

Figure S1. Characteristics and phenotypes of BMSCs. (A) Swirling arranged morphology of BMSCs under microscopy (magnification, x100). (B-D) Phenotypic analysis of surface antigens related to BMSC, including CD29, CD45 and CD90 by flow cytometry. BMSC, bone marrow stem cells; CD, cluster of differentiation.

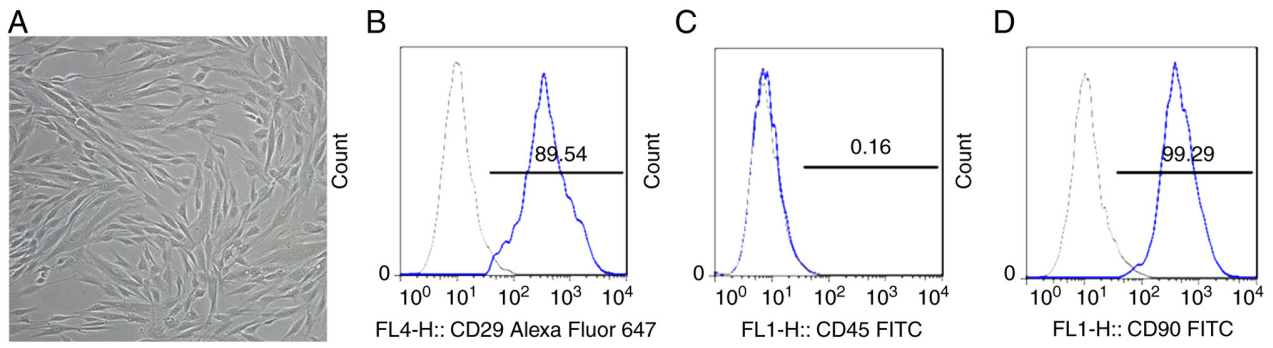


Table SI. Demographic characteristics of the patients and controls.

Number	Sex	Age	Height (cm)	Weight (kg)	Diagnosis	Stage	Underlying disease	Duration of the usage of glucocorticoid
ONFH1	F	32	162	67	Steroid-induced ONFH	ARCO III	SLE	35
ONFH2	F	26	157	49	Steroid-induced ONFH	ARCO IV	SLE	6
ONFH3	F	33	165	68	Steroid-induced ONFH	ARCO IV	SLE	17
ONFH4	F	54	160	60	Steroid-induced ONFH	ARCO IV	SLE	24
ONFH5	F	38	158	56	Steroid-induced ONFH	ARCO III	SLE	19
ONFH6	F	25	164	58	Steroid-induced ONFH	ARCO IV	SLE	39
ONFH7	F	44	166	60	Steroid-induced ONFH	ARCO IV	SLE	13
NORMAL1	F	26	154	47	DDH (Left hip)	Crowe IV	-	-
NORMAL2	F	29	157	44	DDH (Bilateral hip)	Crowe IV	-	-
NORMAL3	F	54	162	57	Femoral neck fracture (right)	Garden III	-	-
NORMAL4	F	67	167	72	Femoral neck fracture (left)	Garden IV	-	-
NORMAL5	F	75	163	65	Femoral neck fracture (right)	Garden IV	-	-
NORMAL6	F	48	161	67	DDH (right hip)	Crowe II	-	-
NORMAL7	F	32	158	46	DDH (bilateral hip)	Crowe IV	-	-

Table SII. Primers used in this study.

Primers	Sequence
U6-F	CTCGCTTCGGCAGCACA
U6-R	ACGCTTCACGAATTTGCGT
GAPDH-F	GGTCTCCTCTGACTTCAACA
GAPDH-R	GTGAGGGTCTCTCTCTTCCT
Hsa_circ_0000219-F	CTGGACGCAAGGGTTTGTGTTTA
Hsa_circ_0000219-R	ATGGTTAAGAGGAAAGACAAC
Hsa_circ_0004588-F	ACTACACGGAGATTAAGTGGCTC
Hsa_circ_0004588-R	GTATGACCTGATCCGGGTGTTT
Hsa_circ_0005936-F	ATGCAGGGATCTTTCACCTCCA
Hsa_circ_0005936-R	CTGCAAAAAGGCTCTCTCCTTG
Circ, circular.	

Table SIII. Functional analysis of differentially expressed microRNAs.

