

1 Supplementary information

3 **METTL18 functions as a Phenotypic Regulator in Src-Dependent** 4 **Oncogenic Responses of HER2-Negative Breast Cancer**

5
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23 24 **Supplementary Figure legends**

25 **Figure S1.** Clinical profile of METTL18 in breast tumor dataset. (A) The gene expression
26 profiles of 23 methyltransferases, including METTL18, PKMTs, and PRMTs, in HER2-
27 negative and HER2-positive breast cancer. We used the publicly available gene expression
28 profiling interactive analysis 2 (GEPIA2) dataset (n=442). (B) Gene expression comparison of
29 METTL13 and METTL18 in HER2-negative and HER2-positive breast cancer. TCGA data
30 were used (n=1080). (C) Kaplan-Meier curve showing the survival probability of HER2-
31 positive breast cancer patients with high or low expression of METTL18 (best cutoff). (D)
32 DMFS of HER2-positive breast cancer patients with low or high expression of METTL18 (best
33 cutoff).

34
35 **Figure S2.** (A) Immunoblotting of METTL18 protein in shScramble-, shMETTL18-, Myc, and
36 METTL18 WT-transfected MDA-MB-231 cells. (B) Migration capacity of METTL18-
37 knockdown MCF-7 cells.

38
39 **Figure S3.** Body weight of xenograft mice intravenously injected with shScramble- or
40 shMETTL18-expressing MDA-MB-231 cells.

41
42 **Figure S4.** Signaling pathway activated by METTL18. (A) Immunoblotting for phospho- and
43 total proteins, p65, p50, c-Jun, c-Fos, Syk, JAK2, and ATF25, in Myc-METTL18-
44 overexpressing MDA-MB-231 cells. The transfection efficacy of the Myc-METTL18 construct
45 was verified by immunoblotting with anti-Myc. β -actin was used as the loading control. (B)
46 Immunoblotting of METTL18, p-Src (Y419), and Src expression in three types of breast cancer
47 cells (SK-BR3, MDA-MB-453, and MDA-MB-231). β -actin was used as the loading control.
48 ns: not significant; * $P < 0.05$; ** $P < 0.01$.

49

50 **Figure S5.** Levels of METTL18 and p-Src in breast tumor patients. Immunoblotting for
51 phospho- and total Src and METTL18 in breast cancer patients from Samsung's cohort. β -actin
52 was used as the loading control.

53
54 **Figure S6.** Gene expression levels of METTL18 and Src in breast tumor patients. Scatterplot
55 showing the gene expression of Src and METTL18 in breast cancer patients from TCGA data.
56 P -values and the correlation coefficient (R) were calculated using the Pearson test.

57
58 **Figure S7.** Role of Src in metastatic potential of breast tumor cells. (A,B) Invasion (A) and
59 migration (B) ability of MDA-MB-231 cells transfected with shScramble or shSrc. (C) The
60 transfection efficacy of the shRNA was verified by Western blotting with anti-Src. ** $P < 0.01$.

61
62 **Figure S8.** (A) Invasion ability of MDA-MB-231 cells transfected with siScramble,
63 siHSP90AA1, or Myc-METTL18. (B) The invasive capacity of MDA-MB-231 cells
64 transfected with siScramble, siActin, or Myc-METTL18. The transfection efficacy of siRNA
65 and METTL18 was identified by immunoblotting with anti-HSP90AA1, anti- β -actin and anti-
66 Myc. Invasive cell numbers were measured by ImageJ. ## $P < 0.01$; ** $P < 0.01$.

67
68 **Figure S9.** Relevance of involvement of HSP90, actin, and p-Src in human and mice. (A)
69 Kaplan-Meier plots of distant relapse-free survival (DMFS) based on low or high expression
70 of HSP90 and β -actin expressions in the HER2-negative breast cancer cohort (median cutoff)
71 (GSE25066). (B) Tumor volume of MDA-MB2310 cells expressing scrambled RNA or
72 shRNA to METTL18 (ShMETTL18). The long and short axes (D and d , respectively) of the
73 tumors were determined using calipers. Tumor volume (mm^3) was subsequently estimated
74 utilizing the formula: $V = 0.5 \times D \times d^2$. (C) F-actin level in sliced tumor tissues expressing
75 shScramble RNA or shMETTL18 RNA from mice. (D). Level of p-Src from tumor tissues
76 expressing shScramble or shMETTL18 RNA. * $P < 0.05$, ** $P < 0.01$, ns: not significant.

77
78 **Figure S10.** (A) Immunoblotting for Myc, β -actin, HSP90, HSP70, Src, GAPDH, JAK2, γ -
79 tubulin, and β -tubulin in MDA-MB-231 cells transfected with METTL18 for 48 hours. (B)
80 Immunoblotting for HSP90 in HA-RPL3 wild type or HA-RPL3 H245A overexpressing MDA-
81 MB-231 cells. The transfection efficacy of the HA-RPL3 wild type and HA-RPL3-H245A
82 construct was verified by immunoblotting with anti-HA. β -actin was used as the loading
83 control. (C) The mRNA expression level of METTL18, HSP90AA, β -actin, HSP70, Src, β -
84 tubulin and γ -tubulin was detected by quantitative real-time PCR in MDA-MB-231 cells
85 transfected with siMETTL18 for 48 hours. GAPDH was used as a control gene. (D)
86 Immunoblotting for JAK2, phospho-Src (Y419), phospho-Src (Y530), and Src in MDA-MB-
87 231 cells transfected with siScramble, siMETTL18, or JAK2. siRNAs and plasmids were
88 transfected for 48 hours and 24 hours, respectively. The transfection efficacy of the siRNA and
89 JAK2 was verified by Western blotting with METTL18 and anti-JAK2. β -actin was used as
90 the loading control.

91
92 **Figure S11.** (A) Immunoblotting of METTL18, HSP90, and Actin proteins in siScramble-,
93 siMETTL18, siHSP90, and siActin-transfected MDA-MB-231. The observed decrease in
94 HSP90 levels following siMETTL18 treatment is attributed to the diminished Rpl3 methylation.
95 (B-D) Actin polymerization level of MDA-MB-231 and HAP-1 cells. (B,D) The F/G actin
96 assay was performed with a G-actin/F-actin *in vivo* assay biochem kit (Cytoskeleton) in
97 siHSP90 (B), siActin (B), siMETTL18 (D), or HSP90 (D)-transfected cells. (C) Confocal
98 microscopy images showing polymerized actin (red) in HAP-1 wild type (WT) and HAP-1

99 METTL18 knockout (KO) cells. Carl Zeiss Zen blue edition calculated the relative intensity of
100 the polymerized actin. (E) Immunoprecipitation analysis for interactions between actin and Src
101 in siMETTL18-transfected MDA-MB-231 cells. (F-G) Effect of METTL18 in MCF-7 cells
102 (F) Immunoblotting for p-Src (Y419), Src, and HSP90 in shMETTL18-expressing MCF-7. The
103 transfection efficacy of the shMETTL18 was verified by Western blotting with anti-METTL18.
104 β -actin was used as the loading control. (G) Confocal microscopy images of polymerized actin
105 (Red) in shMETTL18-expressing MCF-7 cells. * $P < 0.05$, ** $P < 0.01$.

106
107 **Figure S12.** p-Src level of HAP-1 cells. Immunoblotting for HSP90, phospho-Src (Y419),
108 phospho-Src (Y530), Src, and β -actin in HAP-1 wild type and HAP-1 METTL18 knockout
109 cells. METTL18 knockout and transfection efficacy was tested by immunoblotting with anti-
110 METTL18.

111
112 **Figure S13.** Pharmacological inhibition of HSP90AA1. (A) p-Src level of MDA-MB-231 cells
113 transfected with Myc-METTL18 during 17-AAG treatment was analyzed by immunoblotting
114 analysis. (B) Cell migration was examined with Myc-METTL18-overexpressed MDA-MB-
115 231 cells treated with 17-AAG for 19 h. c Invasion level of MDA-MB-231 cells was evaluated
116 under transfection of Myc-METTL18 and 17-AAG exposure.

