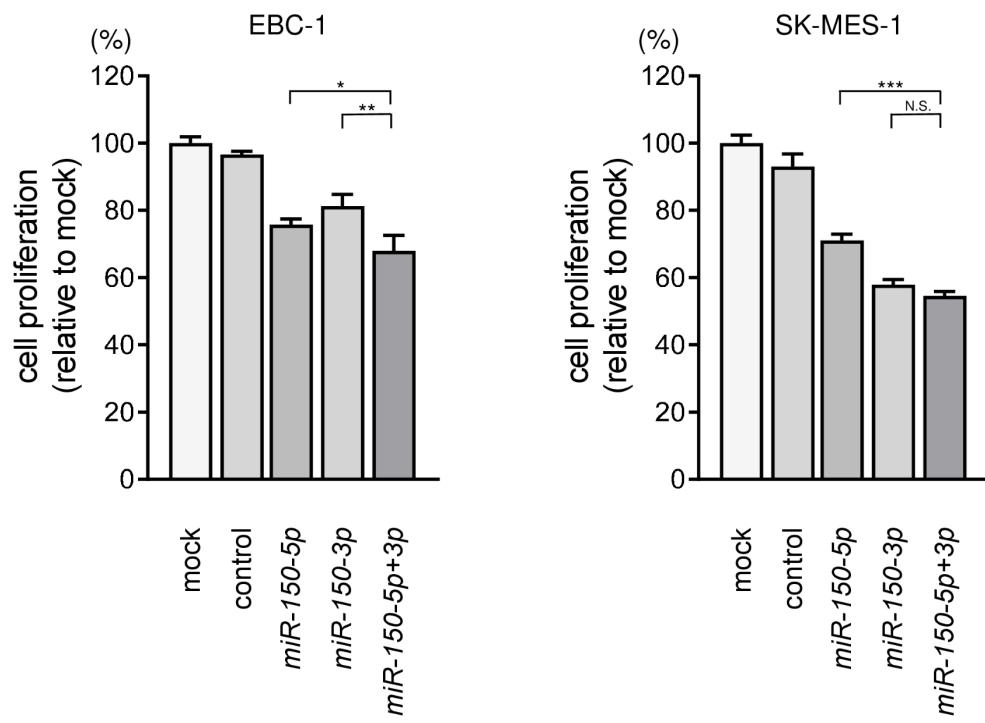
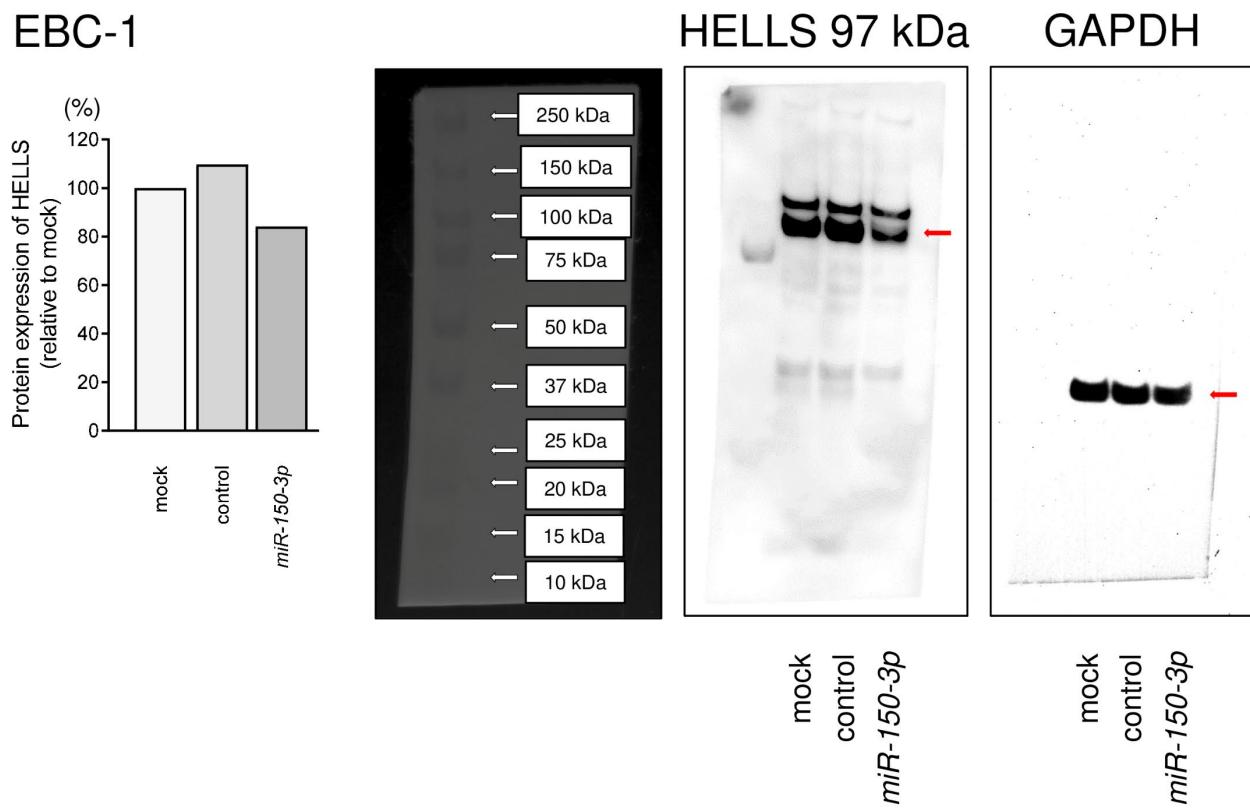


