

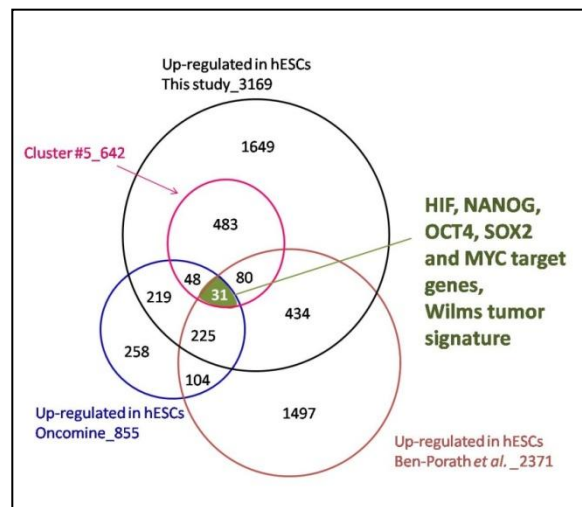
Supplemental Figure 1

A

	Oncomine Upregulated in hESC (855*)	HIF2A target gene (434*)	Combined ES genes and Nanog, Oct4, Sox2 and Myc targets (2371*) (Ben-Porath et al.,2008)	Consensus genes positively correlated with leukemic stem cell frequency (204*) (Somerville et al., 2009)
Upregulatd in hESC (3169*) in our study	528 (1.36 E-294)	70 (2.97 E-6)	770 (2.42 E-196)	88 (7.47 E-37)
Cluster #5 (642*)	79 (4.32 E-29)	36 (4.47 E-13)	111 (7.28 E-17)	10 (0.006)
Oncomine_Upregulate d in hESC (855*)	855 (0)	22 (0.0018)	360 (8.80 E-143)	3 (0.497)
Overlap between Oncomine_Upregulate d in hESC and our hESC upregulated genes (528*)	528 (0)	13 (0.0028)	256 (4.90 E-176)	3 (1)
Overlap between Oncomine_Upregulate d in hESC and cluster #5 of our hESC upregulated genes (79*)	79 (2.10 E-84)	7 (0.202)	31 (6.34 E-5)	2 (0.359)

* number of genes in the gene sets

B



C

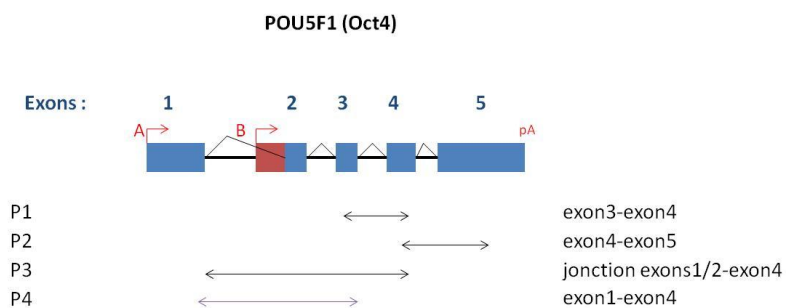
List of the 31 genes overlapping between hESC signature defined by Oncomine and Ben-Porath et al. and our cluster #5

