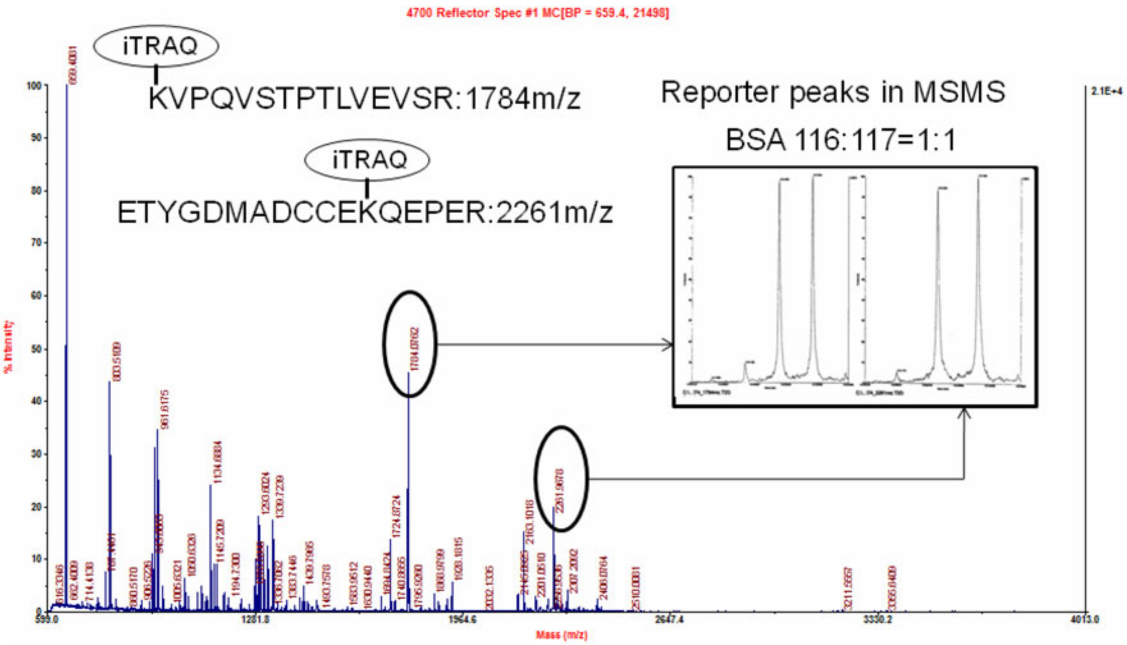

SUPPLEMENTARY FIG. 1. Representative precursor peak of BSA labeled with iTRAQ in MS.

