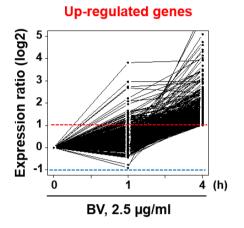
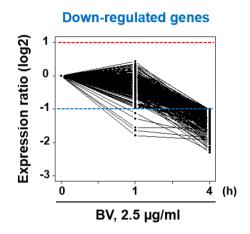
Supplementary Figure 1

Α





B Up-regulated genes

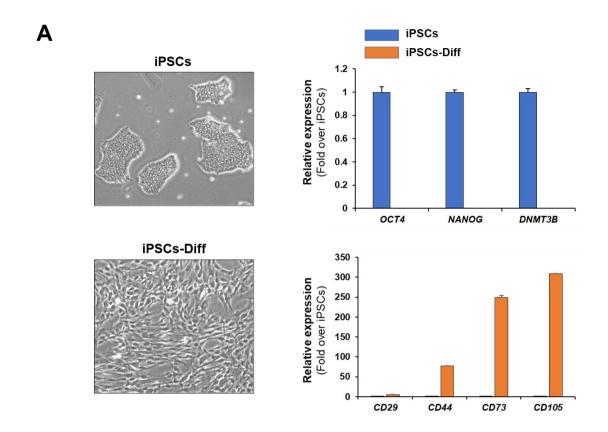
Signal transduction Regulation of cell migration								Development Differentiation				
Positive regulation of cell migration				egulation e activity	Histone H3-K4 methylation ph		phos	Protein phorylation	Nervous sy developm	stem region of epit meser		Positive regulation epithelial to esenchymal transition
Cell adhesion via plasma	Apoptotic process		Glutamate secretion		Negative regulation of cell growth		reg Rh	egative ulation of o protein signal naduction	Lung development	in utero embryonic development		Endoderm development
membrane adhesion molecules	Intracellular signal transduction	TGFβ receptor pathway		Response to mechanical stimulus	Regulation of actin cytoskeleton reorganization	Transcription from RNA polymerase II		Negative regulation of cell proliferation	memory	Bone mineralization		Positive regulation of astrocyte
Integrin- mediated signaling pathway	Response to stress	C	ell-cell		Regulation of small GTPase mediated signal transduction	Peptidyl- serine phospho- rytation		Negative regulation of cell cycle	Skeletal muscle cell differentiation	Negative regulation of		differentiation Endodermal cell
Cellular response to mechanical stimulus	e to regulation of pre-miRNA transcription		gnaling No gnaling	calcium	Extracellular matrix organization	Cell junction assembly		Regulation of PI3-kinase	Cell-mati	differentiati		

Down-regulated genes

Nucle asse	DNA metabolism				
Nucleosome assembly	Chromatin silencing at rDNA	Protein Hetero- tetramerization	Regulation of transcription, DNA-templated		
			Interstrand cross-link repair		
Telomere organization	Intraciliary transport	spliceosomal complex assembly	Acyl-CoA metabolism		

Supplementary Figure 1. QuentSeq analysis of BV-treated iPSCs. (A) iPSCs were treated with 2.5 μ g/ml BV for 1 and 4 h. After measurement of expression level of genes using QuantSeq analysis, time-dependently upregulated 567 genes and time-dependent down-regulated 333 genes were identified as DEGs. Threshold line for 2 or 0.5-fold ratio was shown in red or blue color, respectively. (B) Redundancy removed GO terms associated with DEGS were presented as treemap. Functionally related GO terms were represented with the same color. The area is proportional to the statistical significance of each GO term.

Supplementary Figure 2



В

Gene	Forward primer (5'_ 3')	Reverse primer (5'_ 3')			
OCT4	GGGAGGAGCTAGGGAAAGAAAA	ATTGAACTTCACCTTCCCTCCA			
NANOG	TTAATAACCTTGGCTGCCGTCT	AATAAGCAAAGCCTCCCAATCC			
DNMT3B	TCTCACGGTTCCTGGAGTGTAA	GTAGGTTGCCCCAGAAGTATCG			
CD29	GTAACCAACCGTAGCAAAGGA	TCCCCTGATCTTAATCGCAAAAC			
CD105	TGCACTTGGCCTACAATTCCA	AGCTGCCCACTCAAGGATCT			
CD73	GCCTGGGAGCTTACGATTTTG	TAGTGCCCTGGTACTGGTCG			
CD44	CTGCCGCTTTGCAGGTGTA	CATTGTGGGCAAGGTGCTATT			
GAPDH	CCTCAACGACCACTTTGTCAAG	тсттсстсттдтдстсттдстд			

Supplementary Figure 2. Characterization of iPSCs-derived differentiated cells (iPSCs-Diff). **(A)** Cell morphology of iPSCs and iPSCs-Diff was observed under an inverted microscope. Expression levels of pluripotent markers (e.g., OCT4, NANOG, DNMT3B) and mesenchymal progenitor cell markers (e.g., CD29, CD44, CD73, CD105) in iPSCs and iPSCs-Diff were analyzed by qPCR using specific primers **(B)**.