117
118 **Figure S14.** Tumor-suppressive activity of METTL21B. (A) Colony formation was assessed
119 by colony forming assay with Flag-METTL21B-overexpressed MKN-1 cells for 48 h. (B) Cell
120 migration was examined with Flag-METTL21B-overexpressed MKN-1 cells treated for 24 h.
121 c Invasion level of Flag-METTL21B-overexpressed MKN-1 cells for 24 h was evaluated by
122 invasion assay. * $P < 0.05$, ** $P < 0.01$.

123
124 **Figure S15.** Tumor-suppressive activity of METTL22. (A) Cell migration was examined with
125 Myc-METTL22-overexpressed HCT-116 cells treated for 24 h and 48 h. (B) Invasion level of
126 Myc-METTL22-overexpressed HCT-116 cells for 48 h was evaluated by invasion assay.
127 ** $P < 0.01$.

128
129 **Figure S16.** Tumor promoting activity of CAMKMT. (A) Colony formation was assessed by
130 colony forming assay with Myc-CAMKMT-overexpressed MKN-1 cells for 48 h. (B,C)
131 Invasion levels of Myc-CAMKMT-overexpressed (B) or shCAMKMT-expressing (C) MKN-
132 1 cells for 24 h were evaluated by invasion assay. (D) Levels of p-Src was confirmed by
133 immunoblotting analysis with lysates of Myc-CAMKMT-overexpressed or shCAMKMT-
134 expressing MKN-1 cells. (D) Level of complex formation between CAMKMT and Src was
135 detected by immunoblotting analysis with beads prepared by immunoprecipitation with anti-
136 Myc with lysates of MKN-1 cells transfected with Myc-CAMKMT and/or HA-Src. * $P < 0.05$,
137 ** $P < 0.01$.

138
139 **Figure S17.** Molecular complex formation between METTL18, HSP90, actin and Src. (A-F)
140 Levels of complex formation between actin and HSP90 (A), METTL18 and actin (B),
141 METTL18 and HSP90AA1 (C), actin and Src (D), HSP90 and Src (E), and METTL18 and
142 HSP90 (F) were detected by immunoblotting analysis with beads prepared by
143 immunoprecipitation with anti-GFP, anti-Flag, and anti-HA, with lysates of MDA-MB-231
144 cells transfected with GFP-Actin, HA-Actin, HA-HSP90, Flag-METTL18, or HA-Src. **g**
145 Construct map of HSP90AA1 deletion mutation.

146
147

148 **Supplementary Tables**

149

150 **Table S1. List of primers used for siRNA against METTL18, HSP90AA1, actin, PIMT,**
 151 **EEF2KMT, PRMT1, GRWD1, and RPL3.**

152

Name of siRNA	Forward (5'-3')	Reverse (5'-3')
METTL18	CCAGAUUAUUUAGUAAUUUU	AAUUACUAUAAUAAUCUGGUU
HSP90AA1	GAAACAUUCUCAGUUUAAUUUU	AAUAAACUGAGAAUGUUUCUU
Actin	CGAGAAGAUGACCCAGAUCUUU	AUGAUCUGGGUCAUCUUCUCGUU
PIMT	CUCGGAGCUAAUCCACAAUUU	AUUGUGGAUUAGCUCCGAGUU
EEF2KMT	CUUAGAAGCAAAGUUAAGAUU	UCUUAACUUUGCUUCUAAGUU
PRMT1	CGUCAAGCCAACAAGUUAAU	UAACUUGUUGGCUUUGACGUU
GRWD1	GGGAUGAGCAGGCCCAAUGAA GCCUU	GGCUUCAUUUGGCCUGCUCAU CCCUU
RPL3	CCAAGUCAUCCGUGUCAUUUU	AAUGACACGGAUGACUUGGUU
Scramble	CCUACGCCACCAAUUUCGUUU	ACGAAAUUGGUGGCGUAGGUU

153

154

155 **Table S2. List of primers used to produce shRNA constructs against the METTL18 and**
 156 **Src genes.**

Name of shRNA	Forward (5'-3')	Reverse (5'-3')
shMETTL18	CCGGCATTTCACAACCCAGATT ATTACTCGAGTAATAATCTGG GTTGTAAATGTTTTTG	AATTCAAAAACATTTACAACC CAGATTATTACTCGAGTAATA ATCTGGGTTGTAAATG
shSrc #1	CCGGGCTCGGCTCATTGAAG ACAATCTCGAGATTGTCTTCA ATGAGCCGAGCTTTTTG	AATTCAAAAAGCTCGGCTCAT TGAAGACAATCTCGAGATTGT CTTCAATGAGCCGAGC
shSrc #2	CCGGGACAGACCTGTCCTTCA AGAACTCGAGTTCTTGAAGG ACAGGTCTGTCTTTTTG	AATTCAAAAAGACAGACCTG TCCTTCAAGAACTCGAGTTCT TGAAGGACAGGTCTGTC