SUPPLEMENTARY TABLE S1. CARBONYLATED PROTEINS DETECTED IN YEAST SAMPLES

N	*Accession*	*Name*	*Cov (%)*	*115:114*	*116:114*	*117:114*	*# of unique peptides (99% confidence)*	*Sequence*	*Modifications*
1	P02994 | EF1A_YEAST	Elongation factor 1-alpha	36.9	0.688	0.403	0.311	15	AFSEYPPLGRF	iTRAQ4plex(S)@3
								AFSEYPPLGRFA	
								AIDAIEQPSRPTDKPLRLPLQD	iTRAQ4plex(K)@14
								AIDAIEQPSRPTDKPLRLPLQDVY	iTRAQ4plex(K)@14
								AIDAIEQPSRPTDKPLRLPLQDVYK	iTRAQ4plex(K)@14; iTRAQ4plex(K)@25
								ATTNAPWYKGWE	iTRAQ4plex(K)@9
								ATTNAPWYKGWEKE	iTRAQ4plex(K)@9; iTRAQ4plex(K)@13
								HALLAFTLGVRQLIVAVNKMDSVKWDE	iTRAQ4plex(K)@19; iTRAQ4plex(K)@24
								LGKGSFKYAWVLD	iTRAQ4plex(K)@3; iTRAQ4plex(K)@7
								LGKGSFKYAWVLDKLKAERE	iTRAQ4plex(K)@3; iTRAQ4plex(K)@7; iTRAQ4plex(K)@14; iTRAQ4plex(K)@16
								RGITIDIALWKFE	Methyl(L)@9; FormaldehydeAdduct(W)@10; No iTRAQ4plex(K)@11; Oxidation(F)@12
								TSNFIKKVGYNPKTVPFVPISGWNGDNMIE	iTRAQ4plex(K)@6; iTRAQ4plex(K)@7; iTRAQ4plex(K)@13
								TTNAPWYKGWE	Carbamyl@N-term; iTRAQ4plex(K)@8
								TTNAPWYKGWEKE	Carbamyl@N-term; iTRAQ4plex(K)@8; iTRAQ4plex(K)@12
								VYKIGGIGTVPVGRVE	iTRAQ4plex(K)@3
2	P00925 | ENO2_YEAST	Enolase 2	25.2	1.555	1.633	2.215	5	AWSHFFKTAGIQIVADDLTVTNPARIATAIE	iTRAQ4plex(K)@7
								DTFIADLVVGLRTGQIKTGAPARSE	iTRAQ4plex(K)@17
								FFKDGKYDLDFKNPE	iTRAQ4plex(K)@3; iTRAQ4plex(K)@6; iTRAQ4plex(K)@12
								RLAKLNQLLRIEEE	iTRAQ4plex(K)@4
								SIKAAQDSFAANWGVMVSHRSGETE	iTRAQ4plex(K)@3
3	P10592 | HSP72_YEAST	Heat shock protein SSA2	12.1	1.227	1.324	1.578	7	AEKFKEEDEKE	iTRAQ4plex(K)@3; iTRAQ4plex(K)@5; iTRAQ4plex(K)@10
								LSGIPPAPRGVPQIE	
								LSGIPPAPRGVPQIE	Methyl(L)@1
								SIAYSLKNTISE	iTRAQ4plex(K)@7
								TIAWLDSNTTATKEE	iTRAQ4plex(K)@13
								TIAWLDSNTTATKEEFDDQLKE	iTRAQ4plex(K)@13; iTRAQ4plex(K)@21
								VANPIMSKLYQAGGAPE	iTRAQ4plex(K)@8

4	P34760 | TSA1_YEAST	Peroxiredoxin TSA1	21.4	0.388	0.327	0.329	5	GGLGPINIPLLADTNHSLSRD	
								GGLGPINIPLLADTNHSLSRDYGVLIEEE	
								YSLLAWTNIPRKE	iTRAQ4plex(K)@12
								YSLLAWTNIPRKE	Oxidation(W)@6; iTRAQ4plex(K)@12
								YSLLAWTNIPRKE	Dioxidation(W)@6; iTRAQ4plex(K)@12
5	P22803 | TRX2_YEAST	Thioredoxin II	64.4	2.37	2.278	2.088	4	KFAEQYSDAAFYKLDVDE	iTRAQ4plex(K)@1; iTRAQ4plex(K)@13
								QYSDAAFYKLDVDE	iTRAQ4plex(K)@9
								VSSMPTLIFYKGGKE	iTRAQ4plex(K)@11; iTRAQ4plex(K)@14
								VTRVVGANPAAIKQAIASNV	iTRAQ4plex(K)@13
6	P00549 | KPYK1_YEAST	Pyruvate kinase 1	22	1.132	1.169	1.322	7	DLRFGVK	iTRAQ4plex(K)@7
								IRTGTTTNDVDYPIPPNHE	
								KEPVSDWTDDVEARINFGIE	iTRAQ4plex(K)@1
								KEPVSDWTDDVEARINFGIEKAKE	iTRAQ4plex(K)@1; iTRAQ4plex(K)@21; iTRAQ4plex(K)@23
								LDTKGPEIRTGTTTNDVDYPIPPNHE	iTRAQ4plex(T)@3; iTRAQ4plex(K)@4
								LYPGRPLAIALDTKGPE	iTRAQ4plex(K)@14
								TGTTTNDVDYPIPPNHE	iTRAQ4plex(T)@5
7	P00950 | PMG1_YEAST	Phosphoglycerate mutase 1	30.8	0.841	0.489	0.577	4	KADRLWIPVNRSWRLNE	iTRAQ4plex(K)@1
								KKVYPDVLYTSKLSRAIQTANIALE	iTRAQ4plex(K)@1; iTRAQ4plex(K)@2; iTRAQ4plex(K)@12
								KNLFTGWVDVKLSAKGQQE	iTRAQ4plex(K)@1; iTRAQ4plex(K)@11; iTRAQ4plex(K)@15
								PKLVLVRHGQSEWNE	Protein Terminal iTRAQ4plex@N-term; iTRAQ4plex(K)@2
8	P06169 | PDC1_YEAST	Pyruvate decarboxylase isozyme 1	11.5	0.963	0.578	0.466	4	IQGWDHLSLLPTFGAKDYE	iTRAQ4plex(K)@16
								KLIHGPKAQYNE	iTRAQ4plex(K)@1; iTRAQ4plex(K)@7
								QHPRYGGVYVGTLSKPE	iTRAQ4plex(K)@15
								WDKLTQDKSFNDNSKIR	iTRAQ4plex(K)@3; iTRAQ4plex(K)@8; iTRAQ4plex(K)@15
9	P07284 | SYSC_YEAST	Seryl-tRNA synthetase,	3	2.133	2.454	3.142	1	IISDYKDWVKTRFE	iTRAQ4plex(K)@6; iTRAQ4plex(K)@10

