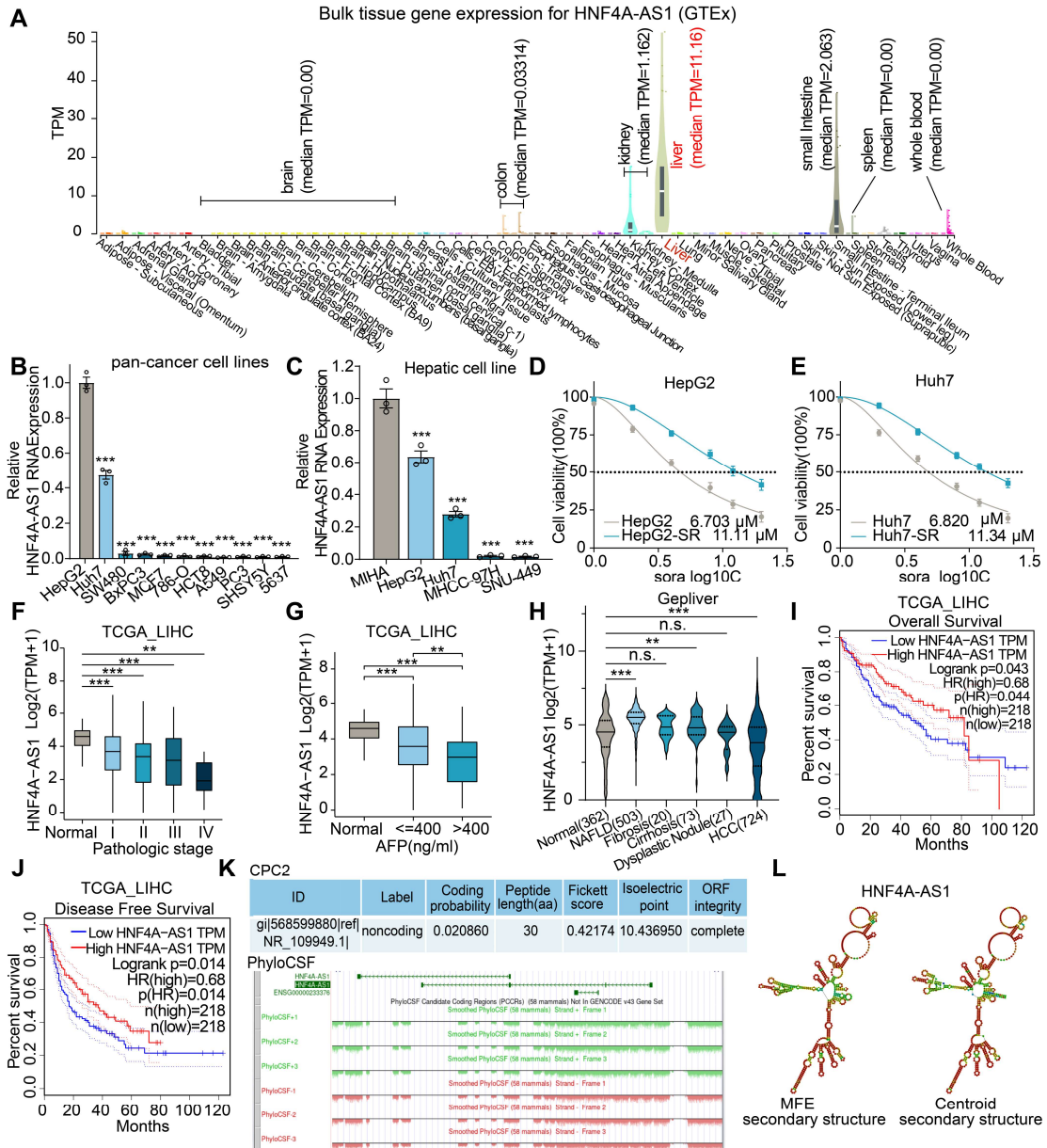
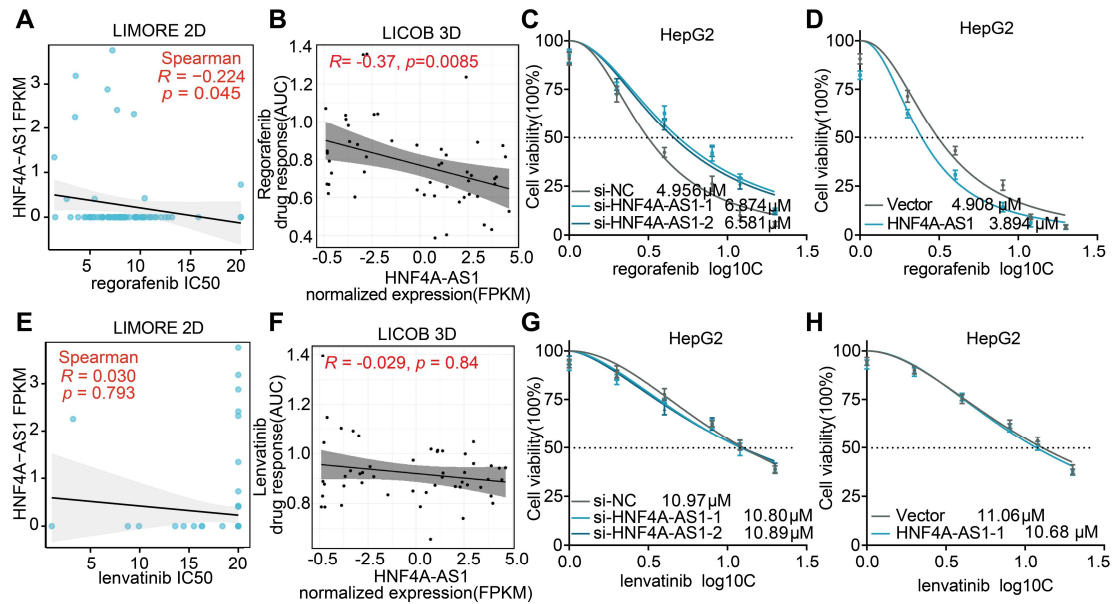


