

Supplementary Material

corresponding to:

The stem cell transcription factor ZFP296 transforms NIH3T3 cells and promotes anchorage-independent growth of cancer cells

YUMI MIZOUE, TOMOMI IKEDA¹, TAKAKO IKEGAMI, OLEKSANDRA RIABETS, YOSHIE OISHI, MORIKUNI TOBITA, HIDENORI AKUTSU, KOICHI HATTORI, BEATE HEISSIG, HIROSHI KOIDE

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Supplemental Information

"The stem cell transcription factor ZFP296 transforms NIH3T3 cells and promotes anchorage-independent growth of cancer cells." by Mizoue, Y. *et al.*

Materials and methods

Cell culture

TIG-114 cells were obtained from JCRB. HeLa, HepG2 and TIG-114 cells were cultured in DMEM containing 10% FBS. hTERT-HME1 were from ATCC and cultured in mammary epithelial cell basal medium MEBM (Lonza). AGS cells were from European Collection of Cell Cultures and cultured in F-12 medium (Life Technologies) containing 10% FBS and 2 mM glutamine. Human umbilical vein endothelial cells (HUVECs) and human dermal lymphatic endothelial cells (HDLECs) were purchased from PromoCell (Heidelberg, Germany) and Takara, respectively, and cultured in endothelial cell growth medium 2 (PromoCell) and endothelial cell growth medium MV2 (PromoCell), respectively. BMEC1, hFOB and U266 cells were cultured in M199 medium (Life Technologies) containing 10% FBS, and RPMI1640 (Nacalai Tesque) containing 15% FBS, respectively. All cells were cultured in a humidified atmosphere with 5% CO₂ at 37°C.

Table S1 Primer sets for qPCR

Gene	Forward primer (5' to 3')	Reverse primer (5' to 3')
mouse β-actin	TCCTTCTTGGGTATGGAATCCTG	GAGGTCTTTACGGATGTCAACG
mouse Zfp296	AGCTTCTCCAAGTCTCCGACC	GTGGCACAGCAACTTCCAAGG
human β-actin	AGCACAGAGCCTCGCCTTT	CGCGGCGATATCATCATCCA
human ZFP296	CTGGACCGACAAACACCCAG	GTGAACTGTTTGCCACAGCG

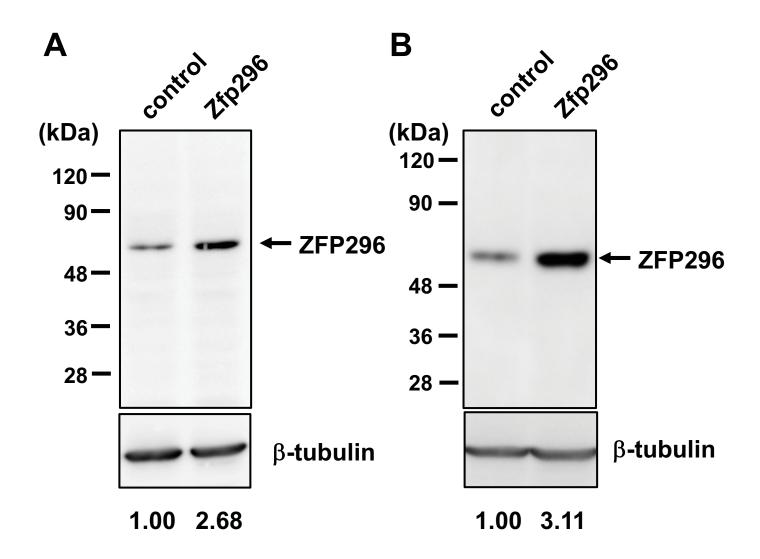


Fig. S1 Western blot analysis

- (A) Confirmation of mouse ZFP296 overexpression in NIH3T3 cells.
- (B) Confirmation of mouse ZFP296 overexpression in C2C12 cells.

Representative data from multiple experiments are shown. The numbers below the gel indicate the expression level of ZFP296, relative to control cells, which was calculated by dividing the density of ZFP296 bands by that of β -tubulin bands, followed by setting the value of control cells as 1.

