# Expanded View Figures

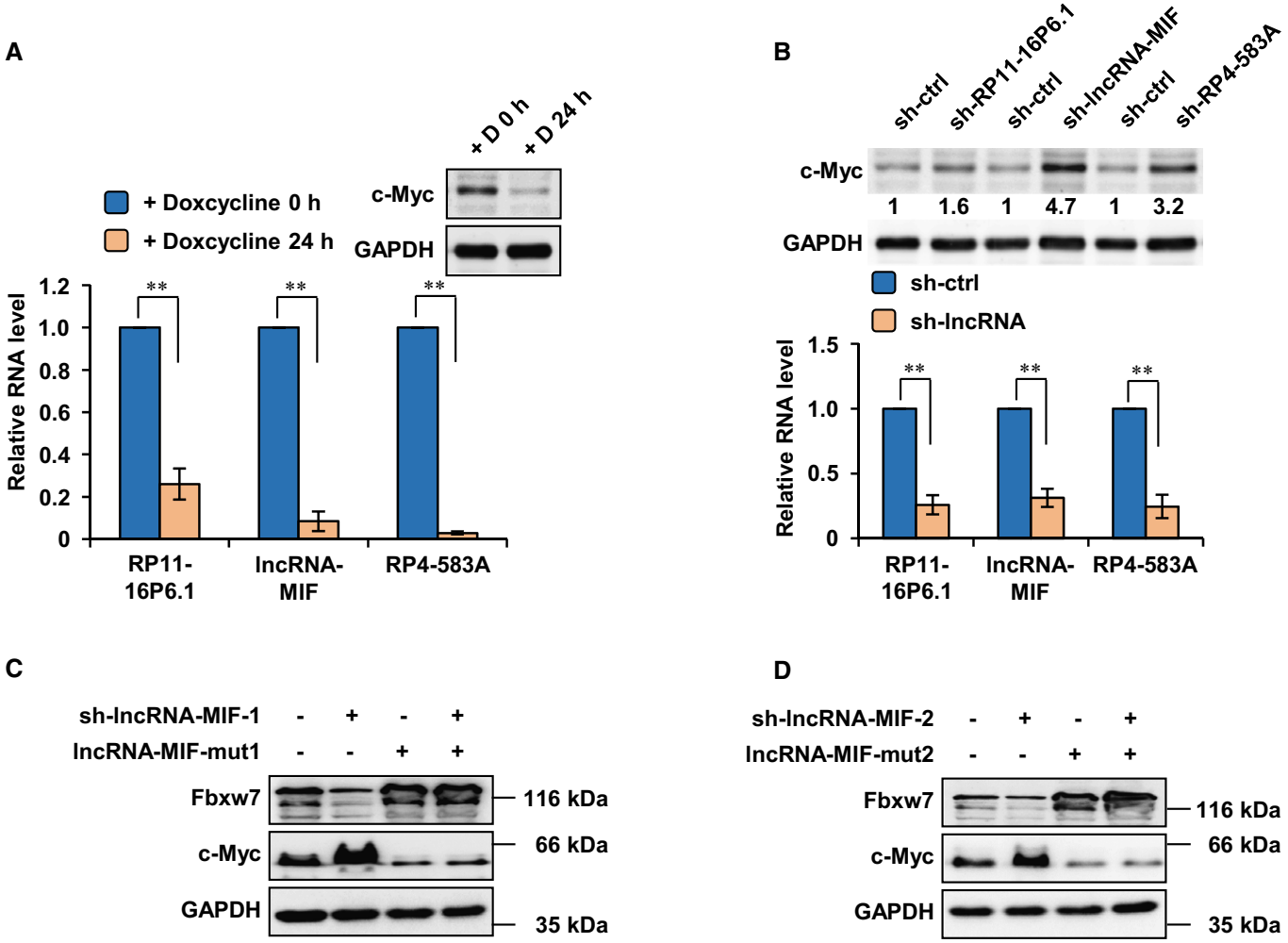


**Figure EV1. Knockdown of lncRNA-MIF by shRNA leads to increased expression of c-Myc.**

A P493-6 cells were treated with doxycycline for 0 and 24 h. Total RNA was analyzed by real-time RT–PCR to examine the levels of RP11-16P6.1, lncRNA-MIF, and RP4-583A. Data shown are mean ± SD ($n$ = 3; $^{**}P < 0.01$, two-tailed $t$-test). Cell lysates were also analyzed by Western blotting using anti-c-Myc and anti-GAPDH antibodies.