**Supplement figure:**



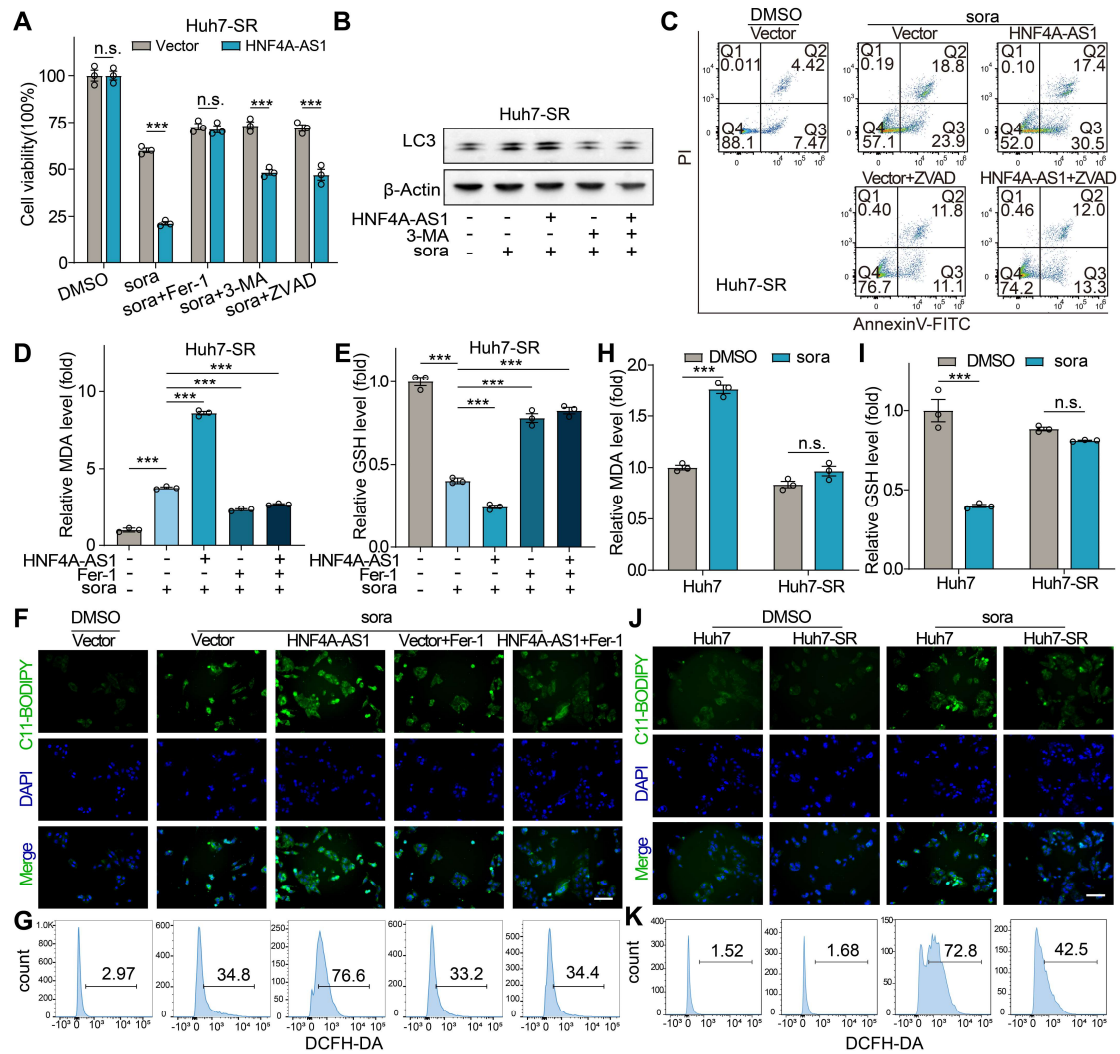
**Fig. S1 HNF4A-AS1 is a liver-specific lncRNA and associated with HCC progression.** (A) Analysis of HNF4A-AS1 expression in bulk tissues with GTEx database (<https://www.gtexportal.org>). (B) Expression levels of HNF4A-AS1 in cancer cells derived from different tissues. (C) HNF4A-AS1 expression in hepatic cell lines. (D-E) Sorafenib IC50 values in parental and resistant HepG2 and Huh7 cells. SR: sorafenib resistance. (F) Relationship between AFP expression and HNF4A-AS1 expression in TCGA LIHC database. (G) Expression levels of HNF4A-AS1 in different liver diseases according to the Gepliver website (<http://www.gepliver.org>). (H-I) Kaplan-Meier survival analysis, using the online tool GEPIA, assessing the overall

survival (OS) and disease-free survival (DFS) implications of HNF4A-AS1. (J) Expression levels of HNF4A-AS1 in different pathologic stages according to TCGA LIHC database. (K) The coding potential of HNF4A-AS1 was predicted using CPC2 (<http://cpc2.gao-lab.org/>) and PhyloCSF (<https://github.com/mlin/PhyloCSF>). (L) The secondary structure of HNF4A-AS1 was predicted using the RNAfold WebServer (<http://rna.tbi.univie.ac.at/cgi-bin/RNAWebSuite/RNAfold.cgi>).



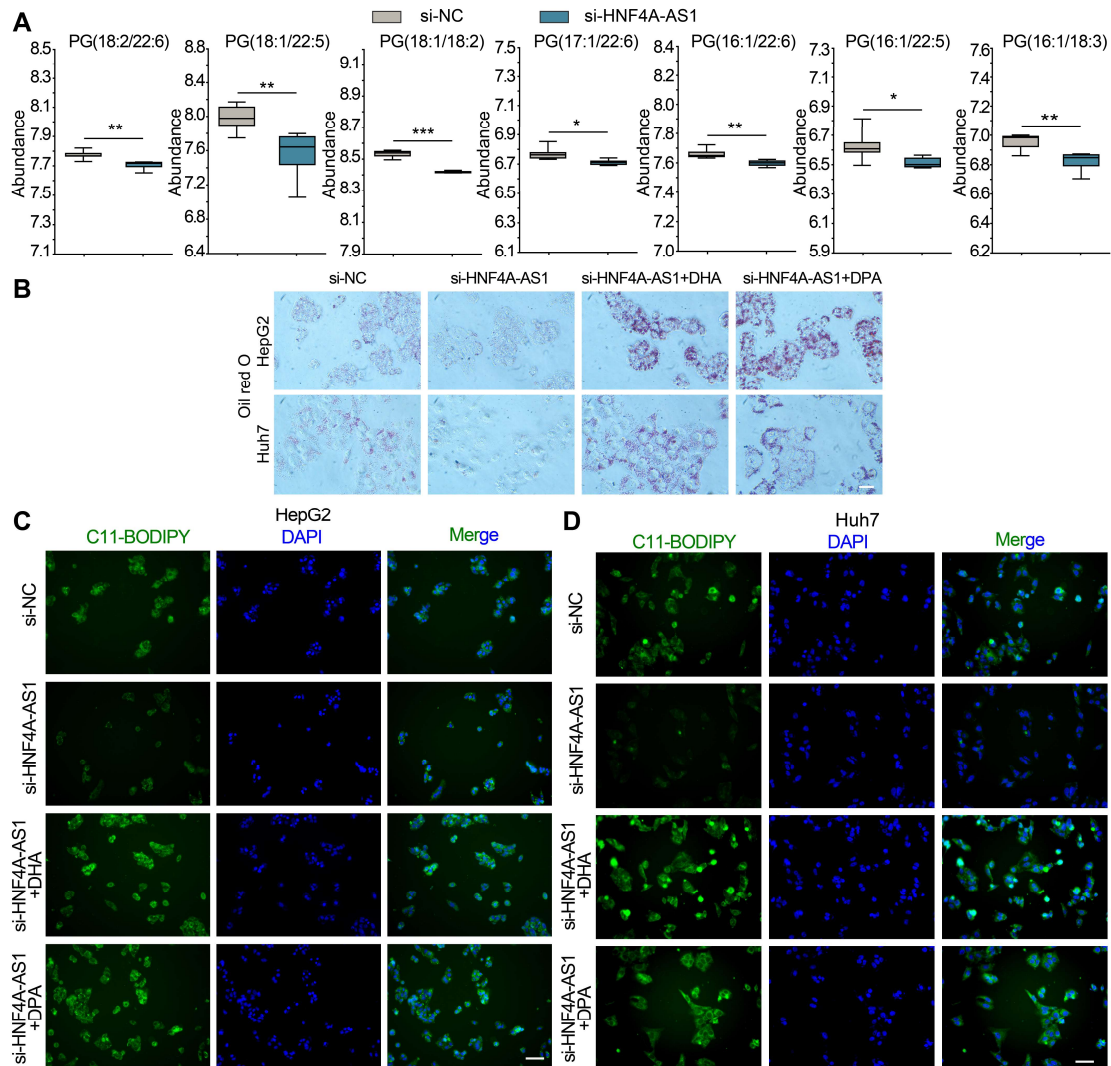
**Fig. S2 The influence of HNF4A-AS1 on regorafenib and lenvatinib response.**

