Metabolomics study on *Arabidopsis thaliana* abiotic stress responses for priming, recovery, and stress combinations

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Dedication

This dissertation is dedicated to my father Bin Xu and my mother Chunli Yang.

Abstract

Temperature, water, and light are three stress factors that have major influences on plant growth, development, and reproduction. Plants can be primed to an acclimated state by a prior mild stress to enhance their resistance to future stress. ‘Priming’ is related to plant stress ‘memory’ during recovery. Plants may need to balance between keeping the memory for enhanced stress defense and resetting for maximum growth and development during recovery. In the field, plants are more often to encounter a combination of different abiotic stresses rather than a specific single stress condition. Plant responses to a combination of stresses may exhibit quite unique defense and acclimation responses as compared to the response elicited by each individual stress, which should not be simply considered as the sum of the two different stresses. However, the simultaneous occurrence of multiple stress events is rarely studied experimentally, especially by metabolomics methods. Metabolomics, the comprehensive, quantitative and qualitative analysis of small molecules, is an emerging 'omics' platform that is an important next-generation systems biology approach. By providing an instantaneous “snapshot” of metabolic processes that occur in an organism, metabolomics can potentially provide insightful *molecular mechanism information* to questions about physiological function in complex biological systems.

The objective of this thesis research was to use both untargeted and targeted metabolomics approaches to investigate plant shared and unique metabolic features in responses to single as well as multiple abiotic stresses, the priming effect of temperature stresses, plant memory during recovery phase, and the relationships between combined stress with each of individual stresses. An ultra-high pressure liquid chromatography-high resolution mass spectrometry (UHPLC-HR-MS)-based metabolomics approach was utilized. In chapter two, a metabolomics study on *Arabidopsis thaliana* 11-day-old seedling’s abiotic stress responses including heat (basal and acquired), cold (basal and acquired), drought and high light with 2-day-recovery was performed using a standardized reference system. In chapter three, *Arabidopsis thaliana* 11-day-old seedlings that were induced by the combination of different abiotic stresses including heat, cold, drought, salinity, and high light, that mimics field environment was studied.

From this thesis research, a number of potential stress signatures determined from the untargeted analysis were identified, quantified and clustered by stress response patterns. Central metabolism were found to undergo a complex regulatory process in response to stress. Shared and unique metabolic signatures were identified across different abiotic single and combined stresses. The majority of stress signatures clustered together and exhibited shared response patterns. However, cysteine, glutathione, and maltose showed unique and dramatic patterns, demonstrating large changes in glutathione biosynthesis, glutathione oxidation, and starch degradation. The results showed that only two combined stresses, including high light x cold and cold x salinity, had metabolic effects that reflected both of their constituent single stresses. Most combined stresses had one dominant stress that had a defining impact on the plant metabolic profile. Drought stress is the dominant stress for all of its stress combinations. Two combined stresses, including high light x heat and high light x salinity, showed unique metabolic stress response patterns that are not similar to any of their individual stresses. Most of these metabolic features were specifically changed only in the combined stress, which should thus be considered as novel stress conditions. In summary, this work utilized metabolomics to study plant priming effects, recovery processes, and combined stress responses. It led to an improved understanding of how plants respond to abiotic stresses and may support subsequent studies on plant abiotic stress metabolic flux analyses.

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List of Abbreviations

AC–acquired cold stress

ACR–acquired cold recovery

AH–acquired heat stress

AHR–acquired heat recovery

BC–basal cold stress

BCR–basal cold recovery

BH–basal heat stress

BHR–basal heat recovery

D–drought stress

DR–drought recovery

GSH–glutathione

GSSG–glutathione disulfide

GSTs–glutathione s-transferases

HCA–hierarchical clustering analysis

HILIC–hydrophilic interaction liquid chromatography

HL–high light stress

HLR–high light recovery

HPLC–high performance liquid chromatography

LC-HRMS–liquid chromatography–high resolution mass spectrometry

MS media, Murashige & Skoog medium

MS/MS, tandem mass spectrometry

m/z, mass-to-charge ratio

OPLS–the orthogonal projection was introduced to latent structures

OPLS-DA–orthogonal projections to latent structures discriminant analysis

OSC–orthogonal signal correction

PCA–principle component analysis

ROS–reactive oxygen species

TCA–tricarboxylic acid

Chapter 1. Introduction: plant abiotic stress and metabolomics

The importance of studying plant responses to abiotic stress, priming, recovery, and a combination of stress events

Stress in plants can be described as anything that can cause a change from ideal growth and optimal developmental conditions (Shulaev et al., 2008). Stresses can be classified as abiotic or biotic (Wardlaw, 1972) where abiotic stresses are caused by nonliving factors in the surrounding environment such as extremes in temperature and light intensity, draught, high salinity, and deficiency or toxic levels of nutrients (Dietz and Sunkar, 2010). Biotic stresses are caused by other competing or pathogenic organisms such as bacteria, viruses, fungi, herbivores, and nearby cultivated or native plants (Wardlaw, 1972). Plant are especially dependent on their environment due to their inability to move to optimize conditions. Therefore, abiotic stress is essentially unavoidable and harmful to plants (Rizhsky, 2004). The yield reduction of food crops that has been caused by abiotic stress worldwide (Ahmad and Prasad, 2012) is considered the major factor in reduced agricultural productivity. Many abiotic stress factors have been predicted to increase in the future due to global climate change, as reported by the Intergovernmental Panel on Climate Change (http://www.ipcc.ch/). Thus, understanding abiotic stress and plant responses to various stress events is an important topic in plant research.

Plants can be primed to an acclimated state for enhanced future stress resistance by a pretreatment with a mild stress; this process is also known as 'hardening off'. Because of this priming effect, it is widely accepted that plants may have a type of environmental 'memory'. However, plants may also need to seek a balance between keeping that memory or forgetting the hardening events, because constantly staying in the acclimated state may sacrifice a plant's optimal growth and orderly development (Crisp et al., 2016). In addition to a specific stress effect, the pretreatment with one abiotic stress may lead to a plant priming for enhanced resistance to another stressor, a phenomenon called plant 'cross hardening'. 'Cross hardening' suggests that different abiotic stresses may share common stress responses or that synergistic effects mediated by co-activation of stress signaling pathways may be result in observed plant 'cross memory' effects (Firtzlaff et al., 2016). Several previous metabolomics studies have reported that specific plant abiotic stress responses, such as heat (Kaplan et al., 2004), cold (Kaplan et al., 2004, 2007), freezing

(Hannah, 2006; Korn et al., 2010), drought (Urano et al., 2009), high light (Wulff-Zottele et al., 2010; Caldana et al., 2011), and heat and drought combination (Rizhsky, 2004) result in significant metabolic responses. Still, less has been done to integrate these stresses together into some uniform understanding of shared and specific stress targets, recovery, and crosstalk between different stresses.

Rather than a particular single stress, plants under typical field conditions most often encounter a combination of stress conditions simultaneously and the metabolic costs of responding to multiple stresses has been shown to severely affect crop production worldwide (Smith and Matthews, 2015). Some combinations of stresses cause more severe damage than each individual stress (Craufurd and Peacock, 1993; Savin and Nicolas, 1996). The National Centers for Environmental Information (NCEI) reported that the combination of heat waves and the accompanying drought has become one of the most common weather disasters resulting in damage worth more than $210 billion annually (Smith and Matthews, 2015). In recognition of these issues, a well-researched goal for maize breeding is to generate resistant lines against stress combinations. However, studies on combination stress response mechanisms is an extremely neglected area as compared to single stress studies. Transgenic plants tested under laboratory conditions that are resistant to one specific stress had only limited success when evaluated for enhanced resistance in the field (Gao et al., 2000; McKersie et al., 1999; Mohamed et al., 2001). These results indicate that the effect of a combined stress event should not be assumed to be simply the sum of any two individual stresses. Two different stresses may have an antagonistic effect with each other and, alternatively, may cause a novel and unique plant response to their combination (Pandey et al., 2017). A massive and complex challenge exists to fully describe and understand the key mechanisms for plant responses to stress combinations as found under typical conditions in the natural environment.

Complex mechanisms for plant abiotic stress responses

Stress leads to complex regulatory responses including changes in global gene expression, protein modifications, and the changes in metabolite composition (Wardlaw, 1972; Gilmour et al., 2000). Abiotic stress can induce physiological, biochemical, and morphological changes in membrane structure and function, tissue water content, protein, lipid, and primary and secondary metabolite composition (Hallberg et al., 1985; Hirayama and Shinozaki, 2010). Abiotic stress may disrupt cellular osmotic homeostasis and cause osmotic or oxidative secondary stresses (Vinocur and Altman, 2005). Second messengers such as Ca^{2+}, phosphatidic acid (PtdOH), reactive oxygen species (ROS), or osmosensors like *Arabidopsis thaliana* histidine kinase-1 (AtHK1) can trigger downstream signaling cascades including mitogen-activated protein kinases (MAPK), overly sensitive (SOS) kinases, and calcium dependent protein kinases (CDPKs) (Mittler, 2002; Qiu et al., 2002; Shou et al., 2004; Schachtman and Schroeder, 1994; Shi et al., 2002). Those signaling cascades can induce important stress responsive transcription factors including heat shock factor (HSF), C-repeat-binding factor/dehydration-responsive element binding protein (CBF/DREB), inducer of CBF expression 1 (ICE1), ABA-responsive element binding factor/ABA-responsive element (ABF/ABRE) families, basic leucine zipper transcription factor (Bzip), and MYC/MYB (Zhang et al., 2004; Jaglo-Ottosen et al., 1998; Chinnusamy et al., 2003; Shen and Ho, 1995). Once induced the stress-inducible transcription factors can regulate genes encoding both functional and regulatory proteins that are directly or indirectly involved in implementing plant abiotic stress defenses (Hirayama and Shinozaki, 2010). For example, heat shock protein (Hsp) and late embryogenesis abundant (LEA) proteins function as chaperones (Wang et al., 2003, 2004) and protect protein structures from denaturation events during stress exposure. Superoxide dismutase (SOD) and peroxidase (PX) function in detoxification (Yoshimura et al., 2004) of oxygen radicals that increase under stress and would otherwise damage the cell. Proteins involved in ion and water transport like aquaporin and ion transporter (Vera-Estrella, 2004) similarly protect the osmotic integrity of the cell. Finally, proteins important for generation of stress-associated metabolites will be synthesized to function in abiotic stress defenses (Vinocur and Altman, 2005). These include metabolites that function as osmoprotectants or compatible solutes for protein and membrane stabilization and turgor pressure maintenance such as amino acids and derivatives, sugars and derivatives, phosphodiesters, quaternary ammonium compounds, and polyols (Yancey et al., 1982; Shahjee et al., 2002; Kang et al., 2002). Metabolites also have antioxidant roles complementary to SOD and PX function for ROS detoxification, protein redox regulation, and cellular component protection and these include sugars and sugar alcohols as well as glutathione (Alscher, 1989; Chiang et al., 2005; Nishizawa et al., 2008).

Using metabolomics as a tool to study plant abiotic stress

Metabolomics is a powerful tool for the post-genomic era that is a rapidly expanding area of research that enables scientists to better understand an organism's physiological state and response to stimuli. Metabolomics is the comprehensive, quantitative and qualitative analysis of the metabolome, the complete set of small molecules in a biological system (Dettmer et al., 2007). Because metabolites are the final product of cellular regulatory processes, and unlike gene and protein whose functions that are affected by epigenetic regulation and posttranslational modifications, metabolomics studies are potentially a more direct indicator of chemical phenotype (Shulaev et al., 2008). Metabolomic analyses can be classified as either untargeted and targeted where untargeted analysis focuses on pattern-based classification of as many metabolites as possible in the system with unbiased and global screening. Untargeted metabolomics is more commonly used for discovery-based questions such as characterization of the metabolic changes following treatment, genetic perturbation, or disease (Patti et al., 2012). In contrast, targeted metabolomic analysis focuses on identification and quantification of metabolites in a selected biochemical pathway or a specific class of compounds, and is more often employed to address questions in a hypothesis-driven manner (Dudley et al., 2010).

The plant kingdom is estimated to contain between 200,000 and 1,000,000 metabolites. *Arabidopsis thaliana* has about 8,000 (Pichersky and Lewinsohn, 2011; Obata and Fernie, 2012). Due to this huge chemical diversity, as well as the wide range in concentrations, there is no single instrumental platform currently for the comprehensive examination of whole metabolome (Bino et al., 2004). Only 1,000 and 2,000 metabolic features (mass-over-charge ratio (*m/z*) and retention time (rt) pairs) can be detected using the most comprehensive methods (Obata and Fernie, 2012). Importantly, a particular metabolic feature is not always a unique metabolite, but can also be an isotope, adduct, or neutral loss (Schrimpe-Rutledge et al., 2016). To increase the number of features or to focus on particular physical properties of the metabolite, metabolomics can be performed with a variety of separation methods such as liquid chromatography (LC) and gas chromatography (GC), and utilizing detection platforms such as mass spectrometry (MS) and nuclear magnetic resonance (NMR). Among them, LC-high resolution MS has become a leading technology for untargeted metabolomics because of the speed of the analyses and the structural information it provides (Schrimpe-Rutledge et al., 2016). Untargeted metabolomics provides a broader exploration and a global view of the metabolism in the system with no or limited preexisting knowledge of the metabolites of interests (Shulaev et al., 2008). However, this is accompanied by major challenges in data analysis, quantification accuracy, and feature annotation because of the high volume and high complexity dataset (Johnson et al., 2015). Therefore, it is important that the hypotheses generated from untargeted metabolomics, based on the relative quantification of both known and unknown metabolites, can be further studied with the tools provided by targeted metabolomics (Shulaev et al., 2008).

Methodologies for untargeted metabolomics

The workflow of untargeted metabolomics incorporate five steps including experimental design and sample collection, data collection, data preprocessing, statistical analysis, and feature annotation (Guitton et al., 2017). First, experimental design should define the biological questions to be addressed with appropriate quality controls such as reagent blanks and sample pools (Guitton et al., 2017). After sample collection and extraction, the data is collected from different analytical instruments. The choice of instrument should be based on the predicted chemical properties of metabolites of interest. For example, LC-MS can analyze a wide variety of metabolites from polar to non-polar, from low to high molecular weight using reversed phase, hydrophobic interaction, or ion exchange columns (Schrimpe-Rutledge et al., 2016). Electrospray ionization (ESI) utilized in LC-MS has advantages in that it is able to generate multiple charged ions for larger molecules and it can generate and be operated in both positive and negative modes (Allwood et al., 2008). However, LC-MS generates adducts that can complicate analyses and it has less consistent retention indices and spectra libraries compared to GC-MS (Dettmer et al., 2007). In comparison, GC-MS has higher reproducibility with larger spectral libraries for metabolite annotation. Nevertheless, GC-MS is only suitable for volatile compounds that can be ionized typically in the positive ion mode, not for large, polar, and/or heat-labile compounds directly. Chemical derivatization thus is typically required as the vast majority of metabolites that are polar non-volatile compounds (amino acids, sugars and organic acids etc.) that cannot be analyzed by GC-MS without derivatization (Allwood et al., 2008).

After data collection, the raw data can be preprocessed for peak detection, retention time alignment, noise filtering, and adduct and isotope annotation. The matrix of peak relative abundance are generated for further statistical analysis to detect metabolic changes between groups of interests. A variety of statistical approaches can then be performed from multivariate to univariate, from unsupervised to supervised. Combining both multivariate modeling and univariate hypothesis testing has become popular to build prediction models and to determine the features of interest (Wang et al., 2012; Thévenot et al., 2015). Univariate statistics, like the t-test and ANOVA, perform hypothesis testing on each individual variable and measure significance, which is particularly useful for non-normal data and outlier intensity measurements (Vinaixa et al., 2012). In comparison, multivariate statistics, such as principal component analysis (PCA), partial least squares discriminant analysis (PLS-DA), orthogonal projections to latent structures discriminant analysis (OPLS-DA), and hierarchical cluster analysis (HCA), generate models for the entire dataset. Among them, PCA and HCA are unsupervised, whereas PLS-DA and OPLS-DA are supervised. OPLS-DA has a greater discrimination power compared to PLS-DA by introducing the OPLS algorithm to improve interpretation between predictive components and the systematic variation (Trygg et al., 2001). Unsupervised PCA is a useful clustering method particularly useful early in the analysis in order to show groups of observations, trends, and outliers. It allows large multivariate data tables to be graphically visualized without overwhelming the analyses by reducing the dimensionality of original variables into two or three principal components (Wold et al., 1987). Once the differences between groups of interests are identified by PCA, it is worthwhile to use supervised OPLS-DA to discover biomarkers or signatures that contribute to the differences. The S-plot of OPLS-DA visualizes both the covariance (variable magnitude) and correlation (reliability) of each variable. The most positive and negative loadings in the S-plot represent variables as ideal biomarkers with both high magnitude and high reliability. The variable importance in projection (VIP) scores for OPLS-DA that reflect the importance of each variable in the projection can also be used for feature selection (Guitton et al., 2017).

After data analysis, a selection of features as potential biomarkers can be identified to draw biological conclusions. First, putative identification can be performed by query of MS1 compounds and spectral databases such as METLIN (Smith et al., 2005), ChemSpider (http://www.chemspider.com), Human Metabolome DataBase (HMDB) (Wishart et al., 2013), KEGG (Ogata et al., 1999), MassBank (Horai et al., 2010), mzCloud (https://www.mzcloud.org), GNPS (http://gnps. ucsd.edu/), etc. The development of high-resolution high-mass accuracy mass spectrometry has significantly improved the MS1 database searching by lowering the mass tolerance window for potential candidates (Schrimpe-Rutledge et al., 2016). However, even the high mass accuracy measurement with less than 1 ppm error is not sufficient to always fully determine elemental composition (Kind and Fiehn, 2006). Further information such as isotope ratio and MS2 fragmentation data are need. Nonetheless, the spectra databases for MS2 searching are currently considered incomplete because the fragmentation patterns are greatly affected by instrument, collision energy, and ionization source. Therefore, the scores for MS2 searching can often result in false positive and false negative results (Cajka and Fiehn, 2016). As a consequence, reference standards are always recommended for confident metabolic feature identification by validating MS1, retention time, and MS2 fragmentation data. Those confidently identified features may be linked back to metabolic networks to give insight as to their biological functions (Guitton et al., 2017).

Metabolome dynamics and metabolic flux analysis

Measurement of metabolite abundance alone, in most cases, cannot accurately describe the situation in vivo. For example, the explanation for metabolite abundance changes is typically complicated, and may need to be integrated with metabolic flux information to correctly model the observed changes. Metabolic flux is the flow of the carbon skeleton of a target metabolite through an organism's metabolic pathways (Roscher et al., 2000). It is affected by the rate of biosynthesis and degradation in a metabolic pathway during complex plant behaviors including plant growth, development, and responses to multiple environments (Pratt et al., 2002). Even though two metabolites have the same absolute abundance at a particular time, their metabolic fluxes may be very different. Some metabolites may be very active metabolically and have high flux rates to channel large quantities of metabolites through them, others have metabolic roles as enzyme intermediates where low steady-state levels remain part of the substrate-enzyme complex, whereas some metabolites may be the final products and thus have very low flux rates (Yang et al., 2010). Therefore, metabolic flux analysis may add additional information often necessary for the complete understanding of plant metabolic behaviors.

Chapter 2. Metabolic signatures of *Arabidopsis thaliana* abiotic stress responses elucidate patterns in stress priming, acclimation and recovery.

Introduction

Stress in plants has been described as any condition that causes a change in optimal growth, development, and reproduction (Wardlaw, 1972). Stress can be classified as abiotic and biotic (Guy, 1999). Abiotic stress is caused by nonliving factors in the environment such as temperature, the supply of water, and light intensity. In comparison, living factors such as bacteria, fungi, parasites, and herbivores cause biotic stress. Abiotic stress is particularly constraining to plants because, unlike animals, plants are not able to move and are thus particularly dependent on environmental factors (Rizhsky, 2004). Temperature, the supply of water, and light intensity are three major abiotic stress factors that have significant impact on plant growth, development, and reproduction. Increased climatic variability and more frequent extreme conditions can lead to plants being exposed to multiple stresses simultaneously.

Despite the fact that abiotic stresses arising at different stages of plant growth increases damage risk, earlier mild stress events can prime plants to an acclimated state to enhance their resistance against future stress by stronger or more rapid responses (Hallberg et al., 1985). Since different stressors often share common response pathways, sometimes a specific preceding stress may also prime a plant for an unrelated, different type of upcoming future stress, which is called the ‘cross stress tolerance/memory’ (Firtzlaff et al., 2016). Because of the priming effect, it has been widely accepted that plants have memory, which can occur at any developmental stage with various modifications from epigenetics to transcription level, and proteome to metabolome levels (Li and Liu, 2016).

By retaining stress memories, plants benefit by enhanced defense against future stress from a stronger or more rapid activation of defense responses. However, keeping the stress memory may also impede plant recovery and cause delayed growth and development (Crisp et al., 2016). Therefore, as soon as the favorable conditions return, it may be more adventitious for plants to reset, or to ‘forget’ in order to obtain the maximum growth. Plants need to seek a balance between resetting (growth) and memory maintenance (defense) during the recovery processes. Plant stress memory studies have been described in terms of epigenetics (Crisp et al., 2016), as changes in transcript levels (Avramova, 2015;

Firtzlaff et al., 2016), and protein changes (Li and Liu, 2016). However, plant memory has been less frequently defined in metabolomic terms. Metabolomics is a post-genomic biology with goals to identify and quantify the metabolome, the small molecules that participate in metabolic reactions and represent the most direct phenotype of a biological system (Freund and Hegeman, 2017).

In this study, metabolic changes induced by three abiotic stressors including temperature, water, and light in *Arabidopsis thaliana* 11-day-old seedlings with and without priming and a 2-day-recovery treatment were measured using a liquid chromatography–mass spectrometry based metabolomics approach. Treatments were performed under identical growth conditions to minimize the influence of non-stress factors. Our focus was on primary metabolites since they best represent plant growth and development conditions and have important roles during plant stress resistant. Primary metabolites can function as energy sources, precursors of secondary metabolites, signaling molecules, osmoprotectants, and antioxidants. Therefore, hydrophilic interaction liquid chromatography (HILIC) was used for best retention and separation of the polar metabolites in primary metabolism. Precursors, intermediates, and products in the same metabolic pathways were monitored simultaneously. This study provides a unique contribution to our understanding of plant priming and memory, as well as shared and unique metabolic stress signatures for different abiotic stresses measured using closely matched parallel workflows.

Results

We conducted a comprehensive characterization of priming and recovery effects of *Arabidopsis thaliana* metabolome physiological variations in abiotic stresses including cold, heat, drought, and high light. The most statistically significant metabolic differences between stressed and control plants were identified using an untargeted metabolomics approach. Untargeted metabolomics is a pattern-based classification approach for as many metabolites as possible in the system using a global unbiased screening (De Vos et al., 2007). It is commonly used for discovery-based studies to characterize metabolic changes in disease, environmental or genetic perturbations (Patti et al., 2012). In this study, we executed a comprehensive analysis using both multivariate and univariate statistics.

Multivariate statistics modeling PCA and OPLS-DA were performed for clustering and potential stress metabolic signature selection. The top five most contributed metabolic features for different treatments were reported in **Supplemental Table 2-1**. The identified potential stress metabolic signatures with loadings of |p[1]|>0.07 from OPLS-DA were reported in **Supplemental Table 2-2**. In order to monitor the changes of precursors, intermediates, and products of those stress metabolic signatures in the same metabolic pathway, the univariate statistics ANOVA test was performed for metabolites in the same class or metabolic pathway. Because of their ability to define differences, both univariate and OPLS methods have increased in popularity for metabolic signature studies and been suggested to complement each other (Zhang and Watson, 2015). Overall, we comprehensively examined the changes of metabolites as stress metabolic signatures and their precursors, intermediates, and products in key central metabolic pathways.

Multivariate statistical comparisons using PCA and OPLS-DA

In this study, principle components analysis (PCA) was performed in a hierarchical manner to assess the extent of divergence between metabolites under different conditions (**Figure 2-1**). First, PCA of all the stress and recovery samples was performed (**Figure 2-1A**), which resulted in two large clusters consisting of the stress and stress-control group well separated from recovery and recovery-control group. This clustering pattern indicates that significant metabolic changes occur during the 2-day growth recovery period. Reanalysis of stress and stress-control (**Figure 2-1B**) and recovery and recovery-control (**Figure 2-1C**) subgroups were performed in an attempt to separate these groups into additional sub-clusters. In the stress group, both AH and BH heat stresses cluster together and are well separated from the other stresses and control, thus indicating that heat stress has the most dramatically different metabolic response within this group (**Figure 2-1B**). Additional reanalysis of subgroup (HL, D, AC, BC & control) in **Figure 2-1B1** shows the control is well separated from stresses in PC2 (18%), indicating that all of the stress groups have metabolic changes compared to control. Drought stress (D) is also well separated from the other stresses in this subgroup, while AC, BC and HL have more similar metabolic signatures. PCA of the basal and acquired heat subgroup (**Figure 2-1B2**) showed these two sets of samples are not well separated in both PC1 and PC2, indicating priming treatment of heat stress has a relatively minor effect right after the stress treatment. Subsequent PCA of the acquired cold, basal cold, and high light subgroup (**Figure 2-1B1a**) showed that acquired and basal cold cluster together but are separated from high light, indicating high light stress has a different response than cold stress. While priming treatment for cold, similar to what was observed for heat, has little significant difference from the unprimed treatment right after the stress treatment.

In the PCA of the recovery subgroup, drought recovery, basal heat recovery, and acquired heat recovery were well separated from another subgroup composed of acquired cold, basal cold, high light, together with the control, indicating that drought and heat have the most distinct metabolic responses (**Figure 2-1C**), and that the priming treatment for heat has a large and significant impact during 2-day-recovery. Subgroup PCA (**Figure 2-1C1**) showed acquired cold recovery and control recovery are separated from basal cold recovery and high light recovery. Additional subgroup PCAs (**Figure 2-1C1a** and **Figure 2-1C1b**) showed minor separation for acquired cold and control, and basal cold and high light. These results indicated the priming effect has dramatic influence during 2-day-recovery. Cold stress with priming treatment is more similar to the control than the unprimed cold stress following the 2-day-recovery period. Cold stress without the priming treatment is, interestingly, more similar to the high light after 2-day-recovery. It is known that *Arabidopsis* is more resilient to cold stress after priming with cold, and it seems likely, given the PCA results, that priming leads to faster recovery from cold stress. Whereas the observation of co-clustering of unprimed (basal) cold and high-light stress responses indicates that the plant's metabolic response for these stresses are similar, and may form the metabolic basis for cross stress tolerance/memory behavior.

Using the clustering hierarchy from the above PCA, we then performed Partial Least Squares Discriminant Analysis (PLS-DA) Orthogonal Projections to Latent Structures Discriminant Analysis (OPLS-DA) to identify which metabolic features were the most important drivers of differentiation. Compared to unsupervised PCA modeling, Both PLS-DA and OPLS-DA are supervised techniques that request a response value to be assigned. However, PLS approaches are often hard to interpret for complex datasets as uncorrelated variation is always present in the scores. To solve this problem, Trygg et al., 2001 introduced the orthogonal projection to latent structures (OPLS) algorithm by incorporating an Orthogonal Signal Correction (OSC) filter into a PLS model to separate the correlated (predictive) variation from uncorrelated (orthogonal) variation. In doing so, OPLS-DA helps identify correlated components in the presence of systematic variation (Thévenot et al., 2015). The clustering results from PCA was used to perform a corresponding hierarchical OPLS-DA for all the subgroups (**Supplemental Figure 2-1**) and all the treatment compared with their corresponding control (**Supplemental Figure 2-2**). The combination of both PCA and OPLS-DA produced novel information regarding general metabolic trends and stress-specific metabolic signatures.

Targeted metabolite analysis and hierarchical clustering

Metabolites that were identified as having significant abundance changes in one or more stress conditions as well as precursors, intermediates, and products in the same metabolic pathways were selected for further targeted analysis in order to provide a better representation of the central metabolic stress response. To do this, putative identities of the selected metabolites were confirmed by: 1) comparison chromatographic retention by co-injection; and 2) by comparison of MS/MS fragmentation behavior (**Supplemental Figures 4.1** & **4.2)** with standard compounds (**Supplemental Table 2-5**). After metabolite identities were confirmed, their corresponding LC-HRMS peaks were manually integrated in both positive and negative ionization modes and the fold change in the average intensities across replicates between stress and control samples were calculated. Fold-changes in intensities for metabolites observed in both ionization modes were averaged if they were deemed indistinguishable by ANOVA, otherwise the values derived from the most intense signals were used on the assumption that the values derived from lower signals were so due to ion-suppression. These confirmed metabolite abundance fold-change values (**Supplemental Table 2-4**) and treatments were then clustered by hierarchical clustering analysis (HCA) to provide relationships between stressors, priming, and recovery using this targeted central metabolism dataset. **Figure 2-2** shows a heatmap of an HCA analysis performed using the complete linkage with maximum distance measurement method. The clustering and distance methods were chosen based on De Souza et al., 2006 who tested three of the most popular clustering methods including single linkage, complete linkage and centroid methods, and found complete linkage and centroid methods performed better than single linkage. They explained that both complete linkage and centroid methods have a tendency to create compact, spherical clusters, whereas single linkage has a tendency to make elongated clusters. In addition, Edelbrock, 1979 reported that complete linkage was more accurate than single linkage when using Euclidean distance as the measure of similarity. We also tested complete linkage using other distance methods including Euclidean (**Supplemental Figure 2-5A**), Manhattan (**Supplemental Figure 2-5B**), and Minkowski (**Supplemental Figure 2-5C**), and other clustering methods including Ward's method (**Supplemental Figure 2-5D**) and McQuitty's method (**Supplemental Figure 2-5E**), and got comparable clustering results.

HCA elucidated five distinct clusters of the six stress and six recovery treatments (detailed in **Table 2-1**) that we named A-E as well as seven clusters of metabolites named 1-7. Group A contained treatments AC and D. It displayed increased abundance of metabolites in clusters 6 & 7 and decreased abundance in clusters 1, 4 & 5. Group B consisted of treatments AH and BH. It displayed a decreased abundance in metabolites in cluster 7 and an increased abundance of metabolites clusters 3, 5 & 6. Group C included treatments BC and HL. It displayed a decreased abundance of metabolites in clusters 1, 4, 5, & 7 and an increased abundance in clusters 2 & 6. Group D included treatments ACR, BCR, and HLR. It displayed decreased abundance in clusters 5, 6, & 7, and increased abundance in clusters 2 & 4. Group E was composed by treatments DR, AHR, and BHR, which displayed decreased abundance in clusters 2, 6 & 7 and increased abundance in cluster 4.

Discussion

Shared stress metabolic signatures

We found many metabolites showed similar responses to different stresses. These metabolites may function as shared stress metabolic signatures, indicating their common participation and general response patterns in multiple stresses. In **Figure 2-2**, metabolites in clusters 1, 2, 3, and 5 are shared stress metabolic signatures and exhibited similar response patterns across different abiotic stresses. Cluster 1 contained three metabolites in sugar metabolism (sucrose) and purine metabolism (adenine and adenosine). Their abundance increased in ACR, DR, AHR, BHR, BH, but decreased in BCR, HLR, AC, BC, AH. Previous studies showed that sucrose might function as signal molecules and osmotic regulators during plant stress responses (Kaplan et al., 2004; Rizhsky, 2004). The increase of sucrose may suggest its roles in stress signaling and osmotic stress responses.

Cluster 2 includes fifteen metabolites in aspartate family amino acids (aspartic acid, asparagine), glycolysis (DHAP, fructose 6−phosphate, glucose 6− phosphate), TCA cycle (DHAP, α−ketoglutaric acid.), glutathione metabolism (glutamic acid, GSSG), purine metabolism (guanosine monophosphate, ribose 5-phosphate), urea cycle (citrulline, arginine, ornithine, urea), and serine family amino acids (serine). They are increased in ACR, BCR, HLR, AC, BC, HL, AH, BH, and decreased in DR, BHR. Major nitrogen transport amino acids glutamate, asparagine, and aspartic acid are in cluster 2. While glutamine, another primary nitrogen assimilation amino acid, is in cluster 3. Most of glycolysis intermediates and two TCA cycle intermediates are in cluster 2. The increase of GSSG in AC, BC, D, HL may be caused by plant oxidative stress defense. During oxidative stress, reduced glutathione GSH can be oxidized to GSSG to detoxify ROS (Foyer et al., 1997). The decrease of GSSG in BHR and DR may indicate the severe level of oxidative stress decreased during recovery.

Cluster 3 was composed by seventeen metabolites in TCA cycle (oxaloacetic acid, succinic acid, malic acid, citric acid, fumaric acid), GABA shunt (γ-aminobutyric acid, shikimate pathway (shikimic acid), glutamate family amino acids (proline, glutamine, histidine), pyruvate family amino acids (alanine, pyruvic acid), oxaloacetate family of amino acids (threonine), glutathione metabolism (glycine), and sugar metabolism (glucose, xylose, fructose). They are increased in D, HL, AH, BH, decreased in DR, BHR. We found most of analyzed TCA cycle intermediates, including oxaloacetate, succinate, malate, citrate, and fumarate clustered together with the non-proteinogenic amino acid GABA. The radial plots for ratio changes of these metabolites were reported in **Figure 2-3D**. TCA cycle generates energy with reducing power, and is responsible for the most part of carbohydrate, amino acid, and fatty acid (Fernie et al., 2004). GABA is known to drive TCA cycle via GABA shunt (Caldana et al., 2011). During GABA shunt, succinate can be synthesized from GABA via succinic semialdehyde. Previous studies showed that GABA synthesis increased during temperature stress including heat and cold (Kinnersley and Turano, 2000). In addition, GABA shunt was reported to coordinate with general N and C metabolism

(Weigelt et al., 2008). The increase of both TCA cycle intermediates and GABA in AH, BH, D, HL may indicate that GABA may fuel central metabolism via TCA cycle for increased energy demand during stress.

We also noticed that proline and sugars including glucose, fructose, and xylose in cluster 3 are all known osmoprotectants or compatible solutes. Proline is synthesized from glutamate by the enzymes P5CS (1-pyrroline-5-carboxylate synthase) that contributes to osmotic adjustment, free radical scavenging, and subcellular structure stabilization (Hare and Cress, 1997). Previous studies showed that proline concentration increased in drought, salinity, and extreme temperatures (Kaplan et al., 2004, 2007; Sanchez et al., 2008). Glucose, fructose, and xylose were known to function as both stress signal and osmoprotectants molecules (Koch, 1996; Roitsch, 1999; Rizhsky, 2004). The increase of proline and sugars in AH, BH, and D may indicate their roles as osmolytes to help plant survive from osmotic stress.

Cluster 5 was consisted of nine metabolites in aromatic amino acids (phenylalanine, tyrosine, and tryptophan), pyruvate family of amino acids (valine, leucine), sugar alcohol (mannitol), sugar metabolism (raffinose), oxaloacetate family amino acids (lysine), and purine metabolism (guanine). **Figure 2-3A** showed similar pattern of metabolites in cluster 5 that increased in BHR, AH, BH, but decreased in ACR, BCR, HLR, AC, BC. Aromatic amino acids (tryptophan, tyrosine, and phenylalanine) are known to be precursors of pigments, alkaloids, hormones, and cell wall components (Dixon, 2001). While branched-chain amino acids (isoleucine, leucine and valine) are precursors of cyanogenic glycosides (Vetter, 2000). Both aromatic amino acids (tryptophan, tyrosine, and phenylalanine) and branched-chain amino acids (leucine and valine) are grouped in cluster 5, indicating they may act as precursors of secondary metabolites during stress responses. In addition, osmotic stress can induce the accumulation of branched-chain amino acids by abscisic acid-regulated protein degradation in *Arabidopsis thaliana* (Huang and Jander, 2017).

Primary metabolites have important roles during stress response

Primary metabolites are directly involved in plant normal growth, development, and reproduction. They act as building blocks and primary source of energy, carbon, and nitrogen. For example, sugar is an important energy source. To be able to fuel energy, sugar will move to glycolysis and thereby into the TCA cycle. Plant cell needs incoming solutes to cover the growing demand energy for both anabolism and catabolism. TCA cycle generates energy with reducing power, and is responsible for the most part of carbohydrate, amino acid, and fatty acid (Fernie et al., 2004). Amino acids are essential for protein synthesis and nitrogen balance. Inorganic nitrogen is incorporated into glutamine and glutamate, and function as nitrogen source to be converted into other amino acids or nitrogenous compounds.

Primary metabolites are known to be precursors of many secondary metabolites that function as defense compounds against biotic stresses elicited by pest, bacteria, and fungi (Kaplan et al., 2004). For example, aromatic amino acids are precursors of indole glucosinolates, phytoalexins, alkaloids, lignins, flavonoids, isoflavonoids, and hydroxycinnamic acids (Dixon, 2001). Branched-chain amino acids are precursors of cyanogenic glycosides, glucosinolates, and acyl-sugars (Vetter, 2000). In our study, both aromatic amino acids (tryptophan, tyrosine, and phenylalanine) and branched-chain amino acids (leucine and valine) are increased in BHR, AH, BH in cluster 5. They may act as precursors of secondary metabolites to accumulate in response against the opportunistic attack by pathogens on heat stress weakened host.

Previous studies show that primary metabolites could also function as signal molecules during stress responses. Many soluble sugars such as glucose, fructose, and sucrose have roles in plant stress signaling (Chiou and Bush, 1998; Koch, 1996; Roitsch, 1999). In our study, sucrose in cluster 1, glucose, xylose, and fructose in cluster 3 may be participated in stress signaling in plant.

Besides, primary metabolites act as osmolytes or compatible solutes to stabilize proteins and membranes and to maintain cellular turgor pressure. Major compatible solutes include amino acids and derivatives, sugars and derivatives, phosphodiesters, quaternary ammonium compounds, and polyols (Yancey et al., 1982; Shahjee et al., 2002). In this study, sucrose in cluster 1, asparagine, ornithine, and serine in cluster 2, GABA, alanine, proline, glycine, glucose, succinate, fructose, and malate in cluster 3, mannitol and raffinose in cluster 5, maltose in cluster 6 have both known compatible solutes properties and compatible solute-like properties. The accumulation of these metabolites indicated that multiple compatible solutes may act synergistically in response to osmotic stress induced by abiotic stresses.

Moreover, primary metabolites can function as antioxidant to detoxify ROS and prevent oxidative damage during oxidative stress. Carbohydrates like raffinose (Nishizawa et al., 2008) and sugar alcohols such as mannitol (Chiang et al., 2005) have been reported to improve plant abiotic stress tolerance by acting as antioxidants. Glutathione (GSH) is also known to be an important plant antioxidant to regulate protein redox and to prevent cellular component damage caused by reactive oxygen species (ROS) (Alscher, 1989). In our study, raffinose and mannitol in cluster 5 and GSH in cluster 6 may be connected to plant defense against oxidative stress.

Unique stress metabolic signatures

Three clusters each containing one single metabolite in HCA (**Figure 2-2**) attracted our attention: cluster 4 with GSH only, cluster 6 with cysteine only, and cluster 7 with maltose only. The separation of these three metabolites from all the other clusters was consistent using different clustering and distance methods including Euclidean (**Supplemental Figure 2-5A**), Manhattan (**Supplemental Figure 2-5B**), and Minkowski (**Supplemental Figure 2-5C**), and other clustering methods including Ward's method (**Supplemental Figure 2-5D**) and McQuitty's method (**Supplemental Figure 2-5E**). Cysteine, GSH, and maltose were always isolated in separate clusters. The unique clustering pattern for these three metabolites may be caused by their unique changing trend and ratio changes as shown in **Figure 2-3B** and **3C**. We found cysteine increased dramatically in stress groups up to 339 fold but had minor changes in the recovery groups. In contrast, GSH decreased tremendously in stress groups up to 66 fold but had little changes in the recovery groups. Both cysteine and GSH are critical compounds in glutathione metabolism. In addition, cysteine is one of the precursors for GSH. The big increase of cysteine may also lead to the increase of the GSH pool. However, GSH may be quickly consumed by oxidation to GSSG in order to detoxify the reactive oxygen species (ROS) produced from oxidative stress, which serves as a secondary stress of different abiotic stresses. This may be the account for the measured large decrease of GSH in the stress groups. On the other hand, maltose, the direct product of starch degradation, showed different responses from other sugars such as glucose, fructose, and sucrose and formed its own single cluster, indicating the potential differences between catabolism and anabolism during plant stress responses. In summary, cysteine, GSH, and maltose may function as unique stress metabolic signatures that has special role in stress responses.

Cysteine, GSH, and GSSG in glutathione metabolism

Glutathione (GSH) is a main low molecular mass plant non-protein thiol compound that is important for regulation of the redox state of the cells (Alscher, 1989). It also functions as an antioxidant in plant defense systems. The biosynthesis of glutathione consists of two enzymatic reactions (Strohm et al., 1995). First, glutamic acid and cysteine form γ-glutamylcysteine. Second, γ-glutamylcysteine and glycine form GSH. Under stress conditions, GSH functions as an antioxidant for reactive oxygen species (ROS) via the ascorbate-glutathione cycle to form the glutathione disulfide (GSSG), resulting in the increase for GSSG and GSSG/GSH ratio (Foyer et al., 1997). Along with its function as an antioxidant, GSH also performs other roles such as thiol disulfide exchange, detoxification, and cell signaling. Thus, alteration of GSH concentration may function together with the changes in amino acids such as glutamate and glutamine, which are GSH-dependent through the γ-glutamyl cycle. Glutathione S-transferases (GSTs) can function in processes to detoxify xenobiotics (Marrs, 1996) through forming phytochelatins that are important for heavy metal detoxification (Chen and Goldsbrough, 1994), and can also activate genes for acclimation, stress tolerance, and pathogen defense response (Wingate et al., 1988).

Glutathione has previously been reported to play important roles for plant abiotic stress defense responses including chilling and cold (Foster and Hess, 1980), heat (Nieto-Sotelo et al., 1999), drought (Gamble and Burke, 1984), salt (Roxas et al., 1997), high light (Cakmak and Marschner, 1992), and UV irradiation (Strid et al., 1994). In this study, the radial plots for ratio changes of cysteine, reduced glutathione (GSH), and oxidized glutathione (GSSG) were reported in **Figure 2-3C.** Cysteine, as one of the precursors of GSH, increased in all the stress groups, especially with a dramatic increase in the AH and BH with fold changes of 339 and 297. GSH decreased in all the stress groups, especially in AC, BC, and HL, with ratio changes of 66, 66 and 20, respectively. In contrast, GSSG had minor changes compared to GSH and cysteine. The increase of cysteine in stress groups may be related to GSH biosynthesis. The decreased GSH in all the stress groups may result from the oxidation of GSH through its function as an antioxidant. However, it is also possible that the biosynthesis pathway from cysteine to GSH is blocked during AH and BH, which leads to the accumulation of cysteine and decrease of GSH. Cysteine, GSH, and GSSG all showed minor changes during recovery, indicating resetting is the predominant strategy for glutathione metabolism during recovery.

Maltose from starch degradation

Maltose is the direct product from starch breakdown by -amylase. The radial plots for ratio changes of maltose and other sugars including glucose, fructose, xylose, mannitol, and raffinose were reported in **Figure 2-3B**. In our study, maltose elevated in AC and D up to 33 and 36 fold, but decreased in BH, HL, BHR, and BHL. The increase of maltose may be caused by starch degradation. Previous work showed that the activity and transcription of -amylase can be induced during temperature stress (Dreier et al., 1995). Kaplan and Guy, 2005 reported maltose was accumulated in *Arabidopsis* by starch degradation in cold shock in order to protect photosynthetic electron transport chain and proteins in chloroplast stroma. Rizhsky, 2004 reported that both maltose abundance and the expression of starch degradation transcripts were elevated in response to drought and heat combination stress. Maltose is also reported to function as compatible solutes and contributed to the protection of plant from freezing stress (Kaplan et al., 2004). It was suggested that moderate level of drought stress is occurred with elevated proline and Glycine-betaine, whereas severe level of drought stress is together with sugar accumulation (Hoekstra et al., 2001). In our study, maltose increased in AC and D of 33 and 36 fold, whereas proline increased in AH and BH. This result indicated that AC and D may induce more severe drought stress compared to AH and BH. Maltose is also involved in the production of glucose and sucrose from starch (Lu and Sharkey, 2004). However, in our study, the increase of maltose did not result in the increase of glucose and sucrose, indicating the accumulation of maltose may be occurred only in the plastids, spatially isolated from cytosolic primary sugar metabolism.

Overcompensation/overcorrection for recovery of basal heat and drought, may be caused by a slow recovery process or an adjusted metabolic baseline

Stress recovery is the process involved after a plant is returned to the favorable conditions until it has achieved a new state of homeostasis (Crisp et al., 2016). This period determines whether plants will keep the stress memory or reset. The group D, including ACR, BCR, and HLR, had lower metabolic fold changes compared to group E, indicating group D during a 2-day-recovery tends to reset to a pre-stress state. If memory dominates, the recovery groups should be more similar to its corresponding stress group. However, none of the recovery groups clustered together with stress group, indicating memory is an exception rather than the rule for most metabolites during plant stress recovery. Group E including DR, AHR, and BHR, showed higher metabolic changes compared to group D. Interestingly, BHR and DR showed opposite metabolic changes with their corresponding stress groups especially in metabolite cluster 2 and 3. The general trend for cluster 2 and 3 increased in BH and D, but decreased in BHR and DR. We call this phenomenon as overcompensation or overcorrection. It is possible that the resetting processes for BH and D during recovery are slow. In order to return to the pre-stress metabolic state faster, plant overcorrected their metabolic changes at beginning to decrease the increased metabolites induced by stress responses. However, it is also possible that a new distinct post-stress homeostasis was achieved during recovery process. Plant may keep the balance between memory and forgetfulness to adjust the metabolic baseline of some key signaling metabolites (cluster 2 and 3) in order to better adapt and survive from future recurring stress with minor cost of growth and development.

Common stress responses between AC and D, BC and HL, AH and BH

For cold stress, priming effect has bigger impact than stressors. AC and D, BC and HL showed common stress responses and clustered together in groups A and C. Crosstalk has been found between cold and drought stress responses at transcription level (Seki et al., 2002). Both cold and drought can activate the expression of genes containing the drought responsive and abscisic-acid-responsive promoter elements (DRE and ABRE) cis-acting element and drought-responsive-element-binding (DRE-binding) transcription factors DREB/CBF (Knight and Knight, 2001). Compared to cross talk between cold and drought stress, the relationship between cold and light stress is less studied.

In addition, no previous work showed that the priming treatment of cold stress will lead to different shared responses from high light stress to drought stress. The biggest different between group A and C is cluster 7 that composed by maltose only, which increased 33 fold in AC and 36 fold in D, but has minor change in BC and decreased in HL. This difference may suggest that the priming treatment of cold stress imposed on plant a different type of internal stress similar to drought stress, indicating AC and D may require increased maltose as osmoprotectant and elevated catabolism through starch degradation.

Cross memory/resistance may happen between heat and drought, cold and high light

In recovery groups, DR clustered together with AH and BH, whereas HL clustered together with AC and BC. The priming treatment for heat and cold has no effect on the metabolic cross talk between different stresses. This may indicate the potential of plant cross memory between drought and heat, high light and cold. Plants exposed to different stresses may keep similar memories after 2-day-recovery. In that way, the prior exposure of one stress may enhance plant future resistance to the other. For example, Rajashekar and Panda, 2014 reported that drought stress can trigger cold tolerance in *Arabidopsis*, wheat, oats, rye, and strawberry. This potential cross memory is important for plants to better survive in nature since the reoccur stress may not be identical and predictable. Thus, the appearance of one stress may serves as an indicator that prepares for the other types of stress. In addition, the memory formation or depletion may be similar between heat and drought, and cold and high light. For CR and HLR, metabolites had smaller fold changes compared to HR and DR, indicating they may tend to forget/reset in order to maximum their growth and development. For HR and DR, plant may prefer to keep the memory or adjust the metabolic baseline to a new state of homeostasis in order to prepare for stronger and quicker defense for reoccurring future stress. This balance mechanism may indicate plant have the ability to acknowledge different stresses to different severe level. Heat and drought may considered being more severe, easier reoccurring stress compared to cold and high light.

Measurements of precursors, intermediates, and products of important metabolic pathways in central metabolism

In this study, we monitored entire metabolic pathways from precursors and intermediates to products simultaneously in order to reveal the subtle interplay of functionally related metabolites. A clear example of substrate and product relationship of identified metabolites that play critical roles in metabolism, stress tolerance, priming, and memory during recovery processes can be observed in **Figure 2-4**. (Larger versions of the radial plots used in **Figure 2-4** are provided in **Supplemental Figure 5**). It also shows the important transitions that regulate stress and recovery processes. The biosynthesis rate of product is largely depended on the availability of precursors and intermediates. However, the possible explanations for the metabolite abundance changes is complicated, and may need to be integrated with metabolic flux information in future studies to give a better picture of the processes measured. Metabolic flux is the flow of the carbon of a metabolite through an organism's metabolic pathways (Roscher et al., 2000) as determined by the rate of biosynthesis and degradation (Pratt et al., 2002). Some metabolites may be very active and have a high flux rate to channel large quantities of metabolites through them or play roles as intermediates that are never released by the enzyme complex, whereas some metabolites may be the end products that accumulate to high levels yet have very low fluxes (Yang et al., 2010).

We showed that in some cases, in the same metabolic pathway, the substrate increased, however the products synthesized from it decreased. One good example is cysteine increased dramatically in all the stress treatments, but GSH synthesized from it decreased notably in AC, BC, and HL. The low abundance of the GSH pool may be caused by the high demand and high flux rate of GSH because of its function as an antioxidant to detoxify the ROS during oxidative stress defense and repair responses. In contrast, we also saw that the substrate decreased, while the products synthesized from it increased. For instance, glutamate decreased in basal heat stress treatments, however amino acids synthesized from it (arginine, glutamine, and proline) increased. Similarly, aspartate decreased in basal heat, drought, and high light stress treatments, whereas amino acids derived from it (asparagine, lysine, and threonine) increased in those treatments. Similarly, serine decreased in BH and HL, however amino acids synthesized from serine (cysteine and glycine) increased in these treatments. Moreover, pyruvate decreased in BH, but amino acids synthesized from it (alanine, leucine, and valine) increased. These results are consistent with the hypothesis that the low abundance of substrate may be caused by a high flux rate to more stable product pools, whereas the high abundance of product may be caused by the low flux rate in utilization pathways (Bateman et al., 2007). These results again suggest that it will be important to incorporate full metabolic flux analysis into future studies to better explain the increase or decrease of those metabolites' abundance.

Materials and Methods

Plant materials, growth conditions, and treatments

Arabidopsis thaliana wild-type (Col-0) seeds were obtained from Lehle Seeds and were sterilized with 30% (v/v) bleach containing 0.1% (v/v) Triton X-100 and vernalized at 4 °C for 2 days. Seedlings were germinated on 1/2 x MS media made from MS Salts (PhytoTechnology Laboratories, M524 Murashige & Skoog (MS) Basal Salt Mixture, 4.33 g/L for 1 x MS) with 1.5% agar. Plants were grown prior to stress, during recovery, and as unstressed controls, vertically, at 22°C under a 16-h-light/8-h-dark photoperiod, with ~80 μmol m^{-2} s^{-1} illumination from cool-white fluorescent tube lights (control conditions). Eleven-day-old seedlings were treated with abiotic stress conditions described in **Table 2-1**. After the stress treatments, plants were removed back to the 'control conditions' for two days. Whole seedlings were harvested for stress and recovery groups, frozen in liquid nitrogen, and stored at -80°C. Experiments were performed using three biological replicates, and each replicate consisted of 25 seedlings grown together on a single plate and pooled. The recovery group for drought stress was obtained by moving the desiccated seedlings back to the agar medium under 'control conditions' for 2 days prior to harvest.

Sample extraction and LC-HRMS analysis

About 100 mg (fresh weight) of frozen seedlings were ground in 1 mL of 70% isopropanol alcohol with one 2.5 mm tungsten carbide ball in a Geno/Grinder™ (OPS Diagnostics) for 7 minutes at an intensity of 10,956 *x g* on -20°C chilled blocks. After centrifugation for 5 minutes at 100,956 *x g*, 1 μL of supernatant was injected onto a UHPLC

(Ultimate 3000, Dionex) with ZIC-cHILIC column (100 mm ×2.1 mm, 3 μm particle size, EMD Millipore Corporation, Billerica, MA). Solvents A (0.1% (v/v) formic acid in water) and B (0.1% (v/v) formic acid in acetonitrile) were used as mobile phases for gradient separation. Extract corresponding to 100 µg of plant material (fresh weight) was loaded onto the column with at a flow rate of 0.4 mL/min, followed by the following gradient separation: 2 min from 98% B, 30 min to 55% B, 2 min to 95% B and maintained for 3 min. The column was equilibrated for 2 min with 98% B prior to the next run. The samples were analyzed using a hybrid quadrupole Orbitrap mass spectrometer (Q Exactive, Thermo Fisher Scientific, San Jose CA). Full scan MS (range 50−750 *m/z*) were acquired with 35 k resolution for both positive and negative mode in polarity switching. The target value based on predictive automatic gain control was 1.0×10^6 with 200 ms of maximum injection time. The flow rate for sheath gas, aux gas, and sweep gas was 50, 20, and 1 separately. The capillary temperature was 350 °C. The S-lens RF was set to 55. The Aux gas heater temperature was 300 °C. Targeted MS/MS acquisition was used during metabolite identification with similar settings to (Fan et al., 2016) with minor modifications. Briefly, the precursor ions were sequentially fragmented in the HCD collision cell with normalized collision energy of 10%, 20%, 40%. MS/MS scans were acquired with 17.5 k resolution and the target value was 2.0×10^5 with 100 ms of maximum injection time. An isolation width of 2.0 *m/z* was used for precursor ion selection in MS/MS mode.

Data analysis

Thermo RAW files were converted to *mzXML* format using *MSConvert* (Chambers et al., 2012). Peak detection, grouping, and retention time correction were performed in *XCMS* in *R*. Statistics analysis including multivariate modeling PCA, OPLSDA and hierarchical clustering were performed in Workflow4Metabolomics.org online resource for computational metabolomics (Giacomoni et al., 2015). Annotation was first performed by databases including *BMRB* (Markley et al., 2008), *METLIN* (Smith et al., 2005), and *HMDB* (Wishart et al., 2013) public databases, and identities were confirmed with authentic standards for *m/z*, retention time, and fragmentation data listed in **Supplemental Table 2-5**. Univariate testing ANOVA was performed using both

Workflow4Metabolomics.org online resource (Giacomoni et al., 2015) and Excel 2016 (Microsoft). The peak area for each targeted metabolites was exported from the *Quan Browser* module of the *Xcalibur* software (Thermo Fisher Scientific) after visual confirmation of mass and retention times to validate the *XCMS* feature extraction. Metabolic pathways were generated by reference to the *KEGG* pathway Database (Kanehisa et al., 2017). Radial plots were generated using *KaleidaGraph*. S-plots of OPLS-DA were generated to select variables with both high correlation and high covariance as metabolic signature candidates (Wiklund et al., 2008). To generate these plots the covariance $p[1]$ was plotted on the x-axis whereas the correlation profile $p(\mathrm{corr})[1]$ is plotted on the y-axis; the most positive and negative loadings in $p[1]$ and $p(\mathrm{corr})[1]$ of the S-plot represent variables with both high magnitude and high reliability. The S-plots for all the subgroups (**Supplemental Figure 2-3**) and all the treatments with their corresponding controls (**Supplemental Figure 2-4**) are included in the Supplemental Materials. The top 5 most contributed variables to OPLS-DA S-plot with both high correlation and high covariance in different groups were reported in **Supplemental Table 2-1**. The potential stress metabolic signatures whose $|p[1]|>0.07$ identified with reference standards were reported by **Supplemental Table 2-2**. Metabolites as potential stress metabolic signatures and their corresponding precursors, intermediates, or products in the same metabolic pathway that were identified by authentic standards with *m/z*, retention time, and fragmentation (**Supplemental Figure 2-6, Supplemental Figure 2-7, Supplemental Table 2-3)**.

Tables

Table 2-1. Abiotic stress conditions

Stress treatment	**Conditions**	**Time**	**Reference**[1]
Drought (D)	remove seedling grown on nylon membrane from medium and desiccate in air for 2h	9:00 AM	Li et al., 2008
Basal heat (BH)	45°C for 5h	9:00 AM	Kaplan et al., 2004;
Acquired heat (AH)	38°C for 1.5h, 22°C for 2h, 45°C for 5h	9:00 AM	Kaplan et al., 2004; Larkindale, 2005
Basal cold (BC)	4°C for 3h	9:00 AM	Kaplan et al., 2004
Acquired cold (AC)	4°C for 3 h, 22°C for 1h, -15°C for 1 h	9:00 AM	Kaplan et al., 2004
High light (HL)	902 μmol m^{-2} s^{-1} metal halide light for 1h	9:00 AM	Rossel et al., 2002
Recovery treatment	**Recovery Conditions**[2]		
Drought (DR)	seedlings transferred back to agar medium in control chamber for 48h	11:00 AM	
Basal heat (BHR)	plates of seedlings moved from stress to control chamber for 48h	2:00 PM	
Acquired heat (AHR)	plates of seedlings moved from stress to control chamber for 48h	5:30 PM	
Basal cold (BCR)	plates of seedlings moved from stress to control chamber for 48h	11:00 AM	
Acquired cold (ACR)	plates of seedlings moved from stress to control chamber for 48h	2:00 PM	
High light (HLR)	plates of seedlings moved from stress to control chamber for 48h	10:00 AM	

[1] Source from which stress conditions, with minor modifications, were derived.

[2] All recovery treatments were identical to the above stress treatments, but were sampled after a 48 hr recovery period at ‘control conditions’ (22°C, 16-h-light/8-h-dark photoperiod with lights on at 8:00 AM., and ~80 μmol m^{-2} s^{-1} from cool-white fluorescent lights)

Figures

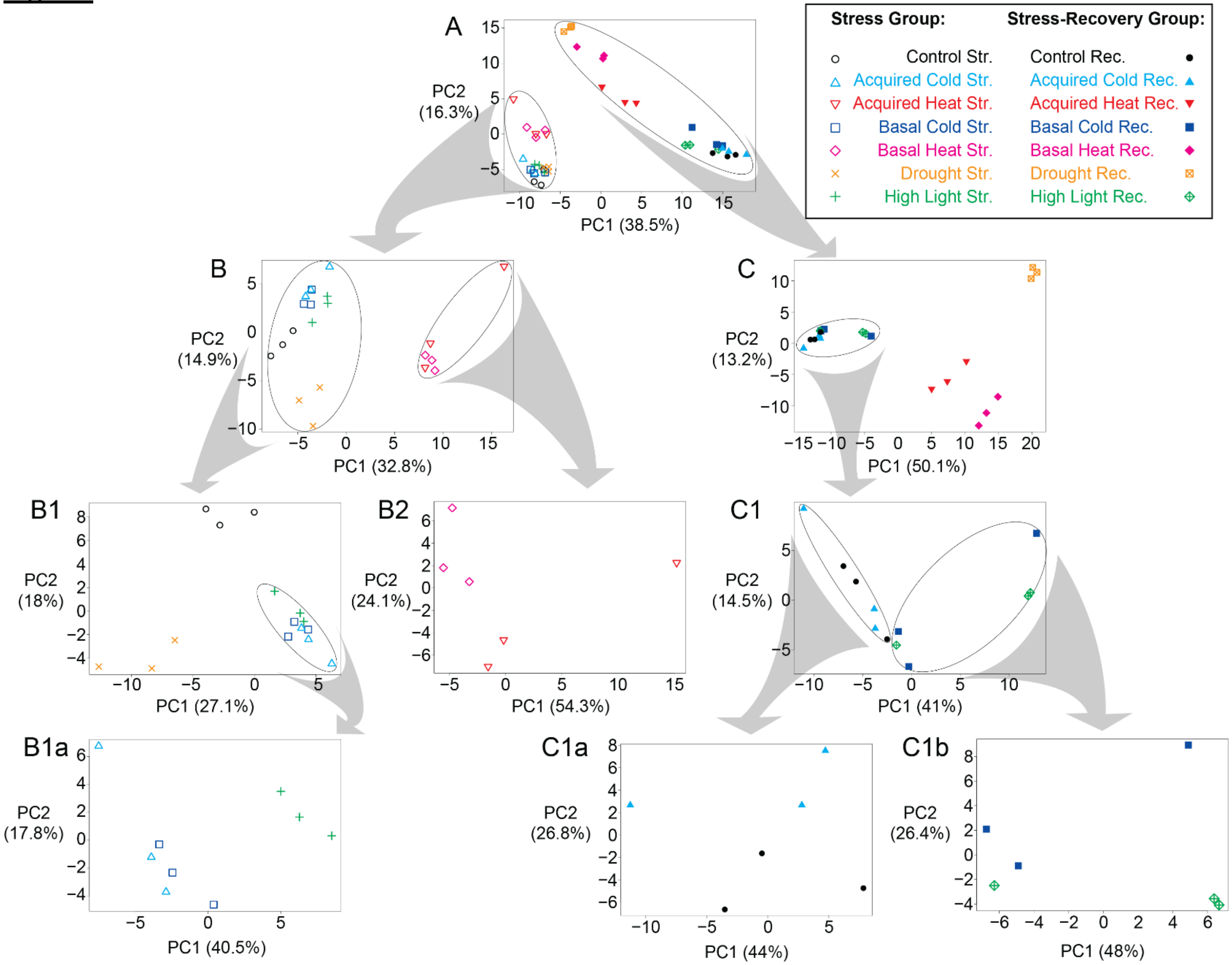

A
PC2 (16.3%)
PC1 (38.5%)
Stress Group:
Stress-Recovery Group:
Control Str.
Acquired Cold Str.
Acquired Heat Str.
Basal Cold Str.
Basal Heat Str.
Drought Str.
High Light Str.
Control Rec.
Acquired Cold Rec.
Acquired Heat Rec.
Basal Cold Rec.
Basal Heat Rec.
Drought Rec.
High Light Rec.
B
PC2 (14.9%)
PC1 (32.8%)
C
PC2 (13.2%)
PC1 (50.1%)
B1
PC2 (18%)
PC1 (27.1%)
B2
PC2 (24.1%)
PC1 (54.3%)
C1
PC2 (14.5%)
PC1 (41%)
B1a
PC2 (17.8%)
PC1 (40.5%)
C1a
PC2 (26.8%)
PC1 (44%)
C1b
PC2 (26.4%)
PC1 (48%)

Figure 2-1. PCA score plots of treatments in subgroups with hierarchical manner for clustering identification.
In the score plot, the symbols and colors corresponded to treatments in stress and recovery groups. (A) All groups. (B) Stress groups. (C) Recovery groups. (B1) Control, acquired cold, basal cold, drought, high light groups. (B2) Basal heat and acquired heat groups. (C1) Control recovery, acquired cold recovery, basal cold recovery, and high light recovery groups. (B1a) Acquired cold, basal cold, and high light groups. (C1a) Control recovery and acquired cold recovery groups. (C1b) Basal cold recovery and high light recovery groups.

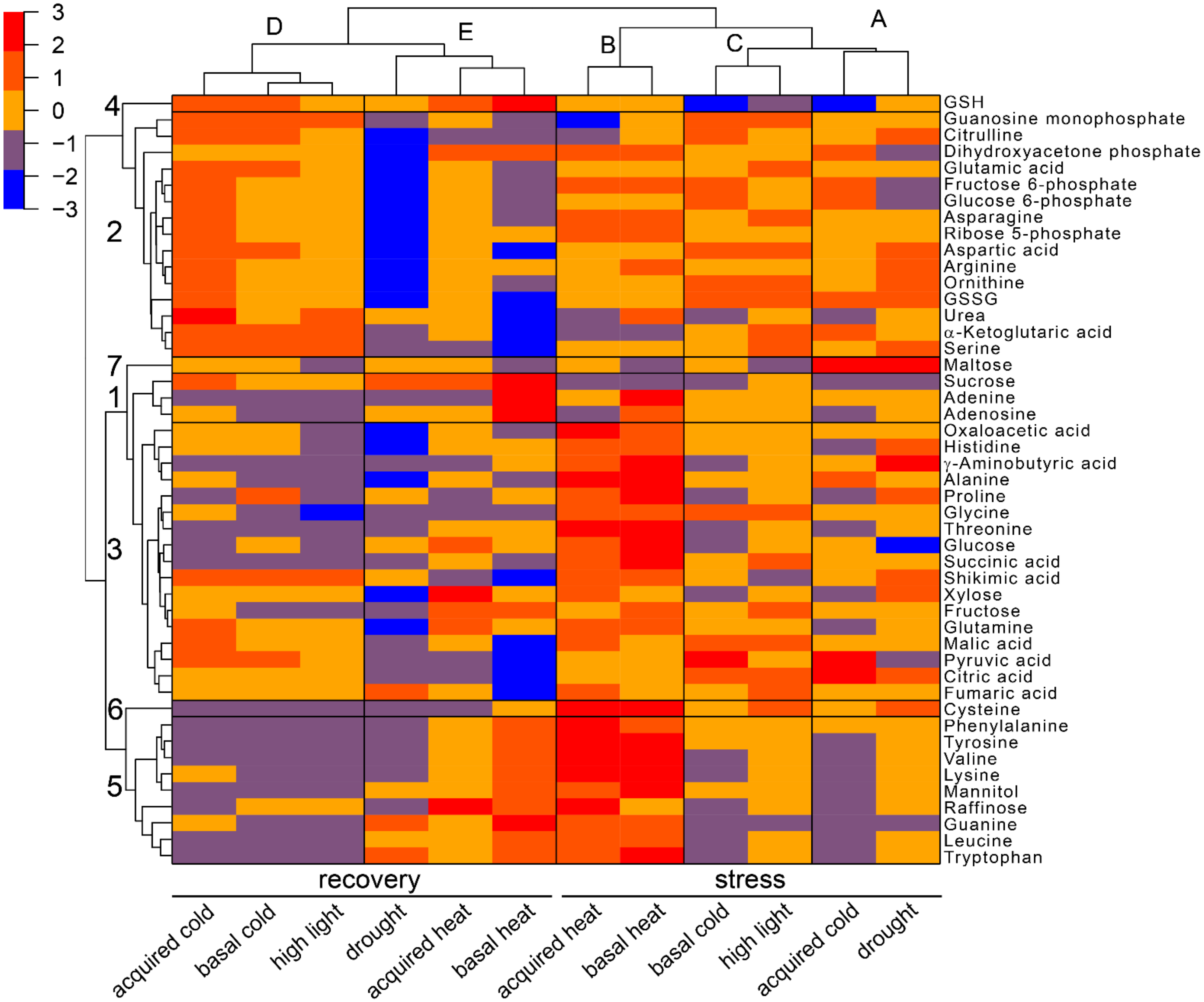

3
2
1
0
−1
−2
−3
D
E
B
C
A
4
2
7
1
3
6
5
GSH
Guanosine monophosphate
Citrulline
Dihydroxyacetone phosphate
Glutamic acid
Fructose 6-phosphate
Glucose 6-phosphate
Asparagine
Ribose 5-phosphate
Aspartic acid
Arginine
Ornithine
GSSG
Urea
α-Ketoglutaric acid
Serine
Maltose
Sucrose
Adenine
Adenosine
Oxaloacetic acid
Histidine
γ-Aminobutyric acid
Alanine
Proline
Glycine
Threonine
Glucose
Succinic acid
Shikimic acid
Xylose
Fructose
Glutamine
Malic acid
Pyruvic acid
Citric acid
Fumaric acid
Cysteine
Phenylalanine
Tyrosine
Valine
Lysine
Mannitol
Raffinose
Guanine
Leucine
Tryptophan
recovery
stress
acquired cold
basal cold
high light
drought
acquired heat
basal heat
acquired heat
basal heat
basal cold
high light
acquired cold
drought

Figure 2-2. Hierarchical clustering analysis (HCA) for potential stress metabolic signatures and their precursors, intermediates, or products in the same pathway.

The top horizontal side bar reflects the log2-transformed fold changes of average for both positive and negative observations as reported in **Supplemental Table 2-4**. Clusters were generated using the complete linkage and maximum distance measurement. Five clusters of treatments were labeled by A-E. Seven clusters of metabolites were labeled by 1-7.

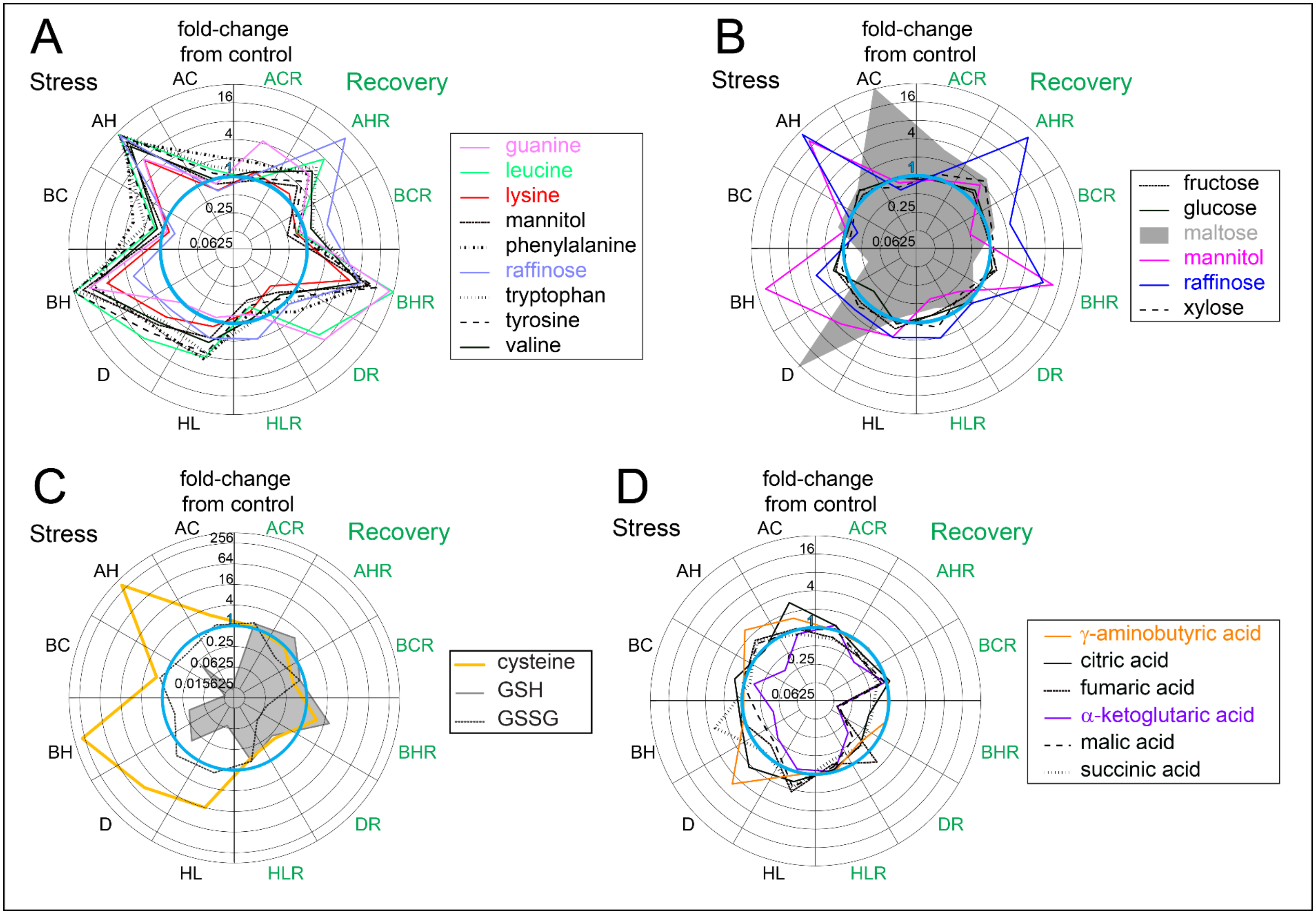

A
fold-change from control
Stress
Recovery
AC
ACR
AHR
BCR
BHR
DR
HLR
HL
D
BH
BC
AH
16
4
1
0.25
0.0625
guanine
leucine
lysine
mannitol
phenylalanine
raffinose
tryptophan
tyrosine
valine
B
fold-change from control
Stress
Recovery
fructose
glucose
maltose
mannitol
raffinose
xylose
C
fold-change from control
Stress
Recovery
256
64
16
4
1
0.25
0.0625
0.015625
cysteine
GSH
GSSG
D
fold-change from control
Stress
Recovery
γ-aminobutyric acid
citric acid
fumaric acid
α-ketoglutaric acid
malic acid
succinic acid

Figure 2-3. Radial plots for ratio changes of tryptophan, phenylalanine, tyrosine, leucine, valine, lysine, mannitol, raffinose, and guanine.
(A) maltose, glucose, fructose, xylose, mannitol, and raffinose (B) cysteine, GSH, and GSSG (C), GABA, succinate, fumarate, malate, citrate, and α-ketoglutaric acid (D) in different treatment compared to control. The ratio change 1 as no change with control was shown as blue circle.

