

Supplementary informations for Additional file 2

- 1) Figure S1a: The promoter regions of the *ICAM1*, *KLF6*, and *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% O₂ 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

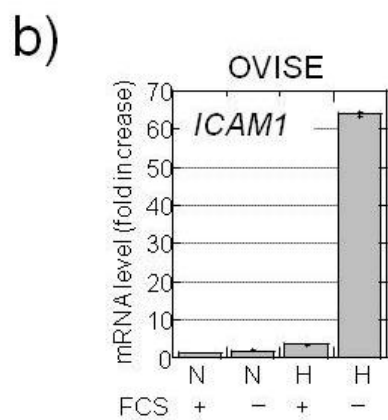
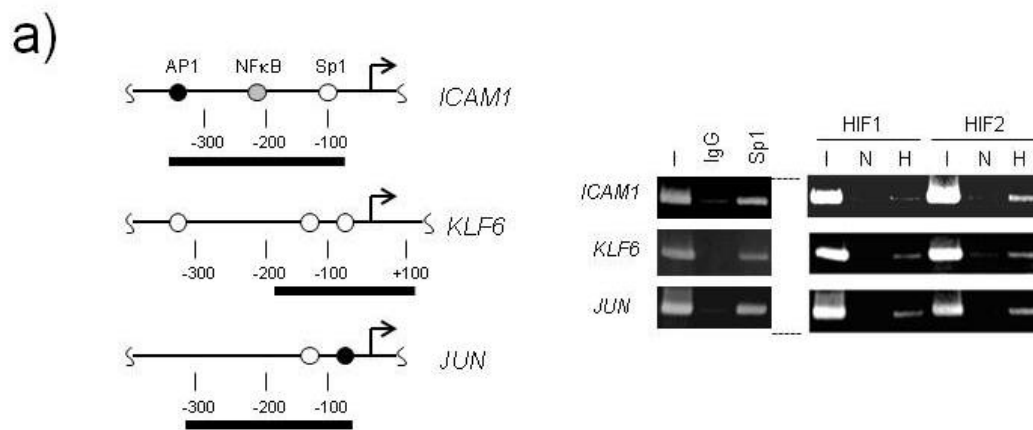


Figure S2

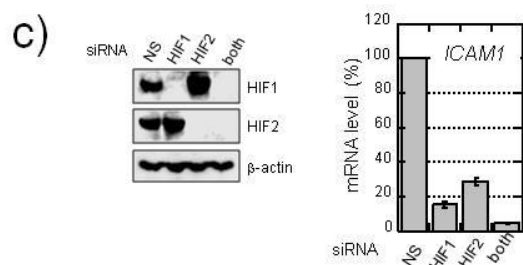
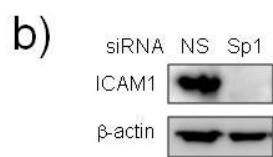
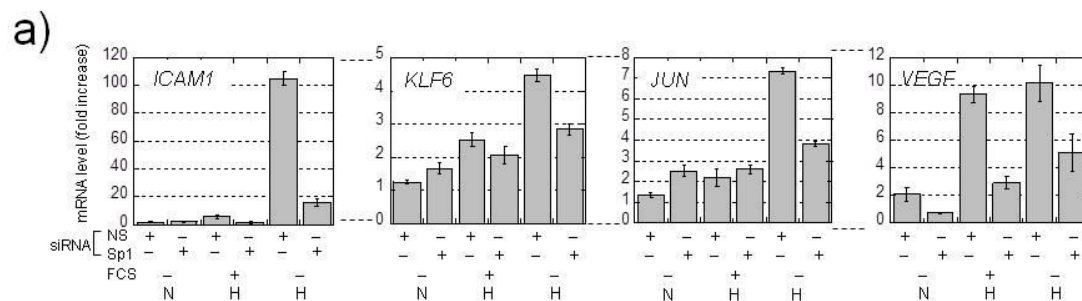


