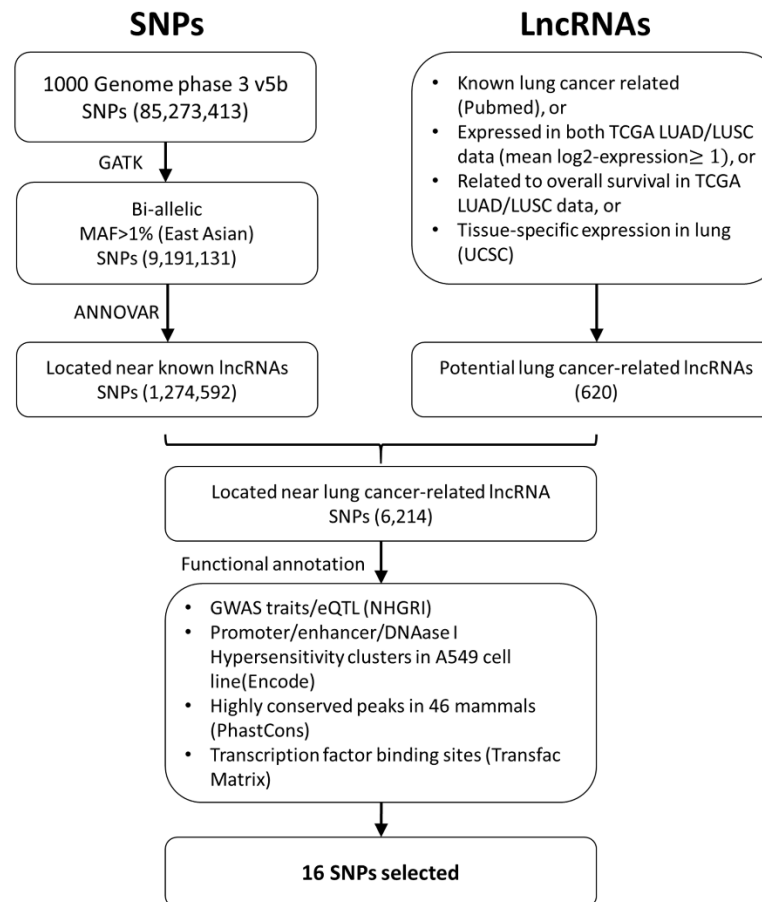
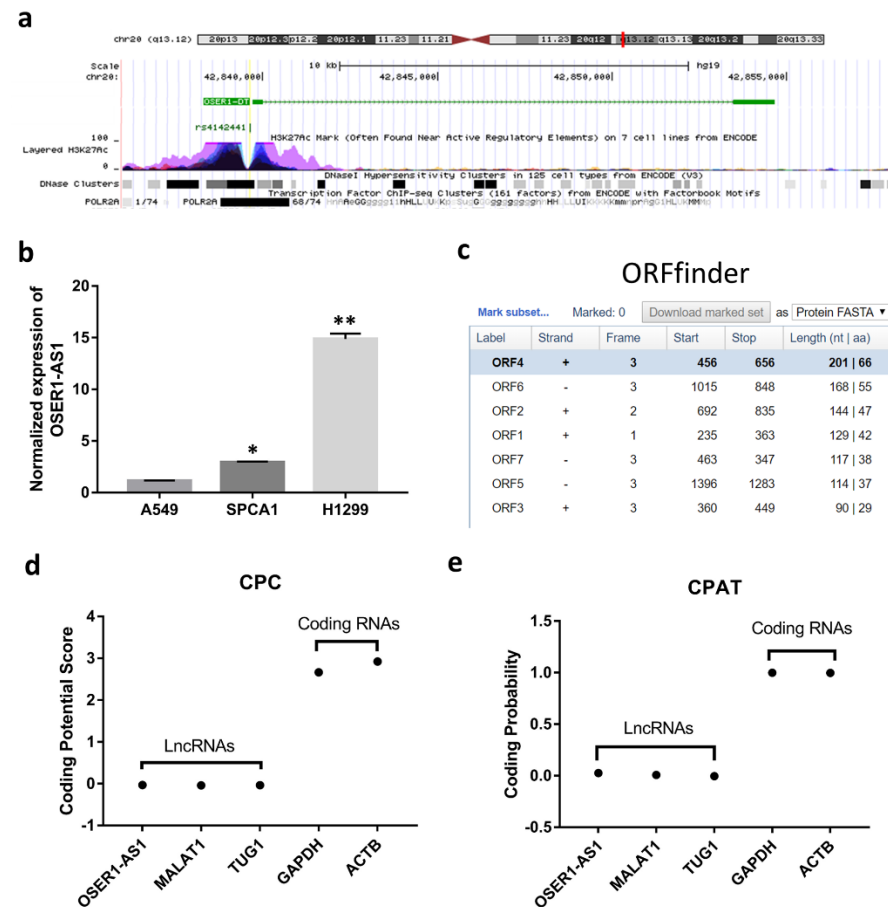




