

## **Supplementary Data**

### **Supplementary Figure 1:**

(A) Representative 2-DE gels of membrane protein extracts of Glc mitochondria and Lac mitochondria. Membrane proteins were enriched from mitochondria by sodium carbonate treatment and resolved by 2-DE (sample load 50  $\mu$ g, IPG 3-10 NL, SDS-PAGE 9-14%T). Spot numbers indicate the identified proteins (Table 1, STable 2), which showed prominent alterations.

(B) Comparisons of the mean spot intensities of selected protein spots from (A). Quantitative values are given in STable 1 (n.d. = not detectable).

### **Supplementary Figure 2:**

Annotated MALDI-TOF spectra of trypsin treated outer mitochondrial membrane proteins separated by SDS/PAGE (Fig. 6A).

**Supplementary Table 1:**

Quantitative analysis (Proteomweaver software V.2.2) of selected protein spots of the 2-DE analysis of membrane protein extracts from Glc and Lac mitochondria. Abbreviations: n.d. = not detectable, n.q. = not quantifiable due to staining saturation. P-values < 0.05 indicate significant alterations. Three representative gels for Lac and three gels for Glc were evaluated.

Spot-No.	SwissProt Identifier	Mean spot intensity Glc mitochondria	Standard deviation	Mean spot intensity Lac mitochondria	Standard deviation	Lac vs. Glc	TTest (unpaired) p-value
1	TOM70	4.913	1.460	1.447	0.249	0.29	0.01543064
2	DLD1	0.146	0.020	3.125	0.354	21.36	0.00013040
3	DLD1	0.122	0.026	4.219	0.863	34.68	0.00119299
4	DLD1	0.266	0.044	3.203	0.754	12.06	0.00252789
5	DHSA	n.d	-----	1.498	0.268	-----	-----
6	DHSA	n.d	-----	1.940	0.544	-----	-----
7	DHSA	n.d	-----	1.705	0.455	-----	-----
8	OM45	1.193	0.379	2.059	0.536	1.73	0.08419855
9	OM45	1.297	0.368	2.228	0.350	1.72	0.03363099
10	UQCR1	0.842	0.093	0.879	0.111	1.04	0.67858124
11	UQCR2	0.350	0.150	0.933	0.202	2.67	0.01593878
12	MCR1	2.251	0.614	5.400	1.589	2.40	0.03285800
13	MCR1	1.289	0.527	3.703	0.715	2.87	0.00924318
14	MPCP	7.500	4.283	22.474	7.316	3.00	0.03768733
15	VDAC1	16.393	0.947	n.q.	-----	-----	-----
16	VDAC1	13.133	0.856	n.q.	-----	-----	-----
17	VDAC1	4.202	0.240	9.476	1.284	2.26	0.00220168
18	CY1	0.439	0.240	2.176	0.232	4.96	0.00083879
19	CY1	0.247	0.036	3.393	0.280	13.74	0.00004232
20	CY1	0.164	0.032	1.762	0.588	10.74	0.00931084
21	COX5A	n.d.	-----	3.627	1.057	-----	-----
22	COX13	n.d.	-----	1.493	0.247	-----	-----
23	UCR7	0.261	0.179	2.014	0.348	7.71	0.00149161

## Supplementary Table 2:

MS analysis of the mitochondrial membrane proteins extracted by sodium carbonate treatment from Lac/Glc mitochondria and separated by 2-DE (Fig. 2B, SFig. 1). Data were obtained on the **ABI** 4700 Proteomics Analyzer and analyzed by GPS Explorer 2.0 software.

