Table S1 Ferroptosis-related genes

ABCC1	ULK2	LGMN	PIR	PEDS1
ACACA	EGFR	SMPD1	HCAR1	ADAMTS13
ACO1	MAPK3	MYCN	SLC16A1	CDC25A
ACSF2	MAPK1	IFNA1	RRM2	CircFNDC3B
ACSL1	BID	IFNA2	NR4A1	PPARD
ACSL3	CDKN2A	IFNA4	RPTOR	ENO3
ACSL4	SOCS1	IFNA5	SREBF1	LCN2
ACLS5	CDO1	IFNA6	SREBF2	MARCHF5
ACSL6	MYB	IFNA7	FZD7	TRIB2
AIFM2	MAPK8	IFNA8	P4HB	DHODH
AKR1C1	MAPK9	IFNA10	NT5DC2	MIR545
AKR1C2	MAPK14	IFNA13	BCAT2	PDK4
AKR1C3	LINC00472	IFNA14	PLA2G6	CircPVT1
ALOX12	PRKAA2	IFNA16	MIR424	MIR9-3HG
ALOX15	PRKAA1	IFNA17	PARK7	ADIPOQ
ALOX5	ELAVL1	IFNA21	FXN	circDTL
ATG5	BAP1	SMG9	SUV39H1	PTPN18
ATG7	MIR6852	PPARG	ATF2	ABCC5
ATP5MC3	ACVR1B	MIR335	ACOT1	CISD3
BACH1	TGFBR1	SNX5	ALDH3A2	MS4A15
CARS	EPAS1	PAQR3	STK11	FURIN
CBS	HILPDA	MICU1	FNDC5	circRHBG
CD44	HIF1A	TOR2A	CircIL4R	GALNT14
CHAC1	IFNG	MIR375	CDH1	KLHDC3
CISD1	ANO6	MAP3K14	NEDD4L	LINC01833
CP	LPIN1	CircKDM4C	BRD2	circGFRA1
CRYAB	HMGB1	MIR324	BRD3	MAPKAP1
CS	TNFAIP3	QSOX1	BRDT	PRR5
CYBB	TLR4	MIB2	DECR1	RICTOR
DPP4	ATF3	CLTRN	GLRX5	GSTM1
EMC2	ATM	KLF2	NCOA3	TERT
FADS2	YY1AP1	MIR5096	NR5A2	circ0097009
FANCD2	EGLN2	HOTAIR	PANX2	TMEM161B-DT
FDFT1	MIOX	H19	RHEBP1	circEPSTI1
FTH1	TAFAZZIN	FOXO4	TFAP2A	MIR18A
FTL	MTDH	YTHDC2	ARF6	RARRES2
FTMT	IDH1	DDR2	GDF15	DUSP1
G6PD	SIRT1	SLC39A7	ABHD12	NCF2
GCLC	FBXW7	TRIM46	PPP1R13L	MT3
GCLM	PANX1	KDM5A	TFAM	UBC
GLS2	DNAJB6	TRIM21	KDM3B	ALB
GOT1	LONP1	DPEP1	RNF113A	TXNRD1
GPX4	CD82	CYGB	AHCY	SRXN1
GSS	IL1B	IDO1	circ-TTBK2	GPX2
HMGCR	CTSB	GSTZ1	MIR522	BNIP3
HMOX1	POR	GJA1	IDH2	OXSR1
HSBP1	CYB5R1	PGRMC1	PPARA	SELENOS
HSPB1	ELOVL5	CIRBP	NOS2	ANGPTL7
IREB2	FADS1	circPSEN1	SIAH2	DDIT4
KEAP1	PTEN	USP11	RELA	LOC284561
LPCAT3	NR1D1	YAP1	VDR	ASNS
MAP1LC3A	NR1D2	MIR135B	NEDD4	TSC22D3
MAP1LC3B	TBK1	TRIM26	PRDX1	DDIT3
MAP1LC3C	IL6	NDRG1	AR	JDP2
MT1G	USP7	MIR302A	MTF1	SLC1A4
NCOA4	miR-182-5p	ASMTL-AS1	COPZ1	PCK2
NFE2L2	miR-378a-3p	PIEZO1	NUPR1	TXNIP
NFS1	ATF4	LIFR	USP35	VLDLR
NOX1	AQP3	PTPN6	NEAT1	GPT2
NQO1	AQP5	MIR15A	PARP1	PSAT1
NRF2	AQP8	EGR1	PARP2	LURAP1L
OTUB1	LINC00618	ADAM23	PARP3	SLC7A5
PCBP1	MT1DP	ARHGEF26-AS1	PARP4	HERPUD1
PCBP2	PEX10	CPEB1	PARP6	XBP1
PEBP1	AGPAT3	COX4I2	PARP8	ZNF419
PGD	PEX12	lncRNA AABR07017145.1	PARP9	KLHL24
PHKG2	CHP1	TIMP1	PARP10	TRIB3