(*Continued*)

Supplementary Table S1. Continued

N	*Accession*	*Name*	*Cov (%)*	*115:114*	*116:114*	*117:114*	*# of unique peptides (99% confidence)*	*Sequence*	*Modifications*
10	P00359 | G3P3_YEAST	Glyceraldehyde-3-phosphate dehydrogenase 3	7.5	0.844	0.849	0.883	2	RDPANLPWGSSNVDIAIDSTGVFKE	iTRAQ4plex(K)@24
								RDPANLPWGSSNVDIAIDSTGVFKE	Deamidated(N)@12; iTRAQ4plex(K)@24
11	P00815 | HIS2_YEAST	Histidine biosynthesis trifunctional protein	1.6	0.923	0.815	0.861	1	QLNVPKERVVVEE	iTRAQ4plex(K)@6
12	Q02642 | NACB1_YEAST	Nascent polypeptide-associated complex subunit beta-1	19.7	0.949	0.548	0.764	2	KNLQDLFPGIISQLGPE	iTRAQ4plex(K)@1
								VFRSAGGNYVVFGE	
13	P00560 | PGK_YEAST	Phosphoglycerate kinase	37.3	0.584	0.41	0.485	8	AFGTAHRAHSSMVGFDLPQRAAGFLLE	
								HHPRYVVLASHLGRPNGERNE	
								LKYFGKALE	iTRAQ4plex(K)@2; iTRAQ4plex(K)@6
								LQSLLGKDVTFLNDCVGPEVE	iTRAQ4plex(K)@7; No Carbamidomethyl(C)@15
								NLRYHIEEE	
								NPTRPFLAILGGAKVAD	iTRAQ4plex(K)@14
								SRKLFAATVAKAKTIVWNGPPGVFE	iTRAQ4plex(K)@3; iTRAQ4plex(K)@11; iTRAQ4plex(K)@13
								VVLPVDFIIADAFSADANTKTVTDKE	iTRAQ4plex(K)@20; iTRAQ4plex(K)@25
14	P00330 | ADH1_YEAST	Alcohol dehydrogenase 1	15.5	0.926	0.465	0.252	3	ALDFFARGLVKSPIKVVGLSTLPE	iTRAQ4plex(K)@11; iTRAQ4plex(K)@15
								KGQIVGRYVVDTSK	iTRAQ4plex(K)@1; iTRAQ4plex(K)@14
								LFRSIGGEVFIDFTKE	iTRAQ4plex(K)@15
15	P16474 | GRP78_YEAST	78 kDa glucose-regulated protein homolog precursor	4	2.224	2.155	2.288	2	LTGIPPAPRGVPQIE	
								TAIAEDFDEKFE	iTRAQ4plex(K)@10
16	P14540 | ALF_YEAST	Fructose-bisphosphate aldolase	5	1.227	1.143	1.786	1	EKPLFLVFHGGSGSTVQE	iTRAQ4plex(K)@2
17	P12398 | HSP77_YEAST	Heat shock protein SSC1, mitochondrial precursor	3	1.911	2.009	1.51	1	STNGDTHLGGEDFDIYLLRE	iTRAQ4plex(T)@2; Deamidated(N)@3