Spot no.	SwissProt Identifier	Accession Number	Peptide Count <sup>a</sup>	Intensity Coverage <sup>b</sup>	MS/MS Spectra <sup>c</sup>	Total Ion Score <sup>d</sup>	MS/MS Score <sup>e</sup>	Peptide Sequence <sup>f</sup>
1	TOM70_YEAST	P07213	13	26.5	1	33	33	GQMNFILQNYDQAGK
2	DLD1_YEAST	P32891	23	35.7	2	105	54 51	SPNIVNALVDEVK IILFPHTTEEVSK
3	DLD1_YEAST	P32891	17	32.9	2	92	58 35	IILFPHTTEEVSK AVAQLNHCNSFQFAK
4	DLD1_YEAST	P32891	12	18.6	0	0	-	-
5	DHSA_YEAST	Q00711	18	46.7	3	194	53 95 46	GEGGFLVNSEGER LGANSLDLVVFGR SIIELEHYGVPSR
6	DHSA_YEAST	Q00711	17	42.7	3	173	51 58 64	AAFGLAEAGYK GEGGFLVNSEGER SIIELEHYGVPSR
7	DHSA_YEAST	Q00711	14	30.4	2	72	36 36	GEGGFLVNSEGER LGANSLDLVVFGR
8	OM45_YEAST	P16547	18	28.3	4	232	33 87 76 36	GEQSEQQIAER SVQGWGDTAQEFGR DSSSQSIFNWGFSEAER EGNV SAYYNGQEY GSSAPPQLGK
9	OM45_YEAST	P16547	15	23.4	3	182	35 95 52	GEQSEQQIAER SVQGWGDTAQEFGR DSSSQSIFNWGFSEAER
10	UQCR1_YEAST	P07256	10	31.3	2	118	49 69	SLDFLNQSFQQK QVQDFEENDHPNR
11	UQCR2_YEAST	P07257	14	45.3	4	206	41 58 66 42	FFLGEENR FNFQNTNTR GLGNPLLYDGVER SAEDQLYAITFR
12	MCR1_YEAST	P36060	20	37.4	6	364	32 35 76 87 93 41	TPQDILLR FNVTYFVDDK DFIQEHVPGPK NQHSFVFNESNK DQGELIGILNNGYSK GSNVVRPYTPVSDLSQK
13	MCR1_YEAST	P36060	16	27.3	4	149	60 43 45	GHFQLVVK DFIQEHVPGPK NQHSFVFNESNK
14	MPCP_YEAST	P23641	16	70.4	6	527	40 101 118 74 136 60	FGGYEVFK ASEFYGFAGPK QLGFFGSFAGLPTR FFIDNLGYDTASR LVSQPQFANGLVGGFSR EEGIGSFYSGFTPIILFK
15	VDAC1_YEAST	P04840	19	69.3	7	548	75 59	SPPVYSDISR YAMALSYFAK

							75	LEFANLTPGLK
							129	LPNSNVNIEFATR
							89	SAVLNTTFTQPFFTAR
							56	QLLRPGVTLGVGSSFDALK
							65	DFYHATPAAFDVQTTTANGIK
<b>16</b>	VDAC1_YEAST	P04840	18	66.2	7	523	51	SPPVYSDISR
							57	YAMALSYFAK
							75	LEFANLTPGLK
							114	LPNSNVNIEFATR
							112	SAVLNTTFTQPFFTAR
							54	QLLRPGVTLGVGSSFDALK
							60	DFYHATPAAFDVQTTTANGIK
<b>17</b>	VDAC1_YEAST	P04840	11	52.0	6	356	34	SPPVYSDISR
							34	YAMALSYFAK
							57	LEFANLTPGLK
							107	LPNSNVNIEFATR
							91	SAVLNTTFTQPFFTAR
							33	QLLRPGVTLGVGSSFDALK
<b>18</b>	CY1_YEAST	P07143	7	22.2	1	51	51	LSDYIPGPYPNEQAAR
<b>19</b>	CY1_YEAST	P07143	7	32.6	2	140	57	AANQGALPPDLSLIVK
							82	LSDYIPGPYPNEQAAR
<b>20</b>	CY1_YEAST	P07143	6	14.0	0	0	-	-
<b>21</b>	COX5A_YEAST	P00424	6	18.2	3	192	68	NANPWGGYSQVQSK
							45	QKLPWAQLTEPEK
							80	QAVWYISYGEWGPR
<b>22</b>	COX13_YEAST	P32799	5	22.7	2	77	43	DYEFMNIR
							34	TLFWNPVVNR
<b>23</b>	UCR7_YEAST	P00128	8	35.5	4	182	67	AHQTELTHLLPR
							44	LCVPVANQFINLAGYK
							71	FDDLIAEENPIMQTALR
								FDDLIAEENPIMQTALR
							36	Oxidation (M)

<sup>a)</sup> Number of peptides that match identified protein

<sup>b)</sup> Intensity coverage, expressed as cumulative intensity of the peaks assigned to the hit divided by the cumulative intensity of all peaks of respective spectrum, given in %