**Figure S1.** Cell migration and invasion assays in LUSQ cells with ectopic expression of *miR-150-5p* or *miR-150-3p*. (A) In wound healing assay, Phase-contrast micrographs of EBC-1 and SK-MES-1 cell lines transfected with *miR-150-5p* or *-3p* are shown. (B) Micrographs of LUSQ cells after transfection with *miR-150-5p* or *miR-150-3p* in Matrigel invasion assays are shown.



**Figure S2.** Cell proliferation was assessed with XTT assays after transfection of *miR-150-5p*, *-3p* or *5p + 3p*. Synergistic effects were not observed by combination of *miR-150-5p* and *miR-150-3p*. \*  $p < 0.05$ , \*\*  $p < 0.001$ , \*\*\*  $p < 0.01$ , N.S.: not significant.

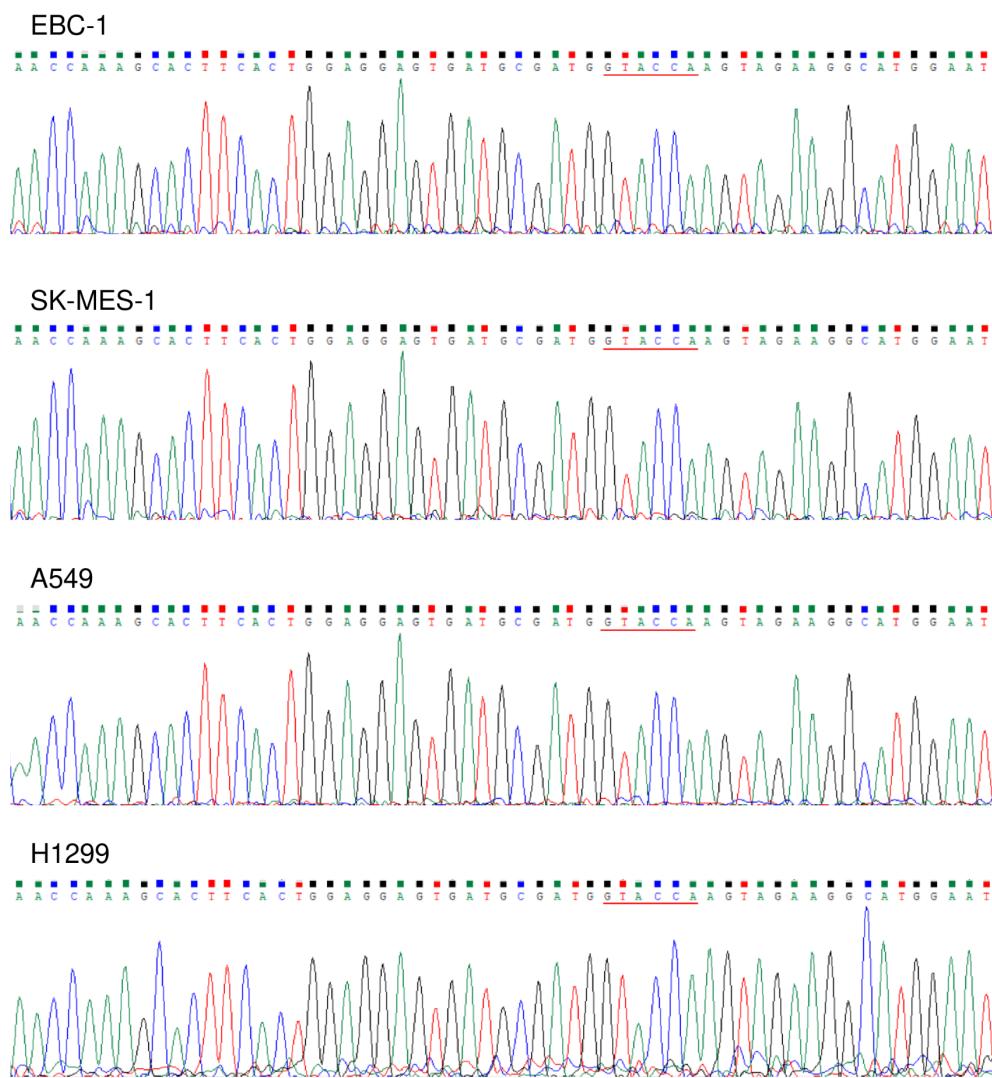


**Figure S3.** Downregulation of HELLs protein expression by *miR-150-3p*. Western blotting was performed to assay expression of HELLs protein. Full images of western blotting are shown. The western blotting results were quantified by ImageJ.

Homo sapiens helicase, lymphoid specific (HELLS), transcript variant 2, mRNA  
NCBI Reference Sequence: NM\_001289067.2  
CDS 135-2789

