

A

Result of STR matching analysis by your data.

DSMZ Profile Database

A graphical presentation is shown at the bottom of this page.

EV	Cell No.	Cell name	Locus names								Figures	
			D5S818	D13S317	D7S820	D16S539	VWA	TH01	AM	TPOX		CSF1PO
		Query (Your Cell)	8,10	11,12	11,11	9,9	14,18	9,9	X,X	11,11	11,12	

Expassy

Cellosaurus

Cellosaurus TPC-1 (CVCL_6298)

[Text version]

Cell line name

TPC-1

Synonyms

TPC1

Accession

CVCL_6298

Resource Identification Initiative

To cite this cell line use: TPC-1 (RRID:CVCL_6298)

Source(s):

Millipore; PubMed=18713817; PubMed=21868764; PubMed=30737244

Markers:

Amelogenin

X

CSF1PO

11,12

D3S1358

16,17

D5S818

8,10

D7S820

11

D8S1179

11,17

D13S317

11,12

D16S539

9

D18S51

13,16

D21S11

30,31.2

FGA

20,21

Penta D

9,13

Penta E

18

TH01

9

TPOX

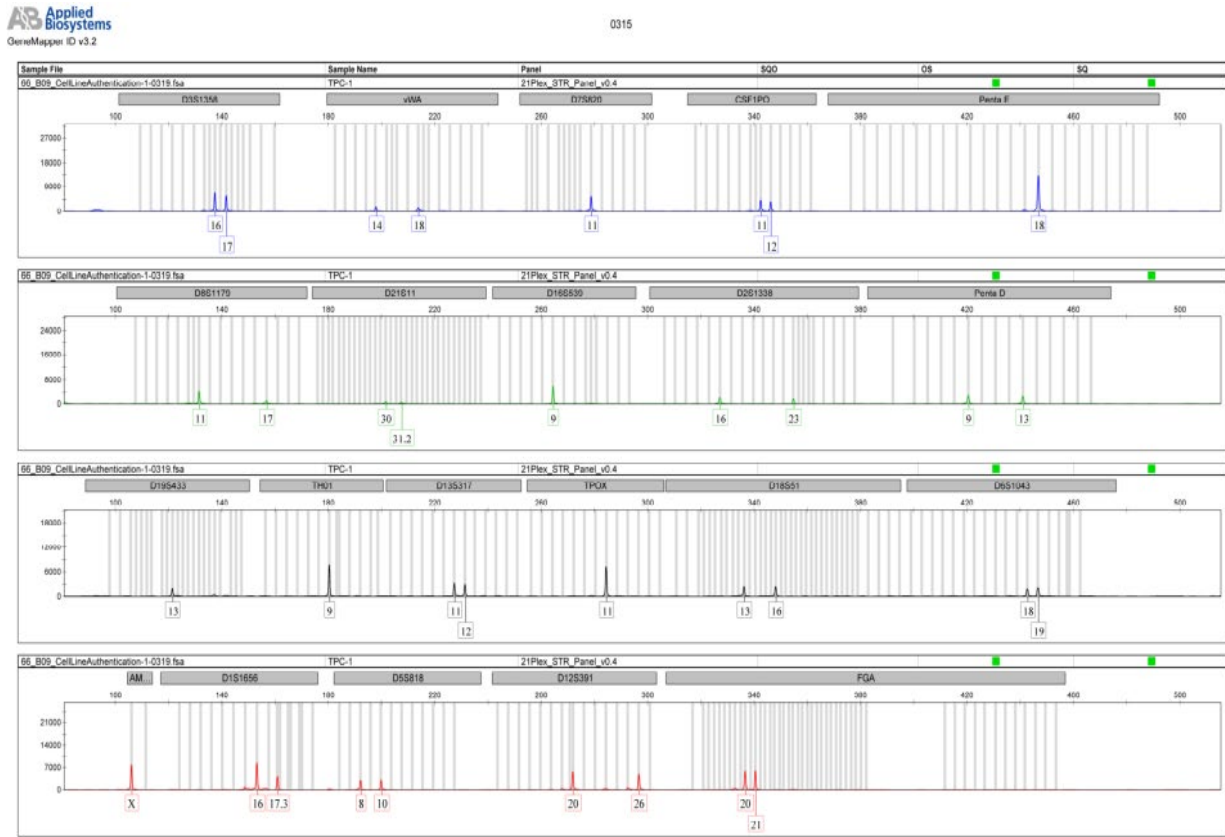
11

VWA

14,18

Run an STR similarity search on this cell line

B



Supplementary Figure 1 Authentication of TPC-1 cell line we used by STR profile.