PRNP	GPAT4	KDM6B	PARP11	ZFP69B
PROM2	BRPF1	METTL14	PARP12	ATP6V1G2
PTGS2	OSBPL9	MIB1	PARP14	VEGFA
RPL8	INTS2	KDM5C	PARP15	TUBE1
SAT1	MMD	MEG3	PARP16	ARRDC3
SAT2	CYP4F8	CCDC6	PDSS2	CEBPG
SLC11A2	MLLT1	CFL1	TXN	SNORA16A
SLC1A5	TTPA	MIR539	SENP1	RGS4
SLC39A14	GRIA3	KMT2D	OIP5-AS1	BLOC1S5-TXNDC5
SLC39A8	EPT1	RB1	MIR190A	LOC390705
SLC3A2	POM121L12	HSF1	FGF21	EIF2S1
SLC40A1	LIG3	SQSTM1	CREB1	KIM-1
SLC7A11	AEBP2	MUC1	CREB3	CXCL2
SQLE	AGPS	HSPA5	CREB5	HSD17B11
STEAP3	CDCA3	HELLS	MIR130B	SETD1B
TF	PEX2	SCD	BEX1	MAFG
TFRC	PEX6	SRC	ASAH2	IL33
TP53	TIMM9	STAT3	FABP4	HAMP
VDAC2	DCAF7	PML	AKT1S1	DRD5
VDAC3	LCE2C	MTOR	MLST8	DRD4
ZEB1	FAR1	TP63	TYRO3	MAP3K5
NOX3	PHF21A	CDKN1A	SIRT6	SLC2A1
NOX4	SMAD7	MIR137	TMSB4X	SLC2A3
NOX5	LYRM1	ENPP2	TMSB4Y	SLC2A6
DUOX1	AMN	FH	KIF20A	SLC2A8
DUOX2	PEX3	CISD2	ECH1	SLC2A12
PIK3CA	MTCH1	MIR9-1	circRHOT1	GLUT13
FLT3	ACADSB	MIR9-2	ETV4	SLC2A14
SCP2	PVT1	MIR9-3	MEG8	EIF2AK4
NRAS	hsa_circ_0008367	ISCU	VCP	TFAP2C
KRAS	MAP3K11	LINC00336	circ_0007142	SP1
HRAS	GSK3B	BRD4	RBMS1	HBA1
TFR2	BRD7	PRDX6	KDM4A	NNMT
SLC38A1	SLC25A28	MIR17	MGST1	PLIN4
CARS1	MFN2	SESN2	circKIF4A	HIC1
ALOX12B	ZFAS1	NF2	miR-7-5p	STMN1
ALOX15B	TSC1	ARNTL	circ_0067934	CAPG
ALOXE3	TGFB1	JUN	MPC1	HNF4A
G6PDX	SNCA	CA9	CHMP1A	NGB
ULK1	SIRT3	TMBIM4	CAMKK2	YWHAE
ATG3	CGAS	PLIN2	SOX2	GABPB1
ATG4D	STING1	MIR212	SRSF9	AURKA
BECN1	HDDC3	Fer1HCH	PROK2	MIR4715
GABARAPL2	MIR761	LAMP2	MIR4443	RIPK1
GABARAPL1	MDM2	ZFP36	SIRT2	MIR30B
ATG16L1	MDM4	CHMP5	circRNA1615	MMP13
WIPI1	MIR214	CHMP6	MIR27A	LRRFIP1
WIPI2	DLD	CAV1	MIR670	CBR1
SNX4	WWTR1	GCH1	MEF2C	
ATG13	PRKCA	DAZAP1	EZH2	

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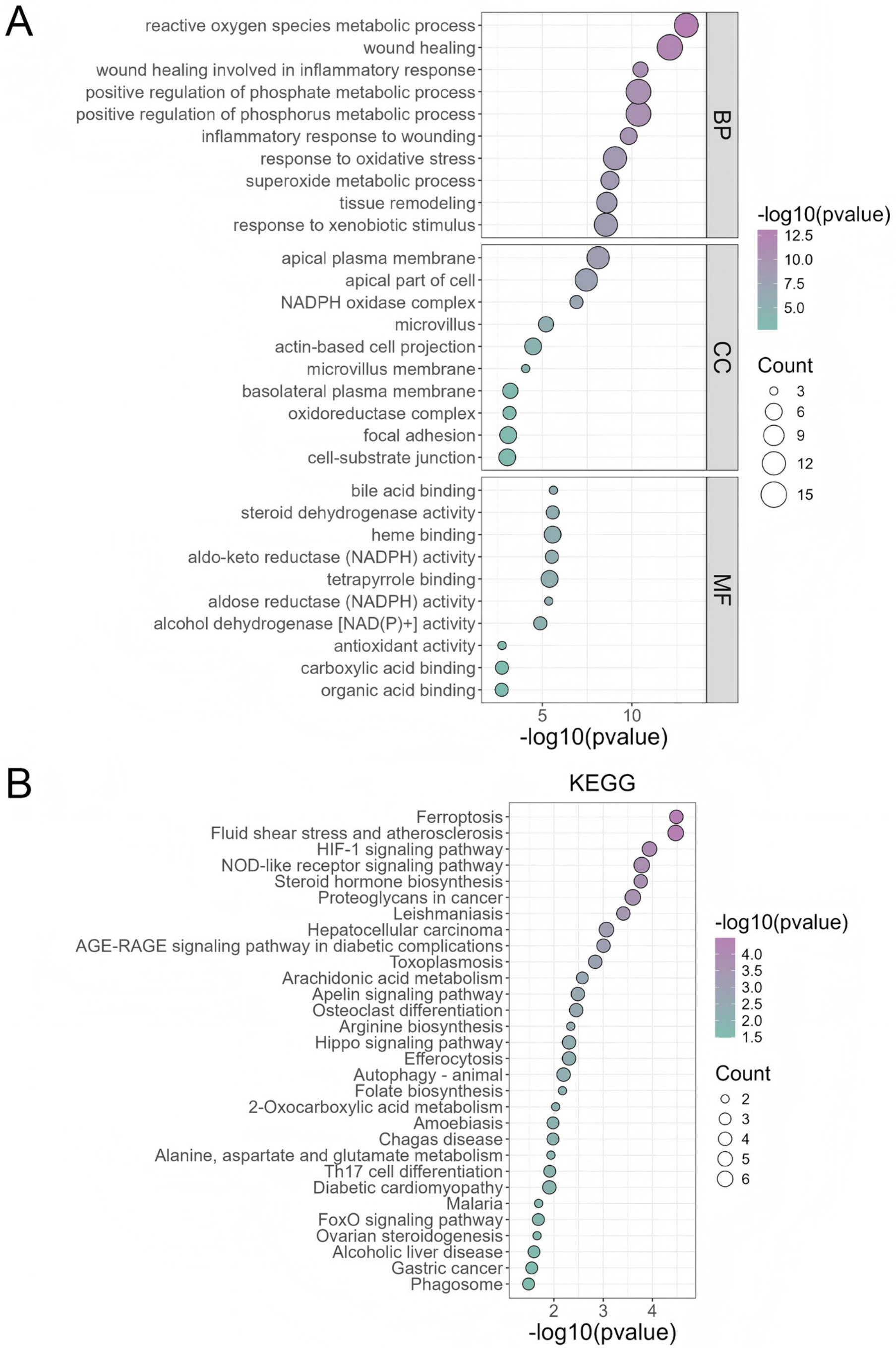

Figure S1 Functional enrichment analysis of ferroptosis-related hub genes. (A) GO enrichment analysis showing significant biological processes, cellular components, and molecular functions. (B) KEGG pathway enrichment analysis.

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Table S2 Varying of transcriptional remodeling caused by virtual knockout of five model genes

Model gene	gene	distance	Z	p.value	p.adj	logFC
AKR1C1	GLUL	2.35814E-05	1.9120157	5.361E-09	1.713E-06	5.0897483
