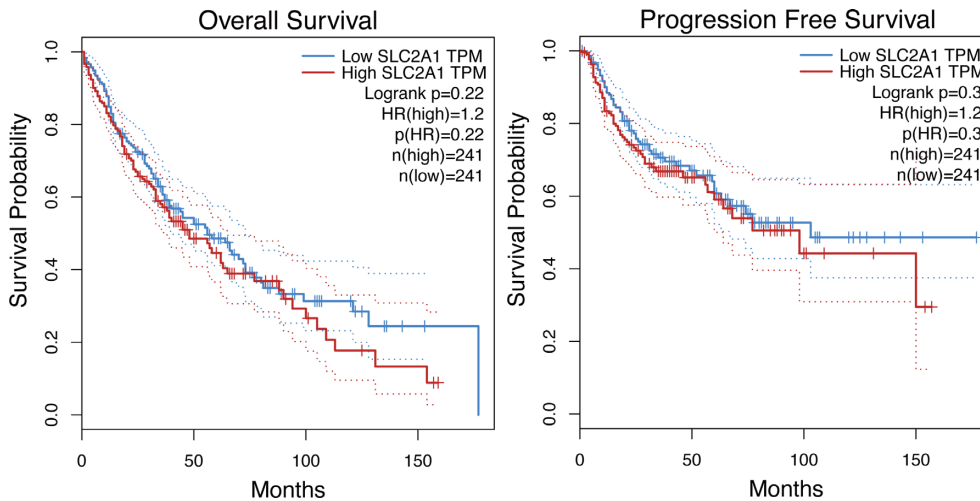


Figure S6 The survival curves of LUSC patients with high and low SLC2A1 expression in GEPIA. LUSC, lung squamous cell carcinoma; GEPIA, Gene Expression Profiling Interactive Analysis.