

A novel lncRNA AC112721.1 promotes the progression of triple-negative breast cancer by directly binding to THBS1 and regulating miR-491-5p/C2CD2L axis

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Supplementary Table 1. Basic clinical data of 30 patients with triple-negative breast cancer

No	Age(y)	Histology	Tumor size (cm)	Molecular classification	Lymph node metastasis status
1	43	IDC	3.5*3	TNBC	+
2	61	IDC	2*2	TNBC	+
3	59	IDC	1.5*1.5	TNBC	—
4	47	IDC	1.5*1	TNBC	—
5	30	IDC	1*1	TNBC	—
6	68	IDC	4.5*2.5	TNBC	—
7	60	IDC	1*1	TNBC	—
8	40	IDC	3*2	TNBC	+
9	33	IDC	1*1	TNBC	—
10	54	IDC	2*2	TNBC	—
11	30	IDC	2*1.5	TNBC	+
12	48	IDC	2*2	TNBC	—
13	54	IDC	N	TNBC	—
14	48	IDC	1.5*1	TNBC	+
15	33	IDC	3*2	TNBC	—
16	44	IDC	3*3	TNBC	+
17	35	IDC	1*1	TNBC	+
18	45	IDC	3*2.5	TNBC	+
19	51	IDC	2*1.5	TNBC	—
20	38	IDC	3*2.5	TNBC	+
21	39	IDC	4.5*3	TNBC	+
22	60	IDC	1.5*1	TNBC	—
23	35	IDC	2*2	TNBC	+
24	24	IDC	4*3	TNBC	—
25	62	IDC	2*2	TNBC	+
26	29	IDC	3*3	TNBC	+
27	42	IDC	3*2	TNBC	+
28	40	IDC	2*2	TNBC	—
29	65	IDC	1.0*1.0	TNBC	—
30	57	IDC	1.9*1.5	TNBC	+

Abbreviations: IDC, invasive ductal carcinoma. TNBC, triple-negative breast cancer.

Supplementary Table 2. Primers and siRNA sequence

Gene	For primer (5'→ 3')	Rew primer (5'→ 3')
hsa-miR-491-5p	GCAGAGGGGAACCCAACC	AGTGCAGGGTCCGAGGTATT
hsa-miR-24-1-5p	GCGAGCCAACAGAGCAGAA	AGTGCAGGGTCCGAGGTATT
hsa-miR-3926-1-5p	GCGAGGCCAAAAAGCAGG	AGTGCAGGGTCCGAGGTATT
hsa-miR-483-5p	GCGAAGACGGGAGGAAAGA	AGTGCAGGGTCCGAGGTATT
hsa-miR-489-5p	GCGGGACGAAAGAGAGACG	AGTGCAGGGTCCGAGGTATT
hsa-miR-6788-5p	GCGCAGGGAGAAGAGAGG	AGTGCAGGGTCCGAGGTATT
hsa-U6	CTCGCTTCGGCAGCACA	AACGCTTCACGAATTTGCGT
hsa-AC112721.1	CTGCCAGGTGGAAGTGAGG	GAGGTGACGCCAAAATGAAGC
hsa-THBS1	AGACTCCGCATCGCAAAGG	TCACCACGTTGTTGTCAAGGG
hsa-C2CD2L	CGCCCAGAACTCAGCCTAAA	GGGTAGGTCTGGGGATGGAT
hsa-GAPDH	GGTGGTCTCCTCTGACTTCAACA	GTTGCTGTAGCCAAATTCGTTGT

Gene	Sequence
AC112721.1 siRNA	GCGATCTGTTATCACTGCA
THBS1 siRNA	GACGGAAGGTGCTGAGAAA
C2CD2L siRNA	GGCCATCTGTGGATGATAT
miR-491-5p mimic	AGUGGGGAACCCUCCAUGAGG
miR-491-5p inhibitor	CCUCAUGGAAGGGUCCCCACU

Supplementary Table 3. The sequence of AC112721.1

Name	Sequence
The exact sequence cloned into pcDNA-AC112721.1,	GACAGAAACTACACCTTGGAGACTGCACACAATTCCTTCTACTGCTGTTTTGAAAGGT GACCCTGTTTGTAGCACGTTGTTACAGCAGCCCTAGCAAATAACACAGAGAGTGTGTGT GCCCCACTGCTGCCCCAACATGCTGGCCAATGGGACAGGAGCTTGACGGCCTCAGCTCAGTC TTGGAAAATAACGGGAGCCTCCAGTTCCTGAGCGATCTGTTATCACTGCAGATCGGATTT CCAGTTTACACGTTCCCTCAGGGCTTCCTGCCAGGTGGAAGTGAGGGCGCCCTCTTCTGGC GTCTCCAGCATCCTCCCGGCCCCGTCTCGGCCGGCCCCCTTAGCTCCGGTTCTCCGCGGGTC TGCAATGAGATCCTCGAGGTCCACGCCTGCTTCATTTTGGCGTCACCTCCACTTCCTAGG GCAGGGCTTCCCCACACAATAGCCCCTCAGTGCACATTTGTTGAGTAAGTGAAGGAATGA AGGAGTTGAGATGACTTTGAAGCTAAAATGAGTAGACATCTGACTTTGTGCCTAAGAGAA AATTCTTCCTAAGGCTAAGATTGTTAAATAAAGGAACTGGTCCACCCA
The exact sequence used for RNA-pulldown / mass spec	GCTAGCGACAGAAACTACACCTTGGAGACTGCACACAATTCCTTCTAC TGCTGTTTTGAAAGGTGACCCTGTTTGTAGCACGTTGTTACAGCAGCCCTA GCAAATAACACAGAGAGTGTGTGTGCCCCACTGCTGCCCCAACATGCTGGC CAATGGGACAGGAGCTTGACGGCCTCAGCTCAGTCTTGAAAATAACGGG AGCCTCCAGTTCCTGAGCGATCTGTTATCACTGCAGATCGGATTTCCAGTT TACACGTTCCCTCAGGGCTTCCTGCCAGGTGGAAGTGAGGGCGCCCTCTTCT GGCGTCTCCAGCATCCTCCCGGCCCCGTCTCGGCCGGCCCCCTTAGCTCCGGT TCTCCGCGGGTCTGCAATGAGATCCTCGAGGTCCACGCCTGCTTCATTTG GCGTCACCTCCACTTCCTAGGGCAGGGCTTCCCCACACAATAGCCCCTCAG TGCACATTTGTTGAGTAAGTGAAGGAATGAAGGAGTTGAGATGACTTTGA AGCTAAAATGAGTAGACATCTGACTTTGTGCCTAAGAGAAAATTCTTCCT AAGGCTAAGATTGTTAAATAAAGGAACTGGTCCACCCAAAGCTT

