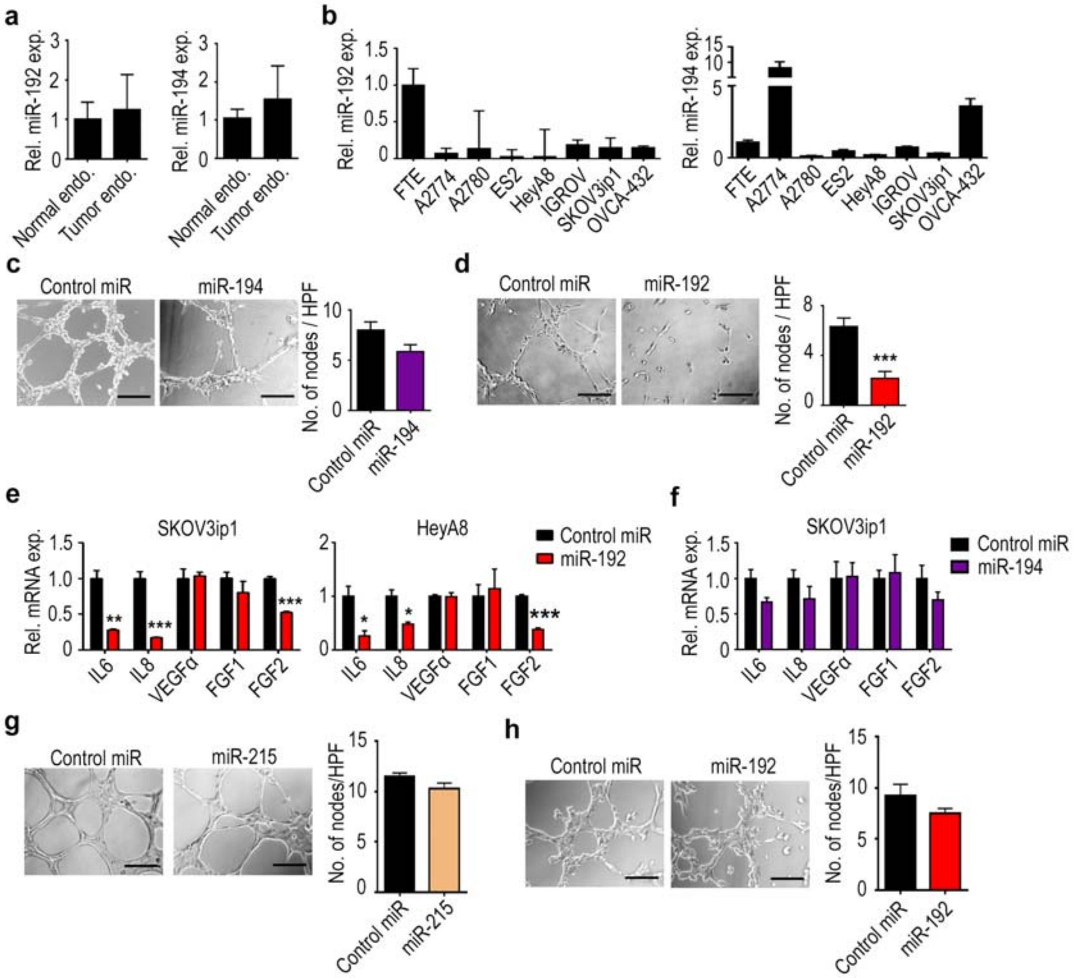
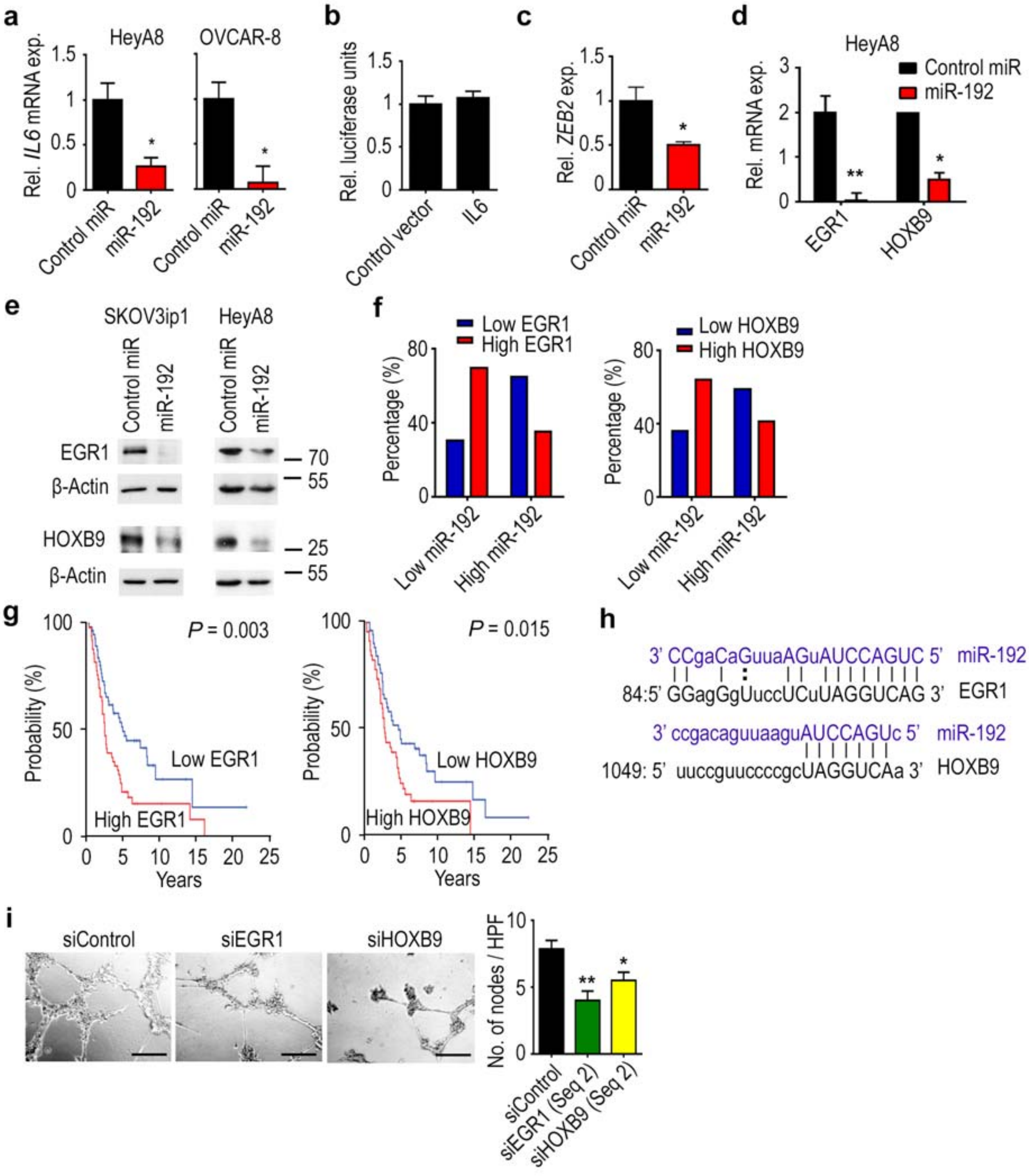
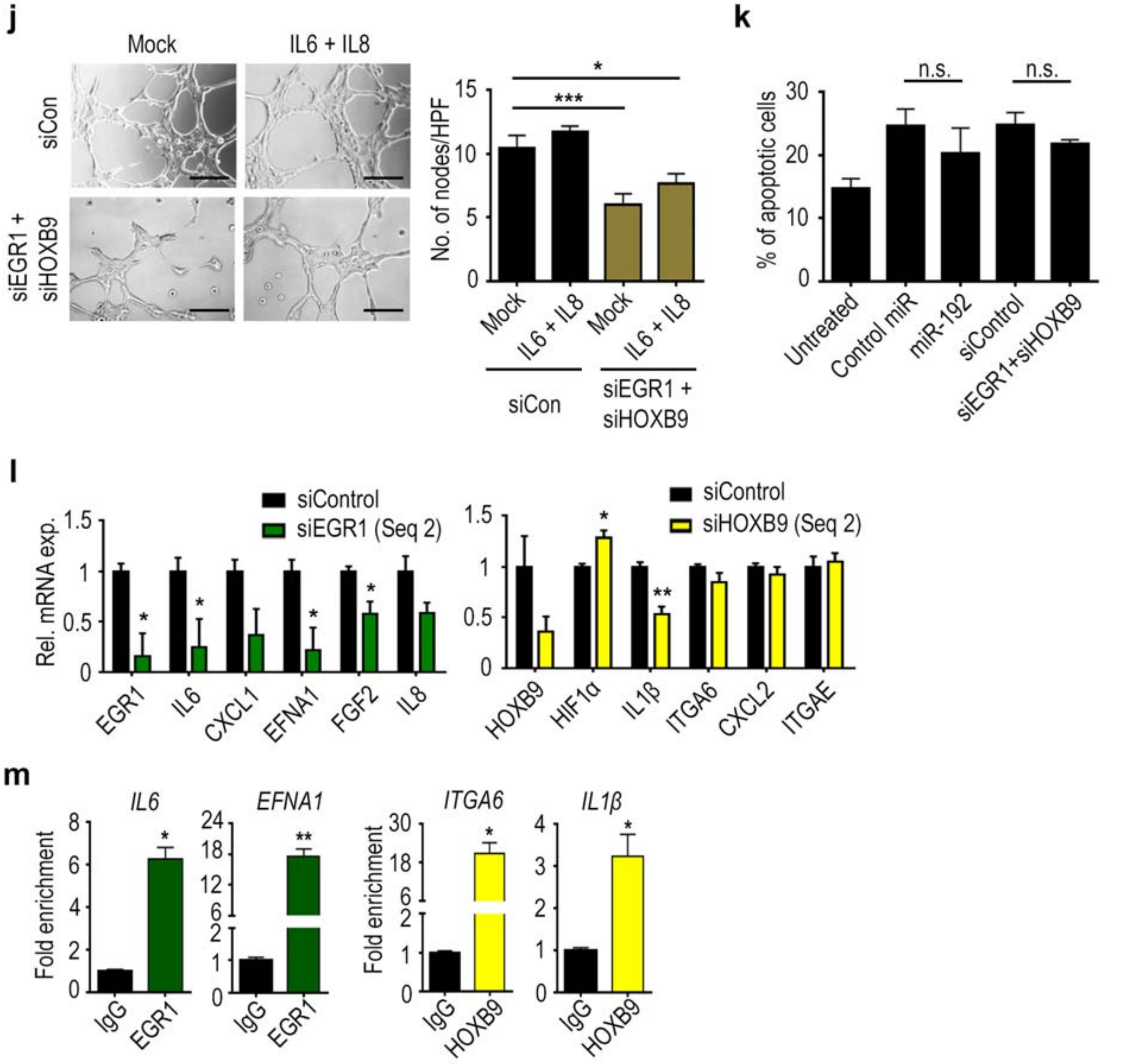
Supplementary Figures



