TMEFF2 deregulation contributes to gastric carcinogenesis and indicates poor survival outcome

**Short title:** TMEFF2 and tumorigenesis signatures in gastric cancer

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**Abbreviations:** GC, gastric cancer; TMEFF2, the transmembrane protein with epidermal growth factor and two follistatin motifs 2; TCGA, the Cancer Genome Atlas; GSEA, Gene Set
Enrichment Analysis; PTPs, the tyrosine phosphatase; GO, Gene Ontology.

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Transcript Profiling: The gene expression data have been deposited in NCBI's Gene Expression Omnibus (GEO, http://www.ncbi.nlm.nih.gov/geo/) and are accessible through GEO Series accession number GES49052.
Translational relevance

The mRNA expression microarray show TMEFF2 is decreased in gastric cancer tissues, however, its role and clinical implication in gastric cancer is poorly understood. We demonstrate for the first time that TMEFF2 may be a potential biomarker to predict gastric carcinogenesis via altering tumorigenesis gene signatures and acts as a tumor suppressor in gastric cancer (GC) through direct interaction with SHP-1. TMEFF2 expression was gradually decreased from normal gastric tissue through to precancerous lesions and then to GC, and its expression was negatively correlated with the poor pathologic stage, large tumor size and poor prognosis. Gene Set Enrichment Analysis (GSEA) revealed that cell proliferation, apoptosis and DNA damage-related genes were enriched in TMEFF2-lower expression patients. The protein tyrosine phosphatase SHP-1 was identified as a binding partner of TMEEF2 and mediator of TMEFF2 function. A favorable prognosis was more likely in GC patients with higher levels of both TMEFF2 and SHP-1.
Abstract

**Purpose:** The role and clinical implication of the transmembrane protein with epidermal growth factor and two follistatin motifs 2 (TMEFF2) in gastric cancer (GC) is poorly understood.

**Experimental Design:** Gene expression profile analyses were performed and Gene Set Enrichment Analysis (GSEA) was used to explore its gene signatures. AGS and MKN45 cells were transfected with TMEFF2 or control plasmids and analyzed for gene expression patterns, proliferation, and apoptosis. TMEFF2 expression was knocked down with small hairpin RNAs and the effects on genome stability were assessed. Interactions between TMEFF2 and SHP1 were determined by mass spectrometry and immunoprecipitation assays.

**Results:** Integrated analysis revealed TMEFF2 expression was significantly decreased in GC cases and its expression was negatively correlated with the poor pathologic stage, large tumor size and poor prognosis. Gene Set Enrichment Analysis (GSEA) in the TCGA and Jilin datasets revealed that cell proliferation, apoptosis and DNA damage-related genes were enriched in TMEFF2-lower expression patients. Gain of TMEFF2 function decreased cell proliferation by increasing of apoptosis and blocking of cell cycle in GC cells. The protein tyrosine phosphatase SHP-1 was identified as a binding partner of TMEEF2 and mediator of TMEFF2 function. TMEFF2 expression positively correlated with SHP-1 and a favorable prognosis was more likely in GC patients with higher levels of both TMEFF2 and SHP-1.

**Conclusion:** TMEFF2 acts as a tumor suppressor in GC through direct interaction with SHP-1 and can be a potential biomarker of carcinogenesis.

**KEYWORDS:** GSEA; biomarker; stomach cancer; carcinogenesis; tumor suppressor
Introduction

Gastric cancer (GC) is the fourth most highly diagnosed type of cancer and the second most common cause of cancer-related death worldwide (1). Most patients are only diagnosed at an advanced stage due to a lack of early specific symptoms. Patients with advanced gastric cancer have a poor prognosis and eventually die after surgery as a result of cancer recurrence and metastasis (2, 3). Pathological classification is currently the most important tool used to assess prognosis and inform the treatment of GC. The roles of genetic changes, epigenetic alterations, and signaling pathways involved in cancer have recently been studied intensively (4-6). The use of gene expression data to predict tumorigenesis holds promise in GC diagnosis. However, many putative pro-cancer genetic changes occur in histologically normal tissue well before the onset of dysplasia. Therefore, more research is needed to discover and develop more effective biomarkers for GC diagnosis.

The transmembrane protein with epidermal growth factor and two follistatin motifs 2 (TMEFF2) gene encodes a putative transmembrane protein containing two follistatin-like domains and an epidermal growth factor (EGF)-like domain (7). It is expressed in the embryo and selectively in the adult brain and prostate (8-10). As a recently discovered gene, TMEFF2 is epigenetically silenced in a number of tumor types (11-13). In contrast, the shed form of TMEFF2 is able to induce ERK1/2 phosphorylation and contribute to cell proliferation in prostate cancer cells in response to phorbol ester treatment (14). Therefore, the biological function of TMEFF2 remains poorly understood because conflicting reports indicate both a positive and a negative association between TMEFF2 and human cancers.

In this study, we show that TMEFF2 expression is significantly decreased in GC tissues
when compared with normal gastric tissues. Functional assays and Genome Set Enrichment Analysis (GSEA) confirmed that TMEFF2 acts as a tumor suppressor by regulating cell proliferation, apoptosis and genomic stability. We also evaluated the biological function and clinical application of TMEFF2 in GC and identified the protein tyrosine phosphatase (PTP) SHP-1 as the major interacting protein with TMEFF2.
Materials and methods

The three individual datasets collection

Tumor, the adjacent and normal gastric specimens were obtained from GC patients who underwent surgery at Shanghai Renji Hospital from Feb 1995 to May 2004. The study protocol was approved by the ethics committee of Shanghai Jiao Tong University School of Medicine, Renji Hospital. Written informed consents were obtained from all participants in this study. All the research was carried out in accordance with the provisions of the Helsinki Declaration of 1975. None of these patients had received radiotherapy or chemotherapy. The percentage of tumor cellularity in the GC patient’s tissue section is at least 70 % via pathological examination of histology slides in Renji patient’s cohort. A written informed consent was obtained from all patients in Jinlin dataset, which was approved by the Institutional Review Board (IRB) at the University of Georgia, Athens, GA, USA. All samples in TCGA have been collected and utilized following strict human subjects protection guidelines, informed consent and IRB review of protocols.

Bioinformatics analysis

Six gastric mucosal tissues (including three normal gastric mucosa and three tumor tissues) with written informed consent were obtained. Total RNA from each sample was isolated and Agilent Array platform was employed for microarray analysis. RNA from human gastric cancer cells (AGS) respectively transfection with TMEFF2 overexpression plasmid or control plasmid was also isolated and used HOA v6 Human One Array for microarray analysis. The gene expression data have been deposited in NCBI’s Gene Expression Omnibus (GEO, http://www.ncbi.nlm.nih.gov/geo/) and are accessible through GEO Series accession
number GES49052.

