

Table 1: Relationship between the expression of FAM3C in pancreatic carcinoma tissues and the clinical characteristics of pancreatic carcinoma patients (n = 115).

Parameters	TMA		χ^2	p value
	High, n(%)	Low, n (%)		
Gender				
Male	51 (58.6)	36 (41.4)	2.125	0.145
Female	12 (42.9)	16 (57.1)		
Age, years				
≤60	39 (54.2)	33 (45.8)	0.029	0.864
>60	24 (55.8)	19 (44.2)		
Tumor location				
Head	50 (52.6)	45 (47.4)	1.020	0.312
Body or tail	13 (65.0)	7 (35.0)		
Tumor size, cm				
≤2	17 (42.5)	23 (57.5)	3.735	0.053
>2	46 (61.3)	29 (38.7)		
Neural invasion				
Yes	30 (63.8)	17 (36.2)	2.626	0.105
No	33 (48.5)	35 (51.5)		
Duodenal invasion				
Yes	13 (81.3)	3 (18.8)	5.256	0.022
No	50 (50.5)	49 (49.5)		
Differentiation				
Low	20 (74.1)	7 (25.9)	7.317	0.026
Median	39 (52.0)	36 (36.0)		
High	4 (30.8)	9 (69.2)		
Lymphatic invasion				
Yes	26 (65.0)	14 (35.0)	2.585	0.108
No	37 (49.3)	38 (50.7)		
Vascular invasion				
Yes	20 (64.5)	11 (35.5)	1.623	0.203
No	43 (51.2)	41 (48.8)		
Liver metastasis				
Yes	12 (80.0)	3 (20.0)	4.428	0.035
No	51 (51.0)	49 (49.0)		
TNM stage (UICC)				
I or IIA	32 (48.5)	34 (51.5)	2.480	0.115
IIB or III, IV	31 (63.3)	18 (36.7)		

UICC, Union for International Cancer Control. Bold indicates statistically significant at p value < 0.05.

Table. S1 Full results of the correlation analysis of FAM3 family genes expression and drug sensitivity in CellMiner.

Gene	Drug name	Cor	<i>p</i> -value
FAM3B	Barasertib	0.651	0.000
FAM3D	Elesclomol	0.561	0.000
FAM3D	GSK-1904529A	0.559	0.000
FAM3D	Linsitinib	0.535	0.000
FAM3B	AMG-900	0.526	0.000
FAM3B	LDK-378	0.516	0.000
FAM3B	PF-06873600	0.505	0.000
FAM3B	Dexrazoxane	0.480	0.000
FAM3D	PI-103	-0.476	0.000
FAM3B	AM-5992	0.467	0.000
FAM3B	CFI-400945	0.453	0.000
FAM3B	CG-806	0.443	0.000
FAM3B	CCT-271850	0.443	0.000
FAM3B	TAE-684	0.439	0.001
FAM3B	LEE-011	0.435	0.001
FAM3B	Palbociclib	0.431	0.001
FAM3B	NTRC-0066-0	0.428	0.001
FAM3B	CEP-37440	0.417	0.001
FAM3B	CT-GSK183	0.416	0.001
FAM3B	GSK-1070916	0.413	0.001
FAM3B	R-547	0.413	0.001
FAM3B	CEP-14083	0.407	0.001
FAM3D	BAY-876	0.407	0.001
FAM3D	AEW-541	0.406	0.001
FAM3B	CX-5461	0.404	0.002
FAM3B	BAY-1161909	0.403	0.002
FAM3D	BMS-754807	0.402	0.002
FAM3D	ADW-742	0.401	0.002
FAM3B	AZD-3463	0.401	0.002
FAM3A	Rapamycin	0.398	0.002
FAM3B	CC-671	0.397	0.002
FAM3B	SOMCL-12-81	0.395	0.002
FAM3A	SNS-314	0.392	0.002
FAM3C	CC-90003	0.39	0.002
FAM3C	ARRY-704	0.386	0.003
FAM3B	BOS-172722	0.385	0.003
FAM3C	Cobimetinib (isomer 1)	0.385	0.003
FAM3A	Olaparib	0.382	0.003
FAM3A	XL-147	0.379	0.003
FAM3D	Ribavirin	0.378	0.003
FAM3C	RO-4987655	0.377	0.003
FAM3A	Sabutoclax	0.375	0.003
FAM3C	TAK-733	0.374	0.004

