

Supplementary Tables

Increased expression and altered cellular localization of fibroblast growth factor receptor like 1 (FGFRL1) are associated with prostate cancer progression

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Table S1: Association of FGFRL1 IHC staining and clinico-pathological features of primary PCA in TMA I (n=139).

	Membranous Staining				Cytoplasmic Staining			Nuclear Staining		
	No. of patients (%)	FGFRL1 low	FGFRL1 high	<i>p</i> value	FGFRL1 low	FGFRL1 high	<i>p</i> value	FGFRL1 low	FGFRL1 high	<i>p</i> value
Age (years)										
< 65	88(63)	45(51)	43(49)	0.668	45(51)	43(49)	0.643	58(66)	30(34)	0.570
≥ 65	51(37)	28(55)	23(45)		24(47)	27(53)		36(71)	15(29)	
Gleason score										
≤7	117(84)	56(48)	61(52)	0.011	60(51)	57(49)	0.372	86(74)	31(26)	0.001
8-9	22(16)	17(77)	5(23)		9(41)	13(59)		8(36)	22(64)	
pre-operative PSA (ng/ml)										
<10	87(63)	43(49)	44(51)	0.345	43(49)	44(51)	0.948	65(75)	22(25)	0.021
≥10	52(37)	30(58)	22(42)		26(50)	26(50)		29(56)	23(44)	
pT-category										
pT2a-T2c	59(42)	30(51)	29(49)	0.735	28(47)	31(53)	0.658	44(75)	15(25)	0.133
pT3a-T4	80(58)	43(54)	37(46)		41(51)	39(49)		50(63)	30(37)	
Positive surgical margin (PSM)										
NO	74(53)	39(53)	35(47)	0.963	38(51)	36(49)	0.667	56(76)	18(24)	0.030
YES	65(47)	34(52)	31(48)		31(48)	34(52)		38(58)	27(42)	

Table S2: Univariable and multivariable Cox regression analysis of FGFR1 staining and clinicopathological parameters regarding to BCR-free survival in primary PCa, (n = 117, no neoadjuvant or adjuvant treatment)

	Univariate		Multivariate	
	HR (95%)	P	HR (95%)	P
FGFR1 plasma membrane (high vs. low)	1.721 (0.848-3.490)	0.133		
FGFR1 cytoplasm (low vs. high)	1.797 (0.886-3.644)	0.104		
FGFR1 nucleus (low vs. high)	3.486 (1.732-7.017)	<0.0001	3.535 (1.747-7.153)	<0.0001
Age (<65 vs. ≥65)	1.346 (0.668-2.709)	0.406		
Preoperative PSA (<10ng/mL vs. ≥10ng/mL)	1.140 (0.557-2.333)	0.720		
Gleason score (≤7 vs. >8)	2.137 (0.923-4.946)	0.076	2.186 (0.937-5.100)	0.070
pT-category (T2 vs. T3)	1.388 (0.678-2.842)	0.370		
Surgical margin (negative vs. positive)	0.867 (0.428-1.757)	0.693		

Table S3A: Genes significantly and reproducibly up-regulated in FGFR1-KD cells – xenografts and 2D monolayer cultures (corresponding to Venn diagram in Fig. 5C).