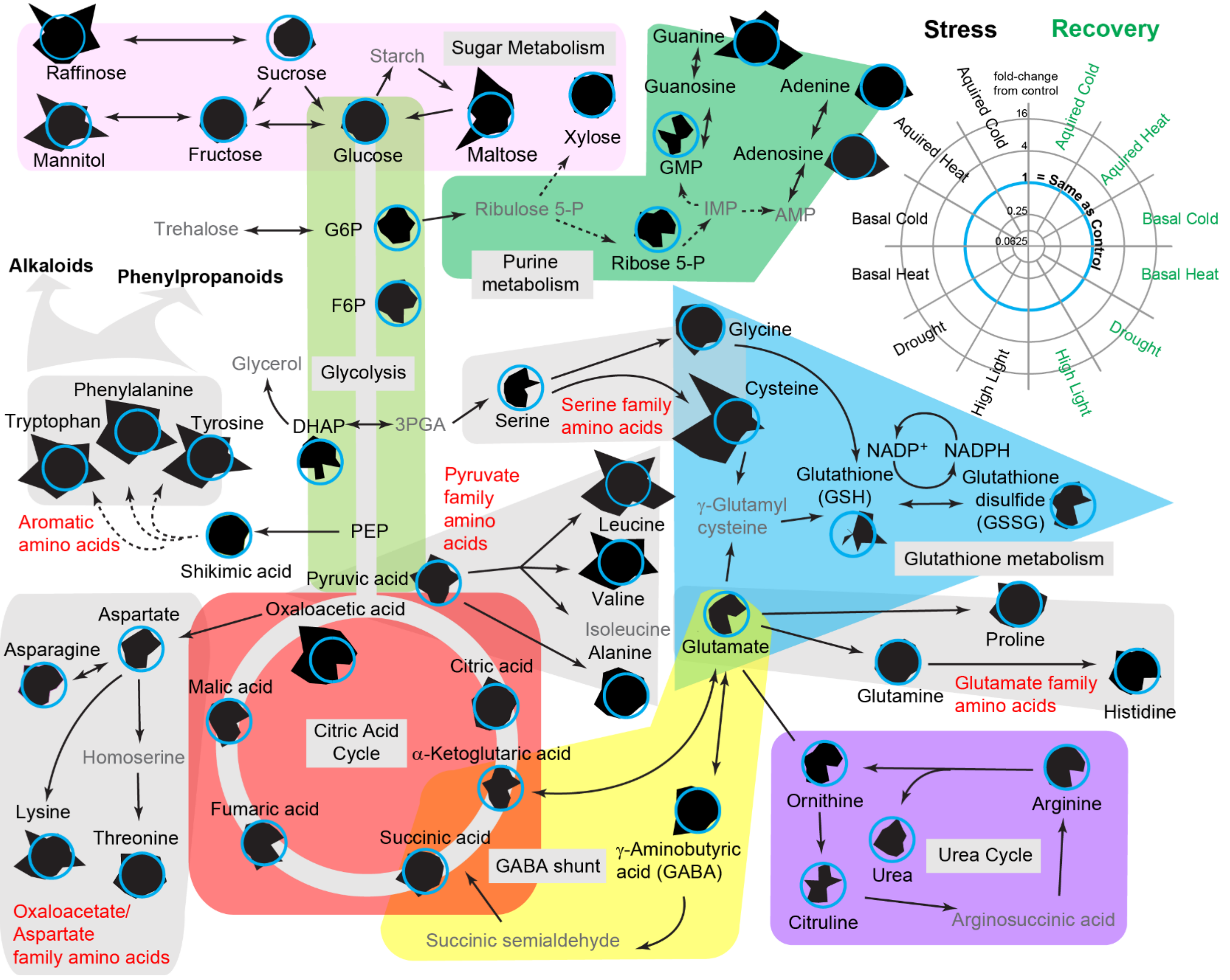
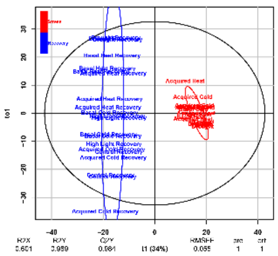

Stress
Recovery
fold-change from control
16
4
1 = Same as Control
0.25
0.0625
Aquired Cold
Aquired Heat
Basal Cold
Basal Heat
Drought
High Light
Aquired Cold
Aquired Heat
Basal Cold
Basal Heat
Drought
High Light
Sugar Metabolism
Raffinose
Sucrose
Starch
Mannitol
Fructose
Glucose
Maltose
Xylose
Trehalose
G6P
F6P
Glycerol
Glycolysis
DHAP
3PGA
PEP
Pyruvic acid
Alkaloids
Phenylpropanoids
Phenylalanine
Tryptophan
Tyrosine
Aromatic amino acids
Shikimic acid
Guanine
Guanosine
Adenine
GMP
Adenosine
IMP
AMP
Ribulose 5-P
Ribose 5-P
Purine metabolism
Glycine
Serine
Serine family amino acids
Cysteine
NADP+
NADPH
Glutathione (GSH)
Glutathione disulfide (GSSG)
γ-Glutamyl cysteine
Glutathione metabolism
Pyruvate family amino acids
Leucine
Valine
Isoleucine
Alanine
Glutamate
Proline
Glutamine
Glutamate family amino acids
Histidine
Aspartate
Asparagine
Homoserine
Lysine
Threonine
Oxaloacetate/ Aspartate family amino acids
Oxaloacetic acid
Malic acid
Citric acid
Citric Acid Cycle
α-Ketoglutaric acid
Fumaric acid
Succinic acid
GABA shunt
γ-Aminobutyric acid (GABA)
Succinic semialdehyde
Ornithine
Arginine
Urea
Urea Cycle
Citruline
Arginosuccinic acid

Figure 2-4. Metabolic pathways and radial plots for identified potential stress metabolic signatures with their precursors, intermediates, or products in the same metabolic pathway.
Radial plots were generated using the ratio change of each metabolite compared to control. The ratio change 1 has no change with control, as shown as a blue circle.

Supplemental materials

A



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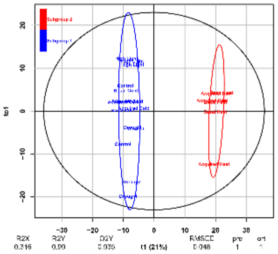

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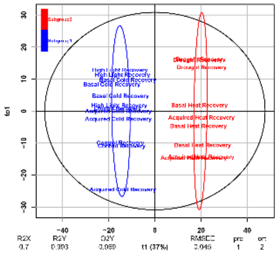
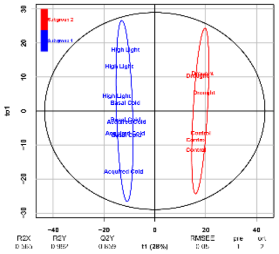


B1



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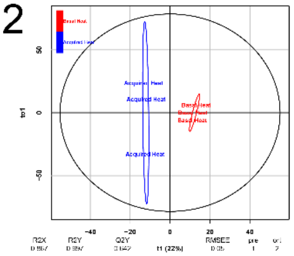
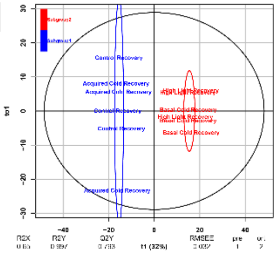
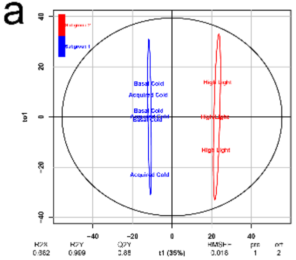


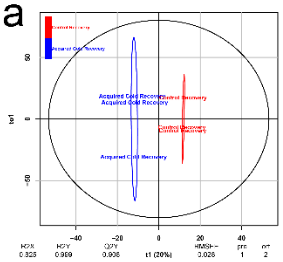
C1



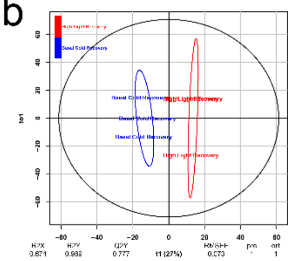
B1a



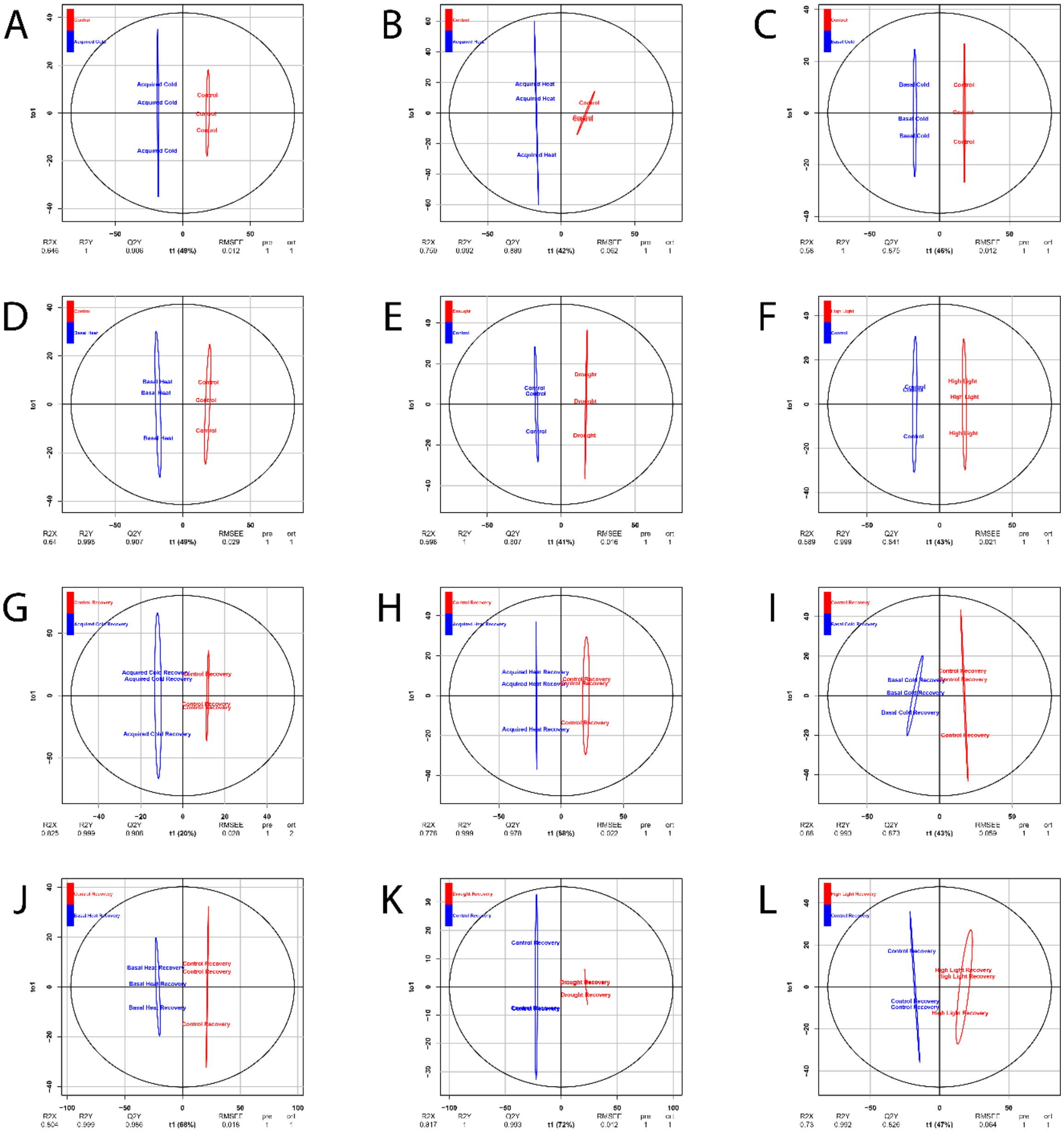
C1a



C1b

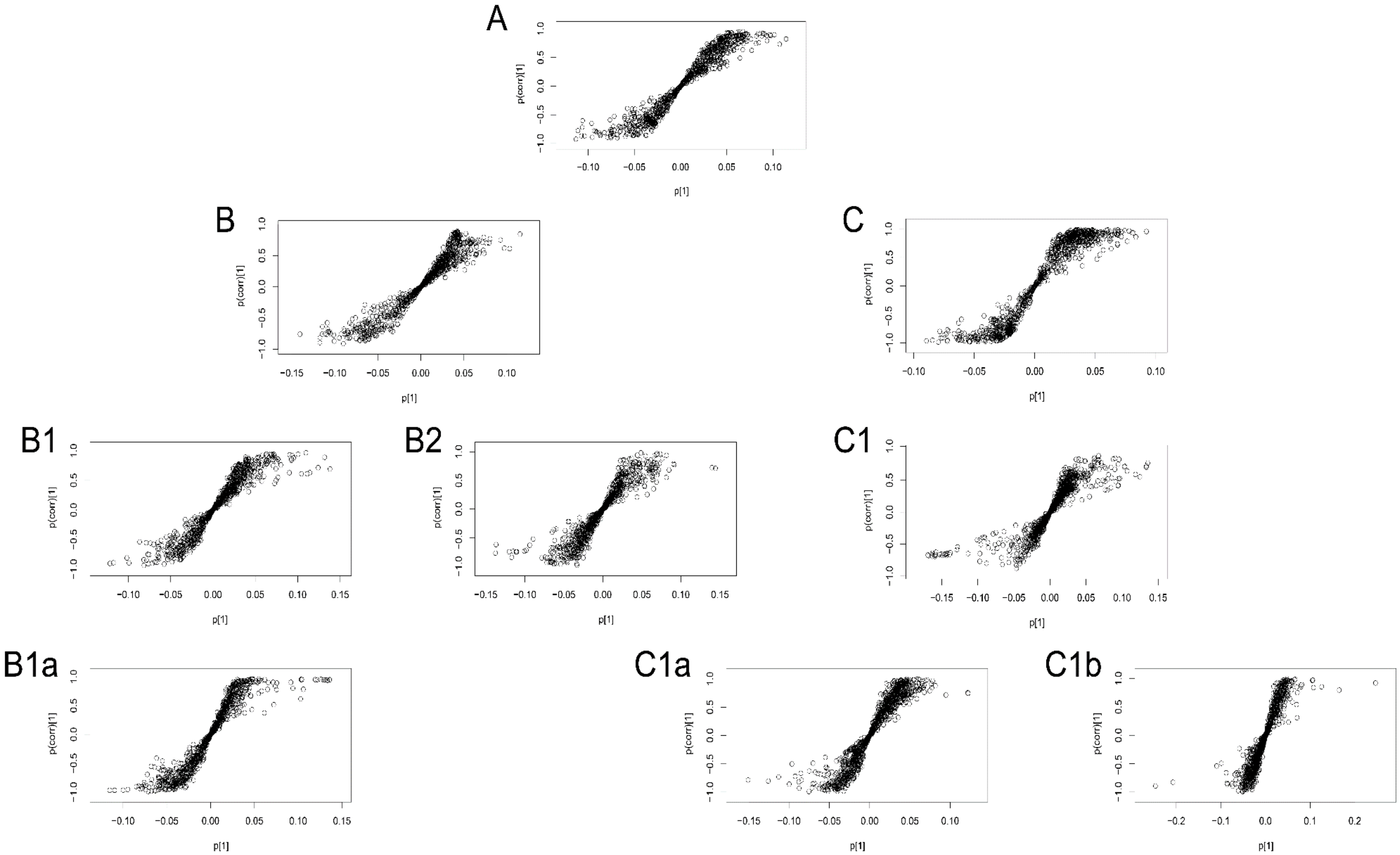


Supplemental Figure 2-1. OPLS-DA score plots of treatments in subgroups with hierarchical manner for clustering identification corresponded to Figure 2-1.
In the score plot, the colors corresponded to different supervised subgroups based on clustering results from PCA. (A) Stress groups and recovery groups. (B) Control, acquired cold, basal cold, drought, high light groups and basal heat and acquired heat groups. (C) Control recovery, acquired cold recovery, basal cold recovery, and high light recovery groups and drought recovery, basal heat recovery, and acquired heat recovery groups. (B1) Acquired cold, basal cold, and high light groups and control and drought groups. (B2) Basal heat group and acquired heat group. (C1) Control recovery and acquired cold recovery groups and basal cold recovery and, high light recovery groups. (B1a) Acquired cold and basal cold groups and high light group. (C1a) control recovery group and acquired cold recovery group. (C1b) Basal cold recovery group and high light recovery group.



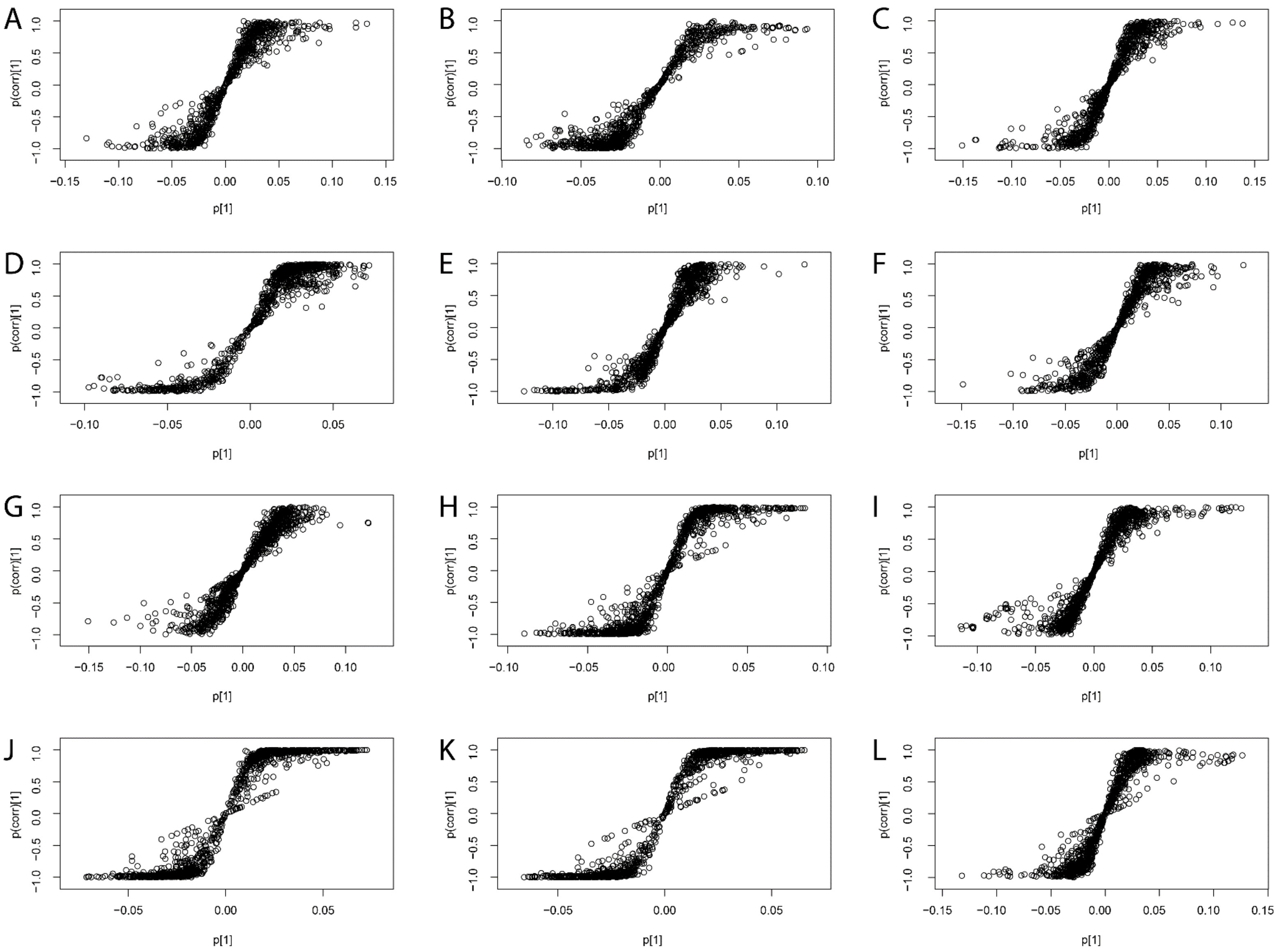
Supplemental Figure 2-1. OPLS-DA score plots of treatment compared to corresponding control.

(A) Acquired cold and control. (B) Acquired heat and control. (C) Basal cold and control. (D) Basal heat and control. (E) Drought and control. (F) High light and control. (G) Acquired cold recovery and control recovery. (H) Acquired heat recovery and control recovery. (I) Basal cold recovery and control recovery. (J) Basal heat recovery and control recovery. (K) Drought recovery and control recovery. (L) High light recovery and control recovery.



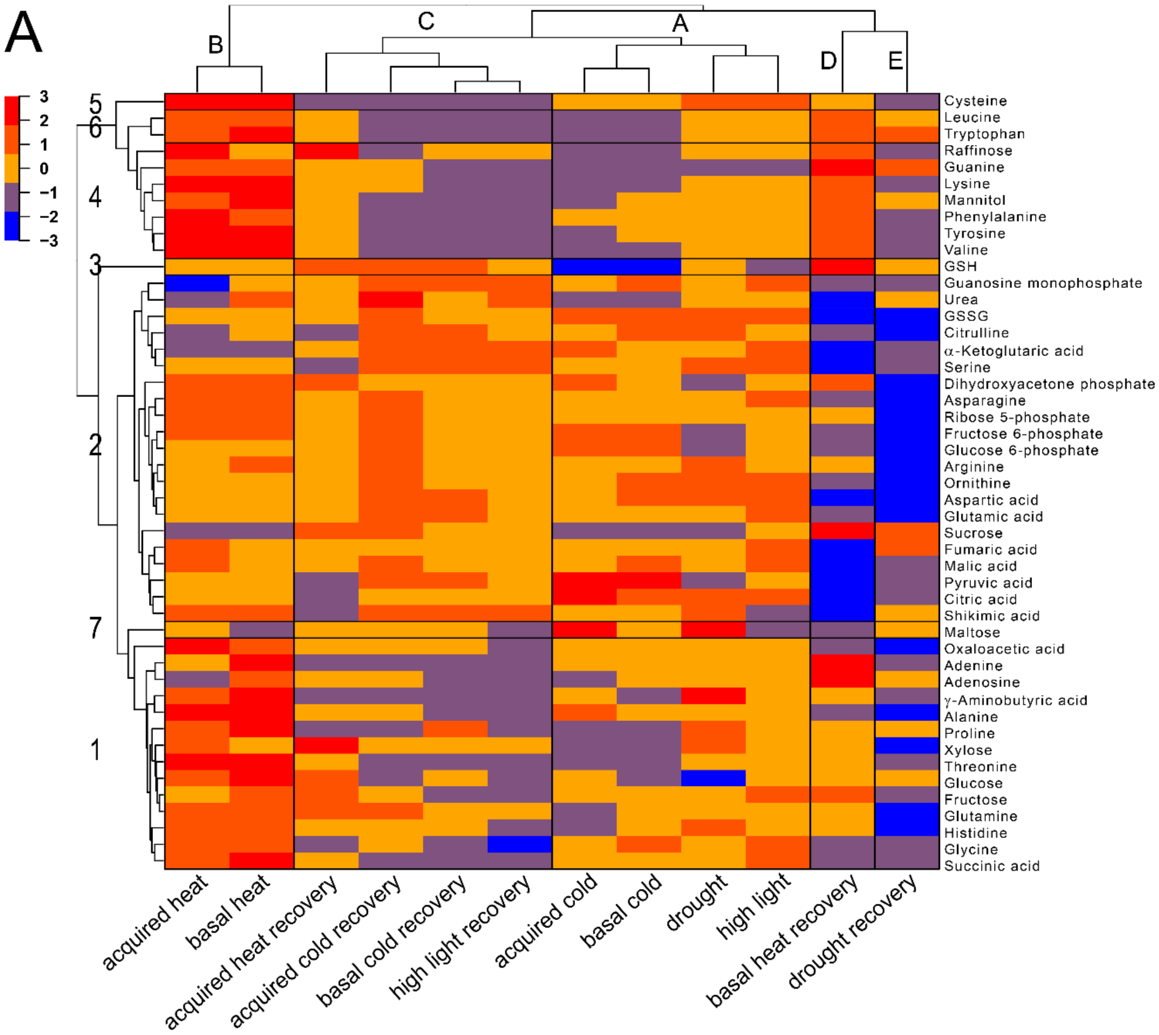
Supplemental Figure 2-2. OPLS-DA S-plot of treatments in subgroups with hierarchical manner for clustering identification corresponded to Figure 2-1.

The representative OPLS-DA loadings S-pot showing relative contribution of metabolic features to the corresponding supervised clusters. (A) Stress groups and recovery groups. (B) Control, acquired cold, basal cold, drought, high light groups and basal heat and acquired heat groups. (C) Control recovery, acquired cold recovery, basal cold recovery, and high light recovery groups and drought recovery, basal heat recovery, and acquired heat recovery groups. (B1) Acquired cold, basal cold, and high light groups and control and drought groups. (B2) Basal heat group and acquired heat group. (C1) Control recovery & acquired cold recovery groups and basal cold recovery and, high light recovery groups. (B1a) Acquired cold and basal cold groups and high light group. (C1a) control recovery group and acquired cold recovery group. (C1b) Basal cold recovery group and high light recovery group. The p[1] and p(corr)[1] axises represents the covariance and the correlation of features towards the predictive variation shown in the corresponding OPLS-DA loading score.



A
B
C
D
E
F
G
H
I
J
K
L
p(corr)[1]
p[1]
-1.0
-0.5
0.0
0.5
1.0
-0.15
-0.10
-0.05
0.00
0.05
0.10
0.15

Supplemental Figure 2-3. OPLS-DA S-plot of treatment compared to corresponding control.
The representative OPLS-DA loadings S-pot showing relative contribution of metabolic features to the corresponding supervised clusters. (A) Acquired cold and control. (B) Acquired heat and control. (C) Basal cold and control. (D) Basal heat and control. (E) Drought and control. (F) High light and control. (G) Acquired cold recovery and control recovery. (H) Acquired heat recovery and control recovery. (I) Basal cold recovery and control recovery. (J) Basal heat recovery and control recovery. (K) Drought recovery and control recovery. (L) High light recovery and control recovery. The p[1] and p(corr)[1] axises represents the covariance and correlation of features towards the predictive variation shown in the corresponding OPLS-DA loading score.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B
C
A
D
E
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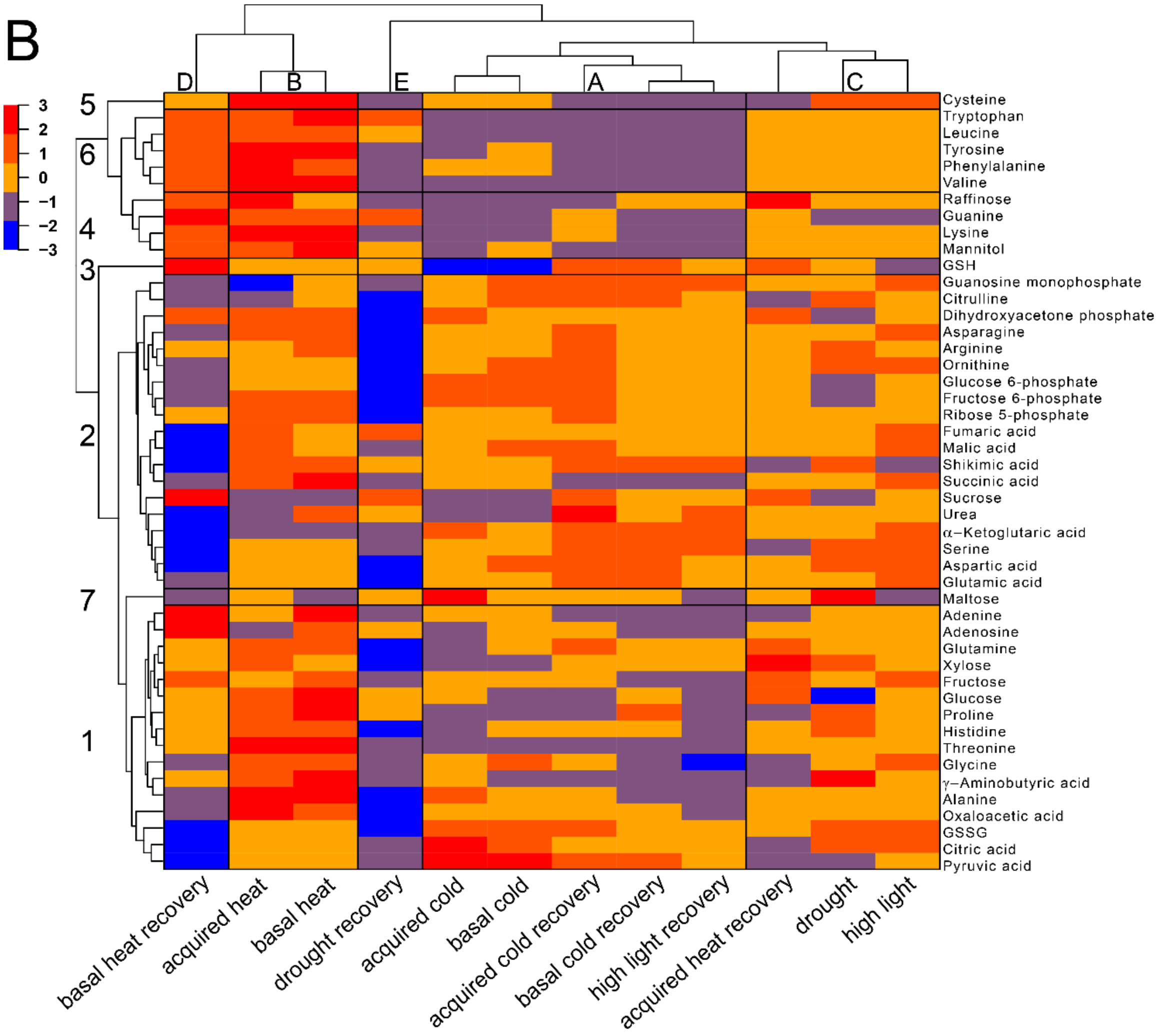
2
7
1
Cysteine
Leucine
Tryptophan
Raffinose
Guanine
Lysine
Mannitol
Phenylalanine
Tyrosine
Valine
GSH
Guanosine monophosphate
Urea
GSSG
Citrulline
α-Ketoglutaric acid
Serine
Dihydroxyacetone phosphate
Asparagine
Ribose 5-phosphate
Fructose 6-phosphate
Glucose 6-phosphate
Arginine
Ornithine
Aspartic acid
Glutamic acid
Sucrose
Fumaric acid
Malic acid
Pyruvic acid
Citric acid
Shikimic acid
Maltose
Oxaloacetic acid
Adenine
Adenosine
γ-Aminobutyric acid
Alanine
Proline
Xylose
Threonine
Glucose
Fructose
Glutamine
Histidine
Glycine
Succinic acid
acquired heat
basal heat
acquired heat recovery
acquired cold recovery
basal cold recovery
high light recovery
acquired cold
basal cold
drought
high light
basal heat recovery
drought recovery


B
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−3
D
B
E
A
C
5
6
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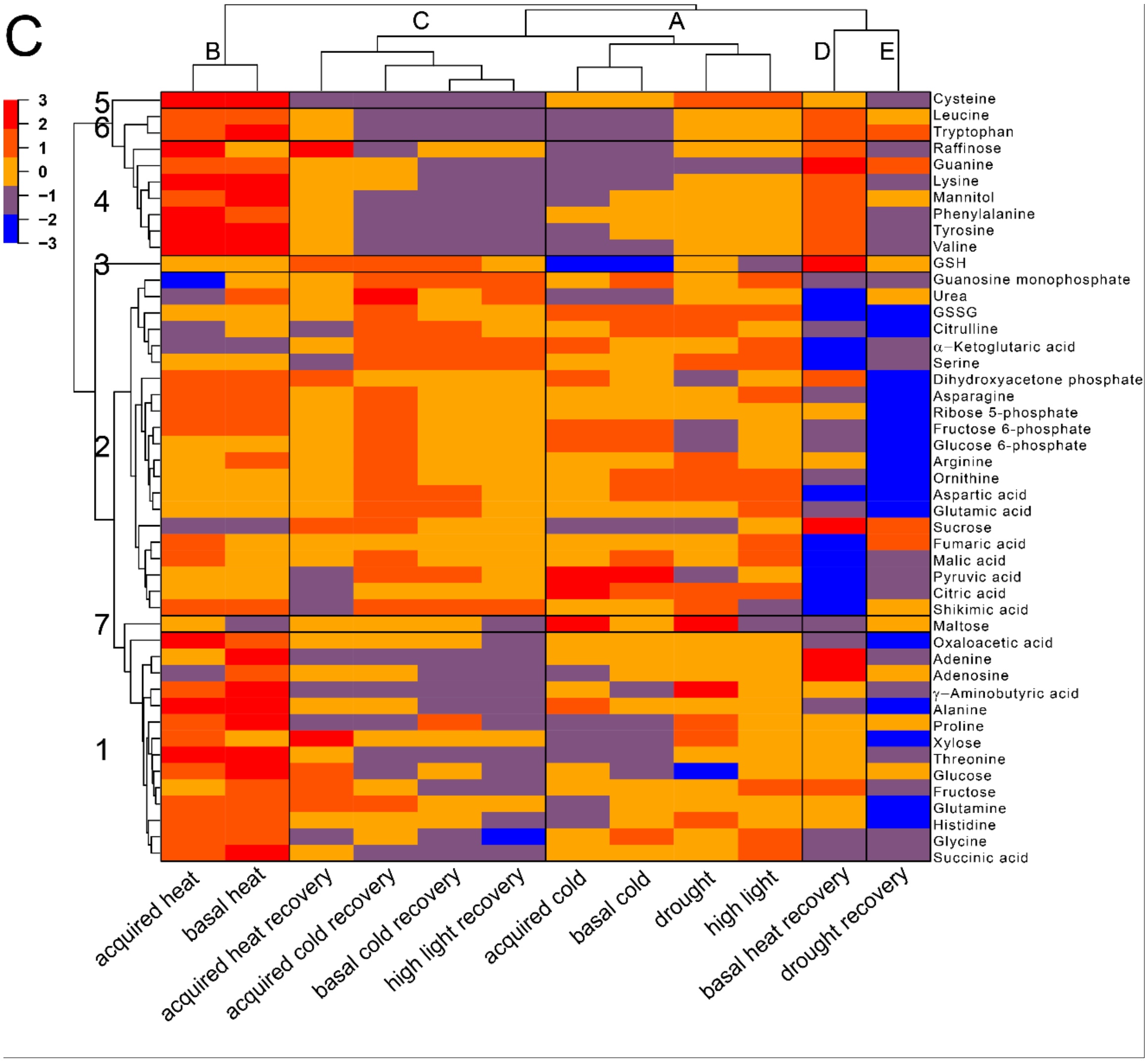
3
2
7
1
Cysteine
Tryptophan
Leucine
Tyrosine
Phenylalanine
Valine
Raffinose
Guanine
Lysine
Mannitol
GSH
Guanosine monophosphate
Citrulline
Dihydroxyacetone phosphate
Asparagine
Arginine
Ornithine
Glucose 6-phosphate
Fructose 6-phosphate
Ribose 5-phosphate
Fumaric acid
Malic acid
Shikimic acid
Succinic acid
Sucrose
Urea
α−Ketoglutaric acid
Serine
Aspartic acid
Glutamic acid
Maltose
Adenine
Adenosine
Glutamine
Xylose
Fructose
Glucose
Proline
Histidine
Threonine
Glycine
γ−Aminobutyric acid
Alanine
Oxaloacetic acid
GSSG
Citric acid
Pyruvic acid
basal heat recovery
acquired heat
basal heat
drought recovery
acquired cold
basal cold
acquired cold recovery
basal cold recovery
high light recovery
acquired heat recovery
drought
high light


C
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2
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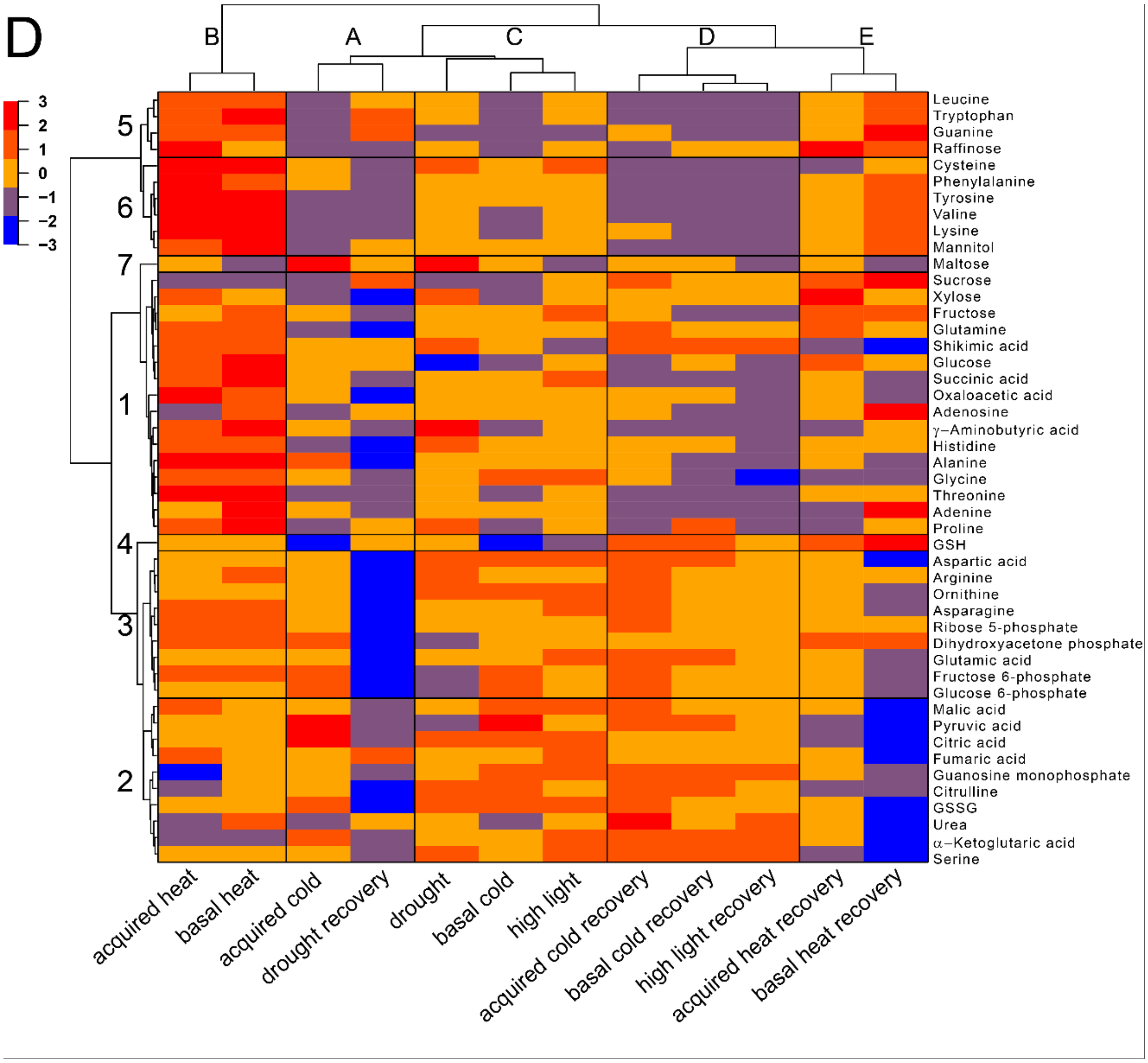
−2
−3
B
C
A
D
E
5
6
4
3
2
7
1
Cysteine
Leucine
Tryptophan
Raffinose
Guanine
Lysine
Mannitol
Phenylalanine
Tyrosine
Valine
GSH
Guanosine monophosphate
Urea
GSSG
Citrulline
α−Ketoglutaric acid
Serine
Dihydroxyacetone phosphate
Asparagine
Ribose 5-phosphate
Fructose 6-phosphate
Glucose 6-phosphate
Arginine
Ornithine
Aspartic acid
Glutamic acid
Sucrose
Fumaric acid
Malic acid
Pyruvic acid
Citric acid
Shikimic acid
Maltose
Oxaloacetic acid
Adenine
Adenosine
γ−Aminobutyric acid
Alanine
Proline
Xylose
Threonine
Glucose
Fructose
Glutamine
Histidine
Glycine
Succinic acid
acquired heat
basal heat
acquired heat recovery
acquired cold recovery
basal cold recovery
high light recovery
acquired cold
basal cold
drought
high light
basal heat recovery
drought recovery



D
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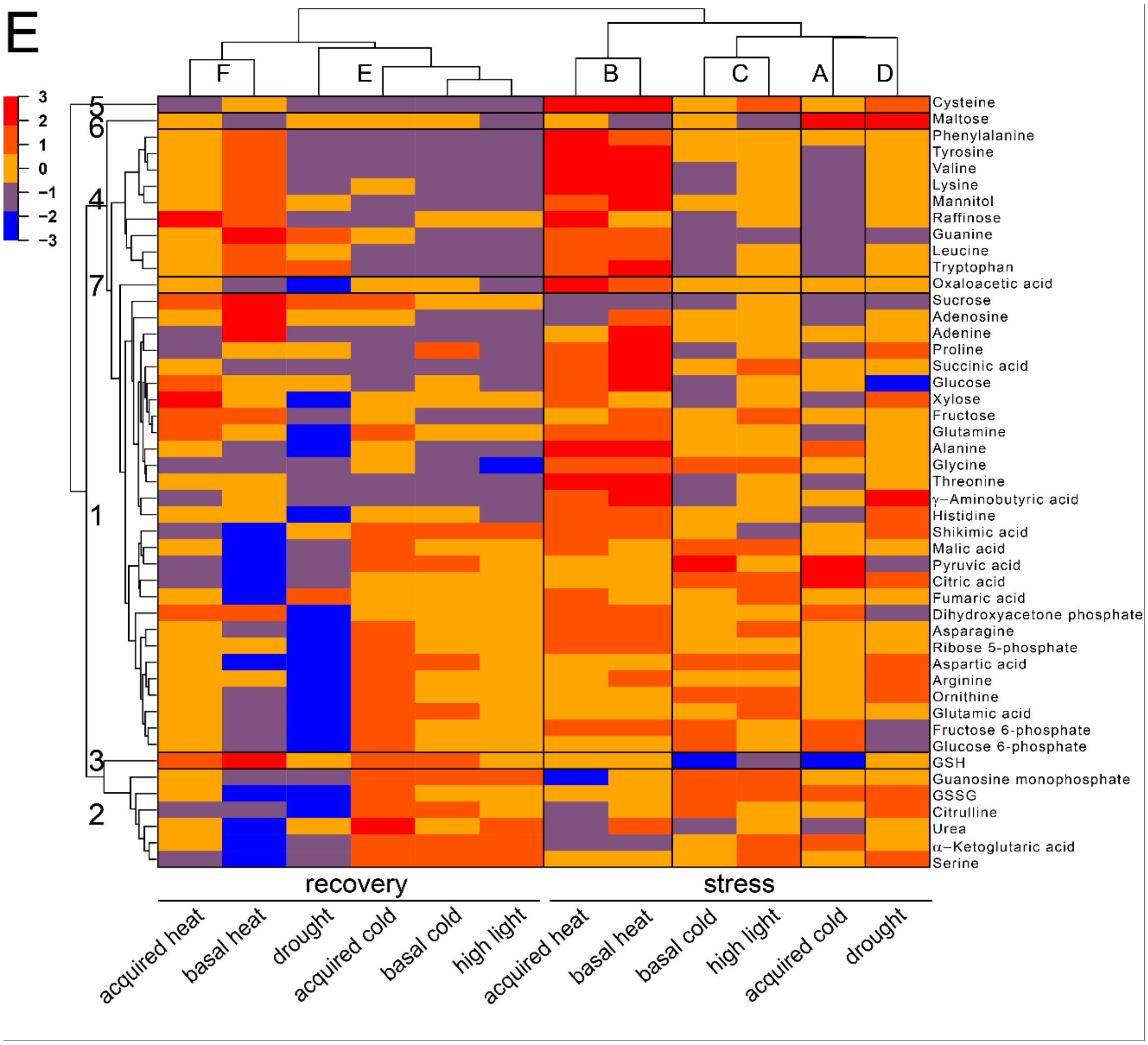
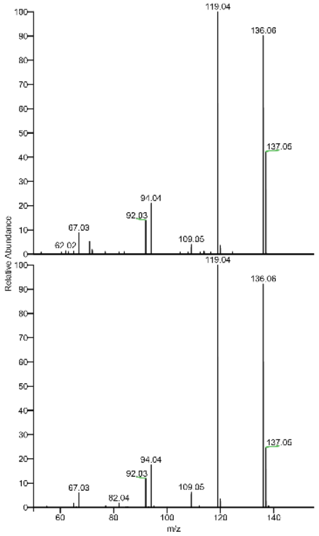
1
0
−1
−2
−3
B
A
C
D
E
5
6
7
1
4
3
2
Leucine
Tryptophan
Guanine
Raffinose
Cysteine
Phenylalanine
Tyrosine
Valine
Lysine
Mannitol
Maltose
Sucrose
Xylose
Fructose
Glutamine
Shikimic acid
Glucose
Succinic acid
Oxaloacetic acid
Adenosine
γ−Aminobutyric acid
Histidine
Alanine
Glycine
Threonine
Adenine
Proline
GSH
Aspartic acid
Arginine
Ornithine
Asparagine
Ribose 5-phosphate
Dihydroxyacetone phosphate
Glutamic acid
Fructose 6-phosphate
Glucose 6-phosphate
Malic acid
Pyruvic acid
Citric acid
Fumaric acid
Guanosine monophosphate
Citrulline
GSSG
Urea
α−Ketoglutaric acid
Serine
acquired heat
basal heat
acquired cold
drought recovery
drought
basal cold
high light
acquired cold recovery
basal cold recovery
high light recovery
acquired heat recovery
basal heat recovery



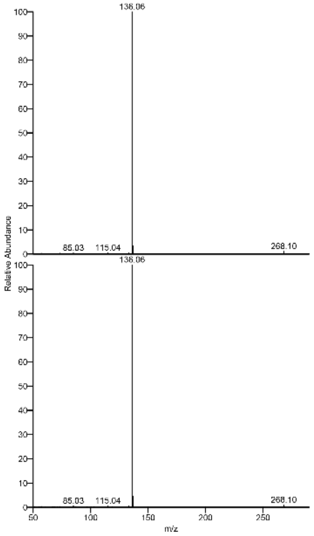
Supplemental Figure 2-4. Hierarchical clustering analysis (HCA) for potential stress metabolic signatures and their precursors, intermediates, or products in the same pathway.

The top horizontal side bar reflects the log2-transformed fold changes of average for both positive and negative observations as reported in **Supplemental Table 2-4**. Clusters were generated using the complete linkage and Euclidean distance measurement (A), complete linkage and Manhattan distance measurement (B), complete linkage and Minkowski distance measurement (C), Wards's method and maximum distance measurement (D), and McQuitty's method with maximum distance measurement (E). Clusters of treatments were labeled by A-E. Clusters of metabolites were labeled by 1-7.

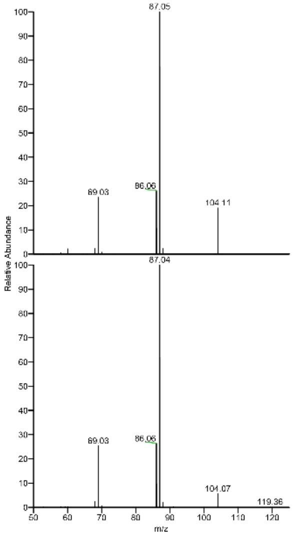
A


Relative Abundance
m/z
119.04
136.06
137.05
94.04
92.03
67.03
62.02
109.05
119.04
136.06
137.05
94.04
92.03
67.03
82.04
109.05

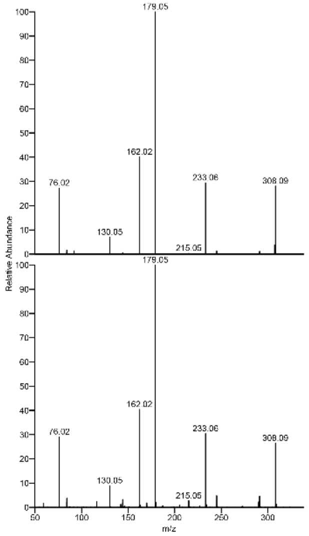
B


Relative Abundance
m/z
136.06
85.03
115.04
268.10
136.06
85.03
115.04
268.10

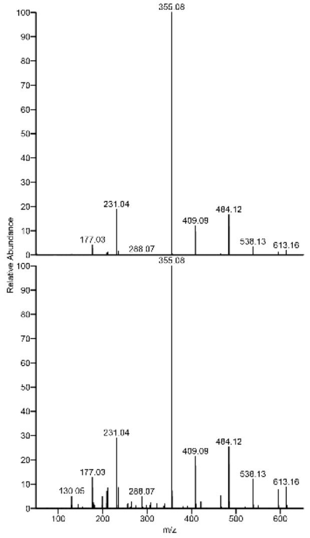
C


Relative Abundance
m/z
87.05
69.03
86.06
104.11
87.04
69.03
86.06
104.07
119.36

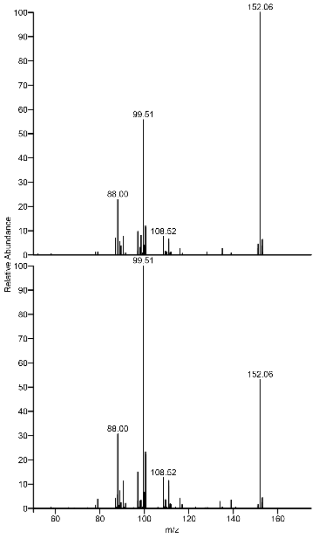
D


Relative Abundance
m/z
179.05
76.02
162.02
233.06
308.09
130.05
215.05
179.05
76.02
162.02
233.06
308.09
130.05
215.05

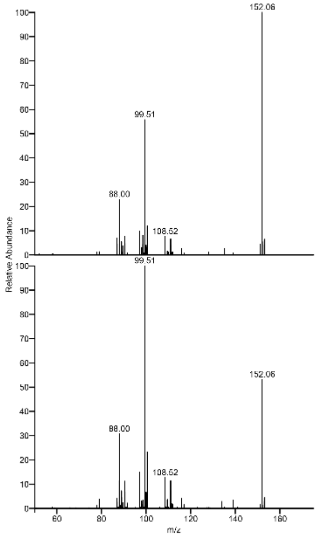
E


Relative Abundance
m/z
355.08
231.04
484.12
409.09
177.03
288.07
538.13
613.16
355.08
231.04
484.12
409.09
177.03
130.05
288.07
538.13
613.16

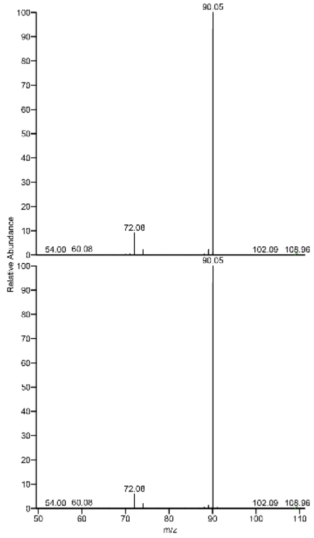
F


Relative Abundance
m/z
152.06
99.51
88.00
108.52
99.51
152.06
88.00
108.52

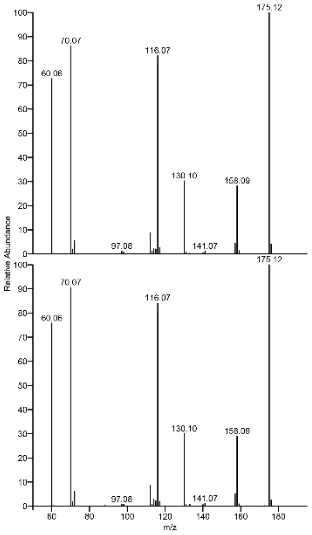
G


Relative Abundance
m/z
152.06
99.51
88.00
108.52
99.51
152.06
88.00
108.52

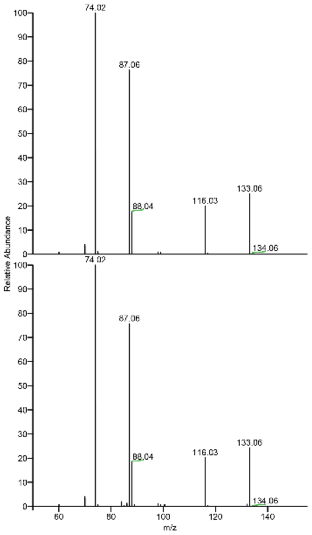
H


Relative Abundance
m/z
90.05
72.08
54.00
60.08
102.09
108.96
90.05
72.08
54.00
60.08
102.09
108.96

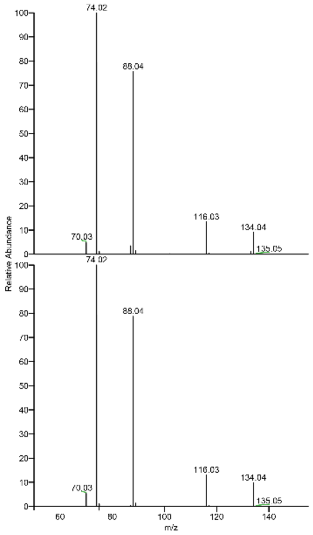
I


175.12
70.07
60.06
116.07
130.10
158.09
97.08
141.07
175.12
70.07
60.06
116.07
130.10
158.09
97.08
141.07
Relative Abundance
m/z

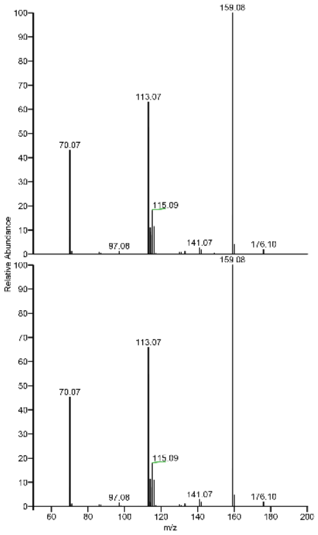
J


74.02
87.06
88.04
116.03
133.06
134.06
74.02
87.06
88.04
116.03
133.06
134.06
Relative Abundance
m/z

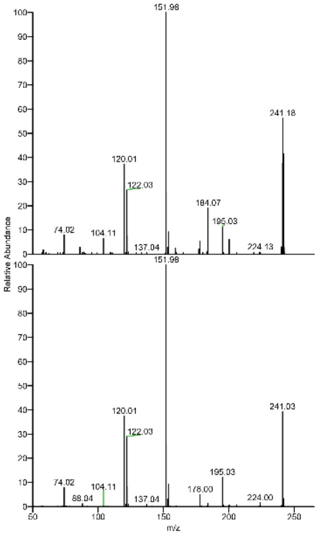
K


74.02
88.04
70.03
116.03
134.04
135.05
74.02
88.04
70.03
116.03
134.04
135.05
Relative Abundance
m/z

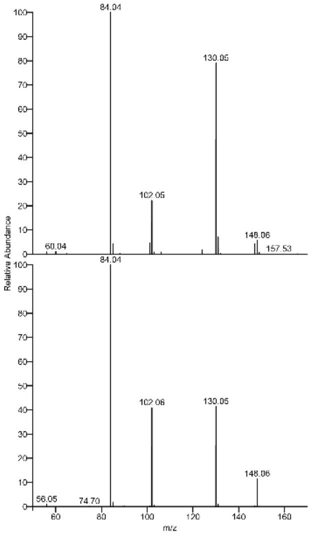
L


159.08
113.07
70.07
115.09
97.08
141.07
176.10
159.08
113.07
70.07
115.09
97.08
141.07
176.10
Relative Abundance
m/z

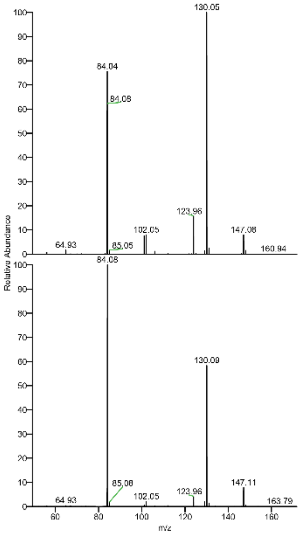
M


151.98
241.18
120.01
122.03
184.07
74.02
104.11
195.03
137.04
224.13
151.98
120.01
122.03
241.03
195.03
74.02
104.11
88.04
178.03
137.04
224.00
Relative Abundance
m/z

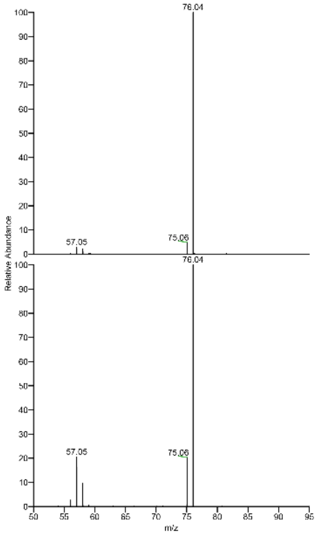
N


84.04
130.05
102.05
148.06
60.04
157.53
84.04
102.06
130.05
148.06
56.05
74.70
Relative Abundance
m/z

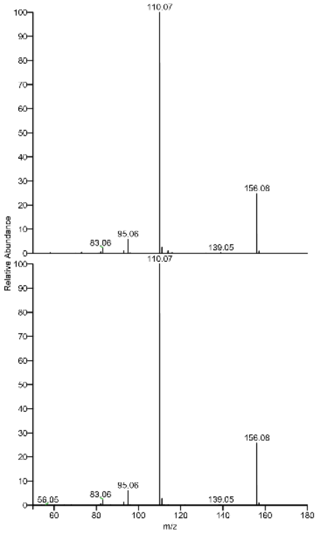
O


130.05
84.04
84.08
123.96
102.05
147.08
64.93
85.05
160.94
84.08
130.09
147.11
85.08
64.93
102.05
123.96
163.79
Relative Abundance
m/z

P

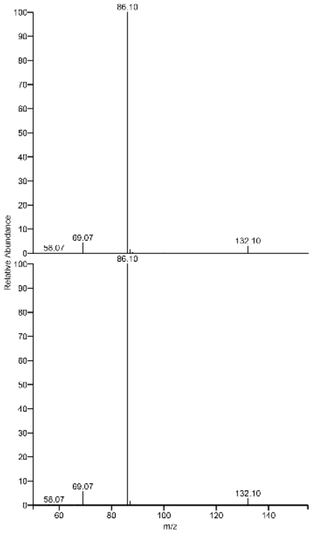

76.04
57.05
75.06
76.04
57.05
75.06
Relative Abundance
m/z

Q



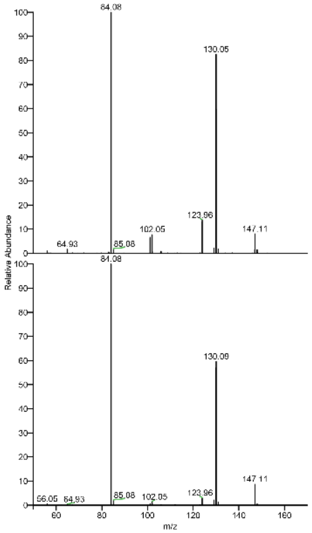
110.07
156.08
83.06
95.06
139.05
110.07
156.08
56.05
83.06
95.06
139.05
Relative Abundance
m/z
60
80
100
120
140
160
180

R



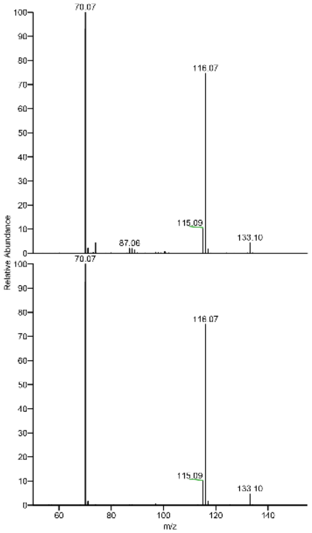
86.10
58.07
69.07
132.10
86.10
58.07
69.07
132.10
Relative Abundance
m/z
60
80
100
120
140

S



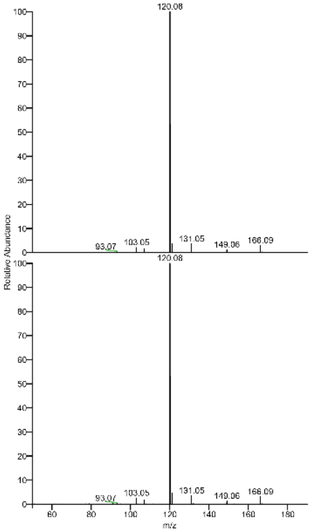
84.08
130.05
64.93
85.08
102.05
123.96
147.11
84.08
130.09
56.05
64.93
85.08
102.05
123.96
147.11
Relative Abundance
m/z
60
80
100
120
140
160

T



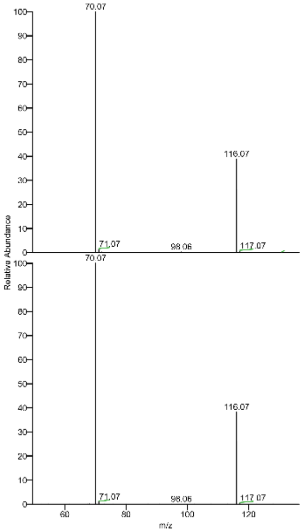
70.07
116.07
87.06
115.09
133.10
70.07
116.07
115.09
133.10
Relative Abundance
m/z
60
80
100
120
140

U



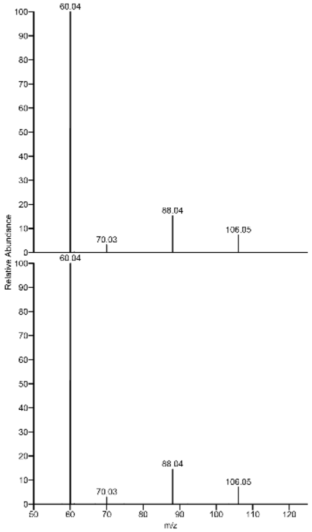
120.08
93.07
103.05
131.05
149.06
166.09
120.08
93.07
103.05
131.05
149.06
166.09
Relative Abundance
m/z
60
80
100
120
140
160
180

V



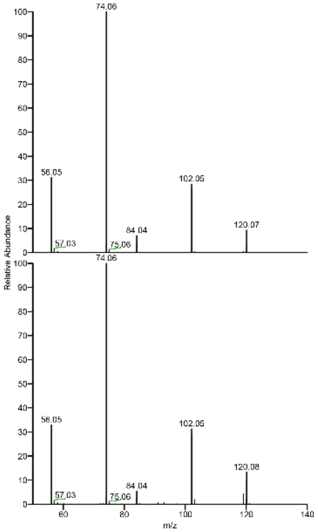
70.07
116.07
71.07
98.06
117.07
70.07
116.07
71.07
98.06
117.07
Relative Abundance
m/z
60
80
100
120

W



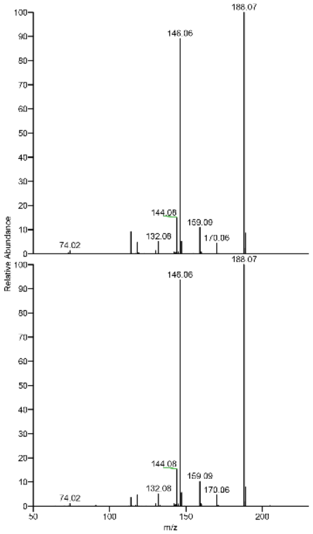
60.04
70.03
88.04
106.05
60.04
70.03
88.04
106.05
Relative Abundance
m/z
50
60
70
80
90
100
110
120

X

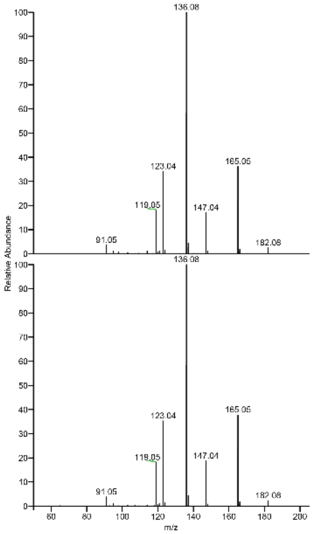


74.06
56.05
57.03
75.06
84.04
102.05
120.07
74.06
56.05
57.03
75.06
84.04
102.05
120.08
Relative Abundance
m/z
60
80
100
120
140

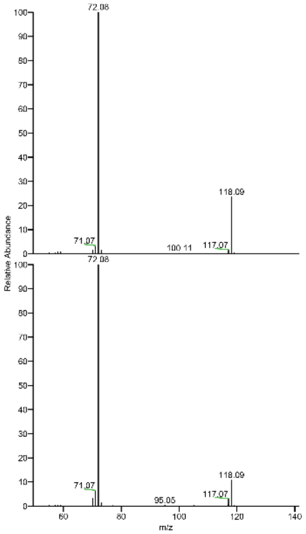
Y


188.07
146.06
144.08
132.08
159.09
170.06
74.02
188.07
146.06
144.08
132.08
159.09
170.06
74.02
Relative Abundance
m/z
50
100
150
200

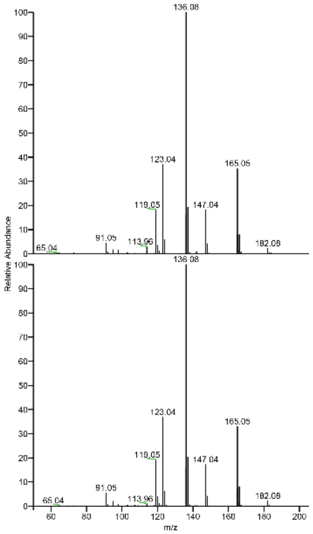
Z


136.08
123.04
165.05
119.05
147.04
91.05
182.08
136.08
123.04
165.05
119.05
147.04
91.05
182.08
Relative Abundance
m/z
60
80
100
120
140
160
180
200

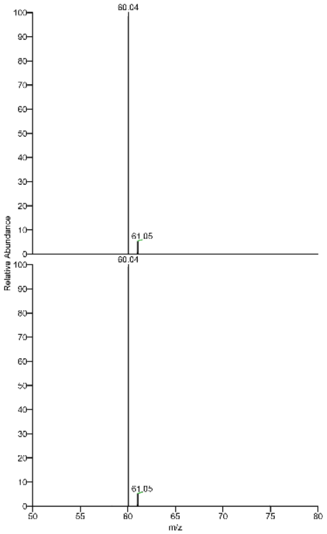
AA


72.08
118.09
71.07
100.11
117.07
72.08
118.09
71.07
95.05
117.07
Relative Abundance
m/z
60
80
100
120
140

AB

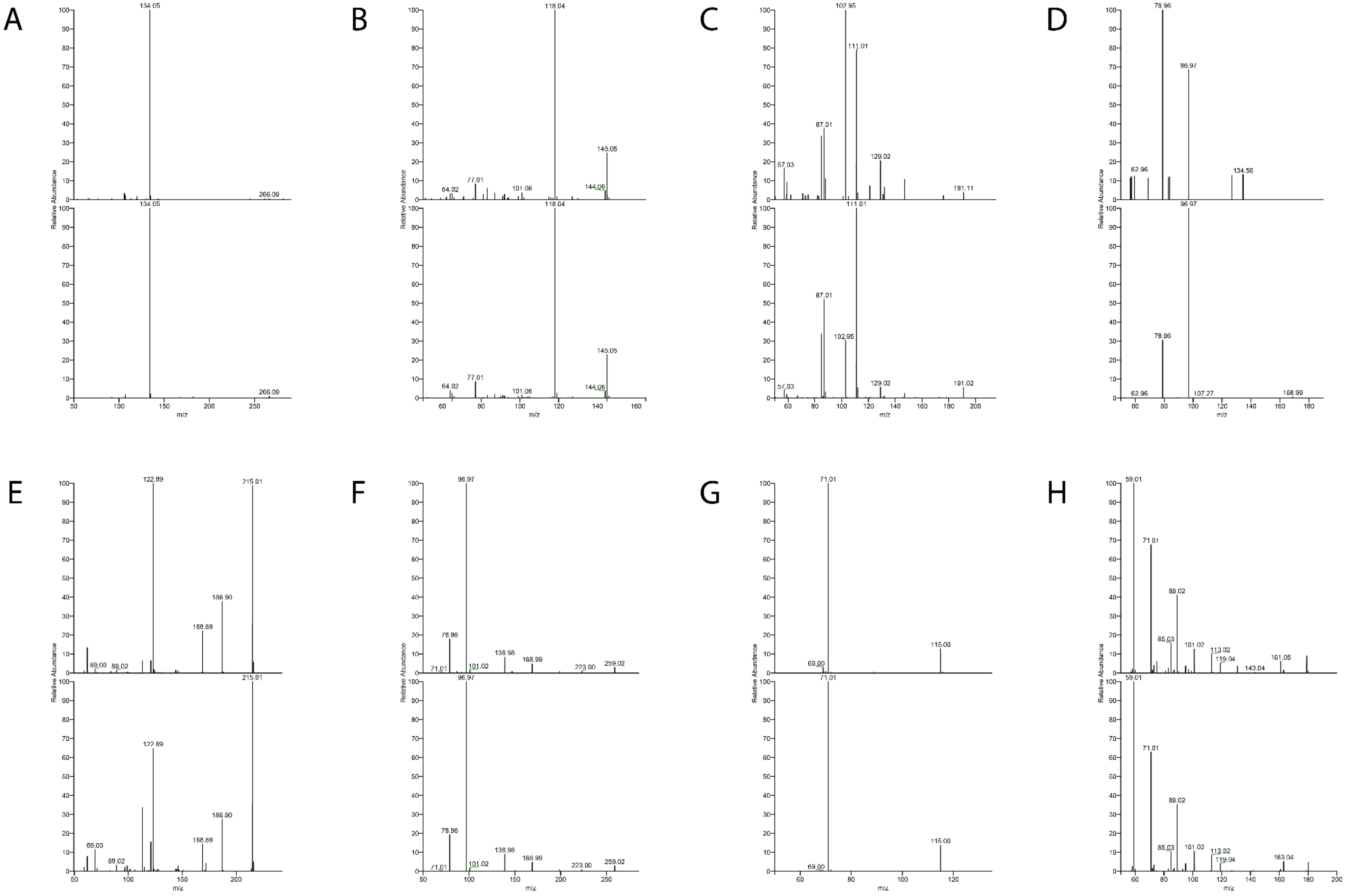

136.08
123.04
165.05
119.05
147.04
91.05
113.96
65.04
182.08
136.08
123.04
165.05
119.05
147.04
91.05
113.96
65.04
182.08
Relative Abundance
m/z
60
80
100
120
140
160
180
200

AC


60.04
61.05
60.04
61.05
Relative Abundance
m/z
50
55
60
65
70
75
80

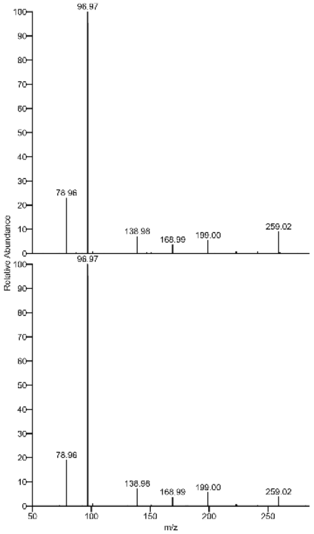
Supplemental Figure 2-5. Metabolites that were identified by authentic standards with *m/z*, retention time, and fragmentation in positive mode.

