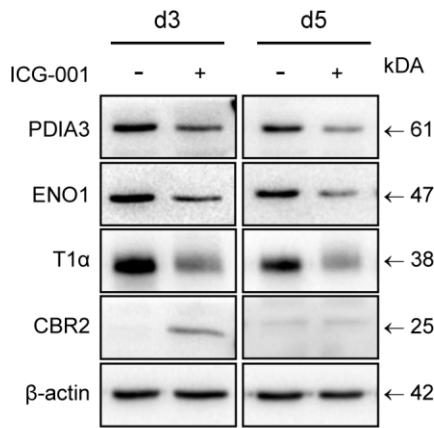
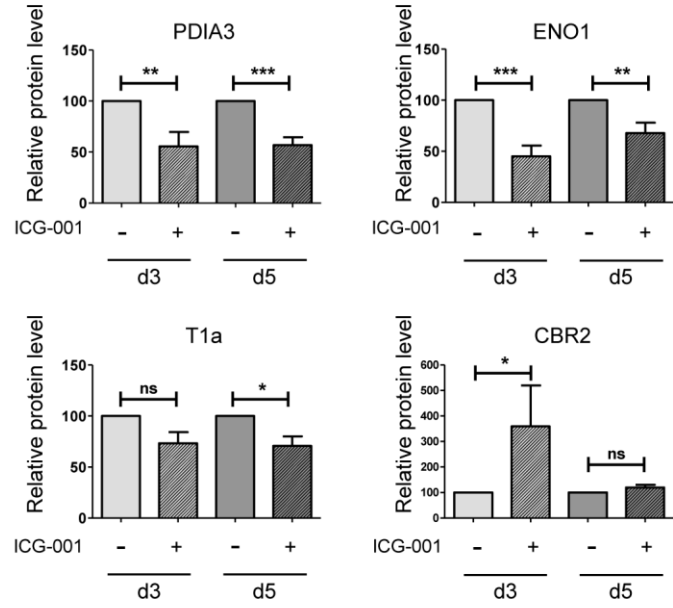