Accession	Description	Adj. P
Top 10 BP terms		
GO:0032501	Multicellular organismal process	1.1×10^{-111}
GO:0051239	Regulation of multicellular organismal process	1.8×10^{-106}
GO:0023051	Regulation of signaling	1.8×10^{-106}
GO:0010646	Regulation of cell communication	1.5×10^{-103}
GO:0032502	Developmental process	7.04×10^{-94}
GO:0048856	Anatomical structure development	1.76×10^{-90}
GO:0050794	Regulation of cellular process	3.4×10^{-88}
GO:0009966	Regulation of signal transduction	4.76×10^{-87}
GO:0065007	Biological regulation	6.04×10^{-86}
GO:0050789	Regulation of biological process	7.46×10^{-71}
Top 10 BP terms		
GO:0005515	Protein binding	2.54×10^{-61}
GO:0043167	Ion binding	5.89×10^{-54}
GO:0000981	RNA polymerase II transcription factor activity, sequence-specific DNA binding	5.51×10^{-49}
GO:0043169	Cation binding	3.7×10^{-45}
GO:0003700	DNA binding transcription factor activity	1.37×10^{-44}
GO:0046872	Metal ion binding	5.6×10^{-43}
GO:0000982	Transcription factor activity, RNA polymerase II proximal promoter sequence-specific DNA binding	4.93×10^{-41}
GO:0140110	Transcription regulator activity	4.49×10^{-39}
GO:0001228	Transcriptional activator activity, RNA polymerase II transcription regulatory region sequence-specific DNA binding	7.5×10^{-39}
GO:0098772	Molecular function regulator	1.15×10^{-32}
Top 10 Kyoto Encyclopedia of Genes and Genomes terms		
map04080	Neuroactive ligand-receptor interaction	2.27×10^{-27}
map04024	cAMP signaling pathway	2.62×10^{-20}
map04010	MAPK signaling pathway	1.45×10^{-18}
map04911	Insulin secretion	7.06×10^{-18}
map05165	Human papillomavirus infection	7.9×10^{-18}
map05226	Gastric cancer	8.05×10^{-17}
map04550	Signaling pathways regulating pluripotency of stem cells	8.05×10^{-17}
map04931	Insulin resistance	6.78×10^{-16}
map05200	Pathways in cancer	7.09×10^{-15}
map05224	Breast cancer	1.11×10^{-14}

Table SIV. Functional analysis of differentially expressed circularRNAs.

Accession	Description	Adj. P
Top 10 BP terms		
GO:0031585	Regulation of inositol 1,4,5-trisphosphate-sensitive calcium-release channel activity	7.96x10 ⁻⁰⁵
GO:0010469	Regulation of receptor activity	0.009601
GO:0016485	Protein processing	0.028804
GO:0048856	Anatomical structure development	0.028804
GO:0044767	Single-organism developmental process	0.028804
GO:0048731	System development	0.028804
GO:0051604	Protein maturation	0.028804
GO:0070076	Histone lysine demethylation	0.028804
GO:0016577	Histone demethylation	0.028804
GO:0007275	Multicellular organism development	0.028804
Top 10 MF terms		
GO:0043167	Ion binding	5.9x10 ⁻⁰⁵
GO:0004597	Peptide-aspartate beta-dioxygenase activity	0.006738
GO:0043169	Cation binding	0.007439
GO:0070300	Phosphatidic acid binding	0.008211
GO:0046872	Metal ion binding	0.008422
GO:0030742	GTP-dependent protein binding	0.008422
GO:0032454	Histone demethylase activity (H3-K9 specific)	0.009475
GO:0043168	Anion binding	0.009475
GO:0005085	Guanyl-nucleotide exchange factor activity	0.01778
GO:0008270	Zinc ion binding	0.019792
Top 10 Kyoto Encyclopedia of Genes and Genomes terms		
map00900	Terpenoid backbone biosynthesis	0.001889
map05100	Bacterial invasion of epithelial cells	0.002747
map04012	ErbB signaling pathway	0.003748
map04510	Focal adhesion	0.01167
map05200	Pathways in cancer	0.017482
map04810	Regulation of actin cytoskeleton	0.025801
map00500	Starch and sucrose metabolism	0.028838
map00410	beta-Alanine metabolism	0.038221
map04670	Leukocyte transendothelial migration	0.038956
map04391	Hippo signaling pathway - fly	0.040731
map00970	Aminoacyl-tRNA biosynthesis	0.049059