FAM3A	LGK-974	0.373	0.004
FAM3A	Quizartinib	0.371	0.004
FAM3D	PLX-8394	0.369	0.004
FAM3C	PD-0325901	0.367	0.004
FAM3C	LXH-254	0.367	0.004
FAM3B	TAS-116	0.367	0.004
FAM3B	ensartinib	0.365	0.005
FAM3C	CCT-251545	-0.364	0.005
FAM3D	AZD-3463	0.360	0.005
FAM3C	AZ-628	0.360	0.005
FAM3C	AZD-0364	0.359	0.005
FAM3C	Acetalax	-0.358	0.005
FAM3A	RAPAMYCIN	0.358	0.005
FAM3B	P-529	-0.355	0.006
FAM3B	ABT-348	0.355	0.006
FAM3D	BMS-536924	0.354	0.006
FAM3C	Pimasertib	0.354	0.006
FAM3B	TAE-226	0.353	0.006
FAM3D	P-529	-0.352	0.006
FAM3C	Simvastatin	0.352	0.006
FAM3C	DIGOXIN	-0.352	0.006
FAM3B	Telatinib	-0.351	0.006
FAM3A	Itraconazole	0.349	0.007
FAM3B	Alisertib	0.349	0.007
FAM3A	AZD-5363	0.347	0.007
FAM3B	PYRAZOLOACRIDINE	0.346	0.007
FAM3B	CCT-251545	0.345	0.007
FAM3C	SCH-772984	0.345	0.008
FAM3C	ARRY-162	0.344	0.008
FAM3B	Danuserib	0.344	0.008
FAM3C	Refametinib	0.343	0.008
FAM3A	FH-535	0.341	0.008
FAM3B	Volasertib	0.340	0.009
FAM3B	BX-912	0.339	0.009
FAM3B	VX-689	0.339	0.009
FAM3C	AMD-070	0.338	0.009
FAM3A	Cpd-401	0.336	0.009
FAM3B	Ifosfamide	0.332	0.010
FAM3C	SEL-120	0.332	0.010
FAM3B	PX-316	0.332	0.010
FAM3A	Irinotecan	0.331	0.010
FAM3A	Axitinib	0.330	0.011
FAM3B	LY-3154567	0.330	0.011
FAM3D	CT-GSK183	0.329	0.011

FAM3C	FGF-401	0.329	0.011
FAM3D	Barasertib	0.328	0.011
FAM3C	RO-5126766	0.327	0.011
FAM3D	Cisplatin	-0.327	0.012
FAM3B	BAY-1217389	0.326	0.012
FAM3B	GSK-1904529A	0.326	0.012
FAM3B	TAK-901	0.323	0.013
FAM3C	AZ-505	0.323	0.013
FAM3A	ARRY-704	-0.322	0.013
FAM3D	SR16157	0.320	0.013
FAM3C	PD 184352	0.320	0.013
FAM3D	TAE-684	0.320	0.014
FAM3C	Procarbazine	0.319	0.014
FAM3C	Kahalide F	0.319	0.014
FAM3A	Temsirolimus	0.319	0.014
FAM3B	EXEL-2280	0.319	0.014
FAM3B	EMD-534085	0.318	0.014
FAM3B	By-Product of CUDC-305	0.317	0.014
FAM3C	Trametinib	0.317	0.014
FAM3A	EMD-1204831	0.315	0.015
FAM3B	KW-2449	0.313	0.016
FAM3B	AT-9283	0.313	0.016
FAM3B	PF-562271	0.313	0.016
FAM3D	Lapachone	-0.312	0.016
FAM3D	DOLASTATIN 10	0.311	0.017
FAM3B	KPT-9274	0.310	0.017
FAM3A	Bosutinib	-0.310	0.017
FAM3D	Vemurafenib	0.309	0.017
FAM3B	Crizotinib	0.308	0.017
FAM3A	pyridoclax	0.308	0.018
FAM3A	Ipatasertib	0.308	0.018
FAM3C	Fluorouracil	-0.308	0.018
FAM3C	ulixertinib	0.307	0.018
FAM3A	5-Fluoro deoxy uridine 10mer	0.306	0.018
FAM3C	CEP-40783	0.306	0.018
FAM3A	Hydrastinine HCl	0.306	0.018
FAM3C	JNJ-38877605	0.305	0.019
FAM3B	AMG-458	-0.304	0.019
FAM3C	RG-7602	-0.304	0.019
FAM3B	AT-13387	0.304	0.019
FAM3A	7-Ethyl-10-hydroxycamptothecin	0.304	0.019
FAM3B	A-911	0.304	0.019
FAM3B	Elesclomol	0.303	0.020
FAM3B	TP-0903	0.303	0.020