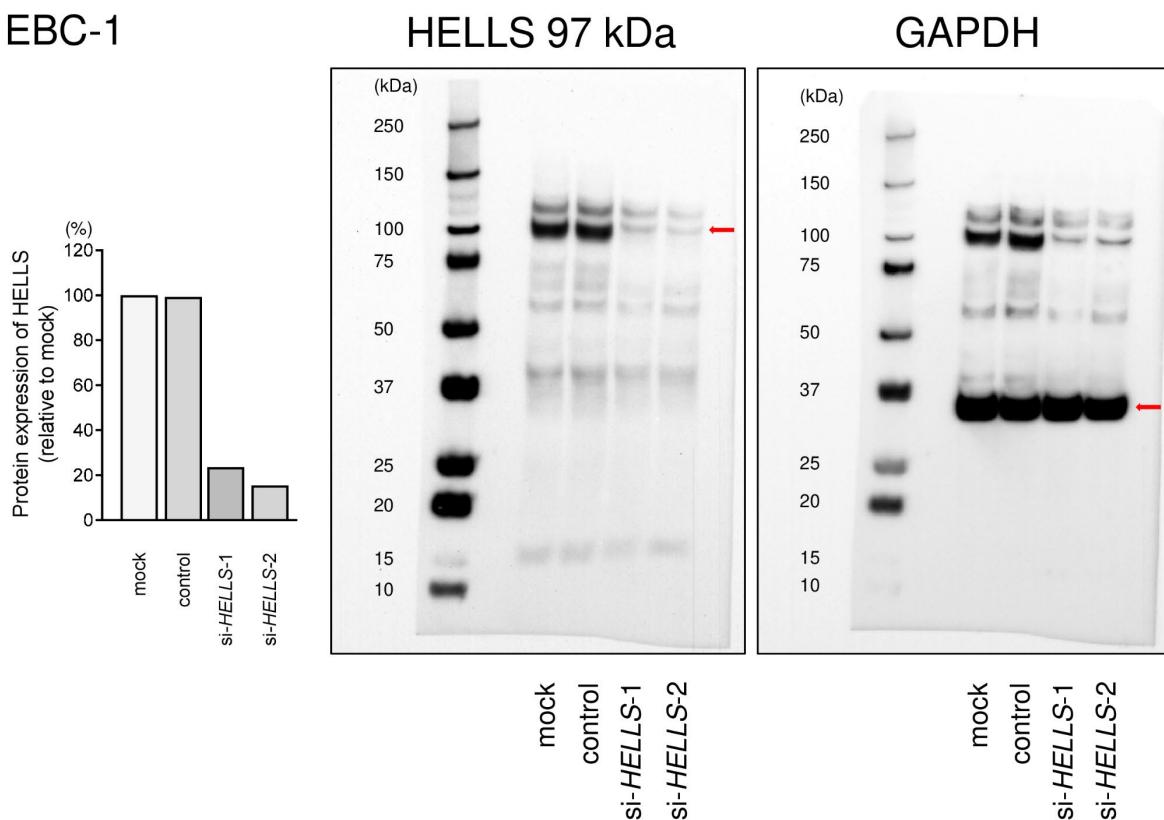
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**Figure S4.** The nucleotide sequence of *HELLS* gene (NM\_001289067.2). The first methionine (atg) and stop codon (taa) are shown in red. The binding sequences of *miR-150-3p* (gtacca) is shown in bold red.

