**INVESTIGATING THE ROLE OF RESPIRATION IN PLANT SALINITY
TOLERANCE BY ANALYSING MITOCHONDRIAL PROTEOMES FROM WHEAT
AND A SALINITY TOLERANT AMPHIPLOID (WHEAT × LOPHOPYRUM
ELONGATUM).**

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Running title: Wheat mitochondrial proteomics and salinity tolerance.

Keywords: Mitochondria, Respiration, Salinity, Wheat, MnSOD, Proteomics, 2D-DIGE, Mass
spectrometry, *De novo* sequencing, Beta-cyanoalanine synthase.

ABSTRACT

The effect of salinity on mitochondrial properties was investigated by comparing the reference wheat variety Chinese Spring (CS) to a salt tolerant amphiploid (AMP). The octoploid AMP genotype was previously generated by combining hexaploid bread wheat (CS) with the diploid wild wheatgrass adapted to salt marshes, *Lophopyrum elongatum*. Here we used a combination of physiological, biochemical and proteomic analyses to explore the mitochondrial and respiratory response to salinity in these two genotypes. The AMP showed greater growth tolerance to salinity treatments and altered respiration rate in both roots and shoots. A proteomic workflow of 2D-DIGE and MALDI TOF/TOF mass spectrometry was used to compare the protein composition of isolated mitochondrial samples from roots and shoots of both genotypes, following control or salt treatment. A large set of mitochondrial proteins were identified as responsive to salinity in both genotypes, notably enzymes involved in detoxification of reactive oxygen species. Genotypic differences in mitochondrial composition were also identified, with AMP exhibiting a higher abundance of manganese superoxide dismutase, serine hydroxymethyltransferase, aconitase, malate dehydrogenase and beta-cyanoalanine synthase compared to CS. We present peptide fragmentation spectra derived from some of these AMP-specific protein spots, which could serve as biomarkers to track superior protein variants.

INTRODUCTION

There are strong links between respiratory function and plant salinity tolerance, illustrated both by comparative studies in a range of plant species¹, and by higher salt tolerance conferred through transgenic manipulation of respiratory gene expression²⁻⁷. Mechanistically, several mitochondrial processes contribute to salinity tolerance. For instance, a plant's capacity to exclude Na⁺ ions is strongly linked to its rate of root respiration^{8, 9}, due to the energetic costs associated with actively transporting Na⁺ and Cl⁻ ions against concentration gradients^{10, 11}. Mitochondrial metabolism also plays a role in regulating the accumulation of osmolytes, such as GABA, proline and glycine betaine¹²⁻¹⁴ and the portion of fixed carbon that is allocated to respiration is a key determinant of whole-plant carbon balance under salinity^{15, 16}. Furthermore, the high abundance of mitochondrial ROS defences can be linked to salinity tolerance^{17, 18}, presumably by limiting the extent of ROS-induced damage to mitochondrial components, and perhaps by modulating mitochondrial ROS signalling¹. The deleterious impact of salinity on plant growth is well characterised, and there is a substantial physiological understanding of how plants deploy strategies to cope with the stress¹⁹. However, breeding approaches to incorporate higher salt tolerance into commercially relevant crop varieties have proved difficult^{20, 21}. Some authors argue that future efforts to breed or engineer salinity tolerance into elite crop varieties will require a mechanistic understanding of salinity stress at the molecular and cellular level²⁰. Also, molecular analyses of tolerant genotypes could discover superior alleles of genes linked to salinity tolerance, which can then be targeted in crop breeding programs²².

Comparative studies between tolerant versus sensitive plants are a well described approach in the salinity literature. In a breeding context, these comparisons are framed as gene discovery approaches, which aim to identify the genes and physiological mechanisms that are specifically

present in the tolerant plants but absent in the sensitive lines. These favourable alleles can subsequently be incorporated into elite agronomic lines through marker-assisted selection²³, or genetic transformation²⁴. Compared to other crop species, wheat is well suited to comparative experiments aiming to identify novel sources of salinity tolerance, due to the large number of salt-tolerant wild species that are closely related to wheat²⁵. One such relative is tall wheatgrass (taxonomic names: *Lophopyrum elongatum*, *Thopyrum elongatum*, *Elytrigia elongate*, *Agropyron elongatum*, *Agropyron rigidum*, *Elymus elognatus*, *Triticum rigidum*). This species is defined as salt tolerant both from its ecological location in salt marshes around the Mediterranean sea²⁶, as well as laboratory studies showing that it displays few visible signs of salt-induced injury under high NaCl treatments compared to other Triticeae species²⁷. The diploid tall wheatgrass genome ($2n \times 7 = 14$) is orthologous to the three genomes of wheat ($3 \times 2n \times 7 = 42$)²⁸. This genetic similarity was exploited to create an amphiploid containing the entire tall wheatgrass genome alongside the entire genome of the model wheat variety Chinese Spring ($4 \times 2n \times 7 = 56$)²⁹. This amphiploid (AMP) successfully combines much of the salinity tolerance observed in tall wheatgrass, with several of the agronomic characteristics of wheat, such as yield and grain size³⁰. Subsequently, AMP has become a widely used plant for investigating the specific traits that underpin its salt tolerance. Experiments have shown that AMP deploys a Na^+ exclusion strategy^{30, 31}, and that it uses a dramatically different osmotic strategy to CS, by accumulating less Na^+ but more glycine betaine in young leaves³². This tolerance was shown to be mediated through the synergistic action of all tall wheatgrass chromosomes, because adding any single chromosome in isolation did not substantially boost tolerance, but adding the entire genome does³⁰. This adds weight to the assertion that due to the complexity of the physiochemical impact of salt on plants, engineering plants for robust salt

tolerance in the field will require the introduction of large networks of interacting genes, rather than one single gene added in isolation³³.

Comparative proteomic investigations of salinity responses have been used to dissect the molecular effects of salt stress and also to analyse molecular differences between tolerant and sensitive lines. Such comparisons have investigated commercial crop varieties^{34, 35}, closely related wild species adapted to saline environments³⁶, and somatic hybrids that incorporate genetic material from closely related wild species^{37, 38}. Typically these investigations have compared the protein profiles of whole-cell extracts, which have identified that some highly abundant mitochondrial proteins exhibit differential abundance following salt treatment^{34, 38}. However, the limited dynamic range of proteomic techniques, as well as the relatively low abundance of mitochondria compared to other cellular compartments, means that only a very small fraction of mitochondrial proteins were sufficiently abundant to be profiled in these whole-cell studies. In contrast, comparisons between enriched mitochondrial fractions isolated from different wheat varieties and following stress treatments can provide a deeper understanding of the compositional differences within this organelle¹⁸.

Here we analyse the mitochondrial role in salinity tolerance by comparing the salinity responses of bread wheat (CS) against a wheat $\times$ *Lophopyrum elongatum* amphiploid (AMP). This work combines physiology and biochemistry respiratory data with a proteomics comparison of mitochondrial protein abundance between CS and AMP in order to better characterise the molecular mechanisms that could contribute to the higher salinity tolerance of AMP.

EXPERIMENTAL PROCEDURES

Plant growth

Plants were grown in a controlled environment growth cabinet (Conviron) using an unsupported hydroponic system where the roots were flooded and drained every 30 min, modified from the designs of Munns et al.³⁹ and Genc et al.⁴⁰. Seeds were sterilised by incubating in 5% (v/v) bleach 0.1% (v/v) Tween-20 for 2 min, before being thoroughly rinsed and germinated in the hydroponic system. Nutrient concentrations were: 5 mM $\text{Ca}(\text{NO}_3)_2$, 1 mM KH_2PO_4 , 1 mM MgSO_4 , 1 mM NH_4NO_3 , 100 μM Fe-EDTA, 50 μM KCl, 25 μM H_3BO_3 , 2 μM MnSO_4 , 2 μM ZnSO_4 , 500 nM CuSO_4 , 500 nM MoO_4 . Light intensity was 500 $\mu\text{mol m}^{-2} \text{s}^{-1}$, and humidity was 65%. Photoperiod was 12 h for plants grown for physiological experiments in order to mimic environmental conditions at the sowing date of most wheats, whereas 16 h photoperiod was chosen for plants grown for mitochondrial isolation in order to facilitate rapid growth of tissue. Day temperature was 28° C, night temperature was 22° C. Salt treatment was imposed by applying 50 mM NaCl on days one, two, three and four after sowing, and the NaCl concentration remained at 200 mM until harvest. Nutrient solutions were changed once weekly. For biomass measurements, plants were harvested after seven weeks growth. Shoots were separated from roots and both were thoroughly rinsed in ddH₂O, then tissue was dried at 65° C for four days and weighed.

Photosynthetic, transpirational and respiratory measurements of intact tissue

Photosynthesis measurements were recorded using an open gas exchange system with IRGA head (Licor) within four hours of the middle of the light period. Measurements of A, E, g_s and C_i were taken with chamber settings of 400 ppm CO_2 , PAR 500 and ~60% humidity, block temperature 28° C. Measurements of V_{cmax} , J_{max} and CO_2 compensation point were calculated by analysing A- C_i curves recorded at 1500 PAR according to the method of Farquhar et al.⁴¹, curves were fitted using the kinetic parameters of Bernacchi et al.⁴². Respiration measurements were recorded within four hours of the middle of the light period using an oxygen electrode (Hansatech) and an IRGA (Licor). For shoots, single leaves were excised from plants, and divided into two pieces, each 6-8 cm² in area. One section was immediately sealed into the IRGA chamber (23° C, 0 PAR, 65% RH) where CO_2 efflux was logged every minute for 30 min, with CO_2 efflux rate calculated as the average rate over the period 20-30 min after tissue harvest. The other section of the leaf was incubated in respiration buffer (10 mM TES, 5 mM $MgSO_4$, 10 mM NaCl, pH 7.2) for 15 min in darkness, then placed into the reaction vessel where O_2 consumption was measured in 2 ml respiration buffer for 15 minutes, with O_2 consumption rate calculated as the average rate over the period 20-30 min after tissue harvest. For roots, ~60 mg of root tissue was chopped into five millimetre sections and incubated in respiration buffer (as above) for ~15 min in darkness, then placed into the reaction vessel where O_2 consumption was measured in 2 ml respiration buffer for 15 min. Where inhibitors were used, they were added 15 min after the start of measurement, which then proceeded for another 15 min. Inhibitor concentrations were 1 mM KCN and 20 mM SHAM for shoots and 0.5 mM KCN and 10 mM SHAM for roots, according to the method of Lambers et al.⁴³.

Mitochondrial isolation and respiration measurements of isolated mitochondria

Shoot mitochondria were isolated using a procedure identical to Jacoby et al.¹⁸, based on the method of Day et al.⁴⁴. The isolation procedure for root mitochondria was the same, except that the first centrifugation step was conducted at 2500× g and only two density gradients were employed (28% Percoll, 0-4.4% PVP-40). Isolated mitochondrial respiration rates were recorded using an oxygen electrode (Hansatech). Mitochondria (50-100 µg protein) were added to respiration buffer (300 mM sucrose, 10 mM KH₂PO₄, 5 mM MgSO₄, 10 mM NaCl, 0.1% BSA) at 25° C, 1 mM NADH and 5 mM succinate were used as respiratory substrates, in the presence of 500 µM ATP to activate succinate dehydrogenase. State 3 respiration rates were attained by adding 200 µM ADP. Following measurement of state 3 rate, AOX capacity was assessed by inhibiting COX with 1 mM KCN and stimulating AOX with 10 mM pyruvate and 5 mM DTT.

2D-DIGE

For quantitative proteomics on shoot mitochondrial samples, 50 µg of protein was precipitated with 100% acetone at -20° C overnight, then centrifuged at 20,000 g for 20 min, and this pellet was rinsed twice with 100% acetone. For root mitochondrial samples, we found that acetone precipitation alone was incompatible with IEF separation, and hence refined our methods to include a TCA precipitation, such that 50 µg of protein was precipitated overnight with 10% (w/v) TCA at 4° C, then centrifuged at 20,000 g for 20 min, and this pellet was rinsed once with 10% (w/v) TCA, then twice with 100% acetone. Following protein precipitation, 2D-DIGE was conducted with all labelling, separation and scanning techniques identical to Jacoby et al.¹⁸. Gel images were statistically analysed using the DeCyder program (v6, GE Healthcare), with Cy3 and Cy5 images normalised to Cy2-labelled internal standard, which contained a pooled mixture

of all samples undergoing comparison. Protein spots were deemed statistically significant if they exhibited p-value <0.05 for G, T, or G×T effects following two-way ANOVA comparison. For each experimental grouping, three independently prepared biological replicates were analysed.

Peptide mass spectrometry, database searching and de novo sequencing

For identification of protein spots deemed as significantly different from analysis of the DIGE images, spots were excised from preparative gels (500 µg protein loading) where the three biological replicates for each sample in the quantitative experiment were pooled, and identified using an Ultraflex III MALDI TOF/TOF (Bruker Daltonics) according to the method of Li et al.⁴⁵. Briefly, gel-bound proteins were excised, destained and digested with trypsin, before proteolytic peptides were extracted from gel spots and dried down in a vacuum centrifuge. Dried peptides were then resuspended in 5% ACN, 0.1% TFA, and transferred onto a steel plate. When evaporation had reduced the sample volume to around 1 µl, 1 µl of saturated HCCA matrix diluted in 90% ACN was added, and the spot left to dry completely, before being briefly washed with 10 mM $\text{NH}_4\text{H}_2\text{PO}_4$ + 0.1% TFA at 4° C, then left to dry once again. Tandem mass spectra were then acquired from spots using a MALDI-TOF/TOF (Bruker Daltonics) and Flex Control software v3.3 (Bruker Daltonics, with 600 laser shots fired to acquire the MS spectrum (~30% laser power), and the 10 most intense precursor ions then selected for MS/MS analysis via 1800 laser shots using LIFTTM method to detect the fragmentation spectra of the targeted precursors (~33% laser power). Tandem mass spectra were searched against the wheat TC database (DFCI release 12; 221,925 sequences)⁴⁶ as well as the wheat EST database (1,282,166 sequences,

accessed July 2012)⁴⁷ using Mascot version 2.2.03⁴⁸, with precursor ion tolerance ± 1.2 Da, variable modifications oxidation (M), and carbamidomethyl (C), with one allowed missed cleavage and a product ion tolerance ± 0.6 Da. For the TC database, peptide fragmentation spectra with ions scores above 49 were considered to be statistically significant matches ($p < 0.05$); for the EST database, this threshold was an ions score of 56.

For deeper investigation of protein spots specific to AMP, these spots were excised from gels and digested with trypsin and then analysed using Agilent 6510 Q-TOF mass spectrometer with an HPLC Chip Cube source controlled by MassHunter Workstation Data Acquisition for Q-TOF (ver B.01.04), Agilent Technologies) according to the method of Taylor et al.⁴⁹, exploiting the more comprehensive coverage obtained from online LC separation of peptides. MS/MS spectra were extracted using MassHunter Workstation Qualitative Analysis (ver B.01.04), Agilent Technologies) were matched against the both the wheat TC database (DFCI release 12, 221,925 sequences)⁴⁶ and the wheat EST database (1,282,166 sequences, accessed July 2012)⁴⁷ using the same parameters detailed above. For the TC database, peptide fragmentation spectra with ions scores above 53 were considered to be statically significant matches ($p < 0.05$); for the EST database, this threshold was an ions score of 59. Protein hits were deemed significant if the protein score derived from summation of ions scores of all matched peptides were above these thresholds. Unmatched spectra were then re-searched with variable modifications now including oxidation (W) and phosphorylation (S, T, Y). Spectra which were still unmatched following this second round of searching were then ranked for spectral quality using the Scanranker program⁵⁰, with spectra attributed a score higher than 0.25 retained for further analysis. To determine whether high quality unmatched spectra were specific to AMP, spectral data from unmatched

AMP protein spots with Scanranker score exceeding 0.25 were manually compared to data from CS spots that matched to the same protein. From this process, any high-scoring unmatched spectra which were deemed to be present in the spots excised from AMP gels but absent in the spots excised from CS gels were then submitted to *de novo* sequencing with PEAKS software⁵¹. *De novo* peptide sequence assignments were considered significant above a confidence threshold of 60% assigned by PEAKS scoring criteria. Output peptide sequences from PEAKS were then homology searched via MS-BLAST⁵² in order to refine outputs from *de novo* sequencing (ie: I/L and K/Q miss assignments). Refined *de novo* peptide sequences were then aligned against the wheat TC that matched the protein spot, and this sequence was aligned against homologous sequences from a range of species (*Oryza sativa*, *Arabidopsis thaliana*, *Brachypodium distachyon*, *Physcomitrella patens*, *Chlamydomonas reinhardtii*).

Immunoblotting

Mitochondrial samples isolated from shoot and root tissue were precipitated as described above. Proteins were then separated via Criterion AnyKD SDS-PAGE (Bio-Rad), and transferred to nitrocellulose membranes by standard procedures. Membranes were blocked overnight at 4° C with 1% blocking solution (Amersham), incubated with anti-AOX antibody⁵³ (1:5000) for 1 h at RT, then with POD-labelled anti-rabbit secondary antibody (1:20000) for 1 h at RT. Chemiluminescence was visualized using an Amersham ImageQuant RT-ECL camera (GE Healthcare) and band intensity quantified using Amersham Image-Quant TLTM software (GE Healthcare).

RESULTS AND DISCUSSION

Growth, physiological and biochemical comparisons of salinity responses between CS and AMP

To assess the whole-plant impact of the salinity treatment on hydroponically grown CS and AMP plants, biomass accumulation and the rates of several physiological processes were measured in seven-week old plants where the salt treated plants had undergone long-term 200 mM NaCl treatment (Table 1). The impact of the 200 mM NaCl treatment is illustrated by the dramatically lower percentage of shoot biomass elicited by salt treatment in both genotypes when expressed as $(\text{shoot biomass [salt]} \div \text{shoot biomass [control]} \times 100)$. This calculation showed that CS retained 28% of shoot biomass under salinity, whereas AMP retained 39% (data from Table 1). The lower magnitude of the salt-induced reduction in shoot biomass is indicative of the higher salt tolerance in AMP, and is corroborated by its maintenance of baseline leaf elongation rates under salinity stress (Table 1). Statistically, root biomass, shoot biomass and leaf elongation rate all exhibited statistically significant genotype x treatment (G×T) interactions according to ANOVA tests. This shows that the growth response of AMP to salinity is fundamentally different to that of CS. However, the slow growth rate of AMP under control treatment indicates that the presence of wild genetic material within this genotype confers a significant growth penalty which probably renders this broad transfer of genetic material poorly suited to an agronomic context²⁵. The photosynthetic responses to salinity revealed no significant differences in the net rate of CO₂ assimilation between control and salinity treatments. However, the slower growing AMP did display higher photosynthetic rates compared to CS, reiterating results of previous studies where photosynthetic rate alone was found to be a poor proxy for growth rate

between genotypes⁵⁴. Analysis of A-C_i curves revealed that salinity treatment induced a higher CO₂ compensation point, which could be indicative of higher photorespiratory rates⁵⁵. Interestingly, V_{cmax} and J_{max} were in fact higher under salt treatment in both genotypes, showing that the salinity treatment did not diminish the biochemical efficiency of the photosynthetic apparatus when supplied with saturating substrate. It has been documented that NaCl treated plants can display higher density of chloroplasts per unit leaf area, but dramatically lower leaf area per plant. This combination makes maximum photosynthetic rate a poor proxy for growth rate⁵⁶. Reduced growth under salt treatment is likely to involve transpirational limitation of water flux, as stomatal conductance was dramatically decreased by NaCl treatment, with the reduction being highly significant by ANOVA in both genotypes (Table 1). Although ANOVA tests did not reveal significant genotype effects on stomatal conductance (p=0.055), AMP leaves exhibited higher conductance values under salinity treatment compared to CS, deemed significant by Student's t-test (p<0.01). Thus, it can be suggested that the tolerance of AMP could relate to superior osmotic adjustment compared to CS, which fits with a previous report that stomatal conductance under salinity stress is a good proxy for genotypic salinity tolerance⁵⁶.

Respiratory responses to salinity in CS and AMP

In order to determine the impact of salinity upon respiration rates in the two genotypes, respiratory responses to NaCl treatment were assessed in seven week old plants as well as five day old plants (Table 2). By assessing both five day old and seven week old plants, we are able to differentiate the short-term adjustments induced to cope with the onset of stress from the longer-term impacts of NaCl (Table 2). In seven week old plants, salinity induced slower rates of

respiratory O₂ consumption, perhaps linked to slower provision of substrate. Meanwhile, root respiratory oxygen consumption rates increased under salinity stress in both genotypes, probably reflecting the energetic demands of ion exclusion. Interestingly, AMP leaves exhibited higher rates of respiratory CO₂ efflux compared to CS, under both control and salt treatments. Although the relationship between respiration rate and growth rate is complex, perhaps this respiratory property is one factor that contributes to the inherently slow growth of AMP under control conditions, because the rapid expenditure of fixed carbon by fast leaf respiration would diminish the pool of sugars that can be allocated to the synthesis of new tissue⁵⁴. Respiratory measurements in young tissues revealed that five day old leaves from both genotypes exhibited dramatically higher rates of respiratory O₂ consumption under salinity treatment compared to control. Interestingly, CS increased this parameter to a greater extent than AMP (Table 2). This genotypic difference in salt-induced respiratory increases in CS corroborates the results of Kasai et al.¹⁵ in their investigation of these same two genotypes. This perhaps implies that the superior tolerance of AMP could involve judicious allocation of stored carbon reserves during the initial response to salinity. Respiratory increases under short term salt stress were less pronounced in root tissue, perhaps indicating that faster respiratory rates in older salt treated roots presented in Table 2 resulted from shifts occurring over a longer timescale.

Dissecting the respiratory response to salinity through application of inhibitors and assays of isolated mitochondria

The plant mitochondrial electron transport chain contains a classical cytochrome oxidase (COX) as well as an energetically dissipative quinol oxidase, the alternative oxidase (AOX). Insights

into potential contributions of these two respiratory oxidases to respiratory rate can be gathered by measuring rates of oxygen consumption of intact tissue in the presence of specific chemical inhibitors. Application of respiratory inhibitors KCN (inhibits COX) and SHAM (inhibits AOX) indicated that the alternative oxidase had a greater capacity in shoot tissues compared to root tissues (Table 2). To determine salinity effects upon respiratory properties without *in situ* effects such as altered substrate provision, we measured oxygen consumption rates and AOX abundance in mitochondrial samples isolated from CS and AMP plants following control and salt treatments. In terms of maximal activity (substrate + ADP), there were no significant differences between the two genotypes or according to salt treatment (Figure 1). However, mitochondria isolated from shoots of salt treated plants showed higher rates of maximal AOX activity (substrate + KCN + pyruvate + DTT), highlighting the prominence of AOX capacity in shoot mitochondria following salt treatment. This result is consistent with the body of literature that links AOX function to supporting photosynthesis in leaves under abiotic stress, shown by the impaired growth and photosynthetic performance of Arabidopsis AOX knockouts under a combination of drought and high light⁵⁷. Although accumulation of AOX protein under salinity stress has been observed across a number of species^{4, 18, 58}, the measurements in this study did not detect higher AOX activity in mitochondria isolated from salt-treated root tissues. This was shown by respiration rates in isolated mitochondria as well as intact root tissues treated with inhibitors (Figure 1; Table 2). One explanation for this difference between tissues is that the high energetic cost of ion exclusion demanded continual ATP supply in roots^{10, 11}. AOX activity does not contribute to proton pumping across the inner mitochondrial membrane, and thus does not lead to ATP synthesis, so its activity in root tissue could diminish the exclusion capacity of the plant. To further investigate the role of AOX under salinity treatment, the abundance of this

protein was assessed using immunoblotting (Figure 2), because the poor solubility of this protein in IEF buffers renders it unsuitable to analysis by 2D-DIGE⁵⁹. This showed that salinity treatment induced higher abundance of AOX protein in isolated shoot mitochondria in both genotypes, with AMP containing higher baseline abundance of the protein. Immunoblotting against AOX in isolated root mitochondrial samples gave an indication that salinity treatment induced lower abundance in this protein in CS, but the high degree of variability between biological replicates precluded confident interpretation of these data. A far longer exposure time was required for visualisation of the luminescent signal in root samples, suggesting that the baseline AOX abundance in root mitochondria was considerably lower than in shoot mitochondria.

Analysing the proteomic response of wheat mitochondria to salt stress in different genotypes.

To examine the impact of salt stress on mitochondrial composition and function, we undertook a detailed study of the proteomic response to salinity exhibited by mitochondrial samples isolated from the wheat genotypes CS (sensitive) and AMP (tolerant) via 2D-DIGE. Mitochondria isolated from shoots and roots were analysed in two independent comparisons. Following statistical analysis of 2D-DIGE images, differentially abundant proteins determined by ANOVA $p < 0.05$ for treatment (T), genotype (G) or interaction (G×T) effects were excised from preparative gels, digested with trypsin and analysed by peptide mass spectrometry using a MALDI-TOF/TOF (quantitative abundance data and top scoring protein matches summarised in Tables 3-8, representative 2D-DIGE images highlighting statistically significant mitochondrial protein differences in Figures 3 and 4, all 12 2D-DIGE images in Supplementary Figure 1, and

detailed peptide MS/MS data in Supplementary Tables 3 and 4). Significant differences according to treatment effect ($p < 0.05$) were evident in 55 mitochondrial protein spots deemed significant by the root comparison, but only 15 mitochondrial protein spots deemed significant in the shoot comparison (Tables 3-8). This could suggest that root tissue was undergoing a more severe salinity scenario due to direct physical contact between root tissue and the saline nutrient solution, or that root mitochondria are endowed with a greater flexibility at the protein level. The 2D-DIGE comparisons also identified several differentially abundant protein spots of non-mitochondrial origin between control versus salt treatments, particularly with regard to the presence of plastidic proteins within mitochondrial samples isolated from shoot tissue (Supplementary Figure 6, Supplementary Table 1). These contaminating proteins were not further investigated. The dataset enables a detailed comparison of mitochondrial protein composition between two genotypes with contrasting salinity tolerance, CS (sensitive) and AMP (tolerant). A major aim of this study was to identify proteins of higher abundance within mitochondria of the salt-tolerant AMP, as these could derive from the wild genetic background of *Lophopyrum elongatum*. The molecular functions of these proteins could contribute to the higher salt tolerance of AMP, and potentially could serve as molecular targets for breeding wheat varieties with higher salt tolerance. Highly significant genotypic effects were more numerous in the shoot mitochondrial comparison, where seven protein spots exhibited $p < 0.001$ for the G effect, compared to only four protein spots with this degree of significance in the root data set (Tables 3-8). One interpretation of this data is that genotypic differences in mitochondrial composition are more likely to be revealed in illuminated leaves, where mitochondrial function is geared towards supporting photosynthetic metabolism, although this hypothesis would need to be confirmed across a larger set of genotypes. Prominent protein spots of higher abundance in shoot

mitochondria isolated from AMP included MnSOD, beta-cyanoalanine synthase (β -CAS), malate dehydrogenase (MDH) and serine hydroxymethyltransferase (SHMT). For these particular spots, we undertook detailed interrogation of peptide mass spectrometry data derived from RP-nano-HPLC/Q-TOF MS/MS, in an attempt to characterise amino acid sequences of these proteins that were specific to AMP (Supplemental Figures 2-5).

Overall, there were a small number of significant G×T interactions across the two data sets (one in the shoot data set and two in the root data set), suggesting that the two genotypes deployed similar molecular strategies to cope with the detrimental effects of salinity stress. Other studies in the literature involving whole-tissue proteomic investigations into genotypic salinity responses have typically revealed a larger number of proteins with significant G×T interactions^{34, 60}. This suggests that compared to other cellular sub-proteomes, the mitochondrial proteome exhibits more consistency in its salinity response across genotypes. The discussion of this dataset is divided according to the molecular function of the identified proteins that exhibited significant differences in abundance according to treatment, genotype or genotype × treatment interaction ($p < 0.05$ from ANOVA).

Salinity induces changes in mitochondrial enzymes of carbon, nitrogen and phosphorous metabolism

In addition to their well established role in catabolising organic acids, mitochondria contain a suite of enzymes that can catabolise and interconvert amino acids, in order to provide energy and

supply metabolic intermediates. Several studies have defined mitochondrial metabolism as a key intersection of C/N fluxes in plant tissues^{61, 62}, and some of the mitochondrial enzymes that metabolise amino acids have been linked to salinity tolerance in the literature^{12, 13}. The data presented in Table 3 outline several components of mitochondrial C, N, and P metabolism that differ according to salt treatment, or according to genotype. It seems there is divergence in glutamate dehydrogenase (GDH) responses to salinity between root and shoot mitochondria, with salt treatment inducing higher abundance of GDH in shoots but lower abundance of this enzyme in roots (Table 3). Another mitochondrial enzyme involved in amino acid metabolism, aspartate aminotransferase (AspAT), was also lower under salinity treatment in roots (Table 3). Taken together, these data suggest that amino acid catabolism by root mitochondria proceeds at a diminished rate under salinity treatment. By contrast, GDH abundance increases in salt treated shoot mitochondria. Transgenic experiments have defined that GDH can be a key mediator of salinity tolerance, which coordinates the rebalancing of cellular nitrogen metabolism under salt stress⁶³. Furthermore, control versus stress experiments have repeatedly shown that GDH abundance can increase following salt treatment^{38, 64}. Although most of the data on GDH shows that this enzyme acts in the deaminating direction to catabolise glutamate^{65, 66}, there are some suggestions that GDH could potentially play an aminating role in illuminated leaves under photorespiratory conditions. This is driven by high NH_4^+ concentrations present in the mitochondrial matrix due to the high flux of photorespiratory glycine through the glycine decarboxylase complex (GDC)⁶⁷. These differing physiological roles of GDH between shoot and root tissues could provide a potential explanation for the divergence in GDH abundance under salinity stress. It can be posited that wheat plants may respond to salinity stress by lowering their

rates of glutamate catabolism in root tissue, but increasing their rates of 2-OG amination in shoot tissue.