(A) Searching for the matching results of locus for TPC-1 cell line we used in the DSMZ profile and Cellosaurus database (in red frame). (B) Sequencing for locus for TPC-1 cell line we used and presentation of each characteristic locus.

A

Result of STR matching analysis by your data.

- DSMZ Profile Database -

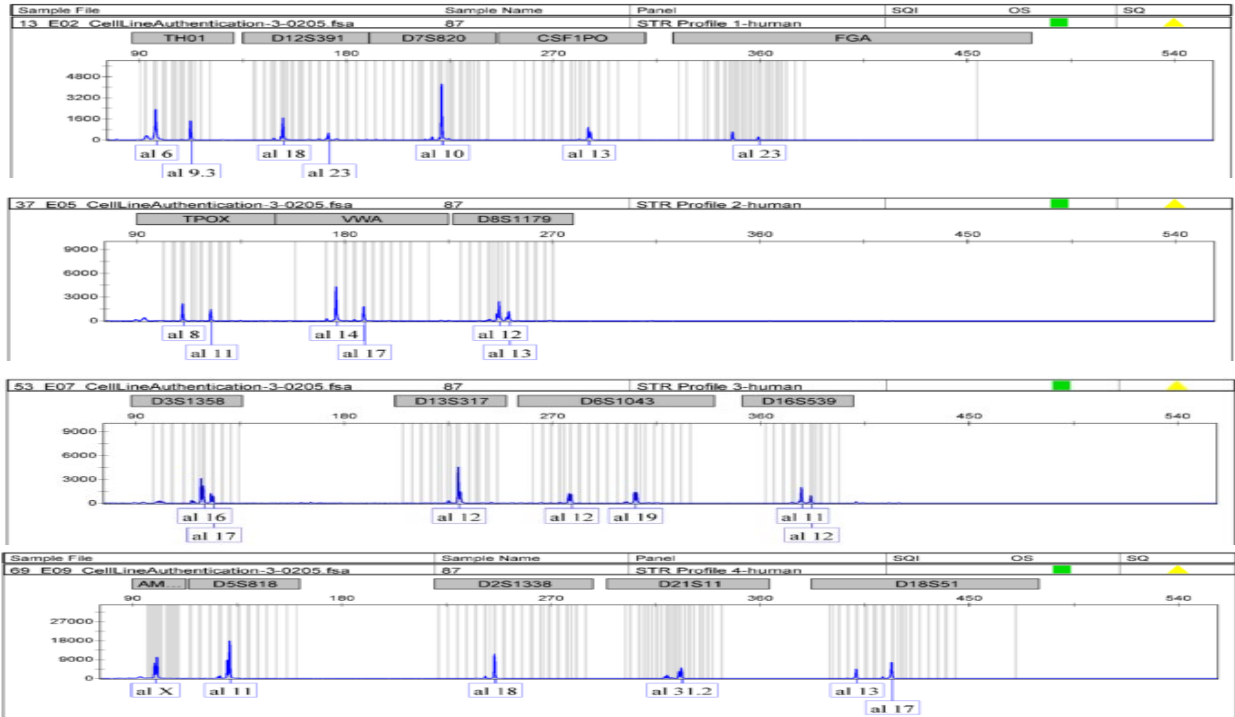
A graphical presentation is shown at the bottom of this page.