1

2 **Supplementary Figure S1. The bioinformatics workflow for selecting SNPs associated with lung cancer and located near**
 3 **lncRNAs.**

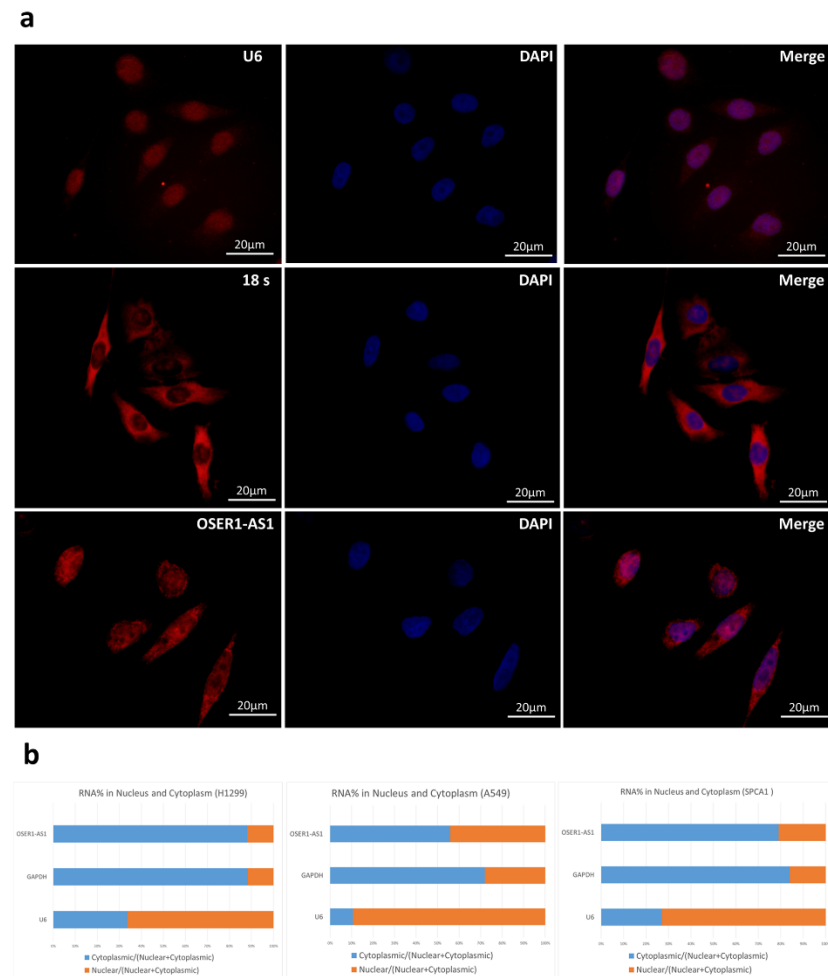


4

5 **Supplementary Figure S2. Genomic location and coding capability prediction of OSER1-AS1.** (a) The localization of OSER1-

6 AS1 on the UCSC genome browser. (b) The relative expression of OSER1-AS1 in non-small cell lung cancer lines. Error bars
7 represent the SD of three independent experiments. (* Mann-Whitney U-test, $P < 0.05$; ** Mann – Whitney U test, $P < 0.01$). (c) Open
8 reading frame on OSER1-AS1. (d) The coding potential of OSER1-AS1 predicted in CPC. (e) The coding potential of OSER1-AS1
9 predicted in CPAT. CPC: Coding Potential Calculator; CPAT: Coding Potential Assessment Tool.

