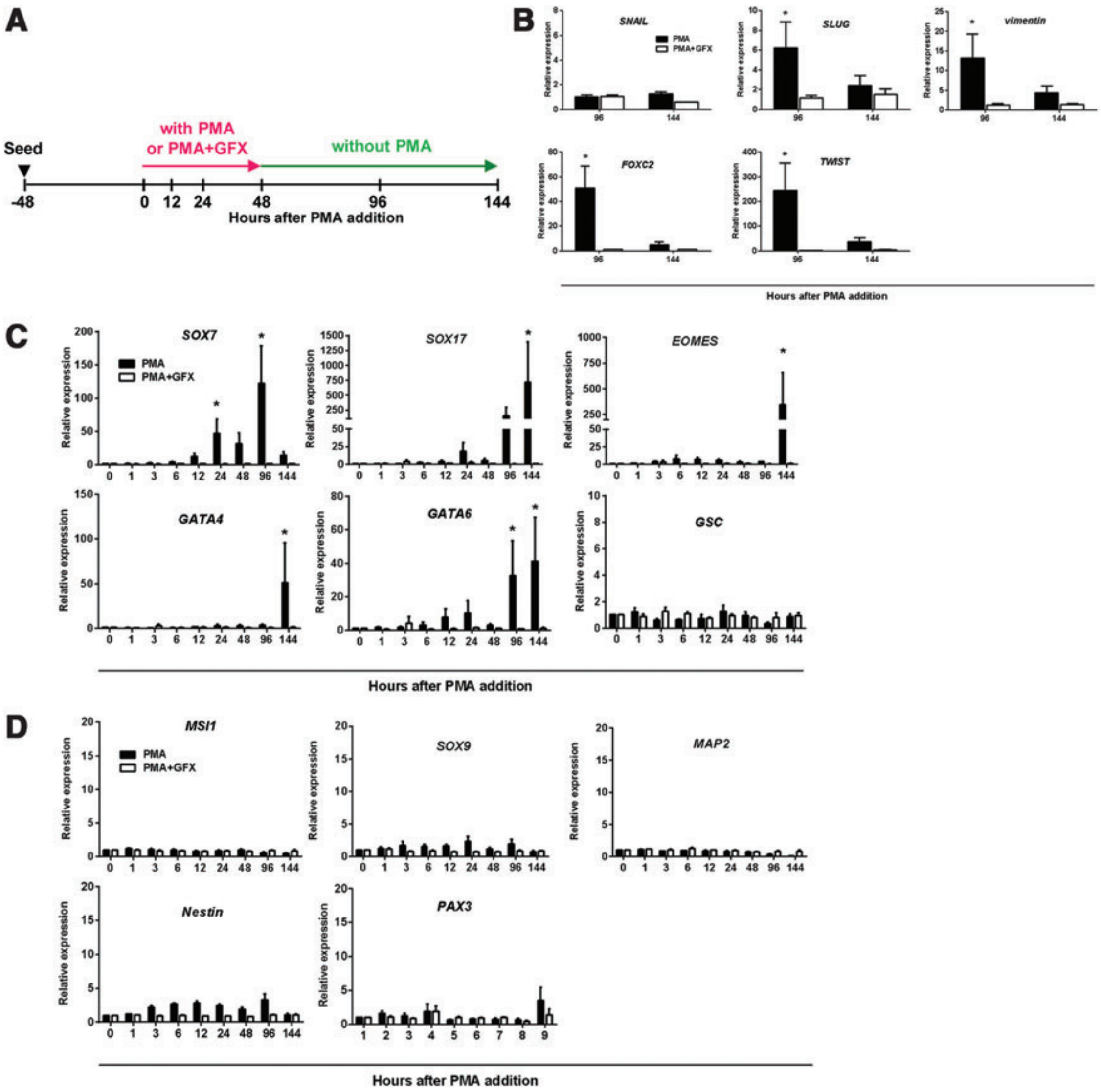
# Supplementary Data



**SUPPLEMENTARY FIG. S1.** Quantitative reverse transcription–polymerase chain reaction analysis of the expression levels of lineage-related genes in the cells after a 48-h phorbol 12-myristate 13-acetate (PMA) treament. The cells were treated with PMA (*black bars*) or PMA together with GFX (*white bars*) in the hESF9 medium for 48 h, and then the cells were grown in the hESF9 medium without PMA for more than 96 h. **(A)** Scheme of experiment. **(B)** The expression levels of epithelial–mesenchymal transition-related genes. **(C)** The expression levels of extraendoderm/endoderm or primitive streak maker genes. **(D)** The expression levels of ectoderm maker genes. Expression levels were all normalized against *GAPDH*. The relative expression levels of each gene were calculated from the undifferentiated H9 human embryonic stem cells untreated with PMA or PMA together with GFX. The data are represented as mean ± standard error (SE, $n = 3$). $^{*}P < 0.05$.