EV	Cell No.	Cell name	Locus names									Figures
			D5S818	D13S317	D7S820	D16S539	VWA	TH01	AM	TPOX	CSF1PO	
	Query (Your Cell)		11,11	12,12	10,10	11,12	14,17	6,9,3	x,x	8,11	13,13	
0.94(34/36)	273	B-CPAP	10,11	12,12	10,10	11,12	14,17	6,9,3	X,X	8,11	13,13	-
0.70(26/37)	CRL-5803	NCI-H1299	11,11	12,12	10,10	12,13	16,17,18	6,9,3	X,X	8,8	12,12	-
0.67(24/36)	266	S-117	11,11	12,12	11,11	11,14	14,14	6,6	X,X	8,8	13,13	-
0.67(24/36)	446	CAL-27	11,12	10,11	10,10	11,12	14,17	6,9,3	X,X	8,8	10,12	-
0.67(24/36)	572	SU-DHL-6	12,12	12,14	10,10	11,12	14,17	6,9,3	X,X	11,12	10,10	-
0.67(24/36)	687	MINO	11,12	12,12	10,11	11,12	14,17	9,3,9,3	X,Y	8,11	9,11	-
0.67(24/36)	766	PGA-1	11,12	8,12	10,11	12,12	17,17	6,9,3	X,Y	8,11	13,13	-
0.67(24/36)	768	U-2904	11,11	12,12	12,12	11,13	16,17	6,9,3	X,X	8,11	12,14	-
0.67(24/36)	776	PG-EBV	11,12	8,12	10,11	9,12	17,17	6,9,3	X,Y	8,11	13,13	-
0.67(24/36)	781	HS-578T	11,11	11,11	10,10	12,12	17,17	9,9,3	X,X	8,8	13,13	-
0.67(24/36)	CCL-251	NCI-H716 [H716]	11,11	8,11	10,11	11,12	16,17	6,9,3	X,X	8,11	11,11	-
0.67(24/36)	CRL-1486	HEPM	11,13	8,12	8,10	11,12	17,18	6,9,3	X,X	8,11	10,11	-
0.67(24/36)	CRL-2095	CAL 27	11,12	10,11	10,10	11,12	14,17	6,9,3	X,X	8,8	10,12	-

B

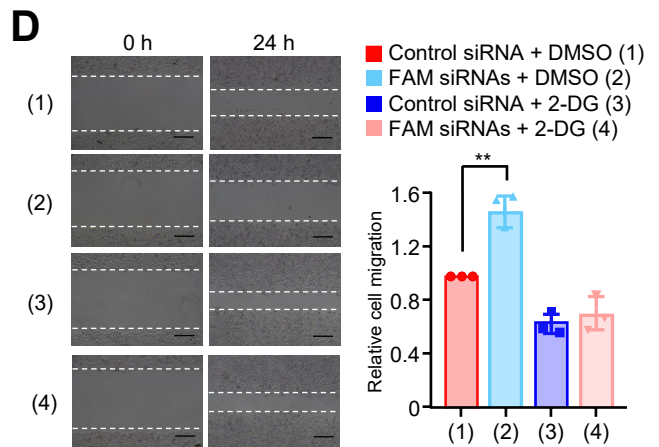
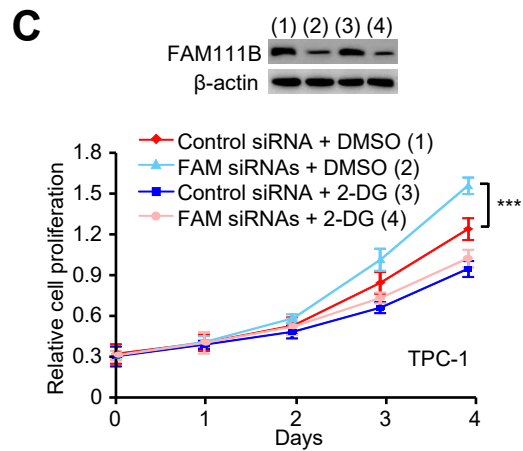
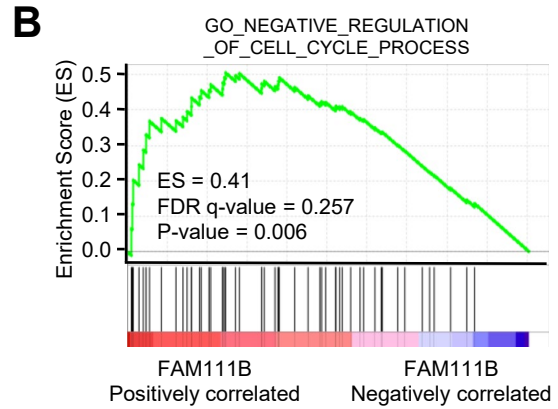
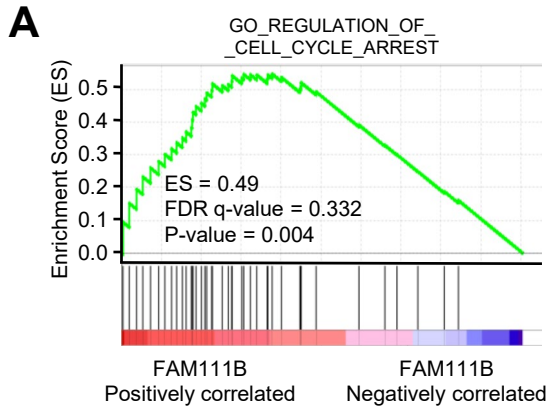
Applied Biosystems
GeneMapper 4.0