Gene Symbol	Gene Name	Genes down-regulated by HIF1B siRNA under hypoxia in U251 cells (1598*)	HIF2A target gene (434*)	MYC targets (976*) (Ben-Porath et al.,2008)	Nanog, Oct4, Sox2 targets (1289*) (Ben-Porath et al.,2008)	Wilms_tumors_vs_Stratagene_Universal_Reference (3235*) (NextBio)
ABCB7	ATP-binding cassette, sub-family B (MDR/TAP), member 7	ABCB7			ABCB7	ABCB7
ADD2	adducin 2 (beta)					
ATP1A2	ATPase, Na+/K+ transporting, alpha 2 (+) polypeptide					ATP1A2
C12orf11	chromosome 12 open reading frame 11	C12orf11				
C1orf38	chromosome 1 open reading frame 38	C1orf38				
CER1	cerberus 1, cysteine knot superfamily, homolog (Xenopus laevis)				CER1	
CYP26A1	cytochrome P450, family 26, subfamily A, polypeptide 1					
DPYSL2	dihydropyrimidinase-like 2	DPYSL2	DPYSL2		DPYSL2	DPYSL2
EIF4B	eukaryotic translation initiation factor 4B	EIF4B			EIF4B	EIF4B
FGFR1	fibroblast growth factor receptor 1	FGFR1			FGFR1	FGFR1
JARID2	jumonji, AT rich interactive domain 2			JARID2	JARID2	JARID2
LTA4H	leukotriene A4 hydrolase	LTA4H		LTA4H		LTA4H
NANOG	Nanog homeobox				NANOG	NANOG
NMU	neuromedin U				NMU	
OAZ2	ornithine decarboxylase antizyme 2				OAZ2	OAZ2
PAICS	phosphoribosylaminoimidazole succinocarboxamide synthetase			PAICS		PAICS
PAPSS2	3';-phosphoadenosine 5';-phosphosulfate synthase 2	PAPSS2			PAPSS2	PAPSS2
PIM2	pim-2 oncogene	PIM2		PIM2	PIM2	PIM2
POLR1D	polymerase (RNA) I polypeptide D, 16kDa			POLR1D		POLR1D
POU5F1	POU class 5 homeobox 1		POU5F1		POU5F1	POU5F1
RARRES2	retinoic acid receptor responder (tazarotene induced) 2		RARRES2			RARRES2
SFRS18	splicing factor, arginine/serine-rich 18				SFRS18	SFRS18
SILV	silver homolog (mouse)				SILV	SILV
SLC16A1	solute carrier family 16, member 1 (monocarboxylic acid transporter 1)					SLC16A1
SORL1	sortilin-related receptor, L(DLR class) A repeats-containing					
SPRY1	sprouty homolog 1, antagonist of FGF signaling (Drosophila)	SPRY1			SPRY1	SPRY1
STC1	stanniocalcin 1	STC1	STC1		STC1	
SYNGR3	synaptogyrin 3	SYNGR3				SYNGR3
TMEFF1	transmembrane protein with EGF-like and two follistatin-like domains 1	TMEFF1				TMEFF1
TNNT1	troponin T type 1 (skeletal, slow)	TNNT1				TNNT1
USO1	USO1 homolog, vesicle docking protein (yeast)			USO1	USO1	
Overlapping gene number		14	4	6	17	22
p value		5.23 E-9	9.30 E-4	4.96E-04	4.27E-13	1.19 E-10

* number of genes in the gene sets

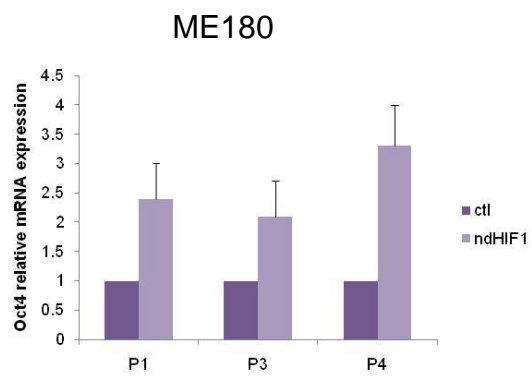
Supplemental Figure 2

A

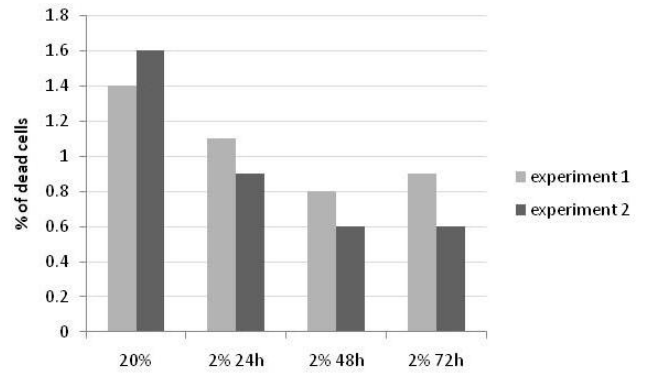
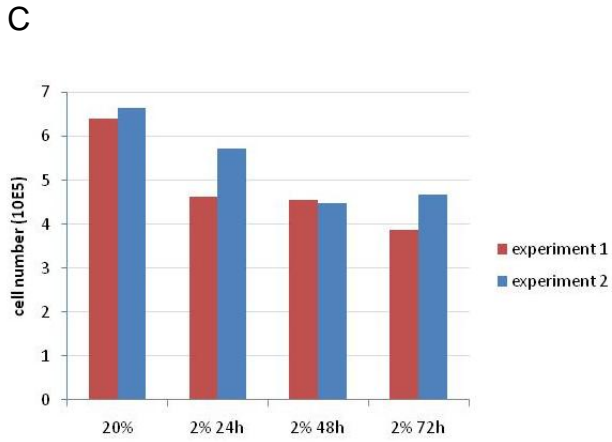
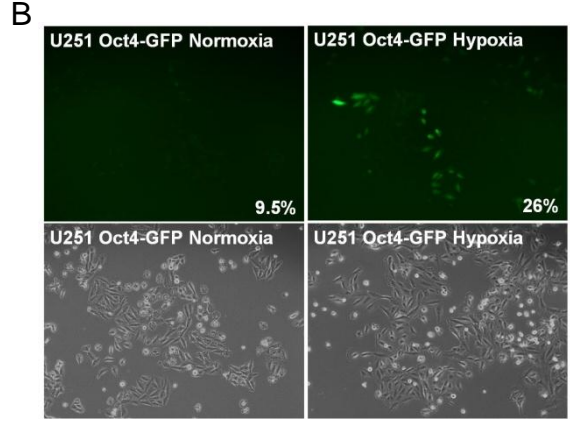
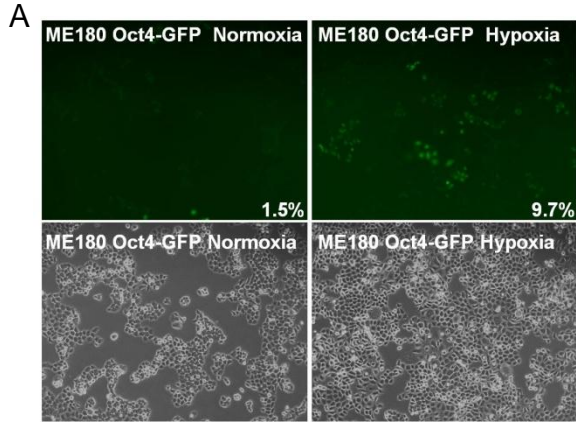


