

# **Genomic Relevance of FGF14 and associated genes on the prognosis of Pancreatic Cancer**

Aroosha Raja, Muhammad Faraz Arshad Malik, Farhan Haq<sup>#</sup>

COMSATS University, Islamabad, Pakistan.

## **#Corresponding author**

Farhan Haq, PhD

COMSATS University, Islamabad

Email: [farhan.haq@comsats.edu.pk](mailto:farhan.haq@comsats.edu.pk)

Tel: +92-334-9540954

**S1 Fig.** Overall Workflow of the study.

**S2 Fig.** Kaplan Meier Analysis of genes in cohort 1. FGF14, FGFR1 overexpression was associated with better overall (A) (B) and overexpression of IGF2BP2, IGF2BP3 associated with lower overall survival (C) (D) of PDAC patients. (**\*p ≤ 0.05**) Red represents expression ≥ the median, while green represents expression < the median.

**S3 Fig.** Kaplan Meier Analysis of genes in cohort 2. FGF9, FGF13, FGF14, FGF17, FGFBP3, IGFBPL1 overexpression was associated with better overall survival (A) (B) (C) (D) (E) (H) and overexpression of FGFR1, IGFBP3, IGFL1 associated with lower overall survival (F) (G) (I) of PDAC patients. (**\*p ≤ 0.05**) Red represents expression ≥ the median, while green represents expression < the median.

**S4 Fig.** Kaplan Meier Analysis of genes in cohort 2. FGF9, FGF12, FGF13, FGF14, FGF17, FGFBP3, IGFBPL1 overexpression was associated with increased DFS (A) (C) (D) (E) (F) (G) (I) and overexpression of FGF10, FGFR1, IGFBP3, IGFL1 associated with reduced DFS (B) (H) (J) of PDAC patients. (**\*p ≤ 0.05**) Red represents expression ≥ the median, while green represents expression < the median.

**S5 Fig.** Common FGF14-Specific signature genes associated with survival in cohort 1 and 2 (**\*p ≤ 0.05**) Red represents expression ≥ the median, while green represents expression < the median.