18	P17967 | PDI_YEAST	Protein disulfide-isomerase precursor	3.6	2.79	1.213	0.628	1	SVVYQGSRSLDSLFDFIKE	iTRAQ4plex(K)@18
19	P05749 | RL22A_YEAST	60S ribosomal protein	32.2	0.779	0.529	0.281	2	NGVFDPASYAKYLIDHIKVE	iTRAQ4plex(K)@11; iTRAQ4plex(K)@18
								YRLAFYQVTPEEDEEEDEE	

20	P10591 | HSP71_YEAST	Heat-shock protein SSA1	9.3	0.674	0.686	0.649	5	AEKFKEEDEKE	iTRAQ4plex(K)@3;
									iTRAQ4plex(K)@5;
									iTRAQ4plex(K)@10

								LSGIPPAPRGVPQIE	
								SIAYSLKNTISE	iTRAQ4plex(K)@7
								TISWLDSNTTASKEE	iTRAQ4plex(K)@13

								TISWLDSNTTASKEEFDDKLKE	iTRAQ4plex(K)@13;
									iTRAQ4plex(K)@19;
									iTRAQ4plex(K)@21

21	P32589 | HSP7F_YEAST	Heat-shock protein homolog SSE1	4.8	0.96	0.785	0.793	2	GFDSIKAKYIAKYEE	iTRAQ4plex(K)@6;
									iTRAQ4plex(K)@8;
									iTRAQ4plex(K)@12

								LASLGNIIRGRYLAKEEE	iTRAQ4plex(K)@15

22	P25294 | SIS1_YEAST	Protein SIS1	12.8	2.301	1.424	2.746	2	DLFVGKKKSFKIGRKGPHGASE	iTRAQ4plex(K)@6;
									iTRAQ4plex(K)@7;
									iTRAQ4plex(K)@8;
									iTRAQ4plex(K)@11;
									iTRAQ4plex(K)@15

								KSHPNFKRDGDDLIYTLPLSFKE	iTRAQ4plex(K)@1;
									iTRAQ4plex(K)@7;
									iTRAQ4plex(K)@22

23	P46672 | G4P1_YEAST	GU4 nucleic-binding protein 1	3.7	0.624	0.354	0.346	1	SLIISKYPVSFTKE	iTRAQ4plex(K)@6; iTRAQ4plex(K)@13
24	P16140 | VATB_YEAST	Vacuolar ATP synthase subunit B	2.9	0.583	0.349	0.095	1	SLDQAWSLLRIYPKE	iTRAQ4plex(K)@14
25	P11076 | ARF1_YEAST	ADP-ribosylation factor 1	9.4	0.556	0.293	0.218	1	LRNAAWLVFANKQDLPE	iTRAQ4plex(K)@12

26	Q3E841 | YN034_YEAST	Uncharacterized protein YNR034W-A	27.6	1.109	0.184	0.806	1	DAQYIGHAFKKAGHFIVYFTPKNKNRE	Deamidated(Q)@3;
									iTRAQ4plex(K)@10;
									iTRAQ4plex(K)@11;
									iTRAQ4plex(K)@22;
									iTRAQ4plex(K)@24

