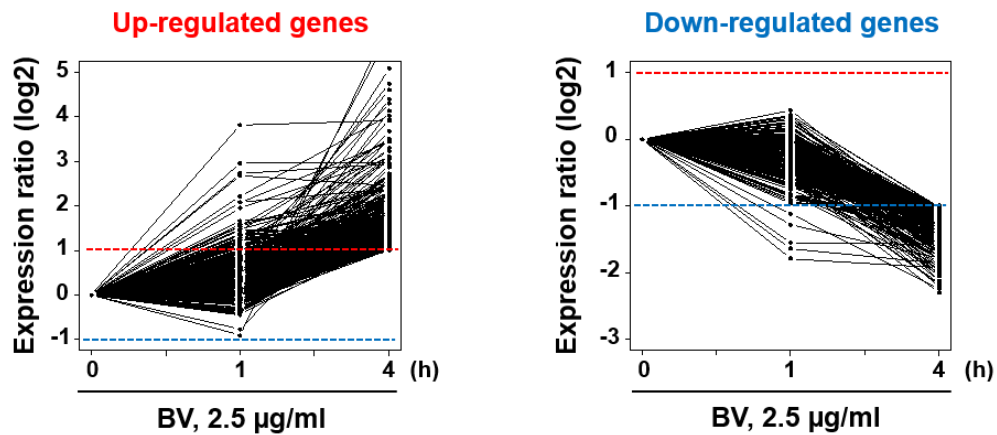
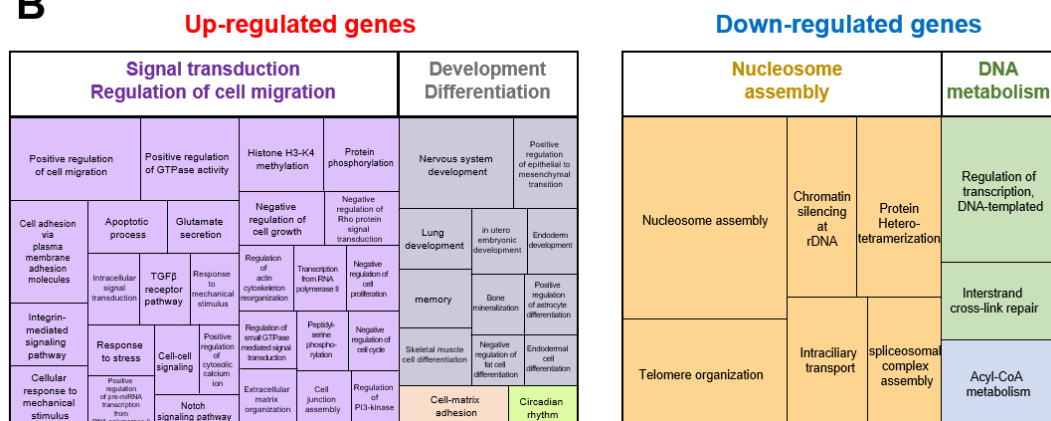


# Supplementary Figure 1

**A**

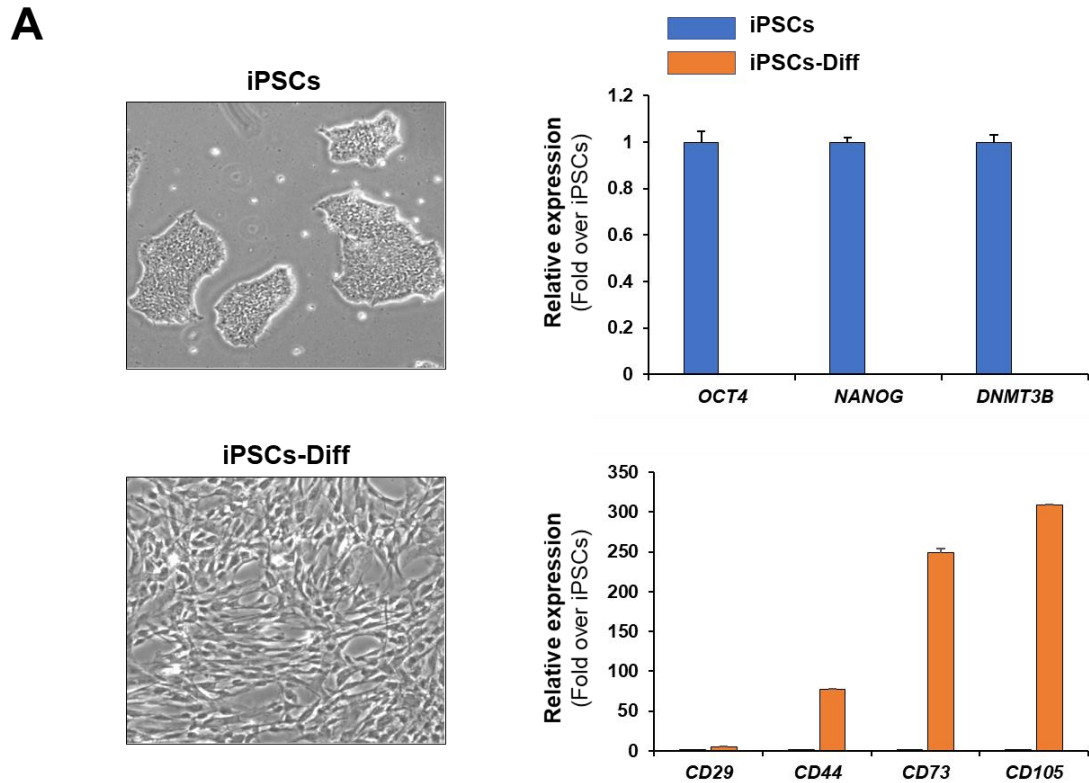


**B**



**Supplementary Figure 1.** QuentSeq analysis of BV-treated iPSCs. **(A)** iPSCs were treated with 2.5 µg/ml BV for 1 and 4 h. After measurement of expression level of genes using QuantSeq analysis, time-dependently up-regulated 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



## B

Gene	Forward primer (5'– 3')	Reverse primer (5'– 3')
<i>OCT4</i>	GGGAGGAGCTAGGGAAAGAAAA	ATTGAACTTCACCTTCCCTCCA
<i>NANOG</i>	TTAATAACCTTGGCTGCCGTCT	AATAAGCAAAGCCTCCCAATCC
<i>DNMT3B</i>	TCTCACGGTTCCTGGAGTGTA	GTAGGTTGCCCCAGAAGTATCG
<i>CD29</i>	GTAACCAACCGTAGCAAAGGA	TCCCCTGATCTTAATCGCAAAC
<i>CD105</i>	TGCACTTGGCCTACAATTCCA	AGCTGCCCACTCAAGGATCT
<i>CD73</i>	GCCTGGGAGCTTACGATTTTG	TAGTGCCCTGGTACTGGTCG
<i>CD44</i>	CTGCCGCTTTCAGGTGTA	CATTGTGGCAAGGTGCTATT
<i>GAPDH</i>	CCTCAACGACCACTTTGTCAAG	TCTTCCTCTTGTGCTCTTGCTG

**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)**.