

Table S1. Oligonucleotide primers used in the study.

Primer	Sequences	
TUFM	(forward)	5' - GTT CTC CCT GAC TTG GGA CA -3'
	(reverse)	5' - CCA GCG TGT TGG TGA CTA GA -3'
HNRNPH3	(forward)	5' - GCT ATG GTG GAG CTG GTG AT -3'
	(reverse)	5' - TCT GCT TCT CCT GTG GCT CT -3'
LDHB	(forward)	5' - TGC TCT TGT GGA TGT TTT GG -3'
	(reverse)	5' - GAC TCT CCC CTT CTT GCT GA -3'
HNRNPK	(forward)	5' - TTC AGT CCC AGA CAG CAG TG -3'
	(reverse)	5' - TCC ACA GCA GCA GAT TCG AG -3'
OXCT1	(forward)	5' - GGG TCC ATA TCC ACG ACA AC -3'
	(reverse)	5' - CCA GTT AGC CAG GTC ACC AT -3'
CCT2	(forward)	5' - GAA CAT GCG GAA AAG GAA AA - 3'
	(reverse)	5' - AGA GGC AAT TTC ACC ACC TG - 3'
ACPP	(forward)	5' - GAC GTT GAC CGG ACT TTG AT - 3'
	(reverse)	5' - TTC TTG AAA ACG AGG GCA GT - 3'
IMPDH2	(forward)	5' - CCG GAC AGA CCT GAA GAA GA -3'
	(reverse)	5' - TGG GAA GAG TCC AAA ACC AC -3'

Table S2. List of proteins identified by MS

Treatment	Gene name	Acc. No. ¹	Protein name	MW ² (KDa)	pI ³	Cellular component	Biological process
DHT	TUFM	P49411	elongation factor Tu, mitochondrial	49.510	7.61	membrane; mitochondrion	metabolic process; response to stimulus
	HNRNPH3	P31942	Heterogeneous nuclear ribonucleoprotein H3	36.903	6.87	nucleus; spliceosomal complex	cell differentiation; metabolic process
	LDHB	P07195	L-lactate dehydrogenase B chain	36.615	6.05	cytoplasm; cytosol; membrane; mitochondrion	metabolic process
FSK	IMPDH2	P12268	inosine-5'-monophosphate dehydrogenase 2	55.770	6.90	cytoplasm; cytosol; extracellular; membrane; nucleus; organelle lumen	cell organization and biogenesis; cell proliferation; metabolic process; response to stimulus; transport
	HNRNPK	P61978	Heterogeneous nuclear ribonucleoprotein K	50.996	5.33	cytoplasm; membrane; nucleus; spliceosomal complex	metabolic process; regulation of biological process; response to stimulus
	OXCT1	P55809	Succinyl-CoA:3-ketoacid coenzyme A transferase 1, mitochondrial	56.122	7.46	mitochondrion; organelle lumen	metabolic process; regulation of biological process; response to stimulus
	CCT2	P78371	T-complex protein 1 subunit beta	57.452	6.46	cytoplasm; cytosol; extracellular; organelle lumen	cell organization and biogenesis; metabolic process; regulation of biological process; transport
	ACPP	P15309	Prostatic acid phosphatase	48.305	7.02	membrane; nucleus	metabolic process; regulation of biological process; transport

¹ Acc. No., UniProt accession number ² MW, Molecular weight ³ pI, Isoelectric point