Supplementary material

***In vitro* induced pluripotency from urine-derived cells in porcine**

Supplementary Table 1 Primers used for pluripotency characterization and EBs differentiation. Porcine specific primers' names are preceded by "p"

Primers	Forward	Reverse	bp
pOCT4	GGGTTCTCTTTGGGAAGGTGT	CTCCAGGTTGCCTCTCACTC	224
pSOX2	CTCAGTGGTCAAGTCCGAGG	AGAGAGAGGCAGTGTACCGT	223
pNANOG	TCCTTCCTCCATGGATCTGCT	GGGTCTGCGAGAACACAGTT	155
pGAPDH	GTCGGTTGTGGATCTGACCT	ACCAGGAAATGAGCTTGACGA	221
mOSKM	ACGAGCCACAAGCTCACCTCT	GGCATTAAAGCAGCGTATCC	221
β-ACTIN3	GAAGATCAAGATCATCGCGCCT	GTGGAATGCAACTAACAGTCCG	177
AFP	GGAATGCTGCAGAGGAAACG	TTCAAGTGTGGTGGGCAACTT	130
VIMENTIN	GTGATGTCCGCCAGCAG	CGCTTCCAGAGACTCGTT	217
β-TUBULINIII	CAGAGCAAGAACAGCAGCTACTT	GTGAACTCCATCTCGTCCATGCCCTC	227

Supplementary Table 2 Number of AP positive, partially positive, and negative UDC-derived iPSCs colonies at p0 for both human and murine reprogramming factors

	Colonies	%	Positive	%	Partially positive	Negative
hOSKM	1541	7.71%	38	2.47%	889	614
mOSKM	1691	8.46%	57	3.37%	1175	460

Supplementary Table 3 Summary of pluripotency detection through immunofluorescence in iPSCs derived from UDCs. The weakly positive cells were represented with "+", the positive cells were represented with "++", partially positive cells with +/- and negative cells were represented with "-"

	C1		C2		C3	
	EP	IP	EP	IP	EP	IP
OCT4	++	++	++	++	+	+
SOX2	++	++	++	++	+	+
NANOG	+	+/-	+	+/-	+/-	+/-
SSEA1	-	+	-	+	+/-	+/-
TRA-1-81	-	-	-	-	+/-	+/-

Supplementary Table 4 Statistical analysis of mRNA relative abundance (mean ± SD) of UDCs and iPSCs for endogenous and exogenous gene expression. $^{A-C}$Superscript capital letters represent differences ($P < 0.05$) between columns in the same line

Gene	UDC	Clonal lineages		
		C1	C2	C3
OCT4	0 ± 0^{B}	0.0671 ± 0.0593^{A}	0.0298 ± 0.0198^{A}	0.0670 ± 0.0248^{A}
SOX2	$4.2896 \times 10^{-5} \pm 1.9131 \times 10^{-5}$ C	0.1213 ± 0.0485^{A}	0.0689 ± 0.0328^{ABC}	0.0689 ± 0.0244^{B}
NANOG	$1.1777 \times 10^{-4} \pm 1.0832 \times 10^{-4}$ B	0.0034 ± 0.0023^{A}	0.0042 ± 0.0023^{A}	0.0031 ± 0.0018^{A}
mOSKM	0 ± 0^{C}	0.5369 ± 0.1253^{B}	0.4733 ± 0.1258^{B}	0.7430 ± 0.1685^{A}

Supplementary Table 5 Statistical analysis of mRNA relative abundance (mean ± SD) of UDCs and iPSCs for endogenous and exogenous gene expression. $^{A-C}$Superscript capital letters represent differences ($P < 0.05$) between columns in the same line

GENE	UDC	iPSCs		
		EP	IP	LP
OCT4	0 ± 0^{B}	0.0481 ± 0.0343^{A}	0.0593 ± 0.0486^{A}	0.0698 ± 0.0513^{A}
SOX2	$4.2896 \times 10^{-5} \pm 1.9131 \times 10^{-5\ B}$	0.0716 ± 0.0442^{AB}	0.0979 ± 0.0448^{A}	0.0998 ± 0.0411^{A}
NANOG	$1.1777 \times 10^{-4} \pm 1.0832 \times 10^{-4\ C}$	0.0046 ± 0.0021^{A}	0.0018 ± 0.0004^{B}	0.0042 ± 0.0021^{AB}
mOSKM	0 ± 0^{B}	0.4778 ± 0.0998^{A}	0.6509 ± 0.2067^{A}	0.7002 ± 0.1470^{A}