The top scheme represents metabolite in sample. The bottom scheme represents metabolite in standard. Standard compounds include: adenine (A), adenosine (B), γ-aminobutyric acid (C), GSH (D), GSSG (E), guanine (F), guanosine monophosphate (G), L-alanine (H), L-arginine (I), L-asparagine (J), L-aspartic acid (K), L-citrulline (L), L-cysteine (M), L-glutamic acid (N), L-glutamine (O), L-glycine (P), L-histidine (Q), L-leucine (R), L-lysine (S), L-ornithine (T), L-phenylalanine (U), L-proline (V), L-serine (W), L-threonine (X), L-tryptophan (Y), L-tyrosine (Z), L-valine (AA), mannitol (AB), urea (AC). It should be noted that while standard compounds of the specified stereochemistry were used, analytical procedures that would resolve enantiomers were not employed. Because of this absolute stereo-assignments for each of these compounds were not included as part of the assignment, though it is likely that the vast majority of amino acids identified are of the L-configuration as D-amino acids are unusual in plants and typically occur in specialized metabolic contexts.

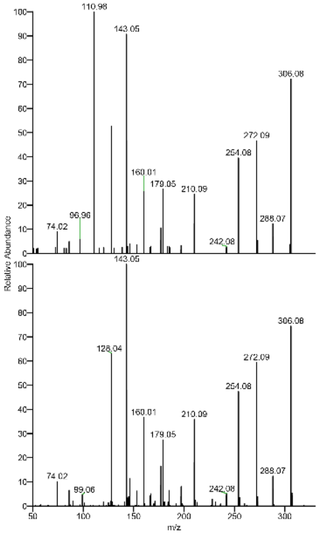


A
134.05
266.09
134.05
266.09
B
118.04
145.05
64.02
77.01
101.06
144.06
118.04
145.05
64.02
77.01
101.06
144.06
C
102.95
111.01
87.01
57.03
129.02
191.11
111.01
87.01
102.95
57.03
129.02
191.02
D
78.96
96.97
62.96
134.56
96.97
78.96
62.96
107.27
168.99
E
122.89
215.01
186.90
168.89
69.00
89.02
215.01
122.89
186.90
69.00
89.02
168.89
F
96.97
78.96
71.01
101.02
138.98
168.99
223.00
259.02
96.97
78.96
71.01
101.02
138.98
168.99
223.00
259.02
G
71.01
115.00
69.00
71.01
115.00
69.00
H
59.01
71.01
89.02
85.03
101.02
113.02
119.04
143.04
161.05
59.01
71.01
89.02
85.03
101.02
113.02
119.04
163.04
Relative Abundance
m/z

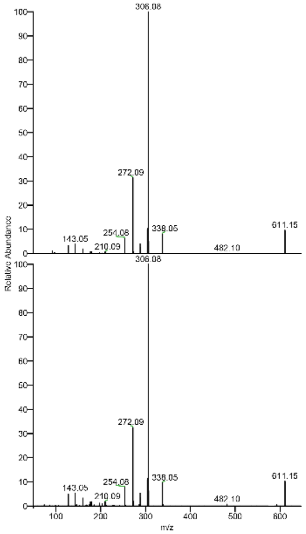
I


96.97
78.96
138.98
168.99
199.00
259.02
96.97
78.96
138.98
168.99
199.00
259.02
Relative Abundance
m/z

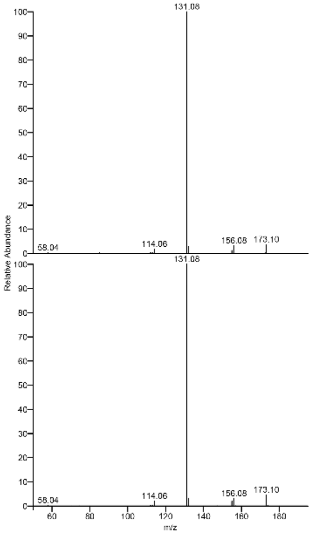
J


110.98
143.05
306.08
272.09
254.08
160.01
179.05
210.09
74.02
96.96
242.08
288.07
143.05
306.08
272.09
128.04
254.08
160.01
210.09
179.05
74.02
99.06
242.08
288.07
Relative Abundance
m/z

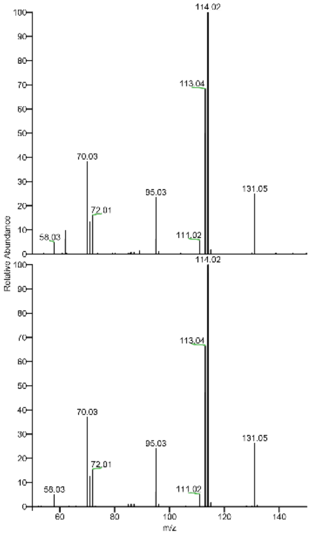
K


306.08
272.09
143.05
254.08
210.09
338.05
482.10
611.15
306.08
272.09
143.05
254.08
210.09
338.05
482.10
611.15
Relative Abundance
m/z

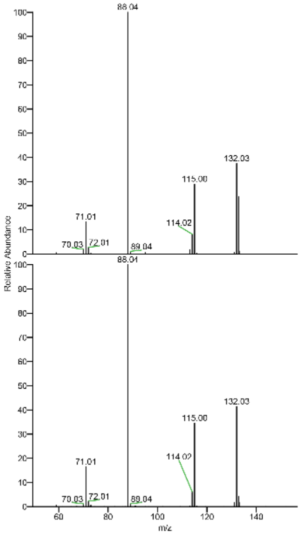
L


131.08
58.04
114.06
156.08
173.10
131.08
58.04
114.06
156.08
173.10
Relative Abundance
m/z

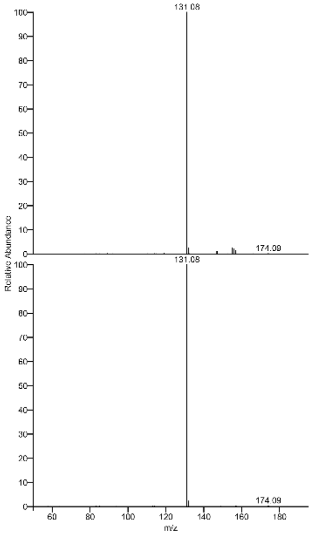
M


114.02
113.04
70.03
95.03
131.05
72.01
58.03
111.02
114.02
113.04
70.03
95.03
131.05
72.01
58.03
111.02
Relative Abundance
m/z

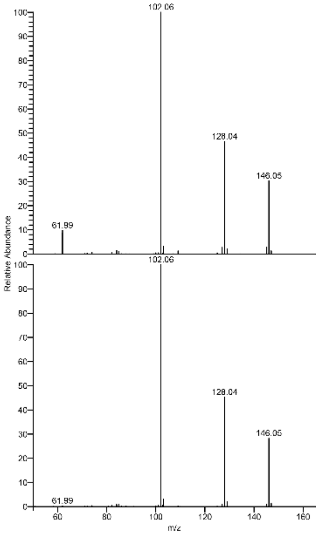
N


88.04
132.03
115.00
71.01
114.02
70.03
72.01
89.04
88.04
132.03
115.00
71.01
114.02
70.03
72.01
89.04
Relative Abundance
m/z

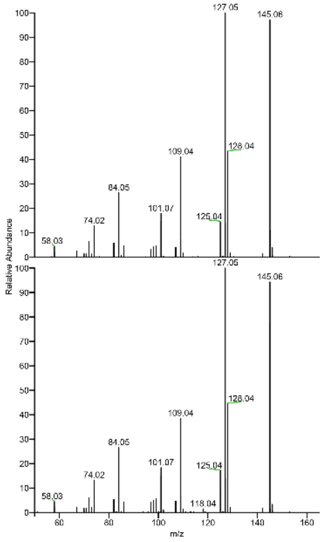
O


131.08
174.09
131.08
174.09
Relative Abundance
m/z

P


102.06
128.04
146.05
61.99
102.06
128.04
146.05
61.99
Relative Abundance
m/z

Q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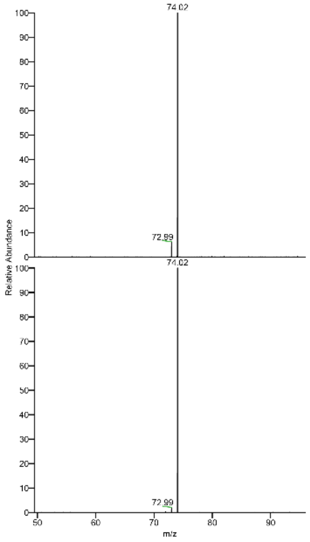
109.04
84.05
101.07
125.04
74.02
58.03
118.04
Relative Abundance
m/z

R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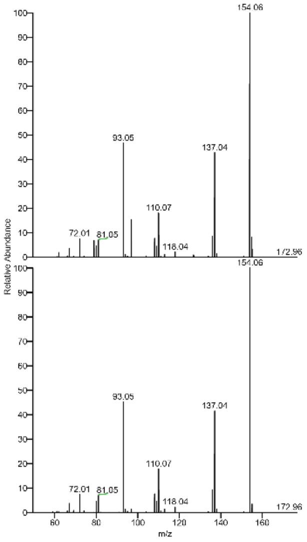
Relative Abundance
m/z

S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137.04
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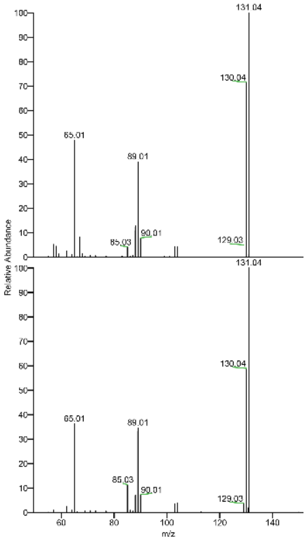
81.05
118.04
172.96
Relative Abundance
m/z

T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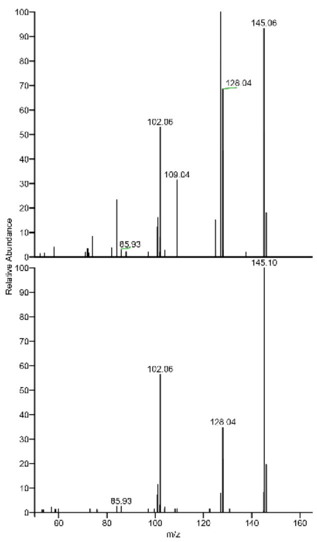
Relative Abundance
m/z

U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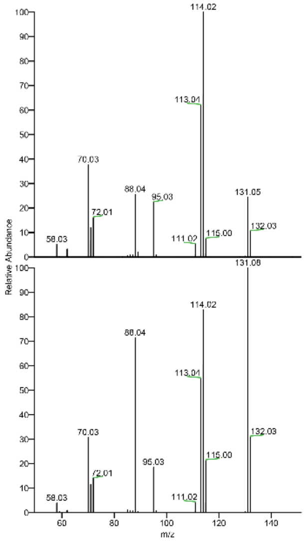
102.06
109.04
85.93
145.10
Relative Abundance
m/z

V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113.01
70.03
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131.05
72.01
58.03
111.02
115.00
132.03
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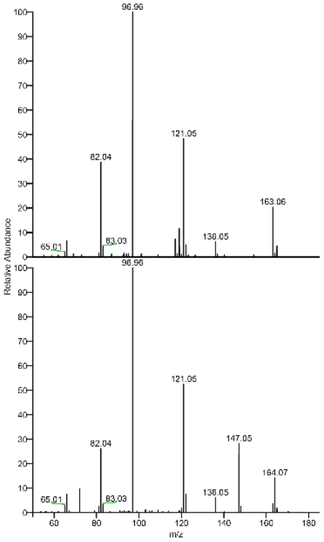
Relative Abundance
m/z

W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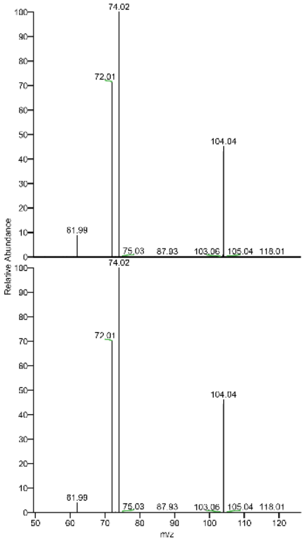
65.01
83.03
147.05
164.07
Relative Abundance
m/z

X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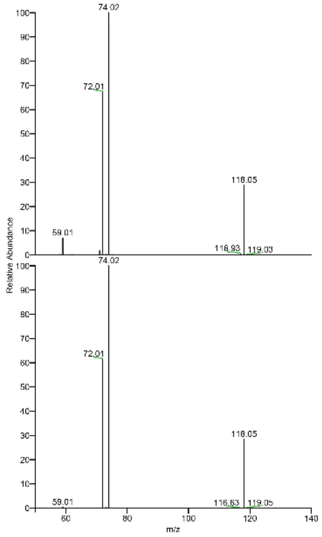
72.01
104.04
81.99
75.03
87.93
103.06
105.04
118.01
Relative Abundance
m/z

Y



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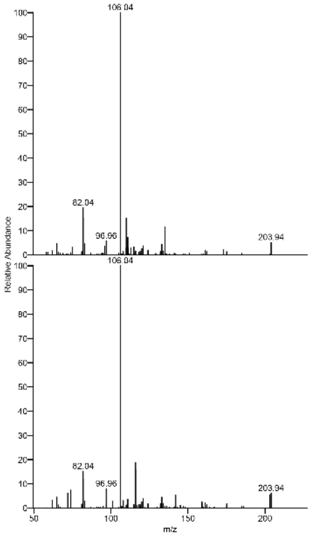

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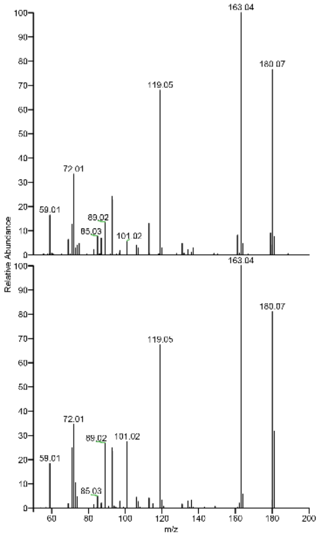

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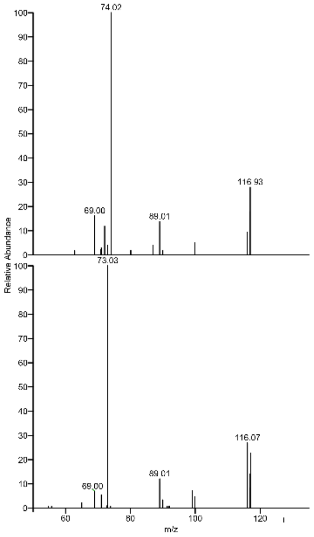

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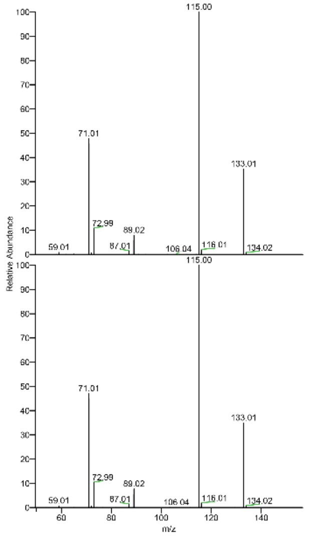

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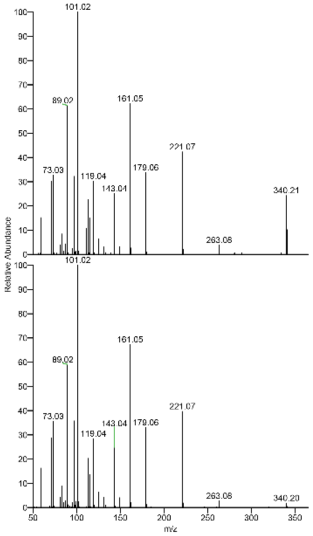

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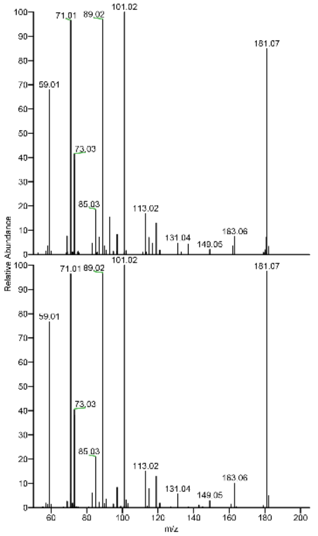

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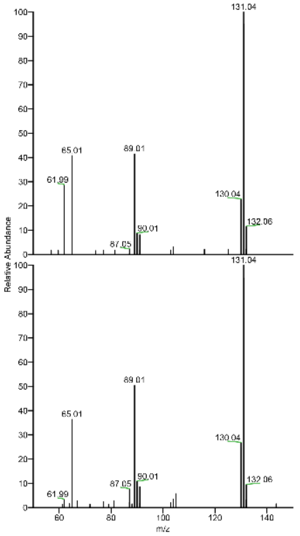

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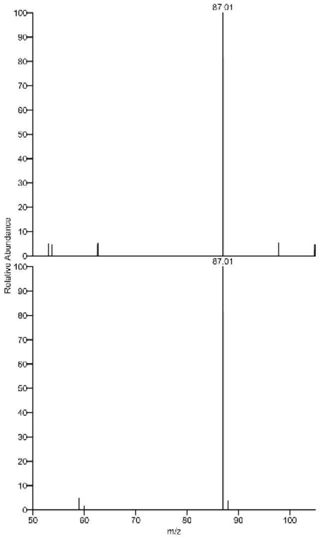

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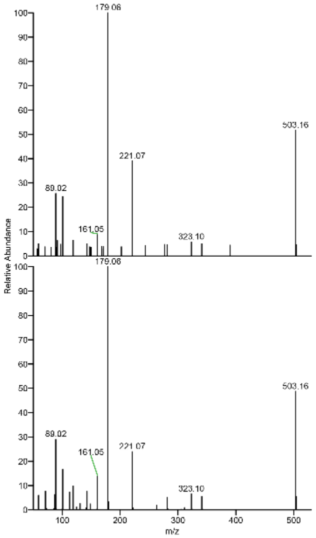

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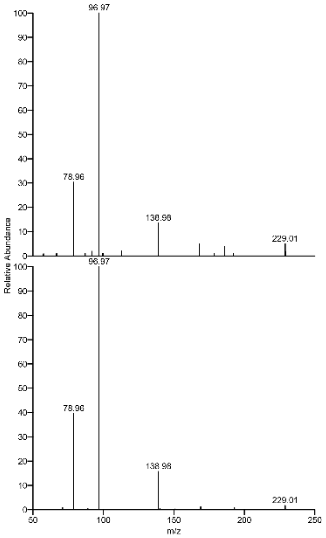

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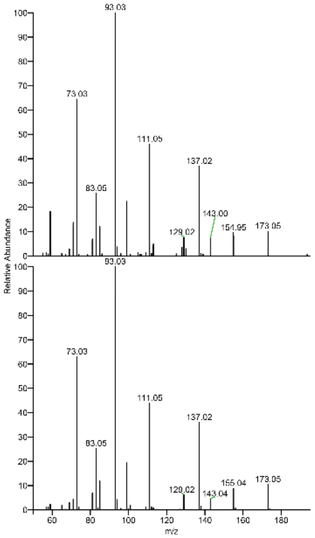

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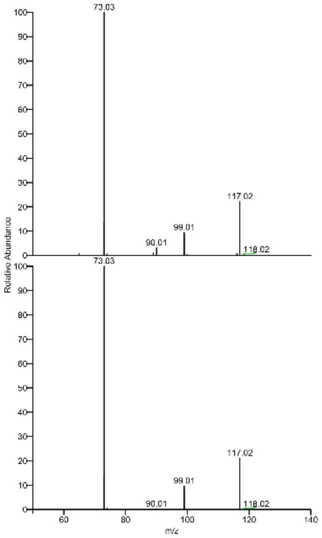
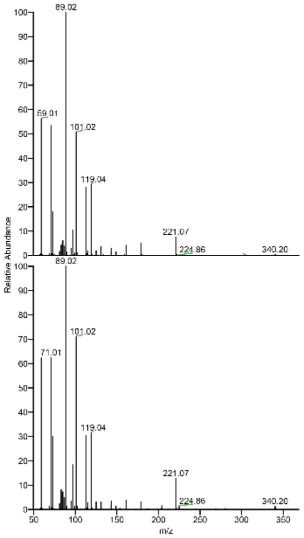


AL



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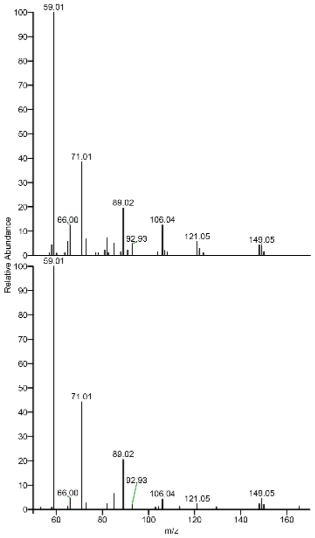


Supplemental Figure 2-6. Metabolites that were identified by authentic standards with *m/z*, retention time, and fragmentation in negative mode.

The top scheme represents metabolite in sample. The bottom scheme represents metabolite in standard. Standard compounds include: adenosine (A), α-ketoglutaric acid (B), citric acid (C), dihydroxyacetone phosphate (D), fructose (E), fructose 6-phosphate (F), fumaric acid (G), glucose (H), glucose 6-phosphate (I), GSH (J), GSSG (K), L-arginine (L), L-asparagine (M), L-aspartic acid (N), L-citrulline (O), L-glutamic acid (P), L-glutamine (Q), L-glycine (R), L-histidine (S), L-leucine (T), L-lysine (U), L-ornithine (V), L-phenylalanine (W), L-serine (X), L-threonine (Y), L-tryptophan (Z), L-tyrosine (AA), L-valine (AB), malic acid (AC), maltose (AD), mannitol (AE), oxoloacetate (AF), pyruvic acid (AG), raffinose (AH), ribose 5-phosphate (AI), shikimic acid (AJ), succinic acid (AK), sucrose (AL), xylose (AM). As noted above, while standard compounds of the specified stereochemistry were used, analytical procedures that would resolve enantiomers were not employed.

Supplemental Table 2-1. Top five most contributed variables to OPLS-DA S-plot with both high correlation and high covariance in different groups

M/z	**Retention time (min)**	**Polarity**	**Groups or stress that contributed the most**	**P[1]**	**P(corr)[1]**	**Identified with reference standard**	**Potential mass (5 ppm)**	**Potential Heuristical Formula (5 ppm)**	**Potential identification by KEGG or PubChem (5 ppm)**
226.9806	8.45	negative	(a) all groups	-0.11	-0.77		227.9851	$C_6H_5ClN_2O_3S$	m-Benzenesulfonium diazonium chloride
248.9613	9.20	negative	(a) all groups	-0.11	-0.92		249.966276997	$C_5H_{11}NS_5$	7-N,N-Dimethylamino-1,2,3,4,5-pentathiocyclooctane
293.0525	8.00	negative	(a) all groups	-0.11	-0.87		294.0617	$C_9H_{15}N_2O_7P$	Pyrimidine 5'-nucleotide
316.2819	5.22	positive	(a) all groups	0.11	0.73				
318.2974	5.25	positive	(a) all groups	0.11	0.82		317.293	$C_{18}H_{39}NO_3$	Phytosphingosine
94.5733	14.37	positive	(b) stress groups only	-0.11	-0.76	Lysine (M+ACN+2H)			
118.0862	6.97	positive	(b) stress groups only	-0.11	-0.64	Valine			
189.1514	10.89	positive	(b) stress groups only	0.12	0.84		188.1442	$C_{10}H_{14}N_2O$	(R)-6-Hydroxynicotine
276.1136	12.19	positive	(b) stress groups only	-0.14	-0.76		275.1044	$C_{13}H_{11}NO_5$	Oxolinic acid
294.9360	3.08	positive	(b) stress groups only	0.10	0.61				
126.9055	6.04	negative	(c) recovery groups only	0.08	0.86				
273.0404	8.84	negative	(c) recovery groups only	0.08	0.93		274.0477	$C_{14}H_{10}O_6$	Isoathyriol
380.8439	5.53	negative	(c) recovery groups only	0.09	0.95				
404.8459	5.77	negative	(c) recovery groups only	-0.09	-0.96				
360.8383	5.80	positive	(c) recovery groups only	-0.08	-0.95				
57.9757	8.70	negative	(d) control, acquired cold, basal cold, drought, high light groups	0.13	0.89		58.98297	CHNS	Thiocyanate
306.0774	11.62	negative	(d) control, acquired cold, basal cold, drought, high light groups	-0.09	-0.54	GSH			
178.1261	4.52	positive	(d) control, acquired cold, basal cold, drought, high light groups	0.14	0.69				

447.1921	14.23	positive	(d) control, acquired cold, basal cold, drought, high light groups	-0.12	-0.89		446.1812	$C_{21}H_{36}INO$	Tridihexethyl iodide
454.2921	7.82	positive	(d) control, acquired cold, basal cold, drought, high light groups	-0.12	-0.91		453.2875	$C_{23}H_{30}N_2O_6$	Cinegalline
505.1671	14.89	negative	(e) basal heat and acquired heat groups	-0.14	-0.77		506.175	$C_{16}H_{23}N_6O_{10}P$	L-2-Aminoadipate adenylate
539.1376	14.89	negative	(e) basal heat and acquired heat groups	-0.12	-0.75	Raffinose (M+Cl)			
551.1711	14.90	negative	(e) basal heat and acquired heat groups	-0.11	-0.74	Raffinose (M+FA-H) [M+2]			
137.0532	5.46	positive	(e) basal heat and acquired heat groups	0.09	0.78				
205.0963	7.35	positive	(e) basal heat and acquired heat groups	0.14	0.71	Tryptophan			
255.0192	7.33	negative	(f) control recovery, acquired cold recovery, basal cold recovery, and high light recovery groups	0.13	0.70				
551.7563	6.13	negative	(f) control recovery, acquired cold recovery, basal cold recovery, and high light recovery groups	-0.17	-0.68				
107.9674	6.41	positive	(f) control recovery, acquired cold recovery, basal cold recovery, and high light recovery groups	0.14	0.77				
123.9393	6.40	positive	(f) control recovery, acquired cold recovery, basal cold recovery, and high light recovery groups	0.13	0.72				
629.6773	6.12	positive	(f) control recovery, acquired cold recovery, basal cold recovery, and high light recovery groups	-0.17	-0.67				

221.0692	12.42	negative	(g) acquired cold, basal cold, and high light groups	0.14	0.95		222.077249175	$C_8H_9N_3O_4$	
302.1022	12.83	negative	(g) acquired cold, basal cold, and high light groups	-0.12	-0.97				
455.1034	12.97	negative	(g) acquired cold, basal cold, and high light groups	0.14	0.95		456.113926926	$C_{23}H_{22}N_2O_6S$	Carfecillin
216.0619	14.17	positive	(g) acquired cold, basal cold, and high light groups	-0.11	-0.97		215.0559	$C_5H_{14}NO_6P$	sn-glycero-3-Phosphoethanolamine
365.1027	12.97	positive	(g) acquired cold, basal cold, and high light groups	0.13	0.95	Sucrose (M+Na)			
163.0220	7.98	negative	(h) control recovery & acquired cold recovery groups	-0.13	-0.81		164.0273	$C_5H_9NO_3S$	Acetylcysteine
66.0682	12.54	positive	(h) control recovery & acquired cold recovery groups	-0.15	-0.79				
82.5371	22.55	positive	(h) control recovery & acquired cold recovery groups	0.12	0.75				
90.0549	8.66	positive	(h) control recovery & acquired cold recovery groups	-0.10	-0.50	Alanine			
94.0450	22.54	positive	(h) control recovery & acquired cold recovery groups	0.12	0.75				
227.8576	6.12	negative	(i) basal cold recovery and, high light recovery groups	-0.25	-0.89				
333.9394	6.31	negative	(i) basal cold recovery and, high light recovery groups	0.25	0.92			$C_8H_2N_2O_{11}P_0S_1$	
401.9273	6.38	negative	(i) basal cold recovery and, high light recovery groups	-0.21	-0.83			$C_8H_{18}N_0O_4P_0S_7$	
117.0738	7.56	positive	(i) basal cold recovery and, high light recovery groups	0.11	0.97	Proline [M+1]			
122.5831	23.45	positive	(i) basal cold recovery and, high light recovery groups	0.17	0.80				
221.0692	12.42	negative	acquired cold	-0.11	-0.93		222.0772	$C_8H_9N_3O_4$	Nicorandil
306.0774	11.62	negative	acquired cold	0.12	0.97	GSH			

341.1117	13.00	negative	acquired cold	-0.10	-0.97	Maltose			
379.9210	4.66	negative	acquired cold	0.12	0.90				
193.1440	4.42	positive	acquired cold	-0.11	-0.90				
162.9404	6.10	negative	acquired cold recovery	-0.13	-0.81				
66.0682	12.54	positive	acquired cold recovery	-0.15	-0.79				
82.5371	22.55	positive	acquired cold recovery	0.12	0.75				
90.0549	8.66	positive	acquired cold recovery	-0.10	-0.50	Alanine			
94.0450	22.54	positive	acquired cold recovery	0.12	0.75				
503.1613	14.88	negative	acquired heat	0.08	0.88	Raffinose			
539.1376	14.89	negative	acquired heat	0.09	0.87	Raffinose (M+Cl)			
550.1691	14.89	negative	acquired heat	0.09	0.86	Raffinose (M+FA-H) [M+1]			
551.1711	14.90	negative	acquired heat	0.09	0.86	Raffinose (M+FA-H) [M+2]			
442.7732	6.15	positive	acquired heat	-0.08	-0.88				
126.9055	6.04	negative	acquired heat recovery	-0.09	-0.99				
315.8734	6.19	negative	acquired heat recovery	0.08	0.98				
394.8930	9.26	negative	acquired heat recovery	-0.08	-0.97				
359.8495	6.38	positive	acquired heat recovery	0.09	0.98				
402.8205	5.41	positive	acquired heat recovery	0.08	0.98				
161.0469	12.44	negative	basal cold	-0.11	-0.98		162.052	$C_6H_6N_2O_3$	Imidazol-5-yl-pyruvate
306.0774	11.62	negative	basal cold	0.13	0.97	GSH			
379.9210	4.66	negative	basal cold	0.11	0.95				
455.1034	12.97	negative	basal cold	-0.11	-0.99		456.1139	$C_{23}H_{22}N_2O_6S$	Carfecillin
136.0791	5.33	positive	basal cold	-0.15	-0.95				
330.8636	6.16	negative	basal cold recovery	0.13	0.98				
401.9273	6.38	negative	basal cold recovery	-0.11	-0.89				
450.8088	6.16	negative	basal cold recovery	0.12	1.00				
324.8255	6.15	positive	basal cold recovery	0.12	0.99				
359.8495	6.38	positive	basal cold recovery	-0.11	-0.85				
248.0549	9.15	negative	basal heat	-0.09	-0.91		249.0596	$C_{13}H_{10}Cl_2$	Bis(4'-chlorophenyl)methane
468.8975	5.45	negative	basal heat	0.07	0.98				
188.0708	7.36	positive	basal heat	-0.09	-0.95		187.0625	$C_6H_{10}ClN_5$	Deethylatrazine
276.1136	12.19	positive	basal heat	-0.10	-0.93		275.104370253	$C_{13}H_{11}NO_5$	Oxolinic acid
526.7586	4.82	positive	basal heat	0.07	0.80				

448.8060	6.15	negative	basal heat recovery	-0.07	-0.99				
136.0621	6.02	positive	basal heat recovery	0.07	1.00	Adenine			
359.8495	6.38	positive	basal heat recovery	0.07	1.00				
402.8205	5.41	positive	basal heat recovery	0.07	1.00				
494.7613	6.18	positive	basal heat recovery	-0.07	-1.00				
402.1015	11.91	negative	drought	-0.12	-0.97		403.1067	$C_{17}H_{12}F_4N_2O_2S$	SC-58125
422.0435	12.71	negative	drought	-0.13	-1.00		423.0465	$C_{13}H_{12}N_5NaO_5S_2$	Ceftizoxime sodium
94.0573	22.72	positive	drought	0.10	0.84				
324.0928	12.70	positive	drought	-0.11	-0.98		323.084374874	$C_{13}H_{12}N_2O_5S$	Nimesulide
398.1643	11.13	positive	drought	0.12	0.99		397.1547	$C_{14}H_{17}N_5O_8$	Succinoadenosine
246.9367	10.91	negative	drought recovery	-0.06	-1.00				
380.8439	5.53	negative	drought recovery	-0.07	-1.00				
402.8205	5.41	positive	drought recovery	0.07	1.00				
442.7732	6.15	positive	drought recovery	-0.06	-0.99				
478.8338	6.40	positive	drought recovery	0.06	1.00				
232.0221	5.84	negative	high light	-0.09	-0.97				
306.0774	11.62	negative	high light	0.12	0.98	GSH			
379.9210	4.66	negative	high light	0.10	0.81				
118.0862	6.97	positive	high light	-0.10	-0.72	Valine			
280.0903	12.85	positive	high light	-0.09	-0.99		279.0814	$C_{13}H_{12}Cl_2N_2$	4,4'-Methylene-bis-(2-chloroaniline)
246.9018	6.16	negative	high light recovery	0.12	0.86				
315.8734	6.19	negative	high light recovery	0.13	0.92				
366.8774	6.30	negative	high light recovery	-0.11	-0.97				
275.8880	6.41	positive	high light recovery	0.12	0.93				
324.8255	6.15	positive	high light recovery	-0.13	-0.97				

Supplemental Table 2-2. Potential stress metabolic signatures whose |p[1]|>0.07 identified with reference standards

M/z	**Retention time (min)**	**Polarity**	**Groups or stress that contributed the most**	**P[1]**	**P(corr)[1]**	**Identified with reference standard**
76.0393	10.04	positive	(i) basal cold recovery and, high light recovery groups	0.08	0.88	Glycine
87.0090	4.31	negative	(d) control, acquired cold, basal cold, drought, high light groups	0.09	0.84	Pyruvate
90.0548	8.89	positive	(f) control recovery, acquired cold recovery, basal cold recovery, and high light recovery groups_regroup	-0.10	-0.44	Alanine
90.0548	8.89	positive	(g) acquired cold, basal cold, and high light groups	0.10	0.62	Alanine
90.0548	8.89	positive	(h) control recovery & acquired cold recovery groups	-0.10	-0.50	Alanine
90.0548	8.89	positive	(i) basal cold recovery and, high light recovery groups	0.07	0.31	Alanine
90.0548	8.89	positive	acquired cold recovery	-0.10	-0.50	Alanine
94.5733	14.37	positive	(b) stress groups only	-0.11	-0.76	Lysine (M+ACN+2H)
94.5733	14.37	positive	basal heat	-0.08	-0.96	Lysine (M+ACN+2H)
104.072	7.42	positive	(d) control, acquired cold, basal cold, drought, high light groups	-0.08	-0.75	gamma-Aminobutyric acid
116.0705	7.54	positive	(d) control, acquired cold, basal cold, drought, high light groups	0.09	0.63	Proline
116.0705	7.54	positive	(i) basal cold recovery and, high light recovery groups	0.10	0.97	Proline
116.072	7.01	negative	(b) stress groups only	-0.11	-0.64	Valine
116.072	7.01	negative	acquired cold	-0.08	-0.65	Valine
116.072	7.01	negative	basal cold	-0.09	-0.68	Valine
116.072	7.01	negative	basal heat	-0.08	-0.80	Valine
116.072	7.01	negative	high light	-0.10	-0.72	Valine
117.0738	7.56	positive	(i) basal cold recovery and, high light recovery groups	0.11	0.97	Proline [M+1]
118.0862	6.97	positive	(b) stress groups only	-0.11	-0.64	Valine
118.0862	6.97	positive	acquired cold	-0.08	-0.65	Valine
118.0862	6.97	positive	basal cold	-0.09	-0.68	Valine
118.0862	6.97	positive	basal heat	-0.08	-0.80	Valine
118.0862	6.97	positive	high light	-0.10	-0.72	Valine
120.0654	9.87	positive	(f) control recovery, acquired cold recovery, basal cold recovery, and high light recovery groups_regroup	-0.13	-0.59	Threonine
132.1018	6.44	negative	(b) stress groups only	-0.11	-0.72	Leucine
132.1018	6.44	negative	(g) acquired cold, basal cold, and high light groups	-0.07	-0.88	Leucine
132.1018	6.44	negative	acquired heat	0.08	0.92	Leucine
132.1018	6.44	negative	basal heat	-0.08	-0.98	Leucine
132.1018	6.44	negative	high light	-0.08	-0.95	Leucine

133.0152	7.44	negative	(d) control, acquired cold, basal cold, drought, high light groups	0.07	0.85	Malic acid
133.1050	6.47	positive	(b) stress groups only	-0.11	-0.72	Leucine [M+1]
133.1050	6.47	positive	(g) acquired cold, basal cold, and high light groups	-0.07	-0.88	Leucine [M+1]
133.1050	6.47	positive	acquired heat	0.08	0.92	Leucine [M+1]
133.1050	6.47	positive	basal heat	-0.08	-0.98	Leucine [M+1]
133.1050	6.47	positive	high light	-0.08	-0.95	Leucine [M+1]
136.0621	5.90	positive	(c) recovery groups only	-0.07	-0.87	Adenine
136.0621	5.90	positive	basal heat recovery	0.07	1.00	Adenine
145.0629	10.81	negative	(h) control recovery & acquired cold recovery groups	-0.07	-0.86	Glutamine
145.0629	10.81	negative	acquired cold recovery	-0.07	-0.86	Glutamine
147.076	10.80	positive	(h) control recovery & acquired cold recovery groups	-0.09	-0.93	Glutamine
147.076	10.80	positive	acquired cold recovery	-0.09	-0.93	Glutamine
152.0568	8.29	positive	(b) stress groups only	-0.11	-0.72	Guanine
166.0862	6.74	positive	acquired cold	-0.07	-0.99	Phenylalanine
166.0862	6.74	positive	acquired heat	0.08	0.91	Phenylalanine
166.0862	6.74	positive	basal cold	-0.08	-0.97	Phenylalanine
180.068	9.13	negative	(b) stress groups only	-0.07	-0.85	Tyrosine
182.0812	9.11	positive	(b) stress groups only	-0.11	-0.75	Tyrosine
182.0812	9.11	positive	acquired heat	0.07	0.88	Tyrosine
182.0812	9.11	positive	basal heat	-0.08	-0.97	Tyrosine
183.085	8.81	positive	(b) stress groups only	-0.10	-0.77	Mannitol
205.0963	7.35	positive	(e) basal heat and acquired heat groups	0.14	0.71	Tryptophan
205.0963	7.35	positive	basal heat	-0.08	-0.97	Tryptophan
205.0963	7.35	positive	high light	-0.07	-0.90	Tryptophan
206.1003	7.32	positive	(b) stress groups only	-0.11	-0.76	Tryptophan [M+1]
206.1003	7.32	positive	acquired heat	0.07	0.89	Tryptophan [M+1]
206.1003	7.32	positive	basal heat	-0.08	-0.97	Tryptophan [M+1]
206.1003	7.32	positive	high light	-0.07	-0.89	Tryptophan [M+1]
259.0227	20.13	negative	(d) control, acquired cold, basal cold, drought, high light groups	0.07	0.75	Glucose 6-phosphate
259.0227	20.13	negative	(g) acquired cold, basal cold, and high light groups	0.07	0.90	Glucose 6-phosphate
259.0227	20.13	negative	(g) acquired cold, basal cold, and high light groups	0.08	0.89	Glucose 6-phosphate
259.023	20.69	negative	(d) control, acquired cold, basal cold, drought, high light groups	0.08	0.76	Fructose 6-P
306.0774	11.60	negative	(d) control, acquired cold, basal cold, drought, high light groups	-0.09	-0.54	GSH

306.0774	11.60	negative	acquired cold	0.12	0.97	GSH
306.0774	11.60	negative	basal cold	0.13	0.97	GSH
306.0774	11.60	negative	high light	0.12	0.98	GSH
341.1116	12.94	negative	(d) control, acquired cold, basal cold, drought, high light groups	0.08	0.55	Maltose
341.1116	12.94	negative	(g) acquired cold, basal cold, and high light groups	0.12	0.95	Maltose
341.1116	12.94	negative	acquired cold	-0.10	-0.97	Maltose
341.1116	12.94	negative	basal cold	-0.10	-0.99	Maltose
365.1027	12.97	positive	(g) acquired cold, basal cold, and high light groups	0.13	0.95	Sucrose (M+Na)
365.1027	12.97	positive	basal cold	-0.11	-0.99	Sucrose (M+Na)
377.0880	12.96	negative	(g) acquired cold, basal cold, and high light groups	0.12	0.95	Sucrose (M+Cl)
377.0880	12.96	negative	acquired cold	-0.09	-0.99	Sucrose (M+Cl)
377.0880	12.96	negative	basal cold	-0.10	-0.99	Sucrose (M+Cl)
503.1614	14.89	negative	(b) stress groups only	-0.08	-0.50	Raffinose
503.1614	14.89	negative	(e) basal heat and acquired heat groups	-0.11	-0.75	Raffinose
503.1614	14.89	negative	acquired heat	0.08	0.88	Raffinose
539.1376	14.89	negative	(e) basal heat and acquired heat groups	-0.12	-0.75	Raffinose (M+Cl)
539.1376	14.89	negative	acquired heat	0.09	0.87	Raffinose (M+Cl)
549.1656	14.89	negative	(b) stress groups only	-0.08	-0.52	Raffinose (M+FA-H)
549.1656	14.89	negative	(e) basal heat and acquired heat groups	-0.11	-0.74	Raffinose (M+FA-H)
549.1656	14.89	negative	(g) acquired cold, basal cold, and high light groups	-0.08	-0.95	Raffinose (M+FA-H)
549.1656	14.89	negative	acquired heat	0.08	0.90	Raffinose (M+FA-H)
550.1691	14.90	negative	(e) basal heat and acquired heat groups	-0.11	-0.75	Raffinose (M+FA-H) [M+1]
550.1691	14.90	negative	acquired heat	0.09	0.86	Raffinose (M+FA-H) [M+1]
551.1711	14.90	negative	(b) stress groups only	-0.11	-0.58	Raffinose (M+FA-H) [M+2]
551.1711	14.90	negative	(e) basal heat and acquired heat groups	-0.11	-0.74	Raffinose (M+FA-H) [M+2]
551.1711	14.90	negative	acquired heat	0.09	0.86	Raffinose (M+FA-H) [M+2]
613.163	18.10	positive	(a) all groups	0.07	0.90	GSSG

Supplemental Table 2-3. Metabolites as potential stress metabolic signatures that are identified with reference standard

Identity	***M/z***	**retention time (min)**	**polarity**	**Molecular formula**	**Monoisotopic Mass**	**Adduct**	**Theoretical exact mass (Da)**	**Mass accuracy (ppm)**	**Fragment ions**
Adenine	136.062	7.08	positive	$C_5H_5N_5$	135.055	M+H	136.062	4	119.04, 94.04, 92.03
Adenosine	266.09	5.66	negative	$C_{10}H_{13}N_5O_4$	267.097	M-H	266.09	2	134.05
Adenosine	268.103	5.62	positive	$C_{10}H_{13}N_5O_4$	267.097	M+H	268.104	4	136.06
Alanine	90.0548	8.89	positive	$C_3H_7NO_2$	89.0477	M+H	90.055	2	74.10, 72.08, 72.04, 60.08, 54.00
alpha-Ketoglutaric acid	145.015	7.36	negative	$C_5H_6O_5$	146.022	M-H	145.014	5	118.04, 101.06, 77.01, 64.02
Arginine	173.105	14.25	negative	$C_6H_{14}N_4O_2$	174.112	M-H	173.104	3	156.08, 131.08, 114.06, 58.04
Arginine	175.119	14.22	positive	$C_6H_{14}N_4O_2$	174.112	M+H	175.119	1	158.09, 141.07, 130.10, 116.07, 112.09, 97.08, 72.08, 70.07, 60.06
Asparagine	131.047	11.36	negative	$C_4H_8N_2O_3$	132.054	M-H	131.046	4	131.05, 114.02, 113.04, 111.02, 96.01, 95.03, 72.01, 70.03, 58.03
Asparagine	133.061	11.09	positive	$C_4H_8N_2O_3$	132.054	M+H	133.061	1	116.03, 88.04, 87.06, 74.02, 70.03, 60.04
Aspartic acid	132.031	12.87	negative	$C_4H_7NO_4$	133.038	M-H	132.03	4	115.00, 113.04, 88.04, 71.01
Aspartic acid	134.045	12.25	positive	$C_4H_7NO_4$	133.038	M+H	134.045	0	116.03, 88.04, 74.02, 70.03
Citric acid	191.02	12.44	negative	$C_6H_8O_7$	192.027	M-H	191.02	3	129.02, 111.01, 102.95, 87.01, 57.03
Citrulline	174.089	11.81	negative	$C_6H_{13}N_3O_3$	175.096	M-H	174.088	4	131.08
Citrulline	176.103	11.81	positive	$C_6H_{13}N_3O_3$	175.096	M+H	176.103	0	141.07, 130.10, 115.09, 113.07, 97.08, 70.07
Cysteine	122.027	16.09	positive	$C_3H_7NO_2S$	121.02	M+H	122.027	3	122.03, 120.01, 104.11
Dihydroxyacetone phosphate	168.992	17.35	negative	$C_3H_7O_6P$	169.998	M-H	168.991	4	96.97, 78.96
Fructose	179.057	7.97	negative	$C_6H_{12}O_6$	180.063	M-H	179.056	4	168.89, 122.89, 89.02, 69.00
Fructose 6-phosphate	259.023	19.74	negative	$C_6H_{13}O_9P$	260.03	M-H	259.022	1	223, 199, 168.99, 138.98, 96.97, 78.96
Fumaric acid	115.004	5.84	negative	$C_4H_4O_4$	116.011	M-H	115.004	3	72.02, 71.01, 69.00
Glucose	179.057	9.28	negative	$C_6H_{12}O_6$	180.063	M-H	179.056	4	163.04, 119.04, 113.02, 101.02, 89.02, 85.03, 71.01, 59.01
Glucose	179.057	9.98	negative	$C_6H_{12}O_6$	180.063	M-H	179.056	5	163.04, 119.04, 113.02, 101.02, 89.02, 85.03, 71.01, 59.01
Glucose 6-phosphate	259.023	20.13	negative	$C_6H_{13}O_9P$	260.03	M-H	259.022	1	199.00, 168.99, 138.98, 101.02, 96.97, 78.96
Glutamic acid	146.046	11.17	negative	$C_5H_9NO_4$	147.053	M-H	146.046	4	128.04, 102.06
Glutamic acid	148.06	11.77	positive	$C_5H_9NO_4$	147.053	M+H	148.06	0	130.05, 102.06, 84.04

Glutamine	145.063	10.81	negative	$C_5H_{10}N_2O_3$	146.069	M-H	145.062	7	128.04, 127.05, 125.04, 109.04, 101.07, 99.06, 86.02, 84.05, 74.02, 72.01, 58.03
Glutamine	147.076	10.80	positive	$C_5H_{10}N_2O_3$	146.069	M+H	147.076	1	130.09, 123.96, 102,05, 84.08, 64.93
Glycine	74.0249	9.98	negative	$C_2H_5NO_2$	75.032	M-H	74.0248	2	72.99
Glycine	76.0393	10.04	positive	$C_2H_5NO_2$	75.032	M+H	76.0393	0	57.05, 58.04, 75.06
GSH	306.077	11.60	negative	$C_{10}H_{17}N_3O_6S$	307.084	M-H	306.077	3	288.07, 272.09, 254.08, 242.08, 210.09, 179.05, 160.01, 143.05, 74.02
GSH	308.09	12.47	positive	$C_{10}H_{17}N_3O_6S$	307.084	M+H	308.091	2	291.06, 245.06, 233.06, 179.05, 162.02, 130.05, 84.04, 76.02
GSSG	611.152	18.11	negative	$C_{20}H_{32}N_6O_{12}S_2$	612.152	M-H	611.145	#	593.14, 482.10, 338.05, 306.08, 272.09, 254.08, 210.09, 143.05
GSSG	613.163	18.1	positive	$C_{20}H_{32}N_6O_{12}S_2$	612.152	M+H	613.159	6	538.13, 484.12, 466.11, 409.09, 355.08, 288.07, 324.04, 177.03, 130.05
Guanine	152.057	8.29	positive	$C_5H_5N_5O$	151.049	M+H	152.057	1	108.52, 99.51, 97.01, 88.00, 87.00
Guanosine monophosphate	364.068	19.19	positive	$C_{10}H_{14}N_5O_8P$	363.058	M+H	364.065	6	152.06, 97.03
Histidine	154.063	14.47	negative	$C_6H_9N_3O_2$	155.07	M-H	154.062	5	137.04, 110.07, 96.96, 93.05, 81.05, 72.01
Histidine	156.077	14.47	positive	$C_6H_9N_3O_2$	155.07	M+H	156.077	0	110.07, 95.06, 83.06
Leucine	130.088	6.46	negative	$C_6H_{13}NO_2$	131.095	M-H	130.087	5	89.01, 85.03, 65.01
Leucine	132.102	6.39	positive	$C_6H_{13}NO_2$	131.095	M+H	132.102	0	86.10, 69.07
Leucine [M+1]	133.105	6.47	positive						86.10, 69.07
Lysine	145.099	14.38	negative	$C_6H_{14}N_2O_2$	146.106	M-H	145.098	7	128.04, 127.05, 102.06, 100.95, 85.93
Lysine	147.113	14.37	positive	$C_6H_{14}N_2O_2$	146.106	M+H	147.113	1	130.09, 123.96, 102.05, 84.08
Lysine (M+ACN+2H)	94.5733	14.37	positive	$C_6H_{14}N_2O_2$	146.106	M+ACN+2H	94.5733	0	130.09, 123.96, 102.05, 84.08
Malic acid	133.015	7.41	negative	$C_4H_6O_5$	134.022	M-H	133.014	3	115.00, 89.02, 72.99, 71.01
Maltose	341.111	12.9	negative	$C_{12}H_{22}O_{11}$	342.116	M-H	341.109	6	221.07, 119.04, 161.05, 119.04, 101.02, 89.02
Mannitol	181.073	8.81	negative	$C_6H_{14}O_6$	182.079	M-H	181.072	6	163.06, 149.05, 131.04, 119.04, 113.02, 101.02, 89.02, 85.03, 73.03, 71.01, 59.01
Mannitol	183.085	8.81	positive	$C_6H_{14}O_6$	182.079	M+H	183.086	9	165.05, 147.04, 136.08, 123.04, 119.05, 113.96, 91.05
Ornithine	131.083	14.86	negative	$C_5H_{12}N_2O_2$	132.09	M-H	131.083	4	115.00, 114.02, 113.04, 111.02, 95.03, 88.04, 72.03, 70.03, 58.03
Ornithine	133.097	14.96	positive	$C_5H_{12}N_2O_2$	132.09	M+H	133.097	0	116.07, 115.09, 70.07
Oxoloacetate	130.997	11.32	negative	$C_4H_4O_5$	132.006	M-H	130.999	#	104.03, 89.01, 65.01

Phenylalanine	164.072	6.89	negative	$C_9H_{11}NO_2$	165.079	M-H	164.072	4	136.05, 121.05, 96.96, 82.04, 65.01
Phenylalanine	166.086	6.88	positive	$C_9H_{11}NO_2$	165.079	M+H	166.086	0	149.06, 131.05, 120.08, 103.05
Proline	116.071	7.55	positive	$C_5H_9NO_2$	115.063	M+H	116.071	0	70.07
Proline [M+1]	117.074	7.56	positive						70.07
Pyruvic acid	87.009	4.31	negative	$C_3H_4O_3$	88.016	M-H	87.0088	3	62.63, 59.01
Raffinose	503.161	14.89	negative	$C_{18}H_{32}O_{16}$	504.169	M-H	503.162	1	289.07, 272.09, 254.08, 228.10, 210.09, 179.05, 160.01, 143.05, 128.04, 74.02
Raffinose (M+Cl)	539.138	14.89	negative	$C_{18}H_{32}O_{16}$	504.169	M+Cl	539.138	2	289.07, 272.09, 254.08, 228.10, 210.09, 179.05, 160.01, 143.05, 128.04, 74.03
Raffinose (M+FA-H)	549.166	14.89	negative	$C_{18}H_{32}O_{16}$	504.169	M+FA-H	549.167	2	289.07, 272.09, 254.08, 228.10, 210.09, 179.05, 160.01, 143.05, 128.04, 74.04
Raffinose (M+FA-H) [M+1]	550.169	14.90	negative						289.07, 272.09, 254.08, 228.10, 210.09, 179.05, 160.01, 143.05, 128.04, 74.05
Raffinose (M+FA-H) [M+2]	551.171	14.90	negative						289.07, 272.09, 254.08, 228.10, 210.09, 179.05, 160.01, 143.05, 128.04, 74.06
Ribose 5-phosphate	229.013	18.73	negative	$C_5H_{11}O_8P$	230.019	M-H	229.012	3	138.98, 96.97, 78.96
Serine	104.036	11.42	negative	$C_3H_7NO_3$	105.043	M-H	104.035	5	74.02, 72.01, 61.99
Serine	106.05	11.37	positive	$C_3H_7NO_3$	105.043	M+H	106.05	1	88.04, 70.03, 60.04
Shikimic acid	173.045	6.52	negative	$C_7H_{10}O_5$	174.053	M-H	173.046	1	137.02, 129.02, 111.05, 99.05, 93.03, 83.05, 73.03, 71.01
Succinic acid	117.02	5.42	negative	$C_4H_6O_4$	118.027	M-H	117.019	4	99.01, 73.03
Sucrose	341.111	12.20	negative	$C_{12}H_{22}O_{11}$	342.116	M-H	341.109	5	221.07, 119.04, 101.02, 89.02, 71.01, 59.01
Sucrose (M+Cl)	377.088	12.96	negative	$C_{12}H_{22}O_{11}$	342.116	M+Cl	377.086	6	221.07, 119.04, 101.02, 89.02, 71.01, 59.01
Sucrose (M+Na)	365.103	12.97	positive	$C_{12}H_{22}O_{11}$	342.116	M+Na	365.105	7	221.07, 119.04, 101.02, 89.02, 71.01, 59.01
Threonine	118.052	10.08	negative	$C_4H_9NO_3$	119.058	M-H	118.051	5	74.02, 72.01, 59.01
Threonine	120.066	10.09	positive	$C_4H_9NO_3$	119.058	M+H	120.066	0	102.05, 84.04, 74.06, 56.05
Tryptophan	203.083	7.31	negative	$C_{11}H_{12}N_2O_2$	204.09	M-H	203.083	3	106.04, 96.96, 82.04, 65.01
Tryptophan	205.097	7.33	positive	$C_{11}H_{12}N_2O_2$	204.09	M+H	205.097	0	188.07, 170.06, 159.09, 146.06, 144.08, 132.08, 91.05, 74.02
Tryptophan [M+1]	206.1	7.32	positive						188.07, 170.06, 159.09, 146.06, 144.08, 132.08, 91.05, 74.02
Tyrosine	180.068	9.13	negative	$C_9H_{11}NO_3$	181.074	M-H	180.067	5	163.04, 119.05, 101.02, 93.03, 89.02, 85.03, 72.01, 59.01
Tyrosine	182.081	9.12	positive	$C_9H_{11}NO_3$	181.074	M+H	182.081	1	165.05, 147.04, 136.08, 123.04, 119.05, 113.96, 91.05

Urea	61.0398	2.79	positive	CH_4N_2O	60.0324	M+H	61.0396	3	60.04
Valine	116.072	7.01	negative	$C_5H_{11}NO_2$	117.079	M-H	116.072	6	99.93, 89.01, 74.02, 73.03, 69.00
Valine	118.086	7.09	positive	$C_5H_{11}NO_2$	117.079	M+H	118.086	0	72.08
Xylose	149.046	6.98	negative	$C_5H_{10}O_5$	150.053	M-H	149.046	4	89.02, 71.01, 59.01
γ-Aminobutyric acid	104.072	7.42	positive	$C_4H_9NO_2$	103.063	M+H	104.071	#	87.04, 86.06, 69.03

Supplemental Table 2-4. Average fold change of metabolites identified with reference standards observed between positive and negative mode compared to control

Metabolites	**Acquired cold stress**	**Acquired heat stress**	**Basal cold stress**	**Basal heat stress**	**Drought stress**	**High light stress**	**Acquired cold recovery**	**Acquired heat recovery**	**Basal cold recovery**	**Basal heat recovery**	**Drought recovery**	**High light recovery**
Adenine	1.16	1.20	1.17	2.60	1.38	0.99	0.92	0.79	0.91	3.29	0.70	0.87
Adenosine	1.01	0.98	1.11	3.03	1.17	1.29	1.46	1.17	0.96	6.61	1.95	1.01
Alanine	2.56	3.77	1.54	4.20	1.99	1.26	1.25	1.46	0.95	1.01	0.58	0.74
alpha-Ketoglutaric acid	0.84	0.32	0.69	0.32	0.46	0.91	1.19	0.48	0.94	0.15	0.35	0.99
Arginine	0.84	0.90	0.91	1.16	1.36	1.00	1.08	0.67	0.69	0.55	0.10	0.76
Asparagine	0.71	2.17	0.95	1.87	1.09	1.22	1.24	0.77	0.81	0.32	0.19	0.61
Aspartic acid	0.52	0.50	0.89	0.55	0.90	0.85	1.15	0.60	0.92	0.27	0.20	0.74
Citric acid	2.88	0.93	1.46	1.16	2.17	1.47	1.17	0.75	1.13	0.50	0.68	0.91
Citrulline	0.64	0.14	0.75	0.30	1.25	0.62	1.16	0.27	0.77	0.12	0.11	0.57
Cysteine	2.33	339.19	1.73	297.28	39.84	15.84	1.12	0.92	0.45	2.34	0.36	0.51
Dihydroxyacetone phosphate	1.97	1.36	0.80	1.17	0.18	0.63	0.84	1.07	0.46	1.12	0.09	0.51
Fructose	1.00	1.11	1.02	1.46	1.17	1.43	1.00	1.25	0.92	1.43	0.82	0.81
Fructose 6-phosphate	1.15	1.00	1.06	0.98	0.43	0.65	1.48	0.59	0.79	0.44	0.17	0.87
Fumaric acid	1.05	1.56	1.00	1.15	0.68	2.20	0.74	0.63	0.81	0.14	1.64	0.75
gamma-Aminobutyric acid	1.58	2.71	1.04	5.43	5.30	1.14	0.99	1.06	1.04	2.21	0.62	1.01
Glucose	0.99	1.34	0.91	1.62	0.61	1.20	0.89	1.40	1.00	1.18	1.08	0.84
Glucose 6-phosphate	1.12	0.52	0.91	0.54	0.36	0.50	1.05	0.47	0.65	0.33	0.15	0.62
Glutamic acid	0.50	0.47	0.63	0.58	0.72	0.92	1.02	0.59	0.84	0.21	0.07	0.74
Glutamine	0.80	1.40	0.95	1.38	1.19	1.07	1.34	1.35	1.07	1.22	0.57	1.01
Glycine	1.26	2.38	2.03	1.85	1.51	2.64	0.98	0.76	0.93	0.77	0.86	0.52
GSH	0.02	0.16	0.02	0.18	0.44	0.05	1.37	2.37	0.75	5.59	0.28	0.62
GSSG	1.21	0.60	1.38	0.49	1.86	1.43	1.44	0.37	0.73	0.07	0.07	0.64
Guanine	0.80	7.66	0.85	17.65	1.06	0.90	4.31	3.43	0.83	27.39	7.87	0.79
Guanosine monophosphate	0.54	0.06	0.69	0.41	0.30	0.96	0.89	0.51	0.61	0.26	0.15	0.62
Histidine	0.73	2.47	1.12	2.50	1.58	1.43	1.30	1.23	0.89	1.47	0.21	0.69
Leucine	1.42	28.30	1.35	31.08	7.32	4.27	0.96	7.60	0.74	31.30	5.94	0.59
Lysine	0.63	7.36	0.78	8.77	2.30	1.28	1.25	1.21	0.71	5.70	0.44	0.71
Malic acid	0.97	1.33	1.11	0.59	0.57	1.80	1.03	0.66	0.94	0.16	0.46	0.82

Maltose	33.58	1.49	1.36	0.42	36.11	0.97	3.04	2.60	1.31	0.56	1.27	0.66
Mannitol	0.58	11.67	0.98	15.80	2.65	1.29	0.62	1.63	0.29	9.23	0.85	0.27
Ornithine	0.79	0.49	1.07	0.67	1.65	1.02	1.22	0.68	0.68	0.33	0.09	0.61
Oxaloacetic acid	2.66	13.49	1.82	7.88	2.44	1.09	1.80	0.99	1.14	0.48	0.11	0.77
Phenylalanine	2.51	19.84	3.17	14.86	4.05	4.56	1.80	3.38	0.81	11.08	1.73	0.73
Proline	0.79	2.98	0.85	3.25	1.85	1.34	0.99	0.84	2.46	1.50	1.23	0.99
Pyruvic acid	2.63	0.73	2.63	0.78	0.42	1.16	1.20	0.54	1.20	0.25	0.36	0.82
Raffinose	0.62	27.55	0.63	3.14	1.67	2.00	1.15	23.70	2.39	8.71	1.17	2.06
Ribose 5-phosphate	0.50	1.48	0.88	1.45	0.48	0.63	1.16	0.65	0.65	0.55	0.12	0.61
Serine	0.47	0.51	0.54	0.55	0.74	0.75	0.99	0.28	0.80	0.10	0.22	0.80
Shikimic acid	0.79	1.00	0.83	1.00	0.97	0.76	1.01	0.76	1.03	0.50	0.84	0.97
Succinic acid	0.86	1.44	0.81	3.14	0.95	1.83	0.71	0.76	0.69	0.56	0.70	0.64
Sucrose	0.44	0.47	0.48	0.48	0.50	0.64	1.08	1.21	0.93	1.91	1.04	0.71
Threonine	0.95	2.68	0.91	2.68	1.44	1.34	1.00	1.52	0.95	1.51	0.85	0.74
Tryptophan	2.40	51.88	2.91	58.43	5.71	5.17	1.52	9.41	1.35	41.28	15.79	1.69
Tyrosine	1.23	27.99	1.49	32.75	5.30	3.54	1.02	2.36	0.63	15.94	0.85	0.56
Urea	0.33	0.34	0.35	0.71	0.41	0.44	1.01	0.40	0.40	0.25	0.50	0.58
Valine	0.96	15.32	1.24	16.59	3.19	2.39	1.30	4.04	1.27	8.12	0.72	0.93
Xylose	0.71	1.43	0.80	1.16	1.39	1.09	1.15	2.31	1.16	1.34	0.68	1.35

Supplemental Table 2-5. Standard compounds used for feature identification by retention time and MS/MS fragmentation pattern matching

Adenine
Adenosine
α-Ketoglutaric acid
Citric acid
Dihydroxyacetone phosphate dilithium salt
D-(−)-Fructose
D-Fructose 6-phosphate disodium salt hydrate
Fumaric acid
γ-Aminobutyric acid
D-(+)-Glucose
D-Glucose 6-phosphate sodium salt
L-Glutathione reduced
L-Glutathione oxidized
Guanine
Guanosine 3′-monophosphate disodium salt
L-Alanine
L-Arginine
L-Asparagine
L-Aspartic acid
L-Citrulline
L-Cysteine
L-Glutamic acid
L-Glutamine
Glycine
L-Histidine
L-Leucine
L-Lysine
L-Ornithine monohydrochloride
L-Phenylalanine
L-Proline
L-Serine

L-Threonine
L-Tryptophan
L-Tyrosine
L-Valine
Malic acid
D-(+)-Maltose monohydrate
D-Mannitol
Oxaloacetic acid
Pyruvic acid
D-(+)-Raffinose pentahydrate
D-Ribose 5-phosphate disodium salt hydrate
Shikimic acid
Succinic acid
Sucrose
Urea
D-(+)-Xylose

Chapter 3. Metabolomics study on the response of *Arabidopsis thaliana* to combinations of abiotic stresses that mimic the field environment including heat, cold, drought, salinity, and high light

Introduction

Abiotic stress can have significant effects on plant growth, development, and reproduction. Although plant responses after exposure to one specific stress has been extensively studied, less is known about how a plant responds to a combination of two different stresses. In the field, a complex set of abiotic stresses, including extremes of temperatures, low water availability, high salinity, and high irradiance can and often occur simultaneously. For example, plants in drought-stricken areas may be subjected to drought stress in combination with heat, salinity, or high light stress (Mittler et al., 2001). Plants in arid and semi-arid regions may encounter a combination of salinity and heat stress (Pandey et al., 2017). *Vitis vinifera* (grapes) growing in continental climate regions, like North China, are known to be particularly vulnerable to combined drought and cold stress (Su et al., 2015). The productivity of crops growing in the Mediterranean regions and northern countries like Canada and Sweden are reduced by cold and high light combined stresses (Loreto and Bongi, 1989). In the US, corn and soybean are especially susceptible to drought and heat combinations (Mittler, 2006). High light and heat often accompany each other (Pandey et al., 2017) and thus, plants face a combination of abiotic stresses more often than a specific single stress under natural and crop field conditions.

Combined stresses also cause extensive losses in crop production worldwide (Mittler, 2006). According to the report of National Centers for Environmental Information (NCEI) (https://www.ncdc.noaa.gov/billions/), from 1980 to 2017, the U.S. has sustained 219 weather disasters with a damage cost of more than $1 billion. Among these weather conditions the combination of drought and heat waves occurred most often and caused greatest amount of damage, worth more than $210 billion (Smith and Matthews, 2015). The effect of drought and heat combination stress has been studied on maize, barley, sorghum, and grasses. It was found that the extent of damage caused by combined stresses was more than that of each of the individual stresses (Craufurd and Peacock, 1993; Savin and Nicolas, 1996). Because combined stresses cause significantly more detrimental damages on agricultural crops, it is crucial to develop crop plants that are more resistant to combined stress. A well-known breeding target in maize is to generate resistant lines to a combination of stresses (Rizhsky, 2004). However, the great majority of research remains focused on plant responses to each individual abiotic stress condition. Transgenic plants or crops developed from laboratory experimentation with enhanced resistant to only a single stress typically fail to show enhanced tolerance when tested in the field (Gao et al., 2000; McKersie et al., 1999; Mohamed et al., 2001), likely because such selections are based on unrealistic assumptions about field stress conditions.

Plants can acquire tolerance to one stress after being exposed to another, a phenomenon known as cross hardening, which suggests that different abiotic stresses may have a synergistic effects and may co-activate stress response signal transduction pathways (Mittler, 2006). For example, drought stress enhances plant cold tolerance (Cloutier and Andrews, 1984) and toxic mineral stress improves plant heat tolerance (Bonham-Smith et al., 1987). The synergistic effects between different abiotic stresses may be controlled via calcium and ROS signaling (Bowler and Fluhr, 2000), mitogen-activated protein kinase (MAPK) cascades, stress responsive transcription factors and genes (Cardinale et al., 2002; Xiong, 2003), and stress hormones including abscisic acid (ABA), jasmonic acid (JA), and ethylene (ET) (Anderson, 2004). Both ethylene and the multiprotein bridging factor 1c (MBF1c) transcription factor were found to enhance *Arabidopsis* heat and osmotic stress tolerance (Suzuki, 2005). In addition, Rizhsky (2004) found that the transcripts expressed during a combination of drought and heat overlapped largely with individual drought and heat stress, suggesting that the combined stress of drought and heat may co-activate the same defense pathways for drought or heat stress individually.

In contrast, abiotic stresses may also have an antagonistic effect with each other when they are combined (Mittler, 2006). For instance, plants subjected to heat stress may open stomata to enhance transpiration in order to lower the temperature of leaves. However, when a plant is faced with a combination of heat and drought stress, the stomata would be closed and the leaves thus cannot be cooled (Rizhsky et al., 2002). Similarly, during heat and salinity stress combination, the effect of salinity stress may be aggravated because enhanced transpiration may result in enhanced uptake of salts (Keleş and Öncel, 2002; Wen et al., 2005). High light combined with cold or drought stress may limit CO_2 availability and increase O_2 production, which may in turn lead to ROS production (Mittler, 2002). In such cases, a plant's response to a combined stress may need to be adjusted or compensated account for the synergistic and antagonistic effects of the two individual stresses in order to seek an appropriately balanced response (Mittler, 2006).

Plant responses to a combination of stresses may exhibit quite unique defense and acclimation responses as compared to the response elicited by each individual stress. The effect of combined stress in such cases would not be just the sum or either of the two different stresses, but in contrast may be determined by a set of complex interactions between the two applied stresses (Pandey et al., 2017). A combination of heat and drought stress were found to have a distinct effect on both tobacco and *Arabidopsis* apart from their individual stress responses (Rizhsky et al., 2002; Rizhsky, 2004). The response to heat and drought combined stress has a large number of unique altered transcripts and features (Rizhsky, 2004). It is evident from such studies that it is quite important to explore the interactions that occur when combined stresses are applied. The need for such investigations was envisioned when a 'stress matrix' was developed by to demonstrate the potential interactions among different agriculturally important abiotic and biotic stresses on plant growth and production (Mittler, 2006; Suzuki et al., 2014). The matrix demonstrated that stress combinations could have both negative (enhanced damage) and positive (cross-protection) effects on plants. In comparison to abiotic and biotic stress interactions, unfortunately most of abiotic stress combinations in the 'stress matrix' were not well-studied (Mittler, 2006). It is thus important to determine if a combination of abiotic stresses represents a new state of stress, in some cases notably distinct from the two individual stresses that are compounded. It was therefore essential to further investigate, using untargeted metabolomics, preferential metabolic response pathways, and stress interactions in *Arabidopsis thaliana* in order to gain a greater mechanistic understanding of the adverse effects following a combination of stress challenges.