The interconversion of nucleoside phosphates is a key step in fine tuning *in vivo* rates of mitochondrial metabolism⁶⁸, and the two major mitochondrial enzymes involved in metabolising nucleotide phosphates, NDPK and ADK, have been linked to stress perception⁶⁹. The reaction catalysed by ADK can be positioned as a buffering systems that maintains ADP:ATP ratios within a narrow window in order to regulate the stimulatory effect of ADP upon ETC flux. NDPK can be thought of as a regulator that fine tunes the rates of catabolic versus anabolic processes, because ATP is produced by catabolism and GTP is typically consumed by anabolic reactions⁶⁸. These two functionally related enzymes are both localised within the intermembrane space, and they have been shown to physically associate, perhaps to mediate substrate channelling for fast catalysis⁷⁰. The data gathered on NDPK and ADK in this comparison once again show divergent responses between root and shoot tissues, with shoot mitochondria exhibiting lower abundance of NDPK following salt treatment while ADK was unchanged. Conversely, root mitochondria exhibited lower abundance of ADK under salt treatment with NDPK unchanged (Table 3). These results raise the intriguing possibility that salinity stress alters the stoichiometry of the interaction between these two proteins in a tissue specific manner. Perhaps this serves to fine tune the abundance of nucleoside phosphates within the mitochondrial IMS in order to meet the specific metabolic and signalling requirements of each specific tissue under their different salinity scenarios.

Cyanide is a toxic inhibitor of cytochrome oxidase (CIV), but all plants produce endogenous cyanide in the course of ethylene metabolism, while thousands of plant species defend themselves against herbivore attack by producing cyanide through hydrolysis of cyanogenic glycosides⁷¹. This cyanide must be metabolised to prevent toxicity, and the enzyme primarily responsible for cyanide detoxification is beta cyanoalanine synthase (β -CAS), which is localised to the mitochondrion. It can be presumed that this proximity to cytochrome oxidase is evolutionarily favourable because it protects the ETC from cyanide inhibition⁷². The shoot mitochondrial comparison showed that AMP exhibited differing abundance of a protein spot matching to β -CAS (Table 3). This difference was not observed in isolated root mitochondria, which is probably attributable to lower abundance of β -CAS in root tissue⁷³. Initial database searching of mass spectrometry data derived from CS and AMP did not reveal any compositional differences between the β -CAS proteins identified in the two genotypes. However, *de novo* sequencing of high quality AMP-specific MS/MS spectra following Q-TOF mass spectrometry defined a candidate peptide that could derive from an AMP-specific β -CAS gene (MGLQQEEDHPAPAPGVLNIR, Supplementary Figure 2). Alignment of this peptide against the wheat β -CAS sequence (TC373702) showed significant sequence similarity at both the N and C termini of the peptide, but the APAP sequence within the middle of the peptide was not matched to the ‘canonical’ wheat sequence. This suggests that the protein might be derived from the *Lophopyrum elongatum* genome. Alignment of β -CAS sequences from a range of taxa showed that this peptide is likely to reside within the N-terminal region of the protein. This region shows little conservation between species, perhaps indicating that sequence variations in this region of the enzyme are a likely site for isoform variations. However, the limitations of *de novo* sequencing are well characterised⁷⁴, so it is possible that the amino acid sequence was

misassigned to the spectrum in question, or otherwise this peptide could derive from a wheat gene that is not present in the search databases due to incomplete EST sampling. Therefore, corroborating genetic analysis β -CAS sequences in *Lophopyrum elongatum* would be desirable to confirm the genetic origin of this potentially novel isoform. Although β -CAS abundance was not induced by salinity treatment, the baseline abundance of this protein was higher in the tolerant AMP. Given that *Lophopyrum elongatum* has adapted to a highly saline ecological niche, it could be postulated that higher β -CAS abundance might contribute to salinity tolerance. Due to this identification of a novel β -CAS peptide specifically detected in mitochondria from AMP, we posit that the β -CAS locus on the *Lophopyrum elongatum* genome could be incorporated into elite wheat cultivars as a potential source of salinity tolerance.

Under salinity, it is thought that photorespiration operates at a faster rate because stomatal closure lowers C_i and therefore shifts RuBisCO kinetics towards oxygenation⁷⁵. The SHMT enzyme catalyses one of the mitochondrial steps of the photorespiratory pathway, and Arabidopsis plants where SHMT has been transgenically knocked out exhibit lower salinity tolerance compared to wild type⁷⁶. In the shoot mitochondrial 2D-DIGE comparison, protein spots derived from the highly abundant photorespiratory SHMT enzyme presented as a train of spots (approximate gel position: MW~52 kDa, pI~7-8). In mitochondria isolated from AMP, the basic end of this train contained a highly abundant protein spot which was dramatically less abundant in CS (Figure 3, Table 3). This difference was also observed in root mitochondria, but with a lower magnitude due to the lower abundance of SHMT in this non-photosynthetic tissue. To investigate this protein spot in greater detail, we conducted Q-TOF mass spectrometry, and analysed these data with expanded database search parameters (Supplementary Figure 3).

Although one potential phosphorylated peptide specific to AMP was identified by this analysis, we posit that this is an unlikely explanation for this genotype's more basic SHMT spot, because typically phosphorylation induces an acidic shift to a protein's pI⁷⁷. Therefore further work would be required to investigate the molecular mechanism underpinning the more basic SHMT spot in AMP. Another genotypic difference in the shoot mitochondrial 2D-DIGE comparison was the higher abundance of an SHMT breakdown product in AMP, particularly under salinity stress. This suggests that the rate or pathway through which SHMT is degraded could differ between the two genotypes.

Higher abundance of mitochondrial redox defence enzymes under salinity

Salt treated plants generally exhibit higher abundance of ROS species compared to untreated controls^{63, 78, 79}, and control versus stress experiments have shown that mitochondrial ROS defences are frequently induced by salinity stress (reviewed in Jacoby et al.¹). Compellingly, overexpression of genes encoding mitochondrial antioxidant proteins can enhance salinity tolerance^{2, 3}. The data in this study show that salinity induces accumulation of protein spots matching to MnSOD in both roots and shoots, across both genotypes (Table 4). MnSOD presented as a train of three protein spots (MW~24 kDa, pI~6-7), with all three spots being induced by salt treatment in at least one genotype in isolated root mitochondria, while the two more acidic spots being induced by salt in both genotypes in shoot mitochondria (Table 4). These repeated measurements of higher MnSOD abundance at the protein level show the importance of mitochondrial superoxide detoxification in mediating salinity tolerance across both roots and shoots, and gives further weight to the very strong links between MnSOD abundance and salinity

tolerance. The enzymological reaction catalysed by MnSOD converts $O_2^{\cdot-}$ to H_2O_2 , and two mitochondrial proteins involved in mitochondrial H_2O_2 detoxification, peroxiredoxin and MDHAR, both exhibited higher abundance under salinity treatment in root mitochondria (Table 4). This result fits with the contention that root tissue underwent a more severe salinity scenario than shoot tissue, which perhaps necessitated increased detoxification capacity of H_2O_2 via these reactions. However, these proteins were not induced by salt treatment in isolated shoot mitochondria, suggesting that $O_2^{\cdot-}$ and H_2O_2 may have different roles between these two tissue types. Perhaps $O_2^{\cdot-}$ prevention and detoxification is more important in shoot tissue, shown by the induction of AOX and MnSOD. In contrast, perhaps detoxification of both $O_2^{\cdot-}$ and H_2O_2 are important in root tissue, shown by induction of MnSOD, Prx and MDHAR.

Abundance of MnSOD is strongly linked to genotypic salt tolerance, compellingly shown by transgenic studies where the overexpression of MnSOD has increased the salinity tolerance of *Arabidopsis* and poplar^{2, 3}. Also, correlative studies link MnSOD abundance/activity to whole plant salt tolerance across genotypes^{17, 18, 80}. Differential MnSOD isoform abundance has been linked to salt tolerance of commercial wheat genotypes¹⁸, while in humans there is clinical interest in whether disease susceptibility is linked to naturally occurring sequence variations in the MnSOD protein encoded at the SOD2 locus^{81, 82}. In this study of CS and AMP, wheat MnSOD presented as a train of three protein spots (MW~24 kDa, pI~6-7), with the most acidic spot from this train being more abundant in AMP. Differential abundance of this acidic spot was highly significant for a genotype effect in mitochondria isolated from both roots and shoots (Table 4). In root mitochondria, the salinity response of this spot diverged between two genotypes, with ANOVA tests showing that a highly significant G×T interaction was evident

(Table 4). A thorough investigation of peptide mass spectra derived from this particular MnSOD protein spot in shoot mitochondria was undertaken with the aim of defining more detailed links between MnSOD composition and the higher salinity tolerance of AMP (Supplementary Figure 4). This process did not identify a compositional difference between the more acidic gel spot that was higher in AMP compared to the other MnSOD spots analysed. However, a range of different MnSOD isoforms and tryptophan oxidation products were confidently identified in both genotypes via interrogation of MS/MS data. These molecular properties are potential targets for subsequent investigations into the relationships between MnSOD and salinity tolerance in wheat.

The response of TCA cycle enzymes to salinity treatment

The TCA cycle is a highly flexible component of plant metabolism that can assume a wide range of flux modes depending on tissue type and environmental context⁸³. The central role of the TCA cycle in shaping plant phenotypes is shown by transgenic experiments where differential abundance of specific TCA cycle enzymes can influence biomass accumulation and nutrient use efficiency^{84, 85}. This study revealed differential abundance of TCA cycle components according to salinity treatment, with these effects being particularly pronounced in mitochondria isolated from root tissue (Table 5). Salt treatment of roots elicited higher abundance of several sequential steps of the cycle, with citrate synthase, aconitase, and isocitrate dehydrogenase all displaying higher abundance under salinity. The concerted action of these enzymes is linked to an anaplerotic role where a partial TCA cycle operates to produce 2-OG as a building block for nitrogen assimilation⁸³. The role of malic enzyme is linked to this pathway, and this protein also

exhibited higher abundance in mitochondria isolated from salt treated root tissue (Table 3). Another set of TCA cycle enzymes, which catalyse different portions of the pathway, were of lower abundance in mitochondria isolated from salt treated root tissue, such as several spots matching to malate dehydrogenase, as well as both subunits of succinyl-CoA ligase. These differential salinity responses within the same metabolic pathway are indicative of salinity-induced remodelling of mitochondrial metabolism in root tissue. This contrasts with the data gathered from shoot mitochondria, where the abundance of TCA cycle components was relatively consistent between control and salinity treatments, with only one spot matching succinyl-CoA ligase beta chain exhibiting a reduction under salinity treatment (Table 5). Although protein abundance does not consistently correlate with enzymatic flux, these data provide insights into salinity effects on the steady state abundance of TCA cycle machinery, and could guide future experiments investigating links between metabolism and salinity tolerance.

Malate dehydrogenase (MDH) is a component of the TCA cycle that is widely distributed across biological taxa⁸⁶. In plants, the role of MDH extends beyond this single pathway, as other MDH isoforms are involved in a range of biochemical processes across the cytosol and several organelles⁸⁷. The mitochondrial MDH exhibits complex interactions with photosynthesis in illuminated leaves^{84, 88}. Enzymological analyses have found a correlation between mitochondrial MDH activity and salinity tolerance across rice varieties, with the more tolerant genotype exhibiting higher activity of the mitochondrial MDH enzyme under both control and salt-treated conditions⁸⁹. In our work, MDH presented on 2D gels as a train of highly abundant spots of MW~37 kDa and pI~5-7. The most basic spot (pI~7) exhibited higher abundance in AMP across both shoot and root tissue (Table 5). Although tryptic peptides from this protein spot were

analysed using Q-TOF mass spectrometry and *de novo* sequencing, this process did not find strong evidence to show that the AMP protein spot contained a fundamentally different amino acid composition compared to the CS spot (Supplementary Figure 5). So we cannot conclusively define the molecular basis that underpins these differential MDH patterns between genotypes. However, our data positions mitochondrial MDH as a target for future investigations of the salinity tolerance of AMP.

There are links between aconitase activity, ROS and salinity stress and, as salt treatment has been shown to increase the rate of mitochondrial ROS production⁹⁰, while ROS-dependent inactivation of the aconitase enzyme has been observed across a number of species^{91, 92}. Interestingly, reduction in MnSOD abundance via RNAi in *Arabidopsis* results in lower aconitase activity, presumably due to damage of the ROS-sensitive iron-sulphur cluster in the aconitase enzyme⁹³. In the root mitochondrial comparison, protein spots matching to aconitase exhibited different pI values between genotypes, with the tolerant AMP exhibiting higher abundance of the two more basic protein spots (Table 5). The genotypic differences in aconitase pI values shown in this work is corroborated by previous investigations into pI distributions of aconitase in these same two genotypes⁹⁴. It is interesting to consider that several aconitase protein spots displayed increased abundance in both genotypes in response to salt treatment in roots (Table 5), indicating that higher aconitase abundance in root tissue could be a molecular strategy that enhances the capacity of the mitochondrion to cope with the impact of salinity stress.

Electron transport chain responses to salinity

The ETC couples the oxidation of substrates to proton pumping across the inner mitochondrial membrane in order to drive ATP generation by ATP synthase. There is evidence that the abundance of several ETC proteins is modulated by salt stress^{64, 95, 96}. Further, the biochemical activity of ETC complexes can be directly affected by NaCl, with low concentrations of ionic salts reported to stimulate kinetic activity of certain ETC complexes⁹⁷, whereas high concentrations of salts are inhibitory^{98, 99}. The 2D-DIGE analysis of shoot mitochondrial composition revealed very few salt induced differences in ETC subunit abundance, with a modest increase in one spot matching to the ATP synthase alpha subunit (Table 6). However, immunoblotting revealed that AOX abundance was significantly higher in shoot tissue under salinity (Figure 2). This suggests that the molecular changes induced by salinity to the electron transport chain in shoot mitochondria involve alterations to the alternative respiratory pathway, while the composition of the classical ETC pathway remains relatively stable (Figure 2, Table 6). In contrast, the root 2D-DIGE comparison identified salinity linked induction of several CI subunits and a CII component in the roots of both genotypes under salinity (Table 4). Based upon calculations of ATP yielded per unit substrate oxidised, it is known that electron flow through CI is a 50% more efficient conversion to ATP compared to the flow through non-phosphorylating alternative NADH dehydrogenases and CII to cytochrome oxidase¹⁰⁰. Given that ion exclusion incurs significant energetic costs, it can be asserted that efficient ATP production by root mitochondria is crucial to meeting the energetic demands of ion exclusion strategies. Therefore, higher CI abundance (Table 6) and lack of AOX induction (Table 2; Figures 1 and 2) may be molecular mechanisms that contribute to high respiratory efficiency under salinity in root mitochondria.

In the shoot mitochondrial comparison, several spots matching to the CI 75 kDa subunit were higher in AMP, under both control and salt treatment (Table 6). It is interesting that this protein was induced by both genotypes under salinity treatment in root mitochondria, which were likely undergoing a more severe salinity scenario. Perhaps higher CI abundance in shoot tissues is indicative of a mechanism by which the tolerant AMP genotype is better able to cope with the onset of a dramatic salt stress, by steady-state higher shoot mitochondrial abundance of this salinity responsive protein complex..

Lower abundance of mitochondrial heat shock proteins under salinity

Mitochondrial heat shock proteins play key roles in the synthesis of mitochondrial encoded proteins, the import of nuclear encoded proteins, as well as quality control of damaged or misfolded proteins in order to prevent malfunction and aggregation¹⁰¹. Prohibitins are thought to perform a similar function, as they associate into large complexes in the inner mitochondrial membrane which act as a scaffold via which ETC complexes are assembled¹⁰². In this study, salinity treatment generally induced lower abundance of mitochondrial heat shock proteins and prohibitins, with lower abundance of Hsp60 being measured in both genotypes in both roots and shoots (Table 7). The complementary component of the chaperonin complex, Hsp10, exhibited lower abundance in root mitochondria from both genotypes following salt treatment (Table 7). Furthermore, several spots matching to Hsp70 and prohibitin exhibited lower abundance under salinity treatment in root mitochondria (Table 7). These more pronounced effects in the root again point toward a more severe salinity scenario in roots compared to shoots. Mechanistically,

the diminished abundance of Hsps and prohibitins under salinity is counterintuitive, as *in vitro* experiments have conclusively shown that NaCl stress leads to protein misfolding¹⁰³. One explanation for lower chaperone abundance under salinity stress involves slower rates of mitochondrial protein import, as was noted under cold and paraquat stresses¹⁰⁴. Perhaps further experiments could investigate the effects of salinity stress upon rates of protein synthesis and degradation using metabolic labelling and high throughput proteomics techniques⁴⁵. Such analyses could further our understanding of whether the mitochondrion has a lower demand for the chaperone function of heat shock proteins due to slower protein turnover under salinity conditions.

Salinity responses of spots matching to membrane transporters, translation and uncharacterised proteins

Voltage dependent anion channels (VDACs) are localised in the outer mitochondrial membrane, forming β -barrels that channel molecules <1000 Da into the intermembrane space. Perhaps because such a wide range of molecules that fall within this mass range, research has linked VDAC porin to a wide range of cellular functions and stress responses in the literature¹⁰⁵. In this study we document a general trend of lower VDAC abundance under salinity treatment, although there was some diversity in the abundance profiles of certain VDAC spots across genotypes and treatments (Table 8). A similar trend was noticed in our previous investigation of wheat mitochondria under salinity¹⁸, so it seems evident that VDAC is a flexible component of the mitochondrial proteome which alters during the mitochondrial salt stress response. In mammals, there are extensive links between porin and the signalling cascades that lead to programmed cell

death. There are some indications that similar signalling processes involving VDAC occur in plants¹⁰⁶. Thus, further investigation into VDACS could focus on their role in salinity stress, particularly under ionic stress conditions where the presence of charged Na⁺ and Cl⁻ ions might alter the electrophysiological regulation of VDAC function. The root comparison in this study also documents the salinity-linked induction of several proteins with uncharacterised molecular functions (Table 8). These proteins can now be considered as potential targets of future investigations into the mitochondrial salinity response in wheat.

CONCLUSION

Respiration and mitochondrial metabolism play important roles in mediating salinity tolerance strategies such as ion exclusion and osmotic tolerance, while mitochondrial ROS defences are important for mediating tissue tolerance. This work compares respiratory properties between two genotypes, CS (sensitive) and AMP (tolerant). The tolerant AMP genotype is a genetic hybrid that combines the genome of bread wheat with the genome of a salt tolerant wild wheatgrass, and here we dissect respiratory traits of these two genotypes with the aim of identifying mitochondrial properties that contribute to the superior tolerance of AMP. The major focus of this investigation was two proteomic data sets where 2D-DIGE was used to compare isolated mitochondrial composition between the two genotypes following either control or salt treatment. These data sets identify a suite of mitochondrial proteins that exhibit altered abundance in response to salt treatment, which furthers our understanding of how mitochondrial composition responds to salinity stress. Furthermore, a number of protein spots notably exhibited higher abundance in mitochondria isolated from AMP, and the molecular functions of these proteins could contribute toward the superior salinity tolerance of AMP. Specifically, AMP exhibited higher abundance of the mitochondrial enzymes β -CAS, SHMT, MnSOD, MDH and aconitase. Of particular note is the higher abundance of a specific MnSOD 2D gel spot in the tolerant AMP, because this enzyme has been extensively linked to salinity tolerance in the literature. Also, we provide peptide MS/MS spectra derived from AMP-specific protein spots, which could potentially act as biomarkers in a breeding scenario. These molecular data are framed by physiological and biochemical measurements that analyse the effect of salinity treatment on growth, photosynthesis and respiration. By integrating proteomic data sets with biochemical and physiological assessments of mitochondrial function, this study advances our understanding of

how salinity affects respiratory physiology and mitochondrial biochemistry in wheat. Also, the results of this work could guide future experiments to assess which specific genetic elements mediate the superior tolerance of AMP. One possibility is to identify the genes encoding the mitochondrial proteins that we have identified at higher abundance in AMP mitochondria. These genes could then be transferred into sensitive wheat varieties using conventional breeding or transgenic manipulation, and the progeny screened for superior performance under salinity, to determine whether these genes are causative in mediating tolerance.

Tables and Figures

	CS		AMP		Statistical significance
	Control	Salt	Control	Salt	
Growth measurements					
Shoot dry weight (g) (n=12)	6.13 ± 2.8	1.70 ± 0.26	2.50 ± 1.1	0.98 ± 0.29	G*** / T*** / G×T**
Root dry weight (g) (n=12)	0.46 ± 0.20	0.14 ± 0.02	0.29 ± 0.13	0.19 ± 0.06	T*** / G×T**
Leaf elongation rate (mm d ⁻¹) (n=8)	71.1 ± 15	33.4 ± 6.6	49.2 ± 14	43.4 ± 8.4	T*** / G×T***
Photosynthetic and transpirational measurements					
Photosynthesis rate (μmol CO ₂ m ⁻² s ⁻¹) (n=8)	16.8 ± 1.7	16.4 ± 1.6	18.0 ± 2.4	19.6 ± 1.4	G**
Transpiration rate (mmol H ₂ O m ⁻² s ⁻¹) (n=8)	2.37 ± 0.42	1.62 ± 0.37	2.48 ± 0.70	2.35 ± 0.47	G* / T*
Intracellular CO ₂ (ppm CO ₂) (n=8)	300 ± 14	244 ± 25	298 ± 20	275 ± 13	G* / T*** / G×T*
Stomatal conductance (mmol H ₂ O m ⁻² s ⁻¹) (n=8)	0.40 ± 0.09	0.20 ± 0.05	0.43 ± 0.17	0.31 ± 0.06	T***
V _{cmax} (μmol CO ₂ m ⁻² s ⁻¹) (n=8)	61.4 ± 8.6	86.2 ± 9.9	71.1 ± 10	89.9 ± 6.2	G* / T***
J _{max} (μmol CO ₂ m ⁻² s ⁻¹) (n=8)	118.3 ± 24	172 ± 18	126 ± 23	166 ± 13	T***
CO ₂ compensation point (ppm CO ₂) (n=8)	36.4 ± 2.4	43.4 ± 2.4	38.7 ± 1.5	44.6 ± 2.3	G* / T***

Table 1: Salinity responses of growth, photosynthesis and transpiration in CS and AMP. Means $\pm$ standard deviations of growth, photosynthetic and transpirational parameters measured in CS and AMP plants grown hydroponically in controlled environment conditions for seven weeks. Salt treatment involved 200 mM NaCl applied in four 50 mM/day increments over days one-four after sowing. To determine statistical significance, data were analysed using two way ANOVA, and lower p-values are indicated by more asterisks ($p < 0.05$ *, $p < 0.01$ **, $p < 0.001$ ***). G denotes genotype effect, T denotes treatment effect and G $\times$ T denotes their interaction.

	CS		AMP		Statistical significance
	Control	Salt	Control	Salt	
Respiratory measurements (7 week old plants)					
Leaf respiratory O ₂ consumption (μmol O ₂ m ⁻² s ⁻¹ ml ⁻¹) (n=6)	1.11 ± 0.30	0.96 ± 0.25	1.49 ± 0.37	1.05 ± 0.26	T*
Leaf respiratory CO ₂ release (μmol CO ₂ m ⁻² s ⁻¹) (n=6)	0.52 ± 0.27	0.53 ± 0.19	0.90 ± 0.33	0.76 ± 0.23	G**
Leaf respiratory quotient (CO ₂ released/O ₂ consumed) (n=6)	0.46 ± 0.17	0.55 ± 0.11	0.60 ± 0.15	0.73 ± 0.12	G**
Root respiratory O ₂ consumption (pmol O ₂ mg ⁻¹ min ⁻¹ ml ⁻¹) (n=6)	96.9 ± 36	123 ± 4.7	72.8 ± 16.7	101 ± 38	T*
Respiratory measurements (5 day old plants)					
Leaf respiratory O ₂ consumption (pmol O ₂ mg ⁻¹ min ⁻¹ ml ⁻¹) (n=8)	99.2 ± 28	248 ± 85	87.6 ± 18	175 ± 43	G*/T***
Leaf respiratory O ₂ consumption + KCN (pmol O ₂ mg ⁻¹ min ⁻¹ ml ⁻¹) (n=4)	79.4 ± 9.9	245 ± 5.7	101 ± 6.8	174 ± 48	T***
Leaf respiratory O ₂ consumption + SHAM (pmol O ₂ mg ⁻¹ min ⁻¹ ml ⁻¹) (n=4)	59.1 ± 11	154 ± 69	46.3 ± 27	71.0 ± 13	T*
Root respiratory O ₂ consumption (pmol O ₂ mg ⁻¹	170 ± 35	206 ± 60	182 ± 62	246 ± 44	T*

min ⁻¹ ml ⁻¹) (n=8)					
Root respiratory O ₂ consumption + KCN (pmol O ₂ mg ⁻¹ min ⁻¹ ml ⁻¹) (n=4)	97.4 ± 17	101 ± 22	82.5 ± 31	90.9 ± 27	-
Root respiratory O ₂ consumption + SHAM (pmol O ₂ mg ⁻¹ min ⁻¹ ml ⁻¹) (n=4)	129 ± 35	115 ± 36	99.5 ± 36	128 ± 55	-

Table 2: Respiration rates of intact tissue from CS and AMP plants following control and salt treatments. Means ± standard deviations of respiratory parameters measured in CS and AMP plants grown hydroponically in controlled environment conditions for either seven weeks or five days. Salt treatment involved 200 mM NaCl applied in four 50 mM/day increments over days one-four after sowing. To determine statistical significance, data were analysed using two way ANOVA, and lower p-values are indicated by more asterisks (p<0.05:*, p<0.01:**, p<0.001:***). G denotes genotype effect, T denotes treatment effect and G×T denotes their interaction.

Spot number	Abundance data	ANOVA p-value	Accession	Description	MOWSE (MS/MS)	# matched peptides (MS/MS)	% coverage (MS/MS)	Breakdown product?
Shoot comparison								
11		G***	TC449830	Serine hydroxymethyl-transferase	202	6	12	
12		T**	TC387564	Glutamate dehydrogenase	176	5	17	
13		T***	TC379352	Formate dehydrogenase	129	4	11	
14		T*	TC379352	Formate dehydrogenase	214	5	16	
15		T**	TC390427	Glutamate dehydrogenase	106	3	10	
16		G***	TC381804	β -Cyanoalanine synthase	80	3	8	
17		T*	TC390353	Glycine decarboxylase complex subunit T	67	3	7	Yes
24		G*** T*** G $\times$ T*	TC418201	Serine hydroxymethyl transferase	130	3	13	Yes
27		T**	TC371824	Nucleoside diphosphate kinase	145	3	11	
Root comparison								
21		G* T***	TC388085	Methyl-malonate semialdehyde dehydrogenase	406	7	11	

22		G* T*	TC388085	Methyl-malonate semialdehyde dehydrogenase	505	7	13	
27		G**	TC449830	Serine hydroxymethyl transferase	415	9	13	
35		T**	TC390855	Aspartate aminotransferase	568	10	21	
36		T**	TC387564	Glutamate dehydrogenase	555	10	21	
45		G* T***	TC388991	Adenylate kinase	526	8	25	
46		T**	TC384775	Adenylate kinase	360	5	8	
60		T**	TC417735	Malic enzyme	200	5	5	

Table 3: Protein spots matching to enzymes of C, N, P metabolism that exhibited statistically significant differences in the 2D-DIGE comparisons of mitochondria isolated from shoots and roots. Spot number refers to Figure 3 (shoots) or Figure 4 (roots). Abundance data was quantified with DeCyder software, error bars represent SEM (n=3). White bars represent control treatment, grey bars represent salt treatment. To determine statistical significance, abundance data was analysed using two way ANOVA, and lower p-values are indicated by more asterisks (p<0.05:*, p<0.01:**, p<0.001:***). G denotes genotype effect, T denotes treatment effect and G×T denotes their interaction. Accession is from the Wheat TC database (TaGI release 12). MOWSE,

number of matched peptides, and coverage data are taken from Mascot search engine. Breakdown products were assigned to spots which presented at lower molecular weights compared to a reference map of the wheat mitochondrial proteome¹⁸.

Spot number	Abundance data	ANOVA p-value	Accession	Description	MOWSE (MS/MS)	# matched peptides (MS/MS)	% coverage (MS/MS)	Breakdown product?
Shoot comparison								
25		G*** T***	CA658901	Manganese superoxide dismutase	100	2	20	
26		T*	TC395139	Manganese superoxide dismutase	69	2	6	
Root comparison								
31		T*	TC406872	Monodehydro-ascorbate reductase	262	3	9	
51		G*** G×T***	TC395139	Manganese superoxide dismutase	236	4	16	
52		G* T***	TC395139	Manganese superoxide dismutase	175	4	17	
53		T***	TC395139	Manganese superoxide dismutase	549	7	32	
54		G* T***	TC388331	Peroxiredoxin	235	5	16	

Table 4: Protein spots matching to enzymes of redox defence that exhibited statistically significant differences in the 2D-DIGE comparisons of mitochondria isolated from shoots and roots. Spot number refers to Figure 3 (shoots) or Figure 4 (roots). Abundance data was quantified with DeCyder software, error bars represent SEM (n=3). White bars represent control treatment, grey bars represent salt treatment. To determine statistical significance, abundance data was

analysed using two way ANOVA, and lower p-values are indicated by more asterisks ($p < 0.05$ *, $p < 0.01$ **, $p < 0.001$ ***). G denotes genotype effect, T denotes treatment effect and G×T denotes their interaction. Accession is from the Wheat TC database (TaGI release 12). MOWSE, number of matched peptides, and coverage data are taken from Mascot search engine. Breakdown products were assigned to spots which presented at lower molecular weights compared to a reference map of the wheat mitochondrial proteome¹⁸.