Human exon arrays for gastric cancer and normal adjacent tissue were downloaded from the GEO. The datasets GSE27342 consisted of 80 paired gastric cancer and normal adjacent tissue. All samples were taken from three hospitals affiliated with Jilin University College of Medicine and Jilin Provincial Cancer Hospital, Changchun, China. TCGA RNA-Seq (Level 3) and corresponding clinical data were downloaded from TCGA website https://tcga-data.nci.nih.gov/tcga/ following approval of this project by the consortium. RNA-Seq analysis used data from 274 gastric cancers and 33 adjacent normal tissues. The mutation counts and fraction of copy number altered genome data for each TCGA gastric cancer individual were directly downloaded from the cBioPortal for Cancer Genomics (http://cbioportal.org). To gain further insight into the biological pathways involved in gastric cancer pathogenesis through TMEFF2 pathway, a gene set enrichment analysis (GSEA) was performed. The gene sets showing FDR, 0.25, a well-established cut-off for the identification of biologically relevant gene, were considered enriched between classes under comparison. The GO gene sets biological process database (c5.bp.v4.0) from the Molecular Signatures Database–MsigDB (http://www.broad.mit.edu/gsea/msigdb/index.jsp) were used for enrichment analysis. Only gene sets represented by at least 15 genes were retained.

**Patient specimens**

Human gastric mucosal tissues (normal tissues, tissues diagnosed with IM or DYS) were collected from patients made gastroscope inspection in Renji hospital with written informed consent. None of the patients had taken nonsteroidal anti-inflammatory drugs, H2 receptor antagonists, proton pump inhibitors,
antimicrobials or bismuth compounds in the 4 wk prior to the study. The different extent of inflammation in these tissues was examined according to the updated Sydney System (International Workshop on the Histopathology of Gastritis, Houston 1994) and was listed in Supplementary Table S1.

**Cell culture and treatment**

The human gastric epithelial cell line GES-1 and gastric cancer cells (AGS, MKN45, MGC803, SGC7901, MKN28) were cultured in RPMI-1640 medium (Gibco, USA) supplemented with 10% fetal bovine serum at 37 °C in an atmosphere of 5% CO2. The small interfering RNAs (siRNAs, 50 nM) against human TMEFF2 and SHP-1, were transfected into the gastric cells using the DharmaFECT 1 siRNA transfection reagent (Thermo Scientific Dharmacon Inc., Lafayette, CO, USA), while nonspecific siRNA was used as negative controls. SHP-1 siRNA, TMEFF2 siRNA, and the control siRNA were purchased from Dharmacon RNA Technology (Lafayette, CO, USA). The plasmids and mutagenesis about human TMEFF2 (GenBank accession number NM_016192) and human SHP-1 (GenBank accession number NM_080548) were transfected into the gastric cells using the FuGENE transfection reagent (Life Technologies, Shanghai, China), while nonspecific plasmid was used as negative controls.

**Cell proliferation assay, cell cycle analysis, apoptosis detection and TUNEL reaction**

Cell proliferation was assessed by the BrdU incorporation assay (Roche Molecular Biochemicals, Mannheim, Germany). Briefly, control and treated gastric cancer cells were seeded onto the 96-well plates at an initial density of $5 \times 10^3$ cells per
well. BrdU labeling solution (10 µl/well) was added to the cells at specified time points. After incubating for 2h, culture medium was removed and the cells were fixed. Then DNA was denatured by adding FixDenat (200 µl/well) and then anti-BrdU-POD working solution (100 µl/well) was added to the cells and incubated for 90 min. The immune complexes were detected by the subsequent substrate reaction. The reaction product was quantified by measuring the absorbance at 370 nm (reference wavelength: approx. 492 nm).

Cell cycles were examined using propidium iodide and flow cytometry. Cells were fixed in cold ethanol for 30 min and then incubated with propidium iodide (PI) for 30 min before flow cytometer analysis (BD Biosciences, San Diego, CA).

Apoptosis was also determined by flow cytometry analysis. An annexin-V fluorescein isothiocyanate (FITC)/PI double stain assay (Biovision Inc, Mountain View, CA) were performed following the manufacturer’s protocol. Both floating and trypsinized adherent cells were all collected, resuspended in 500 µl of binding buffer containing 2.5 µl of annexin-V FITC and 5 µl of PI, and then incubated for 5 min in the dark at room temperature before flow cytometer analysis.

Apoptosis of the xenograft model was detected by TUNEL technology using the in situ cell death detection kit (Roche Molecular Biochemicals, Mannheim, Germany) according to standard protocols. The negative control was incubated with label solution (without terminal transferase) instead of TUNEL reaction mixture.

**Immunohistochemical staining**

The expressions of TMEFF2, SHP-1 and Ki67 were examined with primary antibodies...
(TMEFF2: 1:200; SHP-1: 1:400; Ki67:1:100) using the LSAB+ kit (DakoCytomation, Copenhagen, Denmark) according to the manufacturer’s instructions. The tissue slides were examined independently by two investigators blinded to both the clinical and pathologic data. Protein expression was quantified using a visual grading system based on the extent of staining (percentage of positive tumor cells on a scale of 0–4: 0, none; 1, 1–25%; 2, 26–50%; 3, 51–75%; 4, >75%) and the intensity of staining (graded on a scale of 0–3: 0, no staining; 1, weak staining; 2, moderate staining; 3, strong staining). For further analysis, the product of the extent and intensity grades was used to define the cutoff value for higher protein expression. Therefore, protein expression was thus classified into two categories: high level (grades 4–12) and low level (grades 0–3).

**Immunofluorescence**

For immunofluorescence of cultured cells, the AGS cells were plated into 4-well chamber slides and co-transfected with pCDNA3.1-TMEFF2WT and pCDNA3.1-SHP-1WT plasmids. Cells were fixed with 4% formaldehyde forty-eight hours after transfection. Then the cells were permeabilized with 0.2% Triton X-100 and blocked in 1% BSA in PBS. Secondary antibodies (Alexa488-anti-rabbit and Alexa546-anti-mouse) were used to label TMEFF2 and SHP-1.

**RNA extraction and quantitative real-time PCR**

The mRNA levels were measured using a real-time quantitative PCR system. Total RNA was extracted by TRIzol reagent (Invitrogen), and 1 μg of total RNA was reverse-transcribed using the PrimeScript® RT Reagent Kit (Perfect Real Time; Takara, Shiga, Japan). The amplified transcript level of each specific gene was
normalized to that of 18S. The primers were provided by Sheng gong Company, Shanghai. The sequences of forward and reverse primers are shown in Supplementary Table S2.

**Western blot**

Western blot assays were performed using standard techniques as described previously (15). Glyceraldehyde 3-phosphate dehydrogenase (GAPDH) antibody was used as a control for whole cell lysates. Antibodies were purchased from Cell Signaling Technology Inc.(USA), except for GAPDH (Kangchen, Shanghai, China) and TMEFF2 (Abcam, Cambridge, MA, USA).