	MARCKS	2.12619E-05	1.8595175	1.428E-07	3.042E-05	4.7909923
	LMAN1	1.93368E-05	1.8119748	1.708E-06	0.0002323	4.5171387
	VSIG2	1.91434E-05	1.8069727	2.166E-06	0.0002323	4.4881399
	IGFBP2	1.90189E-05	1.803728	2.52E-06	0.0002323	4.4693106
	TCEAL9	1.90107E-05	1.8035142	2.545E-06	0.0002323	4.4680693
	TMEM98	1.82231E-05	1.7825407	6.496E-06	0.0005188	4.3459879
	FOXA2	1.69875E-05	1.7479738	2.625E-05	0.0018219	4.1433965
	CA2	1.69116E-05	1.7457799	2.851E-05	0.0018219	4.1304793
	AZGP1	1.61539E-05	1.7233834	6.401E-05	0.0037184	3.9982109
	ALDH1A1	1.60535E-05	1.7203461	7.107E-05	0.0037846	3.9802157
	MGST1	1.59212E-05	1.7163192	8.151E-05	0.0040064	3.9563371
	GPR160	1.52249E-05	1.6946302	0.0001648	0.0075224	3.8273081
	SH3BGRL2	1.45161E-05	1.6716387	0.0003279	0.013967	3.6897565
	RHOBTB3	1.36394E-05	1.6417948	0.0007374	0.0287779	3.5100063
	RNASE1	1.35976E-05	1.6403319	0.0007656	0.0287779	3.5011599
	TNFRSF12A	1.27501E-05	1.6097514	0.0016038	0.0569356	3.3154733
	CA8	1.26599E-05	1.6063902	0.001731	0.0582172	3.294975
	MT1G	1.25954E-05	1.6039755	0.0018275	0.05839	3.2802376
	MUC5AC	1.25259E-05	1.6013606	0.0019371	0.0589429	3.2642681
	ZKSCAN1	1.20521E-05	1.5831944	0.0028592	0.0830476	3.1530255
	SMIM24	1.196E-05	1.5795898	0.0030795	0.0855568	3.1308902
	SEZ6L2	1.15953E-05	1.5650704	0.0041123	0.109489	3.0415175
	TRNP1	1.14749E-05	1.5601905	0.0045166	0.1112491	3.0114039
	KRT18	1.1472E-05	1.560075	0.0045266	0.1112491	3.0106903
	SMIM6	1.12581E-05	1.5512875	0.0053367	0.126302	2.9563644
	NEDD4L	1.1173E-05	1.5477551	0.0056934	0.1299319	2.934491
	HSPA1A	1.10721E-05	1.5435305	0.0061448	0.1353965	2.9083045
	TFF2	1.07542E-05	1.53	0.0077844	0.1658085	2.8242398
	ANXA10	1.04226E-05	1.5155091	0.0099022	0.2041134	2.7338758
	LIFR	1.0353E-05	1.5124147	0.0104073	0.2078211	2.7145341
	BCAS1	9.86128E-06	1.4900289	0.0146743	0.2841478	2.5741395
	ANXA2	9.62761E-06	1.4790449	0.0171958	0.3231796	2.5049458
	KRT19	9.3582E-06	1.4660861	0.0205679	0.3755113	2.4230505
	SCGB2A1	9.18001E-06	1.4573341	0.023103	0.4015896	2.36758
	RHOB	9.16999E-06	1.4568376	0.0232532	0.4015896	2.364429
	S100A16	9.12866E-06	1.4547844	0.0238821	0.4015961	2.3513952