B HeLa cells were individually infected with lentiviruses expressing either control shRNA, RP11-16P6.1 shRNA, lncRNA-MIF shRNA, or RP4-583A shRNA. Forty-eight hours after infection, cell lysates were analyzed by Western blotting using anti-c-Myc and anti-GAPDH antibodies. Total RNA was analyzed by real-time RT–PCR. Data shown are mean ± SD ($n$ = 3; $^{**}P < 0.01$, two-tailed $t$-test).

C, D HeLa cells were infected with lentiviruses as indicated. Forty-eight hours after infection, cell lysates were analyzed by Western blot analysis using anti-Fbxw7, anti-c-Myc, and anti-GAPDH antibodies.

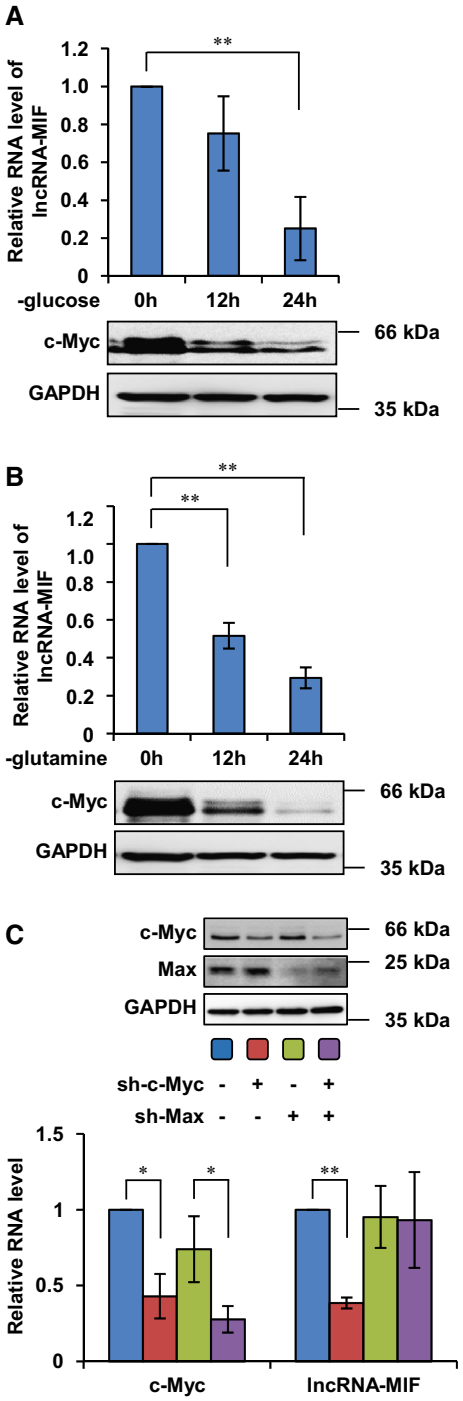


**Figure EV2. c-Myc down-regulates lncRNA-MIF under glucose or glutamine deprivation.**

A HeLa cells were treated with glucose deprivation DMEM medium for 0, 12, or 24 h. Cell lysates were analyzed by Western blotting. Total RNA was analyzed by real-time RT–PCR. Data shown are mean ± SD ($n$ = 3; $^{**}P < 0.01$, two-tailed $t$-test).

B HeLa cells were treated with glutamine deprivation DMEM medium for 0, 12, or 24 h. Cell lysates were analyzed by Western blotting. Total RNA was analyzed by real-time RT–PCR. Data shown are mean ± SD ($n$ = 3; $^{**}P < 0.01$, two-tailed $t$-test).