Figure S3

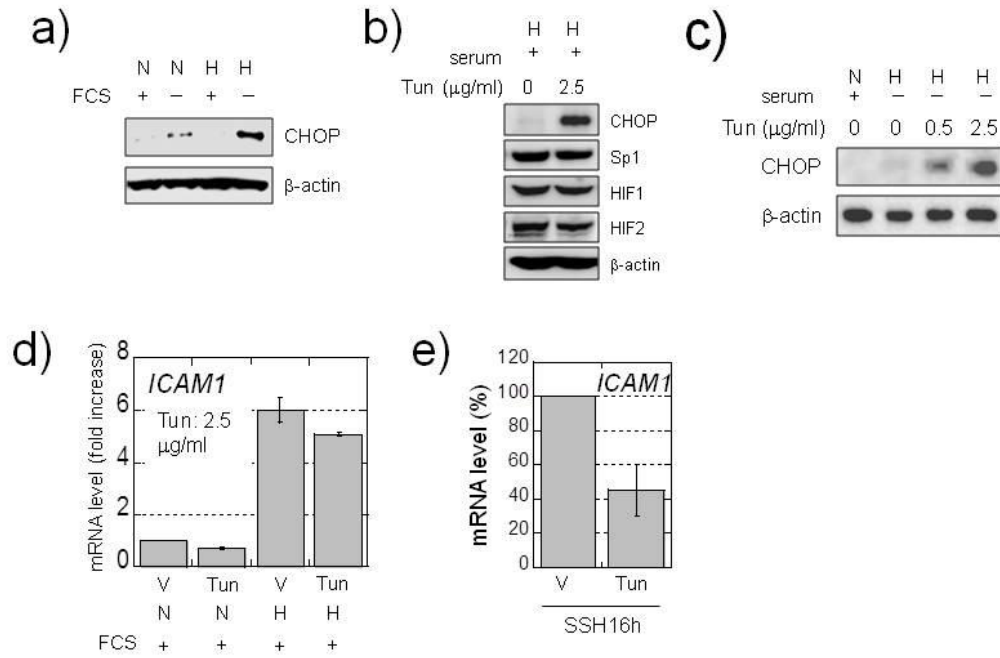


Figure S4

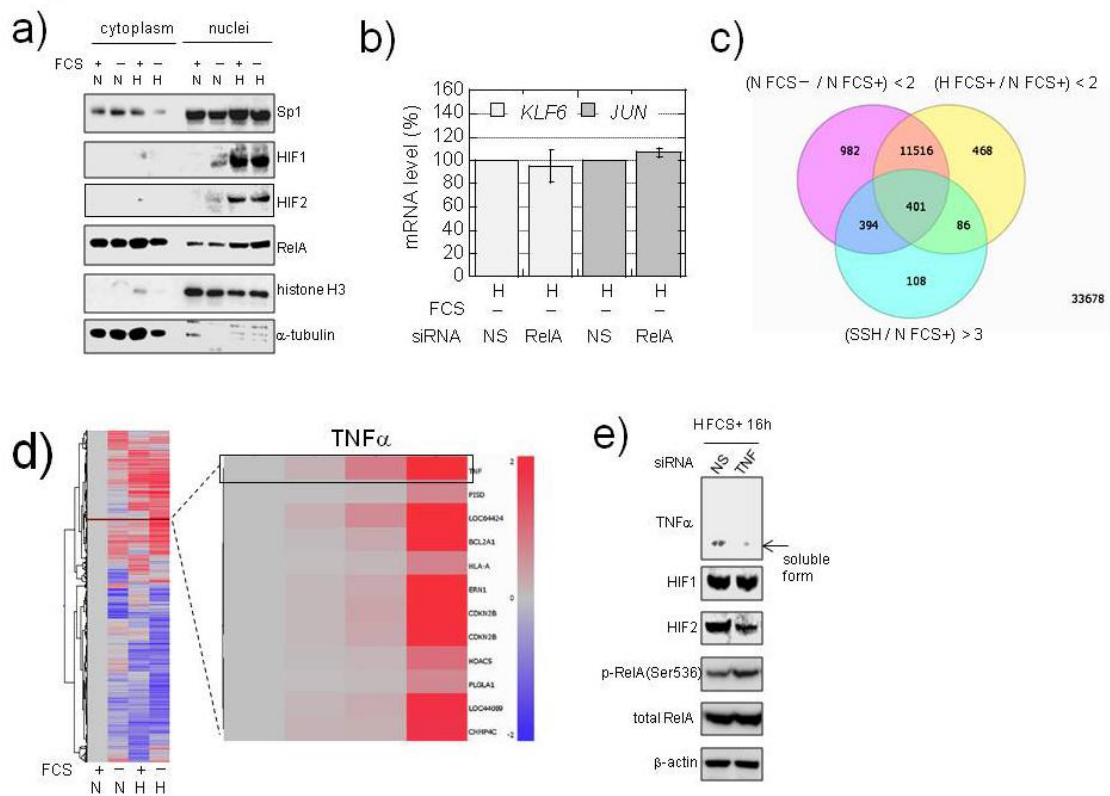