Spot number	Abundance data	ANOVA p-value	Accession	Description	MOWSE (MS/MS)	# matched peptides (MS/MS)	% coverage (MS/MS)	Breakdown product?
Shoot comparison								
18		G***	CA617342	Malate dehydrogenase	121	2	24	
19		G*** T*	TC377226	Succinyl-CoA ligase alpha chain	388	6	38	
Root comparison								
1		T**	BQ238531	Aconitase	419	9	54	
2		T***	TC373025	Aconitase	476	6	15	
3		G** T**	TC373025	Aconitase	210	3	11	
4		G*** G×T*	TC373025	Aconitase	173	3	9	
17		T***	TC382178	Lipoamide dehydrogenase	756	9	31	
32		T**	TC378665	Citrate synthase	429	10	19	
33		T**	TC378665	Citrate synthase	283	5	9	

34		T***	TC378070	Succinyl-CoA ligase β subunit	130	2	5	
37		T***	TC370105	Malate dehydrogenase	448	4	16	
38		T***	TC375673	Malate dehydrogenase	660	4	18	
39		T**	TC445045	Isocitrate dehydrogenase	640	9	24	
40		T**	TC377226	Succinyl-CoA ligase α subunit	313	3	19	
41		T**	TC375936	Pyruvate dehydrogenase E1 α subunit	518	10	23	
42		G**	TC375673	Malate dehydrogenase	928	7	32	
43		G*** T*	TC370105	Malate dehydrogenase	293	3	8	

Table 5: Protein spots matching to TCA cycle components that exhibited statistically significant differences in the 2D-DIGE comparisons of mitochondria isolated from shoots and roots. Spot number refers to Figure 3 (shoots) or Figure 4 (roots). Abundance data was quantified with DeCyder software, error bars represent SEM (n=3). White bars represent control treatment, grey bars represent salt treatment. To determine statistical significance, abundance data was analysed using two way ANOVA, and lower p-values are indicated by more asterisks (p<0.05:*,

$p < 0.01$:**, $p < 0.001$:***). G denotes genotype effect, T denotes treatment effect and $G \times T$ denotes their interaction. Accession is from the Wheat TC database (TaGI release 12). MOWSE, number of matched peptides, and coverage data are taken from Mascot search engine. Breakdown products were assigned to spots which presented at lower molecular weights compared to a reference map of the wheat mitochondrial proteome¹⁸.

Spot number	Abundance data	ANOVA p-value	Accession	Description	MOWSE (MS/MS)	# matched peptides (MS/MS)	% coverage (MS/MS)	Breakdown product?
Shoot comparison								
1		G***	TC412039	Complex I 75 kDa subunit	170	2	15	
2		G***	TC376678	Complex I 75 kDa subunit	187	4	11	
3		G**	TC389811	Complex I 75 kDa subunit	243	4	17	
9		G**	TC404839	ATP synthase beta subunit	308	6	13	
10		T*	TC368629	ATP synthase alpha subunit	244	6	12	
23		G**	TC377466	ATP synthase F _{AD} subunit	224	5	11	
Root comparison								
5		T**	TC376678	Complex I 75 kDa subunit	566	8	21	
6		T**	TC376678	Complex I 75 kDa subunit	523	7	19	
7		T**	TC376678	Complex I 75 kDa subunit	568	8	20	
8		T***	TC389811	Complex I 75 kDa subunit	231	3	15	

9		T***	TC389811	Complex I 75 kDa subunit	301	4	19	
13		T**	TC385839	Succinate dehydrogenase flavoprotein subunit	511	8	17	
14		T***	TC385839	Succinate dehydrogenase flavoprotein subunit	556	10	21	
18		T***	TC404839	ATP synthase beta subunit	1091	11	16	
19		T***	TC404839	ATP synthase beta subunit	1128	10	23	
20		G*	TC411944	ATP synthase beta subunit	1050	10	29	
23		T**	TC373464	Mitochondrial processing peptidase alpha subunit	65	2	10	
24		T*	TC373464	Mitochondrial processing peptidase alpha subunit	556	5	27	
25		T**	TC373464	Mitochondrial processing peptidase alpha subunit	595	5	27	
26		T**	TC425082	Mitochondrial processing peptidase alpha subunit	616	9	17	
28		T**	TC372051	ATP synthase beta subunit	226	5	22	Yes

56		T*	TC381037	Complex I 17 kDa subunit	530	10	19	
57		T*	TC408892	Complex I NDUF5 subunit	482	7	31	
58		T*	TC372910	Complex I 17 kDa subunit	334	6	13	

Table 6: Protein spots matching to electron transport chain components that exhibited statistically significant differences in the 2D-DIGE comparisons of mitochondria isolated from shoots and roots. Spot number refers to Figure 3 (shoots) or Figure 4 (roots). Abundance data was quantified with DeCyder software, error bars represent SEM (n=3). White bars represent control treatment, grey bars represent salt treatment. To determine statistical significance, abundance data was analysed using two way ANOVA, and lower p-values are indicated by more asterisks (p<0.05:*, p<0.01:**, p<0.001:***). G denotes genotype effect, T denotes treatment effect and G×T denotes their interaction. Accession is from the Wheat TC database (TaGI release 12). MOWSE, number of matched peptides, and coverage data are taken from Mascot search engine. Breakdown products were assigned to spots which presented at lower molecular weights compared to a reference map of the wheat mitochondrial proteome¹⁸.

Spot number	Abundance data	ANOVA p-value	Accession	Description	MOWSE (MS/MS)	# matched peptides (MS/MS)	% coverage (MS/MS)	Breakdown product?
Shoot comparison								
4		G**	TC386349	Heat shock protein 70	249	5	13	
5		T**	CK153924	Heat shock protein 60	70	1	10	
6		T***	TC428099	Heat shock protein 60	101	2	2	
7		T**	TC428099	Heat shock protein 60	108	2	2	
Root comparison								
10		G* T***	TC386349	Heat shock protein 70	144	5	7	
11		G* T**	TC386349	Heat shock protein 70	730	7	16	
12		G*	TC386349	Heat shock protein 70	813	10	19	
15		T***	TC428099	Heat shock protein 60	645	9	13	
16		G* T***	TC428099	Heat shock protein 60	704	9	15	

44		T**	TC381621	Prohibitin	560	8	31	
59		G* T***	TC374691	Heat shock protein 10	394	6	21	

Table 7: Spots matching to heat shock proteins and prohibitin that exhibited statistically significant differences in the 2D-DIGE comparisons of mitochondria isolated from shoots and roots. Spot number refers to Figure 3 (shoots) or Figure 4 (roots). Abundance data was quantified with DeCyder software, error bars represent SEM (n=3). White bars represent control treatment, grey bars represent salt treatment. To determine statistical significance, abundance data was analysed using two way ANOVA, and lower p-values are indicated by more asterisks (p<0.05:*, p<0.01:**, p<0.001:***). G denotes genotype effect, T denotes treatment effect and G×T denotes their interaction. Accession is from the Wheat TC database (TaGI release 12). MOWSE, number of matched peptides, and coverage data are taken from Mascot search engine. Breakdown products were assigned to spots which presented at lower molecular weights compared to a reference map of the wheat mitochondrial proteome¹⁸.

Spot number	Abundance data	ANOVA p-value	Accession	Description	MOWSE (MS/MS)	# matched peptides (MS/MS)	% coverage (MS/MS)	Breakdown product?
Shoot comparison								
21		G*	TC369790	Voltage dependent ion channel	221	8	31	
22		G*	TC368846	Voltage dependent ion channel	308	6	26	
Root comparison								
47		G* T**	TC396379	VDAC porin	619	6	25	
48		T**	TC378886	VDAC porin	139	2	8	
49		T***	TC368846	VDAC porin	676	9	26	
50		G* T*	TC368846	VDAC porin	938	9	39	
30		T*	TC415496	Elongation factor Tu	188	5	12	
29		T*	TC373529	Uncharacterised DJ-1 domain protein	151	2	7	
55		T**	CK164007	Uncharacterised CBS domain protein	531	10	28	
61		T***	TC383136	Uncharacterised alcohol dehydrogenase domain protein	401	6	16	

Table 8: Spots matching to proteins involved in membrane transport, translation, and uncharacterised functions that exhibited statistically significant differences in the 2D-DIGE comparisons of mitochondria isolated from shoots and roots. Spot number refers to Figure 3 (shoots) or Figure 4 (roots). Abundance data was quantified with DeCyder software, error bars represent SEM (n=3). White bars represent control treatment, grey bars represent salt treatment. To determine statistical significance, abundance data was analysed using two way ANOVA, and lower p-values are indicated by more asterisks ($p < 0.05$ *, $p < 0.01$ **, $p < 0.001$ ***). G denotes genotype effect, T denotes treatment effect and G×T denotes their interaction. Accession is from the Wheat TC database (TaGI release 12). MOWSE, number of matched peptides, and coverage data are taken from Mascot search engine. Breakdown products were assigned to spots which presented at lower molecular weights compared to a reference map of the wheat mitochondrial proteome¹⁸.

Figure 1: Respiration rates of mitochondria isolated from CS and AMP following control and salt treatments. Rates of oxygen consumption for 100 μ g mitochondrial protein were measured with oxygen electrode. **A.** Mitochondria isolated from shoots, **B.** Mitochondria isolated from roots. White bars represent maximal O₂ consumption rates after addition of NADH, succinate and ADP (state 3), while grey bars represent O₂ consumption rates after addition of NADH, succinate, KCN, DTT and pyruvate (alternative pathway). Error bars represent SEM (n=3).

A) AOX abundance in isolated shoot mitochondria

i) Anti-AOX Western blot

ii) Standardised abundance

B) AOX abundance in isolated root mitochondria

i) Anti-AOX Western blot

ii) Standardised abundance

□ Control ■ Salt

Figure 2: Representative immunoblot images of mitochondria isolated from CS and AMP plants following control and salt treatment with antibodies raised against AOX. Abundance was quantified from Western blot images using Amersham ImageQuant TL (GE Healthcare). White bars represent control treatment, grey bars represent salt treatment. Error bars represent SEM (n=3).

Figure 3: Representative 2D-DIGE comparison of shoot mitochondria from CS and AMP highlighting mitochondrial proteins that exhibited significantly different abundance values across genotypes or treatments. In this image, Cy3 labelled proteins from shoot mitochondrial samples isolated from CS following control treatment (green) are overlaid against Cy5 labelled proteins from shoot mitochondria isolated from AMP following salinity treatment (red). Marked spots are mitochondrial proteins that displayed significant abundance differences between genotypes and/or treatments over the six gel experiment (two-way ANOVA $p < 0.05$). Peptide mass

spectrometry data are shown in Supplementary Table 3, and all six gels in this comparison can be viewed in Supplementary Figure 1A.

Figure 4: Representative 2D-DIGE comparison of root mitochondria from CS and AMP highlighting mitochondrial proteins that exhibited significantly different abundance values across genotypes or treatments. In this image, Cy3 labelled proteins from root mitochondrial samples isolated from CS following salt treatment (green) are overlaid against Cy5 labelled proteins from root mitochondrial samples isolated from AMP following salinity treatment (red). Marked spots are mitochondrial proteins that displayed significant abundance differences between genotypes and/or treatments over the six gel experiment (two-way ANOVA $p < 0.05$). Protein IDs

gathered from peptide mass spectrometry data are shown in Supplementary Table 4 and all six gels in this comparison can be viewed in Supplementary Figure 1B.

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ASSOCIATED CONTENT

Supporting Information

Supplementary Tables 1 and 2, Supplementary Figures 1-6: Tables contain quantitative abundance data and protein match information for contaminating proteins that exhibited statistically significant abundance differences in the 2D-DIGE experiments. Figures contain all DIGE images from the two six-gel DIGE experiments, as well as workflows used to investigate the composition of protein spots that were specific to AMP.

Supplementary Tables 3 and 4: Tables contain MS/MS peptide match information from MALDI-TOF/TOF.

This material is available free of charge via the Internet at <http://pubs.acs.org>.

ACKNOWLEDGMENTS

We thank Tim Colmer (School of Plant Biology, University of Western Australia) for providing the wheat seed used in this study and for helpful discussions. RPJ was supported by a GRDC PhD scholarship (GRS163). This research was funded by the Australian Research Council (ARC) through grants to AHM (CE0561495; LP120200102); AHM is supported as an ARC Future Fellow (FT110100242).

ABBREVIATIONS

2-OG, Two oxoglutarate; A, Photosynthesis rate; ADK, Adenylate kinase; AMP, Amphiploid of wheat v. Chinese Spring with *Lophopyrum elongatum*; AOX, Alternative oxidase; AspAT, Aspartate aminotransferase; β -CAS, Beta-cyanoalanine synthase; CI, Complex one (NADH:Ubiquinone oxidoreductase); C_i, Intracellular CO₂; COX, Cytochrome C oxidase; CS, Wheat v. Chinese Spring; E, Transpiration rate; EST, Expressed sequence tag; ETC, Electron transport chain; G, Genotype; GDC, Glycine decarboxylase complex; GDH, Glutamate dehydrogenase; g_s, Stomatal conductance; HCCA, alpha-Cyano-four-hydroxycinnamic acid; Hsp, Heat shock protein; IMS, Intermembrane space; IRGA, Infra-red gas analyser; J_{max}, Maximum rate of photosynthetic electron transport; KCN, Potassium cyanide; MDH, Malate dehydrogenase; MDHAR, Monodehydroascorbate reductase; MnSOD, Manganese superoxide dismutase; NDPK, Nucleoside diphosphate kinase; PAR, Photosynthetically active radiation; Prx, Peroxiredoxin; RH, Relative humidity; RuBisCO, Ribulose-1,5-bisphosphate carboxylase oxygenase; SHAM, Salicylhydroxamic acid; SHMT, Serine hydroxymethyltransferase; T, Treatment; TC, Tentative consensus; TCA, Tricarboxylic acid; VDAC, Voltage dependent ion channel.

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Supplementary Table 1. Abundance data and protein ID information for proteins from contaminating organelles that exhibited differing abundance values between genotypes and/or treatments in the 2D-DIGE comparison of mitochondria isolated from shoots of CS and AMP after control or salt treatment. Spot number refers to Supplementary Figure 6A. Abundance data was quantified with DeCyder software, error bars represent SEM (n=3). To determine statistical significance, abundance data was analysed using two way ANOVA, and lower p-values are indicated by more asterisks (p<0.05:*, p<0.01:**, p<0.001:***). G denotes genotype effect, T denotes treatment effect and G×T denotes their interaction. Accession is from the Wheat TC database (TaGI release 12). MOWSE, number of matched peptides, and coverage data are taken from Mascot search engine. Breakdown products were assigned to spots which presented at significantly lower molecular weights on 2D gels compared to the annotated molecular weights of Arabidopsis homologous in the TAIR database. Source of contamination was inferred from localisation of Arabidopsis homologues as annotated in the TAIR database.

Spot number	Abundance data	ANOVA p-value	Accession	Description	MOWSE (MS/MS)	# matched peptides (MS/MS)	% coverage (MS/MS)	Breakdown product?	Source of contamination
c1		G* T*	TC410655	Heat shock protein 70	40	1	3		Stroma
c2		G** T**	TC372814	Heat shock protein 60	235	5	16		Stroma
c3		G*** T*** G×T*	TC461954	RuBisCO large subunit	231	5	5		Stroma
c4		G** T**	TC370636	RuBisCO large subunit	250	4	13		Stroma
c5		G*** T**	TC461954	RuBisCO large subunit	262	4	4		Stroma

c6		G*** T*** G×T*	TC369101	Glutamine synthetase	187	3	10		Stroma
c7		G** T***	TC376723	RuBisCO activase	413	8	18		Stroma
c8		G** T*** G×T*	TC376723	RuBisCO activase	433	8	22		Stroma
c9		G* T*	TC377328	Phosphoribulokinase	176	4	15		Stroma
c10		G*** T*	TC370561	Glycolate oxidase	117	3	14		Peroxisome
c11		G***	TC388958	Glycolate oxidase	68	2	10		Peroxisome
c12		G*** T*	TC386809	Glycolate oxidase	280	4	25		Peroxisome
c13		G*** T*** G×T*	TC461954	RuBisCO large subunit	208	7	8	Yes	Stroma
c14		G*** T**	TC378616	Malate dehydrogenase	267	3	16		Peroxisome
c15		G*** T*	TC386997	Malate dehydrogenase	236	5	18		Peroxisome
c16		T*	TC451379	Photosystem II subunit O-2	327	6	29		Thylakoid
c17		T*	TC404320	Photosystem II subunit O-2	326	5	32		Thylakoid

c18		G*** T***	TC417881	Beta carbonic anhydrase	86	4	17		Stroma
c19		G** T**	CK212480	Thioredoxin peroxidase	336	4	17		Stroma
c20		T*	CK208153	Photosystem I reaction centre subunit II	107	2	6		Thylakoid
c21		G*** T*** G×T*	CK212174	RuBisCO small subunit	162	5	18		Stroma
c22		G* T**	CK215598	RuBisCO small subunit	157	4	12		Stroma
c23		G** T**	CK211194	RuBisCO small subunit	98	2	6		Stroma
c24		G*** T*** G×T*	CK211348	RuBisCO small subunit	98	4	17		Stroma
c25		T*	TC385047	Photosystem I subunit N	214	3	17		Thylakoid

Supplementary Table 2. Abundance data and protein ID information for proteins from contaminating sources that exhibited differing abundance values between genotypes and/or treatments in the 2D-DIGE comparison of mitochondria isolated from roots of CS and AMP after control or salt treatment. Spot number refers to Supplementary Figure 6B. Abundance data was quantified with DeCyder software, error bars represent SEM (n=3). To determine statistical significance, abundance data was analysed using two way ANOVA, and lower p-values are indicated by more asterisks (p<0.05:*, p<0.01:**, p<0.001:***). G denotes genotype effect, T denotes treatment effect and G×T denotes their interaction. Accession is from Uniprot database. MOWSE, number of matched peptides, and coverage data are taken from Mascot search engine. Source of contamination was inferred from organism of matched protein.

Spot number	Abundance data	ANOVA p-value	Accession	Description	MOWSE (MS/MS)	# matched peptides (MS/MS)	% coverage (MS/MS)	Breakdown product?	Source of contamination
c1		T**	P02769	Bovine serum albumin	229	6	12		Isolation buffers
c2		T**	P02769	Bovine serum albumin	65	2	4		Isolation buffers

Supplementary Figure 1A. Overlaid Cy3 versus Cy5 images from all six gels in the 2D-DIGE comparison of isolated shoot mitochondria.

AMP control (Cy3, green) versus CS control (Cy5, red)

CS control (Cy3, green) versus AMP salt (Cy5, red)

CS control (Cy3, green) versus CS salt (Cy5, red)

AMP salt (Cy3, green) versus CS salt (Cy5, red)

CS salt (Cy3, green) versus AMP control (Cy5, red)

AMP salt (Cy3, green) versus AMP control (Cy5, red)

Supplementary Figure 1B. Overlaid Cy3 versus Cy5 images from all six gels in the 2D-DIGE comparison of isolated root mitochondria.

AMP control (Cy3, green) versus CS salt (Cy5, red)

CS salt (Cy3, green) versus AMP salt (Cy5, red)

CS control (Cy3, green) versus AMP control (Cy5, red)

AMP control (Cy3, green) versus AMP salt (Cy5, red)

AMP salt (Cy3, green) versus CS control (Cy5, red)

CS salt (Cy3, green) versus CS control (Cy5, red)

Supplementary Figure 2A. Investigating the composition of the β -CAS protein spot of higher abundance in shoot mitochondria isolated from AMP. This diagram depicts the workflow used to investigate the composition of the β -CAS spot of higher abundance in shoot mitochondria isolated from AMP (Table 3, spot 16). The protein spot of interest was excised from the gel, digested with trypsin and analysed with RP-nano-HPLC-Q-TOF MS/MS. Mass spectra were searched against databases (wheat EST and wheat TC), and unmatched spectra were searched with more variable modifications. Remaining unmatched spectra were filtered for quality, and high quality unmatched spectra analysed via *de novo* sequencing. Peptide sequences assigned to spectra were then refined via homology matching with the MS-BLAST program to correct likely I/L or Q/K misassignments. β -CAS spots from CS were also excised and analysed with mass spectrometry to determine whether spectra were specific to AMP.

i) MS/MS spectrum with fragment ions assigned by *de novo* sequencing

iii) Alignment of refined *de novo* peptide A against the homologous region of wheat β -CAS (TC373702)

iv) Alignment of the region of wheat β -CAS (TC373702) homologous to *de novo* peptide A against β -CAS sequences from other taxa

Bradi5g00610	TLGQVDIFVMGIGSGGTVTGVGKYLKEKNPNAKTYGVPEAEANVLINGGKGPGPHLITNGV	282
TC373702	TLGQVDIFVMGIGSGGTVTGVGKYLKEKNPNAK IYGEPAE EANVLINGGKGPGPHLITNGV	282
LOC_0s04g08350	TLGQVDIFVMGTGGSGTGTGVGKYLKSNPNAKTYGVPEAEANVLINGGKGPGPHLITNGV	281
At3g61440	T LGNVDIFVMGTGGSGTGSGVGRYLSKNPNVKVIYGVPEAESNIINGGKGPGPHAITNGV	272
A9RMD3_PHYA	TAGKI DLIVAGTGTGTGTGTGACRLYKSKNPVKVII GVPESSSVLSGGKGPQHQTGIGA	245
A8J434_CHLRE	TAGNIDMFVAGVGTGGTI SGVGYLYLEKQGPGVVAVPEAPSPVISGGAPGYHQIQGIGA	300
	* * . * . : * . * . * . * . * . : . * . * . : . * . * . * . *	

Supplementary Figure 2C. *De novo* assignment of peptide sequence MGLQQQEEDHPAPAPGVLNIR to a high quality AMP-specific unmatched spectrum, and alignment of the orthologous wheat β -CAS sequence against homologous β -CAS sequences from a range of taxa.

i) MS/MS spectrum with fragment ions assigned by *de novo* sequencing

ii) Table of potential fragment ions from peptide highlighting those detected in spectrum, and error plot for assigned ions

#	Immonium	b	b-H2O	b-NH3	b (2+)	Seq	y	y-H2O	y-NH3	y (2+)	#
1	104.05	132.05	114.04	115.02	66.52	M					21
2	30.03	189.09	177.04	172.04	95.03	G	2169.10	2151.09	2152.08	1085.05	20
3	86.10	302.17	284.16	285.13	151.58	L	2112.04	2094.07	2095.06	1056.54	19
4	101.07	430.23	412.22	413.20	215.61	Q	1998.98	1980.96	1981.99	999.97	18
5	101.07	558.28	540.26	541.24	279.64	Q	1870.94	1852.91	1853.91	935.97	17
6	101.07	686.33	668.32	669.30	343.66	Q	1742.86	1724.84	1725.85	874.91	16
7	102.06	815.37	797.36	798.35	408.19	E	1614.81	1596.80	1597.80	807.91	15
8	102.06	944.41	926.40	927.39	472.71	E	1405.78	1467.78	1468.75	743.39	14
9	88.04	1059.44	1041.43	1042.41	530.22	D	1356.71	1338.73	1339.71	678.87	13
10	110.07	1196.51	1178.46	1179.46	598.75	H	1241.65	1223.62	1224.68	621.36	12
11	70.07	1293.55	1275.54	1276.52	647.28	P	1104.65	1086.62	1087.63	552.83	11
12	44.05	1364.61	1346.57	1347.56	682.80	A	1007.59	989.59	990.57	504.30	10
13	70.07	1461.64	1443.63	1444.62	731.32	P	936.53	918.55	919.38	468.78	9
14	44.05	1532.68	1514.67	1515.65	766.84	A	839.50	821.50	822.48	420.25	8
15	70.07	1629.73	1611.72	1612.71	815.37	P	768.46	750.26	751.43	384.74	7
16	30.03	1686.75	1668.74	1669.73	843.88	G	671.41	653.41	654.39	336.21	6
17	72.08	1785.82	1767.81	1768.80	893.41	V	614.40	596.39	597.37	307.70	5
18	86.10	1898.91	1880.90	1881.89	949.95	L	515.33	497.32	498.30	258.12	4
19	87.06	2012.95	1994.94	1995.92	1006.97	N	402.24	384.22	385.22	201.62	3
20	86.10	2126.03	2108.02	2109.01	1063.43	L	288.17	270.19	271.18	144.06	2
21	129.11					R	175.12	157.11	158.09	88.06

iii) Alignment of refined *de novo* peptide B against the homologous region of wheat β -CAS (TC373702)

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>TC373702                PFSTLQQQQEDHP-----GVLNIRDT
>Refined AMP β-CAS de novo B --MGLQQQEEDHP-APAP-GVLNIR--
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iv) Alignment of the region of wheat β -CAS (TC373702) homologous to *de novo* peptide B against β -CAS sequences from other taxa

Bradi5g00610	GAGGS PFFSTQQQQ-----QEDPIL-----PALKIRDTA AHLIGRT PLVYLNKVTEGCGARIAAKLEFLQPSFSVKDR	102
Tc737370	GAAAS P-F S TLQQQ----- PDSH ----- GVLN IRDTA AHLIGRT PLVYLNKVTEGCGARVAAKLEFLQPSFSVKDR	102
LOC_Os04g08350	AAGSP PFFSTLQLQAAAADPVSGPL-----PGLKTRDASALQIGRT PMVYLNKVTEGCCARIAAKLEFLQPSFSVKDR	101
At3g61440	STVGSS PQS AQRLLR-----LPKPF-----PSTNAKR DASLLIGKT PLVFNLVNVTGCBAAYAAKHQHFPTCSIKDR	92
A9RMD3_PHYPA	TSVVSAQSASTKEKL-----ELNIADDTV QLIGKT PMVYLNVTVBGGCT ANIAAKLEIMPECCSVKDR	74
A8J434_CHLRE	RCRGSVTRTVPVRAQAQATQAATPSIAVSVPDPHVGIQPDA TRVLNGT PMVELNV SVTRGCCGARIAAKLESFEECCSVKDR	120

Supplementary Figure 3. Investigating the composition of the SHMT protein spot of higher abundance in shoot mitochondria isolated from AMP. This diagram depicts the workflow used to investigate the composition of the SHMT spot of higher abundance in shoot mitochondria isolated from AMP (Table 3, spot 11). The protein spot of interest was excised from the gel, digested with trypsin and analysed with RP-nano-HPLC-Q-TOF MS/MS. Mass spectra were searched against databases (wheat EST and wheat TC), and unmatched spectra were searched with more variable modifications. Remaining unmatched spectra were filtered for quality, and high quality unmatched spectra analysed via *de novo* sequencing. SHMT spots from CS were also excised and analysed with mass spectrometry to determine whether spectra were specific to AMP.

Supplementary Figure 4A. Investigating the composition of the MnSOD protein spot of higher abundance in shoot mitochondria isolated from AMP. This diagram depicts the workflow used to investigate the composition of the MnSOD spot of higher abundance in shoot mitochondria isolated from AMP (Table 4, spot 25). The protein spot of interest was excised from the gel, digested with trypsin and analysed with RP-nano-HPLC/Q-TOF MS/MS. Mass spectra were searched against databases (wheat EST and wheat TC), and unmatched spectra were searched with more variable modifications. Remaining unmatched spectra were filtered for quality, and high quality unmatched spectra analysed via *de novo* sequencing. MnSOD spots from CS were also excised and analysed with mass spectrometry to determine whether spectra were specific to AMP.

Supplementary Figure 4B. MS/MS spectra for the isoform-specific MnSOD peptides identified in both CS and AMP. Tandem mass spectra for peptides derived from MnSOD were acquired via RP-nano-HPLC-Q-TOF MS/MS. Spectra were searched against wheatTC and wheatEST databases to match against peptide sequences. Singly and doubly charged y and b ions are coloured and annotated.

Supplementary Figure 4C. MS/MS spectra for the isoform-specific MnSOD peptides identified in both CS and AMP. Tandem mass spectra for peptides derived from MnSOD were acquired via RP-nano-HPLC-Q-TOF MS/MS. Spectra were searched against wheatTC and wheatEST databases to match against peptide sequences. Singly and doubly charged y and b ions are coloured and annotated.

Supplementary Figure 4D. MS/MS spectra for the oxidative modifications to the MnSOD peptide LGWAIDEDFGSEIK identified in both CS and AMP. Tandem mass spectra were for peptides derived from MnSOD were acquired via RP-nano-HPLC-Q-TOF MS/MS. Spectra were matched to peptide sequence by searching against wheatTC and wheatEST databases with a number of variable oxidative modifications enabled. Singly and doubly charged y and b ions are coloured and annotated.

i) MS/MS spectrum of LGWAIDEDFGSEIK
(m/z: 790.39, 2+)

ii) MS/MS spectrum of LGWAIDEDFGSEIK
(W-> Kynurenine, m/z: 792.38, 2+)

Supplementary Figure 4D (continued). MS/MS spectra for the oxidative modifications to the MnSOD peptide LGWAIDEDFGSEIK identified in both CS and AMP. Tandem mass spectra were for peptides derived from MnSOD were acquired via RP-nano-HPLC-Q-TOF MS/MS. Spectra were matched to peptide sequence by searching against wheatTC and wheatEST databases with a number of variable oxidative modifications enabled. Singly and doubly charged y and b ions are coloured and annotated.

iii) MS/MS spectrum of LGWAIDEDFGSEIK
(W → Hydroxy-Trp, m/z: 798.38, 2+)

iv) MS/MS spectrum of LGWAIDEDFGSEIK
(W → N-formylkynurenine, m/z: 806.38, 2+)

Supplementary Figure 4E. MS spectrum displaying the oxidative modifications to the MnSOD peptide NVRPDYLTNIWK identified in both CS and AMP. Mass spectrum of tryptic peptides derived from MnSOD were acquired via MALDI-TOF. Annotated mass peaks match to the unmodified peptide NVRPDYLTNIWK (M+H: 1518.76 Da), as well as masses derived from potential oxidative modifications to the tryptophan residue of the peptide. Chemical structures of the tryptophan modifications that correspond to the detected masses are depicted above each peak.

Supplementary Figure 5A. Investigating the composition of the MDH protein spot of higher abundance in shoot mitochondria isolated from AMP. This diagram depicts the workflow used to investigate the composition of the MDH spot of higher abundance in shoot mitochondria isolated from AMP (Table 5, spot 18). The protein spot of interest was excised from the gel, digested with trypsin and analysed with RP-nano-HPLC/Q-TOF MS/MS. Mass spectra were searched against databases (wheat EST and wheat TC), and unmatched spectra were searched with more variable modifications. Remaining unmatched spectra were filtered for quality, and high quality unmatched spectra analysed via *de novo* sequencing. Peptide sequences assigned to spectra were then refined via homology matching with the MS-BLAST program to correct likely I/L or K/Q misassignments. MDH spots from CS were also excised and analysed with mass spectrometry to determine whether spectra were specific to AMP.

