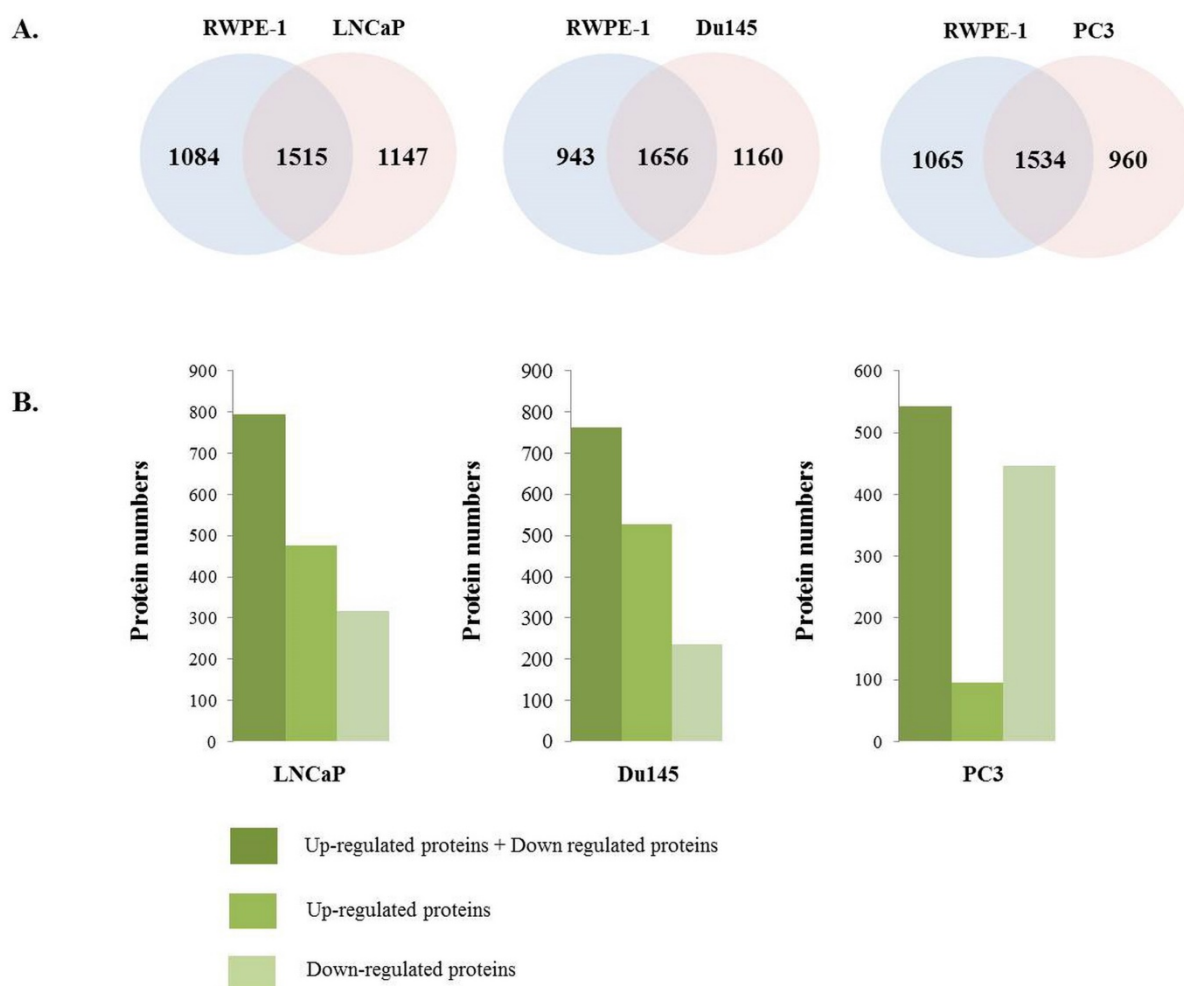


**Figure S1. Schematic representation of the proteomics approach.** Four prostate cell lines, RWPE-1, LNCaP, Du145, and PC3, were cultured in each basic media. Protein samples were digested into peptides with trypsin and fractionated by OFFGEL electrophoresis followed by analysis using high-performance liquid chromatography-mass spectrometry/mass spectrometry (HPLC-MS/MS). Protein sequences were searched using Spectrum Mill and data analysis was performed using GeneGo Metacore software and MPP. The selected proteins were validated by quantitative PCR (Q-PCR).