FAM3D	PLX-4720	0.302	0.020
FAM3B	Tamoxifen	0.302	0.020
FAM3B	VX-944	0.301	0.021
FAM3D	GDC-0994	0.301	0.021
FAM3A	Triethylenemelamine	0.300	0.021
FAM3A	Amuvatinib	0.299	0.021
FAM3D	Dabrafenib	0.299	0.021
FAM3D	IDH-C227	-0.299	0.021
FAM3A	LY-294002	0.299	0.022
FAM3C	RG-6016	0.298	0.022
FAM3C	Milciclib	0.297	0.022
FAM3A	Cisplatin	0.297	0.022
FAM3D	AM-5992	0.297	0.022
FAM3A	AZD-3514	0.297	0.023
FAM3A	Uracil mustard	0.296	0.023
FAM3D	BGB-283	0.295	0.023
FAM3B	PF-06463922	0.295	0.023
FAM3A	Avagacestat	0.295	0.023
FAM3A	Etoposide	0.295	0.024
FAM3D	OTS-964	-0.294	0.024
FAM3B	JNJ-47117096	0.293	0.024
FAM3A	enantiomer of PF-4176340	0.293	0.024
FAM3A	Topotecan	0.292	0.025
FAM3B	brigatinib	0.292	0.025
FAM3C	EPZ-020411	0.292	0.025
FAM3B	KPT-8602	0.291	0.025
FAM3C	Bisacodyl, active ingredient of Viraplex	-0.290	0.026
FAM3A	TAK-733	-0.290	0.026
FAM3A	Chlorambucil	0.289	0.026
FAM3B	Tanespimycin	0.289	0.027
FAM3D	Quercetin	-0.288	0.027
FAM3A	JZL-195	0.287	0.027
FAM3D	CEP-37440	0.287	0.027
FAM3B	Erlotinib	-0.287	0.027
FAM3C	Axitinib	-0.287	0.028
FAM3B	XAV-939	-0.287	0.028
FAM3C	Pelitrexol isomer A	-0.287	0.028
FAM3A	(+)-JQ1	0.286	0.028
FAM3C	P-529	0.286	0.028
FAM3B	SR16157	0.286	0.028
FAM3D	LDK-378	0.285	0.028
FAM3C	By-Product of CUDC-305	-0.285	0.028
FAM3A	BAY-87-2243	0.285	0.029
FAM3B	GNE-617	0.284	0.029

FAM3C	LY-3009120	0.284	0.030
FAM3C	LY-3214996	0.283	0.030
FAM3A	Elliptinium Acetate	0.283	0.030
FAM3A	INCB-047775	0.282	0.030
FAM3A	Teniposide	0.282	0.031
FAM3A	SAR-245409	0.280	0.031
FAM3D	TAE-226	0.280	0.032
FAM3D	Palbociclib	0.280	0.032
FAM3B	BMS-754807	0.280	0.032
FAM3B	Belinostat	0.279	0.032
FAM3A	PD-0325901	-0.279	0.032
FAM3B	YK-4-279	0.279	0.033
FAM3A	LY-3214996	-0.279	0.033
FAM3A	Cobimetinib (isomer 1)	-0.278	0.033
FAM3A	Mitomycin	0.278	0.033
FAM3A	S-49076	0.278	0.033
FAM3B	benzaldehyde (BEN)	0.278	0.033
FAM3A	Trametinib	-0.278	0.033
FAM3B	PI-103	-0.278	0.033
FAM3A	Quercetin	0.278	0.033
FAM3C	SGX-523	0.277	0.034
FAM3A	By-Product of CUDC-305	-0.277	0.034
FAM3B	ARQ-621	0.277	0.034
FAM3A	Thiotepa	0.276	0.034
FAM3A	Pipobroman	0.276	0.034
FAM3C	XAV-939	0.276	0.034
FAM3C	JNJ-54302833	-0.275	0.035
FAM3A	BMN-673	0.272	0.037
FAM3A	Calusterone	0.272	0.037
FAM3B	Teglarinad	0.272	0.037
FAM3A	E-7820	-0.272	0.037
FAM3B	CEP-28122	0.270	0.038
FAM3A	OSI-027	0.269	0.040
FAM3C	benzaldehyde (BEN)	-0.269	0.040
FAM3B	TAK Plk inhibitor	0.268	0.040
FAM3B	ADW-742	0.268	0.040
FAM3D	ST-3595	-0.267	0.041
FAM3B	MLN-0905	0.267	0.041
FAM3B	XR-11576	0.267	0.041
FAM3B	Linsitinib	0.267	0.041
FAM3A	Floxuridine	0.267	0.041
FAM3A	Deforolimus	0.267	0.041
FAM3C	Selumetinib	0.266	0.042
FAM3B	XL-147	-0.266	0.042

