

Supplementary materials

Supplementary Figures

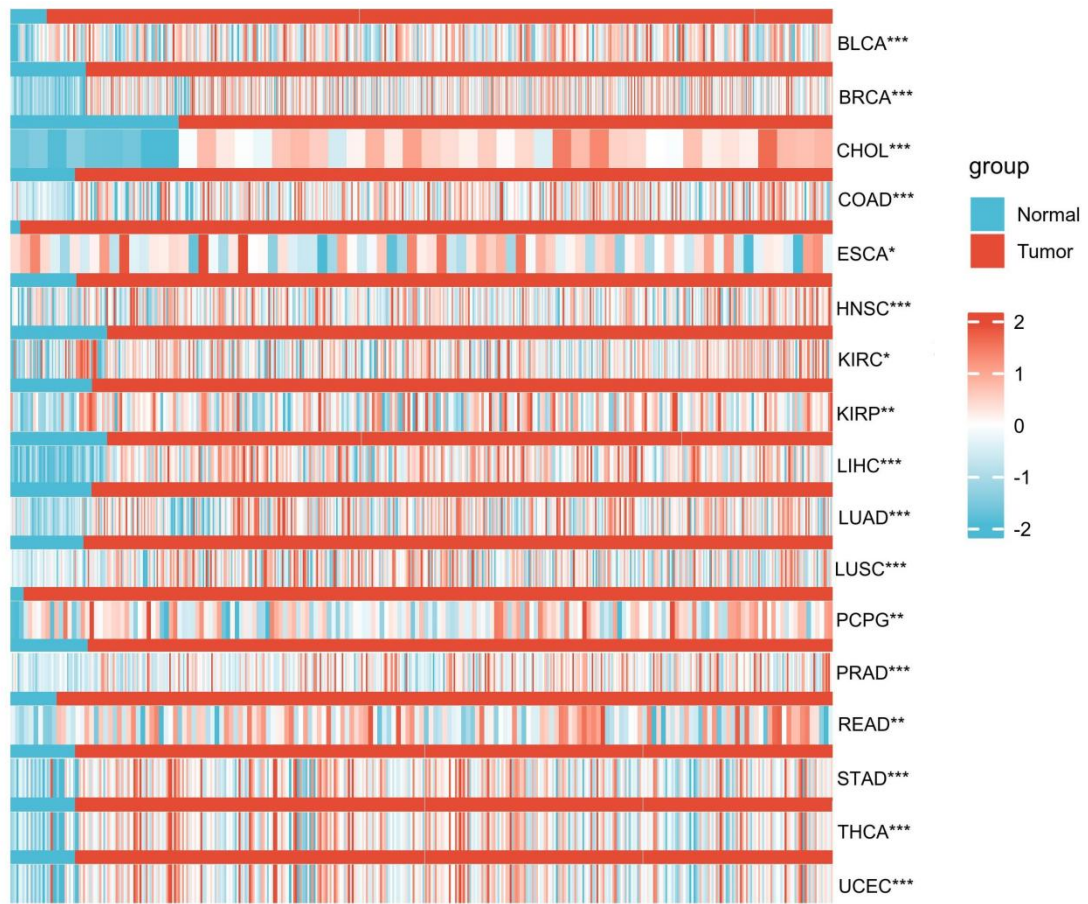


Fig S1 Expression heatmap of ABHD12 in cancer types exhibiting significant differential expression (tumor vs normal). * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$.