Supplementary Table 4. 14 novel lncRNAs related to the survival of patients with triple negative breast cancer

number	ensembl_gene_id	external_gene_name	HR	lower 95%CI	uper 95%CI	p.val	log2 FoldChange	chromosome name
1	ENSG00000254966	AC103974.1	3.152	1.283	7.742	0.012	-1.082325989	11
2	ENSG00000229512	AC068580.1	3.077	1.254	7.548	0.014	1.570521868	11
3	ENSG00000222022	AC112721.1	2.457	1.088	5.545	0.031	3.857537807	2
4	ENSG00000203971	AL354984.1	0.437	0.199	0.96	0.039	3.499946397	20
5	ENSG00000259976	AC093010.3	0.433	0.191	0.983	0.045	-1.122077748	3
6	ENSG00000206249	AL359555.1	0.4	0.177	0.904	0.028	3.254381129	20
7	ENSG00000271888	AL136162.1	0.397	0.16	0.982	0.046	1.823991381	6
8	ENSG00000272853	AC069544.1	0.393	0.181	0.854	0.018	1.404830839	10
9	ENSG00000253348	AC008514.1	0.383	0.165	0.89	0.026	2.858502068	5
10	ENSG00000263884	AP000845.1	0.38	0.155	0.93	0.034	1.406441787	18
11	ENSG00000260645	AL359715.2	0.377	0.167	0.852	0.019	-1.314372795	6
12	ENSG00000235545	AC103923.1	0.37	0.151	0.905	0.029	1.666886824	1
13	ENSG00000263893	AC080037.2	0.362	0.146	0.894	0.028	5.558929685	17
14	ENSG00000275479	AC087741.2	0.224	0.076	0.657	0.006	1.313372332	17

Supplementary Table 5. Proteins specifically bound to LncAC112721.1 were identified using mass spectrometry technology

N	Unused	Total	%Cov	%Cov(50)	%Cov(95)	Accession	Citable Accession	Gene name	Name
73	7.56	7.56	10.31	10.31000018	7.806000113	sp P38646 GRP75_HUMAN	P38646	HSPA9	Stress-70 protein, mitochondrial OS=Homo sapiens OX=9606 GN=HSPA9 PE=1 SV=2
89	6.44	6.44	7.732	5.95600009	4.910999909	sp O75400 PRP40A_HUMAN	O75400	PRPF40A	Pre-mRNA-processing factor 40 homolog A OS=Homo sapiens OX=9606 GN=PRPF40A PE=1 SV=2
104	5.51	5.51	48.11	47.17000127	22.64000028	sp Q969Q0 RL36L_HUMAN	Q969Q0	RPL36AL	60S ribosomal protein L36a-like OS=Homo sapiens OX=9606 GN=RPL36AL PE=1 SV=3
109	5.34	5.34	13.68	13.6800006	13.6800006	sp P01594 KV133_HUMAN	P01594	IGKV1-33	Immunoglobulin kappa variable 1-33 OS=Homo sapiens OX=9606 GN=IGKV1-33 PE=1 SV=2
119	4.67	4.67	6.099	4.941999912	3.680000082	sp Q12872 SFSWA_HUMAN	Q12872	SFSWAP	Splicing factor, suppressor of white-apricot homolog OS=Homo sapiens OX=9606 GN=SFSWAP PE=1 SV=3
134	4.03	4.03	34.11	24.77000058	8.878999949	sp P27635 RL10_HUMAN	P27635	RPL10	60S ribosomal protein L10 OS=Homo sapiens OX=9606 GN=RPL10 PE=1 SV=4
137	4	4	2.995	1.472000033	1.472000033	sp P24928 RPB1_HUMAN	P24928	POLR2A	DNA-directed RNA polymerase II subunit RPB1 OS=Homo sapiens OX=9606 GN=POLR2A PE=1 SV=2
138	4	4	8.523	8.523000032	8.523000032	sp Q9NQ39 RS10L_HUMAN	Q9NQ39	RPS10P5	Putative 40S ribosomal protein S10-like OS=Homo sapiens OX=9606 GN=RPS10P5 PE=5 SV=1
140	3.92	3.92	4.364	3.116999939	3.116999939	sp Q99459 CDC5L_HUMAN	Q99459	CDC5L	Cell division cycle 5-like protein OS=Homo sapiens OX=9606 GN=CDC5L PE=1 SV=2
146	3.7	3.7	5.596	1.703000069	1.703000069	sp Q14683 SMC1A_HUMAN	Q14683	SMC1A	Structural maintenance of chromosomes protein 1A OS=Homo sapiens OX=9606 GN=SMC1A PE=1 SV=2
147	3.62	3.62	9.416	5.838000029	3.954999894	sp Q6P1J9 CDC73_HUMAN	Q6P1J9	CDC73	Parafibromin OS=Homo sapiens OX=9606 GN=CDC73 PE=1 SV=1

