Table S1 Primer list for plasmids construction

Gene Symbol	Genbank No.	3'UTR fragment length (bp)	Primer forward	Primer reverse
HUMAN-3'UTR fragment				
ACTB	NM_001101	589	CATTCTAGAGCGGACTATGACTTAGT	AGCACTAGTGTGTGCACTTTTATTC
ARPC3	NM_005719	206	ATATCTAGACGTCTCCAGAGCCCTG	GCGACTAGTTATTCTTATTAAGCGCC
ATP5B	NM_001686	131	CGGTCTAGAGTCCTCTGTACTGTCTC	TTACTCGAGGTGTACATTTTATTGGA
ATP6AP1	NM_001183	590	ATTTCTAGAGTGGGGGGGTTGAGGGT	TCTCTCGAGAGGAAGGAAACAACCAA
BAG4	NM_004874.3	2551	CCGCTCGAGAAGGATTTAGAACAAAGTGGAAG	CCGCTCGAGTATAAATCCAGAACTGACAACTCTTC
CCND1	NM_053056	3034	AGCTCTAGACTCCTTGTTGTTGGTTGT	AATCTCGAGCTTTTTGTCTTCTGCTGG
CCND3	NM_00113617	919	GGACTAGTCCACACCACATCTAAGCCTGA	CCGCTCGAGGCCAGTTTTATTTCACAATCA
ESRP1	NM_017697.3	1502	TCGCTCGAGAAGAAAACTTCTAGCAAATTCAGG	GGGCTCGAGTTGAGATTAAACAGGCAAGTTTTAT
FN1	NM_212482	1053	TAATCTAGATTTCCAATCCAGAGGAA	ACTCTCGAGCTTTGAACAGAGGTTTA
GAPDH	NM_002046	194	CATTCTAGATAAGACCCCTGGACCA	GGTACTAGTCAGGGTACTTTATTGAT
GATA6	NM_005257.5	1705	TCGCTCGAGGCCCACGCCGCCAGGA	GGGCTCGAGCACAGTTAAAGGCCAT
IGF1R	NM_000875.4	2662	CCGCTCGAGGCTTTTCCCACAGCAGTCCACCT	CCGCTCGAGGGAGAACGCTTCCAGGCAACAT
KLF4	NM_004235	792	ATATCTAGAGGAGCCCAGCCAGAAAG	GCGCTCGAGTTAAAACTTAATTCTCA
LDHA	NM_005566	563	CAATCTAGAAGTCTTCTGATGTCAT	GTAACTAGTGTTCAAGGTTTATTGG
MAPK1	NM_002745.4	2361	CCGCTCGAGTTGACTCCTTTGAGCCGTTTG	CCGCTCGAGAGCACACAACTTATGGCTACAATG
NANOG	NM_024865	943	CGGTCTAGATATTACTCAATTTCAGTCT	ATGCTCGAGCTGTATATTTACTCATTGA
PGK1	NM_000291	989	CATACTAGTTACTTTCCTGCCTTTT	GCGACTAGTGTAAATTTAATCATAGC
POU5F1	NM_002701	243	TGCTCTAGATTCTAGGAATGGGGGAC	GAGCTCGAGTATCTACTGTGTCCCAG
PPARG	NM_138712	168	TATTCTAGACTTCTTCCAGTTGCACTAT	GTCACTAGTTTCATAATATGGTAATTTT
PTN	NM_002825	658	ATATCTAGAGATGTCACCTGTGGAAC	CGGACTAGTGATTTATTTTCCTAGTA

SOX2	NM_003106	1083	ATATCTAGAGAGGGCCGGACAGCGAA	GGCGACTAGTTGCATAATGGAGTAAAA
VCAN	NM_004285	704	TGATCTAGAAAATGGCGAACATGTGT	GAACTCGAGTCCATTCAGGCCTTTCT
VEGFA	NM_001025366	1778	CGTTCTAGAGTTTCGGGAACCAGATCTC	CGTTCTAGACACTAGAGACAAAGACGTGATG
MOUSE-3’UTR fragment				
Actb	NM_007393	664	CTGTCTAGAGCGGACTGTTACTGAGCTG	TCGCTCGAGTGCACTTTTATTGGTCTC
Arpc3	NM_019824	222	CGTTCTAGAGAGGAGCCTGGGCAGCAC	GTTCTCGAGCAATGTCTAACATAAGCAGT
Hand1	NM_008213	879	CGTTCTAGATGAGACCAGGCCAACG	CCAACTAGTTTTTATTAAGTCAAGAGC
Hoxb1	NM_008266	526	GCTTCTAGATGAATTGAACTTCCTAA	CCAACTAGTCAGTCGGTGCTATTGT
Myc	NM_010849	362	CCGTCTAGAACTGACCTAACTCGA	CAAACTAGTTACATGTCTTAAAATC
Nanog	NM_028016	1058	CTGTCTAGATGAGACTTACGCAACA	GCTACTAGTTGTTTAAACTAGTCCAGC
Pou5f1	NM_013633	213	CGTTCTAGAGGCACCAGCCCTCC	ACTACTAGTCCCAGTCTTTATTTAAG
Zfp42	NM_009556	493	CGCTCTAGAAGGTGGAGACAGATTG	GCAACTAGTATCTTCAGATGGATCAAC