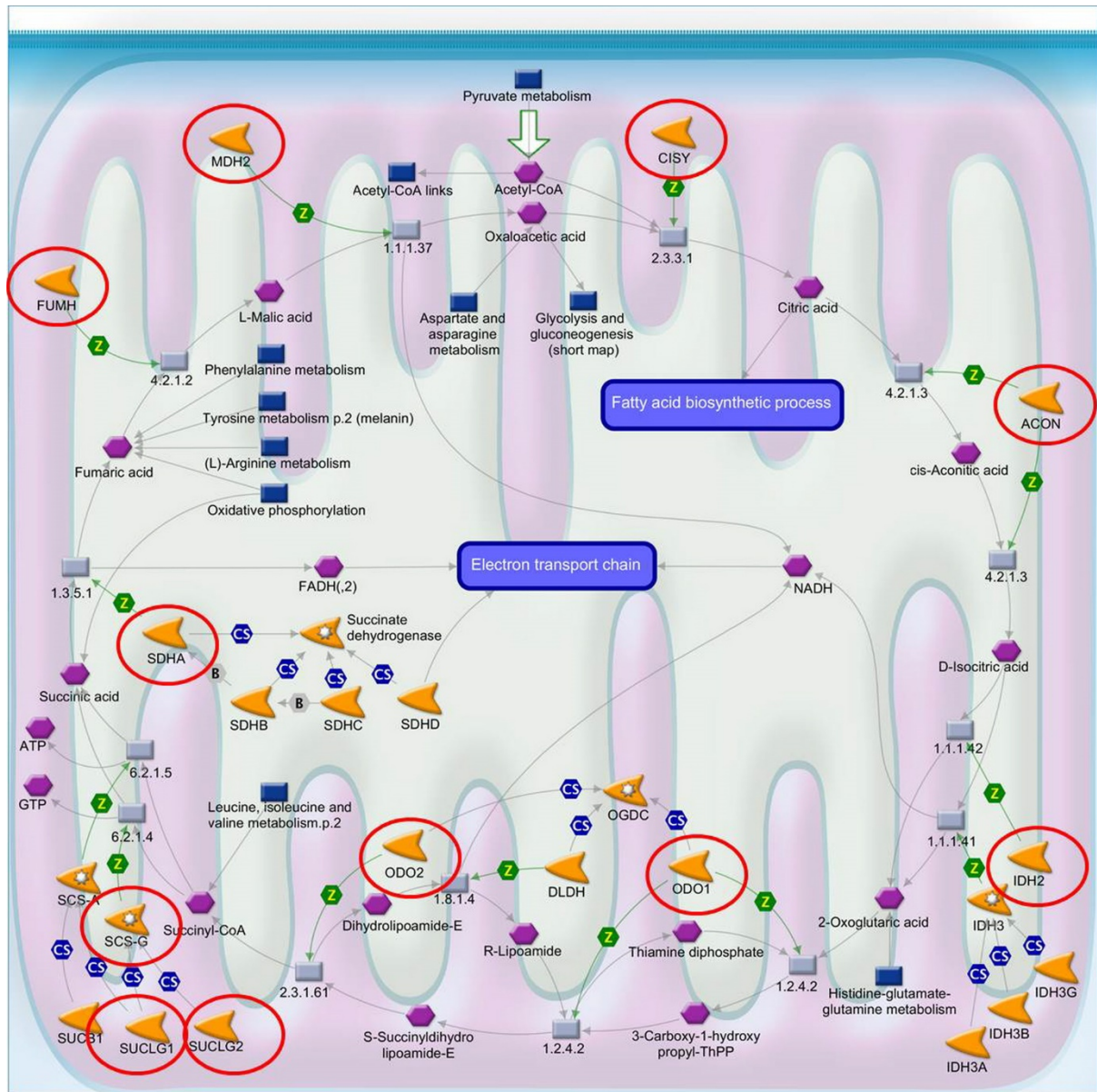


**Figure S2. Protein identification in prostate cancer cell lines compared with that in RWPE-1.** (A) Venn diagram shows the common and specific proteins in cancer cell lines compared with that in RWPE-1. (B) Number of differentially expressed proteins (1.2-fold up- or down-regulated proteins).