	KRT8	9.05366E-06	1.4510378	0.0250609	0.4062482	2.3275927
	GALNT7	9.0136E-06	1.449025	0.0257111	0.4062482	2.3147953
	SELENBP1	8.9921E-06	1.4479417	0.026066	0.4062482	2.307905
	PGC	8.7384E-06	1.4349838	0.0305838	0.4653108	2.2253284
	ID3	8.58869E-06	1.427181	0.0335535	0.4986209	2.1754644
	TMPRSS2	8.51204E-06	1.4231403	0.035167	0.49974	2.1496005
	ARFGEF3	8.51083E-06	1.4230763	0.035193	0.49974	2.1491906
	CST3	8.44643E-06	1.4196553	0.0366005	0.5084292	2.1272712
	ATP8B1	8.31656E-06	1.4126878	0.0395848	0.5381843	2.0825645
	BMP2	8.21486E-06	1.4071641	0.0420638	0.5498946	2.0470617
	TSC22D1	8.20665E-06	1.4067158	0.0422695	0.5498946	2.0441777
	TM9SF3	8.17668E-06	1.4050751	0.0430277	0.5498946	2.0336209
	SPINK1	7.93067E-06	1.3914044	0.0496973	0.6226774	1.9454744
CTSB	KRT19	8.40415E-06	2.0719064	1.158E-09	2.935E-07	5.2109836
	ANXA2	8.36556E-06	2.068993	1.378E-09	2.935E-07	5.1977036
	KRT8	7.94913E-06	2.0368027	8.588E-09	1.372E-06	5.050376
	KRT18	7.53152E-06	2.0030402	4.923E-08	6.292E-06	4.894662
	S100A6	7.1931E-06	1.9744874	1.899E-07	2.022E-05	4.76201
	S100A16	6.95199E-06	1.953436	4.794E-07	4.376E-05	4.6636345
	S100A14	5.66271E-06	1.8289722	4.118E-05	0.0032896	4.071766
	CLDN7	5.3857E-06	1.7991032	9.614E-05	0.0068258	3.9270492
	GPRC5A	5.28479E-06	1.7878961	0.0001297	0.0082866	3.8724751
	MYOF	5.15901E-06	1.7736672	0.000187	0.0108624	3.8029686
	ITGB4	4.94443E-06	1.7486958	0.0003428	0.0168935	3.6803908
	KLK10	4.94353E-06	1.7485887	0.0003437	0.0168935	3.6798633
	TNFRSF12A	4.85291E-06	1.7377627	0.0004409	0.0201239	3.6264828
	KRT7	4.76777E-06	1.7274317	0.0005551	0.0236477	3.575408
	MYH14	4.41336E-06	1.6826623	0.0013935	0.0556517	3.3525352
	PRSS3	4.31225E-06	1.6693271	0.0017915	0.0673403	3.2856605
	CCND1	4.28135E-06	1.6651989	0.0019326	0.0686064	3.2649114
	S100A10	4.11242E-06	1.6421678	0.0029007	0.0975556	3.1487537
	CD9	4.03136E-06	1.6308295	0.0035074	0.1120603	3.0913169
	PLA2G16	3.84648E-06	1.60422	0.0053447	0.1581161	2.9558602
	ITGA2	3.83826E-06	1.6030108	0.0054437	0.1581161	2.9496828
	JUP	3.81179E-06	1.5991049	0.0057737	0.1604096	2.9297144
	LGALS3	3.76286E-06	1.5918236	0.0064315	0.1712396	2.8924372