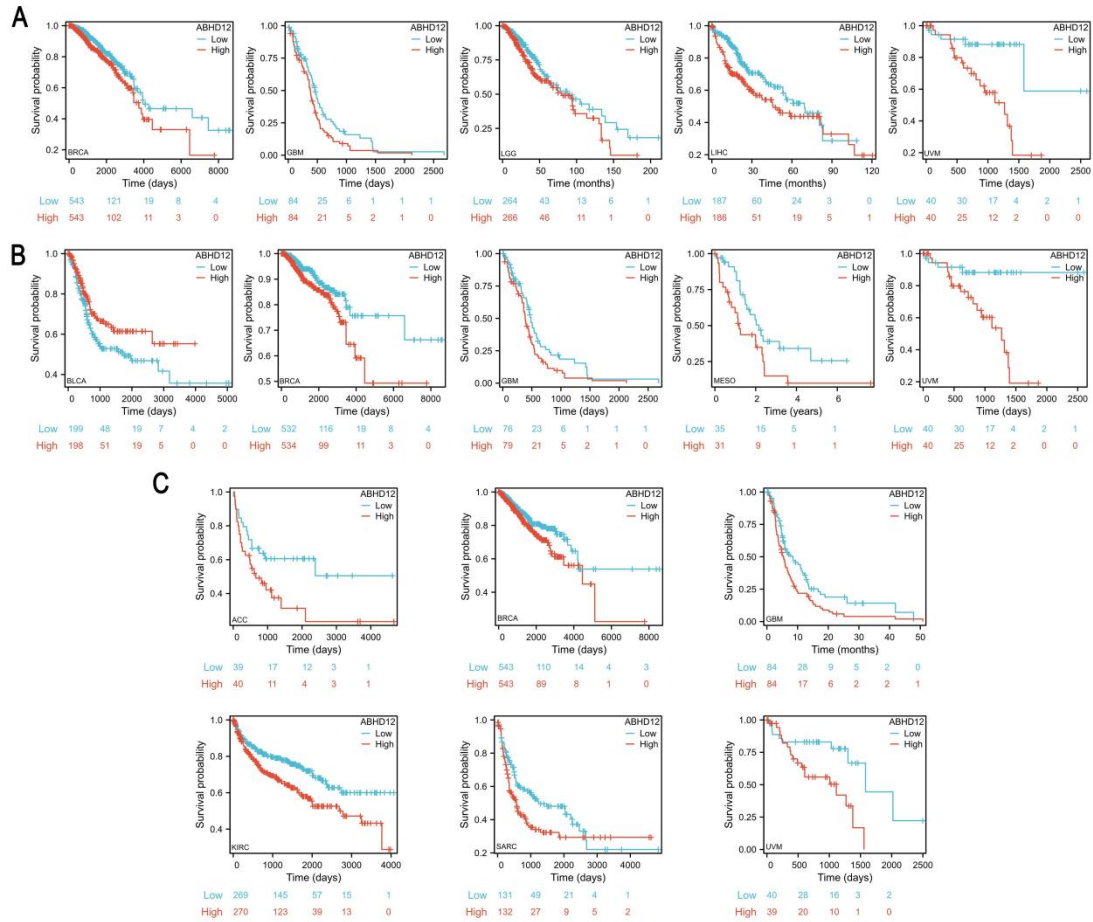


Fig S2 Kaplan-Meier (KM) Curves Showing the Detailed Association Between ABHD12 Expression and Prognosis in Cancer Patients. **(A)** OS in BRCA (HR=1.48, $p=0.016$), GBM (HR=1.44, $p=0.036$), LGG (HR=1.44, $p=0.036$), LIHC (HR=1.52, $p=0.019$), and UVM (HR=4.22, $p=0.005$). **(B)** DSS in BLCA (HR=0.68, $p=0.034$), BRCA (HR=1.72, $p=0.014$), GBM (HR=1.47, $p=0.040$), MESO (HR=1.91, $p=0.036$), and UVM (HR=4.92, $p=0.036$). **(C)** PFS in ACC (HR=1.191, $p=0.045$), BRCA (HR=1.47, $p=0.021$), GBM (HR=1.54, $p=0.013$), KIRC (HR=1.61, $p=0.003$), SARC (HR=1.46, $p=0.024$) and UVM (HR=3.14, $p=0.007$).