27	P32911 | SUI1_YEAST	Eukaryotic translation initiation factor eIF-1	16.7	0.568	0.316	0.19	1	FMISQLGLQKKNIKIHGF	iTRAQ4plex(K)@10;
									iTRAQ4plex(K)@11;
									iTRAQ4plex(K)@14

28	Q12074 | SPEE_YEAST	Spermidine synthase	4.4				1	ITHPTIVDGWFRE	
29	P38013 | AHP1_YEAST	Peroxiredoxin type-2	10.2				1	LAVGDGVYWSGRWAMVVE	
30	P32324 | EF2_YEAST	Elongation factor 2	3.3				2	DLYQTFARTVE	
31	Q01560 | NOP3_YEAST	Nucleolar protein 3	4.1				1	LSNTRLFVRPFPLDVQE	

Supplementary Table S2. Functional and Pathway Analysis of Identified Proteins

#	*Gene*	*Mw (Da)*	*PI*	*Molecules/cell*	*Function**	*Localization***	*Pathway*	*Cofactor*
1	TEF2/TEF1	50,032	9.72	450/377	4	C	translation_elongation of peptide synthesis	
2	ENO2/ENO1	46,914/46,816	5.88/6.6	2,610/76,700	1	C	glycolysis	magnesium
3	SSA2	69,469	4.77	364,000	3,5	W,C,N		
4	TSA1	21,590	4.87	378,000	3	C, PC		
5	TRX2	11,204	4.62	17,200	3	C,N		
6	CDC19	54,544	7.66	291,000	1	C	glycolysis	magnesium, potassium
7	GPM1	27,608	9.65	172,000	1	C	glycolysis	
8	PDC1	61,495	6.12	8,970	1	C,N, A		thiamine pyrophosphate, Mg^{2+}
9	SES1	53,309	5.98		4	C		
10	TDH3	35,746	6.96	169,000	1	C,N	glycolysis	
11	HIS4	87,721	5.04	521	1	C	histidine biosynthesis	
12	EGD1	17,020	6.53	18,000	2	C,N		
13	PGK1	44,738	7.77	314,000	1	C,N	gluconeogenesis,glycolysis	
14	ADH1	36,849	6.66		1	C		zinc
15	KAR2	74,467	4.62	337,000	3,5	ER,A		
16	FBA1	39,620	5.65	1,020,000	1	C	glycolysis	zinc
17	SSC1	70,627	5.34		3	M		
18	PDI1	58,227	4.22		3	C,ER, V		
19	RPL22A	13,693	6.01	60,400	4	C		
20	SSA1	69,657	4.82	269,000	3,5	C,N		
21	SSE1	77,366	4.97	71,700	3	C		
22	SIS1	37,590	9.86	20,300	3	C,N		
23	ARC1	42,084	8.01	57,700	2	C		
24	VMA2	57,749	4.79	131,000	5	V		
25	ARF1	20,529	7.46	19,300	5	G, PC		
26	YNR034W-A	10,781	9.79	2,820	6	C		
27	SUI1	12,312	8.1		4	C		
28	SPE3	33,324	5.33		1	C,N,M	polyamine biosynthesis	
29	AHP1	19,115	4.87	16,200	3	C,N,P	protection against oxidizing agents	Thioredoxin
30	EFT1/EFT2	93,288	6.25	82,700/78,100	4	C	elongation of peptide synthesis	
31	NPL3	45,407	5.35	78,700	2	N	Npl3/Mtr10p nuclear import pathway	

*1: metabolism, 2: transcription, 3: cell defense and protein folding, 4: protein synthesis, 5: cell transport, 6: others and unknown.

**A: Ambiguous, C: Cytoplasm, N: Nucleus, ER: Endoplasmic Reticulum, M: Mitochondria, P: Peroxisome, W: Cell wall PC: Punctate composite, G: Golgi, V: Vacuole.