**Figure S3. Up-regulated pathways in prostate cancer cell lines compared with that in RWPE-1.**

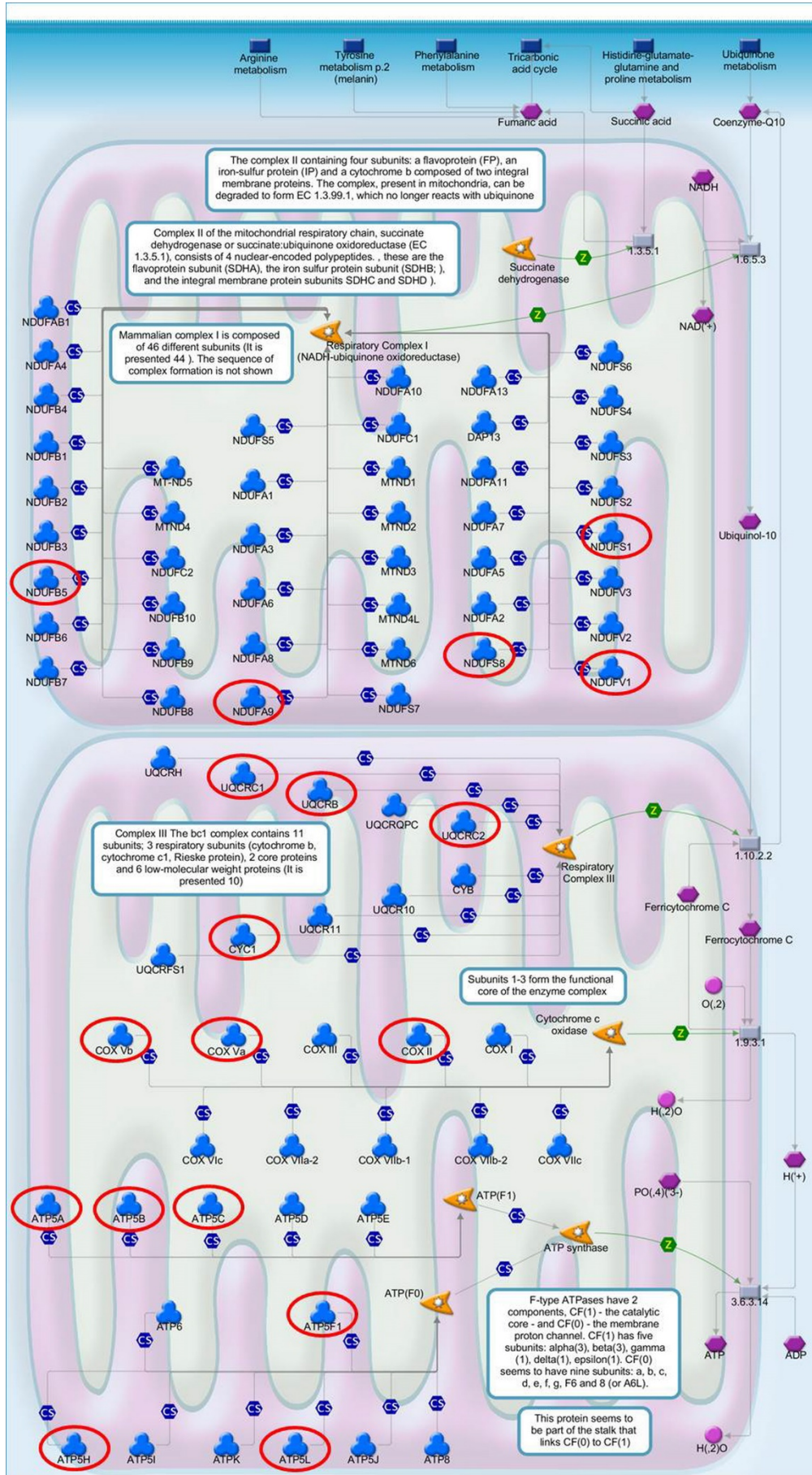
(A) Krebs cycle, (B) electron transport chain, and (C) table showing a list of protein component of the Krebs cycle and electron transport chain. Red circles indicate 1.2-fold up-regulated proteins in cancer cell lines compared with that in RWPE-1.

