

**Supplemental Table S1.** Primer sequences for PCR analysis

Primer name	Primer sequence (5'–3')	Size of amplified DNA (bp)
miR-101-2	Forward: cggattctcagaagttgactgctgggt Reverse: cgggatccttcttctgttcggagagcc	495
<i>ING3</i>	Forward: ccgctcgaggttagccttgattttcagtg Reverse: ataagaatcggccgccactctgtctggatgcagaaa	454

**Supplemental Table S2.** Sequences of the insert fragments

Name	Sequence
miR-101-2 precursor	tcagaagttgactgctgggtttaaagtaggcattctcaaaaagagcagatcctcagaagactgaaatctaaacagca cagtgaaaaagcattactgaaagtaagtgaggttgctgtgaacagccccttgagcactgatatctgtacatgtgtct gtgtgcttaaagattgtctgtagccacatgggtggtagcttgggaggagtgtgccttgggtgcaagggaaatattc aggtagatatgagactgaactgtccttttcggtatcatggtaccgatgctgtatatctgaaaggtagactactgtgata actgaaagatgggtgccatcacattgagaaaaggctgggcactgcagaggggctggcacaccactggaccatgg tgttatgggcagagaccacggtattctctggaggctttttttctgtaagttgatggtggaaggctctccgaaacaa ggaa
<i>ING3</i> -3'UTR	gttagccttgattttcagtgccaacgtatgcagacattgtactcctcaaccattttcceaagtaatgggcattctat aatgtagactcaaagaattccaacgatgaagatttaagaaaagtattttatattcaacaggtatgttctgctgcatgtac tgtactccagagctgttatgtaacactgtatataaatggtgcaaaaaaaaaagtgcttctaaaaagataatggtttttaa atgcctttataataagcttgtttcttggtaaaactaaattcagcgggctgaagcaaatggtcatgtgataaaggggctg atgtcctctagagtacctgggtacataaacagaaactcctgtaggtaaaaacgaatctgggccattagctttatatgttt ctgcatccagacagagtg
<i>ING3</i> -3'UTR-MUT	gttagccttgattttcagtgccaacgtatgcagacattgtactcctcaaccattttcceaagtaatgggcattctat aatgtagactcaaagaattccaacgatgaagatttaagaaaagtattttatattcaacaggtatgttctgctgcatcga gtgactccagagctgttatgtaacactgtatataaatggtgcaaaaaaaaaagtgcttctaaaaagataatggtttttaa atgcctttataataagcttgtttcttggtaaaactaaattcagcgggctgaagcaaatggtcatgtgataaaggggctg atgtcctctagagtacctgggtacataaacagaaactcctgtaggtaaaaacgaatctgggccattagctttatatgttt ctgcatccagacagagtg

**Supplemental Table S3.** Expression stability values of the candidate housekeeping genes in BFF, 513-B1-BFF calculated by the geNorm and Normfinder (ranking in parentheses).

Gene	Full gene name	Stability value geNorm	Stability value NormFinder
GAPDH	glyceraldehyde-3-phosphate dehydrogenase	0.41 (1)	0.16 (1)
ACTB	β-actin	0.46 (2)	0.26 (2)
18S rRNA	18S ribosomal RNA	0.53 (3)	0.33 (3)
EEF1A2	eukaryotic translation elongation factor 1 alpha 2	0.63 (4)	0.54 (5)
H2A	Histone 2 alpha	0.76 (5)	0.38 (4)

**Supplemental Table S4.** Expression stability values of the candidate housekeeping genes in Day-seven blastocysts from IVF, 513-B1-NT, or miR-101-NT groups calculated by the geNorm and Normfinder (ranking in parentheses).