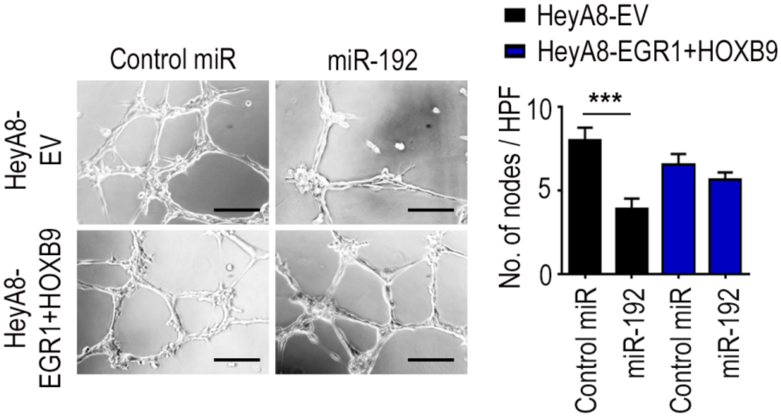
Supplementary Figure 1. The effects of miR-192 and miR-194 on angiogenesis. (**a**) The expression of miR-192 and miR-194 in endothelial cells isolated from normal ovary (n=3) or ovarian tumors (n=3). (**b**) Expression of miR-192 and miR-194 in a panel of ovarian cancer cells. Fallopian tube epithelial (FTE) cells were used as a control. (**c**) Tube formation potential of RF24 cells was assessed after exposure to conditioned media collected from SKOV3ip1 cells treated with control miRNA or miR-194 (48 hrs post transfection). Tube formation was assessed 6 hrs post incubation (n=5). (**d**) The effect of miR-192 on tube formation potential. RF24 cells were exposed to conditioned media collected from HeyA8 cells treated with control miRNA or miR-192 (48 hrs post transfection, n=5, student *t*-test). (**e**) mRNA levels of several important angiogenic factors following control miRNA or miR-192 transfection in SKOV3ip1 or HeyA8 cells (n=3, student *t*-test). (**f**) mRNA levels of angiogenic factors following control miRNA or miR-194 transfection in SKOV3ip1 cells (n=3). (**g**) The effect of miR-215 on tube formation potential. RF24 cells were exposed to conditioned media collected from SKOV3ip1 cells treated with control miRNA or miR-215 (n=5). (**h**) Tube formation potential of RF24-Control miR and RF24-miR-192 stable expressing cells (n=5). Scale bar, 100 μm. All bars and error bars represent mean values and the corresponding SEMs. (*, *P*<0.05; **, *P*<0.01; and ***, *P*<0.001).