Table S2 MiRNAs expressing in normoxic CNE

Name of miRNA	Name of miRNA	Name of miRNA
hsa-miR-20b-5p	hsa-miR-103a-3p	hsa-miR-29b-3p
hsa-miR-26b-5p	hsa-let-7b-5p	hsa-miR-17-3p
hsa-miR-15b-5p	hsa-miR-106b-5p	hsa-miR-25-3p
hsa-let-7g-5p	hsa-miR-26a-5p	hsa-miR-193a-3p
hsa-miR-224-5p	hsa-miR-24-3p	hsa-miR-29c-3p
hsa-let-7a-5p	hsa-let-7i-5p	hsa-miR-100-5p
hsa-let-7d-5p	hsa-miR-23a-3p	hsa-miR-22-3p
hsa-miR-16-5p	hsa-miR-106a-5p	hsa-miR-21-5p
hsa-let-7f-5p	hsa-miR-99a-5p	hsa-miR-221-3p
hsa-miR-30b-5p	hsa-miR-338-3p	hsa-miR-423-3p
hsa-miR-20a-5p	hsa-miR-222-3p	hsa-miR-361-5p
hsa-let-7c	hsa-miR-27a-3p	hsa-miR-30a
hsa-let-7e-5p	hsa-miR-31-5p	hsa-miR-92a-3p
hsa-miR-23b-3p	hsa-miR-30c-5p	hsa-miR-181a-5p
hsa-miR-107	hsa-miR-29a-3p	hsa-miR-193b-3p
hsa-miR-17-5p	hsa-miR-125b-5p	hsa-miR-320a

The miRNAs with ratio of normoxic fluorescence intensity to hypoxic fluorescence intensity > 3 and t test $p < 0.05$ are considered as the specific miRNAs in normoxic CNE, and they are indicated as red colour.

Table S3 MiRNAs expressing in DFOM-induced hypoxic CNE

Name of miRNA	Name of miRNA	Name of miRNA
hsa-miR-155-5p	hsa-let-7i-5p	hsa-miR-193a-3p
hsa-miR-210	hsa-miR-23a-3p	hsa-miR-29c-3p
hsa-miR-188-5p	hsa-miR-106a-5p	hsa-miR-100-5p
hsa-miR-181b-5p	hsa-miR-99a-5p	hsa-miR-22-3p
hsa-miR-30d-5p	hsa-miR-338-3p	hsa-miR-21-5p
hsa-miR-151a-5p	hsa-miR-222-3p	hsa-miR-221-3p
hsa-miR-23b-3p	hsa-miR-27a-3p	hsa-miR-423-3p
hsa-miR-107	hsa-miR-31-5p	hsa-miR-361-5p
hsa-miR-17-5p	hsa-miR-30c-5p	hsa-miR-30a-5p
hsa-miR-103a-3p	hsa-miR-29a-3p	hsa-miR-92a-3p
hsa-let-7b-5p	hsa-miR-125b-5p	hsa-miR-181a-5p
hsa-miR-106b-5p	hsa-miR-29b-3p	hsa-miR-193b-3p
hsa-miR-26a-5p	hsa-miR-17-3p	hsa-miR-320a
hsa-miR-24-3p	hsa-miR-25-3p	

The miRNAs with ratio of normoxic fluorescence intensity to hypoxic fluorescence intensity < 0.33 and t test p < 0.05 are considered as the specific miRNAs in DFOM-induced hypoxic CNE, and they are indicated as red colour.