**S6 Fig.** Correlation of FGF14 with IGF pathway genes

**S7 Fig.** Scatterplot showing correlation between FGF14 and FGFR1 in all three study cohorts

**S1 Table.** Clinicopathological characteristics of 65 PDAC patients of Cohort 1 (**\*p ≤ 0.05**)

**S2 Table.** Clinicopathological characteristics of 179 PDAC patients of Cohort 2 (**\*p ≤ 0.05**)

**S3 Table.** Clinicopathological characteristics of 288 PDAC patients of Cohort 3 (**\*p ≤ 0.05**)

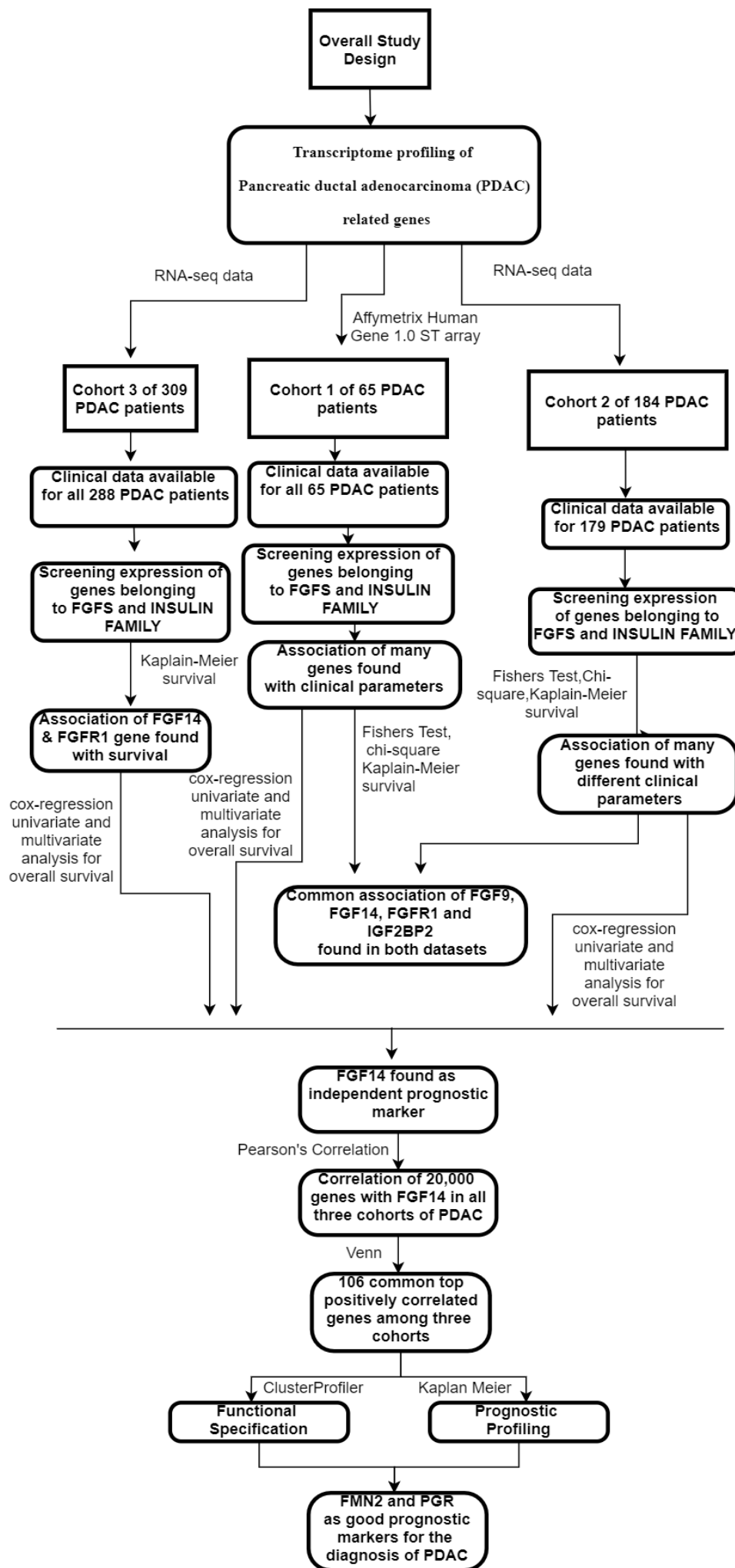
**S4 Table.** Association of genes with clinicopathologic parameters in Cohort 1 (**\*p ≤ 0.05**)

**S5 Table.** Association of genes with clinicopathologic parameters in Cohort 2 (**\*p ≤ 0.05**)

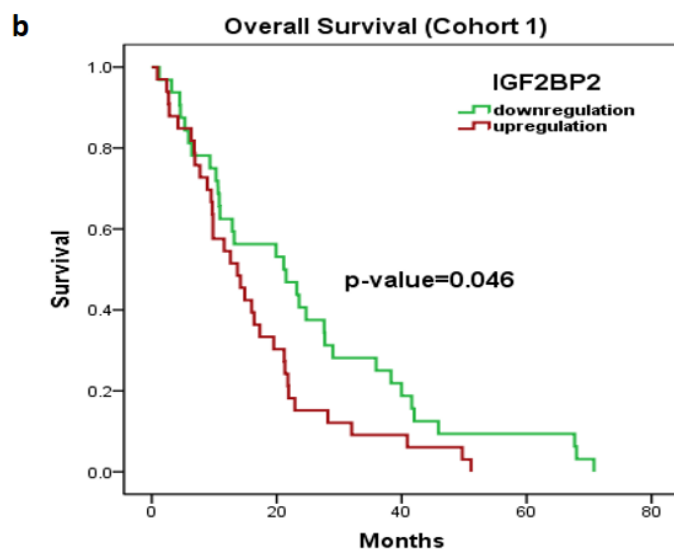
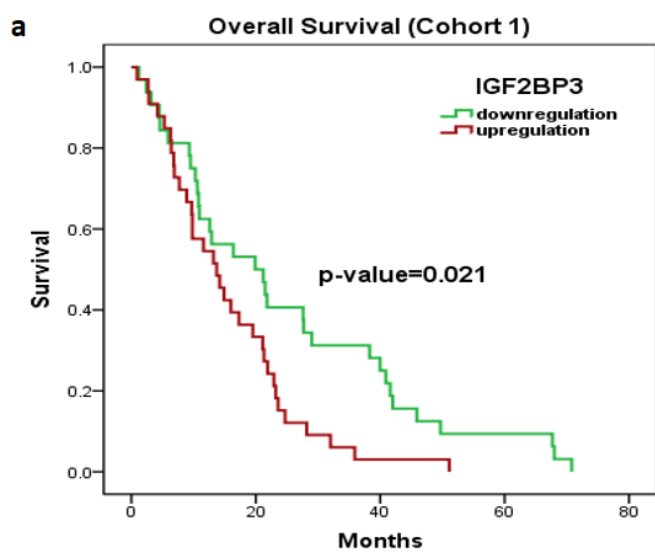
**S6 Table.** Association of common genes with clinicopathologic parameters in Cohort 1 and 2 (**\*p ≤ 0.05**)