CellLineAuthentication-0129



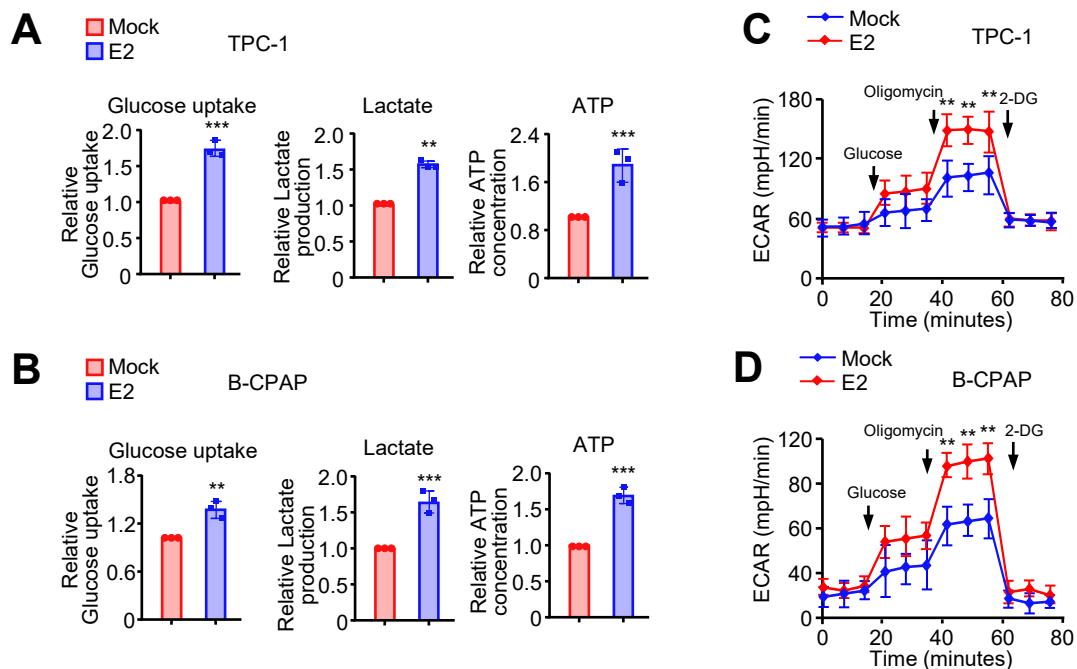
Supplementary Figure 2 Authentication of B-CPAP cell line we used by STR profile.

- (A) Searching for the matching results of locus for B-CPAP cell line we used in the DSMZ profile database (in red frame).
- (B) Sequencing for locus of B-CPAP cell line we used and presentation of each characteristic locus.