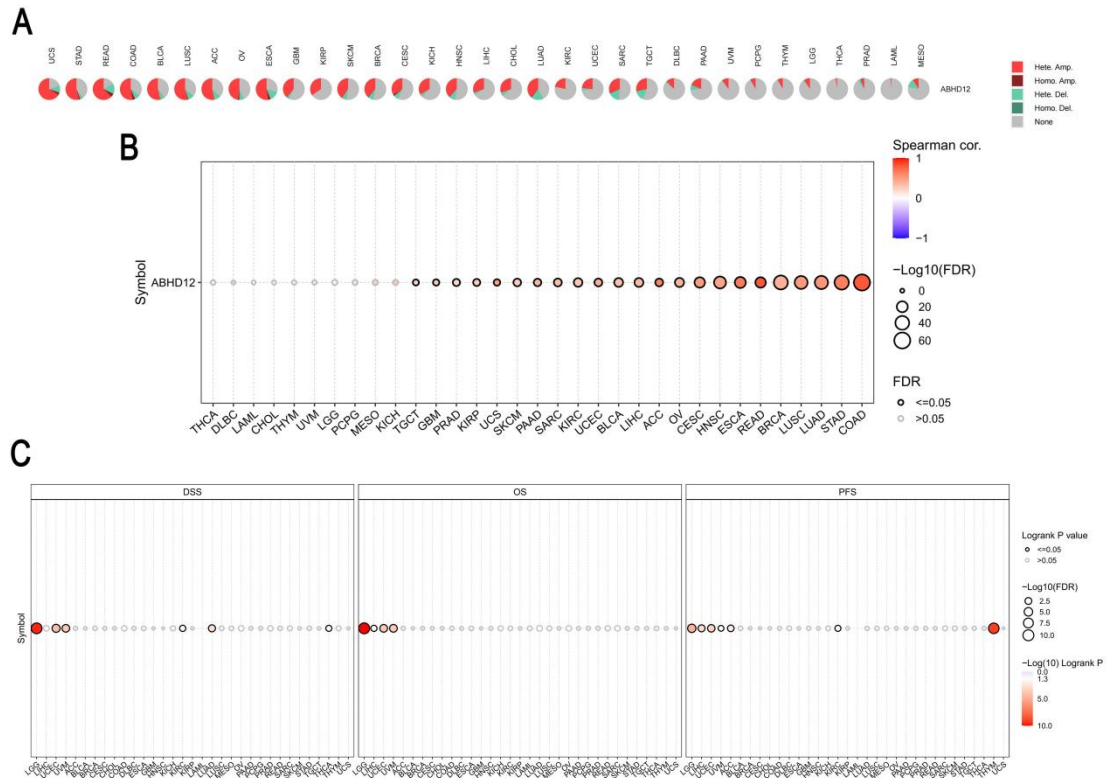


Fig S3 Mutation analysis of ABHD12. **(A)** Percentage of ABHD12 CNVs in each cancer. **(B)** Correlation between ABHD12 mRNA expression and CNVs. **(C)** Effect of ABHD12 CNVs on prognosis in cancer patients.

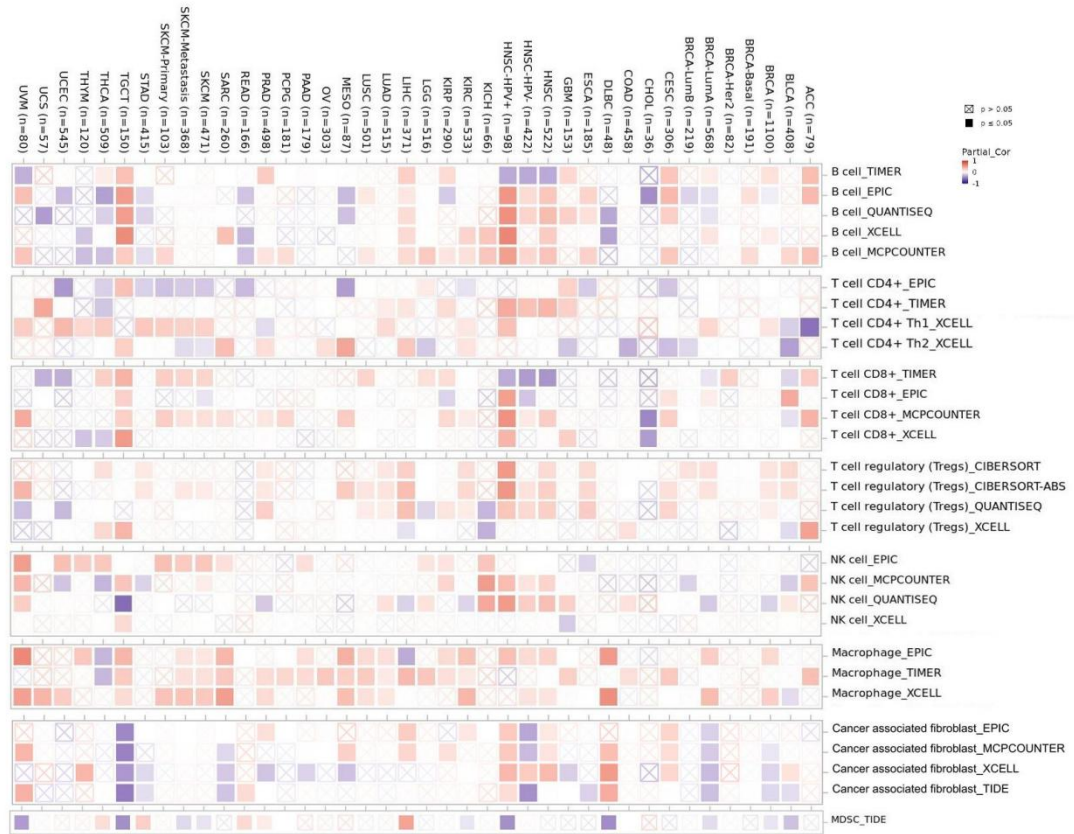


Fig S4 Correlation analysis of ABHD12 expression with multiple immune cell infiltrates in pan-cancer.