**S7 Table.** FGF14-Signature genes associated with survival in cohort 1 (**\*p ≤ 0.05**)

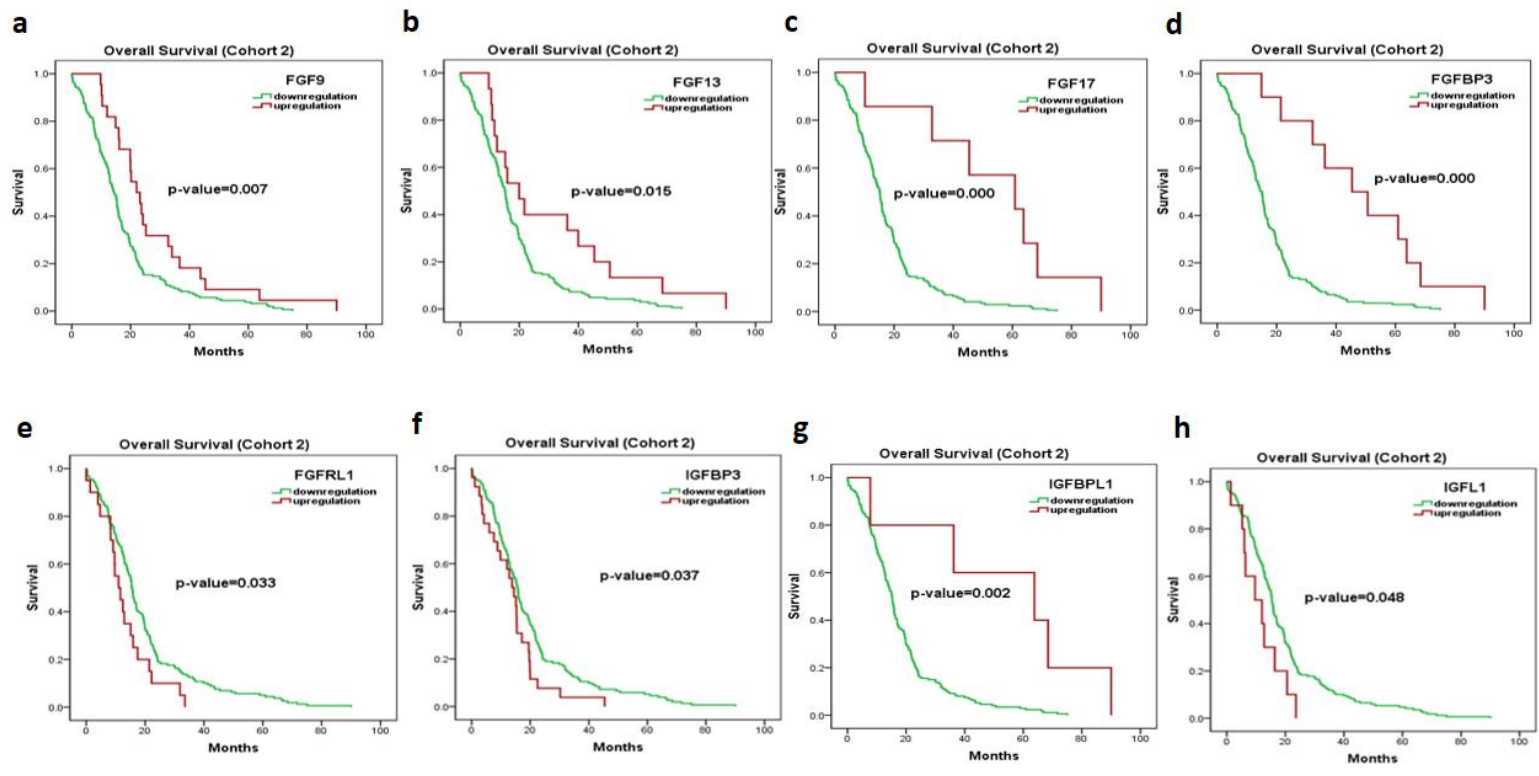
**S8 Table.** FGF14-Signature genes associated with survival in cohort 2 (**\*p ≤ 0.05**)