**Liquid Chromatography-Mass Spectrometry (LC-MS) analysis and Database search and protein identification**

The TMEFF2-flag overexpression plasmid was introduced into AGS cells, and the TMEFF2-interacting complex was purified using anti-FLAG beads. To identify specific TMEFF2 interactors, TMEFF2 and empty vector affinity eluates were compared and the bands that were mainly represented only in the TMEFF2 co-immunoprecipitate sample were chosen. The bands were excised to perform in-gel trypsin digestion, peptide extraction and LC-MS identification. LC-MS analysis was performed on a nano Acquity UPLC system (Waters Corporation, Milford, USA) connected to a LTQ Orbitrap XL mass spectrometer (Thermo Scientific, Bremen, Germany) equipped with an online nano-electrospray ion source (Michrom Bioresources, Auburn, USA). Peptides were resuspended with 12 µl solvent A (5% acetonitrile, 0.1% formic acid in water). 10µl peptide solution was loaded onto the Captrap Peptide column (2mm x 0.5mm, Michrom Bioresources, Auburn, USA) at a 20 µl/min flow
rate of solvent A for 5 min and then was separated on a Magic C18AQ reverse phase column (100μm id×15cm, Michrom Bioresources, Auburn, USA) with a three-step linear gradient. Starting from 5% B (90% acetonitrile, 0.1% formic acid in water) to 45% B (in other words, from 95% A to 55% A, the same below) in 100 min, increased to 80% B in 3 min, and then to 5% B in 2 min. The column was re-equilibrated at initial conditions for 15 min. The column flow rate was maintained at 500 nL/min and column temperature was maintained at 35°C. The electrospray voltage of 1.8 kV versus the inlet of the mass spectrometer was used.

LTQ Orbitrap XL mass spectrometer was operated in the data-dependent mode to switch automatically between MS and MS/MS acquisition. Survey full-scan MS spectra with one microscan (m/z 300-1800) was acquired in the Orbitrap with a mass resolution of 60,000 at m/z 400, followed by MS/MS of the eight most-intense peptide ions in the LTQ analyzer. The automatic gain control (AGC) was set to 1000 000 ions, with maximum accumulation times of 500 ms. For MS/MS, we used an isolation window of 2 m/z and the automatic gain control (AGC) of LTQ was set to 20 000 ions, with maximum accumulation time of 120 ms. Single charge state was rejected and dynamic exclusion was used with two microscans in 10 s and 90 s exclusion duration. For MS/MS, precursor ions were activated using 35% normalized collision energy at the default activation q of 0.25 and an activation time of 30 ms. The spectrum were recorded with Xcalibur (version 2.2.0) software.

The mass spectra were searched using the Mascot Daemon software (Version 2.3.0, Matrix Science, London, UK) based on the Mascot algorithm. The database used to search was the human UniProtKB/Swiss-Prot database (Release 2012_12_14, with 20233 entries). To reduce false positive identification results, a decoy database containing the reverse
sequences was appended to the database. The searching parameters were set up as follows: full trypsin (KR) cleavage with two missed cleavage was considered. Oxidation on methionine and acetylation of the protein N-terminus were set as variable modifications. The peptide mass tolerance was 10 ppm and the fragment ion tolerance was 1.0 Da. Peptides with Mascot scores exceeding the 99% confidence level score were accepted as correct matches (Ions Score≥28).

**Purification of TMEFF2 interacting complex, protein digestion and peptide extraction**

Anti-FLAG beads (A2220) was purchased from Sigma-Aldrich; Sequencing-grade trypsin (V5113) was purchased from Promega. Cells maintained in 10×100 mm dishes were either transfected with empty vector (16 µg) or 3×FLAG-tagged TMEFF2 (16 µg), respectively. 48h later, cells were lysed with lysis buffer (Beyotime, P0013C) supplemented with protease inhibitor cocktail and phosphatase inhibitor cocktail (Kangchen company, KC-440). The cell lysate derived from each group (empty vector versus 3×FLAG-tagged TMEFF2) was pre-cleared by incubation with (30 µl) mouse IgG-beads (Sigma- Aldrich, A0910) at 4°C for 2h, then followed by incubation with anti-FLAG beads (70 µl) at 4°C for 4h, respectively. After immunoprecipitation, anti-FLAG beads were washed for 5 times with TBS buffer (50mM Tris-HCl (pH7.4), 150mM NaCl) to eliminate the non-specific binding, respectively. Immunoprecipitates were then eluted by 100µg/mL of 3 × FLAG peptide (Sigma-Aldrich) and concentrated to the appropriate volume respectively for the following SDS-PAGE separation and Coomassie Blue staining. In contrast to the control (sample pulled-down from empty vector-transfected cells), the bands only in sample pulled-down from TMEFF2-transfected cells were excised for the following in-gel trypsin digestion. The
procedure of visible bands excision, in-gel trypsin digestion, and peptide extraction was performed following the previously described protocol (16).

**Co-immunoprecipitation (Co-IP) and GST-pull down analysis**

Co-immunoprecipitation was performed as described previously (17). Both the input and IP samples were analyzed by Western blot using various antibodies at the following dilutions: TMEFF2 Antibody (1:1000) (Abcam, Cambridge, MA, USA), SHP-1 Antibody (1:1000), Flag-tag Antibody (1:1000), HA-tag Antibody (1:1000) (Cell Signal Technology, Danvers, MA, USA), and normal rabbit/mouse IgG (Upstate, Billerica, MA, USA).

GST protein and GST-SHP-1 fusion proteins were expressed and purified according to manufacturer's instructions (GE Healthcare, London, U.K.). For the pull-down assay, 1–5 mg of the GST or GST fusion proteins were mixed with 40 ml of a 50% suspension of glutathione-Sepharose 4B beads for 2 h in binding buffer [25 mM HEPES-NaOH (pH 7.5), 12.5 mM MgCl210% Glycerol, 5 mM DTT, 0.1% NP-40, 150 mM KCl and 20 mM ZnCl2]. Then 1–5 mg of purified TMEFF2 protein (Abcam, Cambridge, MA, USA) was added followed by incubation for another 2 h. The pellets were washed extensively, and were identified by western blotting TMEFF2 antibody and GST antibody (1:1000) (Cell Signal Technology, Danvers, MA, USA).

**Plasmids and mutagenesis**

The DNA fragment encoding the TMEFF2 gene (GenBank® accession number NM_016192) was amplified from human cDNA with the primers TMEFF2F 5’-GGATCCATGGACTACAAGACCATGACGGTGATTATAAAGATCATGACATC-3’ and GATTACAAGGATGACGATGACAAGATGGTGCTGTGGGAGTCCCC-3’ and
TMEFF2R 5’- CTCGAGATTGATTAACCTCGTGGACGCTCT-3’, which introduced the cloning sites BamHI and XhoI (underlined), respectively. The cDNA fragment obtained above was verified by sequencing and finally cloned into pCDNA3.1 between the BamHI and XhoI sites to obtain pCDNA3.1-TMEFF2WT with Flag tag.

The TMEFF2 ΔID DNA fragment was amplified from pCDNA3.1-TMEFF2WT with the primers ΔID-F 5’- GGATCCATGGACTACAAAGACCATGACGGTGATTAT AAAGATCATGACATCGATTACAAGGATGACGATGACAAGATGGTGCTGTGG GAGTCCCC-3’ and ΔID-R 5’- CTCGAGTTAGATGCAGAGGACC, which introduced the cloning sites BamHI and XhoI (underlined), respectively. The DNA fragment obtained above was verified by sequencing and finally cloned into pCDNA3.1 between the BamHI and XhoI sites to obtain pCDNA3.1-TMEFF2ΔID with Flag tag.