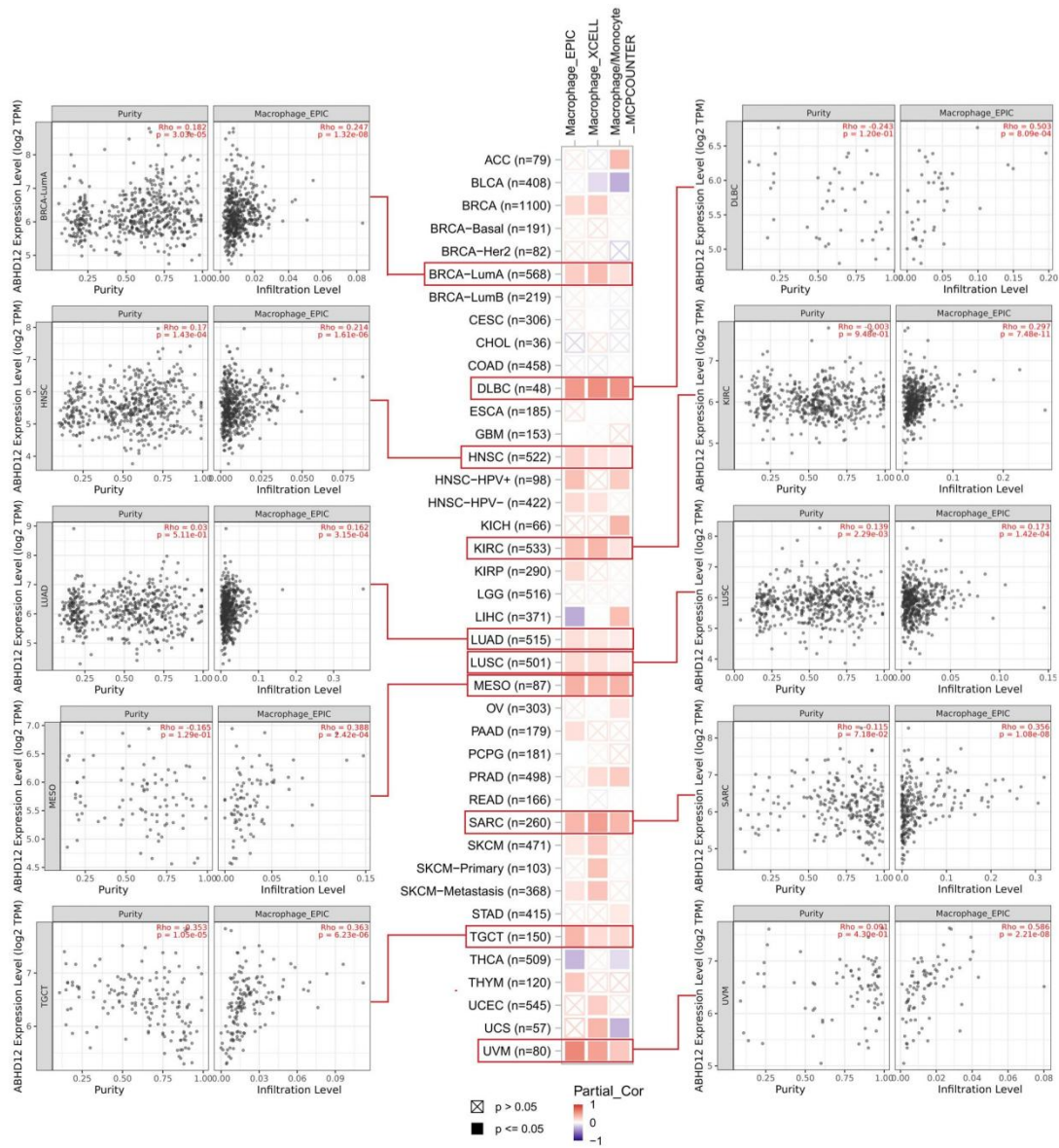
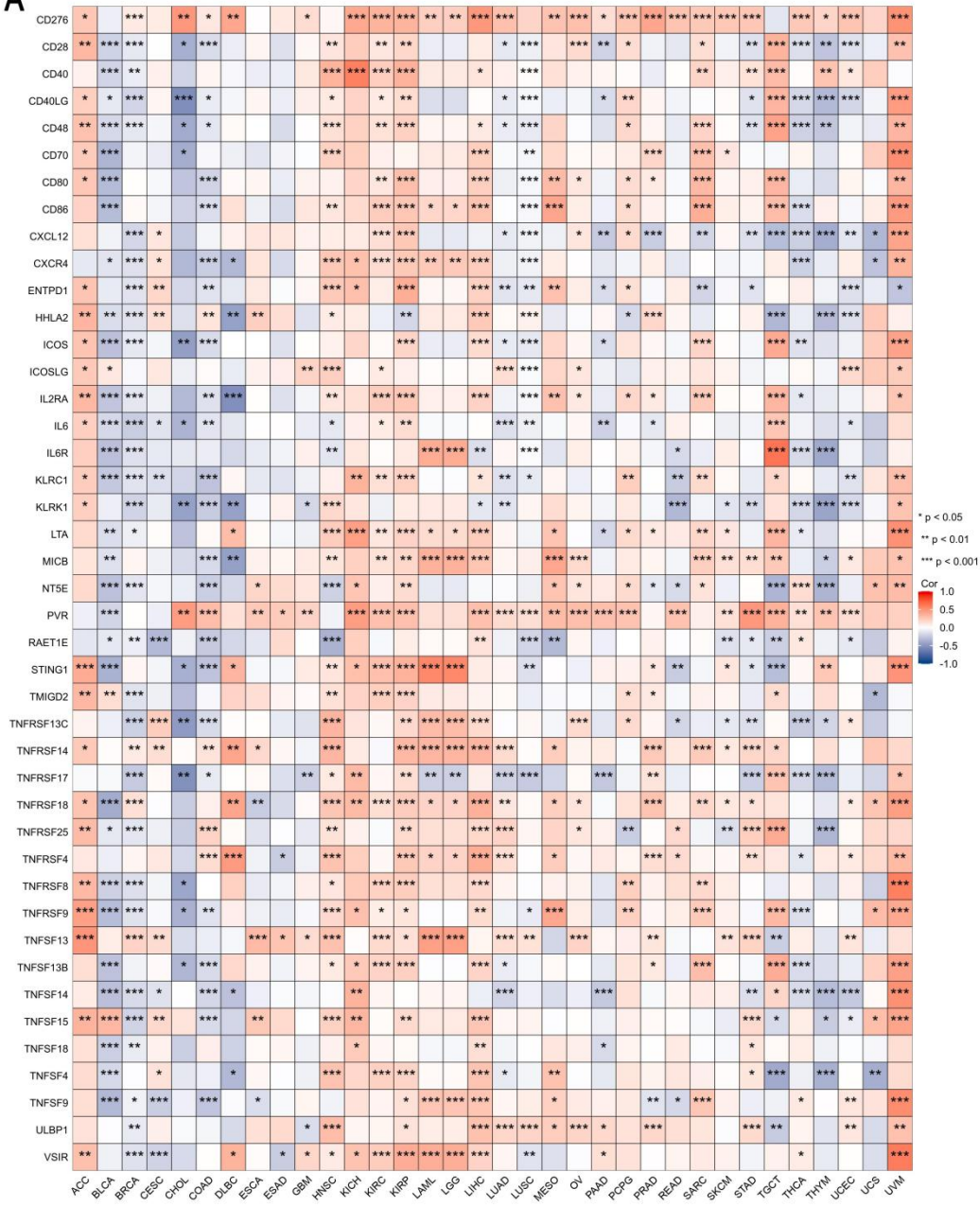