a
HeyA8
OVCAR-8
Rel. IL6 mRNA exp.
1.5
1
0.5
0
*
*
Control miR
miR-192
Control miR
miR-192
b
Rel. luciferase units
1.5
1
0.5
0
Control vector
IL6
c
Rel. ZEB2 exp.
1.5
1
0.5
0
*
Control miR
miR-192
d
HeyA8
Control miR
miR-192
Rel. mRNA exp.
3
2
1
0
**
*
EGR1
HOXB9
e
SKOV3ip1
HeyA8
Control miR
miR-192
Control miR
miR-192
EGR1
β-Actin
HOXB9
β-Actin
70
55
25
55
f
Low EGR1
High EGR1
Percentage (%)
80
40
0
Low miR-192
High miR-192
Low HOXB9
High HOXB9
Percentage (%)
80
40
0
Low miR-192
High miR-192
g
P = 0.003
Probability (%)
100
50
0
Low EGR1
High EGR1
0
5
10
15
20
25
Years
P = 0.015
Probability (%)
100
50
0
Low HOXB9
High HOXB9
0
5
10
15
20
25
Years
h
3' CCgaCaGuuaAGuAUCCAGUC 5' miR-192
84:5' GGagGgUuccUCuUAGGUCAG 3' EGR1
3' ccgacaguuaaguAUCCAGUc 5' miR-192
1049: 5' uuccguuccccgcUAGGUCAa 3' HOXB9
i
siControl
siEGR1
siHOXB9
No. of nodes / HPF
10
5
0
**
*
siControl
siEGR1 (Seq 2)
siHOXB9 (Seq 2)

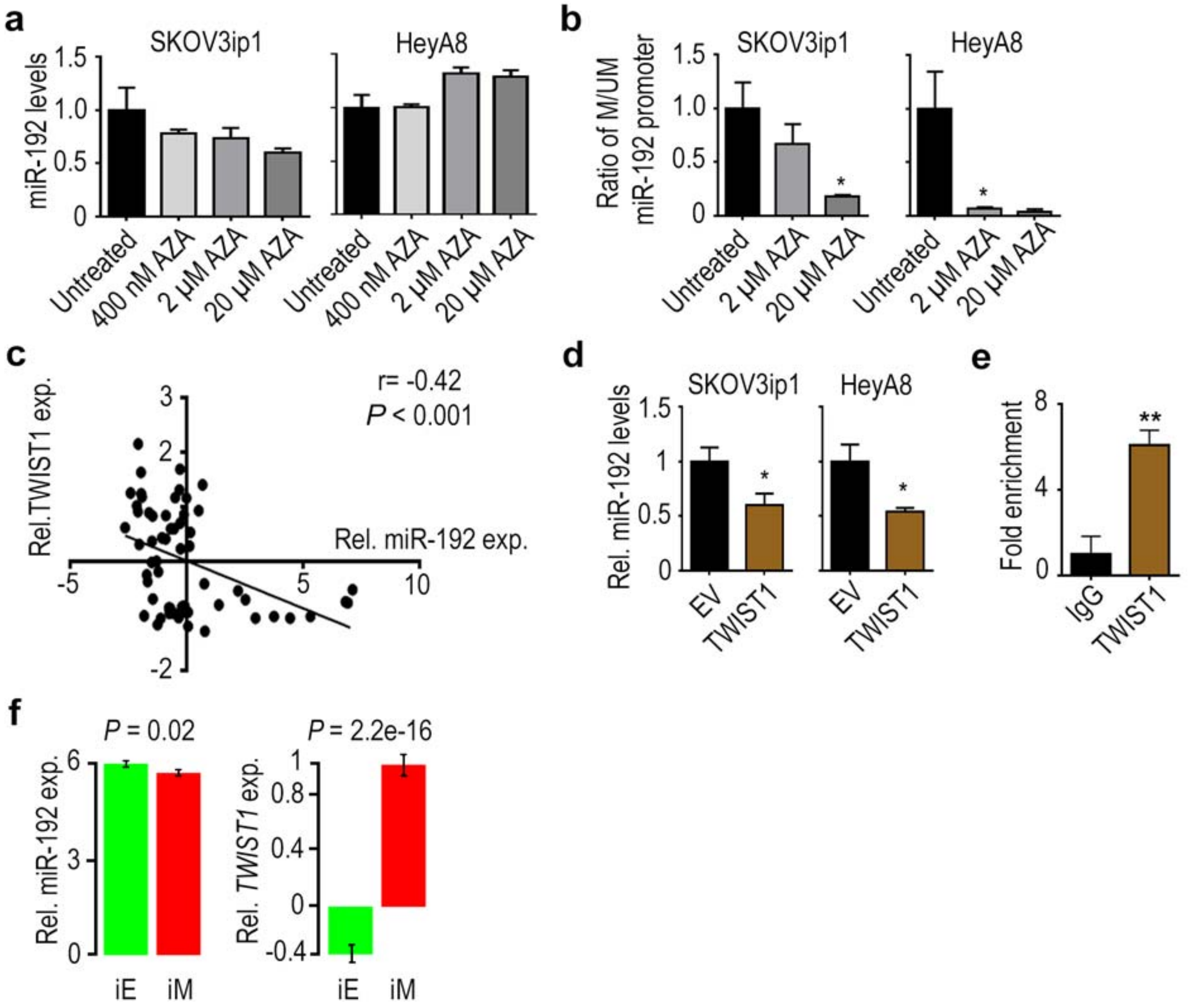


Supplementary Figure 2. The mechanism by which miR-192 mediates its broad anti-angiogenic function. (**a**) The effect of miR-192 on *IL6* level in HeyA8 and OVCAR-8 cells. mRNA levels were assessed at 48 hrs post-transfection (n=3, student *t*-test). (**b**) Relative luciferase activity normalized to empty control for *IL6* 3'-UTR. SKOV3ip1 cells were transfected with miR-192 and UTR luciferase constructs and luciferase assay was performed at 24 hrs post transfection (n=5, student *t*-test). (**c**) Effect of miR-192 treatment on *ZEB2* expression in SKOV3ip1 cells. mRNA levels were assessed at 48 hrs post transfection (n=3, student *t*-test). (**d**) Effect of miR-192 on EGR1 and HOXB9 mRNA levels in HeyA8 cells at 24 hrs post-transfection (n=3, student *t*-test). (**e**) Effect of miR-192 on EGR1 and HOXB9 protein levels at 48 hrs post-transfection in SKOV3ip1 and HeyA8 cells. (**f**) Correlation between miR-192 expression and EGR1 and HOXB9 protein levels in human ovarian epithelial tumors. Tumors were dichotomized into high vs. low