C HeLa cells expressing control shRNA or c-Myc shRNA were infected with lentiviruses expressing control shRNA or Max shRNA. Forty-eight hours after infection, cell lysates were analyzed by Western blotting. Total RNA was analyzed by real-time RT–PCR. Data shown are mean ± SD ($n$ = 3; $^{*}P < 0.05$, $^{**}P < 0.01$, two-tailed $t$-test).

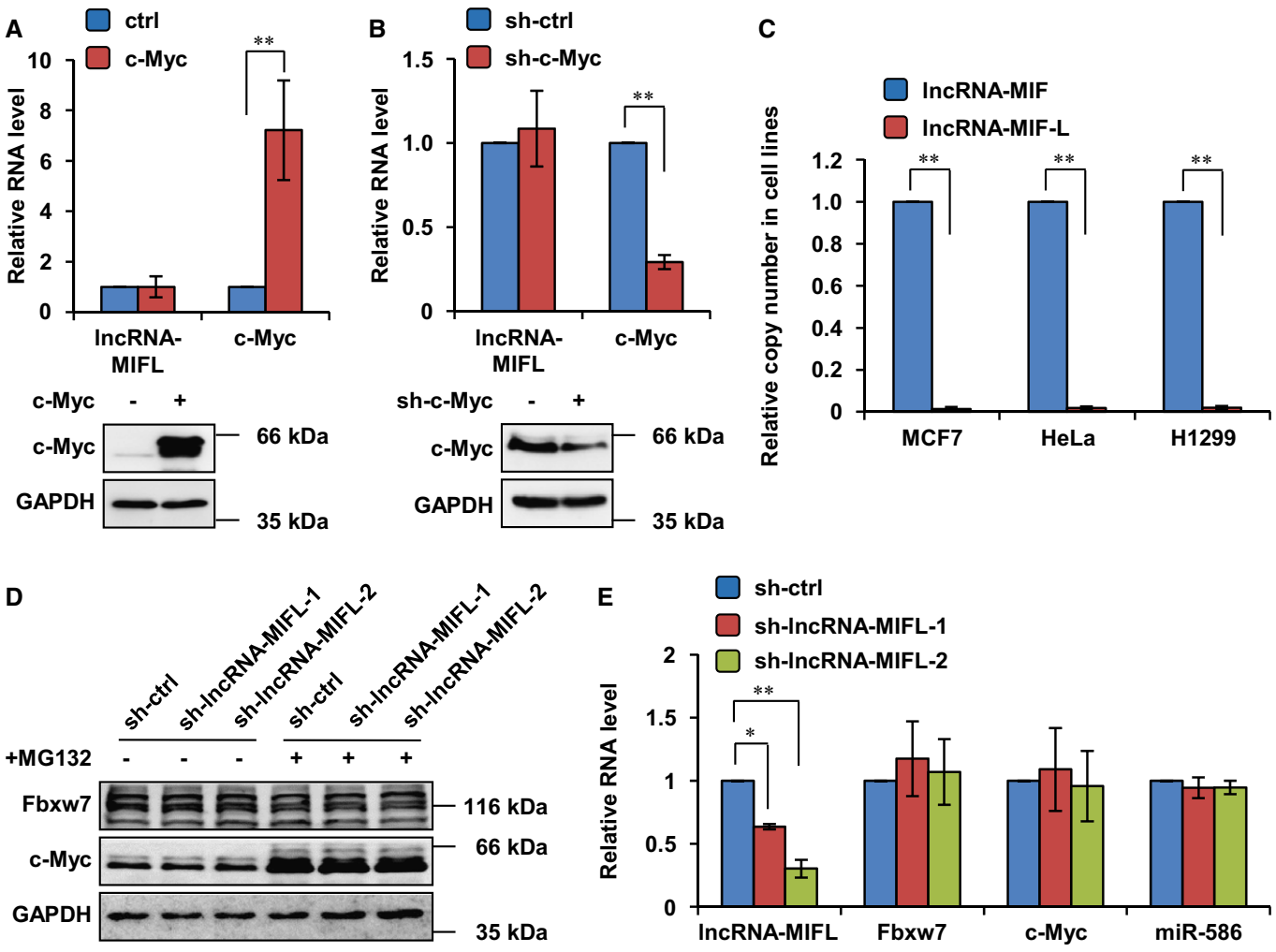


**Figure EV3. LncRNA-MIF-L is not a ceRNA for miR-586 to regulate Fbxw7 expression.**

A HeLa cells were transfected with control vector or Flag-c-Myc. Twenty-four hours after transfection, cell lysates were analyzed by Western blotting, and total RNA was analyzed by real-time RT–PCR. Data shown are mean ± SD ($n$ = 3; $^{**}P < 0.01$, two-tailed $t$-test).