The DNA fragment encoding the SHP-1 gene (GenBank® accession number NM_080548) was amplified from human cDNA with the primers SHP-1F: 5’-AAGCTTATGCTGTCCCGTGGGTGG-3’ and SHP-1R: 5’-CTCGAGTCAGCGTAATCAGGCACATCGTAAGGGTA-3’, which introduced the cloning sites HindIII and XhoI (underlined), respectively. The cDNA fragment obtained above was verified by sequencing and finally cloned into pCDNA3.1 between the HindIII and XhoI sites to obtain pCDNA3.1-SHP-1WT with HA tag.

The SHP-1 ΔSH2D1, ΔSH2D2 and ΔPTPD DNA fragment was amplified from pCDNA3.1-SHP-1WT and the DNA fragments obtained above was verified by sequencing and finally cloned into pCDNA3.1 between the HindIII and XhoI sites to obtain pCDNA3.1-SHP-1ΔID with HA tag.
obtain pCDNA3.1-SHP-1ΔSH2D1, pCDNA3.1-SHP-1ΔSH2D2 and pCDNA3.1-SHP-1ΔPTPD, with HA tag respectively.

**In vivo experiments**

In order to clarify the effect of TMEFF2 in vivo, 4-week-old male BALB/c nude mice obtained from Experimental Animal Centre of SIBS were used in our study. AGS cells (1.0×10^7) were injected subcutaneously into the right flank of these mice to establish the gastric cancer xenograft model. Ten days after subcutaneous inoculation, mice were randomly divided into 3 groups (8 mice/group) and were injected with PBS, or control adenoviruses, or TMEFF2 overexpression adenoviruses by ways of multipoint intratumoural injection every other day for fourteen days. Tumour volume (mm^3) was estimated by the formula: tumour volume (mm^3) = shorter diameter^2×longer diameter/2. The tumour volumes data are presented as means ± SE. All experimental procedures were approved by the Institutional Animal Care and Use Committee.

**Adenovirus and lentivirus transduction**

The control adenovirus, TMEFF2 overexpression adenovirus, control shRNA lentivirus and TMEFF2 shRNA lentivirus were all constructed by Shanghai SBO medical biotechnology company, Shanghai, China.

**SupF mutation assay**

The pSupFG1 plasmid and *E.coli* SY204 strain were kindly provided by Professor Gan Wang (Institute of Environmental Health Sciences, Wayne State University, Detroit, MI, USA). As previously described (18, 19), a total of 6×10^5 cells in 10 ml of culture medium
were plated onto a 100 mm dish. After 16h cell culture, plasmid pSupFG1 (10 µg) was transfected into the GES-1 cells or GES-1 with TMEFF2 depletion cells using lipofectamine 2000 (Life Technolgies, USA) according to the supplier’s recommendations. After 48h, propagated plasmids were extracted from the cells using a QIAprep Spin Miniprep Kit (Qiagen, Germany). The extracted plasmids were digested with DpnI (Takara, Japan) to eliminate unreplicated plasmids, which retained a bacterial methylation pattern. After removal of proteins by Phenol-Chloroform extraction, DNA was purified with an Amicon Ultra-4 Centrifugal Filter Unit with Ultracel-30 membrane (Millipore, Billerica, MA, USA). The plasmid DNAs recovered were introduced into the E.coli SY204 (lacZ amber) with a Gene Pulser II electroporation apparatus (Bio-Rad, Tokyo, Japan). To select E.coli with a mutated supF gene, the transformed cells were plated onto a LB plate containing ampicillin, IPTG and X-gal and were cultured at 37°C for 24 h. As the E.coli SY204 strain carries an amber mutation in the lacZ gene, a functional supF gene suppresses the amber mutation in the lacZ gene and results in blue colonies on the X-gal plate while mutations in the supF reporter gene lead to colorless colonies on the X-gal plates. The mutation frequency of the supF reporter gene was determined as the number of mutant colonies to the number of total colonies on the plates.

**Fish assay**

The FISH method was performed on slides with cells fixed in methanol/acetic acid. The c-MYC gene probe (Abnova, Taipei City, Taiwan) was purchased to detect the c-MYC gene alteration in the GES-1 cells and GES-1 cells with TMEFF2 depletion. The slides were washed in 2x saline sodium citrate solution (SSC) and dehydrated in 70%, 80% and 95%
ethanol. The samples were then denatured with 70% formamide/2x SSC (pH 7.0) at 70°C for 2 min and transferred to an iced ethanol (–20°C) series at 70%, 80% and 95%. The probe was denatured at 96°C for 5 min. Then, 10µL were applied to the slide under a glass coverslip. In situ hybridization occurred at 42°C in a moist chamber overnight. Post-hybridization washings were done, and the nuclei were counterstained with DAPI/antifade (Vector Laboratories, Burlingame, CA, USA). The molecular cytogenetic analysis was carried out under a ZEISS AXIOPHOT fluorescence microscope and an ISIS capture and image analysis system. For each sample, 200 interphase nuclei were analyzed.

**BSP analysis**

Genomic DNA was extracted from the gastric tissues using QIAamp DNA Mini kit (Qiagen, Hilden, Germany). DNA was chemically modified with sodium metabisulphite. The bisulfite-modified DNA was PCR amplified with Pebp1-specific bisulphate sequencing primers (TMEFF2-BSP F1 5’- TGTTATAAGGAGGGAGTTTTGGGA -3’ ; and TMEFF2-BSP R1 5’- CTACATCCTACTCCACCAATCAAAC -3’; TMEFF2-BSP F2 5’- TGCGGGTAGTTTATTTTGAAGTT -3’ ; and TMEFF2-BSP R2 5’- CGTTTTAAAAACACAC AAATCTCAAC; SHP-1-BSP F 5’- AGGGTTGTGGTGAGAAATTAATTAG -3’ ; and SHP-1-BSP R 5’- TTACACACTCCAAACCCCAAATAATAC -3’ ; ). The resulting PCR product was obtained by 1.5% agarose gel electrophoresis, cloned into pMD19-T vector (TaKaRa, Japan) and then 18-20 clones from the control and treated samples were sequenced. Twenty eight CpG sites spanning the -258 and +138 bp regions of TMEFF2 gene promoter and 11 CpG sites spanning the –361 and -140 bp regions of SHP-1 gene promoter were evaluated. Sequences were analyzed by using SeqScape software (Applied Biosystems) and
Biocedit ([http://www.mbio.ncsu.edu/BioEdit/bioedit.html](http://www.mbio.ncsu.edu/BioEdit/bioedit.html)).