P4: Primers and amplicons used in Mueller et al., 2009

B

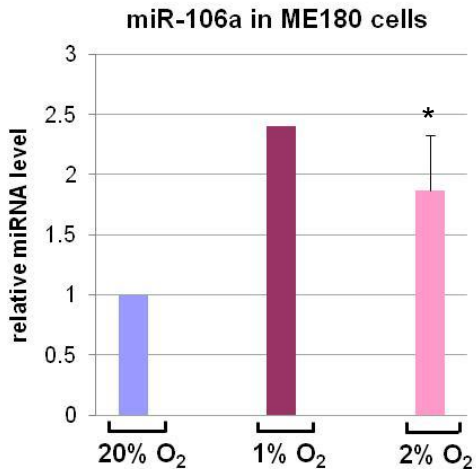


Supplemental Figure 3

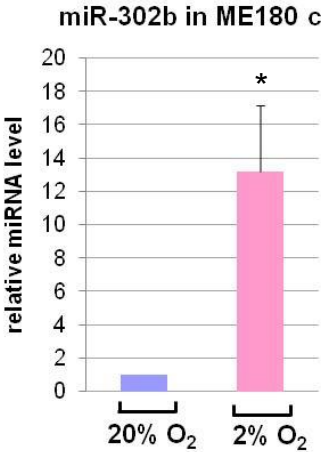


Supplemental Figure 4

A

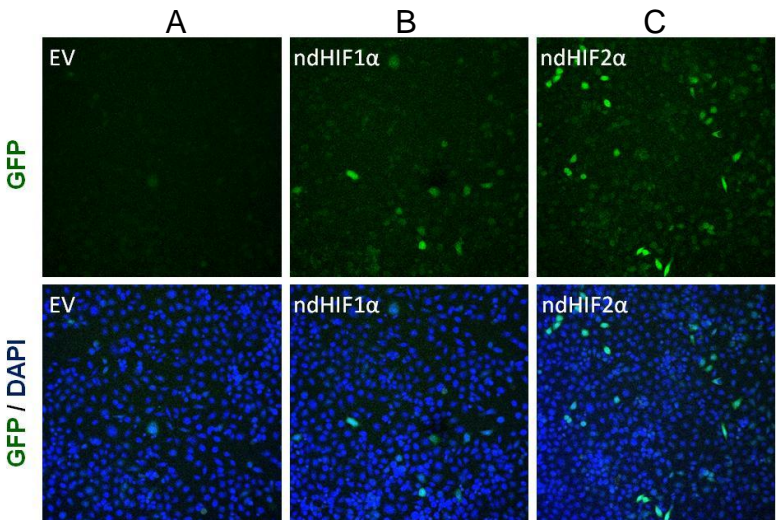


B

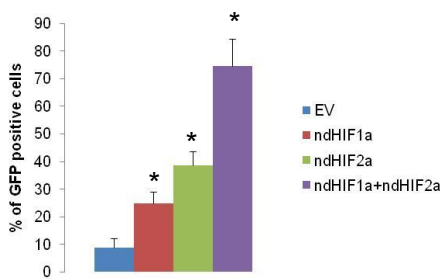


Supplemental Figure 5

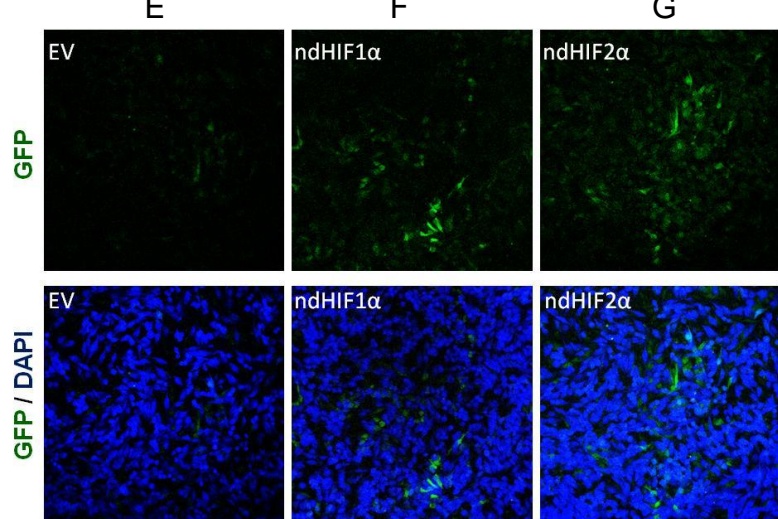
ME180 Oct4-GFP



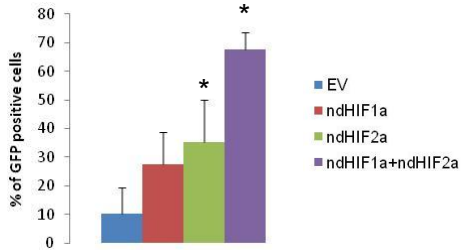
D ME180 Oct4-GFP



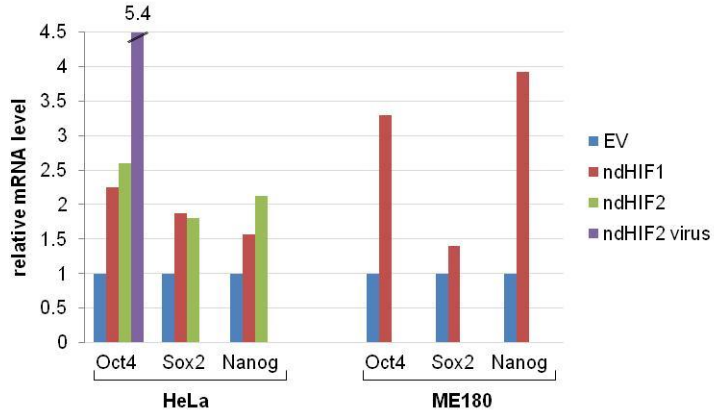
U251 Oct4-GFP