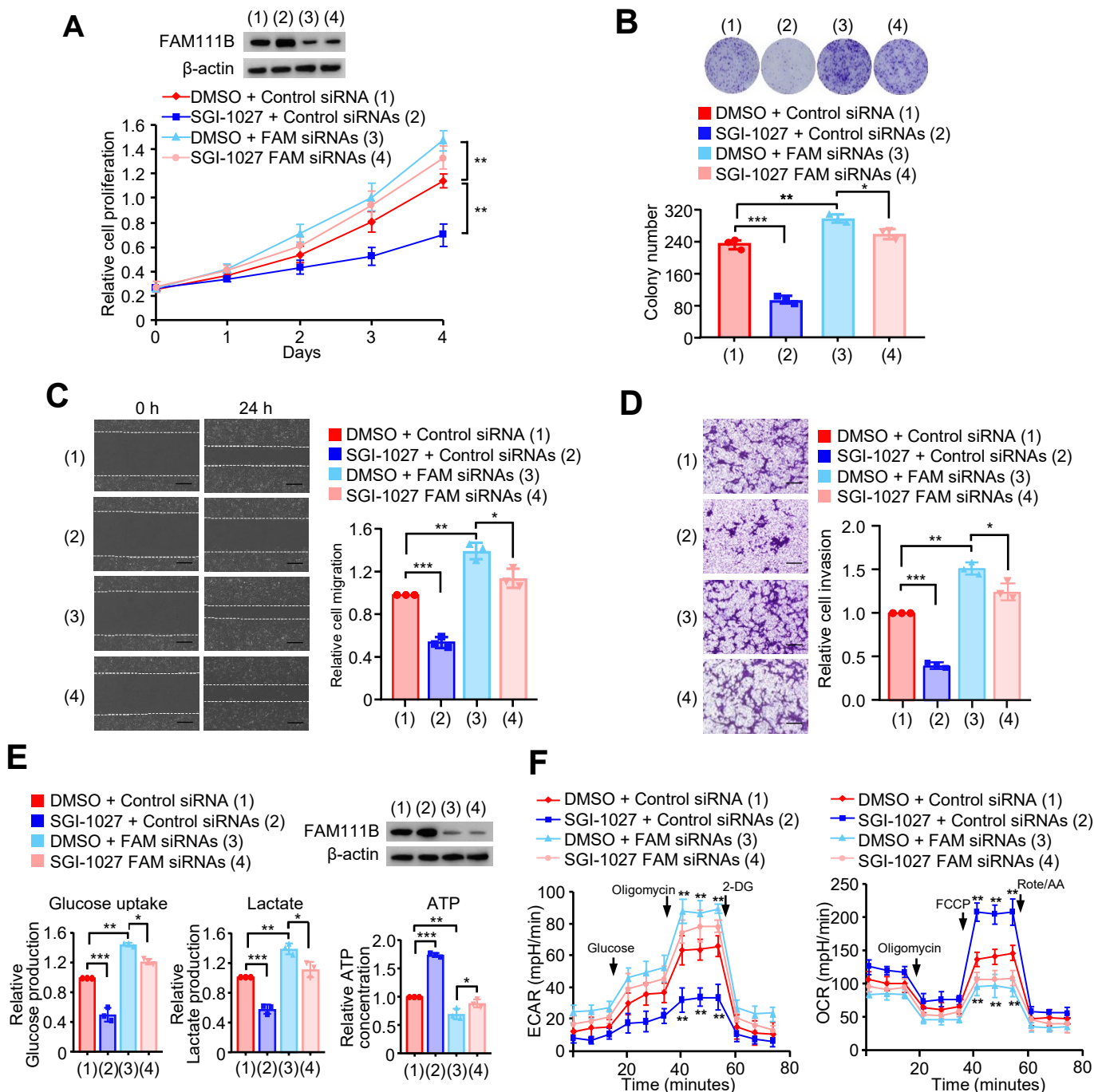
Supplementary Figure 3 2-DG inhibits the growth and migration of PTC.

