

Table S1. Nucleotide sequences of primers used in RT-PCR.

Gene	Direction	Nucleotide Sequence
<i>PDK1</i>	Forward	5'-AACCTCTAGGAATACAGC-3'
	Reverse	5'-CCTTTGAGGAAAATTGACAG-3'
<i>BNIP3</i>	Forward	5'-TGTTGCAAGCTCAGAAGTAA-3'
	Reverse	5'-TTCTGAAAGTTTTCTTCCA-3'
<i>GAPDH</i>	Forward	5'-TGTGGTCATGAGTCCTTCCA-3'
	Reverse	5'-CGAGATCCCTCCAAAATCAA-3'
<i>HIF1A</i>	Forward	5'-CCCAGATTCAGGATCAGACA-3'
	Reverse	5'-ACCATCATGTTCCATTTTTTCG-3'
<i>HIF2A</i>	Forward	5'-TCATCATGTGTGAACCAATC-3'
	Reverse	5'-GAACACCACGTCATTCTTCT-3'

Table S2. Patient information for the prostate cancer tissue array.

No.	Age	Sex	Organ	Diagnosis	Gleason score	Stage	Residual tumor	Follow-up month	Survival status	PSA (ng/ml)
1	60	Male	Prostate	adenocarcinoma	9	3	no	60	alive	11.2
2	64	Male	Prostate	adenocarcinoma	7	2b	no	60	alive	30
3	71	Male	Prostate	adenocarcinoma	9	3	yes	55	alive	60.4
4	64	Male	Prostate	adenocarcinoma	10	3	yes	47	alive	7.4
5	59	Male	Prostate	adenocarcinoma	9	3	yes	44	alive	9.8
6	65	Male	Prostate	adenocarcinoma	8	3	yes	43	alive	34.9
7	73	Male	Prostate	adenocarcinoma	7	2b	yes	42	alive	48.1
8	69	Male	Prostate	adenocarcinoma	7	2b	no	42	alive	10.6
9	62	Male	Prostate	adenocarcinoma	7	2b	yes	39	alive	37.3
10	66	Male	Prostate	adenocarcinoma	9	3	yes	39	alive	1.2
11	60	Male	Prostate	adenocarcinoma	9	3	yes	39	alive	40
12	66	Male	Prostate	adenocarcinoma	7	3	yes	39	alive	8.4
13	70	Male	Prostate	adenocarcinoma	7	3	yes	37	alive	7
14	65	Male	Prostate	adenocarcinoma	9	3	yes	23	dead	17.5
15	67	Male	Prostate	adenocarcinoma	9	3	yes	34	alive	13.1
16	69	Male	Prostate	adenocarcinoma	7	3	yes	33	alive	1.1
17	63	Male	Prostate	adenocarcinoma	9	3	yes	33	alive	11.8
18	69	Male	Prostate	adenocarcinoma	7	3	yes	27	alive	17.6