H U251 Oct4-GFP

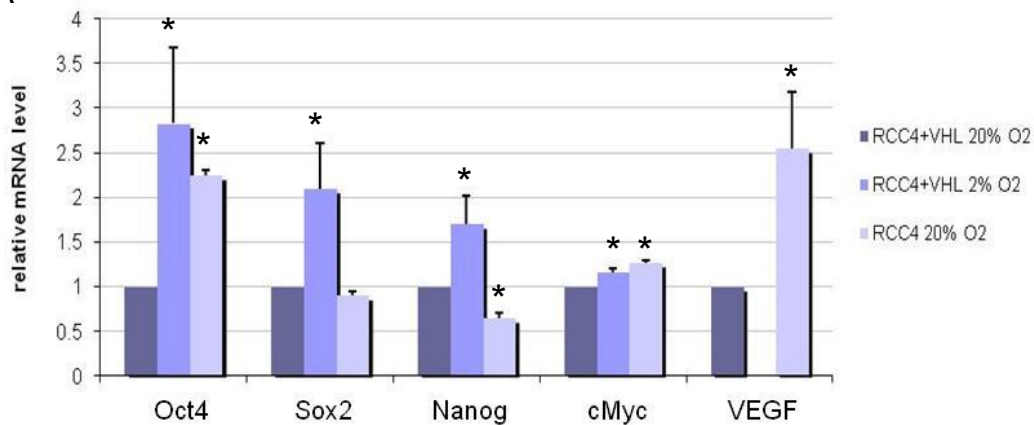


I

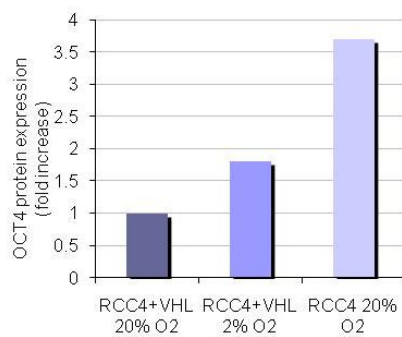


Supplemental figure 6

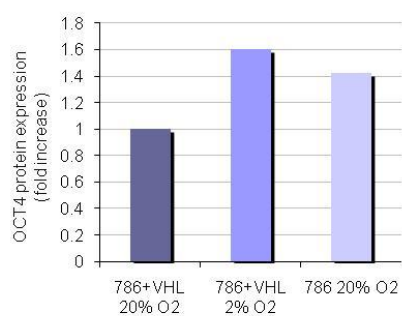
A



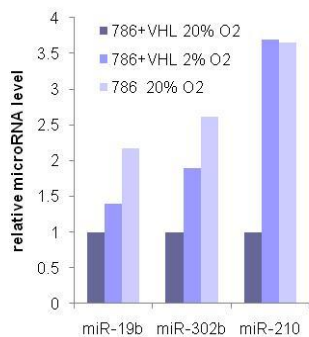
B



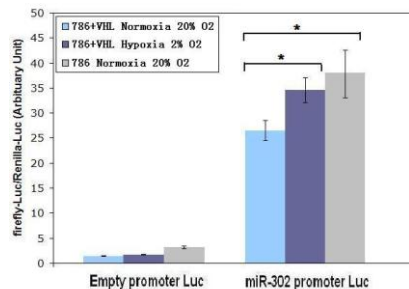
C



D

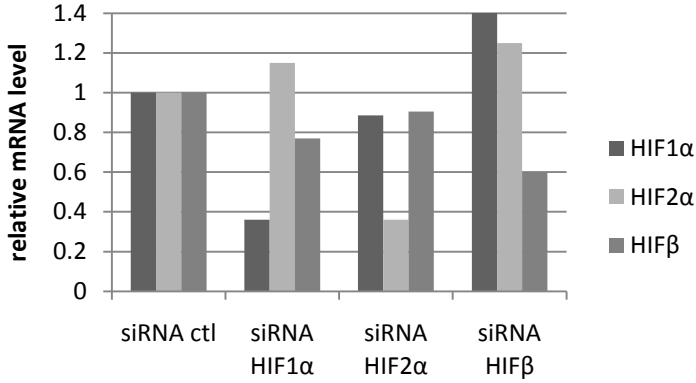


E

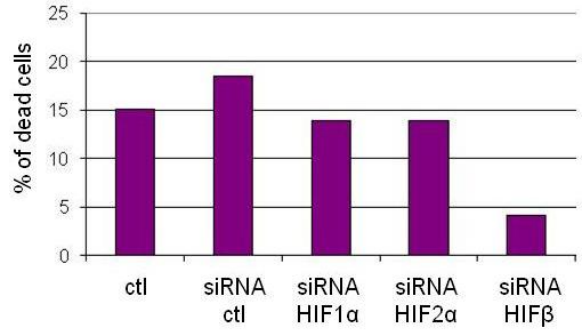


Supplemental figure 7

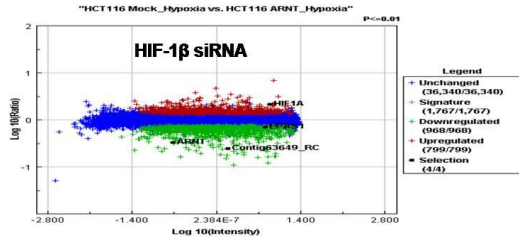
A. HIF qPCR in ME180



B. ME180

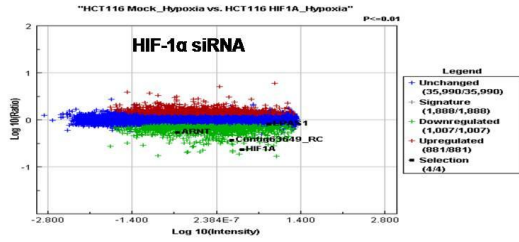