(A, B) GSEA plot showing that FAM111B expression is positively correlated with cell cycle arrest and negatively correlated with cell cycle process in the TCGA THCA dataset. (C) TPC-1 cells were transfected with FAM111B siRNAs and treated with 2-DG. The proliferation of the cells was measured by CCK-8 assay. (D) Wound healing of TPC-1 cells transfected and treated as in (C). Right histograms reveal the relative cell migration. Scale bar, 50 μ m. ** p < 0.01, *** p < 0.001 vs. Control siRNA + DMSO group



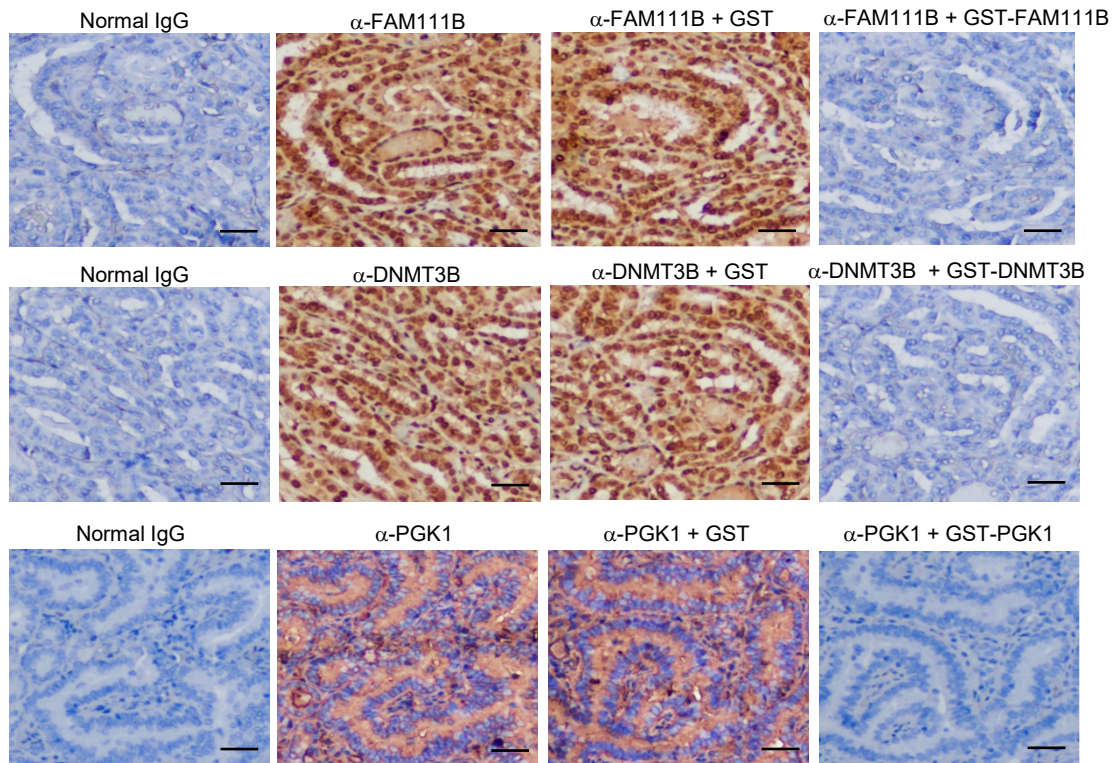
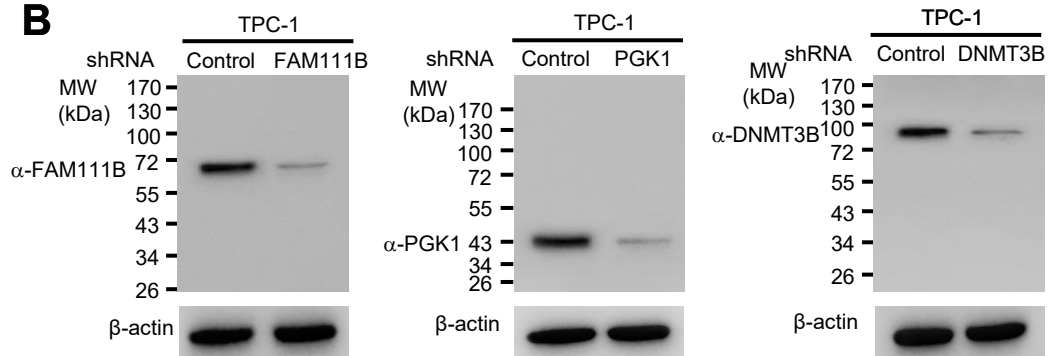
Supplementary Figure 4 E2 upregulates glycolysis in PTC cells.