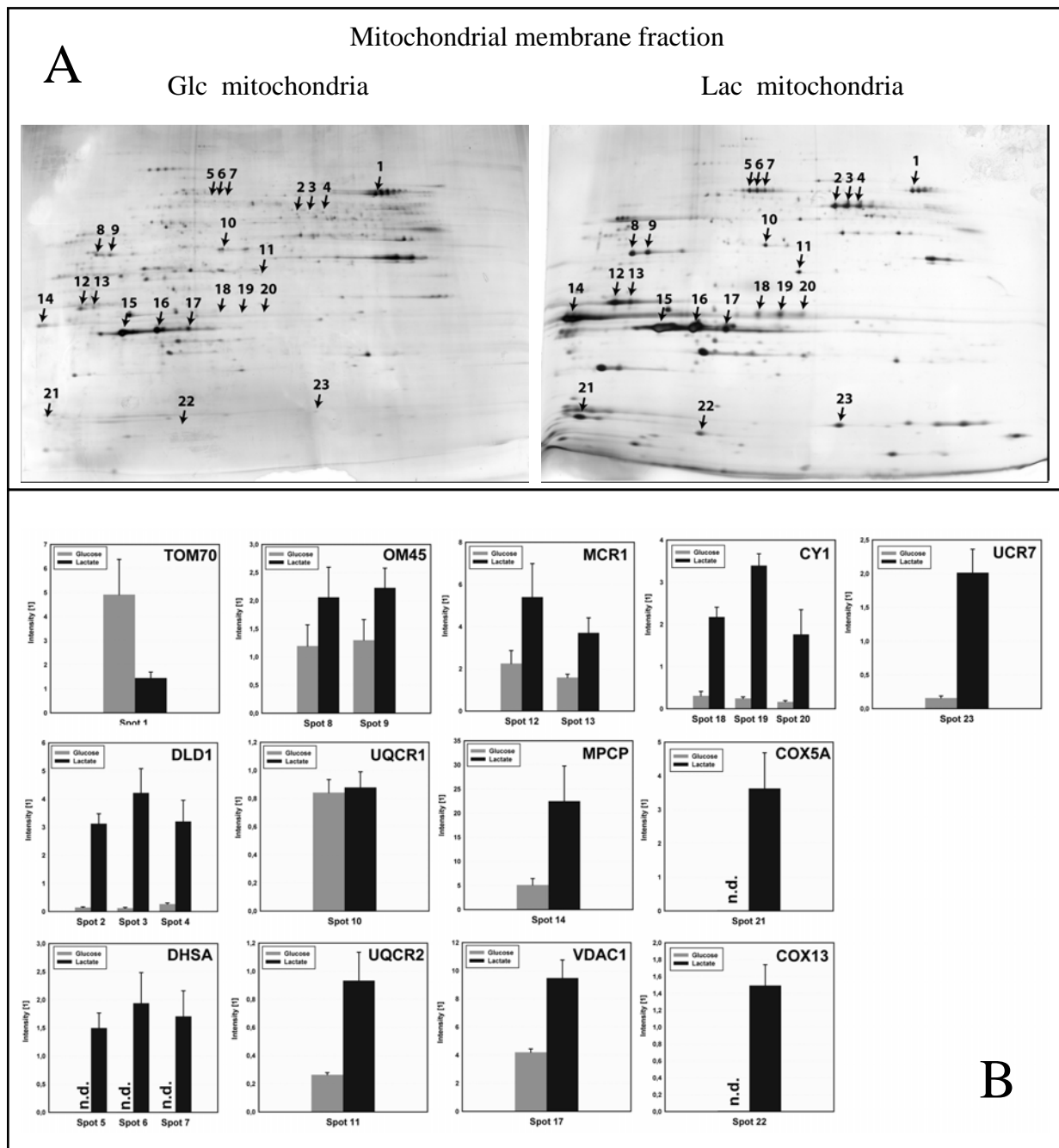
<sup>c)</sup> Number of MS/MS spectra with MS/MS scores > 31 obtained for the identified protein

<sup>d)</sup> Sum of MOWSE scores of the identified protein as given by Mascot for all MS/MS spectra with MS/MS scores > 31

<sup>e)</sup> MOWSE scores as given by Mascot for the respective MS/MS spectrum, only MS/MS scores > 31 were considered