C. Profiling in HCT116



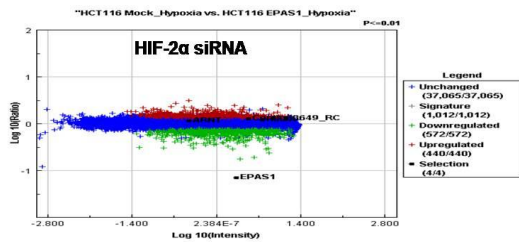
Subunit fold change

HIF1α -1.43
 HIF2α 2.13
 HIFβ -3.08



Subunit fold change

HIF1α -4.38
 HIF2α -1.26
 HIFβ -1.87



Subunit fold change

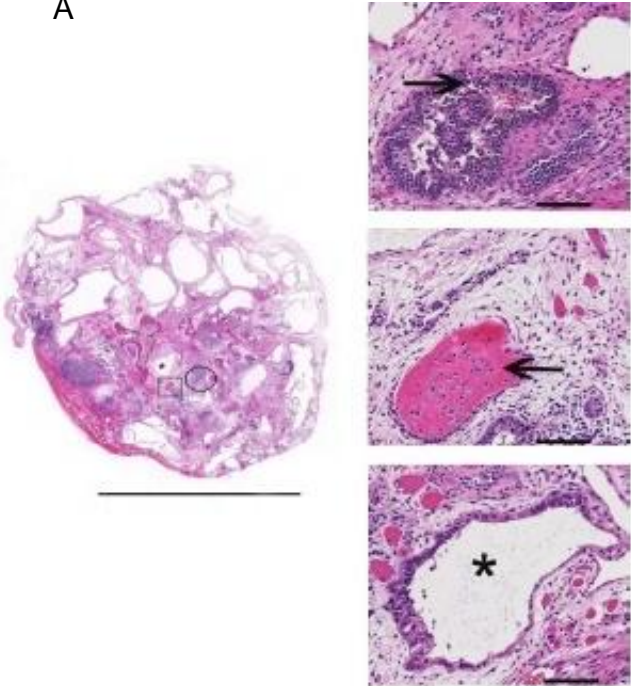
HIF1α 1.18
 HIF2α -14.45
 HIFβ 1.14

D.

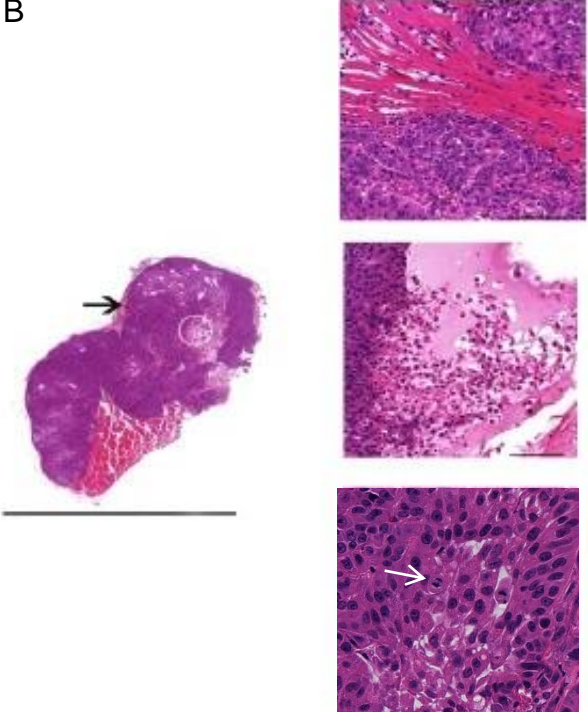
Primary Sequence Name	Entrez Gene ID	Fold change (RCC4-pBABE HIF1A siRNA vs. RCC4-pBABE Mock)	Fold Change (RCC4-VHL Hypoxia vs. RCC4-VHL Normoxia)	AceView Link