Results

Multivariate statistical comparisons using unsupervised principle components analysis (PCA) for clustering and supervised orthogonal projections to latent structures discriminant analysis (OPLS-DA) for potential stress signatures

We report on a comprehensive characterization of multiple stressor effects on the *Arabidopsis thaliana* metabolome that define the physiological variations under abiotic stresses including cold, heat, drought, salinity, and high light. The most statistically significant metabolic differences between stressed and control plants were identified using an untargeted metabolomics approach. Untargeted metabolomics is a pattern-based classification approach for as many metabolites as possible in the system using a global unbiased screening (De Vos et al., 2007). It is commonly used for discovery-based studies to characterize metabolic changes in disease, environmental or genetic perturbations (Patti et al., 2012). In this study, we executed a comprehensive analysis using both multivariate and univariate statistics. Multivariate statistics modeling PCA and OPLS-DA were performed for clustering and potential stress metabolic signature selection. The top ten metabolic features with highest and lowest OPLS-DA S-plot covariance value in different treatments compared to control and subgroups based on the clustering results of PCA were reported in **Supplemental Table 3-1**. Metabolic features increased or decreased more than 2 fold in different treatments compared to control were reported in **Supplemental Table 3-2**. The changes of precursors, intermediates, and products of those stress metabolic signatures in the same metabolic pathway were also monitored by both hierarchical clustering analysis (HCA) and ANOVA. Overall, we comprehensively examined the relationships between combined stress with its individual stresses, and identified stress metabolic signatures exhibiting shared or unique patterns across different single or combined stresses.

In this study, PCA was performed in a hierarchical manner to assess the extent of divergence between metabolites under different conditions (**Figure 3-1**). First, PCA of all the samples were performed (**Figure 3-1A**), which resulted in two large clusters A1 and A2. Combined stresses including heat x drought, high light x drought, and high light x heat cluster together in A2 and are separated from the other groups in A1 in PC2 (15%), thus indicating that these three combined stresses had the most dramatically different metabolic responses within these groups. Additional re-analysis of subgroup A2 in **Figure 3-1**C shows high light x heat in C2 is well separated from heat x drought and high light x drought in C1 in PC1 (50%). In addition, heat x drought is well separated from high light x drought in PC2 (20%). This indicated that all these three combined stresses result in distinctly different metabolic patterns. PCA of cluster A1 was re-analyzed for additional sub-cluster separation (**Figure 3-1B**). Three treatments including heat, heat x salinity, and high light x salinity in B2 were separated from all the other stresses in B1 in PC2 (15%). Additional re-analysis of B2 in **Figure 3-1E** shows high light x salinity in E2 is well separated from two other stresses in E1 in PC1 (48%), indicating that high light x salinity has dramatically different metabolic responses within this sub-cluster. PCA for sub-cluster B1 performed in **Figure 3-1D** shows that three stresses in D2 including drought, salinity, and cold x drought clustered together and were separated from all the other stresses in D1 in PC2 (15%). Further separation of sub-cluster D2 (**Figure 3-1G**) shows that drought is separated from the other two stresses in PC2 (21%); cold x drought is separated from salinity in PC1 (38%), indicating the different metabolic responses between these three treatments. Similarly, to better separate treatments in D1, we performed sub-cluster PCA in **Figure 3-1F**. High light and high light x cold cluster together in F2 and are separated from F1 in PC1 (23%), indicating the similar metabolic responses between these two stresses. Whereas control, cold, and cold x salinity cluster in F1, indicating cold and cold x salinity are less severe stresses that have a minor separation from control. Final re-analysis of sub-cluster F1 in **Figure 3-1H** shows that control is separated from stresses including cold and cold x salinity in PC2 (18%), indicating that all of the stress groups have metabolic changes compared to control. However, cold and cold x salinity are not well separated in both PC1 and PC2, indicating these two treatments cause similar metabolic responses in the plant.

Using the clustering hierarchy from the aforementioned PCA analyses, we then performed orthogonal projections to latent structures discriminant analysis (OPLS-DA) to identify which metabolic features were the most important drivers of differentiation. Compared to unsupervised PCA modeling, OPLS-DA are supervised techniques that request a response value to be assigned. In order to better interpret for complex datasets, Trygg et al., 2001 introduced the orthogonal projection to latent structures (OPLS) algorithm by incorporating an Orthogonal Signal Correction (OSC) filter into a Partial Least Squares Discriminant Analysis (PLS) model to separate the correlated (predictive) variation from uncorrelated (orthogonal) variation. In doing so, OPLS-DA helps identify correlated components in the presence of systematic variation (Thévenot et al., 2015). The clustering results from PCA was used to perform a corresponding hierarchical OPLS-DA for both score plot and s-plot of all the subgroups (**Supplemental Figure 3-1, Supplemental Figure 3-3**) and all the treatment compared with their corresponding control (**Supplemental Figure 3-2, Supplemental Figure 3-4**). The combination of both PCA and OPLS-DA produced novel information regarding general metabolic trends and stress metabolic signatures.

Hierarchical clustering analysis (HCA) for all the metabolic features revealed both dominant and unique metabolic changes for combined stresses with the corresponding individual stresses

All the metabolic features detected were used to represent the entire measured metabolome. The ratio changes for all the features in treatments compared to control (**Supplemental Table 3-4**) were used to perform HCA in order to elucidate the relationship between single and combined stresses. **Figure 3-2** shows a HCA heat map using the complete linkage with the Euclidean distance function. The clustering and distance functions were chosen based on De Souza et al. (2006) who tested three of the most popular clustering methods including single linkage, complete linkage and centroid methods in their metabolomics data, and found complete linkage and the centroid methods performed better than single linkage. They explained that both complete linkage and centroid methods have a tendency to create compact, spherical clusters, whereas single linkage has a tendency to make elongated clusters. In addition, Edelbrock (1979) reported that complete linkage was more accurate than single linkage when using Euclidean distance function.

In **Figure 3-2**, HCA elucidated five distinct clusters of the five single stress and eight combined stress treatments that we named A-E. Group A consisted of the single treatment, high light x heat. Group B consisted of treatments cold x drought, drought, heat x drought, and high light x drought. Group C also consisted of a single treatment, high light x salinity. Group D included treatments heat and heat x salinity. Group E contained treatments salinity, high light, high light x cold, cold, and cold x salinity. Other HCA clustering methods and distance functions were also tested including complete linkage using distance functions including Manhattan (**Supplemental Figure 3-5A**), Minkowski (**Supplemental Figure 3-5B**), Ward's methods using distance functions including Euclidean (**Supplemental Figure 3-5C**), Manhattan (**Supplemental Figure 3-5D**), Minkowski (**Supplemental Figure 3-5E**), McQuitty's methods using distance functions including Euclidean (**Supplemental Figure 3-5F**), Minkowski (**Supplemental Figure 3-5G**), and average linkage using distance functions including Euclidean (**Supplemental Figure 3-5H**), Manhattan (**Supplemental Figure 3-5I**), and Minkowski (**Supplemental Figure 3-5J**). All these HCA methods provided comparable clustering results, demonstrating the consistency of the techniques.

Table 3-2 summarizes which combined stresses are the result of both dominant and unique metabolomic changes when compared with each pair of single component stress conditions. We found only two combined stresses, including high light combined with cold and cold combined with salinity, cluster together with both of their corresponding single stresses. This suggested that for these two combined stresses, both corresponding single stresses are important aspects of the response. Each single stress may have synergistic effect and may co-activate the same stress responses pathway. In that case, the metabolic changes of these two combined stresses are the results of a combined response to the two corresponding single stresses. **Figure 3-3** illustrates Venn diagrams scaled to the numbers of features that are increased or decreased more than 2 fold for each combined and set of corresponding single stresses. Interestingly, cold stress always separate and has no overlap between both its combined stresses and other stresses. This result indicated that cold stress may be the subordinate stress for its combined stresses and may has smaller and distinct impact on plant combined stress responses. When plant is subjected to cold stress combined with other stresses like drought, salinity, and high light, plant may take priority to other stresses and make corresponding metabolic changes.

Most combined stresses cluster together with only one of its individual stresses components but not to the other, indicating that the metabolic profile of combined stress is more similar to one of its individual stresses. This suggested that the single stress is the dominant stress of the combined stresses, and in those cases may have a bigger impact on plant stress responses. This result indicates that when subjected to the combined stresses, the plant's major metabolic responses are to the dominant stress, and that plants may only make minor adjustments to accommodate the non-dominant stress. Interestingly, drought stress is the dominant stress for all of its combined stresses including cold x drought, heat x drought, and high light x drought. This result indicated that water deficit is a more dominant stressor than temperature extremes and high light intensity. When a plant encounters drought coupled with other abiotic stresses, the plant may need to take drought stress as its priority response to defend first, and then it may make adjustment or compensation to other stresses based on its response to drought stress. It has previously been shown that drought stress was accompanied by closed stomata, heat stress was accompanied by opened stomata, whereas drought and heat combined stress accompanied by closed stroma, which is the same as drought stress (Rizhsky, 2004). This physiological characterization may provide one of the possible explanations that why drought stress is always the dominant stress for its combined stress.

One possibility for the noted dominant role of drought stress is that the severity of drought stress may be higher than that of the other stresses tested in our experiments. To test this idea, we determined the numbers of metabolic features decreased or increased more than 2 fold in all treatments compared to control to use as a gauge of over-all metabolic impact of each stress condition/combination (reported in **Table 3-3** and **Supplemental Table 3-2)**. Using this metric drought stress, despite its dominance, actually induced the smallest number of changes compared to other stresses. A total of 54 metabolic features were increased or decreased more than 2 fold in drought stress treatment. In comparison, the number of metabolic features increased or decreased more than 2 fold in cold, heat, salinity, and high light are 98, 101, 57, and 63, respectively. The Van Krevelen diagrams for scatter plot and heat map showed chemical composition changes for all metabolic features in all groups (**Supplemental Figure 3-9, Supplemental Figure 3-10**), and the features changed more than 2 fold in all treatments compared to control (**Supplemental Figure 3-11, Supplemental Figure 3-12**). However, no obvious differences were found for chemical composition of both all the features and features that changed more than 2 fold between drought and other single stresses. Therefore, the dominant role of drought stress is not mainly caused by its higher severity compared to other stresses.

In addition to those combined stresses with both or dominant effects from two single stress responses, we also noticed that two combined stresses, high light x heat and high light x salinity, showed unique metabolic responses. The metabolic profiles of these two combined stresses are not similar to any of their corresponding single stresses, suggesting that the combined stresses may influence plant metabolism in a new response pattern that is distinct from changes caused by each of single stress applied individually. In addition, these two combined stresses are in the two most positive loadings of the top 2 principal components in PCA score plots. In **Figure 3-1A**, high light x heat is in the most positive loading of PC1. Whereas high light x salinity is in the most positive loading of PC2. This result confirmed that these two treatments have unique metabolic profiles compared to other treatments. It is likely that the two single stresses have antagonistic effects with each other so that the plant may need a new defense or acclimation strategy to adjust or compensate for the antagonistic effect. Therefore, high light x heat and high light x salinity should be considered as two novel abiotic stress combinations.

Moreover, high light x heat and high light x salinity induced top 2 maximum number of metabolic features that either increased or decreased more than 2 fold (**Table 3-3**) compared to control as 244 and 179 respectively. The metabolic composition changes for those features reported by the Van Krevelen diagrams for scatter plot and heat map (**Supplemental Figure 3-11, Supplemental Figure 3-12**) also showed most obvious difference compared to all the other treatments. **Figure 3-3** shows Venn diagrams scaled to the numbers of features increased or decreased more than 2 fold for each combined and set of corresponding single stresses. Very limited similarity was found between these two unique combined stresses with their individual stresses and most of changed features are combined stress specific. For high light x heat-combined stress, a total of 103 metabolic features increased and 141 decreased more than 2 fold. However, 47 features specifically increased and 118 specifically decreased in high light x heat. A similar situation was observed with high light and salinity combined stress. Out of 60 metabolic features increased and 119 decreased more than 2 fold, 35 of the increasing and 97 of the decreasing metabolites are high light x salinity-specific. Therefore, plants subjected to these two combined stresses have specific and more severe metabolic changes that are different from that of plant subjected to individual stresses. Some of those combined stress specific changed metabolites were identified using reference standard. For high light x salinity-combined stress, fructose 6-phosphate, sucrose, tyrosine, and urea are identified metabolites that uniquely increased in the combined stress. While adenine, alpha-ketoglutaric acid, arginine, GABA, glucose 6-phosphate, guanosine monophosphate, lysine, maltose, ornithine, proline, ribose 5-phosphate, and xylose are identified metabolites that specifically decreased in the combined stress. For high light x heat-combined stress, adenine, adenosine, GABA, guanine, pyruvic acid, and sucrose are identified metabolites specifically increased in the combined stress. Whereas alpha-ketoglutaric acid, citric acid, glucose 6-phosphate, GSH, GSSG, and ribose 5-phosphate are identified metabolites particularly decreased in the combined stress. It is noteworthy to mention that GSH decreased more than 1076 fold in high light x heat, which may tremendously contributed to the uniqueness of this combined stress.

Targeted metabolite analysis and hierarchical clustering revealed similar stress clustering patterns with untargeted analysis

Metabolites that were identified as having significant abundance changes in one or more stress conditions as well as precursors, intermediates, and products in the same metabolic pathways were selected for further targeted analysis in order to provide a better representation of the central metabolic stress response. To do this, putative identities of the selected metabolites were confirmed by: 1) comparison of chromatographic retention by co-injection; and 2) by comparison of MS/MS fragmentation patterns (**Supplemental Figures 5.1, Supplemental Figure 3-7, Supplemental Figure 3-8)** with standard compounds (**Supplemental Table 3-6**). After metabolite identities were confirmed, their corresponding LC-HRMS peak areas from the polarity with highest intensity were integrated and the average fold change of relative abundances across replicates between stress and control samples were calculated (**Supplemental Table 3-5**). These confirmed metabolite abundance fold-change values and treatments were then clustered by HCA to determine metabolites with shared response across multiple stresses and metabolites with unique and dramatic responses.

Figure 3-4 shows a HCA heat map using complete linkage with Euclidean distance function. The treatment clustering results of **Figure 3-4** are compared with **Figure 3-2**. Three groups in **Figure 3-4** are identical with group A, C, D in **Figure 3-2**, so we named them as group A', C', D'. Group D' included heat and heat x salinity. Group A' and group C' both consisted by one single treatment; high light x heat for Group A', and high light x salinity for group C'. This consistent clustering results indicated that the targeted identified stress signatures may contribute to the unique metabolic patterns of high light x heat and high light x salinity. However, one treatment cold x drought that was in group B in **Figure 3-2** split from group B’ and merge into group E’(B’’) in **Figure 3-4**. Group B’ consisted of treatments drought, heat x drought, and high light x drought. Group E’ (B’’) contained treatments cold x drought, salinity, high light, high light x cold, cold, and cold x salinity. The similar treatment clustering results between **Figure 3-2** and **Figure 3-4** confirmed that these identified targeted compounds are important stress signatures that may determine the metabolic stress responses patterns between different treatments. We also tested complete linkage using distance functions including Manhattan (**Supplemental Figure 3-6A**), Maximum (**Supplemental Figure 3-6B**), Ward’s methods using distance functions including Euclidean (**Supplemental Figure 3-6C**), Manhattan (**Supplemental Figure 3-6D**), Maximum (**Supplemental Figure 3-6E**), McQuitty's methods using distance functions including Euclidean (**Supplemental Figure 3-6F**), Manhattan (**Supplemental Figure 3-6G**), and average linkage using distance functions including Euclidean (**Supplemental Figure 3-6H**) and Manhattan (**Supplemental Figure 3-6I**), and got comparable clustering results.

Discussion

Primary metabolites play important roles during stress response

Primary metabolites have important functions, in addition to core metabolism, as signal molecules, osmolytes, antioxidant, and precursors of secondary metabolites during plant stress responses. Previous studies showed that many soluble sugars such as glucose, fructose, and sucrose have roles in plant stress signaling (Chiou and Bush, 1998; Koch, 1996; Roitsch, 1999). Osmolytes or compatible solutes can stabilize proteins and membranes and function to maintain cellular turgor pressure. Major osmolytes include amino acids and derivatives, sugars and derivatives, phosphodiesters, quaternary ammonium compounds, and polyols (Yancey et al., 1982; Shahjee et al., 2002). Antioxidants play important roles to regulate protein redox and to prevent cellular component damage caused by reactive oxygen species (ROS) (Alscher, 1989). Glutathione (GSH), carbohydrates like raffinose (Nishizawa et al., 2008), and sugar alcohols such as mannitol (Chiang et al., 2005) have been reported to act as plant antioxidants. Moreover, primary metabolites are known to be precursors for many secondary metabolites that function as defense compounds against biotic stresses (Kaplan et al., 2004). For example, aromatic amino acids are precursors of indole glucosinolates, phytoalexins, alkaloids, lignins, flavonoids, isoflavonoids, and hydroxycinnamic acids (Dixon, 2001) and branched-chain amino acids are precursors of cyanogenic glycosides, glucosinolates, and acyl-sugars (Vetter, 2000).

Shared stress metabolic signatures

We found many metabolites had similar responses to different stresses. These metabolites may function as shared stress metabolic signatures with common participation and general response patterns in different stresses. **Figure 3-4** and **Figure 3-5** showed metabolites in cluster 1, 2, 3, 4 and 5 are shared stress metabolites that exhibited similar response patterns across different single and combined stresses. Cluster 1 contained four metabolites in purine metabolism (adenine, adenosine, guanine, and GMP). The significant increase of these purine metabolites in high light x heat may be related to high light induced DNA oxidative damage, which is consistent with the significant decrease of GSH in high light x heat.

Cluster 2 was consisted of seven metabolites including aromatic amino acids (phenylalanine, tryptophan, and tyrosine), sugar alcohol (mannitol), sugar metabolism (raffinose), pyruvate family of amino acids (alanine, leucine). Aromatic amino acids (tryptophan, tyrosine, and phenylalanine) are known to be precursors of pigments, alkaloids, hormones, and cell wall components (Dixon, 2001). While branched-chain amino acids (isoleucine, leucine, and valine) are precursors of the cyanogenic glycosides (Vetter, 2000). All three aromatic amino acids and leucine were increased in all treatments except salinity stress, possibly because they serve as precursors for secondary metabolites that may accumulate during stress responses. Both raffinose (Nishizawa et al., 2008) and mannitol (Chiang et al., 2005) have been reported to have compatible solutes properties and function as antioxidants.

Cluster 3 enclosed fifteen metabolites in the aspartate family of amino acids (aspartic acid and asparagine), the glutamate family of amino acids (glutamate, glutamine), glycolysis (glucose 6− phosphate), TCA cycle (citric acid and α−ketoglutaric acid.), glutathione metabolism (GSSG), purine metabolism (ribose 5-phosphate), urea cycle (arginine, citrulline, and ornithine), and serine family of amino acids (serine). Inorganic nitrogen can be incorporated into glutamine and glutamate as a nitrogen source to be converted into other amino acids or nitrogenous compounds. Primary nitrogen assimilation and transport amino acids glutamate, glutamine, asparagine, and aspartic acid are all in cluster 3. They may play important roles in nitrogen balance during plant abiotic stress responses. The increase of GSSG in heat x drought, high light x drought, cold x drought, drought, heat x salinity, heat, cold, high light x cold, and cold x salinity may relate to plant oxidative stress defenses. During oxidative stress, reduced glutathione GSH can be oxidized to GSSG to detoxify ROS (Foyer et al., 1997).

Cluster 4 was composed by six metabolites in sugar metabolism (glucose, fructose), glycolysis (DHAP and pyruvate), TCA cycle (malic acid), and urea cycle (urea). Sugars, including glucose and fructose, are known as both stress signal molecules and osmoprotectants (Koch, 1996; Roitsch, 1999; Rizhsky, 2004). Sugar is, most centrally, an important energy source. To provide energy, sugars will, of course, be consumed by glycolysis and through the TCA cycle yielding ATP and reducing power. Plant cells may need incoming sugars to cover the growing demand for energy for both anabolism and catabolism during certain stress events.

Cluster 5 contained eleven metabolites in the TCA cycle (succinic acid and fumaric acid), GABA shunt (γ−aminobutyric acid), glutamate family of amino acids (proline and histidine), sugar metabolism (sucrose), glycolysis (fructose 6-phosphate), pyruvate family of amino acids (valine), oxaloacetate family of amino acids (lysine, threonine), and glutathione metabolism (glycine). We found the non-proteinogenic amino acid GABA clustered together with TCA cycle intermediates succinate and fumarate. The TCA cycle generates energy with reducing power, and is responsible for the most part of carbohydrate, amino acid, and fatty acid precursors (Fernie et al., 2004). GABA is known to drive the TCA cycle via GABA shunt (Caldana et al., 2011). During GABA shunt, succinate can be synthesized from GABA via succinic semialdehyde. Previous studies showed that GABA increased during heat and cold stresses (Kinnersley and Turano, 2000). The GABA shunt was also reported to coordinate with general nitrogen and carbon metabolism (Weigelt et al., 2008). The increase of both TCA cycle intermediates and GABA in high light x heat,

heat, heat x salinity, heat x drought, drought, and high light x drought, indicates that GABA may fuel central metabolism via the TCA cycle for increased energy demand during stress. Proline in cluster 5 increased in heat, drought, high light, heat x drought, high light x drought, heat x salinity, high light x heat, high light x cold. Proline is synthesized from glutamate by the enzyme P5CS (1-pyrroline-5-carboxylate synthase) that contributes to osmotic adjustment, free radical scavenging, and subcellular structure stabilization (Hare and Cress, 1997). Previous studies showed that proline concentrations increased in drought, salinity, and extreme temperatures (Kaplan et al., 2004, 2007; Sanchez et al., 2008). Sucrose functions as both a plant stress signal molecule and an osmotic regulator (Kaplan et al., 2004; Rizhsky, 2004). The increase of sucrose may suggest its involvement in stress signaling or as an osmotic stress defense response.

Unique stress metabolic signatures GSH and maltose

Two clusters each containing one single metabolite in HCA **(Figure 3-2)** attracted our attention: cluster 6 with GSH only and cluster 7 with maltose only. The separation of these two metabolites from all the other clusters was consistent using different clustering and distance functions including complete linkage using distance functions including Manhattan (**Supplemental Figure 3-6A**), Maximum (**Supplemental Figure 3-6B**), Ward's methods using distance functions including Euclidean (**Supplemental Figure 3-6C**), Manhattan (**Supplemental Figure 3-6D**), Maximum (**Supplemental Figure 3-6E**), Mcquitty's methods using distance functions including Euclidean (**Supplemental Figure 3-6F**), Manhattan (**Supplemental Figure 3-6G**), and average linkage using distance functions including Euclidean (**Supplemental Figure 3-6H**) and Manhattan (**Supplemental Figure 3-6I**). GSH and maltose were always isolated in separate clusters. The unique clustering pattern for these two metabolites may be caused by their unique and dramatic changing trend shown in **Figure 3-5**. We found GSH decreased in drought, salinity, heat x drought, and dramatically decreased in high light x heat up to 1076 fold, which may contribute to the unique stress response patter of high light x heat.. GSH, of course, is a critical compound in all aspects of glutathione metabolism. During oxidative stress, GSH may be quickly consumed by oxidation to GSSG in order to detoxify the reactive oxygen species (ROS). This may account for the measured large decrease of GSH in the stress groups. On the other hand, maltose increased dramatically in heat x drought, high light x cold, cold x drought and dramatically increased in cold x salinity up to 37 fold. Maltose is the direct product of starch degradation and it showed different responses from other sugars, indicating the potential differences between catabolism and anabolism during plant stress responses. In summary, GSH and maltose may function as unique stress metabolic signatures that highlight special roles in both single and combined stress responses.

GSH and GSSG in glutathione metabolism

Glutathione (GSH) is a main low molecular mass plant non-protein thiol compound that is important for regulation of the redox state of the cells (Alscher, 1989). It also functions as an antioxidant in plant defense systems. The biosynthesis of glutathione consists of two enzymatic reactions (Strohm et al., 1995). First, glutamic acid and cysteine form γ-glutamylcysteine. Second, γ-glutamylcysteine and glycine form GSH. Under stress conditions, GSH functions as an antioxidant for reactive oxygen species (ROS) via the ascorbate-glutathione cycle to form the glutathione disulfide (GSSG), resulting in the increase for the GSSG and GSSG/GSH ratio (Foyer et al., 1997). Along with its function as an antioxidant, GSH also performs other roles such as thiol disulfide exchange, detoxification, and cell signaling. Thus, alteration of GSH concentration may function together with the changes in amino acids such as glutamate and glutamine, which are GSH-dependent through the γ-glutamyl cycle. Glutathione S-transferases (GSTs) can function in processes to detoxify xenobiotics (Marrs, 1996) through forming phytochelatins that are important for heavy metal detoxification (Chen and Goldsbrough, 1994), and can also activate genes for acclimation, stress tolerance, and pathogen defense response (Wingate et al., 1988).

Glutathione has previously been reported to play important roles for plant abiotic stress defense responses including chilling and cold (Foster and Hess, 1980), heat (Nieto-Sotelo et al., 1999), drought (Gamble and Burke, 1984), salt (Roxas et al., 1997), high light (Cakmak and Marschner, 1992), and UV irradiation (Strid et al., 1994). In this study, the ratio changes of metabolites in glutathione metabolism including glycine, glutamate, reduced glutathione (GSH), and oxidized glutathione (GSSG) were reported in **Figure 3-**

5, **Figure 3-6**, **and Supplemental Table 3-5**. Among them, GSH showed unique response pattern that decreased in cold x drought, cold x salinity, drought, salinity, heat, drought, high light x salinity, especially in high light x heat, with ratio change of 9.29 x 10^{-4}, more than a 1076 fold decrease compared to control. The decrease of GSH may be caused by the high demand of GSH for its function as an antioxidant to detoxify ROS during oxidative stress defense and repair responses.

Maltose from starch degradation

Maltose is the direct product from starch breakdown by α-amylase. The ratio changes of maltose and other sugars including glucose, fructose, xylose, mannitol, and raffinose were shown in **Figure 3-5**, **Figure 6**, **and Supplemental Table 3-5**. In our study, maltose showed unique stress response pattern that was elevated in cold x drought, heat x drought, high light x cold, and especially in cold x salinity up to 37 fold, but decreased in high light x drought and high light x salinity. The increase of maltose may be caused by starch degradation or as a potential osmoregulator. Previous work showed that the activity and transcription of α-amylase can be induced during temperature stress (Dreier et al., 1995). Kaplan and Guy (2005) reported maltose accumulated in *Arabidopsis* by starch degradation under cold shock potentially to protect the photosynthetic electron transport chain and proteins in the chloroplast stroma. Rizhsky (2004) reported that both maltose abundance and the expression of starch degradation transcripts were elevated in response to drought and heat combination stress. Maltose is also reported to function as compatible solute and contributed to the protection of plants from freezing stress (Kaplan et al., 2004). It was suggested that with moderate levels of drought stress plant’s respond with elevated proline and glycine-betaine, whereas with more severe levels of drought stress these changes occur together with sugar accumulation (Hoekstra et al., 2001). In our study, proline increased in heat, drought, high light, heat x drought, high light x drought, heat x salinity, high light x heat, high light x cold up to 2.6 fold. Whereas maltose increased in cold, heat, salinity, cold x drought, heat x drought, cold x salinity, high light x heat, high light x cold up to 37 fold. Maltose is also involved in the production of glucose and sucrose from starch (Lu and Sharkey, 2004). However, in our study, the increase in maltose did not result in a measured increase for glucose and sucrose, indicating the accumulation of maltose may occur in the plastids, spatially isolated from cytosolic primary sugar metabolism.

Measurements of precursors, intermediates, and products of important metabolic pathways in central metabolism

We monitored metabolic pathways from precursors and intermediates to products simultaneously in order to reveal the subtle interplay of functionally related metabolites. A clear example of substrate and product relationship and important transitions in primary metabolism that regulate single and combined stresses can be observed in **Figure 6**. The relationships between combined stresses with their individual stresses were also illustrated. The biosynthesis rate of products is, of course, largely dependent on the availability of primary precursors and intermediates. However, the possible explanations for the metabolite abundance changes is often complicated, and may need to be integrated with metabolic flux information in future studies to give a better picture of the processes measured. Metabolic flux is the flow of the carbon of a metabolite through an organism’s metabolic pathways (Roscher et al., 2000) as determined by the rate of biosynthesis and degradation (Pratt et al., 2002). Some metabolites may be very active and have a high flux rate to channel large quantities of metabolites through them or play roles as intermediates that are never released by the enzyme complex, whereas some metabolites may be the end products that accumulate to high levels yet have very low flux rates (Yang et al., 2010).In our study, we saw the phenomenon that fit for the hypothesis that intermediate abundances decreased or had no change caused by the high flux rate, but product abundance increase caused by the low flux rate. For instance, shikimic acid decreased or no change in heat, salinity, and high light x heat, however the three aromatic amino acids derived from it increased dramatically in these three treatments. Similar situation was found in pyruvate with its products pyruvate family amino acids leucine, valine, and alanine. Therefore, it will be important to incorporate full metabolic flux analysis into future studies to better explain the increase or decrease of those metabolites’ abundance.

Plants are more often to encounter in nature a combination of different abiotic stresses rather than a specific single stress condition. However, the simultaneous occurrence of multiple stress events is rarely studied experimentally, especially by metabolomics methods, where the results provide a direct indication of the biochemical adaptations of a stress-responding plant. Our results showed that only two combined stresses including high light x cold and cold x salinity had metabolic effects from both of their individual stresses. Most of the combined stresses exhibited one dominant stress response. Among them, drought stress is the dominant stress for all combined stresses. The dominant effect is not caused by the more severe experimental conditions tested in our study, indicating that water deficiency may either be a more important stress responded to by plant or, alternatively, the one stress that metabolic intervention can partially alleviate. The metabolic response of plants to combined stresses of high light and heat, and high light and salinity are unique and result in more severe metabolic changes that cannot be simply explained by linear combinations of the corresponding single stress responses. Most of metabolic features are specifically changed in these two combined stresses which should be considered as novel stress conditions. Many identified stress signatures contributed to the differences between stress and control showed shared patterns across different abiotic treatments. However, maltose and GSH showed unique stress response patterns. Our study indicated that it is imperative to study plant combination stress tolerance that mimics the field environment that may potentially contribute to future research designed to enhance crop plant tolerance to field abiotic stress conditions.

Materials and Methods

Plant materials, growth conditions, and treatments

Arabidopsis thaliana wild-type (Col-0) seeds were obtained from Lehle Seeds and were sterilized with 30% (v/v) bleach containing 0.1% (v/v) Triton X-100 and vernalized at 4 °C for 2 days. Seedlings were germinated on 1/2 x MS media made from MS Salts (PhytoTechnology Laboratories, M524 Murashige & Skoog (MS) Basal Salt Mixture, 4.33 g/L for 1 x MS) with 1.5% agar. Plants were grown prior to stress, during recovery, and as unstressed controls, vertically, at 22°C under a 16-h-light/8-h-dark photoperiod, with ~80 μmol m^{-2} s^{-1} illumination from cool-white fluorescent tube lights (control conditions). Eleven-day-old seedlings were treated with single and combination stress conditions described in **Table 3-1**. Whole seedlings were harvested, frozen in liquid nitrogen, and stored at -80°C. Experiments were performed using three biological replicates.

Sample extraction and LC-HRMS analysis

Seedlings were lyophilized, weighed, and extracted in 70% isopropanol alcohol with one 2.5 mm tungsten carbide ball in a Geno/Grinder™ (OPS Diagnostics) for 7 minutes at an intensity of 10,956 *x g* on -20°C chilled blocks to make a final concentration of 10 mg/ml (dry weight). After centrifugation for 10 minutes at 100,956 *x g*, 1 µL of supernatant was injected onto a UHPLC (Ultimate 3000, Dionex) with a ZIC-cHILIC column (100 mm ×2.1 mm, 3 µm particle size, EMD Millipore Corporation, Billerica, MA). Solvents A (0.1% (v/v) formic acid in water) and B (0.1% (v/v) formic acid in acetonitrile) were used as mobile phases for gradient separation. Extract corresponding to 100 µg of plant material (fresh weight) was loaded onto the column with at a flow rate of 0.4 mL/min, followed by the following gradient separation: 1 min from 98% B, 17 min to 65% B and maintained for 2 min, then 95% B and maintained for 1.5 min. The column was equilibrated for 1 min with 98% B prior to the next run. The samples were analyzed using a hybrid quadrupole Orbitrap mass spectrometer (Q Exactive, Thermo Fisher Scientific, San Jose CA). Full scan MS (range 50−750 *m/z*) were acquired with 35 k resolution for both positive and negative mode in polarity switching. The target value based on predictive automatic gain control was 1.0×10^6 with 200 ms of maximum injection time. The flow rate for sheath gas, aux gas, and sweep gas was 50, 20, and 1 separately. The capillary temperature was 350 °C. The S-lens RF was set to 55. The Aux gas heater temperature was 300 °C. Targeted MS/MS acquisition was used during metabolite identification with an inclusion list of ions of interest. Briefly, the precursor ions were sequentially fragmented in the HCD collision cell with normalized collision energy of 10%, 20%, 40%. MS/MS scans were acquired with 17.5 k resolution and the target value was 2.0×10^5 with 100 ms of maximum injection time. An isolation width of 2.0 *m/z* was used for precursor ion selection in MS/MS mode.

Data analysis

Thermo RAW files were converted to *mzXML* format using *MSConvert* (Chambers et al., 2012). Preprocessing including peak detection, grouping, and retention time correction and statistics analysis including multivariate modeling PCA, OPLS-DA and hierarchical clustering analysis were performed in Workflow4Metabolomics.org online resource for computational metabolomics (Giacomoni et al., 2015). Annotation was first performed from databases including *BMRB* (Markley et al., 2008), *METLIN* (Smith et al., 2005), and *HMDB* (Wishart et al., 2013) public databases, and identities were confirmed with authentic standards for accurate mass measurement, retention time, and fragmentation data listed in **Supplemental Table 3-6**. Univariate testing ANOVA was performed using both Workflow4Metabolomics.org online resource (Giacomoni et al., 2015) and Excel 2016 (Microsoft). Metabolic pathways were generated by reference to the *KEGG* pathway Database (Kanehisa et al., 2017). S-plots of OPLS-DA were generated to select variables with both high covariance and correlation values as metabolic signature candidates (Wiklund et al., 2008). To generate these S-plots the covariance was plotted on the x-axis whereas the correlation profile is plotted on the y-axis; the most positive and negative loadings in covariance and correlation represent variables with both high magnitude and high reliability. The S-plots for all the subgroups (**Supplemental Figure 3-3**) and all the treatments with their corresponding controls (**Supplemental Figure 3-4**) are included in the Supplemental Materials. The top 10 most positive and negative loadings in S-plot in different groups were reported in **Supplemental Table 3-1**. Metabolic features that increased or decreased more than 2 fold in each treatment compared to control were reported in **Supplemental Table 3-2**. Metabolites as potential stress signatures and their corresponding precursors, intermediates, or products in the same metabolic pathway that were identified by authentic standards with *m/z*, retention time, and fragmentation were reported in **Figure 6**, **Supplemental Table 3-3, Supplemental Table 3-5**.

Tables

Table 3-1. Single and combined stress conditions

Stress treatment	Conditions	Time	Period	Reference[1]
cold	4 °C	9:00 AM	2 h	Kaplan et al., 2004
heat	45 °C	9:00 AM	2 h	Larkindale, 2005
drought	move seedlings grown on nylon membrane from medium to desiccate in air	9:00 AM	2 h	Li et al., 2008
high light	562 µmol m^{-2} s^{-1} cool white fluorescent light	9:00 AM	2 h	Rossel et al., 2002
salinity	remove seedlings grown on nylon membrane to 200 mM NaCl plate	9:00 AM	2 h	Seki et al., 2002
heat x high light	45 °C + 565 µmol m^{-2} s^{-1} cool white fluorescent light	9:00 AM	2 h	
heat x salinity	45 °C + move seedlings to 200 mM NaCl plate	9:00 AM	2 h	
heat x drought	45 °C + move seedlings to desiccate	9:00 AM	2 h	
cold x high light	4 °C + 338 µmol m^{-2} s^{-1}	9:00 AM	2 h	
cold x salinity	4 °C + move seedlings to 200 mM NaCl plate	9:00 AM	2 h	
cold x drought	4 °C + move seedlings to desiccate	9:00 AM	2 h	
high light x salinity	562 µmol m^{-2} s^{-1} + move seedlings to 200 mM NaCl plate	9:00 AM	2 h	
high light x drought	562 µmol m^{-2} s^{-1} + move seedlings to desiccate	9:00 AM	2 h	

[1] Source from which stress conditions, with minor modifications, were derived. Plants were grown on a 16 hr light/8 hr dark photoperiod with lights on at 8:00 AM.

Table 3-2. Relationships between combined stress and each single stresses

Combined stresses	Relationship to Single Stress Responses
cold x salinity	both contribute
high light x cold	both contribute
heat x salinity	heat dominant
drought x heat	drought dominant
drought x cold	drought dominant
drought x high light	drought dominant
high light x heat	Unique
high light x salinity	Unique

Table 3-3. Numbers of metabolic features increased or decreased more than 2 fold compared to control

Treatment	Increase	Decrease	Total
Cold	20	78	98
Drought	34	20	54
Heat	79	22	101
High light	41	16	57
Salinity	24	39	63
Cold x Drought	24	8	32
Cold x Salinity	26	5	31
Heat x Drought	77	29	106
Heat x Salinity	91	17	108
High light x Cold	33	15	48
High light x Drought	56	36	92
High light x Heat	103	141	244
High light x Salinity	60	119	179

Figures

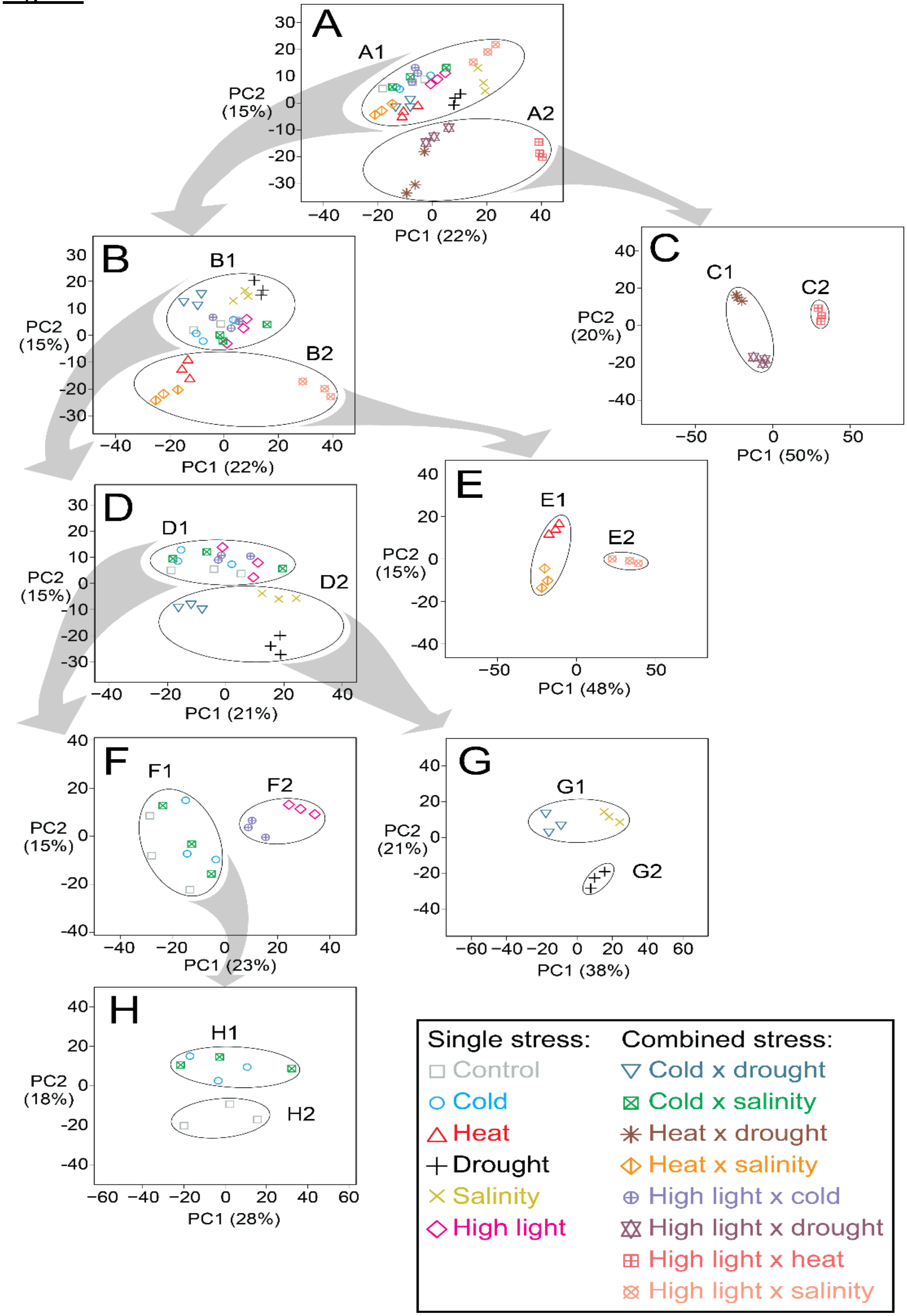

A
A1
A2
PC2 (15%)
PC1 (22%)
30
20
10
0
-10
-20
-30
−40
−20
0
20
40
B
B1
B2
PC2 (15%)
PC1 (22%)
C
C1
C2
PC2 (20%)
PC1 (50%)
40
20
0
-20
-40
−50
0
50
D
D1
D2
PC2 (15%)
PC1 (21%)
E
E1
E2
PC2 (15%)
PC1 (48%)
F
F1
F2
PC2 (15%)
PC1 (23%)
G
G1
G2
PC2 (21%)
PC1 (38%)
−60 −40 −20 0 20 40 60
H
H1
H2
PC2 (18%)
PC1 (28%)
−60 −40 −20 0 20 40 60
Single stress:
□ Control
○ Cold
△ Heat
+ Drought
× Salinity
◇ High light
Combined stress:
▽ Cold x drought
⊠ Cold x salinity
✳ Heat x drought
⟡ Heat x salinity
⊕ High light x cold
✡ High light x drought
⊞ High light x heat
⊠ High light x salinity

Figure 3-1. PCA score plots of treatments in subgroups with hierarchical manner for clustering identification.

In the score plot, the names and colors corresponded to different treatments. Letters and circles indicated subgroups (A) All groups. (B) control, cold, heat, drought, salinity, high light, cold x drought, cold x salinity, heat x salinity, high light x cold, high light x salinity. (C) heat x drought, high light x drought, high light x heat. (D) control, cold, drought, salinity, high light, cold x drought, cold x salinity, high light x cold, high light x salinity. (E) heat, heat x salinity, high light x salinity. (F) control, cold, high light, cold x salinity, high light x cold, high light x salinity. (G) drought, salinity, cold x drought. (H) control, cold, cold x salinity.

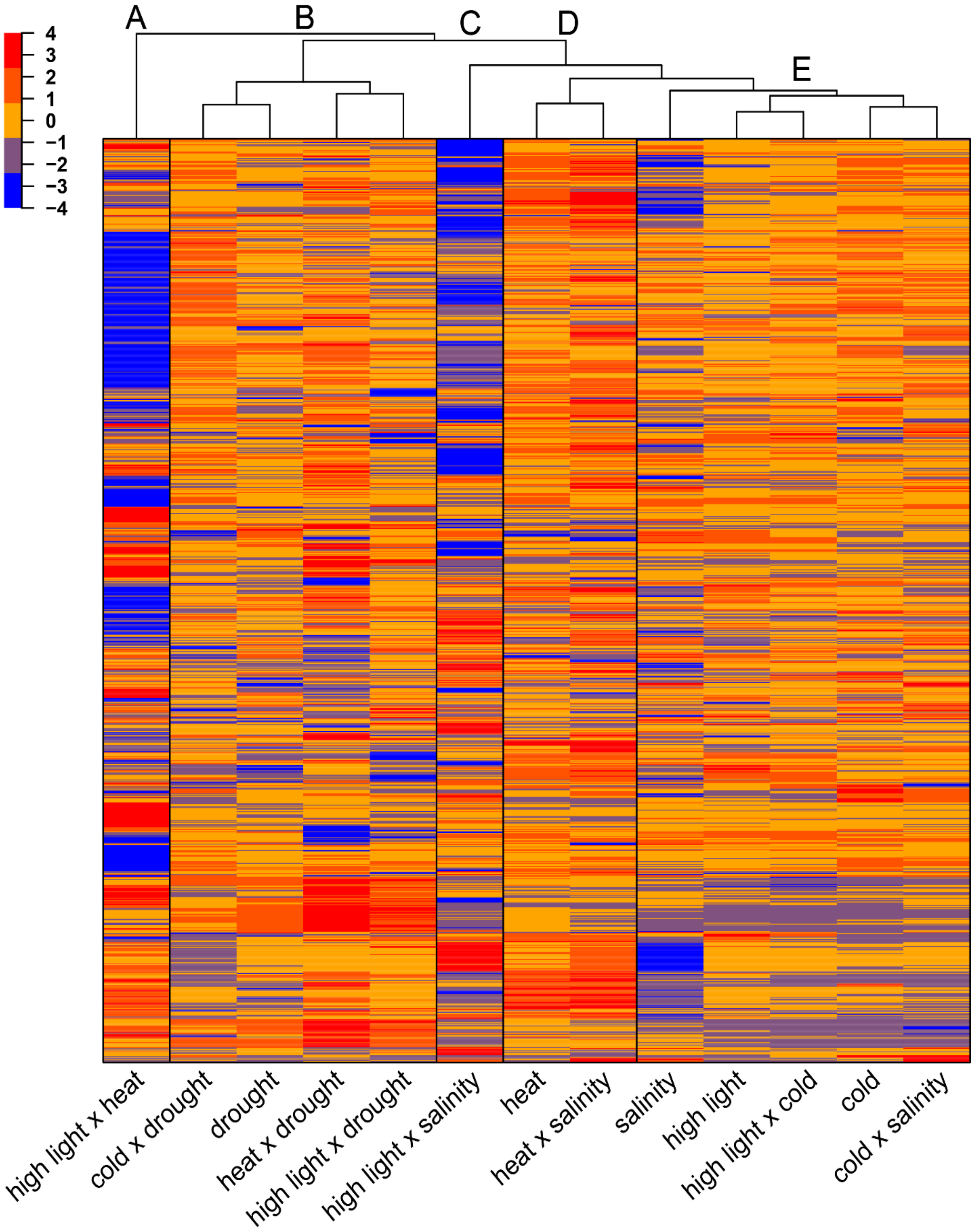


Figure 3-2. Hierarchical clustering analysis (HCA) for all the metabolic features. The top horizontal side bar reflects the $\log_2$-transformed fold changes of metabolic features in different treatments compared to control as reported in **Supplemental Table 3-4**. Clusters were generated using the complete linkage and Euclidean distance function. Five clusters of treatments were labeled A-E.

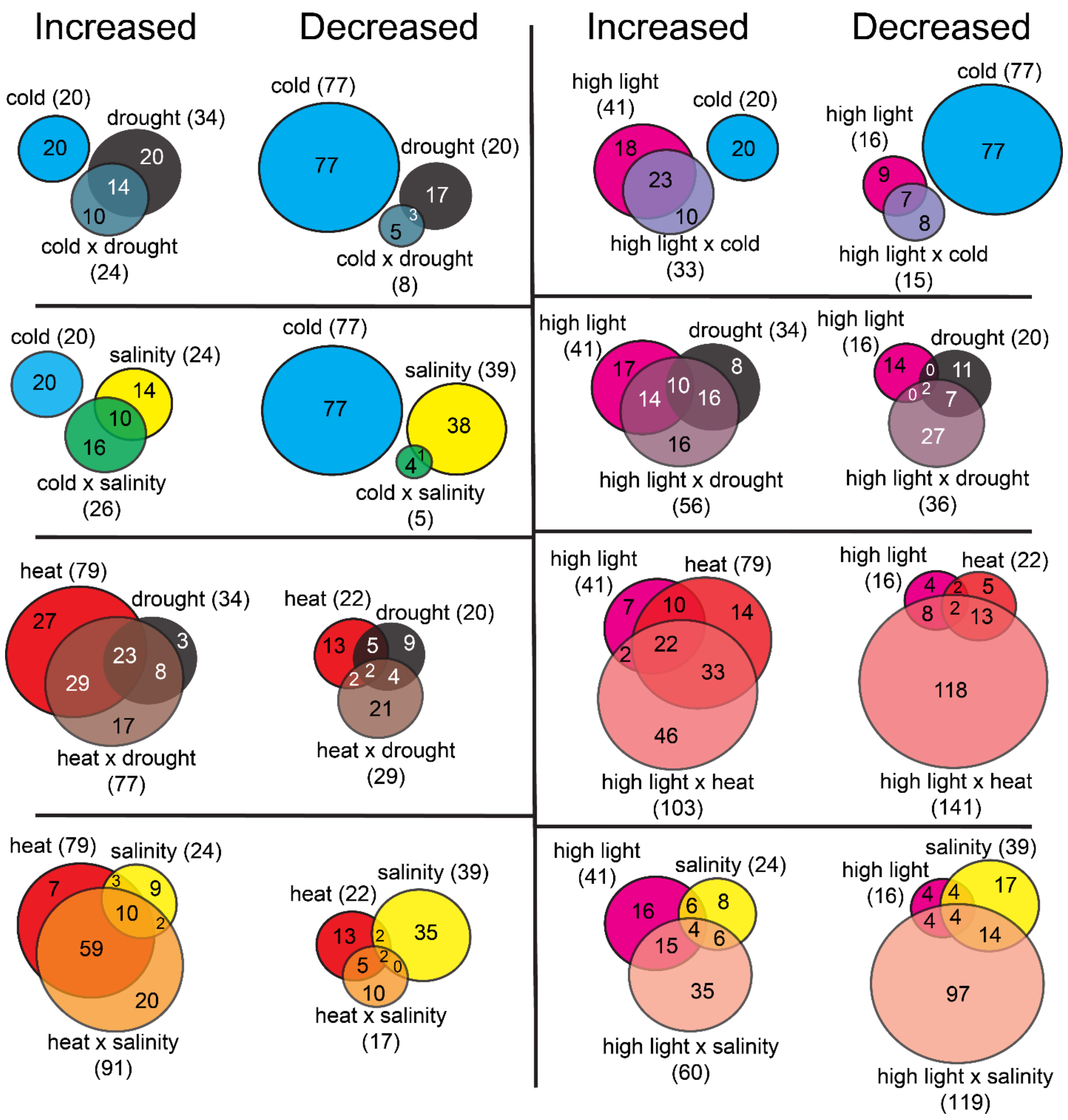


Figure 3-3. Venn diagrams showing the numbers and overlap of metabolic features increased (top) or decreased (bottom) more than 2 fold in plants in responses to stresses/combined stress conditions.

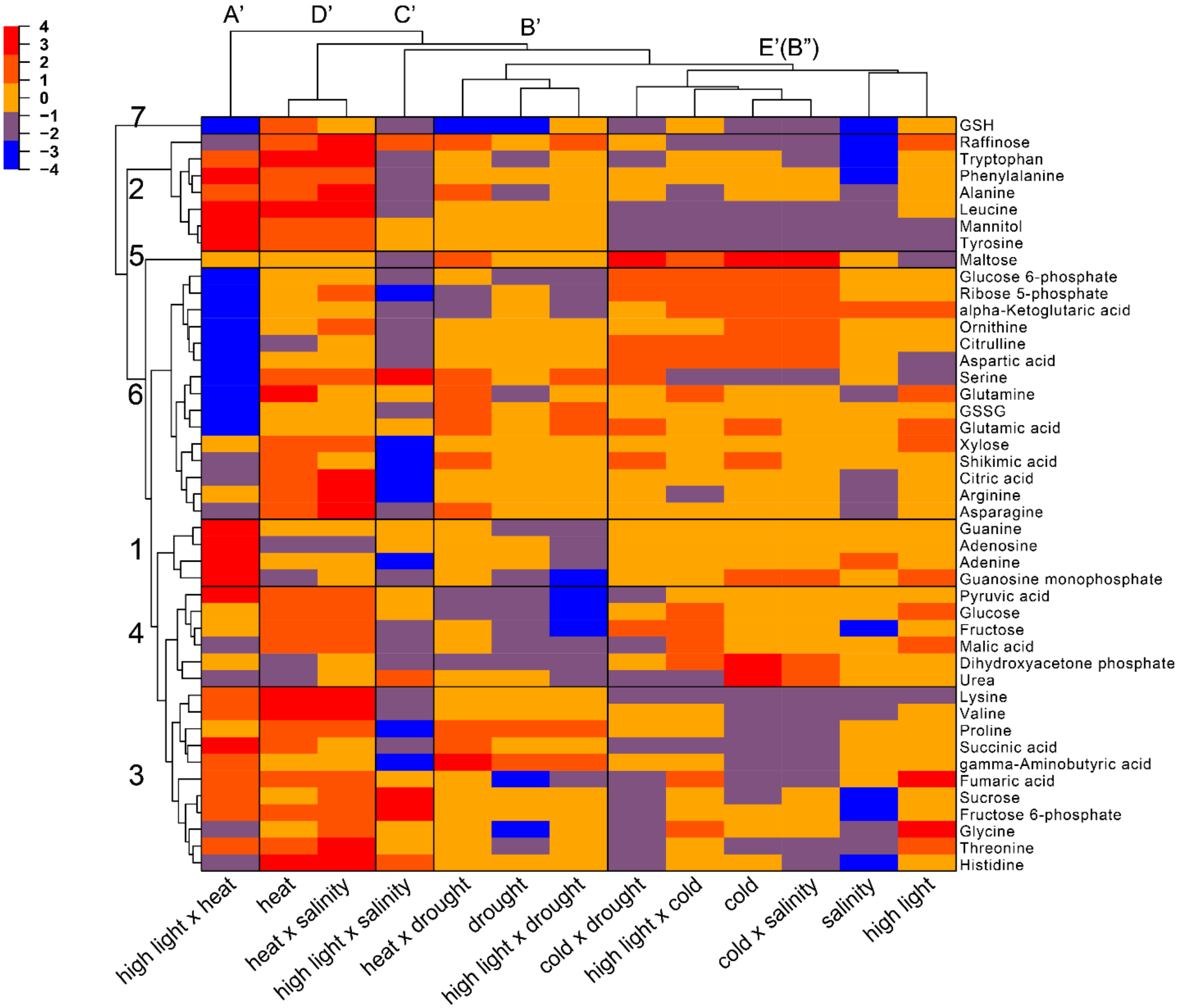

4
3
2
1
0
−1
−2
−3
−4
A'
D'
C'
B'
E'(B")
7
2
5
6
1
4
3
GSH
Raffinose
Tryptophan
Phenylalanine
Alanine
Leucine
Mannitol
Tyrosine
Maltose
Glucose 6-phosphate
Ribose 5-phosphate
alpha-Ketoglutaric acid
Ornithine
Citrulline
Aspartic acid
Serine
Glutamine
GSSG
Glutamic acid
Xylose
Shikimic acid
Citric acid
Arginine
Asparagine
Guanine
Adenosine
Adenine
Guanosine monophosphate
Pyruvic acid
Glucose
Fructose
Malic acid
Dihydroxyacetone phosphate
Urea
Lysine
Valine
Proline
Succinic acid
gamma-Aminobutyric acid
Fumaric acid
Sucrose
Fructose 6-phosphate
Glycine
Threonine
Histidine
high light x heat
heat
heat x salinity
high light x salinity
heat x drought
drought
high light x drought
cold x drought
high light x cold
cold
cold x salinity
salinity
high light

Figure 3-4. Hierarchical clustering analysis (HCA) for potential stress metabolic signatures and their precursors, intermediates, or products in the same pathway.

The top horizontal side bar reflects the $\log_2$-transformed average fold changes of identified metabolites in different treatments compared to control as reported in Supplemental Table 3-5. Clusters were generated using the complete linkage and Euclidean distance function. Five clusters of treatments were labeled A'-E'. Seven clusters of metabolites were labeled 1-7.

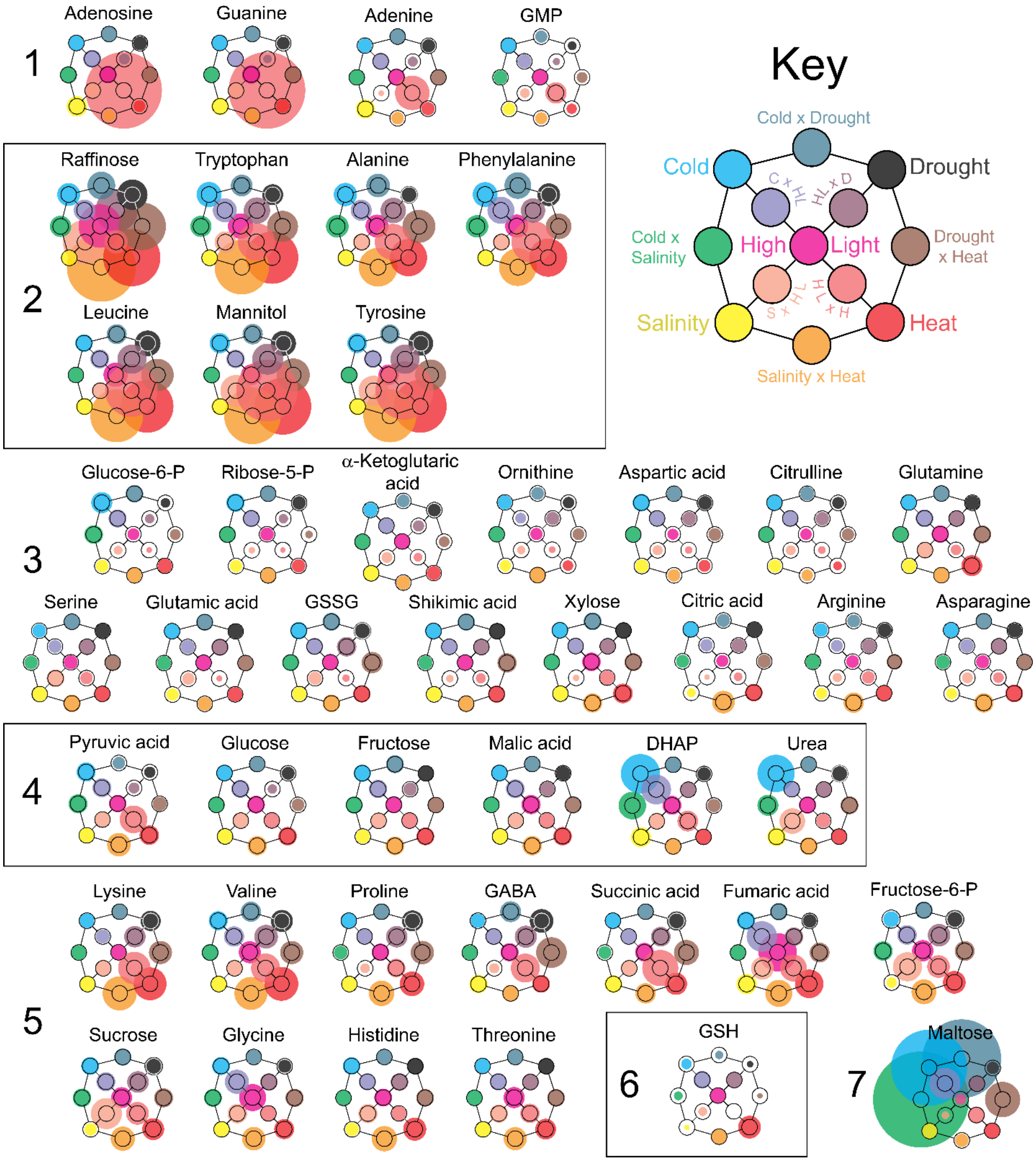


Figure 3-5. Plots for metabolites in cluster 1-7 from Figure 3-4 using the ratio change (Supplemental Table 3-5) in metabolite abundance represented by the colored area for each stress/combined stress condition with the control area shown by the black circles.
Lines are used to connect the stresses to show how they are combined.

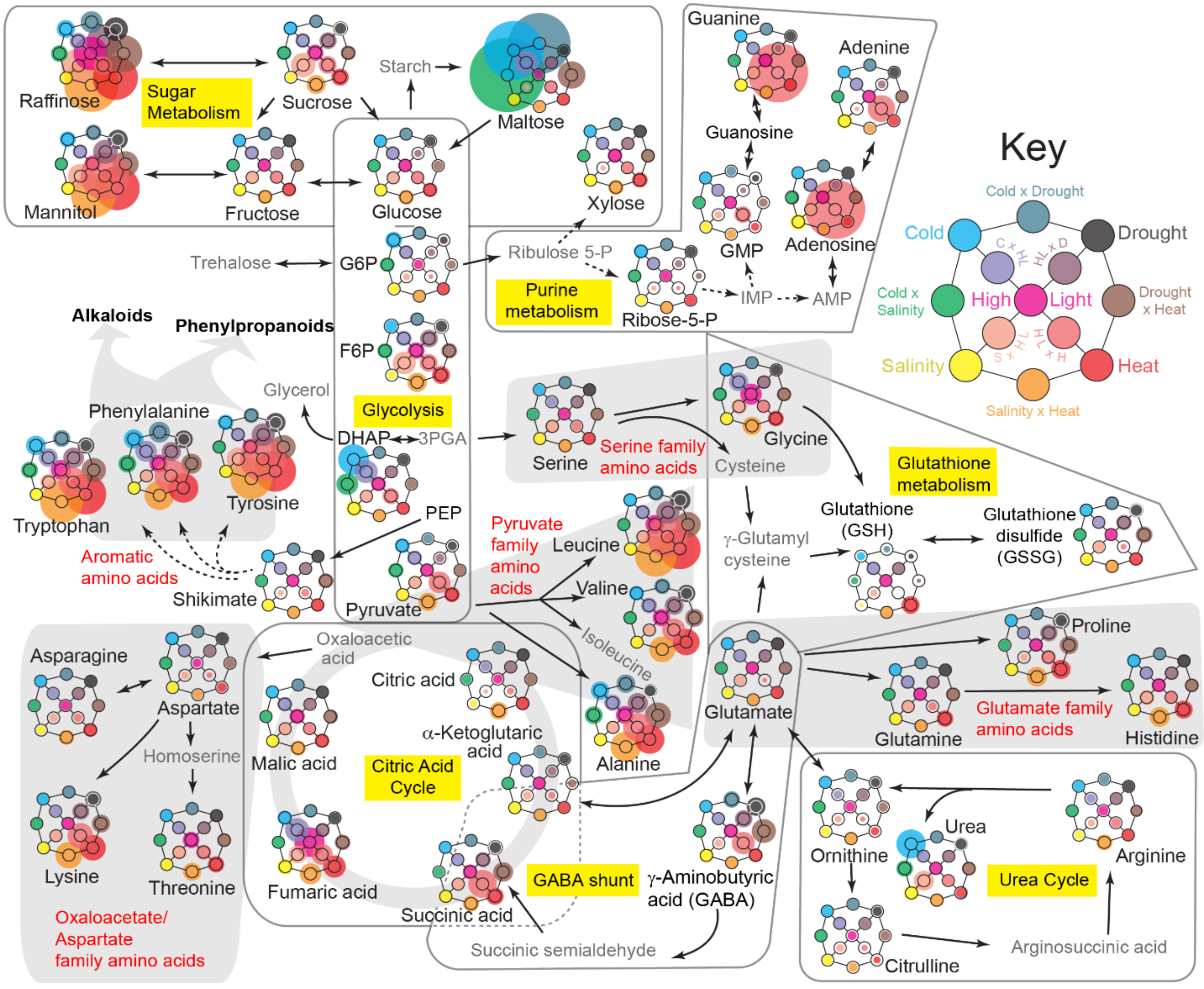
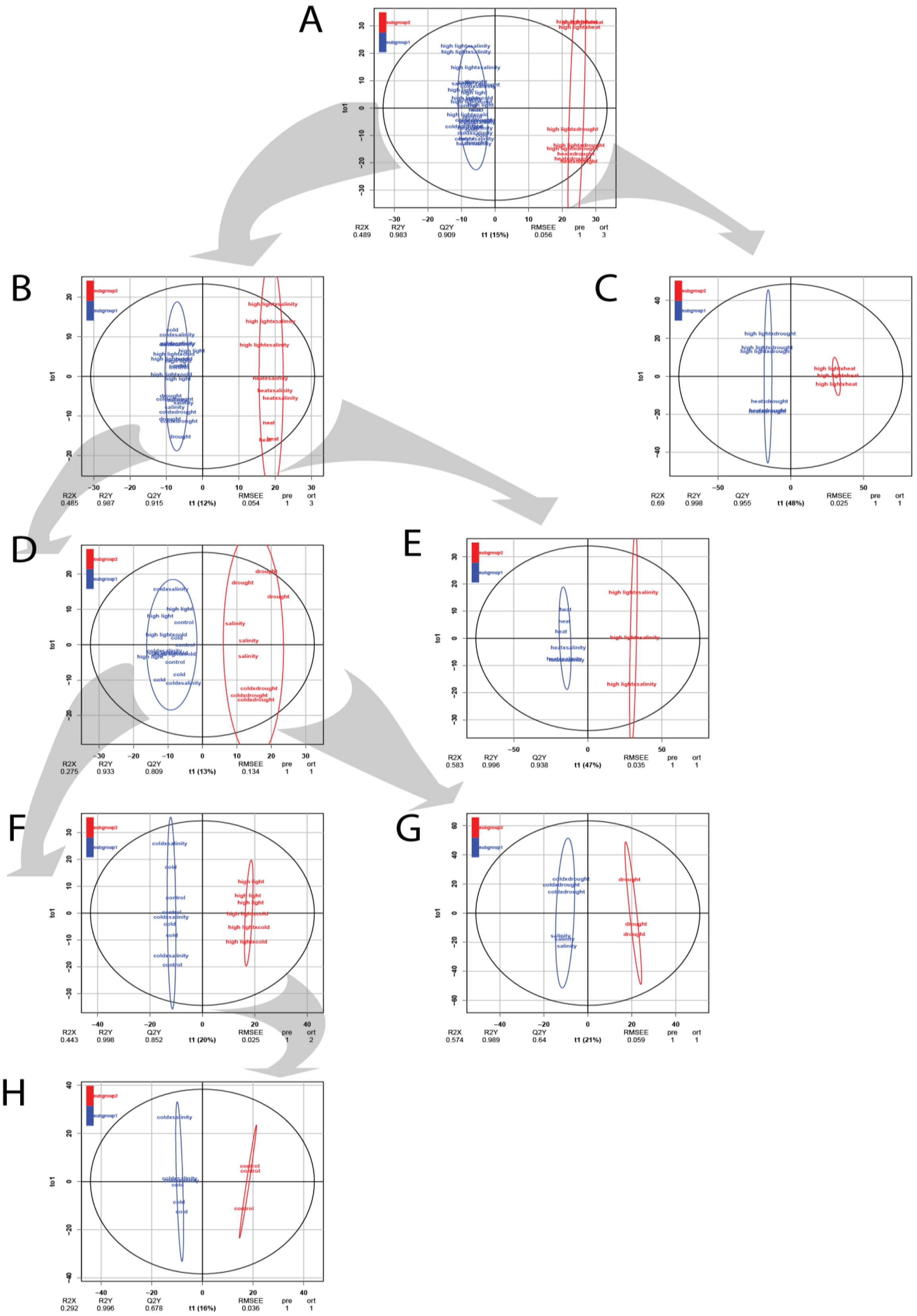
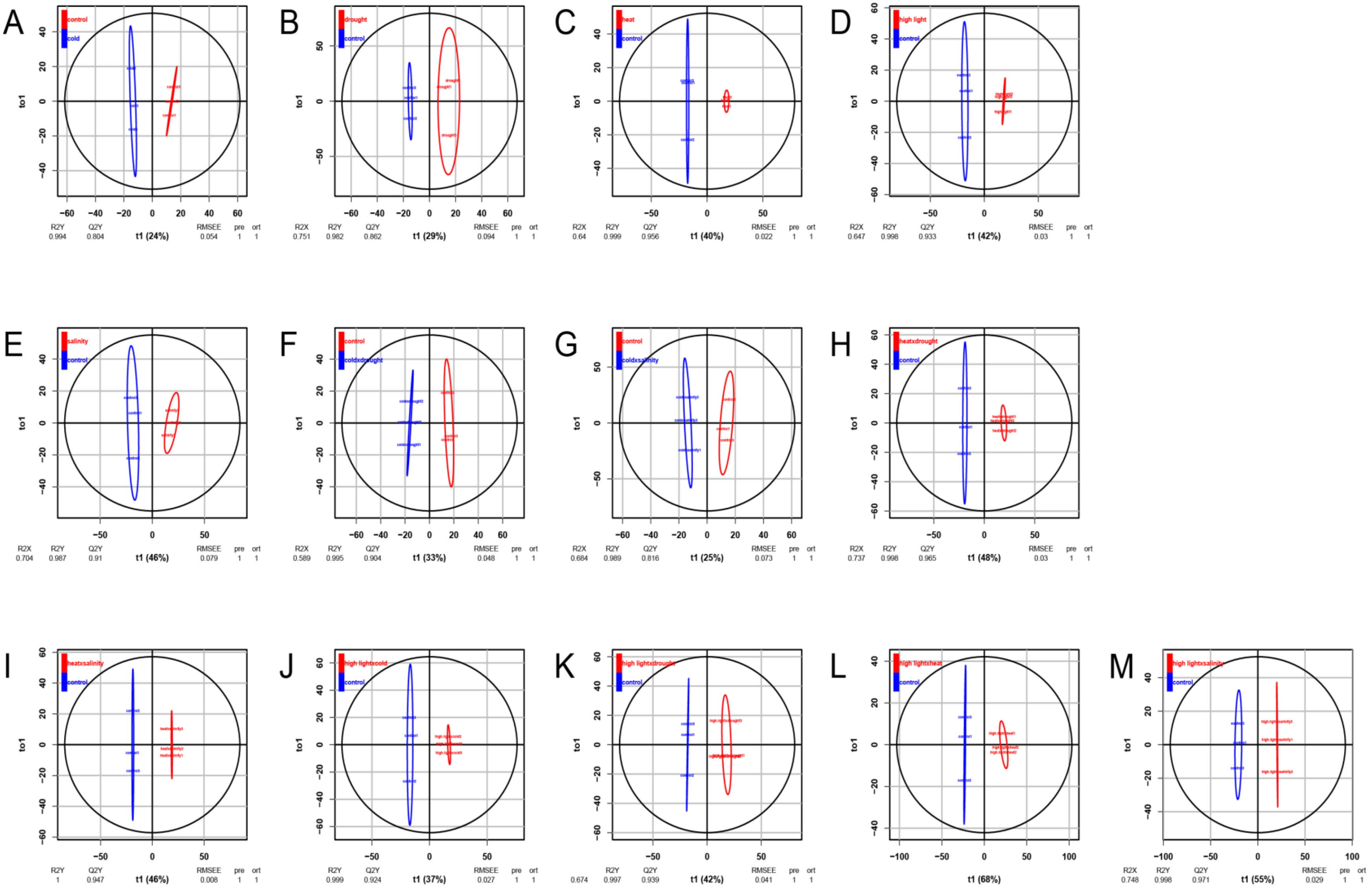

Raffinose
Sugar Metabolism
Sucrose
Starch
Maltose
Mannitol
Fructose
Glucose
Xylose
Trehalose
G6P
Ribulose 5-P
Purine metabolism
Ribose-5-P
Guanine
Guanosine
Adenine
GMP
Adenosine
IMP
AMP
Key
Cold x Drought
Cold
Drought
C x HL
HL x D
Cold x Salinity
High
Light
Drought x Heat
S x HL
HL x H
Salinity
Heat
Salinity x Heat
Alkaloids
Phenylpropanoids
F6P
Glycerol
Glycolysis
Phenylalanine
DHAP
3PGA
Serine
Serine family amino acids
Glycine
Cysteine
Glutathione metabolism
Tryptophan
Tyrosine
PEP
Aromatic amino acids
Shikimate
Pyruvate
Pyruvate family amino acids
Leucine
Valine
Isoleucine
Alanine
γ-Glutamyl cysteine
Glutathione (GSH)
Glutathione disulfide (GSSG)
Asparagine
Aspartate
Homoserine
Lysine
Threonine
Oxaloacetate/ Aspartate family amino acids
Oxaloacetic acid
Citric acid
Malic acid
α-Ketoglutaric acid
Citric Acid Cycle
Fumaric acid
Succinic acid
GABA shunt
Succinic semialdehyde
γ-Aminobutyric acid (GABA)
Glutamate
Proline
Glutamine
Glutamate family amino acids
Histidine
Ornithine
Urea
Arginine
Urea Cycle
Citrulline
Arginosuccinic acid

Figure 3-6. Metabolic pathways and plots for identified potential stress metabolic signatures with their precursors, intermediates, or products.
The fold changes (Supplemental Table 3-5) in metabolite abundance are represented by the colored area for each stress/combined stress condition, with the control area outlined by the black circles. Lines are used to connect the stresses to show how they are combined.