Fig S5 Correlation analysis of ABHD12 expression with macrophage cell infiltrates in pan-cancer.

A



B

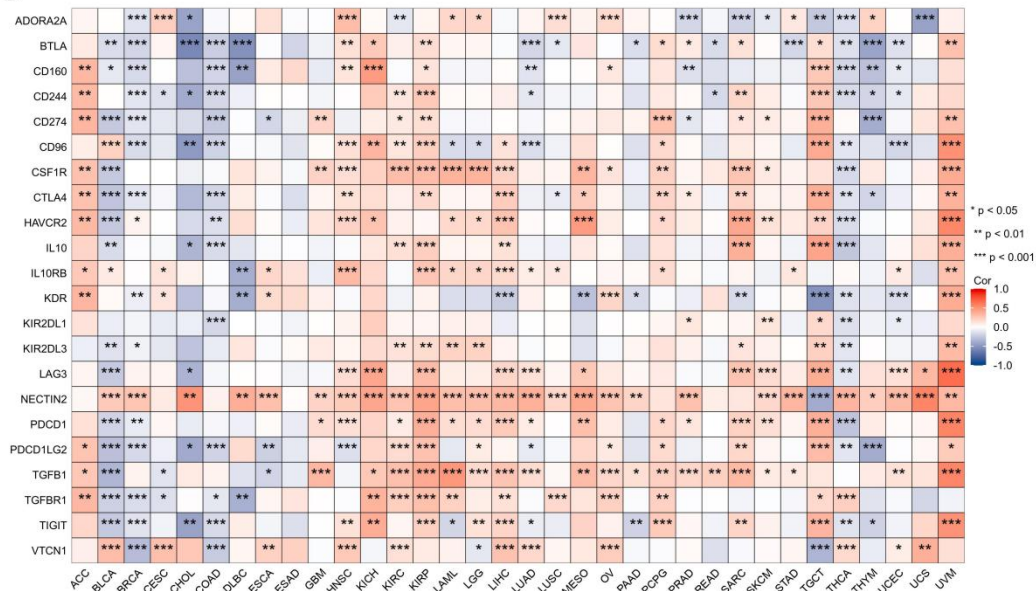


Fig S6 Co-expression of ABHD12 with **(A)** immune activating genes and **(B)** immune suppressive genes. * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$.