(A, B) TPC-1 and B-CPAP cells were treated with Mock or E2 respectively. Glucose uptake, lactate production and ATP production were measured. (C, D) TPC-1 cells (C) and B-CPAP cells (D) were treated as in (A,B), and extracellular acidification rate (ECAR) was then evaluated. The arrows indicate the time of adding glucose, oligomycin, 2-DG. All values shown are mean $\pm$ S.D. of triplicate measurements and have been repeated 3 times with similar results (A-D). ** p < 0.01, *** p < 0.001 vs. Mock group.



Supplementary Figure 5 Methylation of FAM111B by DNMT3B promotes the growth, migration, invasion and glycolysis of PTC.

(A) B-CPAP cells were transfected with FAM111B siRNAs and treated with SGI-1027. The proliferation of the cells was measured by CCK-8 assay. The representative immunoblot indicated FAM111B protein level. (B) Colony formation assay of B-CPAP cells transfected and treated as in (A). Representative images reveal colonies in plates (upper panels). Histograms reveal colony number. (C, D) Wound healing (C) and Transwell (D) assays of B-CPAP cells transfected and treated as in (A). Right histograms reveal the relative cell migration and invasion. (E) Glucose uptake and the production of lactate and ATP were determined. Representative immunoblot shows the expression of FAM111B. (F) B-CPAP cells were transfected and treated as in (A), and extracellular acidification rate (ECAR) (F) and oxygen consumption rate (OCR) were then measured. Scale bar, 50 μ m. * p < 0.05, ** p < 0.01, *** p < 0.001 vs. DMSO + Control siRNA group.

A**B****Supplementary Figure 6 Identification of the specificity of the antibodies used in IHC.**

(A) IHC staining of thyroid cancer specimens incubated with normal IgG, anti-FAM111B, anti-DNMT3B and anti-PGK1. To confirm the antibody specificity, anti-FAM111B, anti-DNMT3B and anti-PGK1 was pre-incubated respectively with the indicated recombinant GST or GST-FAM111B, GST-DNMT3B and GST-PGK1 applied to the tissue for 1 hour. Scale bar, 50 μ m. (B) Western blot analysis of lysates from TPC-1 cells infected with control shRNA or FAM111B, PGK1 and DNMT3B.

Table S1 The sequences of all primers and oligonucleotide used in the study.

Gene	Forward primer (5' to 3')	Reverse primer (5' to 3')
FAM111B	GCCCTTGAAATGCAGAATCCA	GCTGTAAACACACTACGGTCTAA
ALDOA	ATGCCCTACCAATATCCAGCA	GCTCCCAGTGGACTCATCTG
DNMT3B	AGGGAAGACTCGATCCTCGTC	GTGTGTAGCTTAGCAGACTGG
β -ACTIN	GGGACCTGACTGACTACCTC	TCATACTCCTGCTTGCTGAT
GPI	CAAGGACCGCTTCAACCACTT	CCAGGATGGGTGTGTTTGACC
PGAM4	CCTCAGTGCAGAAGAGAGTGATC	TGGTGGGACATCATAGGAGCGC
PGAM2	AGAAGCACCCCTACTACAACCTC	TCTGGGGAACAATCTCCTCGT
PGAM1	GTGCAGAAGAGAGCGATCCG	CGGTTAGACCCCCATAGTGC
LDHA	ATGGCAACTCTAAAGGATCAGC	CCAACCCCAACAACCTGTAATCT
PFKP	GCATGGGTATCTACGTGGGG	CTCTGCGATGTTTGAGCCTC
PFKL	GCTGGGCGGCACTATCATT	TCAGGTGCGAGTAGGTCCG
ENO1	AAAGCTGGTGCCGTTGAGAA	GGTTGTGGTAAACCTCTGCTC
PGM2	GAGGCAGTGAAACGACTAATAGC	CTGTCCCAAACCTCCATTCGGG
PGM1	CCAAACCGACTGAAGATCCGT	CATGTTTCGATCCCCATCTCC
GAPDH	GGAGCGAGATCCCTCCAAAAT	GGCTGTTGTCATACTTCTCATGG
PGK1	TGGACGTAAAGGGAAGCGG	GCTCATAAGGACTACCGACTTGG
HK2	GAGCCACCACTCACCCTACT	CCAGGCATTGCGCAATGTG
PFKM	GGTGCCCGTGTCTTCTTTGT	AAGCATCATCGAAACGCTCTC
ALDH2	ATGGCAAGCCCTATGTCATCT	CCGTGGTACTTATCAGCCCA
PKM	GACCCGGAATCCCCAGACAG	TCACGGCACAGGAACAACACG
Oligonucleotide	Sense (5' to 3')	Antisense (5' to 3')
si-FAM111B -1	CCUGUUGAUCAUUGUCUAUTT	AUAGACAAUGAUCAACAGGTT
si-FAM111B-2	GCAAGUCAGUUGGGUUCAUTT	AUGAACCCAAACUGACUUGCTT
si-FAM111B-3	GCAUGCCCUUAUUGAAUUUTT	AAAUUCAUAAGGGCAUGCTT