149	3.59	3.59	3.743	1.841999963	1.841999963	sp Q8WWI1 LMO7_HUMAN	Q8WWI1	LMO7	LIM domain only protein 7 OS=Homo sapiens OX=9606 GN=LMO7 PE=1 SV=3
150	3.57	3.57	11.57	5.431000143	2.834000066	sp Q8IY81 SPB1_HUMAN	Q8IY81	FTSJ3	pre-rRNA 2'-O-ribose RNA methyltransferase FTSJ3 OS=Homo sapiens OX=9606 GN=FTSJ3 PE=1 SV=2
153	3.49	3.49	35.57	30.86999953	22.14999944	sp P0DP25 CALM3_HUMAN	P0DP25	CALM3	Calmodulin-3 OS=Homo sapiens OX=9606 GN=CALM3 PE=1 SV=1
156	3.44	3.44	2.087	2.087000012	2.087000012	sp Q9H2P0 ADNP_HUMAN	Q9H2P0	ADNP	Activity-dependent neuroprotector homeobox protein OS=Homo sapiens OX=9606 GN=ADNP PE=1 SV=1
168	3.03	3.03	5.897	5.897000059	5.897000059	sp Q14240 EIF4A2_HUMAN	Q14240	EIF4A2	Eukaryotic initiation factor 4A-II OS=Homo sapiens OX=9606 GN=EIF4A2 PE=1 SV=2
170	2.99	3	13.85	13.8500005	8.845999837	sp O95478 NSA2_HUMAN	O95478	NSA2	Ribosome biogenesis protein NSA2 homolog OS=Homo sapiens OX=9606 GN=NSA2 PE=1 SV=1
172	2.98	2.98	24.76	19.05000061	19.05000061	sp Q9Y3U8 RL36_HUMAN	Q9Y3U8	RPL36	60S ribosomal protein L36 OS=Homo sapiens OX=9606 GN=RPL36 PE=1 SV=3
174	2.96	2.96	24.44	17.03999937	17.03999937	sp P62910 RL32_HUMAN	P62910	RPL32	60S ribosomal protein L32 OS=Homo sapiens OX=9606 GN=RPL32 PE=1 SV=2
175	2.94	2.94	15.5	15.50000012	15.50000012	sp Q9BTM1 H2AJ_HUMAN	Q9BTM1	H2AJ	Histone H2A.J OS=Homo sapiens OX=9606 GN=H2AJ PE=1 SV=1
179	2.85	2.85	2.386	1.412000041	1.021999959	sp Q92614 MYO18A_HUMAN	Q92614	MYO18A	Unconventional myosin-XVIIIa OS=Homo sapiens OX=9606 GN=MYO18A PE=1 SV=3
181	2.81	2.81	44.29	34.2900008	31.43000007	sp P63173 RL38_HUMAN	P63173	RPL38	60S ribosomal protein L38 OS=Homo sapiens OX=9606 GN=RPL38 PE=1 SV=2
182	2.78	2.78	3.944	3.943999857	2.676000074	sp P19338 NUCL_HUMAN	P19338	NCL	Nucleolin OS=Homo sapiens OX=9606 GN=NCL PE=1 SV=3
185	2.67	2.67	5.594	5.593999848	5.245000124	sp P52907 CAZA1_HUMAN	P52907	CAPZA1	F-actin-capping protein subunit alpha-1 OS=Homo sapiens OX=9606 GN=CAPZA1 PE=1 SV=3

190	2.51	2.51	2.5	0.714300014	0.312500005	sp Q9BTC0 DIDO1_HUMAN	Q9BTC0	DIDO1	Death-inducer obliterator 1 OS=Homo sapiens OX=9606 GN=DIDO1 PE=1 SV=5
192	2.47	2.47	13.68	13.6800006	13.6800006	sp A0A0C4DH69 KV109_HUMAN	A0A0C4DH69	IGKV1-9	Immunoglobulin kappa variable 1-9 OS=Homo sapiens OX=9606 GN=IGKV1-9 PE=3 SV=1
194	2.42	2.42	5.069	5.068999901	2.765000053	sp Q7L4I2 RSRC2_HUMAN	Q7L4I2	RSRC2	Arginine/serine-rich coiled-coil protein 2 OS=Homo sapiens OX=9606 GN=RSRC2 PE=1 SV=1
200	2.39	2.39	7.277	3.262000158	1.25500001	sp Q9Y4W6 AFG32_HUMAN	Q9Y4W6	AFG3L2	AFG3-like protein 2 OS=Homo sapiens OX=9606 GN=AFG3L2 PE=1 SV=2
203	2.34	2.34	8.201	3.438999876	1.720000058	sp Q5QJE6 TDIF2_HUMAN	Q5QJE6	DNTTIP2	Deoxynucleotidyltransferase terminal-interacting protein 2 OS=Homo sapiens OX=9606 GN=DNTTIP2 PE=1 SV=2
204	2.32	2.32	2.852	2.851999924	0.950600021	sp O60264 SMCA5_HUMAN	O60264	SMARCA5	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5 OS=Homo sapiens OX=9606 GN=SMARCA5 PE=1 SV=1
205	2.31	2.31	20	15.62999934	11.2499997	sp P46778 RL21_HUMAN	P46778	RPL21	60S ribosomal protein L21 OS=Homo sapiens OX=9606 GN=RPL21 PE=1 SV=2
206	2.29	2.29	5.069	5.068999901	2.995000035	sp P06733 ENOA_HUMAN	P06733	ENO1	Alpha-enolase OS=Homo sapiens OX=9606 GN=ENO1 PE=1 SV=2
207	2.27	2.27	30.34	14.04000074	7.864999771	sp Q9Y3C1 NOP16_HUMAN	Q9Y3C1	NOP16	Nucleolar protein 16 OS=Homo sapiens OX=9606 GN=NOP16 PE=1 SV=2
208	2.23	2.23	33.91	33.91000032	7.825999707	sp P62854 RS26_HUMAN	P62854	RPS26	40S ribosomal protein S26 OS=Homo sapiens OX=9606 GN=RPS26 PE=1 SV=3
209	2.2	2.2	7.388	4.123999923	2.404999919	sp Q9NVN8 GNL3L_HUMAN	Q9NVN8	GNL3L	Guanine nucleotide-binding protein-like 3-like protein OS=Homo sapiens OX=9606 GN=GNL3L PE=1 SV=1
211	2.12	2.12	5.778	1.926000044	1.926000044	sp O60506 HNRPQ_HUMAN	O60506	SYNCRIP	Heterogeneous nuclear ribonucleoprotein Q OS=Homo sapiens OX=9606 GN=SYNCRIP PE=1 SV=2

