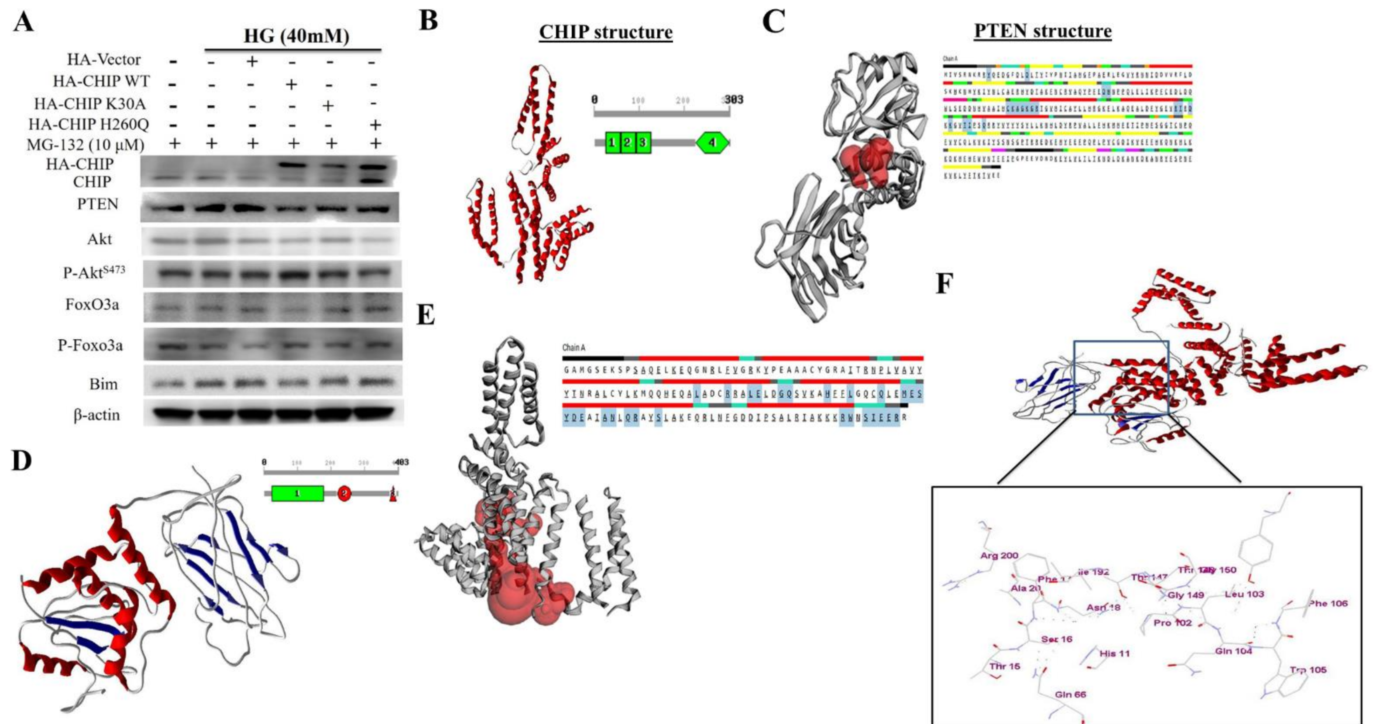

Fig S2. Molecular docking studies of CHIP with PTEN (A) WJMSCs were transfected with pRK5-HA-vector (3 μg), pRK5-HA-CHIP (3 μg), pRK5-HA-K30A (3 μg), or pRK5-HA-H260Q (3 μg) in the presence of MG-132 for 6 h followed by HG incubation for 24 h. Cell lysate was analyzed via immunoblotting. (**B**) The three dimensional structure of CHIP with twenty one helices; four regions including three domains with TPR function (1-3) and one domain with U-box (4). (**C**) Three dimensional structure of PTEN with nine sheets and five helices. Three different domains with dual specificity protein phosphatase (1); cyclic nucleotide binding (2); and ferredoxin like domain (3). (**D**) Prediction of binding sites (red color) in CHIP; amino acids involved in active site were predicted (grey color). (**E**) Prediction of binding sites (red color) in PTEN; amino acids involved in active site were predicted (grey color). (**F**) Molecular docking of CHIP with PTEN; the hydrogen bonding interactions and amino acids involved in docking were predicted.