ENSEMBL GENE_ID	SYMBOL	GENE NAME	logFC xenografts	p-value	p-value adjusted	logFC cell line	p-value	p-value adjusted
ENSG00000087495	PHACTR3	phosphatase and actin regulator 3	8.01	5.14E-37	2.58E-34	8.73	7.30E-06	3.15E-03
ENSG00000160183	TMPRSS3	transmembrane protease, serine 3	11.53	3.39E-37	1.81E-34	8.25	9.06E-10	1.16E-05
ENSG00000155760	FZD7	frizzled class receptor 7	6.35	1.76E-22	2.30E-20	5.77	1.83E-08	5.09E-05
ENSG00000160185	UBASH3A	ubiquitin associated and SH3 domain containing A	5.95	5.02E-07	5.75E-06	5.57	6.59E-08	1.02E-04
ENSG00000131398	KCNC3	potassium voltage-gated channel subfamily C member 3	3.77	4.81E-51	6.13E-48	5.49	1.07E-05	3.79E-03
ENSG00000198223	CSF2RA	colony stimulating factor 2 receptor alpha subunit	6.58	6.65E-13	2.33E-11	5.47	8.12E-09	5.09E-05
ENSG00000160182	TFF1	trefoil factor 1	1.71	1.09E-03	5.31E-03	5.46	1.89E-07	2.19E-04
ENSG00000071073	MGAT4A	mannosyl -glycoprotein beta-1,4-N-acetylglucosaminyl transferase, isozyme A	7.91	2.28E-31	6.59E-29	5.41	3.30E-04	2.58E-02
ENSG00000176788	BASP1	brain abundant membrane attached signal protein 1	4.31	1.13E-15	5.98E-14	5.32	4.51E-06	2.22E-03
ENSG00000077274	CAPN6	calpain 6	3.08	5.35E-04	2.88E-03	5.29	1.03E-07	1.32E-04
ENSG00000177675	CD163L1	CD163 molecule like 1	4.04	7.07E-31	1.97E-28	5.27	2.52E-06	1.70E-03
ENSG00000186310	NAP1L3	nucleosome assembly protein 1 like 3	5.57	7.62E-40	4.59E-37	4.64	1.23E-04	1.59E-02
ENSG00000126752	SSX1	SSX family member 1	4.22	5.04E-11	1.31E-09	4.62	8.91E-06	3.56E-03
ENSG00000148082	SHC3	SHC adaptor protein 3	5.14	4.16E-68	1.29E-64	4.54	1.75E-06	1.40E-03
ENSG00000179083	FAM133A	family with sequence similarity 133 member A	4.11	9.05E-33	3.07E-30	4.48	1.29E-04	1.64E-02
ENSG00000163347	CLDN1	claudin 1	3.33	8.01E-26	1.35E-23	4.3	1.21E-08	5.09E-05
ENSG00000185973	TMLHE	trimethyllysine hydroxylase, epsilon	2.63	3.86E-29	9.30E-27	4.25	5.01E-05	9.49E-03
ENSG00000237442	HNRNPA1 P57	HNRNPA1P57	1.74	7.91E-04	4.05E-03	4.15	3.19E-05	7.03E-03
ENSG00000183287	CCBE1	collagen and calcium binding EGF domains 1	4.99	3.93E-14	1.66E-12	4.03	1.66E-04	1.86E-02
ENSG00000078725	BRINP1	BMP/retinoic acid inducible neural specific 1	5.64	4.39E-12	1.35E-10	3.57	5.99E-06	2.83E-03
ENSG00000196220	SRGAP3	SLIT-ROBO Rho GTPase activating protein 3	3.14	6.88E-24	1.03E-21	3.53	1.32E-06	1.12E-03
ENSG00000169083	AR	androgen receptor	7.77	2.45E-11	6.67E-10	3.45	3.34E-05	7.24E-03
ENSG00000155962	CLIC2	chloride intracellular channel 2	2.99	4.84E-14	2.02E-12	3.21	4.97E-05	9.49E-03
ENSG00000125966	MMP24	matrix metalloproteinase 24	1.7	1.54E-04	9.74E-04	3.16	7.94E-05	1.20E-02
ENSG00000196611	MMP1	matrix metalloproteinase 1	2.58	1.43E-14	6.50E-13	3.05	6.51E-04	3.81E-02
ENSG00000163661	PTX3	pentraxin 3	5.55	4.21E-24	6.47E-22	2.84	1.16E-03	4.97E-02
ENSG00000134193	REG4	regenerating family member 4	2.22	3.65E-04	2.07E-03	2.47	8.15E-05	1.20E-02
ENSG00000198865	CCDC152	coiled-coil domain containing 152	3.51	4.35E-10	9.50E-09	2.41	2.42E-05	6.32E-03
ENSG00000140297	GCNT3	glucosaminyl transferase 3, mucin type	2.2	2.45E-10	5.54E-09	2.31	4.49E-04	3.05E-02
ENSG00000102271	KLHL4	kelch like family member 4	2.71	1.41E-21	1.57E-19	2.21	9.20E-06	3.56E-03
ENSG00000043355	ZIC2	Zic family member 2	3.1	2.20E-13	8.33E-12	2.18	8.63E-04	4.36E-02

ENSG00000139973	SYT16	synaptotagmin 16	1.64	1.03E-05	8.87E-05	2.18	7.40E-06	3.15E-03
ENSG00000149573	MPZL2	myelin protein zero like 2	1.76	1.25E-15	6.59E-14	2.1	9.23E-04	4.46E-02
ENSG00000112299	VNN1	vanin 1	3.89	5.11E-27	9.55E-25	1.92	8.13E-04	4.27E-02
ENSG00000187323	DCC	DCC netrin 1 receptor	2.42	4.19E-27	7.97E-25	1.83	1.62E-04	1.85E-02
ENSG00000131171	SH3BGRL	SH3 domain binding glutamate rich protein like	2.08	1.17E-51	1.69E-48	1.83	2.76E-05	6.69E-03
ENSG00000188404	SELL	selectin L	1.93	4.52E-07	5.23E-06	1.77	8.70E-04	4.36E-02
ENSG00000176463	SLCO3A1	solute carrier organic anion transporter family member 3A1	2.41	4.61E-05	3.36E-04	1.68	1.55E-04	1.82E-02
ENSG00000198157	HMGNS5	high mobility group nucleosome binding domain 5	2.48	2.88E-44	2.50E-41	1.68	3.10E-04	2.53E-02
ENSG00000043591	ADRB1	adrenoceptor beta 1	2.38	1.54E-39	9.06E-37	1.67	1.85E-04	2.00E-02
ENSG00000169740	ZNF32	zinc finger protein 32	2.55	5.31E-39	3.03E-36	1.55	3.51E-04	2.67E-02
ENSG00000120885	CLU	microRNA 6843	2.53	4.85E-40	3.00E-37	1.42	2.71E-05	6.69E-03
ENSG00000087842	PIR	pirin	2.49	5.23E-37	2.58E-34	1.41	8.68E-04	4.36E-02
ENSG00000138829	FBN2	fibrillin 2	1.52	6.65E-21	6.71E-19	1.35	1.17E-03	4.97E-02
ENSG00000147408	CSGALNACT1	chondroitin sulfate N-acetylgalactosaminyl-transferase 1	2.75	3.80E-40	2.42E-37	1.34	9.36E-05	1.33E-02
ENSG00000197410	DCHS2	dachsous cadherin-related 2	1.92	3.79E-03	1.55E-02	1.33	8.04E-04	4.24E-02
ENSG00000178343	SHISA3	shisa family member 3	1.72	2.19E-20	2.11E-18	1.31	6.93E-08	1.02E-04
ENSG00000081923	ATP8B1	ATPase phospholipid transporting 8B1	2.56	1.94E-36	8.75E-34	1.28	1.92E-04	2.04E-02
ENSG00000169760	NLGN1	neuroligin 1	1.82	1.32E-20	1.29E-18	1.15	4.89E-05	9.49E-03
ENSG00000187764	SEMA4D	semaphorin 4D	2	4.21E-06	3.96E-05	1.12	2.98E-04	2.53E-02
ENSG00000168077	SCARA3	scavenger receptor class A member 3	1.52	7.16E-25	1.15E-22	1	5.75E-04	3.54E-02
ENSG00000164733	CTSB	cathepsin B	1.59	6.49E-35	2.41E-32	0.86	9.60E-04	4.57E-02