(A-B) The relationship between regorafenib response and HNF4A-AS1 expression was observed in primary liver cancer cells cultured in 2D (LIMORE, A) and in organoids cultured in 3D (LICOB, B) from the respective databases. Higher IC50 and AUC indicate lower sorafenib response. (C-D) Regorafenib IC50 values in HepG2 cells after knockdown or overexpression of HNF4A-AS1 level. (E-F) The relationship between lenvatinib response and HNF4A-AS1 expression was observed in primary liver cancer cells cultured in 2D (LIMORE, E) and in organoids cultured in 3D (LICOB, F) from the respective databases. Higher IC50 and AUC indicate lower sorafenib response. (G-H) Lenvatinib IC50 values in HepG2 cells after knockdown or overexpression of HNF4A-AS1 level.



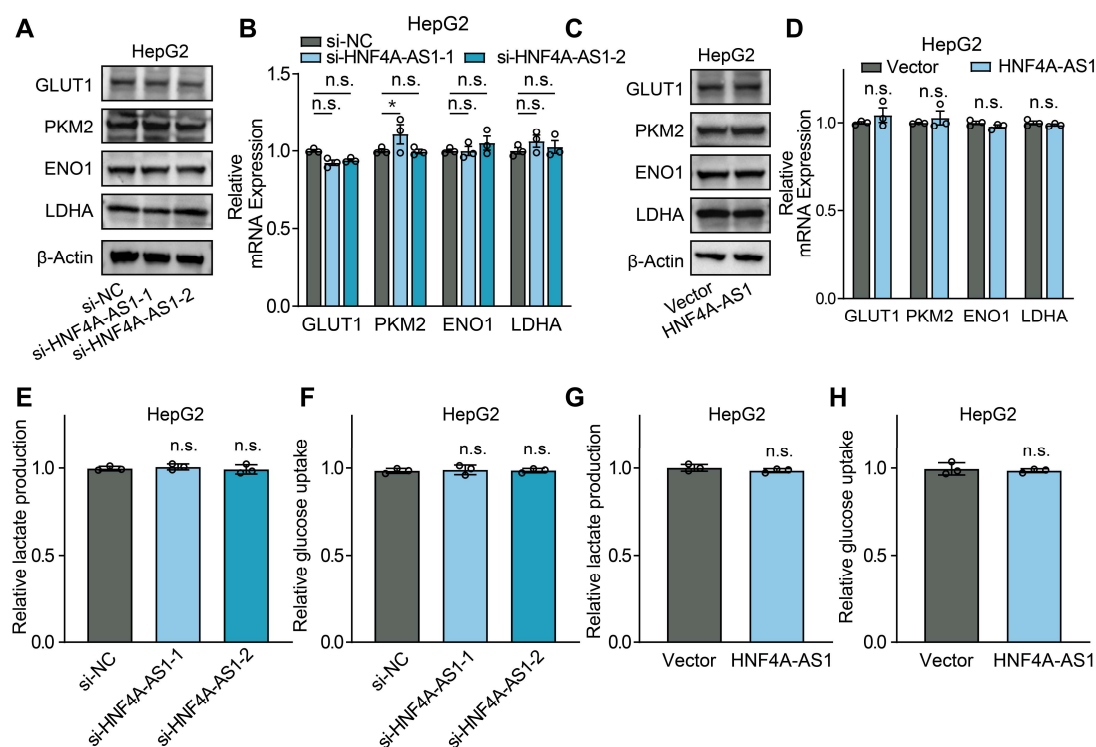
**Fig. S3 HNF4A-AS1 regulates sorafenib response through ferroptosis.** (A) Cell viability experiment assessing the effects of ferroptosis inhibitor ferrostatin-1 (Fer-1, 10  $\mu$ M), autophagy inhibitor 3-methyladenine (3-MA, 10  $\mu$ M) or apoptosis inhibitor Z-VAD-FMK (ZVAD, 50  $\mu$ M) on cell viability after sorafenib treatment in Huh7-SR cells overexpressing HNF4A-AS1 or Vector. (B) Western blot analysis demonstrating the impact of HNF4A-AS1 overexpression and autophagy inhibitor 3-MA (10  $\mu$ M) on autophagy in Huh7-SR cells after sorafenib treatment (10  $\mu$ M). (C) AnnexinV/PI flow cytometry experiment showing the influence of HNF4A-AS1 overexpression and apoptosis inhibitor ZVAD (50  $\mu$ M) on induced apoptosis in Huh7-SR cells after sorafenib treatment (10  $\mu$ M). (D-G) MDA assay (D), GSH assay (E), C11-bodipy labeled LPO (F), and DCFH-DA labeled ROS (G) indicating the effects of HNF4A-AS1 overexpression and ferroptosis inhibitor Fer-1 on induced ferroptosis in Huh7-SR

cells after sorafenib treatment (10  $\mu$ M). Scale bar:50  $\mu$ m. (H-K) MDA assay (H), GSH assay (I), C11-bodipy labeled LPO (J), and DCFH-DA labeled ROS (K) demonstrating that ferroptosis is less prominent in the drug-resistant cell line Huh7-SR compared to the parental Huh7 cells under sorafenib treatment (10  $\mu$ M). Scale bar:50  $\mu$ m. Data shown are means  $\pm$  SD from biological triplicates. \*\*\*: $P < 0.001$ , n.s.: $P > 0.05$