Supplementary Figure 5B. *De novo* assignment of peptide sequence ATAEEVLGLGNQSAKNK to a high quality AMP-specific unmatched spectrum, and alignment of the orthologous wheat MDH sequence against homologous MDH sequences from a range of taxa.

i) MS/MS spectrum with fragment ions assigned by *de novo* sequencing

ii) Table of potential fragment ions from peptide highlighting those detected in spectrum, and error plot for assigned ions

#	Immonium	b	b-H2O	b-NH3	b (2+)	Seq	y	y-H2O	y-NH3	y (2+)	#
1	44.05	72.08	54.03	55.02	36.52	A					17
2	74.06	173.09	155.08	156.07	87.05	T	1658.87	1640.86	1641.84	829.94	16
3	44.05	244.12	226.12	227.10	122.56	A	1557.82	1539.81	1540.80	779.41	15
4	102.06	373.17	355.15	356.15	187.09	E	1486.79	1468.78	1469.76	743.89	14
5	102.06	502.21	484.19	485.19	251.61	E	1357.74	1339.73	1340.72	679.37	13
6	72.08	601.26	583.27	584.26	301.14	V	1228.69	1210.69	1211.67	614.85	12
7	86.10	714.36	696.36	697.34	357.68	L	1129.62	1111.62	1112.61	565.32	11
8	30.03	771.36	753.38	754.36	386.19	G	1016.54	998.54	999.52	508.77	10
9	86.10	884.47	866.46	867.45	442.74	L	959.52	941.52	942.50	480.26	9
10	30.03	941.49	923.48	924.47	471.25	G	846.45	828.43	829.42	423.72	8
11	87.06	1055.54	1037.53	1038.51	528.27	N	789.41	771.36	772.39	395.21	7
12	101.07	1183.60	1165.59	1166.57	592.30	Q	675.38	657.37	658.35	338.19	6
13	60.04	1270.57	1252.62	1253.60	635.81	S	547.30	529.31	530.29	274.16	5
14	44.05	1341.67	1323.65	1324.64	671.33	A	460.28	442.28	443.26	230.64	4
15	101.11	1469.76	1451.75	1452.73	735.38	K	389.23	371.24	372.22	195.13	3
16	87.06	1583.80	1565.79	1566.78	792.40	N	261.16	243.15	244.12	131.08	2
17	101.11					K	147.11	129.10	130.09	74.06	1

iii) Alignment of refined *de novo* peptide A against the homologous region of wheat MDH (TC370105)

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>TC370105                                LGKNGVEEVLGLGQLTQFEKDG
>Refined AMP MDH de novo A  ---ATAEEVLGLGNQSAKNK---
                                .*****: : :*

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iv) Alignment of the region of wheat MDH (TC370105) homologous to *de novo* peptide A against MDH sequences from other taxa

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LOC_Os01g46070      NACLKGLNGVDPVVECSFVQSTVT-ELPFFASKVKLGKNGVEEVLGLGQLSDFEKEGLEN 322
Bradi2g45200        DACLKGLNGVDPDIVECSYVQSTIT-ELPFFASKVRLGKNGVEEVLGLGQLSDFEKEGLE 321
TC370105            DACLKGLNGVDPDIVECSYVQSTVT-ELPFFASKVRLGKNGVEEVLGLGQLTQFEKDGLEA 239
At1g53240           DACLKGLNGVDPDIVECSYVQSTIT-ELPFFASKVRLGKNGVEEVLGLGQLSDFEKEGLEA 323
A9TBX2_PHYPA        ESCLKGLNGAPDIVECSYVASTVVPGLPYFSSKVRLLGNGIEEILGLGSLSDYEQKGLEG 302
A8JHU0_CHLRE        DSCLRLGLNGAP-VVECTYVESTVT-DAPYFASKVKLSTEGVDKIHDGLPLSDYEKAGLKA 354
::*:****.* :*:** **:. *::****.*. :*::: .** *::*: **:
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Supplementary Figure 5C. *De novo* assignment of peptide sequence GLVAALKGHQAGGIGQPLSLLFK to a high quality AMP-specific unmatched spectrum, and alignment of the orthologous wheat MDH sequence against homologous MDH sequences from a range of taxa.

i) MS/MS spectrum with fragment ions assigned by *de novo* sequencing

ii) Table of potential fragment ions from peptide highlighting those detected in spectrum, and error plot for assigned ions

#	Immonium	b	b-H2O	b-NH3	b (2+)	Seq	y	y-H2O	y-NH3	y (2+)	#
1	30.03	58.03	40.02	41.00	29.51	G					23
2	86.09	171.11	153.10	154.09	86.06	L	2218.31	2200.30	2201.28	1109.65	22
3	72.08	270.14	252.17	253.15	135.59	V	2105.22	2087.21	2088.20	1053.11	21
4	44.05	341.21	323.21	324.19	171.11	A	2006.15	1988.14	1989.13	1003.58	20
5	44.05	412.25	394.25	395.10	206.63	A	1935.12	1917.11	1918.09	968.06	19
6	86.10	525.34	507.33	508.31	263.17	L	1864.08	1846.07	1847.05	932.54	18
7	101.11	653.39	635.42	636.41	327.22	K	1751.00	1732.99	1733.97	876.00	17
8	30.03	710.41	692.45	693.43	355.73	G	1622.90	1604.89	1605.87	811.95	16
9	110.07	847.52	829.50	830.49	424.26	H	1565.88	1547.87	1548.85	783.44	15
10	101.07	975.57	957.56	958.55	488.29	Q	1428.75	1410.81	1411.79	714.91	14
11	44.05	1046.61	1028.60	1029.58	523.81	A	1300.71	1282.75	1283.74	650.88	13
12	30.03	1103.63	1085.62	1086.61	552.32	G	1229.67	1211.71	1212.70	615.36	12
13	30.03	1160.65	1142.64	1143.63	580.83	G	1172.64	1154.69	1155.68	586.85	11
14	86.10	1273.74	1255.73	1256.58	637.37	L	1115.61	1097.67	1098.66	558.34	10
15	30.03	1330.76	1312.75	1313.73	665.88	G	1002.54	984.59	985.57	501.80	9
16	101.07	1458.82	1440.81	1441.79	729.91	Q	945.54	927.57	928.55	473.29	8
17	86.10	1571.90	1553.89	1554.88	786.45	L	817.47	799.51	800.49	409.26	7
18	70.07	1668.95	1650.94	1651.93	834.98	P	704.43	686.42	687.41	352.72	6
19	60.04	1755.99	1737.98	1738.96	878.49	S	607.33	589.37	590.35	304.19	5
20	86.10	1869.07	1851.06	1852.04	935.04	L	520.31	502.34	503.32	260.67	4
21	86.10	1982.16	1964.14	1965.13	991.58	L	407.23	389.25	390.24	204.13	3
22	120.08	2129.22	2111.21	2112.20	1065.11	F	294.14	276.17	277.15	147.59	2
23	101.11					K	147.11	129.10	130.08	74.06	1

iii) Alignment of refined *de novo* peptide B against the homologous region of wheat MDH (TC375883)

```
>TC375883      MRSAAQLRRRNYSSASGQPERKVAAILGAAGGIGQPLSLLMKLN
>Refined AMP MDH de novo B  --GLVAALK-----GHQA-----GGIGQPLSLLFK--
      . . * :                * : *                ***** : *
```

iv) Alignment of the region of wheat MDH (TC375883) homologous to *de novo* peptide B against MDH sequences from other taxa