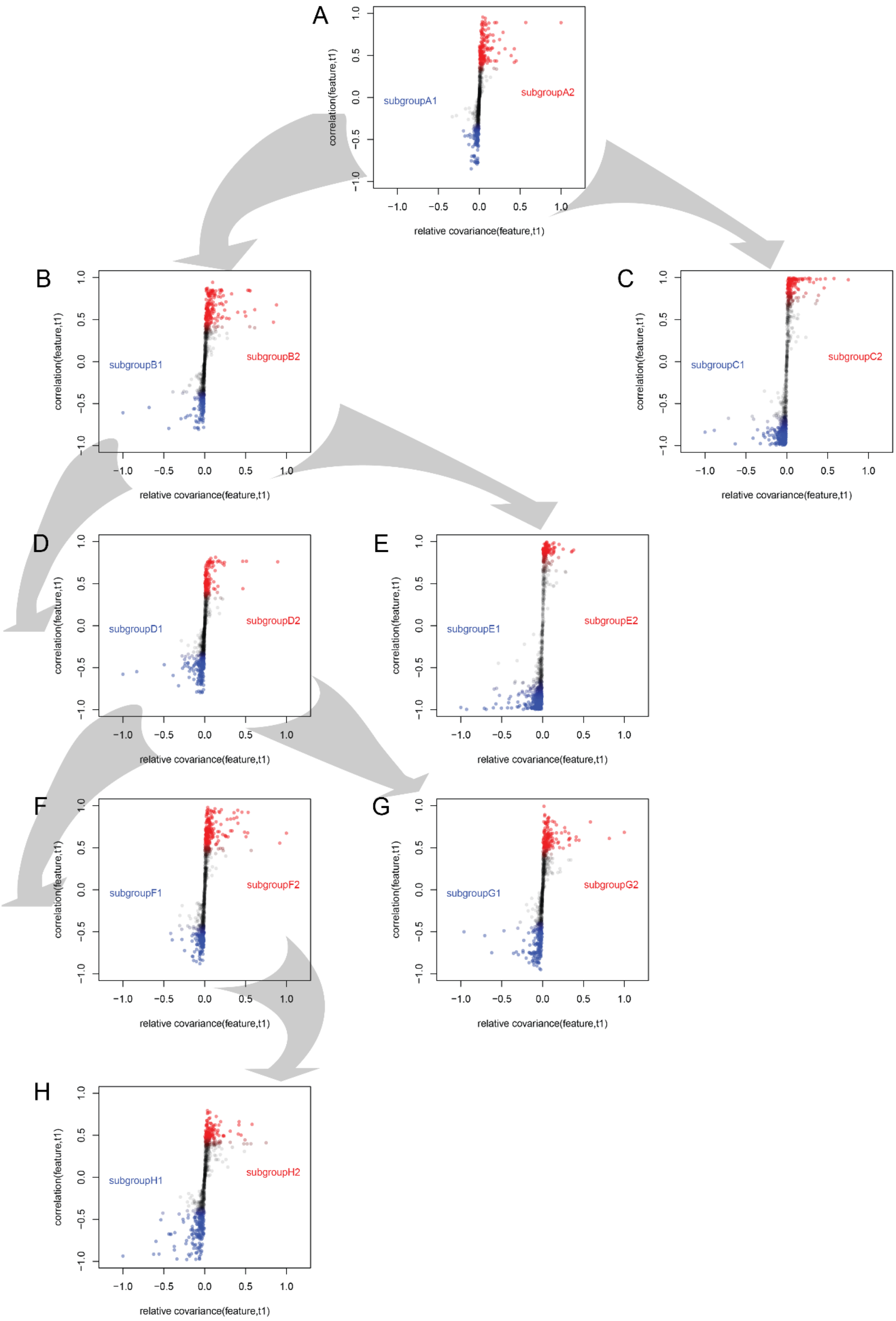
Supplemental Materials



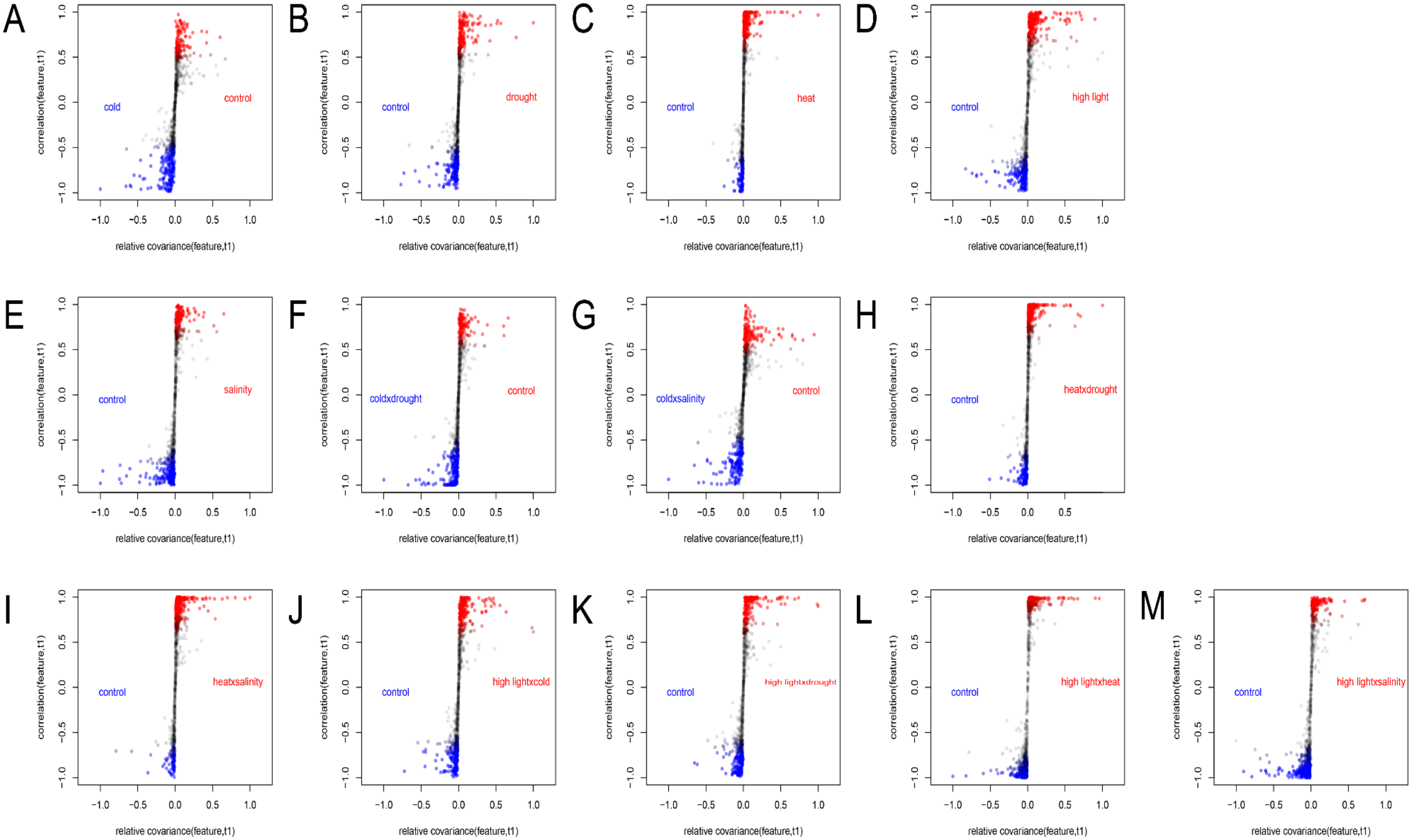
Supplemental Figure 3-1. OPLS-DA score plots of treatments in subgroups with hierarchical clustering identification that corresponds to Figure 3-1.
In the score plot, the names and colors corresponded to different supervised subgroups based on clustering results from PCA. (A) All groups. (B) control, cold, heat, drought, salinity, high light, cold x drought, cold x salinity, heat x salinity, high light x cold, high light x salinity. (C) heat x drought, high light x drought, high light x heat. (D) control, cold, drought, salinity, high light, cold x drought, cold x salinity, high light x cold, high light x salinity. (E) heat, heat x salinity, high light x salinity. (F) control, cold, high light, cold x salinity, high light x cold, high light x salinity. (G) drought, salinity, cold x drought. (H) control, cold, coldxsalinity.


A
control
cold
to1
t1 (24%)
R2Y 0.994 Q2Y 0.804 RMSEE 0.054 pre 1 ort 1
B
drought
control
to1
t1 (29%)
R2X 0.751 R2Y 0.982 Q2Y 0.862 RMSEE 0.094 pre 1 ort 1
C
heat
control
to1
t1 (40%)
R2X 0.64 R2Y 0.999 Q2Y 0.956 RMSEE 0.022 pre 1 ort 1
D
high light
control
to1
t1 (42%)
R2X 0.647 R2Y 0.998 Q2Y 0.933 RMSEE 0.03 pre 1 ort 1
E
salinity
control
to1
t1 (46%)
R2X 0.704 R2Y 0.987 Q2Y 0.91 RMSEE 0.079 pre 1 ort 1
F
control
coldxdrought
to1
t1 (33%)
R2X 0.589 R2Y 0.995 Q2Y 0.904 RMSEE 0.048 pre 1 ort 1
G
control
coldxsalinity
to1
t1 (25%)
R2X 0.684 R2Y 0.989 Q2Y 0.816 RMSEE 0.073 pre 1 ort 1
H
heatxdrought
control
to1
t1 (48%)
R2X 0.737 R2Y 0.998 Q2Y 0.965 RMSEE 0.03 pre 1 ort 1
I
heatxsalinity
control
to1
t1 (46%)
R2Y 1 Q2Y 0.947 RMSEE 0.008 pre 1 ort 1
J
high lightxcold
control
to1
t1 (37%)
R2Y 0.999 Q2Y 0.924 RMSEE 0.027 pre 1 ort 1
K
high lightxdrought
control
to1
t1 (42%)
0.674 R2Y 0.997 Q2Y 0.939 RMSEE 0.041 pre 1 ort 1
L
high lightxheat
control
to1
t1 (68%)
M
high lightxsalinity
control
to1
t1 (55%)
R2X 0.748 R2Y 0.998 Q2Y 0.971 RMSEE 0.029 pre 1 ort 1

Supplemental Figure 3-2. OPLS-DA score plots of treatments compared to control.
(A) cold and control. (B) drought and control. (C) heat and control. (D) high light and control. (E) salinity and control. (F) cold x drought and control. (G) cold x salinity and control. (H) heat x drought and control. (I) heat x salinity and control. (J) high light x cold and control. (K) high light x drought and control. (L) high light x heat and control. (M) high light x salinity and control.

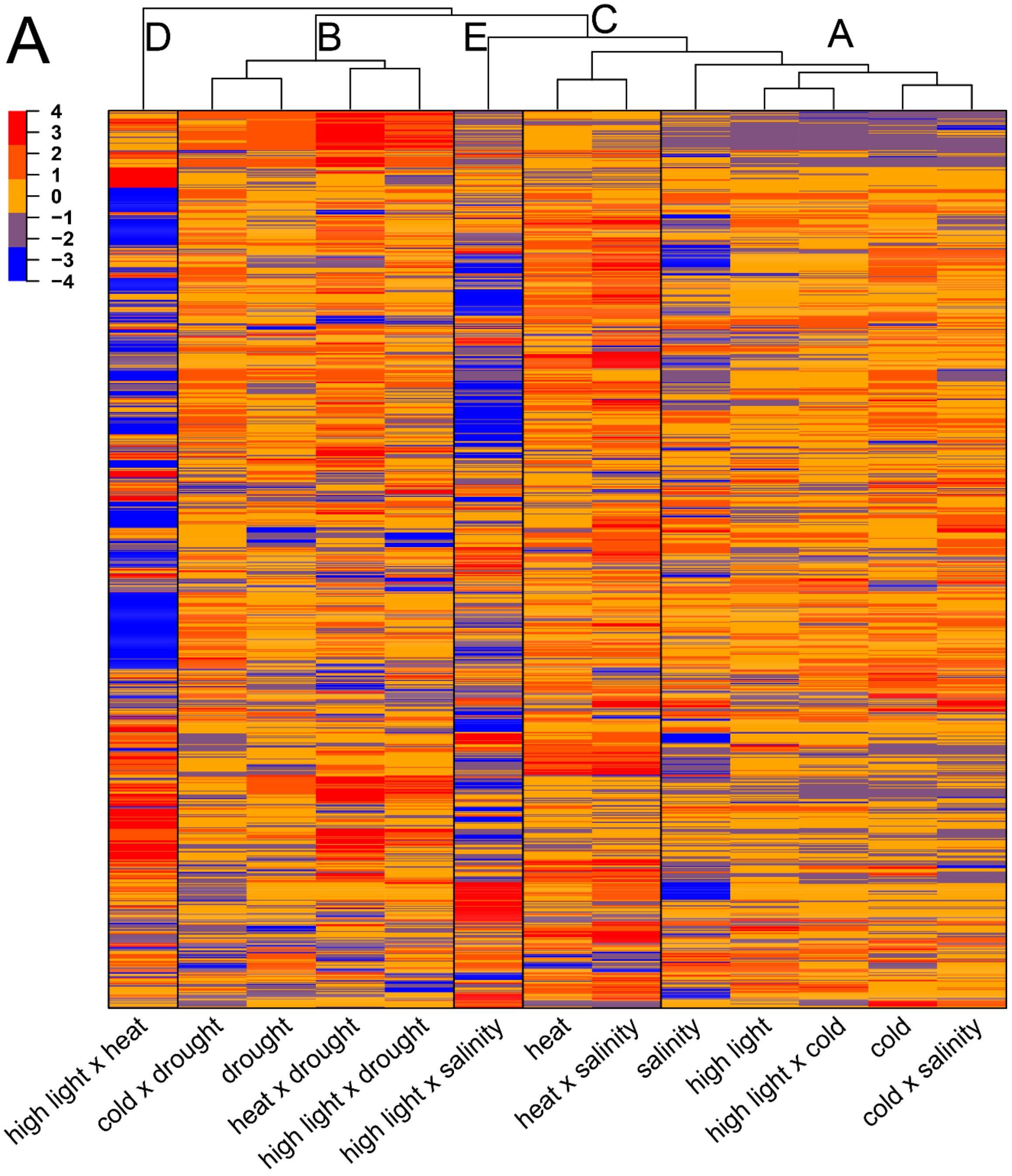

A
subgroupA1
subgroupA2
B
subgroupB1
subgroupB2
C
subgroupC1
subgroupC2
D
subgroupD1
subgroupD2
E
subgroupE1
subgroupE2
F
subgroupF1
subgroupF2
G
subgroupG1
subgroupG2
H
subgroupH1
subgroupH2
correlation(feature,t1)
relative covariance(feature,t1)
−1.0
−0.5
0.0
0.5
1.0

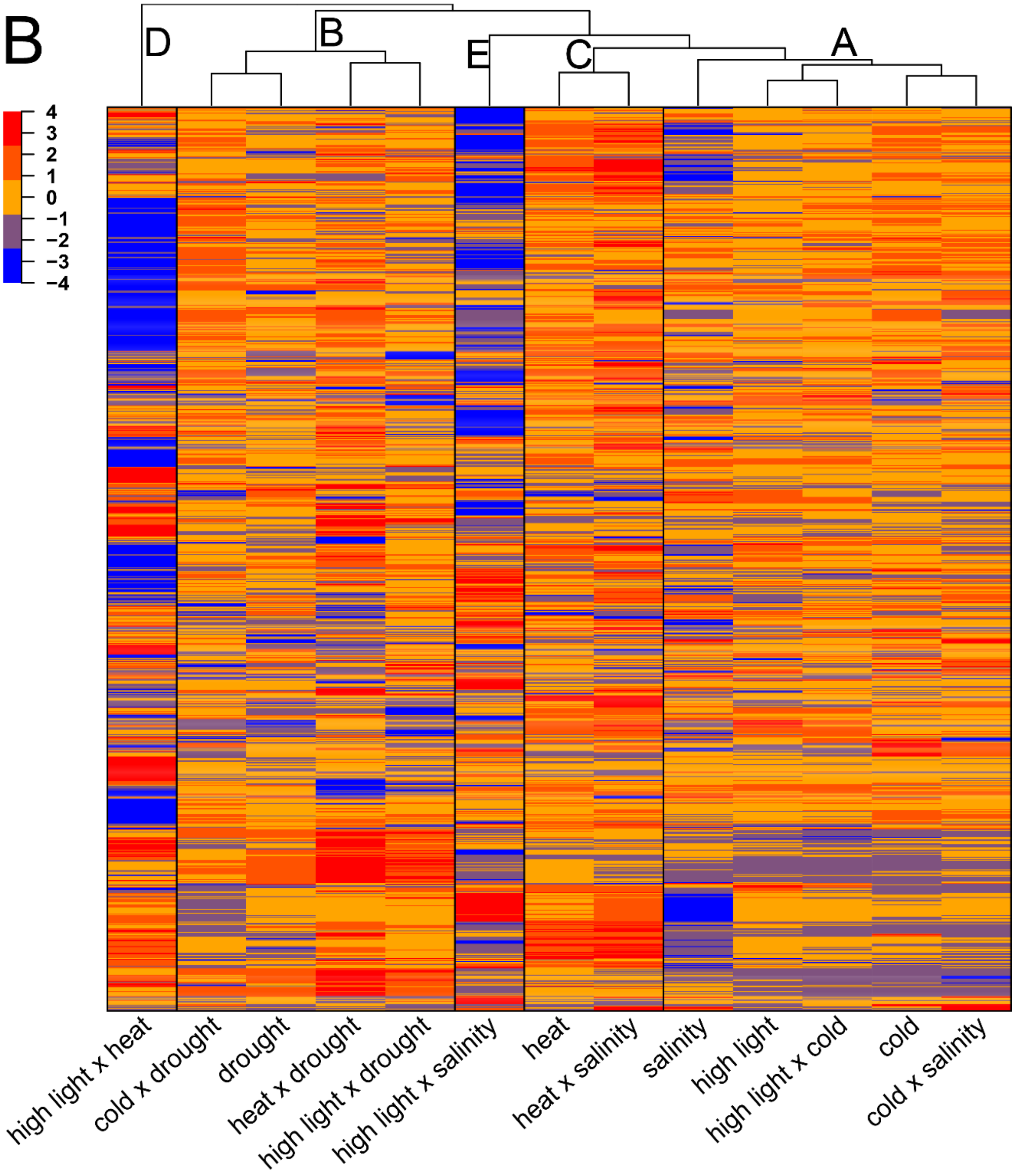
Supplemental Figure 3-3. OPLS-DA S-plot of treatments in subgroups with hierarchical clustering identification that corresponds to Figure 3-1.
The representative OPLS-DA loadings S-pot showing relative contribution of metabolic features to the corresponding supervised clusters. (A) All groups. (B) control, cold, heat, drought, salinity, high light, cold x drought, cold x salinity, heat x salinity, high light x cold, high light x salinity. (C) heat x drought, high light x drought, high light x heat. (D) control, cold, drought, salinity, high light, cold x drought, cold x salinity, high light x cold, high light x salinity. (E) heat, heat x salinity, high light x salinity. (F) control, cold, high light, cold x salinity, high light x cold, high light x salinity. (G) drought, salinity, cold x drought. (H) control, cold, cold x salinity.
The x and y axis represents the covariance and the correlation of features towards the predictive variation shown in the corresponding OPLS-DA loading score.

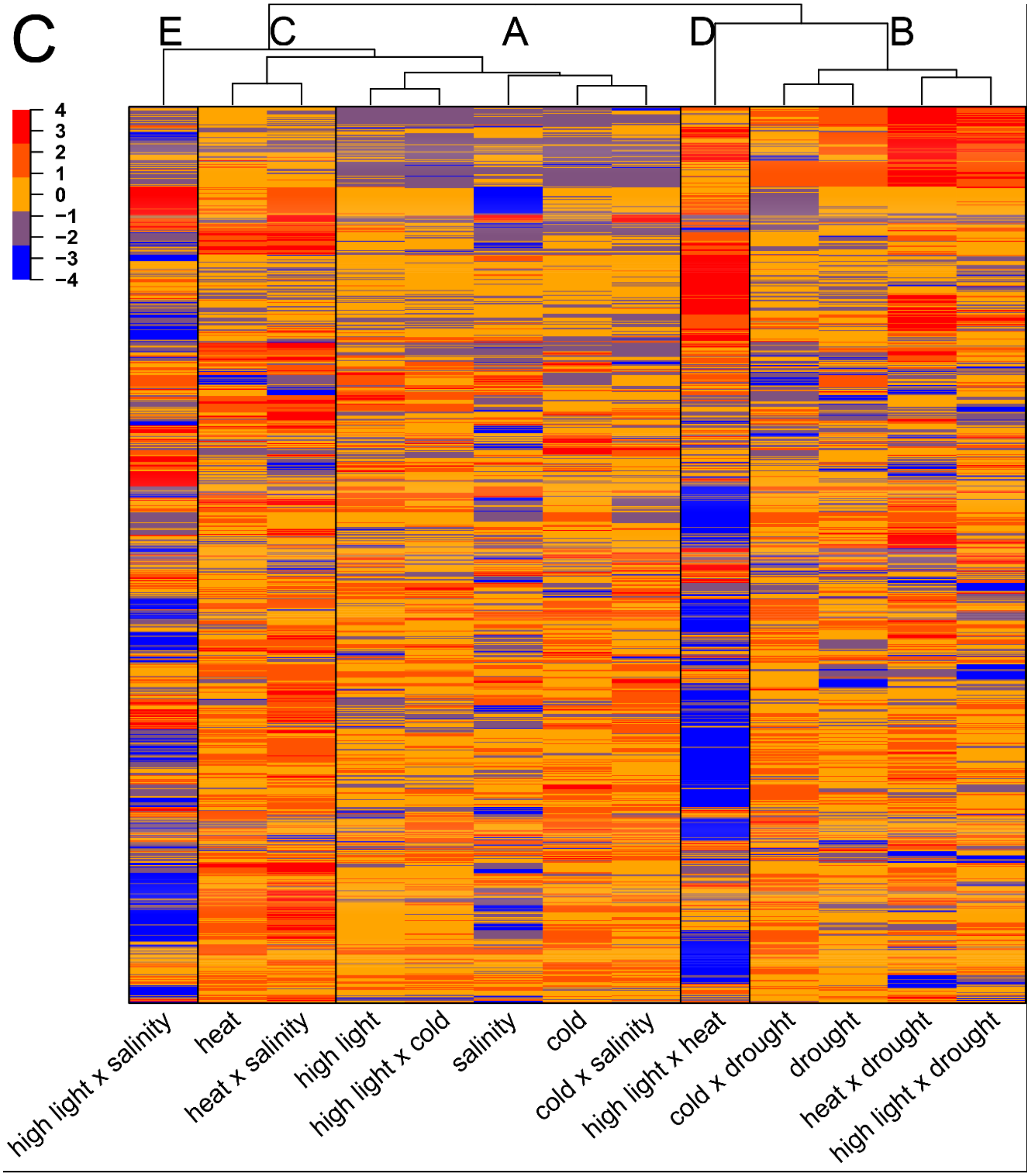


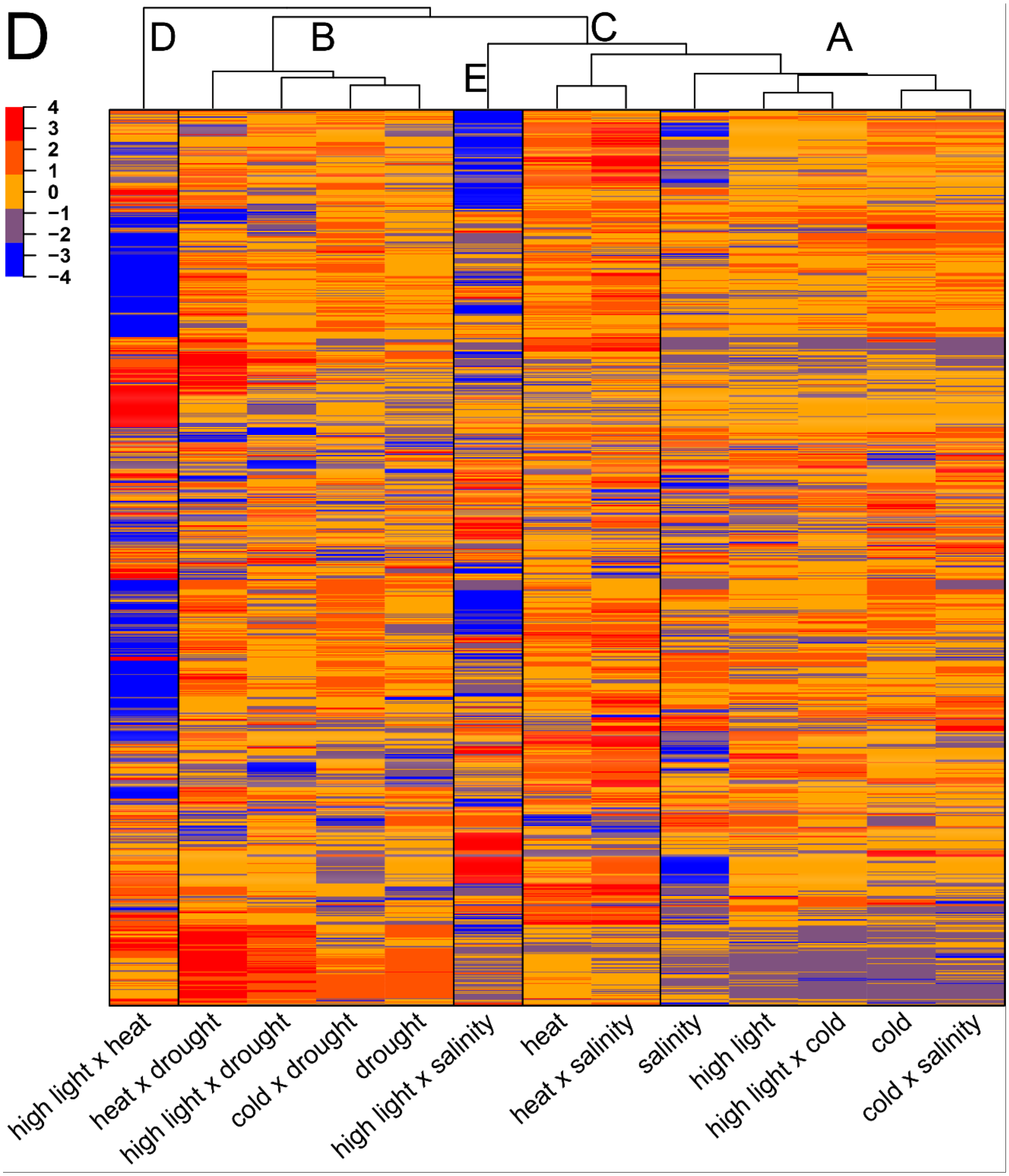
Supplemental Figure 3-4. OPLS-DA S-plot of treatment compared to control.

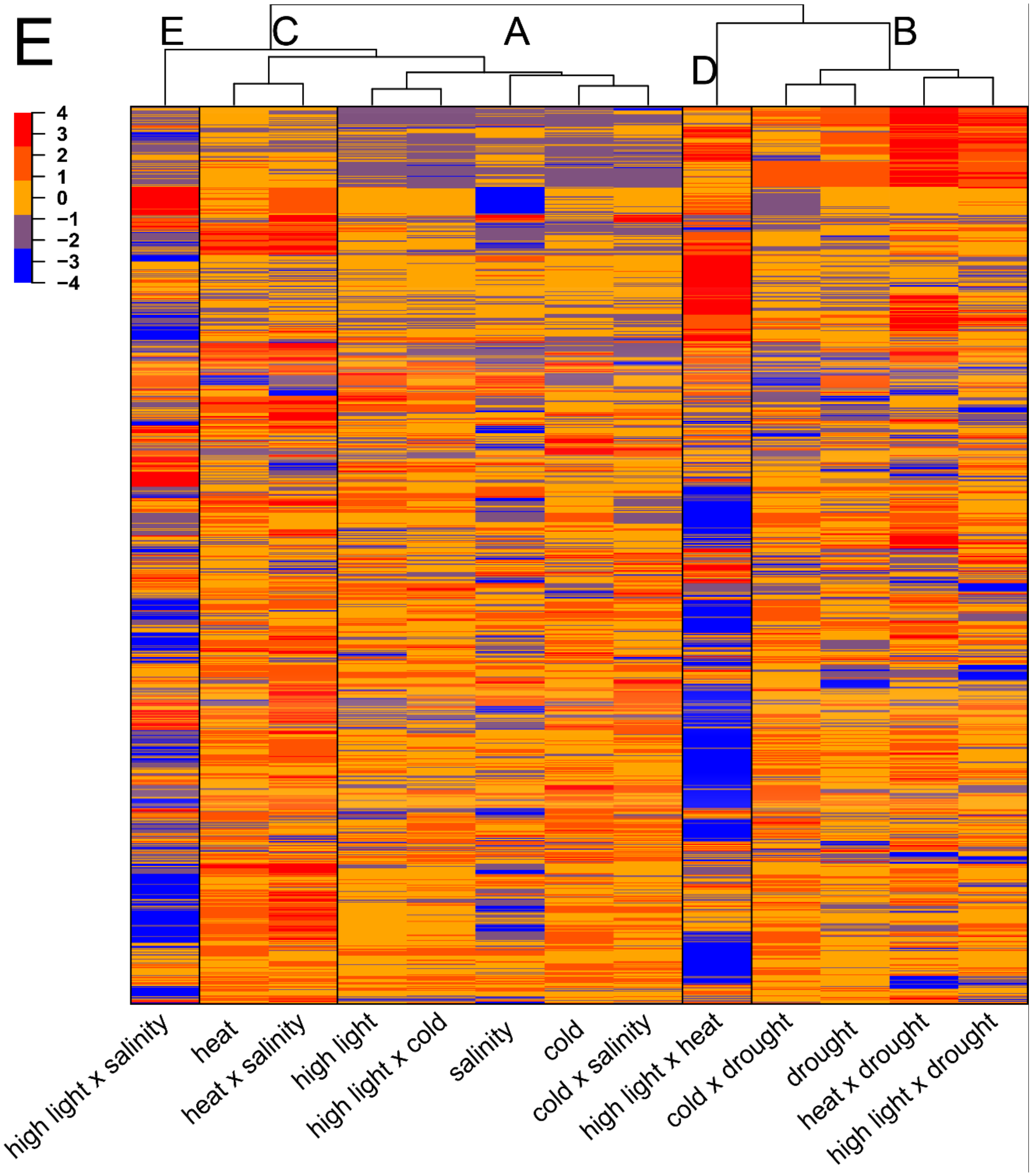
The representative OPLS-DA loadings S-plot showing relative contribution of metabolic features to the corresponding supervised clusters. (A) cold and control. (B) drought and control. (C) heat and control. (D) high light and control. (E) salinity and control. (F) cold x drought and control. (G) cold x salinity and control. (H) heat x drought and control. (I) heat x salinity and control. (J) high light x cold and control. (K) high light x drought and control. (L) high light x heat and control. (M) high light x salinity and control. The x and y axis represents the covariance and the correlation of features towards the predictive variation shown in the corresponding OPLS-DA loading score.

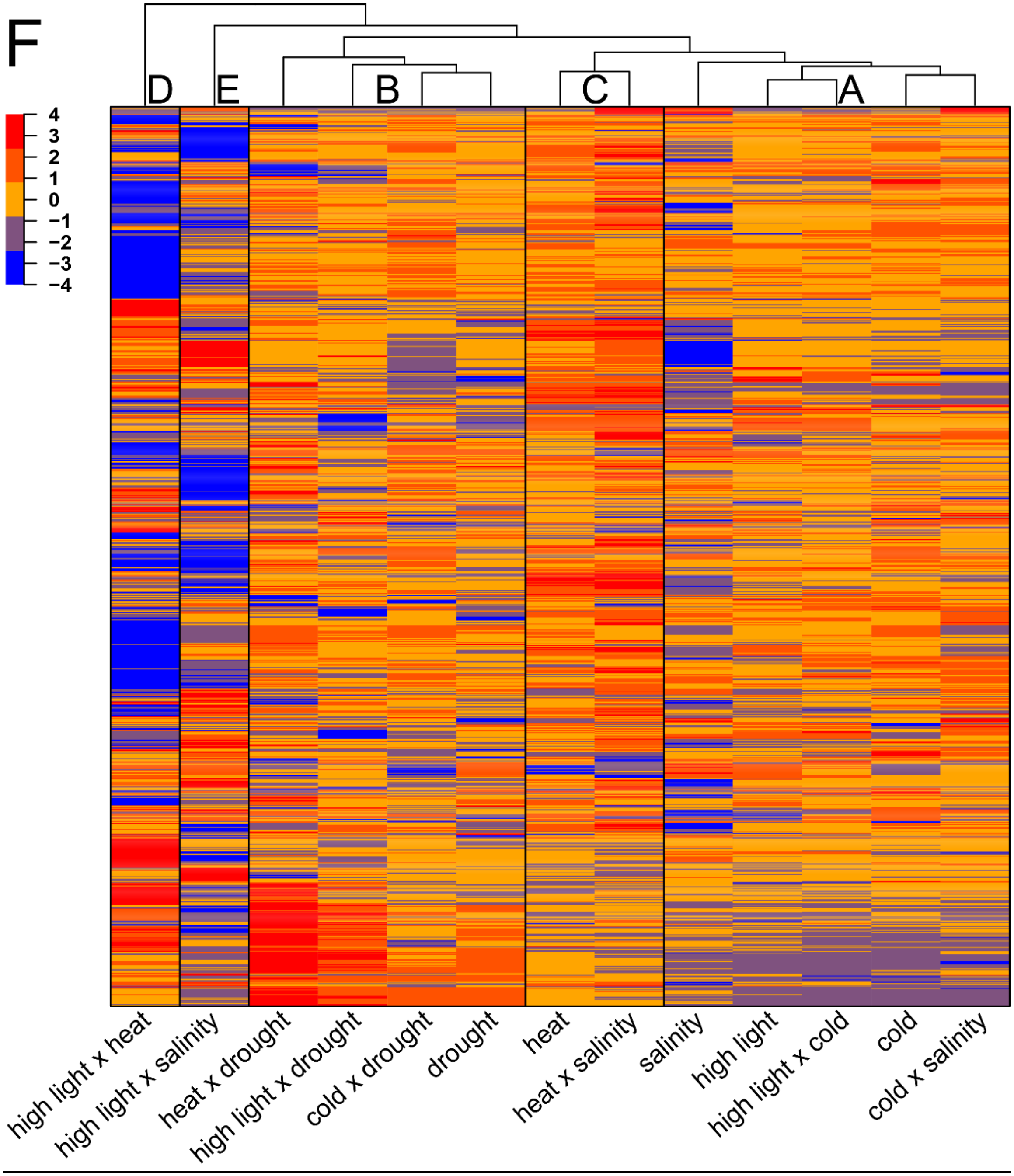

A
D
B
C
E
A
4
3
2
1
0
−1
−2
−3
−4
high light x heat
cold x drought
drought
heat x drought
high light x drought
high light x salinity
heat
heat x salinity
salinity
high light
high light x cold
cold
cold x salinity

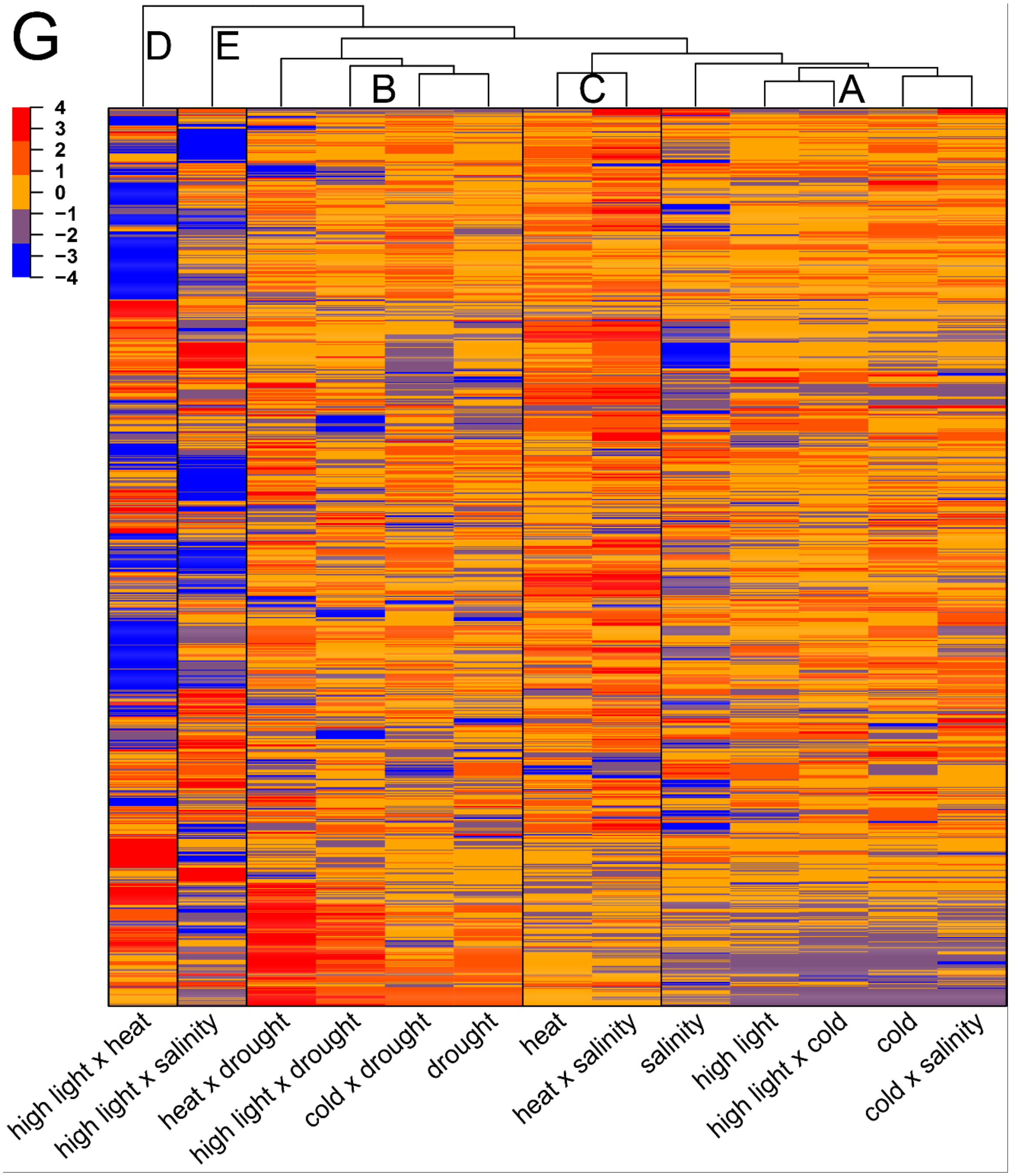

B
D
B
E
C
A
4
3
2
1
0
−1
−2
−3
−4
high light x heat
cold x drought
drought
heat x drought
high light x drought
high light x salinity
heat
heat x salinity
salinity
high light
high light x cold
cold
cold x salinity

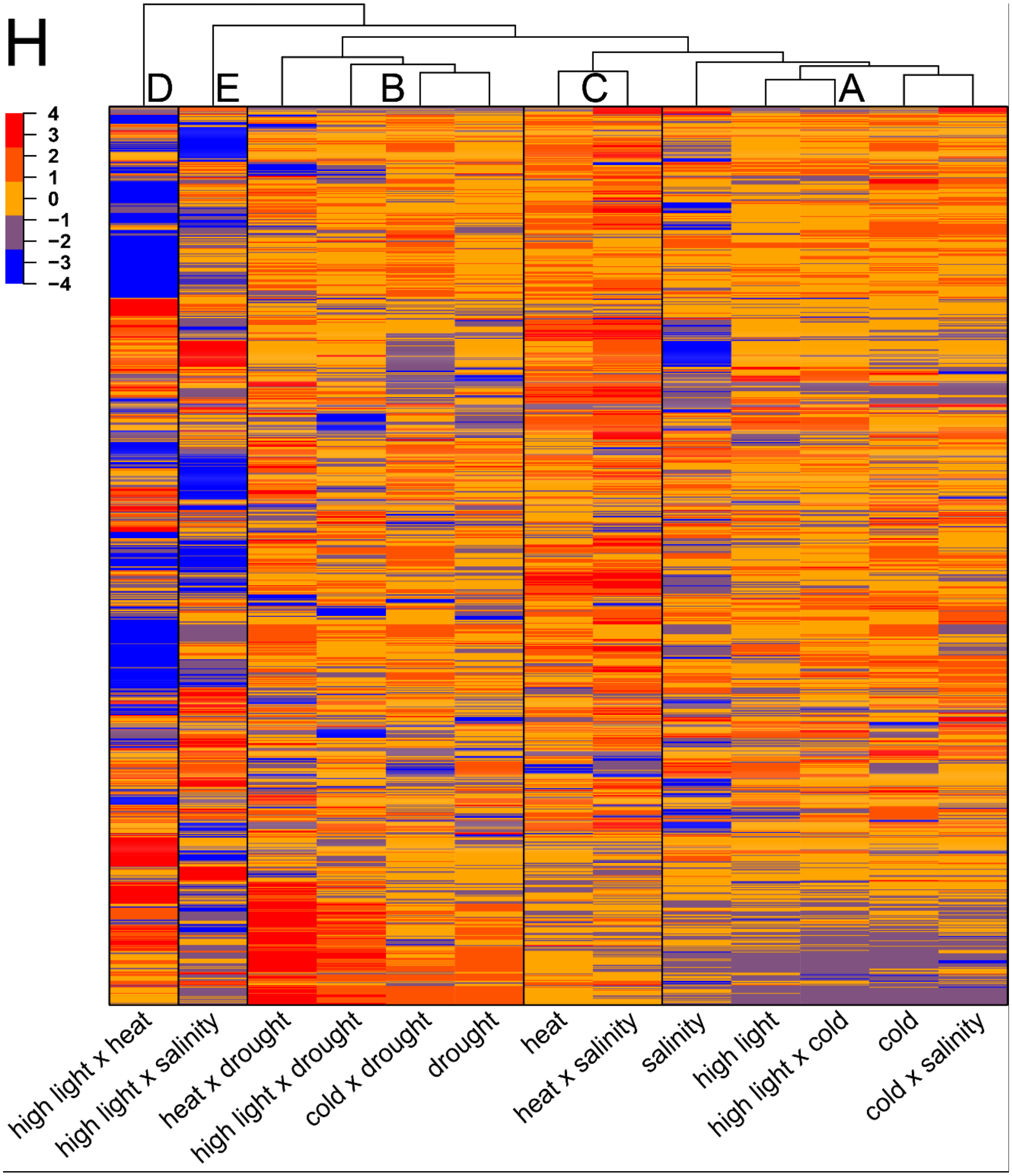

C
4
3
2
1
0
−1
−2
−3
−4
E
C
A
D
B
high light x salinity
heat
heat x salinity
high light
high light x cold
salinity
cold
cold x salinity
high light x heat
cold x drought
drought
heat x drought
high light x drought

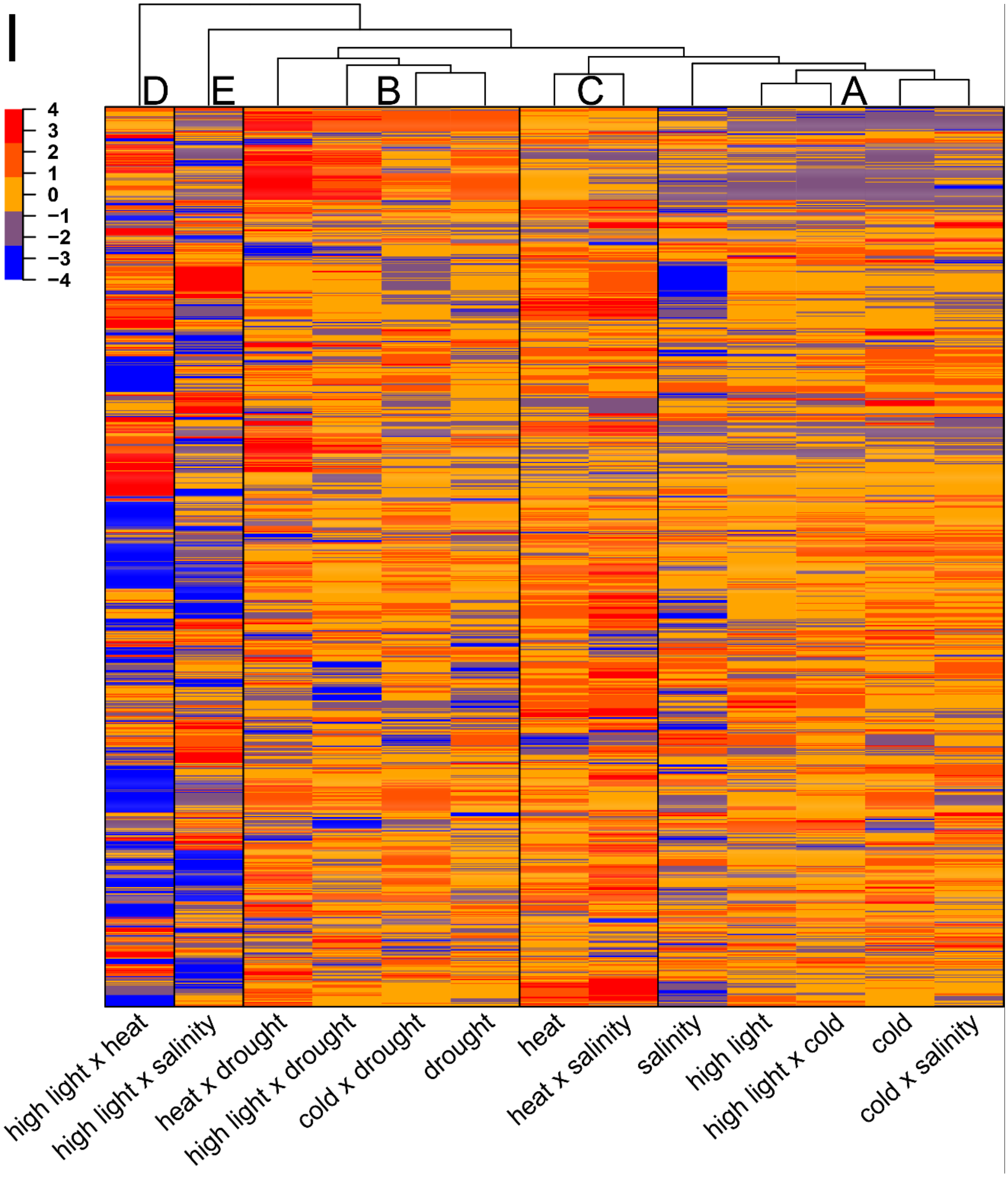

D
4
3
2
1
0
−1
−2
−3
−4
D
B
C
E
A
high light x heat
heat x drought
high light x drought
cold x drought
drought
high light x salinity
heat
heat x salinity
salinity
high light
high light x cold
cold
cold x salinity


E
4
3
2
1
0
−1
−2
−3
−4
E
C
A
D
B
high light x salinity
heat
heat x salinity
high light
high light x cold
salinity
cold
cold x salinity
high light x heat
cold x drought
drought
heat x drought
high light x drought


F
4
3
2
1
0
−1
−2
−3
−4
D
E
B
C
A
high light x heat
high light x salinity
heat x drought
high light x drought
cold x drought
drought
heat
heat x salinity
salinity
high light
high light x cold
cold
cold x salinity


G
D
E
B
C
A
4
3
2
1
0
−1
−2
−3
−4
high light x heat
high light x salinity
heat x drought
high light x drought
cold x drought
drought
heat
heat x salinity
salinity
high light
high light x cold
cold
cold x salinity

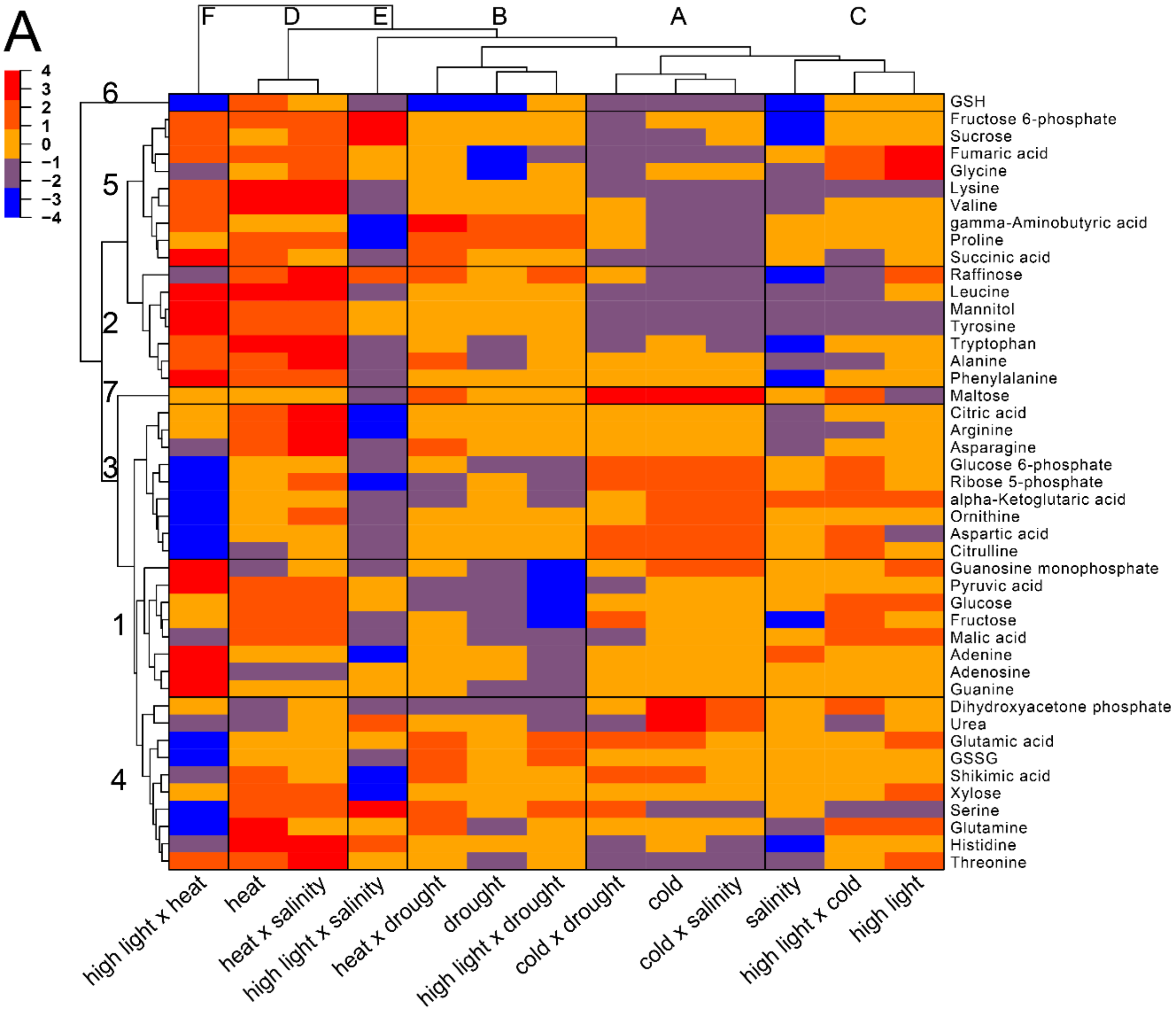

H
D
E
B
C
A
4
3
2
1
0
−1
−2
−3
−4
high light x heat
high light x salinity
heat x drought
high light x drought
cold x drought
drought
heat
heat x salinity
salinity
high light
high light x cold
cold
cold x salinity

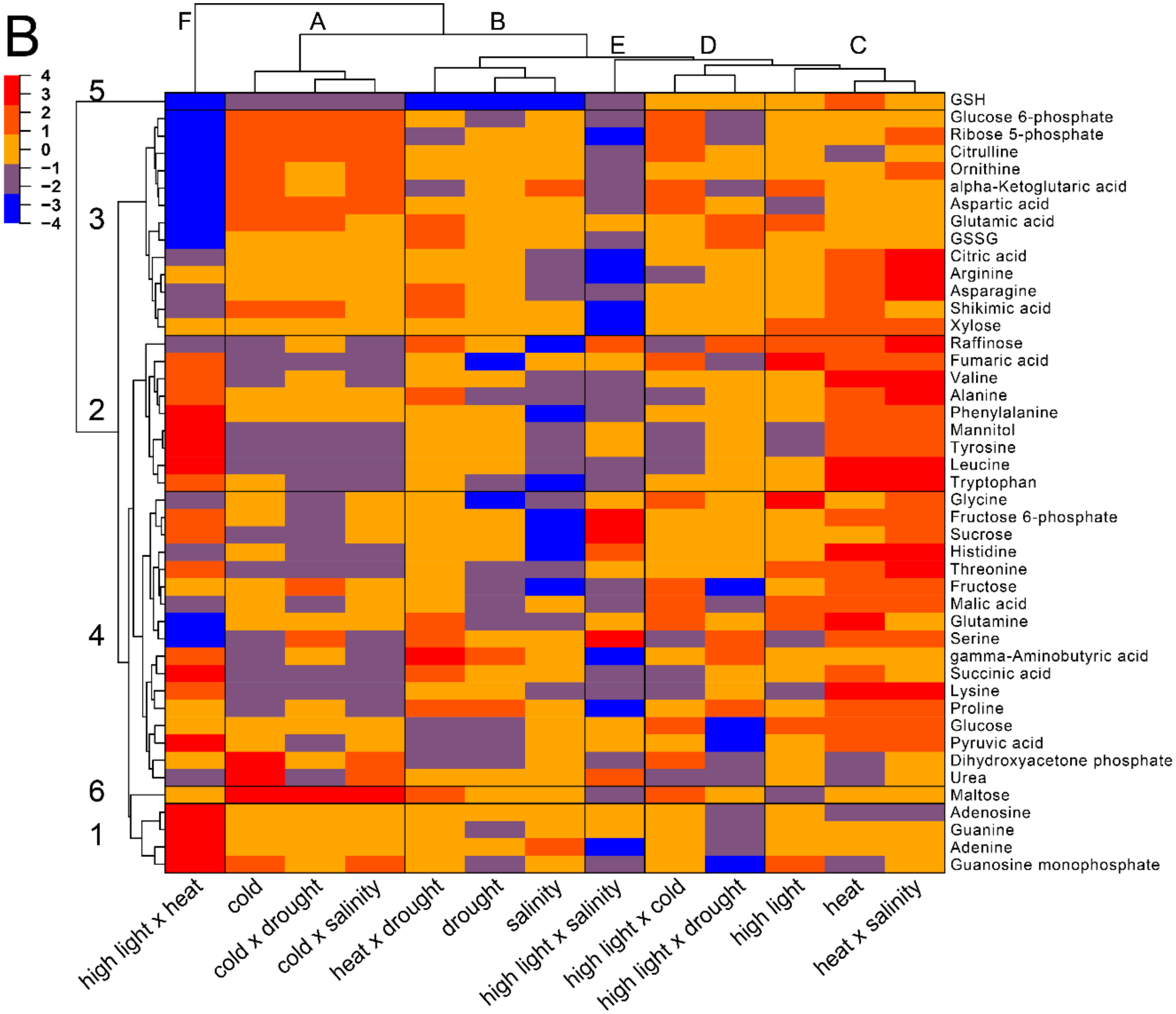


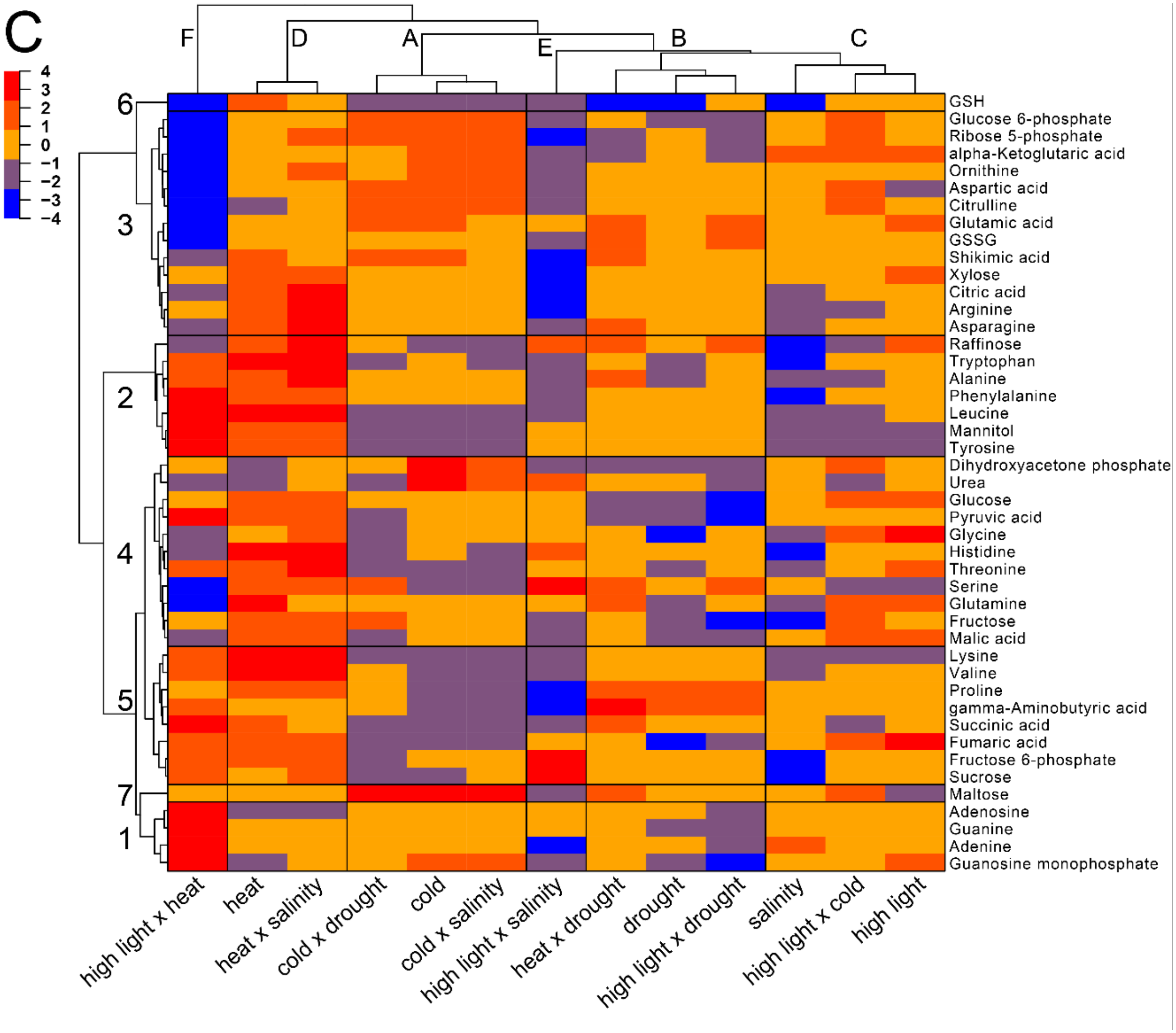
Supplemental Figure 3-5. Hierarchical clustering analysis (HCA) for all the metabolic features.

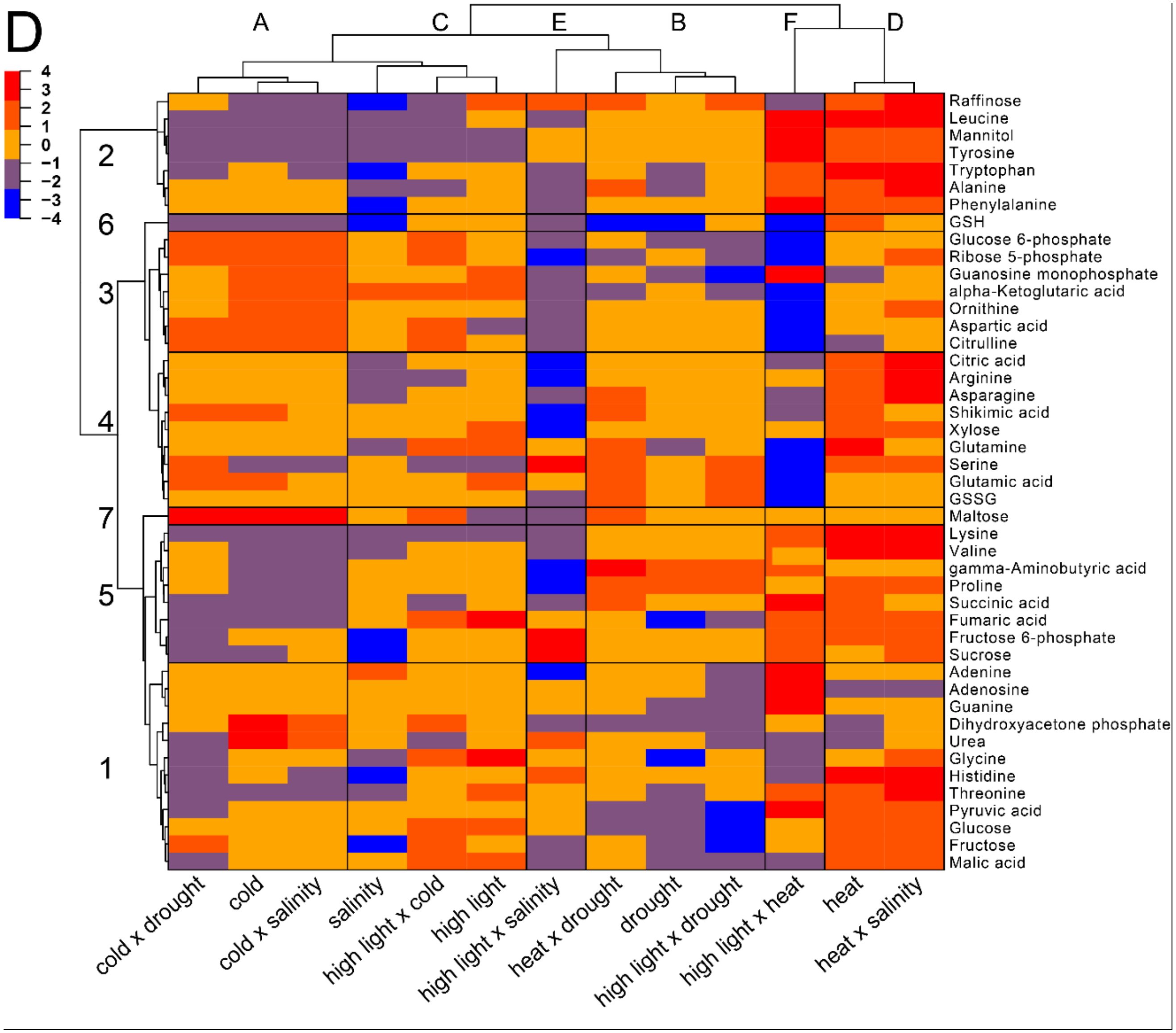
The top horizontal side bar reflects the log2-transformed fold changes of metabolic features in different treatments compared to control reported in Supplemental Table 3-4. Clusters were generated using the complete linkage and Manhattan distance function (Supplemental Figure 3-5A), complete linkage and Minkowski distance function (Supplemental Figure 3-5B), Ward's methods using and Euclidean distance function (Supplemental Figure 3-5C), Ward's methods and Manhattan distance function (Supplemental Figure 3-5D), Ward's methods and Minkowski distance function (Supplemental Figure 3-5E), McQuitty's methods and Euclidean distance function

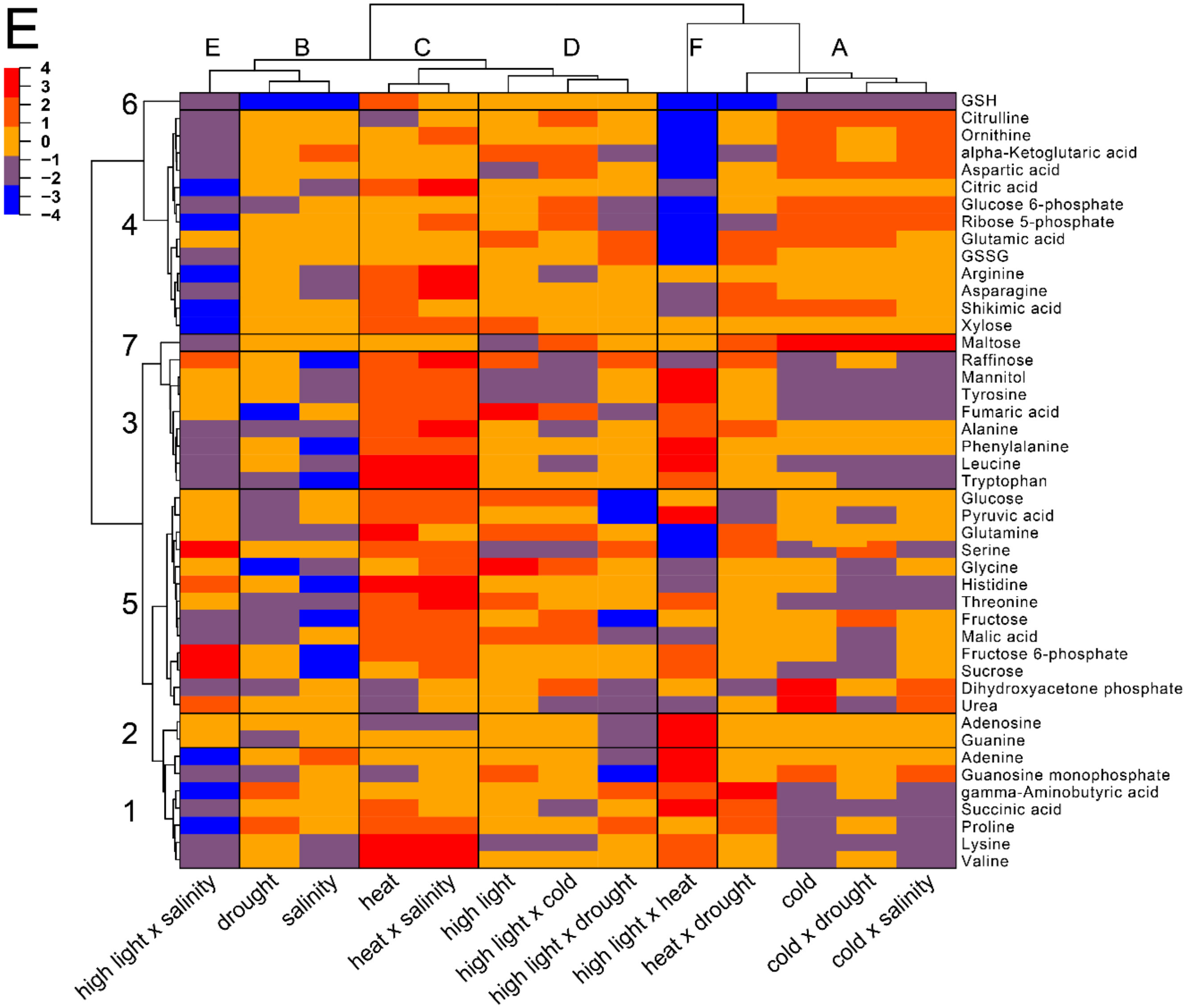
(Supplemental Figure 3-5F), McQuitty’s methods and Minkowski distance function (Supplemental Figure 3-5G), average linkage and Euclidean distance function (Supplemental Figure 3-5H), average linkage and Manhattan distance function (Supplemental Figure 3-5I), average linkage and Minkowski distance function (Supplemental Figure 3-5J).