Table S4 MiRNAs expressing in undifferentiated mESC (reads number> 5000)

Name of miRNA	Name of miRNA	Name of miRNA	Name of miRNA
mmu-miR-294-3p	mmu-miR-381-3p	mmu-let-7f-5p	mmu-miR-101a-3p
mmu-let-7e-5p	mmu-miR-130b-3p	mmu-miR-541-5p	mmu-miR-196a-5p
mmu-miR-96-5p	mmu-miR-20b-5p	mmu-miR-292-5p	mmu-miR-27b-3p
mmu-miR-291a-5p	mmu-miR-9-5p	mmu-miR-7a-5p	mmu-miR-872-5p
mmu-let-7b-5p	mmu-miR-181d-5p	mmu-miR-93-5p	mmu-miR-17-5p
mmu-miR-152-3p	mmu-miR-130a-3p	mmu-miR-103-3p	mmu-miR-411-5p
mmu-miR-369-3p	mmu-miR-148b-3p	mmu-miR-101b-3p	mmu-miR-191-5p
mmu-miR-146a-5p	mmu-miR-27a-5p	mmu-miR-30a-5p	mmu-miR-292-3p
mmu-miR-181c-5p	mmu-let-7g-5p	mmu-miR-30e-5p	mmu-miR-106a-5p
mmu-miR-434-5p	mmu-miR-199a-3p	mmu-let-7c-5p	mmu-miR-151-3p
mmu-miR-192-5p	mmu-miR-199b-3p	mmu-miR-140-3p	mmu-miR-26a-5p
mmu-miR-434-3p	mmu-miR-182-5p	mmu-let-7a-5p	mmu-miR-106b-5p
mmu-miR-708-5p	mmu-miR-183-5p	mmu-miR-127-3p	mmu-miR-25-3p
mmu-miR-1965	mmu-miR-21-5p	mmu-miR-24-3p	mmu-miR-30e-3p
mmu-let-7i-5p	mmu-miR-143-3p	mmu-miR-291a-3p	mmu-miR-200c-3p
mmu-miR-29a-3p	mmu-miR-378-3p	mmu-miR-293-5p	mmu-miR-92a-3p
mmu-miR-382-5p	mmu-miR-379-5p	mmu-miR-134-5p	mmu-miR-672-5p
mmu-miR-363-3p	mmu-miR-295-3p	mmu-miR-30d-5p	mmu-miR-16-5p
mmu-miR-300-3p	mmu-miR-34c-5p	mmu-miR-146b-5p	mmu-miR-28-3p
mmu-miR-30a-3p	mmu-miR-293-3p	mmu-miR-20a-5p	mmu-miR-184-3p
mmu-miR-27a-3p	mmu-miR-148a-3p	mmu-miR-99b-5p	mmu-miR-744-5p

The miRNAs with reads number > 5000 in undifferentiated mESCs and < 5000 in RA-induced differentiated mESCs are considered as specific miRNAs in undifferentiated mESCs, and are indicated as red colour.

Table S5 MiRNAs expressing in RA-induced differentiated mESC (reads number >5000)

Name of miRNA	Name of miRNA	Name of miRNA
mmu-miR-10a-5p	mmu-miR-103-3p	mmu-miR-106b-5p
mmu-miR-21-5p	mmu-miR-291a-3p	mmu-miR-151-3p
mmu-miR-183-5p	mmu-miR-7a-5p	mmu-miR-26a-5p
mmu-miR-379-5p	mmu-miR-30d-5p	mmu-miR-17-5p
mmu-miR-148a-3p	mmu-miR-196a-5p	mmu-miR-293-5p
mmu-miR-293-3p	mmu-let-7f-5p	mmu-miR-200c-3p
mmu-miR-295-3p	mmu-miR-182-5p	mmu-miR-101a-3p
mmu-miR-30a-5p	mmu-let-7a-5p	mmu-miR-30e-3p
mmu-miR-93-5p	mmu-miR-24-3p	mmu-miR-16-5p
mmu-miR-30e-5p	mmu-let-7c-5p	mmu-miR-672-5p
mmu-miR-143-3p	mmu-miR-20a-5p	mmu-miR-28-3p
mmu-miR-378-3p	mmu-miR-127-3p	mmu-miR-292-3p
mmu-miR-99b-5p	mmu-miR-191-5p	mmu-miR-744-5p
mmu-miR-292-5p	mmu-miR-184-3p	mmu-miR-92a-3p
mmu-miR-34c-5p	mmu-miR-27b-3p	mmu-miR-148b-3p
mmu-miR-140-3p	mmu-miR-134-5p	mmu-miR-25-3p
mmu-miR-541-5p	mmu-miR-872-5p	mmu-miR-411-5p
mmu-miR-101b-3p	mmu-miR-146b-5p	

The miRNAs with reads number > 5000 in RA-induced differentiated mESCs and < 5000 in undifferentiated mESCs are considered as specific miRNAs in RA-induced differentiated mESCs, and are indicated as red colour.