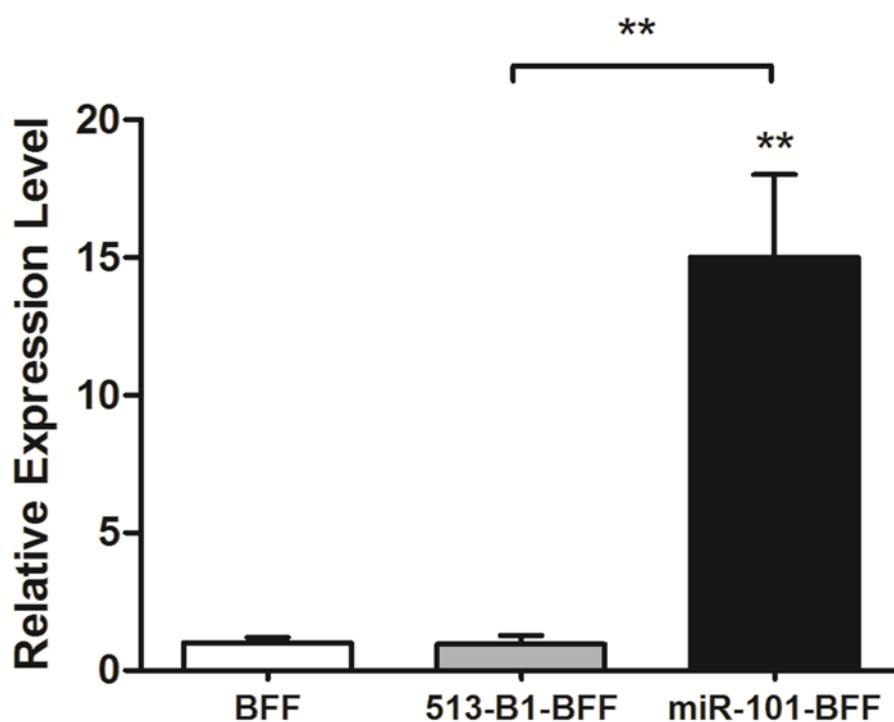
Gene	Full gene name	Stability value geNorm	Stability value NormFinder
GAPDH	glyceraldehyde-3-phosphate dehydrogenase	0.46 (1)	0.21 (1)
H2A	Histone 2 alpha	0.59 (2)	0.31 (2)
ACTB	β-actin	0.68(3)	0.37 (4)
18S rRNA	18S ribosomal RNA	0.69 (4)	0.35 (3)
EEF1A2	eukaryotic translation elongation factor 1 alpha 2	0.91 (5)	0.72 (5)

**Supplemental Table S5.** Primer sequences for real-time PCR analysis.

Primer name	Primer sequence (5'–3')	
	Forward	Reverse
<i>GAPDH</i>	GATGGTGAAGGTCGGAGTGAAC	GTCATTGATGGCGACGATGT
<i>ACTB</i>	ATCACCATCGGCAATGAGCGGTTC	CGGATGTCGACGTCACACTTCATGA
<i>H2A</i>	GAGGAGCTGAACAAGCTGTTG	TTGTGGTGGCTCTCAGTCTTC
<i>18S rRNA</i>	AGAAACGGCTACCACATCCA	CACCAGACTTGCCCTCCA
<i>EEF1A2</i>	GCAGCCATTGTGGAGATG	ACTTGCCCCGCCTTCTGTG
<i>ING3</i>	ACGAGAAGGTTCAAGTTGGCA	TGTCTAATTCCAGAGATCGCCT
<i>TP53</i>	TCCGTCTAGGGTTCCTGCAATC	AGCTGCACTGGGCAGGTCTT
<i>CDKN1A</i>	GAGACCCCCAGAAGAGCCAC	AAAGTCGAAGTTCACCGCT
<i>BAX</i>	TCTGACGGCAACTTCAACTG	TGGGTGTCCCAAAGTAGGAG
<i>BCL2L1</i>	GGTATTGGTGAGTCGGATCG	CAAGACGACCCGAGTGAGAA
U6	CGCTTCGGCAGCACATATACTA	ACGCTTCACGAATTTGCGTGTC
miR-101-2	GGGGGTACAGTACTGTGATAACTGA A	the miscript universal primer
<i>CDX2</i>	GCAAAGGAAAGGAAAATCAACAA	GGGCTCTGGGACGCTTCT
<i>POU5F1</i>	CCACCCTGCAGCAAATTAGC	CCACACTCGGACCACGTCTT
<i>SOX2</i>	GGTTGACATCGTTGGTAATTTATAAT AGC	CACAGTAATTTTCATGTTGGTTTT TCA
<i>NANOG</i>	CGTGTCTTGCAAACGTCAT	CTGTCTCTCCTCTTCCCTCCTC

Annealing temperature is 60°C.

Figure S1



**Supplemental Figure S1.** The expression of miR-101-2 in bovine fetal fibroblasts and clone cells. miR-101-2 expression was assessed by real-time PCR in BFF, 513-B1-BFF (BFFs transfected with empty vectors) and miR-101-BFF (BFFs with miR-101-2 overexpression). Data are shown as mean  $\pm$  standard deviation (SD) from 3 experimental repeats (\*\* $p < 0.01$ ).