19	70	Male	Prostate	adenocarcinoma	7	3	yes	26	alive	9
20	58	Male	Prostate	adenocarcinoma	9	3	no	26	alive	5.8
21	58	Male	Prostate	adenocarcinoma	7	3	yes	24	alive	15.8
22	71	Male	Prostate	adenocarcinoma	7	2b	yes	24	alive	31.4
23	70	Male	Prostate	adenocarcinoma	7	3	yes	19	alive	14.4
24	59	Male	Prostate	adenocarcinoma	6	2a	no	18	alive	18.3
25	63	Male	Prostate	adenocarcinoma	9	3	yes	17	alive	16.6
26	72	Male	Prostate	adenocarcinoma	9	3	yes	16	alive	.
27	66	Male	Prostate	adenocarcinoma	8	2	yes	17	dead	10.8
28	70	Male	Prostate	adenocarcinoma	6	3	yes	16	alive	10.8
29	70	Male	Prostate	adenocarcinoma	7	2b	no	15	alive	.
30	68	Male	Prostate	adenocarcinoma	8	3	yes	15	alive	26.9
31	63	Male	Prostate	adenocarcinoma	10	3	yes	15	alive	.
32	57	Male	Prostate	adenocarcinoma	7	3	yes	15	alive	25
33	72	Male	Prostate	adenocarcinoma	8	2b	yes	15	alive	16.8
34	70	Male	Prostate	adenocarcinoma	8	3	yes	15	alive	0.5
35	75	Male	Prostate	adenocarcinoma	9	3	yes	15	alive	98
36	62	Male	Prostate	adenocarcinoma	9	3	yes	15	alive	.
37	63	Male	Prostate	adenocarcinoma	9	3	yes	14	alive	91
38	53	Male	Prostate	adenocarcinoma	9	3	yes	17	dead	161
39	63	Male	Prostate	adenocarcinoma	8	3	yes	13	alive	13
40	44	Male	Prostate	adenocarcinoma	7	3	yes	11	alive	.
41	69	Male	Prostate	normal
42	62	Male	Prostate	normal
43	66	Male	Prostate	normal
44	65	Male	Prostate	normal
45	69	Male	Prostate	normal
46	70	Male	Prostate	normal
47	70	Male	Prostate	normal
48	63	Male	Prostate	normal
49	44	Male	Prostate	normal

Table S3. Core enriched gene list for the gene set PID_HIF1_TFPATHWAY

Probe	Gene Symbol	Gene Title	Rank in gene list	Rank metric score	Running ES	Core enrichment
HK2	HK2	hexokinase 2	156	0.353764	0.091885	Yes
NCOA1	NCOA1	nuclear receptor coactivator 1	225	0.328689	0.188197	Yes
HIF1A	HIF1A	hypoxia-inducible factor 1, alpha subunit (basic helix-loop-helix transcription factor)	261	0.318103	0.285788	Yes
RORA	RORA	RAR-related orphan receptor A	338	0.299635	0.371595	Yes
TFRC	TFRC	transferrin receptor (p90, CD71)	494	0.266397	0.435452	Yes
HK1	HK1	hexokinase 1	591	0.253815	0.503641	Yes
EGLN1	EGLN1	egl nine homolog 1 (C. elegans)	810	0.225232	0.545267	Yes
ETS1	ETS1	v-ets erythroblastosis virus E26 oncogene homolog 1 (avian)	830	0.223343	0.614579	Yes
NCOA2	NCOA2	nuclear receptor coactivator 2	1148	0.193335	0.631844	Yes
PFKFB3	PFKFB3	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3	1445	0.16977	0.644497	Yes