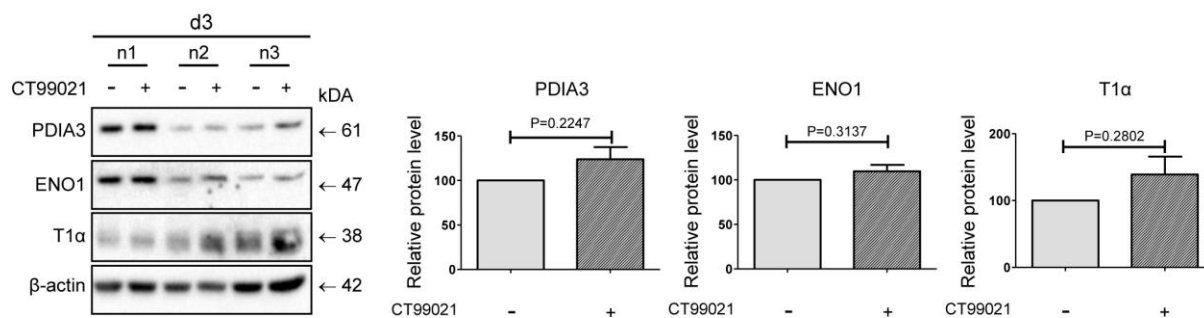
A



B



A



SUPPLEMENTARY TABLE S1

Proteins identified on 2D gel by MALDI-TOF MS						
Number	Name of protein	GI-number	Unique peptides detected	Mascot score	Sequence coverage	Peptide sequences used for MS/MS
1	Calreticulin	6680836	15	181	30%	⁵⁶ FYGDLEKDK ⁶⁴ ¹⁴³ KVHVIFNYK ¹⁵¹ ¹⁴⁴ VHVIFNYK ¹⁵¹
2	Protein disulfide-isomerase	54777	19	318	33%	⁷² LKAEGSEIR ⁸⁰ ⁸⁴ VDATEESDLAQQYGVR ⁹⁹ ²¹¹ FDEGRNNFEGETK ²²⁴ ⁴⁴⁷ FFPASADR ⁴⁵⁴
3	Carbonyl reductase 2	6671688	12	123	34%	¹ MKLNFSGLR ⁹ ¹¹⁰ SVFQVSQMVAR ¹²⁰ ¹⁹⁰ VSADPEFAR ¹⁹⁸
4	ATP synthase subunit β , mitochondrial	74197074	21	337	42%	¹⁴⁴ IMNVIGEPIDER ¹⁵⁵ ²⁶⁵ VALVYQGMNEPPGAR ²⁷⁹ ³¹¹ FTQAGSEVSALLGR ³²⁴ ³⁸⁸ AIAELGIYPAVDPLDSTR ⁴⁰⁶
5	Hspd1 protein	76779273	17	219	31%	⁹⁷ LVQDVANNNEEAGDGTTTATVLR ¹²¹ ¹³⁴ GANPVEIRR ¹⁴² ⁴³⁰ AAVEEGIVLGGCALLR ⁴⁴⁶ ⁴⁶³ IGIEIKR ⁴⁷⁰
6	Putative uncharacterized protein	74191337	10	249	29%	¹³³ LYGPSSVSFADDFVR ¹⁴⁷ ³⁹³ DNQSGSLLFIGR ⁴⁰⁴
7	Protein disulfide isomerase associated 3	23958822	23	339	36%	¹⁰⁸ DGEEAGAYDGPGR ¹¹⁹ ¹⁴⁸ FISDKDASVVGFFR ¹⁶¹ ⁴⁷² ELNDFISYLQR ⁴⁸²
8	Krt8 protein	76779293	26	346	48%	⁸⁴ LEVDPNIQAVR ⁹⁴ ¹⁴⁰ SNMDNMFESYINNL ¹⁵⁴ ²²⁰ LEGLTDEINFLR ²³¹
9	Anxa1	70912321	17	444	44%	¹¹⁴ TPAQFDADEL ¹²⁴ ¹²⁹ GLGTDEDLIEILTTR ¹⁴⁴ ²¹⁴ KGTDVNVFTILTSTR ²²⁸ ²¹⁵ GTDVNVFTILTSTR ²²⁸
10	Caldesmon 1	18043856	24	357	40%	¹⁰⁴ RLQEALER ¹¹¹ ¹¹² QKEFDPTITDGLSLGSPSR ¹²⁹ ¹⁵¹ SGRYEVEETEVIK ¹⁵⁴ ²⁴² QTENAFSPSR ²⁵¹
11	Enolase 1	54673814	12	277	34%	³³ AAVPSGASTGIYEAL ⁵⁰ ¹⁶³ LAMQEFMILPVGASSFR ²¹⁷⁹ ²⁵⁷ YDLDFKSPDDPSR ²⁶⁹ ²⁷⁰ YITPDQLADLYK ²⁸¹
12	Aldehyde dehydrogenase 2	6753036	19	363	38%	¹¹⁰ LADLIERDR ¹¹⁸ ¹⁶² TIPIDGFFSYTR ¹⁷⁴ ³²⁷ TFVQENVYDEFVER ³⁴⁰ ³⁴⁹ VVGNPFDSR ³⁵⁷ ⁴³¹ TIEVVGR ⁴³⁸
13	Serine hydroxymethyl transferase 2	21312298	22	338	39%	⁷⁰ GLELIASENFCSR ⁸² ⁹⁶ YSEGYPGKR ¹⁰⁴ ²²⁰ LIAGTSAYAR ²³⁰ ³⁵⁷ NAQAMADALLKR ³⁶⁸ ⁴²⁶ LGAPALTSR ⁴³⁴