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Bradi2g45200    ---MRPSVMR---SAAQLRRR--SYSSASGQPERKVAAILGAAGGIGQPLSLLMKLNPLVSSLSDYIAATPGVAADISHINSPALVKGFMG 84
TC375883       ---MRPSVMR---SAAQLRRR--NYSSASGQPERKVAAILGAAGGIGQPLSLLMKLNPLVSSLSDYIAATPGVAADVSHINSPALVKGFMG 84
LOC_Os01g46070 ---MRPSLMR---SASQVLRRRRGYSASGQPERKVAAILGAAGGIGQPLSLLMKLNPLVSSLSDYIAGT PGVAADVSHINAPQVKGFMG 85
At1g53240      ---MFRSMLVRSSASAKQAVIRR-SFSSGS--VPERKVAAILGAAGGIGQPLSLLMKLNPLVSSLSDYIANTPGVAADVGHINTRSEVVGFMG 87
A9TBX2_PHYPA   -----MSSQT--PKRKVAVLGAAGGIGQPLSLLMKLNPLVTDLSLYDIAGT PGVASDLSHINTGANVEGFAG 65
A8JHU0_CHLRE   --AMASSTSSAMAKWAAQAARGFAAAAPSSGKGRKVAVLGAAGGIGQPLSLLMKMNSQVSSLSDYIAGT PGVAADVSHINTKAQVKGFD- 119
      : :                * : *                * : *                * : *                * : *
```


Supplementary Figure 6A. Representative 2D-DIGE comparison of shoot mitochondria from CS and AMP highlighting proteins from contaminating organelles that exhibited significantly different abundance values across genotypes or treatments. In this image, Cy3 labelled proteins from shoot mitochondrial samples isolated from CS following control treatment (green) are overlaid against Cy5 labelled proteins from shoot mitochondria isolated from AMP following salinity treatment (red). Marked spots are proteins from contaminating organelles that displayed significant abundance differences between genotypes and/or treatments over the six gel experiment (two-way ANOVA $p < 0.05$). Protein IDs gathered from peptide mass spectrometry data are shown in Supplementary Table 1.

Supplementary Figure 6B. Representative 2D-DIGE comparison of root mitochondria from CS and AMP highlighting proteins from isolation buffers which exhibited significantly different abundance values across genotypes or treatments. In this gel image, Cy3 labelled proteins from root mitochondrial samples isolated from CS salt treatment (green) are overlayed against Cy5 labelled proteins from root mitochondrial samples isolated from AMP salt treatment (red). Marked spots are proteins from isolation buffers that displayed significant abundance differences between genotypes and/or treatments over the six gel experiment (two-way ANOVA $p < 0.05$). Protein IDs gathered from peptide mass spectrometry data are shown in Supplementary Table 2.

Supplementary Table 3

Peptide match information for digested protein spots analysed using MS/MS on MALDI-TOF/TOF. Spots exhibited significant G₁ or GxT effects after ANOVA analysis of the shoot mitochondrial DIGE experiment (Figure 3). Data were searched against the Wheat TC database (v12, DFCI). Spot number refers to Figure 3. Prot_hit_num is the ranking of each protein hit. Prot_score is calculated by Mascot based on combined ions scores of matched peptides. Protein hits presented here were filtered according to prot_score (p<0.05). Prot_acc and prot_desc are accession code and description line of the protein match, copied directly from the database. Prot_mass is the theoretical MW of the protein, calculated by Mascot. Prot_mz is the number of peptides matched to that accession (ions score cut-off of 0). Prot-cover is the percentage of the sequence covered by matched peptides. Pep_exp_mz is the observed m/z of the peptide. Pep_exp_mr is experimental m/z transformed to a relative molecular mass. Pep_calc is the relative molecular mass calculated from the matched peptide sequence. Pep_delta is the difference (error) between the experimental and calculated masses. Pep_miss is the number of missed cleavages. Pep_score is the ions score of each peptide. Pep_res_before, pep_seq, and pep_res_after are sequence of the peptide in 1-letter code, along with the residues that bracket the peptide sequence in the protein (if the peptide forms the protein terminus, then a dash is shown instead). Pep_var_mod details any modifications to the peptide.

prot_number (Figure 3)	Mascoat output																										
1	prot_hit_n	prot_acc	prot_desc	prot_score	prot_mass	prot_matci	prot_matci	prot_sequi	prot_sequi	prot_cover	pep_query	pep_rank	pep_isbold	pep_isuniq	pep_exp_n	pep_exp_n	pep_exp_z	pep_calc_r	pep_delta	pep_miss	pep_score	pep_expect	pep_res_b	pep_seq	pep_res_al	pep_var_mod	
	1	TC412039	homologu	170	26756	2	2	2	2	14.6	21	1	1	1	1817.95	1816.943	1	1816.914	0.0286	0	78.03	1.90E-05	K	GFSVLQACEVAGVDIPR	F	Carbamidomethyl (C)	
	1	TC412039	homologu	170	26756	2	2	2	2	14.6	28	1	1	1	2303.179	2302.172	1	2302.159	0.0127	0	91.93	5.80E-07	R	VELPPNPDALEVFVDGHAVR	I		
	2	TC389811	similar to l	146	36864	3	2	3	2	14.7	8	1	1	0	1356.787	1355.78	1	1355.756	0.0235	0	78.87	1.40E-05	K	NPVIIAGAGLFR	E		
	2	TC389811	similar to l	146	36864	3	2	3	2	14.7	24	1	1	1	1886.026	1885.018	1	1884.995	0.0239	0	54.19	0.0041	R	ALSEVAGAPLPYDSVAAVR	S		
	2	TC389811	similar to l	146	36864	3	2	3	2	14.7	26	3	1	0	1979.102	1978.095	1	1978.074	0.021	1	13.4	43	R	VDEREPSVISA EVKPPVK	Q		
	3	TC376678	similar to l	146	57056	4	1	4	1	11.5	7	1	1	1	1315.762	1314.755	1	1314.73	0.0254	0	22.67	6.5	K	ADVFLLVGTQPR	V		
	3	TC376678	similar to l	146	57056	4	1	4	1	11.5	8	1	0	0	1356.787	1355.78	1	1355.756	0.0235	0	78.87	1.40E-05	K	NPVIIAGAGLFR	E		
	3	TC376678	similar to l	146	57056	4	1	4	1	11.5	25	1	1	1	1916.035	1915.028	1	1915.005	0.0227	0	32.8	0.59	R	ALSEVAGAPLPYDSVTAVR	S		
3	TC376678	similar to l	146	57056	4	1	4	1	11.5	26	3	0	0	1979.102	1978.095	1	1978.074	0.021	1	13.4	43	R	VDEREPSVISA EVKPPVK	Q			
2	prot_hit_n	prot_acc	prot_desc	prot_score	prot_mass	prot_matci	prot_matci	prot_sequi	prot_sequi	prot_cover	pep_query	pep_rank	pep_isbold	pep_isuniq	pep_exp_n	pep_exp_n	pep_exp_z	pep_calc_r	pep_delta	pep_miss	pep_score	pep_expect	pep_res_b	pep_seq	pep_res_al	pep_var_n	pep_var_mod_pos
	1	TC376678	similar to l	187	57056	4	2	4	2	11.4	11	1	1	1	1315.75	1314.743	1	1314.73	0.0129	0	67.4	0.00024	K	ADVFLLVGTQPR	V		
	1	TC376678	similar to l	187	57056	4	2	4	2	11.4	12	1	1	0	1356.778	1355.771	1	1355.756	0.0147	0	86.16	2.90E-06	K	NPVIIAGAGLFR	E		
	1	TC376678	similar to l	187	57056	4	2	4	2	11.4	21	2	1	0	1608.789	1607.782	1	1607.773	0.0092	0	12.33	87	K	VLCEGNGPNPPADIR	S	Carbamidc	0.001000000000000.0
	1	TC376678	similar to l	187	57056	4	2	4	2	11.4	35	1	1	1	1916.024	1915.017	1	1915.005	0.0117	0	23.16	5.6	R	ALSEVAGAPLPYDSVTAVR	S		
	2	TC389811	similar to l	172	36864	2	2	2	2	9.5	12	1	0	0	1356.778	1355.771	1	1355.756	0.0147	0	86.16	2.90E-06	K	NPVIIAGAGLFR	E		
	2	TC389811	similar to l	172	36864	2	2	2	2	9.5	34	1	1	1	1886.015	1885.008	1	1884.995	0.013	0	85.7	3.00E-06	R	ALSEVAGAPLPYDSVAAVR	S		
	3	TC415977	similar to l	106	53351	3	1	3	1	10.9	21	2	0	0	1608.789	1607.782	1	1607.773	0.0092	0	12.33	87	K	VLCEGNGPNPPADIR	S	Carbamidc	0.001000000000000.0
	3	TC415977	similar to l	106	53351	3	1	3	1	10.9	30	1	1	1	1817.935	1816.927	1	1816.914	0.0131	0	74.29	4.70E-05	K	GFSVLQACEVAGVDIPR	F	Carbamidc	0.00000001000000000.0
3	TC415977	similar to l	106	53351	3	1	3	1	10.9	38	2	1	1	2303.168	2302.161	1	2302.159	0.0011	0	19.66	9.8	R	VELPPNPDALEVFVDGHAVR	I			
3	prot_hit_n	prot_acc	prot_desc	prot_score	prot_mass	prot_matci	prot_matci	prot_sequi	prot_sequi	prot_cover	pep_query	pep_rank	pep_isbold	pep_isuniq	pep_exp_n	pep_exp_n	pep_exp_z	pep_calc_r	pep_delta	pep_miss	pep_score	pep_expect	pep_res_b	pep_seq	pep_res_al	pep_var_n	pep_var_mod_pos
	1	TC389811	similar to l	243	36864	4	2	4	2	16.7	10	5	1	0	1099.636	1098.629	1	1098.622	0.0066	0	7.36	2.70E+02	R	ISMVAPNLVR	V		
	1	TC389811	similar to l	243	36864	4	2	4	2	16.7	13	1	1	0	1356.78	1355.773	1	1355.756	0.0165	0	119.36	1.40E-09	K	NPVIIAGAGLFR	E		
	1	TC389811	similar to l	243	36864	4	2	4	2	16.7	26	5	1	0	1601.79	1600.783	1	1600.756	0.0274	0	19.4	18	K	AAVENFYMTDAITR	A		
	1	TC389811	similar to l	243	36864	4	2	4	2	16.7	38	1	1	1	1886.034	1885.027	1	1884.995	0.0322	0	96.63	2.30E-07	R	ALSEVAGAPLPYDSVAAVR	S		
	2	TC376678	similar to l	242	57056	5	2	5	2	13.1	10	5	0	0	1099.636	1098.629	1	1098.622	0.0066	0	7.36	2.70E+02	R	ISMVAPNLVR	V		
	2	TC376678	similar to l	242	57056	5	2	5	2	13.1	12	1	1	1	1315.753	1314.746	1	1314.73	0.0163	0	57.68	0.0022	K	ADVFLLVGTQPR	V		
	2	TC376678	similar to l	242	57056	5	2	5	2	13.1	13	1	0	0	1356.78	1355.773	1	1355.756	0.0165	0	119.36	1.40E-09	K	NPVIIAGAGLFR	E		
	2	TC376678	similar to l	242	57056	5	2	5	2	13.1	26	5	0	0	1601.79	1600.783	1	1600.756	0.0274	0	19.4	18	K	AAVENFYMTDAITR	A		
2	TC376678	similar to l	242	57056	5	2	5	2	13.1	39	1	1	1	1916.044	1915.037	1	1915.005	0.0318	0	40.62	0.095	R	ALSEVAGAPLPYDSVTAVR	S			
3	TC415977	similar to l	143	53351	3	1	3	1	11.1	32	5	1	1	1649.861	1648.854	1	1648.824	0.0296	0	14.66	47	R	FASEVAGVQDLGMLGR	G			
3	TC415977	similar to l	143	53351	3	1	3	1	11.1	36	1	1	1	1817.959	1816.951	1	1816.914	0.0372	0	102.75	6.40E-08	K	GFSVLQACEVAGVDIPR	F	Carbamidc	0.00000001000000000.0	
3	TC415977	similar to l	143	53351	3	1	3	1	11.1	42	1	1	1	2303.181	2302.174	1	2302.159	0.0148	0	25.68	2.4	R	VELPPNPDALEVFVDGHAVR	I			
4	prot_hit_n	prot_acc	prot_desc	prot_score	prot_mass	prot_matci	prot_matci	prot_sequi	prot_sequi	prot_cover	pep_query	pep_rank	pep_isbold	pep_isuniq	pep_exp_n	pep_exp_n	pep_exp_z	pep_calc_r	pep_delta	pep_miss	pep_score	pep_expect	pep_res_b	pep_seq	pep_res_al	pep_var_mod	
	1	TC386349		249	56179	5	3	4	3	13.4	23	2	1	1	1593.944	1592.937	1	1592.893	0.0441	0	10.06	77	K	LLGEFDLVGIPPAPR	G		
	1	TC386349		249	56179	5	3	4	3	13.4	33	1	1	1	1821.961	1820.954	1	1820.902	0.052	0	79.1	1.50E-05	K	SQVVFSTAADNQTVGIR	V		
	1	TC386349		249	56179	5	3	4	3	13.4	36	1	1	1	1939.069	1938.061	1	1937.999	0.0621	0	80.57	8.50E-06	K	GVNPDEAVAMGAALQGGILR	G		
	1	TC386349		249	56179	5	3	4	3	13.4	38	2	1	1	1955.048	1954.041	1	1953.994	0.0469	0	20.18	10	K	GVNPDEAVAMGAALQGGILR	G	Oxidation (M)	
	1	TC386349		249	56179	5	3	4	3	13.4	41	1	1	1	2041.135	2040.128	1	2040.074	0.0538	1	79.38	9.90E-06	R	DKIPAEVATEIETAVADLR	T		
	2	TC398313	similar to l	156	87117	3	2	2	2	4.2	22	1	1	1	1564.857	1563.85	1	1563.805	0.0451	0	75.9	3.50E-05	K	AVITVPAYFNDAQR	Q		
	2	TC398313	similar to l	156	87117	3	2	2	2	4.2	36	1	0	1	1939.069	1938.061	1	1937.999	0.0621	0	80.57	8.50E-06	K	GVNPDEAVAMGAAIQGGILR	G		
2	TC398313	similar to l	156	87117	3	2	2	2	4.2	38	2	0	1	1955.048	1954.041	1	1953.994	0.0469	0	20.18	10	K	GVNPDEAVAMGAAIQGGILR	G	Oxidation (M)		
5	prot_hit_n	prot_acc	prot_desc	prot_score	prot_mass	prot_matci	prot_matci	prot_sequi	prot_sequi	prot_cover	pep_query	pep_rank	pep_isbold	pep_isuniq	pep_exp_n	pep_exp_n	pep_exp_z	pep_calc_r	pep_delta	pep_miss	pep_score	pep_expect	pep_res_b	pep_seq	pep_res_al	pep_var_n	pep_var_mod_pos
	1	CK153924	similar to l	70	20845	1	1	1	1	9.5	42	1	1	1	2040.96	2039.952	1	2040.074	-0.1215	1	69.98	0.00011	R	DKIPAEVATEIETAVADLR	A		
6	prot_hit_n	prot_acc	prot_desc	prot_score	prot_mass	prot_matci	prot_matci	prot_sequi	prot_sequi	prot_cover	pep_query	pep_rank	pep_isbold	pep_isuniq	pep_exp_n	pep_exp_n	pep_exp_z	pep_calc_r	pep_delta	pep_miss	pep_score	pep_expect	pep_res_b	pep_seq	pep_res_al	pep_var_n	pep_var_mod_pos
	1	TC428099	homologu	101	92530	2	2	1	1	2.3	55	1	1	1	2093.086	2092.079	1	2092.011	0.0683	0	101.22	7.70E-08	R	MISTSEEIAQVGTISANGER	E		
	1	TC428099	homologu	101	92530	2	2	1	1	2.3	56	1	1	1	2109.128	2108.121	1	2108.006	0.1154	0	70.56	8.50E-05	R	MISTSEEIAQVGTISANGER	E	Oxidation (	0.2000000000000000000.0
2	TC374031	homologu	101	44751	1	1	1	1	4.8	57	1	1	1	2120.182	2119.174	1	2119.022	0.1529	0	100.74	6.80E-08	R	MINTSEEIAQVGTISANGER	E			
7	prot_hit_n	prot_acc	prot_desc	prot_score	prot_mass	prot_matci	prot_matci	prot_sequi	prot_sequi	prot_cover	pep_query	pep_rank	pep_isbold	pep_isuniq	pep_exp_n	pep_exp_n	pep_exp_z	pep_calc_r	pep_delta	pep_miss	pep_score	pep_expect	pep_res_b	pep_seq	pep_res_al	pep_var_n	pep_var_mod_pos
	1	TC428099	homologu	108	92530	2	2	1	1	2.3	40	1	1	1	2093.086	2092.079	1	2092.011	0.0683	0	108.12	1.60E-08	R	MISTSEEIAQVGTISANGER	E		
	1	TC428099	homologu	108	92530	2	2	1	1	2.3	42	1	1	1	2109.139	2108.131	1	2108.006	0.1258	0	63.94	0.00038	R	MISTSEEIAQVGTISANGER	E	Oxidation (	0.2000000000000000000.0
8	prot_hit_n	prot_acc	prot_desc	prot_score	prot_mass	prot_matci	prot_matci	prot_sequi	prot_sequi	prot_cover	pep_query	pep_rank	pep_isbold	pep_isuniq	pep_exp_n	pep_exp_n	pep_exp_z	pep_calc_r	pep_delta	pep_miss	pep_score	pep_expect	pep_res_b	pep_seq	pep_res_al	pep_var_n	pep_var_mod_pos
	1	TC428099	homologu	205	92530	3	2	3	2	5.1	7	1	1	0	1289.744	1288.736	1	1288.703	0.0335	0	38.1	0.21	R	TVIIEQSFGAPK	V		
	1	TC428099	homologu	205	92530	3	2	3	2	5.1	9	1	1	1	1430.767	1429.759	1	1429.724	0.0352	0	92.17	9.40E-07	R	GYISPYFITNQK	T		
	1	TC428099	homologu	205	92530	3	2	3	2	5.1	19	1	1	1	1901.076	1900.069	1	1900.031	0.0384	0	75.12	2.60E-05	K	AAVEEGIVPGGGVALLYASK	A		
	2	TC385776	homologu	65	26867	2	0	2	0																		

	1	TC404839	UniRef100.	308	75142	6	2	6	2	13.1	29	1	1	1	1676.004	1674.996	1	1674.942	0.0546	0	28.98	0.87 R	LVLVEAQHLGENVVR	T			
	1	TC404839	UniRef100.	308	75142	6	2	6	2	13.1	46	2	1	1	2061.109	2060.102	1	2060.043	0.0593	0	17.5	17 R	QISELGIYPADVPLDSTSR	M			
	1	TC404839	UniRef100.	308	75142	6	2	6	2	13.1	50	1	1	1	2186.218	2185.21	1	2185.138	0.0723	0	91.94	5.00E-07 R	IPSAVGYQPTLATDLGGLQER	I			
10	prot_hit_n_prot_acc	prot_desc	prot_score	prot_mass	prot_matci	prot_matci	prot_sequi	prot_sequi	prot_cover	pep_query	pep_rank	pep_isbold	pep_isuniq	pep_exp_n	pep_exp_n	pep_exp_z	pep_calc_r	pep_delta	pep_miss	pep_score	pep_expect	pep_res_b_i	pep_seq	pep_res_al	pep_var_r	pep_var_mod_pos	
	1	TC368629	ATP synthase	244	77756	6	3	5	3	12	21	8	1	1	1438.884	1437.877	1	1437.842	0.0352	0	8.9	79 R	GIRPAINVGLSVSR	V			
	1	TC368629	ATP synthase	244	77756	6	3	5	3	12	23	1	1	1	1537.79	1536.782	1	1536.736	0.0462	0	110.03	1.50E-08 R	EAFPGDVFLHSR	L			
	1	TC368629	ATP synthase	244	77756	6	3	5	3	12	34	1	1	1	1834.896	1833.889	1	1833.836	0.0534	0	56.56	0.0029 R	MTNFYTNFQVDIGR	V			
	1	TC368629	ATP synthase	244	77756	6	3	5	3	12	35	1	1	1	1850.891	1849.884	1	1849.831	0.0533	0	39.24	0.15 R	MTNFTYNFQVDIGR	V	Oxidation I	0.200000000000000.0	
	1	TC368629	ATP synthase	244	77756	6	3	5	3	12	45	1	1	1	2308.222	2307.215	1	2307.15	0.0653	0	53.43	0.0037 R	EVAFAAQFGSDLAATAQTALLNR	G			
	1	TC368629	ATP synthase	244	77756	6	3	5	3	12	46	2	1	1	2373.295	2372.288	1	2372.259	0.0291	0	14.9	24 K	GIALNLLENENVGVFSGSDTAIK	E			
11	prot_hit_n_prot_acc	prot_desc	prot_score	prot_mass	prot_matci	prot_matci	prot_sequi	prot_sequi	prot_cover	pep_query	pep_rank	pep_isbold	pep_isuniq	pep_exp_n	pep_exp_n	pep_exp_z	pep_calc_r	pep_delta	pep_miss	pep_score	pep_expect	pep_res_b_i	pep_seq	pep_res_al	pep_var_r	pep_var_mod_pos	
	1	TC449830	UniRef100.	202	73856	6	2	5	2	12.1	8	2	1	1	999.4834	998.4761	1	998.4457	0.0304	0	24.45	7.1 K	YSEGYPGAR	Y			
	1	TC449830	UniRef100.	202	73856	6	2	5	2	12.1	11	1	1	1	1091.66	1090.653	1	1090.614	0.0393	0	38.65	0.15 K	LIVAGASAYAR	L			
	1	TC449830	UniRef100.	202	73856	6	2	5	2	12.1	28	1	1	1	1660.901	1659.894	1	1659.833	0.0606	0	55.89	0.0033 K	ISAVSIFFETMPYR	L			
	1	TC449830	UniRef100.	202	73856	6	2	5	2	12.1	29	2	1	1	1676.887	1675.88	1	1675.828	0.0519	0	20.12	13 K	ISAVSIFFETMPYR	L	Oxidation I	0.00000000002000.0	
	1	TC449830	UniRef100.	202	73856	6	2	5	2	12.1	46	1	1	1	2291.19	2290.183	1	2290.117	0.0667	0	17.42	16 R	IMALDLPHGGHLSHGYSQTDTK	K			
	1	TC449830	UniRef100.	202	73856	6	2	5	2	12.1	51	1	1	1	2596.482	2595.475	1	2595.429	0.0463	0	65.37	0.00014 K	INAAVFPLQGPPHNHTITGLAVALK	Q			
12	prot_hit_n_prot_acc	prot_desc	prot_score	prot_mass	prot_matci	prot_matci	prot_sequi	prot_sequi	prot_cover	pep_query	pep_rank	pep_isbold	pep_isuniq	pep_exp_n	pep_exp_n	pep_exp_z	pep_calc_r	pep_delta	pep_miss	pep_score	pep_expect	pep_res_b_i	pep_seq	pep_res_al	pep_var_r	pep_var_mod_pos	
	1	TC387564	homologue	176	56897	5	1	5	1	16.6	21	2	1	1	1300.647	1299.64	1	1299.61	0.0305	0	27.22	3.5 K	DDGTLASYVGFR	V			
	1	TC387564	homologue	176	56897	5	1	5	1	16.6	24	2	1	1	1555.879	1554.872	1	1554.841	0.0314	0	14.71	38 R	GVLFATEALLAEHGK	G			
	1	TC387564	homologue	176	56897	5	1	5	1	16.6	32	1	1	1	1746.887	1745.88	1	1745.825	0.0547	0	92.26	8.10E-07 K	GGIGCSPGDLSISELER	L	Carbamidc	0.00001000000000000.0	
	1	TC387564	homologue	176	56897	5	1	5	1	16.6	36	2	1	1	2210.155	2209.148	1	2209.09	0.0575	0	17.56	16 K	YIIEAANHPTDPEADEILAK	K			
	1	TC387564	homologue	176	56897	5	1	5	1	16.6	37	2	1	1	2214.218	2213.211	1	2213.159	0.0517	0	24.31	3 K	FHGYSPAVVTGKPVDLGGSLGR	D			
13	prot_hit_n_prot_acc	prot_desc	prot_score	prot_mass	prot_matci	prot_matci	prot_sequi	prot_sequi	prot_cover	pep_query	pep_rank	pep_isbold	pep_isuniq	pep_exp_n	pep_exp_n	pep_exp_z	pep_calc_r	pep_delta	pep_miss	pep_score	pep_expect	pep_res_b_i	pep_seq	pep_res_al	pep_var_r	pep_var_mod_pos	
	1	TC379352	homologue	129	51163	4	1	4	1	10.7	12	1	1	1	1209.632	1208.625	1	1208.605	0.0195	0	38.52	0.26 K	GEWNVAGIAHR	A			
	1	TC379352	homologue	129	51163	4	1	4	1	10.7	16	3	1	1	1292.701	1291.694	1	1291.693	0.0012	0	17.47	31 R	NFLPGYQQVVK	G			
	1	TC379352	homologue	129	51163	4	1	4	1	10.7	20	4	1	1	1602.842	1601.835	1	1601.798	0.0362	0	17.92	23 K	NPNFVGCVEGALGIR	D	Carbamidc	0.000000100000000.0	
	1	TC379352	homologue	129	51163	4	1	4	1	10.7	21	1	1	1	1689.898	1688.891	1	1688.846	0.0451	0	57.36	0.0024 R	LKPFNCNLLYHDR	L	Carbamidc	0.0000010000000.0	
14	prot_hit_n_prot_acc	prot_desc	prot_score	prot_mass	prot_matci	prot_matci	prot_sequi	prot_sequi	prot_cover	pep_query	pep_rank	pep_isbold	pep_isuniq	pep_exp_n	pep_exp_n	pep_exp_z	pep_calc_r	pep_delta	pep_miss	pep_score	pep_expect	pep_res_b_i	pep_seq	pep_res_al	pep_var_r	pep_var_mod_pos	
	1	TC379352	homologue	214	51163	5	3	5	3	15.7	8	1	1	1	1209.629	1208.622	1	1208.605	0.0166	0	60.43	0.0017 K	GEWNVAGIAHR	A			
	1	TC379352	homologue	214	51163	5	3	5	3	15.7	14	1	1	1	1381.675	1380.668	1	1380.656	0.0115	0	10.89	1.40E+02 K	GEDFPAENYVK	E			
	1	TC379352	homologue	214	51163	5	3	5	3	15.7	20	1	1	1	1602.821	1601.813	1	1601.798	0.0149	0	67.74	0.00025 K	NPNFVGCVEGALGIR	D	Carbamidc	0.000000100000000.0	
	1	TC379352	homologue	214	51163	5	3	5	3	15.7	24	1	1	1	1689.871	1688.863	1	1688.846	0.0177	0	58.72	0.0019 R	LKPFNCNLLYHDR	L	Carbamidc	0.0000010000000.0	
	1	TC379352	homologue	214	51163	5	3	5	3	15.7	41	1	1	1	2577.301	2576.294	1	2576.285	0.0092	0	21.18	5.7 K	HIEDMHVLITTPFHPAYVTAER	I			
15	prot_hit_n_prot_acc	prot_desc	prot_score	prot_mass	prot_matci	prot_matci	prot_sequi	prot_sequi	prot_cover	pep_query	pep_rank	pep_isbold	pep_isuniq	pep_exp_n	pep_exp_n	pep_exp_z	pep_calc_r	pep_delta	pep_miss	pep_score	pep_expect	pep_res_b_i	pep_seq	pep_res_al	pep_var_r	pep_var_mod_pos	
	1	TC390427	homologue	106	58357	3	2	3	2	10.2	9	1	1	1	1284.663	1283.655	1	1283.615	0.0406	0	50.69	0.016 K	DDGTLASFVGFR	V			
	1	TC390427	homologue	106	58357	3	2	3	2	10.2	26	1	1	1	2202.228	2201.221	1	2201.171	0.0499	0	43.62	0.033 K	FHGHSPAVVTGKPIDLGGSLGR	D			
	1	TC390427	homologue	106	58357	3	2	3	2	10.2	28	10	1	1	2224.169	2223.162	1	2223.106	0.0557	0	13.47	41 K	FIIEAANHPTDPEADEILTK	K			
16	prot_hit_n_prot_acc	prot_desc	prot_score	prot_mass	prot_matci	prot_matci	prot_sequi	prot_sequi	prot_cover	pep_query	pep_rank	pep_isbold	pep_isuniq	pep_exp_n	pep_exp_n	pep_exp_z	pep_calc_r	pep_delta	pep_miss	pep_score	pep_expect	pep_res_b_i	pep_seq	pep_res_al	pep_var_r	pep_var_mod_pos	
	1	TC381804	similar to l	80	39183	3	1	2	1	7.9	7	7	1	1	1278.565	1277.557	1	1277.709	-0.1518	0	15.01	1.90E+02 K	LIVTVHPSAGER	Y			
	1	TC381804	similar to l	80	39183	3	1	2	1	7.9	20	1	1	0	1860.044	1859.036	1	1857.918	1.1182	0	64.63	0.0013 K	GYELVLTMPSYTSLER	R			
	1	TC381804	similar to l	80	39183	3	1	2	1	7.9	21	1	1	0	1876.076	1875.069	1	1873.913	1.156	0	33.65	1.5 K	GYELVLTMPSYTSLER	R	Oxidation I	0.0000000200000000.0	
	2	TC373702	similar to l	76	37787	3	1	2	1	7.9	8	1	1	0	1294.573	1293.566	1	1293.697	-0.1314	0	11.55	4.10E+02 K	LEFLQPSFSVK	D			
	2	TC373702	similar to l	76	37787	3	1	2	1	7.9	20	1	0	0	1860.044	1859.036	1	1857.918	1.1182	0	64.63	0.0013 K	GYELVLTMPSYTSLER	R			
	2	TC373702	similar to l	76	37787	3	1	2	1	7.9	21	1	0	0	1876.076	1875.069	1	1873.913	1.156	0	33.65	1.5 K	GYELVLTMPSYTSLER	R	Oxidation I	0.0000000200000000.0	
	3	TC438181	homologue	53	22345	1	1	1	1	5.4	6	1	1	1	1255.488	1254.48	1	1253.659	0.8213	0	52.53	0.032 R	IFQAACVAYLR	K			
17	prot_hit_n_prot_acc	prot_desc	prot_score	prot_mass	prot_matci	prot_matci	prot_sequi	prot_sequi	prot_cover	pep_query	pep_rank	pep_isbold	pep_isuniq	pep_exp_n	pep_exp_n	pep_exp_z	pep_calc_r	pep_delta	pep_miss	pep_score	pep_expect	pep_res_b_i	pep_seq	pep_res_al	pep_var_r	pep_var_mod_pos	
	1	TC390353	homologue	67	42988	3	0	3	0	6.9	2	1	1	1	1154.661	1153.654	1	1153.624	0.0294	0	21.68	9.7 R	VGIFSQGPPPR	S			
	1	TC390353	homologue	67	42988	3	0	3	0	6.9	4	1	1	1	1310.762	1309.755	1	1309.726	0.0291	1	19.95	12 R	RVGIFSQGPPPR	S			
	1	TC390353	homologue	67	42988	3	0	3	0	6.9	9	1	1	1	1752.888	1751.881	1	1751.853	0.0284	0	25.49	3.8 K	VNDHHVVLVVNAGCR	D	Carbamidc	0.000000000000010.0	
18	prot_hit_n_prot_acc	prot_desc	prot_score	prot_mass	prot_matci	prot_matci	prot_sequi	prot_sequi	prot_cover	pep_query	pep_rank	pep_isbold	pep_isuniq	pep_exp_n	pep_exp_n	pep_exp_z	pep_calc_r	pep_delta	pep_miss	pep_score	pep_expect	pep_res_b_i	pep_seq	pep_res_al	pep_var_r	pep_var_mod_pos	
	1	CA617342	homologue	121	17216	2	2	2	2	23.6	4	1	1	1	1219.477	1218.469	1	1218.697	-0.2279	0	65.8	0.0028 K	LFGVTTLDVVR	A			
	1	CA617342	homologue	121	17216	2	2	2	2	23.6	32	1	1	1	2658.862	2657.855	1	2657.301	0.5541	0	55.12	0.01 K	GFMGDDQLGEALGSDVVIIPAGVPR	K	Oxidation I	0.002000000000000000000000.0	
	2	TC374980	similar to l	51	36862	1	1	1	1	4.2	4	2	0	1	1219.477	1218.469	1	1219.616	-1.1464	0	54.52	0.038 R	ASAAVAGSSTATAR	V			
19	prot_hit_n_prot_acc	prot_desc	prot_score	prot_mass	prot_matci	prot_matci	prot_sequi	prot_sequi	prot_cover	pep_query																	

		1	TC369790	similar to l	221	40548	8	1	8	1	30.7	12	1	1	1	1346.833	1345.826	1	1345.808	0.0174	0	11.91	49	K	LAALLQHEVKPK	S	
		1	TC369790	similar to l	221	40548	8	1	8	1	30.7	17	4	1	1	1471.802	1470.795	1	1470.772	0.0227	1	10.45	1.30E+02	K	KGGLYSLDVASAYK	Y	
		1	TC369790	similar to l	221	40548	8	1	8	1	30.7	20	1	1	1	1500.724	1499.716	1	1499.689	0.0271	0	61.37	0.0012	K	GLAFGGGEAGFDTSSGK	F	
		1	TC369790	similar to l	221	40548	8	1	8	1	30.7	33	1	1	1	2225.161	2224.154	1	2224.116	0.0371	0	30.3	0.89	K	YTGGSFVTKPDFHASAILADK	G	
		1	TC369790	similar to l	221	40548	8	1	8	1	30.7	38	1	1	1	2549.36	2548.353	1	2548.339	0.0141	1	33.59	0.31	R	KLSTNENTLTVGGLYTVDPQTAVK	A	
		1	TC369790	similar to l	221	40548	8	1	8	1	30.7	42	3	1	1	2739.409	2738.402	1	2738.392	0.0101	1	28.07	1	K	YTGGSFVTKPDFHASAILADKGDTIK	V	
22	prot_hit_n	prot_acc	prot_desc	prot_score	prot_mass	prot_matcl	prot_matcl	prot_sequ	prot_sequ	prot_cover	pep_query	pep_rank	pep_isbold	pep_isuniq	pep_exp_n	pep_exp_n	pep_exp_z	pep_calc_r	pep_delta	pep_miss	pep_score	pep_expec	pep_res_b	pep_seq	pep_res_a	pep_var_n	pep_var_mod_pos