Table S3B: Genes significantly and reproducibly down-regulated in FGFR1-KD cells – xenografts and 2D monolayer cultures, corresponding to Venn diagram shown in Fig. 5C.

ENSEMBL GENE_ID	SYMBOL	GENE NAME	logFC xenografts	p-value	p-value adjusted	logFC cell line	p-value	p-value adjusted
ENSG00000166165	CKB	creatine kinase B	-1.56	1.71E-19	1.50E-17	-0.97	3.07E-05	6.87E-03
ENSG00000124615	MOCS1	molybdenum cofactor synthesis 1	-2.23	1.69E-14	7.54E-13	-1.16	7.78E-04	4.19E-02
ENSG00000142173	COL6A2	collagen type VI alpha 2 chain	-2.01	3.60E-36	1.53E-33	-1.67	4.40E-04	3.02E-02
ENSG00000181885	CLDN7	claudin 7	-1.87	4.60E-10	1.00E-08	-1.72	5.65E-04	3.52E-02
ENSG00000121653	MAPK8IP1	mitogen-activated protein kinase 8 interacting protein 1	-1.57	7.89E-31	2.17E-28	-1.77	4.79E-04	3.16E-02
ENSG00000165186	PTCHD1	patched domain containing 1	-2.65	1.87E-53	3.70E-50	-2	4.37E-04	3.02E-02
ENSG00000078114	NEBL	nebullette	-1.84	1.30E-25	2.18E-23	-2.03	1.32E-05	4.27E-03
ENSG00000184292	TACSTD2	tumor-associated calcium signal transducer 2	-2.84	2.42E-21	2.56E-19	-2.05	3.37E-04	2.59E-02
ENSG00000182389	CACNB4	calcium voltage-gated channel auxiliary subunit beta 4	-3.07	1.75E-05	1.42E-04	-2.47	8.42E-06	3.47E-03
ENSG00000141526	SLC16A3	Solute carrier 16 A 3	-1.71	3.47E-40	2.28E-37	-2.48	4.82E-04	3.16E-02
ENSG00000150051	MKX	mohawk homeobox	-2.56	1.35E-36	6.35E-34	-2.62	5.24E-05	9.71E-03
ENSG00000157833	GAREM2	GRB2 associated regulator of MAPK1 subtype 2	-2.25	6.42E-16	3.51E-14	-2.74	6.34E-04	3.77E-02
ENSG00000116016	EPAS1	endothelial PAS domain protein 1	-4.4	5.03E-24	7.63E-22	-2.97	2.41E-04	2.29E-02
ENSG00000012171	SEMA3B	microRNA 6872	-1.57	3.06E-15	1.50E-13	-3.03	5.14E-04	3.31E-02
ENSG00000120784	ZFP30	ZFP30 zinc finger protein	-8.96	1.37E-21	1.55E-19	-4.85	7.97E-05	1.20E-02
ENSG00000198538	ZNF28	zinc finger protein 28	-3.5	4.05E-07	4.74E-06	-4.89	6.43E-04	3.78E-02
ENSG00000244219	TMEM225B	TMEM225B	-8.05	4.10E-17	2.69E-15	-6.01	1.06E-05	3.79E-03
ENSG00000203995	ZYG11A	zyg-11 family member A, cell cycle regulator	-8.88	9.29E-21	9.28E-19	-6.22	1.20E-05	4.13E-03
ENSG00000179542	SLITRK4	SLIT and NTRK like family member 4	-7.31	1.50E-28	3.36E-26	-7.21	7.68E-04	4.16E-02

Table S4A: Top 100 most prominently up-regulated genes in mouse xenograft tumors after stable knock-down of FGFR1.