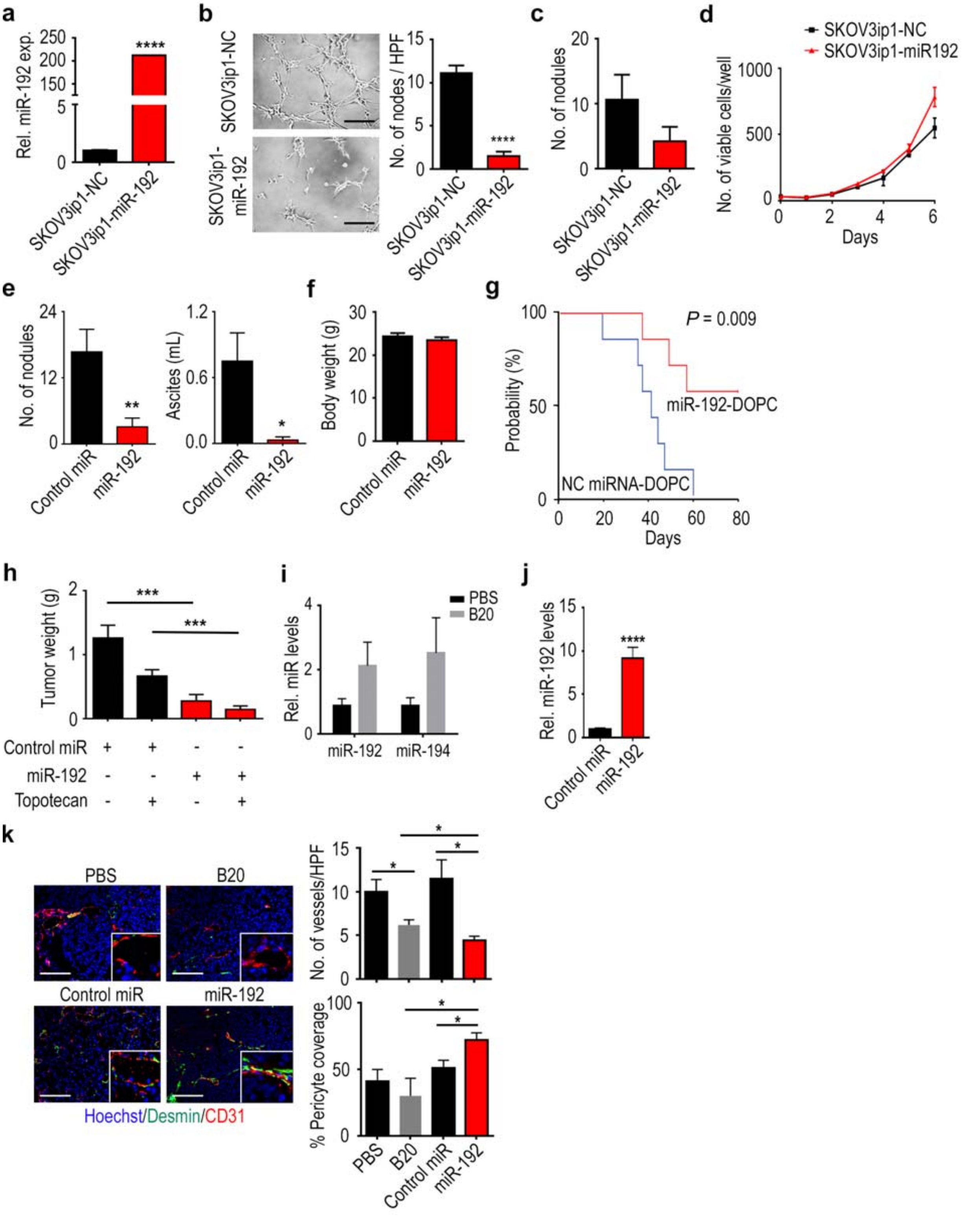
EGR1 or HOXB9 expression groups and the percentages of patients in each of these groups were assessed in tumors with high *vs.* low miR-192 expression (n=98, Chi-square test). (**g**) The impact of tumoral EGR1 or HOXB9 protein expression on overall survival in ovarian cancer patients (n=98, log-rank test). (**h**) Predicted miR-192 binding sites for *EGR1* and *HOXB9*. (**i**) Tube formation potential was assessed in RF24 cells after exposing to conditioned media collected from HeyA8 cells treated with siEGR1 or siHOXB9 (48 hrs post-transfection, n=5, student *t*-test). (**j**) Tube formation assay in RF24 cells following incubation with conditioned media collected from SKOV3ip1 cells treated with control siRNA or siEGR1+siHOXB9 (48 hrs post- transfection). The assay was performed in the presence or absence of IL-6 (8,000 pg/mL) and IL-8 (13,000 pg/mL). Bar graph shows the quantitative analyses of the number of nodes per HPF (n=5, student *t*-test). (**k**) The effect of miR-192 and siEGR1+siHOXB9 treatments on the survival of RF24 cells. RF24 cells were exposed to conditioned media collected from SKOV3ip1 cells treated with miR-192 or siEGR1+siHOXB9 (48 hrs post- treatment). After 6 hrs of exposure, the number of apoptotic cells was assessed *via* Annexin V and propidium iodide staining (n=3, student *t*-test). (**l**) Effect of EGR1 or HOXB9 silencing on levels of angiogenic factors in HeyA8 cells. RNA was isolated at 48 hours post transfection (n=3, student *t*-test). (**m**) Binding of EGR1 or HOXB9 to the promoter regions of *IL6*, *EFNA1*, *ITGA6*, or *IL1β* in SKOV3ip1 cells (n=2, student *t*-test). Scale bar, 100 μm. All bars and error bars represent mean values and the corresponding SEMs (*, $P<0.05$; **, $P<0.01$; and ***, $P<0.001$).

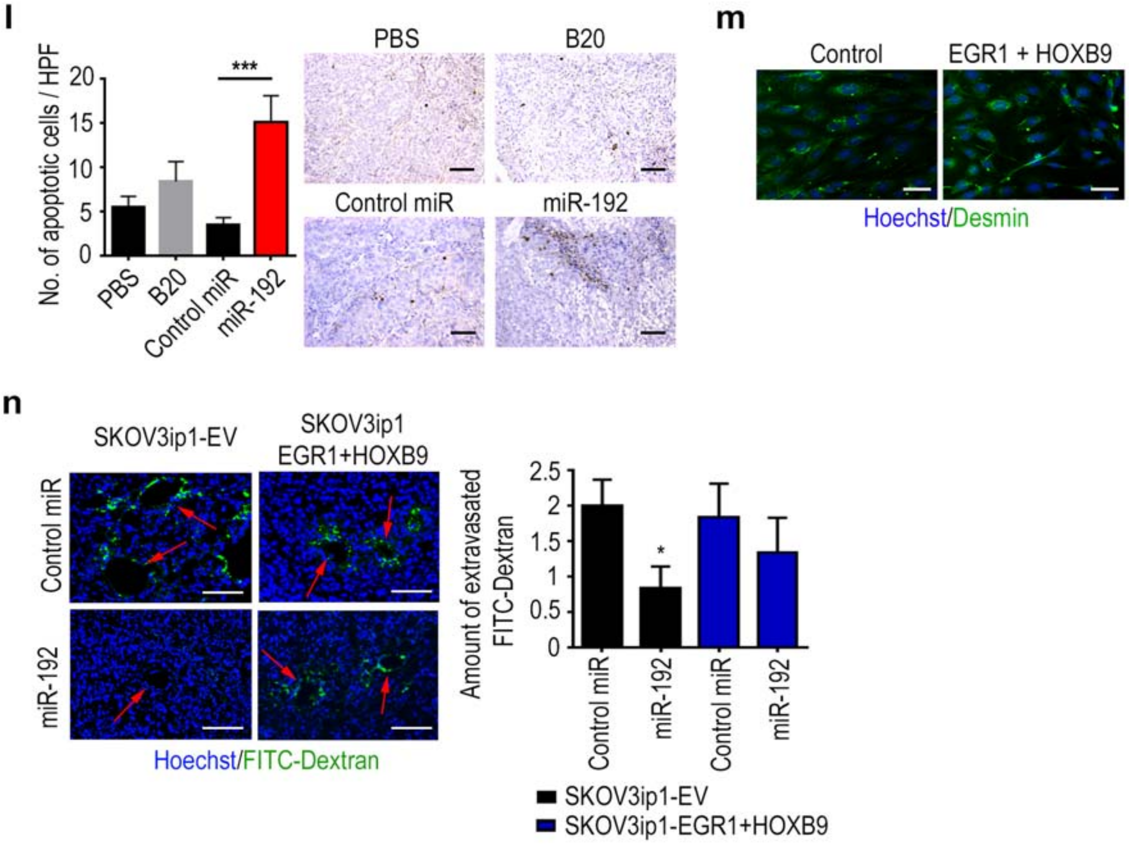


Supplementary Figure 3. The role of EGR1 and HOXB9 in mediating the anti-angiogenic effect of miR-192. RF24 cells were incubated with conditioned media collected from control miRNA or miR-192 treated HeyA8-EV or HeyA8-EGR1+HOXB9 cells (48 hrs post-transfection). Tube formation potential was assessed at 6 hrs post-incubation (n=5, student *t*-test). Scale bar, 100 µm. Bars and error bars represent mean values and the corresponding SEMs (***, *P*<0.001).