**Statistical analysis**

All statistical analyses were carried out using the program R ([www.r-project.org](http://www.r-project.org)) or SPSS for Windows 17.0.1 software (SPSS Inc., Chicago, IL, USA). Data from at least 3 independent experiments performed in triplicate are presented as the means ± standard error (SE). Error bars in the scatter plots and the bar graphs represent SE. Date were examined whether they were normally distributed with the One-Sample Kolmogorov-Smirnor test. If the data were normally distributed, comparisons of measurement data between two groups were performed using the paired-sample t test or independent-sample t test. And the comparisons among three or more groups were firstly performed by One-Way ANOVA test. If the results showed significant difference, the Student Newman Keuls analysis was used to test the difference between two groups. When the data were skewed distribution, comparisons were performed by nonparametric tests. Measurement data between two groups were performed using paired sample Wilcoxon signed rank test or non-parametric Mann-Whitney test. The measurement data among three or more groups were examined by Kruskal Wallis test, and the difference between the two groups were further tested by Mann-Whitney test, adjusted for multiple comparisons using Bonferroni correction. Enumeration data were examined by Chi-square test or Fisher Exact test. Overall survival in relation to TMEFF2 or SHP-1 expression was evaluated by the Kaplan–Meier survival curve and the Mantel-Cox test. The correlation of TMEFF2 and SHP-1 expression were examined by Spearman
correlation test. Statistical tests and $P$-values were two-sided. Differences were considered significant with a value of $P < 0.05$. 
Results

Integrative analysis reveals genes downregulated in gastric cancer tissues

To identify genes that are differentially expressed in gastric cancer (GC) at the genome scale, we compared the gene expression profiles of GC and normal gastric tissues through a microarray analysis. Using mRNA expression arrays containing approximately 27,958 best-defined human genes, we found that 5417 genes were significantly altered in their expression of which 2584 genes were significantly downregulated in GC tissues (Supplementary Fig. S1A. Raw data accessible via GEO number: GSE49052). Functional clustering analysis of the downregulated genes revealed a significant enrichment of genes (17%, 435/2584 genes) related to cell proliferation, apoptosis and cell cycle (Fig. 1A). Further analysis showed that 14 downregulated genes were specifically associated with cell proliferation, cell cycle and apoptosis. Of these 14 genes, RUNX3 and IL1B have been previously studied intensively in GC (20, 21). Of the remaining 12 genes, TMEFF2 exhibited the most significantly decrease in transcriptional level in the microarray data. Furthermore, TMEFF2 expression was significantly decreased in GC tissues when compared with the adjacent tissues of patients in Renji (from South of China), Jilin (from North of China), and TCGA independent dataset (Fig. 1B). To ensure that conclusions derived from these results are reliable, we have compared the TMEFF2 expression between paired GC and normal tissues (n = 66) and tested for statistical significance by Student’s paired t-test. Analysis of tumor/ non-tumor adjacent tissue (T/N) ratios for TMEFF2 expression of 66 patients revealed that TMEFF2 expression was decreased in approximately 70 % GC patient tissues (P < 0.001, Fig. 1C). These results indicate that TMEFF2 may play an important role in gastric
carcinogenesis and therefore we chose to focus our experimental research on TMEFF2.

**Graded decrease in TMEFF2 expression in gastric carcinogenesis correlates with gastric cancer patient survival**

The real-time PCR data and immunohistochemical staining showed that TMEFF2 expression was gradually decreased from normal gastric tissue through to intestinal metaplasia (IM) to dysplasia, and to GC (Supplementary Fig. S1B-D), suggesting that a decrease in TMEFF2 expression is an early event in the multistep progression of gastric carcinogenesis.

Next, we explored whether the lower expression of TMEFF2 in GC was associated with poor prognosis. Evaluation of TMEFF2 expression in 105 GC patients (Renji dataset) with different clinicopathological features revealed that the TMEFF2 expression was negatively correlated with the histological stage ($P < 0.001$) (Supplementary Table S3) and tumor size ($P < 0.05$, Fig. 1D). No correlation was found between TMEFF2 expression and other clinicopathologic features. We also compared the survival time in patients of Renji dataset. The cumulative survival rate was significantly higher in patients with higher-TMEFF2-expressing tumors than in those with lower-TMEFF2-expressing tumors ($P = 0.0148$, HR = 0.57, 95% CI: 0.37-0.90, Fig. 1E). In addition, multivariate analysis revealed that the lower expression of TMEFF2 was found to be significantly associated with poor survival in GC patients independently of the TNM stage ($P = 0.016$, Fig. 1F). These data indicate that TMEFF2 expression could represent a new prognostic factor in GC patients.

**Functional roles of TMEFF2 as a tumor-suppressor in vitro and in vivo**

To elucidate whether TMEFF2 could play a role in preventing GC occurrence, a
microarray analysis was performed to compare the gene expression profiles of TMEFF2 and control plasmid transfectants. A total of 1442 downregulated genes (≥2-fold) and 1395 upregulated genes (≥2-fold) was detected (Raw data accessible via GEO number: GSE49052) after overexpression of TMEFF2 in GC cells. Gene Ontology (GO) analysis revealed changes in gene sets related to cell proliferation, apoptosis and DNA damage in TMEFF2 overexpression cells (Fig. 2A). To gain further insight into the biological pathways involved in GC pathogenesis stratified by the median of TMEFF2 expression level, GSEA analysis was performed in TCGA and Jilin datasets. Enrichment plots of GSEA showed that the gene signatures of cell proliferation and apoptosis were more correlated with patients with TMEFF2-lower expression versus patients with TMEFF2-higher expression in the both individual datasets (Fig. 2B and Supplementary Fig. S2A-C). The top-scoring genes recurring in the two pathways included key cancer genes, such as CDKN1B (p27), Ki67 and FASLG. Further real time PCR data confirmed that alteration of TMEFF2 expression dramatically affected the key gene signatures which are involved in tumorigenesis (Supplementary Fig. S3), suggesting that TMEFF2 may be a key regulator in gastric tumorigenesis.

To validate the GSEA analysis of TMEFF2, we transfected TMEFF2-overexpressing plasmid into the GC cell lines, AGS and MKN45. Both these cell lines display a lower expression of TMEFF2 compared to GES-1 gastric cells (Supplementary Fig. S4A and S4B). Overexpression of TMEFF2 significantly inhibited GC cell proliferation both in vitro and in vivo (Fig. 3A and B; Supplementary Fig. S4C). We also examined the effects of TMEFF2 on GC cell cycle progression and apoptosis. As illustrated in Fig. 3C, overexpression of TMEFF2 dramatically blocked the cell cycle at the G2-M phase. In addition, apoptotic GC
cells were significantly increased after overexpression of TMEFF2 both in vitro and in vivo (Fig. 3D and E). Furthermore, the knockdown of TMEFF2 significantly increased cell proliferation in GES-1 cells (Supplementary Fig. S4D). These data suggest that TMEFF2 may function as a tumor-suppressor in GC through inhibition of cell cycle progression and the induction of cell apoptosis. IHC staining and Western blot analyses showed that alteration of TMEFF2 expression significantly changed the expression of the cell proliferation markers Ki67 and PCNA in gastric cells (Fig. 3F and Supplementary Fig. S4E and S4F). In addition, P27 and FASL (a trigger of apoptosis) were also upregulated following TMEFF2 overexpression (Supplementary Fig. S4E). The data were consistent with the correlation of TMEFF2 with clinicopathological features (especially tumor size) and GSEA analysis in GC.