A
4
3
2
1
0
−1
−2
−3
−4
F
D
E
B
A
C
6
5
2
7
3
1
4
GSH
Fructose 6-phosphate
Sucrose
Fumaric acid
Glycine
Lysine
Valine
gamma-Aminobutyric acid
Proline
Succinic acid
Raffinose
Leucine
Mannitol
Tyrosine
Tryptophan
Alanine
Phenylalanine
Maltose
Citric acid
Arginine
Asparagine
Glucose 6-phosphate
Ribose 5-phosphate
alpha-Ketoglutaric acid
Ornithine
Aspartic acid
Citrulline
Guanosine monophosphate
Pyruvic acid
Glucose
Fructose
Malic acid
Adenine
Adenosine
Guanine
Dihydroxyacetone phosphate
Urea
Glutamic acid
GSSG
Shikimic acid
Xylose
Serine
Glutamine
Histidine
Threonine
high light x heat
heat
heat x salinity
high light x salinity
heat x drought
drought
high light x drought
cold x drought
cold
cold x salinity
salinity
high light x cold
high light


B
4
3
2
1
0
−1
−2
−3
−4
F
A
B
E
D
C
5
3
2
4
6
1
GSH
Glucose 6-phosphate
Ribose 5-phosphate
Citrulline
Ornithine
alpha-Ketoglutaric acid
Aspartic acid
Glutamic acid
GSSG
Citric acid
Arginine
Asparagine
Shikimic acid
Xylose
Raffinose
Fumaric acid
Valine
Alanine
Phenylalanine
Mannitol
Tyrosine
Leucine
Tryptophan
Glycine
Fructose 6-phosphate
Sucrose
Histidine
Threonine
Fructose
Malic acid
Glutamine
Serine
gamma-Aminobutyric acid
Succinic acid
Lysine
Proline
Glucose
Pyruvic acid
Dihydroxyacetone phosphate
Urea
Maltose
Adenosine
Guanine
Adenine
Guanosine monophosphate
high light x heat
cold
cold x drought
cold x salinity
heat x drought
drought
salinity
high light x salinity
high light x cold
high light x drought
high light
heat
heat x salinity


C
4
3
2
1
0
−1
−2
−3
−4
F
D
A
E
B
C
6
3
2
4
5
7
1
GSH
Glucose 6-phosphate
Ribose 5-phosphate
alpha-Ketoglutaric acid
Ornithine
Aspartic acid
Citrulline
Glutamic acid
GSSG
Shikimic acid
Xylose
Citric acid
Arginine
Asparagine
Raffinose
Tryptophan
Alanine
Phenylalanine
Leucine
Mannitol
Tyrosine
Dihydroxyacetone phosphate
Urea
Glucose
Pyruvic acid
Glycine
Histidine
Threonine
Serine
Glutamine
Fructose
Malic acid
Lysine
Valine
Proline
gamma-Aminobutyric acid
Succinic acid
Fumaric acid
Fructose 6-phosphate
Sucrose
Maltose
Adenosine
Guanine
Adenine
Guanosine monophosphate
high light x heat
heat
heat x salinity
cold x drought
cold
cold x salinity
high light x salinity
heat x drought
drought
high light x drought
salinity
high light x cold
high light


D
4
3
2
1
0
−1
−2
−3
−4
A
C
E
B
F
D
2
6
3
4
7
5
1
Raffinose
Leucine
Mannitol
Tyrosine
Tryptophan
Alanine
Phenylalanine
GSH
Glucose 6-phosphate
Ribose 5-phosphate
Guanosine monophosphate
alpha-Ketoglutaric acid
Ornithine
Aspartic acid
Citrulline
Citric acid
Arginine
Asparagine
Shikimic acid
Xylose
Glutamine
Serine
Glutamic acid
GSSG
Maltose
Lysine
Valine
gamma-Aminobutyric acid
Proline
Succinic acid
Fumaric acid
Fructose 6-phosphate
Sucrose
Adenine
Adenosine
Guanine
Dihydroxyacetone phosphate
Urea
Glycine
Histidine
Threonine
Pyruvic acid
Glucose
Fructose
Malic acid
cold x drought
cold
cold x salinity
salinity
high light x cold
high light
high light x salinity
heat x drought
drought
high light x drought
high light x heat
heat
heat x salinity

E
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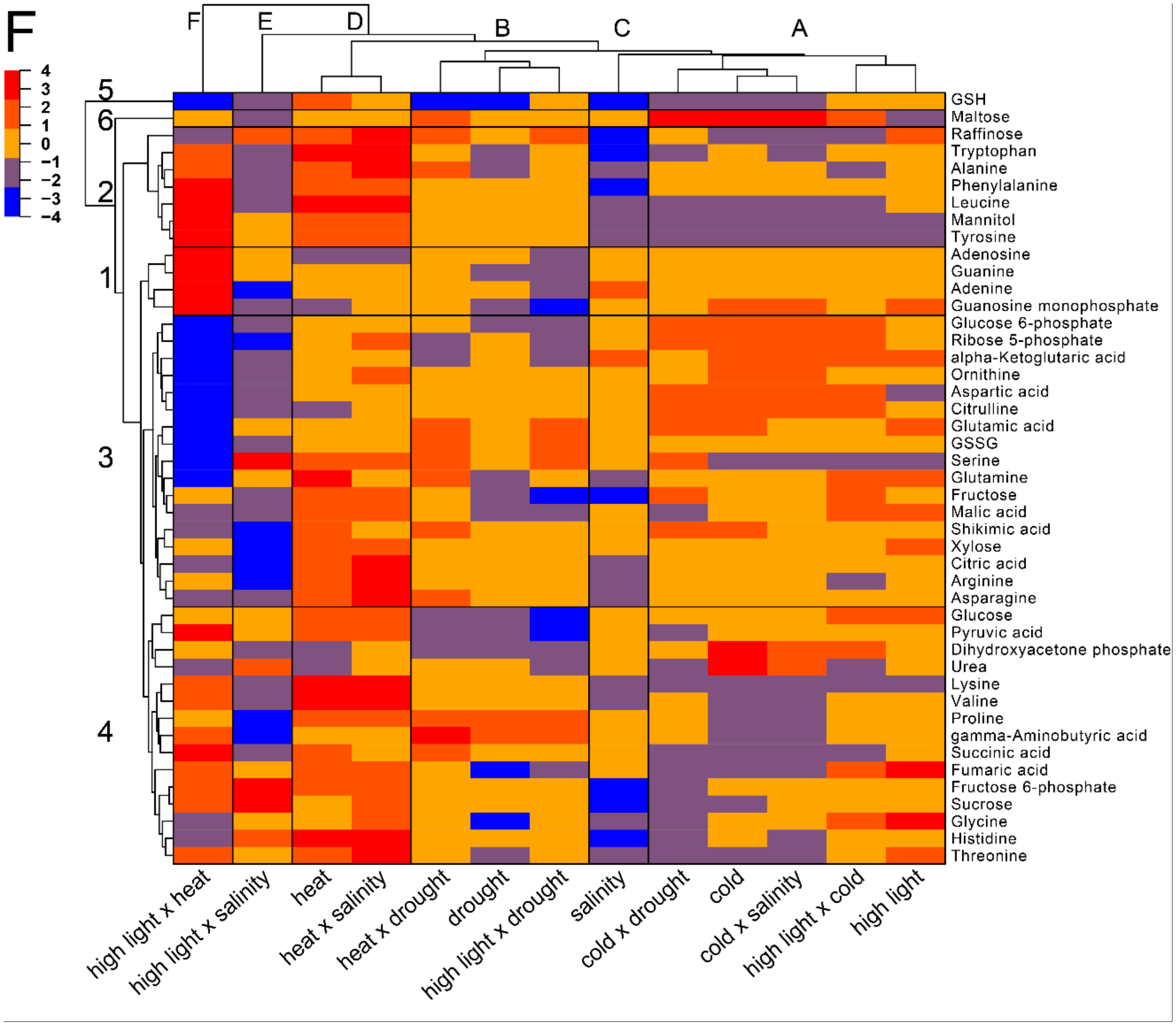
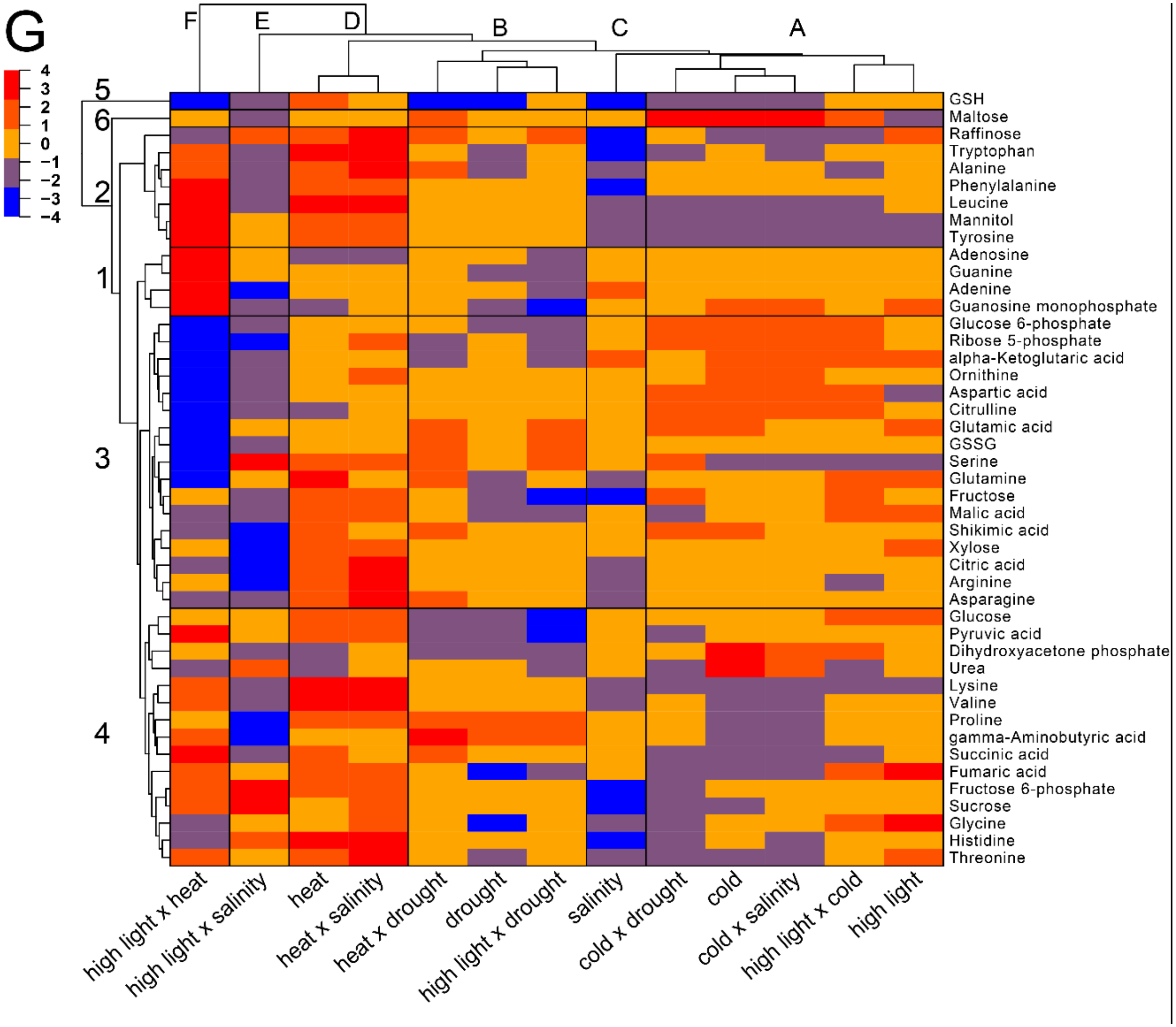
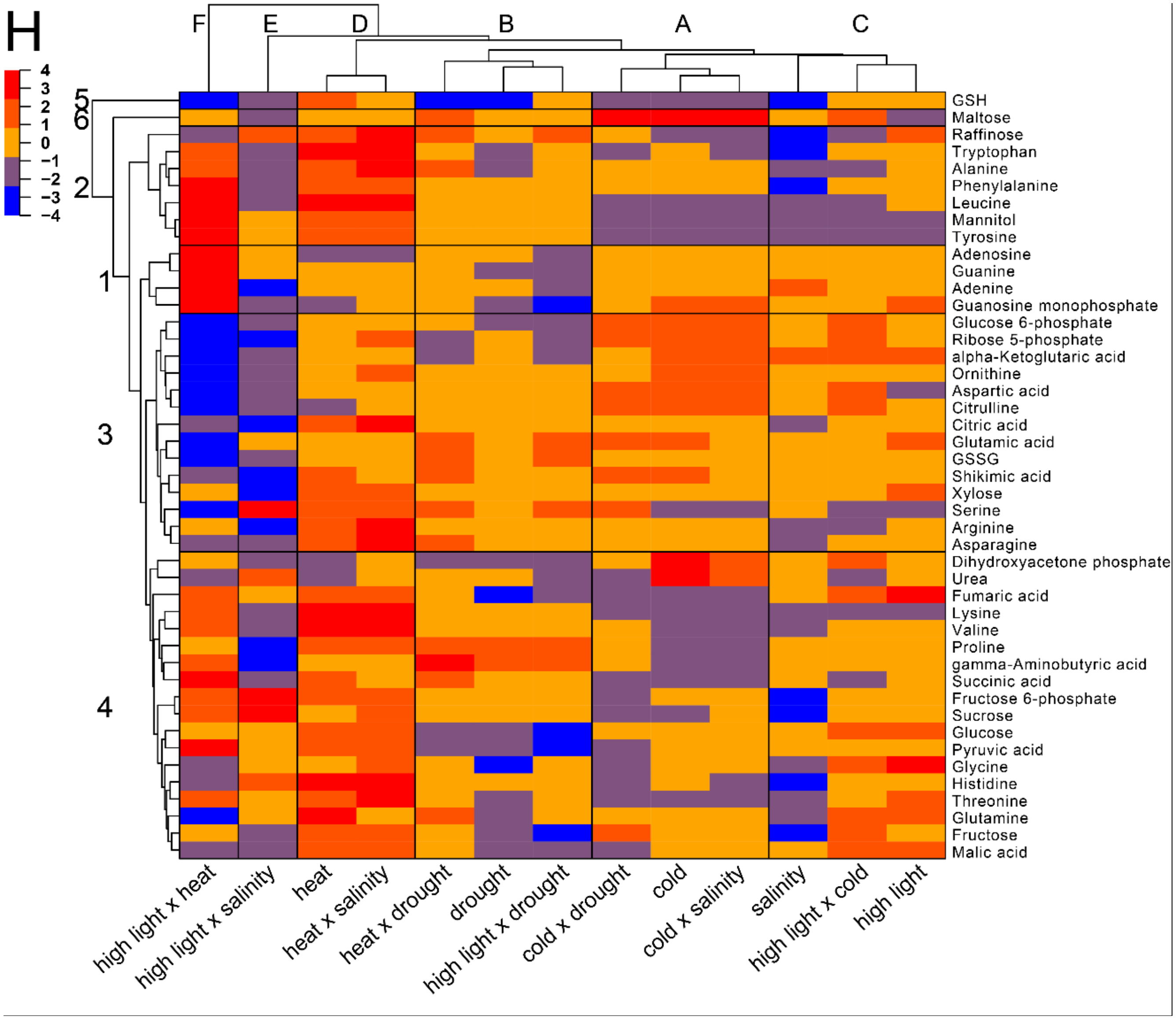
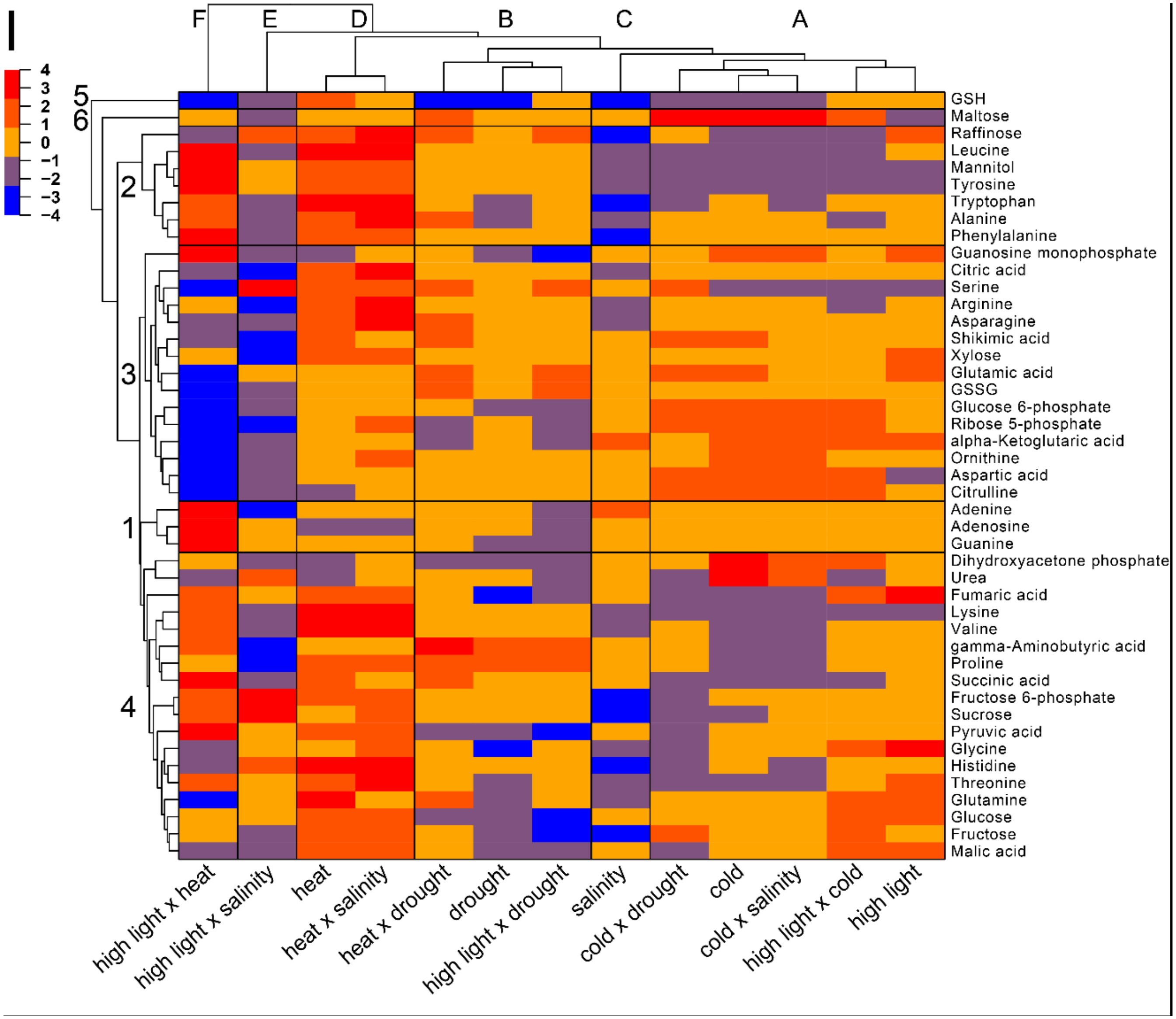
3
2
1
0
−1
−2
−3
−4
E
B
C
D
F
A
6
4
7
3
5
2
1
GSH
Citrulline
Ornithine
alpha-Ketoglutaric acid
Aspartic acid
Citric acid
Glucose 6-phosphate
Ribose 5-phosphate
Glutamic acid
GSSG
Arginine
Asparagine
Shikimic acid
Xylose
Maltose
Raffinose
Mannitol
Tyrosine
Fumaric acid
Alanine
Phenylalanine
Leucine
Tryptophan
Glucose
Pyruvic acid
Glutamine
Serine
Glycine
Histidine
Threonine
Fructose
Malic acid
Fructose 6-phosphate
Sucrose
Dihydroxyacetone phosphate
Urea
Adenosine
Guanine
Adenine
Guanosine monophosphate
gamma-Aminobutyric acid
Succinic acid
Proline
Lysine
Valine
high light x salinity
drought
salinity
heat
heat x salinity
high light
high light x cold
high light x drought
high light x heat
heat x drought
cold
cold x drought
cold x salinity

F
4
3
2
1
0
−1
−2
−3
−4
F
E
D
B
C
A
5
6
2
1
3
4
GSH
Maltose
Raffinose
Tryptophan
Alanine
Phenylalanine
Leucine
Mannitol
Tyrosine
Adenosine
Guanine
Adenine
Guanosine monophosphate
Glucose 6-phosphate
Ribose 5-phosphate
alpha-Ketoglutaric acid
Ornithine
Aspartic acid
Citrulline
Glutamic acid
GSSG
Serine
Glutamine
Fructose
Malic acid
Shikimic acid
Xylose
Citric acid
Arginine
Asparagine
Glucose
Pyruvic acid
Dihydroxyacetone phosphate
Urea
Lysine
Valine
Proline
gamma-Aminobutyric acid
Succinic acid
Fumaric acid
Fructose 6-phosphate
Sucrose
Glycine
Histidine
Threonine
high light x heat
high light x salinity
heat
heat x salinity
heat x drought
drought
high light x drought
salinity
cold x drought
cold
cold x salinity
high light x cold
high light

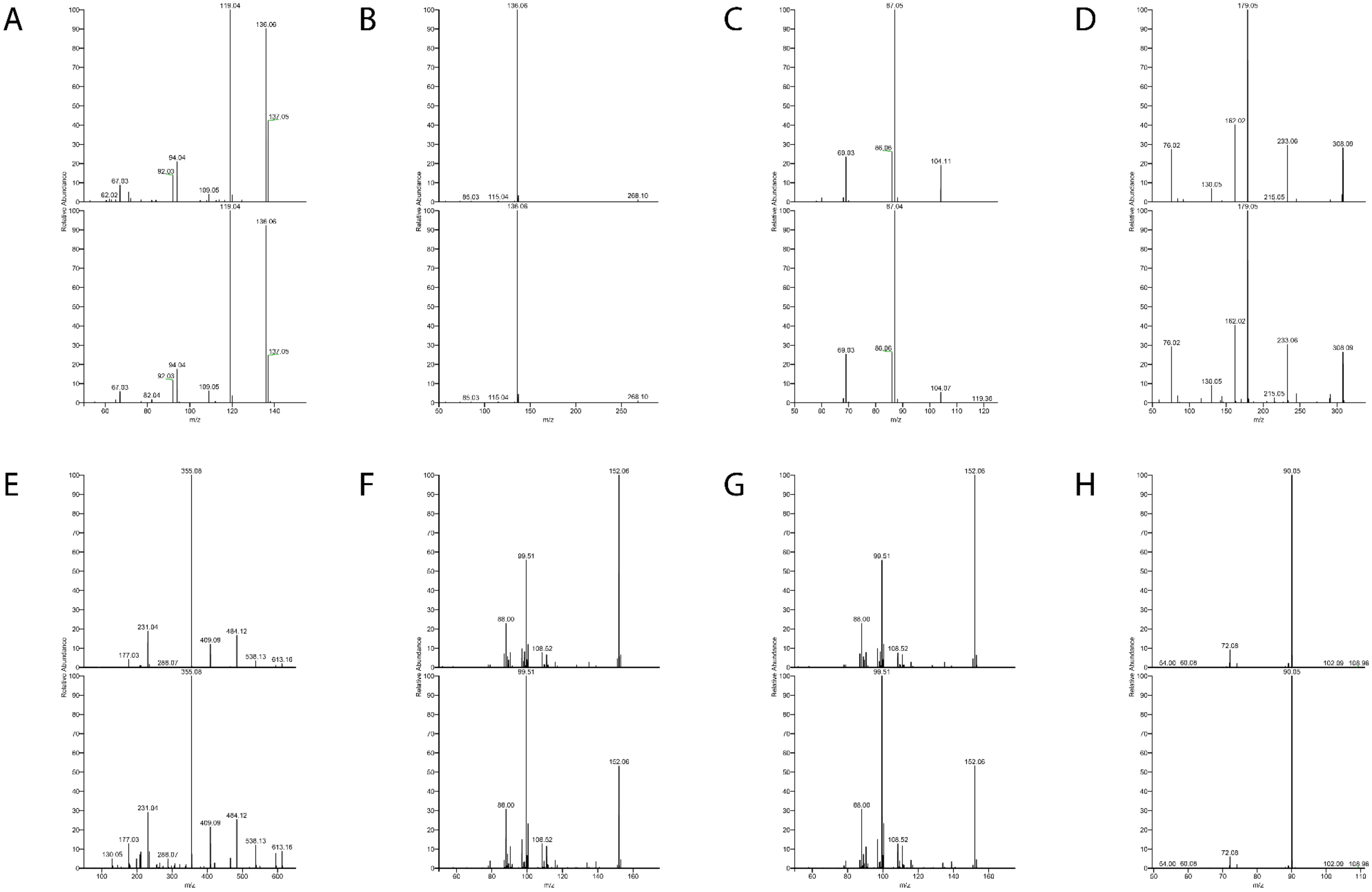

G
4
3
2
1
0
−1
−2
−3
−4
F
E
D
B
C
A
5
6
2
1
3
4
GSH
Maltose
Raffinose
Tryptophan
Alanine
Phenylalanine
Leucine
Mannitol
Tyrosine
Adenosine
Guanine
Adenine
Guanosine monophosphate
Glucose 6-phosphate
Ribose 5-phosphate
alpha-Ketoglutaric acid
Ornithine
Aspartic acid
Citrulline
Glutamic acid
GSSG
Serine
Glutamine
Fructose
Malic acid
Shikimic acid
Xylose
Citric acid
Arginine
Asparagine
Glucose
Pyruvic acid
Dihydroxyacetone phosphate
Urea
Lysine
Valine
Proline
gamma-Aminobutyric acid
Succinic acid
Fumaric acid
Fructose 6-phosphate
Sucrose
Glycine
Histidine
Threonine
high light x heat
high light x salinity
heat
heat x salinity
heat x drought
drought
high light x drought
salinity
cold x drought
cold
cold x salinity
high light x cold
high light

H
4
3
2
1
0
−1
−2
−3
−4
F
E
D
B
A
C
5
6
2
1
3
4
GSH
Maltose
Raffinose
Tryptophan
Alanine
Phenylalanine
Leucine
Mannitol
Tyrosine
Adenosine
Guanine
Adenine
Guanosine monophosphate
Glucose 6-phosphate
Ribose 5-phosphate
alpha-Ketoglutaric acid
Ornithine
Aspartic acid
Citrulline
Citric acid
Glutamic acid
GSSG
Shikimic acid
Xylose
Serine
Arginine
Asparagine
Dihydroxyacetone phosphate
Urea
Fumaric acid
Lysine
Valine
Proline
gamma-Aminobutyric acid
Succinic acid
Fructose 6-phosphate
Sucrose
Glucose
Pyruvic acid
Glycine
Histidine
Threonine
Glutamine
Fructose
Malic acid
high light x heat
high light x salinity
heat
heat x salinity
heat x drought
drought
high light x drought
cold x drought
cold
cold x salinity
salinity
high light x cold
high light

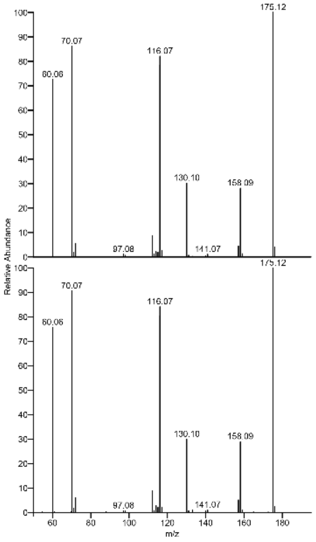

I
4
3
2
1
0
−1
−2
−3
−4
F
E
D
B
C
A
5
6
2
3
1
4
GSH
Maltose
Raffinose
Leucine
Mannitol
Tyrosine
Tryptophan
Alanine
Phenylalanine
Guanosine monophosphate
Citric acid
Serine
Arginine
Asparagine
Shikimic acid
Xylose
Glutamic acid
GSSG
Glucose 6-phosphate
Ribose 5-phosphate
alpha-Ketoglutaric acid
Ornithine
Aspartic acid
Citrulline
Adenine
Adenosine
Guanine
Dihydroxyacetone phosphate
Urea
Fumaric acid
Lysine
Valine
gamma-Aminobutyric acid
Proline
Succinic acid
Fructose 6-phosphate
Sucrose
Pyruvic acid
Glycine
Histidine
Threonine
Glutamine
Glucose
Fructose
Malic acid
high light x heat
high light x salinity
heat
heat x salinity
heat x drought
drought
high light x drought
salinity
cold x drought
cold
cold x salinity
high light x cold
high light

Supplemental Figure 3-6. Hierarchical clustering analysis (HCA) for potential stress metabolic signatures and their precursors, intermediates, or products in the same pathway.

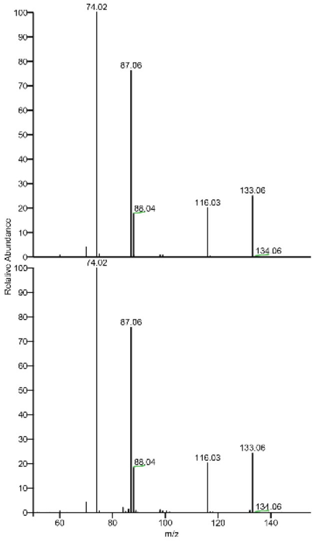
The top horizontal side bar reflects the log2-transformed fold changes of average for both positive and negative observations as reported in Supplemental Table 3-5. Clusters were generated using the complete linkage and Manhattan distance function (Supplemental Figure 3-6A), complete linkage and Maximum distance function (Supplemental Figure 3-6B), ward methods using and Euclidean distance function (Supplemental Figure 3-6C), Ward’s methods and Manhattan distance function (Supplemental Figure 3-6D), Ward’s methods and Maximum distance function (Supplemental Figure 3-6E), McQuitty’s methods and Euclidean distance function (Supplemental Figure 3-6F), McQuitty’s methods and Manhattan distance function (Supplemental Figure 3-6G), average linkage and Euclidean distance function (Supplemental Figure 3-6H), average linkage and Manhattan distance function (Supplemental Figure 3-6I).


A
B
C
D
E
F
G
H
Relative Abundance
m/z
119.04
136.06
137.05
94.04
92.03
67.03
62.02
109.05
82.04
136.06
85.03
115.04
268.10
87.05
87.04
69.03
86.06
104.11
104.07
119.36
179.05
162.02
76.02
130.05
215.05
233.06
308.09
355.08
231.04
177.03
130.05
288.07
409.09
484.12
538.13
613.16
152.06
99.51
88.00
108.52
90.05
72.08
54.00
60.08
102.09
108.96

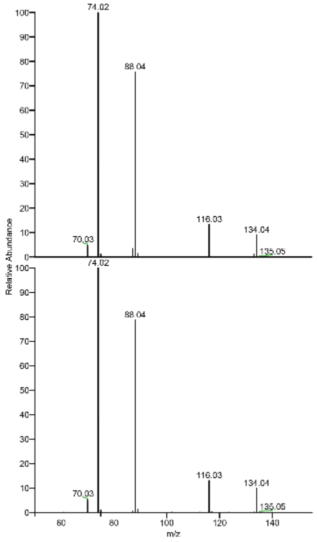
I


175.12
70.07
60.06
116.07
130.10
158.09
97.08
141.07
175.12
70.07
60.06
116.07
130.10
158.09
97.08
141.07
Relative Abundance
m/z
60
80
100
120
140
160
180

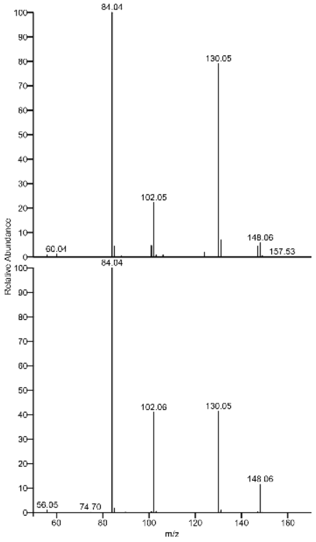
J


74.02
87.06
88.04
116.03
133.06
134.06
74.02
87.06
88.04
116.03
133.06
134.06
Relative Abundance
m/z
60
80
100
120
140

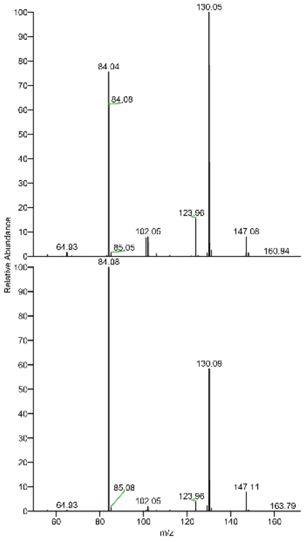
K


74.02
88.04
70.03
116.03
134.04
135.05
74.02
88.04
70.03
116.03
134.04
135.05
Relative Abundance
m/z
60
80
100
120
140

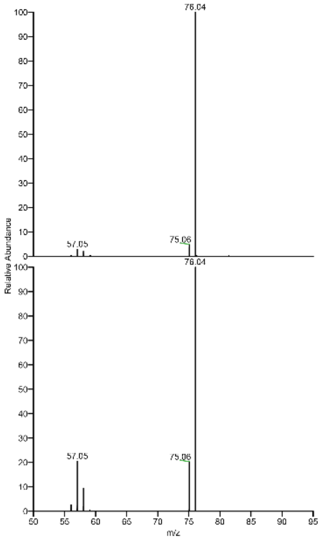
L


84.04
130.05
102.05
60.04
148.06
157.53
84.04
102.06
130.05
148.06
56.05
74.70
Relative Abundance
m/z
60
80
100
120
140
160

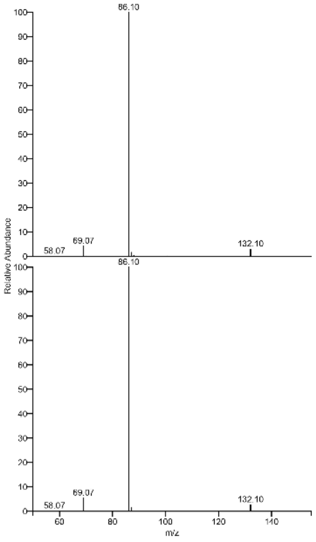
M


130.05
84.04
84.08
123.96
102.05
147.08
64.93
85.05
160.94
84.08
130.09
85.08
147.11
64.93
102.05
123.96
163.79
Relative Abundance
m/z
60
80
100
120
140
160

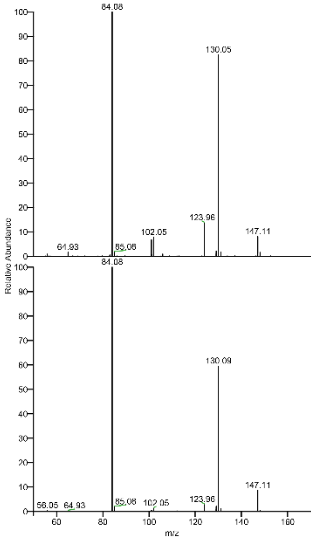
N

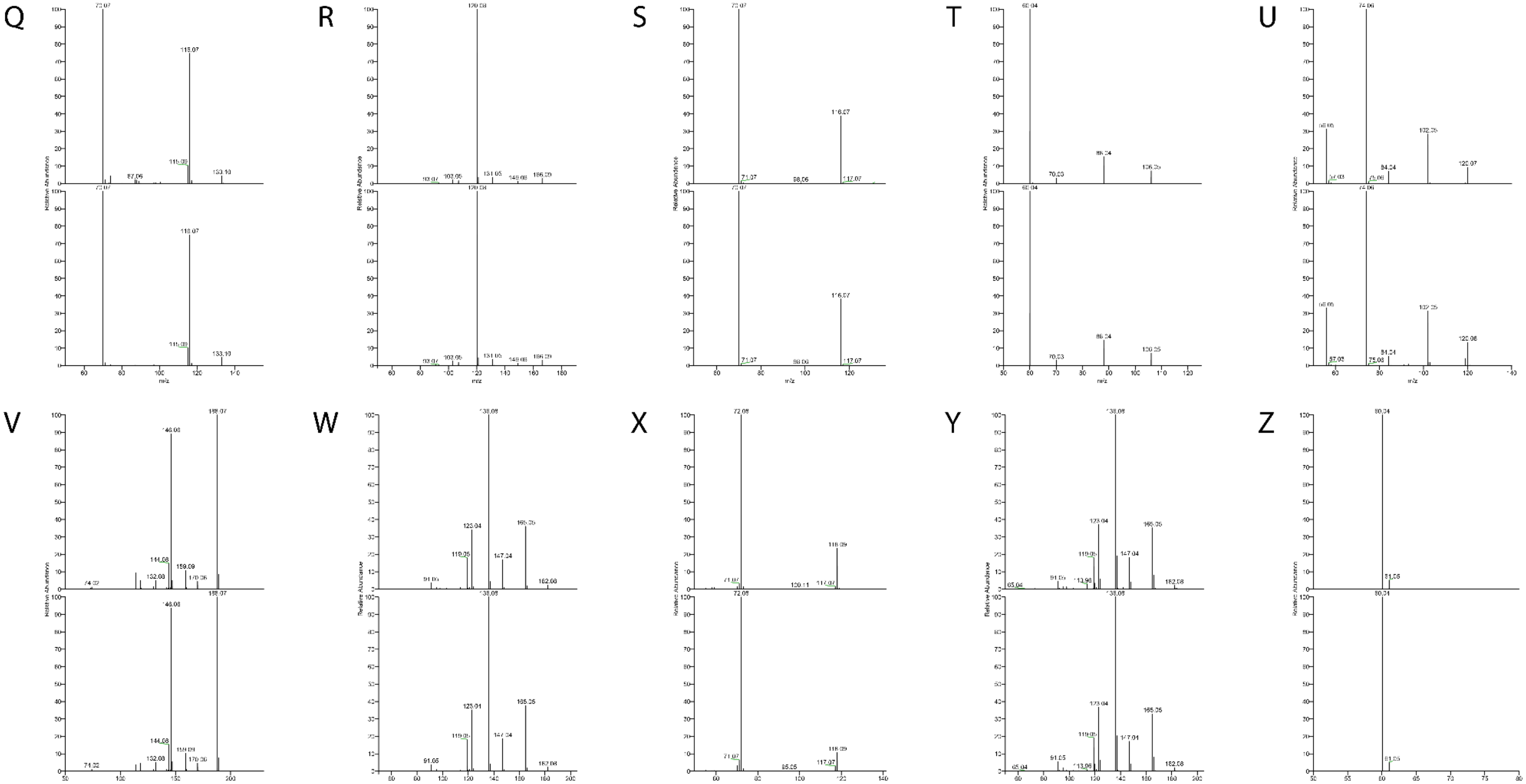

76.04
57.05
75.06
76.04
57.05
75.06
Relative Abundance
m/z
50
55
60
65
70
75
80
85
90
95

O


86.10
58.07
69.07
132.10
86.10
69.07
58.07
132.10
Relative Abundance
m/z
60
80
100
120
140

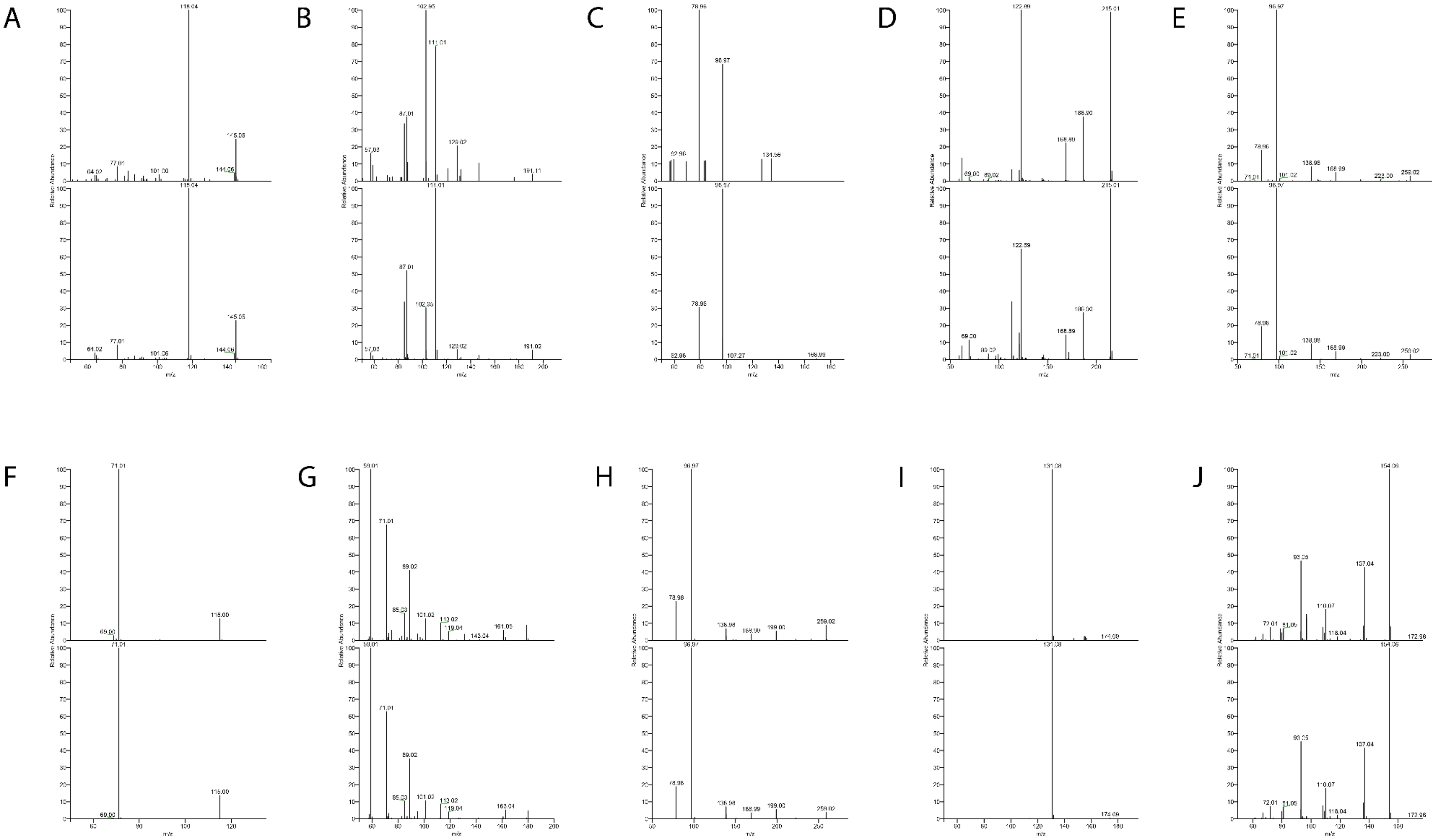
P

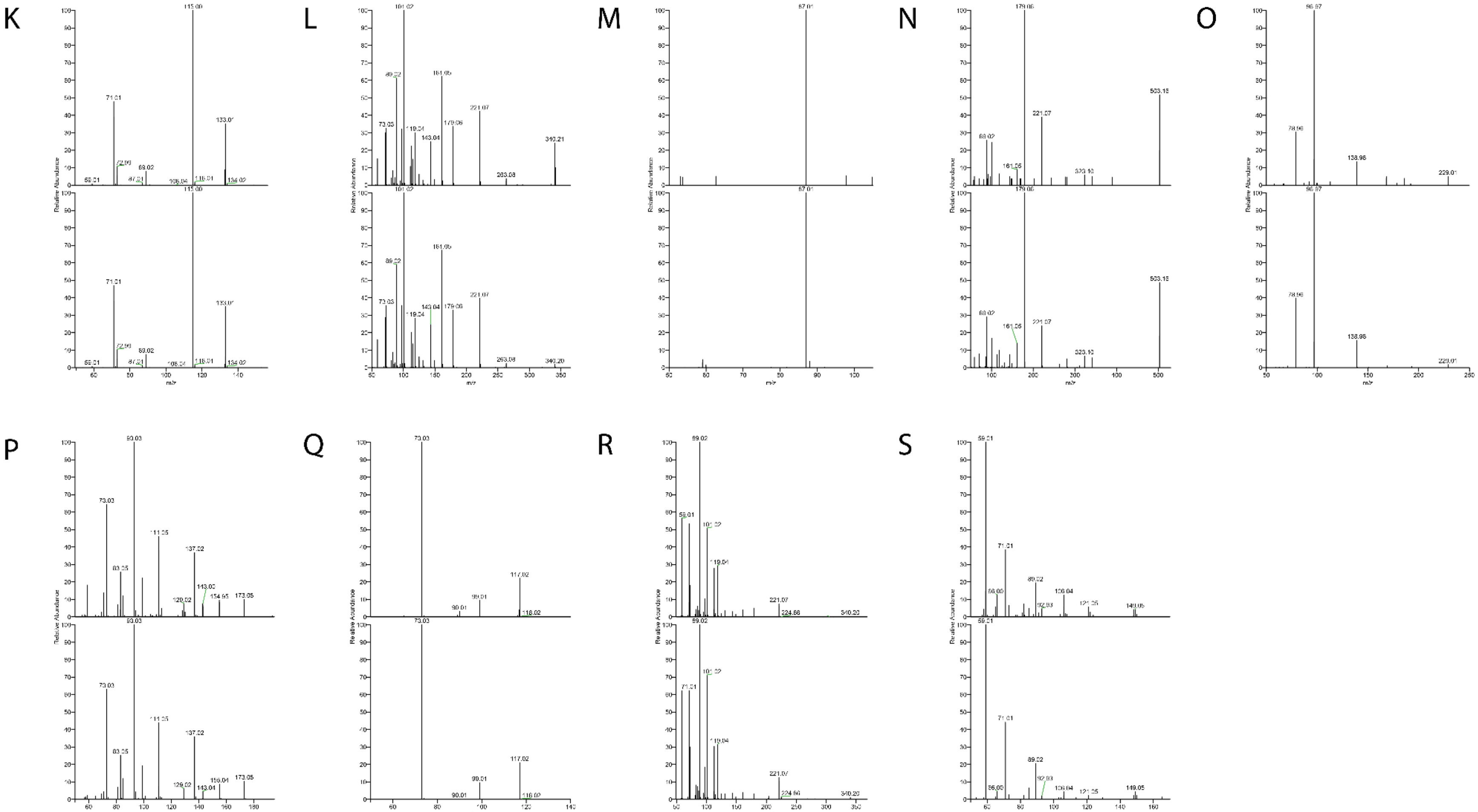

84.08
130.05
123.96
102.05
147.11
64.93
85.08
84.08
130.09
147.11
56.05
64.93
85.08
102.05
123.96
Relative Abundance
m/z
60
80
100
120
140
160



Supplemental Figure 3-7. Metabolites that were identified by authentic standards with *m/z*, retention time, and fragmentation in positive mode.

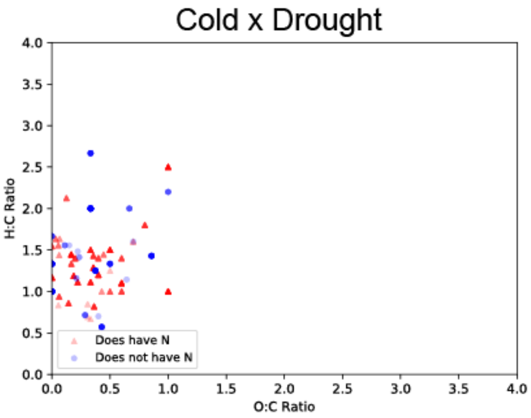
The top scheme represents metabolite in sample. The bottom scheme represents metabolite in standard. Standard compounds include: adenine (A), adenosine (B), γ-aminobutyric acid (C), GSH (D), GSSG (E), guanine (F), guanosine monophosphate (G), L-alanine (H), L-arginine (I), L-asparagine (J), L-aspartic acid (K), L-glutamic acid (L), L-glutamine (M), L-glycine (N), L-leucine (O), L-lysine (P), L-ornithine (Q), L-phenylalanine (R), L-proline (S), L-serine (T), L-threonine (U), L-tryptophan (V), L-tyrosine (W), L-valine (X), mannitol (Y), urea (Z). It should be noted that while standard compounds of the specified stereochemistry were used, analytical procedures that would resolve enantiomers were not employed. Because of this, absolute stereo-assignments for each of these compounds were not included as part of the assignment, though it is likely that the vast majority of amino acids identified are of the L-configuration as D-amino acids are unusual in plants and typically occur in specialized metabolic contexts.

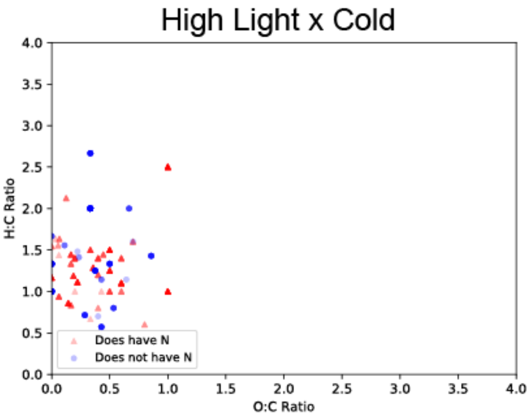

A
118.04
145.05
64.02
77.01
101.06
144.06
118.04
145.05
61.02
77.01
101.06
144.06
B
102.95
111.01
87.01
57.03
129.02
191.11
111.01
87.01
102.96
57.03
129.02
191.02
C
78.96
96.97
62.96
134.56
96.97
78.96
52.96
107.27
168.99
D
122.89
215.01
186.90
168.89
69.00
89.02
215.01
122.89
69.00
89.02
168.89
186.90
E
96.97
78.96
71.01
101.02
138.98
168.99
223.00
259.02
96.97
78.96
71.01
101.02
138.98
168.99
223.00
259.02
F
71.01
115.00
69.00
71.01
115.00
69.00
G
59.01
71.01
89.02
85.03
101.02
113.02
119.04
143.04
161.05
59.01
71.01
89.02
85.03
101.02
113.02
119.04
163.04
H
96.97
78.96
136.98
168.99
199.00
259.02
96.97
78.96
136.98
168.99
199.00
259.02
I
131.08
174.09
131.08
174.09
J
154.06
93.05
137.04
110.07
72.01
91.05
118.04
172.96
154.06
93.05
137.04
110.07
72.01
91.05
118.04
172.96
Relative Abundance
m/z

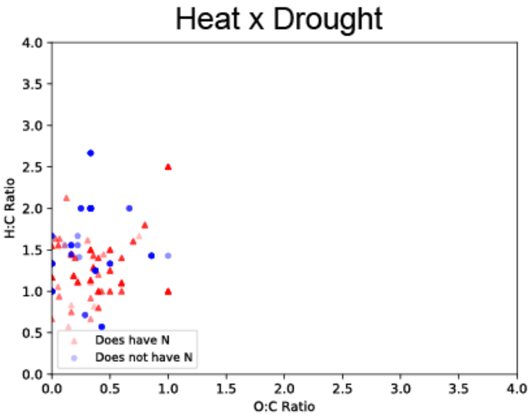


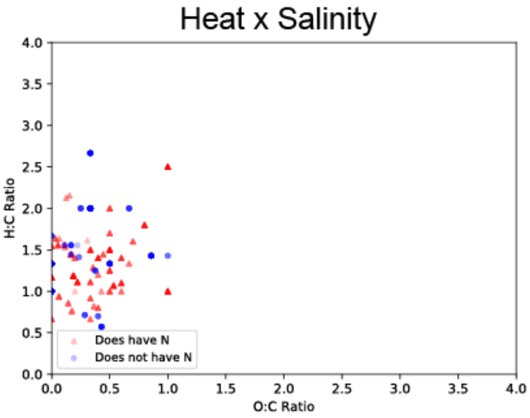
Supplemental Figure 3-8. Metabolites that were identified by authentic standards with *m/z*, retention time, and fragmentation in negative mode.

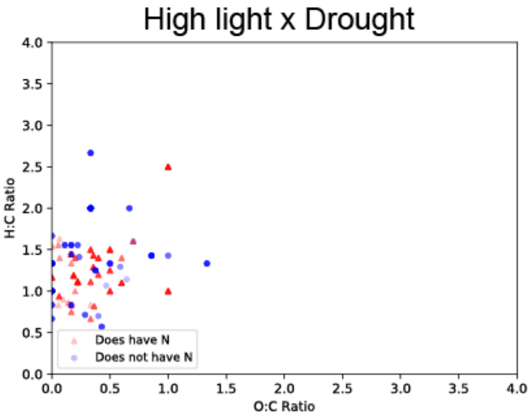
The top scheme represents metabolite in sample. The bottom scheme represents metabolite in standard. Standard compounds include: α-ketoglutaric acid (A), citric acid (B), dihydroxyacetone phosphate (C), fructose (D), fructose 6-phosphate (E), fumaric acid (F), glucose (G), glucose 6-phosphate (H), L-citrulline (I), L-histidine (J), malic acid (K), maltose (L), pyruvic acid (M), raffinose (N), ribose 5-phosphate (O), shikimic acid (P), succinic acid (Q), sucrose (R), xylose (S). As noted above, while standard compounds of the specified stereochemistry were used, analytical procedures that would resolve enantiomers were not employed.

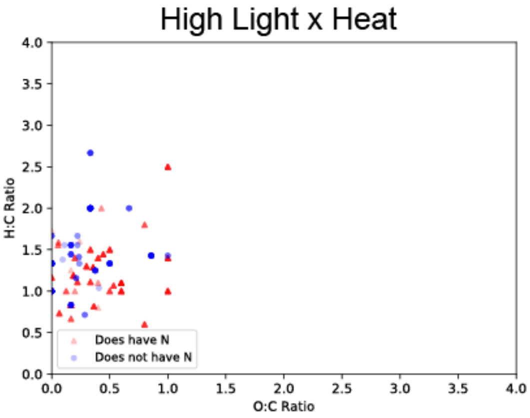

Cold x Drought


High Light x Cold


Heat x Drought


Heat x Salinity


High light x Drought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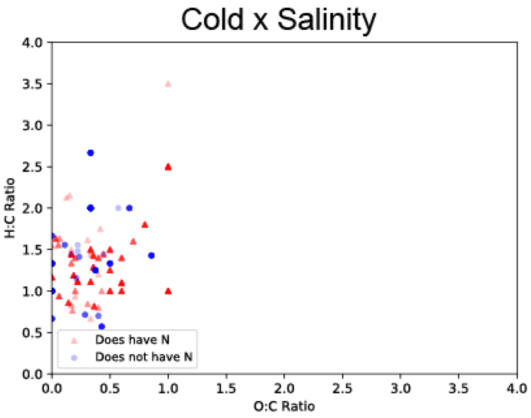
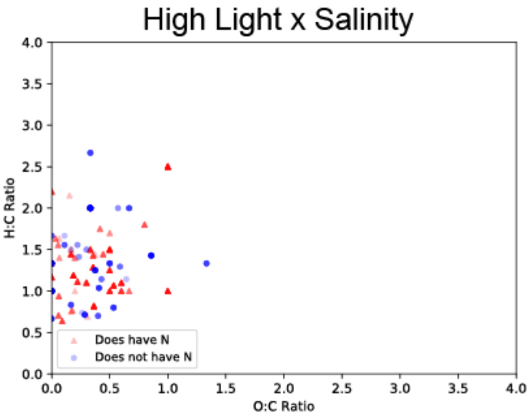
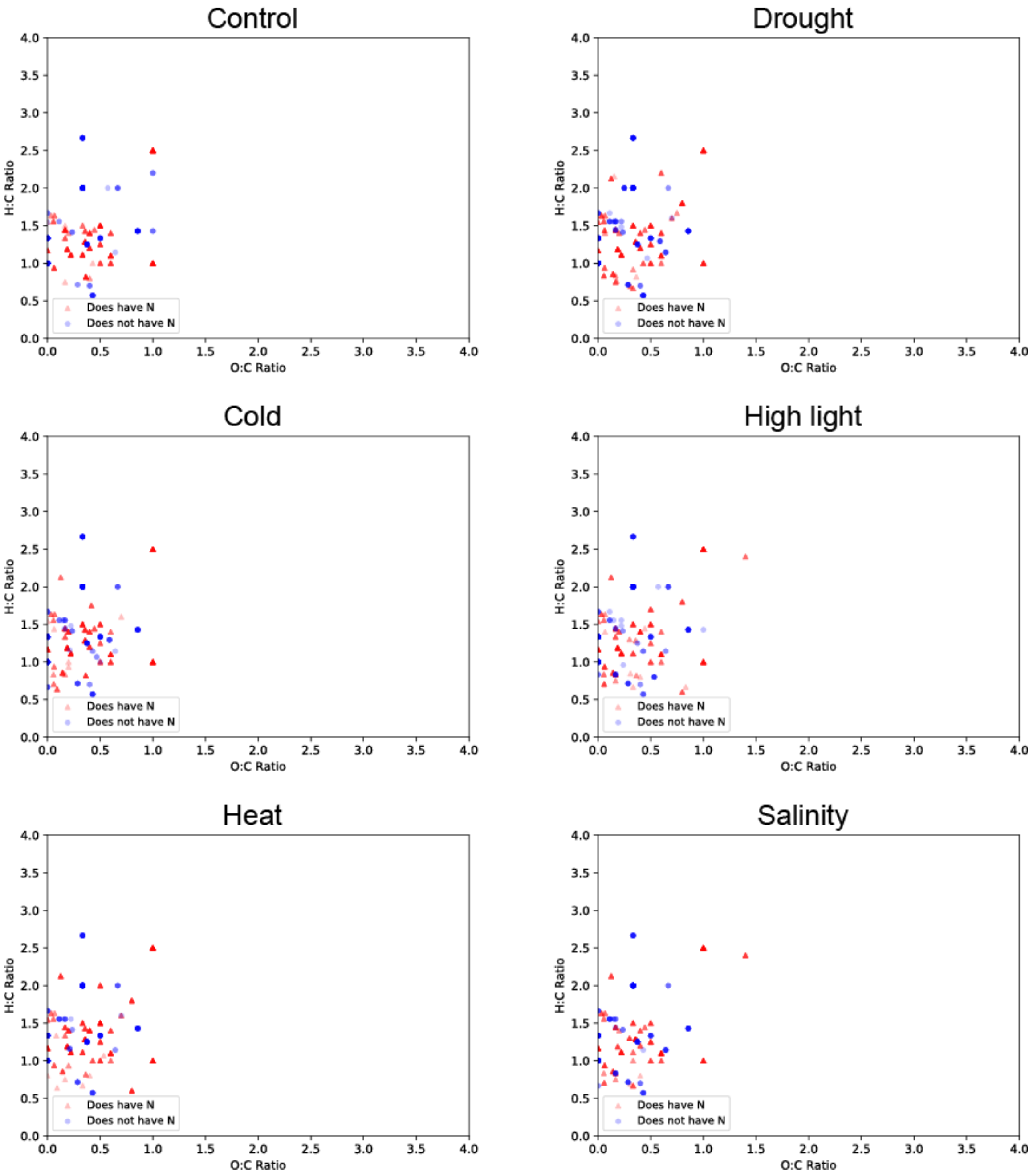
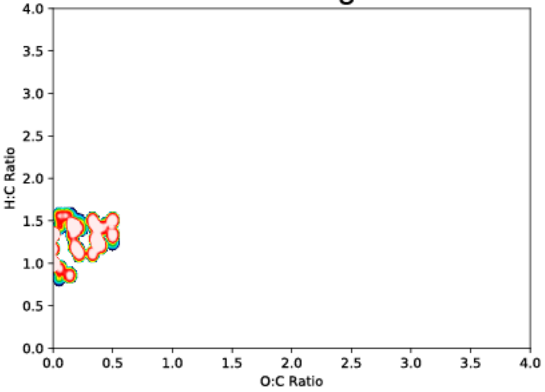

Cold x Salinity


High Light x Salinity

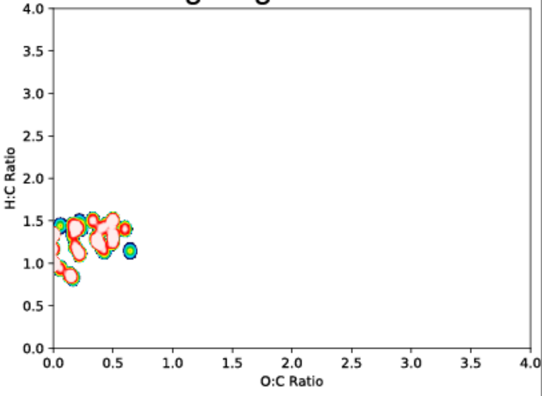


Supplemental Figure 3-9. The Van Krevelen diagrams of scatter plot for metabolic composition changes of all metabolic features.

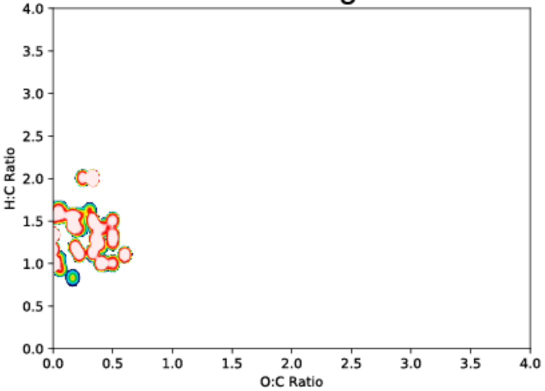
Cold x Drought



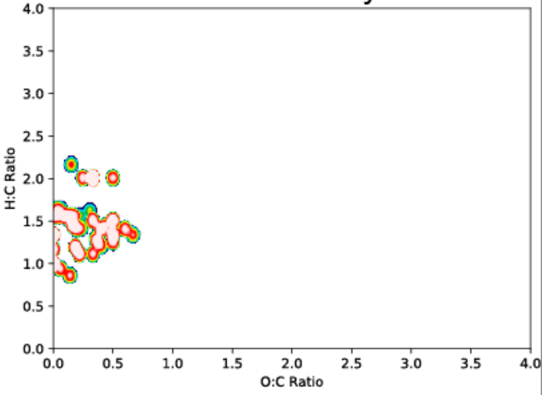
High Light x Cold



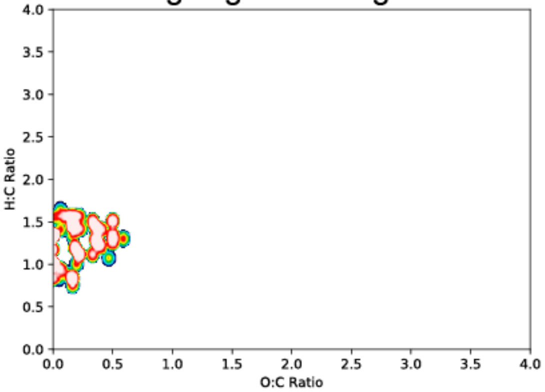
Heat x Drought



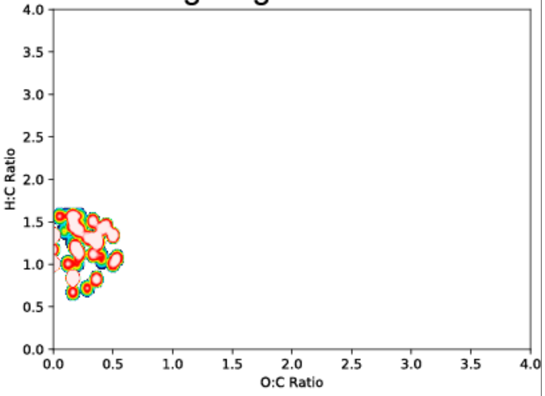
Heat x Salinity



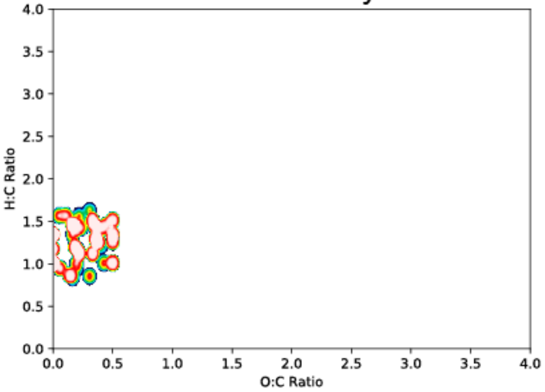
High light x Drought



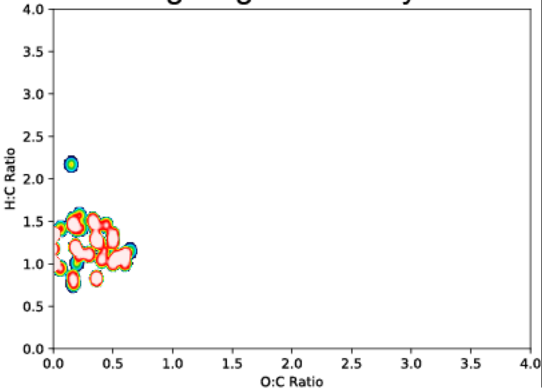
High Light x Heat

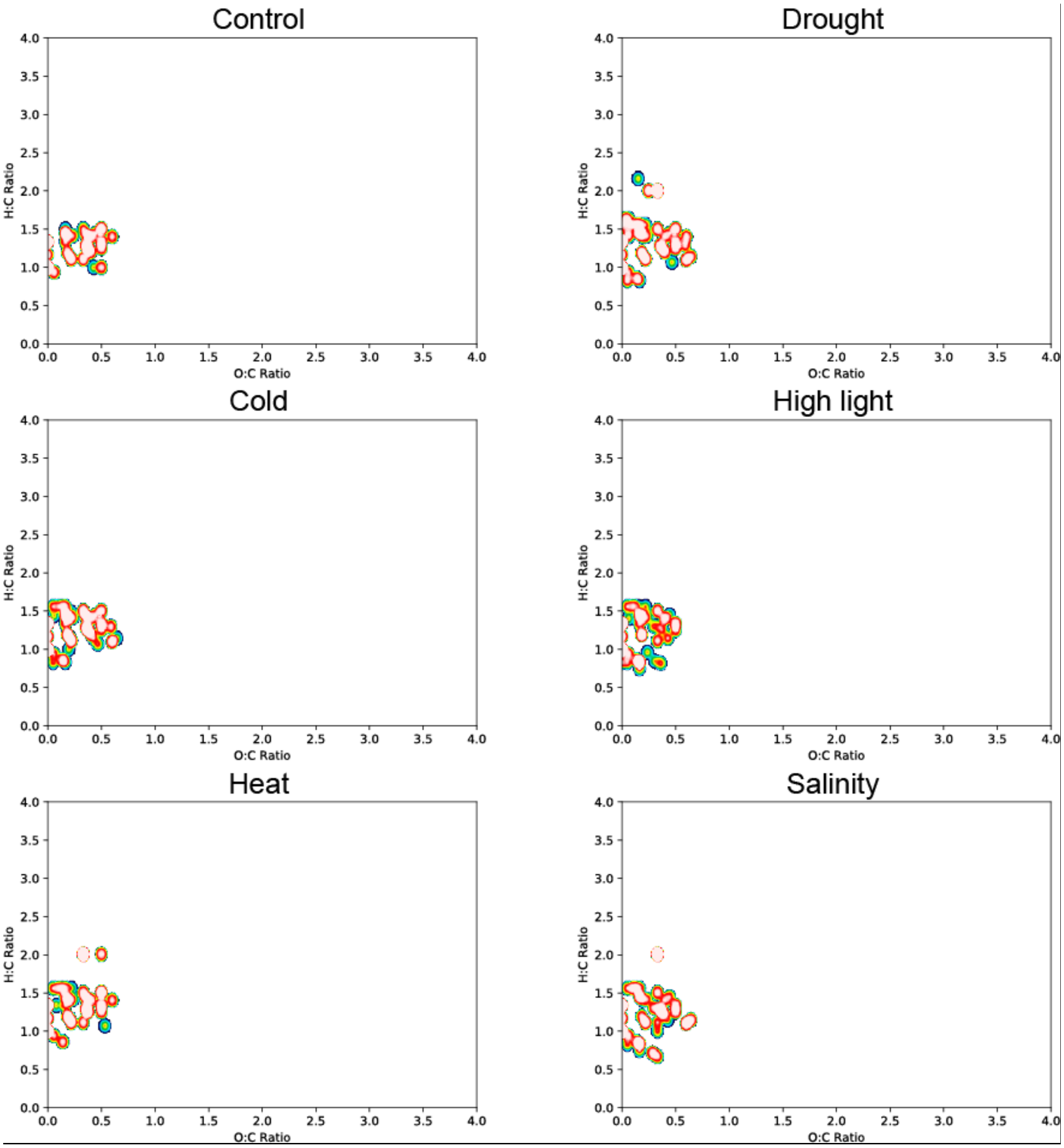


Cold x Salinity

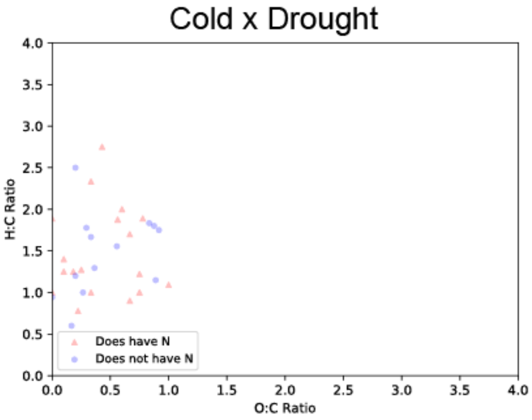


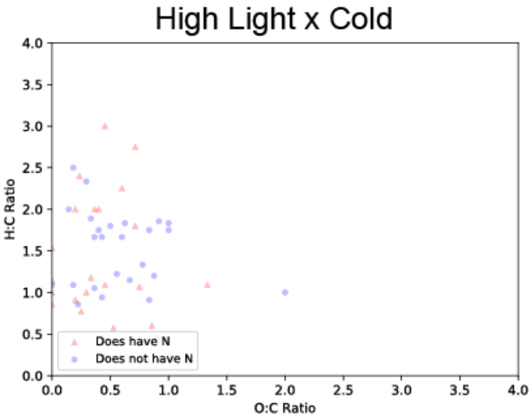
High Light x Salinity

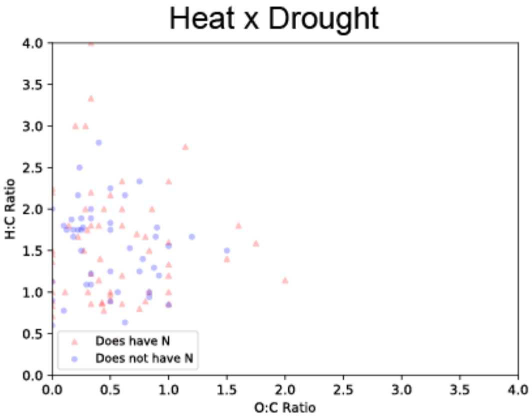


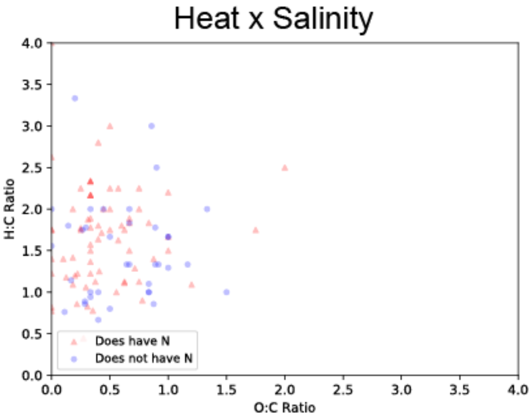


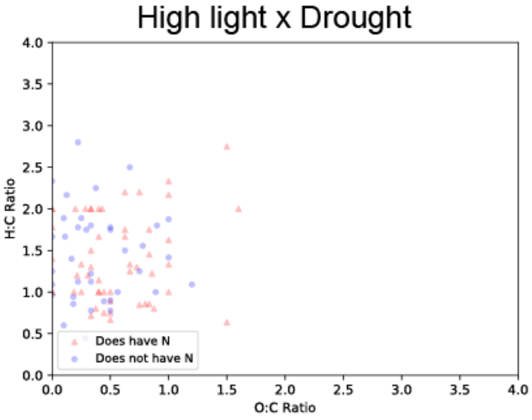
Supplemental Figure 3-10. The Van Krevelen diagrams of heatmap for metabolic composition changes of all metabolic features.

