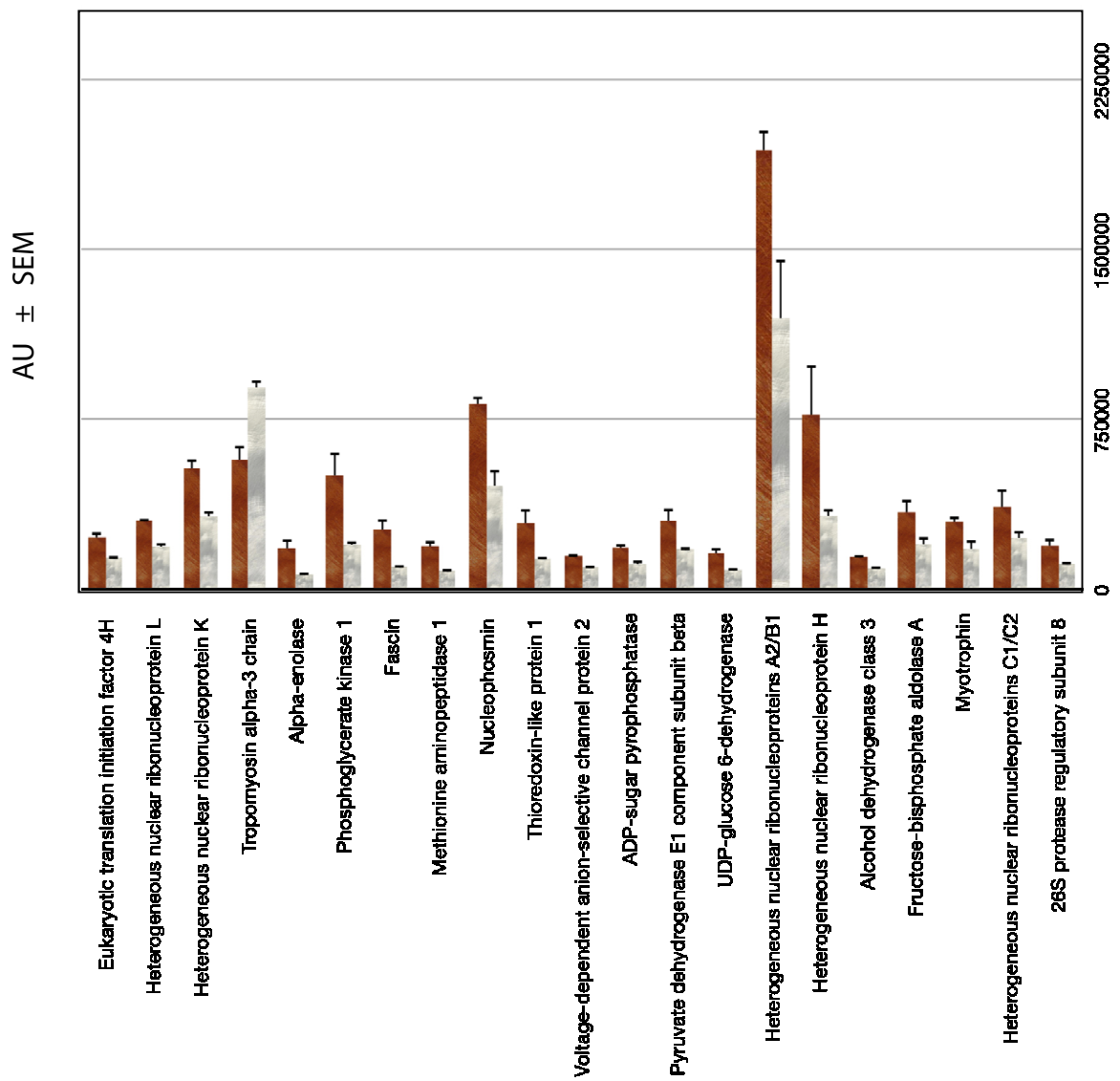


Table 1: Differentially-expressed proteins identified by MALDI-TOF MS by peptide mass fingerprinting