Knockdown of TMEFF2 significantly increased DNA damage, genomic instability and DNA mutation frequency in GES-1 cells

According to the GSEA analysis, DNA damage-related genes were active in patients with TMEFF2-lower expression (Fig. 2B), we next performed functional assay to validate that. The representative data of comet assay showed that knockdown of TMEFF2 significantly increased DNA damage (Fig. 4A), and induced the alteration of DNA-damage related gene signatures in GES-1 cells (Fig. 4B), indicating that knockdown of TMEFF2 may induce DNA damage in GES-1 cells.

Moreover, in TCGA dataset we found that a greater fraction of copy number altered genome and DNA mutations were detected in GC patients with lower TMEFF2 expression than in those with higher TMEFF2 expression (Fig. 4C and D). To explore the role of TMEFF2 in gastric genome stability, we introduced TMEFF2 shRNA lentivirus into GES-1
cells. As *c-MYC* gene amplification was often detected in gastric carcinogenesis (22, 23), we detected the *c-MYC* gene amplification in GES-1 with TMEFF2-depleted cells by Fish assay. More DNA copies of *c-MYC* gene were detected in the GES-1 cells after stable knockdown of TMEFF2 (Fig. 4E), suggesting that downregulation of TMEFF2 may increase genome instability via accumulating of extra copies of DNA in GES-1 cells.

Furthermore, *supF* mutation assay showed that replication of the pSupFG1 vector in GES-1 cells with stable knockdown of TMEFF2 yielded a significantly higher (5-fold) mutant frequency than in the control shRNA cells (TMEFF2 shRNA1 VS Control: 91±16 x 10^{-4} vs. 20±1 x 10^{-4}, *P* = 0.011; TMEFF2 shRNA2 VS Control: 96±13 x 10^{-4} vs. 20±1 x 10^{-4}, *P* = 0.005; Fig. 4F), indicating that the DNA mutation is more frequent in TMEFF2-depleted gastric cells than in normal gastric cells. The data is consistent with our DNA mutation statistic data in patients.

**Association of TMEFF2 with SHP-1**

To dissect the molecular mechanism of the TMEFF2-induced inhibition of GC cell growth, we employed the LC-MS-based proteomic approach to identify protein candidates that functionally associate with TMEFF2. The details of LC-MS identification were shown in Supplementary Table S4. Interestingly, six peptide fragments of protein-tyrosine phosphatase SHP-1 were identified in TMEFF2 pull-down complex as the main fraction. SHP-1 functions as an important regulator of multiple signaling pathways in hematopoietic cells and in tumorigenesis (24, 25). We explored further the nature of the interaction between SHP-1 and TMEFF2. Co-immunoprecipitation experiments in AGS and MKN45 cells confirmed the SHP-1/TMEFF2 interaction (Fig. 5A and B). In addition, immunofluorescence revealed that
TMEFF2 is co-localized with SHP-1 (Fig. 5C) (Fig. 5A - C shows the in vivo data). Second, as shown in Fig. 5D, TMEFF2 was pulled down by the GST-SHP-1 fusion protein, but not by GST alone, suggesting that TMEFF2 may directly interact with SHP-1 (in vitro data). The results obtained from LC-MS-based proteomic screening combined with a variety of biological approaches indicate that SHP-1 directly interacts with TMEFF2.

We next detected whether SHP-1 mediates the biological function of TMEFF2 in GC. The functional assay showed that the downregulation of SHP-1 markedly blocked the TMEFF2-induced decrease in cell proliferation and increase in cell apoptosis (Fig. 5E and F), indicating that SHP-1 may mediate the function of TMEFF2 in GC.

**TMEFF2 functions through its association with SHP-1**

To explore the mechanism of SHP-1-mediated TMEFF2 function in GC, we sought to identify regions within TMEFF2 and SHP-1 that are important for SHP-1/TMEFF2 interaction. The human TMEFF2 protein contains an extracellular domain (ED; residues 41-320), a transmembrane domain (TD; residues 321-341) and an intracellular domain (ID; residues 342-374) (Fig. 6A). The human SHP-1 protein contains two SH2 domains (SH2D1 and SH2D2; residues 4-100 and 110-213, respectively) and a protein tyrosine phosphatase domain (PTPD; residues 244-515; Fig. 6B). To determine the regions of TMEFF2 and SHP-1 responsible for their physical interaction, we generated a truncation mutant of the TMEFF2 intracellular domain (termed TMEFF2ΔID), with a Flag tag and truncation mutants of SHP-1, namely ΔSH2D1, ΔSH2D2, and ΔPTPD, with a HA tag. All the truncation mutants were successfully overexpressed in GC cells (Supplementary Fig. S4G and S4H). Deletion of the ID domain significantly blocked the interaction between TMEFF2 and SHP-1 in a co-IP assay.
(Fig. 6C) as well as the TMEFF2-mediated loss of cell proliferation in GC cells (Fig. 6D), suggesting that the TMEFF2ID domain is important for the TMEFF2/SHP-1 interaction and TMEFF2 function in GC.

In addition, deletion of the SH2D1 or SH2D2 domain but not deletion of the PTP domain significantly blocked TMEFF2/SHP-1 interaction (Fig. 6E) as determined through a co-IP assay, indicating that the two SH2 domains of SHP-1 are required for the interaction between TMEFF2 and SHP-1. A further functional assay showed that the overexpression of SHP-1ΔSH2D1 or ΔSH2D2 but not ΔPTPD significantly blocked the TMEFF2-induced loss of cell proliferation (Fig. 6F and Supplementary Fig. S5A). These data are consistent with the co-IP data and suggest that the two SH2 domains of SHP-1 are important for the tumor-suppressive function of TMEFF2 in GC.

We also analyzed the somatic mutation data of TCGA (320 cases) and Renji datasets (20 cases) (Supplementary Table S5). However, no DNA mutations in the ID domain of TMEFF2 and in the SH2D1, SH2D2 or PTPD domains of SHP-1 were observed, indicating that somatic mutation of TMEFF2 may not be the major cause of deregulation of this gene in gastric carcinogenesis.

**Correlation of TMEFF2 and SHP-1 expression in human GC**

Because it is important to fully clarify the roles of SHP-1 on the function of TMEFF2 in vivo, we further tested the correlation of TMEFF2 and SHP-1 in human gastric mucosal specimens. Similar to TMEFF2, SHP-1 expression was also significantly decreased from normal tissues to pre-cancerous lesions to cancer (Supplementary Fig. S6A). The correlation analysis showed that TMEFF2 expression was significantly correlated with SHP-1 in gastric
carcinogenesis ($r_{\text{Spearman}} = 0.479, P < 0.01$, Supplementary Fig. S6B).