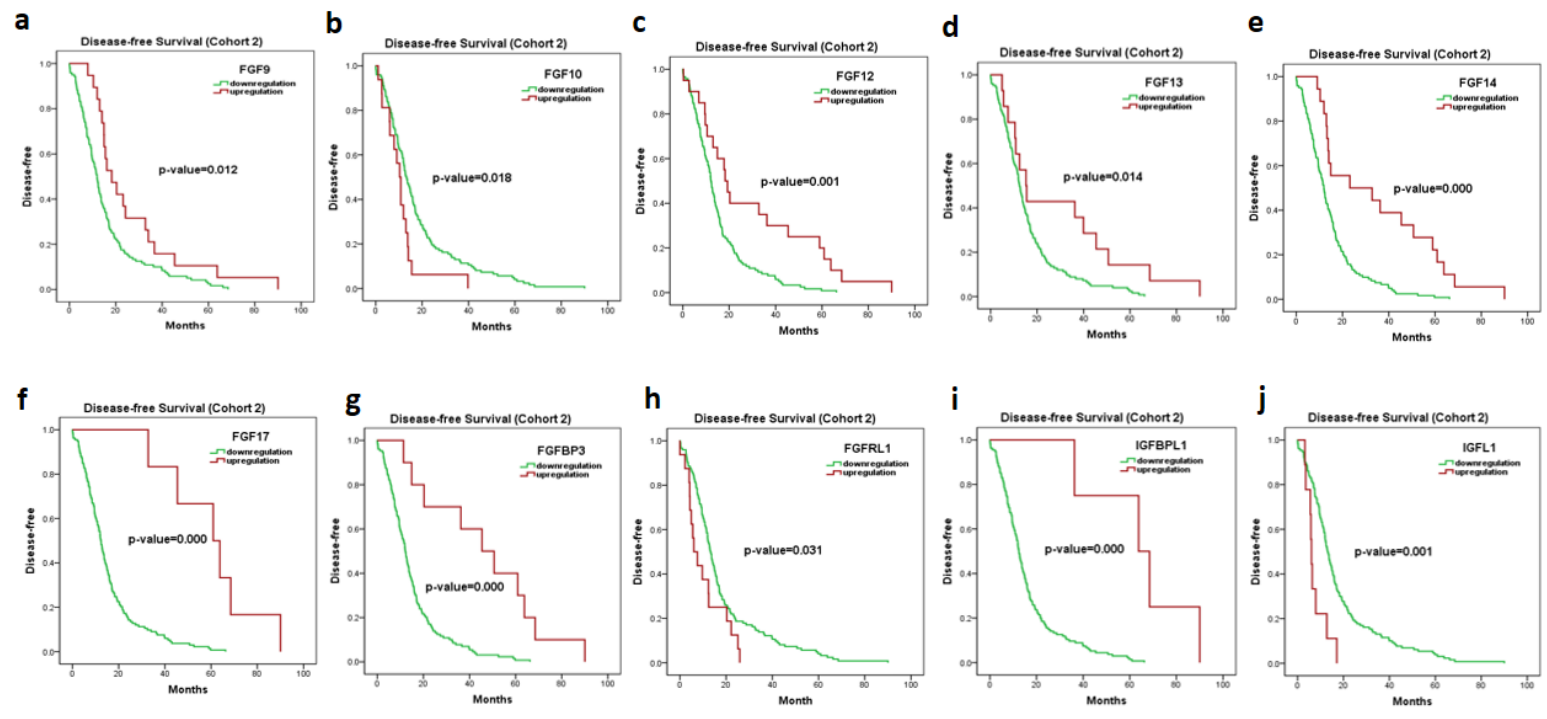
S1 Fig



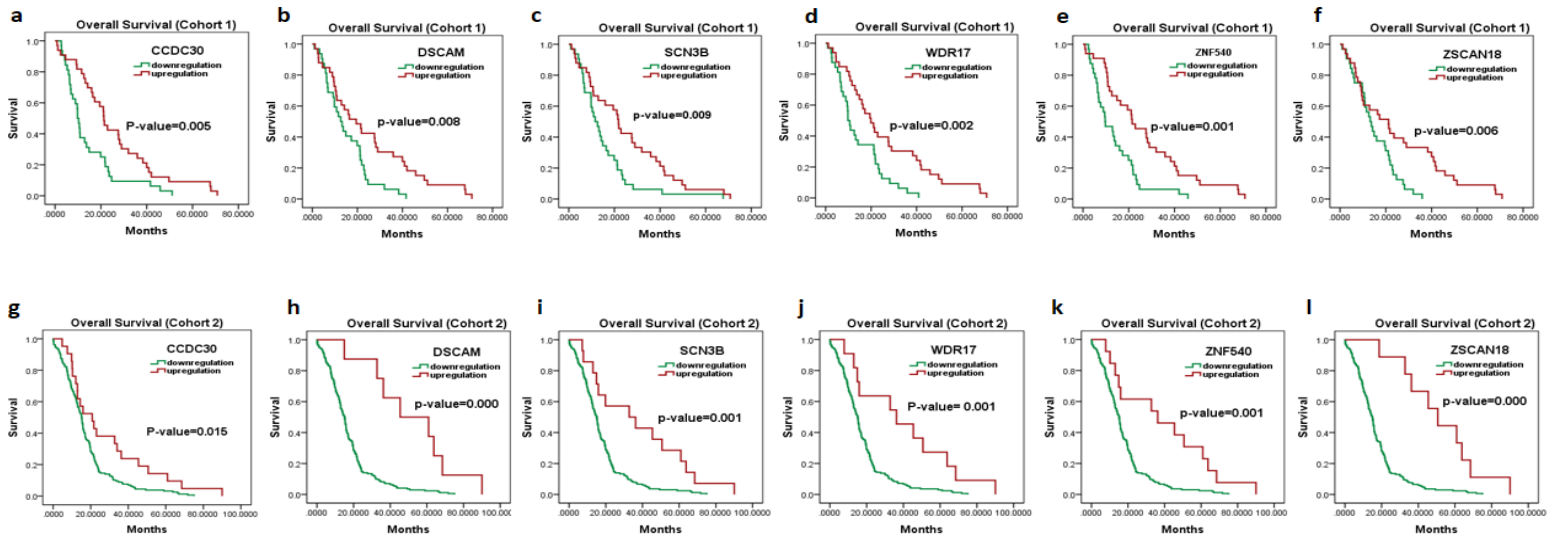