B HeLa, HCT116, and MCF10A cells were separately infected with lentiviruses expressing either control shRNA or c-Myc shRNA. Twenty-four hours after infection, total RNA was analyzed by real-time RT–PCR. Data shown are mean ± SD ($n$ = 3; $^{**}P < 0.01$, two-tailed $t$-test).

C The copy numbers of lncRNA-MIF and lncRNA-MIF-L transcript per million cells in the indicated cells were quantified using a quantitative real-time RT–PCR assay. Data shown are mean ± SD, and lncRNA-MIF as control ($n$ = 3; $^{**}P < 0.01$, two-tailed $t$-test).

D HeLa cells were infected with lentiviruses expressing control shRNA, lncRNA-MIF-L shRNA-1 or -2. Forty-eight hours after infection, cells were treated with MG132 or DMSO for 6 h. Cell lysates were then analyzed by Western blotting with the indicated antibodies.

E HeLa cells were infected with lentiviruses expressing control RNA, lncRNA-MIF, or lncRNA-MIF-AS. Forty-eight hours after infection, total RNA was subjected to real-time RT–PCR analysis. Data shown are mean ± SD ($n$ = 3; $^{*}P < 0.05$, $^{**}P < 0.01$, two-tailed $t$-test).

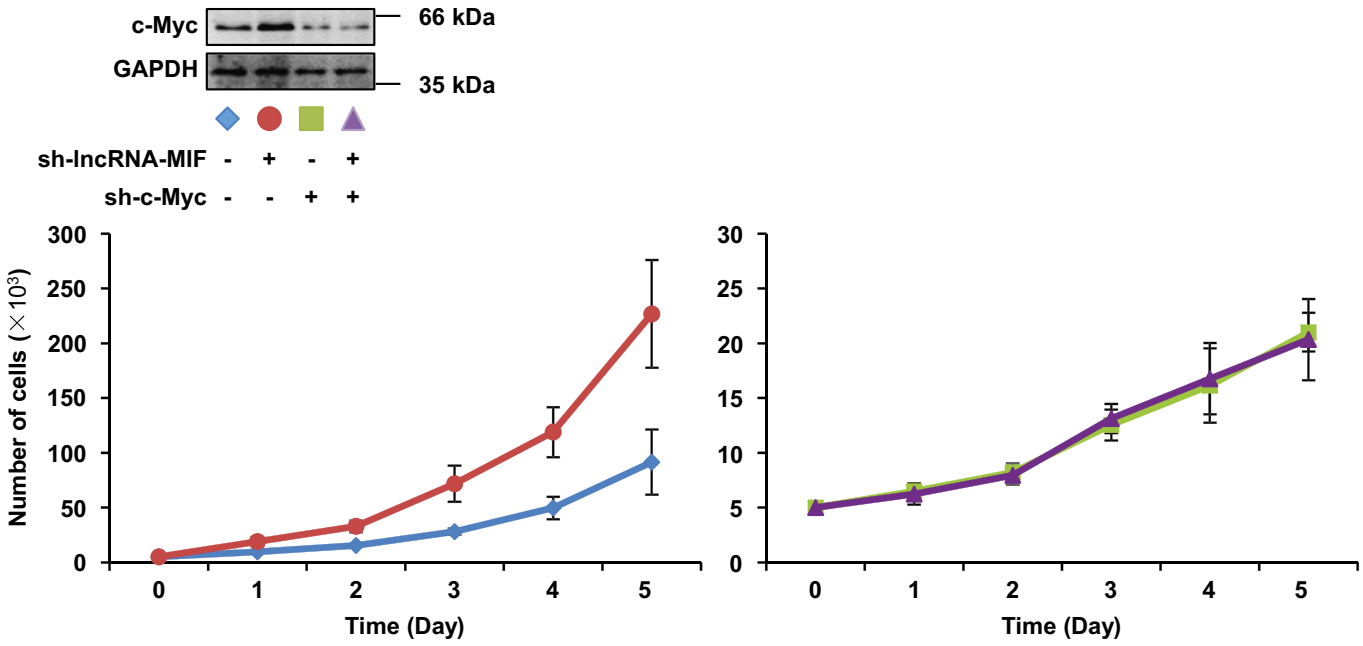