157

158

Fig. S1a

Normal-Like

HER2 positive

HER2 negative

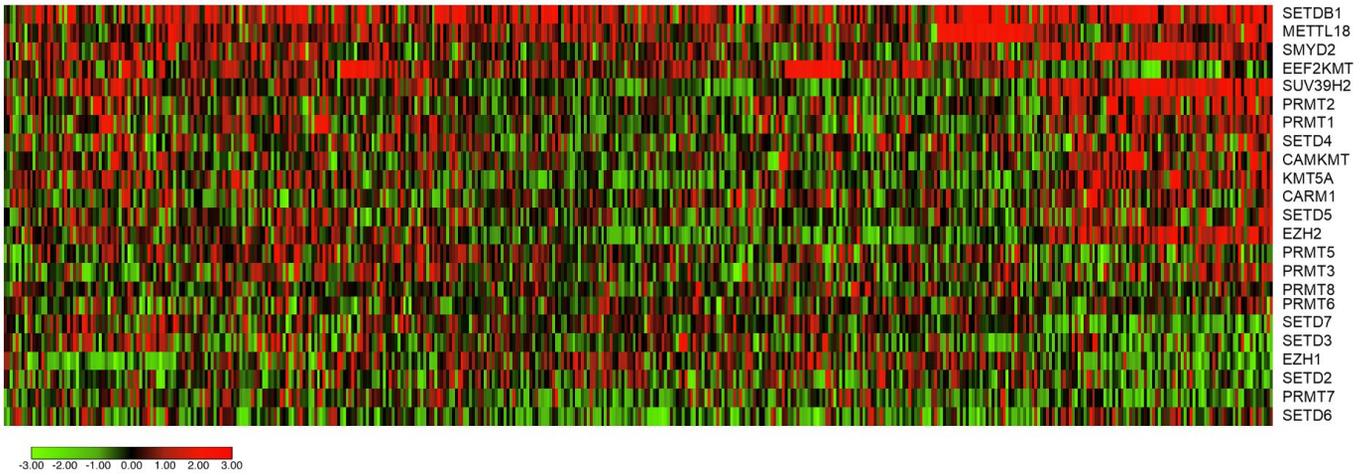


Fig. S1b

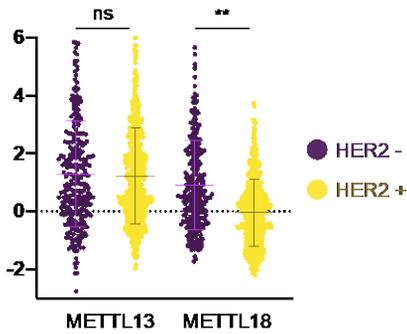


Fig. S1c

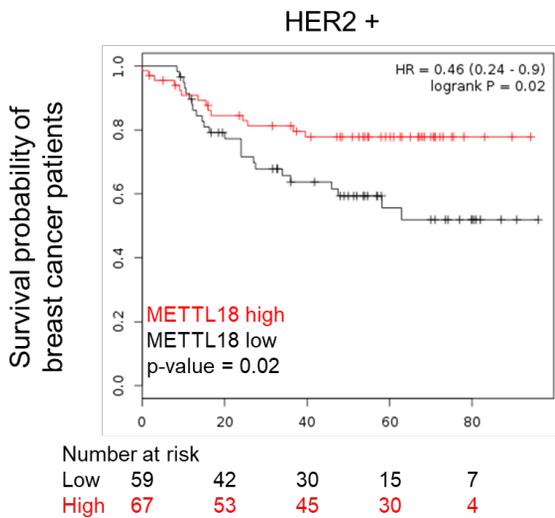


Fig. S1d

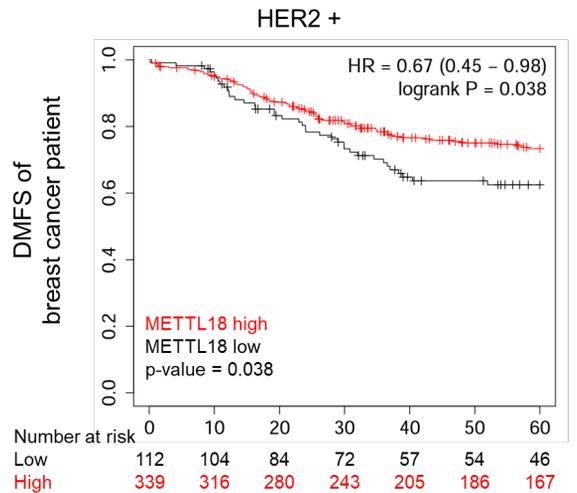


Fig. S2a

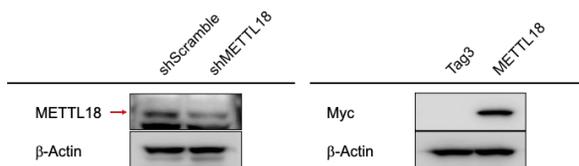


Fig. S3

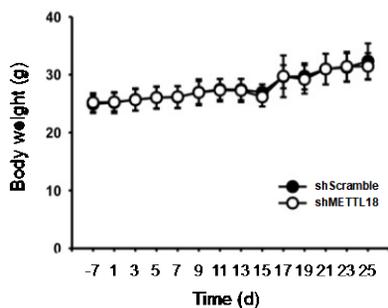


Fig. S2b

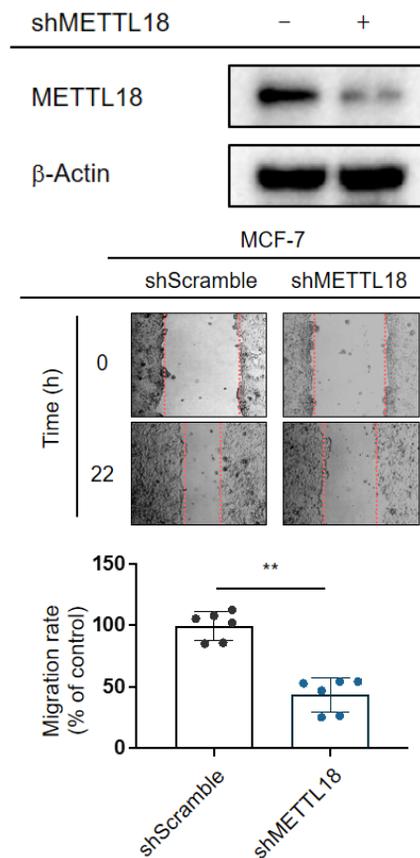


Fig. S4a

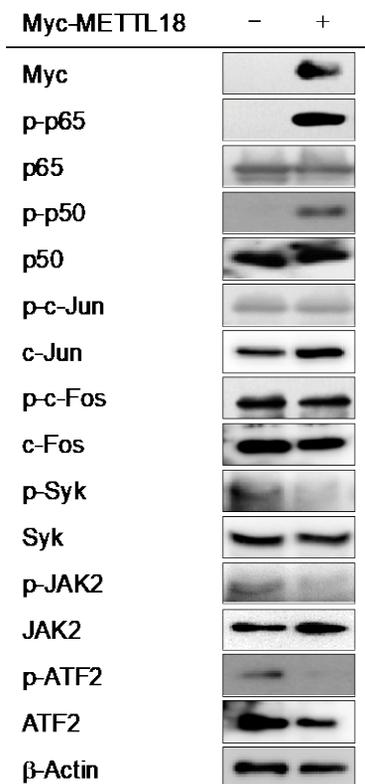


Fig. S4b

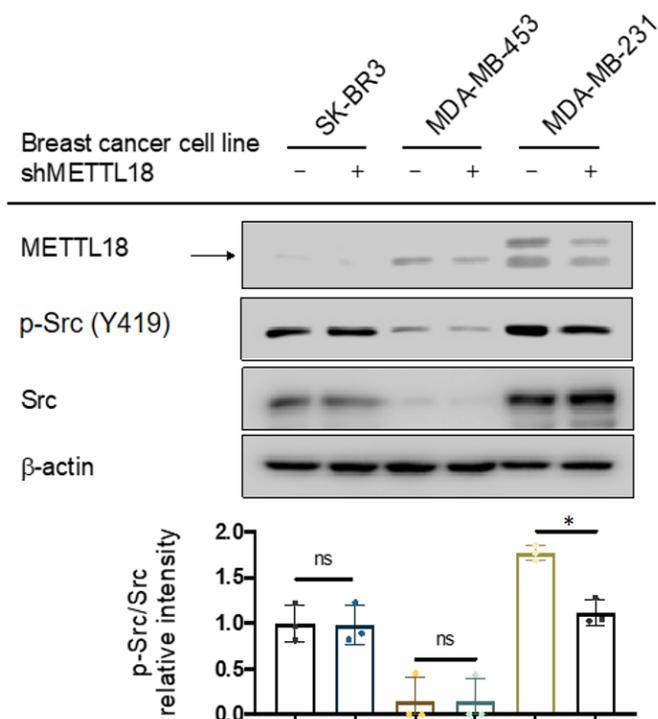