Table S4. Core enriched gene list for the gene set ELVIDGE_HYPOXIA_UP

Probe	Gene Symbol	Gene Title	Rank in gene list	Rank metric score	Running ES	Core enrichment
HEY1	HEY1	hairy/enhancer-of-split related with YRPW motif 1	17	0.459048	0.041123	Yes
DTNA	DTNA	dystrobrevin, alpha	130	0.364195	0.059669	Yes
HK2	HK2	hexokinase 2	156	0.353764	0.08966	Yes
ERO1L	ERO1L	ERO1-like (S. cerevisiae)	219	0.330226	0.11213	Yes
KLHL24	KLHL24	kelch-like 24 (Drosophila)	220	0.330224	0.14346	Yes
DDIT4	DDIT4	DNA-damage-inducible transcript 4	247	0.320453	0.170147	Yes
PDK1	PDK1	pyruvate dehydrogenase kinase, isozyme 1	271	0.316203	0.19686	Yes
ATXN1	ATXN1	ataxin 1	317	0.304557	0.219324	Yes
WSB1	WSB1	WD repeat and SOCS box-containing 1	349	0.296292	0.243004	Yes
TRA2A	TRA2A	-	351	0.295798	0.270925	Yes
DST	DST	dystonin	398	0.285046	0.291395	Yes
RRAGD	RRAGD	Ras-related GTP binding D	402	0.284205	0.31793	Yes
EFNA3	EFNA3	ephrin-A3	480	0.270144	0.332556	Yes
YPEL1	YPEL1	yippee-like 1 (Drosophila)	524	0.26243	0.351309	Yes
KLF7	KLF7	Kruppel-like factor 7 (ubiquitous)	756	0.232209	0.340325	Yes
NR3C1	NR3C1	nuclear receptor subfamily 3, group C, member 1 (glucocorticoid receptor)	801	0.226952	0.355569	Yes
EGLN1	EGLN1	egl nine homolog 1 (C. elegans)	810	0.225232	0.375795	Yes
SAMD4A	SAMD4A	sterile alpha motif domain containing 4A	838	0.222161	0.393014	Yes
TGFBI	TGFBI	transforming growth factor, beta-induced, 68kDa	873	0.219064	0.408938	Yes
STC1	STC1	stanniocalcin 1	877	0.218482	0.429238	Yes
BBX	BBX	bobby sox homolog (Drosophila)	922	0.214723	0.443322	Yes
TMEM45A	TMEM45A	transmembrane protein 45A	946	0.212318	0.460179	Yes
ANKZF1	ANKZF1	ankyrin repeat and zinc finger domain containing 1	1250	0.182756	0.434213	Yes
ITPR1	ITPR1	inositol 1,4,5-triphosphate receptor, type 1	1362	0.174956	0.434949	Yes
STC2	STC2	stanniocalcin 2	1371	0.174458	0.450357	Yes
PFKFB3	PFKFB3	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3	1445	0.16977	0.456031	Yes
YEATS2	YEATS2	YEATS domain containing 2	1452	0.169411	0.471247	Yes

Table S5. Core enriched gene list for the gene set CHANDRAN_METASTASIS_UP

Probe	Gene Symbol	Gene Title	Rank in gene list	Rank metric score	Running ES	Core enrichment
KIAA1267	KIAA1267	KIAA1267	4	0.497317	0.018461	Yes
EIF2C2	EIF2C2	eukaryotic translation initiation factor 2C, 2	5	0.496974	0.037485	Yes
PABPC1	PABPC1	poly(A) binding protein, cytoplasmic 1	6	0.495015	0.056434	Yes
PCBP2	PCBP2	poly(rC) binding protein 2	13	0.468056	0.073487	Yes
COX19	COX19	COX19 cytochrome c oxidase assembly homolog (S. cerevisiae)	22	0.453974	0.089713	Yes
PLXNA1	PLXNA1	plexin A1	27	0.445768	0.106201	Yes
NCAPH2	NCAPH2	non-SMC condensin II complex, subunit H2	30	0.438933	0.122715	Yes
MAP3K8	MAP3K8	mitogen-activated protein kinase kinase kinase 8	32	0.437222	0.139307	Yes
MLL3	MLL3	myeloid/lymphoid or mixed-lineage leukemia 3	37	0.432568	0.15529	Yes
SDCCAG3	SDCCAG3	serologically defined colon cancer antigen 3	39	0.431612	0.171668	Yes
IBTK	IBTK	inhibitor of Bruton agammaglobulinemia tyrosine kinase	54	0.415719	0.185565	Yes
CPEB4	CPEB4	cytoplasmic polyadenylation element binding protein 4	62	0.410953	0.200288	Yes
BIRC6	BIRC6	baculoviral IAP repeat-containing 6 (apollon)	81	0.40106	0.213048	Yes
TRIO	TRIO	triple functional domain (PTPRF interacting)	88	0.395203	0.227313	Yes
MLL5	MLL5	myeloid/lymphoid or mixed-lineage leukemia 5 (trithorax homolog, Drosophila)	93	0.390662	0.241691	Yes
HMBOX1	HMBOX1	homeobox containing 1	103	0.385236	0.255141	Yes
PVT1	PVT1	Pvt1 oncogene homolog, MYC activator (mouse)	111	0.376192	0.268534	Yes
RAB12	RAB12	RAB12, member RAS oncogene family	112	0.375525	0.282909	Yes
MALAT1	MALAT1	metastasis associated lung adenocarcinoma transcript 1 (non-coding RNA)	113	0.374778	0.297255	Yes
CHORDC1	CHORDC1	cysteine and histidine-rich domain (CHORD)-containing 1	114	0.374647	0.311597	Yes
HCG18	HCG18	HLA complex group 18	117	0.372864	0.325582	Yes
TARS	TARS	threonyl-tRNA synthetase	118	0.372496	0.339841	Yes
RASAL2	RASAL2	RAS protein activator like 2	122	0.3708	0.353603	Yes
FNBP4	FNBP4	formin binding protein 4	123	0.369849	0.36776	Yes
MSI2	MSI2	musashi homolog 2 (Drosophila)	127	0.366204	0.381346	Yes
LRRC58	LRRC58	leucine rich repeat containing 58	128	0.366168	0.395363	Yes
SNORA28	SNORA28	small nucleolar RNA, H/ACA box 28	129	0.365658	0.40936	Yes
DONSON	DONSON	downstream neighbor of SON	131	0.36294	0.42311	Yes
TMEM70	TMEM70	transmembrane protein 70	170	0.349713	0.431024	Yes