	SERPINB1	3.71435E-06	1.5845253	0.0071494	0.182739	2.8550014
	ITGA6	3.54946E-06	1.5590899	0.0101583	0.2496608	2.723977
	PHLDA2	3.52997E-06	1.5560182	0.0105797	0.2503866	2.7080947
	AHNAK2	3.40787E-06	1.5364319	0.0135923	0.3101955	2.6065228
	PDZK1IP1	3.3145E-06	1.5210459	0.016384	0.3610137	2.5263652
	CDCP1	3.27656E-06	1.5146875	0.0176553	0.3760577	2.4931436
	LAMC2	3.23944E-06	1.5084058	0.0189818	0.389272	2.4602683
	TM4SF1	3.22571E-06	1.5060669	0.0194941	0.389272	2.4480138
	TPM1	3.16194E-06	1.4950906	0.0220348	0.4164829	2.3904013
	LMO7	3.15576E-06	1.4940162	0.0222959	0.4164829	2.3847531
	GABRP	3.14371E-06	1.4919186	0.0228121	0.4164829	2.3737207
	DSG2	3.03915E-06	1.473411	0.0277471	0.4925113	2.2761129
	SYT13	2.95443E-06	1.4580139	0.0323956	0.5594806	2.1945408
	C19orf33	2.92217E-06	1.4520514	0.0343335	0.5644244	2.1628614
	PLS1	2.9195E-06	1.4515562	0.0344979	0.5644244	2.160228
	MISP	2.90615E-06	1.4490705	0.0353317	0.5644244	2.1470042
	TSPAN1	2.828E-06	1.4343197	0.0405657	0.6322318	2.068349
	FAT1	2.81323E-06	1.4314916	0.0416259	0.6333084	2.0532332
	FXYD3	2.78946E-06	1.4269152	0.0433807	0.6446572	2.0287478
	S100P	2.7536E-06	1.4199497	0.0461452	0.6701539	1.9914219
	SDCBP2	2.7141E-06	1.4121839	0.0493618	0.6947744	1.9497239
EZH2	LCN2	1.49237E-05	2.5309982	9.861E-53	3.151E-50	7.8677932
	PDZK1IP1	5.56235E-06	1.9905813	1.223E-08	2.606E-06	5.0201133
	S100A10	3.86966E-06	1.8077075	7.403E-05	0.0118268	3.9731408
	TNFRSF12A	3.38756E-06	1.7426519	0.000522	0.0667109	3.5892128
	BCAS1	3.27381E-06	1.726123	0.0008002	0.0852228	3.4906648
	TXN	3.21194E-06	1.7169201	0.0010041	0.0916638	3.4356169
	STMN1	3.11942E-06	1.7028617	0.0014002	0.1118421	3.3512769
	HMGB2	2.77934E-06	1.6478313	0.0044226	0.3140036	3.0182093
	LMNA	2.57272E-06	1.6114337	0.0084205	0.5380693	2.7953073
	TOP2A	2.51949E-06	1.6016427	0.0098738	0.5735784	2.7349855
	ANKH	2.38503E-06	1.5760763	0.014585	0.776653	2.5767433

Table S2 *(contuned)*

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Table S2 *(contuned)*

Model gene	gene	distance	Z	p.value	p.adj	logFC
	HMMR	2.305E-06	1.5602508	0.0182474	0.8085966	2.4782579
	SMC4	2.2594E-06	1.5510161	0.0206756	0.8085966	2.420598