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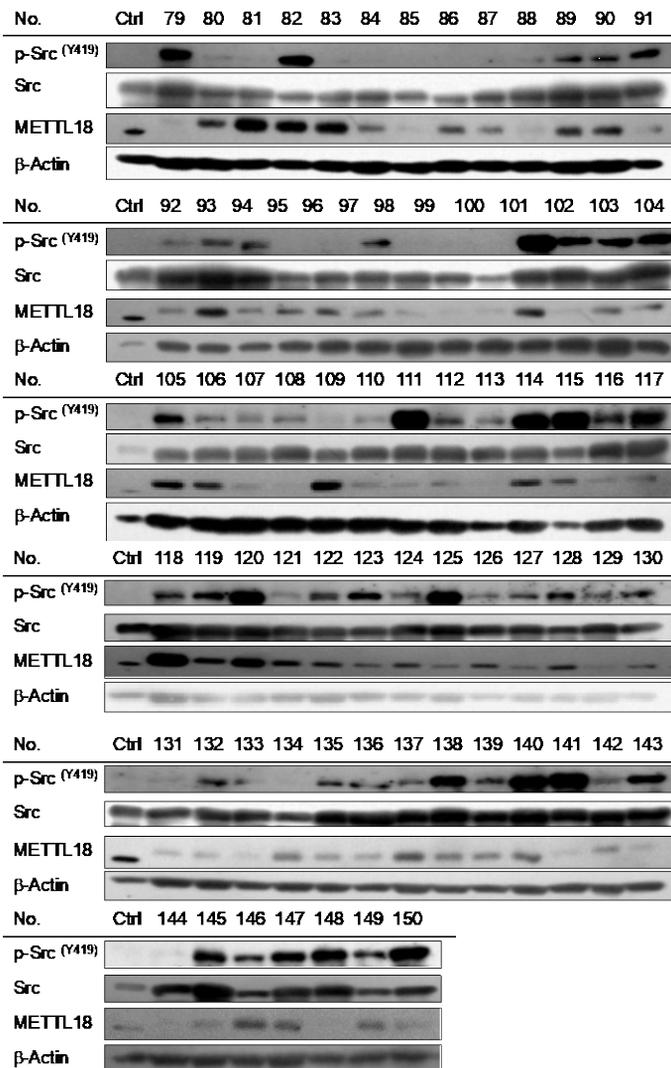
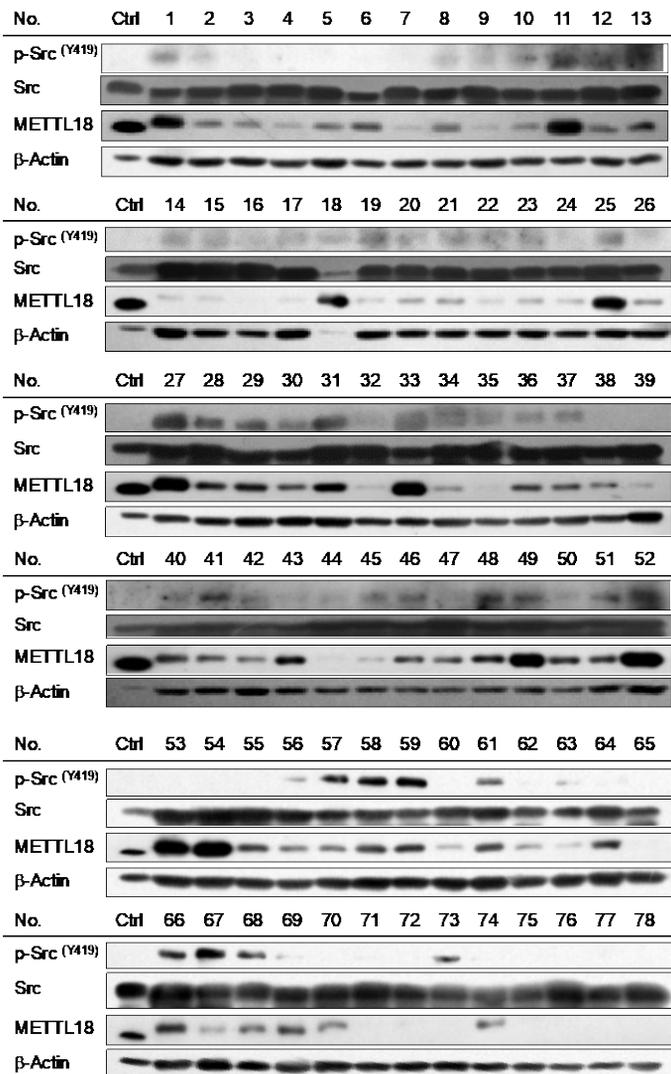
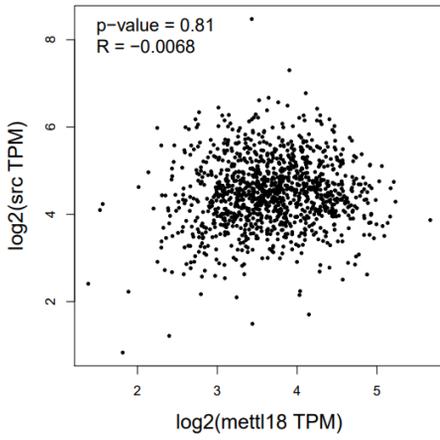
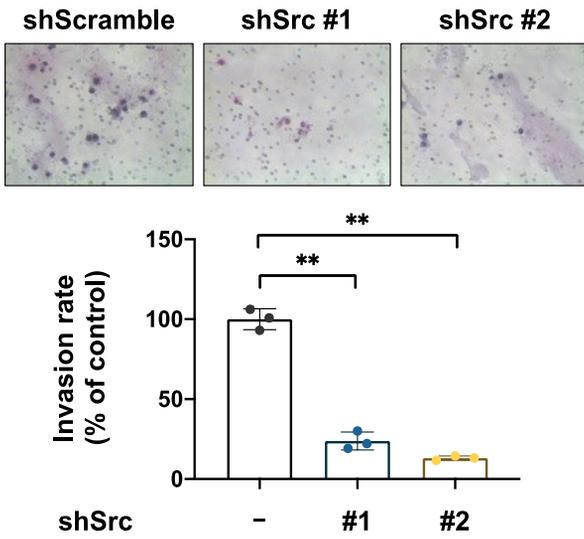
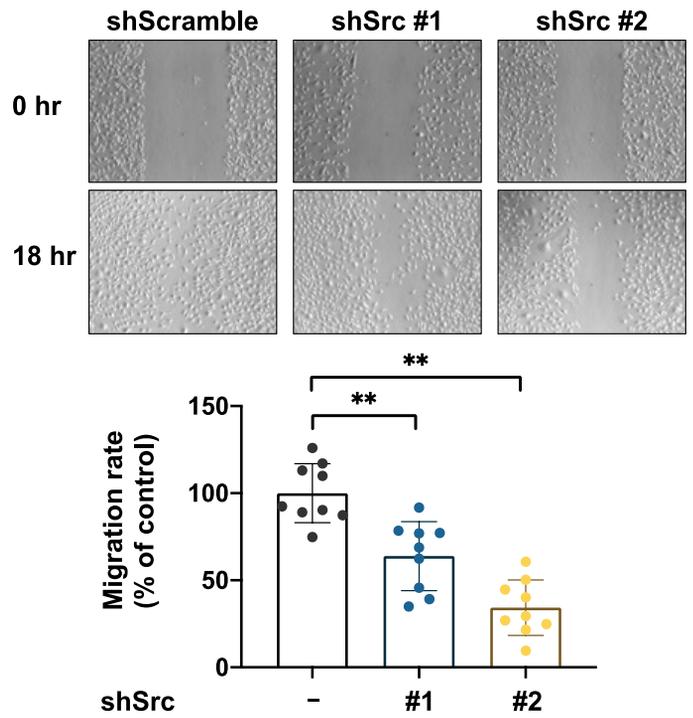


Fig. S6**Fig. S7a****Fig. S7b****Fig. S7c**

shScramble	+	-	-
shSrc #1	-	+	-
shSrc #2	-	-	+



Fig. S8a

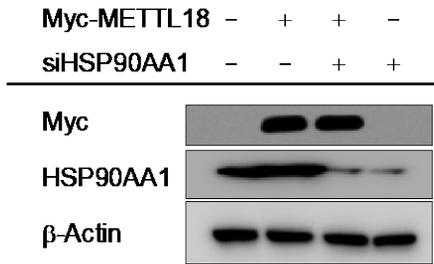
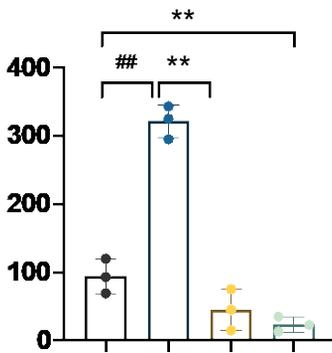
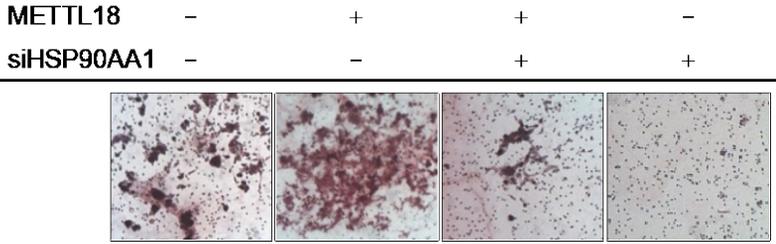