212	2.12	2.12	6.484	3.313999996	1.872999966	sp Q86XJ1 GA2L3_HUMAN	Q86XJ1	GAS2L3	GAS2-like protein 3 OS=Homo sapiens OX=9606 GN=GAS2L3 PE=1 SV=1
214	2.08	2.08	1.765	0.882599968	0.617800001	sp Q8WYP5 ELYS_HUMAN	Q8WYP5	AHCTF1	Protein ELYS OS=Homo sapiens OX=9606 GN=AHCTF1 PE=1 SV=3
216	2.06	2.06	8.568	6.266000122	3.835999966	sp P06396 GELS_HUMAN	P06396	GSN	Gelsolin OS=Homo sapiens OX=9606 GN=GSN PE=1 SV=1
217	2.05	2.05	1.82	1.195000019	0.796400011	sp Q7Z3J3 RGPD4_HUMAN	Q7Z3J3	RGPD4	RanBP2-like and GRIP domain-containing protein 4 OS=Homo sapiens OX=9606 GN=RGPD4 PE=2 SV=3
219	2.04	2.04	20.62	12.06	3.502000123	sp P82914 RT15_HUMAN	P82914	MRPS15	28S ribosomal protein S15, mitochondrial OS=Homo sapiens OX=9606 GN=MRPS15 PE=1 SV=1
220	2.04	2.04	3.493	1.81099996	1.81099996	sp Q96TA2 YME1L1_HUMAN	Q96TA2	YME1L1	ATP-dependent zinc metalloprotease YME1L1 OS=Homo sapiens OX=9606 GN=YME1L1 PE=1 SV=2
224	2.02	2.02	2.542	0.95309997	0.95309997	sp P28290 ITPI2_HUMAN	P28290	ITPRID2	Protein ITPRID2 OS=Homo sapiens OX=9606 GN=ITPRID2 PE=1 SV=3
226	2.02	2.02	10.41	7.69200027	7.69200027	sp Q01130 SRSF2_HUMAN	Q01130	SRSF2	Serine/arginine-rich splicing factor 2 OS=Homo sapiens OX=9606 GN=SRSF2 PE=1 SV=4
227	2.01	2.01	5.018	1.792000048	1.792000048	sp Q9UBB9 TFP11_HUMAN	Q9UBB9	TFIP11	Tuftelin-interacting protein 11 OS=Homo sapiens OX=9606 GN=TFIP11 PE=1 SV=1
228	2.01	2.01	2.654	0.789100025	0.789100025	sp P42704 LRPPRC_HUMAN	P42704	LRPPRC	Leucine-rich PPR motif-containing protein, mitochondrial OS=Homo sapiens OX=9606 GN=LRPPRC PE=1 SV=3
235	2	2.66	6.406	6.406000257	4.270000011	sp P29692 EEF1D_HUMAN	P29692	EEF1D	Elongation factor 1-delta OS=Homo sapiens OX=9606 GN=EEF1D PE=1 SV=5
239	2	2	4.019	1.339999959	1.339999959	sp Q9Y4F1 FARP1_HUMAN	Q9Y4F1	FARP1	FERM, ARHGEF and pleckstrin domain-containing protein 1 OS=Homo sapiens OX=9606 GN=FARP1 PE=1 SV=1
242	2	2	4.04	2.222000062	2.222000062	sp Q9UHK0 NUFIP1_HUMA	Q9UHK0	NUFIP1	Nuclear fragile X mental retardation-interacting protein 1

						N			OS=Homo sapiens OX=9606 GN=NUFIP1 PE=1 SV=2
244	2	2	5.322	2.598999999	2.598999999	sp Q4KMP7 TB10B_HUMAN	Q4KMP7	TBC1D10B	TBC1 domain family member 10B OS=Homo sapiens OX=9606 GN=TBC1D10B PE=1 SV=3
253	2	2	0.9558	0.438100006	0.438100006	sp P49327 FAS_HUMAN	P49327	FASN	Fatty acid synthase OS=Homo sapiens OX=9606 GN=FASN PE=1 SV=3
255	2	2	5.672	4.478000104	4.478000104	sp P04406 G3P_HUMAN	P04406	GAPDH	Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens OX=9606 GN=GAPDH PE=1 SV=3
256	2	2	4.87	4.870000109	4.870000109	sp Q9UHR5 S30BP_HUMAN	Q9UHR5	SAP30BP	SAP30-binding protein OS=Homo sapiens OX=9606 GN=SAP30BP PE=1 SV=1
257	2	2	4.149	4.148999974	4.148999974	sp Q9P031 TAP26_HUMAN	Q9P031	CCDC59	Thyroid transcription factor 1-associated protein 26 OS=Homo sapiens OX=9606 GN=CCDC59 PE=1 SV=2
258	2	2	2.113	2.112999931	2.112999931	sp Q9BRS2 RIOK1_HUMAN	Q9BRS2	RIOK1	Serine/threonine-protein kinase RIO1 OS=Homo sapiens OX=9606 GN=RIOK1 PE=1 SV=2
265	2	2	5.882	5.882000178	5.882000178	sp P61353 RL27_HUMAN	P61353	RPL27	60S ribosomal protein L27 OS=Homo sapiens OX=9606 GN=RPL27 PE=1 SV=2
271	2	2	0.9402	0.940200035	0.940200035	sp P07996 TSP1_HUMAN	P07996	THBS1	Thrombospondin-1 OS=Homo sapiens OX=9606 GN=THBS1 PE=1 SV=2
273	2	2	1.977	1.977000013	1.977000013	sp P04843 RPN1_HUMAN	P04843	RPN1	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1 OS=Homo sapiens OX=9606 GN=RPN1 PE=1 SV=1
274	1.96	2	0.9455	0.945500005	0.945500005	sp Q8IY17 PLPL6_HUMAN	Q8IY17	PNPLA6	Patatin-like phospholipase domain-containing protein 6 OS=Homo sapiens OX=9606 GN=PNPLA6 PE=1 SV=3
276	1.92	1.92	12.73	12.72999942	12.72999942	sp P81605 DCD_HUMAN	P81605	DCD	Dermcidin OS=Homo sapiens OX=9606 GN=DCD PE=1 SV=2
279	1.89	1.89	3.863	3.863000125	3.863000125	sp Q13283 G3BP1_HUMAN	Q13283	G3BP1	Ras GTPase-activating protein-binding protein 1 OS=Homo sapiens OX=9606 GN=G3BP1 PE=1 SV=1