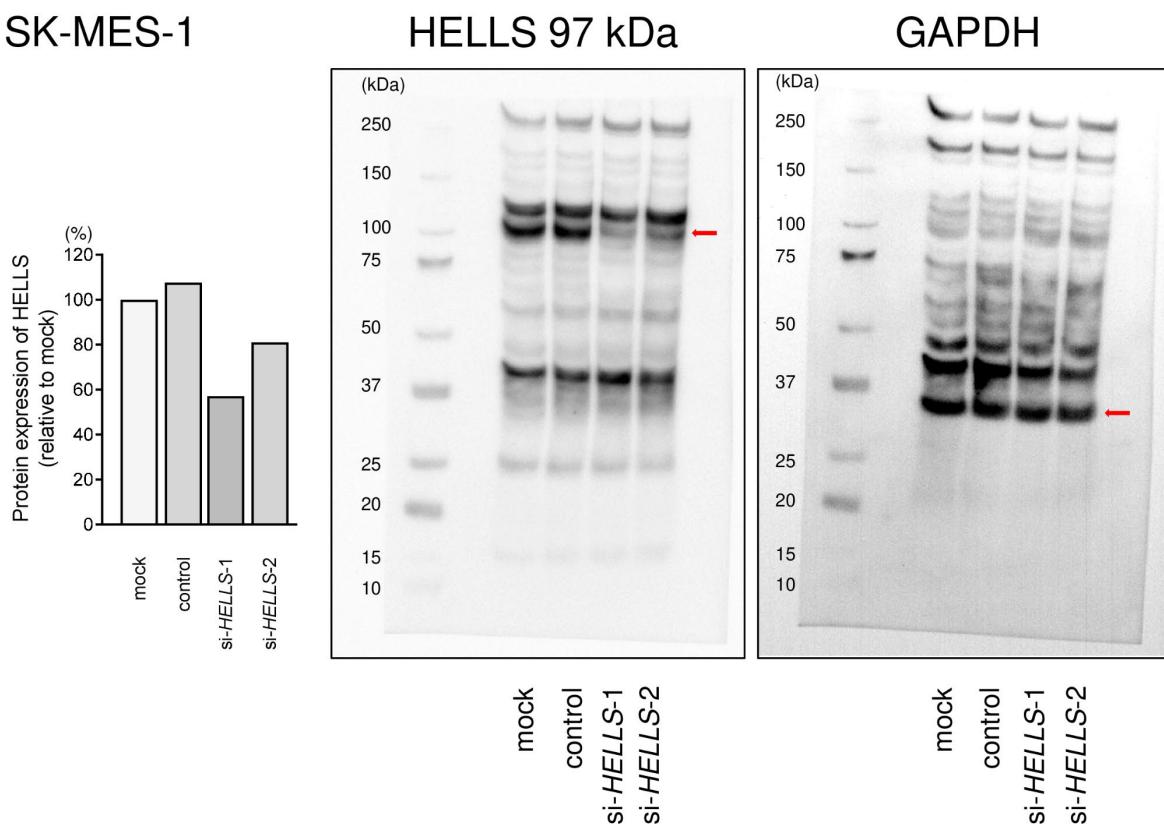


**Figure S5.** The sequence of the region containing the *miR-150-3p* binding site of each cell line. In each cell, a *miR-150-3p* binding sequence (gtacca) is present (red underline). This sequence was inserted into the luciferase reporter assay vector.