SYMBOL	ENSEMBL_GENE_ID	Gene Name (ENSEMBL)	log2 Fold Change	p-value adjusted
TMPRSS3	ENSG00000160183	transmembrane serine protease 3	11.53	1.81E-30
CNNM1	ENSG00000119946	cyclin and CBS domain divalent metal cation transport mediator 1	10.51	3.73E-23
ATF7IP2	ENSG00000166669	activating transcription factor 7 interacting protein 2	9.56	4.68E-19
MAGEB16	ENSG00000189023	MAGE family member B16	9.56	2.76E-17
BMP7	ENSG00000101144	bone morphogenetic protein 7	9.02	3.19E-17
PDPN	ENSG00000162493	podoplanin	8.80	2.27E-12
NCAM1	ENSG00000149294	neural cell adhesion molecule 1	8.34	1.75E-03
FAM155B	ENSG00000130054	family with sequence similarity 155 B	8.19	4.71E-08
ZNF536	ENSG00000198597	zinc finger protein 536	8.18	1.91E+01
LRP3	ENSG00000130881	LDL receptor related protein 3	8.14	6.87E-10
PHACTR3	ENSG00000087495	phosphatase and actin regulator 3	8.01	2.58E-30
LARGE1	ENSG00000133424	LARGE xylosyl- and glucuronyltransferase 1	8.00	7.06E-01
SLFN11	ENSG00000172716	schlafen family member 11	7.92	4.91E+01
MGAT4A	ENSG00000071073	alpha-1,3-mannosyl-glycoprotein 4-beta-N-acetylglucosaminyltransferase A	7.91	6.59E-25
TBX5-AS1	ENSG00000255399	TBX5 antisense RNA 1	7.82	2.75E+01
GOLGA8G	ENSG00000183629	golgin A8 family member G	7.79	1.41E-08
ANKRD30B	ENSG00000180777	ankyrin repeat domain 30B	7.79	3.66E-03
FGF23	ENSG00000118972	fibroblast growth factor 23	7.77	3.55E-07
AR	ENSG00000169083	androgen receptor	7.77	6.67E-06
COL22A1	ENSG00000169436	collagen type XXII alpha 1 chain	7.68	5.21E-02
CRMP1	ENSG00000072832	collapsin response mediator protein 1	7.67	8.35E-01
DLGAP2	ENSG00000198010	DLG associated protein 2	7.64	2.13E-01
TIMP3	ENSG00000100234	TIMP metalloproteinase inhibitor 3	7.60	1.52E+00
LPL	ENSG00000175445	lipoprotein lipase	7.52	2.10E-01
FOXF1	ENSG00000103241	forkhead box F1	7.42	4.47E-05
CXADR3	ENSG00000265766	CXADR pseudogene 3	7.42	1.27E+02
PPP1R14C	ENSG00000198729	protein phosphatase 1 regulatory inhibitor subunit 14C	7.29	2.31E-05
LRIG1	ENSG00000144749	leucine rich repeats and immunoglobulin like domains 1	7.17	2.07E-11
TBX5	ENSG00000089225	T-box transcription factor 5	7.06	4.15E+00
ROR2	ENSG00000169071	receptor tyrosine kinase like orphan rec. 2	6.96	1.25E-01
GABRA5	ENSG00000186297	gamma-aminobutyric acid type A receptor alpha5 subunit	6.96	1.99E-02

CLRN3	ENSG00000180745	clarin 3	6.95	8.03E+00
NDRG2	ENSG00000165795	NDRG family member 2	6.92	1.44E+01
WNT3A	ENSG00000154342	Wnt family member 3A	6.89	1.41E+01
OR10J3	ENSG00000196266	olfactory receptor family 10 subfamily J member 3	6.89	6.97E-05
LINC00993	ENSG00000235687	long intergenic non-protein coding RNA 993	6.86	2.10E-04
FAM189A1	ENSG00000104059	family with sequence similarity 189 member A1	6.84	2.34E+00
CECR2	ENSG00000099954	CECR2 histone acetyl-lysine reader	6.79	1.73E+01
TMEM132D-AS1	ENSG00000249196	TMEM132D antisense RNA 1	6.78	5.14E-03
TSHZ2	ENSG00000182463	teashirt zinc finger homeobox 2	6.72	2.68E-04
EMP2	ENSG00000213853	epithelial membrane protein 2	6.61	3.12E-43
CSF2RA	ENSG00000198223	colony stimulating factor 2 receptor alpha subunit	6.58	2.33E-07
LITAF	ENSG00000189067	lipopolysaccharide induced TNF factor	6.57	2.29E-03
TFAP2C	ENSG00000087510	transcription factor AP-2 gamma	6.56	4.60E-03
CHST15	ENSG00000182022	carbohydrate sulfotransferase 15	6.56	1.60E-03
LDLRAD4	ENSG00000168675	low density lipoprotein receptor class A domain containing 4	6.55	2.69E-03
CRNDE	ENSG00000245694	colorectal neoplasia differentially expressed	6.54	4.10E-11
IRX5	ENSG00000176842	iroquois homeobox 5	6.53	3.73E-05
SYT8	ENSG00000149043	synaptotagmin 8	6.51	9.75E+00
MAGEA5	ENSG00000242520	MAGE family member A5	6.49	5.75E-05
IRX4	ENSG00000113430	iroquois homeobox 4	6.48	5.78E-03
TMC3-AS1	ENSG00000259343	TMC3 antisense RNA 1	6.43	2.49E-04
ADARB2	ENSG00000185736	adenosine deaminase RNA specific B2 (inactive)	6.41	5.79E-02
ATRNL1	ENSG00000107518	attractin like 1	6.37	2.25E-16
FZD7	ENSG00000155760	frizzled class receptor 7	6.35	2.30E-16
MYO18B	ENSG00000133454	myosin XVIIIIB	6.35	3.43E-01
FAM20C	ENSG00000177706	FAM20C golgi associated secretory pathway kinase	6.34	7.01E-01
LPAR4	ENSG00000147145	lysophosphatidic acid receptor 4	6.26	7.82E-07
DIRAS2	ENSG00000165023	DIRAS family GTPase 2	6.25	2.57E-03
EZH1P	ENSG00000187690	EZH inhibitory protein	6.25	2.21E-02
SNTG2	ENSG00000172554	syntrophin gamma 2	6.23	1.02E-02
MAN1C1	ENSG00000117643	mannosidase alpha class 1C member 1	6.22	3.70E-03
LRRC38	ENSG00000162494	leucine rich repeat containing 38	6.20	1.89E-01
ADGRE1	ENSG00000174837	adhesion G protein-coupled receptor E1	6.19	5.84E-16
XKR3	ENSG00000172967	XK related 3	6.17	3.31E-04
TPO	ENSG00000115705	thyroid peroxidase	6.14	3.16E-01
ADAMTS16	ENSG00000145536	ADAM metalloproteinase with thrombospondin type 1 motif 16	6.12	2.28E-01