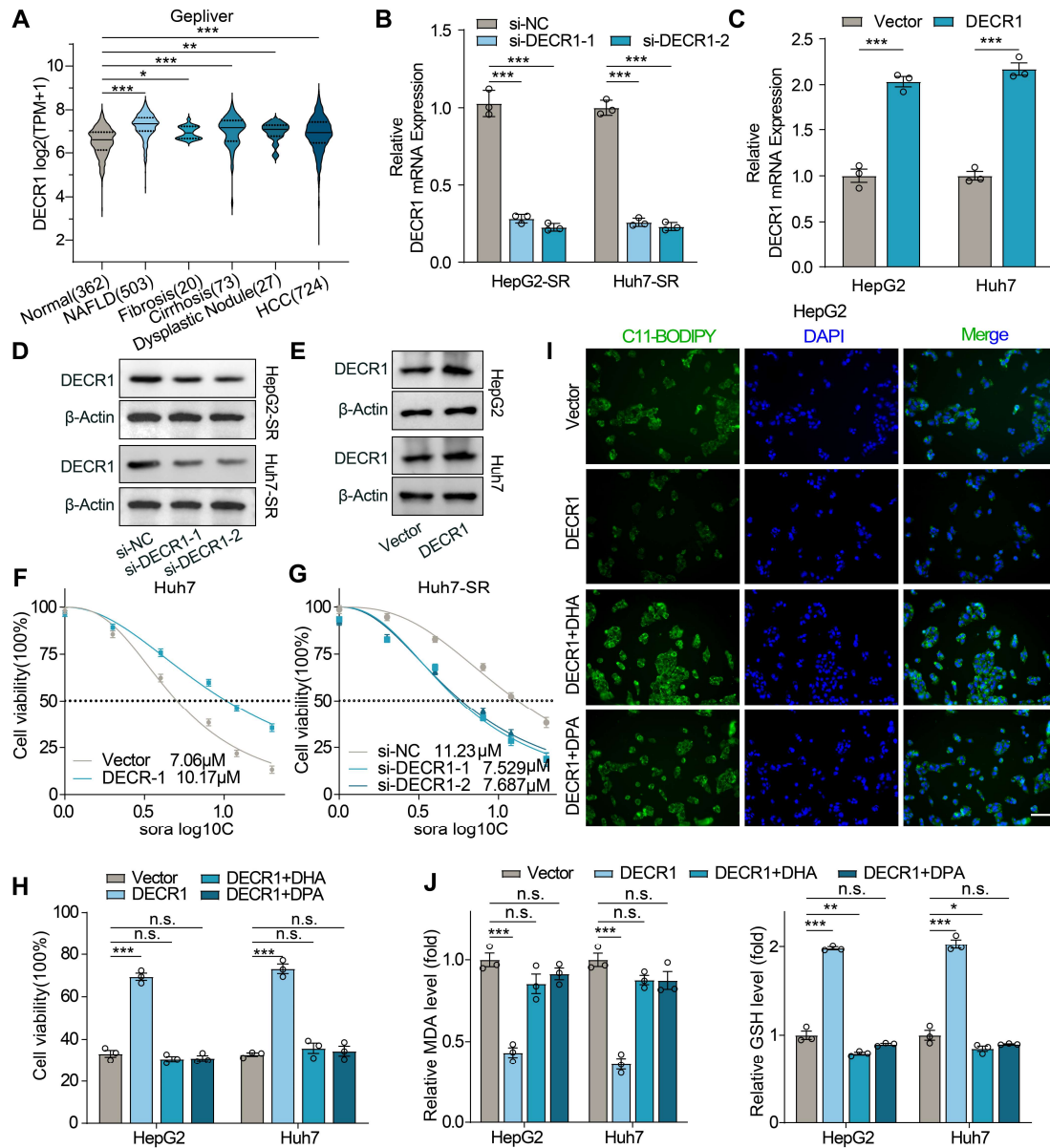


**Fig. S4 Exogenous PUFA reverses the reduction in sorafenib-dependent ferroptosis caused by si-HNF4A-AS1.** (A) Abundance of different phospholipids that contain PUFA are shown based on lipidomic in Figure 3A. (B) Oil red O staining of HepG2 and Huh7 cells transfected with si-NC or si-HNF4A-AS1 and treated with DHA or DPA (50  $\mu$ M). Scale bar:10  $\mu$ m. (C-D) C11-BODIPY staining of HepG2 and Huh7 cells transfected with si-NC or si-HNF4A-AS1 and treated with DHA or DPA (50  $\mu$ M)

under sorafenib treatment (10  $\mu$ M). Scale bar:50  $\mu$ m. Data shown are means  $\pm$  SD from 6 biological plicates. \*: $P < 0.05$ , \*\*: $P < 0.01$ , \*\*\*: $P < 0.001$