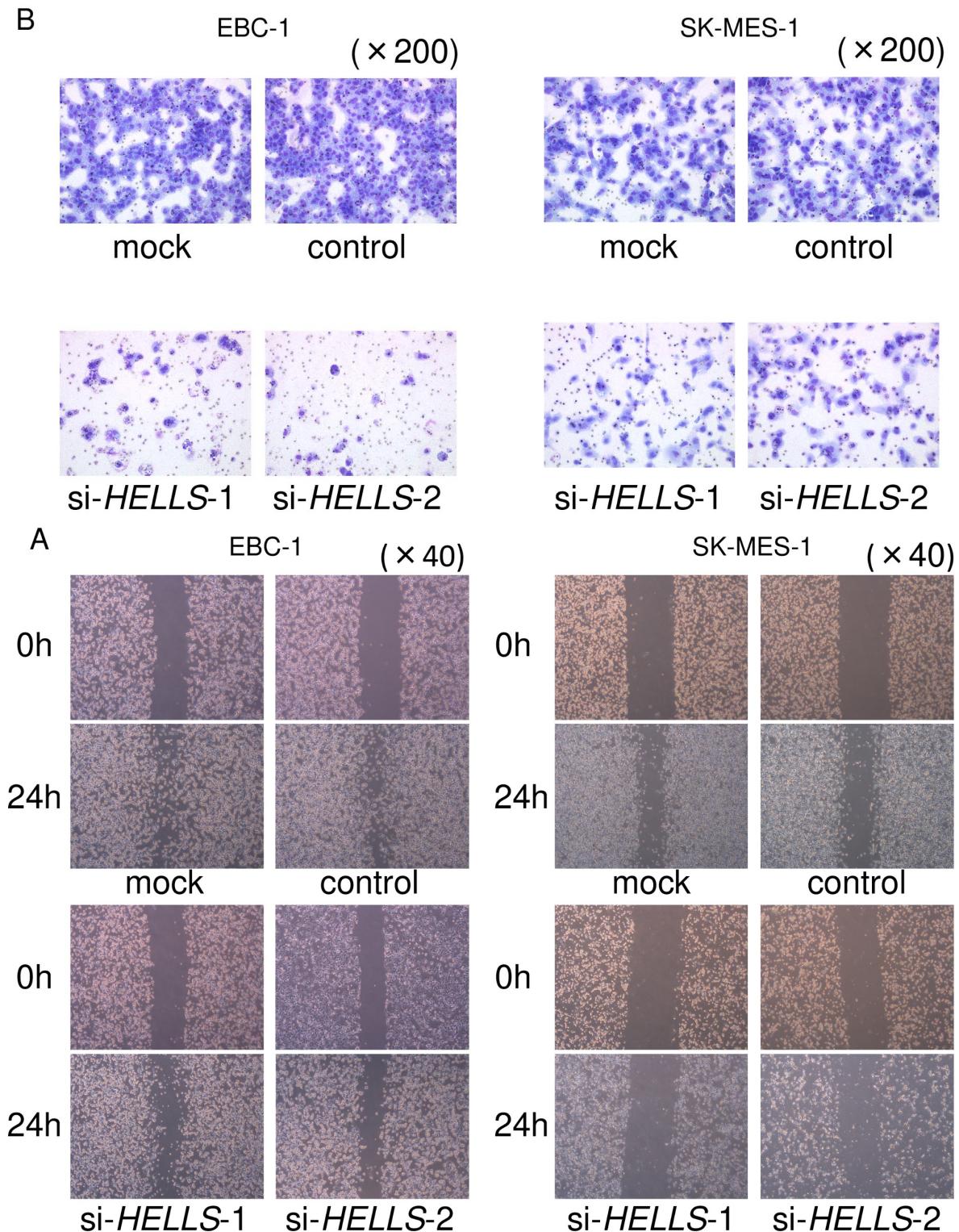
## EBC-1



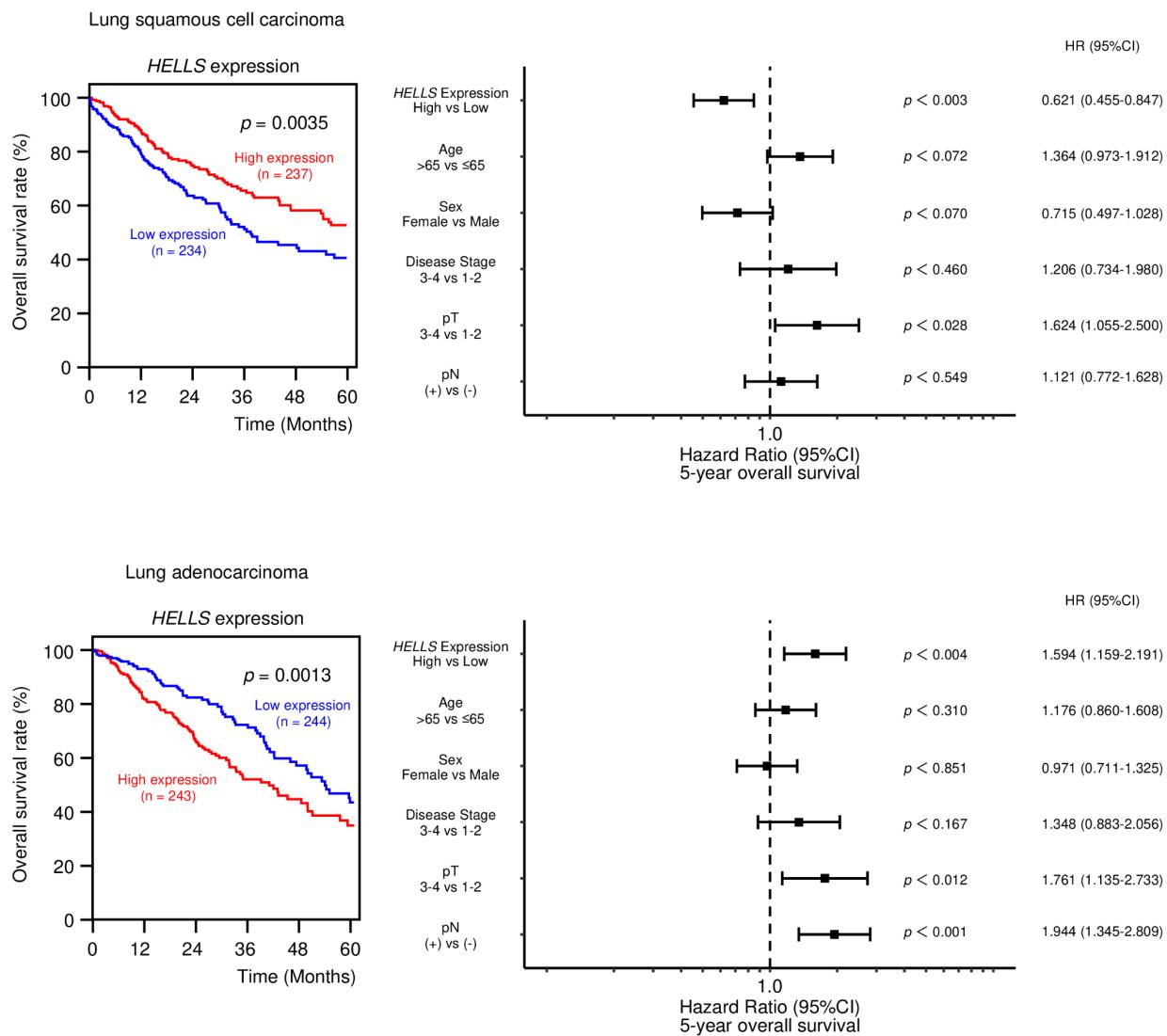
## SK-MES-1



**Figure S6.** HELLs protein expression downregulated by si-HELLs. HELLs protein expression was evaluated by western blot. Full western blot images of HELLs are shown. The western blotting results were quantified by ImageJ.



**Figure S7.** Cell migration and invasion assays in EBC-1 and SK-MES-1 after knockdown of HELLS by si-HELLS. (A) Phase-contrast micrographs of wound healing assay are shown after transfection with si-HELLS in EBC-1 and SK-MES-1. (B) Micrographs of Matrigel invasion assays for LUSQ cells transfected with si-HELLS are shown.



**Figure S8.