H19	ENSG00000130600	H19 imprinted maternally expressed transcript	6.11	2.33E-07
CRYZL2P	ENSG00000242193	crystallin zeta like 2, pseudogene	6.10	3.15E-02
EMX1	ENSG00000135638	empty spiracles homeobox 1	6.08	2.28E+02
SDK1	ENSG00000146555	sidekick cell adhesion molecule 1	6.07	4.80E+00
KAZN	ENSG00000189337	kazrin, periplakin interacting protein	6.02	3.52E-01
MNX1-AS1	ENSG00000243479	MNX1 antisense RNA 1 (head to head)	6.02	3.82E-14
LILRA2	ENSG00000239998	leukocyte immunoglobulin like receptor A2	5.98	2.53E-01
UBASH3A	ENSG00000160185	ubiquitin associated and SH3 domain containing A	5.95	5.75E-02
RIMKLB	ENSG00000166532	ribosomal modification protein rimK like family member B	5.90	2.39E-01
TRIM22	ENSG00000132274	tripartite motif containing 22	5.88	3.31E-02
SHANK2	ENSG00000162105	SH3 and multiple ankyrin repeat domains 2	5.88	1.03E+02
FOXI1	ENSG00000168269	forkhead box I1	5.87	1.34E+01
LINC02152	ENSG00000261319	long intergenic non-protein coding RNA 2152	5.86	5.66E-01
TESC	ENSG00000088992	tescalcin	5.85	4.87E-01
GAS7	ENSG00000007237	growth arrest specific 7	5.84	4.28E+02
LINC01257	ENSG00000204603	long intergenic non-protein coding RNA 1257	5.83	1.80E+00
ERO1B	ENSG00000086619	endoplasmic reticulum oxidoreductase 1 beta	5.78	5.29E-20
CYTL1	ENSG00000170891	cytokine like 1	5.78	1.30E+00
C7orf33	ENSG00000170279	chromosome 7 open reading frame 33	5.77	1.88E+00
THBS2	ENSG00000186340	thrombospondin 2	5.71	1.80E-09
ZNF516	ENSG00000101493	zinc finger protein 516	5.70	5.07E-06
LINC01484	ENSG00000253686	long intergenic non-protein coding RNA 1484	5.70	6.00E-02
BRINP1	ENSG00000078725	BMP/retinoic acid inducible neural specific 1	5.64	1.35E-06
PIEZO2	ENSG00000154864	piezo type mechanosensitive ion channel component 2	5.61	1.62E-01
ZNF157	ENSG00000147117	zinc finger protein 157	5.57	6.19E+00
NKD1	ENSG00000140807	NKD inhibitor of WNT signaling pathway 1	5.57	6.60E-01
NAP1L3	ENSG00000186310	nucleosome assembly protein 1 like 3	5.57	4.59E-33
EYA2	ENSG00000064655	EYA transcriptional coactivator and phosphatase 2	5.56	2.92E-02
ZMAT1	ENSG00000166432	zinc finger matrin-type 1	5.55	5.18E-11
ZNF423	ENSG00000102935	zinc finger protein 423	5.55	5.86E-05

PTX3	ENSG00000163661	pentraxin 3	5.55	6.47E-18
SPATA48	ENSG00000164500	spermatogenesis associated 48	5.55	3.75E+00
SDC2	ENSG00000169439	syndecan 2	5.54	4.83E-01

Table S4B: Top 100 most prominently down-regulated genes in mouse xenograft tumors after stable knock-down of FGFR1.