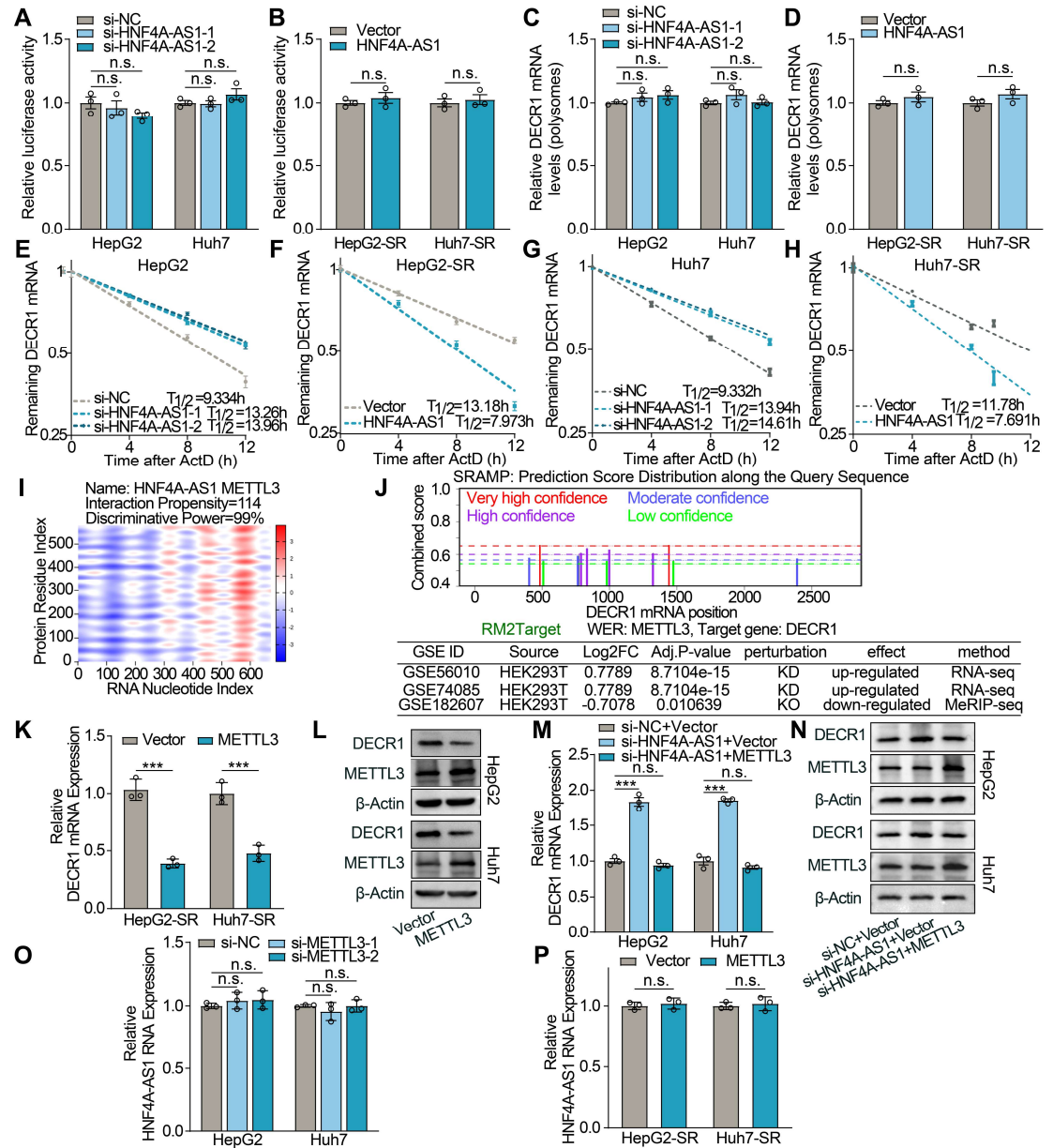


**Fig. S5 HNF4A-AS1 have no influence on glycolysis.** (A-B) The protein and RNA levels of glycolysis enzymes (GLUT1, PKM2, ENO1, LDHA) were detected after interference of HNF4A-AS1 by WB or qRT-PCR, respectively. (C-D) The protein and RNA levels of glycolysis enzymes (GLUT1, PKM2, ENO1, LDHA) were detected after overexpression of HNF4A-AS1 by WB or RT-PCR, respectively. (E-F) The levels of glucose uptake and lactate production in HepG2 transfected with si-NC or si-HNF4A-AS1 were measured. (G-H) Measurement of glucose uptake and lactate production levels in HepG2 transfected with HNF4A-AS1 overexpression. n.s.: $P > 0.05$



**Fig. S6 HNF4A-AS1 mediates the tolerance of sorafenib-induced ferroptosis through DECR1.** (A) Expression levels of DECR1 in different liver diseases from the Gepliver database. (B-E) RT-qPCR and western blot analysis of DECR1 expression in parental and resistant cells transfected with si-DECR1 or DECR1 overexpression plasmid respectively. (F-G) IC<sub>50</sub> values of sorafenib were measured in Huh7 cells with overexpressing DECR1 and Huh7-SR cells with si-DECR1 interference. (H-J) Cell viability (H), LPO (I), MDA, and GSH (J) assays showed that DECR1 overexpression decreased ferroptosis under sorafenib treatment (10 μM) in HepG2 and Huh7 cells, and these effects were reversed by supplementing of DHA or DPA (50 μM). Scale bar: 50 μm. Data shown are means ± SD from biological triplicates. \*:  $P < 0.05$ , \*\*:  $P < 0.01$ ,

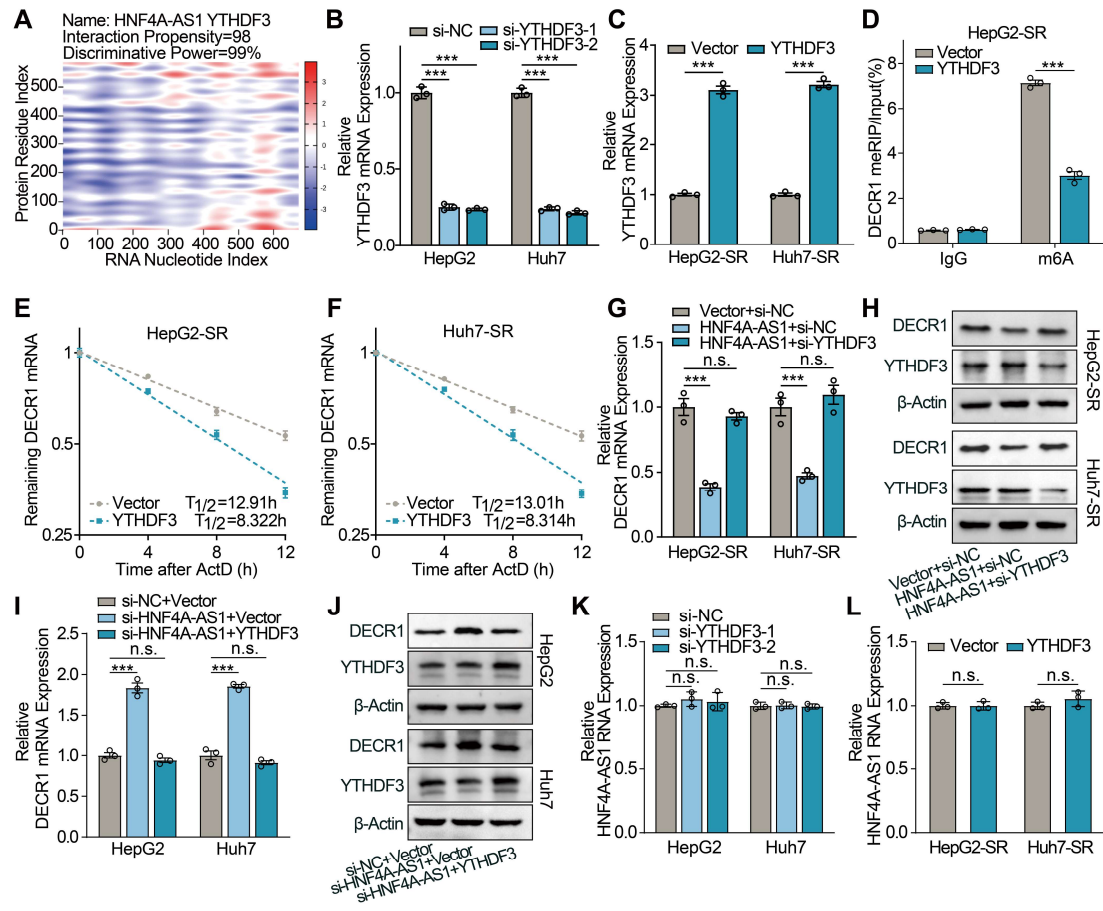
\*\*\*:  $P < 0.001$ , n.s.:  $P > 0.05$



