

Supplementary Information

Establishment of Bactrian Camel Induced Pluripotent Stem Cells and Prediction of Their Unique Pluripotency Genes

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Table S1-S7

Table S1. Primers used in the construction of pMXS-EGFP and corrected pMXS-SOX2

Gene	Primer	Enzyme loci	Annealing temp(°C)	Fragment size(bp)
<i>EGFP</i>	TTTAAGCTTTTACTTGTACAGCTCGTCC TAAGGATCCATGGTGAGCAAGGGCGAG	HidIII BamI	57	738
<i>EGFP-J</i>	GGTGGGGTCTTTCATTCC CGCCGACACCAGACTAAG		57	1006
pMXC-F	CCGCTCGAGTTTAAATAGTACA	Xho I	57	
<i>Sox2-R1</i>	TAAGGATCCCAGTGTGGTGGTACGGGA AATCACAAGTTTG	BamI	58	1174
<i>Sox2-R2</i>	CACAAGTTTGTACAAAAAAGCAGGCTA TGTATAACATGAT		58	1144
<i>Sox2-jian</i>	GGTGGGGTCTTTCATTCC CGCCGACACCAGACTAAG		57	1430

Table S2. The composition of 6 different culture protocols

Protocol	OSKG	M	Trophoblast	VTN-N	E8	E8+LIF
1	√	√	√		√	
2	√	√	√			√
3	√	√		√	√	
4	√		√		√	
5	√		√			√
6	√			√	√	

O: Pseudovirus of *Oct4* gene

S: Pseudovirus of *Sox2* gene

K: Pseudovirus of *Klf4* gene

M: Pseudovirus of c-*Myc* gene

G: Pseudovirus of *EGFP* gene

Trophoblast: Mouse embryo fibroblasts treated with mitomycin C

VTN-N: Vitronectin (VTN-N) Recombinant Human Protein, Truncated

E8:Essential 8™ medium

LIF: 1000 U/ml leukemia inhibitory factor

Table S3. Primers used to detect endogenous genes and three germ layer genes

Gene	Primer	Annealing temperature(°C)	Fragment size(bp)
<i>Endo Sox2</i>	AGAGAACCCCAAGATGCACA	57	104
	GCTTGGCCTCGTCGATAAAC		
<i>Endo Nanog</i>	GATGCCTGGCGAATACTTCC	63	329
	CTGCTGGGGACTGACATACT		
<i>FoxA2</i>	ACAACCTCATGTCCTCGGAG	60	225
	TAATGGGTCGGGAGTACACC		
<i>MYOD1</i>	GGAGCTAGAGAGGACGAGCA	55	172
	TCTCAAAGGCCTCGTTGACT		
<i>DES</i>	CCATCGCGGCTAAGAACATC	55	184
	GAATCGTTGGTGCCCTTGAG		
<i>MYF5</i>	ACTTGCAAGGCTCAGACGAG	60	165
	TGACCTTCTTCAGGCGTCTT		
<i>GFAP</i>	ACATTGAGAAGGTGCGCTTC	55	190
	TGTGCCAGATTGTCCCTCTC		
<i>PAX6</i>	TCAGCACCAGTGTCTACCAG	55	243
	AGGTATCATAACTCCGCCCCG		
<i>TERT</i>	AGAAGCTAGTCTCCCTGGGA	57	174
	CCATCAACCAGCACAGGAAC		
<i>β-Actin</i>	CTGGACTTGGAGCAGGAGATG	55	234
	CACCGTGTTGGCGTAGAGG		

Table S4. Primers used to detect RNA-Seq sequencing data

Gene	Primer	Annealing temperature(°C)	Fragment size(bp)
<i>CCNB2</i>	AGTACCTGAGGCAGCTTGAG	53	231
	GCAGAGCTGTAATCCCAACC		
<i>CDC20</i>	AGAATCAGCCCGAAAACAGC	57	220
	AGGGAAGGAATGTAACGGCA		
<i>ICAM1</i>	TGATACCCTCCGGATTGTGG	56	247
	ATTCTCCAGTCTACTCCGCG		
<i>IFK67</i>	CCGTCATACCCAGCAGTGAA	56	208
	CCTGGCGCTTTCTGGAATTT		
<i>MMP9</i>	GCAAACCAATCTCACCGACA	53	223
	GGTCAGAAATTTGCCACGT		
<i>PCNA</i>	CGGACACCTTGGCACTAGTA	56	215
	CACCCCATCTTTTGCACAGG		
<i>PLK1</i>	CTCGACACGCCTTATCCTCT	53	206
	GGGCTAGCTCATCACCTTCA		
<i>RRM2</i>	TGCCTGCCTGATGTTCAAAC	53	182
	GCATAAGTCTGTCTGCCACG		
<i>S100A4</i>	TTCCACAAGTACTCGGGCAA	56	242
	TTATCCGGGAAGCCTTCGAA		
<i>TP3</i>	GAGGACGCCAGTGGTAATCT	56	197
	AGCGGCTTCTTCTTTTGTGG		
<i>VEGFC</i>	CTCTCTCTCAAGGCCCAAA	53	244
	GGGTCATCTCCAGCGTTAGA		
<i>VIM</i>	GATTCAGGAACAGCACGTCC	56	207
	TTGGATTCTTGCTTCGCCTG		