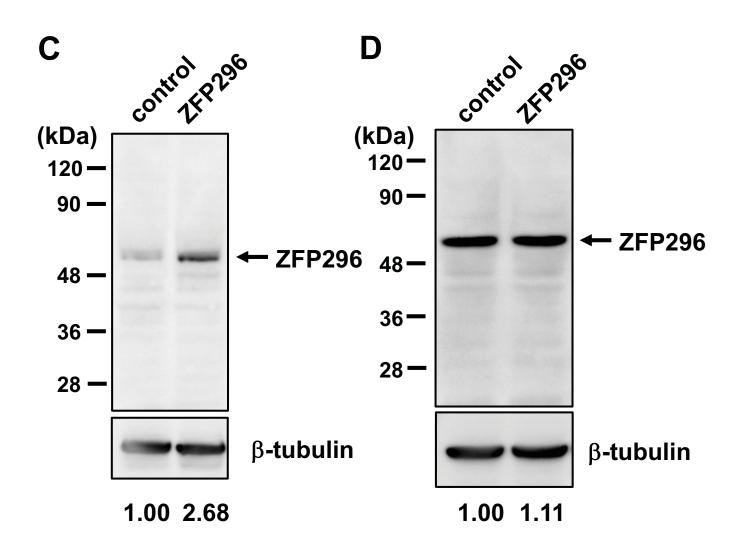


Fig. S1 Western blot analysis

- (C) Confirmation of human ZFP296 overexpression in HT1080 cells.
- (D) Confirmation of human ZFP296 overexpression in HCT116 cells.

Representative data from multiple experiments are shown. The numbers below the gel indicate the expression level of ZFP296, relative to control cells.

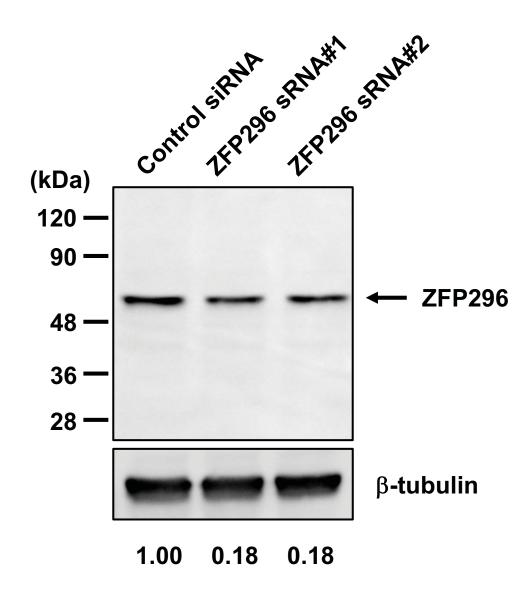


Fig. S1 Western blot analysis

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(E) Confirmation of ZFP296 knockdown in MCF7 cells.

Representative data from multiple experiments are shown. The numbers below the gel indicate the expression level of ZFP296, relative to control cells.

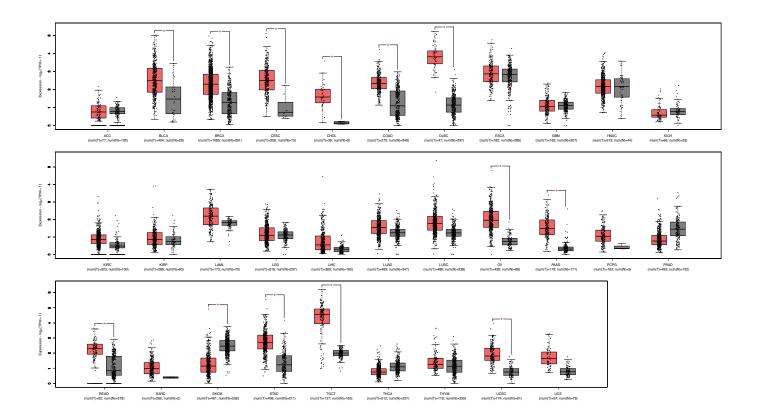


Fig. S2 Expression of ZFP296 in several human tumors (red box) and normal tissues (grey box).

Data from the Cancer Genome Atlas (TCGA) and the Genotype-Tissue Expression (GTEx) were analyzed by using GEPIA2. The abbreviations for each cancer in the figure are as follows.

- ACC Adrenocortical carcinoma BLCA Bladder urothelial carcinoma BRCA Breast invasive carcinoma CESC Cervical squamous cell carcinoma and endocervical adenocarcinoma CHOL Cholangiocarcinoma COAD Colon adenocarcinoma DLBC Lymphoid neoplasm diffuse large B-cell lymphoma ESCA Esophageal carcinoma GBM Glioblastoma multiforme HNSC Head and Neck squamous cell carcinoma KICH Kidney chromophobe KIRC Kidney renal clear cell carcinoma KIRP Kidney renal papillary cell carcinoma LAML Acute myeloid leukemia LGG Brain lower grade glioma LIHC Liver hepatocellular carcinoma
- LUAD Lung adenocarcinoma LUSC Lung squamous cell carcinoma MESO Mesothelioma OV Ovarian serous cystadenocarcinoma PAAD Pancreatic adenocarcinoma PCPG Pheochromocytoma and paraganglioma PRAD Prostate adenocarcinoma **READ** Rectum adenocarcinoma SARC Sarcoma SKCM Skin cutaneous melanoma STAD Stomach adenocarcinoma TGCT Testicular germ cell tumors THCA Thyroid carcinoma THYMThymoma UCEC Uterine corpus endometrial carcinoma UCS Uterine carcinosarcoma
 - UVM Uveal melanoma