SYMBOL	ENSEMBL_GENE_ID	Gene Name (ENSEMBL)	log2 Fold Change	p-value adjusted
TMEM168	ENSG00000146802	transmembrane protein 168	-10.90	8.10E-26
ZFP30	ENSG00000120784	ZFP30 zinc finger protein	-8.96	1.55E-15
ZYG11A	ENSG00000203995	zyg-11 family member A, cell cycle regulator	-8.88	9.28E-15
SMO	ENSG00000128602	smoothened, frizzled class receptor	-8.31	1.89E-35
MIR548XHG	ENSG00000224141	MIR548X host gene	-8.10	6.51E-11
TMEM225B	ENSG00000244219	transmembrane protein 225B	-8.05	2.69E-11
SERPINB9	ENSG00000170542	serpin family B member 9	-7.88	4.03E-10
ZSCAN18	ENSG00000121413	zinc finger and SCAN domain containing 18	-7.83	3.44E-13
SLITRK4	ENSG00000179542	SLIT and NTRK like family member 4	-7.31	3.36E-22
PTGS2	ENSG00000073756	prostaglandin-endoperoxide synthase 2	-6.81	5.65E-06
SLC26A4-AS1	ENSG00000233705	SLC26A4 antisense RNA 1	-6.30	1.29E-03
PPDPFL	ENSG00000168333	pancreatic progenitor cell differentiation and proliferation factor like	-6.19	4.44E-14
CXCL1	ENSG00000163739	C-X-C motif chemokine ligand 1	-6.19	3.87E-03
CLDN10-AS1	ENSG00000223392	CLDN10 antisense RNA 1	-6.14	3.77E-04
RAB6B	ENSG00000154917	RAB6B, member RAS oncogene family	-6.14	1.41E-65
DNAJC15	ENSG00000120675	DnaJ heat shock protein family (Hsp40) member C15	-5.93	9.72E-05
CD79B	ENSG00000007312	CD79b molecule	-5.86	1.16E-02
ZNF347	ENSG00000197937	zinc finger protein 347	-5.75	6.91E-02
IL1RAPL1	ENSG00000169306	interleukin 1 receptor accessory protein like 1	-5.72	1.08E-02
ENG	ENSG00000106991	endoglin	-5.70	8.47E-02
LINC02820	ENSG00000258815	long intergenic non-protein coding RNA 2820	-5.63	2.16E-01
KCNH5	ENSG00000140015	potassium voltage-gated channel subfamily H member 5	-5.54	3.39E+00
LAG3	ENSG00000089692	lymphocyte activating 3	-5.51	1.78E-159
ZNF607	ENSG00000198182	zinc finger protein 607	-5.44	1.97E-03
SLC10A4	ENSG00000145248	solute carrier family 10 member 4	-5.36	5.74E+00
BCL2A1	ENSG00000140379	BCL2 related protein A1	-5.12	1.36E+01

ZNF256	ENSG00000152454	zinc finger protein 256	-5.09	1.63E-15
RPS6KL1	ENSG00000198208	ribosomal protein S6 kinase like 1	-5.05	1.89E+00
FGG	ENSG00000171557	fibrinogen gamma chain	-4.87	3.34E+01
IGFBP3	ENSG00000146674	insulin like growth factor binding protein 3	-4.85	7.80E-20
OTOGL	ENSG00000165899	otogelin like	-4.84	7.24E-05
CDH5	ENSG00000179776	cadherin 5	-4.84	1.54E+01
LINC01357	ENSG00000224167	long intergenic non-protein coding RNA 1357	-4.81	1.20E-09
TMPRSS15	ENSG00000154646	transmembrane serine protease 15	-4.73	2.01E-18
XIST	ENSG00000229807	X inactive specific transcript	-4.71	6.74E+00
C6orf223	ENSG00000181577	chromosome 6 open reading frame 223	-4.70	2.89E-03
DAAM2	ENSG00000146122	dishevelled associated activator of morphogenesis 2	-4.64	4.10E+01
MT1M	ENSG00000205364	metallothionein 1M	-4.62	1.09E+02
OGN	ENSG00000106809	osteoglycin	-4.57	8.01E-02
CDC42P2	ENSG00000234844	cell division cycle 42 pseudogene 2	-4.57	1.69E+01
SYN1	ENSG00000008056	synapsin I	-4.48	2.40E+01
HPN	ENSG00000105707	hepsin	-4.46	1.25E-01
UGT2B10	ENSG00000109181	UDP glucuronosyltransferase family 2 member B10	-4.41	2.63E-01
PRG4	ENSG00000116690	proteoglycan 4	-4.40	1.75E-03
EPAS1	ENSG00000116016	endothelial PAS domain protein 1	-4.40	7.63E-18
NXF3	ENSG00000147206	nuclear RNA export factor 3	-4.36	2.54E-02
TNFSF14	ENSG00000125735	TNF superfamily member 14	-4.35	2.89E+00
SCNN1G	ENSG00000166828	sodium channel epithelial 1 gamma subunit	-4.35	1.66E-13
LRRK2	ENSG00000188906	leucine rich repeat kinase 2	-4.34	1.25E-03
ACSL5	ENSG00000197142	acyl-CoA synthetase long chain family member 5	-4.33	1.70E-05
CYP2C18	ENSG00000108242	cytochrome P450 family 2 subfamily C member 18	-4.32	1.30E+02
TREM1	ENSG00000124731	triggering receptor expressed on myeloid cells 1	-4.31	7.07E-04
AQP1	ENSG00000240583	aquaporin 1 (Colton blood group)	-4.26	2.86E-13
EVI2A	ENSG00000126860	ecotropic viral integration site 2A	-4.26	4.47E+01
PDZK1IP1	ENSG00000162366	PDZK1 interacting protein 1	-4.24	2.18E+01
SLC35G2	ENSG00000168917	solute carrier family 35 member G2	-4.21	1.85E-25
CDH13	ENSG00000140945	cadherin 13	-4.12	6.42E-04
TGM2	ENSG00000198959	transglutaminase 2	-4.11	6.17E-05
SCNN1B	ENSG00000168447	sodium channel epithelial 1 beta subunit	-4.11	2.10E-05