Supplementary Table S1 Number of Samples in Each Cancer Type

cancer	TGCA	
	group	n
ACC	Tumor	79
BLCA	Normal	19
BLCA	Tumor	412
BRCA	Normal	113
BRCA	Tumor	1113
CESC	Normal	3
CESC	Tumor	306
CHOL	Normal	9
CHOL	Tumor	35
COAD	Normal	41
COAD	Tumor	480
DLBC	Tumor	48
ESCA	Normal	11
ESCA	Tumor	163
GBM	Normal	5
GBM	Tumor	169
HNSC	Normal	44
HNSC	Tumor	504
KICH	Normal	25
KICH	Tumor	65
KIRC	Normal	72

KIRC	Tumor	541
KIRP	Normal	32
KIRP	Tumor	291
LAML	Tumor	150
LGG	Tumor	532
LIHC	Normal	50
LIHC	Tumor	374
LUAD	Normal	59
LUAD	Tumor	539
LUSC	Normal	49
LUSC	Tumor	502
MESO	Tumor	87
OV	Tumor	381
PAAD	Normal	4
PAAD	Tumor	179
PCPG	Normal	3
PCPG	Tumor	184
PRAD	Normal	52
PRAD	Tumor	501
READ	Normal	10
READ	Tumor	167
SARC	Normal	2
SARC	Tumor	263
SKCM	Normal	1
SKCM	Tumor	472
STAD	Normal	32
STAD	Tumor	375

TGCT	Tumor	156
THCA	Normal	59
THCA	Tumor	512
THYM	Normal	2
THYM	Tumor	120
UCEC	Normal	35
UCEC	Tumor	554
UCS	Tumor	57
UVM	Tumor	80

TCGA+GTEx

cancer	group	n
ACC	Normal	128
ACC	Tumor	77
BLCA	Normal	28
BLCA	Tumor	407
BRCA	Normal	292
BRCA	Tumor	1099
CESC	Normal	13
CESC	Tumor	306
CHOL	Normal	9
CHOL	Tumor	36
COAD	Normal	349
COAD	Tumor	290
DLBC	Normal	444
DLBC	Tumor	47
ESCA	Normal	666
ESCA	Tumor	182

GBM	Normal	1157
GBM	Tumor	166
HNSC	Normal	44
HNSC	Tumor	520
KICH	Normal	53
KICH	Tumor	66
KIRC	Normal	100
KIRC	Tumor	531
KIRP	Normal	60
KIRP	Tumor	289
LAML	Normal	70
LAML	Tumor	173
LGG	Normal	1152
LGG	Tumor	523
LIHC	Normal	160
LIHC	Tumor	371
LUAD	Normal	347
LUAD	Tumor	515
LUSC	Normal	338
LUSC	Tumor	498
MESO	Tumor	87
OV	Normal	88
OV	Tumor	427
PAAD	Normal	171
PAAD	Tumor	179
PCPG	Normal	3
PCPG	Tumor	182

PRAD	Normal	152
PRAD	Tumor	496
READ	Normal	318
READ	Tumor	93
SARC	Normal	2
SARC	Tumor	262
SKCM	Normal	813
SKCM	Tumor	469
STAD	Normal	210
STAD	Tumor	414
TGCT	Normal	165
TGCT	Tumor	154
THCA	Normal	338
THCA	Tumor	512
THYM	Normal	446
THYM	Tumor	119
UCEC	Normal	101
UCEC	Tumor	181
UCS	Normal	78
UCS	Tumor	57
UVM	Tumor	79

Supplementary Table S2 Clinical Characteristics of 16 Paired Clinical Samples

ID	Age (year)	Molecular subtype	TNM	ER	PR	HER	Menopausal status	Preoperative Chemotherapy, Radiotherapy, or Hormone Therapy
BC01	39	Luminal B	T2N1M0	+	+	+	Premenopausal	No
BC02	46	Luminal A	T1cN0M0	+	+	-	Premenopausal	No
BC03	52	Luminal B	T2N0M0	++	++	+	Postmenopausal	No
BC04	60	Triple-negative	T2N1M0	-	-	-	Postmenopausal	No
BC05	31	Luminal B	T1cN0M0	+	+	-	Premenopausal	No
BC06	67	Luminal A	T1aN0M0	+	+	-	Postmenopausal	No
BC07	55	Triple-negative	T2N0M0	-	-	-	Postmenopausal	No
BC08	35	HER2-enriched	T2N1M0	-	-	+++	Premenopausal	No
BC09	45	Luminal A	T2N1M0	+	++	-	Premenopausal	No
BC10	49	HER2-enriched	T2N1M0	+	-	+++	Premenopausal	No
BC11	39	Triple-negative	T3N2M0	-	-	-	Premenopausal	No
BC12	67	HER2-enriched	T2N1M0	-	-	+++	Postmenopausal	No
BC13	51	HER2-enriched	T3N2M0	-	-	++	Postmenopausal	No
BC14	41	Triple-negative	T3N1M0	-	-	-	Premenopausal	No
BC15	63	Luminal A	T1aN0M0	++	++	-	Postmenopausal	No
BC16	58	Luminal B	T3N1M0	++	+	-	Postmenopausal	No