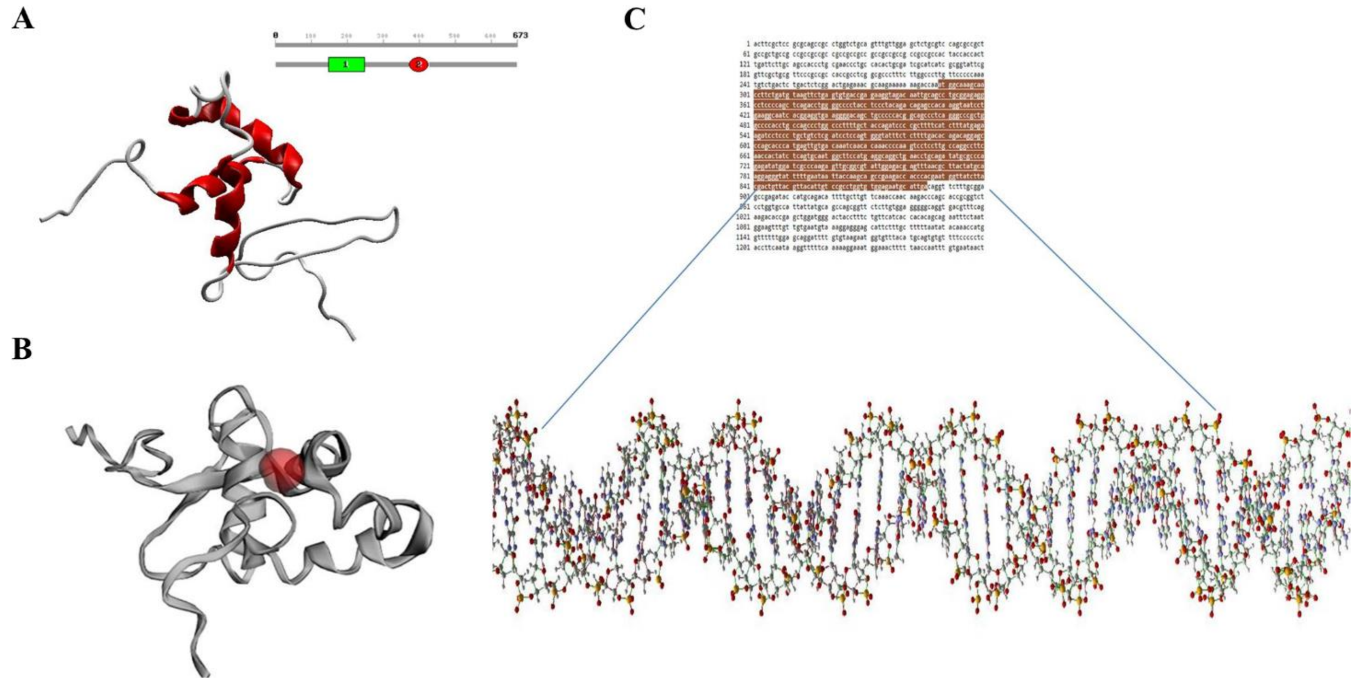

Fig S5. Insilico analysis of binding FOXO3a with the *bim* promoter region (A) The three dimensional structure of FoxO3a with three helices; two different domains fork head transcription factor (1); and unknown function (2). **(B)** Prediction of binding sites for FOXO3a using Castp server (red color). **(C)** Prediction of *bim* promoter region binding with FOXO3a; include residues from 289-885.

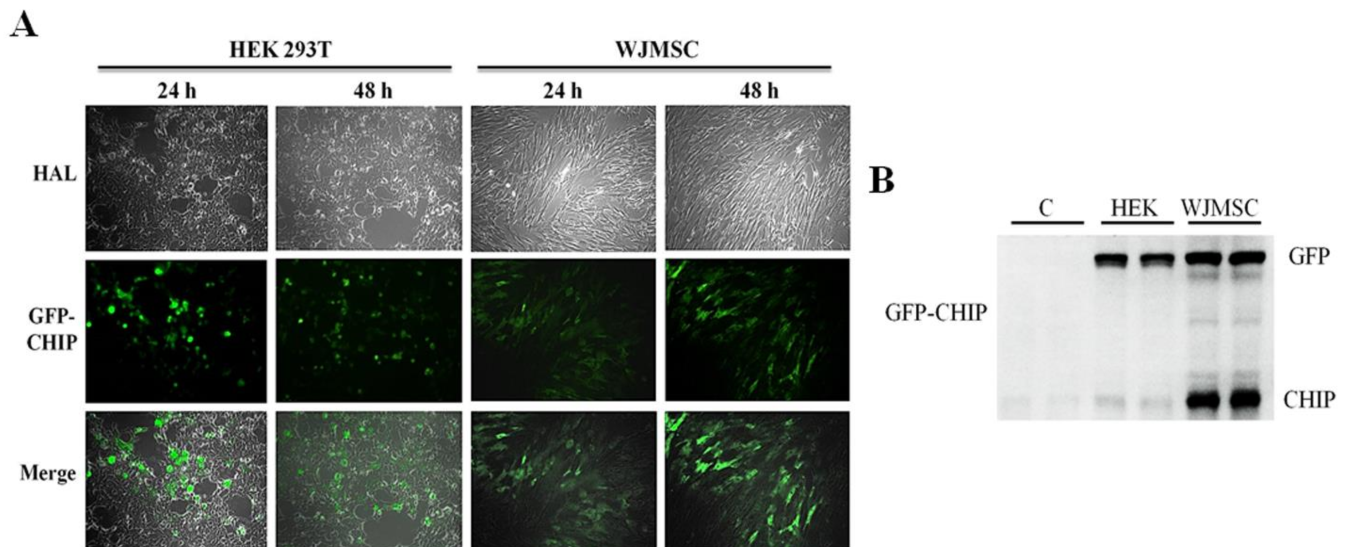

Fig S7. Establishment of stable cell line (A) Lentiviral particles from HEK293T cells were transduced into WJMSCs for 24 and 48 h, and examined under fluorescence microscope. **(B)** Total cell lysate from HEK293T and WJMSCs was harvested and immunoblotted to analyze the expression of GFP-CHIP.