ARHGAP1	ARHGAP1	Rho GTPase activating protein 1	179	0.344033	0.443041	Yes
ADD1	ADD1	adducin 1 (alpha)	184	0.342645	0.455582	Yes
SMCR3	SMCR3	Smith-Magenis syndrome chromosome region, candidate 3	196	0.338658	0.466961	Yes
LONRF2	LONRF2	LON peptidase N-terminal domain and ring finger 2	209	0.333435	0.477997	Yes
GNL3L	GNL3L	guanine nucleotide binding protein-like 3 (nucleolar)-like	223	0.328949	0.488717	Yes
CBX4	CBX4	chromobox homolog 4 (Pc class homolog, Drosophila)	229	0.32713	0.500519	Yes
HN1	HN1	hematological and neurological expressed 1	231	0.325315	0.512828	Yes
MORF4L2	MORF4L2	mortality factor 4 like 2	234	0.324261	0.524953	Yes
DDIT4	DDIT4	DNA-damage-inducible transcript 4	247	0.320453	0.535491	Yes
FUS	FUS	fusion (involved in t(12;16) in malignant liposarcoma)	253	0.31945	0.547	Yes
RPL37	RPL37	ribosomal protein L37	270	0.316271	0.556802	Yes
NFATC2IP	NFATC2IP	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 2 interacting protein	300	0.308669	0.564442	Yes
MINA	MINA	MYC induced nuclear antigen	326	0.303237	0.572449	Yes
TMSB10	TMSB10	thymosin, beta 10	333	0.300665	0.583095	Yes
LIMD1	LIMD1	LIM domains containing 1	353	0.29568	0.591677	Yes
THBS2	THBS2	thrombospondin 2	367	0.291194	0.600951	Yes
SLC35B3	SLC35B3	solute carrier family 35, member B3	375	0.290295	0.611056	Yes
ZNF621	ZNF621	zinc finger protein 621	382	0.289706	0.621282	Yes
RBBP6	RBBP6	retinoblastoma binding protein 6	416	0.282136	0.627329	Yes
FN1	FN1	fibronectin 1	419	0.281591	0.63782	Yes
HPN	HPN	hepsin (transmembrane protease, serine 1)	439	0.277839	0.64572	Yes
TBC1D24	TBC1D24	TBC1 domain family, member 24	485	0.268276	0.649509	Yes
RBM39	RBM39	RNA binding motif protein 39	529	0.261961	0.653344	Yes
GSK3B	GSK3B	glycogen synthase kinase 3 beta	561	0.257611	0.658741	Yes
LYN	LYN	v-yes-1 Yamaguchi sarcoma viral related oncogene homolog	568	0.256619	0.6677	Yes
KIAA1147	KIAA1147	KIAA1147	713	0.236468	0.656015	Yes
ZNF281	ZNF281	zinc finger protein 281	743	0.233149	0.660764	Yes
SOX4	SOX4	SRX (sex determining region Y)-box 4	786	0.228941	0.663479	Yes
ATG4D	ATG4D	ATG4 autophagy related 4 homolog D (S. cerevisiae)	834	0.222563	0.66523	Yes
TAOK1	TAOK1	TAO kinase 1	857	0.220173	0.67049	Yes
CDC26	CDC26	cell division cycle 26	859	0.219976	0.678767	Yes
ABHD5	ABHD5	abhydrolase domain containing 5	870	0.219402	0.685725	Yes
FGFR1OP2	FGFR1OP2	FGFR1 oncogene partner 2	885	0.217776	0.692045	Yes
PRKAB2	PRKAB2	protein kinase, AMP-	932	0.213831	0.693606	Yes