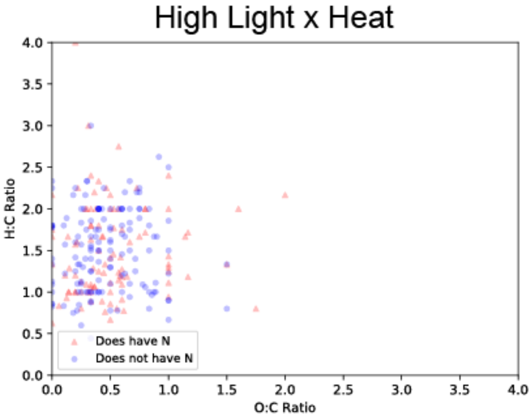

Cold x Drought

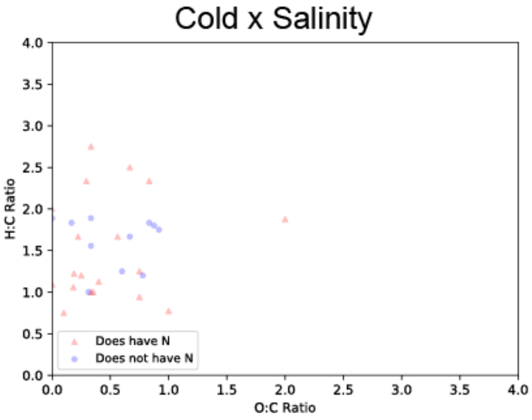

High Light x Cold

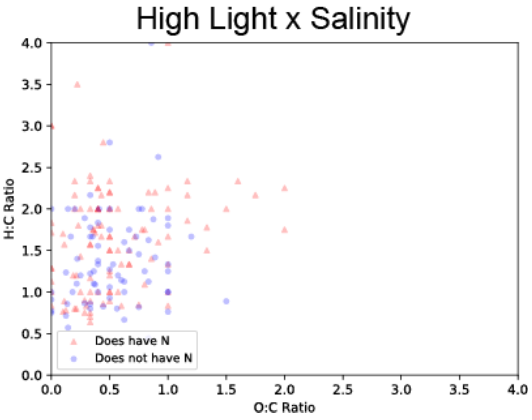

Heat x Drought

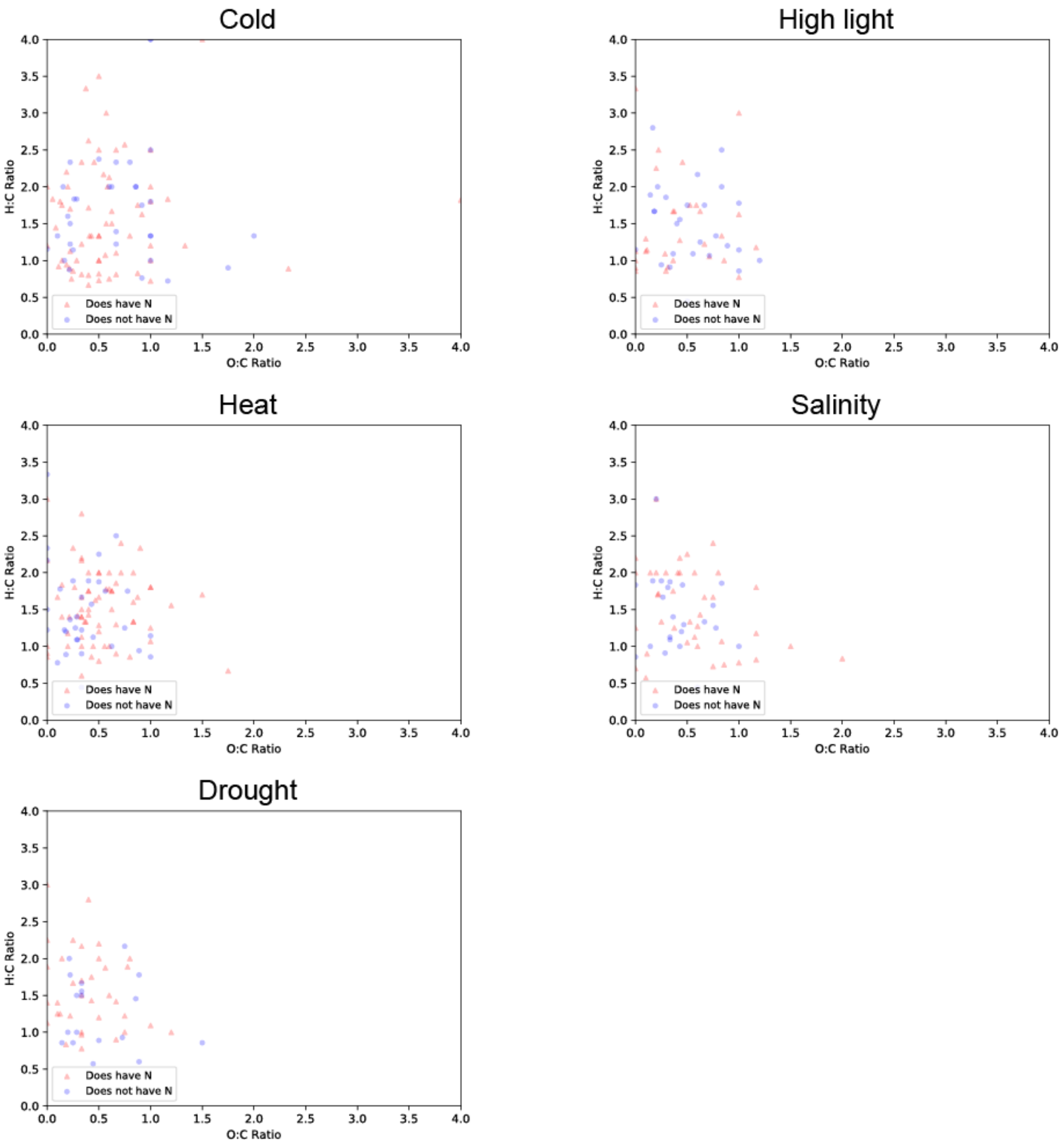

Heat x Salinity


High light x Drought

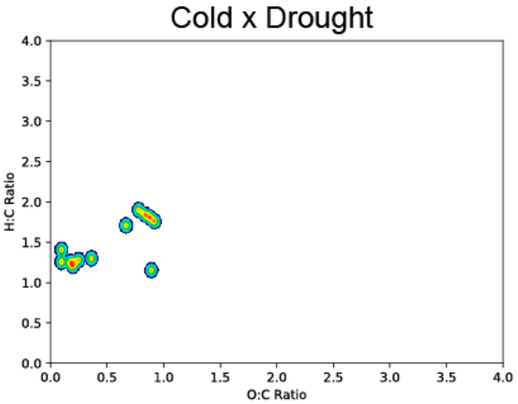

High Light x Heat

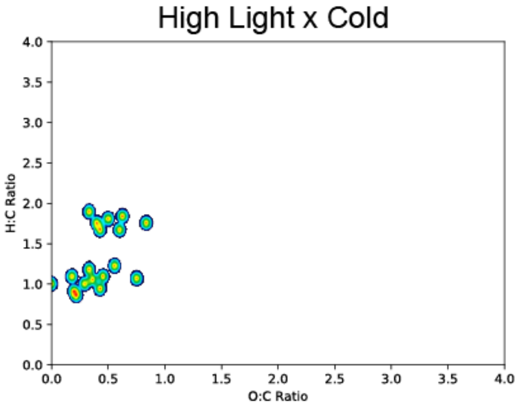

Cold x Salinity

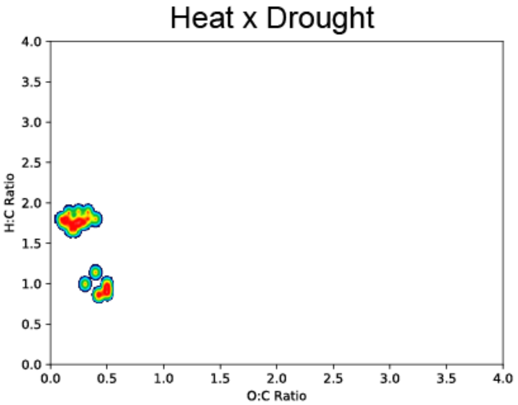

High Light x Salinity

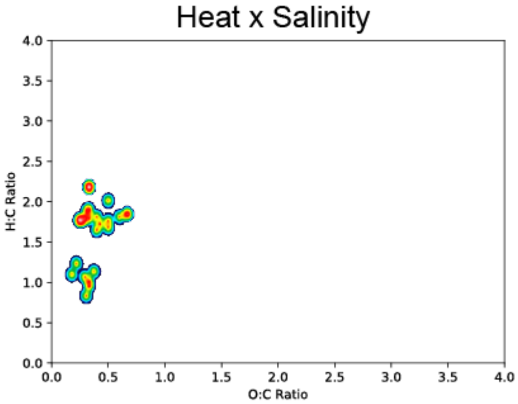


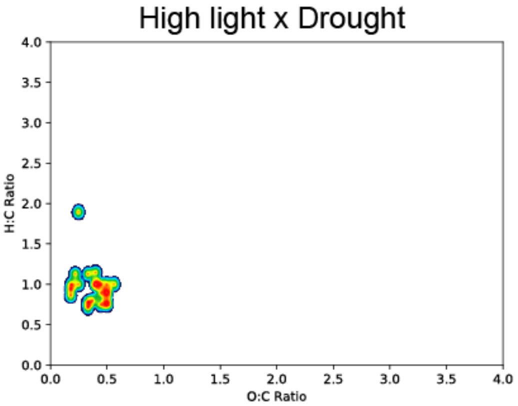
Supplemental Figure 3-11. The Van Krevelen diagrams of scatter plot for metabolic composition changes of metabolic features increased or decreased more than 2 fold in all treatments.

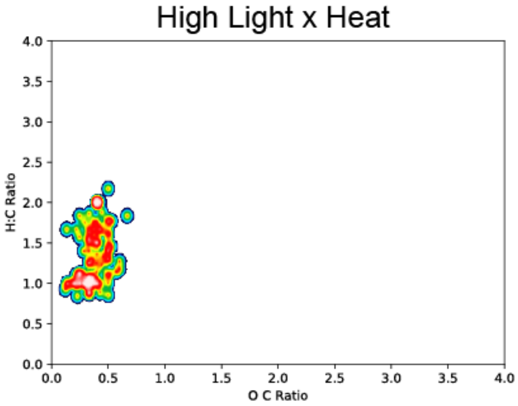

Cold x Drought

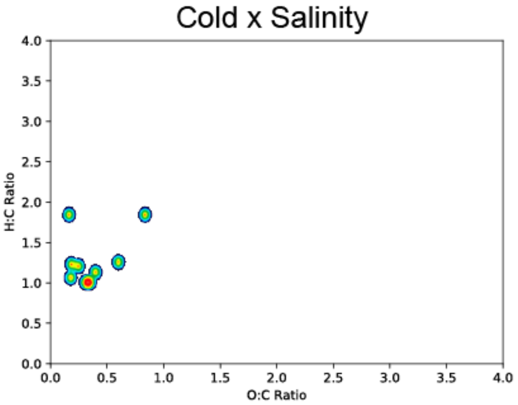

High Light x Cold

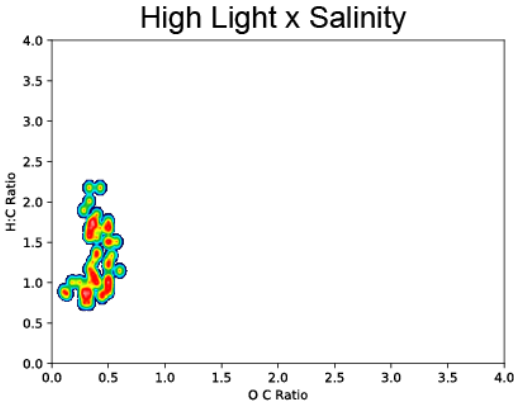

Heat x Drought

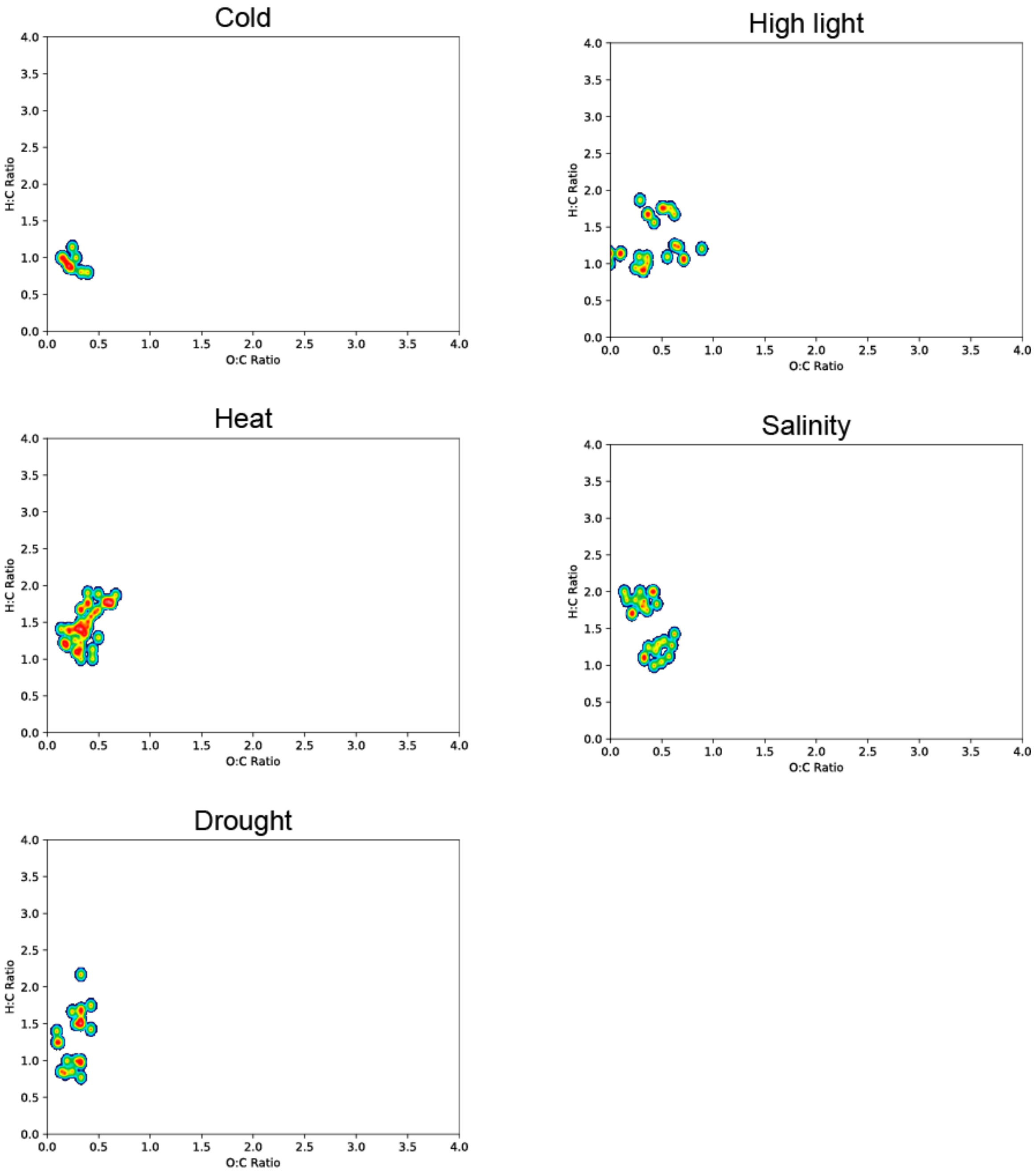

Heat x Salinity


High light x Drought


High Light x Heat


Cold x Salinity


High Light x Salinity



Supplemental Figure 3-12. The Van Krevelen diagrams of heatmap for metabolic composition changes of metabolic features increased or decreased more than 2 fold in all treatments.

Supplemental Table 3-1. Metabolic features with top 10 most positive and negative covariance loadings to OPLS-DA S-plot in different groups

M/z	**Retention time**	**Polarity**	**Covariance**	**Correlation**	**Vip_prediction**	**Treatment**	**Potential heuristical formula**	**Identified with reference standard**
132.1018	6.47	positive	3078	0.5	2.0	all treatments	$C_6H_{13}NO_2$	Leucine
116.0704	7.43	positive	2842	0.5	1.8	all treatments	$C_5H_9NO_2$	Proline
90.0548	8.59	positive	2663	0.6	2.3	all treatments	$C_3H_7NO_2$	Alanine
104.0704	6.65	positive	2557	0.4	1.5	all treatments	$C_4H_9NO_2$	gamma-Aminobutyric acid
86.0600	6.60	positive	2402	0.6	2.2	all treatments	C_4H_7NO	
118.0861	6.96	positive	2016	0.6	2.1	all treatments	$C_5H_{11}NO_2$	Valine
147.0762	10.56	positive	1848	0.2	0.8	all treatments	$C_5H_{10}N_2O_3$	Glutamine
72.0808	6.93	positive	1682	0.6	2.1	all treatments	C_4H_9N	
87.0440	6.65	positive	1454	0.4	1.5	all treatments	$C_4H_6O_2$	
166.0860	6.75	positive	1366	0.5	1.9	all treatments	$C_9H_{11}NO_2$	Phenylalanine
259.0226	19.06	negative	-535	-0.4	1.6	all treatments	$C_6H_{13}O_9P$	Glucose 6-phosphate
148.0603	11.01	positive	-573	-0.2	0.6	all treatments	$C_5H_9NO_4$	Glutamic acid
176.1028	11.61	positive	-576	-0.6	2.1	all treatments	$C_6H_{13}N_3O_3$	Citrulline
234.0194	7.40	positive	-613	-0.3	1.3	all treatments		
134.0446	12.03	positive	-766	-0.5	2.0	all treatments	$C_4H_7NO_4$	Aspartic acid
391.1194	7.38	positive	-826	-0.4	1.4	all treatments		
194.0501	7.42	negative	-1056	-0.3	1.3	all treatments		
88.0756	5.12	positive	-1373	-0.6	2.2	all treatments	C_4H_9NO	
196.0635	7.40	positive	-1399	-0.3	1.2	all treatments		
61.9882	10.57	negative	-2579	-0.4	1.3	all treatments		
175.1186	14.01	positive	804	0.5	1.0	cold	$C_6H_{14}N_4O_2$	Arginine
114.1025	12.22	positive	720	0.7	1.5	cold		
196.0635	7.40	positive	681	0.3	0.6	cold		
130.0497	10.55	positive	652	0.4	0.8	cold	$C_5H_7NO_3$	
98.9840	14.99	positive	569	0.5	1.1	cold	$C_2H_3KO_2$	
66.0683	12.22	positive	507	0.8	1.6	cold		
106.0498	11.45	positive	503	0.7	1.3	cold	$C_3H_7NO_3$	Serine
194.0501	7.42	negative	466	0.3	0.6	cold		

104.0704	6.65	positive	446	0.3	0.6	cold	$C_4H_9NO_2$	gamma-Aminobutyric acid
81.0447	1.94	positive	425	0.8	1.6	cold	$C_4H_4N_2$	
341.1104	12.04	negative	-514	-0.8	1.7	cold	$C_{12}H_{22}O_{11}$	Sucrose
259.0226	19.06	negative	-549	-1.0	1.9	cold	$C_6H_{13}O_9P$	Glucose 6-phosphate
133.0151	7.34	negative	-556	-0.6	1.3	cold	$C_4H_6O_5$	Malic acid
72.0808	6.93	positive	-567	-0.8	1.6	cold	C_4H_9N	
118.0861	6.96	positive	-659	-0.8	1.6	cold	$C_5H_{11}NO_2$	Valine
120.0807	6.75	positive	-707	-0.9	1.9	cold		
439.0775	12.05	negative	-722	-0.9	1.9	cold		
89.0248	2.53	negative	-779	-0.5	1.0	cold	$C_3H_6O_3$	
166.0860	6.75	positive	-787	-0.9	1.9	cold	$C_9H_{11}NO_2$	Phenylalanine
90.0548	8.59	positive	-1200	-1.0	1.9	cold	$C_3H_7NO_2$	Alanine
175.1186	14.01	positive	1070	0.9	1.5	coldxdrought	$C_6H_{14}N_4O_2$	Arginine
196.0635	7.40	positive	979	0.7	1.1	coldxdrought		
147.0762	10.56	positive	970	0.8	1.3	coldxdrought	$C_5H_{10}N_2O_3$	Glutamine
114.1025	12.22	positive	619	0.8	1.3	coldxdrought		
194.0501	7.42	negative	567	0.5	0.9	coldxdrought		
130.0497	10.55	positive	551	0.5	0.9	coldxdrought	$C_5H_7NO_3$	
391.1194	7.38	positive	514	0.7	1.2	coldxdrought		
66.0683	12.22	positive	423	0.8	1.4	coldxdrought		
311.1265	7.41	positive	366	0.6	1.0	coldxdrought	$C_{20}H_{14}N_4$	
65.0605	14.01	positive	357	0.9	1.5	coldxdrought		
339.0736	5.91	negative	-644	-0.8	1.4	coldxdrought	$C_{15}H_{16}O_9$	
132.1018	6.47	positive	-658	-1.0	1.7	coldxdrought	$C_6H_{13}NO_2$	Leucine
120.0807	6.75	positive	-714	-1.0	1.7	coldxdrought		
118.0861	6.96	positive	-750	-1.0	1.7	coldxdrought	$C_5H_{11}NO_2$	Valine
166.0860	6.75	positive	-795	-1.0	1.7	coldxdrought	$C_9H_{11}NO_2$	Phenylalanine
86.0600	6.60	positive	-838	-0.9	1.6	coldxdrought	C_4H_7NO	
87.0440	6.65	positive	-923	-0.9	1.6	coldxdrought	$C_4H_6O_2$	
112.9862	7.82	negative	-928	-0.5	0.8	coldxdrought		
90.0548	8.59	positive	-1084	-1.0	1.7	coldxdrought	$C_3H_7NO_2$	Alanine
104.0704	6.65	positive	-1611	-0.9	1.6	coldxdrought	$C_4H_9NO_2$	gamma-Aminobutyric acid
196.0635	7.40	positive	1073	0.7	1.3	coldxsalinity		

116.0704	7.43	positive	904	0.6	1.2	coldxsalinity	$C_5H_9NO_2$	Proline
112.9862	7.82	negative	898	0.3	0.7	coldxsalinity		
147.0762	10.56	positive	820	0.4	0.8	coldxsalinity	$C_5H_{10}N_2O_3$	Glutamine
133.0606	11.13	positive	782	0.6	1.2	coldxsalinity	$C_4H_8N_2O_3$	Asparagine
98.9840	14.99	positive	744	0.7	1.3	coldxsalinity	$C_2H_3KO_2$	
194.0501	7.42	negative	744	0.6	1.3	coldxsalinity		
148.0603	11.01	positive	717	0.5	1.0	coldxsalinity	$C_5H_9NO_4$	Glutamic acid
311.1265	7.41	positive	602	0.7	1.5	coldxsalinity	$C_{20}H_{14}N_4$	
88.0756	5.12	positive	577	0.6	1.3	coldxsalinity	C_4H_9NO	
130.0862	6.83	positive	-483	-1.0	2.0	coldxsalinity	$C_6H_{11}NO_2$	
89.0248	2.53	negative	-498	-0.8	1.5	coldxsalinity	$C_3H_6O_3$	
139.0079	9.13	negative	-505	-0.4	0.8	coldxsalinity		
387.1156	12.04	negative	-547	-0.7	1.5	coldxsalinity		
341.1104	12.04	negative	-547	-0.7	1.4	coldxsalinity	$C_{12}H_{22}O_{11}$	Sucrose
120.0807	6.75	positive	-604	-1.0	1.9	coldxsalinity		
166.0860	6.75	positive	-679	-1.0	1.9	coldxsalinity	$C_9H_{11}NO_2$	Phenylalanine
68.9958	7.55	negative	-688	-0.5	1.1	coldxsalinity		
439.0775	12.05	negative	-744	-0.8	1.6	coldxsalinity		
90.0548	8.59	positive	-1135	-0.9	1.9	coldxsalinity	$C_3H_7NO_2$	Alanine
104.0704	6.65	positive	2131	0.9	1.6	drought	$C_4H_9NO_2$	gamma-Aminobutyric acid
116.0704	7.43	positive	1642	0.7	1.3	drought	$C_5H_9NO_2$	Proline
87.0440	6.65	positive	1200	0.9	1.6	drought	$C_4H_6O_2$	
132.1018	6.47	positive	1115	0.9	1.7	drought	$C_6H_{13}NO_2$	Leucine
86.0600	6.60	positive	1094	0.9	1.6	drought	C_4H_7NO	
118.0861	6.96	positive	917	0.9	1.6	drought	$C_5H_{11}NO_2$	Valine
139.0079	9.13	negative	893	0.7	1.3	drought		
112.9862	9.14	negative	838	0.5	1.0	drought		
72.0808	6.93	positive	766	0.9	1.6	drought	C_4H_9N	
420.0473	12.65	negative	622	1.0	1.8	drought		
234.0194	7.40	positive	-634	-0.8	1.5	drought		
175.1186	14.01	positive	-751	-0.5	0.9	drought	$C_6H_{14}N_4O_2$	Arginine
104.1068	0.99	positive	-757	-0.5	0.9	drought		
391.1194	7.38	positive	-831	-0.9	1.7	drought		

98.9840	14.99	positive	-851	-0.7	1.3	drought	$C_2H_3KO_2$	
194.0501	7.42	negative	-1114	-0.9	1.6	drought		
130.0497	10.55	positive	-1234	-0.8	1.4	drought	$C_5H_7NO_3$	
61.9882	10.57	negative	-1406	-0.5	0.9	drought		
147.0762	10.56	positive	-1557	-0.8	1.4	drought	$C_5H_{10}N_2O_3$	Glutamine
196.0635	7.40	positive	-1642	-0.9	1.7	drought		
147.0762	10.56	positive	3242	1.0	1.5	heat	$C_5H_{10}N_2O_3$	Glutamine
132.1018	6.47	positive	2466	1.0	1.6	heat	$C_6H_{13}NO_2$	Leucine
116.0704	7.43	positive	2161	1.0	1.5	heat	$C_5H_9NO_2$	Proline
90.0548	8.59	positive	1896	1.0	1.6	heat	$C_3H_7NO_2$	Alanine
86.0600	6.60	positive	1704	1.0	1.6	heat	C_4H_7NO	
118.0861	6.96	positive	1626	1.0	1.6	heat	$C_5H_{11}NO_2$	Valine
130.0497	10.55	positive	1455	0.5	0.8	heat	$C_5H_7NO_3$	
72.0808	6.93	positive	1348	1.0	1.6	heat	C_4H_9N	
166.0860	6.75	positive	1166	1.0	1.6	heat	$C_9H_{11}NO_2$	Phenylalanine
120.0807	6.75	positive	1034	1.0	1.6	heat		
159.0762	11.61	positive	-369	-1.0	1.6	heat	$C_6H_{10}N_2O_3$	
196.0635	7.40	positive	-384	-0.2	0.4	heat		
114.1025	12.22	positive	-402	-0.6	1.0	heat		
176.1028	11.61	positive	-407	-1.0	1.6	heat	$C_6H_{13}N_3O_3$	Citrulline
134.0446	12.03	positive	-431	-0.9	1.4	heat	$C_4H_7NO_4$	Aspartic acid
148.0603	11.01	positive	-472	-0.5	0.7	heat	$C_5H_9NO_4$	Glutamic acid
110.9763	10.75	negative	-497	-0.5	0.9	heat	CH_4O_4S	
104.1068	0.99	positive	-664	-0.6	1.0	heat		
88.0756	5.12	positive	-831	-0.9	1.5	heat	C_4H_9NO	
61.9882	10.57	negative	-1305	-0.5	0.7	heat		
104.0704	6.65	positive	2559	1.0	1.4	heatxdrought	$C_4H_9NO_2$	gamma-Aminobutyric acid
130.0497	10.55	positive	1802	0.9	1.3	heatxdrought	$C_5H_7NO_3$	
116.0704	7.43	positive	1722	0.9	1.3	heatxdrought	$C_5H_9NO_2$	Proline
147.0762	10.56	positive	1619	0.8	1.1	heatxdrought	$C_5H_{10}N_2O_3$	Glutamine
90.0548	8.59	positive	1466	1.0	1.4	heatxdrought	$C_3H_7NO_2$	Alanine
87.0440	6.65	positive	1456	1.0	1.4	heatxdrought	$C_4H_6O_2$	
86.0600	6.60	positive	1327	1.0	1.4	heatxdrought	C_4H_7NO	

132.1018	6.47	positive	1245	1.0	1.4	heatxdrought	$C_6H_{13}NO_2$	Leucine
436.0427	15.70	negative	942	1.0	1.4	heatxdrought		
420.0473	12.65	negative	862	1.0	1.4	heatxdrought		
218.0454	7.41	positive	-459	-1.0	1.4	heatxdrought		
234.0194	7.40	positive	-462	-0.8	1.2	heatxdrought		
112.9862	7.82	negative	-488	-0.3	0.4	heatxdrought		
88.0756	5.12	positive	-585	-0.8	1.2	heatxdrought	C_4H_9NO	
110.9763	10.75	negative	-594	-0.7	1.0	heatxdrought	CH_4O_4S	
391.1194	7.38	positive	-665	-0.9	1.4	heatxdrought		
175.1186	14.01	positive	-668	-0.7	1.0	heatxdrought	$C_6H_{14}N_4O_2$	Arginine
61.9882	10.57	negative	-847	-0.3	0.5	heatxdrought		
194.0501	7.42	negative	-908	-0.9	1.3	heatxdrought		
196.0635	7.40	positive	-1301	-0.9	1.3	heatxdrought		
132.1018	6.47	positive	2284	1.0	1.5	heatxsalinity	$C_6H_{13}NO_2$	Leucine
116.0704	7.43	positive	2128	1.0	1.4	heatxsalinity	$C_5H_9NO_2$	Proline
90.0548	8.59	positive	1837	1.0	1.5	heatxsalinity	$C_3H_7NO_2$	Alanine
86.0600	6.60	positive	1597	1.0	1.5	heatxsalinity	C_4H_7NO	
118.0861	6.96	positive	1437	1.0	1.4	heatxsalinity	$C_5H_{11}NO_2$	Valine
175.1186	14.01	positive	1224	0.8	1.1	heatxsalinity	$C_6H_{14}N_4O_2$	Arginine
72.0808	6.93	positive	1200	1.0	1.4	heatxsalinity	C_4H_9N	
166.0860	6.75	positive	1060	1.0	1.5	heatxsalinity	$C_9H_{11}NO_2$	Phenylalanine
133.0606	11.13	positive	1008	0.8	1.2	heatxsalinity	$C_4H_8N_2O_3$	Asparagine
120.0807	6.75	positive	947	1.0	1.5	heatxsalinity		
62.0602	6.00	positive	-299	-0.8	1.2	heatxsalinity	C_2H_7NO	
68.9958	7.55	negative	-311	-0.3	0.5	heatxsalinity		
136.0617	6.00	positive	-329	-0.8	1.2	heatxsalinity	$C_5H_5N_5$	Adenine
134.0446	12.03	positive	-377	-0.9	1.3	heatxsalinity	$C_4H_7NO_4$	Aspartic acid
112.9862	9.14	negative	-522	-0.6	0.9	heatxsalinity		
148.0603	11.01	positive	-587	-0.6	0.9	heatxsalinity	$C_5H_9NO_4$	Glutamic acid
110.9763	10.75	negative	-745	-0.7	1.1	heatxsalinity	CH_4O_4S	
88.0756	5.12	positive	-833	-0.9	1.4	heatxsalinity	C_4H_9NO	
112.9862	7.82	negative	-1327	-0.7	1.0	heatxsalinity		
61.9882	10.57	negative	-1803	-0.7	1.0	heatxsalinity		

130.0497	10.55	positive	1257	0.5	0.8	high light	$C_5H_7NO_3$	
147.0762	10.56	positive	1175	0.5	0.7	high light	$C_5H_{10}N_2O_3$	Glutamine
112.9862	9.14	negative	1132	0.9	1.4	high light		
133.0151	7.34	negative	910	0.9	1.4	high light	$C_4H_6O_5$	Malic acid
90.0548	8.59	positive	889	1.0	1.5	high light	$C_3H_7NO_2$	Alanine
132.1018	6.47	positive	873	1.0	1.5	high light	$C_6H_{13}NO_2$	Leucine
104.0704	6.65	positive	823	0.7	1.0	high light	$C_4H_9NO_2$	gamma-Aminobutyric acid
118.0861	6.96	positive	809	1.0	1.5	high light	$C_5H_{11}NO_2$	Valine
115.0043	5.74	negative	731	1.0	1.5	high light	$C_4H_4O_4$	Fumaric acid
139.0079	9.13	negative	730	0.7	1.1	high light		
391.1194	7.38	positive	-545	-0.8	1.2	high light		
114.1025	12.22	positive	-549	-0.8	1.2	high light		
98.9840	14.99	positive	-583	-0.7	1.0	high light	$C_2H_3KO_2$	
61.9882	10.57	negative	-614	-0.3	0.4	high light		
88.0756	5.12	positive	-695	-0.9	1.4	high light	C_4H_9NO	
133.0606	11.13	positive	-778	-0.8	1.2	high light	$C_4H_8N_2O_3$	Asparagine
104.1068	0.99	positive	-855	-0.8	1.2	high light		
194.0501	7.42	negative	-862	-0.8	1.3	high light		
175.1186	14.01	positive	-934	-0.8	1.2	high light	$C_6H_{14}N_4O_2$	Arginine
196.0635	7.40	positive	-1043	-0.7	1.1	high light		
147.0762	10.56	positive	1636	0.6	1.0	high lightxcold	$C_5H_{10}N_2O_3$	Glutamine
130.0497	10.55	positive	1604	0.7	1.1	high lightxcold	$C_5H_7NO_3$	
112.9862	9.14	negative	1041	0.8	1.4	high lightxcold		
133.0151	7.34	negative	904	0.9	1.5	high lightxcold	$C_4H_6O_5$	Malic acid
90.0548	8.59	positive	787	0.9	1.5	high lightxcold	$C_3H_7NO_2$	Alanine
112.9862	7.82	negative	783	0.4	0.7	high lightxcold		
166.0860	6.75	positive	761	1.0	1.6	high lightxcold	$C_9H_{11}NO_2$	Phenylalanine
84.0443	10.68	positive	756	0.9	1.5	high lightxcold		
339.0736	5.91	negative	713	0.9	1.5	high lightxcold	$C_{15}H_{16}O_9$	
118.0861	6.96	positive	710	1.0	1.6	high lightxcold	$C_5H_{11}NO_2$	Valine
234.0194	7.40	positive	-470	-0.7	1.2	high lightxcold		
66.0683	12.22	positive	-487	-0.9	1.5	high lightxcold		
106.0498	11.45	positive	-505	-0.8	1.3	high lightxcold	$C_3H_7NO_3$	Serine

148.0603	11.01	positive	-665	-0.6	1.0	high lightxcold	$C_5H_9NO_4$	Glutamic acid
133.0606	11.13	positive	-719	-0.7	1.2	high lightxcold	$C_4H_8N_2O_3$	Asparagine
104.1068	0.99	positive	-720	-0.7	1.1	high lightxcold		
114.1025	12.22	positive	-736	-0.9	1.4	high lightxcold		
194.0501	7.42	negative	-771	-0.7	1.2	high lightxcold		
196.0635	7.40	positive	-891	-0.6	1.0	high lightxcold		
175.1186	14.01	positive	-1187	-0.9	1.5	high lightxcold	$C_6H_{14}N_4O_2$	Arginine
116.0704	7.43	positive	1579	0.9	1.4	high lightxdrought	$C_5H_9NO_2$	Proline
104.0704	6.65	positive	1562	0.9	1.4	high lightxdrought	$C_4H_9NO_2$	gamma-Aminobutyric acid
132.1018	6.47	positive	1163	1.0	1.5	high lightxdrought	$C_6H_{13}NO_2$	Leucine
90.0548	8.59	positive	1085	1.0	1.5	high lightxdrought	$C_3H_7NO_2$	Alanine
118.0861	6.96	positive	931	1.0	1.5	high lightxdrought	$C_5H_{11}NO_2$	Valine
87.0440	6.65	positive	878	0.9	1.4	high lightxdrought	$C_4H_6O_2$	
420.0473	12.65	negative	828	1.0	1.5	high lightxdrought		
86.0600	6.60	positive	798	0.9	1.4	high lightxdrought	C_4H_7NO	
112.9862	7.82	negative	787	0.5	0.7	high lightxdrought		
439.0775	12.05	negative	784	1.0	1.5	high lightxdrought		
62.0602	6.00	positive	-420	-0.8	1.2	high lightxdrought	C_2H_7NO	
194.0501	7.42	negative	-432	-0.5	0.8	high lightxdrought		
391.1194	7.38	positive	-434	-0.6	1.0	high lightxdrought		
136.0617	6.00	positive	-448	-0.9	1.4	high lightxdrought	$C_5H_5N_5$	Adenine
114.1025	12.22	positive	-551	-0.7	1.1	high lightxdrought		
175.1186	14.01	positive	-556	-0.5	0.8	high lightxdrought	$C_6H_{14}N_4O_2$	Arginine
98.9840	14.99	positive	-593	-0.7	1.0	high lightxdrought	$C_2H_3KO_2$	
196.0635	7.40	positive	-751	-0.6	0.9	high lightxdrought		
104.1068	0.99	positive	-972	-0.9	1.3	high lightxdrought		
147.0762	10.56	positive	-1032	-0.8	1.3	high lightxdrought	$C_5H_{10}N_2O_3$	Glutamine
104.0704	6.65	positive	1966	1.0	1.2	high lightxheat	$C_4H_9NO_2$	gamma-Aminobutyric acid
132.1018	6.47	positive	1860	1.0	1.2	high lightxheat	$C_6H_{13}NO_2$	Leucine
90.0548	8.59	positive	1373	1.0	1.2	high lightxheat	$C_3H_7NO_2$	Alanine
86.0600	6.60	positive	1272	1.0	1.2	high lightxheat	C_4H_7NO	
268.1038	5.50	positive	1198	1.0	1.2	high lightxheat	$C_{10}H_{13}N_5O_4$	Adenosine
87.0440	6.65	positive	1119	1.0	1.2	high lightxheat	$C_4H_6O_2$	

118.0861	6.96	positive	998	1.0	1.2	high lightxheat	$C_5H_{11}NO_2$	Valine
166.0860	6.75	positive	993	1.0	1.2	high lightxheat	$C_9H_{11}NO_2$	Phenylalanine
136.0617	6.00	positive	957	1.0	1.2	high lightxheat	$C_5H_5N_5$	Adenine
112.9862	9.14	negative	956	0.9	1.1	high lightxheat		
114.1025	12.22	positive	-681	-0.9	1.1	high lightxheat		
196.0635	7.40	positive	-690	-0.7	0.9	high lightxheat		
88.0756	5.12	positive	-727	-0.9	1.1	high lightxheat	C_4H_9NO	
175.1186	14.01	positive	-817	-1.0	1.2	high lightxheat	$C_6H_{14}N_4O_2$	Arginine
133.0606	11.13	positive	-852	-0.9	1.1	high lightxheat	$C_4H_8N_2O_3$	Asparagine
104.1068	0.99	positive	-1013	-0.9	1.1	high lightxheat		
148.0603	11.01	positive	-1220	-1.0	1.2	high lightxheat	$C_5H_9NO_4$	Glutamic acid
61.9882	10.57	negative	-1614	-0.7	0.9	high lightxheat		
130.0497	10.55	positive	-1694	-1.0	1.2	high lightxheat	$C_5H_7NO_3$	
147.0762	10.56	positive	-2056	-1.0	1.2	high lightxheat	$C_5H_{10}N_2O_3$	Glutamine
439.0775	12.05	negative	1136	1.0	1.3	high lightxsalinity		
341.1104	12.04	negative	1121	1.0	1.3	high lightxsalinity	$C_{12}H_{22}O_{11}$	Sucrose
387.1156	12.04	negative	1077	1.0	1.3	high lightxsalinity		
130.0497	10.55	positive	996	0.7	0.9	high lightxsalinity	$C_5H_7NO_3$	
147.0762	10.56	positive	837	0.5	0.7	high lightxsalinity	$C_5H_{10}N_2O_3$	Glutamine
365.1042	12.03	positive	709	1.0	1.3	high lightxsalinity	Sucrose (M+Na)	
112.9862	9.14	negative	655	0.8	1.1	high lightxsalinity		
248.9608	5.41	negative	435	0.9	1.3	high lightxsalinity		
440.0809	12.05	negative	429	1.0	1.3	high lightxsalinity		
388.1191	12.04	negative	413	1.0	1.3	high lightxsalinity	$C_{23}H_{19}NO_5$	
104.0704	6.65	positive	-930	-0.7	1.0	high lightxsalinity	$C_4H_9NO_2$	gamma-Aminobutyric acid
194.0501	7.42	negative	-938	-1.0	1.3	high lightxsalinity		
133.0606	11.13	positive	-957	-0.9	1.2	high lightxsalinity	$C_4H_8N_2O_3$	Asparagine
98.9840	14.99	positive	-959	-0.9	1.2	high lightxsalinity	$C_2H_3KO_2$	
104.1068	0.99	positive	-1053	-0.9	1.2	high lightxsalinity		
116.0704	7.43	positive	-1070	-0.8	1.1	high lightxsalinity	$C_5H_9NO_2$	Proline
112.9862	7.82	negative	-1180	-0.7	0.9	high lightxsalinity		
175.1186	14.01	positive	-1248	-1.0	1.3	high lightxsalinity	$C_6H_{14}N_4O_2$	Arginine
196.0635	7.40	positive	-1421	-0.9	1.3	high lightxsalinity		

61.9882	10.57	negative	-1578	-0.6	0.8	high lightxsalinity		
112.9862	9.14	negative	1008	0.9	1.3	salinity		
104.0704	6.65	positive	862	0.7	1.0	salinity	$C_4H_9NO_2$	gamma-Aminobutyric acid
139.0079	9.13	negative	799	0.8	1.1	salinity		
112.9862	7.82	negative	662	0.4	0.6	salinity		
68.9958	9.12	negative	599	0.9	1.3	salinity		
339.0736	5.91	negative	583	0.9	1.3	salinity	$C_{15}H_{16}O_9$	
110.9763	10.75	negative	541	0.6	0.9	salinity	CH_4O_4S	
87.0440	6.65	positive	496	0.7	1.0	salinity	$C_4H_6O_2$	
223.0618	5.90	negative	487	0.9	1.3	salinity	$C_{11}H_{12}O_5$	
86.0600	6.60	positive	453	0.7	1.0	salinity	C_4H_7NO	
98.9840	14.99	positive	-716	-0.7	1.1	salinity	$C_2H_3KO_2$	
88.0756	5.12	positive	-718	-0.9	1.3	salinity	C_4H_9NO	
391.1194	7.38	positive	-737	-1.0	1.4	salinity		
148.0603	11.01	positive	-937	-0.8	1.2	salinity	$C_5H_9NO_4$	Glutamic acid
133.0606	11.13	positive	-1007	-0.9	1.3	salinity	$C_4H_8N_2O_3$	Asparagine
194.0501	7.42	negative	-1115	-1.0	1.4	salinity		
130.0497	10.55	positive	-1140	-0.8	1.2	salinity	$C_5H_7NO_3$	
175.1186	14.01	positive	-1149	-0.9	1.4	salinity	$C_6H_{14}N_4O_2$	Arginine
147.0762	10.56	positive	-1497	-0.8	1.2	salinity	$C_5H_{10}N_2O_3$	Glutamine
196.0635	7.40	positive	-1548	-1.0	1.5	salinity		
104.0704	6.65	positive	3705	0.9	2.6	subgroupA	$C_4H_9NO_2$	
87.0440	6.65	positive	2109	0.9	2.6	subgroupA	$C_4H_6O_2$	
132.1018	6.47	positive	1670	0.4	1.3	subgroupA	$C_6H_{13}NO_2$	Leucine
116.0704	7.43	positive	1590	0.4	1.2	subgroupA	$C_5H_9NO_2$	Proline
86.0600	6.60	positive	1589	0.6	1.7	subgroupA	C_4H_7NO	
90.0548	8.59	positive	1446	0.5	1.4	subgroupA	$C_3H_7NO_2$	Alanine
268.1038	5.50	positive	1168	0.6	1.7	subgroupA	$C_{10}H_{13}N_5O_4$	Adenosine
436.0427	15.70	negative	1078	0.8	2.2	subgroupA		
420.0473	12.65	negative	922	0.7	2.0	subgroupA		
136.0617	6.00	positive	890	0.5	1.5	subgroupA	$C_5H_5N_5$	Adenine
134.0446	12.03	positive	-425	-0.4	1.3	subgroupA	$C_4H_7NO_4$	Aspartic acid
112.9862	7.82	negative	-458	-0.1	0.4	subgroupA		

259.0226	19.06	negative	-471	-0.6	1.6	subgroupA	$C_6H_{13}O_9P$	Glucose 6-phosphate
133.0151	7.34	negative	-494	-0.3	0.8	subgroupA	$C_4H_6O_5$	Malic acid
223.0618	5.90	negative	-523	-0.5	1.3	subgroupA	$C_{11}H_{12}O_5$	
130.0497	10.55	positive	-621	-0.1	0.4	subgroupA	$C_5H_7NO_3$	
339.0736	5.91	negative	-650	-0.5	1.3	subgroupA	$C_{15}H_{16}O_9$	
68.9958	7.55	negative	-714	-0.4	1.1	subgroupA		
61.9882	10.57	negative	-1037	-0.2	0.6	subgroupA		
147.0762	10.56	positive	-1227	-0.2	0.7	subgroupA	$C_5H_{10}N_2O_3$	Glutamine
132.1018	6.47	positive	2227	0.7	1.7	subgroupB	$C_6H_{13}NO_2$	Leucine
147.0762	10.56	positive	2131	0.5	1.2	subgroupB	$C_5H_{10}N_2O_3$	Glutamine
90.0548	8.59	positive	1553	0.6	1.6	subgroupB	$C_3H_7NO_2$	Alanine
130.0497	10.55	positive	1552	0.4	1.0	subgroupB	$C_5H_7NO_3$	
439.0775	12.05	negative	1410	0.8	2.1	subgroupB		
116.0704	7.43	positive	1397	0.4	1.0	subgroupB	$C_5H_9NO_2$	Proline
341.1104	12.04	negative	1381	0.8	2.1	subgroupB	$C_{12}H_{22}O_{11}$	Sucrose
387.1156	12.04	negative	1340	0.8	2.1	subgroupB		
86.0600	6.60	positive	1271	0.5	1.4	subgroupB	C_4H_7NO	
118.0861	6.96	positive	1242	0.6	1.5	subgroupB	$C_5H_{11}NO_2$	Valine
134.0446	12.03	positive	-535	-0.6	1.6	subgroupB	$C_4H_7NO_4$	Aspartic acid
87.0440	6.65	positive	-563	-0.4	0.9	subgroupB	$C_4H_6O_2$	
136.0617	6.00	positive	-595	-0.7	1.7	subgroupB	$C_5H_5N_5$	Adenine
104.1068	0.99	positive	-647	-0.4	0.9	subgroupB		
148.0603	11.01	positive	-681	-0.4	1.0	subgroupB	$C_5H_9NO_4$	Glutamic acid
62.0602	6.00	positive	-735	-0.7	1.7	subgroupB	C_2H_7NO	
104.0704	6.65	positive	-987	-0.4	0.9	subgroupB	$C_4H_9NO_2$	gamma-Aminobutyric acid
88.0756	5.12	positive	-1114	-0.8	2.0	subgroupB	C_4H_9NO	
112.9862	7.82	negative	-1724	-0.5	1.4	subgroupB		
61.9882	10.57	negative	-2534	-0.6	1.5	subgroupB		
132.1018	6.47	positive	1731	1.0	1.4	subgroupC	$C_6H_{13}NO_2$	Leucine
268.1038	5.50	positive	1329	1.0	1.4	subgroupC	$C_{10}H_{13}N_5O_4$	Adenosine
136.0617	6.00	positive	1085	1.0	1.4	subgroupC	$C_5H_5N_5$	Adenine
110.9763	10.75	negative	1050	0.9	1.2	subgroupC	CH_4O_4S	
166.0860	6.75	positive	944	1.0	1.4	subgroupC	$C_9H_{11}NO_2$	Phenylalanine

112.9862	9.14	negative	893	0.8	1.1	subgroupC		
86.0600	6.60	positive	853	0.7	1.0	subgroupC	C_4H_7NO	
120.0807	6.75	positive	838	1.0	1.4	subgroupC		
90.0548	8.59	positive	814	0.7	1.0	subgroupC	$C_3H_7NO_2$	Alanine
118.0861	6.96	positive	756	0.9	1.3	subgroupC	$C_5H_{11}NO_2$	Valine
145.0627	10.50	negative	-654	-0.9	1.2	subgroupC	$C_5H_{10}N_2O_3$	Glutamine
420.0473	12.65	negative	-742	-1.0	1.4	subgroupC		
68.9958	7.55	negative	-823	-0.8	1.1	subgroupC		
104.1068	0.99	positive	-931	-0.7	1.0	subgroupC		
133.0606	11.13	positive	-947	-0.9	1.3	subgroupC	$C_4H_8N_2O_3$	Asparagine
116.0704	7.43	positive	-968	-0.7	0.9	subgroupC	$C_5H_9NO_2$	Proline
148.0603	11.01	positive	-1449	-1.0	1.4	subgroupC	$C_5H_9NO_4$	Glutamic acid
61.9882	10.57	negative	-1637	-0.7	0.9	subgroupC		
130.0497	10.55	positive	-2037	-0.8	1.1	subgroupC	$C_5H_7NO_3$	
147.0762	10.56	positive	-2298	-0.8	1.2	subgroupC	$C_5H_{10}N_2O_3$	Glutamine
104.0704	6.65	positive	2318	0.8	2.1	subgroupD	$C_4H_9NO_2$	gamma-Aminobutyric acid
87.0440	6.65	positive	1325	0.8	2.2	subgroupD	$C_4H_6O_2$	
116.0704	7.43	positive	1213	0.4	1.2	subgroupD	$C_5H_9NO_2$	Proline
86.0600	6.60	positive	1207	0.8	2.2	subgroupD	C_4H_7NO	
420.0473	12.65	negative	626	0.8	2.1	subgroupD		
477.0651	11.95	negative	618	0.7	2.0	subgroupD		
110.9763	10.75	negative	568	0.3	0.9	subgroupD	CH_4O_4S	
436.0427	15.70	negative	561	0.7	2.1	subgroupD		
132.1018	6.47	positive	510	0.3	0.9	subgroupD	$C_6H_{13}NO_2$	Leucine
105.0738	6.65	positive	488	0.8	2.1	subgroupD		
90.0548	8.59	positive	-635	-0.4	1.1	subgroupD	$C_3H_7NO_2$	Alanine
145.0627	10.50	negative	-639	-0.5	1.4	subgroupD	$C_5H_{10}N_2O_3$	Glutamine
439.0775	12.05	negative	-703	-0.5	1.4	subgroupD		
194.0501	7.42	negative	-717	-0.4	1.0	subgroupD		
61.9882	10.57	negative	-740	-0.2	0.5	subgroupD		
76.0393	9.69	positive	-828	-0.7	2.0	subgroupD	$C_2H_5NO_2$	Glycine
133.0151	7.34	negative	-1002	-0.6	1.7	subgroupD	$C_4H_6O_5$	Malic acid
196.0635	7.40	positive	-1283	-0.5	1.3	subgroupD		

130.0497	10.55	positive	-2159	-0.5	1.5	subgroupD	$C_5H_7NO_3$	
147.0762	10.56	positive	-2595	-0.6	1.6	subgroupD	$C_5H_{10}N_2O_3$	Glutamine
341.1104	12.04	negative	821	0.9	1.2	subgroupE	$C_{12}H_{22}O_{11}$	Sucrose
387.1156	12.04	negative	777	0.9	1.2	subgroupE		
439.0775	12.05	negative	765	0.9	1.2	subgroupE		
110.9763	10.75	negative	611	0.6	0.9	subgroupE	CH_4O_4S	
112.9862	9.14	negative	600	0.6	0.9	subgroupE		
365.1042	12.03	positive	543	0.9	1.2	subgroupE		Sucrose (M+Na)
248.9608	5.41	negative	435	1.0	1.3	subgroupE		
89.0248	2.53	negative	423	0.8	1.1	subgroupE	$C_3H_6O_3$	
68.9958	7.55	negative	370	0.5	0.7	subgroupE		
68.9958	9.12	negative	358	0.7	0.9	subgroupE		
104.0704	6.65	positive	-1136	-0.8	1.1	subgroupE	$C_4H_9NO_2$	gamma-Aminobutyric acid
147.0762	10.56	positive	-1166	-0.4	0.6	subgroupE	$C_5H_{10}N_2O_3$	Glutamine
196.0635	7.40	positive	-1214	-0.7	1.0	subgroupE		
133.0606	11.13	positive	-1230	-0.9	1.3	subgroupE	$C_4H_8N_2O_3$	Asparagine
175.1186	14.01	positive	-1277	-0.8	1.0	subgroupE	$C_6H_{14}N_4O_2$	Arginine
118.0861	6.96	positive	-1298	-1.0	1.3	subgroupE	$C_5H_{11}NO_2$	Valine
86.0600	6.60	positive	-1487	-1.0	1.4	subgroupE	C_4H_7NO	
90.0548	8.59	positive	-1539	-1.0	1.3	subgroupE	$C_3H_7NO_2$	Alanine
132.1018	6.47	positive	-2003	-1.0	1.4	subgroupE	$C_6H_{13}NO_2$	Leucine
116.0704	7.43	positive	-2156	-1.0	1.3	subgroupE	$C_5H_9NO_2$	Proline
130.0497	10.55	positive	2090	0.7	1.4	subgroupF	$C_5H_7NO_3$	
147.0762	10.56	positive	1921	0.6	1.2	subgroupF	$C_5H_{10}N_2O_3$	Glutamine
112.9862	7.82	negative	1189	0.5	1.0	subgroupF		
133.0151	7.34	negative	1110	0.9	2.0	subgroupF	$C_4H_6O_5$	Malic acid
112.9862	9.14	negative	1099	0.7	1.4	subgroupF		
104.0704	6.65	positive	1058	0.6	1.3	subgroupF	$C_4H_9NO_2$	gamma-Aminobutyric acid
116.0704	7.43	positive	1021	0.7	1.5	subgroupF	$C_5H_9NO_2$	Proline
339.0736	5.91	negative	952	0.9	2.0	subgroupF	$C_{15}H_{16}O_9$	
132.1018	6.47	positive	850	0.8	1.7	subgroupF	$C_6H_{13}NO_2$	Leucine
115.0043	5.74	negative	846	0.9	2.0	subgroupF	$C_4H_4O_4$	Fumaric acid
89.0248	2.53	negative	-398	-0.3	0.7	subgroupF	$C_3H_6O_3$	

114.1025	12.22	positive	-434	-0.4	0.9	subgroupF		
134.0446	12.03	positive	-513	-0.7	1.5	subgroupF	$C_4H_7NO_4$	Aspartic acid
61.9882	10.57	negative	-576	-0.2	0.4	subgroupF		
88.0756	5.12	positive	-582	-0.6	1.3	subgroupF	C_4H_9NO	
133.0606	11.13	positive	-586	-0.5	1.0	subgroupF	$C_4H_8N_2O_3$	Asparagine
196.0635	7.40	positive	-635	-0.3	0.7	subgroupF		
194.0501	7.42	negative	-641	-0.4	0.9	subgroupF		
104.1068	0.99	positive	-831	-0.6	1.3	subgroupF		
175.1186	14.01	positive	-869	-0.5	1.1	subgroupF	$C_6H_{14}N_4O_2$	Arginine
116.0704	7.43	positive	1857	0.7	1.6	subgroupG	$C_5H_9NO_2$	Proline
104.0704	6.65	positive	1516	0.6	1.4	subgroupG	$C_4H_9NO_2$	gamma-Aminobutyric acid
132.1018	6.47	positive	1087	0.8	1.9	subgroupG	$C_6H_{13}NO_2$	Leucine
87.0440	6.65	positive	828	0.6	1.4	subgroupG	$C_4H_6O_2$	
118.0861	6.96	positive	766	0.6	1.5	subgroupG	$C_5H_{11}NO_2$	Valine
86.0600	6.60	positive	756	0.6	1.4	subgroupG	C_4H_7NO	
175.1186	14.01	positive	644	0.4	0.8	subgroupG	$C_6H_{14}N_4O_2$	Arginine
72.0808	6.93	positive	622	0.6	1.4	subgroupG	C_4H_9N	
439.0775	12.05	negative	612	0.5	1.2	subgroupG		
387.1156	12.04	negative	605	0.6	1.4	subgroupG		
259.0226	19.06	negative	-446	-0.7	1.7	subgroupG	$C_6H_{13}O_9P$	Glucose 6-phosphate
90.0548	8.59	positive	-508	-0.4	0.9	subgroupG	$C_3H_7NO_2$	Alanine
223.0618	5.90	negative	-548	-0.8	1.8	subgroupG	$C_{11}H_{12}O_5$	
133.0151	7.34	negative	-561	-0.5	1.1	subgroupG	$C_4H_6O_5$	Malic acid
136.0617	6.00	positive	-595	-0.7	1.7	subgroupG	$C_5H_5N_5$	Adenine
339.0736	5.91	negative	-660	-0.8	1.8	subgroupG	$C_{15}H_{16}O_9$	
104.1068	0.99	positive	-877	-0.5	1.1	subgroupG		
68.9958	7.55	negative	-1156	-0.7	1.8	subgroupG		
112.9862	7.82	negative	-1314	-0.5	1.3	subgroupG		
61.9882	10.57	negative	-1785	-0.5	1.2	subgroupG		

Supplemental Table 3-2. Metabolic features increased or decreased more than 2 fold in different treatments compared to control

M/z	**Retention time (min)**	**Polarity**	**Ratio change**	**Treatment**	**Increase or decrease**	**Potential heuristical formula**	**Identified with reference standard**
341.1109	12.90	negative	33.58	cold	increase	$C_{12}H_{22}O_{11}$	
365.1027	12.97	positive	32.01	cold	increase	$C_{21}H_{16}O_6$	
221.0675	12.91	negative	22.26	cold	increase	$C_8H_{14}O_7$	
196.0238	4.73	negative	10.06	cold	increase	$C_8H_7NO_5$	
115.0403	3.86	negative	3.09	cold	increase	$C_5H_8O_3$	Fumaric acid
191.0203	12.44	negative	2.88	cold	increase	$C_6H_8O_7$	
166.0863	6.80	positive	2.76	cold	increase	$C_9H_{11}NO_2$	
231.1001	5.07	positive	2.68	cold	increase	$C_{14}H_{14}O_3$	
87.0089	4.33	negative	2.68	cold	increase	$C_3H_4O_3$	
166.0862	6.88	positive	2.66	cold	increase	$C_9H_{11}NO_2$	
87.0090	4.31	negative	2.63	cold	increase	$C_3H_4O_3$	
91.0582	8.73	positive	2.62	cold	increase	$C_4H_{10}S$	
90.0549	8.74	positive	2.57	cold	increase	$C_3H_7NO_2$	Alanine
90.0548	8.89	positive	2.56	cold	increase	$C_3H_7NO_2$	
90.0549	8.66	positive	2.56	cold	increase	$C_3H_7NO_2$	Alanine
96.0444	3.91	positive	2.46	cold	increase	C_5H_5NO	
164.0723	6.89	negative	2.36	cold	increase	$C_9H_{11}NO_2$	
241.0308	16.09	positive	2.33	cold	increase	$C_6H_{12}N_2O_4S_2$	
191.0204	12.15	negative	2.27	cold	increase	$C_6H_8O_7$	
131.0816	8.73	positive	2.26	cold	increase	$C_5H_{10}N_2O_2$	
218.1171	1.06	positive	0.50	cold	decrease	$C_{13}H_{15}NO_2$	
307.0773	7.06	positive	0.50	cold	decrease	$C_{14}H_{14}N_2O_4S$	
228.9940	7.33	negative	0.50	cold	decrease	$C_9H_8Cl_2N_2O$	
133.0338	12.25	negative	0.49	cold	decrease	$C_5H_{10}O_2S$	
141.0660	8.86	positive	0.49	cold	decrease	$C_6H_8N_2O_2$	
110.9764	10.98	negative	0.49	cold	decrease	CH_4O_4S	
146.0465	11.17	negative	0.48	cold	decrease	$C_5H_9NO_4$	
171.0069	16.97	negative	0.48	cold	decrease	$C_3H_9O_6P$	

379.0841	13.91	negative	0.47	cold	decrease	$C_{21}H_{17}ClN_2O_3$	
132.0501	11.19	negative	0.47	cold	decrease	$C_5H_{11}NOS$	
379.0843	12.21	negative	0.47	cold	decrease	$C_{21}H_{17}ClN_2O_3$	
187.0731	8.69	negative	0.47	cold	decrease	$C_7H_{12}N_2O_4$	
145.0496	12.20	positive	0.46	cold	decrease	$C_6H_8O_4$	
132.0308	12.87	negative	0.46	cold	decrease	$C_4H_7NO_4$	
89.0246	3.05	negative	0.46	cold	decrease	$C_3H_6O_3$	
132.0308	12.26	negative	0.46	cold	decrease	$C_4H_7NO_4$	
124.9560	8.24	negative	0.46	cold	decrease	$C_2H_6S_3$	
382.0810	12.18	positive	0.46	cold	decrease	$C_{14}H_{15}N_5O_6S$	
341.1116	12.99	negative	0.44	cold	decrease	$C_{12}H_{22}O_{11}$	
113.0358	11.15	negative	0.44	cold	decrease	$C_4H_6N_2O_2$	
104.0357	11.63	negative	0.43	cold	decrease	$C_3H_7NO_3$	
104.0358	11.42	negative	0.43	cold	decrease	$C_3H_7NO_3$	
73.0649	5.37	positive	0.43	cold	decrease	C_4H_8O	
341.1104	12.20	negative	0.43	cold	decrease	$C_{12}H_{22}O_{11}$	
343.1156	12.20	negative	0.43	cold	decrease	$C_8H_{21}N_6O_7P_2$	
254.0157	7.33	negative	0.43	cold	decrease	$C_{12}H_{11}Cl_2NO$	
182.9711	7.34	negative	0.42	cold	decrease	$C_3H_5O_7P$	
389.1206	12.20	negative	0.41	cold	decrease	$C_{20}H_{22}O_8$	
131.0471	11.30	negative	0.41	cold	decrease	$C_4H_8N_2O_3$	Asparagine
85.0284	12.21	positive	0.41	cold	decrease	$C_4H_4O_2$	
388.1192	12.20	negative	0.41	cold	decrease	$C_{23}H_{19}NO_5$	
300.0823	11.25	negative	0.41	cold	decrease	$C_7H_{18}N_4O_7P$	
187.0236	5.36	negative	0.41	cold	decrease	$C_7H_8O_6$	
305.1441	9.98	positive	0.40	cold	decrease	$C_{11}H_{20}N_4O_6$	
315.0818	11.19	negative	0.39	cold	decrease	$C_{16}H_{16}N_2O_3S$	
157.0608	11.22	positive	0.39	cold	decrease	$C_6H_8N_2O_3$	
265.0763	7.95	negative	0.39	cold	decrease	$C_{16}H_{12}NO_3$	
285.0824	11.32	negative	0.38	cold	decrease	$C_{12}H_{16}NO_7$	
285.1100	7.44	positive	0.38	cold	decrease	$C_{17}H_{16}O_4$	
361.1515	12.19	positive	0.38	cold	decrease	$C_{16}H_{24}O_9$	
325.1110	12.20	positive	0.37	cold	decrease	$C_{19}H_{17}ClN_2O$	

223.9852	11.64	negative	0.37	cold	decrease	$C_6H_{11}NO_3Se$	
453.0930	12.21	negative	0.36	cold	decrease	$C_{22}H_{18}N_2O_9$	
97.0284	12.23	positive	0.36	cold	decrease	$C_5H_4O_2$	
103.0866	5.47	positive	0.35	cold	decrease	$C_4H_{10}N_2O$	
124.0081	11.07	negative	0.35	cold	decrease	$C_2H_7NO_3S$	
117.0198	5.42	negative	0.35	cold	decrease	$C_4H_6O_4$	
74.0248	11.64	negative	0.33	cold	decrease	$C_2H_5NO_2$	
61.0398	2.79	positive	0.33	cold	decrease	CH_4N_2O	Urea
185.0079	5.44	negative	0.32	cold	decrease	$C_7H_6O_6$	
61.0398	2.76	positive	0.32	cold	decrease	CH_4N_2O	
109.0285	12.22	positive	0.32	cold	decrease	$C_6H_4O_2$	
189.0887	11.18	negative	0.32	cold	decrease	$C_7H_{14}N_2O_4$	
339.0454	7.27	positive	0.31	cold	decrease	$C_9H_{13}N_3O_9P$	
127.0391	12.21	positive	0.31	cold	decrease	$C_6H_6O_3$	
180.0327	11.33	positive	0.30	cold	decrease	$C_5H_9NO_4S$	
275.1340	11.25	positive	0.29	cold	decrease	$C_{10}H_{18}N_4O_5$	
178.0552	9.41	negative	0.29	cold	decrease	$C_6H_{13}NO_3S$	
204.0866	12.20	positive	0.25	cold	decrease	$C_8H_{13}NO_5$	
156.0422	5.68	positive	0.21	cold	decrease	$C_3H_{10}NO_4P$	
139.0503	6.89	positive	0.20	cold	decrease	$C_6H_6N_2O_2$	
211.9973	4.66	negative	0.20	cold	decrease	$C_4H_8NO_7P$	
299.0485	11.63	negative	0.19	cold	decrease	$C_{10}H_{12}N_4O_5S$	
150.1125	1.20	positive	0.18	cold	decrease	$C_6H_{15}NO_3$	
437.0455	15.86	negative	0.12	cold	decrease	$C_{15}H_{20}NO_{10}S_2$-	
130.1591	1.14	positive	0.11	cold	decrease	$C_8H_{19}N$	
551.1711	14.90	negative	0.09	cold	decrease	$C_{23}H_{32}N_6O_6S_2$	
181.0153	7.35	negative	0.08	cold	decrease	$C_8H_6O_5$	
166.0514	6.14	negative	0.05	cold	decrease	$C_8H_9NO_3$	
247.0342	11.63	negative	0.04	cold	decrease	$C_{11}H_8N_2O_5$	
129.1023	5.11	positive	0.04	cold	decrease	$C_6H_{12}N_2O$	
160.0758	4.52	positive	0.02	cold	decrease	$C_{10}H_9NO$	
308.0894	11.55	positive	0.02	cold	decrease	$C_{10}H_{17}N_3O_6S$	
306.0774	11.61	negative	0.01	cold	decrease	$C_{18}H_{13}NO_4$	

306.0774	11.60	negative	0.01	cold	decrease	$C_{18}H_{13}NO_4$	
144.1384	11.48	positive	0.01	cold	decrease	$C_8H_{17}NO$	
145.0146	5.62	negative	0.01	cold	decrease	$C_5H_6O_5$	
113.0245	7.98	negative	0.00	cold	decrease	$C_5H_6O_3$	
236.1135	11.06	positive	329.94	coldxdrought	increase	$C_9H_{17}NO_6$	
281.0884	12.72	negative	135.38	coldxdrought	increase	$C_{10}H_{18}O_9$	
222.0978	11.36	positive	88.27	coldxdrought	increase	$C_8H_{15}NO_6$	
254.0843	11.66	positive	62.23	coldxdrought	increase	$C_{12}H_{15}NO_3S$	
221.0674	12.74	negative	37.61	coldxdrought	increase	$C_8H_{14}O_7$	
162.0404	12.66	positive	35.69	coldxdrought	increase	$C_5H_7NO_5$	
252.1084	13.36	positive	35.66	coldxdrought	increase	$C_9H_{17}NO_7$	
130.0650	11.96	positive	26.98	coldxdrought	increase	C_9H_7N	
341.1103	12.66	negative	25.47	coldxdrought	increase	$C_{12}H_{22}O_{11}$	Maltose
161.0465	12.72	negative	23.87	coldxdrought	increase	$C_6H_{10}O_5$	
447.0548	13.82	negative	13.02	coldxdrought	increase	$C_{16}H_{20}N_2O_9S_2$	
207.0584	13.80	positive	12.88	coldxdrought	increase	$C_{10}H_{10}N_2OS$	
160.0755	11.94	positive	6.83	coldxdrought	increase	$C_{10}H_9NO$	
303.0037	10.78	negative	3.66	coldxdrought	increase	$C_{15}H_9ClO_5$	
293.2107	0.90	positive	3.43	coldxdrought	increase	$C_{18}H_{28}O_3$	
596.1678	8.43	positive	3.28	coldxdrought	increase	$C_{27}H_{31}O_{15}$	
503.1611	14.65	negative	3.16	coldxdrought	increase	$C_{18}H_{32}O_{16}$	Raffinose
301.1057	8.67	positive	3.16	coldxdrought	increase	$C_{17}H_{16}O_5$	
166.0860	6.75	positive	2.93	coldxdrought	increase	$C_9H_{11}NO_2$	Phenylalanine
203.0835	7.20	negative	2.52	coldxdrought	increase	$C_{11}H_{12}N_2O_2$	
91.0582	8.59	positive	2.34	coldxdrought	increase	$C_4H_{10}S$	
90.0548	8.59	positive	2.29	coldxdrought	increase	$C_3H_7NO_2$	Alanine
163.0752	5.90	positive	2.27	coldxdrought	increase	$C_{10}H_{10}O_2$	
595.2917	12.05	negative	2.07	coldxdrought	increase	$C_{34}H_{44}O_9$	
122.0811	9.07	positive	0.45	coldxdrought	decrease	$C_4H_{11}NO_3$	
175.1074	8.25	positive	0.43	coldxdrought	decrease	$C_7H_{14}N_2O_3$	
93.0463	1.99	negative	0.43	coldxdrought	decrease	$C_5H_6N_2$	
150.0430	8.17	negative	0.40	coldxdrought	decrease	$C_5H_5N_5O$	
209.0819	13.99	negative	0.40	coldxdrought	decrease	$C_{11}H_{14}O_4$	

139.0501	2.00	positive	0.34	coldxdrought	decrease	$C_6H_6N_2O_2$	
139.0501	6.84	positive	0.31	coldxdrought	decrease	$C_6H_6N_2O_2$	
308.0905	11.42	positive	0.28	coldxdrought	decrease	$C_{10}H_{17}N_3O_6S$	GSH
281.0884	12.72	negative	206.92	coldxsalinity	increase	$C_{10}H_{18}O_9$	
221.0674	12.74	negative	54.50	coldxsalinity	increase	$C_8H_{14}O_7$	
341.1103	12.66	negative	37.85	coldxsalinity	increase	$C_{12}H_{22}O_{11}$	Maltose
161.0465	12.72	negative	34.45	coldxsalinity	increase	$C_6H_{10}O_5$	
236.1135	11.06	positive	9.24	coldxsalinity	increase	$C_9H_{17}NO_6$	
93.0463	1.99	negative	6.82	coldxsalinity	increase	$C_5H_6N_2$	
252.1084	13.36	positive	5.71	coldxsalinity	increase	$C_9H_{17}NO_7$	
130.0862	6.83	positive	5.32	coldxsalinity	increase	$C_6H_{11}NO_2$	
293.2107	0.90	positive	5.05	coldxsalinity	increase	$C_{18}H_{28}O_3$	
139.0501	2.00	positive	4.68	coldxsalinity	increase	$C_6H_6N_2O_2$	
351.1035	6.16	positive	4.57	coldxsalinity	increase	$C_{16}H_{18}N_2O_5S$	
125.0363	10.83	negative	4.29	coldxsalinity	increase	$C_5H_6N_2O_2$	
254.0843	11.66	positive	3.42	coldxsalinity	increase	$C_{12}H_{15}NO_3S$	
222.0978	11.36	positive	3.16	coldxsalinity	increase	$C_8H_{15}NO_6$	
168.9915	16.50	negative	3.11	coldxsalinity	increase	$C_3H_7O_6P$	Dihydroxyacetone phosphate
301.1057	8.67	positive	2.71	coldxsalinity	increase	$C_{17}H_{16}O_5$	
122.0811	9.07	positive	2.70	coldxsalinity	increase	$C_4H_{11}NO_3$	
139.0501	6.84	positive	2.63	coldxsalinity	increase	$C_6H_6N_2O_2$	
379.0991	6.02	positive	2.53	coldxsalinity	increase	$C_{17}H_{18}N_2O_6S$	
203.0835	7.20	negative	2.37	coldxsalinity	increase	$C_{11}H_{12}N_2O_2$	
345.1145	5.85	positive	2.35	coldxsalinity	increase	$C_{22}H_{17}ClN_2$	
89.0248	2.53	negative	2.30	coldxsalinity	increase	$C_3H_6O_3$	
91.0582	8.59	positive	2.12	coldxsalinity	increase	$C_4H_{10}S$	
90.0548	8.59	positive	2.10	coldxsalinity	increase	$C_3H_7NO_2$	Alanine
325.1121	12.05	positive	2.09	coldxsalinity	increase	$C_{12}H_{20}O_{10}$	
166.0860	6.75	positive	2.07	coldxsalinity	increase	$C_9H_{11}NO_2$	Phenylalanine
265.0718	5.60	negative	0.47	coldxsalinity	decrease	$C_{16}H_{12}NO_3$	
207.0584	13.80	positive	0.45	coldxsalinity	decrease	$C_{10}H_{10}N_2OS$	
229.1443	5.58	positive	0.41	coldxsalinity	decrease	$C_{12}H_{20}O_4$	
447.0548	13.82	negative	0.41	coldxsalinity	decrease	$C_{16}H_{20}N_2O_9S_2$	