**Fig. S7 METTL3-mediated m6A modification decreases DECR1 mRNA stability.** (A-B) DECR1 promoter sequence luciferase reporter activity in parental and resistant cells respectively transfected with si-NC/si-HNF4A-AS1 or vector/HNF4A-AS1 were measured by luciferase reporter assay. Renilla luciferase served as a control. (C-D) The polysomes-conjunct DECR1 mRNA was measured in parental and resistant cells respectively transfected with si-NC/si-HNF4A-AS1 or vector/HNF4A-AS1. (E-H) RNA stability assay of DECR1 in parental and resistant cells respectively transfected with si-NC/si-HNF4A-AS1 or vector/HNF4A-AS1. (I) Heatmap showing the predicted

interaction between HNF4A-AS1 and METTL3 protein in catRAPID website ([http://service.tartaglialab.com/page/catrapid\\_group](http://service.tartaglialab.com/page/catrapid_group)). The colors represent the interaction scores ranging from -3 to 3 for individual amino acid and nucleotide pairs. The interaction propensity between HNF4A-AS1 and METTL3 protein is 114, and the discriminative power is 99%. (J) SRAMP (<http://www.cuilab.cn/sramp>) and RM2Target (<http://rm2target.canceromics.org>) databases suggested that DECR1 has two very high confident m6A modification sites and is negatively regulated by METTL3. (K-L) RT-qPCR and western blot analysis of DECR1 expression in HepG2-SR and Huh7-SR cells transfected with vector or METTL3 plasmid. (M-N) RT-qPCR and western blot analysis of DECR1 expression in HepG2 and Huh7 cells transfected with si-NC+vector, si-HNF4A-AS1+vector, or si-HNF4A-AS1+METTL3. (O-P) RT-qPCR analysis of HNF4A-AS1 expression in parental and resistant cells transfected with si-NC/si-METTL3 or vector/METTL3, respectively. Data shown are means  $\pm$  SD from biological triplicates. \*\*\*: $P < 0.001$ , n.s.: $P > 0.05$





**Fig. S8 YTHDF3-mediated m6A modification decreases DECR1 mRNA stability.**

(A) The heatmap shows the predicted interaction between HNF4A-AS1 and YTHDF3 protein in catRAPID website. The colors indicate the interaction scores (-3 to 3) of individual amino acid and nucleotide pairs. The interaction propensity between HNF4A-AS1 and YTHDF3 protein is 98, and the discriminative power is 99%. (B-C) RT-qPCR analysis to determine the knockdown efficiency of si-YTHDF3 and overexpression efficiency of YTHDF3 plasmid. (D) MeRIP-PCR of DECR1 mRNA using anti-m6A or anti-IgG antibodies in HepG2-SR cells transfected with vector or YTHDF3 plasmid. (E-F) RNA stability assay of DECR1 in HepG2 and Huh7 cells transfected with vector or YTHDF3 plasmid. (G-H) RT-qPCR and western blot analyses of DECR1 expression in HepG2-SR and Huh7-SR cells transfected with vector+si-NC, HNF4A-AS1+si-NC, or HNF4A-AS1+si-YTHDF3. (I-J) RT-qPCR and western blot analyses of DECR1 expression in HepG2 and Huh7 cells transfected with si-NC+vector, si-HNF4A-AS1+vector, or si-HNF4A-AS1+YTHDF3. (K-L) RT-qPCR analysis of

HNF4A-AS1 expression in parental and resistant cells transfected with si-NC/si-YTHDF3 or vector/YTHDF3, respectively. Data shown are means  $\pm$  SD from biological triplicates. \*\*\*: $P < 0.001$ , n.s.: $P > 0.05$

**Supplement table S1. The unsaturated fatty acid metabolism geneset.**

ABCD1	CYP2A6	ELOVL1	PLA2G10	HADHB
ABCD2	CYP2A7	ELOVL2	PLA2G2F	ACSL1
ABHD12	CYP2B6	ELOVL3	PLA2G3	HSD17B4
ABHD6	CYP2C18	ELOVL4	PLA2G4A	MIR1908
ACAA1	CYP2C19	ELOVL5	PLA2G4B	MIR6734
ACOT8	CYP2C8	ELOVL6	PLA2G4C	ACADS
ACOX1	CYP2C9	ELOVL7	PLA2G4F	ACADVL
AKR1B1	CYP2D6	EPHX1	PLAA	ACSM3
AKR1C1	CYP2D7	FAAH	PNPLA8	ACSM6
AKR1C2	CYP2E1	FAAH2	PRXL2B	ECHS1
AKR1C3	CYP2F1	FABP5	PTGDS	HADH
AKR1C4	CYP2G1P	FADS1	PTGES	
ALOX12	CYP2J2	FADS2	PTGES2	
ALOX12B	CYP2S1	FADS2B	PTGES3	
ALOX15	CYP2U1	FADS3	PTGIS	
ALOX15B	CYP4A11	GPX1	PTGR1	
ALOX5	CYP4A22	GPX4	PTGR2	
ALOXE3	CYP4F11	GSTA1	PTGS1	
ANXA1	CYP4F12	GSTM1	PTGS2	
ATP6V1B1	CYP4F2	GSTM2	SCD	
AVP	CYP4F3	GSTP1	SCD5	
AVPR1A	CYP4F8	HPGD	SCP2	
AWAT1	CYP4Z1	HPGDS	SIRT1	
CBR1	DAGLA	IL1B	TBXAS1	
CD74	DAGLB	MGLL	TNFRSF1A	
CES2	DECR1	MIF	ZADH2	
CYP1A1	DECR2	MIR132	ACADL	
CYP1A2	DEGS1	MIR204	ACADM	
CYP1B1	EDN1	MIR766	ECI1	
CYP2A13	EDN2	PIBF1	HADHA	