Moreover, to test the possibility that inhibition of the tumor suppressive function of TMEFF2 (and associated SHP-1) could be through an increase in the methylation level of TMEFF2 and SHP-1 gene promoters, we analyzed the gene promoter methylation patterns of the relevant gene promoters using bisulfite-sequencing PCR (BSP) analysis (26). The promoter methylation levels of TMEFF2 and SHP-1 were gradually increased from normal gastric tissue, IM, dysplasia through to GC (Supplementary Fig. S6C), suggesting that the synchronous expression of SHP-1 and TMEFF2 may be regulated by methylation in GC development.

Importantly, the cumulative survival rate was significantly better in patients with higher-SHP-1-expressing tumors than in those with lower-SHP-1-expressing tumors ($P = 0.031$, HR = 0.62, 95% CI: 0.41-0.96, Supplementary Fig. S6D), indicating that SHP-1 downregulation is also significantly associated with poor survival in GC. We further investigated the survival difference in GC patients with combined higher/lower expressions of TMEFF2 and SHP-1. The prognosis is better in patients with higher expression levels of both TMEFF2 and SHP1 (TMEFF2$^H +$ SHP-1$^H$) than in patients with lower expression levels of both TMEFF2 and SHP-1 (TMEFF2$^L +$ SHP-1$^L$) ($P = 0.0039$, HR = 0.45, 95% CI: 0.26-0.78, Supplementary Fig. S6E), indicating that higher levels of TMEFF2 and SHP-1 may predict better overall survival in GC patients.
Discussion

The deregulation of TMEFF2 has been demonstrated in various tumor types (10, 12, 27). However, the biological functions and clinical implication of TMEFF2 in GC remain unknown. In the present study, we highlight a functional role for TMEFF2 in gastric carcinogenesis.

We compared TMEFF2 expression between GC tissues and adjacent non-tumor tissues in relation to GC pathogenesis in Renji, Jilin and TCGA datasets. TMEFF2 expression is significantly decreased in GC tissues when compared with adjacent tissues in the three individual datasets, and the expression of TMEFF2 is higher in male patients than in female patients. It is possible that the expression of TMEFF2 may be associated with hormone metabolism and strongly associated with androgen. Our data is consistent with previous report that TMEFF2 is initially identified as an androgen-regulated gene in prostate cancer cells and is regulated by androgens (10). Recently, another group also illustrate that androgen may regulate the translation of TMEFF2 in prostate cancer via promoting the phosphorylation level of eIF2α (28). In addition, TMEFF2 is progressively downregulated from normal gastric tissues through to pre-cancerous tissues to GC tissues and TMEFF2-higher expression in GC is associated with a favorable prognosis. Moreover, the downregulation of TMEFF2 in GC was found to be negatively correlated with the histological grade and tumor size. These data suggest that TMEFF2 may play important roles in GC.

GO analysis and GSEA analyses demonstrated that the cell proliferation, apoptosis and DNA repair pathways were significantly enriched in response to TMEFF2 alteration in GC cells and patients. The bioinformatics analyses were further validated in the subsequently
performed in vitro and in vivo experiments. In cultured GC cells and xenograft mouse models, TMEFF2 markedly suppressed cell growth through induction of cell cycle arrest and increase of cell apoptosis. Moreover, TMEFF2 may participate in maintaining gastric genomic stability, since greater numbers of extra copies of DNA and frequently DNA mutation were detected in normal gastric cells and patients with TMEFF2 depletion. These data consistently indicate that aggressive gastric cancer cells are addicted to lower TMEFF2 expression, which explains the important role that TMEFF2 plays in the progression of GC. Although TMEFF2 has been reported to mediate tumor suppression in CRC (29), this study provides the first demonstration of its crucial functions in GC development by combining high-throughput data analysis and functional assays. The strong correlation between TMEFF2 expression and GC patient survival, tumor size and pathologic stage highlights the potential value of TMEFF2 as a novel biomarker for GC prognosis.

Several studies have indicated that TMEFF2 is a tumor-suppressor in human cancer cells (11-13), whereas others reports have demonstrated that the elevated TMEFF2 expression is associated with higher prostate cancer grade and hormone independence (9, 30). Truncated TMEFF2 (without the cytoplasmic domain) may promote cell proliferation through the induction of ERK1/2 phosphorylation (14). Therefore, the role of TMEFF2 in carcinogenesis requires further study.

The TMEFF2 protein has been found to interact with multiple proteins. In prostate cancer cells, TMEFF2 binds to sarcosine dehydrogenase (SARDH) and modulates cellular sarcosine levels (31). It has been suggested that TMEFF2 and SARDH may cooperate to modulate one-carbon metabolism and invasion in cancer cells (32). The extracellular domain of
TMEFF2 interacts with PDGF-AA and regulates PDGF signaling (12). In this study, using a combination of MS analysis, confocal microscopy and immunoprecipitation assays, we reveal that TMEFF2 directly binds to the SH2 domains of SHP-1. Importantly, we show that the intracellular domain of TMEFF2 mediates the TMEFF2/SHP-1 interaction and the TMEFF2-mediated decrease in cell proliferation in GC. The tumor-suppressive function of TMEFF2 is mediated by SHP-1, particularly the SH2 domains of SHP-1. SHP-1 is primarily expressed in hematopoietic cells and behaves as a key regulator of the intracellular phosphotyrosine levels in lymphocytes (33, 34). SHP-1 regulates the intracellular signaling of different transmembrane receptors, including growth factor receptors and cytokine receptors. For example, decreased or abolished SHP-1 expression or activity results in increased JAK kinase activity and can directly cause abnormal cell growth (35, 36). SHP-1 has therefore been considered a tumor suppressor in different cancers.

The clinical relevance of the interaction of TMEFF2 and SHP-1 was further supported by the analysis of human tissues along the gastric carcinogenic cascade. The expression of TMEFF2 was positively correlated with that of SHP-1 in human pre-cancerous lesions and GC. Furthermore, higher expressions of TMEFF2 and SHP-1 cases exhibited the best prognosis. The synchronous expression of SHP-1 and TMEFF2 may be regulated by methylation of their gene promoters during GC development.

In conclusion, our findings have provided additional insight into the mechanisms of gastric carcinogenesis. As represented in Supplementary Fig. 6G, TMEFF2 may play an important role in the progression of gastric tumorigenesis and it is identified as a potential biomarker and therapeutic target for gastric cancer.
Disclosure of Potential Conflicts of Interest

The authors declare no potential conflict that is relevant to the manuscript.

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**Figure Legends**

**Figure 1. TMEFF2 downregulation correlates with poor survival in gastric cancer patients.**

(A) Overview of the microarray analysis used to identify the differential gene expression between gastric cancer (GC) and normal gastric tissues.

(B) Analysis of TMEFF2 expression in GC and their preneoplastic adjacent mucosa in three independent dataset. Renji dataset (non-parametric Mann-Whitney test), Jilin dataset (non-parametric Mann-Whitney test). Generalized linear model (GLM) analysis was performed for TCGA RNA-sequence data.

(C) Analysis of TMEFF2 expression in GC and their matched adjacent mucosa in Renji dataset. n = 66, paired-sample t test.

