

Table S1. Primers or sequences used in the study.

<i>siRNAs</i>	
si-SP1	GUGCAAACCAACAGAUUAUTT AUAACUCUGUUGGUUUGCACTT
si-YY1	CAUGCUAAGGCCAAAAACATT UGUUUUUGGCCUUAGCAUGTT
<i>Q-RT-PCR primers</i>	
lncRNA-AFAP1-AS1	FW: 5'-AATGGTGGTAGGAGGGAGGA-3' RV: 5'-CACACAGGGGAATGAAGAGG-3'
GAPDH	FW: 5'-ATGACATCAAGAAGGTGGTGAAGCAGG-3' RV: 5'-GCGTCAAAGGTGGAGGAGTGGGT-3'
YY1	FW: 5'-TGGCAGAATTTGCTAGAATGAAGC-3' RV: 5'-TGGCCGAGTTATCCCTGAAC-3'
SP1	FW: 5'-TTGCTGCTATGCCAAACCTA-3' RV: 5'-CCTGAGAGCTGGGAGTCAAG-3'
EIF4B	FW: 5'-CTTCCCAAATCGCCACCC-3' RV: 5'-CGAGCCCTCCAGTCTGTATCT-3'
MAPKAP1	FW: 5'-AACAGTTCAAGGGCAGACGG-3' RV: 5'-CAGCAAGGTCACAGGCACA-3'
SGK1	FW: 5'-ACCATCTCCAGAGGGAACGC-3' RV: 5'-GCAGGCCATACAGCATCTCATA-3'
SEH1L	FW: 5'-TCAGCAGGGAACCTCAAATC-3' RV: 5'-GGCATAACTGGACCATCTCG-3'
SKP2	FW: 5'-GCTCAACTACCTCCAACACCT-3' RV: 5'-TCTGGCACGATTCCAAAA-3'
NEDD4L	FW: 5'-CGACCCTATACATTAAAGGACTTTC-3' RV: 5'-TGGTGCTGAGAAGCCGAGT-3'
<i>CHIP primers</i>	
P1 primer for ChIP	5'-GAGACAGCGTCCATTCACTCCC-3' 5'-ACAAAGATTTCTCCTAACCTTCC-3'
P2 primer for ChIP	5'-GACCCACGTGACACGCC-3' 5'-CCCACGACACCCGTAAGA-3'
P3 primer for ChIP	5'-GTACGTGCCCAATACTTGACG-3' 5'-GGCTTTGTTCCAGGTGCTT-3'
P4 primer for ChIP	5'-AGCCAGTGCTAGACAGCAACAA-3' 5'-AGCCAAACCATATCACCTCCTT-3'
P5 primer for ChIP	5'-GCACCTGTGCAGGAAGAG-3' 5'-TGAGATTTGGATGGGGATAC-3'
P6 primer for ChIP	5'-CATCCAAATCTCAGCTTGAATT-3' 5'-CCTTGATAAACCTCCAGGTA-3'
<i>FISH probes</i>	
AFAP1-AS1	AAGGGGCTCAAAGATACACCAAAGT

ATGTTGGATGTCTAATCAGGGAGCC
 CACCCTCTTCCCTTCCCTGTAGTAG
 CAGAGAAGCATTAAGACATGAGACACT
 TGAGAAAAGAATCACCAAGAGAGTAAG

Table S2. The potential binding sites of Sp1 towards lncRNA AFAP1-AS1 promoter regions (hg38_knownGene_ENST00000608442.2, range = chr4:7752077-7779028) by JASPAR with relative profile score threshold of 80 %.

<i>Matrix ID</i>	<i>Name</i>	<i>Score</i>	<i>Relative score</i>	<i>Start</i>	<i>End</i>	<i>Strand</i>	<i>Predicted sequence</i>
MA0079.1	MA0079.1.SP1	9.304687	0.911425279	1175	1184	+	CGGGCGTGGT
MA0079.3	MA0079.3.SP1	9.048192	0.894977296	790	800	+	TTCTCTCCCCA
MA0079.1	MA0079.1.SP1	8.938865	0.89866482	1792	1801	+	GAGGCAGGGA
MA0079.5	MA0079.5.SP1	8.318838	0.863441621	1878	1886	+	TGGGAGGGA
MA0079.1	MA0079.1.SP1	8.311052	0.876765707	1037	1046	+	TGGGCCGGGT
MA0079.3	MA0079.3.SP1	8.113572	0.883218707	766	776	+	GCCCATCCCCC
MA0079.5	MA0079.5.SP1	8.020701	0.858261002	1245	1253	+	GAGGCGGAG
MA0079.1	MA0079.1.SP1	7.197659	0.837928744	1877	1886	+	GTGGGAGGGA
MA0079.1	MA0079.1.SP1	6.957125	0.829538534	1911	1920	+	GGGGGCTGGT
MA0079.1	MA0079.1.SP1	6.7868495	0.823599042	273	282	+	TGGGGATGGA
MA0079.5	MA0079.5.SP1	6.593582	0.833462442	1798	1806	+	GGGAAGGAG
MA0079.3	MA0079.3.SP1	6.4261227	0.861988661	1509	1519	+	CGCCTGCCCCC
MA0079.1	MA0079.1.SP1	6.1590366	0.801699912	160	169	+	TGGGGAAGGT
MA0079.5	MA0079.5.SP1	5.623053	0.816597892	274	282	+	GGGGATGGA
MA0079.4	MA0079.4.SP1	5.5256863	0.845683731	758	772	+	CGTGACACGCCCATC
MA0079.5	MA0079.5.SP1	5.255307	0.810207699	1037	1045	+	TGGGCCGGG
MA0079.3	MA0079.3.SP1	5.1665006	0.846141173	100	110	+	TTCACTCCCCC
MA0079.3	MA0079.3.SP1	2.6205626	0.814110358	765	775	+	CGCCCATCCCC
MA0079.3	MA0079.3.SP1	2.4257746	0.811659703	1918	1928	+	GGTCTTCCCCG
MA0079.3	MA0079.3.SP1	2.1372697	0.808029981	770	780	+	ATCCCCCCCCAT
MA0079.4	MA0079.4.SP1	0.9273069	0.804953733	1690	1704	+	CAGAACACGCACCTG
MA0079.4	MA0079.4.SP1	0.9273069	0.804953733	1722	1736	+	CAGAACACGCACCTG
MA0079.4	MA0079.4.SP1	0.7430556	0.803321733	763	777	+	CACGCCCATCCCCC