Table S2 The sequences of FAM111B-R

ATGAATTCCATGAAGACTGAAGAAAACAAGTCATTTAGCGCTATGGAAGATGACCAGA
GGACTAGACCTGAAGTTTCAAAGGATACTGTCATGAAGCAGACACATGCTGACACACC
TGTGATCACTGTCTATCTGGCATAAGAAAGTGTAGCAGCACCTTTAAGCTTAAAAGTG
AAGTCAACAAGCATGAAACAGCCCTTGAAATGCAGAATCCAAATTTGAACAATAAAGA
ATGTTGTTTCACCTTTACGTTGAATGGAACTCCAGAAAATTAGACCGTAGTGTGTTTA
CAGCATATGGTAAACCCAGCGAGAGTATCTACTCAGCCCTGAGTGCTAATGACTATTTT
AGTGAAAGGATAAAGAATCAGTTTAATAAGAACATTATTGTTTATGAAGAAAAGACAAT
AGATGGACATATAAATTTAGGAATGCCTCTCAAGTGCCTGCCTAGTGATTCTCATTTTAA
AATTACATTTGGTCAAAGAAAGAGTAGCAAAGAAGATGGACACATATTACGCCAATGT
GAAAATCCAAACATGGAATGCATTCTTTTCATGTTGTTGCTATAGGAAGGACAAGAAA
GAAGATTGTTAAGATCAACGAACTTCATGAAAAAGGAAGTAACTTTGTATTTATGCCT
TGAAGGGTGAGACTATTGAAGGAGCCTTATGCAAGGATGGCCGTTTTCCGTCTGACAT
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TAAAACTAAAAGAAAATGGAAATGCGTTTCCTCCAGGACTATGGCGACAGATTTCTCC
TCAACCATCTACTGGTTTGATTTATTTAATTGGTCATCCTGAAGGCCAGATCAAGAAAAT
AGATGGTTGTACTGTGATTCTCTAAACGAACGATTGAAAAAATATCCAAACGATTGTC
AAGATGGGTTGGTAGATCTCTATGATACCACCAGTAATGTATACTGTATGTTTACCCAAA
GAAGTTTCCTATCAGAGGTTTGGAAACACACACACGCTTAGTTATGATACTTGTTTCTCT
GATGGGTCCTCAGGCTCCCCAGTGTTTAATGCATCTGGCAAATTGGTTGCTTTGCATAC
CTTTGGGCTTTTTTATCAACGAGGATTTAATGTGATGCCCTATTGAATTTGGTTATTCT
ATGGATTCTATTCTTTGTGATATTA AAAAGACAAATGAGAGCTTGTATAAATCATTAAAT
GATGAGAACTTGAGACCTACGATGAAGAGAAAGGTAAACAAGAGTCATCACTTCAA
GATCATCAGATTGAACCCATGGAATGTTAG

The red font represents the target sequence of siRNAs and the yellow font represents the mutation sites.