Supplementary Table S3 Sequence information of the shRNA used

Name	Sequence (5'→3')
sh-ABHD12-1	CCACAGGATCAAGGTTTGAAT
sh-ABHD12-2	CCTTGGCTACAGGCACAAATA
sh-ABHD12-3	CCCTTATATTGGAATCTCCAT
ABHD12-OE-F	TGACATGGAGACCAAGAAAGACC
ABHD12-OE-R	ATGCTAGGAAGAGGGGCTCA
ABHD12-F	TGGCAGAGACCTTATGGTATTGG
ABHD12-R	AGGTCTTTGCCAAATGCTTCTC
GAPDH-F	GAAGGTGAAGGTCGGAGTCA
GAPDH-R	GGAAGATGGTGATGGGATTT

Supplementary Table S4A Univariate and Multivariate Cox Analysis for BRCA

Characteristics	Total(N)	Univariate analysis		Multivariate analysis	
		Hazard ratio (95% CI)	P value	Hazard ratio (95% CI)	P value
Pathologic T stage	1,083				
T1&T2	908	Reference		Reference	
T3&T4	175	1.588 (1.096 - 2.301)	0.014	0.805 (0.451 - 1.438)	0.464
Pathologic N stage	1,067				
N0	516	Reference		Reference	
N1	358	1.947 (1.322 - 2.865)	< 0.001	1.370 (0.855 - 2.194)	0.191
N2	116	2.522 (1.484 - 4.287)	< 0.001	1.046 (0.430 - 2.548)	0.920
N3	77	4.191 (2.318 - 7.580)	< 0.001	1.945 (0.816 - 4.640)	0.133
Pathologic stage	1,062				
Stage I	181	Reference		Reference	
Stage II	619	1.703 (0.989 - 2.933)	0.055	1.465 (0.792 - 2.712)	0.224
Stage III&Stage IV	262	3.566 (2.042 - 6.228)	< 0.001	2.930 (1.080 - 7.948)	0.035
ABHD12	1,086				
Low	543	Reference		Reference	
High	543	1.484 (1.077 - 2.046)	0.016	1.436 (1.017 - 2.029)	0.040

Supplementary Table S4B Univariate and Multivariate Cox Analysis for LGG

Characteristic s	Total(N)	Univariate analysis		Multivariate analysis	
		Hazard ratio (95% CI)	P value	Hazard ratio (95% CI)	P value
Primary therapy outcome	460				
PR&CR	203	Reference		Reference	
PD&SD	257	5.052 (2.833 - 9.011)	< 0.001	5.150 (2.887 - 9.185)	< 0.001
ABHD12	530				
Low	264	Reference		Reference	
High	266	1.445 (1.025 - 2.036)	0.036	1.632 (1.135 - 2.346)	0.008

Supplementary Table S4C Univariate and Multivariate Cox Analysis for UVM

Characteristic s	Total(N)	Univariate analysis		Multivariate analysis	
		Hazard ratio (95% CI)	P value	Hazard ratio (95% CI)	P value
Clinical T stage	78				
T2&T3	40	Reference		Reference	
T4	38	2.416 (0.964 - 6.055)	0.060	3.180 (1.178 - 8.584)	0.022
Age	80				
<= 60	40	Reference		Reference	
> 60	40	2.123 (0.914 - 4.933)	0.080	3.780 (1.489 - 9.598)	0.005
ABHD12	80				
Low	40	Reference		Reference	
High	40	4.221 (1.561 - 11.413)	0.005	4.229 (1.523 - 11.742)	0.006

Supplementary Table S5A Association between ABHD12 mRNA expression levels and drug sensitivity in CTRP

drug	CTRP	
	cor	fdr
alvocidib	0.35287075	8.55799E-11
BI-2536	0.371975381	4.36306E-26
BRD-K66453893	0.361784299	1.27002E-23
CD-437	0.362057354	1.29523E-23
clofarabine	0.386985518	8.69921E-28
cytarabine hydrochloride	0.398527232	2.44245E-29
docetaxel	0.365586061	3.35199E-11
doxorubicin	0.357483762	5.45353E-24
etoposide	0.384242156	5.60276E-27
gemcitabine	0.374019581	2.60383E-23
GSK461364	0.387577743	3.90483E-27
indisulam	0.36875148	2.56862E-23
isoevodiamine	0.371766453	3.6437E-25
KX2-391	0.370724609	1.0189E-24
leptomycin B	0.343156262	4.12593E-22
LY-2183240	0.370809421	3.06162E-25
mitomycin	0.385113258	1.27327E-26
nakiterpiosin	0.358237073	4.22384E-23
omacetaxine mepesuccinate	0.355112009	1.2606E-16
parbendazole	0.377018091	1.12534E-26
PF-3758309	0.368887365	2.93215E-12
rigosertib	0.374407443	1.64833E-24
SB-225002	0.362331516	1.46439E-24