Accession No.	Gene Name	Protein Description	Fold Change	% Coverage	Peptides Matched	Predicted Mw(kDa)/pI	Observed Mw(kDa)/pI	MOWSE Score
P06748	NPM1	Nucleophosmin (NPM)	-1.8	12.2	6 (25)	32.6/4.6	38.8/4.8	7.1x10 ³
P04075	ALDOA	Fructose-bisphosphate aldolase A	-3.17	49.7	12	39.4/8.3	40.7/9.3	7.1x10 ⁵
P22626	HNRNPA2B1	Heterogeneous nuclear ribonucleoprotein A2/B1	-1.72	44.8	11 (29)	37.4/9.0	35.6/8.8	2.9x10 ⁷
P61978	HNRNPK	Heterogeneous nuclear ribonucleoprotein K	-1.77	25.1	12 (17)	51.0/5.4	59.4/5.7	3.1x10 ⁴
P06733	ENO1L1	Alpha-enolase	-2.78	12.7	6 (12)	47.2/7.0	48.6/7.5	1.9x10 ⁴
P45880	VDAC2	Voltage-dependent anion-selective channel protein 2	-1.53	36.3	8 (22)	38.0/6.3	31.9/7.8	4.5x10 ⁵
P06753	TPM3	Tropomyosin alpha-3 chain	-1.56	27.5	11 (20)	32.8/4.7	31.0/4.5	9.4x10 ²
Q9UUK9	NUDT5	ADP-sugar pyrophosphatase	-1.7	38.8	9 (25)	24.38/4.9	30.9/4.8	1.1x10 ⁴
P00558	PGK1	Phosphoglycerate kinase 1	-2.58	30.2	8 (21)	44.6/8.3	45/9	8.1x10 ⁴
P62195	PSMC5	26S protease regulatory subunit 8	-1.71	42.4	16 (48)	45.6/7.1	46.2/7.2	6.2x10 ⁷
P07910	HNRNPC	Heterogeneous nuclear ribonucleoprotein	-1.61	38.6	15 (25)	33.7/5.0	38.3/5.2	7.1x10 ⁴
O43396	TXNL1	Thioredoxin-like protein 1	-2.17	49.1	13 (18)	32.3/4.8	35.2/5.0	1.4x10 ⁶
P31943	HNRNPH1	Heterogeneous nuclear ribonucleoprotein H	-2.39	61	21 (22)	49.2/5.9	53.8/4.6	3.9x10 ¹⁰
P14866	HNRNPL	Heterogeneous nuclear ribonucleoprotein L	-1.62	32.1	16 (57)	60.2/6.7	60.8/7.1	3.5x10 ⁷

Table 1: Differentially-expressed proteins identified by MALDI-TOF MS by peptide mass fingerprinting (cont'd.)								
Accession No.	Gene Name	Protein Description	Fold Change	% Coverage	Peptides Matched	Predicted Mw(kDa)/pI	Observed Mw(kDa)/pI	MOWSE Score
P11766	ADH5	Alcohol dehydrogenase class 3	-1.56	24.1	8 (32)	39.7/7.5	39.3/7.9	5.5x10 ⁵
Q15056	EIF4H	Eukaryotic translation initiation factor 4H	-1.65	43.5	9 (21)	27.4/6.7	25.3/7.8	1.2x10 ⁴
P58546	MTPN	Myotrophin	-1.68	60.2	7 (16)	12.9/5.3	10.0/5.0	2.7x10 ²
P11177	PDHB	Pyruvate dehydrogenase E1 component subunit beta, mitochondrial precursor	-1.7	29.2	8 (11)	39.2/6.2	36.6/5.6	1.4x10 ⁴
Q16658	FSCN1	Fascin	-2.69	9.6	4 (6)	54.5/6.8	53.6/7.2	4.4x10 ²
O60701	UGDH	UDP-glucose 6-dehydrogenase	-1.9	55.5	25 (35)	55.0/6.7	56.2/7.2	3.8x10 ¹⁰
P53582	METAP1	Methionine aminopeptidase 1	-2.36	23.6	5 (9)	43.2/6.8	45.2/7.0	3.0x10 ³

Table 1: List of differentially-expressed proteins identified by MALDI-TOF MS.



(Supplemental Figure 1): Bar graph illustration of fold-changes for each of the differentially-expressed proteins identified from PB-treated and control samples. The y-axis is given in Arbitrary Units (AU) from the densitometry analysis, and error is reflected as standard error measurement (SEM) for n=5 replicates. Orange bars represent control samples, and grey bars are from PB-treated cultures.