Figure S5

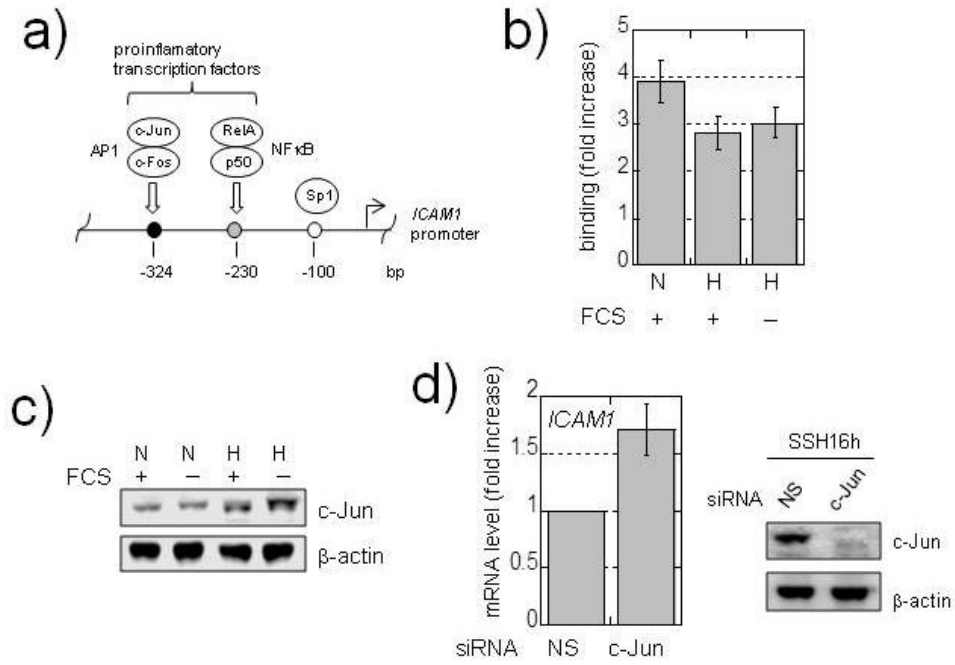


Figure S6

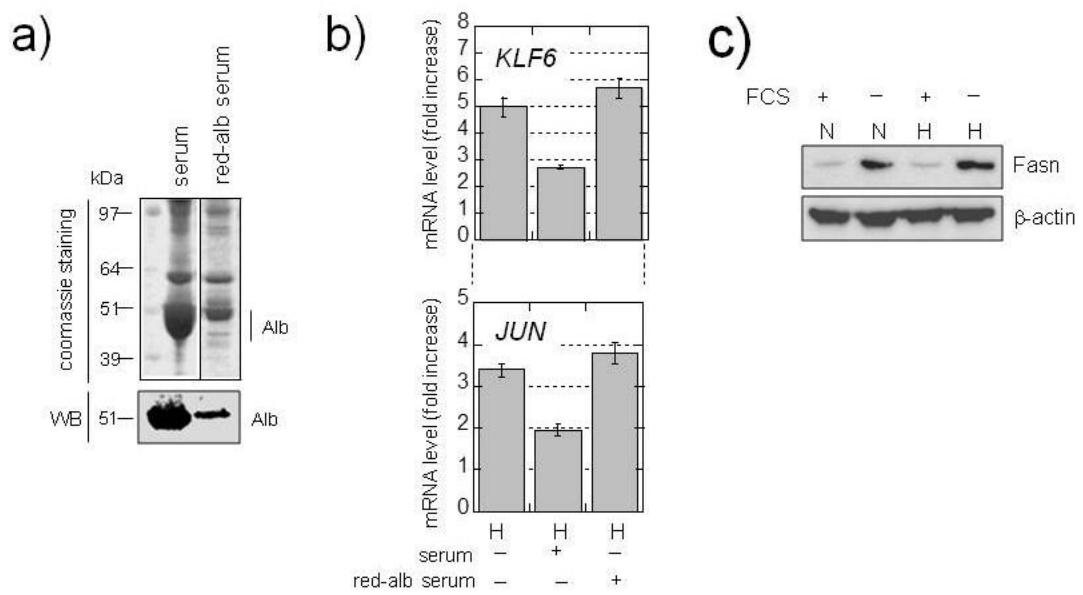