**A.**





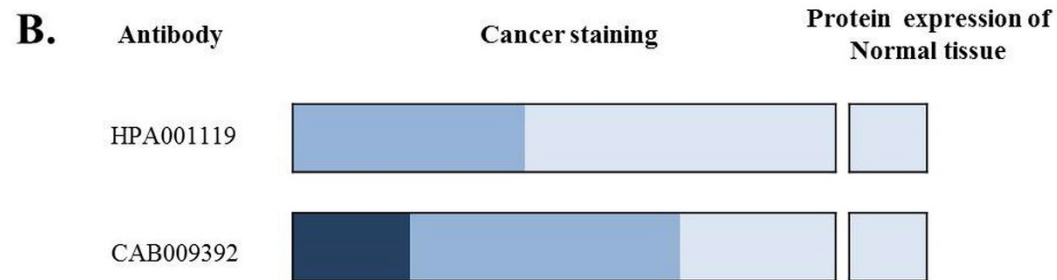
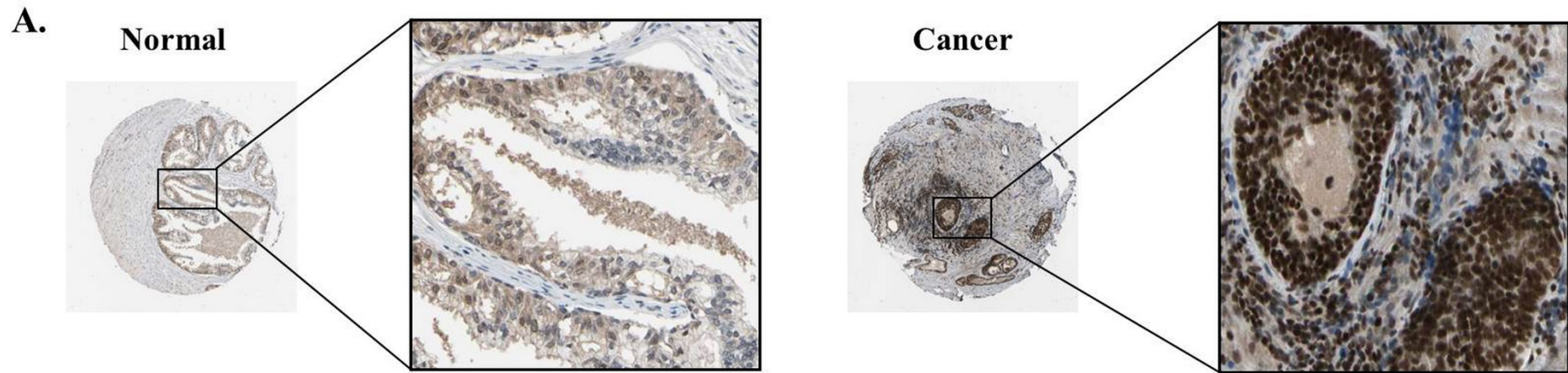
B.



## C.

Cellular pathway	Gene symbol	Protein name	Swiss-Prot ID	PI <sup>a</sup>	Mass (Da) <sup>b</sup>
<b>Krebs cycle</b>					
	ACON	Aconitate hydratase, mitochondrial	Q99798	7.45	86165.5
	CISY	Citrate synthase, mitochondrial	O75390	8.69	51939.7
	FUMH	Fumarate hydratase, mitochondrial	P07954	9.02	54807.2
	IDH2	Isocitrate dehydrogenase [NADP], mitochondrial	P48735	9.21	51364.8
	MDH2	Malate dehydrogenase, mitochondrial	P40926	9.38	35959.1
	ODO1	2-oxoglutarate dehydrogenase, mitochondrial	Q02218	6.4	117131.3
	ODO2	Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial	P36957	9.44	49096.8
	SCS-G	Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial	Q96199	6.15	46852.1
	SDHA	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial	P31040	7.11	73717.2
	SUCLG1	Succinyl-CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial	P53597	9.46	36648.5
	SUCLG2	Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial	Q96199	6.15	46852.1
<b>Electron transport chain</b>					
	ATP5A	ATP synthase subunit alpha, mitochondrial	P25705	9.25	59863.7
	ATP5B	ATP synthase subunit beta, mitochondrial	P06576	5.26	56558.9
	ATP5C	ATP synthase subunit gamma, mitochondrial	P36542	9.28	33052.5
	ATP5F1	ATP synthase F(0) complex subunit B1, mitochondrial	P24539	9.43	28965.2
	ATP5H	ATP synthase subunit d, mitochondrial	O75947	5.21	18547.9
	ATP5L	ATP synthase subunit g, mitochondrial	O75964	9.64	11428.3
	COX II	Cytochrome c oxidase subunit 2	P00403	4.67	25735.7
	COX Va	Cytochrome c oxidase subunit 5A, mitochondrial	P20674	6.3	16933
	COX Vb	Cytochrome c oxidase subunit 5B, mitochondrial	P10606	9.77	13923.7
	CYC1	Cytochrome c1, heme protein, mitochondrial	P08574	9.52	35763.7
	NDUFA9	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial	Q16795	9.96	42679.9
	NDUFB5	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 5, mitochondrial	O43674	9.62	21749.9
	NDUFS1	NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	P28331	5.89	80493.1
	NDUFS8	NADH dehydrogenase [ubiquinone] iron-sulfur protein 8, mitochondrial	O00217	6	24218.2
	NDUFV1	NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial	P49821	9.11	51500.8
	UQCRCB	Cytochrome b-c1 complex subunit 7	P14927	8.73	13530.2
	UQCRC1	Cytochrome b-c1 complex subunit 1, mitochondrial	P31930	5.94	53329.5
	UQCRC2	Cytochrome b-c1 complex subunit 2, mitochondrial	P22695	8.94	48613.3

