Figure S1. Reverse transcription-quantitative PCR analysis of ATF3 mRNA expression in exATF3 and exNC cells. GAPDH was used as an internal control. Data are presented as the mean ± SD from ≥3 independent experiments, and were analyzed using a one-tailed Student's t-test. ***P<0.001. ATF3, activating transcriptional factor 3; NC, negative control.

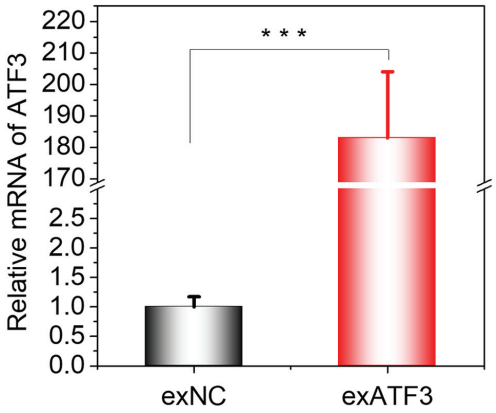

Figure S2. Assessment of JunB overexpression using western blotting in HEC-1B before and after transient transfection. Data are presented as the mean ± SD (n=3) and were analyzed using a one-tailed Student's t-test. **P<0.01.

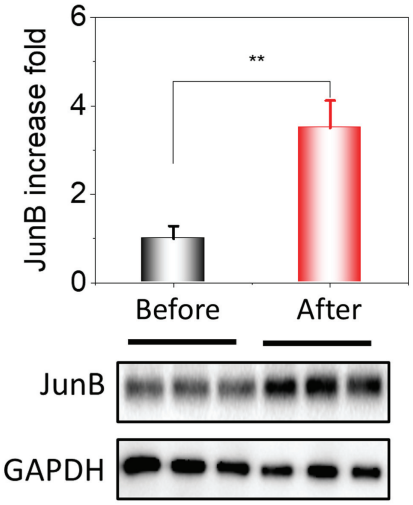

Figure S3. Verification of ATF3-JunB interaction *in vitro*. (A) HEC-1B genome library screening using ATF3 using Y2H. (B) P.C. mating between Y2HGold [pGBKT7-53] and Y187 [pGADT7-T]. N.C. mating between Y2HGold [pGBKT7-Lam] and Y187 [pGADT7-T]. Protein-protein interactions between ATF3 and JunB were evaluated by the ability of the yeast cells to grow on minimal medium in the presence of X-α-GAL. (C) Co-immunoprecipitation of endogenous ATF3 of 293T cells with JunB, and WB using anti-ATF3, anti-JunB antibodies indicated the binding of ATF3 and JunB. (D) HIS-tag pull-down of purified rhHIS-ATF3 by JunB and WB using anti-HIS tag antibodies identified the binding of HIS-ATF3 and JunB. ATF3, activating transcriptional factor 3; WB, western blotting; Y2H, yeast two-hybrid; P.C., positive control; N.C., negative control; HIS, polyhistidine.

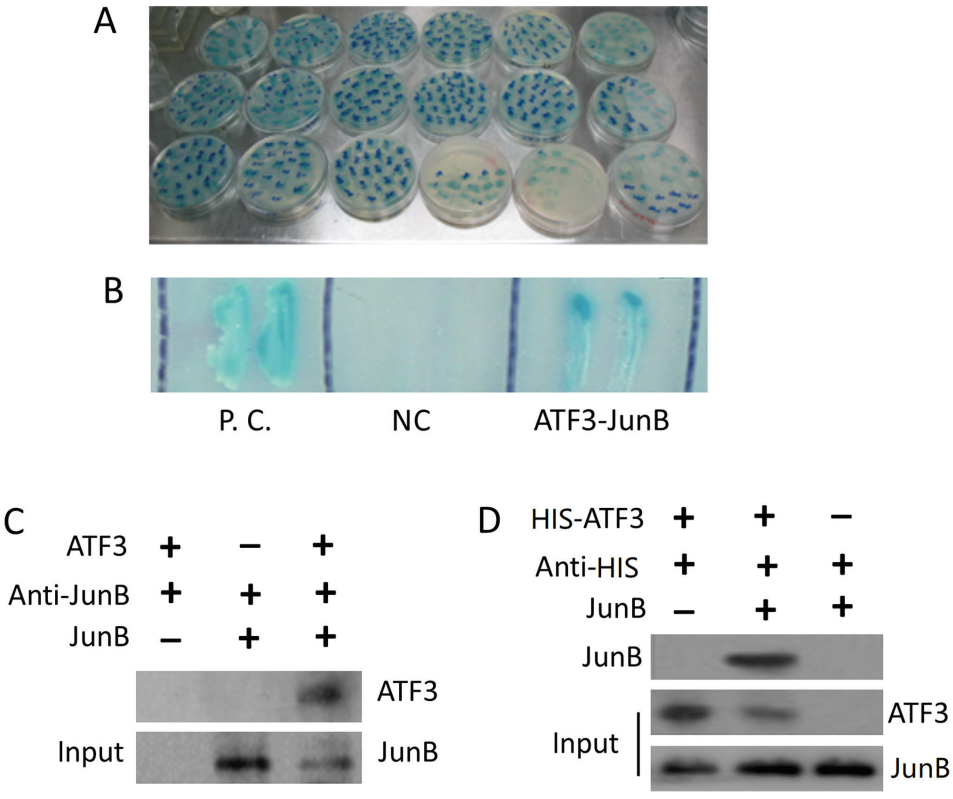

Figure S4. Reverse transcription-quantitative PCR analysis of JunB mRNA expression in exATF3 and exNC cells. GAPDH was used as an internal control. Data are presented as the mean ± SD from ≥3 independent experiments and were analyzed using a one-tailed Student's t-test. **P<0.01. ATF3, activating transcriptional factor 3; NC, negative control.