Fig. S8b

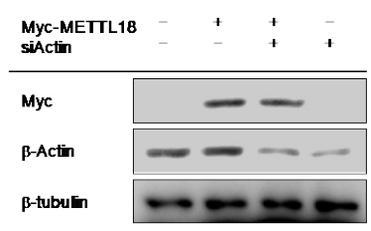
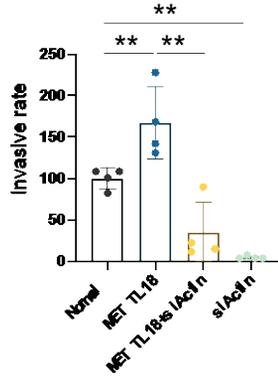
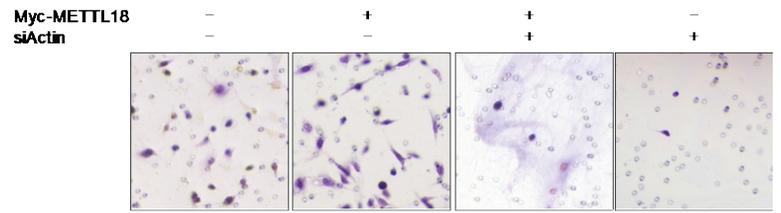
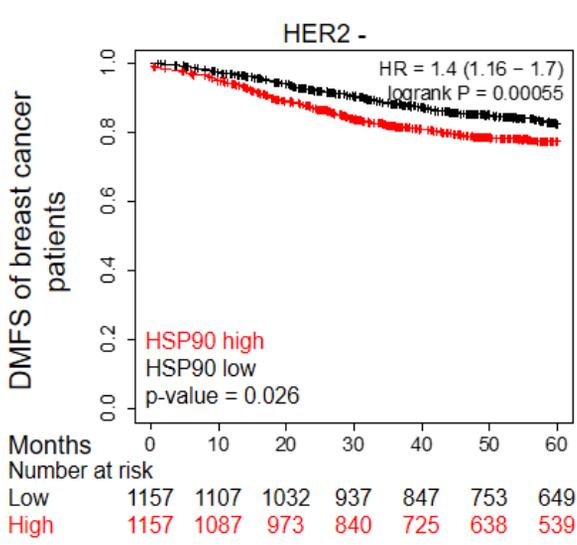
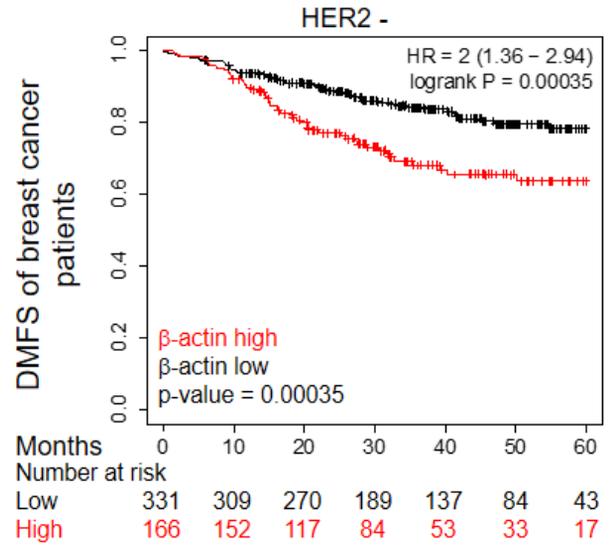


Fig. S9a



DMFS : Distant Metastasis Free Survival



DMFS : Distant Metastasis Free Survival

Fig. S9b

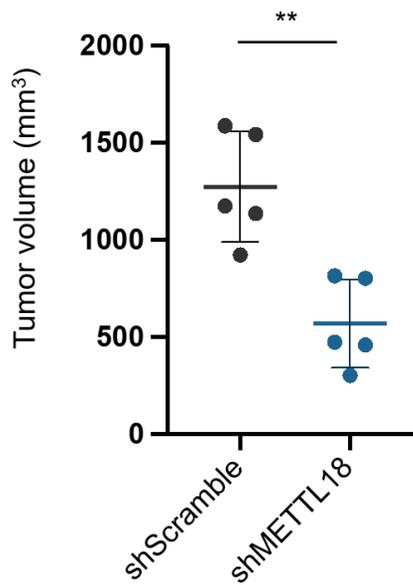
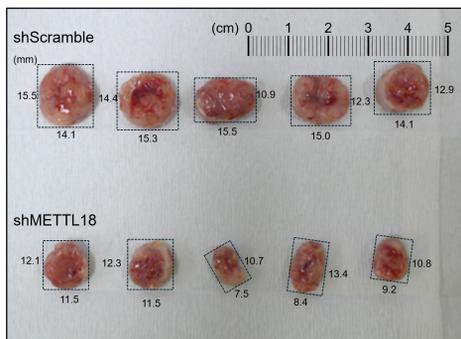


Fig. S9c

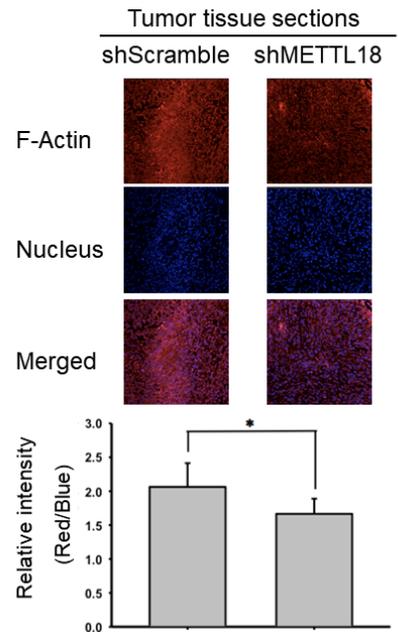


Fig. S9d

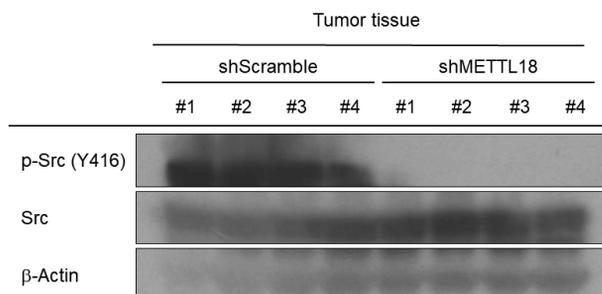


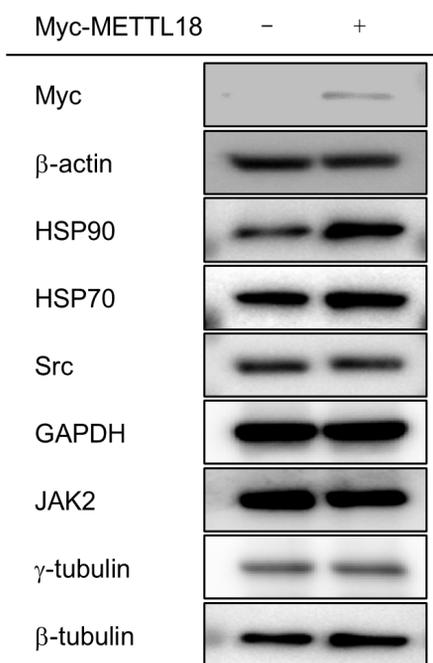
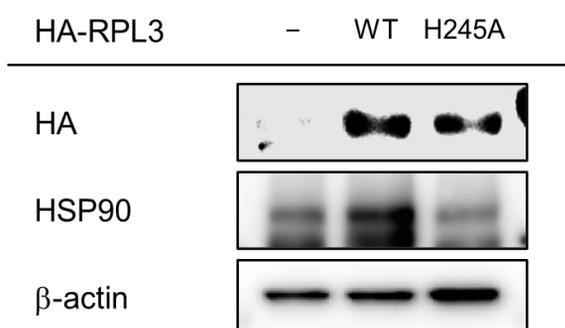
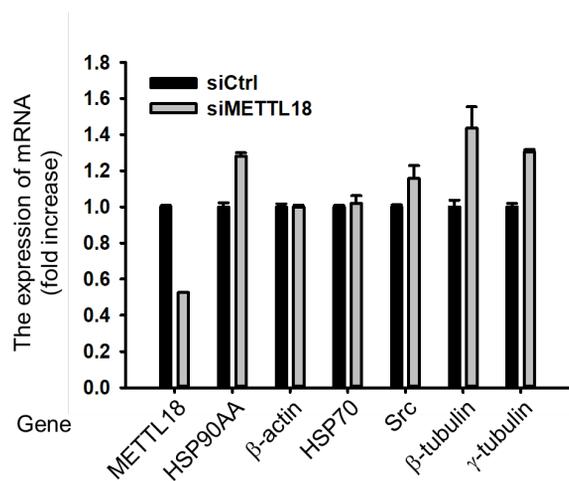
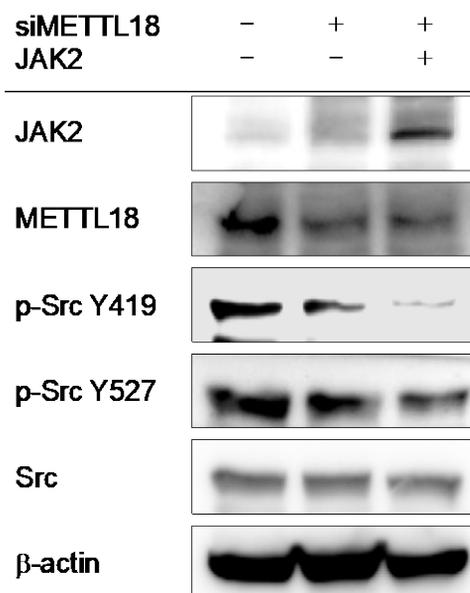
Fig. S10a**Fig. S10b****Fig. S10c****Fig. S10d**