TAF9B	51616	2.49	-2.018935	http://www.ncbi.nlm.nih.gov/IEB/Research/AceView/av.cgi?exdb=AceView&db=36a&term=taf9b&submit=Go
AREG	374	1.44	-2.177243	http://www.ncbi.nlm.nih.gov/IEB/Research/AceView/av.cgi?exdb=AceView&db=36a&term=areg&submit=Go
SGK3	56260	1.34	-1.504768	http://www.ncbi.nlm.nih.gov/IEB/Research/AceView/av.cgi?exdb=AceView&db=36a&term=sgk3&submit=Go

Supplemental Figure 8

A

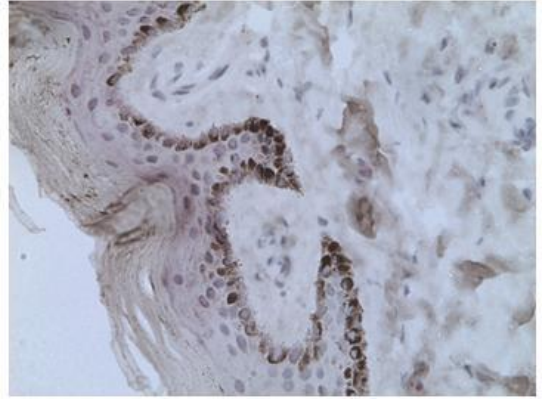
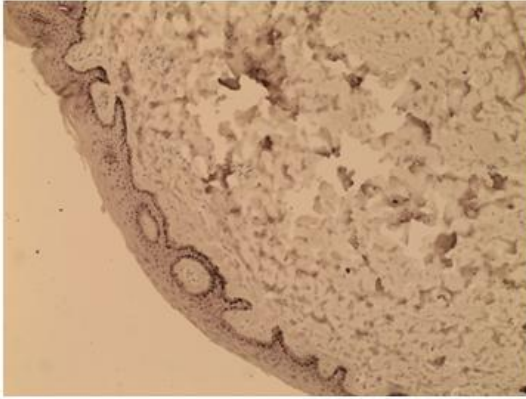


