Supplementary informations for Additional file 2

1) Figure S1a: The promoter regions of the \textit{ICAM1}, \textit{KLF6}, and \textit{JUN} genes and the positions of Sp1, NFκB, and AP1 binding sites based on the current literature [19-21] are shown in the diagram. Black bars indicate PCR amplicon sizes for the ChIP assay. I: Input control lysate without immunoprecipitation. IgG: negative control using IgG. N and H indicate normoxia and hypoxia (1% O$_2$ for 16 h), respectively.

2) Figure S1, S2a,c, S3, S4, and S6: Cells were cultured for 16h.

3) Figure S2b, S5, S7a, and S8a: Cells were cultured for 24h.

4) Figure S2a,c, S3d,e, S4b, S5b,d, S6b, and S9a: Data shown are the mean (n = 3) ± SD.

5) Figure S1b: Data shown are the mean (n = 2) ± SD.

6) Figure S4a: α-tubulin and histone H3 were used as markers for cytoplasm and nuclei, respectively.

7) Figure S6a: Lanes were run on the same gel but were noncontiguous (separated by black line).

8) Figure S7a: Subsequently, cell blocks containing cells embedded in agarose and fixed in 10% neutral formaldehyde were prepared.

9) Figure S8b,c: Data shown are the mean (n = 3) ± SD. *$P = 0.002$; **$P = 0.03$.

10) Figure S9a: Cells were cultured under normoxia with FCS treatment, and then cell viability was determined by MTS assay.

11) Figure S9b, Tumors derived from OVISE cells transfected with shRNAs were isolated at day 27 post-cell injection.

12) Figure S10e: Data shown are the mean ± SD (N = 8). *$P < 0.0001$. 
Figure S1

a) 

b) 

OVISE

ICAM1

mRNA level (fold of control)

FCS: + - + -

H: - - - -
Figure S2

(a) 

(b) 

(c)
Figure S7

(a) 

(b) Vascular core area, Necrotic area, Necrotic area, Necrotic area

CD31, CD31, CD31, CD31

ICAM1, ICAM1, ICAM1, ICAM1
Figure S8

(a) Western blot analysis showing ICAM1 expression in OVSAVO cells with Sc#1 and ICAM1sh#1, and Sc#2 and ICAM1sh#2 under normoxia (N) and hypoxia (H) conditions.

(b) Graphs illustrating the percentage survival of Sc#1 and ICAM1sh#1, and Sc#2 and ICAM1sh#2 under normoxia and hypoxia conditions over 6, 24, 48, and 72 hours.

Figure S9

(a) Graphs showing the cell number (ordinate) over time (abscissa) for Sc#1, ICAM1sh#1, Sc#2, and ICAM1sh#2. The graphs are divided into two panels for each condition.

(b) Western blot analysis showing ICAM1 expression in tumor samples under Sc#2 and ICAM1-sh#2 conditions with β-actin as a loading control.
Figure S10

(a) pimo, HIF1, HIF2, ICAM1

(b) view 1, view 2, pimo, ICAM1

(c) pimo, HIF1, ICAM1 (mRNA)

(d) ICAM1, Scr, Ki67, CD44

(e) ICAM1, ICAM1 (mRNA)

Figure S11

(a) DAPI, CD31, Merge

(b) DAPI, ICAM1, Merge