S2 Fig



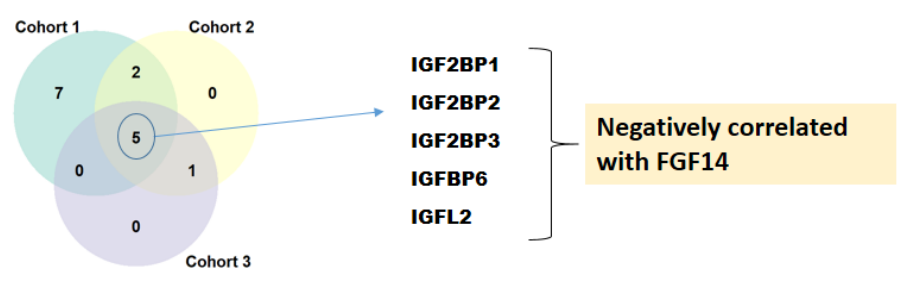
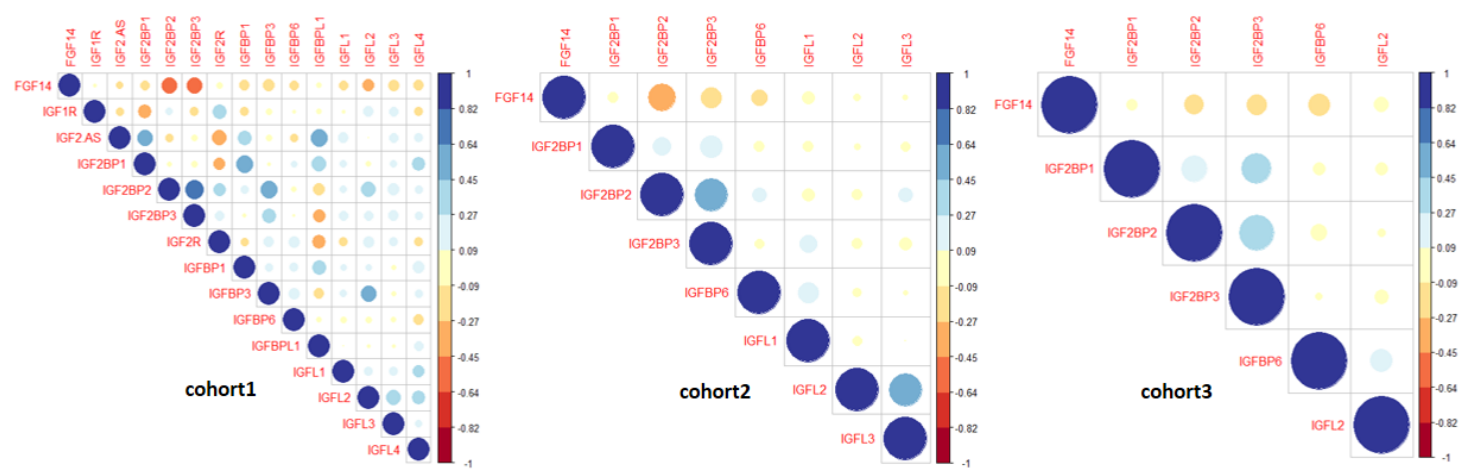
S3 Fig