Table S5. Inducible genes collection

Gene	Author	Gene	Author	Gene	Author
<i>c-Myc</i>	Takahashi K et al ^[1]	<i>Sox15</i>	Nakagawa M et al ^[2]	<i>PAX1</i>	Shu J et al ^[3]
<i>L-Myc</i>	Nakagawa M et al ^[4]	<i>Sox18</i>	Nakagawa M et al ^[2]	<i>GATA4</i>	Shu J et al ^[3]
<i>N-Myc</i>	Nakagawa M et al ^[4]	<i>Rcor2</i>	Yang P et al ^[5]	<i>CEBPa</i>	Shu J et al ^[3]
<i>Glis1</i>	Maekawa M et al ^[6]	<i>Obox1</i>	Wu L et al ^[7]	<i>HNF4a</i>	Shu J et al ^[3]
<i>Klf4</i>	Takahashi K et al ^[1]	<i>GMNN</i>	Shu J et al ^[3]	<i>GRB2</i>	Shu J et al ^[3]
<i>Klf1</i>	Lee B C et al ^[8]	<i>TH2A</i>	Toshie et al ^[9]	<i>Tet1</i>	Gao Y et al ^[10]
<i>Klf2</i>	Lee B C et al ^[8]	<i>TH2B</i>	Toshie et al ^[9]	<i>Jhdm1b</i>	Liu J et al ^[11]
<i>Klf5</i>	Lee B C et al ^[8]	<i>Oct4</i>	Takahashi K et al ^[1]	<i>Bmi1</i>	Moon JH et al ^[12]
<i>Esrrb</i>	Bo F et al ^[13]	<i>Nr5a1</i>	Heng J et al ^[14]	<i>Sall4</i>	Liu J et al ^[11]
<i>Bmp4</i>	Chen J et al ^[15]	<i>Nr5a2</i>	Heng J et al ^[14]	<i>Dppa2</i>	Buganim Y et al ^[16]
<i>Nanog</i>	Yu J et al ^[17]	<i>CDH1</i>	Redmer T et al ^[18]	<i>Lrh1</i>	Liu J et al ^[11]
<i>Lin28</i>	Yu J et al ^[17]	<i>TCL-1A</i>	Picano-Castro V et al ^[19]	<i>Jdp2</i>	Liu J et al ^[11]
<i>Sox2</i>	Takahashi K et al ^[1]	<i>Brn4</i>	Bar-Nur O et al ^[20]	<i>Id1</i>	Liu J et al ^[11]
<i>Sox1</i>	Nakagawa M et al ^[2]	<i>GATA6</i>	Shu J et al ^[3]		
<i>Sox3</i>	Nakagawa M et al ^[2]	<i>Sox7</i>	Shu J et al ^[3]		

Table S6. Annotation information in the GO term and KEGG pathway where the induced gene is located

Database	Detailed information
Pathway	ko04550//Signaling pathways regulating pluripotency of stem cells ko04390//Hippo signaling pathway ko05200//Pathways in cancer ko04350//TGF-beta signaling pathway ko04218//Cellular senescence ko05202//Transcriptional misregulation in cancers ko04950//Maturity onset diabetes of the young ko04934//Cushing syndrome
GO Component	GO:0043231//intracellular membrane-bounded organelle GO:0043232//intracellular non-membrane-bounded organelle GO:0044451//nucleoplasm part GO:0090575//RNA polymerase II transcription factor complex GO:0044424//intracellular part
GO Function	GO:0000982//transcription factor activity, RNA polymerase II core promoter proximal region sequence-specific binding GO:0000977//RNA polymerase II regulatory region sequence-specific DNA binding GO:0003712//transcription cofactor activity GO:0046983//protein dimerization activity GO:0003723//RNA binding GO:0000976//transcription regulatory region sequence-specific DNA binding GO:0008134//transcription factor binding GO:0005515//protein binding GO:0046914//transition metal ion binding GO:0001071//nucleic acid binding transcription factor activity GO:0043169//cation binding GO:0000975//regulatory region DNA binding GO:0003700//transcription factor activity, sequence-specific DNA binding GO:0000981//RNA polymerase II transcription factor activity, sequence-specific DNA binding GO:0003677//DNA binding GO:0003676//nucleic acid binding GO:0019904//protein domain specific binding
GO Process	GO:0001101//response to acid chemical GO:0006357//regulation of transcription from RNA polymerase II promoter GO:0001708//cell fate specification GO:0019827//stem cell population maintenance GO:0008284//positive regulation of cell proliferation GO:0003006//developmental process involved in reproduction GO:0045597//positive regulation of cell differentiation GO:0060795//cell fate commitment involved in formation of primary germ layer GO:0008285//negative regulation of cell proliferation GO:0008283//cell proliferation GO:0042981//regulation of apoptotic process GO:0006355//regulation of transcription, DNA-templated GO:0043009//chordate embryonic development GO:0010468//regulation of gene expression
No information	No information

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