<sup>a</sup>PI, isoelectric point, <sup>b</sup>Da,dalton

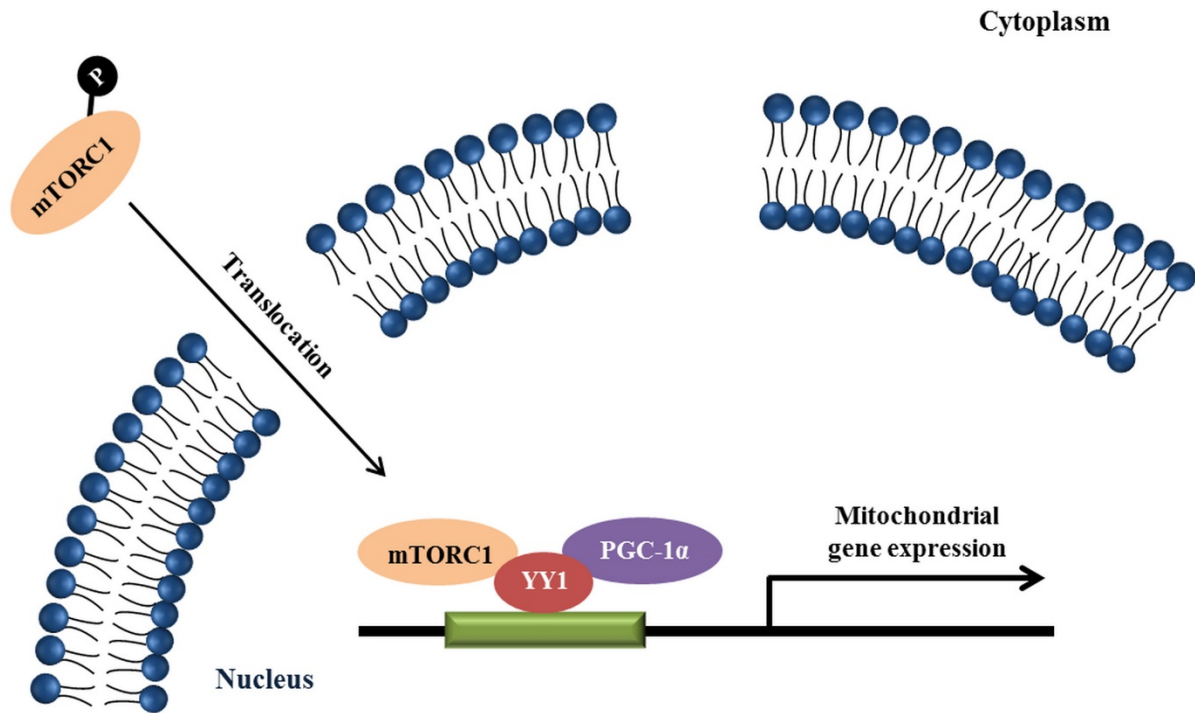


**C.**

Cancer type	Accession no.	Protein name	Gene symbol	HPA Antibody	IHC staining in HPA				
					Tumor tissue			Normal tissue	
					Strong	Moderate	Weak	Intensity	Quantity (%)
Prostate cancer	P2540	Yin yang 1	YY1	HPA01119	-	3	4	Moderate	>75
				CAB009392	2	3	2	Moderate	<25

**Figure S4. Data from the human protein atlas on YY1 expression in the nucleus.** (A) Immunochemistry images showing differentially expressed YY1 in

normal and prostate cancer tissue. (B) Detection of YY1 expression using HAP001119 and CAB009392 antibodies. (C) Table showing the YY1 expression profile in human protein atlas.



