

## **Supplemental Information**

### **The MicroRNA-92a/Sp1/MyoD Axis Regulates Hypoxic Stimulation of Myogenic Lineage Differentiation in Mouse Embryonic Stem Cells**

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## **Supplementary Figure legends**

**Supplementary Figure S1. Effect of HIF1 $\alpha$  or HIF2 $\alpha$  overexpression on HIF-responsive genes in C57 ESCs under normoxia.** Quantitative real-time PCR for bFGF and VEGF suggests that HIF plasmids were functional ( $n = 3$ ; \*\* $p < 0.01$ , \*\*\* $p < 0.001$ ). ESCs were transfected with 1  $\mu$ g pEGFP-HIF1 $\alpha$  or pEGFP-HIF2 $\alpha$  for 24 h, allowed to form EBs for 3 days under normoxic conditions, and real-time PCR were performed.

**Supplementary Figure S2. Real-time PCR for *Sp1* and *MyoD*.** (A) *Sp1* mRNA was significantly decreased by the transient transfection of shSp1 compared to that with the non-target shRNA control (shMock) ( $n = 4$ ). (B) Sp1 knockdown suppressed the increased expression of *MyoD* mRNA even under hypoxia ( $n = 4$ ). \*\*\* $p < 0.001$  versus Nor-EBs ### $p < 0.001$  versus Hyp-shMock-EBs. ESCs were transfected with 1  $\mu$ g shMock or shSp1 for 24 h, formed EBs for 3 days under normoxia, and further incubated for 16 h under normoxic or hypoxic conditions.

**Supplementary Figure S3. Generation of Sp1-knockdown stable cells.** *Sp1* mRNA was remarkably reduced in all four Sp1 knockdown C57 EB clones. C57 ESCs were transfected with 1  $\mu$ g shMock or shSp1 for 24 h, and further selected by puromycin treatment.

**Supplementary Figure S4.** Quantification of western blotting for Sp1. C57 ESCs were transfected with miRNA mimic-oligomer for 2 days under normoxic conditions, and western blotting was performed. miR-NC: miRNA-negative control;  $n=3$ , \*\* $p < 0.01$ , \*\*\* $p < 0.001$ ).

**Supplementary Table 1.** Primers used for real-time PCR and ChIP assay

Primer		Sequence	Size (bp)
Sp1	Forward	5'-CACCTAACACCCATTGCCT-3'	187
	Reverse	5'-TCCATGATCACCTGGGGTGT-3'	
MyoD	Forward	5'-TGGAGATCCTGCGAACGCC-3'	138
	Reverse	5'-TGTAGTGCTCGCTGCCACGG-3'	
Myf5	Forward	5'-CCACCATGCGCGAGCGTAGA-3'	194
	Reverse	5'-GCTCTGTCCCAGGCTGTA-3'	
MyoG	Forward	5'-CTGCGCAGCGCCATCCAGTA-3'	222
	Reverse	5'-GGCGTCTGTAGGGTCAGCCG-3'	
AP2 $\alpha$	Forward	5'-CTCCAGAAGGGTTGTGCAT-3'	171
	Reverse	5'-CGGGCCTGAAGAGGTTACTC-3'	
HIF1 $\alpha$	Forward	5'-TCCTGGAAACGAGTGAAAGG-3'	176
	Reverse	5'-CTGCCTTGTATGGGAGCATT-3'	
HIF2 $\alpha$	Forward	5'-CTTGGAGGGTTCATGCTG-3'	246
	Reverse	5'-ACCGTGCACCCATCCTCAT-3'	
18s rRNA	Forward	5'-GTAACCCGTTAACCTT-3'	151
	Reverse	5'-CCATCCAATCGGTAGTAGCG-3'	
OCT4	Forward	5'-GAAGCCCTCCCTACAGCAGA-3'	437
	Reverse	5'-CAGAGCAGTGACGGGAACAG-3'	
VEGF	Forward	5'-CGGATCAAACCTCACCAAAG-3'	131
	Reverse	5'-TTTCTCCGCTCTGAACAAGG-3'	
bFGF	Forward	5'-TCAAGGACCCAAGCGGCTC-3'	170
	Reverse	5'-GTACCGGTTGGCACACACTC-3'	
ChIP-MyoD	Forward	5'-GTCTCTCTGCCCTCCTCCTA-3'	185
	Reverse	5'-TATCCAGGGTAGCCTAAAAGCC-3'	
ChIP-NC	Forward	5'-GCCAACCCAACCCATCTT-3'	226
	Reverse	5'-CCTCTTCCTGAACTTGCCCT-3'	