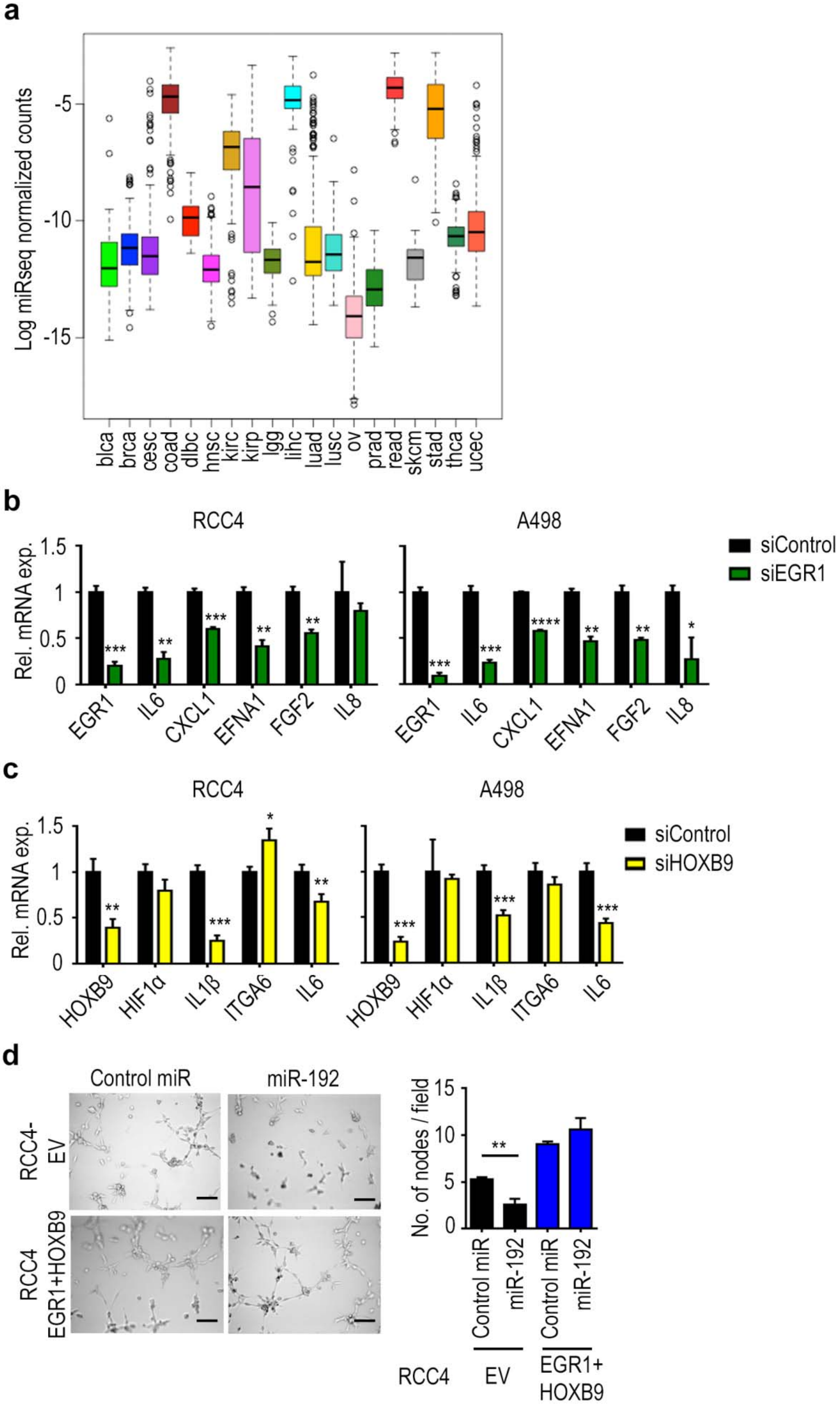
Supplementary Figure 4. Upstream regulation of miR-192. (**a**) MiR-192 expression level at 72 hrs following azacitidine (AZA) treatment in SKOV3ip1 and HeyA8 cells. (**b**) The effect of azacitidine on the ratios of methylated (M) / unmethylated (UM) miR-192 promoter levels (n=3, student *t*-test). (**c**) Correlation between miR-192 and *TWIST1* expression in NCI-60 cell line database (*P*<0.001, Spearman correlation test). (**d**) Effect of TWIST1 expression on miR-192 levels in SKOV3ip1 and HeyA8 cells. Empty vector transfected cells were used as the control (n=3, student *t*-test). (**e**) Binding of TWIST1 to the promoter regions of miR-192 in OVCA-432 high-grade serous ovarian cancer cells (n=2, student *t*-test). (**f**) Relative TWIST1 and miR-192 expression in integrative epithelial (iE) *vs.* integrative mesenchymal (iM) subtype of ovarian tumors (n=459, Wilcoxon rank-sum test). All bars and error bars represent mean values and the corresponding SEMs (*, *P*<0.05; **, *P*<0.01).


a
Rel. miR-192 exp.
250
200
150
5
0
****
SKOV3ip1-NC
SKOV3ip1-miR-192
b
SKOV3ip1-NC
SKOV3ip1-miR-192
No. of nodes / HPF
15
10
5
0
****
SKOV3ip1-NC
SKOV3ip1-miR-192
c
No. of nodules
20
10
0
SKOV3ip1-NC
SKOV3ip1-miR-192
d
SKOV3ip1-NC
SKOV3ip1-miR192
No. of viable cells/well
1000
500
0
0
2
4
6
Days
e
No. of nodules
24
12
0
**
Control miR
miR-192
Ascites (mL)
1.2
0.6
0.0
*
Control miR
miR-192
f
Body weight (g)
30
20
10
0
Control miR
miR-192
g
Probability (%)
100
50
0
P = 0.009
miR-192-DOPC
NC miRNA-DOPC
0
20
40
60
80
Days
h
Tumor weight (g)
2
1
0
***
***
Control miR + + - -
miR-192 - - + +
Topotecan - + - +
i
PBS
B20
Rel. miR levels
4
2
0
miR-192
miR-194
j
Rel. miR-192 levels
15
10
5
0
****
Control miR
miR-192
k
PBS
B20
Control miR
miR-192
Hoechst/Desmin/CD31
No. of vessels/HPF
15
10
5
0
*
*
*
% Pericyte coverage
100
50
0
*
*
PBS
B20
Control miR
miR-192

