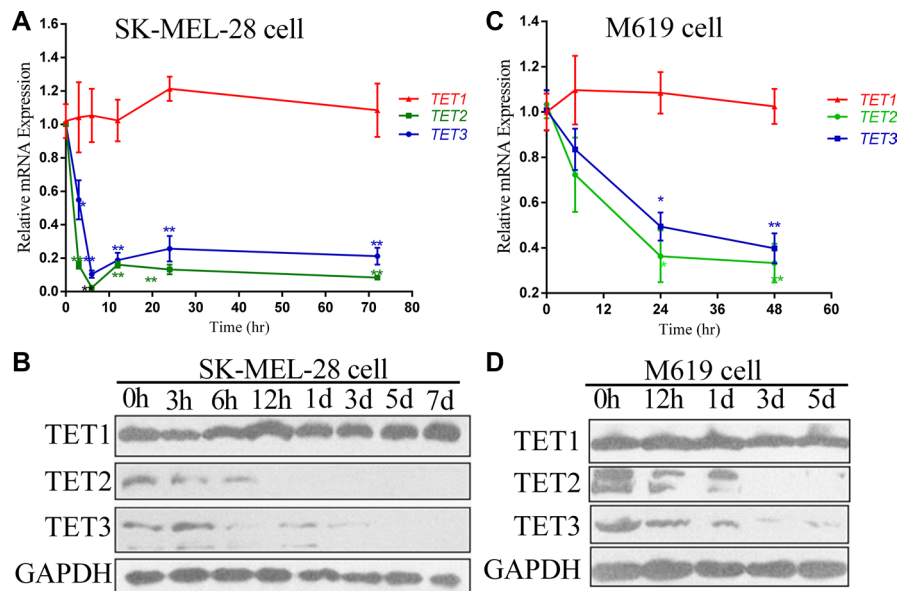# Epigenetic silencing of TET2 and TET3 induces an EMT-like process in melanoma

Supplementary Materials

Supplementary Figure S1: TGF-β1 induces the down regulation of TET2 and TET3 in SK-MEL-28 cells and M619 cells. The expression levels of TET1, TET2 and TET3 mRNA and protein in SK-MEL-28 cells and M619 cells cultured with TGF-β1 for different times were measured by RT-qPCR (**A–C**) and immunoblotting (**B–D**). For RT-qPCR, the data are displayed as the fold change in the expression levels in untreated cells and were normalized by *GAPDH* (Student's *t* test, *$p < 0.05$, **$p < 0.01$); for immunoblotting, GAPDH was used to show that equal amounts of proteins were loaded on the gel.
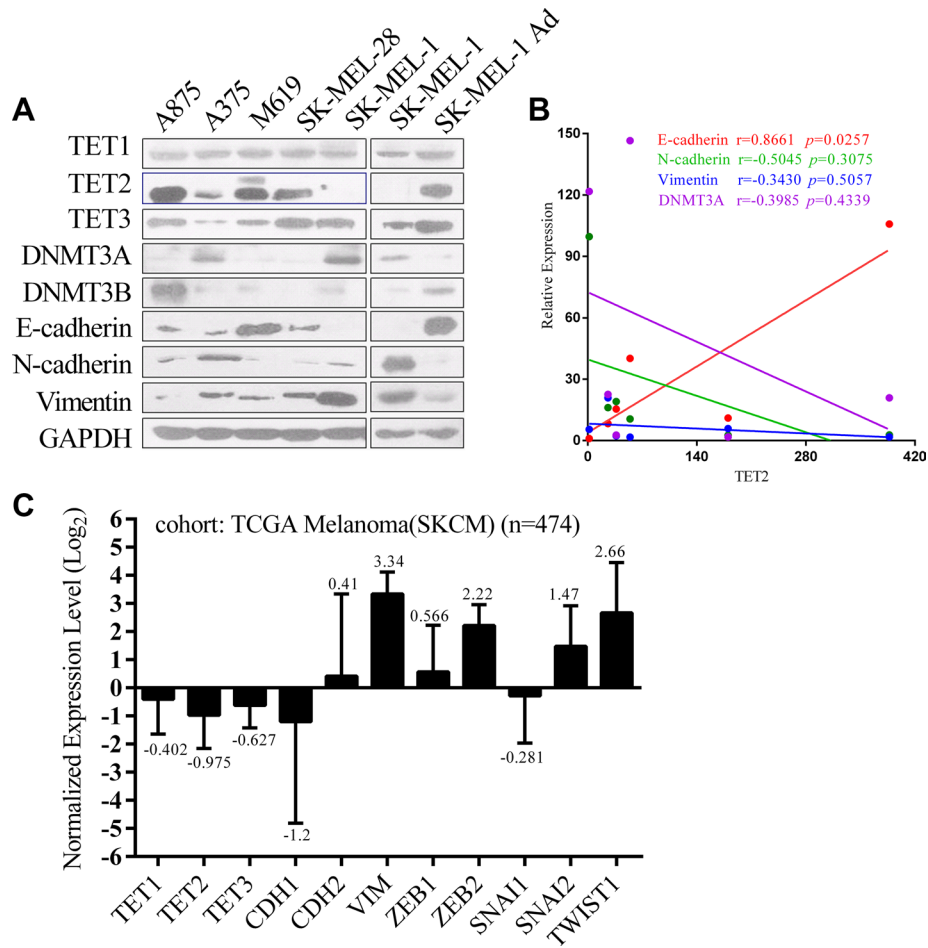
Supplementary Figure S2: Expression of the TET protein family in different cell lines and human melanomas. (**A**) The expression levels of the indicated proteins were detected in 6 different melanoma cell lines by immunoblotting, and GAPDH was used to show that equal amounts of proteins were loaded on the gel; (**B**) Scatter plots show the Pearson correlations of E-cadherin, N-cadherin, Vimentin, the DNMT3A levels and the TET2 level. The Y-axis represents the relative expression levels of the indicated genes in different cell lines, while the X-axis represents the relative expression levels of TET2 in different cell lines. Correlations (r) and corresponding *p*-values are indicated in different colors: r > 0 indicates a positive correlation, r < 0 indicates a negative correlation, and *p* < 0.05 is considered a significant correlation; (**C**) The expression levels of TET gene family and EMT related genes of TCGA melanoma comprising 474 samples. The X-axis represents different genes and the Y-axis represents the normalized expression levels (Log$_2$) of the indicated genes.