S4 Fig

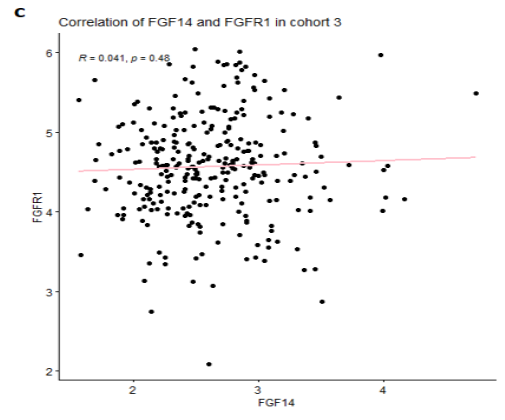
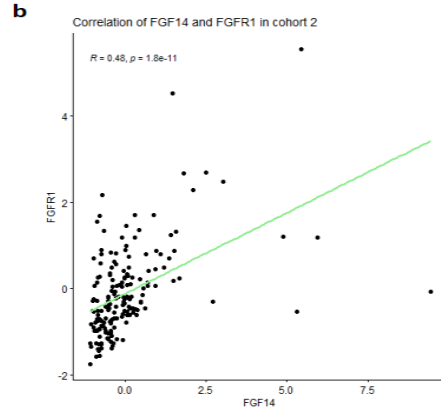
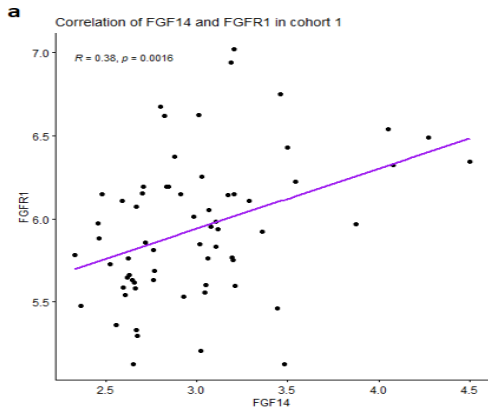


S5 Fig



S6 Fig





**S7 Fig**

**S1 Table**

<b>Characteristics</b>	<b>No.</b>	<b>Percentage</b>
<b>Stage</b>		
Stage I, IA, IB, IIA, IIB	49	75%
Stage III, IV	16	25%
<b>Grade</b>		
G1 & G2	34	52%
G3 & G4	30	46%
GX	1	2%
<b>Dead/Alive</b>		
Alive	16	25%
Dead	49	75%

**S2 Table**

<b>Characteristics</b>	<b>No.</b>	<b>Percentage</b>
<b>Age</b>		
<=50	24	13%
>50	155	87%
<b>Gender</b>		
Male	99	55%
Female	80	45%
<b>Stage</b>		
Stage I, IA, IB, IIA, IIB	168	94%
Stage III, IV	8	4%
Discrepancy or (NA)	3	2%
<b>Tumor (T)-stage</b>		
T1, T2	31	17%
T3, T4	146	82%
Tx	2	1%
<b>Nodes</b>		
N0	50	27%
N1 or greater	124	70%
Nx	5	3%
<b>Metastasis</b>		
M0	80	45%
M1 or greater	5	2%
Mx	94	53%
<b>Residual</b>		
R0	107	60%
R1 & R2	58	33%
Rx	14	7%
<b>Dead/Alive</b>		
Alive	86	48%

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Dead	93	52%
<b>Type-2 Diabetes (T2D)</b>		
Yes	38	21%
No	109	61%
NA	32	18%
<b>ALCOHOL</b>		
Yes	102	57%
No	65	36%
NA	12	7%
<b>Grade</b>		
G1 & G2	127	71%
G3 & G4	50	28%
GX	2	1%
<b>Recurrence</b>		
DiseaseFree	57	32%
Recurred/Progressed	82	45%
NA	40	23%