DENND2D	ENSG00000162777	DENN domain containing 2D	-4.09	6.00E-53
VWA1	ENSG00000179403	von Willebrand factor A domain containing 1	-4.07	2.54E-02
GJB4	ENSG00000189433	gap junction protein beta 4	-4.02	8.94E+01
PDE8B	ENSG00000113231	phosphodiesterase 8B	-3.99	1.95E-15
RSPO2	ENSG00000147655	R-spondin 2	-3.98	3.08E+02
ACKR3	ENSG00000144476	atypical chemokine receptor 3	-3.95	2.11E-11
CSF2	ENSG00000164400	colony stimulating factor 2	-3.94	7.82E+00
SIRPG-AS1	ENSG00000237914	SIRPG antisense RNA 1	-3.93	3.22E+02
LINC01714	ENSG00000227634	long intergenic non-protein coding RNA 1714	-3.92	2.56E+02
ANKRD60	ENSG00000124227	ankyrin repeat domain 60	-3.86	7.11E-06
NDUFA4L2	ENSG00000185633	NDUFA4 mitochondrial complex associated like 2	-3.85	3.05E-06
HHLA2	ENSG00000114455	HERV-H LTR-associating 2	-3.85	2.09E-01
AGTR1	ENSG00000144891	angiotensin II receptor type 1	-3.84	6.87E+01
LGI2	ENSG00000153012	leucine rich repeat LGI family member 2	-3.83	1.80E-11
GFAP	ENSG00000131095	glial fibrillary acidic protein	-3.71	3.05E+02
ELOVL3	ENSG00000119915	ELOVL fatty acid elongase 3	-3.69	2.89E+02
C6orf132	ENSG00000188112	chromosome 6 open reading frame 132	-3.68	1.34E-02
ASB14	ENSG00000239388	ankyrin repeat and SOCS box containing 14	-3.67	3.46E+02
RTL4	ENSG00000187823	retrotransposon Gag like 4	-3.65	2.32E-02
CLDN24	ENSG00000185758	claudin 24	-3.64	5.84E-02
P4HA3-AS1	ENSG00000246211	P4HA3 antisense RNA 1	-3.62	3.99E+02
FGB	ENSG00000171564	fibrinogen beta chain	-3.60	1.26E+01
ZNF518A	ENSG00000177853	zinc finger protein 518A	-3.59	3.24E+02
CD86	ENSG00000114013	CD86 molecule	-3.59	9.20E-02
OASL	ENSG00000135114	2'-5'-oligoadenylate synthetase like	-3.57	1.48E-11
CSPG4	ENSG00000173546	chondroitin sulfate proteoglycan 4	-3.56	1.47E+01
SCGB1D2	ENSG00000124935	secretoglobin family 1D member 2	-3.56	4.53E+02
FAM225A	ENSG00000231528	family with sequence similarity 225 member A	-3.56	1.83E+01
PLA2G3	ENSG00000100078	phospholipase A2 group III	-3.55	9.34E+00
ANO3	ENSG00000134343	anoctamin 3	-3.55	7.61E+00
CPA5	ENSG00000158525	carboxypeptidase A5	-3.50	2.16E+02
ZNF28	ENSG00000198538	zinc finger protein 28	-3.50	4.74E-02
LINC01356	ENSG00000215866	long intergenic non-protein coding RNA 1356	-3.49	2.43E+00
KCNJ15	ENSG00000157551	potassium voltage-gated channel subfamily J member 15	-3.45	8.01E-02
CCN4	ENSG00000104415	cellular communication network factor 4	-3.44	3.10E-30

ANGPTL4	ENSG00000167772	angiotensin like 4	-3.44	1.90E-07
FREM1	ENSG00000164946	FRAS1 related extracellular matrix 1	-3.43	8.18E-01
NYNRIN	ENSG00000205978	NYN domain and retroviral integrase containing	-3.38	2.55E-02
TINAGL1	ENSG00000142910	tubulointerstitial nephritis antigen like 1	-3.37	1.75E-03
SPTLC3	ENSG00000172296	serine palmitoyltransferase long chain base subunit 3	-3.32	3.91E+00
TBPL2	ENSG00000182521	TATA-box binding protein like 2	-3.29	4.38E+02

Table S5: Significantly enriched tumor/stroma interactions detected by the CASTIN algorithm in PC-3M xenografts derived from FGFR1-KD versus control cells.