		1	TC368846	homologu	308	39777	6	3	6	3	26	5	4	1	0	1218.655	1217.648	1	1217.666	-0.0181	0	15.57	50	K	TILSFAVPDQK	S	
		1	TC368846	homologu	308	39777	6	3	6	3	26	11	1	1	1	1396.764	1395.757	1	1395.762	-0.0055	0	49.04	0.018	K	ASALIQHEFRPK	S	
		1	TC368846	homologu	308	39777	6	3	6	3	26	13	1	1	0	1555.901	1554.894	1	1554.898	-0.0039	1	125.67	2.60E-10	K	KADLILGEIQSQIK	N	
		1	TC368846	homologu	308	39777	6	3	6	3	26	15	1	1	0	1582.78	1581.772	1	1581.768	0.0048	0	38.11	0.23	K	GDSLTSASYHIVEK	S	
		1	TC368846	homologu	308	39777	6	3	6	3	26	22	1	1	0	2143.14	2142.132	1	2142.117	0.0155	0	60.21	0.0009	K	ANSASNVITTITADDLAAPGLK	T	
		1	TC368846	homologu	308	39777	6	3	6	3	26	24	4	1	0	2340.173	2339.165	1	2339.176	-0.0103	0	19.04	11	K	YNAALSYTNQDLIASLNLNNK	G	
		2	TC378886	homologu	296	33820	6	2	6	2	30.6	5	4	0	0	1218.655	1217.648	1	1217.666	-0.0181	0	15.57	50	K	TILSFAVPDQK	S	
		2	TC378886	homologu	296	33820	6	2	6	2	30.6	10	1	1	1	1387.702	1386.695	1	1386.697	-0.0015	0	37.52	0.3	K	ASALIQHEFMPK	R	Oxidation 0.000000000200.0
		2	TC378886	homologu	296	33820	6	2	6	2	30.6	13	1	0	0	1555.901	1554.894	1	1554.898	-0.0039	1	125.67	2.60E-10	K	KADLILGEIQSQIK	N	
		2	TC378886	homologu	296	33820	6	2	6	2	30.6	15	1	0	0	1582.78	1581.772	1	1581.768	0.0048	0	38.11	0.23	K	GDSLTSASYHIVEK	S	
		2	TC378886	homologu	296	33820	6	2	6	2	30.6	22	1	0	0	2143.14	2142.132	1	2142.117	0.0155	0	60.21	0.0009	K	ANSASNVITTITADDLAAPGLK	T	
		2	TC378886	homologu	296	33820	6	2	6	2	30.6	24	4	0	0	2340.173	2339.165	1	2339.176	-0.0103	0	19.04	11	K	YNAALSYTNQDLIASLNLNNK	G	
23	prot_hit_n	prot_acc	prot_desc	prot_score	prot_mass	prot_matcl	prot_matcl	prot_sequ	prot_sequ	prot_cover	pep_query	pep_rank	pep_isbold	pep_isuniq	pep_exp_n	pep_exp_n	pep_exp_z	pep_calc_r	pep_delta	pep_miss	pep_score	pep_expec	pep_res_b	pep_seq	pep_res_a	pep_var_n	pep_var_mod_pos
		1	TC377466	UniRef100	224	42074	5	3	3	3	10.7	5	1	1	1	1250.672	1249.665	1	1249.667	-0.0018	0	57.76	0.003	R	TYLDTLQQLR	K	
		1	TC377466	UniRef100	224	42074	5	3	3	3	10.7	14	1	1	0	1465.666	1464.659	1	1464.656	0.0035	1	56.01	0.0039	R	EEFKDEAMPDVR	K	
		1	TC377466	UniRef100	224	42074	5	3	3	3	10.7	16	2	1	0	1481.653	1480.645	1	1480.65	-0.0051	1	12.89	73	R	EEFKDEAMPDVR	K	Oxidation 0.000000020000.0
		1	TC377466	UniRef100	224	42074	5	3	3	3	10.7	22	1	1	1	2090.043	2089.036	1	2089.015	0.021	0	110.34	9.90E-09	K	ITIDPDDPTAVANYAQVMR	T	
		1	TC377466	UniRef100	224	42074	5	3	3	3	10.7	24	3	1	1	2106.035	2105.028	1	2105.01	0.0181	0	25.73	2.9	K	ITIDPDDPTAVANYAQVMR	T	Oxidation 0.000000000000000020.0
		2	CK154460	homologu	77	29067	3	1	2	1	8.7	5	6	0	0	1250.672	1249.665	1	1249.638	0.0272	0	20.69	15	K	NMGLLLAEFDK	I	
		2	CK154460	homologu	77	29067	3	1	2	1	8.7	14	1	0	0	1465.666	1464.659	1	1464.656	0.0035	1	56.01	0.0039	R	EEFKDEAMPDVR	K	
		2	CK154460	homologu	77	29067	3	1	2	1	8.7	16	2	0	0	1481.653	1480.645	1	1480.65	-0.0051	1	12.89	73	R	EEFKDEAMPDVR	K	Oxidation 0.000000020000.0
24	prot_hit_n	prot_acc	prot_desc	prot_score	prot_mass	prot_matcl	prot_matcl	prot_sequ	prot_sequ	prot_cover	pep_query	pep_rank	pep_isbold	pep_isuniq	pep_exp_n	pep_exp_n	pep_exp_z	pep_calc_r	pep_delta	pep_miss	pep_score	pep_expec	pep_res_b	pep_seq	pep_res_a	pep_var_n	pep_var_mod_pos
		1	TC418201	UniRef100	130	28955	3	2	3	2	13.3	10	1	1	1	999.4557	998.4484	1	998.4457	0.0027	0	52.21	0.011	K	YSEGYPGAR	Y	
		1	TC418201	UniRef100	130	28955	3	2	3	2	13.3	11	1	1	1	1091.623	1090.616	1	1090.614	0.0025	0	50.7	0.014	K	LIVAGASAYAR	L	
		1	TC418201	UniRef100	130	28955	3	2	3	2	13.3	24	1	1	1	1738.84	1737.833	1	1737.831	0.002	0	27.43	2.4	R	LDESTGLIDYDQLEK	S	
25	prot_hit_n	prot_acc	prot_desc	prot_score	prot_mass	prot_matcl	prot_matcl	prot_sequ	prot_sequ	prot_cover	pep_query	pep_rank	pep_isbold	pep_isuniq	pep_exp_n	pep_exp_n	pep_exp_z	pep_calc_r	pep_delta	pep_miss	pep_score	pep_expec	pep_res_b	pep_seq	pep_res_a	pep_var_n	pep_var_mod_pos
		1	gi2523742	gbCA65890	100	15315	2	1	2	1	20.1	12	1	1	1	1582.767	1581.76	1	1579.715	2.0445	0	58.94	0.033	K	LGWANDEDFGSIEK	X	
		1	gi2523742	gbCA65890	100	15315	2	1	2	1	20.1	13	1	1	0	1600.788	1599.78	1	1598.774	1.006	0	41.49	1.8	K	FNGGGHVNHSIFWK	N	
		2	gi1995707	gbBJ21720	90	23847	2	0	2	0	12	7	1	1	1	1518.815	1517.808	1	1517.799	0.0087	0	48.45	0.39	K	NVRPDYLTNIWK	V	
		2	gi1995707	gbBJ21720	90	23847	2	0	2	0	12	13	1	0	0	1600.788	1599.78	1	1598.774	1.006	0	41.49	1.8	K	FNGGGHVNHSIFWK	N	
26	prot_hit_n	prot_acc	prot_desc	prot_score	prot_mass	prot_matcl	prot_matcl	prot_sequ	prot_sequ	prot_cover	pep_query	pep_rank	pep_isbold	pep_isuniq	pep_exp_n	pep_exp_n	pep_exp_z	pep_calc_r	pep_delta	pep_miss	pep_score	pep_expec	pep_res_b	pep_seq	pep_res_a	pep_var_n	pep_var_mod_pos
		1	TC395139	UniRef100	69	35012	2	1	2	1	6.3	2	9	1	1	988.4357	987.4284	1	987.4185	0.0099	0	5.75	4.50E+02	K	YAGEEYEK	V	
		1	TC395139	UniRef100	69	35012	2	1	2	1	6.3	11	1	1	1	1518.825	1517.818	1	1517.799	0.0187	0	63.45	0.00063	K	NVRPDYLTNIWK	V	
	prot_hit_n	prot_acc	prot_desc	prot_score	prot_mass	prot_matcl	prot_matcl	prot_sequ	prot_sequ	prot_cover	pep_query	pep_rank	pep_isbold	pep_isuniq	pep_exp_n	pep_exp_n	pep_exp_z	pep_calc_r	pep_delta	pep_miss	pep_score	pep_expec	pep_res_b	pep_seq	pep_res_a	pep_var_n	pep_var_mod_pos
		1	TC371824	homologu	145	35679	3	1	3	1	11.4	2	9	1	1	973.5742	972.5669	1	972.5604	0.0066	0	19.26	19	R	GLISEIVSR	F	
		1	TC371824	homologu	145	35679	3	1	3	1	11.4	10	1	1	1	1344.765	1343.758	1	1343.756	0.002	0	104.67	4.50E-08	R	TFIAIKPDGVQR	G	
		1	TC371824	homologu	145	35679	3	1	3	1	11.4	13	1	1	1	1625.893	1624.886	1	1624.89	-0.0042	1	20.6	11	K	SEPGTIRGD LAVVVGR	N	

Supplementary Table 4

Peptide match information for digested protein spots analysed using MS/MS on MALDI-TOF/TOF. Spots exhibited significant G, T or GxT effects after ANOVA analysis of the root mitochondrial DIGE experiment (Figure 4). Data were searched against the Wheat TC database (v12, DFCI). Spot number refers to Figure 4. Prot_hit_num is the ranking of each protein hit. Prot_score is calculated by Mascot based on combined ions scores of matched peptides. Protein hits presented here were filtered according to prot_score (p<0.05). Prot_acc and prot_desc are accession code and description line of the protein match, copied directly from the database. Prot_mass is the theoretical MW of the protein, calculated by Mascot. Prot_match is the number of peptides matched to that accession (ions score cut-off of 0). Prot-cover is the percentage of the sequence covered by matched peptides. Pep_exp_mz is the observed m/z of the peptide. Pep_exp_mr is experimental m/z transformed to a relative molecular mass. Pep_calc is the relative molecular mass calculated from the matched peptide sequence. Pep_delta is the difference (error) between the experimental and calculated masses. Pep_miss is the number of missed cleavages. Pep_score is the ions score of each peptide. Pep_res_before, pep_seq, and pep_res_after are sequence of the peptide in 1-letter code, along with the residues that bracket the peptide sequence in the protein (if the peptide forms the protein terminus, then a dash is shown instead). Pep_var_mod details any modifications to the peptide.

number (Figure 4)	Mascot output																											
1	prot_hit_nu	prot_acc	prot_desc	prot_score	prot_mass	prot_match	prot_match	prot_seque	prot_seque	prot_cover	pep_query	pep_rank	pep_isbold	pep_isuniq	pep_exp_r	pep_exp_r	pep_exp_z	pep_calc_n	pep_delta	pep_miss	pep_score	pep_expect	pep_res_b	pep_seq	pep_res_af	pep_var_m	pep_var_m	pep_scan_title
	1	BQ238531	similar to U	419	20976	9	3	8	3	53.9	5	1	1	1	914.5595	913.5523	1	913.5596	-0.0074	0	45.8	0.19	R	ILLESAIR	N			
	1	BQ238531	similar to U	419	20976	9	3	8	3	53.9	17	6	1	1	1132.645	1131.638	1	1131.64	-0.0025	1	23	33	R	IDRLPYsir	I			
	1	BQ238531	similar to U	419	20976	9	3	8	3	53.9	22	1	1	1	1184.677	1183.669	1	1183.671	-0.0021	0	73.63	0.00027	K	QVEIPFKPAR	V			
	1	BQ238531	similar to U	419	20976	9	3	8	3	53.9	24	1	1	1	1197.547	1196.54	1	1196.513	0.0265	0	33.5	2.8	R	NCDEFQVTGK	D	Carbamido	0.0100000000.0	
	1	BQ238531	similar to U	419	20976	9	3	8	3	53.9	26	1	1	1	1265.66	1264.653	1	1264.645	0.0077	0	69.15	0.00075	K	YYSLPALADPR	I			
	1	BQ238531	similar to U	419	20976	9	3	8	3	53.9	47	1	1	1	1724.797	1723.79	1	1723.784	0.0061	0	45.82	0.11	R	SENAVQANMELEFSR	N			
	1	BQ238531	similar to U	419	20976	9	3	8	3	53.9	48	1	1	1	1740.8	1739.792	1	1739.778	0.0139	0	107.38	7.90E-08	R	SENAVQANMELEFSR	N	Oxidation (I	0.000000002000000.0	
	1	BQ238531	similar to U	419	20976	9	3	8	3	53.9	59	1	1	1	2120.082	2119.075	1	2119.081	-0.0061	0	21.5	23	R	VLLQDFTGVPVVDLACMR	D	Carbamido	0.0000000000000000120.0	
	1	BQ238531	similar to U	419	20976	9	3	8	3	53.9	60	1	1	1	2140.054	2139.047	1	2139.048	-0.0012	0	45.35	0.092	K	NSYDEILTSIAKPGGGADFGK	Y			
	2	TC373025		297	40168	4	2	4	2	14.9	7	1	1	1	945.4051	944.3978	1	944.3988	-0.001	0	36.16	1.9	K	DFNSYSGSR	R			
	2	TC373025		297	40168	4	2	4	2	14.9	32	1	1	1	1381.685	1380.678	1	1380.671	0.0065	0	64.14	0.0022	K	STYIHEPPYFK	D			
	2	TC373025		297	40168	4	2	4	2	14.9	40	3	1	1	1542.733	1541.726	1	1540.712	1.0142	0	23.74	21	K	AGEDADTLGLTGHER	Y			
	2	TC373025		297	40168	4	2	4	2	14.9	66	1	1	1	2325.123	2324.116	1	2324.103	0.0125	1	172.71	1.50E-14	K	YKNEGHDITILAGAEYSGSSR	D			
	3	TC389108	similar to U	95	45748	2	0	2	0	4.7	2	1	1	1	855.4357	854.4285	1	854.4286	-0.0002	0	49.94	0.076	K	VAEFSFR	G			
	3	TC389108	similar to U	95	45748	2	0	2	0	4.7	40	1	0	1	1542.733	1541.726	1	1542.724	-0.9976	0	45.11	0.16	R	SDETVAMIETYLr	A	Oxidation (I	0.0000002000000.0	
	4	TC388049	similar to U	59	65390	1	1	1	1	1.7	22	2	0	1	1184.677	1183.669	1	1183.683	-0.0133	1	58.64	0.0085	-	RAEIPFKPAR	V			
2	prot_hit_nu	prot_acc	prot_desc	prot_score	prot_mass	prot_match	prot_match	prot_seque	prot_seque	prot_cover	pep_query	pep_rank	pep_isbold	pep_isuniq	pep_exp_r	pep_exp_r	pep_exp_z	pep_calc_n	pep_delta	pep_miss	pep_score	pep_expect	pep_res_b	pep_seq	pep_res_af	pep_var_m	pep_var_m	pep_scan_title
	1	TC373025		476	40168	6	3	6	3	14.9	10	1	1	1	945.3642	944.357	1	944.3988	-0.0418	0	49.74	0.083	K	DFNSYSGSR	R			
	1	TC373025		476	40168	6	3	6	3	14.9	13	1	1	1	1073.455	1072.448	1	1072.494	-0.0462	1	47.14	0.13	R	KDFNSYSGSR	R			
	1	TC373025		476	40168	6	3	6	3	14.9	25	1	1	1	1381.632	1380.625	1	1380.671	-0.0466	0	58.62	0.0077	K	STYIHEPPYFK	D			
	1	TC373025		476	40168	6	3	6	3	14.9	31	7	1	1	1522.726	1521.718	1	1521.768	-0.0501	0	18.11	80	R	SNLAGMGIVPLCFK	A	Carbamido	0.00000200000100.0	
	1	TC373025		476	40168	6	3	6	3	14.9	51	1	1	1	2033.896	2032.889	1	2032.945	-0.0563	0	128.86	4.40E-10	K	NEGHDITILAGAEYSGSSR	D			
	1	TC373025		476	40168	6	3	6	3	14.9	60	1	1	1	2325.053	2324.046	1	2324.103	-0.0577	1	173.12	1.30E-14	K	YKNEGHDITILAGAEYSGSSR	D			
	2	BQ238531	similar to U	185	20976	3	2	3	2	15.2	8	1	1	1	914.5262	913.5189	1	913.5596	-0.0408	0	38.02	1.2	R	ILLESAIR	N			
	2	BQ238531	similar to U	185	20976	3	2	3	2	15.2	17	1	1	1	1184.633	1183.626	1	1183.671	-0.0452	0	76.25	0.00015	K	QVEIPFKPAR	V			
	2	BQ238531	similar to U	185	20976	3	2	3	2	15.2	21	1	1	1	1265.611	1264.603	1	1264.645	-0.0417	0	70.79	0.00051	K	YYSLPALADPR	I			
	3	TC389108	similar to U	142	45748	2	2	2	2	4.7	5	1	1	1	855.3971	854.3898	1	854.4286	-0.0388	0	54.7	0.025	K	VAEFSFR	G			
	3	TC389108	similar to U	142	45748	2	2	2	2	4.7	36	1	1	1	1543.686	1542.679	1	1542.724	-0.045	0	86.81	1.00E-05	R	SDETVAMIETYLr	A	Oxidation (I	0.0000002000000.0	
	4	TC388049	similar to U	61	65390	1	1	1	1	1.7	17	2	0	1	1184.633	1183.626	1	1183.683	-0.0564	1	60.81	0.0053	-	RAEIPFKPAR	V			
3	prot_hit_nu	prot_acc	prot_desc	prot_score	prot_mass	prot_match	prot_match	prot_seque	prot_seque	prot_cover	pep_query	pep_rank	pep_isbold	pep_isuniq	pep_exp_r	pep_exp_r	pep_exp_z	pep_calc_n	pep_delta	pep_miss	pep_score	pep_expect	pep_res_b	pep_seq	pep_res_af	pep_var_m	pep_var_m	pep_scan_title
	1	TC373025		210	40168	3	1	3	1	10.9	8	1	1	0	945.4047	944.3974	1	944.3988	-0.0014	0	35.76	2.1	K	DFNSYSGSR	R			
	1	TC373025		210	40168	3	1	3	1	10.9	24	1	1	1	1381.673	1380.666	1	1380.671	-0.0058	0	34.64	1.9	K	STYIHEPPYFK	D			
	1	TC373025		210	40168	3	1	3	1	10.9	50	1	1	0	2325.099	2324.092	1	2324.103	-0.0118	1	140.06	2.70E-11	K	YKNEGHDITILAGAEYSGSSR	D			
	2	BQ238531	similar to U	209	20976	5	2	5	2	27.7	6	1	1	1	914.5571	913.5499	1	913.5596	-0.0098	0	33.26	3.5	R	ILLESAIR	N			
	2	BQ238531	similar to U	209	20976	5	2	5	2	27.7	15	6	1	1	1132.637	1131.63	1	1131.64	-0.01	1	23.75	28	R	IDRLPYsir	I			
	2	BQ238531	similar to U	209	20976	5	2	5	2	27.7	17	1	1	1	1184.672	1183.665	1	1183.671	-0.0065	0	56.76	0.013	K	QVEIPFKPAR	V			
	2	BQ238531	similar to U	209	20976	5	2	5	2	27.7	21	1	1	1	1265.65	1264.643	1	1264.645	-0.0025	0	39.41	0.7	K	YYSLPALADPR	I			
	2	BQ238531	similar to U	209	20976	5	2	5	2	27.7	41	1	1	1	1740.781	1739.774	1	1739.778	-0.0046	0	55.52	0.012	R	SENAVQANMELEFSR	N	Oxidation (I	0.000000002000000.0	
	3	CA640484	similar to U	182	20862	2	1	2	1	19.5	29	1	1	0	1527.705	1526.698	1	1526.696	0.0013	0	42.03	0.32	K	AGEDADSLGLTGHER	Y			
	3	CA640484	similar to U	182	20862	2	1	2	1	19.5	50	1	0	0	2325.099	2324.092	1	2324.103	-0.0118	1	140.06	2.70E-11	K	YKNEGHDITILAGAEYSGSSR	D			
	4	TC378471	similar to U	78	41254	2	0	2	0	6.1	8	1	0	0	945.4047	944.3974	1	944.3988	-0.0014	0	35.							

6	prot_hit_nu	prot_acc	prot_desc	prot_score	prot_mass	prot_match	prot_match	prot_seque	prot_seque	prot_cover	pep_query	pep_rank	pep_isbold	pep_isuniq	pep_exp_r	pep_exp_r	pep_exp_z	pep_calc_n	pep_delta	pep_miss	pep_score	pep_expect	pep_res_b	pep_seq	pep_res_af	pep_var_m	pep_var_m	pep_scan_title
	1	TC376678	similar to U	523	57056	7	5	7	5	18.8	12	4	1	1	0	1115.575	1114.568	1	1114.617	-0.049	0	24.63	23 R	ISMVAPNLVR	V			
	1	TC376678	similar to U	523	57056	7	5	7	5	18.8	17	1	1	1	1	1315.692	1314.685	1	1314.73	-0.0445	0	87.97	9.30E-06 K	ADVFLLVGTQPR	V			Oxidation (f0.0020000000.0
	1	TC376678	similar to U	523	57056	7	5	7	5	18.8	19	1	1	0	0	1356.724	1355.716	1	1355.756	-0.0399	0	118.72	7.60E-09 K	NPVIAAGLFR	E			
	1	TC376678	similar to U	523	57056	7	5	7	5	18.8	37	1	1	0	0	1609.746	1608.738	1	1607.773	0.9658	0	32.85	2.5 K	VLCEGNGPNPPADIR	S	Carbamidoi	0.001000000000000.0	
	1	TC376678	similar to U	523	57056	7	5	7	5	18.8	38	1	1	0	0	1617.723	1616.716	1	1616.75	-0.0344	0	71.05	0.00037 K	AAVENFYMTDAITR	A			Oxidation (f0.000000002000000.0
	1	TC376678	similar to U	523	57056	7	5	7	5	18.8	54	1	1	1	1	1915.978	1914.971	1	1915.005	-0.0346	0	122.93	2.00E-09 R	ALSEVAGAPLPYDSVTAVR	S			
	1	TC376678	similar to U	523	57056	7	5	7	5	18.8	56	1	1	0	0	1979.045	1978.037	1	1978.074	-0.0361	1	68.52	0.0005 R	VDEREPSVISAEVKPPVK	Q			
	2	TC389811	similar to U	437	36864	5	4	5	4	21.8	12	4	0	0	0	1115.575	1114.568	1	1114.617	-0.049	0	24.63	23 R	ISMVAPNLVR	V			Oxidation (f0.0020000000.0
	2	TC389811	similar to U	437	36864	5	4	5	4	21.8	19	1	0	0	0	1356.724	1355.716	1	1355.756	-0.0399	0	118.72	7.60E-09 K	NPVIAAGLFR	E			
	2	TC389811	similar to U	437	36864	5	4	5	4	21.8	38	1	0	0	0	1617.723	1616.716	1	1616.75	-0.0344	0	71.05	0.00037 K	AAVENFYMTDAITR	A			Oxidation (f0.000000002000000.0
	2	TC389811	similar to U	437	36864	5	4	5	4	21.8	52	1	1	1	1	1885.963	1884.956	1	1884.995	-0.0385	0	153.63	1.70E-12 R	ALSEVAGAPLPYDSVAAVR	S			
	2	TC389811	similar to U	437	36864	5	4	5	4	21.8	56	1	0	0	0	1979.045	1978.037	1	1978.074	-0.0361	1	68.52	0.0005 R	VDEREPSVISAEVKPPVK	Q			
	3	TC415977	similar to U	207	53351	4	1	4	1	10.9	4	1	1	1	1	869.3384	868.3311	1	868.365	-0.0339	0	37.32	1.3 R	FCYHSR	L	Carbamidoi	0.010000.0	
	3	TC415977	similar to U	207	53351	4	1	4	1	10.9	37	1	0	0	0	1609.746	1608.738	1	1607.773	0.9658	0	32.85	2.5 K	VLCEGNGPNPPADIR	S	Carbamidoi	0.001000000000000.0	
	3	TC415977	similar to U	207	53351	4	1	4	1	10.9	43	1	1	1	1	1665.794	1664.787	1	1664.819	-0.0326	0	94.93	1.50E-06 R	FASEVAGVQDLGMLGR	G			Oxidation (f0.00000000000002000.0
	3	TC415977	similar to U	207	53351	4	1	4	1	10.9	48	1	1	1	1	1816.914	1816.871	1	1816.914	-0.0437	0	43.65	0.18 K	GFSVLQACEVAGVDIPR	F	Carbamidoi	0.00000001000000000.0	
	4	CA680986	similar to U	50	21592	1	0	1	0	5	17	2	0	0	1	1315.692	1314.685	1	1314.612	0.0731	0	49.88	0.06 R	WVFIXLXLYPR	X			
7	prot_hit_nu	prot_acc	prot_desc	prot_score	prot_mass	prot_match	prot_match	prot_seque	prot_seque	prot_cover	pep_query	pep_rank	pep_isbold	pep_isuniq	pep_exp_r	pep_exp_r	pep_exp_z	pep_calc_n	pep_delta	pep_miss	pep_score	pep_expect	pep_res_b	pep_seq	pep_res_af	pep_var_m	pep_var_m	pep_scan_title
	1	TC376678	similar to U	568	57056	8	5	8	5	20.3	12	1	1	0	0	1001.489	1000.482	1	1000.516	-0.0348	0	40.19	0.7 R	HPFCSILK	S	Carbamidoi	0.00010000.0	
	1	TC376678	similar to U	568	57056	8	5	8	5	20.3	16	6	1	0	0	1115.58	1114.573	1	1114.617	-0.044	0	22.57	37 R	ISMVAPNLVR	V			Oxidation (f0.0020000000.0
	1	TC376678	similar to U	568	57056	8	5	8	5	20.3	19	1	1	0	0	1315.699	1314.692	1	1314.73	-0.0378	0	91.99	3.70E-06 K	ADVFLLLVGTQPR	V			
	1	TC376678	similar to U	568	57056	8	5	8	5	20.3	22	1	1	0	0	1356.727	1355.72	1	1355.756	-0.0365	0	114.73	1.90E-08 K	NPVIAAGLFR	E			
	1	TC376678	similar to U	568	57056	8	5	8	5	20.3	39	1	1	0	0	1609.744	1608.737	1	1607.773	0.9639	0	45.91	0.12 K	VLCEGNGPNPPADIR	S	Carbamidoi	0.001000000000000.0	
	1	TC376678	similar to U	568	57056	8	5	8	5	20.3	40	1	1	0	0	1617.726	1616.719	1	1616.75	-0.0318	0	68.09	0.00073 K	AAVENFYMTDAITR	A			Oxidation (f0.000000002000000.0
	1	TC376678	similar to U	568	57056	8	5	8	5	20.3	57	1	1	1	1	1915.98	1914.972	1	1915.005	-0.0328	0	110.25	3.60E-08 R	ALSEVAGAPLPYDSVTAVR	S			
	1	TC376678	similar to U	568	57056	8	5	8	5	20.3	59	1	1	0	0	1979.047	1978.04	1	1978.074	-0.0334	1	80.58	3.10E-05 R	VDEREPSVISAEVKPPVK	Q			
	2	TC389811	similar to U	499	36864	6	4	6	4	24.2	12	1	0	0	0	1001.489	1000.482	1	1000.516	-0.0348	0	40.19	0.7 R	HPFCSILK	S	Carbamidoi	0.00010000.0	
	2	TC389811	similar to U	499	36864	6	4	6	4	24.2	16	6	0	0	0	1115.58	1114.573	1	1114.617	-0.044	0	22.57	37 R	ISMVAPNLVR	V			Oxidation (f0.0020000000.0
	2	TC389811	similar to U	499	36864	6	4	6	4	24.2	22	1	0	0	0	1356.727	1355.72	1	1355.756	-0.0365	0	114.73	1.90E-08 K	NPVIAAGLFR	E			
	2	TC389811	similar to U	499	36864	6	4	6	4	24.2	40	1	0	0	0	1617.726	1616.719	1	1616.75	-0.0318	0	68.09	0.00073 K	AAVENFYMTDAITR	A			Oxidation (f0.000000002000000.0
	2	TC389811	similar to U	499	36864	6	4	6	4	24.2	54	1	1	0	0	1885.968	1884.961	1	1884.995	-0.034	0	174.68	1.30E-14 R	ALSEVAGAPLPYDSVAAVR	S			
	2	TC389811	similar to U	499	36864	6	4	6	4	24.2	59	1	0	0	0	1979.047	1978.04	1	1978.074	-0.0334	1	80.58	3.10E-05 R	VDEREPSVISAEVKPPVK	Q			
	3	TC370854	similar to U	379	32820	5	3	5	3	23	12	2	0	0	0	1001.489	1000.482	1	1000.534	-0.0525	0	33.46	3.3 K	QQVSPAPFK	A			
	3	TC370854	similar to U	379	32820	5	3	5	3	23	16	6	0	0	0	1115.58	1114.573	1	1114.617	-0.044	0	22.57	37 R	ISMVAPNLVR	V			Oxidation (f0.0020000000.0
	3	TC370854	similar to U	379	32820	5	3	5	3	23	40	1	0	0	0	1617.726	1616.719	1	1616.75	-0.0318	0	68.09	0.00073 K	AAVENFYMTDAITR	A			Oxidation (f0.000000002000000.0
	3	TC370854	similar to U	379	32820	5	3	5	3	23	54	1	0	0	0	1885.968	1884.961	1	1884.995	-0.034</								

[illegible]

2	TC374031	homologue	325	44751	5	4	5	4	15.3	78	1	1	1	2120.997	2119.99	1	2119.022	0.9682	0	69.06	0.00041	R	MINTSEEIAQVGTISANGER	E					
	3 TC385776	homologue	136	26867	3	1	3	1	17.3	26	6	0	0	1267.554	1266.547	1	1266.57	-0.0228	0	23.1	29	K	SVAAGMNAMDLR	R	2 Oxidation (0.000002002000.0				
	3 TC385776	homologue	136	26867	3	1	3	1	17.3	28	1	0	0	1289.685	1288.678	1	1288.703	-0.0252	0	81.32	4.50E-05	R	TVIEQSFQAPK	V					
	3 TC385776	homologue	136	26867	3	1	3	1	17.3	75	2	0	1	2092.987	2091.979	1	2091.063	0.9162	1	31.43	2.4	R	MISTSKEIAQVGTISANGER	E					
	4 TC404839	UniRef100_	106	75142	2	1	2	1	4.1	33	1	1	1	1390.653	1389.646	1	1389.679	-0.0331	0	88	9.00E-06	K	AHGGFSVFAGVGGER	T					
	4 TC404839	UniRef100_	106	75142	2	1	2	1	4.1	51	1	1	1	1675.912	1674.905	1	1674.942	-0.037	0	17.95	72	R	LVLEVAQHLGENVVVR	T					
5	TC420589		54	44875	1	1	1	1	2.2	5	2	0	1	847.3753	846.368	1	846.4018	-0.0338	0	53.7	0.037	R	ACAAASTPR	A					
17	prot_hit_nu	prot_acc	prot_desc	prot_score	prot_mass	prot_match	prot_match	prot_seque	prot_seque	prot_cover	pep_query	pep_rank	pep_isbold	pep_isuniqui	pep_exp_r	pep_exp_r	pep_exp_z	pep_calc_n	pep_delta	pep_miss	pep_score	pep_expect	pep_res_b	pep_seq	pep_res_af	pep_var_m	pep_var_m	pep_scan_title	
	1	TC382178	similar to U	756	45413	9	7	9	7	30.6	3	1	1	1	917.4878	916.4805	1	916.513	-0.0325	0	57.67	0.014	K	FPLANSR	A				
	1	TC382178	similar to U	756	45413	9	7	9	7	30.6	25	1	1	1	1450.69	1449.682	1	1449.703	-0.0213	0	87.3	1.00E-05	R	TCHAHPTVSEALK	E	Carbamido	0.01000000000000.0		
	1	TC382178	similar to U	756	45413	9	7	9	7	30.6	36	1	1	1	1725.857	1724.85	1	1724.892	-0.042	0	40.34	0.4	K	GYYAIGDAIPGPMLAHK	A	Oxidation	(0.000000000000020000.0		
	1	TC382178	similar to U	756	45413	9	7	9	7	30.6	42	1	1	1	1818.922	1817.915	1	1817.941	-0.0266	0	99.04	5.00E-07	R	VPYTAGIGLDAIGVETDK	G				
	1	TC382178	similar to U	756	45413	9	7	9	7	30.6	53	1	1	1	2089.065	2088.058	1	2088.085	-0.0271	1	150.32	3.10E-12	R	VPYTAGIGLDAIGVETDKGGR	V				
	1	TC382178	similar to U	756	45413	9	7	9	7	30.6	66	1	1	0	2476.201	2475.194	1	2475.22	-0.0268	0	46.01	0.063	R	LGSEVTVVEFADPIVPSMDGEIR	K	Oxidation	(0.000000000000000200000.0		
	1	TC382178	similar to U	756	45413	9	7	9	7	30.6	67	1	1	0	2481.278	2480.271	1	2480.312	-0.0413	0	79.69	2.60E-05	K	LTVEPAAGGEQTVEADVLVSAGR	V				
	1	TC382178	similar to U	756	45413	9	7	9	7	30.6	70	1	1	1	2555.22	2554.212	1	2554.234	-0.0217	0	166.87	4.90E-14	R	EGHVDTYDTPGVGVYTHPEVASVGK	T				
	1	TC382178	similar to U	756	45413	9	7	9	7	30.6	73	1	1	0	2604.299	2603.292	1	2603.315	-0.0233	1	30.96	1.8	R	LGSEVTVVEFADPIVPSMDGEIRK	Q	Oxidation	(0.0000000000000002000000.0		
	2	TC382394	similar to U	202	40553	4	2	4	2	16.7	30	1	1	1	1538.714	1537.707	1	1538.73	-1.023	0	45.39	0.15	K	ALLHSSHHMYHEAK	S	Oxidation	(0.0000000200000.0		
	2	TC382394	similar to U	202	40553	4	2	4	2	16.7	66	1	0	0	2476.201	2475.194	1	2475.22	-0.0268	0	46.01	0.063	R	LGSEVTVVEFADPIVPSMDGEIR	K	Oxidation	(0.000000000000000200000.0		
	2	TC382394	similar to U	202	40553	4	2	4	2	16.7	67	1	0	0	2481.278	2480.271	1	2480.312	-0.0413	0	79.69	2.60E-05	K	LTVEPAAGGEQTVEADVLVSAGR	V				
	2	TC382394	similar to U	202	40553	4	2	4	2	16.7	73	1	0	0	2604.299	2603.292	1	2603.315	-0.0233	1	30.96	1.8	R	LGSEVTVVEFADPIVPSMDGEIRK	Q	Oxidation	(0.0000000000000002000000.0		
	3	TC393672	homologue	76	26400	1	1	1	1	4.6	22	1	0	0	1384.599	1383.592	1	1383.624	-0.0321	0	75.55	0.00015	K	FLENFCGDQVR	F	Carbamido	0.0000100000.0		