**Supplement table S2. Mass spectrometry data of proteins and peptides pulled down by HNF4A-AS1.**

Accession	Gene	Description	Mw(kDa)	Antise nse	Sense	log2(S/ A)	Dif f Sig
P06702	S100A9	Protein S100-A9	13.242	19.690 3	25.02 75	5.3372	++
P12273	PIP	Prolactin-inducible protein	16.572	20.739 2	25.78 64	5.0472	++
H0YKU1	TMOD 3	Tropomodulin-3 (Fragment)	20.79	19.768 9	24.75 65	4.9876	++
P68363	TUBA1 B	Tubulin alpha-1B chain	50.151	21.321 9	26.05 54	4.7335	++
Q15125	EBP	3-beta-hydroxysteroid- Delta(8),Delta(7)- isomerase	26.352	21.012 6	25.31 77	4.3051	++
O75131	CPNE3	Copine-3	60.13	19.722 7	23.96 12	4.2385	++
C9JRC4	PPP1R7	Protein phosphatase 1 regulatory subunit 7 (Fragment)	21.156	19.744 4	23.85 15	4.1071	++
A0A024R 7W5	YTHDF 3	YTH domain family, member 3, isoform CRA_a	58.311	19.108 9	22.99 89	3.89	++
B8ZZ77	PPIL3	Peptidyl-prolyl cis-trans isomerase	17.696	20.953 9	24.54 95	3.5956	++
Q02318	CYP27 A1	Sterol 26-hydroxylase, mitochondrial	60.234	19.850 5	23.41 93	3.5688	++
Q14966	ZNF638	Zinc finger protein 638	220.62	25.76 22.3	92	3.4692	++
H7C0D5	YIPF4	Protein YIPF4 (Fragment)	6.447	19.516 7	22.89 42	3.3775	++
A8MU39	PPP5C	Serine/threonine-protein phosphatase	42.394	20.344 8	23.52 65	3.1817	++
P35914	HMGC L	Hydroxymethylglutaryl- CoA lyase, mitochondrial	34.36	19.752 8	22.65 37	2.9009	++
C9JLU1	POLR2 H	DNA-directed RNA polymerases I, II, and III subunit RPABC3 (Fragment)	16.925	20.362 8	23.14 82	2.7854	++
Q5T760	SRSF11	Serine/arginine-rich- splicing factor 11 (Fragment)	42.316	20.083 5	22.64 7	2.5635	++
Q9UBV8	PEF1	Peflin	30.381	20.202 8	22.72 67	2.5239	++

				20.883	23.33		
C9JAX1	FXN	Frataxin intermediate form	14.91	5	67	2.4532	++
		N6-adenosine-					
	METTL	methyltransferase catalytic		20.277	22.67		
F5H6D8	3	subunit	26.266	2	44	2.3972	++
		Double-stranded RNA-					
A0A3B3I		specific adenosine		21.242	23.60		
RQ9	ADAR	deaminase (Fragment)	128.27	1	31	2.361	++
A0A087X				19.434	21.72		
208	AGRN	Agurin	202.29	8	18	2.287	++
		Ubiquitin-associated		20.531	22.80		
Q5T6F2	UBAP2	protein 2	117.11	5	55	2.274	++
	DNAJC	DnaJ homolog subfamily			22.13		
Q9H3Z4	5	C member 5	22.149	20.09	52	2.0452	++
		Cleavage and					
		polyadenylation specific					
		factor 3, 73kDa, isoform		19.559	21.59		
G5E9W3	CPSF3	CRA_b	73.476	1	91	2.04	++
		Lipoma-preferred partner		20.781	22.76		
C9JXK9	LPP	(Fragment)	26.706	1	36	1.9825	++
A0A5H1Z		Polyglutamine-binding		20.648	22.38		
RR1	PQBP1	protein 1 (Fragment)	24.935	9	8	1.7391	++
	MRPL5	39S ribosomal protein		21.088			
Q96EL3	3	L53, mitochondrial	12.107	4	22.69	1.6016	++
	ABRA	Costars family protein		20.956	22.46		
Q5SZC9	CL	ABRACL	7.5164	7	34	1.5067	++
				20.745	22.22		
H0Y6T7	NCSTN	Nicastrin (Fragment)	30.045	6	91	1.4835	++
	SACM1	Phosphatidylinositol-3-		20.293	21.64		
Q9NTJ5	L	phosphatase SAC1	66.966	2	67	1.3535	++
		Heat shock cognate 71		20.872	22.17		
A8K7Q2	HSPA8	kDa protein	45.338	8	37	1.3009	++
					22.90		
O75663	TIPRL	TIP41-like protein	31.444	21.607	18	1.2948	++
		<i>RNA-binding motif,</i>					
		<i>single-stranded-</i>					
		<i>interacting protein 1</i>		21.083	22.36		
E7EPF2	RBMS1	(Fragment)	13.713	6	98	1.2862	++
	PRXL2			19.582	24.74		
Q9BRX8	A	Peroxiredoxin-like 2A	25.764	6	77	5.1651	++
				18.481	21.29		
B0YJC4	VIM	Vimentin	49.653	8	29	2.8111	++
	PPP1R1	E3 ubiquitin-protein ligase		21.260	23.75		
O60927	1	PPP1R11	13.952	6	39	2.4933	++

Q53S08	RAB6D	Ras-related protein Rab-6D	28.242	22.973	25.09	9	87	2.1248	++
					25.61				
Q9NU22	MDN1	Midasin	632.81	23.618	55	1.9975		++	
					23.56				
Q02413	DSG1	Desmoglein-1	113.75	21.586	3	1.977		++	
					25.42				
Q8WXE9	STON2	Stonin-2	101.16	23.556	92	1.8732		++	
		Ras-related protein Rab-		23.459	25.13				
Q9H0U4	RAB1B	1B	22.171	8	45	1.6747		++	
		Purine nucleoside		23.873	25.51				
J3QSB7	MTAP	phosphorylase	26.777	1	39	1.6408		++	
				26.567	28.15				
P81605	DCD	Dermeidin	11.284	3	86	1.5913		++	
				22.745	24.29				
P16104	H2AX	Histone H2AX	15.144	7	15	1.5458		++	
		Methylcrotonoyl-CoA		22.785	24.31				
G5E9X5	MCCC1	carboxylase subunit alpha, mitochondrial	48.216	1	41	1.529		++	
		Eukaryotic translation		22.642	24.16				
Q7L2H7	EIF3M	initiation factor 3 subunit M	42.502	7	08	1.5181		++	
		Acylpyruvase FAHD1,		22.284	23.77				
Q6P587	FAHD1	mitochondrial	24.843	6	76	1.493		++	
		40S ribosomal protein		20.626	22.09				
H3BN98		S15a (Fragment)	27.168	1	77	1.4716		++	
				22.749	24.20				
Q5T8U5	SURF4	Surfeit locus protein 4	21.127	4	52	1.4558		++	
		Peptidyl-prolyl cis-trans		24.461	25.90				
Q9Y3C6	PPIL1	isomerase-like 1	18.237	1	99	1.4488		++	
				25.511	26.94				
D6RFH4	CYB5B	Cytochrome b5 type B	15.208	8	6	1.4342		++	
	CSNK2	Casein kinase II subunit		25.070	26.46				
P68400	A1	alpha	45.143	7	5	1.3943		++	
		Phosphopantothenate--		20.749	22.14				
Q9HAB8	PPCS	cysteine ligase	34.005	3	23	1.393		++	
		2-deoxynucleoside 5-		23.233	24.62				
O43598	DNPH1	phosphate N-hydrolase 1	19.108	4	23	1.3889		++	
		Developmentally-			23.28				
J3QKW7	DRG2	regulated GTP-binding protein 2	26.624	21.915	39	1.3689		++	
		Elongation factor Ts,		22.005					
P43897	TSFM	mitochondrial	35.39	3	23.37	1.3647		++	