		activated, beta 2 non-catalytic subunit				
LOC642852	LOC642852	-	941	0.212835	0.700602	Yes
LRCH3	LRCH3	leucine-rich repeats and calponin homology (CH) domain containing 3	947	0.212217	0.708005	Yes

Table S6. Core enriched gene list for the gene set HALLMARK_HYPOXIA

Probe	Gene Symbol	Gene Title	Rank in gene list	Rank metric score	Running ES	Core enrichment
EXT1	EXT1	exostoses (multiple) 1	10	0.474807	0.038659	Yes
TPD52	TPD52	tumor protein D52	91	0.392801	0.060388	Yes
DTNA	DTNA	dystrobrevin, alpha	130	0.364195	0.085705	Yes
HK2	HK2	hexokinase 2	156	0.353764	0.112	Yes
ERO1L	ERO1L	ERO1-like (S. cerevisiae)	219	0.330226	0.131018	Yes
KLHL24	KLHL24	kelch-like 24 (Drosophila)	220	0.330224	0.1589	Yes
DDIT4	DDIT4	DNA-damage-inducible transcript 4	247	0.320453	0.182239	Yes
PDK1	PDK1	pyruvate dehydrogenase kinase, isozyme 1	271	0.316203	0.205649	Yes
B4GALNT2	B4GALNT2	beta-1,4-N-acetyl-galactosaminyl transferase 2	273	0.315813	0.232171	Yes
RORA	RORA	RAR-related orphan receptor A	338	0.299635	0.24832	Yes
WSB1	WSB1	WD repeat and SOCS box-containing 1	349	0.296292	0.271907	Yes
RRAGD	RRAGD	Ras-related GTP binding D	402	0.284205	0.28847	Yes
LARGE	LARGE	like-glycosyltransferase	441	0.277505	0.306467	Yes
EFNA3	EFNA3	ephrin-A3	480	0.270144	0.323844	Yes
HK1	HK1	hexokinase 1	591	0.253815	0.329548	Yes
KLF7	KLF7	Kruppel-like factor 7 (ubiquitous)	756	0.232209	0.325709	Yes
NR3C1	NR3C1	nuclear receptor subfamily 3, group C, member 1 (glucocorticoid receptor)	801	0.226952	0.338581	Yes
ETS1	ETS1	v-ets erythroblastosis virus E26 oncogene homolog 1 (avian)	830	0.223343	0.353435	Yes
LXN	LXN	latexin	846	0.221438	0.369987	Yes
TGFBI	TGFBI	transforming growth factor, beta-induced, 68kDa	873	0.219064	0.384767	Yes
STC1	STC1	stanniocalcin 1	877	0.218482	0.402785	Yes
TMEM45A	TMEM45A	transmembrane protein 45A	946	0.212318	0.41099	Yes