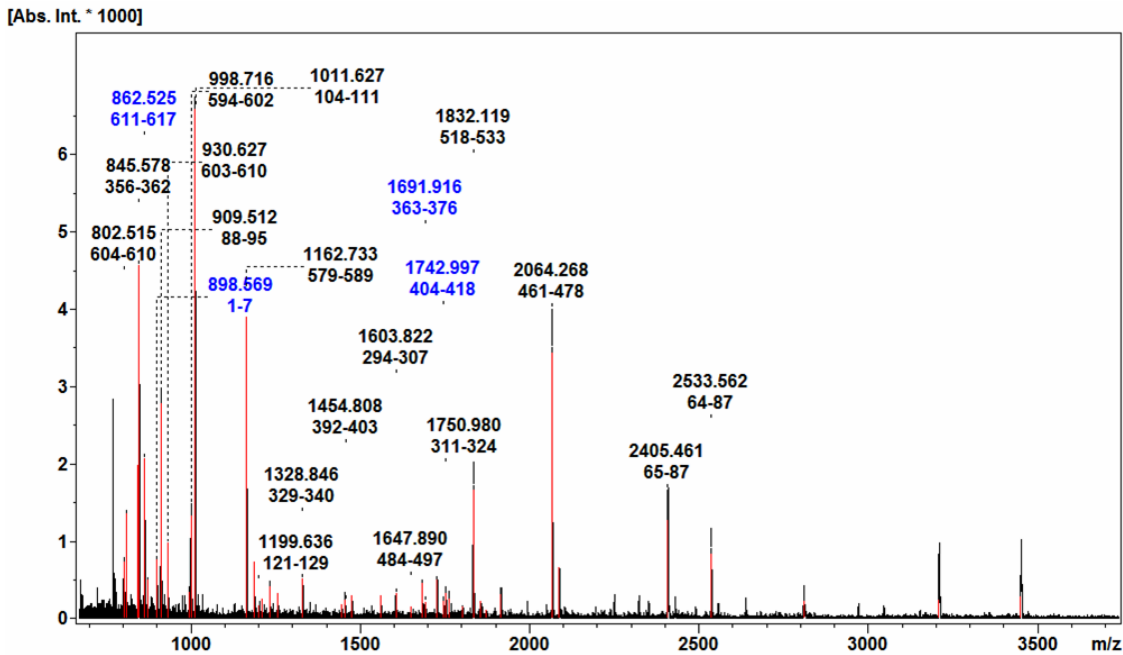
<sup>f)</sup> Peptide sequence (Oxidation (M): methionine was considered oxidized)

# Supplementary Figure 1

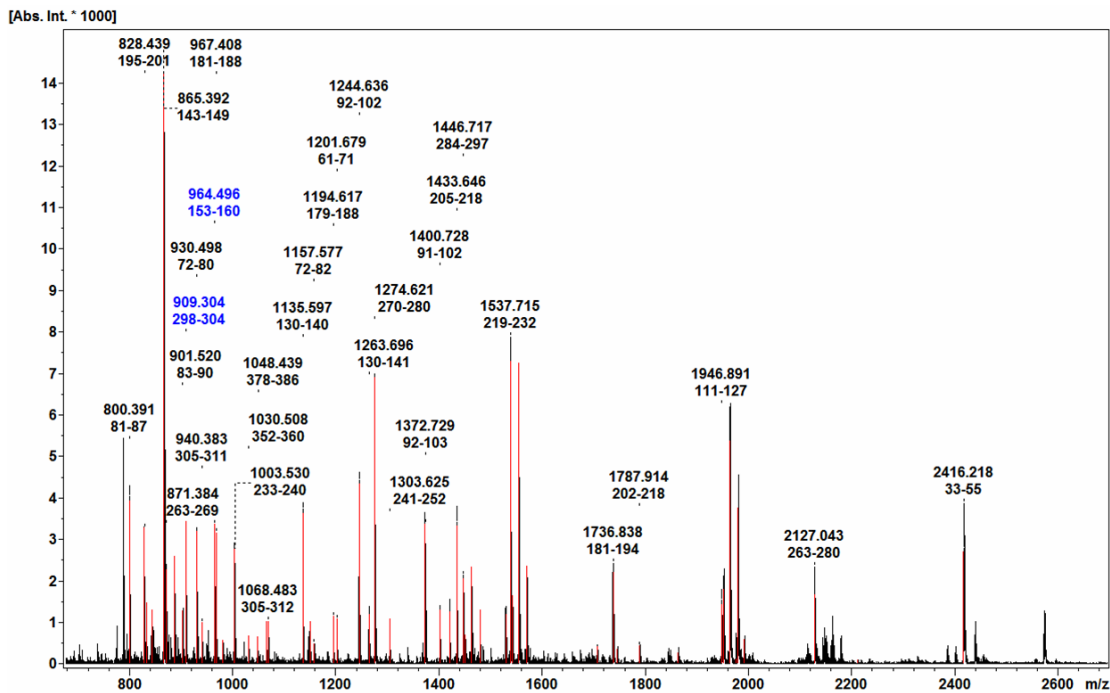


# Supplementary Figure 2

- A Annotated Spectrum of the trypsin treated protein band 1 in Figure 6 (TOM70):**  
 All peaks belonging to top hit are labelled with first line indicating the mass and second line giving amino-acid positions covered by the respective peptide. Black color labelling indicates unmodified peptides, blue color labelling indicates peptides carrying an oxidized methionine.



- B Annotated Spectrum of the trypsin treated protein band 2 in Figure 6 (OM45):**



# Supplementary Figure 2

## C Annotated Spectrum of the trypsin treated protein band 3 in Figure 6 (VDAC1):