	MKI67	2.2319E-06	1.5453686	0.0222721	0.8085966	2.3852667
	NCAPG	2.22167E-06	1.5432529	0.0228925	0.8085966	2.372017
	CENPE	2.18816E-06	1.536258	0.0250325	0.8085966	2.3281581
	NUSAP1	2.1822E-06	1.5350053	0.0254303	0.8085966	2.3202949
	GTSE1	2.174E-06	1.5332752	0.0259871	0.8085966	2.3094308
	CDK1	2.1544E-06	1.5291155	0.0273613	0.8085966	2.2832897
	KIF20B	2.14367E-06	1.5268252	0.0281395	0.8085966	2.2688843
	TUBB	2.1206E-06	1.5218671	0.0298772	0.8085966	2.2376686
	KIF11	2.11011E-06	1.5195956	0.0306979	0.8085966	2.2233543
	BIRC5	2.10838E-06	1.519221	0.0308347	0.8085966	2.2209925
	DSTN	2.07143E-06	1.5111389	0.0338912	0.8085966	2.1699841
	MAD2L1	2.06371E-06	1.5094333	0.0345619	0.8085966	2.1592056
	CENPF	2.05558E-06	1.5076313	0.0352804	0.8085966	2.1478126
	CCNA2	2.04748E-06	1.5058312	0.0360082	0.8085966	2.1364261
	ECT2	2.03206E-06	1.5023843	0.0374304	0.8085966	2.1146071
	SFN	2.02205E-06	1.5001355	0.0383785	0.8085966	2.1003613
	ANLN	1.98455E-06	1.4916215	0.0421146	0.8085966	2.0463484
	TYMS	1.96398E-06	1.486892	0.0442912	0.8085966	2.0162912
	KIF23	1.96028E-06	1.4860353	0.0446933	0.8085966	2.0108426
	CKS1B	1.9521E-06	1.4841386	0.045592	0.8085966	1.9987752
	DLGAP5	1.94531E-06	1.4825605	0.0463488	0.8085966	1.9887297
	BUB1	1.94127E-06	1.4816183	0.0468045	0.8085966	1.9827301
	PLK1	1.93426E-06	1.4799779	0.0476049	0.8085966	1.9722811
	CEP55	1.93009E-06	1.4790013	0.0480856	0.8085966	1.9660587
IDO1	ANXA2	7.4313E-07	1.7804566	2.262E-10	7.226E-08	5.3300678
	KRT19	7.21937E-07	1.7695143	7.204E-10	1.534E-07	5.2465856
	KRT8	6.93661E-07	1.7544482	3.215E-09	5.136E-07	5.1313011
	KRT18	6.7699E-07	1.7453	7.563E-09	9.665E-07	5.0611056
	S100A6	5.99592E-07	1.6999319	3.098E-07	3.3E-05	4.7108017
	S100A16	5.84674E-07	1.6905756	6.037E-07	5.511E-05	4.6381004
	S100A14	4.72149E-07	1.6120104	5.586E-05	0.0044614	4.0213238
	MYOF	4.51055E-07	1.5953982	0.0001183	0.0083989	3.8894428
	CLDN7	4.45337E-07	1.5907728	0.0001442	0.0092151	3.8526306
	GPRC5A	4.22849E-07	1.5720401	0.0003075	0.0178622	3.7031258
	TNFRSF12A	4.1258E-07	1.5631806	0.0004295	0.0228707	3.6321863
	KLK10	4.02763E-07	1.5545206	0.0005872	0.0288615	3.5626978
	ITGB4	3.9495E-07	1.54749	0.0007495	0.0330179	3.5061782