18	prot_hit_nu	prot_acc	prot_desc	prot_score	prot_mass	prot_match	prot_match	prot_seque	prot_seque	prot_cover	pep_query	pep_rank	pep_isbold	pep_isuniqui	pep_exp_r	pep_exp_r	pep_exp_z	pep_calc_n	pep_delta	pep_miss	pep_score	pep_expect	pep_res_b	pep_seq	pep_res_af	pep_var_m	pep_var_m	pep_scan_title	
	1	TC404839	UniRef100_	1091	75142	11	10	11	10	22.8	4	1	1	1	1135.638	1134.631	1	1134.593	0.0374	0	66.63	0.0015	K	THDFLPIHR	E				
	1	TC404839	UniRef100_	1091	75142	11	10	11	10	22.8	6	1	1	1	1173.7	1172.692	1	1172.655	0.0369	0	77.07	0.00012	K	VVDLLAPYQR	G				
	1	TC404839	UniRef100_	1091	75142	11	10	11	10	22.8	13	1	1	1	1390.732	1389.724	1	1389.679	0.0454	0	112.59	3.10E-08	K	AHGGFSVFAGVGGER	T				
	1	TC404839	UniRef100_	1091	75142	11	10	11	10	22.8	14	1	1	1	1399.818	1398.81	1	1398.762	0.0482	0	100	5.30E-07	R	VGLTGLTVAEHFR	D				
	1	TC404839	UniRef100_	1091	75142	11	10	11	10	22.8	15	1	1	1	1409.897	1408.89	1	1408.804	0.0856	0	79.16	5.60E-05	K	VLNTGSPITVPVGR	A				
	1	TC404839	UniRef100_	1091	75142	11	10	11	10	22.8	17	1	1	1	1492.846	1491.839	1	1491.768	0.0709	0	138.87	6.50E-11	R	FTQANSEVSALLGR	I				
	1	TC404839	UniRef100_	1091	75142	11	10	11	10	22.8	24	1	1	1	1662.815	1661.807	1	1661.765	0.0419	0	21.05	36	K	CALVYGQMNPEPPGAR	A	Carbamido	0.1000000000000000.0		
	1	TC404839	UniRef100_	1091	75142	11	10	11	10	22.8	25	1	1	1	1676.006	1674.998	1	1674.942	0.0566	0	92.76	2.10E-06	R	LVLEVAQHLGENVVVR	T				
	1	TC404839	UniRef100_	1091	75142	11	10	11	10	22.8	31	1	1	1	1825.987	1824.98	1	1824.894	0.086	0	51.23	0.029	R	MLSPHVLGDVHYNTAR	G	Oxidation	(0.0.2000000000000000.0		
	1	TC404839	UniRef100_	1091	75142	11	10	11	10	22.8	37	1	1	1	2061.145	2060.137	1	2060.043	0.0948	0	178.51	4.40E-15	R	QISELGIYPAVDPLDSTSR	M				
	1	TC404839	UniRef100_	1091	75142	11	10	11	10	22.8	40	1	1	1	2186.264	2185.257	1	2185.138	0.1188	0	172.8	1.40E-14	R	IPSAVGYQPTLATDLGGLQER	I				
	2	TC386629	ATP synth	73	77756	1	1	1	1	1.8	18	1	1	1	1537.795	1536.788	1	1536.736	0.0515	0	72.73	0.00027	R	EAFPGDVLYLHSR	L				
	3	CJ783822	similar to U	57	12569	1	1	1	1	12.5	26	1	1	1	1677.927	1676.92	1	1676.921	-0.0013	0	56.76	0.0091	R	LVLEVAQHLGENTVR	T				
	19	prot_hit_nu	prot_acc	prot_desc	prot_score	prot_mass	prot_match	prot_match	prot_seque	prot_seque	prot_cover	pep_query	pep_rank	pep_isbold	pep_isuniqui	pep_exp_r	pep_exp_r	pep_exp_z	pep_calc_n	pep_delta	pep_miss	pep_score	pep_expect	pep_res_b	pep_seq	pep_res_af	pep_var_m	pep_var_m	pep_scan_title
1		TC404839	UniRef100_	1128	75142	10	9	10	9	22.8	13	1	1	1	1173.664	1172.657	1	1172.655	0.0011	0	69.81	0.00067	K	VVDLLAPYQR	G				
1		TC404839	UniRef100_	1128	75142	10	9	10	9	22.8	26	1	1	1	1390.688	1389.681	1	1389.679	0.002	0	110.14	5.50E-08	K	AHGGFSVFAGVGGER	T				
1		TC404839	UniRef100_	1128	75142	10	9	10	9	22.8	27	1	1	1	1399.777	1398.77	1	1398.762	0.0075	0	92.41	3.10E-06	R	VGLTGLTVAEHFR	D				
1		TC404839	UniRef100_	1128	75142	10	9	10	9	22.8	28	1	1	1	1409.821	1408.814	1	1408.804	0.0098	0	84.09	2.00E-05	K	VLNTGSPITVPVGR	A				
1		TC404839	UniRef100_	1128	75142	10	9	10	9	22.8	34	1	1	1	1492.789	1491.782	1	1491.768	0.014	0	134.79	1.70E-10	R	FTQANSEVSALLGR	I				
1		TC404839	UniRef100_	1128	75142	10	9	10	9	22.8	40	1	1	1	1622.722	1621.714	1	1620.739	0.9755	0	48.81	0.062	K	CALVYGQMNPEPPGAR	A	Oxidation	(0.0000000020000000.0		
1		TC404839	UniRef100_	1128	75142	10	9	10	9	22.8	44	1	1	1	1675.972	1674.965	1	1674.942	0.0231	0	90.41	3.80E-06	R	LVLEVAQHLGENVVVR	T				
1		TC404839	UniRef100_	1128	75142	10	9	10	9	22.8	60	1	1	1	2061.085	2060.078	1	2060.043	0.0352	0	175.32	9.70E-15	R	QISELGIYPAVDPLDSTSR	M				
1		TC404839	UniRef100_	1128	75142	10	9	10	9	22.8	64	1	1	1	2186.191	2185.184	1	2185.138	0.0459	0	184.67	1.00E-15	R	IPSAVGYQPTLATDLGGLQER	I				
1		TC404839	UniRef100_	1128	75142	10	9	10	9	22.8	74	1	1	1	2591.372	2590.365	1	2590.306	0.0587	0	137.76	3.60E-11	K	ITDEFTGAGSIGQVCQVIGAVVDVR	F	Carbamido	0.000000000000010000000000.0		
2		CJ795732	similar to U	88	27004	1	1	1	1	7.6	58	1	1	1	2044.052	2043.044	1	2044.048	-1.0033	0	88.29	5.10E-06	R	QIAELGIYPAVDPLDSTSR	M				
3		CJ783822	similar to U	57	12569	1	1	1	1	12.5	45	1	1	1	1678.811	1677.803	1	1676.921	0.8823	0	57.2	0.0085	R	LVLEVAQHLGENTVR	T				
20		prot_hit_nu	prot_acc	prot_desc	prot_score	prot_mass	prot_match	prot_match	prot_seque	prot_seque	prot_cover	pep_query	pep_rank	pep_isbold	pep_isuniqui	pep_exp_r	pep_exp_r	pep_exp_z	pep_calc_n	pep_delta	pep_miss	pep_score	pep_expect	pep_res_b	pep_seq	pep_res_af	pep_var_m	pep_var_m	pep_scan_title
		1	TC411944	homologue	1050	59655	10	9	10	9	28.9	17	1	1	1	1173.631	1172.624	1	1172.655	-0.0313	0	73.62	0.00028	K	VVDLLAPYQR	G			
	1	TC411944	homologue	1050	59655	10	9	10	9	28.9	27	1	1	1	1390.654	1389.647	1	1389.679	-0.0322	0	122.87	2.90E-09	K	AHGGFSVFAGVGGER	T				
	1	TC411944	homologue	1050	59655	10	9	10	9	28.9	28	1	1	1	1399.738	1398.731	1	1398.762	-0.0311	0	104.86	1.80E-07	R	VGLTGLTVAEHFR	D				

	3	TC368629	ATP synth	159	77756	2	1	2	1	3.3	37	1	1	1	1340.627	1339.62	1	1340.698	-1.0779	0	40.01	0.57 K	QPQYEPLPIEK	Q				
		3	TC368629	ATP synth	159	77756	2	1	2	1	3.3	48	1	1	1	1537.71	1536.703	1	1536.736	-0.0334	0	119.17	6.00E-09 R	EAFPGDVFYLHSR	L			
		4	TC373464	similar to U	110	33420	1	1	1	1	5.8	78	1	1	1	1971.96	1970.953	1	1970.991	-0.038	0	110.31	3.40E-08 R	ELTSLATPGQVDQTQLDR	A			
23	prot_hit_nu	prot_acc	prot_desc	prot_score	prot_mass	prot_match	prot_match	prot_seque	prot_seque	prot_cover	pep_query	pep_rank	pep_isbold	pep_isuniqui	pep_exp_r	pep_exp_r	pep_exp_z	pep_calc_n	pep_delta	pep_miss	pep_score	pep_expect	pep_res_bc	pep_seq	pep_res_af	pep_var_m	pep_var_m	pep_scan_title
		2	TC373464	similar to U	65	33420	2	0	2	0	9.6	37	1	1	0	1429.721	1428.714	1	1428.761	-0.0476	0	32.09	3.4 R	LNPLVNEFDQIK	S			
		2	TC373464	similar to U	65	33420	2	0	2	0	9.6	55	1	1	1	1971.945	1970.938	1	1970.991	-0.0527	0	32.66	2 R	ELTSLATPGQVDQTQLDR	A			
		3	TC370081	similar to U	54	37603	2	0	2	0	6	15	1	1	1	1029.466	1028.459	1	1028.493	-0.0336	0	21.81	47 K	SVYVGGEYR	R			
		3	TC370081	similar to U	54	37603	2	0	2	0	6	37	1	0	0	1429.721	1428.714	1	1428.761	-0.0476	0	32.09	3.4 R	LNPLVNEFDQIK	S			
24	prot_hit_nu	prot_acc	prot_desc	prot_score	prot_mass	prot_match	prot_match	prot_seque	prot_seque	prot_cover	pep_query	pep_rank	pep_isbold	pep_isuniqui	pep_exp_r	pep_exp_r	pep_exp_z	pep_calc_n	pep_delta	pep_miss	pep_score	pep_expect	pep_res_bc	pep_seq	pep_res_af	pep_var_m	pep_var_m	pep_scan_title
		1	TC373464	similar to U	556	33420	5	5	5	5	26.8	7	1	1	0	891.436	890.4287	1	890.461	-0.0323	0	55.68	0.022 R	QALAFGER	K			
		1	TC373464	similar to U	556	33420	5	5	5	5	26.8	37	1	1	0	1429.734	1428.726	1	1428.761	-0.0349	0	69.95	0.00055 R	LNPLVNEFDQIK	S			
		1	TC373464	similar to U	556	33420	5	5	5	5	26.8	56	1	1	1	1971.959	1970.951	1	1970.991	-0.0395	0	152.62	2.00E-12 R	ELTSLATPGQVDQTQLDR	A			
		1	TC373464	similar to U	556	33420	5	5	5	5	26.8	65	1	1	1	2297.118	2296.111	1	2296.16	-0.0492	0	152.01	1.80E-12 K	NVHSNTGIFGIHASTEAAFPVK	V			
		1	TC373464	similar to U	556	33420	5	5	5	5	26.8	75	1	1	1	2585.3	2584.293	1	2584.332	-0.0393	0	126.13	5.60E-10 K	IISPLTMASHGNVINVPAYETVR	G		Oxidation (I 0.00000002000000000000000.0	
		2	TC425082	similar to U	459	68096	8	6	7	6	16	7	1	0	0	891.436	890.4287	1	890.461	-0.0323	0	55.68	0.022 R	QALAFGER	N			
		2	TC425082	similar to U	459	68096	8	6	7	6	16	12	1	1	0	1029.465	1028.458	1	1028.493	-0.0348	0	61.8	0.0047 K	SVYVGGEYR	R			
		2	TC425082	similar to U	459	68096	8	6	7	6	16	37	1	0	0	1429.734	1428.726	1	1428.761	-0.0349	0	69.95	0.00055 R	LNPLVNEFDQIK	S			
		2	TC425082	similar to U	459	68096	8	6	7	6	16	50	4	1	1	1856.826	1855.819	1	1855.852	-0.0332	0	19.32	46 K	TYMPMEMVEVLVDCVR	N		Carbamido (0.00002000000100.0	
		2	TC425082	similar to U	459	68096	8	6	7	6	16	52	1	1	1	1872.822	1871.815	1	1871.847	-0.0319	0	57.39	0.007 K	TYMPMEMVEVLVDCVR	N		Carbamido (0.002002000000100.0	
		2	TC425082	similar to U	459	68096	8	6	7	6	16	57	1	1	0	1985.966	1984.959	1	1985.007	-0.0477	0	44.5	0.13 R	ELTSLATPGQVDQTQLER	A			
		2	TC425082	similar to U	459	68096	8	6	7	6	16	60	1	1	1	2095.021	2094.014	1	2094.063	-0.0496	0	118.68	4.50E-09 R	LNTDVLLEEFLALNYTSPR	I			
		2	TC425082	similar to U	459	68096	8	6	7	6	16	68	1	1	0	2327.118	2326.111	1	2326.171	-0.0601	0	52.73	0.015 K	NVHSNTGIFGIHTSTEAFAFPVK	V			
		3	TC370081	similar to U	408	37603	6	5	6	5	26.5	7	1	0	0	891.436	890.4287	1	890.461	-0.0323	0	55.68	0.022 R	QALAFGER	K			
		3	TC370081	similar to U	408	37603	6	5	6	5	26.5	12	1	0	0	1029.465	1028.458	1	1028.493	-0.0348	0	61.8	0.0047 K	SVYVGGEYR	R			
		3	TC370081	similar to U	408	37603	6	5	6	5	26.5	37	1	0	0	1429.734	1428.726	1	1428.761	-0.0349	0	69.95	0.00055 R	LNPLVNEFDQIK	S			
		3	TC370081	similar to U	408	37603	6	5	6	5	26.5	57	1	0	0	1985.966	1984.959	1	1985.007	-0.0477	0	44.5	0.13 R	ELTSLATPGQVDQTQLER	A			
		3	TC370081	similar to U	408	37603	6	5	6	5	26.5	68	1	0	0	2327.118	2326.111	1	2326.171	-0.0601	0	52.73	0.015 K	NVHSNTGIFGIHTSTEAFAFPVK	V			
		4	TC370081	similar to U	408	37603	6	5	6	5	26.5	75	2	0	1	2585.3	2584.293	1	2584.332	-0.0393	0	123.76	9.60E-10 K	IISPLTMASHGNVLNVPAYETVR	G		Oxidation (I 0.00000002000000000000000.0	
		4	TC368629	ATP synth	92	77756	1	1	1	1	1.8	43	1	1	1	1537.706	1536.699	1	1536.736	-0.0373	0	91.7	3.40E-06 R	EAFPGDVFYLHSR	L			
		5	TC422222	homologue	51	26484	1	0	1	0	3.3	7	2	0	1	891.436	890.4287	1	890.5338	-0.1051	1	50.51	0.073 -	KIAAFVSR	D			
25	prot_hit_nu	prot_acc	prot_desc	prot_score	prot_mass	prot_match	prot_match	prot_seque	prot_seque	prot_cover	pep_query	pep_rank	pep_isbold	pep_isuniqui	pep_exp_r	pep_exp_r	pep_exp_z	pep_calc_n	pep_delta	pep_miss	pep_score	pep_expect	pep_res_bc	pep_seq	pep_res_af	pep_var_m	pep_var_m	pep_scan_title
		1	TC373464	similar to U	595	33420	5	5	5	5	26.8	9	1	1	0	891.4457	890.4385	1	890.461	-0.0225	0	55.7	0.022 R	QALAFGER	K			
		1	TC373464	similar to U	595	33420	5	5	5	5	26.8	37	1	1	0	1429.751	1428.744	1	1428.761	-0.0172	0	80.8	4.50E-05 R	LNPLVNEFDQIK	S			
		1	TC373464	similar to U	595	33420	5	5	5	5	26.8	58	1	1	1	1971.99	1970.983	1	1970.991	-0.0084	0	160.87	3.00E-13 R	ELTSLATPGQVDQTQLDR	A			
		1	TC373464	similar to U	595	33420	5	5	5	5	26.8	66	1	1	1	2297.147	2296.14	1	2296.16	-0.0205	0	145.83	7.50E-12 K	NVHSNTGIFGIHASTEAAFPVK	V			
		1	TC373464	similar to U	595	33420	5	5	5	5	26.8	76	1	1	1	2585.344	2584.337	1	2584.332	0.0049	0	151.74	1.50E-12 K	IISPLTMASHGNVINVPAYETVR	G		Oxidation (I 0.00000002000000000000000.0	
		2	TC425082	similar to U	519	68096	8	5	8	5	14.6	1	1	1	1	809.4269	808.4196	1	808.4443	-0.0247	0	40.66	0.68 K	LAFTTTR	N			
		2	TC425082	similar to U	519	68096	8	5	8	5	14.6	9	1	0	0	891.4457	890.4385	1	890.461	-0.0225	0	55.7	0.022 R	QALAFGER	N			
		2	TC425082	similar to U	519	68096	8	5	8	5	14.6	15	1	1	0	1029.479	1028.472	1	1028.493	-0.021	0	65.68	0.0019 K	SVYVGGEYR	R			
		2	TC425082	similar to U	519	68096	8	5	8	5	14.6	28	1	1	1	1277.591	1276.584	1	1276.601	-0.0168	0	37.69	1 R	ELMSYSYGALK	T		Oxidation (I 0.002000000000.0	
		2	TC425082	similar to U	519	68096	8	5	8	5	14.6	29	1	1	1	1308.635	1307.628	1	1307.662	-0.0346	0	33.58	2.6 R	SSGGFLGLWTGAR	S			
		2	TC425082	similar to U	519	68096	8	5	8	5	14.6	37	1	0	0	1429.751	1428.744	1	1428.761	-0.0172	0	80.8	4.50E-05 R	LNPLVNEFDQIK	S			
		2	TC425082	similar to U	519	68096	8	5	8	5	14.6	52	1	1	1	1872.844	1871.837	1	1871.847	-0.0101	0	57.21	0.0073 K	TYMPMEMVEVLVDCVR	N		Carbamido (0.002002000000100.0	
		2	TC425082	similar to U	519	68096	8	5	8	5	14.6	62	1	1	1	2095.043	2094.035	1	2094.063	-0.028	0	149.94	3.40E-12 R	LNTDVLLEEFLALNYTSPR	I			
		3	TC370081	similar to U	351	37603	4	4	4	4	15.1	9	1	0	0	891.4457	890.4385	1	890.461	-0.0225	0	55.7	0.022 R	QALAFGER	K			
		3	TC370081	similar to U	351	37603	4	4	4	4	15.1	15	1	0	0	1029.479	1028.472	1	1028.493	-0.021	0	65.68	0.0019 K	SVYVGGEYR	R			
		3	TC370081	similar to U	351	37603	4	4	4	4	15.1	37	1	0	0	1429.751	1428.744	1	1428.761	-0.0172	0	80.8	4.50E-05 R	LNPLVNEFDQIK	S			
		3	TC370081	similar to U	351	37603	4	4	4	4	15.1	76	2	0	1	2585.344	2584.337	1	2584.332	0.0049	0	149.1	2.70E-12 K	IISPLTMASHGNVLNVPAYETVR	G		Oxidation (I 0.00000002000000000000000.0	
26	prot_hit_nu	prot_acc	prot_desc	prot_score	prot_mass	prot_match	prot_match	prot_seque	prot_seque	prot_cover	pep_query	pep_rank	pep_isbold	pep_isuniqui	pep_exp_r	pep_exp_r	pep_exp_z	pep_calc_n	pep_delta	pep_miss	pep_score	pep_expect	pep_res_bc	pep_seq	pep_res_af	pep_var_m	pep_var_m	pep_scan_title
		1	TC425082	similar to U	616	68096	9	6	8	6	16.4	1	3	1	1	809.4124	808.4051	1	808.4443	-0.0392	0	20.84	65 K	LAFTTTR	N			
		1	TC425082	similar to U	616	68096	9	6	8	6	16.4	10	1	1	0	891.438	890.4307	1	890.461	-0.0303	0	58.17	0.012 R	QALAFGER	N			
		1	TC425082	similar to U	616	68096	9	6	8	6	16.4	17	1	1	0	1029.471	1028.464	1	1028.493	-0.0291	0	61.87	0.0046 K	SVYVGGEYR	R			
		1	TC425082	similar to U	616	68096	9	6	8	6	16.4	38	1	1	1	1308.628	1307.621	1	1307.662	-0.0414	0	28.92	7.6 R	SSGGFLGLWTGAR	S			
		1	TC425082	similar to U	616	68096	9	6	8	6	16.4	46	1	1	0	1429.744	1428.737	1	1428.761	-0.0243								

[illegible]

		1	TC387564	homologue	555	56897	10	5	8	5	20.6	72	1	1	1	2128.004	2126.996	1	2127.031	-0.0345	1	39.27	0.38	K	VECTIPKDDGTLASVVGFR	V	Carbamidoi 0.001000000000000000.0	
		1	TC387564	homologue	555	56897	10	5	8	5	20.6	77	1	1	1	2210.081	2209.074	1	2209.09	-0.0161	0	22.47	17	K	YIEAANHPTDPEADEILAK	K		
		1	TC387564	homologue	555	56897	10	5	8	5	20.6	78	1	1	1	2214.143	2213.136	1	2213.159	-0.0237	0	96.15	7.30E-07	K	FHGYSPAVVTGKPVDLGGSGLGR	D		
		2	TC451875	homologue	172	33724	3	2	2	2	9.6	15	1	0	0	1065.52	1064.513	1	1064.544	-0.031	0	47.79	0.12	R	MGAFTLGVNR	V		
		2	TC451875	homologue	172	33724	3	2	2	2	9.6	16	1	0	0	1081.521	1080.514	1	1080.539	-0.0251	0	53.41	0.031	R	MGAFTLGVNR	V	Oxidation (I 0.2000000000.0	
		2	TC451875	homologue	172	33724	3	2	2	2	9.6	83	1	1	1	2324.116	2323.109	1	2323.133	-0.0247	0	118.7	3.80E-09	K	YIEAANHPTDPEADEILANK	G		
		3	TC390427	homologue	171	58357	4	2	3	2	5.3	3	2	0	0	845.4989	844.4917	1	844.5171	-0.0254	0	47.42	0.15	K	SLIPFR	E		
		3	TC390427	homologue	171	58357	4	2	3	2	5.3	15	1	0	0	1065.52	1064.513	1	1064.544	-0.031	0	47.79	0.12	R	MGAFTLGVNR	V		
		3	TC390427	homologue	171	58357	4	2	3	2	5.3	16	1	0	0	1081.521	1080.514	1	1080.539	-0.0251	0	53.41	0.031	R	MGAFTLGVNR	V	Oxidation (I 0.2000000000.0	
		3	TC390427	homologue	171	58357	4	2	3	2	5.3	36	1	1	1	1284.595	1283.587	1	1283.615	-0.0273	0	73.98	0.00024	K	DDGTLASFVGFR	V		
		4	TC423271	homologue	73	56677	2	0	2	0	4	28	1	1	1	1217.579	1216.572	1	1216.599	-0.0268	0	29.05	7.8	R	HLQFPFADR	L		
		4	TC423271	homologue	73	56677	2	0	2	0	4	45	1	1	1	1423.637	1422.629	1	1422.657	-0.0276	0	45.5	0.15	K	YAFEYAYLNNR	K		
		5	TC374104	homologue	51	31241	1	1	1	1	4.6	59	1	0	1	1689.823	1688.815	1	1688.846	-0.0303	0	51.08	0.035	R	LKPFNCNLLYHDR	L	Carbamidoi 0.0000010000000.0	
37	prot_hit_nu	prot_acc	prot_desc	prot_score	prot_mass	prot_match	prot_match	prot_seq	prot_seq	prot_cover	pep_query	pep_rank	pep_isbold	pep_isuniq	pep_exp_r	pep_exp_r	pep_exp_z	pep_calc_r	pep_delta	pep_miss	pep_score	pep_expect	pep_res_b	pep_seq	pep_res_af	pep_var_m	pep_var_m	pep_scan_title
		1	TC370105	similar to U	448	37312	4	4	4	4	15.6	3	1	1	0	1219.697	1218.689	1	1218.697	-0.0079	0	102.67	3.40E-07	R	LFGVTTLDVVR	A		
		1	TC370105	similar to U	448	37312	4	4	4	4	15.6	11	1	1	1	1375.8	1374.793	1	1374.798	-0.0054	1	67.69	0.00092	K	RLFGVTTLDVVR	A		
		1	TC370105	similar to U	448	37312	4	4	4	4	15.6	19	1	1	1	1861.957	1860.95	1	1859.963	0.9872	0	103.05	2.00E-07	K	NGVEEVLGLGQLTQFEK	D		
		1	TC370105	similar to U	448	37312	4	4	4	4	15.6	40	1	1	1	2670.371	2669.363	1	2669.337	0.0262	0	174.27	7.80E-15	K	GFMADDQLAEALDGADLVIIIPAGVPR	K	Oxidation (I 0.00200000000000000000000000.0	
		2	TC375673	homologue	275	38885	2	2	2	2	9.8	3	1	0	0	1219.697	1218.689	1	1218.697	-0.0079	0	102.67	3.40E-07	K	LFGVTTLDVVR	A		
		2	TC375673	homologue	275	38885	2	2	2	2	9.8	37	1	1	1	2608.367	2607.36	1	2607.354	0.0056	0	172.67	1.20E-14	K	GFVGDDQLGEALEGADLVIIIPAGVPR	K		
		3	CA485584	similar to U	116	24473	2	1	2	1	15.6	3	1	0	0	1219.697	1218.689	1	1218.697	-0.0079	0	102.67	3.40E-07	K	LFGVTTLDVVR	A		
		3	CA485584	similar to U	116	24473	2	1	2	1	15.6	40	4	0	1	2670.371	2669.363	1	2669.337	0.0262	0	13.44	95	K	GFMGEEQLGEALEGSDVVIIPAGVPR	K		
		4	TC378952	similar to U	85	25939	1	1	1	1	4.5	4	1	1	1	1255.662	1254.654	1	1254.661	-0.0065	0	84.84	2.00E-05	R	YLSSALFEGLR	K		
38	prot_hit_nu	prot_acc	prot_desc	prot_score	prot_mass	prot_match	prot_match	prot_seq	prot_seq	prot_cover	pep_query	pep_rank	pep_isbold	pep_isuniq	pep_exp_r	pep_exp_r	pep_exp_z	pep_calc_r	pep_delta	pep_miss	pep_score	pep_expect	pep_res_b	pep_seq	pep_res_af	pep_var_m	pep_var_m	pep_scan_title
		1	TC375673	homologue	660	38885	4	4	4	4	17.8	8	1	1	0	1219.697	1218.689	1	1218.697	-0.0332	0	101.37	4.60E-07	K	LFGVTTLDVVR	A		
		1	TC375673	homologue	660	38885	4	4	4	4	17.8	14	1	1	0	1347.77	1346.763	1	1346.792	-0.0292	1	107.39	1.00E-07	K	KLFGVTTLDVVR	A		
		1	TC375673	homologue	660	38885	4	4	4	4	17.8	59	1	1	1	2608.334	2607.327	1	2607.354	-0.0277	0	241.41	1.60E-21	K	GFVGDDQLGEALEGADLVIIIPAGVPR	K		
		1	TC375673	homologue	660	38885	4	4	4	4	17.8	64	1	1	1	2994.584	2993.577	1	2993.582	-0.0054	0	210.24	1.50E-18	K	LNPLVSSLSLYDIAATPGVAADVSHINA	A		
		2	CA486629	similar to U	225	21912	3	2	3	2	16.9	8	1	0	0	1219.671	1218.664	1	1218.697	-0.0332	0	101.37	4.60E-07	K	LFGVTTLDVVR	A		
		2	CA486629	similar to U	225	21912	3	2	3	2	16.9	14	1	0	0	1347.77	1346.763	1	1346.792	-0.0292	1	107.39	1.00E-07	K	KLFGVTTLDVVR	A		
		2	CA486629	similar to U	225	21912	3	2	3	2	16.9	53	1	1	1	2288.103	2287.096	1	2286.143	0.9534	1	16.09	71	K	AGAGSATLSMAYAAARFVESSLR	A		
		3	TC378952	similar to U	77	25939	1	1	1	1	4.5	9	1	1	1	1255.661	1254.624	1	1254.661	-0.0372	0	76.53	0.00014	R	YLSSALFEGLR	K		
39	prot_hit_nu	prot_acc	prot_desc	prot_score	prot_mass	prot_match	prot_match	prot_seq	prot_seq	prot_cover	pep_query	pep_rank	pep_isbold	pep_isuniq	pep_exp_r	pep_exp_r	pep_exp_z	pep_calc_r	pep_delta	pep_miss	pep_score	pep_expect	pep_res_b	pep_seq	pep_res_af	pep_var_m	pep_var_m	pep_scan_title
		1	TC445045	similar to U	640	46145	9	8	9	8	23.6	8	1	1	0	1198.556	1197.549	1	1197.582	-0.0329	0	65.6	0.0017	R	VAEYAFHYAK	A		
		1	TC445045	similar to U	640	46145	9	8	9	8	23.6	9	1	1	0	1207.592	1206.585	1	1206.625	-0.0399	0	57.54	0.011	R	YDDVNLVTIR	E		
		1	TC445045	similar to U	640	46145	9	8	9	8	23.6	12	1	1	1	1243.544	1242.537	1	1242.574	-0.037	0	77.18	0.00012	R	HLQFNDQADR	I		
		1	TC445045	similar to U	640	46145	9	8	9	8	23.6	23	1	1	0	1464.742	1463.734	1	1463.773	-0.039	1	67.32	0.00098	K	TRYDDVNLVTIR	E		
		1	TC445045	similar to U	640	46145	9	8	9	8	23.6	25	1	1	1	1683.773	1682.766	1	1682.815	-0.0493	0	53.13	0.022	R	TESFLTWESLESVR	R		
		1	TC445045	similar to U	640	46145	9	8	9	8	23.6	32	1	1	0	1800.889	1799.881	1	1799.931	-0.0491	0	80.98	3.30E-05	R	ATLFPDGDIGPEIAESVK	Q		
		1	TC445045	similar to U	640	46145	9	8	9	8	23.6	36	1	1	1	1846.815	1845.808	1	1845.849	-0.0418	0	137.61	6.80E-11	R	ENTEGEYSGLEHQVVR	G		
		1	TC445045	similar to U	640	46145	9	8	9	8	23.6	44	1	1	0	2050.992	2049.985	1	2050.031	-0.0455	0	81.58	2.40E-05	K	ELGLYANVRPCNSLPGYK	T	Carbamidoi 0.000000000010000000.0	
		1	TC445045	similar to U	640	46145	9	8	9	8	23.6	48	1	1	0	2179.073	2178.066	1	2178.126	-0.0597	1	18.8	41	R	KELGLYANVRPCNSLPGYK	T	Carbamidoi 0.00000000000100000000.0	
		2	TC423153	homologue	401	31482	7	5	7	5	25.9	8	1	0	0	1198.556	1197.549	1	1197.582	-0.0329	0	65.6	0.0017	R	VAEYAFHYAK	A		
		2	TC423153	homologue	401	31482	7	5	7	5	25.9	9	1	0	0	1207.592	1206.585	1	1206.625	-0.0399	0	57.54	0.011	R	YDDVNLVTIR	E		
		2	TC423153	homologue	401	31482	7	5	7	5	25.9	23	1	0	0	1464.742	1463.734	1	1463.773	-0.039	1	67.32	0.00098	K	TRYDDVNLVTIR	E		
		2	TC423153	homologue	401	31482	7	5	7	5	25.9	25	2	0	1	1683.773	1682.766	1	1681.831	0.9347	0	29.12	5.5	R	TQSFLTWESLESVR	R		
		2	TC423153	homologue	401	31482	7	5	7	5	25.9	32	1	0	0	1800.889	1799.881	1	1799.931	-0.0491	0	80.98	3.30E-05	R	ATLFPDGDIGPEIAESVK	Q		
		2	TC423153	homologue	401	31482	7	5	7	5	25.9	44	1	0	0	2050.992	2049.985	1	2050.031	-0.0455	0	81.58	2.40E-05	K	ELGLYANVRPCNSLPGYK	T	Carbamidoi 0.000000000010000000.0	
		2	TC423153	homologue	401	31482	7	5	7	5	25.9	48	1	0	0	2179.073	2178.066	1	2178.126	-0.0597	1	18.8	41	R	KELGLYANVRPCNSLPGYK	T	Carbamidoi 0.00000000000100000000.0	
40	prot_hit_nu	prot_acc	prot_desc	prot_score	prot_mass	prot_match	prot_match	prot_seq	prot_seq	prot_cover	pep_query	pep_rank	pep_isbold	pep_isuniq	pep_exp_r	pep_exp_r	pep_exp_z	pep_calc_r	pep_delta	pep_miss	pep_score	pep_expect	pep_res_b	pep_seq	pep_res_af	pep_var_m	pep_var_mod_pos	
		1	TC377226	homologue	313	27969	3	3	3	3	18.6	28	1	1	0	1454.755	1453.748	1	1453.786	-0.0384	0	52.28	0.031	K	IGIMPGYIHKPGR	I	Oxidation (I 0.00020000000000.0	
		1	TC377226	homologue	313	27969	3	3	3	3	18.6	46	1	1	1	1823.984	1822.977	1	1823.031	-0.054	0	111.56	2.80E-08	K	TEKPVVAFIAGLTAPPGR	R		
		1	TC377226	homologue	313	27969	3	3	3	3	18.6	49	1	1	0	1953.985	1952.978	1	1953.032	-0.0543	1	151.37	2.70E-12	K	KGGTEHLGLPVFNVSVAEAK	A		
		2	TC399318	homologue	299	37773	3	3	3	3	15.6	28	1</															

43	prot_hit_nu	prot_acc	prot_desc	prot_score	prot_mass	prot_match	prot_match	prot_seque	prot_seque	prot_cover	pep_query	pep_rank	pep_isbold	pep_isuniq	pep_exp_rr	pep_exp_rr	pep_exp_z	pep_calc_n	pep_delta	pep_miss	pep_score	pep_expect	pep_res_bt	pep_seq	pep_res_af	pep_var_m	pep_var_m	pep_scan_title	
		1	TC370105	similar to U	293	37312	3	3	3	8.2	27	1	1	0	1219.664	1218.657	1	1218.697	-0.0403	0	100.37	5.80E-07	R	LFGVTTLDVVVR	A				
		1	TC370105	similar to U	293	37312	3	3	3	8.2	43	1	1	0	1375.765	1374.757	1	1374.798	-0.0411	1	86.56	1.20E-05	K	RLFGVTTLDVVVR	A				
		1	TC370105	similar to U	293	37312	3	3	3	8.2	67	1	1	1	1861.908	1860.901	1	1859.963	0.9377	0	106.05	1.00E-07	K	NGVEEVLGLQLTQFEK	D				
		2	TC375883	similar to U	225	37986	3	2	3	8.6	27	1	0	0	1219.664	1218.657	1	1218.697	-0.0403	0	100.37	5.80E-07	R	LFGVTTLDVVVR	A				
		2	TC375883	similar to U	225	37986	3	2	3	8.6	43	1	0	0	1375.765	1374.757	1	1374.798	-0.0411	1	86.56	1.20E-05	K	RLFGVTTLDVVVR	A				
		2	TC375883	similar to U	225	37986	3	2	3	8.6	64	1	1	1	1823.983	1822.976	1	1824.054	-1.0781	0	38.15	0.61	K	VAILGAAGGIGQPLSLLMK	L	Oxidation (I0.000000000000000020.0			
		3	CA486629	similar to U	117	21912	2	1	2	16.4	27	1	0	0	1219.664	1218.657	1	1218.697	-0.0403	0	100.37	5.80E-07	K	LFGVTTLDVVVR	A				
		3	CA486629	similar to U	117	21912	2	1	2	16.4	82	2	1	1	2288.075	2287.067	1	2286.143	0.9247	1	16.18	69	K	AGAGSATLSMAYAAARFVESSLR	A				
44	prot_hit_nu	prot_acc	prot_desc	prot_score	prot_mass	prot_match	prot_match	prot_seque	prot_seque	prot_cover	pep_query	pep_rank	pep_isbold	pep_isuniq	pep_exp_rr	pep_exp_rr	pep_exp_z	pep_calc_n	pep_delta	pep_miss	pep_score	pep_expect	pep_res_bt	pep_seq	pep_res_af	pep_var_m	pep_var_m	pep_scan_title	