**S3 Table**

<b>Characteristics</b>	<b>No.</b>	<b>Percentage</b>
<b>Gender</b>		
Male	166	58%
Female	122	42%
<b>Nodes</b>		
N0	76	26%
N1 or greater	212	74%
<b>Dead/Alive</b>		
Alive	107	37%
Dead	181	63%
<b>T-stage</b>		
T1, T2	51	18%
T3, T4	237	82%

S4 Table

Genes	Classification	Stage	Grade	Alive/Dead
FGF6	FGF Ligands	NA	U	NA
FGF9		NA	U	NA
FGF14		NA	U	NA
FGFR1	FGF Receptors	U	U	U
FGFR1OP2		NA	U	NA
FGFR4	IGF binding protein genes	NA	U	NA
IGFBP4		U	NA	NA
IGF2BP3		NA	U	NA
IGF2BP2		NA	U	NA
IGFL2		Insulin growth factor gene	NA	U
IRS1	Insulin receptor substrate	NA	U	NA

**U** = upregulated in

advance stages, dead;

**U** = upregulated in early stages, living;

NA = no significant association;

S5 Table

Genes	Classification	Gender	Age	Grade	Stage	Recurrence	Residual	Nodes	Dead/Alive	Diabetes	Alcohol
FGF1	FGF Ligands	NA	NA	NA	NA	NA	NA	U	NA	NA	NA
FGF2		U	NA	NA	NA	U	NA	NA	U	NA	NA
FGF4		NA	U	NA	NA	NA	NA	NA	NA	NA	NA
FGF7		NA	NA	U	NA	NA	NA	NA	NA	U	NA
FGF9		NA	NA	U	NA	NA	NA	U	NA	NA	NA
FGF12		NA	NA	NA	U	U	NA	NA	U	NA	NA
FGF13		NA	NA	NA	NA	U	NA	NA	NA	NA	NA
FGF14		NA	NA	U	U	U	U	U	U	NA	NA
FGF17		NA	NA	NA	U	U	NA	NA	NA	NA	NA
FGF18		NA	NA	U	NA	NA	NA	NA	NA	NA	NA
FGFR1	FGF Receptors	NA	NA	NA	U	U	U	NA	U	NA	NA
FGFR2		NA	NA	NA	NA	NA	NA	NA	NA	U	NA
FGFR4		NA	NA	NA	NA	U	NA	NA	NA	U	NA
FGFBP1	FGFs Binding protein genes	NA	NA	U	NA	NA	NA	NA	NA	NA	NA
FGFBP3		NA	NA	NA	U	U	NA	NA	U	NA	NA
IGF1R	Insulin growth factor receptor	NA	NA	NA	U	NA	NA	NA	NA	NA	NA
IGF1	Insulin growth factor genes	NA	NA	U	NA	NA	NA	NA	NA	NA	NA
IGFL3		U	NA	NA	NA	NA	U	NA	NA	NA	NA
IGFL4		U	NA	NA	NA	U	NA	NA	NA	NA	NA
IGFBP6		NA	NA	NA	NA	U	NA	NA	NA	NA	NA
IGF2BP2	IGF binding protein genes	NA	NA	NA	U	U	NA	NA	NA	NA	NA
IGF2BP3		NA	U	NA	NA	U	NA	NA	NA	NA	NA
IGFBPL1		NA	NA	NA	U	U	NA	NA	NA	NA	NA
INSR	Insulin receptor gene	NA	NA	NA	NA	U	NA	NA	U	NA	NA
INSRR		U	NA	NA	U	NA	NA	NA	NA	NA	NA
IRS2	Insulin receptor substrate	NA	NA	NA	NA	NA	NA	NA	NA	NA	U

**U** = upregulated in advance stages, yes, >50, female, dead, recurred;

**U** = upregulated in early stages, no, <=50, male, living, disease-free;

NA = no significant association;

S6 Table

Genes	Classification	Grade	Stage	Nodes	Residual	Dead/Alive	Recurrence
FGF9	FGF Ligands	U	NA	U	NA	NA	NA
FGF14		U	U	U	U	U	U
FGFR1	FGF Receptor	U	U	NA	U	U	U
IGF2BP2	IGF binding protein genes	U	U	NA	NA	NA	U

U = upregulated in advance stages, dead, recurred;  
U = upregulated in early stages, living, disease-free;  
 NA = no significant association;