B

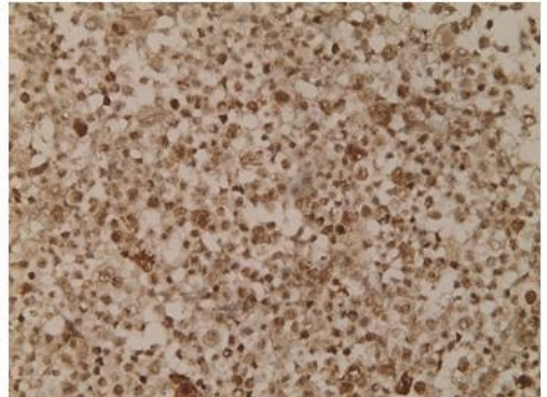
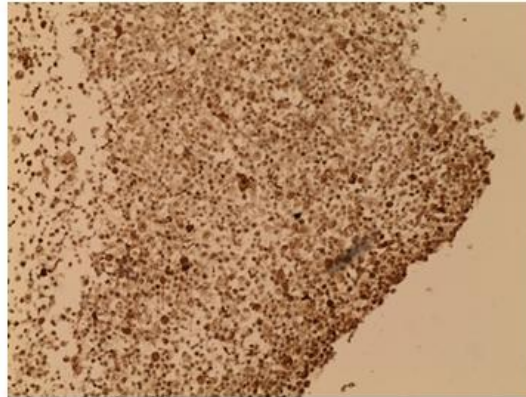


Supplemental Figure 9

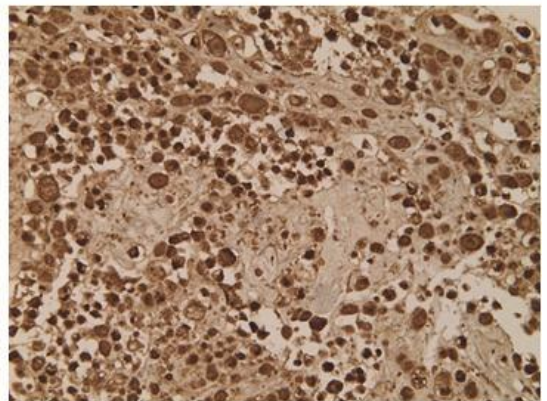
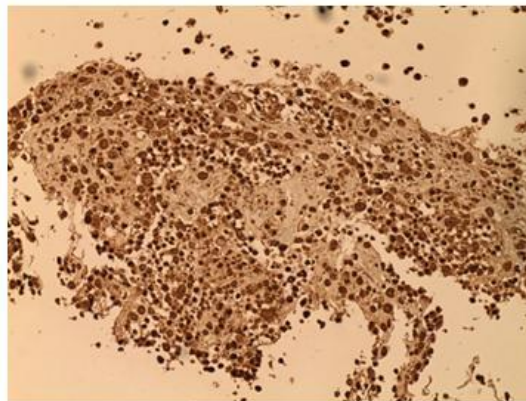
**Skin
HIF1 α**