**Supplementary Table 2.** Primers for cloning

pcDNA3.1-Sp1
For: 5'-GGTACCCACCATGAGCGACCAAGATCACTCCAT-3'
Rev: 5'-CTCGAGCCTCTAATCTTAGAAACCATTGCCAC-3'
pGL4-MyoD promoter region
For: 5'- GGTACCTTTAATGATGATTCCCACTA-3'
Rev: 5'- CTCGAGCGTGAGAGTCGTCTAAC TTT -3'
pGL4-MyoD promoter region- Δ1mt
For: 5'- GGTACCTACACTCCTATTGGC -3'
Rev: 5'- CTCGAG CGTGAGAGTCGTCTAAC TTT -3'
pGL4-MyoD promoter region- Δ2mt
For: 5'- GGTACCTTTAATGATGATTCCCACTA -3'
Rev: 5'- CTCGAGGCCTCAAGCCAATAG -3'
psiCHECK-2-Sp1-3'UTR-WT-Fragment A
For: 5'-GGTACCGATTAGACACCCAGTGCCAGAGACA-3'
Rev: 5'-CTCGAGTGAGCGGCTCACAGACAGGGAG-3'
psiCHECK-2-Sp1-3'UTR-WT-Fragment B
For: 5'-GGATCCAGTTACAAGCCGGCTCGAGATGC-3'
Rev: 5'-AAGCTTACAAAGGAGCTACAGACTACATTG-3'
psiCHECK-2-Sp1-3'UTR-Fragment B – mt1 (3737–3765)
For: 5'-GACGCTGCAGAT <u>CTTGTA</u> <u>AAATT</u> AACCTA-3'
Rev: 5'- <u>TAGGTTA</u> <u>ATT</u> ACAAAGATCTGCAGCGTC-3'
(Underline indicates mutations introduced at the miR-92a seed region of the <i>Sp1</i> 3'UTR)

psiCHECK-2-Sp1-3'UTR-Fragment B – mt2 (4983–5011)

For: 5'-CCAGTTATCTTCTTAATAACTAATCCGGACC-3'

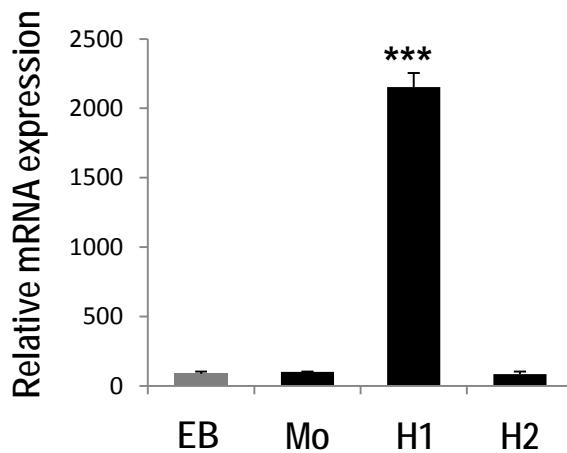
Rev: 5'-GGTCCGGATTAGTTATTAAGAAAGATAAACTGG-3'

(Underline indicates mutations introduced at the miR-92a seed region  
of the *Sp1* 3'UTR)

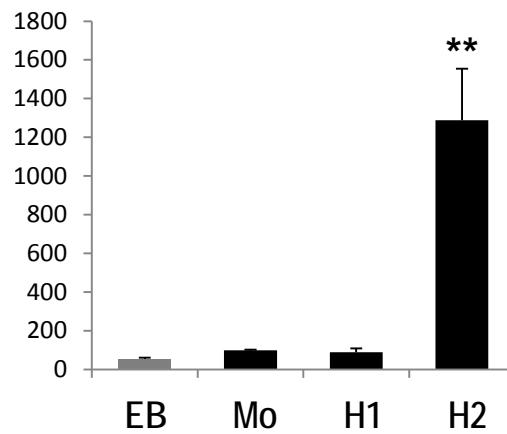
# Supplementary Figure S1

(A)

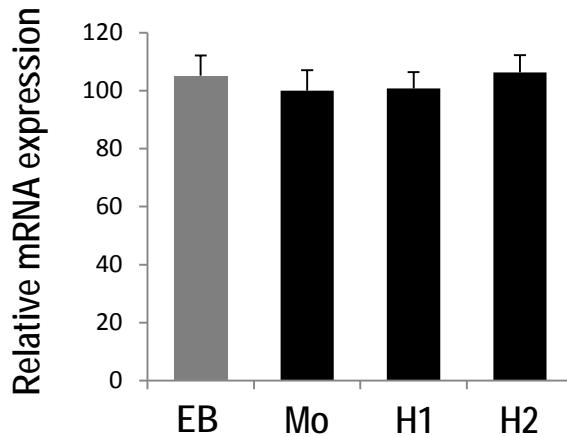
[HIF1 $\alpha$ ]