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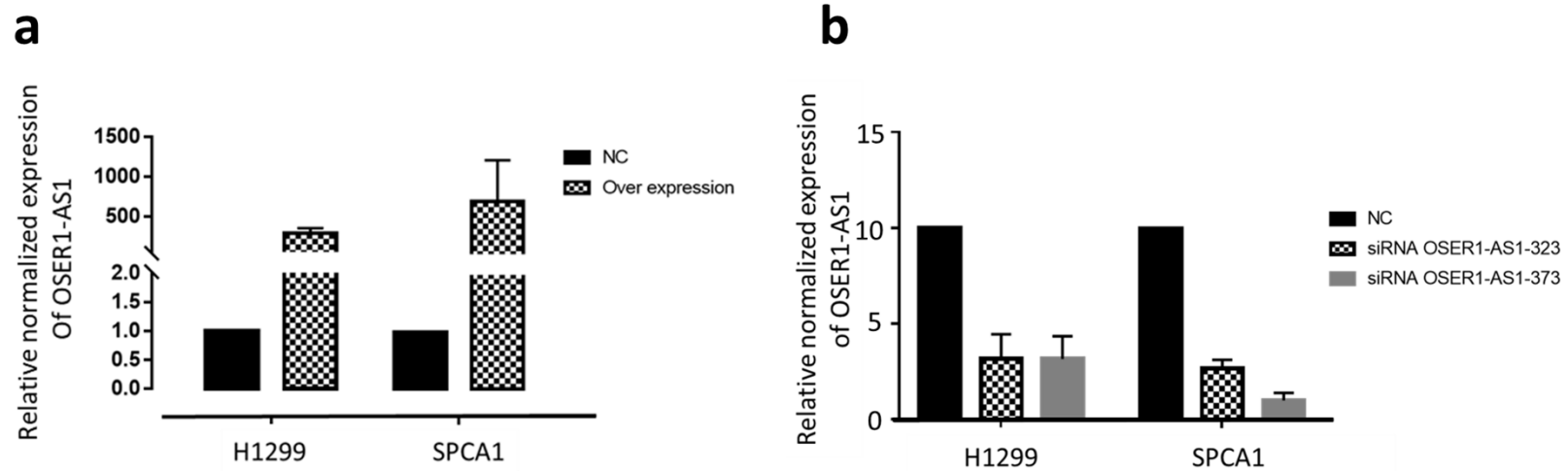
12 **Supplementary Figure S3. The subcellular localization of OSER1-AS1 in NSCLC cells. (a) The subcellular localization of**

13 OSER1-AS1 by RNA-FISH in A549 cells. 18s and U6 were used as the localization controls of cytoplasm and nucleus, respectively.

14 (b) Cytoplasmic and nuclear separation results of H1299, A549, and SPCA1. GAPDH and U6 were used as the localization controls

15 of cytoplasm and nucleus, respectively.