SB-743921	0.350173512	4.97712E-23
teniposide	0.422540614	2.9107E-17
tivantinib	0.387124633	1.83167E-13
topotecan	0.367558297	3.92269E-25
triazolothiadiazine	0.390326124	1.06521E-28
vincristine	0.369585093	3.37753E-26
YK 4-279	0.364364198	2.38919E-24

Supplementary Table S5B Association between ABHD12 mRNA expression levels and drug sensitivity in GDSC

drug	GDSC	
	cor	fdr
5-Fluorouracil	0.27120755	0
AR-42	0.255199803	6.81171E-14
AT-7519	0.285259279	0
AZD8055	0.262890276	4.69152E-13
BX-912	0.305812356	0
CAY10603	0.26029922	1.99245E-14
CP466722	0.304097747	0
CX-5461	0.28654432	0
FK866	0.33329482	0
GSK1070916	0.275702753	0
I-BET-762	0.289619195	0
Ispinesib Mesylate	0.334916082	0
JW-7-24-1	0.264192523	7.04545E-15
KIN001-102	0.275140373	0
Methotrexate	0.304580309	0

NG-25	0.268022337	0
NPK76-II-72-1	0.279578725	0
PHA-793887	0.325534063	0
PI-103	0.274554903	0
PIK-93	0.297599465	0
SNX-2112	0.258926242	3.07688E-14
TG101348	0.250502981	1.39679E-13
THZ-2-102-1	0.26762615	7.29334E-15
TL-1-85	0.251168682	1.46694E-13
TPCA-1	0.309055388	0
Tubastatin A	0.303264559	0
Vorinostat	0.292447539	0
WZ3105	0.254703349	5.33286E-14
XMD13-2	0.280820476	0
ZSTK474	0.257187594	5.13482E-14

Supplementary Table S6 List of the top genes associated with ABHD12

Gene Symbol	Gene ID	PCC
HSCB	ENSP00000216027	0.292
B3GAT2	ENSP00000230053	0.163
CANX	ENSP00000247461	0.19
SRSF1	ENSP00000258962	0.292
GYS2	ENSP00000261195	0.282
ALG1	ENSP00000262374	0.282
DPP9	ENSP00000262960	0.376
PLEKHA4	ENSP00000263265	0.292
LMBR1L	ENSP00000267102	0.292

SLC39A4	ENSP00000301305	0.224
GYS1	ENSP00000317904	0.282
DNAJB12	ENSP00000345575	0.165
VAPA	ENSP00000345656	0.224
UGT1A9	ENSP00000346768	0.165
PEX19	ENSP00000357051	0.225
IRAK1	ENSP00000358997	0.155
PLAC9	ENSP00000361337	0.163
HLA-DRB5	ENSP00000364114	0.186
B3GALT4	ENSP00000390784	0.161
SLC39A12	ENSP00000366586	0.196
ALG1L	ENSP00000482705	0.282
PIGA	ENSP00000369820	0.282
ALG1L2	ENSP00000479850	0.282
ALG11	ENSP00000430236	0.282
PIGW	ENSP00000482202	0.282
CPVL	ENSP00000387164	0.252
ALG2	ENSP00000417764	0.282

Supplementary Table S7 GO terms and KEGG pathways enriched in the analysis

ONTOLOGY	ID	Description	GeneRatio	p.adjust
BP	GO:0097502	mannosylation	5/104	0.001632753
BP	GO:0006486	protein glycosylation	9/104	0.001632753
BP	GO:0043413	macromolecule glycosylation	9/104	0.001632753
BP	GO:0070085	glycosylation	9/104	0.00213848
BP	GO:0006488	dolichol-linked oligosaccharide biosynthetic process	3/104	0.023417714
CC	GO:0033176	proton-transporting V-type ATPase complex	4/112	0.003111657
CC	GO:0033180	proton-transporting V-type ATPase, V1 domain	3/112	0.003111657

CC	GO:0005765	lysosomal membrane	10/112	0.004057763
CC	GO:0030134	COPII-coated ER to Golgi transport vesicle	4/112	0.034024005
CC	GO:0000421	autophagosome membrane	3/112	0.047796755
MF	GO:0016758	hexosyltransferase activity	12/111	6.34983E-07
MF	GO:0016757	glycosyltransferase activity	13/111	1.13136E-06
MF	GO:0000030	mannosyltransferase activity	5/111	2.23943E-05
MF	GO:0008194	UDP-glycosyltransferase activity	7/111	0.0015872
KEGG	hsa00510	N-Glycan biosynthesis	4/47	0.025609498
KEGG	hsa00563	Glycosylphosphatidylinositol (GPI)-anchor biosynthesis	3/47	0.028651017
KEGG	hsa04152	AMPK signaling pathway	5/47	0.028651017
KEGG	hsa00513	Various types of N-glycan biosynthesis	3/47	0.038716535
KEGG	hsa04145	Phagosome	5/47	0.038716535