						⁴⁷⁰ SFLKDPETSQR ⁴⁸¹
14	ATP synthase,	6680748	19	327	37%	⁵⁹ ILGADTSVDLEETGR ⁷³ ¹³⁴ TGAIVDVPVGEELLGR ¹⁴⁹ ¹⁹⁵ AVDSLVPGR ²⁰⁴ ³³⁵ EAYPGDVVFLHSR ⁴⁴¹
15/16	Lamin A/C	1794160	44	728	55%	¹² SGAQASSTPLSPTR ²⁵ ²⁹ LQEKEDLQELNDR ⁴¹ ⁵¹ SLETENAGLR ⁶⁰ ²⁸¹ NSNLVGAHEELQQR ²⁹⁶ ³²⁰ IRIDLSAQLSQLQK ³²⁹ ³⁷⁹ LLEGEERLR ³⁸⁸ ⁴⁴⁰ VAVEEVDEEGKFVR ⁴⁵³
17	Mitochondrial phosphoenolpyruvate carboxykinase 2	28077029	22	225	35%	¹⁴⁵ DTVPLLAGGAR ¹⁵⁵ ²⁶² TLIGHVPDQR ²⁷¹ ²⁶² FDSEGQLR ²⁶⁹ ⁴⁹⁷ HGVFVGSAMR ⁵⁰⁶ ⁵⁸⁸ RLEGEDSAQETPIGLVPK ⁶⁰⁵ ⁶²⁸ DFWEQEVV ⁶³⁵
18	Mitochondrial phosphoenolpyruvate carboxykinase 2	28077029	21	228	35%	¹⁴⁵ DTVPLLAGGAR ¹⁵⁵ ²⁶² TLIGHVPDQR ²⁷¹ ³⁶² FDSEGQLR ³⁶⁹ ⁴⁹⁶ HGVFVGSAMR ⁵⁰⁶ ⁵⁸⁸ RLEGEDSAQETPIGLVPK ⁶⁰⁵ ⁶²⁸ DFWEQEVV ⁶³⁵
19	Dihydrolipoyl dehydrogenase,	6014973	12	154	23%	¹³³ ALTGGIAHLFK ¹⁴³ ³³⁵ GRIPVNNR ³⁴² ⁴¹⁸ IGKFPFAANSR ⁴²⁸ ⁴⁸³ VCHAHPTLSEAFR ⁴⁹⁵
20	Glutamate dehydrogenase 1	6680027	8	150	16%	⁶⁹ MVEGFFDR ⁷⁶ ¹²⁵ DDGSWEVIEGYR ¹³⁶ ⁴⁸¹ HGGTIPVVPVTAEFQDR ⁴⁹⁶
21	Annexin A11	7304885	18	112	33%	³⁵⁸ DVQELYAAGENR ³⁶⁹ ³⁸⁷ AHLVAVFNEYQR ³⁹⁸
22	Heat shock 70kD protein 5	29748016	27	548	36%	⁶² ITPSYVAVFTPEGER ⁷⁵ ¹⁶⁶ VTHAVVTVPAYFNDAQR ¹⁸² ¹⁹⁹ IINEPTAAAIAAYGLDKR ²¹⁵ ³²⁶ AKFEELNMDLFR ³³⁷ ³⁵⁴ KSDIDEIVLVGGSTR ³⁶⁸
23	Electron transferring flavoprotein,	38142460	13	241	49%	⁶⁰ EIIAVSCGPSQCQETIR ⁷⁶ ¹⁶⁵ EIDGGLETLR ¹⁷⁴ ¹⁷⁵ LKLPVAVVTADLR ¹⁸⁶ ²²² VSVISVEEPPQR ²³³
24	Malate dehydrogenase 2	31982186	6	203	21%	⁹² GCDVVVIPAGVPR ¹⁰⁴ ¹⁶⁶ IFGVTTLDIVR ¹⁷⁶ ²¹⁶ VDFPQDQLATLTGR ²²⁹
25	Heterogeneous nuclear ribonucleoprotein A2/B1/B0	23266713	8	155	28%	¹³⁸ IDTIEITDR ¹⁴⁷ ²⁰⁴ GGNFGFGDSR ²¹³ ²¹⁴ GGGNGFGPGGSNFR ²²⁸
26	Caldesmon 1	18043856	25	233	43%	¹¹² QKEFDPTITDGSLSGPSR ¹²⁹ ²⁴² QTENAFSPSR ²⁵¹ ³⁴² LKEEIER ³⁴⁸
27	Ornithine aminotransferase	8393866	9	237	21%	³² KTEQGPPSSEYIFER ⁴⁶ ³³ TEQGPPSSEYIFER ⁴⁶ ⁴¹⁴ LAPPLVIKEDEIR ⁴²⁶