**Supplementary Figures**

**C:\Users\Jinlong Yin\2011년3월국립암센터\실험관련\TGase 2\Manuscript_160217\170206 CR\Revision_170316\최종\Supplemental Fig. 1.tif**

**Supplementary Figure 1.**

**TGM2 is highly expressed in the necrotic region of MES GBM. (A)** Showing the expression fold change of TGM2 in non-MES and MES tissues as determined by RNA sequencing. IHC results from GBM patients samples were analyzed for TGM2 expression level by TissueFAX. (**B)** Comparing the expression fold changes of TGM2 in non-necrotic versus necrotic tissues. (**C)** IHC analysis of TGM2 staining in GBM patient tissues. Scale bar, 100μm. N: necrotic region, PN: perinecrotic region. Scale bar, 500 μm.

**C:\Users\Jinlong Yin\2011년3월국립암센터\실험관련\TGase 2\Manuscript_160217\170206 CR\Revision_170316\최종\Supplemental Fig. 2.tif**

**Supplementary Figure 2.**

**TGM2 regulates stemness of MES, PN, and CL GSC. (A)** IB analysis of TGM2, CD44, TAZ, C/EBPβ, pSTAT3, and STAT3 in GSC (131) infected with shTGM2-expressing lentiviral or control construct. α-tubulin was used as a loading control. **(B)** LDA was performed in 131-Con, 131-shTGM2-B, and 131-shTGM2-C cells. **(C)** IB analysis of TGM2, CD44, TAZ, C/EBPβ, pSTAT3, and STAT3 in GSC (84NS) infected with TGM2-expressing lentiviral or control construct. α-tubulin was used as a loading control. **(D)** LDA was performed in 84NS-Con and 84NS-TGM2 cells. (**E)** IB analysis of TGM2, CD44, and C/EBPβ in 047T cells infected with TGM2-expressing lentiviral or control construct. α-tubulin was used as a loading control. (**F)** LDA was performed in 047T-Con and 047T-TGM2 cells. (**G)** IB analysis of TGM2, CD44, and C/EBPβ in 352T2 cells infected with TGM2-expressing lentiviral or control construct. Α-tubulin was used as a loading control. **(H)** LDA was performed in 352T2-Con and 352T2-TGM2 cells.

**C:\Users\Jinlong Yin\2011년3월국립암센터\실험관련\TGase 2\Manuscript_160217\170206 CR\Revision_170316\Supplementary Fig.3.tif**

**Supplementary Figure 3.**

**A negative correlation between C/EBPβ and GADD153. (A)** A dot plot of MES subtype-associated genes that are correlated with TGM2 in TCGA database. **(B** and **C)** IB analysis of TGM2 and GADD153 in 131 cells treated with the proteasome inhibitor MG132 (10 μM, 12 h) **(B)** and epoxomicin (2 μM, 12 h) **(C).** α-tubulin was used as a loading control.