281	1.79	1.85	23.86	6.863000244	6.863000244	sp P07910 HNRPC_HUMAN	P07910	HNRNPC	Heterogeneous nuclear ribonucleoproteins C1/C2 OS=Homo sapiens OX=9606 GN=HNRNPC PE=1 SV=4
286	1.72	1.72	4.202	2.101000026	2.101000026	sp P61619 S61A1_HUMAN	P61619	SEC61A1	Protein transport protein Sec61 subunit alpha isoform 1 OS=Homo sapiens OX=9606 GN=SEC61A1 PE=1 SV=2
287	1.7	1.7	4.967	2.197000012	2.197000012	sp Q9Y5B9 SP16H_HUMAN	Q9Y5B9	SUPT16H	FACT complex subunit SPT16 OS=Homo sapiens OX=9606 GN=SUPT16H PE=1 SV=1
289	1.68	1.68	3.867	3.866999969	3.866999969	sp Q9P035 HACD3_HUMAN	Q9P035	HACD3	Very-long-chain (3R)-3-hydroxyacyl-CoA dehydratase 3 OS=Homo sapiens OX=9606 GN=HACD3 PE=1 SV=2
291	1.65	1.65	6.87	4.070999846	4.070999846	sp Q99536 VAT1_HUMAN	Q99536	VAT1	Synaptic vesicle membrane protein VAT-1 homolog OS=Homo sapiens OX=9606 GN=VAT1 PE=1 SV=2
292	1.62	1.62	3.803	1.123999991	1.123999991	sp Q8IY37 DHX37_HUMAN	Q8IY37	DHX37	Probable ATP-dependent RNA helicase DHX37 OS=Homo sapiens OX=9606 GN=DHX37 PE=1 SV=1
293	1.59	1.59	2.841	1.025999989	1.025999989	sp Q92610 ZNF592_HUMAN	Q92610	ZNF592	Zinc finger protein 592 OS=Homo sapiens OX=9606 GN=ZNF592 PE=1 SV=2
295	1.54	1.54	6.478	3.156000003	3.156000003	sp Q07065 CKAP4_HUMAN	Q07065	CKAP4	Cytoskeleton-associated protein 4 OS=Homo sapiens OX=9606 GN=CKAP4 PE=1 SV=2
296	1.53	1.53	2.947	1.472999994	1.472999994	sp P07947 YES_HUMAN	P07947	YES1	Tyrosine-protein kinase Yes OS=Homo sapiens OX=9606 GN=YES1 PE=1 SV=3
297	1.5	1.5	7.062	2.763999999	1.023999974	sp Q96T37 RBM15_HUMAN	Q96T37	RBM15	RNA-binding protein 15 OS=Homo sapiens OX=9606 GN=RBM15 PE=1 SV=2
299	1.48	1.48	6.726	6.725999713	6.725999713	sp Q5T3I0 GPTC4_HUMAN	Q5T3I0	GPATCH4	G patch domain-containing protein 4 OS=Homo sapiens OX=9606 GN=GPATCH4 PE=1 SV=2
300	1.47	1.48	4.405	4.405000061	4.405000061	sp P00403 COX2_HUMAN	P00403	MT-CO2	Cytochrome c oxidase subunit 2 OS=Homo sapiens OX=9606 GN=MT-CO2 PE=1 SV=1
303	1.42	1.42	3.684	3.297999874	3.297999874	sp Q86YZ3 HORN_HUMAN	Q86YZ3	HRNR	Hornerin OS=Homo sapiens OX=9606 GN=HRNR PE=1 SV=2

304	1.39	1.39	1.525	1.525000017	1.525000017	sp Q02413 DSG1_HUMAN	Q02413	DSG1	Desmoglein-1 OS=Homo sapiens OX=9606 GN=DSG1 PE=1 SV=2
306	1.35	1.35	5.228	1.854999922	1.854999922	sp Q8WXI9 P66B_HUMAN	Q8WXI9	GATAD2B	Transcriptional repressor p66-beta OS=Homo sapiens OX=9606 GN=GATAD2B PE=1 SV=1
308	1.3	1.3	2.412	2.411999926	2.411999926	sp P50991 TCPD_HUMAN	P50991	CCT4	T-complex protein 1 subunit delta OS=Homo sapiens OX=9606 GN=CCT4 PE=1 SV=4

Supplementary Table 6. Correlation analysis between LncRNAs and miRNAs.