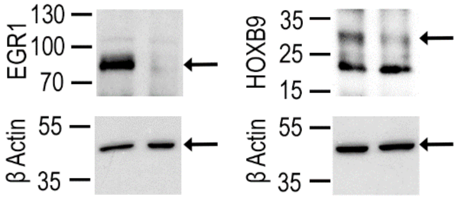


Supplementary Figure 5. *In vivo* effects of miR-192 in mouse models of ovarian cancer. (**a**) Expression of miR-192 in SKOV3ip1-NC and SKOV3ip1-miR-192 cells (n=3, student *t*-test). (**b**) Tube formation potential of RF24 cells treated with conditioned media collected from SKOV3ip1-NC and SKOV3ip1-miR-192 cells (n=5, student *t*-test). Both cell lines were seeded at 300,000 cells per well and conditioned media was collected at 48 hrs post seeding. Scale bar, 100 µm. (**c**) Number of tumor nodules in mice bearing SKOV3ip1-NC or SKOV3ip1-miR-192 tumors. (**d**) The effect of miR-192 expression on growth of SKOV3ip1 cells *in vitro* (n=3). (**e**) The effect of miR-192-DOPC therapy on the number of tumor nodules and volume of ascites in SKOV3ip1 tumor bearing mice (n=10, student *t*-test). (**f**) The effects of miR-192-DOPC therapy on mouse body weight (n=10). (**g**) The impact of miR-192-DOPC treatment on survival in mice. Mice bearing SKOV3ip1 tumors were treated with control miRNA-DOPC or miR-192-DOPC twice weekly. A Kaplan Meier curve was used to analyze the survival difference between control and treatment groups (n=7, log-rank test). (**h**) The effect of miR-192-DOPC on tumor burden in mice bearing SKOV3ip1 tumors treated with control miRNA-DOPC, miR-192-DOPC, and/or topotecan (n=10, student *t*-test). The effect of (**i**) B20 or (**j**) miR-192-DOPC treatment on tumoral miR-192 and/or miR-194 expression (n=5, student *t*-test). The impact of B20 and miR-192-DOPC treatment on (**k**) MVD and vessel pericyte coverage and (**l**) tumor cell apoptosis (n=5, student *t*-test). (**m**) The effect of EGR1 and HOXB9 expression on desmin levels in pericyte-like 10T1/2 cells. 10T1/2 cells were exposed to conditioned media collected from control or EGR1+HOXB9 expressing SKOV3ip1 cells for 48 hrs and desmin expression was assessed *via* immunofluorescence. (**n**)

Representative images of Hoechst 33342 (blue) and FITC-dextran (green) in SKOV3ip1-EV and EGR1+HOXB9 tumors (n=3, student *t*-test). 0 points, no staining; 1 point, focal or <25%; 2 points, 25–50%, 3 points, 50-75%, and 4 points, 75-100% FITC-dextran. Red arrows indicate the location of blood vessels. Scale bar, 50 µm. All bars and error bars represent mean values and the corresponding SEMs (*, *P*<0.05; **, *P*<0.01; ***, *P*<0.001; and ****, *P*<0.0001).


a
Log miRseq normalized counts
-5
-10
-15
blca
brca
cesc
coad
dlbc
hnsc
kirc
kirp
lgg
lihc
luad
lusc
ov
prad
read
skcm
stad
thca
ucec
b
RCC4
A498
siControl
siEGR1
Rel. mRNA exp.
1.5
1
0.5
0
***
**
***
**
**
***
***
****
**
**
*
EGR1
IL6
CXCL1
EFNA1
FGF2
IL8
c
RCC4
A498
siControl
siHOXB9
Rel. mRNA exp.
1.5
1
0.5
0
**
***
*
**
***
***
***
HOXB9
HIF1α
IL1β
ITGA6
IL6
d
Control miR
miR-192
RCC4-EV
RCC4 EGR1+HOXB9
No. of nodes / field
15
10
5
0
**
Control miR
miR-192
RCC4
EV
EGR1+ HOXB9

Supplementary Figure 6. The expression and functional effect of miR-192 in renal tumors. (**a**) The expression of miR-192 in tumors across 19 cancer types in TCGA databases. The horizontal lines represent the median normalized expression levels. The bottom and the top lines in each individual box represent the first and the third quartile expression levels, respectively. Bladder urothelial carcinoma, BLCA; Breast invasive carcinoma, BRCA; Cervical squamous cell carcinoma and endocervical adenocarcinoma, CESC; Colon adenocarcinoma, COAD; Lymphoid neoplasm diffuse large B-cell lymphoma, DLBC; Head and neck squamous cell carcinoma, HNSC; Kidney renal clear cell carcinoma, KIRC; Kidney renal papillary cell carcinoma, KIRP; Brain lower grade glioma, LGG; Liver hepatocellular carcinoma, LIHC; Lung adenocarcinoma, LUAD; Lung squamous cell carcinoma, LUSC; Ovarian serous cystadenocarcinoma, OV; Prostate adenocarcinoma, PRAD; Rectum adenocarcinoma, READ; Skin Cutaneous Melanoma, SKCM; Stomach adenocarcinoma, STAD; Thyroid carcinoma, THCA; Uterine corpus endometrial carcinoma, UCEC. The levels of angiogenic factors at 48 hrs following (**b**) siEGR1 and (**c**) siHOXB9 treatment in RCC4 and A498 cells (n=3, student *t*-test). (**d**) Tube formation potential of RF24 cells following incubation with conditioned media collected from control miRNA or miR-192 treated RCC4-EV or RCC4-EGR1+HOXB9 cells. Bar graph (right) shows the quantitative analyses of number of nodes per field (n=5, student *t*-test). Scale bar, 100 μm. All bars and error bars represent mean values and the corresponding SEMs (*, $P<0.05$; **, $P<0.01$; ***, $P<0.001$; and ****, $P<0.0001$).



Supplementary Fig. 7. Full scans of Western blots. Full scans of blots from Supplementary Figure 2e.

Supplementary Tables

Supplementary Table 1. Correlation between miRNA levels and angiogenic scores in HGSC tumors (Spearman correlation tests).

	Correlation coefficient (with angiogenic scores)	***P*-values**
miR-96	-0.2	<0.0001
miR-181c	-0.07	0.0873
miR-182	-0.13	0.0018
miR-191	-0.09	0.0319
miR-192	-0.24	<0.0001
miR-194	-0.17	<0.0001
miR-200b	-0.18	<0.0001
miR-205	0.01	0.7908
miR-522	0.02	0.6511
miR-663	0.02	0.7103

Supplementary Table 2. Correlation of clinical and pathological features with miR-192 levels in 128 patients with invasive epithelial ovarian carcinoma.

Variable		**miR-192 Expression**		***P* value**	**Statistical Tests**
		Low (N=40)	**High (N=88)**		
Tumor grade – no. (%)	Low High	2 38	6 82	0.69	Chi-square test
Tumor stage – no. (%)	I or II III or IV	5 35	14 74	0.62	Chi-square test
Histology – no. (%)	Serous Others	36 4	78 10	0.82	Chi-square test
Cytoreduction – no. (%)	Optimal Suboptimal	19 21	43 45	0.89	Chi-square test
Median OS (Yrs.)		3.86	6.85	0.001	Log-rank test
Microvessel density		106.1	34.6	<0.0001	Student *t*-test

Supplementary Table 3. Top pathways affected by miR-192. Pathway analysis of genes that are negatively associated with miR-192 expression in TCGA ovarian dataset (*P* values were generated using the Fisher Exact Test).