**hESC
Nanog**

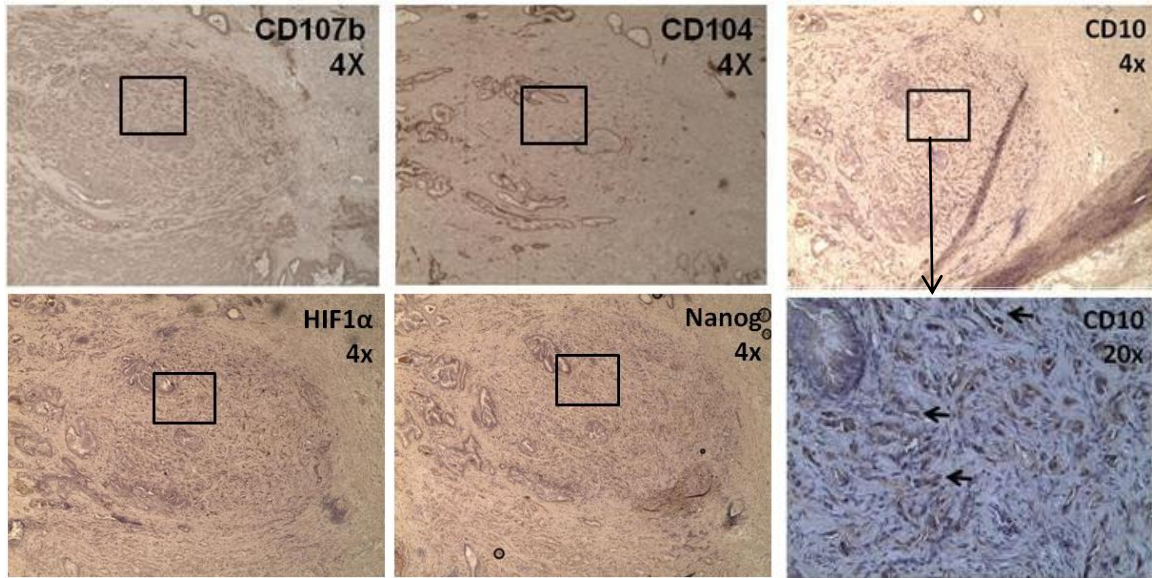


**hESC
Oct4**

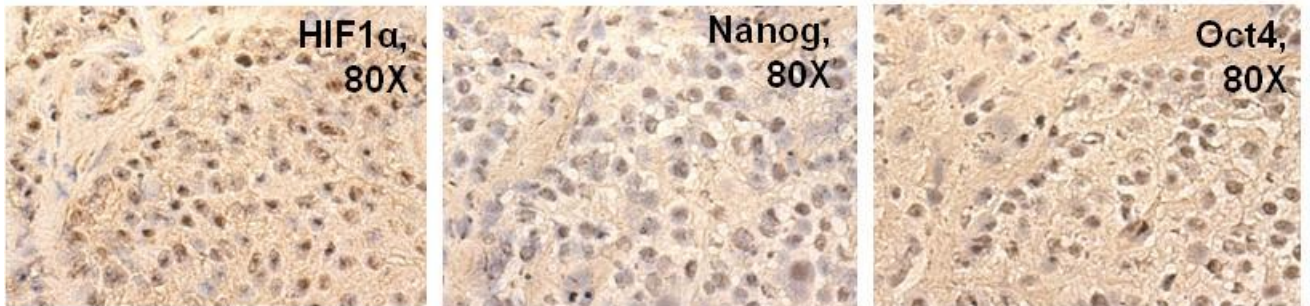


Supplemental Figure 10

A Prostate 09-066C

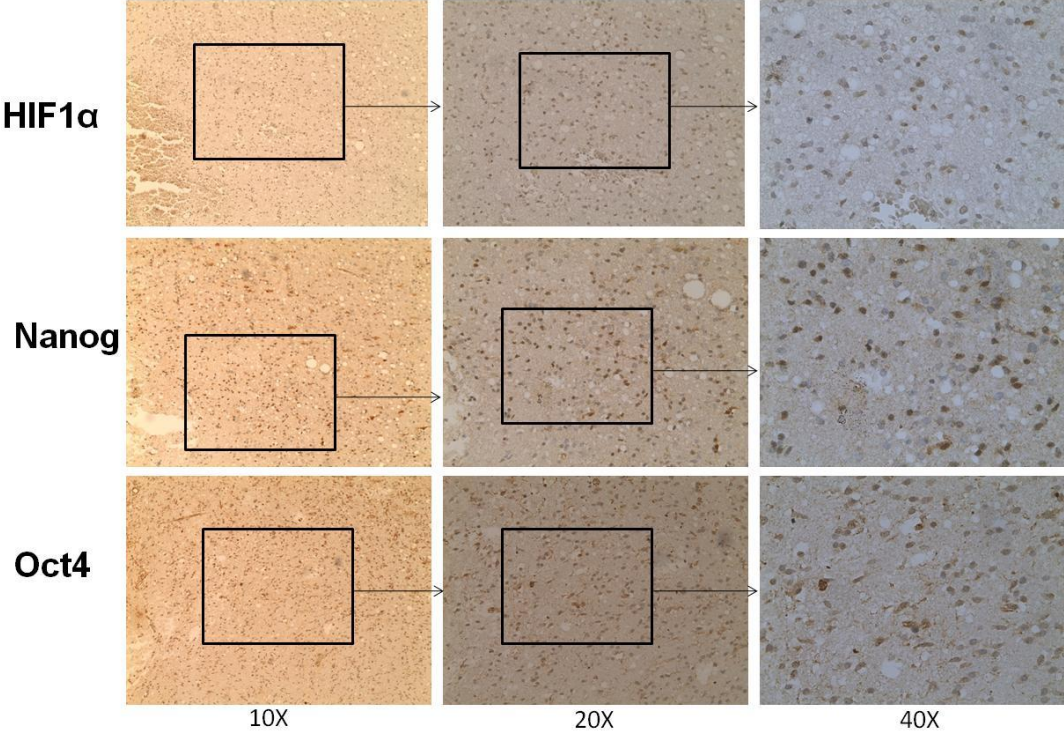


B Prostate 07-020C



Supplemental figure 11

glioma NP07-3-SC1



Supplemental figure 12

