

Table SI.Markers identified in cell authentication analysis by short tandem repeat.

Cell line	Amelogenins		D5S818		D13S317		D7S820		D16S539		vWA		TH01		TPOX		CSF1P0	
HaCaT	X	X	12		8	9	11	12	11		15	17	8		11		12	
HeLa	X		11	12	12	14	11		9	10	16	18	7	9	8	12	9	10
SiHa	X		9		11		9		12		14	17	6	9	8		12	
CasKi	X		13		8		8	11	11	12	17		7		8		10	
C4-I	X		9	11	11	12	10	11	11		14		9	3	10	11	12	
C33-A	X		11	12	13		11	12	13	14	18	19	7	8	9		12	
HCB-514	X		10		9	11	9		9		16		7		8	12	12	

Table SII. Dilution of the siPORT™ NeoFX™ transfection reagent used in the present study.

Medium/reagent used	96-well plate	24-well plate	12-well plate	6-well plate
Opti-MEM culture medium	10	25 μ L	50 μ L	100 μ L
siPORT NeoFX transfection agent	0.625 μ L	1.25 μ L	2.5 μ L	5 μ L

Table SIII. Number of cells and transfection volume used for transfection.

Cells/volume	96-well plate	24-well plate	12-well plate	6-well plate
Cell volume	80 μ l	450 μ l	900 μ l	2.3 ml
Total no. of cells	6×10^3	4×10^4	8×10^4	2×10^5
Final volume of transfection	100 μ l	500 μ l	1 ml	2.5 ml

Table SIV.Primers used for the evaluation of microRNA expression in the present study.

microRNA	Mature sequence	Concentration (mg/ml)	Cat.no.	Accession no.
RNU6-1	GUGCUCGCUUCGGCAGCACAUAUACUAAAAUUGGAACGAUACAGAGAAGAUUAGCAU GGCCCCUGCGCAAGGAUGACACGCAAAUUCGUGAAGCGUCCAUUUUU	10	MIRCP00001	NR_004394.1 ^a
miR-130a	CAGUGCAAUGUUAAAAGGGCAU	10	MIRAP00149	MI0000448 ^b

^aNCBI reference sequence; ^bmiRBase accession no.

Table SV. Thermocycling conditions use for RT-qPCR in the present study.

Poly A tailing Reaction	cDNA Reaction	qPCR (40 cycles)
37°C, 60 min	42°C, 20 min	95°C, 2 min
70°C, 5 min	85°C, 5 min	95°C, 15 sec
		60°C, 1 min

Table SVI.Enriched pathways for the *DLL1* and *WNT10A* genes.

Enriched pathways	P-value	FDR	Genes
Proteolysis and signaling pathway of notch(B)	1.01E-03	0.0152	<i>DLL1</i>
Pathways in cancer(K)	2.00E-03	0.0169	<i>WNT10A, DLL1</i>
WNT ligand biogenesis and trafficking(R)	4.38E-03	0.0169	<i>WNT10A</i>
Signaling by NOTCH2(R)	4.88E-03	0.0169	<i>DLL1</i>
Signaling by NOTCH3(R)	7.40E-03	0.0169	<i>DLL1</i>
Presenilin action in Notch and Wnt signaling(N)	7.57E-03	0.0169	<i>DLL1</i>
Notch signaling pathway(N)	8.74E-03	0.0169	<i>DLL1</i>
Notch signaling pathway(K)	8.91E-03	0.0169	<i>DLL1</i>
Signaling by NOTCH1(R)	0.0103	0.0169	<i>DLL1</i>
Basal cell carcinoma(K)	0.0106	0.0169	<i>WNT10A</i>
Th1 and Th2 cell differentiation(K)	0.0154	0.0169	<i>DLL1</i>
Endocrine resistance(K)	0.0163	0.0169	<i>DLL1</i>
Cadherin signaling pathway(P)	0.0168	0.0169	<i>WNT10A</i>
Signaling pathways regulating pluripotency of stem cells(K)	0.0239	0.0239	<i>WNT10A</i>
mTOR signaling pathway(K)	0.0259	0.0259	<i>WNT10A</i>
Hippo signaling pathway(K)	0.0263	0.0263	<i>WNT10A</i>
Wnt signaling pathway(K)	0.0268	0.0268	<i>WNT10A</i>
Hepatocellular carcinoma(K)	0.0281	0.0281	<i>WNT10A</i>
Proteoglycans in cancer(K)	0.0342	0.0342	<i>WNT10A</i>
Wnt signaling pathway(P)	0.0453	0.0453	<i>WNT10A</i>

The letter in parentheses after each pathway gene set name corresponds to the source of the pathway annotations: B, BioCarta; K, Kyoto Encyclopedia of Genes and Genomes (KEGG); R, Reactome; P, Panther.