16

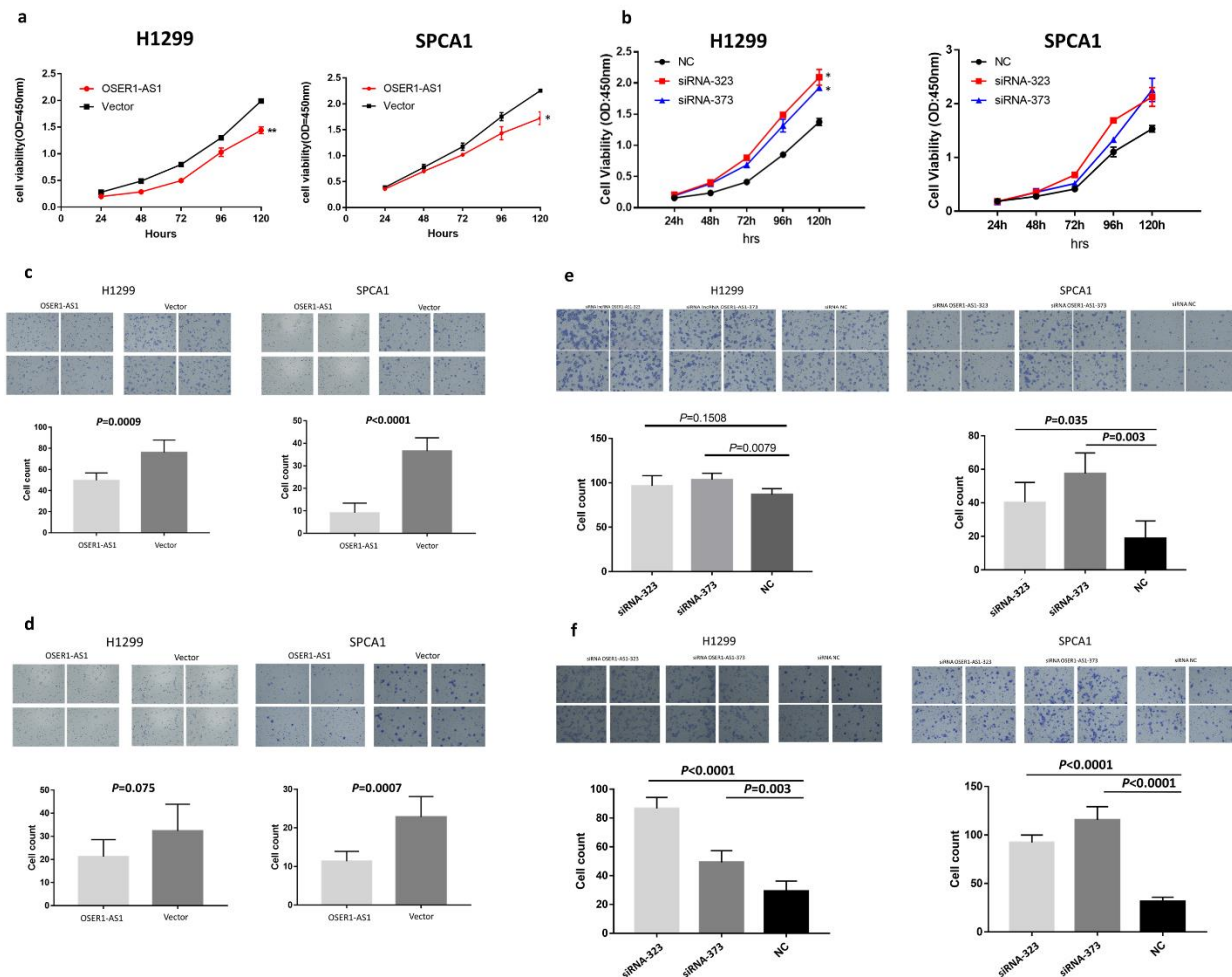


17

18 **Supplementary Figure S4. Knockdown and overexpression of lncRNA OSER1-AS1 in non-small cell lung cancer lines were**
 19 **verified by qRT-PCR.** (a) Knockdown of OSER1-AS1 expression in H1299 and SPCA1 cells were qualified by qRT-PCR. (b)

20 Overexpression of OSER1-AS1 expression in H1299 and SPCA1 cells were qualified by qRT-PCR. Error bars represent the SD of
21 three independent experiments.

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23

24 **Supplementary Figure S5. OSER1-AS1 influences proliferation, migration, and invasion *in vitro*.** (a) Growth curves of H1299

25 and SPCA1 cells after transfection with OSER1-AS1 or vector control were examined by CCK-8 assays. (b) Growth curves of H1299
26 and SPCA1 cells after transfection with two OSER1-AS1 siRNAs (siRNA-323 and siRNA-373) or negative control si-NC were
27 examined by CCK-8 assays (c & d) Migration and invasion of H1299 and SPCA1 cells transfection with OSER1-AS1 or vector control
28 were determined by transwell assays. Magnification, $\times 200$. Error bars represent the SD of three independent experiments. OSER1-
29 AS1 vs. vector control groups were compared by two-tailed Student's t-test: *, $P < 0.05$; **, $P < 0.01$. (e & f) Migration and invasion
30 of H1299 and SPCA1 cells transfection with siRNA-323, siRNA-373 or si-NC were determined by transwell assays. Magnification,
31 $\times 200$. Error bars represent the SD of three independent experiments. Two-tailed Student's t-test: *, $P < 0.05$; **, $P < 0.01$.