** Kaplan–Meier curves of 5-year overall survival due to difference in *HELLS* expression in LUSQ and LUAD patients from TCGA database and forest plot presenting the results of a multivariate Cox regression analysis of the prognostic value of *HELLS* in TCGA-LUSQ and TCGA-LUAD. 5-year overall survival showed that low expression of *HELLS* was poor prognosis in LUSQ patients, but on the other hand high expression of *HELLS* was poor prognosis in LUAD. The expression level of *HELLS* was determined to be independent prognostic factors in terms of the 5-year overall survival rate after adjustments for age, sex, disease stage, pathological T and N stage ( $p < 0.05$ ). HR: hazard ratio, CI: confidence interval.

**Table S1:** Reagents used in this study.

Primer and probe		Assay ID	Company
<i>miR-150-5p</i>		000473	Applied Biosystem (Foster City, CA, USA)
<i>miR-150-3p</i>		002637	Applied Biosystem
<i>RNU48</i>		001006	Applied Biosystem
<i>HELLS</i>		Hs00934778_m1	Applied Biosystem
<i>GUSB</i>		Hs00939627_m1	Applied Biosystem
miRNA	Concentration	Catalog Number/Assay ID	Company
<i>miR-150-5p</i>	10nM	AM17100 / PM10070	Invitrogen (Carlsbad, CA, USA)
<i>miR-150-3p</i>	10nM	AM17100 / PM12324	Invitrogen
anti-miR Negative Control #1	10nM	AM17010 / AM1--100	Invitrogen
siRNA	Concentration	Primer Name	Company
si- <i>HELLS</i>	10nM	HSS104740, HSS104741, HSS179196	Invitrogen (Carlsbad, CA, USA)
Antibody	Dilution	Catalog number	Company
HELLS (SMARCA6)	WB 1:500	ab3851	Abcam (Cambridge, UK)
GAPDH	WB 1:10000	MAB374	EMD Millipore (Billerica, MA, USA)
HELLS	IHC 1:200	HPA063242	Sigma Aldrich (St. Louis, MO, USA)