(D) Statistical analysis on the tumor size of GC in TMEFF2-higher expression (n = 32) and lower expression (n = 73) groups ($P < 0.05$, non-parametric Mann-Whitney test).

(E) Survival analysis showed that TMEFF2-higher expression tumors have a favorable prognosis compared to TMEFF2-lower expression tumors ($P = 0.0148$, HR = 0.57, 95% CI: 0.37-0.90, Mantel-Cox test).

(F) Multivariable analysis was performed in the Renji dataset. All the error bars in the scatter plots represent SE.

**Figure 2. Gene Ontology (GO) and Gene Set Enrichment Analysis (GSEA) in TMEFF2-higher/lower expression GC cells and patients.**

(A) Overview of the GO analysis used to identify the differential gene expression between TMEFF2- overexpression and control GC cells.

(B) Gene Set enrichment Analysis (GSEA) comparing TMEFF2 lower expression group (red) against TMEFF2 higher expression group (blue) of GC patients in the TCGA dataset, illustrating distinct pathways and biological processes between both subgroups. Cytoscape and Enrichment map were used for visualization of the GSEA results (1% FDR, $P = 0.005$). Nodes represent enriched gene sets, which are grouped and annotated by their similarity
according to related gene sets. Enrichment results were mapped as a network of gene sets (nodes). Node size is proportional to the total number of genes within each gene set. Proportion of shared genes between gene sets is represented as the thickness of the green line between nodes. This network map was manually curated removing general and uninformative sub-networks, resulting in a simplified network map shown in Figure 2B. Enrichment plots are shown for a set of activated genes related to cell proliferation and apoptosis and DNA damage in TCGA patients’ dataset. The enrichment score (ES, green line) means the degree to which the gene set is over-represented at the top or bottom of the ranked list of genes. Black bars indicate the position of genes belonging to the gene set in the ranked list of genes included in the analysis. A positive value indicates more correlation with “TMEFF2 lower expression”-patients and a negative value indicates more correlation with “TMEFF2 higher expression”-patients.

**Figure 3. Functional roles of TMEFF2 in vitro and in vivo.**

(A) TMEFF2 overexpression inhibited GC cell growth *in vitro*. n = 3, *P < 0.01*, non-parametric Mann-Whitney test.

(B) Representative data showed that overexpression of TMEFF2 significantly inhibited tumor growth in nude mice xenograft model. Tumor volume was measured after TMEFF2 overexpression adenoviruses treatments. n = 8, *P < 0.01*, non-parametric Mann-Whitney test.

(C) Cell cycle arrest after TMEFF2 overexpression in AGS and MKN45 GC cells was assessed by flow cytometry. n = 3.

(D) Cell apoptosis after TMEFF2 overexpression in AGS and MKN45 GC cells was assessed by flow cytometry. n = 3.

(E) Higher percentage of apoptotic cells in TMEFF2 overexpression group tumors were detected compared to PBS or control groups by the TUNEL reaction. n = 8.

(F) IHC staining of Ki-67 of the three group xenografts was shown. n = 3, *P < 0.05*, independent-sample t test. Error bars in the scatter plots represent SE.
**Figure 4. Detection of the genomic instability and DNA mutation frequency in GES-1 cells with TMEFF2 depletion.**

(A) Representative images for comet assay in GES-1 cells after introduction of control shRNA and TMEFF2 shRNA virus. n = 3.

(B) The mRNA levels of DNA-damage related genes were measured in GES-1 cells after introduction of control shRNA and TMEFF2 shRNA virus. n = 3, *P < 0.05.

(C) Genome instability (DNA copy number alteration and mutation) were detected in TCGA GC patients with TMEFF2-lower expression (P < 0.05, non-parametric Mann-Whitney test). Error bars in the scatter plots represent SE.

(D) The immunofluorescence data revealed that more DNA copies of c-MYC gene were detected in GES-1 cells with TMEFF2 stable knockdown. (The Fish probe of c-MYC is labeled with Texas Red).

(E) TMEFF2 depletion significantly increased the supF mutant frequencies in GES-1 cells. n = 3, P < 0.01, independent-sample t test. Error bars in the scatter plots represent SE.

**Figure 5. TMEFF2 binds to SHP-1 in vitro and in vivo.**

(A) and (B) Co-immunoprecipitation showed that TMEFF2 interacts with SHP-1 in the GC cell lines AGS and MKN45. n = 3.

(C) Immunofluorescence revealed that TMEFF2 is co-localized with SHP-1. n = 3.

(D) TMEFF2 was pulled down by GST-SHP-1 fusion protein, but not by GST alone. n = 3.

(E) and (F) Downregulation of SHP-1 dramatically blocked TMEFF2-induced decrease in cell proliferation and increase in cell apoptosis in GC cell line AGS and MKN45. n = 3, non-parametric Mann-Whitney test. Control plasmid: pCDNA3.1; TMEFF2 plasmid: pCDNA3.1-TMEFF2WT.

**Figure 6. TMEFF2 functions through its intracellular domain that associates with the two SH2 domains of SHP-1.**

(A) Schematic representation of TMEFF2 protein and the truncated mutant. TMEFF2 protein
includes the extracellular domain (ED in pale blue), the transmembrane domain (TD in tan) and the intracellular domain (ID in orange). The TMEFF2 mutant without the ID was named as TMEFF2ΔID.

(B) Schematic representation of SHP-1 protein and the truncated mutants. SHP-1 protein includes the SH2 domain-1/2 (SH2D1 and SH2D2 in pale blue) and the protein-tyrosine phosphatase (PTP) domain (PTPD in tan). The SHP-1 mutant without the SH2D1, SH2D2 or PTPD was named as SHP-1ΔSH2D1, ΔSH2D2 or ΔPTPD, respectively.

(C) Co-IP was performed after co-expression of TMEFF2ΔID with Flag tag and SHP-1 in AGS and MKN45 cells. n = 3.

(D) Cell proliferation assays were performed in GC cells after overexpression of TMEFF2WT/ΔID with or without SWT. n = 3, non-parametric Mann-Whitney test. TWT: TMEFF2WT; SWT: SHP-1WT.

(E) Co-IP was performed after co-expression of SHP-1ΔSH2D1/ΔSH2D2/ΔPTPD with HA tag and TMEFF2 WT in GC cells. n = 3.

(F) Cell proliferation assays were performed in AGS cells after overexpression of SHP-1WT/ΔSH2D1/ΔSH2D2/ΔPTPD or these constructs combined with TMEFF2. n = 3, non-parametric Mann-Whitney test.

(G) Schematic representation the biological role of TMEFF2 in gastric carcinogenesis. TMEFF2 may act as a tumor suppressor by regulating cell proliferation, apoptosis and genomic stability in gastric carcinogenesis. TMEFF2 directly interacts with SHP-1 via its intercellular domain. The SH2 1/2 domains of SHP-1 are important for its interaction with TMEFF2 and the tumor-suppressive function of TMEFF2.
TMEFF2 deregulation contributes to gastric carcinogenesis and indicates poor survival outcome

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