	KRT7	3.93867E-07	1.546505	0.0007751	0.0330179	3.4982521
	PRSS3	3.77475E-07	1.5312923	0.0012746	0.0509024	3.3755989
	CCND1	3.53901E-07	1.5083196	0.002524	0.0948728	3.1895261
	MYH14	3.49838E-07	1.5042203	0.0028286	0.1004146	3.1562136
	CD9	3.40216E-07	1.4943339	0.0036884	0.124046	3.075737
	PLA2G16	3.28828E-07	1.4822987	0.0050088	0.1600324	2.9775079
	JUP	3.10466E-07	1.462065	0.0080551	0.2327986	2.811712
	AHNAK2	3.09844E-07	1.4613606	0.0081826	0.2327986	2.805925
	S100A10	3.08901E-07	1.4602902	0.0083793	0.2327986	2.7971296
	PHLDA2	3.07184E-07	1.4583328	0.0087484	0.2329269	2.7810401
	SERPINB1	3.04317E-07	1.4550434	0.009397	0.240187	2.7539845
	PDZK1IP1	3.01201E-07	1.4514365	0.0101501	0.2494586	2.724292
	ITGA2	2.99613E-07	1.4495849	0.0105543	0.2497851	2.7090389
	ITGA6	2.93826E-07	1.4427611	0.0121509	0.2773002	2.6527667
	LGALS3	2.91002E-07	1.4393858	0.0130052	0.2865625	2.6248974
	TM4SF1	2.69954E-07	1.4132443	0.0212235	0.4520599	2.408263
	LAMC2	2.58835E-07	1.3986734	0.0271684	0.5580937	2.2869039
	GABRP	2.56955E-07	1.3961527	0.0283045	0.5580937	2.2658643
	CDCP1	2.5612E-07	1.3950284	0.0288217	0.5580937	2.2564761
	TPM1	2.47258E-07	1.3828803	0.0348344	0.6421082	2.1548667
	LMO7	2.46802E-07	1.3822455	0.0351702	0.6421082	2.149549
	TIMP1	2.35466E-07	1.3660845	0.0444693	0.7893309	2.0138736
	GLUL	2.32109E-07	1.3611627	0.0475922	0.7932063	1.9724452
	FAT1	2.32016E-07	1.3610254	0.0476814	0.7932063	1.9712883
	SYT13	2.31259E-07	1.3599061	0.0484117	0.7932063	1.9618595
TIMP1	KRT19	2.16965E-05	2.0183624	2.394E-10	7.65E-08	5.3260687
	ANXA2	2.1267E-05	2.0071755	5.357E-10	1.141E-07	5.2683819
	KRT8	2.02775E-05	1.9806332	3.231E-09	5.161E-07	5.1309091
	KRT18	1.9462E-05	1.9578985	1.336E-08	1.708E-06	5.0124759
	S100A6	1.81275E-05	1.9188397	1.211E-07	1.29E-05	4.8075157
	S100A16	1.76022E-05	1.9027739	2.77E-07	2.529E-05	4.7226576
	S100A14	1.43239E-05	1.791899	2.897E-05	0.0023137	4.1280024
	CLDN7	1.32954E-05	1.752537	0.0001039	0.0073803	3.9129966
	TNFRSF12A	1.28755E-05	1.7357053	0.0001708	0.0107775	3.8204175
	MYOF	1.27851E-05	1.7320183	0.0001898	0.0107775	3.8000857
	GPRC5A	1.27295E-05	1.729739	0.0002024	0.0107775	3.7875076