**Table S2:** Characteristics of the patients used for normal lung tissue near the tumor in Figure 2A.

Age	Sex	T	N	M	Pathological stage	Type
64	M	1a	1	0	IIA	LUSQ
70	M	2a	1	0	IIA	LUSQ
69	M	3	0	0	IIB	LUSQ
78	M	1a	1	0	IIA	LUSQ
78	M	2b	2a	0	IIIA	LUSQ
79	M	3	1	0	IIIA	LUSQ
61	M	3	1	0	IIIA	LUSQ
75	M	1a	0	0	IA	LUSQ
50	M	1a	2	0	IIIA	LUSQ
73	M	2a	0	0	IB	LUSQ
64	M	2a	0	0	IB	LUSQ
88	M	3	0	0	IIB	LUSQ
68	M	3	0	0	IIB	LUSQ
76	M	1b	0	0	IA	LUSQ
73	M	2a	0	0	IB	LUSQ
76	M	2a	0	0	IB	LUSQ
65	M	1b	0	0	IA	LUSQ
69	M	1b	0	0	IA	LUSQ
50	M	2a	0	0	IB	LUSQ
65	M	2a	0	0	IB	LUSQ
69	M	1a	0	0	IA	LUSQ
65	M	2a	0	0	IB	LUSQ

LUSQ: lung squamous cell carcinoma.

**Table S3:** Characteristics of the patients used for lung cancer tissue in Figure 2A.

Age	Sex	T	N	M	Pathological stage	Type
69	M	3	0	0	IIB	LUSQ
65	M	3	0	0	IIB	LUSQ
71	M	3	2	0	IIIA	LUSQ
78	M	2b	2a	0	IIIA	LUSQ
56	M	2a	1	0	IIA	LUSQ
79	M	3	1	0	IIIA	LUSQ
61	M	3	1	0	IIIA	LUSQ
50	M	1a	2	0	IIIA	LUSQ
74	M	3	0	0	IIB	LUSQ
73	M	2a	0	0	IB	LUSQ
64	M	2a	0	0	IB	LUSQ
88	M	3	0	0	IIB	LUSQ
68	M	3	0	0	IIB	LUSQ
65	F	1b	2	0	IIB	LUSQ
72	M	2a	1	0	IIA	LUSQ
76	M	1b	0	0	IA	LUSQ
71	M	2a	2	0	IIIA	LUSQ
73	M	2a	0	0	IB	LUSQ
73	M	2a	0	0	IB	LUSQ
71	M	2b	2	0	IIIA	LUSQ
77	M	1a	0	0	IA	LUSQ
73	F	3a	0	0	IIB	LUSQ
82	M	2a	0	0	IB	LUSQ
76	M	2a	0	0	IB	LUSQ
65	M	1b	0	0	IA	LUSQ
69	M	1b	0	0	IA	LUSQ
50	M	2a	0	0	IB	LUSQ
65	M	2a	0	0	IB	LUSQ
69	M	1a	0	0	IA	LUSQ
50	M	4	2	0	IIIB	LUSQ
65	M	2a	0	0	IB	LUSQ

LUSQ: lung squamous cell carcinoma.

**Table S4:** Characteristics of the patients used for immunostaining.

Patients	Age	Sex	T	N	M	Pathological stage	Type
A	69	M	1	0	0	IA	LUSQ
B	48	M	2	0	0	IB	LUSQ
C	54	M	3	0	0	IIB	LUSQ
D	30	M	-	-	-	-	Normal lung tissue
E	24	M	-	-	-	-	Normal lung tissue
F	48	M	-	-	-	-	Normal lung tissue

LUSQ: lung squamous cell carcinoma.