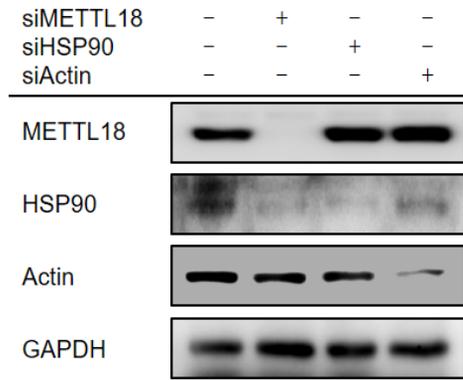
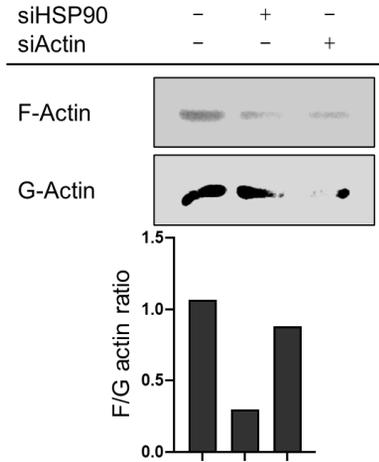
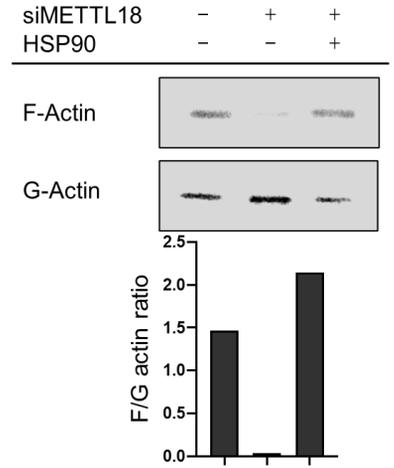
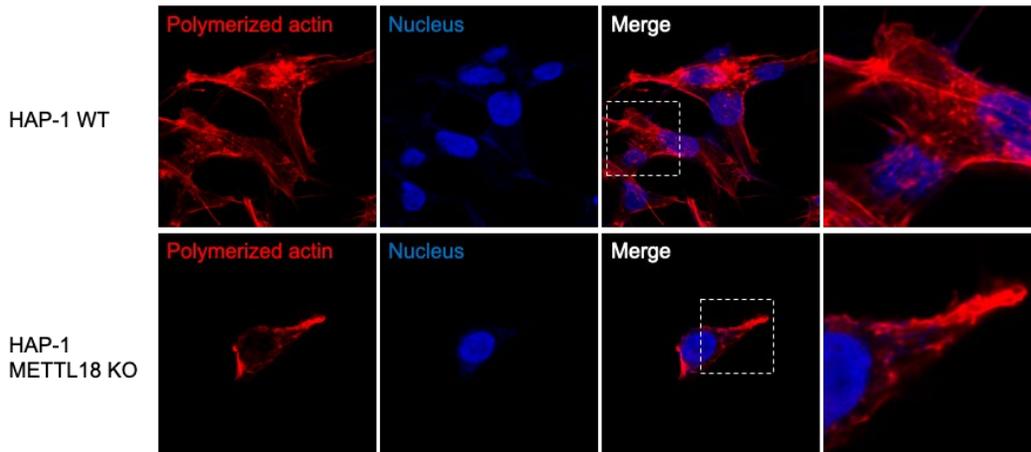
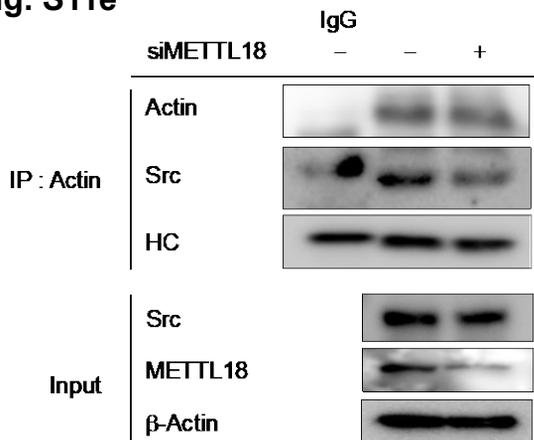
Fig. S11a**Fig. S11b****Fig. S11d****Fig. S11c****Fig. S11e**