32

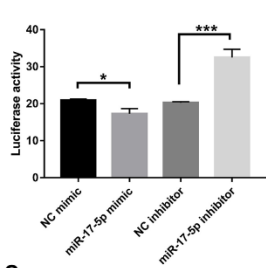
a

MicroRNA	LncRNA	Target site (hg19)	Alignment
Hsa-miR-17-5p	OSER1-AS1	chr20:42854367-42854385[+]	Target: 5' gaACAUGCCC----AGCACUUUg 3' miRNA : 3' gaUGGACGUGACAUUCGUGAAAc 5'

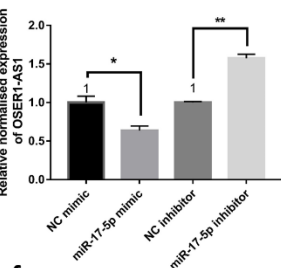
b

RBP	LncRNA	Binding site (hg19)	Sequencing type	Cell	GEO accession
ELAVL1	OSER1-AS1	chr20:42854116-42854147[+]	PAR-CLIP	HEK293	GSM738185
ELAVL1	OSER1-AS1	chr20:42854187-42854212[+]	PAR-CLIP	HEK293	GSM1234284
ELAVL1	OSER1-AS1	chr20:42854597-42854628[+]	iCLIP	Huvec	GSM2033153
ELAVL1	OSER1-AS1	chr20:42854621-42854628[+]	iCLIP	Huvec	GSM738185

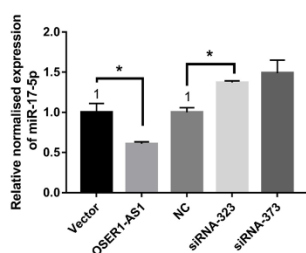
c



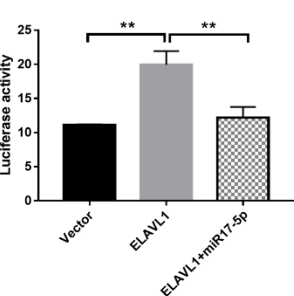
d



e



f



33

34 **Supplementary Figure S6. OSER1-AS1 functions as a sponge for both miR-17-5p and ELAVL1. (a) Potential miRNA binding**

35 site predicted to target OSER1-AS1 with miRanda algorithm. (b) RBP-binding sites in the 3'-end region of OSER1-AS1 detected by
36 ELAVL1 PAR-CLIP deep sequencing experiments in GEO database. (c) Luciferase assays of H1299 cells co-transfected with
37 Pischeck-2 reporter containing the OSER1-AS1 3'-end region and hsa-miR-17-5p mimic, NC mimic, inhibitor and NC-inhibitor. Error
38 bars represent the SD of three independent experiments. Two-tailed Student's t-test: *, $P < 0.05$; ***, $P < 0.001$. (d) OSER1-AS1
39 expression levels in H1299 cells after transfection with hsa-miR-17-5p mimic, NC mimic, inhibitor and NC-inhibitor. Error bars
40 represent the SD of three independent experiments. Two-tailed Student's t-test: *, $P < 0.05$; **, $P < 0.01$. (e) MiR-17-5p expression
41 levels in H1299 cells after overexpression or knockdown of OSER1-AS1. Error bars represent the SD of three independent
42 experiments. Two-tailed Student's t-test: *, $P < 0.05$. (f) Luciferase assays of H1299 cells co-transfected with ELAVL1 plasmids, or
43 with both ELAVL1 and hsa-miR-17-5p mimics. Error bars represent the SD of three independent experiments. Two-tailed Student's
44 t-test: **, $P < 0.01$.

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