	KLK10	1.24741E-05	1.7191595	0.0002711	0.0133256	3.7290319
	ITGB4	1.21025E-05	1.7034213	0.0004109	0.0187561	3.6417565
	KRT7	1.18139E-05	1.6909093	0.0005632	0.0239941	3.5721257
	PRSS3	1.08343E-05	1.6463526	0.0015628	0.062414	3.3223716
	MYH14	1.06534E-05	1.6377429	0.0018712	0.070334	3.2737855
	CCND1	1.0423E-05	1.6265913	0.0023447	0.0832377	3.2106962
	CD9	9.72313E-06	1.5913504	0.0045343	0.1524961	3.0101357
	PLA2G16	9.46049E-06	1.5775543	0.00575	0.1797386	2.9311237
	ITGA2	9.43033E-06	1.5759487	0.0059069	0.1797386	2.9219097
	S100A10	9.33736E-06	1.5709713	0.0064153	0.1863343	2.8933224
	PDZK1IP1	9.12957E-06	1.5596889	0.0076964	0.213826	2.8283862
	JUP	8.99698E-06	1.5523725	0.0086293	0.2228388	2.7861744
	LGALS3	8.98501E-06	1.5517078	0.0087183	0.2228388	2.7823352
	SERPINB1	8.89401E-06	1.5466259	0.0094222	0.2297915	2.7529628
	PHLDA2	8.8586E-06	1.5446362	0.0097095	0.2297915	2.7414522
	AHNAK2	8.53291E-06	1.5260038	0.0127409	0.2907652	2.6333702
	ITGA6	8.4755E-06	1.5226555	0.0133545	0.2942603	2.6138917
	LAMC2	7.728E-06	1.4771552	0.0240731	0.5127564	2.3474844
	CDCP1	7.66751E-06	1.4733075	0.0252014	0.5194743	2.3248085
	TM4SF1	7.60895E-06	1.4695577	0.026337	0.5259162	2.3026874
	GABRP	7.56421E-06	1.4666764	0.0272339	0.5273479	2.2856743
	LMO7	7.409E-06	1.4565626	0.0305535	0.5742265	2.2258533
	TPM1	7.33627E-06	1.4517595	0.0322251	0.5883383	2.1973878
	SYT13	7.07466E-06	1.434134	0.0389006	0.6904857	2.0926144
	DSG2	6.9928E-06	1.4285024	0.041217	0.7118291	2.0590333
	C19orf33	6.94699E-06	1.4253259	0.0425635	0.7157396	2.0400693
	MISP	6.90914E-06	1.4226875	0.043704	0.7160733	2.0243058
	TSPAN1	6.85234E-06	1.4187045	0.0454638	0.7262846	2.000487
	PLS1	6.74401E-06	1.4110281	0.0489858	0.7634612	1.9545092

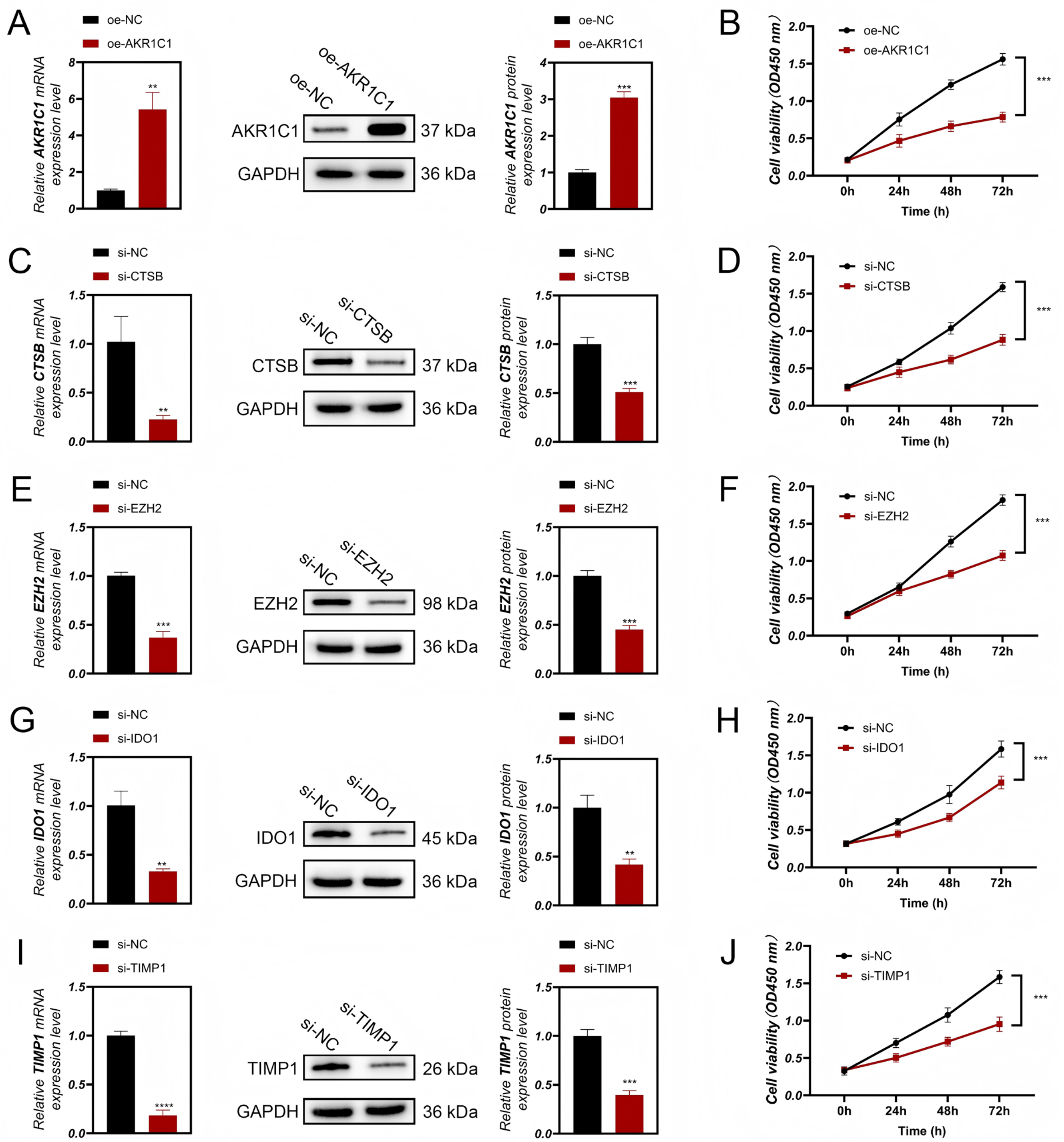

Figure S2 Validation of gene overexpression or knockdown in HGC-27 cells and effects on proliferation. (A) qRT-PCR and Western blot confirmed effective overexpression of AKR1C1 (oe-AKR1C1) and knockdown of CTSB, EZH2, IDO1, and TIMP1 (siRNAs). (B) CCK-8 assays showed that AKR1C1 overexpression or knockdown of the other four genes significantly inhibited cell proliferation. **, P<0.01; ***, P<0.001.