

Supplementary Materials: Alpha6-Integrin Regulates FGFR1 Expression Through the ZEB1/YAP1 Transcription Complex in Glioblastoma Stem Cells Resulting in Enhanced Proliferation and Stemness

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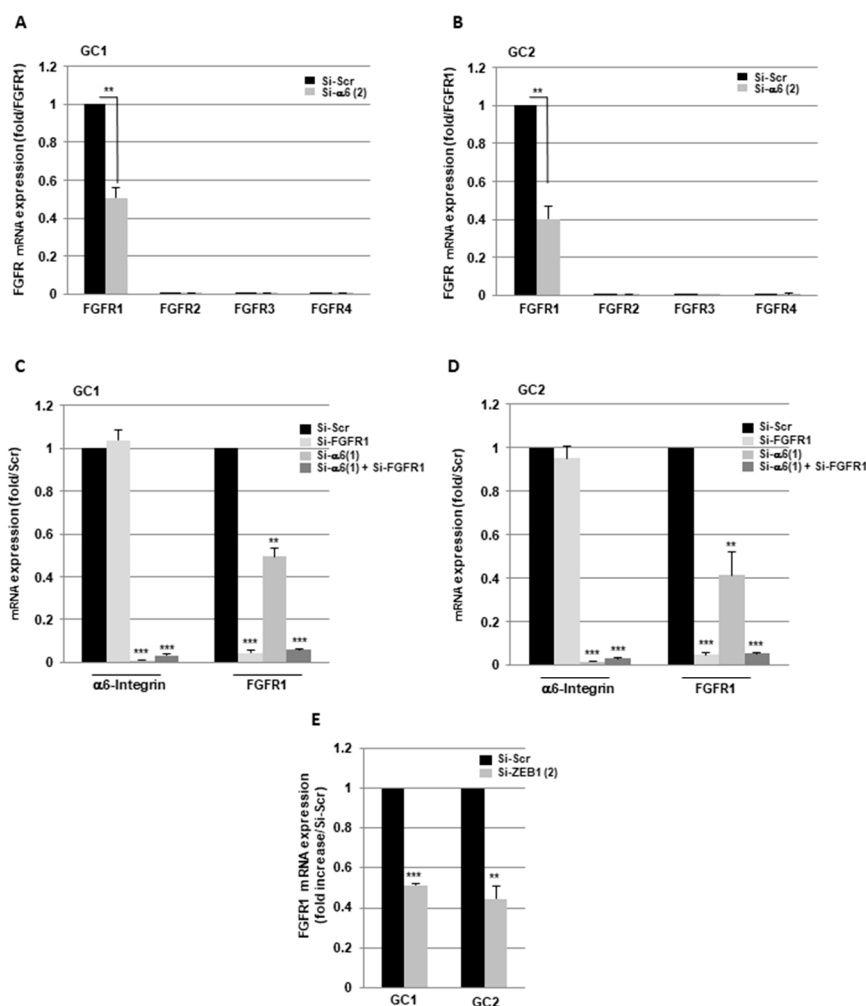


Figure S1. (A–E) GBMSC derived from GBM biopsy specimens (GC1, GC2) were transfected with an $\alpha 6$ -integrin siRNA (si- $\alpha 6$ (1) or si- $\alpha 6$ (2)), a FGFR1 siRNA (si-FGFR1), a combination of both siRNA (si- $\alpha 6$ (1) + si-FGFR1), a scramble control (si-Scr) or a ZEB1 siRNA (si-ZEB1 (2)) as indicated. FGFRs or $\alpha 6$ -integrin expression was analyzed by real time PCR. Quantifications of 3 independent experiments are presented as means \pm SD. *** $p < 0.001$; ** $0.001 < p < 0.01$.

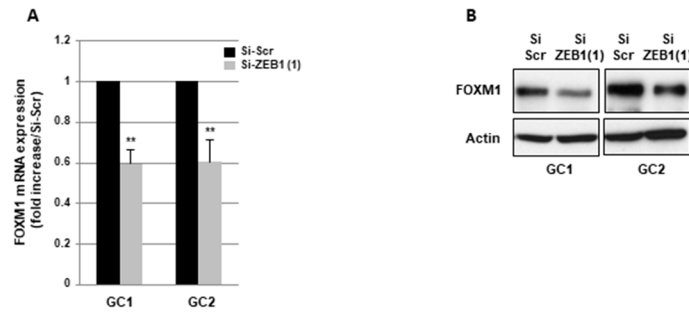


Figure S2. (A,B) GBMSC derived from GBM biopsy specimens (GC1, GC2) were transfected with a ZEB1 siRNA (si-ZEB1 (1)) or a scramble control (si-Scr). (A) FOXM1 expression was analyzed by real time PCR. Quantifications of 3 independent experiments are presented as means \pm SD. $** 0.001 < p < 0.01$. (B) FOXM1 protein expression was analyzed by western blot. Images are representative of 3 independent experiments. Actin was used as a loading control.

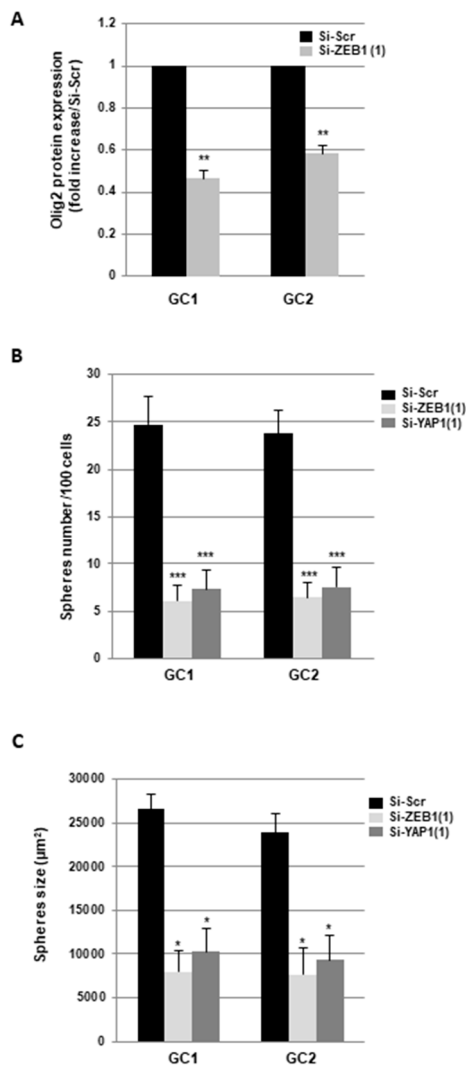


Figure S3. GBMSC derived from GBM biopsy specimens (GC1, GC2) were transfected with a ZEB1 siRNA (si-ZEB1(1)), a YAP1 siRNA (si-YAP1(1)) or a scramble control (si-Scr). (A) Olig2 protein expression was analyzed by western blot. (B,C) Spheres formation was analyzed as described in “methods”. (B). Neurospheres number was counted under the microscope. (A,C) Western blot images and the spheres size were quantified using the Image J software. Quantifications of 3 experiments are presented as means \pm SD. $*** p < 0.001$; $** 0.001 < p < 0.01$; $* 0.01 < p < 0.05$.



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