Pathway	**No. of molecules**	***P* values**
Integrin signaling pathway	49	<0.001
Angiogenesis	38	0.004
Notch signaling pathway	12	0.017
Alzheimer disease-presenilin pathway	22	0.048
Wnt signaling pathway	46	0.067
Cadherin signaling pathway	24	0.085

Supplementary Table 4. Transcription factors predicted to be targeted by miR-192.

Transcription Factor	**Number of predicted angiogenic factors**
ZNF263	18
ZBTB7	17
PLAG1	16
STAT3	14
WT1	14
EGR1	11
TAL1_E2A	11
E2F3	8
GLIS2	8
TEAD	7
HOXB9	6
ZNF217	5
CRX	5

Supplementary Table 5. Correlations between promoter methylation and miR-192 expression levels in TCGA databases. Spearman correlation analysis was used to generate *P* values.

Cancer Types		**Methylation Probe**			
		MiR192-cg02258444-11-64658622	MiR192-cg09349409-11-64658765	MiR192-cg18262830-11-64658819	MiR192-cg27083891-11-64658726
BLCA	**Correlation**	-0.077	-0.112	-0.164	0.031
	***P* values**	0.131	0.029	0.001	0.546
BRCA	**Correlation**	-0.031	0.018	0.231	0.001
	***P* values**	0.432	0.651	<0.0005	0.974
CESC	**Correlation**	-0.093	-0.245	-0.236	0.027
	***P* values**	0.135	<0.0005	<0.0005	0.662
COAD	**Correlation**	-0.594	-0.563	-0.546	-0.576
	***P* values**	<0.0005	<0.0005	<0.0005	<0.0005
DLBC	**Correlation**	0.106	0.012	0.124	-0.051
	***P* values**	0.478	0.934	0.404	0.732
HNSC	**Correlation**	0.225	0.236	0.258	0.188
	***P* values**	<0.0005	<0.0005	<0.0005	<0.0005
KIRC	**Correlation**	-0.627	-0.613	-0.573	-0.612
	***P* values**	<0.0005	<0.0005	<0.0005	<0.0005
KIRP	**Correlation**	-0.84	0.764	-0.702	-0.764
	***P* values**	<0.0005	<0.0005	<0.0005	<0.0005
LGG	**Correlation**	0.031	0.039	0.16	0.121
	***P* values**	0.477	0.377	<0.0005	0.005
LIHC	**Correlation**	-0.652	-0.621	-0.556	-0.642
	***P* values**	<0.0005	<0.0005	<0.0005	<0.0005
LUAD	**Correlation**	-0.39	-0.396	-0.364	-0.369
	***P* values**	<0.0005	<0.0005	<0.0005	<0.0005
LUSC	**Correlation**	0.164	0.127	0.021	0.221
	***P* values**	0.003	0.02	0.699	<0.0005
PRAD	**Correlation**	-0.084	-0.109	0.143	0.123
	***P* values**	0.073	0.02	0.002	0.009
READ	**Correlation**	-0.599	-0.605	-0.57	-0.631
	***P* values**	<0.0005	<0.0005	<0.0005	<0.0005
SKCM	**Correlation**	-0.039	0.064	0.056	0.094
	***P* values**	0.418	0.179	0.242	0.049
STAD	**Correlation**	-0.63	-0.585	-0.553	-0.635
	***P* values**	<0.0005	<0.0005	<0.0005	<0.0005
THCA	**Correlation**	-0.101	-0.013	-0.032	-0.05
	***P* values**	0.016	0.753	0.455	0.232
UCEC	**Correlation**	-0.124	-0.144	-0.07	-0.126
	***P* values**	0.009	0.003	0.146	0.008

Bladder urothelial carcinoma, BLCA; Breast invasive carcinoma, BRCA; Cervical squamous cell carcinoma and endocervical adenocarcinoma, CESC; Colon adenocarcinoma, COAD; Lymphoid neoplasm diffuse large B-cell lymphoma, DLBC; Head and neck squamous cell carcinoma, HNSC; Kidney renal clear cell carcinoma, KIRC; Kidney renal papillary cell carcinoma, KIRP; Brain lower grade glioma, LGG; Liver hepatocellular carcinoma, LIHC; Lung adenocarcinoma, LUAD; Lung squamous cell carcinoma, LUSC; Ovarian serous cystadenocarcinoma, OV; Prostate adenocarcinoma, PRAD; Rectum adenocarcinoma, READ; Skin Cutaneous Melanoma, SKCM; Stomach adenocarcinoma, STAD; Thyroid carcinoma, THCA; Uterine corpus endometrial carcinoma, UCEC.

Supplementary Table 6. The list of samples used for miRNA-angiogenic factor correlation analyses.

TCGA-04-1331	TCGA-04-1649	TCGA-09-2054	TCGA-13-0765	TCGA-13-0903
TCGA-04-1332	TCGA-04-1651	TCGA-09-2055	TCGA-13-0766	TCGA-13-0904
TCGA-04-1335	TCGA-04-1652	TCGA-09-2056	TCGA-13-0768	TCGA-13-0905
TCGA-04-1336	TCGA-04-1654	TCGA-10-0925	TCGA-13-0791	TCGA-13-0906
TCGA-04-1337	TCGA-04-1655	TCGA-10-0926	TCGA-13-0792	TCGA-13-0908
TCGA-04-1338	TCGA-09-0364	TCGA-10-0927	TCGA-13-0793	TCGA-13-0910
TCGA-04-1342	TCGA-09-0365	TCGA-10-0928	TCGA-13-0794	TCGA-13-0911
TCGA-04-1343	TCGA-09-0366	TCGA-10-0930	TCGA-13-0795	TCGA-13-0912
TCGA-04-1346	TCGA-09-0367	TCGA-10-0931	TCGA-13-0797	TCGA-13-0913
TCGA-04-1347	TCGA-09-0369	TCGA-10-0933	TCGA-13-0799	TCGA-13-0916
TCGA-04-1348	TCGA-09-1659	TCGA-10-0934	TCGA-13-0800	TCGA-13-0919
TCGA-04-1349	TCGA-09-1661	TCGA-10-0935	TCGA-13-0801	TCGA-13-0920
TCGA-04-1350	TCGA-09-1662	TCGA-10-0936	TCGA-13-0802	TCGA-13-0921
TCGA-04-1351	TCGA-09-1664	TCGA-10-0937	TCGA-13-0803	TCGA-13-0923
TCGA-04-1356	TCGA-09-1665	TCGA-10-0938	TCGA-13-0804	TCGA-13-0924
TCGA-04-1361	TCGA-09-1666	TCGA-13-0714	TCGA-13-0805	TCGA-13-1403
TCGA-04-1362	TCGA-09-1667	TCGA-13-0717	TCGA-13-0807	TCGA-13-1404
TCGA-04-1364	TCGA-09-1668	TCGA-13-0720	TCGA-13-0883	TCGA-13-1405
TCGA-04-1365	TCGA-09-1669	TCGA-13-0723	TCGA-13-0884	TCGA-13-1407
TCGA-04-1367	TCGA-09-1670	TCGA-13-0724	TCGA-13-0885	TCGA-13-1408
TCGA-04-1369	TCGA-09-1672	TCGA-13-0725	TCGA-13-0886	TCGA-13-1409
TCGA-04-1371	TCGA-09-1673	TCGA-13-0726	TCGA-13-0887	TCGA-13-1410
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TCGA-61-2614