FAM3B	PF-03758309	0.265	0.042
FAM3D	AMG-900	0.265	0.042
FAM3A	Mitoxantrone	0.265	0.043
FAM3A	Salinomycin	0.264	0.043
FAM3B	MPC-3100	0.264	0.043
FAM3C	Pelitrexol	-0.264	0.044
FAM3B	Pipamperone	0.264	0.044
FAM3A	Neratinib	-0.263	0.044
FAM3A	WORTMANNIN	0.263	0.044
FAM3A	ZM-336372	0.263	0.044
FAM3A	Melphalan	0.263	0.044
FAM3A	PKM2 (9)	0.262	0.045
FAM3C	CC-671	-0.262	0.045
FAM3C	Encorafenib	0.262	0.045
FAM3A	AZD-3229	0.261	0.046
FAM3B	5-aza-T-dCyd	0.261	0.046
FAM3A	SR16157	0.261	0.046
FAM3A	Everolimus	0.261	0.046
FAM3D	Everolimus	-0.261	0.046
FAM3A	MK-2206	0.260	0.046
FAM3D	Bleomycin	-0.260	0.047
FAM3A	MITOXANTRONE	0.260	0.047
FAM3B	BMS-387032	0.259	0.047
FAM3B	B-7100	0.259	0.048
FAM3D	IDF-11774	0.258	0.048
FAM3A	AMG-176	0.258	0.049
FAM3B	VS-4718	0.258	0.049
FAM3B	MI-503	0.257	0.050

Table. S2 Univariate and multivariate analysis of the relationship between FAM3C expression and overall survival in PAAD.

Parameters	Univariate analysis			Multivariate analysis		
	HR	95%CI	p value	HR	95%CI	p value
Age	1.029	1.008-1.051	0.008	1.016	0.986-1.047	0.293
Gender (Female/Male)	0.809	0.537-1.219	0.311			
Grade (G1/G2/G3/G4)	1.453	1.091-1.934	0.010	1.575	0.986-2.516	0.057
Stage (I/II/III/IV)	1.213	0.842-1.747	0.299			
T (T1/T2/T3/T4)	1.556	1.003-2.413	0.048	1.002	0.494-2.032	0.995
N (N0/N1)	2.153	1.281-3.617	0.004	2.326	0.942-5.743	0.067

M (M0/M1)	0.756	0.181-3.157	0.701			
Family history of cancer (Yes/No)	0.894	0.520-1.537	0.686			
History of chronic pancreatitis (Yes/No)	0.849	0.406-1.778	0.665			
History of diabetes (Yes/No)	1.079	0.619-1.879	0.789			
Alcohol history (Yes/No)	0.872	0.561-1.355	0.543			
Lymph nodes examined count	0.997	0.975-1.019	0.782	1.008	0.9-1.129	0.891
Number of positive lymph nodes	1.062	1.007-1.121	0.027			
Cancer status (Tumor free/With tumor)	7.666	3.260-18.029	0.000	4.317	1.422-13.101	0.010
Race (White/Black/Asian)	0.902	0.593-1.371	0.630			
Tissue of origin (Head of pancreas/Body of pancreas/Tail of pancreas/Overlapping lesion of pancreas)	0.610	0.395-0.941	0.026	0.837	0.509-1.378	0.484
FAM3C expression	1.761	1.287-2.411	0.000	1.393	0.899-2.158	0.137

Table. S3 Gene sets enriched in phenotype high.

MSigDB collection	Gene set name	NES	NOM p-value	FDR q-val
C2.cp.kegg.v	KEGG_P53_SIGNALING_PATHWAY	1.913	0.000	0.043
7.4.symbols. gmt	KEGG_AXON_GUIDANCE	1.741	0.008	0.137
[Curated]	KEGG_UBIQUITIN_MEDIATED_PROTEOLYSIS	1.835	0.000	0.057
	KEGG_NUCLEOTIDE_EXCISION_REPAIR	1.970	0.000	0.037
	KEGG_CELL_CYCLE	1.864	0.002	0.048
	KEGG_MISMATCH_REPAIR	1.870	0.000	0.060

C5.all.v7.4.symbols.gmt [Gene ontology]	GOBP_EXIT_FROM_MITOSIS	2.132	0.000	0.023
	GOBP_REGULATION_OF_EXIT_FROM_MITOSIS	2.071	0.000	0.053
	GOCC_CHROMOSOMAL_REGION	1.940	0.002	0.055
	GOCC_PHOSPHATASE_COMPLEX	1.957	0.002	0.063
	GOMF_CADHERIN_BINDING	2.143	0.000	0.037
	GOMF_CELL_CELL_ADHESION_MEDIATOR_ACTIVITY	2.046	0.000	0.063

NES=normalized enrichment score, NOM=nominal, FDR=false discovery rate, NOM p value < 0.05 and FDR q-val <0.25 are considered as significant.