Table S3. The intersection of down-regulated genes in MDA-MB-231 and MDA-MB-468 cells after knockdown of lncRNA AFAP1-AS1, and the relative KEGG pathways of these 17 down-regulated genes which appeared more than twice.

<i>Overlapped down-regulated genes</i>	<i>Relative KEGG pathways</i>
<i>ARSD</i>	hsa00500: Starch and sucrose metabolism
<i>UBE2I</i>	hsa04120: Ubiquitin mediated proteolysis
<i>KLF6</i>	hsa04960: Aldosterone-regulated sodium reabsorption
<i>COMT</i>	hsa04121: Ubiquitin system BR
<i>DUSP1</i>	hsa03019: Messenger RNA biogenesis BR
<i>NANOS1</i>	hsa04150: mTOR signaling pathway
<i>GYG2</i>	hsa04151: PI3K-Akt signaling pathway
<i>C6orf120</i>	hsa04990: Domain-containing proteins not elsewhere classified BR
<i>NEDD4L</i>	hsa03000: Transcription factors BR
<i>ENPP1</i>	
<i>SGK1</i>	
<i>FAM172A</i>	
<i>MATN2</i>	
<i>EIF4B</i>	
<i>LMO4</i>	
<i>FOSB</i>	
<i>CPA4</i>	

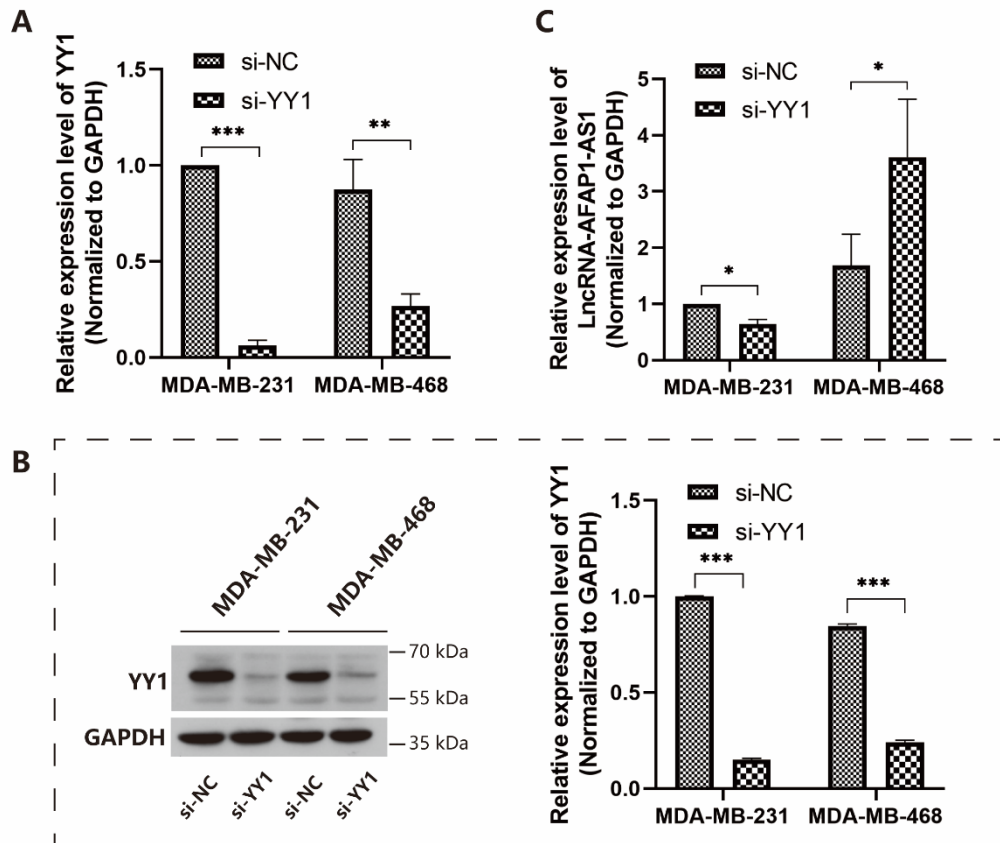


Figure S1 The regulation of YY1 towards the expression of lncRNA AFAP1-AS1. (A) Q-RT-PCR and (B) western blot assays confirmed the silencing efficiency of YY1 by siRNA; (C) lncRNA AFAP1-AS1 expression was decreased in MDA-MB-231 cell after YY1 silencing and increased in MDA-MB-468 cell. Unpaired student's t-tests were used for the statistical analyses. * $p < 0.05$; ** $p < 0.01$; *** $p < 0.005$; ns, no significant.