		1	TC381621	homologue	560	33145	8	6	7	5	30.8	3	1	1	872.4277	871.4204	1	871.4763	-0.0559	0	45.71	0.22	K	EIAAELAR	S				
		1	TC381621	homologue	560	33145	8	6	7	5	30.8	11	1	1	0	1058.467	1057.46	1	1057.515	-0.0554	0	58.66	0.0095	K	QVAQQEAEER	S			
		1	TC381621	homologue	560	33145	8	6	7	5	30.8	20	1	1	0	1218.604	1217.597	1	1217.644	-0.0473	0	37.03	1.3	K	DLQMVNLTLR	L	Oxidation (I0.0002000000.0		
		1	TC381621	homologue	560	33145	8	6	7	5	30.8	24	1	1	1	1276.626	1275.619	1	1275.676	-0.0566	0	106.74	1.30E-07	K	MLLGLNAAAGFGGR	-			
		1	TC381621	homologue	560	33145	8	6	7	5	30.8	26	1	1	1	1292.642	1291.635	1	1291.671	-0.0361	0	98.17	9.10E-07	K	MLLGLNAAAGFGGR	-	Oxidation (I0.20000000000000.0		
		1	TC381621	homologue	560	33145	8	6	7	5	30.8	31	1	1	0	1432.637	1431.629	1	1431.686	-0.0562	0	81.87	3.60E-05	R	TRPHNFSNSGK	D			
		1	TC381621	homologue	560	33145	8	6	7	5	30.8	46	1	1	1	1727.941	1726.934	1	1726.983	-0.049	0	139.35	4.90E-11	R	LISEATAIAGTGILIELR	R			
		1	TC381621	homologue	560	33145	8	6	7	5	30.8	74	1	1	0	2520.316	2519.308	1	2519.361	-0.0524	0	92.83	1.20E-06	K	AVVAQFNADQLLTDRPHVSALVR	D			
		2	TC380420	homologue	497	29929	5	4	5	4	28.3	11	1	0	0	1058.467	1057.46	1	1057.515	-0.0554	0	58.66	0.0095	K	QVAQQEAEER	S			
		2	TC380420	homologue	497	29929	5	4	5	4	28.3	20	1	0	0	1218.604	1217.597	1	1217.644	-0.0473	0	37.03	1.3	K	DLQMVNLTLR	L	Oxidation (I0.0002000000.0		
		2	TC380420	homologue	497	29929	5	4	5	4	28.3	31	1	0	0	1432.637	1431.629	1	1431.686	-0.0562	0	81.87	3.60E-05	R	TRPHNFSNSGK	D			
		2	TC380420	homologue	497	29929	5	4	5	4	28.3	60	1	1	1	2221.084	2220.076	1	2220.139	-0.0623	0	226.51	6.70E-20	K	AAAGLGAASLLSASLYTVDGGER	A			
		2	TC380420	homologue	497	29929	5	4	5	4	28.3	74	1	0	0	2520.316	2519.308	1	2519.361	-0.0524	0	92.83	1.20E-06	K	AVVAQFNADQLLTDRPHVSALVR	D			
45	prot_hit_nu	prot_acc	prot_desc	prot_score	prot_mass	prot_match	prot_match	prot_seque	prot_seque	prot_cover	pep_query	pep_rank	pep_isbold	pep_isuniq	pep_exp_rr	pep_exp_rr	pep_exp_z	pep_calc_n	pep_delta	pep_miss	pep_score	pep_expect	pep_res_bt	pep_seq	pep_res_af	pep_var_m	pep_var_m	pep_scan_title	
		1	TC388991	homologue	526	40826	8	5	8	5	24.9	5	1	1	0	939.4403	938.4331	1	938.4722	-0.0392	0	46.05	0.18	R	WIHPSSGR	S			
		1	TC388991	homologue	526	40826	8	5	8	5	24.9	13	1	1	0	1021.511	1020.504	1	1020.539	-0.0355	0	54.04	0.029	K	GFILDGFPR	T			
		1	TC388991	homologue	526	40826	8	5	8	5	24.9	38	1	1	1	1582.766	1581.759	1	1581.8	-0.0407	0	136.02	1.20E-10	K	TPGVDDVSGEPLIQR	K			
		1	TC388991	homologue	526	40826	8	5	8	5	24.9	40	1	1	0	1617.807	1616.8	1	1616.841	-0.0412	0	83.07	2.30E-05	K	VLNFAIDDAILEER	I			
		1	TC388991	homologue	526	40826	8	5	8	5	24.9	55	1	1	1	2052.974	2051.966	1	2052.02	-0.0541	0	97.75	5.70E-07	R	LEAFHIQTEPVIDYYSK	N			
		1	TC388991	homologue	526	40826	8	5	8	5	24.9	59	1	1	1	2123.049	2122.042	1	2122.106	-0.0643	1	25.27	9.6	K	FAPPKTPGVDDVSGEPLIQR	K			
		1	TC388991	homologue	526	40826	8	5	8	5	24.9	62	1	1	1	2296.104	2295.097	1	2295.154	-0.0567	1	59.48	0.0032	K	SRLEAFHIQTEPVIDYYSK	N			
		1	TC388991	homologue	526	40826	8	5	8	5	24.9	71	1	1	0	2694.206	2693.199	1	2693.261	-0.0624	1	26.74	4.3	K	GTQSPLIKDEYCLCHLATGDMLR	A	2 Carbamic 0.00000000000101000000200.0		
		2	TC384775	homologue	281	82506	5	3	5	3	9	5	1	0	0	939.4403	938.4331	1	938.4722	-0.0392	0	46.05	0.18	R	WIHPSSGR	S			
		2	TC384775	homologue	281	82506	5	3	5	3	9	13	1	0	0	1021.511	1020.504	1	1020.539	-0.0355	0	54.04	0.029	K	GFILDGFPR	T			
		2	TC384775	homologue	281	82506	5	3	5	3	9	39	1	1	1	1596.775	1595.768	1	1595.816	-0.0479	0	72.71	0.00026	K	TPGVDDVTGEPLIQR	K			
		2	TC384775	homologue	281	82506	5	3	5	3	9	40	1	0	0	1617.807	1616.8	1	1616.841	-0.0412	0	83.07	2.30E-05	K	VLNFAIDDAILEER	I			
		2	TC384775	homologue	281	82506	5	3	5	3	9	71	1	0	0	2694.206	2693.199	1	2693.261	-0.0624	1	26.74	4.3	K	GTQSPLIKDEYCLCHLATGDMLR	A	2 Carbamic 0.00000000000101000000200.0		
46	prot_hit_nu	prot_acc	prot_desc	prot_score	prot_mass	prot_match	prot_match	prot_seque	prot_seque	prot_cover	pep_query	pep_rank	pep_isbold	pep_isuniq	pep_exp_rr	pep_exp_rr	pep_exp_z	pep_calc_n	pep_delta	pep_miss	pep_score	pep_expect	pep_res_bt	pep_seq	pep_res_af	pep_var_m	pep_var_m	pep_scan_title	
		1	TC384775	homologue	360	82506	5	3	5	3	8.5	8	1	1	1	939.4394	938.4321	1	938.4722	-0.0401	0	50.53	0.064	R	WIHPSSGR	S			
		1	TC384775	homologue	360	82506	5	3	5	3	8.5	19	1	1	1	1021.509	1020.501	1	1020.539	-0.038	0	53.69	0.031	K	GFILDGFPR	T			
		1	TC384775	homologue	360	82506	5	3	5	3	8.5	48	1	1	1	1596.778	1595.773	1	1595.816	-0.043	0	135.47	1.40E-10	K	TPGVDDVTGEPLIQR	K			
		1	TC384775	homologue	360	82506	5	3	5	3	8.5	49	1	1	1	1617.798	1616.79	1	1616.841	-0.0508	0	85.48	1.30E-05	K	VLNFAIDDAILEER	I			
		1	TC384775	homologue	360	82506	5	3	5	3	8.5	74	1	1	1	2330.046	2329.038	1	2329.105	-0.0666	1	37.03	0.54	K	SRLEAFHMQTEPVIDYYSK	N	Oxidation (I0.0000000200000000000.0		
		2	TC374069		146	45611	2	2	2	6.4	30	1	1	1	1338.638	1337.631	1	1337.665	-0.0342	1	59.09	0.0071	R	TVMSIFDKEPR	I	Oxidation (I0.00200000000.0			
		2	TC374069		146	45611	2	2	2	6.4	59	1	1	1	1911.847	1910.84	1	1910.883	-0.0433	1	87.23	7.20E-06	K	FAHKDEEYDSMLGVVR	E	Oxidation (I0.0000000002000000.0			
47	prot_hit_nu	prot_acc	prot_desc	prot_score	prot_mass	prot_match	prot_match	prot_seque	prot_seque	prot_cover	pep_query	pep_rank	pep_isbold	pep_isuniq	pep_exp_rr	pep_exp_rr	pep_exp_z	pep_calc_n	pep_delta	pep_miss	pep_score	pep_expect	pep_res_bt	pep_seq	pep_res_af	pep_var_m	pep_var_m	pep_scan_title	
		1	TC396379	homologue	619	42912	6	5	6	5	24.6	12	1	1	1	1226.661	1225.654	1	1225.703	-0.0492	0	95.15	1.90E-06	K	SILSLVVPDQR	S			
		1	TC396379	homologue	619	42912	6	5	6	5	24.6	31	1	1	1	1634.824	1633.816	1	1633.868	-0.0512	1	116.63	1.00E-08	R	KNESIFGELQTLK	N			
		1	TC396379	homologue	619	42912	6	5	6	5	24.6	38	1	1	1	1796.829	1795.822	1	1795.86	-0.0382	0	151.76	2.80E-12	K	SHSSTAVGAELSHNFPK	N			
		1	TC396379	homologue	619	42912	6	5	6	5	24.6	49	1	1	1	1966.946	1965.939	1	1965.983	-0.0443	0	157.33	6.80E-13	K	FTLTTCCTPEGVAITAAGTR	K	Carbamidol 0.0000010000000000000.0		
		1	TC396379	homologue	619	42912	6	5	6	5	24.6	61	3	1	1	2163.981	2162.973	1	2163.032	-0.0586	0	11.83	2.00E+02	R	FNNYGMASALVQHEWRPK	S	Oxidation (I0.000002000000000000.0		
		1	TC396379	homologue	619	42912	6	5	6	5	24.6	66	1	1	1	2197.027	2196.019	1	2196.081	-0.0619	0	86.77	6.50E-06	R	NESTLIFGSQHSLDPHTSVK	A			</

		2	TC378886	homologue	921	33820	9	8	9	8	45.8	17	1	0	0	1218.64	1217.633	1	1217.666	-0.0327	0	67.66	0.0011	K	TILSFAVPDQK	S		
		2	TC378886	homologue	921	33820	9	8	9	8	45.8	28	1	1	1	1387.678	1386.67	1	1386.697	-0.0262	0	68.3	0.00083	K	ASALIQHEFMPK	R	Oxidation (I0.000000000200.0	
		2	TC378886	homologue	921	33820	9	8	9	8	45.8	33	1	0	0	1427.777	1426.769	1	1426.803	-0.0338	0	91.78	3.60E-06	K	ADLILGEIQSQIK	N		
		2	TC378886	homologue	921	33820	9	8	9	8	45.8	37	1	0	0	1555.877	1554.87	1	1554.898	-0.0282	1	116.12	1.20E-08	K	KADLILGEIQSQIK	N		
		2	TC378886	homologue	921	33820	9	8	9	8	45.8	40	1	0	0	1582.752	1581.745	1	1581.768	-0.023	0	68.64	0.00066	K	GDSLTSASYHIVEK	S		
		2	TC378886	homologue	921	33820	9	8	9	8	45.8	53	1	0	0	1933.951	1932.943	1	1931.984	0.9594	0	91.94	2.40E-06	K	FTLTYYTANGAAITATSTK	K		
		2	TC378886	homologue	921	33820	9	8	9	8	45.8	57	1	0	0	2143.093	2142.086	1	2142.117	-0.0313	0	221.15	2.40E-19	K	ANSASNVTITITADDLAAPGLK	T		
		2	TC378886	homologue	921	33820	9	8	9	8	45.8	65	1	0	0	2340.147	2339.14	1	2339.176	-0.0358	0	187.94	4.50E-16	K	YNAALSYTNQDLIASLNLNNK	G		
		2	TC378886	homologue	921	33820	9	8	9	8	45.8	85	2	0	0	3659.901	3658.894	1	3658.812	0.0825	0	7.46	1.60E+02	K	SGTAVGAELTHSFSSNENSLFTGTQI	A		
		3	TC370164	similar to U	78	41534	1	1	1	1	3.8	45	1	1	1	1739.849	1738.841	1	1738.883	-0.0418	0	77.53	7.60E-05	K	IHPVVYAFQEFSEFR	W		
51	prot_hit_nu	prot_acc	prot_desc	prot_score	prot_mass	prot_match	prot_match	prot_seque	prot_seque	prot_cover	pep_query	pep_rank	pep_isbold	pep_isuniq	pep_exp_r	pep_exp_r	pep_exp_z	pep_calc_r	pep_delta	pep_miss	pep_score	pep_expect	pep_res_b	pep_seq	pep_res_af	pep_var_m	pep_var_m	pep_scan_title
		1	TC395139	UniRef100	236	35012	8	3	4	2	15.7	22	1	1	1	1317.589	1316.582	1	1316.626	-0.0442	0	76.25	0.00025	K	HHATYVANYNK	A		
		1	TC395139	UniRef100	236	35012	8	3	4	2	15.7	31	1	1	0	1518.751	1517.743	1	1517.799	-0.0557	0	50.94	0.081	K	NVRPDYLTNIWK	V		
		1	TC395139	UniRef100	236	35012	8	3	4	2	15.7	32	1	1	0	1522.751	1521.743	1	1521.794	-0.0514	0	57.8	0.017	K	NVRPDYLTNIWK	V	Trp->Kynur 0.0000000000050.0	
		1	TC395139	UniRef100	236	35012	8	3	4	2	15.7	37	1	1	0	1550.752	1549.745	1	1549.789	-0.0444	0	59.98	0.01	K	NVRPDYLTNIWK	V	Dioxidation 0.0000000000030.0	
		1	TC395139	UniRef100	236	35012	8	3	4	2	15.7	44	1	1	0	1583.715	1582.708	1	1582.752	-0.0438	0	51.79	0.065	K	LGWAIDEDFGSIEK	L	Trp->Kynur 0.005000000000000.0	
		1	TC395139	UniRef100	236	35012	8	3	4	2	15.7	52	1	1	1	1604.724	1603.716	1	1602.769	0.9472	0	20.21	94	K	FNGGGHVNHSIFWK	N	Trp->Kynur 0.000000000000050.0	
		1	TC395139	UniRef100	236	35012	8	3	4	2	15.7	53	1	1	0	1611.71	1610.703	1	1610.746	-0.0433	0	38.32	1.4	K	LGWAIDEDFGSIEK	L	Dioxidation 0.003000000000000.0	
		1	TC395139	UniRef100	236	35012	8	3	4	2	15.7	59	1	1	1	1632.721	1631.714	1	1630.764	0.9496	0	48.2	0.15	K	FNGGGHVNHSIFWK	N	Dioxidation 0.000000000000030.0	
		2	GH727141	homologue	110	26461	5	2	2	1	10.6	31	1	0	0	1518.751	1517.743	1	1517.799	-0.0557	0	50.94	0.081	K	NVRPDYLTNIWK	V		
		2	GH727141	homologue	110	26461	5	2	2	1	10.6	32	1	0	0	1522.751	1521.743	1	1521.794	-0.0514	0	57.8	0.017	K	NVRPDYLTNIWK	V	Trp->Kynur 0.0000000000050.0	
		2	GH727141	homologue	110	26461	5	2	2	1	10.6	37	1	0	0	1550.752	1549.745	1	1549.789	-0.0444	0	59.98	0.01	K	NVRPDYLTNIWK	V	Dioxidation 0.00000000000030.0	
		2	GH727141	homologue	110	26461	5	2	2	1	10.6	44	1	0	1	1583.715	1582.708	1	1582.752	-0.0438	0	51.79	0.065	-	LGWALDEDFGSIEK	L	Trp->Kynur 0.005000000000000.0	
		2	GH727141	homologue	110	26461	5	2	2	1	10.6	53	1	0	1	1611.71	1610.703	1	1610.746	-0.0433	0	38.32	1.4	-	LGWALDEDFGSIEK	L	Dioxidation 0.003000000000000.0	
		3	CA616257	UniRef100	78	19614	4	0	2	0	14.5	32	9	0	1	1522.751	1521.743	1	1522.814	-1.0718	0	11.04	8.00E+02	R	TLRPDYLTNIWK	V	Trp->Kynur 0.0000000000050.0	
		3	CA616257	UniRef100	78	19614	4	0	2	0	14.5	37	2	0	1	1550.752	1549.745	1	1550.809	-1.0648	0	26.44	23	R	TLRPDYLTNIWK	V	Dioxidation 0.000000000000030.0	
		3	CA616257	UniRef100	78	19614	4	0	2	0	14.5	44	1	0	0	1583.715	1582.708	1	1582.752	-0.0438	0	51.79	0.065	K	LGWAIDEDFGSIEK	L	Trp->Kynur 0.005000000000000.0	
		3	CA616257	UniRef100	78	19614	4	0	2	0	14.5	53	1	0	0	1611.71	1610.703	1	1610.746	-0.0433	0	38.32	1.4	K	LGWAIDEDFGSIEK	L	Dioxidation 0.003000000000000.0	
		4	CA616252	homologue	77	18061	3	0	2	0	15.1	37	3	0	1	1550.752	1549.745	1	1548.725	1.0193	0	25.61	28	R	TXRPDYLTNIWK	V	Dioxidation 0.00000000000030.0	
		4	CA616252	homologue	77	18061	3	0	2	0	15.1	44	1	0	0	1583.715	1582.708	1	1582.752	-0.0438	0	51.79	0.065	K	LGWAIDEDFGSIEK	L	Trp->Kynur 0.005000000000000.0	
		4	CA616252	homologue	77	18061	3	0	2	0	15.1	53	1	0	0	1611.71	1610.703	1	1610.746	-0.0433	0	38.32	1.4	K	LGWAIDEDFGSIEK	L	Dioxidation 0.003000000000000.0	
52	prot_hit_nu	prot_acc	prot_desc	prot_score	prot_mass	prot_match	prot_match	prot_seque	prot_seque	prot_cover	pep_query	pep_rank	pep_isbold	pep_isuniq	pep_exp_r	pep_exp_r	pep_exp_z	pep_calc_r	pep_delta	pep_miss	pep_score	pep_expect	pep_res_b	pep_seq	pep_res_af	pep_var_m	pep_var_m	pep_scan_title
		1	TC395139	UniRef100	175	35012	8	3	4	1	17.2	22	1	1	0	1518.757	1517.75	1	1517.799	-0.0491	0	56.46	0.037	K	NVRPDYLTNIWK	V		
		1	TC395139	UniRef100	175	35012	8	3	4	1	17.2	23	1	1	0	1522.751	1521.743	1	1521.794	-0.0507	0	57.13	0.032	K	NVRPDYLTNIWK	V	Trp->Kynur 0.0000000000050.0	
		1	TC395139	UniRef100	175	35012	8	3	4	1	17.2	25	1	1	0	1534.75	1533.742	1	1533.794	-0.0517	0	47.95	0.26	K	NVRPDYLTNIWK	V	Oxidation (I0.0000000000030.0	
		1	TC395139	UniRef100	175	35012	8	3	4	1	17.2	28	1	1	0	1550.756	1549.749	1	1549.789	-0.0398	0	59.26	0.02	K	NVRPDYLTNIWK	V	Dioxidation 0.00000000000040.0	
		1	TC395139	UniRef100	175	35012	8	3	4	1	17.2	34	1	1	0	1583.716	1582.708	1	1582.752	-0.0432	0	46.85	0.34	K	LGWAIDEDFGSIEK	L	Trp->Kynur 0.005000000000000.0	
		1	TC395139	UniRef100	175	35012	8	3	4	1	17.2	41	1	1	0	1611.716	1610.709	1	1610.746	-0.0376	0	53.32	0.076	K	LGWAIDEDFGSIEK	L	Dioxidation 0.004000000000000.0	
		1	TC395139	UniRef100	175	35012	8	3	4	1	17.2	51	1	1	1	1632.717	1631.709	1	1630.764	0.9454	0	26.76	35	K	FNGGGHVNHSIFWK	N	Dioxidation 0.000000000000040.0	
		1	TC395139	UniRef100	175	35012	8	3	4	1	17.2	58	1	1	0	1797.924	1796.917	1	1796.963	-0.0465	1	38.77	2.1	K	RLSVETTPNQDPLVTK	G		
		2	CA616257	UniRef100	117	19614	5	0	3	0	23.5	23	4	0	1	1522.751	1521.743	1	1522.814	-1.0711	0	14.28	6.20E+02	R	TLRPDYLTNIWK	V	Trp->Kynur 0.0000000000050.0	
		2	CA616257	UniRef100	117	19614	5	0	3	0	23.5	28	2	0	1	1550.756	1549.749	1	1550.809	-1.0602	0	24.61	57	R	TLRPDYLTNIWK	V	Dioxidation 0.00000000000040.0	
		2	CA616257	UniRef100	117	19614	5	0	3	0	23.5	34	1	0	0	1583.716	1582.708	1	1582.752	-0.0432	0	46.85	0.34	K	LGWAIDEDFGSIEK	L	Trp->Kynur 0.005000000000000.0	
		2	CA616257	UniRef100	117	19614	5	0	3	0	23.5	41	1	0	0	1611.716	1610.709	1	1610.746	-0.0376	0	53.32	0.076	K	LGWAIDEDFGSIEK	L	Dioxidation 0.004000000000000.0	
		2	CA616257	UniRef100	117	19614	5	0	3	0	23.5	58	1	0	0	1797.924	1796.917	1	1796.963	-0.0465	1	38.77	2.1	K	RLSVETTPNQDPLVTK	G		
		3	GH727141	homologue	113	26461	6	3	2	1	10.6	22	1	0	0	1518.757	1517.75	1	1517.799	-0.0491	0	56.46	0.037	K	NVRPDYLTNIWK	V		
		3	GH727141	homologue	113	26461	6	3	2	1	10.6	23	1	0	0	1522.751	1521.743	1	1521.794	-0.0507	0	57.13	0.032	K	NVRPDYLTNIWK	V	Trp->Kynur 0.0000000000050.0	
		3	GH727141	homologue	113	26461	6	3	2	1	10.6	25	1	0	0	1534.75	1533.742	1	1533.794	-0.0517	0	47.95	0.26	K	NVRPDYLTNIWK	V	Oxidation (I0.0000000000030.0	
		3	GH727141	homologue	113	26461	6	3	2	1	10.6	28	1	0	0	1550.756	1549.749	1	1549.789	-0.0398	0	59.26	0.02	K	NVRPDYLTNIWK	V	Dioxidation 0.00000000000040.0	
		3	GH727141	homologue	113	26461	6	3	2	1	10.6	34	1	0	1	1583.716	1582.708	1	1582.752	-0.0432	0	46.85	0.34	-	LGWALDEDFGSIEK	L	Trp->Kynur 0.005000000000000.0	
		3	GH727141	homologue	113	26461	6	3	2	1	10.6	41	1	0	1	1611.716	1610.709	1	1610.746	-0.0376	0	53.32	0.076	-	LGWALDEDFGSIEK	L	Dioxidation 0.004000000000000.0	
		4	CA616252	homologue	76	18061	4	0	2	0	15.1	23	9	0	1	1522.751	1521.743	1	1520.73	1.013								

		5 CA616252	homologue	96	18061	4	0	3	0	23.8	25	3	0	1	1550.767	1549.76	1	1548.725	1.0346	0	24.89	54	R	TXRPDYLTNIWK	V	Dioxidation (W)		
		5 CA616252	homologue	96	18061	4	0	3	0	23.8	30	1	0	0	1583.731	1582.724	1	1582.752	-0.0276	0	31.01	13	K	LGWAIDEDFGSIEK	L	Trp->Kynurenin (W)		
		5 CA616252	homologue	96	18061	4	0	3	0	23.8	45	1	0	0	1641.845	1640.838	1	1640.862	-0.0246	0	40.34	1.5	K	LSVETTPNQDPLVTK	G			
54	prot_hit_nu	prot_acc	prot_desc	prot_score	prot_mass	prot_match	prot_match	prot_seque	prot_seque	prot_cover	pep_query	pep_rank	pep_isbold	pep_isuniq	pep_exp_r	pep_exp_r	pep_exp_z	pep_calc_n	pep_delta	pep_miss	pep_score	pep_expect	pep_res_b	pep_seq	pep_res_af	pep_var_m	pep_var_m	pep_scan_title
		1 TC388331	similar to U	235	35620	6	2	5	2	16.1	6	1	1	1	1024.446	1023.439	1	1023.466	-0.0272	0	64.51	0.0049	R	WSAFVDDGK	I			
		1 TC388331	similar to U	235	35620	6	2	5	2	16.1	11	1	1	1	1265.622	1264.615	1	1264.645	-0.0306	1	50.92	0.11	R	WSAFVDDGKIK	A			
		1 TC388331	similar to U	235	35620	6	2	5	2	16.1	12	1	1	1	1269.616	1268.609	1	1268.64	-0.0316	1	77.16	0.00027	R	WSAFVDDGKIK	A	Trp->Kynur	0.50000000000.0	
		1 TC388331	similar to U	235	35620	6	2	5	2	16.1	20	1	1	0	1490.761	1489.752	1	1489.793	-0.0407	1	48.94	0.17	K	FSTTPLKDFH GK	K			
		1 TC388331	similar to U	235	35620	6	2	5	2	16.1	23	9	1	1	1585.832	1584.825	1	1584.872	-0.0472	0	15.96	3.40E+02	K	SLDLIELDLSAALLGR	R			
		1 TC388331	similar to U	235	35620	6	2	5	2	16.1	26	1	1	1	1713.732	1712.725	1	1712.768	-0.0433	0	32.25	7.8	K	DAIEFYGDLDG SFHK	S			
		2 CA647979	similar to U	93	22142	2	0	2	0	10.5	6	2	0	0	1024.446	1023.439	1	1023.451	-0.012	0	43.92	0.56	R	SWDEGVATK	F	Dioxidation	0.040000000.0	
		2 CA647979	similar to U	93	22142	2	0	2	0	10.5	20	1	0	0	1490.76	1489.752	1	1489.793	-0.0407	1	48.94	0.17	K	FSTTPLKDFH GK	K			
55	prot_hit_nu	prot_acc	prot_desc	prot_score	prot_mass	prot_match	prot_match	prot_seque	prot_seque	prot_cover	pep_query	pep_rank	pep_isbold	pep_isuniq	pep_exp_r	pep_exp_r	pep_exp_z	pep_calc_n	pep_delta	pep_miss	pep_score	pep_expect	pep_res_b	pep_seq	pep_res_af	pep_var_m	pep_var_mod_pos	
		1 CK164007	similar to U	531	35560	10	6	8	4	27.6	1	1	1	1	813.4863	812.4791	1	812.5232	-0.0441	1	32.82	4.1	R	KIIVQGR	S			
		1 CK164007	similar to U	531	35560	10	6	8	4	27.6	11	1	1	1	945.4975	944.4902	1	944.5291	-0.0389	0	61.41	0.0057	K	SIAGIVTER	D			
		1 CK164007	similar to U	531	35560	10	6	8	4	27.6	19	1	1	1	1056.602	1055.594	1	1055.634	-0.0396	0	48.33	0.1	K	LITVKPETR	V			
		1 CK164007	similar to U	531	35560	10	6	8	4	27.6	28	1	1	1	1410.69	1409.683	1	1409.726	-0.0431	1	91.24	4.10E-06	R	AVVSEHK EELNR	L			
		1 CK164007	similar to U	531	35560	10	6	8	4	27.6	34	1	1	1	1492.761	1491.753	1	1491.805	-0.0512	1	48.6	0.072	K	SIAGIVTERDYLR	K			
		1 CK164007	similar to U	531	35560	10	6	8	4	27.6	43	1	1	1	2008.976	2007.969	1	2008.041	-0.0723	0	50.69	0.03	K	SMTQHNVGALVVVKPGEDK	S			
		1 CK164007	similar to U	531	35560	10	6	8	4	27.6	44	1	1	1	2024.989	2023.982	1	2024.036	-0.0542	0	110.83	2.90E-08	K	SMTQHNVGALVVVKPGEDK	S	Oxidation (I	0.020000000000000000.0	
		1 CK164007	similar to U	531	35560	10	6	8	4	27.6	51	1	1	1	2173.082	2172.075	1	2172.146	-0.0709	0	107.81	5.10E-08	K	VGDIMTEENKLITVKPETR	V			
		1 CK164007	similar to U	531	35560	10	6	8	4	27.6	53	1	1	1	2189.092	2188.085	1	2188.141	-0.0562	1	124.87	1.00E-09	K	VGDIMTEENKLITVKPETR	V	Oxidation (I	0.0000200000000000000.0	
		1 CK164007	similar to U	531	35560	10	6	8	4	27.6	66	2	1	1	2276.051	2275.043	1	2275.101	-0.0577	0	14.94	92	R	HIPVISGTEMMGMV SIGDVVR	A	3 Oxidation	0.0000000002020200000000.0	
56	prot_hit_nu	prot_acc	prot_desc	prot_score	prot_mass	prot_match	prot_match	prot_seque	prot_seque	prot_cover	pep_query	pep_rank	pep_isbold	pep_isuniq	pep_exp_r	pep_exp_r	pep_exp_z	pep_calc_n	pep_delta	pep_miss	pep_score	pep_expect	pep_res_b	pep_seq	pep_res_af	pep_var_m	pep_var_m	pep_scan_title
		1 TC381037	similar to U	530	47944	10	4	9	3	18.9	1	1	1	1	820.4502	819.4429	1	819.4603	-0.0174	0	42.02	0.53	K	GLTNFLR	Y			
		1 TC381037	similar to U	530	47944	10	4	9	3	18.9	3	3	1	1	845.4461	844.4388	1	844.4555	-0.0168	0	27.62	15	R	SVWQGIR	E			
		1 TC381037	similar to U	530	47944	10	4	9	3	18.9	18	1	1	1	949.4773	948.47	1	948.489	-0.0189	0	49.74	0.083	K	GHALNPGQR	D			
		1 TC381037	similar to U	530	47944	10	4	9	3	18.9	22	1	1	1	989.4736	988.4663	1	988.4726	-0.0063	0	54.4	0.027	K	LHDTQYGR	H			
		1 TC381037	similar to U	530	47944	10	4	9	3	18.9	23	1	1	1	990.4471	989.4398	1	988.4726	0.9672	0	54.96	0.024	K	LHDTQYGR	H			
		1 TC381037	similar to U	530	47944	10	4	9	3	18.9	29	1	1	1	1077.583	1076.576	1	1076.598	-0.0222	1	45.45	0.2	R	EKGLTNFLR	Y			
		1 TC381037	similar to U	530	47944	10	4	9	3	18.9	32	1	1	1	1123.538	1122.531	1	1122.546	-0.0153	1	27.81	11	R	WVEYADKGR	Y			
		1 TC381037	similar to U	530	47944	10	4	9	3	18.9	34	1	1	1	1128.554	1127.546	1	1127.561	-0.0147	1	34.96	2.1	R	YAREEGYLK	C			
		1 TC381037	similar to U	530	47944	10	4	9	3	18.9	56	1	1	1	1738.79	1737.783	1	1737.796	-0.0129	0	113.16	2.10E-08	R	QNYTGQGGDLIYH SK	G			
		1 TC381037	similar to U	530	47944	10	4	9	3	18.9	58	1	1	1	1755.916	1754.908	1	1754.932	-0.0231	0	134.33	1.60E-10	K	IHNIGATLVGVDTFGNK	Y			
57	prot_hit_nu	prot_acc	prot_desc	prot_score	prot_mass	prot_match	prot_match	prot_seque	prot_seque	prot_cover	pep_query	pep_rank	pep_isbold	pep_isuniq	pep_exp_r	pep_exp_r	pep_exp_z	pep_calc_n	pep_delta	pep_miss	pep_score	pep_expect	pep_res_b	pep_seq	pep_res_af	pep_var_m	pep_var_m	pep_scan_title
		1 TC408892		482	25214	7	5	7	5	31.2	4	1	1	1	879.3944	878.3872	1	878.4246	-0.0374	1	35.9	2.1	R	DKFEANR	N			
		1 TC408892		482	25214	7	5	7	5	31.2	20	1	1	1	1172.557	1171.55	1	1171.583	-0.0335	0	74.83	0.00021	R	LIEDAEAQQR	N			
		1 TC408892		482	25214	7	5	7	5	31.2	21	1	1	0	1186.569	1185.562	1	1185.599	-0.037	0	61.83	0.0042	R	NVENLDVIDR	L			
		1 TC408892		482	25214	7	5	7	5	31.2	27	1	1	1	1378.66	1377.653	1	1377.668	-0.0152	0	86.29	1.30E-05	R	HLFYQDASELR	D			
		1 TC408892		482	25214	7	5	7	5	31.2	48	1	1	1	1621.772	1620.765	1	1620.79	-0.0245	1	73.1	0.00023	R	HLFYQDASELRDK	F			
		1 TC408892		482	25214	7	5	7	5	31.2	60	1	1	0	2023.956	2022.949	1	2022.995	-0.0465	0	42.82	0.18	R	NFQHPDPYIVPWAPGGTK	F			
		1 TC408892		482	25214	7	5	7	5	31.2	78	1	1	1	2173.016	2172.008	1	2172.038	-0.0293	1	107.18	5.90E-08	R	NPPPPPEGIEIINYGKEDQ	-			
		2 TC447761		212	43836	3	2	3	2	11.9	21	1	0	0	1186.569	1185.562	1	1185.599	-0.037	0	61.83	0.0042	R	NVENLDVIDR	L			
		2 TC447761		212	43836	3	2	3	2	11.9	60	1	0	0	2023.956	2022.949	1	2022.995	-0.0465	0	42.82	0.18	R	NFQHPDPYIVPWAPGGTK	F			
		2 TC447761		212	43836	3	2	3	2	11.9	78	1	0	1	2173.016	2172.008	1	2172.001	0.0071	0	107.18	5.90E-08	R	NPPPPPEGIEIINYGQEDQ	-			
		3 CD490698	homologue	88	15675	2	0	2	0	26.2	60	1	0	0	2023.956	2022.949	1	2022.995	-0.0465	0	42.82	0.18	R	NFQHPDPYIVPWAPGGTK	F			
		3 CD490698	homologue	88	15675	2	0	2	0	26.2	78	3	0	1	2173.016	2172.008	1	2171.054	0.9547	1	45.03	0.097	R	NPPPPQGEIINYGKEDQ	-			
58	prot_hit_nu	prot_acc	prot_desc	prot_score	prot_mass	prot_match	prot_match	prot_seque	prot_seque	prot_cover	pep_query	pep_rank	pep_isbold	pep_isuniq	pep_exp_r	pep_exp_r	pep_exp_z	pep_calc_n	pep_delta	pep_miss	pep_score	pep_expect	pep_res_b	pep_seq	pep_res_af	pep_var_m	pep_var_m	pep_scan_title
		1 TC372910		334	50399	6	3	6	3	13	10	3	1	1	988.4853	987.4781	1	987.5389	-0.0608	0	24.81	25	K	WQIETAK	I			
		1 TC372910		334	50399	6	3	6	3	13	22	1	1	1	1314.596	1313.589	1	1313.648	-0.0588	0	59.27	0.0069	K	DHRPADLHEPK	K			
		1 TC372910		334	50399	6	3	6	3	13	25	1	1	1	1360.629	1359.622	1	1359.678	-0.0565	0	86.22	1.40E-05	R	HLVDQYLESTR	G			
		1 TC372910		334	50399	6	3	6	3	13	38	1	1	1	1540.654	1539.647	1	1539.703	-0.056	0	75.98	0.00012	K	NPYGDPAVAMLEYR	E	Oxidation (I	0.00000000020000.0	
		1 TC372910		334	50399	6	3	6	3	13	44	1	1	1	1705.714	1704.706	1	1704.763	-0.0567	0	40.73	0.35	K	VEFDERPPDDFDPK	N			
		1 TC372910		334	50399	6	3	6	3	13	49	1	1	1	1904.839	1903.832	1	1903.895	-0.0634	1	47.47	0.067	K	AKVEFDERPPDDFDPK	N			
59	prot_hit_nu	prot_acc	prot_desc	prot_score	prot_mass	prot_match	prot_match	prot_seque	prot_seque	prot_cover	pep_query	pep_rank	pep_isbold	pep_isuniq	pep_exp_r	pep_exp_r	pep_exp_z	pep_calc_n	pep_delta	pep_miss	pep_score	pep_expect	pep_res_b	pep_seq	pep_res_af	pep_var_m	pep_var_m	pep_scan_title
		1 TC374691																										