Figure S7

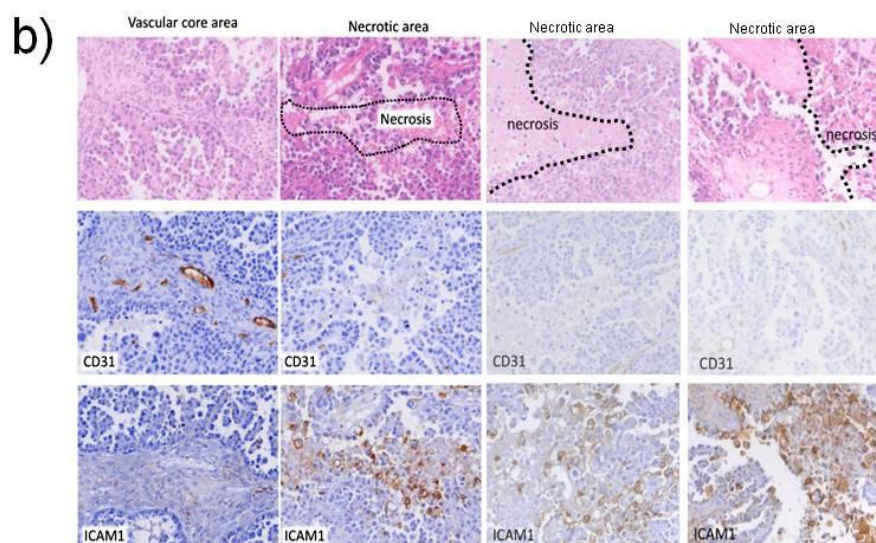
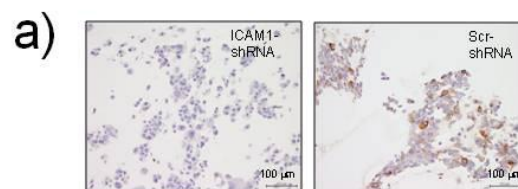