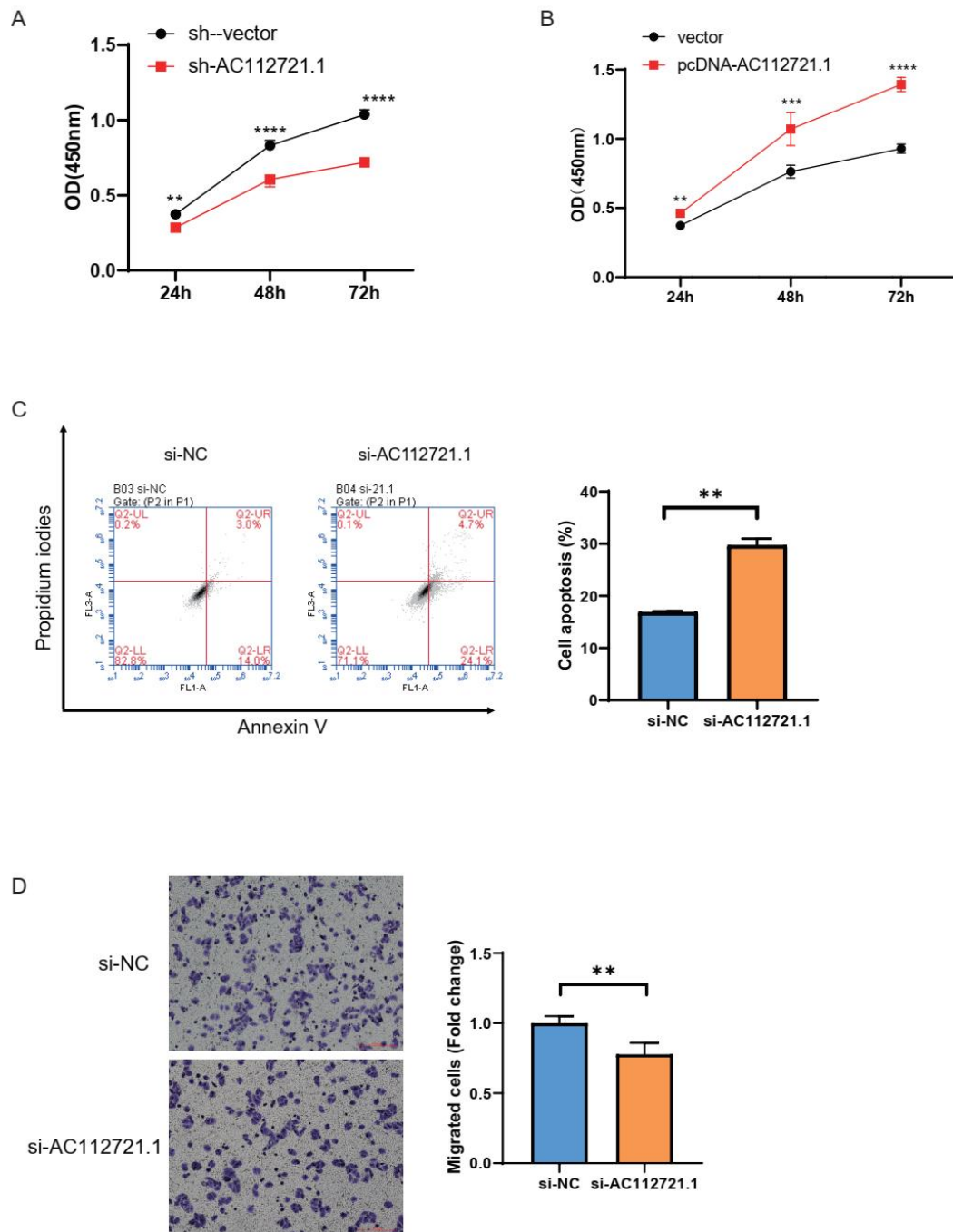
Symbol	Correlation
AC112721.1	1
Has-miR-24-1-5p	-0.159931035
Has-miR-3926-1	-0.230807672
Has-miR-483-5p	-0.341861952
Has-miR-489-5p	-0.27903169
has-miR-491-5p	-0.305601253
Has-miR-6788-5p	-0.353105424

Supplementary Table 7. Target genes of miR-491-5p

Genes	TargetScan	PolymiRTs	RNA22	MiRBase	Sum
SYNGAP1	1	1	1	1	4
GATAD2B	1	1	1	1	4
FOXP4	1	1	0	1	3
ELOVL1	1	0	1	1	3
DERL3	1	1	0	1	3
NOVA2	1	0	1	1	3
TAF10	1	0	1	1	3
ZNF703	1	1	0	1	3
DNAJB5	1	1	0	1	3
PEA15	1	1	0	1	3
CREB3L2	1	1	0	1	3
B4GALT5	1	1	0	1	3
SYT2	1	1	0	1	3
CYP26B1	1	1	0	1	3
CNN2	1	1	1	0	3
BCL6B	1	0	1	1	3
ZBTB4	1	0	1	1	3
GIPC1	1	0	1	1	3
ZBTB8A	1	1	0	1	3
CLIP2	1	0	1	1	3
C2CD2L	1	0	1	1	3
CELF3	1	0	1	1	3
IQGAP3	1	0	1	1	3
RASL10B	1	0	1	1	3
PADI2	1	1	0	1	3
PDGFRA	1	1	0	1	3
LRRC4B	1	0	1	1	3

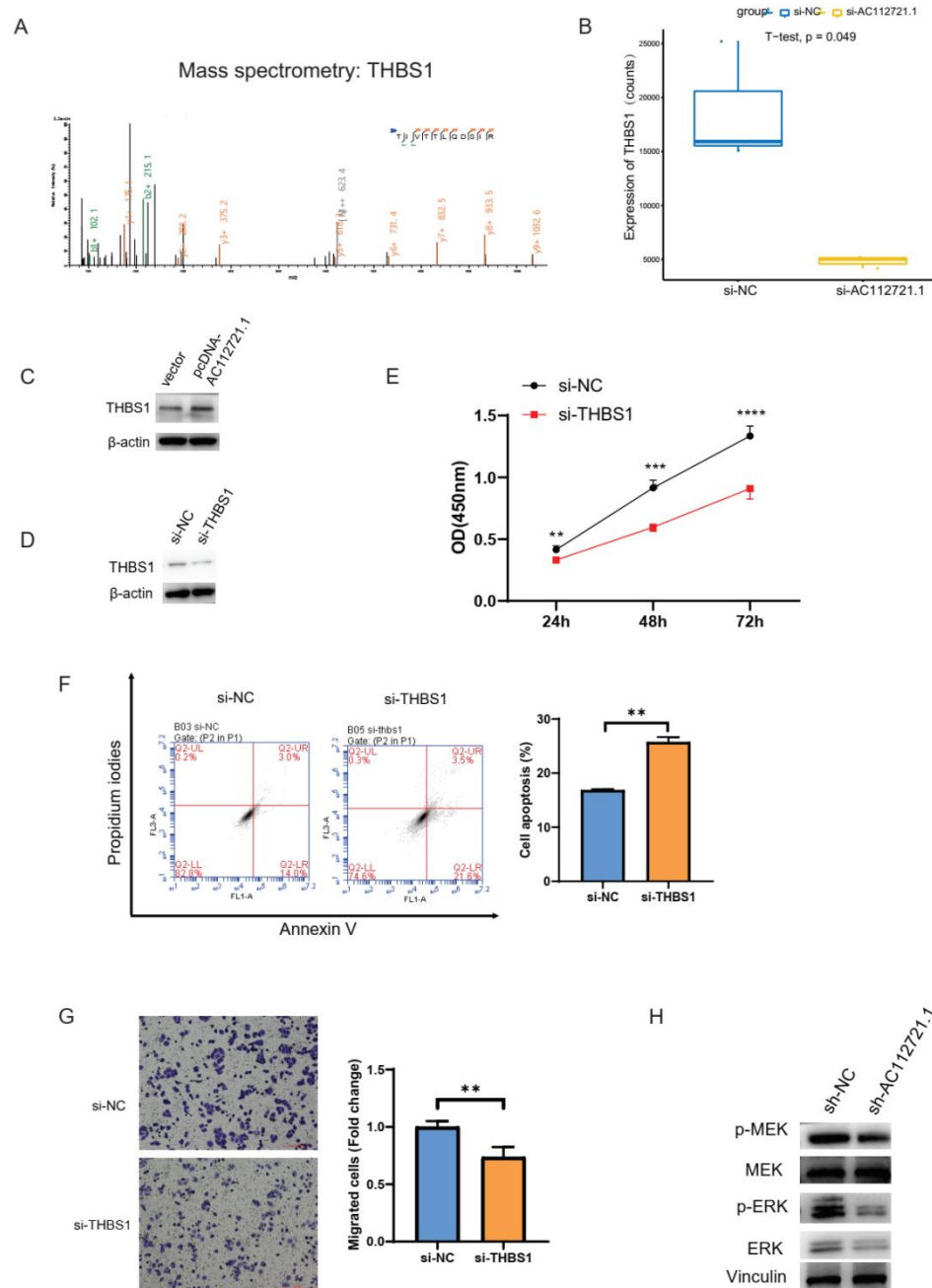
CDYL2	1	1	0	1	3
SRGAP3	1	1	0	1	3
CHD3	1	0	1	1	3
CSMD2	1	0	1	1	3
SFTPB	0	1	1	1	3
CRX	0	1	1	1	3
PKD1L2	0	1	1	1	3
SRC	0	1	1	1	3
HSPG2	0	1	1	1	3
SH3PXD2A	0	1	1	1	3
LRRTM2	0	1	1	1	3
KIF21B	0	1	1	1	3
TBC1D22B	0	1	1	1	3
SLC6A20	0	1	1	1	3
C6orf106	0	1	1	1	3
ELFN2	0	1	1	1	3
C11orf45	0	1	1	1	3
PTK7	0	1	1	1	3