Table S6 The parameters output by CoPrediction under normoxic conditions in CNE cells.

Name of 3'UTR fragment	Fluorescence repression ratio %	Potential MER	Total MRE	The density of potential MRE per kb	The density of total MRE per kb	The length of 3’UTR fragments (bp)	The average free energy of potential MREs (kcal/mol)
ACTB	13.01	5	14	8.49	23.77	589	-19.50
ARPC3	18.77	5	17	24.27	82.52	206	-19.66
ATP5B	8.01	0	0	0.00	0.00	131	0.00
ATP6AP1	43.95	16	26	27.12	44.07	590	-20.30
BAG4	71.26	41	92	16.07	36.06	2551	-19.06
CCND1	76.90	57	178	18.79	58.67	3034	-19.69
CCND3	70.07	13	22	14.15	23.94	919	-21.48
ESRP1	67.00	35	75	23.30	49.93	1502	-18.56
FN1	57.40	15	27	14.25	25.64	1053	-18.90
GAPDH	20.26	0	0	0.00	0.00	194	0.00
GATA6	64.01	31	89	18.18	52.20	1705	-18.50
IGF1R	86.42	40	107	15.03	40.20	2662	-19.90
KLF4	58.94	15	43	18.94	54.29	792	-18.53
LDHA	39.27	5	14	8.88	24.87	563	-24.22
MAPK1	74.21	56	226	23.72	95.72	2361	-20.17
NANOG	51.19	10	19	10.60	20.15	943	-20.69
PGK1	64.82	15	29	15.17	29.32	989	-18.68
POU5F1	10.27	2	3	8.23	12.35	243	-24.50
PPARG	1.58	2	6	11.90	35.71	168	-17.10
PTN	30.14	2	10	3.04	15.20	658	-19.90
SOX2	25.25	6	8	5.54	7.39	1083	-19.58
VCAN	47.03	7	13	9.94	18.47	704	-17.64
VEGFA	61.09	24	64	13.50	36.00	1778	-21.32

Table S7 The parameters output by CoPrediction under DFOM-induced hypoxic conditions in CNE cells.

Name of 3'UTR fragment	Fluorescence repression ratio %	Potential MER	Total MRE	The density of potential MRE per kb	The density of total MRE per kb	The length of 3'UTR fragments (bp)	The average free energy of potential MREs (kcal/mol)
ACTB	6.49	6	10	10.19	16.98	589	-18.83
ARPC3	19.49	5	11	24.27	53.40	206	-19.38
ATP5B	13.29	1	1	7.63	7.63	131	-17.30
ATP6AP1	43.86	15	20	25.42	33.90	590	-20.50
BAG4	72.87	41	73	16.07	28.62	2551	-19.50
CCND1	78.55	56	122	18.46	40.21	3034	-20.12
CCND3	72.75	15	21	16.32	22.85	919	-21.98
ESRP1	82.72	32	60	21.30	39.95	1502	-18.63
FN1	65.85	14	20	13.30	18.99	1053	-18.92
GAPDH	23.23	0	0	0.00	0.00	194	0.00
GATA6	75.45	34	67	19.94	39.30	1705	-18.72
IGF1R	85.26	56	103	21.04	38.69	2662	-20.50
KLF4	38.62	12	22	15.15	27.78	792	-18.08
LDHA	49.07	6	17	10.66	30.20	563	-23.45
MAPK1	73.21	50	130	21.18	55.06	2361	-19.86
NANOG	56.34	11	14	11.66	14.85	943	-20.85
PGK1	53.76	16	27	16.18	27.30	989	-19.46
POU5F1	12.68	2	3	8.23	12.35	243	-24.50
PPARG	6.19	2	4	11.90	23.81	168	-17.00
PTN	11.27	3	5	4.56	7.60	658	-17.67
SOX2	26.09	8	9	7.39	8.31	1083	-18.73
VCAN	39.77	7	10	9.94	14.20	704	-17.60
VEGFA	69.75	25	52	14.06	29.25	1778	-21.27

Table S8 The parameters output by CoPrediction under undifferentiated mESCs .

Name of 3'UTR fragment	Fluorescence repression ratio %	Potential MER	Total MRE	The density of potential MRE per kb	The density of total MRE per kb	The length of 3’UTR fragments (bp)	The average free energy of potential MREs (kcal/mol)
Actb	28.25	17	50	25.60	75.30	664	-20.28
Arpc3	16.25	3	4	13.51	18.02	222	-20.57
Hand1	54.30	19	58	21.62	65.98	879	-21.70
Hoxb1	73.23	14	26	26.62	49.43	526	-20.78
Myc	27.70	7	34	19.34	93.92	362	-21.41
Nanog	74.41	21	57	19.85	53.88	1058	-19.80
Pou5f1	1.24	4	13	18.78	61.03	213	-21.65
Zfp42	4.68	3	6	6.06	12.12	493	-19.60

Table S9 The parameters output by CoPrediction under RA-induced differentiated mESC condition.