Fig. S11f

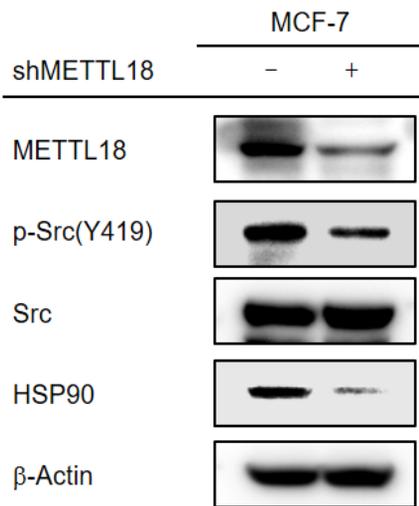


Fig. S11g

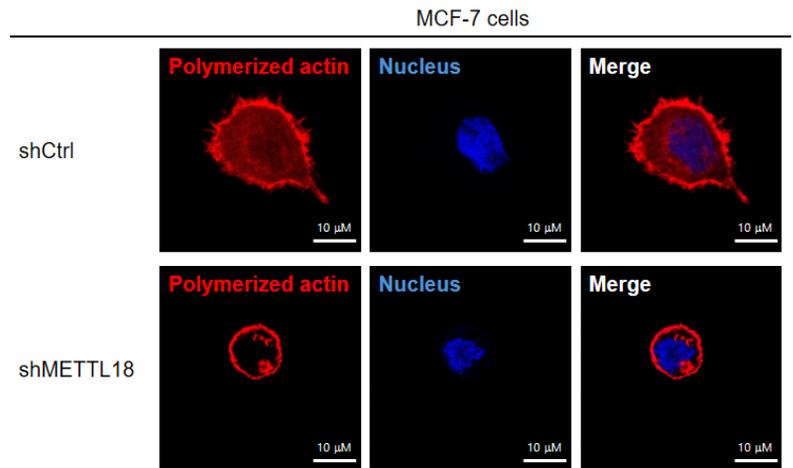


Fig. S12

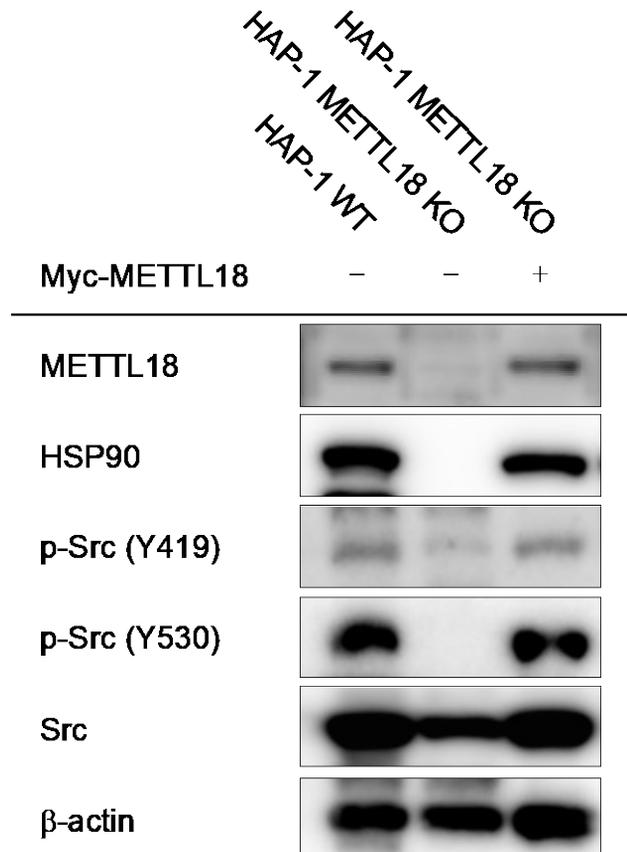


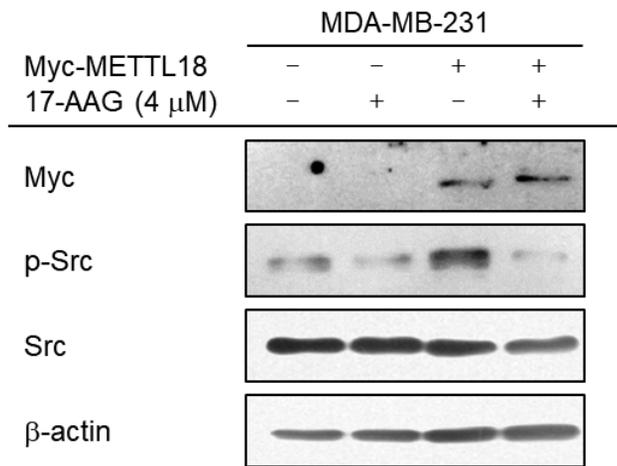
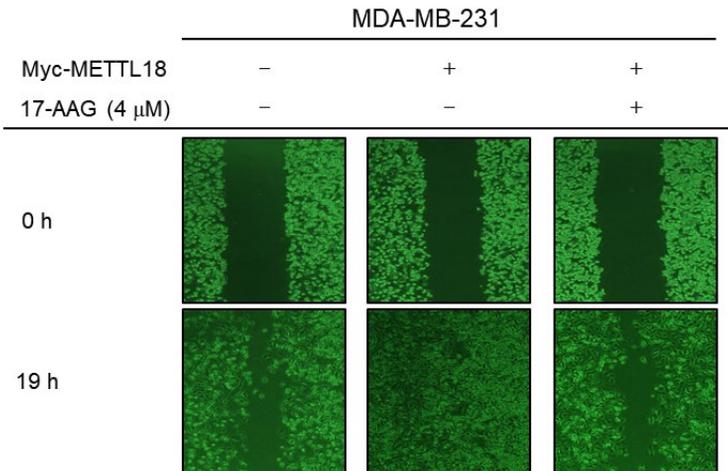
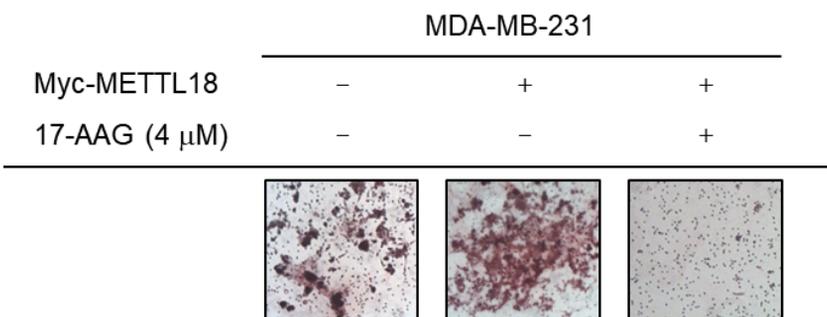
Fig. S13a**Fig. S13b****Fig. S13c**