**Figure EV4. The effect of lncRNA-MIF on cell proliferation is dependent on c-Myc.**
HeLa cells expressing control shRNA or lncRNA-MIF shRNA were infected with lentiviruses expressing control shRNA or c-Myc shRNA. Forty-eight hours after infection, growth curves were measured for the indicated periods of time. Data shown are mean ± SD ($n$ = 3). Cell lysates were analyzed by Western blotting with the indicated antibodies.

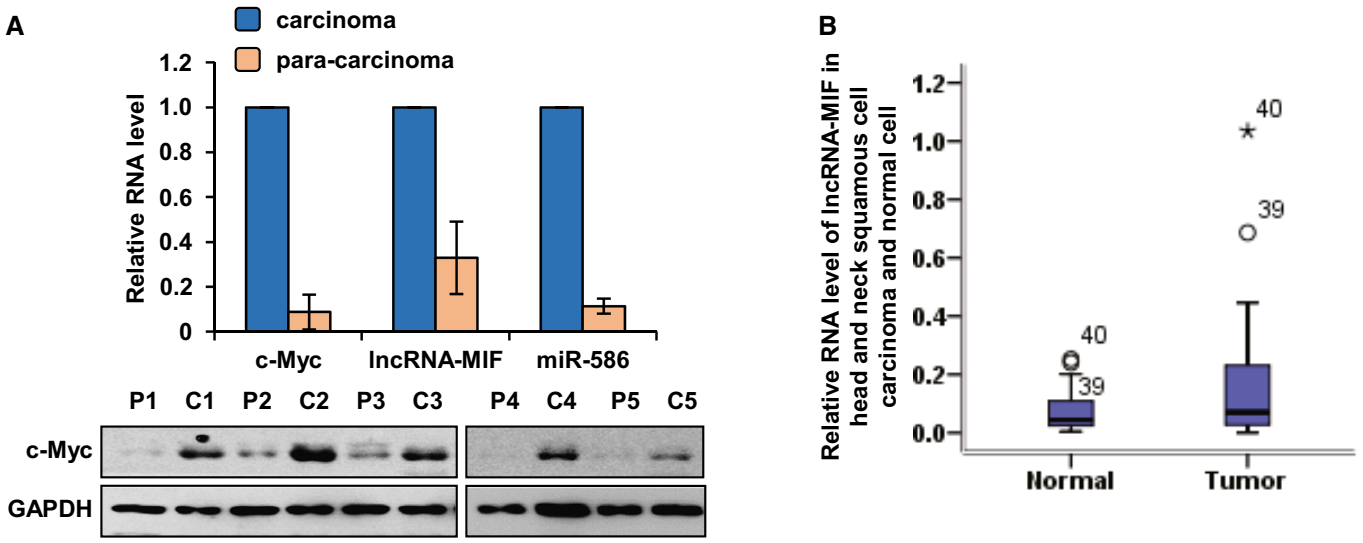


**Figure EV5. lncRNA-MIF and miR-586 show higher expression in carcinoma than in para-carcinoma or normal cells.**

A Proteins and total RNA were extracted from five pairs of colorectal carcinoma and para-carcinoma tissues. Protein samples were analyzed by Western blotting and total RNA was subjected to real-time RT–PCR analysis. Data shown are mean ± SD ($n$ = 3).

B Data of lncRNA-MIF expression level in HNSC (head and neck squamous cells) carcinoma and normal tissues were downloaded from TCGA dataset. Box plots showing the differential expression (mean ± SD) of lncRNA-MIF between normal and tumor samples ($n$ = 40).