Name of 3'UTR fragment	Fluorescence repression ratio %	Potential MER	Total MRE	The density of potential MRE per kb	The density of total MRE per kb	The length of 3’UTR fragments (bp)	The average free energy of potential MREs (kcal/mol)
Actb	40.71	14	32	21.08	48.19	664	-19.95
Arpc3	9.88	2	3	9.01	13.51	222	-19.70
Hand1	68.60	15	34	17.06	38.68	879	-19.55
Hoxb1	54.09	11	20	20.91	38.02	526	-20.76
Myc	15.79	6	18	16.57	49.72	362	-20.68
Nanog	57.03	16	33	15.12	31.19	1058	-19.04
Pou5f1	38.98	4	8	18.78	37.56	213	-21.65
Zfp42	14.36	3	3	6.06	6.06	493	-18.50

Table S11 microarray fluorescence intensity data

NAME	Fluorescence intensity in normoxic CNE	Fluorescence intensity in hypoxic CNE
ACTB	51767	38199
ARPC3	12907	10612
ATP5B	319	312
ATP6AP1	4779	5067
BAG4	100	57
CCND1	1369	620
CCND3	6918	3176
ESRP1	-79	-92
FN1	357	377
GAPDH	52720	101628
GATA6	399	1086
IGF1R	50	129
KLF4	99	-5
LDHA	45239	69423
MAPK1	460	912
NANOG	148	182
PGK1	39984	134855
POU5F1	3334	13047
PPARG	-66	-127
PTN	-15	27
SOX2	217	301
VCAN	266	295
VEGF	6449	26644

According to the methods, the gene will be considered as ‘expression’ when its microarray fluorescence intensity is above 1000.

Table S12 The largest fold increase in gene expression and the basal level of endogenous gene expression as indicated by fluorescence intensity.

Gene name	Fluorescence Intensity	The largest fold increase in gene expression	SD
ACTB	51767	3.75	0.08
ARPC3	12907	4.97	0.10
ATP6AP1	4779	6.23	0.19
CCND1	1369	5.86	0.29
CCND3	6918	5.09	0.29
LDHA	45239	4.35	0.06
PGK1	39984	3.23	0.10
POU5F1	3334	8.74	0.35
VEGFA	6449	7.68	0.71

Table S13 Primer list for mRNA expression detection

Gene Symbol	Genbank No.	Species	Primer forward	Primer reverse
ACTB	NM_001101	homo sapiens	CATGTACGTTGCTATCCAGGC	CTCCTTAATGTCACGCACGAT
ARPC3	NM_005719	homo sapiens	GTGCAATTCCAAAAGCCAAGG	GGCTCTCATCACTTCATCTTCC
ATP6AP1	NM_001183	homo sapiens	CAGCGACTTGCAGCTCTCTAC	TGAAATCCTCAATGCTCAGCTTG
B2M	NM_004048	homo sapiens	GAGGCTATCCAGCGTACTCCA	CGGCAGGCATACTCATCTTTT
CCND1	NM_053056	homo sapiens	GCATGTTCGTGGCCTCTAAG	CGGATGGAGTTGTCGGTGTAG
CCND3	NM_00113617	homo sapiens	TACCCGCCATCCATGATCG	AGGCAGTCCACTTCAGTGC
GAPDH	NM_002046	homo sapiens	AAGGTGAAGGTCGGAGTCAAC	GGGGTCATTGATGGCAACAATA
LDHA	NM_005566	homo sapiens	TTGACCTACGTGGCTTGGAAG	GGTAACGGAATCGGGCTGAAT
PGK1	NM_000291	homo sapiens	GGAGAACCTCCGCTTTCATG	GCTGGCTCGGCTTTAACCT
POU5F1	NM_002701	homo sapiens	GGGAGATTGATAACTGGTGTGTT	GTGTATATCCCAGGGTGATCCTC
VEGFA	NM_001025366	homo sapiens	GAGGGCAGAATCATCACGAAG	GGTCTCGATTGGATGGCAGTA
Renilla Luciferase	M63501.1	renilla reniformis	CCTCGTGAAATCCCGTTAGT	TTGGCACCTTCAACAATAGC