GENE SYMBOLS	MEAN Tumor (human)	MEAN Stroma (mouse)	SD Tumor	SD Stroma	P-VALUE
Enriched in PC-3M xenografts					
SEMA4F (tumor) / NRP2 (stroma)	1.121	0.987	0.028	0.026	0.0001
COL2A1 (tumor) / ITGA2B (stroma)	0.031	-0.644	0.057	0.174	0.003
VEGFC (tumor) / FLT4 (stroma)	1.243	1.481	0.122	0.075	0.009
FGF23 (tumor) / FGFR3 (stroma)	0.101	-0.593	0.304	0.080	0.015
EFNB3 (tumor) / EPHB3 (stroma)	0.669	0.386	0.147	0.097	0.018
FGF2 (tumor) / FGFR3 (stroma)	0.593	0.360	0.111	0.089	0.028
CCL26 (tumor) / CCR1 (stroma)	1.206	1.377	0.112	0.094	0.032
JAG2 (tumor) / NOTCH3 (stroma)	1.304	1.427	0.052	0.088	0.034
DKK1 (tumor) / KREMEN1 (stroma)	2.290	2.132	0.086	0.106	0.034
FGF2 (tumor) / GPC4 (stroma)	1.193	0.965	0.029	0.087	0.034
EGF (tumor) / EGFR (stroma)	0.907	0.723	0.113	0.013	0.045
VEGFC (tumor) / KDR (stroma)	1.568	1.719	0.055	0.099	0.048
Enriched in stromal (mouse) tissue					
NTN1 (stroma) / DCC (tumor)	0.903	0.421	0.104	0.116	0.0001
ADAM12 (stroma) / EGF (tumor)	1.214	0.928	0.047	0.029	0.0002
LAMA1 (stroma) / ITGA2 (tumor)	0.998	0.747	0.113	0.084	0.005
EPHB3 (stroma) / EFNB3 (tumor)	0.669	0.386	0.147	0.097	0.018
TNFSF10 (stroma) / TNFRSF10C (tumor)	0.509	0.182	0.042	0.195	0.018
INHBA (stroma) / ACVR1B (tumor)	1.311	1.552	0.090	0.092	0.018

Stroma: corresponds to reads matched to the mouse genome (= mouse stromal cells in xenografts)
Tumour: corresponds to reads matched to human genome (= PC3M cells in xenografts)

Table S6: The sequencing coverage and quality statistics of next generation sequencing (NGS) data for PC3M control and FGFR1 knock down cell line and xenografts.

Sample set*	Sample ID	RNA integrity number (RIN)	Total number of sequenced reads	Total number of uniquely mapped reads	Ratio of all reads aligned to rRNA regions to total uniquely mapped reads (rRNA rate) [%]	Ratio of exon-mapped reads to total uniquely mapped reads (Expression Profile Efficiency) [%]	Total number of detected transcripts with reads ≥ 1	Reference genome
I	21_492_ctrl_sh5 (PC3M control clone 5)	9.5	9771694	8214742	0.2	33.5	25375	GRCh38.81
I	22_493_ctrl_sh5 (PC3M control clone 5)	10	7335684	6153615	0.3	33.9	23575	GRCh38.81
I	23_609_ctrl_sh8 (PC3M control clone 8)	10	14943012	12643362	0.1	32.9	27798	GRCh38.81
I	24_610_ctrl_sh8 (PC3M control clone 8)	10	14578922	12418712	0.1	32.9	27909	GRCh38.81
I	33_615_FGFR5sh11 (PC3M KD clone 11)	10	8407203	7164026	0.1	32.8	21871	GRCh38.81
I	34_616_FGFR5sh11 (PC3M KD clone 11)	10.0	9660825	8216287	0.1	32.7	23394	GRCh38.81
II	T1-5 (PC3M xenograft control)	9.4	23608595	16479360	2.1	78.0	34155	hg19
II	T1-6 (PC3M xenograft control)	9.7	36899072	26794663	1.9	78.8	34583	hg19
II	T2-1 (PC3M xenograft control)	9.5	26237705	19159521	2.1	80.2	34295	hg19
II	T2-3 (PC3M xenograft control)	9.6	48997888	35939600	1.8	79.0	34182	hg19
II	T2-4 (PC3M xenograft control)	9.9	40784423	29528974	1.6	78.0	35128	hg19
II	T5-2 (PC3M KD xenograft)	9.5	21535877	14669665	1.6	78.1	35168	hg19
II	T5-5 (PC3M KD xenograft)	9.7	37293152	26795537	1.9	77.3	34614	hg19
II	T6-1 (PC3M KD xenograft)	8.7	19846462	10891409	3.8	75.4	34222	hg19
II	T6-4 (PC3M KD xenograft)	9.5	27343702	19357981	1.7	77.1	35757	hg19
II	T6-5 (PC3M KD xenograft)	9.8	22550288	16665003	1.5	79.0	35130	hg19

*Set I, cell lines; Set II, xenografts