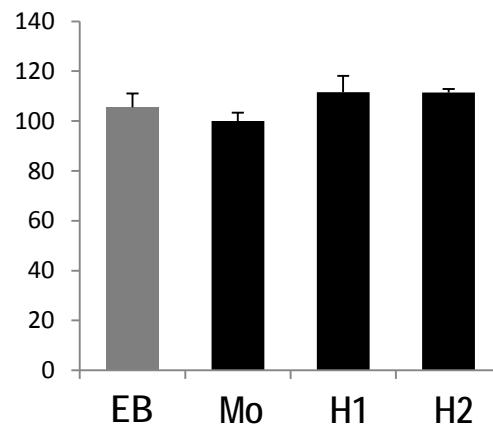
[HIF2 $\alpha$ ]



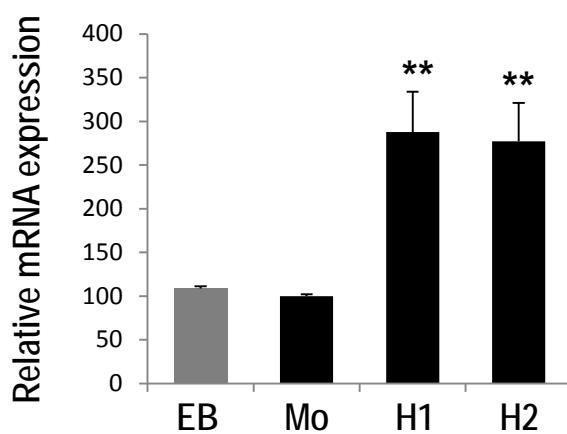
[MyoD]



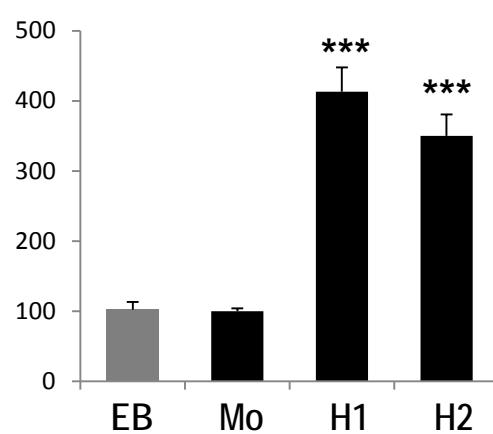
[Myf5]



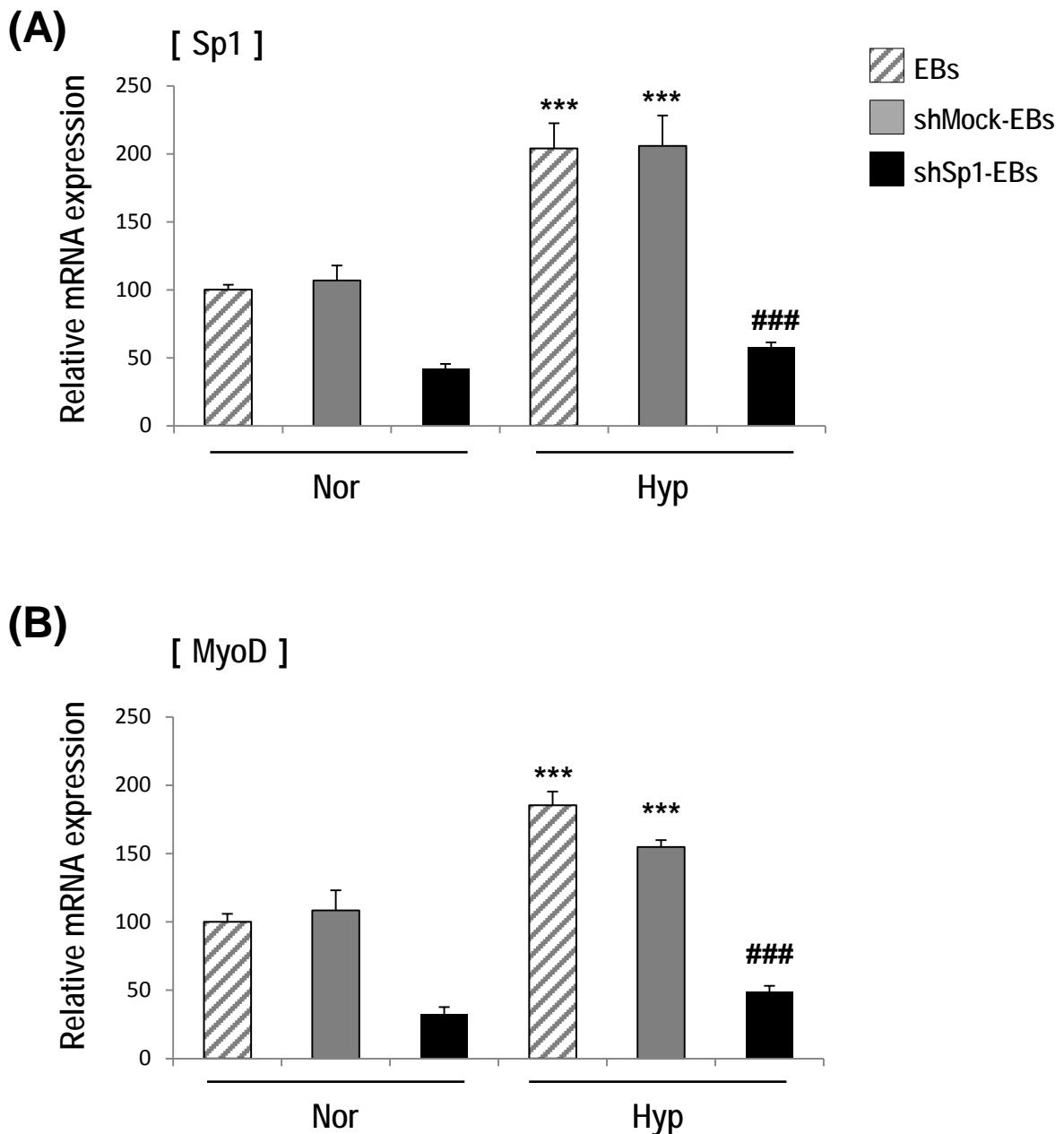
[bFGF]