Figure S8

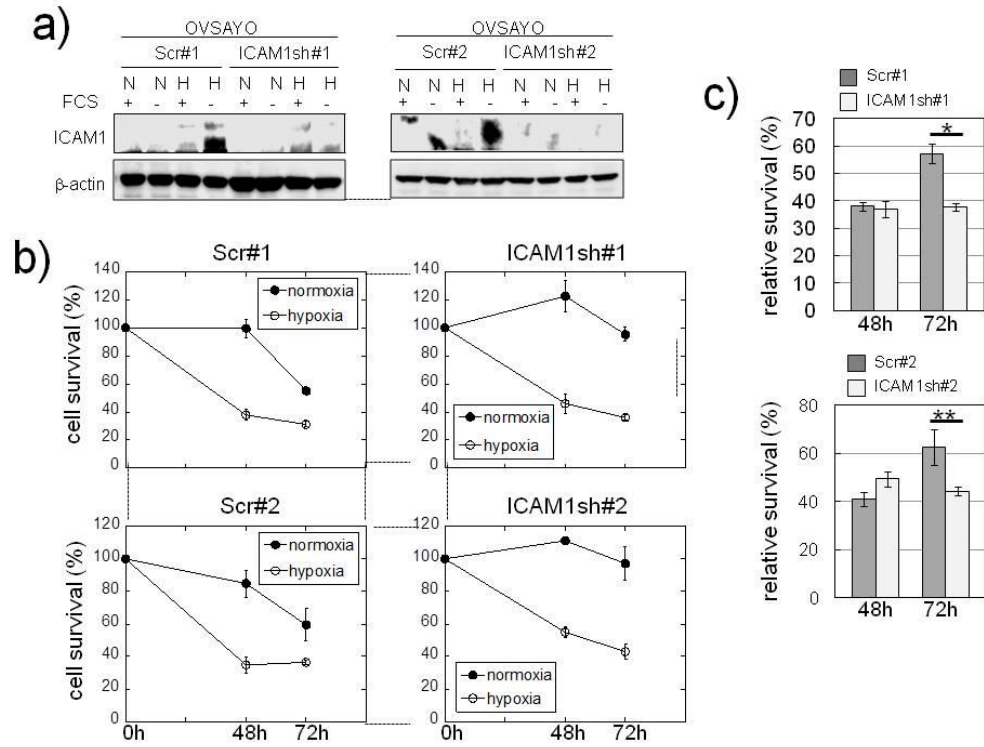


Figure S9

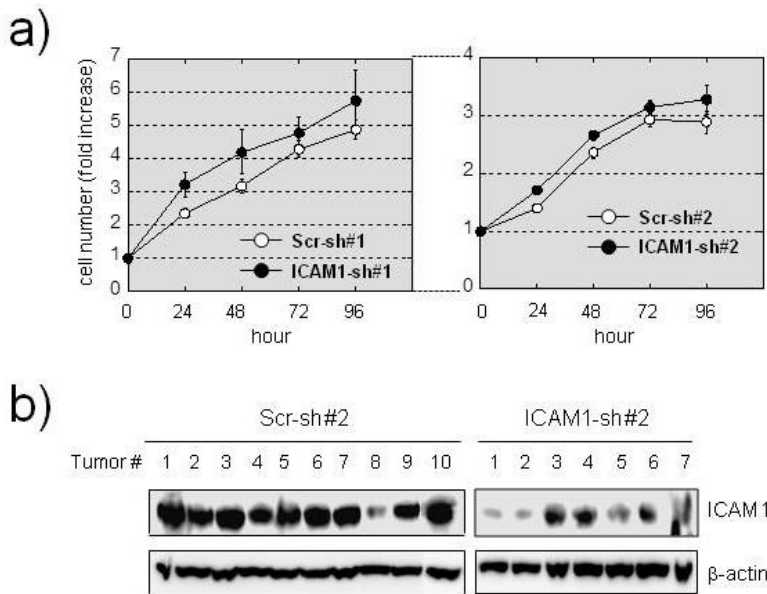


Figure S10

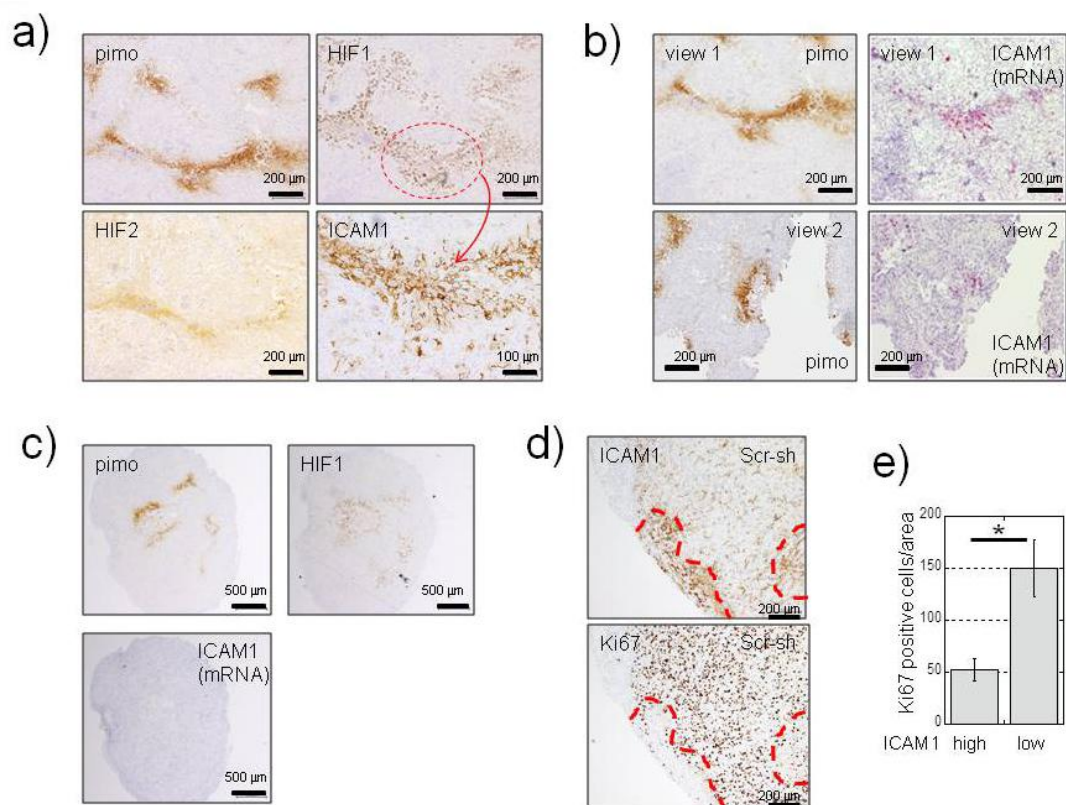


Figure S11

