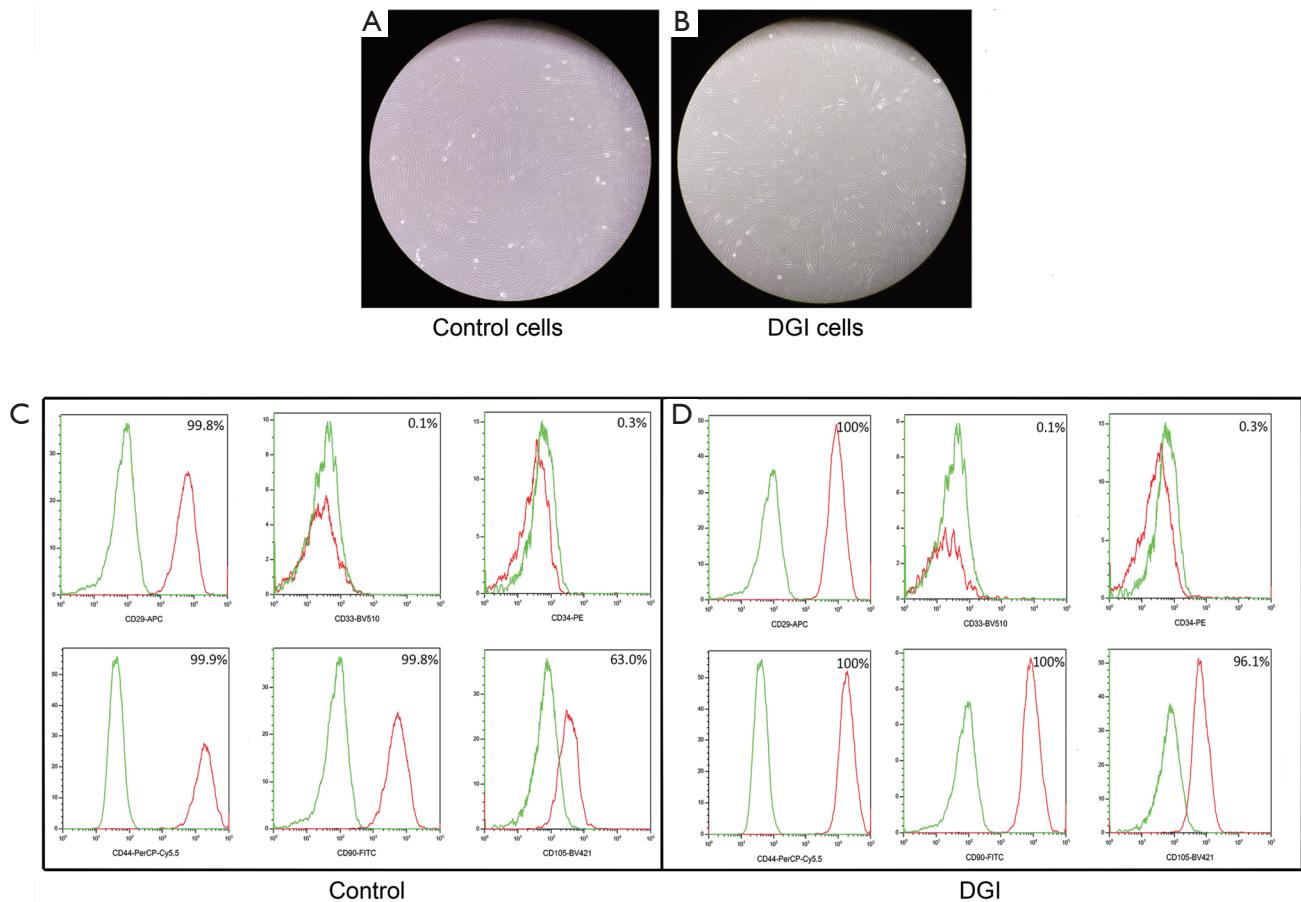


## Supplementary



**Figure S1** Isolation and Identification of hDPSCs. (A) The morphology of the control cells culture ( $\times 100$ ). (B) The morphology of the patient' cells culture ( $\times 100$ ). (C) Flow cytometric analysis of control cells. Control cells are positive for CD29, CD44, CD90, and CD105 and negative for CD33 and CD34. (D) Flow cytometric analysis of patient' cells. DGI cells are positive for CD29, CD44, CD90, CD105 and negative for CD33 and CD34. hDPSCs, human dental pulp stem cells; DGI, dentinogenesis imperfecta.

**Table S1** Primers used for *DSPP* gene verification and qPCR

Amplicon	Primers sequence (5' to 3')	Amplicon size (bp)
DSPP, c.53T>G	F-GGGCTGATCTAACACGTCCA R-CCACTGGCATTAACTCATCCT	500
DSPP-qPCR	F-ACACCCAGAACGCTAACCAT R-TACCTTCGTTGCCCTTCCCA	168
ALP	F-TAAGGACATCGCCTACCAGCTC R-TCTTCCAGGTGTCAACGAGGT	169
RUNX2	F- CTGTGGTTACTGTCATGGCG R- AGGTAGCTACTGGGGAGGA	183
GAPDH	CTTGGTATCGTGGAGGACTC GTAGAGGCAGGGATGATGTTCT	136

**Table S2** The element content in DGI teeth and control

Variable	C/%	O/%	Mg/%	Ca/%	P/%	Ratio (Ca/P)
DGI	43.40±9.04	22.29±3.49	0.43±0.12	23.01±3.48	10.45±1.37	2.20±0.09
Control	58.00±9.76	18.57±5.48	0.37±0.20	15.52±2.79	7.52±1.48	2.07±0.08
P value	0.130	0.377	0.672	0.044	0.066	0.140

DGI, dentinogenesis imperfecta.

**Table S3** Pathogenicity prediction of *DSPP* mutation in the study

Nucleotide changes	Amino acid changes	SIFT	PolyPhen-2
c.53T > G	p.V18G	Deleterious	Probably damaging

*DSPP*, dentin sialophosphoprotein (NM\_014208).**Table S4** Mineralized calcium depositions of DGI and control

Variable	mineralized calcium deposition
DGI	23.32±4.27
Control	38.77±2.05
P value	0.012

DGI, dentinogenesis imperfecta.

**Table S5** The expression of *DSPP*, *ALP*, and *RUNX2* in patient and control cells

Variable	DSPP	ALP	RUNX2
Patient	0.38±0.18	723.56±40.92	2302.97±213.14
Control	0.96±0.27	710.72±92.51	3075.85±36.35
P value	0.022	0.866	0.007

*DSPP*, dentin sialophosphoprotein; *ALP*, alkaline phosphatase.