**S7 Table**

<b>Genes</b>	<b>P-value</b>	<b>Association</b>
CCDC30	0.005	Overexpression with good OS
DSCAM	0.008	Overexpression with good OS
FGF14	0.001	Overexpression with good OS
FMN2	0.01	Overexpression with good OS
SCN3B	0.009	Overexpression with good OS
WDR17	0.002	Overexpression with good OS
ZNF540	0.001	Overexpression with good OS
ZSCAN18	0.006	Overexpression with good OS
ANKS1B	0.002	Overexpression with good OS
CNTN5	0.005	Overexpression with good OS
KCTD16	0.009	Overexpression with good OS
KIAA0319	0.025	Overexpression with good OS
KRT222	0.029	Overexpression with good OS
NCAM1	0.05	Overexpression with good OS
PCSK1	0.027	Overexpression with good OS
PGR	0	Overexpression with good OS
PPM1E	0.01	Overexpression with good OS
RGN	0.002	Overexpression with good OS
SNAP91	0.007	Overexpression with good OS
TRPM3	0.045	Overexpression with good OS

**S8 Table**

<b>Genes</b>	<b>P-value</b>	<b>Association</b>
ACTL6B	0.000	Overexpression with good OS
AK9	0.003	Overexpression with good OS
APBB1	0.000	Overexpression with good OS
ARNT2	0.002	Overexpression with good OS
ASTN1	0.001	Overexpression with good OS
ATP8A1	0.019	Overexpression with good OS
ATRNL1	0.001	Overexpression with good OS
CDIP1	0.001	Overexpression with good OS
CAMK2B	0.000	Overexpression with good OS
CCDC30	0.015	Overexpression with good OS
CES4A	0.001	Overexpression with good OS
CLGN	0.000	Overexpression with good OS
CPEB1	0.05	Overexpression with good OS
DDX25	0.002	Overexpression with good OS
DPY19L2	0.001	Overexpression with good OS
DSCAM	0.000	Overexpression with good OS
EFR3B	0.000	Overexpression with good OS
ELAC1	0.000	Overexpression with good OS
ELAVL4	0.024	Overexpression with good OS
EML5	0.004	Overexpression with good OS
EPHA5	0.013	Overexpression with good OS
FAM135B	0.001	Overexpression with good OS
FGF14	0.000	Overexpression with good OS
FMN2	0.001	Overexpression with good OS

GDAP1	0.002	Overexpression with good OS
GRIA3	0.001	Overexpression with good OS
HFM1	0.000	Overexpression with good OS
HYDIN	0.004	Overexpression with good OS
KCNH6	0.000	Overexpression with good OS
KCNMB2	0.002	Overexpression with good OS
KCNT2	0.002	Overexpression with good OS
KIAA1324	0.001	Overexpression with good OS
LRRTM4	0.017	Overexpression with good OS
MCF2L2	0.001	Overexpression with good OS
MLXIPL	0.004	Overexpression with good OS
MTMR7	0.001	Overexpression with good OS
MTUS2	0.028	Overexpression with good OS
NAP1L2	0.001	Overexpression with good OS
NEURL1	0.000	Overexpression with good OS
NLGN1	0.006	Overexpression with good OS
NPAS3	0.007	Overexpression with good OS
TENM1	0.019	Overexpression with good OS
PTPRS	0.006	Overexpression with good OS
RBM11	0.000	Overexpression with good OS
REEP2	0.000	Overexpression with good OS
SCG3	0.001	Overexpression with good OS
SCN3B	0.001	Overexpression with good OS
SLC7A14	0.004	Overexpression with good OS
SNAP25	0.000	Overexpression with good OS
SPTB	0.004	Overexpression with good OS
SSTR2	0.000	Overexpression with good OS
ST18	0.001	Overexpression with good OS
SYT4	0.000	Overexpression with good OS
SYT5	0.000	Overexpression with good OS
TMEM175	0.000	Overexpression with good OS
TMEM63C	0.000	Overexpression with good OS
UNC80	0.000	Overexpression with good OS
VWDE	0.041	Overexpression with good OS
WDR17	0.001	Overexpression with good OS
ZNF540	0.001	Overexpression with good OS
ZSCAN18	0.001	Overexpression with good OS
CTNND2	0.015	Overexpression with good OS
KCNK16	0.005	Overexpression with good OS
LRRTM2	0.014	Overexpression with good OS
PGR	0.028	Overexpression with good OS
RGS9	0.008	Overexpression with good OS
ULK4	0.005	Overexpression with good OS