Supplementary Figure 1



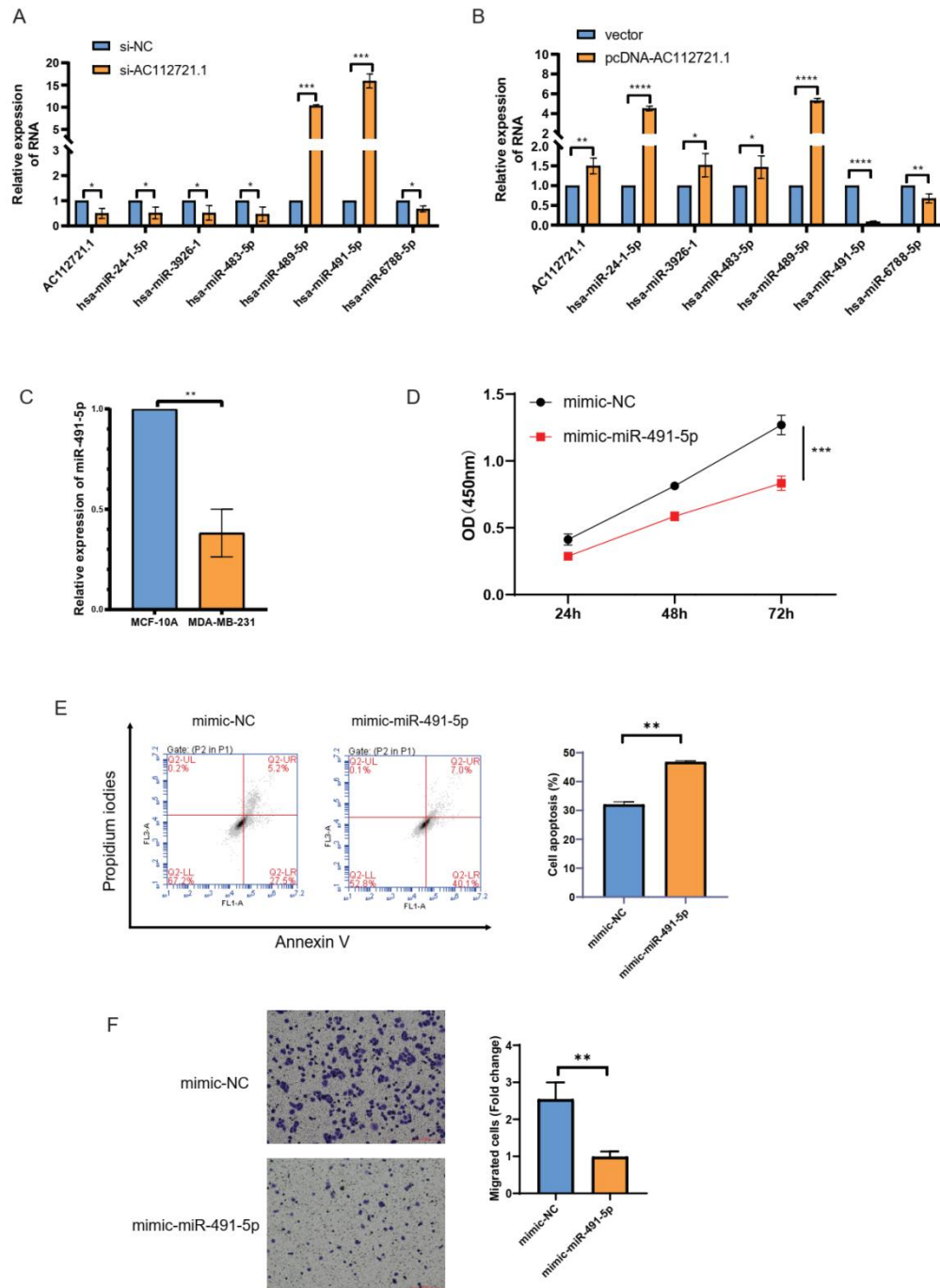
Supplementary Figure 1. A. CCK-8 assays showing the growth of MDA-MB-468 cells treated with sh-AC112721.1. B. CCK-8 assays assessed proliferation of MDA-MB-468 cells transfected with pcDNA-AC112721.1. C. Knockdown of AC112721.1 promoted MDA-MB-468 cell apoptosis. D. Knockdown of AC112721.1 inhibited MDA-MB-468 cell migration. All experiments were performed at least thrice with triplicate samples. ** $p < 0.01$, *** $p < 0.001$, **** $p < 0.0001$.