Fig. S14a

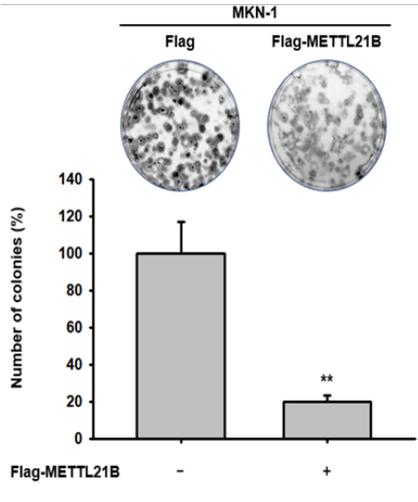


Fig. S14b

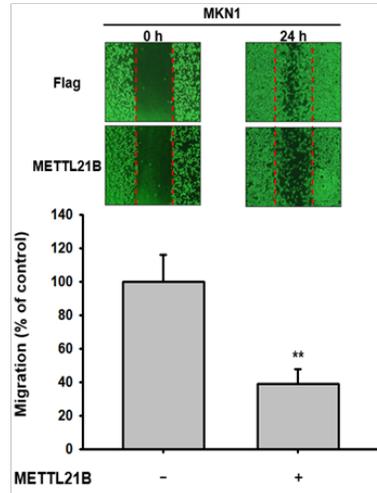


Fig. S14c

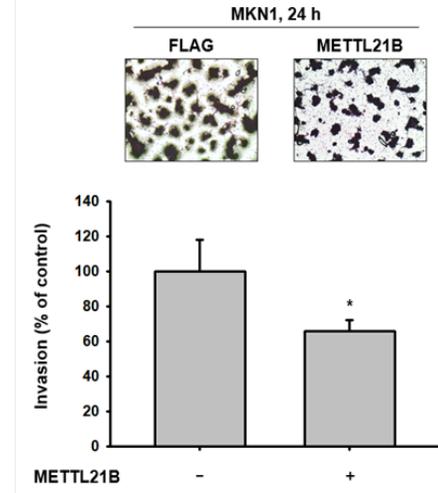


Fig. S15a

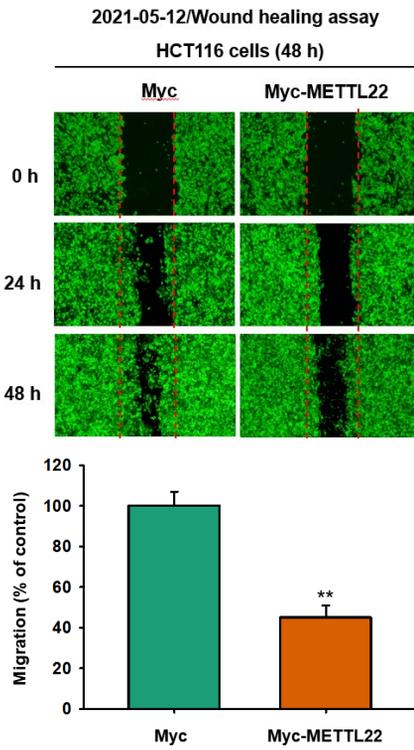


Fig. S15b

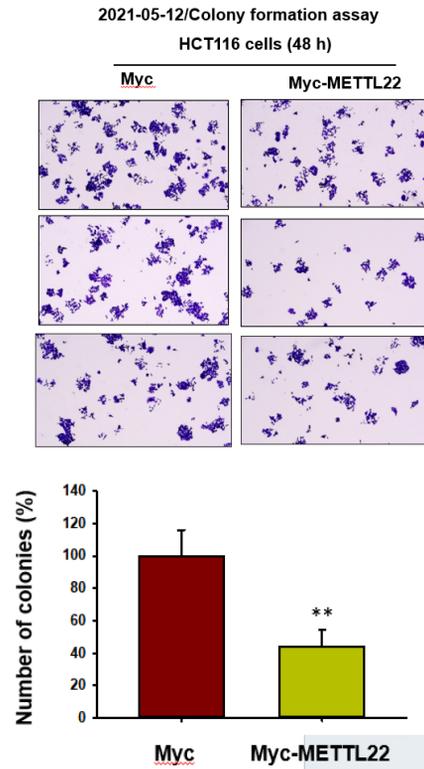


Fig. S16a

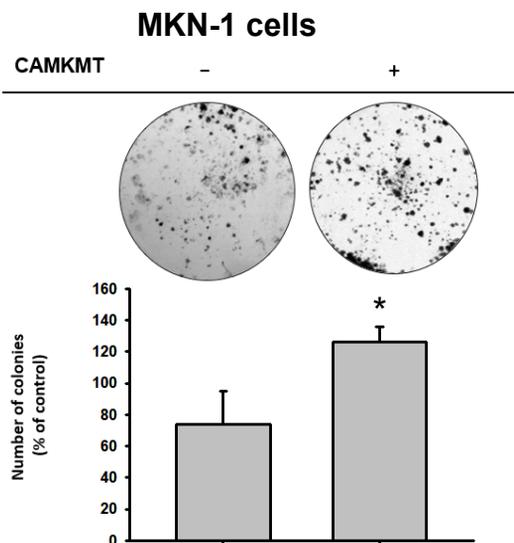


Fig. S16b

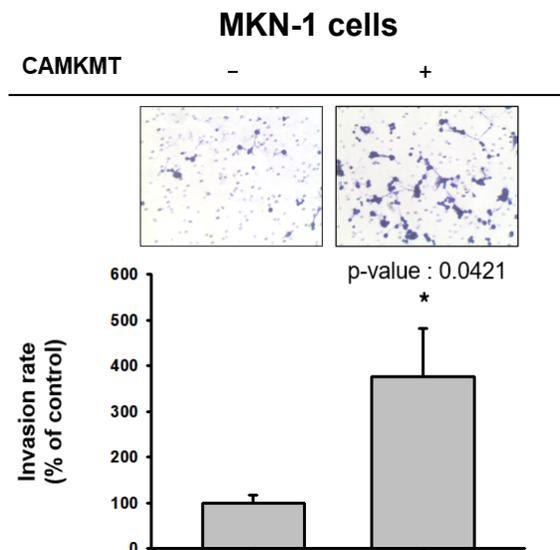


Fig. S16c

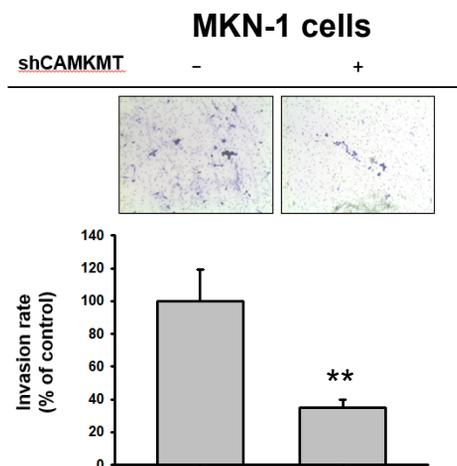


Fig. S16d

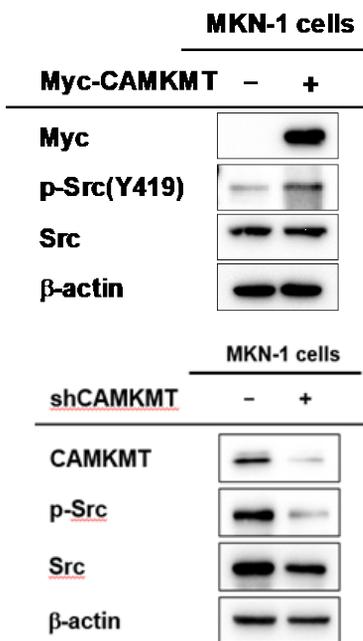


Fig. S16e

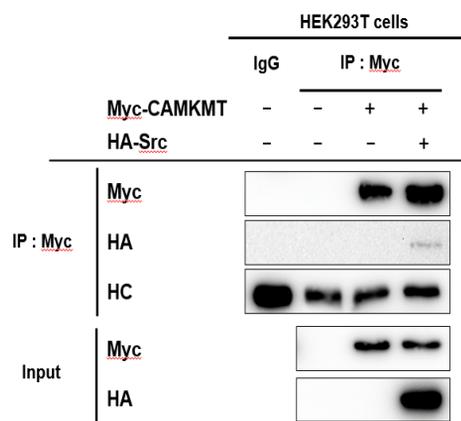


Fig. S17a

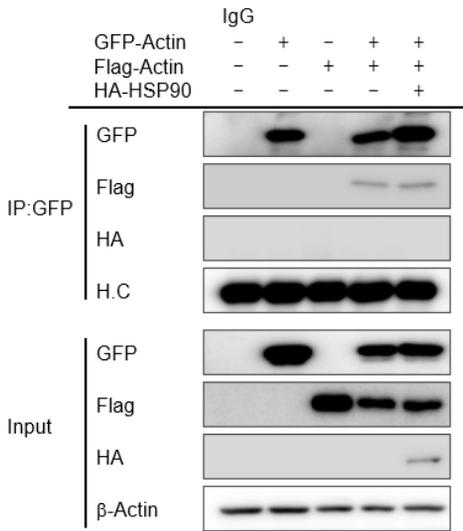


Fig. S17b

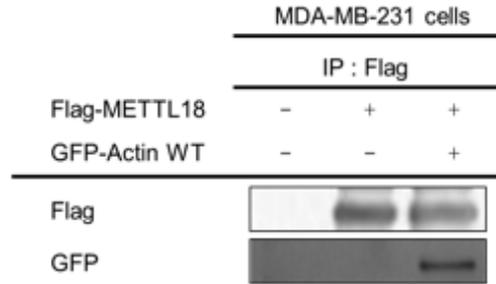


Fig. S17c

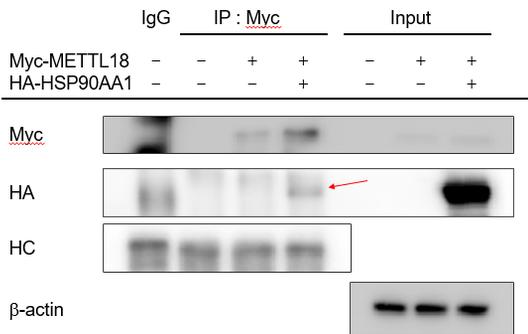


Fig. S17d

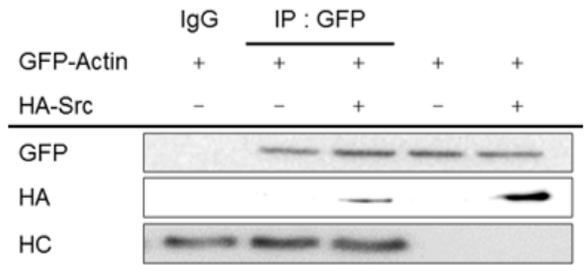


Fig. S17f

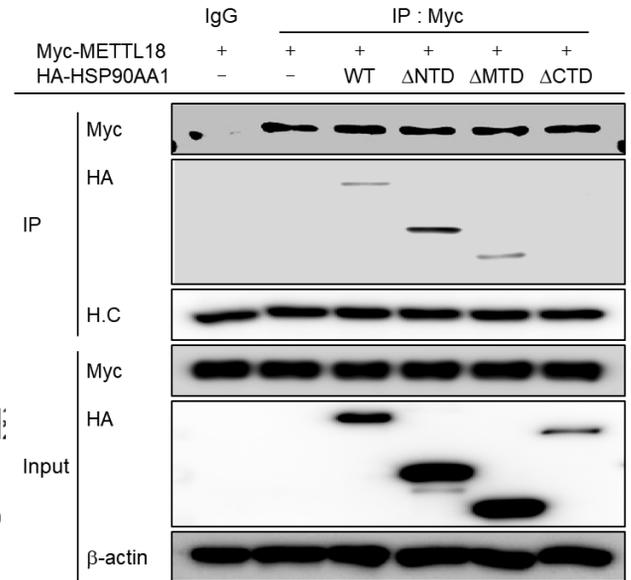


Fig. S17e

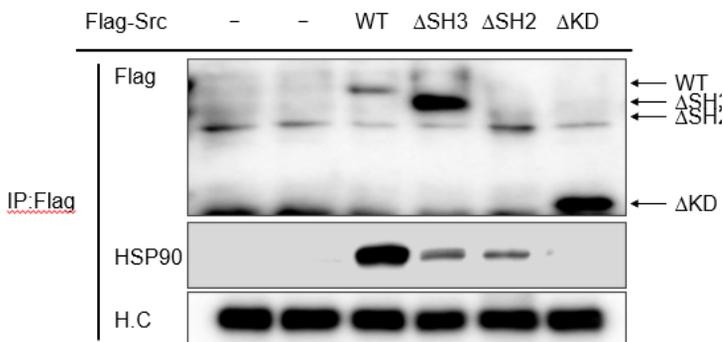


Fig. S17g