				20.556	21.91		
Q08554	DSC1	Desmocollin-1	99.986	7	77	1.361	++
				25.732	27.09		
P62854	RPS26	40S ribosomal protein S26	13.015	9	19	1.359	++
	RXYLT	Ribitol-5-phosphate		24.534	25.84		
G3V1K2	1	xylosyltransferase 1	21.208	8	67	1.3119	++
		Nebulin-related-anchoring		24.43			
Q86VF7	NRAP	protein	197.07	23.133	89	1.3059	++
		Histidine triad nucleotide-		23.655	24.94		
Q9BX68	HINT2	mitochondrial	17.162	8	56	1.2898	++
		Serine--tRNA ligase,		18.583	19.83		
B4DJM9	SARS2	mitochondrial	26.313	1	89	1.2558	++
		KH domain-containing,					
	KHDR	transduction-associated		25.947	27.18		
Q07666	BS1	protein 1	48.227	5	27	1.2352	++
		Succinate--CoA ligase					
		[ADP/GDP-forming]					
	SUCLG	subunit alpha,		23.564	24.79		
P53597	1	mitochondrial	36.249	8	99	1.2351	++
	SNRPD	Small nuclear		24.112	25.29		
P62314	1	ribonucleoprotein Sm D1	13.281	5	57	1.1832	++
		Catechol O--		21.535	22.70		
P21964	COMT	methyltransferase	30.037	8	37	1.1679	++
		m-AAA protease-		21.932	23.08		
Q8WWC4	MAIP1	mitochondrial	32.544	4	54	1.153	+
		U6 snRNA-associated		22.402	23.54		
F2Z2Y6	LSM8	Sm-like protein LSm8	7.3713	2	52	1.143	+
		Glutamine					
		amidotransferase-like					
A0A096L	GATD3	protein 3B, mitochondrial		22.290	23.41		
NJ1	B	(Fragment)	11.004	5	62	1.1257	+
		WD repeat-containing		21.135	22.24		
H0YL19	WDR61	protein 61	23.241	1	43	1.1092	+
		Signal sequence receptor		23.725	24.81		
C9JA28	SSR3	subunit gamma	20.161	6	43	1.0887	+
		Deoxyuridine 5-		25.258	26.34		
H0YMM5	DUT	nucleotidohydrolase	14.306	7	49	1.0862	+

		Guanine nucleotide-binding protein subunit		22.185	23.25		
Q14344	GNA13	alpha-13	44.049	4	1	1.0656	+
		Phosphoribosylformylglyc		23.565	24.61		
O15067	PFAS	inamidine synthase	144.73	2	83	1.0531	+
	DYNL	Dynein light chain		26.408	27.41		
Q9NP97	RB1	roadblock-type 1	10.921	7	76	1.0089	+
		Nucleoporin p58/p45		21.433	22.44		
Q5JRG1	NUP58	(Fragment)	49.095	5	13	1.0078	+

### Supplement table S3. The sequence of siRNA

SiRNA Targets	Sequences (5' - 3')
HNF4A-AS1#1	Sense: GGAGCUGGGAUCUGACACUTT Antisense: AGUGUCAGAUCCCAGCUCCTT
HNF4A-AS1#2	Sense: CCUGGGCAGAAGCUUUAATT Antisense: UUUAAGCUUCUGCCCAGGTT
METTL3#1	Sense: CCUGCAAGUAUGUUCACUATT Antisense: UAGUGAACAUACUUGCAGGTT
METTL3#2	Sense: GCUACCUGGACGUCAGUAUTT Antisense: AUACUGACGUCCAGGUAGCTT
YTHDF3#1	Sense: UCCAUCCAUUGGAUUCCAUAUUTT Antisense: AAUAUGGAAAUCCAAUGGAUGGATT
YTHDF3#2	Sense: GACCUGAAAGGGCAAGGAAAUAATT Antisense: UUUAUUUCCUUGCCCUUAGGUCTT
DEC1#1	Sense: AUGCUACCACCUAUAGUUTT Antisense: AACUAUUAGGUGGUAGCAUCG
DEC1#2	Sense: AGAAGAACUCGCAAUCUUTT Antisense: AAGAUUUGCGAGUUCUUCUAC

### Supplement table S4. Primers of RT-qPCR

Gene	Sequence (5' to 3')
HNF4A-AS1	F: TCCTTTAGCGGCTTCCAAGG R: GCCTGTCTTCAAGTCACCGA

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HNF4A	F: TGC GACTCTCCAAAACCCTC R: ATTGCCCATCGTCAACACCT
DECR1	F: TCTTCAAAAAGCGATGCTACCA R: CTATCACGCACTGAGCACCT
SCP2	F: ACTGATTTGCCAAGCTCGTTT R: TCAGGCCAGATTTCTCATAGCA
ALOX5	F: CTCAAGCAACACCGACGTAAA R: CCTTGTGGCATTGTCATCG
ELOVL5	F: ATGGTTTGTCGTCAGTCCCTT R: AGCTGGTCTGGATGATTGTCA
ACSL1	F: CGACGAGCCCTTGGTGTATTT R: GGTTTCCGAGAGCCTAAACAA
GLUT1	F: ATTGGCTCCGGTATCGTCAAC R: GCTCAGATAGGACATCCAGGGTA
ENO1	F: TGGTGTCTATCGAAGATCCCTT R: CCTTGGCGATCCTCTTTGG
PKM2	F: ATAACGCCTACATGGAAAAGTGT R: TAAGCCCATCATCCACGTAGA
LDHA	F: TTGACCTACGTGGCTTGGAAG R: GGTAACGGAATCGGGCTGAAT
GAPDH	F: CTGGGCTACACTGAGCACC R: AAGTGGTCGTTGAGGGCAATG
ACTB	F: CATGTACGTTGCTATCCAGG R: CTCCTTAATGTCACGCACGAT
U6	F: CTCGCTTCGGCAGCACAT R: TTTGCGTGTCATCCTTGCG
METTL3	F: TTGTCTCCAACCTTCCGTAGT R: CCAGATCAGAGAGGTGGTGTAG

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YTHDF3	F: TCAGAGTAACAGCTATCCACCA
	R: GGTTGTCAGATATGGCATAGGCT

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**Supplement table S5. Antibodies used for western blotting.**

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Antibody	Company	Catalog number	Dilution
DECR1	Abcam	Ab198848	1:1000
METTL3	Proteintech	15073-1-AP	1:1000
YTHDF3	Proteintech	25537-1-AP	1:1000
$\beta$ -actin	Proteintech	66009-1-Ig	1:3000
GLUT1	Proteintech	21829-1-AP	1:1000
PKM2	Proteintech	60268-1-Ig	1:1000
ENO1	Proteintech	11204-1-AP	1:1000
LDHA	Proteintech	19987-1-AP	1:1000
HRP-conjugated Affinipure Goat Anti-Rabbit IgG(H+L)	Proteintech	SA00001-2	1:3000
HRP-conjugated Affinipure Goat Anti-Mouse IgG(H+L)	Proteintech	SA00001-1	1:3000

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