[VEGF]

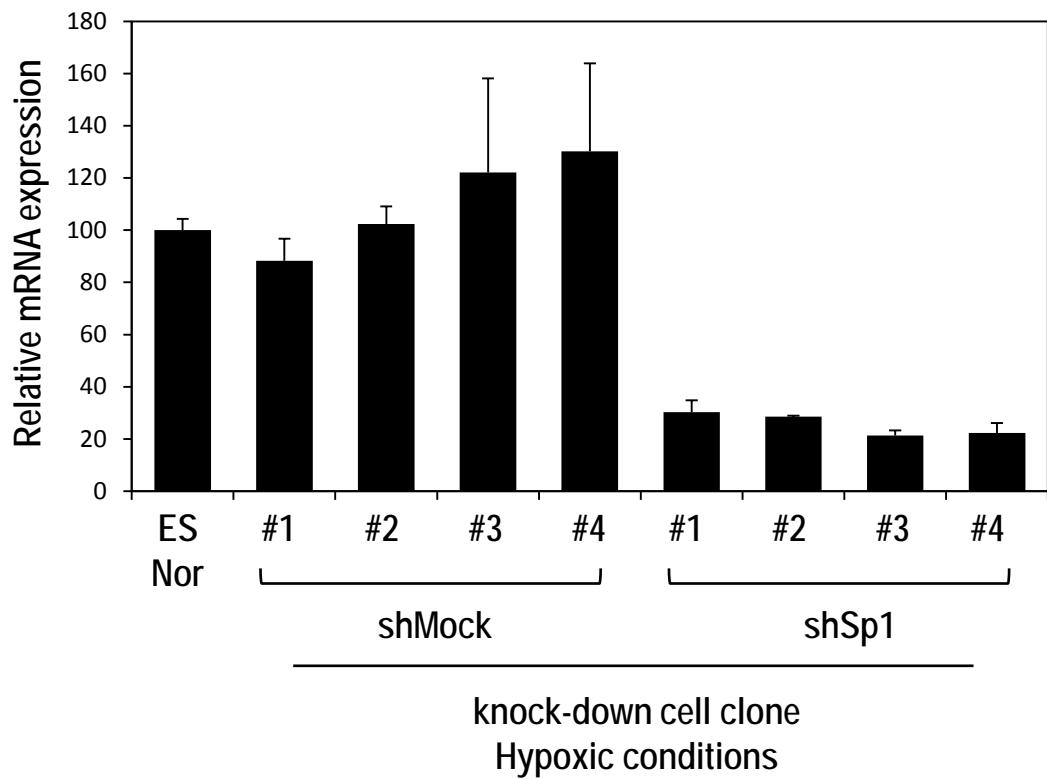


# Supplementary Figure S2



# Supplementary Figure S3

(A) Sp1 mRNA



# Supplementary Figure S4

(A) Sp1 protein