Supplementary Figure 2



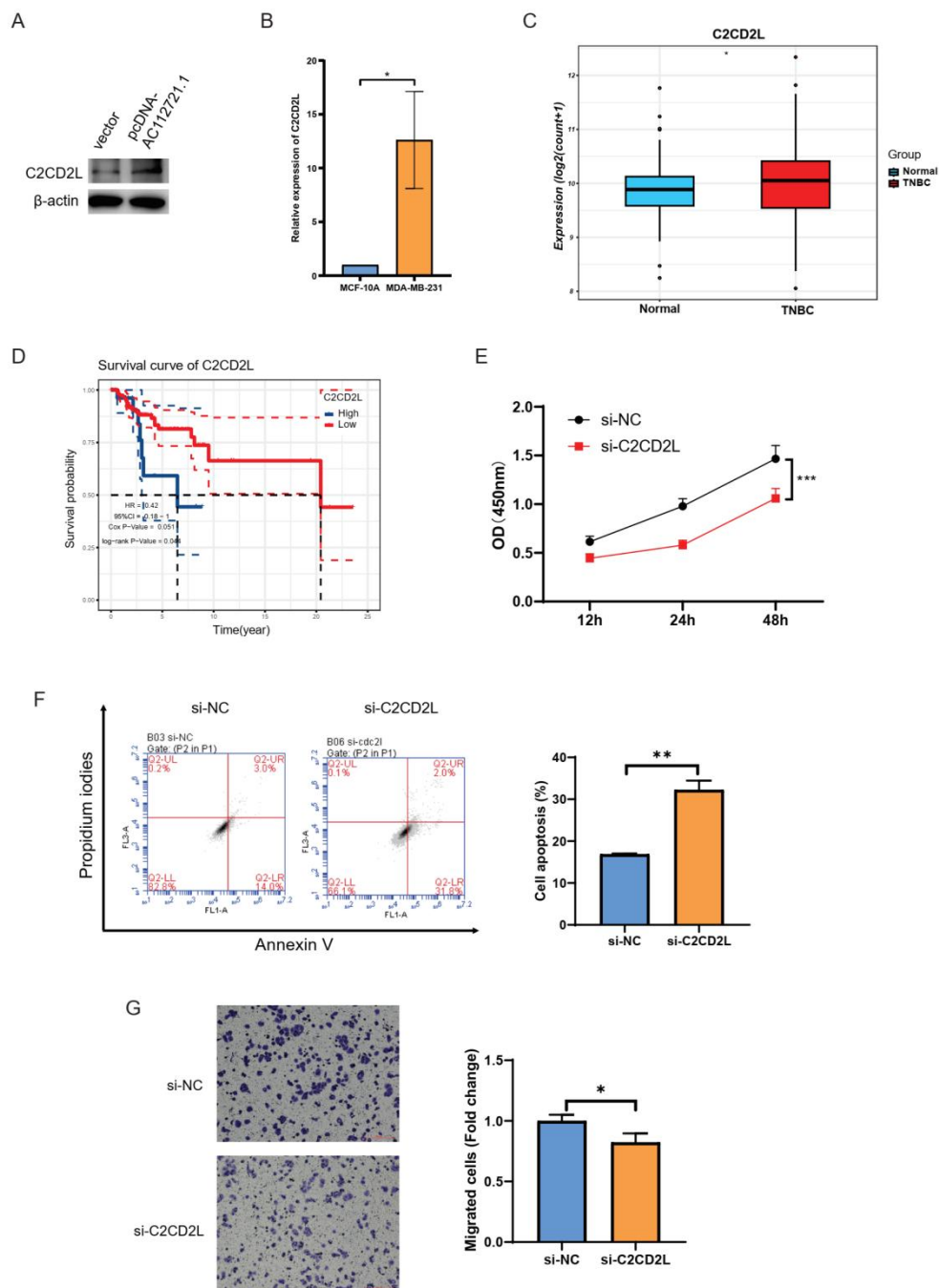
Supplementary Figure 2. A. Mass spectrometry analysis of THBS1. B. The relative expression of AC112721.1 based on RNA-sequencing. C. The relative expression level of THBS1 after AC112721.1 overexpression. D. The knockdown efficiency of THBS1 was assessed using western blot. E. Cell proliferation of MDA-MB-468 cells was detected by CCK-8 assay with the indicated treatment. F. FACS was performed to determine the apoptosis rate of MDA-MB-468 cells after knockdown of THBS1. G. Cell migration ability of MDA-MB-468 cells was determined after transfection with si-THBS1. H. The impact of knocking down AC112721.1 on the Ras pathway was measured using Western blot. All experiments were performed at least thrice with triplicate samples. ** $p < 0.01$, *** $p < 0.001$, **** $p < 0.0001$.

Supplementary Figure 3



Supplementary Figure 3. qRT-PCR analysis of miRNAs expression in MDA-MB-231 cells transfected with si-AC112721.1 (A) or pcDNA- AC112721.1 (B). C. The relative expression level of miR-491-5p in different cell lines. D. Overexpression of miR-491-5p inhibited MDA-MB-468 cell proliferation. D. Overexpression of miR-491-5p promoted MDA-MB-468 cell apoptosis. E. Overexpression of miR-491-5p inhibited MDA-MB-468 cell migration. All experiments were performed at least thrice with triplicate samples. * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$, **** $p < 0.0001$.

Supplementary Figure 4



Supplementary Figure 4. A. The relative expression level of C2CD2L after AC112721.1 overexpression. B. The relative expression level of C2CD2L in different cell lines. C. The expression levels of C2CD2L in TNBC tissues and normal tissues in the TCGA database. D. Kaplan-Meier survival analysis of TNBC patients stratified by C2CD2L expression level. E. Cell proliferation of MDA-MB-468 cells was detected by CCK-8 assay with the indicated treatment. F. FACS was performed to determine the apoptosis rate of MDA-MB-468 cells after knockdown of C2CD2L. G. Cell migration ability of MDA-MB-468 cells was determined after transfection with si-C2CD2L. ** $p < 0.01$, *** $p < 0.001$.

Western blot Raw data