**Figure S5. YY1 transcription factor forms a complex to regulate mitochondrial gene expression in the nucleus.** mTOR controls mitochondrial oxidative function through a YY1/PGC-1  $\alpha$  transcriptional complex. Nature 450:736-740.



**Table S1. Primer sequences and conditions used for quantitative PCR.**

Gene	Amplicon (bp)		Primer	Annealing temperature
ACO2	121	F R	5'-CCCTACAGCCTACTGGTGACT-3' 5'-TGTA CTCTGTTGGGCTCAAAGT-3'	58°C
IDH2	104	F R	5'-CCCGTATTATCTGGCAGTTCATC-3' 5'-ATCAGTCTGGTCACGGTTTGG-3'	60°C
OGDH	159	F R	5'-TTGGCTGGAAAACCCCAAAG-3' 5'-TGTGCTTCTACCAGGGACTGT-3'	59°C
DLD	77	F R	5'-CACTGCTACGAAAGCTGATGG-3' 5'-TAACTTCTGAACCCGTGGCTA-3'	58°C
SUCLA2	108	F R	5'-TCTCCGTTCCCAAAGGATATGT-3' 5'-CACCAGCTAAAACCTGTGCC-3'	58°C
FH	133	F R	5'-GGAGGTGTGACAGAACGCAT-3' 5'-CATCTGCTGCCTTCATTATTGC-3'	59°C
NDUFA9	129	F R	5'-CCGACGAGTAGTACAACACAGC-3' 5'-GCTTCCTTGACAGTTGAGCA-3'	60°C
NDUFS1	108	F R	5'-TTAGCAAATCACCCATTGGACTG-3' 5'-CCCCTCTAAAAATCGGCTCCTA-3'	58°C
SDHA	119	F R	5'-CAGCATGTGTTACCAAGCTGT-3' 5'-GGTGTCGTAGAAATGCCACCT-3'	58°C
SDHB	113	F R	5'-GACACCAACCTCAATAAGGTCTC-3' 5'-GGCTCAATGGATTGTACTGTGC-3'	58°C
UQCRC2	120	F R	5'-TTCAGCAATTTAGGAACCACCC-3' 5'-GGTCACACTTAATTTGCCACCAA-3'	58°C
COX2	375	F R	5'-CCATCCCTACGCATCCTTTAC-3' 5'-GTTTGCTCCACAGATTTACAGAG-3'	54°C
COX4I1	113	F R	5'-CAGGGTATTTAGCCTAGTTGGC-3' 5'-GCCGATCCATATAAGCTGGGA-3'	59°C
COX5B	91	F R	5'-TGTGAAGAGGACAATACCAGCG-3' 5'-CCAGGCATCTATATCTGGCTTG-3'	59°C
ATP5A1	149	F R	5'-AACTGATTATTGGTGACCGACAG-3' 5'-GGCAACAGTGGATCTCTTTTGA-3'	58°C

ATB5B	90	F R	5'-AAACAATTTGCTCCCATTCATGC-3' 5'-GACAACCTTGATACCAGTCACC-3'	58°C
ATP5F1	117	F R	5'-AGGTCCAGGGTATTGCAG-3' 5'-TCCTCAGGGATCAGTCCATAAC-3'	58°C

**Table S5. Transcriptional regulation analysis of proteins associated with glycolysis and gluconeogenesis in the GeneGo database.**

Key network objects	p-Value	z Score	g Score
CREB1	1.10e-72	262.39	262.39
c-Myc	6.43e-69	255.42	255.42
SP1	3.63e-65	248.26	248.26
HIF1A	3.63e-65	248.26	248.26
ERR1	5.42e-43	200.09	200.09
SP3	2.38e-39	190.90	190.90
HNF4-alpha	1.01e-35	181.26	181.26
HNF3-beta	1.01e-35	181.26	181.26
ESR1(nuclear)	1.01e-35	181.26	181.26
PPAR-gamma	4.11e-32	171.10	171.10