Supplementary Table 7. List of siRNA sequences used in this study

Gene	SiRNA Sequences
siControl	5'-UUAUGCCGAUCGCGUCACA**TT**-3' 3'-**TT**AAUACGGCUAGCGCAGUGU-5'
siEGR1 (Seq 1)	5'-CCAACGACAGCAGUCCCAU**TT**-3' 3'-**TT**GGUUGCUGUCGUCAGGGUA-5'
siEGR1 (Seq 2)	5'-CAAAGAACUUGAUUUGCAU**TT**-3' 3'-**TT**GUUUCUUGAACUAAACGUA-5'
siHOXB9 (Seq 1)	5'-CUAAGAAUGUGAUGGGCCA**TT**-3' 3'-**TT**GAUUCUUACACUACCCGGU-5'
siHOXB9 (Seq 2)	5'-CUUGCCUGUUUCUUCUCUA**TT**-3' 3'-**TT**GAACGGACAAAGAAGAGAU-5'

Supplementary Table 8. Primer sequences for RT-PCR.

Gene	Primer Sequences
β-actin	5’-AGCCTCGCCTTTGCCGA-3’
	5’-CTGGTGCCTGGGGCG-3’
EGR1	5’-GTTTGGCTGGGGTAACTGGT-3’
	5’-AGCCCTACGAGCACCTGAC-3’
HOXB9	5’-TCCAGCGTCTGGTATTTGGT-3’
	5’-GAAGCGAGGACAAAGAGAGG-3’
CRX	5’-GACACTGAGGCCCAAGTCAG-3’
	5’-TGTTTCCTTCAGCCTCTGCT-3’
E2F3	5’-CTAGCTCCAGCCTTCGCTTT-3’
	5’-AGCCTCCTCTACACCACGC-3’
GLIS2	5’-TGTGCTTAAAGCGGTCACTG-3’
	5’-AACCTGAAGATCCACAACCG-3’
STAT3	5’-CTGCTCCAGGTACCGTGTGT-3’
	5’-CCTCTGCCGGAGAAACAG-3’
TEAD1	5’-CTTGAATGTGCAATGAAGCG-3’
	5’-CGAAGTTTGCCTCGGACTC-3’
WT1	5’-TTGTGTGGTTATCGCTCTCG-3’
	5’-CAAATGACATCCCAGCTTGA-3’
ZNF217	5’-TCTCTTTTGTGCCATGCTGT-3’
	5’-TTGTGTGCCTGCTGGTAGTC-3’
ZNF263	5’-CTTTCCTCCTTGTCCCACCT-3’
	5’-CACGGTGCAGGAGAGTTATG-3’

Gene	Primer Sequences
IL6	5’-GTCAGGGGTGGTTATTGCAT-3’
	5’-AGTGAGGAACAAGCCAGAGC-3’
CXCL1	5’-CTTCCTCCTCCCTTCTGGTC-3’
	5’-GAAAGCTTGCCTCAATCCTG-3’
ITGB1	5’-CAGTCCAATCCAGAAAATTGG-3’
	5’-GAGTCGCGGAACAGCAG-3’
EFNA1	5’-TCAGCTGCACATGTATGGTGT-3’
	5’-TCTCTTGGGTCTGTGCTGC-3’
ITGAV	5’-TCCAAACCACTGATGGGACT-3’
	5’-GTGACTGGTCTTCTACCCGC-3’
NRP1	5’-TTGCAGTCTCTGTCCTCCAA-3’
	5’-GAAAAATGCGAATGGCTGAT-3’
FGF2	5’-AGCCAGGTAACGGTTAGCAC-3’
	5’-GGAGAAGAGCGACCCTCAC-3’
IL8	5’-AAATTTGGGGTGGAAAGGTT-3’
	5’-TCCTGATTTCTGCAGCTCTGT-3’
HIF1α	5’-TGGCTGCATCTCGAGACTTT-3’
	5’-GAAGACATCGCGGGGAC-3’
IL1β	5’-AAGCCCTTGCTGTAGTGGTG-3’
	5’-GAAGCTGATGGCCCTAAACA-3’
ITGA6	5’-GTTGGCTCTCTGCAGTGGAA-3’
	5’-CCTCTTCGGCTTCTCGCT-3’
CXCL2	5’-GCTTCCTCCTTCCTTCTGGT-3’
	5’-GGGCAGAAAGCTTGTCTCAA-3’
ITGAE	5’-CTATGCAGAGCAGAGTGTGGA-3’
	5’-TGAGGGGAAGCTGAGTGG-3’
VEGF	5’-AGCTGCGCTGATAGACATCC-3’
	5’-CTACCTCCACCATGCCAAGT-3’
FGF1	5’-AAGGTGGTGATTTCCCCTTC-3’
	5’-TGTGGAGAGAGGTACAGCCC-3’
TWIST1	5’-TCCATTTTCTCCTTCTCTGGAA-3’
	5’-GTCCGCGTCCCACTAGC-3’
ZEB2	5'-CAATACCGTCATCCTCAGCA-3'
	5'-CCAATCCCAGGAGGAAAAAC-3'
miR-192 promoter (methylated); HeyA8	5’-ATGGGATATTTTTTAGAGTTTTGTC-3’
	5’-CTTCTTCGTAAATACTAACCCTCG-3’

Gene	**Primer Sequences**
miR-192 promoter (unmethylated); HeyA8	5’-GGGATATTTTTTAGAGTTTTGTTGA-3’
	5’-TTCTTCATAAATACTAACCCTCACC-3’
miR-192 promoter (methylated); SKOV3ip1	5’-GTTTCGGTTTTTAATTGGTTTTC-3’
	5’-CTTCTTCGTAAATACTAACCCTCG-3’
miR-192 promoter (unmethylated); SKOV3ip1	5’-GTTTTGGTTTTTAATTGGTTTTTGT-3’
	5’-CTTCTTCATAAATACTAACCCTCACC-3’
ChIP - miR-192	5’-TCACCGAGGCTTCTTATCATC
	5’-GACTTTGCCCAGGAAGGAG
ChIP - IL6	5’-GCGATGGAGTCAGAGGAAAC-3’
	5’-GGCTAGAATTTAGCGTTCCAG-3’
ChIP - EFNA1	5’-AGACCCACAAGTGAGCGAAC-3’
	5’-TGCAGGAAAGAGCGAAGC-3’
ChIP - IL1β	5’-TTTCTCAGCCTCCTACTTCTGC-3’
	5’-TTGTGCCTCGAAGAGGTTTG-3’
ChIP - ITGA6	5’-CCCACATCTGCAAGAACAGG-3’
	5’-AGCGAGGGAGACTTTACTACCC-3’
ChIP - Control	5’-TTGCCAGTGGTGCATACAG-3’
	5’-CACTTCGGGAAGGTTGTTG-3’