308.0905	11.42	positive	0.32	coldxsalinity	decrease	$C_{10}H_{17}N_3O_6S$	GSH
236.1135	11.06	positive	326.28	drought	increase	$C_9H_{17}NO_6$	
254.0843	11.66	positive	114.05	drought	increase	$C_{12}H_{15}NO_3S$	
222.0978	11.36	positive	112.75	drought	increase	$C_8H_{15}NO_6$	
252.1084	13.36	positive	45.95	drought	increase	$C_9H_{17}NO_7$	
162.0404	12.66	positive	44.61	drought	increase	$C_5H_7NO_5$	
130.0650	11.96	positive	31.44	drought	increase	C_9H_7N	
207.0584	13.80	positive	17.77	drought	increase	$C_{10}H_{10}N_2OS$	
447.0548	13.82	negative	17.74	drought	increase	$C_{16}H_{20}N_2O_9S_2$	
293.2107	0.90	positive	16.72	drought	increase	$C_{18}H_{28}O_3$	
160.0755	11.94	positive	7.71	drought	increase	$C_{10}H_9NO$	
111.0206	1.94	negative	4.93	drought	increase	$C_4H_4N_2O_2$	
303.0037	10.78	negative	4.81	drought	increase	$C_{15}H_9ClO_5$	
258.1098	12.64	positive	3.93	drought	increase	$C_{10}H_{15}N_3O_5$	
503.1611	14.65	negative	3.79	drought	increase	$C_{18}H_{32}O_{16}$	Raffinose
214.0494	13.95	negative	3.13	drought	increase	$C_5H_{14}NO_6P$	
93.0463	1.99	negative	3.11	drought	increase	$C_5H_6N_2$	
132.1018	6.47	positive	2.70	drought	increase	$C_6H_{13}NO_2$	Leucine
182.0810	8.96	positive	2.51	drought	increase	$C_9H_{11}NO_3$	Tyrosine
309.2079	0.99	negative	2.50	drought	increase	$C_{18}H_{30}O_4$	
165.0544	8.96	positive	2.47	drought	increase	$C_9H_8O_3$	
136.0756	8.94	positive	2.45	drought	increase	C_8H_9NO	
431.2220	8.51	negative	2.34	drought	increase	$C_{29}H_{28}N_4$	
139.0501	2.00	positive	2.31	drought	increase	$C_6H_6N_2O_2$	
203.0835	7.20	negative	2.30	drought	increase	$C_{11}H_{12}N_2O_2$	
104.0704	6.65	positive	2.29	drought	increase	$C_4H_9NO_2$	gamma-Aminobutyric acid
72.0808	6.93	positive	2.27	drought	increase	C_4H_9N	
87.0440	6.65	positive	2.27	drought	increase	$C_4H_6O_2$	
86.0600	6.60	positive	2.26	drought	increase	C_4H_7NO	
121.0303	5.56	negative	2.24	drought	increase	$C_7H_6O_2$	
69.0335	6.65	positive	2.18	drought	increase	C_4H_4O	
166.0860	6.75	positive	2.11	drought	increase	$C_9H_{11}NO_2$	Phenylalanine
128.0705	6.63	positive	2.05	drought	increase	$C_6H_9NO_2$	

123.0440	8.94	positive	2.02	drought	increase	$C_7H_6O_2$	
118.0861	6.96	positive	2.01	drought	increase	$C_5H_{11}NO_2$	Valine
279.0274	10.85	negative	0.50	drought	decrease	$C_{14}H_{13}ClO_2S$	
275.0756	3.23	negative	0.50	drought	decrease	$C_{11}H_{16}O_8$	
175.1073	9.56	positive	0.49	drought	decrease	$C_7H_{14}N_2O_3$	
134.0481	6.05	negative	0.48	drought	decrease	$C_5H_5N_5$	
131.0471	11.19	negative	0.47	drought	decrease	$C_4H_8N_2O_3$	Asparagine
182.9920	5.75	negative	0.46	drought	decrease	$C_7H_4O_6$	
285.1022	9.04	positive	0.46	drought	decrease	$C_{12}H_{17}N_2O_4P$	
187.0986	3.08	negative	0.45	drought	decrease	$C_9H_{16}O_4$	
255.1080	9.64	positive	0.44	drought	decrease	$C_9H_{18}O_8$	
229.0867	1.15	positive	0.44	drought	decrease	$C_{14}H_{12}O_3$	
154.0156	6.20	negative	0.42	drought	decrease	$C_6H_5NO_4$	
259.0226	19.06	negative	0.38	drought	decrease	$C_6H_{13}O_9P$	Glucose 6-phosphate
101.0249	9.86	negative	0.35	drought	decrease	$C_4H_6O_3$	
229.1443	5.58	positive	0.35	drought	decrease	$C_{12}H_{20}O_4$	
277.1671	5.82	positive	0.34	drought	decrease	$C_{14}H_{20}N_4O_2$	
364.0647	18.38	positive	0.32	drought	decrease	$C_{10}H_{14}N_5O_8P$	Guanosine monophosphate
76.0757	5.16	positive	0.31	drought	decrease	C_3H_9NO	
308.0905	11.42	positive	0.17	drought	decrease	$C_{10}H_{17}N_3O_6S$	GSH
175.1074	8.25	positive	0.12	drought	decrease	$C_7H_{14}N_2O_3$	
150.0430	8.17	negative	0.08	drought	decrease	$C_5H_5N_5O$	
236.1135	11.06	positive	64.27	heat	increase	$C_9H_{17}NO_6$	
254.0843	11.66	positive	31.90	heat	increase	$C_{12}H_{15}NO_3S$	
222.0978	11.36	positive	26.24	heat	increase	$C_8H_{15}NO_6$	
102.0549	10.49	positive	17.63	heat	increase	$C_4H_7NO_2$	
252.1084	13.36	positive	17.28	heat	increase	$C_9H_{17}NO_7$	
125.0363	10.83	negative	17.09	heat	increase	$C_5H_6N_2O_2$	
203.0835	7.20	negative	14.21	heat	increase	$C_{11}H_{12}N_2O_2$	
301.1057	8.67	positive	14.06	heat	increase	$C_{17}H_{16}O_5$	
503.1611	14.65	negative	13.55	heat	increase	$C_{18}H_{32}O_{16}$	Raffinose
136.0756	8.94	positive	11.81	heat	increase	C_8H_9NO	
231.0154	5.74	negative	11.59	heat	increase	$C_9H_4N_4O_4$	

182.0810	8.96	positive	11.48	heat	increase	$C_9H_{11}NO_3$	Tyrosine
132.1018	6.47	positive	11.42	heat	increase	$C_6H_{13}NO_2$	Leucine
188.0705	7.20	positive	11.39	heat	increase	$C_6H_{10}ClN_5$	
165.0544	8.96	positive	11.39	heat	increase	$C_9H_8O_3$	
205.0969	7.21	positive	11.23	heat	increase	$C_{11}H_{12}N_2O_2$	Tryptophan
123.0461	6.39	negative	10.31	heat	increase	$C_7H_8O_2$	
162.0404	12.66	positive	9.84	heat	increase	$C_5H_7NO_5$	
123.0440	8.94	positive	8.97	heat	increase	$C_7H_6O_2$	
167.0359	6.40	negative	7.93	heat	increase	$C_3H_{10}N_3O_3S$	
130.0650	11.96	positive	7.93	heat	increase	C_9H_7N	
207.0584	13.80	positive	7.13	heat	increase	$C_{10}H_{10}N_2OS$	
217.0837	10.98	negative	7.07	heat	increase	$C_8H_{14}N_2O_5$	
447.0548	13.82	negative	6.94	heat	increase	$C_{16}H_{20}N_2O_9S_2$	
298.0955	14.04	positive	6.18	heat	increase	$C_{11}H_{15}N_5O_3S$	
166.0860	6.75	positive	5.96	heat	increase	$C_9H_{11}NO_2$	Phenylalanine
91.0582	8.59	positive	5.87	heat	increase	$C_4H_{10}S$	
90.0548	8.59	positive	5.69	heat	increase	$C_3H_7NO_2$	Alanine
72.0808	6.93	positive	5.61	heat	increase	C_4H_9N	
258.1098	12.64	positive	5.58	heat	increase	$C_{10}H_{15}N_3O_5$	
144.0807	7.28	positive	5.52	heat	increase	$C_{10}H_9N$	
180.0666	8.95	negative	5.40	heat	increase	$C_9H_{11}NO_3$	Tyrosine
293.2107	0.90	positive	5.17	heat	increase	$C_{18}H_{28}O_3$	
214.0494	13.95	negative	5.16	heat	increase	$C_5H_{14}NO_6P$	
145.0991	14.13	negative	5.14	heat	increase	$C_6H_{14}N_2O_2$	Lysine
86.0600	6.60	positive	4.82	heat	increase	C_4H_7NO	
118.0861	6.96	positive	4.72	heat	increase	$C_5H_{11}NO_2$	Valine
147.1126	14.14	positive	4.43	heat	increase	$C_6H_{14}N_2O_2$	Lysine
281.0884	12.72	negative	3.41	heat	increase	$C_{10}H_{18}O_9$	
115.0043	5.74	negative	3.35	heat	increase	$C_4H_4O_4$	Fumaric acid
84.0807	14.14	positive	3.13	heat	increase	C_5H_9N	
595.2917	12.05	negative	2.97	heat	increase	$C_{34}H_{44}O_9$	
162.0759	9.98	positive	2.97	heat	increase	$C_6H_{11}NO_4$	
275.0215	7.34	negative	2.92	heat	increase	$C_{14}H_{12}O_2S_2$	

158.0832	5.75	negative	2.80	heat	increase	$C_7H_{13}NO_3$	
71.0139	5.78	negative	2.61	heat	increase	$C_3H_4O_2$	
168.0654	12.05	positive	2.55	heat	increase	$C_8H_9NO_3$	
76.0757	5.16	positive	2.51	heat	increase	C_3H_9NO	
70.0651	7.43	positive	2.51	heat	increase	C_4H_7N	
116.0704	7.43	positive	2.48	heat	increase	$C_5H_9NO_2$	Proline
119.0347	12.03	negative	2.46	heat	increase	$C_4H_8O_4$	
325.1121	12.05	positive	2.45	heat	increase	$C_{12}H_{20}O_{10}$	
221.0674	12.74	negative	2.41	heat	increase	$C_8H_{14}O_7$	
219.0972	10.97	positive	2.35	heat	increase	$C_8H_{14}N_2O_5$	
204.0865	12.03	positive	2.34	heat	increase	$C_8H_{13}NO_5$	
311.1144	6.02	negative	2.28	heat	increase	$C_{15}H_{20}O_7$	
163.0599	12.04	positive	2.25	heat	increase	$C_6H_{10}O_5$	
109.0283	12.09	positive	2.23	heat	increase	$C_6H_4O_2$	
211.9975	4.44	negative	2.22	heat	increase	$C_4H_8NO_7P$	
161.0916	9.05	positive	2.20	heat	increase	$C_6H_{12}N_2O_3$	
128.0361	4.44	negative	2.20	heat	increase	$C_5H_7NO_3$	
154.0631	14.24	negative	2.19	heat	increase	$C_6H_9N_3O_2$	Histidine
97.0284	12.06	positive	2.17	heat	increase	$C_5H_4O_2$	
127.0389	12.07	positive	2.12	heat	increase	$C_6H_6O_3$	
308.0905	11.42	positive	2.12	heat	increase	$C_{10}H_{17}N_3O_6S$	GSH
259.0131	12.03	negative	2.11	heat	increase	$C_6H_{12}O_9S$	Fructose 6-phosphate
85.0283	12.05	positive	2.10	heat	increase	$C_4H_4O_2$	
233.1131	8.87	positive	2.10	heat	increase	$C_9H_{16}N_2O_5$	
339.0736	5.91	negative	2.07	heat	increase	$C_{15}H_{16}O_9$	
147.0308	6.40	negative	2.06	heat	increase	$C_5H_8O_5$	
161.0465	12.72	negative	2.05	heat	increase	$C_6H_{10}O_5$	
160.0755	11.94	positive	2.04	heat	increase	$C_{10}H_9NO$	
145.0494	12.05	positive	2.03	heat	increase	$C_6H_8O_4$	
159.0309	6.54	negative	2.03	heat	increase	$C_6H_8O_5$	
207.0650	5.88	positive	2.03	heat	increase	$C_{11}H_{10}O_4$	
110.0712	14.25	positive	2.01	heat	increase	$C_5H_7N_3$	
156.0766	14.25	positive	2.01	heat	increase	$C_6H_9N_3O_2$	Histidine

213.0501	10.91	negative	2.00	heat	increase	$C_8H_{10}N_2O_5$	
117.0201	5.31	negative	2.00	heat	increase	$C_4H_6O_4$	Succinic acid
303.0037	10.78	negative	0.50	heat	decrease	$C_{15}H_9ClO_5$	
285.1022	9.04	positive	0.48	heat	decrease	$C_{12}H_{17}N_2O_4P$	
365.1193	5.90	positive	0.48	heat	decrease	$C_{17}H_{20}N_2O_5S$	
115.0865	14.72	positive	0.46	heat	decrease	$C_5H_{10}N_2O$	
133.0970	14.72	positive	0.45	heat	decrease	$C_5H_{12}N_2O_2$	Ornithine
169.0152	7.89	negative	0.45	heat	decrease	$C_7H_6O_5$	
364.0647	18.38	positive	0.44	heat	decrease	$C_{10}H_{14}N_5O_8P$	Guanosine monophosphate
277.1671	5.82	positive	0.43	heat	decrease	$C_{14}H_{20}N_4O_2$	
114.0550	11.60	positive	0.42	heat	decrease	$C_5H_7NO_2$	
229.0867	1.15	positive	0.41	heat	decrease	$C_{14}H_{12}O_3$	
134.0481	6.05	negative	0.38	heat	decrease	$C_5H_5N_5$	
187.0986	3.08	negative	0.37	heat	decrease	$C_9H_{16}O_4$	
170.0469	6.41	negative	0.36	heat	decrease	$C_7H_9NO_4$	
159.0762	11.61	positive	0.36	heat	decrease	$C_6H_{10}N_2O_3$	
176.1028	11.61	positive	0.36	heat	decrease	$C_6H_{13}N_3O_3$	Citrulline
93.0463	1.99	negative	0.32	heat	decrease	$C_5H_6N_2$	
174.0893	11.61	negative	0.32	heat	decrease	$C_6H_{13}N_3O_3$	Citrulline
139.0501	2.00	positive	0.29	heat	decrease	$C_6H_6N_2O_2$	
139.0501	6.84	positive	0.25	heat	decrease	$C_6H_6N_2O_2$	
115.0865	6.90	positive	0.24	heat	decrease	$C_5H_{10}N_2O$	
188.0575	6.42	negative	0.18	heat	decrease	$C_7H_{11}NO_5$	
175.1074	8.25	positive	0.07	heat	decrease	$C_7H_{14}N_2O_3$	
236.1135	11.06	positive	593.92	heatxdrought	increase	$C_9H_{17}NO_6$	
254.0843	11.66	positive	287.25	heatxdrought	increase	$C_{12}H_{15}NO_3S$	
222.0978	11.36	positive	230.47	heatxdrought	increase	$C_8H_{15}NO_6$	
293.2107	0.90	positive	157.88	heatxdrought	increase	$C_{18}H_{28}O_3$	
162.0404	12.66	positive	108.97	heatxdrought	increase	$C_5H_7NO_5$	
252.1084	13.36	positive	100.96	heatxdrought	increase	$C_9H_{17}NO_7$	
303.0037	10.78	negative	82.12	heatxdrought	increase	$C_{15}H_9ClO_5$	
130.0650	11.96	positive	60.49	heatxdrought	increase	C_9H_7N	
207.0584	13.80	positive	57.98	heatxdrought	increase	$C_{10}H_{10}N_2OS$	

447.0548	13.82	negative	57.93	heatxdrought	increase	$C_{16}H_{20}N_2O_9S_2$	
102.0549	10.49	positive	19.65	heatxdrought	increase	$C_4H_7NO_2$	
311.2237	0.99	negative	19.30	heatxdrought	increase	$C_{18}H_{32}O_4$	
281.0884	12.72	negative	16.74	heatxdrought	increase	$C_{10}H_{18}O_9$	
160.0755	11.94	positive	13.84	heatxdrought	increase	$C_{10}H_9NO$	
279.1182	11.50	positive	12.13	heatxdrought	increase	$C_{22}H_{14}$	
217.0837	10.98	negative	12.13	heatxdrought	increase	$C_8H_{14}N_2O_5$	
111.0206	1.94	negative	12.12	heatxdrought	increase	$C_4H_4N_2O_2$	
180.0868	12.10	positive	10.81	heatxdrought	increase	$C_6H_{13}NO_5$	
309.2079	0.99	negative	10.71	heatxdrought	increase	$C_{18}H_{30}O_4$	
503.1611	14.65	negative	9.27	heatxdrought	increase	$C_{18}H_{32}O_{16}$	Raffinose
595.2917	12.05	negative	9.23	heatxdrought	increase	$C_{34}H_{44}O_9$	
221.0674	12.74	negative	8.77	heatxdrought	increase	$C_8H_{14}O_7$	
203.0835	7.20	negative	8.62	heatxdrought	increase	$C_{11}H_{12}N_2O_2$	
301.1057	8.67	positive	6.91	heatxdrought	increase	$C_{17}H_{16}O_5$	
161.0465	12.72	negative	6.14	heatxdrought	increase	$C_6H_{10}O_5$	
214.0494	13.95	negative	6.08	heatxdrought	increase	$C_5H_{14}NO_6P$	
125.0363	10.83	negative	5.15	heatxdrought	increase	$C_5H_6N_2O_2$	
341.1103	12.66	negative	5.11	heatxdrought	increase	$C_{12}H_{22}O_{11}$	Maltose
258.1098	12.64	positive	5.08	heatxdrought	increase	$C_{10}H_{15}N_3O_5$	
75.0089	3.66	negative	4.66	heatxdrought	increase	$C_2H_4O_3$	
91.0582	8.59	positive	4.57	heatxdrought	increase	$C_4H_{10}S$	
293.1762	1.01	negative	4.50	heatxdrought	increase	$C_{17}H_{26}O_4$	
90.0548	8.59	positive	4.47	heatxdrought	increase	$C_3H_7NO_2$	Alanine
103.0407	2.08	negative	4.34	heatxdrought	increase	$C_4H_8O_3$	
132.1018	6.47	positive	4.30	heatxdrought	increase	$C_6H_{13}NO_2$	Leucine
219.0972	10.97	positive	4.26	heatxdrought	increase	$C_8H_{14}N_2O_5$	
136.0756	8.94	positive	4.01	heatxdrought	increase	C_8H_9NO	
188.0705	7.20	positive	4.00	heatxdrought	increase	$C_6H_{10}ClN_5$	
205.0969	7.21	positive	3.95	heatxdrought	increase	$C_{11}H_{12}N_2O_2$	Tryptophan
182.0810	8.96	positive	3.94	heatxdrought	increase	$C_9H_{11}NO_3$	Tyrosine
165.0544	8.96	positive	3.88	heatxdrought	increase	$C_9H_8O_3$	
104.0704	6.65	positive	3.86	heatxdrought	increase	$C_4H_9NO_2$	gamma-Aminobutyric acid

87.0440	6.65	positive	3.86	heatxdrought	increase	$C_4H_6O_2$	
86.0600	6.60	positive	3.84	heatxdrought	increase	C_4H_7NO	
69.0335	6.65	positive	3.72	heatxdrought	increase	C_4H_4O	
431.2220	8.51	negative	3.57	heatxdrought	increase	$C_{29}H_{28}N_4$	
275.1348	11.15	positive	3.41	heatxdrought	increase	$C_{10}H_{18}N_4O_5$	
128.0361	4.44	negative	3.37	heatxdrought	increase	$C_5H_7NO_3$	
358.1843	13.98	positive	3.35	heatxdrought	increase	$C_{17}H_{27}NO_7$	
211.9975	4.44	negative	3.29	heatxdrought	increase	$C_4H_8NO_7P$	
123.0440	8.94	positive	3.20	heatxdrought	increase	$C_7H_6O_2$	
137.0253	2.13	negative	3.20	heatxdrought	increase	$C_7H_6O_3$	
128.0705	6.63	positive	3.17	heatxdrought	increase	$C_6H_9NO_2$	
159.0309	6.54	negative	2.86	heatxdrought	increase	$C_6H_8O_5$	
147.0308	6.40	negative	2.75	heatxdrought	increase	$C_5H_8O_5$	
177.0414	6.47	negative	2.74	heatxdrought	increase	$C_6H_{10}O_6$	
166.0860	6.75	positive	2.71	heatxdrought	increase	$C_9H_{11}NO_2$	Phenylalanine
145.0991	14.13	negative	2.66	heatxdrought	increase	$C_6H_{14}N_2O_2$	Lysine
117.0201	5.31	negative	2.58	heatxdrought	increase	$C_4H_6O_4$	Succinic acid
298.0955	14.04	positive	2.54	heatxdrought	increase	$C_{11}H_{15}N_5O_3S$	
72.0808	6.93	positive	2.52	heatxdrought	increase	C_4H_9N	
130.0650	5.13	positive	2.48	heatxdrought	increase	C_9H_7N	
231.0154	5.74	negative	2.34	heatxdrought	increase	$C_9H_4N_4O_4$	
596.1678	8.43	positive	2.33	heatxdrought	increase	$C_{27}H_{31}O_{15}$	
70.0651	7.43	positive	2.32	heatxdrought	increase	C_4H_7N	
215.1386	5.77	positive	2.25	heatxdrought	increase	$C_{10}H_{18}N_2O_3$	
116.0704	7.43	positive	2.23	heatxdrought	increase	$C_5H_9NO_2$	Proline
76.0757	5.16	positive	2.23	heatxdrought	increase	C_3H_9NO	
123.0461	6.39	negative	2.21	heatxdrought	increase	$C_7H_8O_2$	
118.0861	6.96	positive	2.19	heatxdrought	increase	$C_5H_{11}NO_2$	Valine
147.1126	14.14	positive	2.19	heatxdrought	increase	$C_6H_{14}N_2O_2$	Lysine
291.1297	15.85	positive	2.17	heatxdrought	increase	$C_{10}H_{18}N_4O_6$	
275.0215	7.34	negative	2.14	heatxdrought	increase	$C_{14}H_{12}O_2S_2$	
167.0359	6.40	negative	2.07	heatxdrought	increase	$C_3H_{10}N_3O_3S$	
124.0392	8.53	positive	2.03	heatxdrought	increase	$C_6H_5NO_2$	

144.0807	7.28	positive	2.02	heatxdrought	increase	$C_{10}H_9N$	
131.0722	1.23	negative	2.02	heatxdrought	increase	$C_6H_{12}O_3$	
179.0359	6.04	negative	0.49	heatxdrought	decrease	$C_9H_8O_4$	
364.0647	18.38	positive	0.48	heatxdrought	decrease	$C_{10}H_{14}N_5O_8P$	Guanosine monophosphate
259.0226	19.06	negative	0.48	heatxdrought	decrease	$C_6H_{13}O_9P$	Glucose 6-phosphate
85.0298	7.26	negative	0.48	heatxdrought	decrease	$C_4H_6O_2$	
145.0151	7.32	negative	0.47	heatxdrought	decrease	$C_6H_{10}S_2$	alpha-Ketoglutaric acid
129.0202	7.25	negative	0.45	heatxdrought	decrease	$C_5H_6O_4$	
111.0094	7.27	negative	0.43	heatxdrought	decrease	$C_5H_4O_3$	
122.0811	9.07	positive	0.38	heatxdrought	decrease	$C_4H_{11}NO_3$	
219.0154	7.28	negative	0.38	heatxdrought	decrease	$C_7H_8O_8$	
140.0115	8.39	negative	0.35	heatxdrought	decrease	$C_2H_8NO_4P$	
139.0501	6.84	positive	0.34	heatxdrought	decrease	$C_6H_6N_2O_2$	
83.0141	7.27	negative	0.33	heatxdrought	decrease	$C_4H_4O_2$	
228.9940	7.23	negative	0.30	heatxdrought	decrease	$C_9H_8Cl_2N_2O$	
93.0463	1.99	negative	0.30	heatxdrought	decrease	$C_5H_6N_2$	
173.0101	7.27	negative	0.29	heatxdrought	decrease	$C_6H_6O_6$	
254.9172	5.49	negative	0.24	heatxdrought	decrease	$C_4H_8Cl_3O_4P$	
132.0653	10.44	positive	0.24	heatxdrought	decrease	$C_5H_9NO_3$	
229.0122	18.08	negative	0.23	heatxdrought	decrease	$C_5H_{11}O_8P$	Ribose 5-phosphate
316.9492	5.43	negative	0.21	heatxdrought	decrease	$C_{14}H_{10}Cl_4$	
116.0512	5.07	negative	0.19	heatxdrought	decrease	C_8H_7N	
175.1074	8.25	positive	0.14	heatxdrought	decrease	$C_7H_{14}N_2O_3$	
185.0077	5.32	negative	0.13	heatxdrought	decrease	$C_7H_6O_6$	
308.0905	11.42	positive	0.12	heatxdrought	decrease	$C_{10}H_{17}N_3O_6S$	GSH
275.0756	3.23	negative	0.11	heatxdrought	decrease	$C_{11}H_{16}O_8$	
124.9558	6.49	negative	0.08	heatxdrought	decrease	$C_2H_6S_3$	
150.0430	8.17	negative	0.05	heatxdrought	decrease	$C_5H_5N_5O$	
157.0152	5.05	negative	0.05	heatxdrought	decrease	$C_6H_6O_5$	
244.0620	5.05	negative	0.02	heatxdrought	decrease	$C_{13}H_{11}NO_4$	
168.0451	0.91	positive	0.01	heatxdrought	decrease	$C_3H_9N_3O_3S$	
311.1144	6.02	negative	98.16	heatxsalinity	increase	$C_{15}H_{20}O_7$	
503.1611	14.65	negative	19.59	heatxsalinity	increase	$C_{18}H_{32}O_{16}$	Raffinose

254.0843	11.66	positive	17.73	heatxsalinity	increase	$C_{12}H_{15}NO_3S$	
125.0363	10.83	negative	17.13	heatxsalinity	increase	$C_5H_6N_2O_2$	
203.0835	7.20	negative	16.58	heatxsalinity	increase	$C_{11}H_{12}N_2O_2$	
301.1057	8.67	positive	15.53	heatxsalinity	increase	$C_{17}H_{16}O_5$	
252.1084	13.36	positive	14.98	heatxsalinity	increase	$C_9H_{17}NO_7$	
188.0705	7.20	positive	12.40	heatxsalinity	increase	$C_6H_{10}ClN_5$	
205.0969	7.21	positive	12.17	heatxsalinity	increase	$C_{11}H_{12}N_2O_2$	Tryptophan
236.1135	11.06	positive	11.96	heatxsalinity	increase	$C_9H_{17}NO_6$	
136.0756	8.94	positive	11.87	heatxsalinity	increase	C_8H_9NO	
182.0810	8.96	positive	11.53	heatxsalinity	increase	$C_9H_{11}NO_3$	Tyrosine
132.1018	6.47	positive	11.45	heatxsalinity	increase	$C_6H_{13}NO_2$	Leucine
165.0544	8.96	positive	11.37	heatxsalinity	increase	$C_9H_8O_3$	
123.0440	8.94	positive	8.91	heatxsalinity	increase	$C_7H_6O_2$	
258.1098	12.64	positive	8.72	heatxsalinity	increase	$C_{10}H_{15}N_3O_5$	
222.0978	11.36	positive	7.72	heatxsalinity	increase	$C_8H_{15}NO_6$	
231.0154	5.74	negative	7.60	heatxsalinity	increase	$C_9H_4N_4O_4$	
298.0955	14.04	positive	7.46	heatxsalinity	increase	$C_{11}H_{15}N_5O_3S$	
351.1035	6.16	positive	7.34	heatxsalinity	increase	$C_{16}H_{18}N_2O_5S$	
123.0461	6.39	negative	7.32	heatxsalinity	increase	$C_7H_8O_2$	
217.0837	10.98	negative	6.93	heatxsalinity	increase	$C_8H_{14}N_2O_5$	
214.0494	13.95	negative	6.76	heatxsalinity	increase	$C_5H_{14}NO_6P$	
130.0862	6.83	positive	6.52	heatxsalinity	increase	$C_6H_{11}NO_2$	
293.2107	0.90	positive	6.46	heatxsalinity	increase	$C_{18}H_{28}O_3$	
91.0582	8.59	positive	6.35	heatxsalinity	increase	$C_4H_{10}S$	
102.0549	10.49	positive	6.30	heatxsalinity	increase	$C_4H_7NO_2$	
90.0548	8.59	positive	6.15	heatxsalinity	increase	$C_3H_7NO_2$	Alanine
144.0807	7.28	positive	6.04	heatxsalinity	increase	$C_{10}H_9N$	
167.0359	6.40	negative	5.98	heatxsalinity	increase	$C_3H_{10}N_3O_3S$	
166.0860	6.75	positive	5.82	heatxsalinity	increase	$C_9H_{11}NO_2$	Phenylalanine
145.0991	14.13	negative	5.60	heatxsalinity	increase	$C_6H_{14}N_2O_2$	Lysine
72.0808	6.93	positive	5.33	heatxsalinity	increase	C_4H_9N	
180.0666	8.95	negative	5.15	heatxsalinity	increase	$C_9H_{11}NO_3$	Tyrosine
86.0600	6.60	positive	4.93	heatxsalinity	increase	C_4H_7NO	

147.1126	14.14	positive	4.78	heatxsalinity	increase	$C_6H_{14}N_2O_2$	Lysine
118.0861	6.96	positive	4.45	heatxsalinity	increase	$C_5H_{11}NO_2$	Valine
162.0759	9.98	positive	4.35	heatxsalinity	increase	$C_6H_{11}NO_4$	
281.0884	12.72	negative	4.32	heatxsalinity	increase	$C_{10}H_{18}O_9$	
275.0215	7.34	negative	3.74	heatxsalinity	increase	$C_{14}H_{12}O_2S_2$	
162.0404	12.66	positive	3.45	heatxsalinity	increase	$C_5H_7NO_5$	
84.0807	14.14	positive	3.41	heatxsalinity	increase	C_5H_9N	
168.0654	12.05	positive	3.29	heatxsalinity	increase	$C_8H_9NO_3$	
221.0674	12.74	negative	3.08	heatxsalinity	increase	$C_8H_{14}O_7$	
595.2917	12.05	negative	3.03	heatxsalinity	increase	$C_{34}H_{44}O_9$	
115.0043	5.74	negative	2.99	heatxsalinity	increase	$C_4H_4O_4$	Fumaric acid
325.1121	12.05	positive	2.92	heatxsalinity	increase	$C_{12}H_{20}O_{10}$	
119.0347	12.03	negative	2.91	heatxsalinity	increase	$C_4H_8O_4$	
204.0865	12.03	positive	2.88	heatxsalinity	increase	$C_8H_{13}NO_5$	
109.0283	12.09	positive	2.83	heatxsalinity	increase	$C_6H_4O_2$	
76.0757	5.16	positive	2.78	heatxsalinity	increase	C_3H_9NO	
97.0284	12.06	positive	2.71	heatxsalinity	increase	$C_5H_4O_2$	
127.0389	12.07	positive	2.67	heatxsalinity	increase	$C_6H_6O_3$	
70.0651	7.43	positive	2.66	heatxsalinity	increase	C_4H_7N	
116.0704	7.43	positive	2.64	heatxsalinity	increase	$C_5H_9NO_2$	Proline
163.0599	12.04	positive	2.64	heatxsalinity	increase	$C_6H_{10}O_5$	
85.0283	12.05	positive	2.64	heatxsalinity	increase	$C_4H_4O_2$	
154.0631	14.24	negative	2.63	heatxsalinity	increase	$C_6H_9N_3O_2$	Histidine
379.0991	6.02	positive	2.58	heatxsalinity	increase	$C_{17}H_{18}N_2O_6S$	
453.0928	12.08	negative	2.54	heatxsalinity	increase	$C_{22}H_{18}N_2O_9$	
259.0131	12.03	negative	2.54	heatxsalinity	increase	$C_6H_{12}O_9S$	Fructose 6-phosphate
130.0650	11.96	positive	2.51	heatxsalinity	increase	C_9H_7N	
145.0494	12.05	positive	2.42	heatxsalinity	increase	$C_6H_8O_4$	
341.1104	12.04	negative	2.40	heatxsalinity	increase	$C_{12}H_{22}O_{11}$	Sucrose
71.0139	5.78	negative	2.39	heatxsalinity	increase	$C_3H_4O_2$	
343.1153	12.04	negative	2.39	heatxsalinity	increase	$C_8H_{21}N_6O_7P_2$	
219.0972	10.97	positive	2.39	heatxsalinity	increase	$C_8H_{14}N_2O_5$	
211.9975	4.44	negative	2.39	heatxsalinity	increase	$C_4H_8NO_7P$	

128.0361	4.44	negative	2.39	heatxsalinity	increase	$C_5H_7NO_3$	
141.0202	3.90	negative	2.38	heatxsalinity	increase	$C_6H_6O_4$	
156.0766	14.25	positive	2.37	heatxsalinity	increase	$C_6H_9N_3O_2$	Histidine
389.1206	12.04	negative	2.37	heatxsalinity	increase	$C_{20}H_{22}O_8$	
110.0712	14.25	positive	2.37	heatxsalinity	increase	$C_5H_7N_3$	
388.1191	12.04	negative	2.36	heatxsalinity	increase	$C_{23}H_{19}NO_5$	
180.0868	12.10	positive	2.35	heatxsalinity	increase	$C_6H_{13}NO_5$	
322.1124	8.19	positive	2.28	heatxsalinity	increase	$C_{13}H_{23}NO_4S_2$	
76.0393	9.69	positive	2.26	heatxsalinity	increase	$C_2H_5NO_2$	Glycine
233.1131	8.87	positive	2.26	heatxsalinity	increase	$C_9H_{16}N_2O_5$	
161.0465	12.72	negative	2.26	heatxsalinity	increase	$C_6H_{10}O_5$	
87.0091	4.09	negative	2.25	heatxsalinity	increase	$C_3H_4O_3$	Pyruvic acid
239.1486	0.95	positive	2.22	heatxsalinity	increase	$C_{11}H_{18}N_4O_2$	
120.0654	9.76	positive	2.18	heatxsalinity	increase	$C_4H_9NO_3$	Threonine
161.0916	9.05	positive	2.11	heatxsalinity	increase	$C_6H_{12}N_2O_3$	
187.0734	8.61	negative	2.11	heatxsalinity	increase	$C_7H_{12}N_2O_4$	
345.1145	5.85	positive	2.11	heatxsalinity	increase	$C_{22}H_{17}ClN_2$	
191.0207	13.99	negative	2.09	heatxsalinity	increase	$C_6H_8O_7$	Citric acid
118.0517	9.77	negative	2.09	heatxsalinity	increase	$C_4H_9NO_3$	Threonine
164.0738	12.52	positive	2.08	heatxsalinity	increase	$C_6H_{13}NO_2S$	
102.0549	12.57	positive	2.07	heatxsalinity	increase	$C_4H_7NO_2$	
327.0678	8.19	positive	2.07	heatxsalinity	increase	$C_{14}H_{14}O_9$	
207.0584	13.80	positive	2.05	heatxsalinity	increase	$C_{10}H_{10}N_2OS$	
381.0936	5.90	positive	0.49	heatxsalinity	decrease	$C_{21}H_{16}O_7$	
283.2647	1.84	negative	0.49	heatxsalinity	decrease	$C_{18}H_{36}O_2$	
365.1193	5.90	positive	0.48	heatxsalinity	decrease	$C_{17}H_{20}N_2O_5S$	
105.0199	5.82	negative	0.48	heatxsalinity	decrease	$C_3H_6O_4$	
387.1310	5.91	negative	0.47	heatxsalinity	decrease	$C_{18}H_{20}N_4O_6$	
187.0986	3.08	negative	0.47	heatxsalinity	decrease	$C_9H_{16}O_4$	
285.1022	9.04	positive	0.46	heatxsalinity	decrease	$C_{12}H_{17}N_2O_4P$	
88.0756	5.12	positive	0.46	heatxsalinity	decrease	C_4H_9NO	
150.0430	8.17	negative	0.38	heatxsalinity	decrease	$C_5H_5N_5O$	
253.0933	4.42	negative	0.37	heatxsalinity	decrease	$C_9H_{18}O_8$	

175.1074	8.25	positive	0.31	heatxsalinity	decrease	$C_7H_{14}N_2O_3$	
140.0115	8.39	negative	0.29	heatxsalinity	decrease	$C_2H_8NO_4P$	
170.0469	6.41	negative	0.28	heatxsalinity	decrease	$C_7H_9NO_4$	
188.0575	6.42	negative	0.24	heatxsalinity	decrease	$C_7H_{11}NO_5$	
115.0865	6.90	positive	0.22	heatxsalinity	decrease	$C_5H_{10}N_2O$	
124.9558	6.49	negative	0.16	heatxsalinity	decrease	$C_2H_6S_3$	
185.0077	5.32	negative	0.08	heatxsalinity	decrease	$C_7H_6O_6$	
231.0154	5.74	negative	29.55	high light	increase	$C_9H_4N_4O_4$	
102.0549	10.49	positive	13.80	high light	increase	$C_4H_7NO_2$	
258.1098	12.64	positive	9.64	high light	increase	$C_{10}H_{15}N_3O_5$	
125.0363	10.83	negative	9.17	high light	increase	$C_5H_6N_2O_2$	
503.1611	14.65	negative	7.73	high light	increase	$C_{18}H_{32}O_{16}$	Raffinose
115.0043	5.74	negative	6.02	high light	increase	$C_4H_4O_4$	Fumaric acid
214.0494	13.95	negative	5.79	high light	increase	$C_5H_{14}NO_6P$	
293.2107	0.90	positive	5.67	high light	increase	$C_{18}H_{28}O_3$	
158.0832	5.75	negative	5.37	high light	increase	$C_7H_{13}NO_3$	
301.1057	8.67	positive	4.94	high light	increase	$C_{17}H_{16}O_5$	
254.0843	11.66	positive	4.84	high light	increase	$C_{12}H_{15}NO_3S$	
217.0837	10.98	negative	4.47	high light	increase	$C_8H_{14}N_2O_5$	
71.0139	5.78	negative	3.97	high light	increase	$C_3H_4O_2$	
252.1084	13.36	positive	3.75	high light	increase	$C_9H_{17}NO_7$	
275.0215	7.34	negative	3.31	high light	increase	$C_{14}H_{12}O_2S_2$	
76.0393	9.69	positive	3.01	high light	increase	$C_2H_5NO_2$	Glycine
161.0465	5.61	negative	2.81	high light	increase	$C_6H_{10}O_5$	
203.0835	7.20	negative	2.79	high light	increase	$C_{11}H_{12}N_2O_2$	
596.1678	8.43	positive	2.78	high light	increase	$C_{27}H_{31}O_{15}$	
188.0705	7.20	positive	2.68	high light	increase	$C_6H_{10}ClN_5$	
205.0969	7.21	positive	2.66	high light	increase	$C_{11}H_{12}N_2O_2$	Tryptophan
207.0650	5.88	positive	2.45	high light	increase	$C_{11}H_{10}O_4$	
132.1018	6.47	positive	2.40	high light	increase	$C_6H_{13}NO_2$	Leucine
339.0736	5.91	negative	2.33	high light	increase	$C_{15}H_{16}O_9$	
171.0308	5.81	negative	2.32	high light	increase	$C_7H_8O_5$	
119.0347	12.03	negative	2.31	high light	increase	$C_4H_8O_4$	

325.1121	12.05	positive	2.26	high light	increase	$C_{12}H_{20}O_{10}$	
168.0654	12.05	positive	2.23	high light	increase	$C_8H_9NO_3$	
72.0808	6.93	positive	2.22	high light	increase	C_4H_9N	
163.0752	5.90	positive	2.21	high light	increase	$C_{10}H_{10}O_2$	
185.0077	5.32	negative	2.21	high light	increase	$C_7H_6O_6$	
124.9558	6.49	negative	2.21	high light	increase	$C_2H_6S_3$	
167.0359	6.40	negative	2.20	high light	increase	$C_3H_{10}N_3O_3S$	
91.0582	8.59	positive	2.19	high light	increase	$C_4H_{10}S$	
166.0860	6.75	positive	2.19	high light	increase	$C_9H_{11}NO_2$	Phenylalanine
90.0548	8.59	positive	2.15	high light	increase	$C_3H_7NO_2$	Alanine
223.0618	5.90	negative	2.11	high light	increase	$C_{11}H_{12}O_5$	
123.0461	6.39	negative	2.09	high light	increase	$C_7H_8O_2$	
242.0786	12.06	positive	2.06	high light	increase	$C_9H_{12}ClN_5O$	
163.0599	12.04	positive	2.05	high light	increase	$C_6H_{10}O_5$	
204.0865	12.03	positive	2.04	high light	increase	$C_8H_{13}NO_5$	
134.0446	12.03	positive	0.50	high light	decrease	$C_4H_7NO_4$	Aspartic acid
385.1154	5.66	negative	0.49	high light	decrease	$C_{17}H_{22}O_{10}$	
207.0584	13.80	positive	0.48	high light	decrease	$C_{10}H_{10}N_2OS$	
345.1145	5.85	positive	0.48	high light	decrease	$C_{22}H_{17}ClN_2$	
132.0311	12.05	negative	0.48	high light	decrease	$C_4H_7NO_4$	Aspartic acid
409.1094	5.63	positive	0.48	high light	decrease	$C_{19}H_{20}O_{10}$	
169.0152	7.89	negative	0.46	high light	decrease	$C_7H_6O_5$	
365.1193	5.90	positive	0.43	high light	decrease	$C_{17}H_{20}N_2O_5S$	
193.0366	7.18	negative	0.43	high light	decrease	$C_6H_{10}O_7$	
205.0500	5.62	negative	0.41	high light	decrease	$C_{11}H_{10}O_4$	
351.1035	6.16	positive	0.41	high light	decrease	$C_{16}H_{18}N_2O_5S$	
160.0755	11.94	positive	0.38	high light	decrease	$C_{10}H_9NO$	
134.0481	6.05	negative	0.37	high light	decrease	$C_5H_5N_5$	
209.0819	13.99	negative	0.35	high light	decrease	$C_{11}H_{14}O_4$	
175.1074	8.25	positive	0.16	high light	decrease	$C_7H_{14}N_2O_3$	
231.1004	5.12	positive	0.15	high light	decrease	$C_{14}H_{14}O_3$	
231.0154	5.74	negative	15.78	high lightxcold	increase	$C_9H_4N_4O_4$	
281.0884	12.72	negative	13.01	high lightxcold	increase	$C_{10}H_{18}O_9$	

102.0549	10.49	positive	10.97	high lightxcold	increase	$C_4H_7NO_2$	
125.0363	10.83	negative	8.94	high lightxcold	increase	$C_5H_6N_2O_2$	
221.0674	12.74	negative	6.86	high lightxcold	increase	$C_8H_{14}O_7$	
161.0465	12.72	negative	4.95	high lightxcold	increase	$C_6H_{10}O_5$	
158.0832	5.75	negative	4.73	high lightxcold	increase	$C_7H_{13}NO_3$	
341.1103	12.66	negative	3.99	high lightxcold	increase	$C_{12}H_{22}O_{11}$	Maltose
115.0043	5.74	negative	3.84	high lightxcold	increase	$C_4H_4O_4$	Fumaric acid
168.9915	16.50	negative	3.62	high lightxcold	increase	$C_3H_7O_6P$	Dihydroxyacetone phosphate
301.1057	8.67	positive	3.34	high lightxcold	increase	$C_{17}H_{16}O_5$	
175.1073	9.56	positive	3.27	high lightxcold	increase	$C_7H_{14}N_2O_3$	
275.0215	7.34	negative	3.21	high lightxcold	increase	$C_{14}H_{12}O_2S_2$	
166.0860	6.75	positive	3.01	high lightxcold	increase	$C_9H_{11}NO_2$	Phenylalanine
596.1678	8.43	positive	2.94	high lightxcold	increase	$C_{27}H_{31}O_{15}$	
71.0139	5.78	negative	2.89	high lightxcold	increase	$C_3H_4O_2$	
252.1084	13.36	positive	2.75	high lightxcold	increase	$C_9H_{17}NO_7$	
130.0862	6.83	positive	2.60	high lightxcold	increase	$C_6H_{11}NO_2$	
217.0837	10.98	negative	2.53	high lightxcold	increase	$C_8H_{14}N_2O_5$	
76.0393	9.69	positive	2.39	high lightxcold	increase	$C_2H_5NO_2$	Glycine
203.0835	7.20	negative	2.36	high lightxcold	increase	$C_{11}H_{12}N_2O_2$	
205.0969	7.21	positive	2.35	high lightxcold	increase	$C_{11}H_{12}N_2O_2$	Tryptophan
188.0705	7.20	positive	2.35	high lightxcold	increase	$C_6H_{10}ClN_5$	
207.0650	5.88	positive	2.33	high lightxcold	increase	$C_{11}H_{10}O_4$	
161.0465	5.61	negative	2.31	high lightxcold	increase	$C_6H_{10}O_5$	
339.0736	5.91	negative	2.25	high lightxcold	increase	$C_{15}H_{16}O_9$	
122.0811	9.07	positive	2.25	high lightxcold	increase	$C_4H_{11}NO_3$	
171.0308	5.81	negative	2.20	high lightxcold	increase	$C_7H_8O_5$	
124.9558	6.49	negative	2.19	high lightxcold	increase	$C_2H_6S_3$	
223.0618	5.90	negative	2.12	high lightxcold	increase	$C_{11}H_{12}O_5$	
225.0755	5.70	positive	2.09	high lightxcold	increase	$C_{11}H_{12}O_5$	
105.0199	5.82	negative	2.08	high lightxcold	increase	$C_3H_6O_4$	
163.0752	5.90	positive	2.01	high lightxcold	increase	$C_{10}H_{10}O_2$	
297.0585	5.99	positive	0.49	high lightxcold	decrease	$C_{10}H_{20}N_2S_4$	
205.0500	5.62	negative	0.49	high lightxcold	decrease	$C_{11}H_{10}O_4$	

115.0865	14.72	positive	0.48	high lightxcold	decrease	$C_5H_{10}N_2O$	
133.0970	14.72	positive	0.48	high lightxcold	decrease	$C_5H_{12}N_2O_2$	Ornithine
293.1762	1.01	negative	0.47	high lightxcold	decrease	$C_{17}H_{26}O_4$	
345.1145	5.85	positive	0.45	high lightxcold	decrease	$C_{22}H_{17}ClN_2$	
203.1499	10.54	positive	0.43	high lightxcold	decrease	$C_8H_{18}N_4O_2$	
132.0653	10.44	positive	0.43	high lightxcold	decrease	$C_5H_9NO_3$	
169.0152	7.89	negative	0.41	high lightxcold	decrease	$C_7H_6O_5$	
134.0481	6.05	negative	0.39	high lightxcold	decrease	$C_5H_5N_5$	
365.1193	5.90	positive	0.38	high lightxcold	decrease	$C_{17}H_{20}N_2O_5S$	
303.0037	10.78	negative	0.37	high lightxcold	decrease	$C_{15}H_9ClO_5$	
182.9920	5.75	negative	0.35	high lightxcold	decrease	$C_7H_4O_6$	
409.1094	5.63	positive	0.33	high lightxcold	decrease	$C_{19}H_{20}O_{10}$	
209.0819	13.99	negative	0.25	high lightxcold	decrease	$C_{11}H_{14}O_4$	
236.1135	11.06	positive	487.02	high lightxdrought	increase	$C_9H_{17}NO_6$	
254.0843	11.66	positive	188.28	high lightxdrought	increase	$C_{12}H_{15}NO_3S$	
222.0978	11.36	positive	170.94	high lightxdrought	increase	$C_8H_{15}NO_6$	
162.0404	12.66	positive	96.66	high lightxdrought	increase	$C_5H_7NO_5$	
293.2107	0.90	positive	61.23	high lightxdrought	increase	$C_{18}H_{28}O_3$	
252.1084	13.36	positive	49.72	high lightxdrought	increase	$C_9H_{17}NO_7$	
207.0584	13.80	positive	35.58	high lightxdrought	increase	$C_{10}H_{10}N_2OS$	
447.0548	13.82	negative	34.80	high lightxdrought	increase	$C_{16}H_{20}N_2O_9S_2$	
130.0650	11.96	positive	32.11	high lightxdrought	increase	C_9H_7N	
303.0037	10.78	negative	11.26	high lightxdrought	increase	$C_{15}H_9ClO_5$	
160.0755	11.94	positive	7.82	high lightxdrought	increase	$C_{10}H_9NO$	
111.0206	1.94	negative	7.43	high lightxdrought	increase	$C_4H_4N_2O_2$	
503.1611	14.65	negative	7.36	high lightxdrought	increase	$C_{18}H_{32}O_{16}$	Raffinose
102.0549	10.49	positive	6.99	high lightxdrought	increase	$C_4H_7NO_2$	
258.1098	12.64	positive	6.23	high lightxdrought	increase	$C_{10}H_{15}N_3O_5$	
217.0837	10.98	negative	5.58	high lightxdrought	increase	$C_8H_{14}N_2O_5$	
301.1057	8.67	positive	5.36	high lightxdrought	increase	$C_{17}H_{16}O_5$	
203.0835	7.20	negative	5.31	high lightxdrought	increase	$C_{11}H_{12}N_2O_2$	
214.0494	13.95	negative	5.16	high lightxdrought	increase	$C_5H_{14}NO_6P$	
311.2237	0.99	negative	4.55	high lightxdrought	increase	$C_{18}H_{32}O_4$	

309.2079	0.99	negative	4.39	high lightxdrought	increase	$C_{18}H_{30}O_4$	
144.0464	0.93	negative	4.10	high lightxdrought	increase	C_9H_7NO	
275.1348	11.15	positive	3.60	high lightxdrought	increase	$C_{10}H_{18}N_4O_5$	
281.0884	12.72	negative	3.55	high lightxdrought	increase	$C_{10}H_{18}O_9$	
182.0810	8.96	positive	3.52	high lightxdrought	increase	$C_9H_{11}NO_3$	Tyrosine
132.1018	6.47	positive	3.47	high lightxdrought	increase	$C_6H_{13}NO_2$	Leucine
136.0756	8.94	positive	3.47	high lightxdrought	increase	C_8H_9NO	
165.0544	8.96	positive	3.47	high lightxdrought	increase	$C_9H_8O_3$	
231.0154	5.74	negative	2.94	high lightxdrought	increase	$C_9H_4N_4O_4$	
123.0440	8.94	positive	2.87	high lightxdrought	increase	$C_7H_6O_2$	
205.0969	7.21	positive	2.85	high lightxdrought	increase	$C_{11}H_{12}N_2O_2$	Tryptophan
188.0705	7.20	positive	2.80	high lightxdrought	increase	$C_6H_{10}ClN_5$	
431.2220	8.51	negative	2.79	high lightxdrought	increase	$C_{29}H_{28}N_4$	
91.0582	8.59	positive	2.72	high lightxdrought	increase	$C_4H_{10}S$	
90.0548	8.59	positive	2.66	high lightxdrought	increase	$C_3H_7NO_2$	Alanine
72.0808	6.93	positive	2.59	high lightxdrought	increase	C_4H_9N	
168.0654	12.05	positive	2.53	high lightxdrought	increase	$C_8H_9NO_3$	
166.0860	6.75	positive	2.43	high lightxdrought	increase	$C_9H_{11}NO_2$	Phenylalanine
185.0077	5.32	negative	2.34	high lightxdrought	increase	$C_7H_6O_6$	
325.1121	12.05	positive	2.34	high lightxdrought	increase	$C_{12}H_{20}O_{10}$	
118.0861	6.96	positive	2.30	high lightxdrought	increase	$C_5H_{11}NO_2$	Valine
219.0972	10.97	positive	2.24	high lightxdrought	increase	$C_8H_{14}N_2O_5$	
163.0599	12.04	positive	2.24	high lightxdrought	increase	$C_6H_{10}O_5$	
204.0865	12.03	positive	2.23	high lightxdrought	increase	$C_8H_{13}NO_5$	
119.0347	12.03	negative	2.21	high lightxdrought	increase	$C_4H_8O_4$	
97.0284	12.06	positive	2.12	high lightxdrought	increase	$C_5H_4O_2$	
221.0674	12.74	negative	2.12	high lightxdrought	increase	$C_8H_{14}O_7$	
181.0152	6.57	negative	2.11	high lightxdrought	increase	$C_8H_6O_5$	
85.0283	12.05	positive	2.09	high lightxdrought	increase	$C_4H_4O_2$	
279.1182	11.50	positive	2.08	high lightxdrought	increase	$C_{22}H_{14}$	
259.0131	12.03	negative	2.08	high lightxdrought	increase	$C_6H_{12}O_9S$	Fructose 6-phosphate
145.0991	14.13	negative	2.07	high lightxdrought	increase	$C_6H_{14}N_2O_2$	Lysine
254.9172	5.49	negative	2.07	high lightxdrought	increase	$C_4H_8Cl_3O_4P$	

316.9492	5.43	negative	2.07	high lightxdrought	increase	$C_{14}H_{10}Cl_4$	
109.0283	12.09	positive	2.05	high lightxdrought	increase	$C_6H_4O_2$	
127.0389	12.07	positive	2.03	high lightxdrought	increase	$C_6H_6O_3$	
87.0091	4.09	negative	0.50	high lightxdrought	decrease	$C_3H_4O_3$	Pyruvic acid
135.0461	6.05	negative	0.49	high lightxdrought	decrease	$C_8H_8O_2$	
268.1038	5.50	positive	0.49	high lightxdrought	decrease	$C_{10}H_{13}N_5O_4$	Adenosine
139.0501	2.00	positive	0.48	high lightxdrought	decrease	$C_6H_6N_2O_2$	
265.0718	5.60	negative	0.47	high lightxdrought	decrease	$C_{16}H_{12}NO_3$	
179.0359	6.04	negative	0.46	high lightxdrought	decrease	$C_9H_8O_4$	
161.0918	7.24	positive	0.45	high lightxdrought	decrease	$C_6H_{12}N_2O_3$	
139.0501	6.84	positive	0.44	high lightxdrought	decrease	$C_6H_6N_2O_2$	
187.0986	3.08	negative	0.42	high lightxdrought	decrease	$C_9H_{16}O_4$	
136.0617	6.00	positive	0.41	high lightxdrought	decrease	$C_5H_5N_5$	Adenine
119.0357	9.81	negative	0.37	high lightxdrought	decrease	$C_5H_4N_4$	
189.1231	6.38	positive	0.37	high lightxdrought	decrease	$C_8H_{16}N_2O_3$	
179.0570	9.82	negative	0.37	high lightxdrought	decrease	$C_7H_8N_4O_2$	Glucose
233.1493	6.64	positive	0.37	high lightxdrought	decrease	$C_{10}H_{20}N_2O_4$	
229.0122	18.08	negative	0.37	high lightxdrought	decrease	$C_5H_{11}O_8P$	Ribose 5-phosphate
122.0811	9.07	positive	0.36	high lightxdrought	decrease	$C_4H_{11}NO_3$	
259.0226	19.06	negative	0.35	high lightxdrought	decrease	$C_6H_{13}O_9P$	Glucose 6-phosphate
89.0248	9.82	negative	0.34	high lightxdrought	decrease	$C_3H_6O_3$	
134.0481	6.05	negative	0.34	high lightxdrought	decrease	$C_5H_5N_5$	
112.0505	9.17	positive	0.34	high lightxdrought	decrease	$C_4H_5N_3O$	
71.0139	9.83	negative	0.33	high lightxdrought	decrease	$C_3H_4O_2$	
143.0358	9.80	negative	0.32	high lightxdrought	decrease	$C_6H_8O_4$	
59.0137	9.82	negative	0.31	high lightxdrought	decrease	$C_2H_4O_2$	
175.1074	8.25	positive	0.30	high lightxdrought	decrease	$C_7H_{14}N_2O_3$	
152.0566	9.00	positive	0.30	high lightxdrought	decrease	$C_5H_5N_5O$	Guanine
284.0985	9.05	positive	0.30	high lightxdrought	decrease	$C_{10}H_{13}N_5O_5$	
275.0756	3.23	negative	0.28	high lightxdrought	decrease	$C_{11}H_{16}O_8$	
157.0152	5.05	negative	0.28	high lightxdrought	decrease	$C_6H_6O_5$	
125.0363	10.83	negative	0.25	high lightxdrought	decrease	$C_5H_6N_2O_2$	
229.0867	1.15	positive	0.24	high lightxdrought	decrease	$C_{14}H_{12}O_3$	

364.0647	18.38	positive	0.22	high lightxdrought	decrease	$C_{10}H_{14}N_5O_8P$	Guanosine monophosphate
93.0463	1.99	negative	0.20	high lightxdrought	decrease	$C_5H_6N_2$	
244.0620	5.05	negative	0.16	high lightxdrought	decrease	$C_{13}H_{11}NO_4$	
101.0249	9.86	negative	0.16	high lightxdrought	decrease	$C_4H_6O_3$	
285.1022	9.04	positive	0.08	high lightxdrought	decrease	$C_{12}H_{17}N_2O_4P$	
168.0451	0.91	positive	0.06	high lightxdrought	decrease	$C_3H_9N_3O_3S$	
293.2107	0.90	positive	136.76	high lightxheat	increase	$C_{18}H_{28}O_3$	
303.0037	10.78	negative	66.47	high lightxheat	increase	$C_{15}H_9ClO_5$	
254.0843	11.66	positive	38.43	high lightxheat	increase	$C_{12}H_{15}NO_3S$	
285.1022	9.04	positive	30.59	high lightxheat	increase	$C_{12}H_{17}N_2O_4P$	
152.0566	9.00	positive	24.16	high lightxheat	increase	$C_5H_5N_5O$	Guanine
268.1038	5.50	positive	24.08	high lightxheat	increase	$C_{10}H_{13}N_5O_4$	Adenosine
284.0985	9.05	positive	23.23	high lightxheat	increase	$C_{10}H_{13}N_5O_5$	
595.2917	12.05	negative	22.77	high lightxheat	increase	$C_{34}H_{44}O_9$	
148.0974	9.05	positive	21.09	high lightxheat	increase	$C_6H_{13}NO_3$	
203.0835	7.20	negative	16.33	high lightxheat	increase	$C_{11}H_{12}N_2O_2$	
252.1084	13.36	positive	15.95	high lightxheat	increase	$C_9H_{17}NO_7$	
136.0756	8.94	positive	14.66	high lightxheat	increase	C_8H_9NO	
112.0505	9.17	positive	14.34	high lightxheat	increase	$C_4H_5N_3O$	
165.0544	8.96	positive	14.18	high lightxheat	increase	$C_9H_8O_3$	
182.0810	8.96	positive	13.84	high lightxheat	increase	$C_9H_{11}NO_3$	Tyrosine
217.0837	10.98	negative	13.08	high lightxheat	increase	$C_8H_{14}N_2O_5$	
236.1135	11.06	positive	12.82	high lightxheat	increase	$C_9H_{17}NO_6$	
222.0978	11.36	positive	11.60	high lightxheat	increase	$C_8H_{15}NO_6$	
231.0154	5.74	negative	11.39	high lightxheat	increase	$C_9H_4N_4O_4$	
132.1018	6.47	positive	11.37	high lightxheat	increase	$C_6H_{13}NO_2$	Leucine
123.0440	8.94	positive	11.30	high lightxheat	increase	$C_7H_6O_2$	
130.0650	11.96	positive	10.53	high lightxheat	increase	C_9H_7N	
231.1004	5.12	positive	10.29	high lightxheat	increase	$C_{14}H_{14}O_3$	
301.1057	8.67	positive	9.59	high lightxheat	increase	$C_{17}H_{16}O_5$	
243.0628	5.51	negative	9.14	high lightxheat	increase	$C_9H_{12}N_2O_6$	
166.0860	6.75	positive	7.27	high lightxheat	increase	$C_9H_{11}NO_2$	Phenylalanine
144.0464	0.93	negative	7.04	high lightxheat	increase	C_9H_7NO	

447.0548	13.82	negative	6.66	high lightxheat	increase	$C_{16}H_{20}N_2O_9S_2$	
171.0308	5.81	negative	6.60	high lightxheat	increase	$C_7H_8O_5$	
233.1493	6.64	positive	6.58	high lightxheat	increase	$C_{10}H_{20}N_2O_4$	
111.0206	1.94	negative	6.46	high lightxheat	increase	$C_4H_4N_2O_2$	
124.0392	8.53	positive	6.38	high lightxheat	increase	$C_6H_5NO_2$	
207.0584	13.80	positive	6.26	high lightxheat	increase	$C_{10}H_{10}N_2OS$	
311.2237	0.99	negative	5.98	high lightxheat	increase	$C_{18}H_{32}O_4$	
188.0705	7.20	positive	5.79	high lightxheat	increase	$C_6H_{10}ClN_5$	
149.0252	5.93	negative	5.73	high lightxheat	increase	$C_8H_6O_3$	
205.0969	7.21	positive	5.70	high lightxheat	increase	$C_{11}H_{12}N_2O_2$	Tryptophan
91.0582	8.59	positive	5.47	high lightxheat	increase	$C_4H_{10}S$	
162.0404	12.66	positive	5.46	high lightxheat	increase	$C_5H_7NO_5$	
180.0666	8.95	negative	5.42	high lightxheat	increase	$C_9H_{11}NO_3$	Tyrosine
117.0201	5.31	negative	5.35	high lightxheat	increase	$C_4H_6O_4$	Succinic acid
145.0991	14.13	negative	5.34	high lightxheat	increase	$C_6H_{14}N_2O_2$	Lysine
90.0548	8.59	positive	5.31	high lightxheat	increase	$C_3H_7NO_2$	Alanine
215.1386	5.77	positive	5.19	high lightxheat	increase	$C_{10}H_{18}N_2O_3$	
136.0617	6.00	positive	4.89	high lightxheat	increase	$C_5H_5N_5$	Adenine
86.0600	6.60	positive	4.76	high lightxheat	increase	C_4H_7NO	
110.0255	6.56	negative	4.46	high lightxheat	increase	$C_5H_5NO_2$	
147.1126	14.14	positive	4.32	high lightxheat	increase	$C_6H_{14}N_2O_2$	Lysine
72.0808	6.93	positive	4.14	high lightxheat	increase	C_4H_9N	
261.1441	7.39	positive	3.77	high lightxheat	increase	$C_{15}H_{20}N_2S$	
75.0089	3.66	negative	3.72	high lightxheat	increase	$C_2H_4O_3$	
73.0296	5.34	negative	3.70	high lightxheat	increase	$C_3H_6O_2$	
298.0955	14.04	positive	3.57	high lightxheat	increase	$C_{11}H_{15}N_5O_3S$	
118.0861	6.96	positive	3.47	high lightxheat	increase	$C_5H_{11}NO_2$	Valine
219.0972	10.97	positive	3.46	high lightxheat	increase	$C_8H_{14}N_2O_5$	
87.0440	6.65	positive	3.42	high lightxheat	increase	$C_4H_6O_2$	
104.0704	6.65	positive	3.42	high lightxheat	increase	$C_4H_9NO_2$	gamma-Aminobutyric acid
150.0430	8.17	negative	3.41	high lightxheat	increase	$C_5H_5N_5O$	
221.0674	12.74	negative	3.41	high lightxheat	increase	$C_8H_{14}O_7$	
189.1231	6.38	positive	3.30	high lightxheat	increase	$C_8H_{16}N_2O_3$	

69.0335	6.65	positive	3.29	high lightxheat	increase	C_4H_4O	
168.0654	12.05	positive	3.27	high lightxheat	increase	$C_8H_9NO_3$	
144.0807	7.28	positive	3.25	high lightxheat	increase	$C_{10}H_9N$	
87.0091	4.09	negative	3.14	high lightxheat	increase	$C_3H_4O_3$	Pyruvic acid
84.0807	14.14	positive	3.14	high lightxheat	increase	C_5H_9N	
325.1121	12.05	positive	3.09	high lightxheat	increase	$C_{12}H_{20}O_{10}$	
309.2079	0.99	negative	3.08	high lightxheat	increase	$C_{18}H_{30}O_4$	
281.0884	12.72	negative	3.06	high lightxheat	increase	$C_{10}H_{18}O_9$	
116.0512	5.07	negative	3.03	high lightxheat	increase	C_8H_7N	
109.0283	12.09	positive	2.99	high lightxheat	increase	$C_6H_4O_2$	
119.0347	12.03	negative	2.96	high lightxheat	increase	$C_4H_8O_4$	
158.0832	5.75	negative	2.95	high lightxheat	increase	$C_7H_{13}NO_3$	
115.0043	5.74	negative	2.94	high lightxheat	increase	$C_4H_4O_4$	Fumaric acid
128.0361	4.44	negative	2.89	high lightxheat	increase	$C_5H_7NO_3$	
127.0389	12.07	positive	2.75	high lightxheat	increase	$C_6H_6O_3$	
244.0620	5.05	negative	2.73	high lightxheat	increase	$C_{13}H_{11}NO_4$	
494.2581	6.70	positive	2.64	high lightxheat	increase	$C_{26}H_{39}NO_6S$	
97.0284	12.06	positive	2.63	high lightxheat	increase	$C_5H_4O_2$	
163.0599	12.04	positive	2.63	high lightxheat	increase	$C_6H_{10}O_5$	
204.0865	12.03	positive	2.57	high lightxheat	increase	$C_8H_{13}NO_5$	
85.0283	12.05	positive	2.51	high lightxheat	increase	$C_4H_4O_2$	
161.0465	12.72	negative	2.49	high lightxheat	increase	$C_6H_{10}O_5$	
76.0757	5.16	positive	2.48	high lightxheat	increase	C_3H_9NO	
128.0705	6.63	positive	2.45	high lightxheat	increase	$C_6H_9NO_2$	
145.0494	12.05	positive	2.43	high lightxheat	increase	$C_6H_8O_4$	
293.1762	1.01	negative	2.43	high lightxheat	increase	$C_{17}H_{26}O_4$	
139.0501	6.84	positive	2.43	high lightxheat	increase	$C_6H_6N_2O_2$	
431.2220	8.51	negative	2.41	high lightxheat	increase	$C_{29}H_{28}N_4$	
185.0077	5.32	negative	2.28	high lightxheat	increase	$C_7H_6O_6$	
134.0481	6.05	negative	2.27	high lightxheat	increase	$C_5H_5N_5$	
503.1611	14.65	negative	2.27	high lightxheat	increase	$C_{18}H_{32}O_{16}$	Raffinose
130.0650	5.13	positive	2.26	high lightxheat	increase	C_9H_7N	
131.0722	1.23	negative	2.26	high lightxheat	increase	$C_6H_{12}O_3$	

130.0518	6.37	negative	2.25	high lightxheat	increase	$C_5H_9NO_3$	
160.0755	11.94	positive	2.21	high lightxheat	increase	$C_{10}H_9NO$	
177.0414	6.47	negative	2.17	high lightxheat	increase	$C_6H_{10}O_6$	
343.1153	12.04	negative	2.13	high lightxheat	increase	$C_8H_{21}N_6O_7P_2$	
341.1104	12.04	negative	2.12	high lightxheat	increase	$C_{12}H_{22}O_{11}$	Sucrose
337.1098	11.88	positive	2.10	high lightxheat	increase	$C_{20}H_{16}O_5$	
259.0131	12.03	negative	2.10	high lightxheat	increase	$C_6H_{12}O_9S$	Fructose 6-phosphate
129.0657	6.88	positive	2.09	high lightxheat	increase	$C_5H_8N_2O_2$	
389.1206	12.04	negative	2.05	high lightxheat	increase	$C_{20}H_{22}O_8$	
388.1191	12.04	negative	2.02	high lightxheat	increase	$C_{23}H_{19}NO_5$	
151.0623	7.23	positive	0.50	high lightxheat	decrease	$C_6H_{14}S_2$	
359.1480	0.95	positive	0.49	high lightxheat	decrease	$C_{20}H_{22}O_6$	
101.0709	10.54	positive	0.49	high lightxheat	decrease	$C_4H_8N_2O$	
145.0627	10.50	negative	0.49	high lightxheat	decrease	$C_5H_{10}N_2O_3$	Glutamine
101.0249	7.31	negative	0.48	high lightxheat	decrease	$C_4H_6O_3$	
127.0521	10.50	negative	0.48	high lightxheat	decrease	$C_5H_8N_2O_2$	
109.0413	10.49	negative	0.48	high lightxheat	decrease	$C_5H_6N_2O$	
130.0497	10.55	positive	0.48	high lightxheat	decrease	$C_5H_7NO_3$	
72.0808	12.22	positive	0.48	high lightxheat	decrease	C_4H_9N	
133.0606	11.13	positive	0.47	high lightxheat	decrease	$C_4H_8N_2O_3$	Asparagine
150.0582	7.25	positive	0.47	high lightxheat	decrease	$C_5H_{11}NO_2S$	
116.0341	11.13	positive	0.47	high lightxheat	decrease	$C_4H_5NO_3$	
134.0639	11.12	positive	0.47	high lightxheat	decrease	$C_5H_{11}NOS$	
305.0992	3.55	positive	0.46	high lightxheat	decrease	$C_{11}H_{16}N_2O_8$	
132.0653	10.44	positive	0.45	high lightxheat	decrease	$C_5H_9NO_3$	
147.0762	10.56	positive	0.45	high lightxheat	decrease	$C_5H_{10}N_2O_3$	Glutamine
131.0471	11.19	negative	0.45	high lightxheat	decrease	$C_4H_8N_2O_3$	Asparagine
133.0317	7.24	positive	0.45	high lightxheat	decrease	$C_5H_8O_2S$	
102.0549	10.49	positive	0.43	high lightxheat	decrease	$C_4H_7NO_2$	
357.1204	6.02	negative	0.43	high lightxheat	decrease	$C_{17}H_{18}N_4O_5$	
135.0647	11.13	positive	0.43	high lightxheat	decrease	$C_5H_{10}O_4$	
174.0418	6.78	negative	0.42	high lightxheat	decrease	$C_6H_9NO_5$	
254.9172	5.49	negative	0.42	high lightxheat	decrease	$C_4H_8Cl_3O_4P$	

210.0759	9.20	positive	0.42	high lightxheat	decrease	$C_{10}H_{11}NO_4$	
141.0202	6.67	negative	0.41	high lightxheat	decrease	$C_6H_6O_4$	
208.0623	9.19	negative	0.41	high lightxheat	decrease	$C_{10}H_{11}NO_4$	
275.1348	11.15	positive	0.40	high lightxheat	decrease	$C_{10}H_{18}N_4O_5$	
133.0515	3.54	negative	0.40	high lightxheat	decrease	$C_6H_6N_4$	
175.1073	9.56	positive	0.40	high lightxheat	decrease	$C_7H_{14}N_2O_3$	
172.0625	4.45	negative	0.40	high lightxheat	decrease	$C_7H_{11}NO_4$	
283.2647	1.84	negative	0.39	high lightxheat	decrease	$C_{18}H_{36}O_2$	
128.0361	11.02	negative	0.39	high lightxheat	decrease	$C_5H_7NO_3$	
188.0575	6.42	negative	0.39	high lightxheat	decrease	$C_7H_{11}NO_5$	
88.0756	5.12	positive	0.38	high lightxheat	decrease	C_4H_9NO	
187.0986	3.08	negative	0.38	high lightxheat	decrease	$C_9H_{16}O_4$	
258.1098	12.64	positive	0.38	high lightxheat	decrease	$C_{10}H_{15}N_3O_5$	
163.0622	6.53	negative	0.37	high lightxheat	decrease	$C_6H_{12}O_5$	
114.0550	11.60	positive	0.37	high lightxheat	decrease	$C_5H_7NO_2$	
144.1018	5.50	positive	0.37	high lightxheat	decrease	$C_7H_{13}NO_2$	
130.0862	6.83	positive	0.37	high lightxheat	decrease	$C_6H_{11}NO_2$	
213.0413	8.29	negative	0.37	high lightxheat	decrease	$C_9H_{10}O_6$	
253.0933	4.42	negative	0.36	high lightxheat	decrease	$C_9H_{18}O_8$	
129.0656	10.55	positive	0.35	high lightxheat	decrease	$C_5H_8N_2O_2$	
229.0867	1.15	positive	0.35	high lightxheat	decrease	$C_{14}H_{12}O_3$	
113.0339	5.95	positive	0.35	high lightxheat	decrease	$C_4H_4N_2O_2$	
115.0865	0.95	positive	0.35	high lightxheat	decrease	$C_5H_{10}N_2O$	
85.0298	7.26	negative	0.34	high lightxheat	decrease	$C_4H_6O_2$	
289.0686	4.63	positive	0.32	high lightxheat	decrease	$C_{15}H_{12}O_6$	
595.1644	8.44	positive	0.32	high lightxheat	decrease	$C_{27}H_{30}O_{15}$	
163.0422	9.22	positive	0.32	high lightxheat	decrease	$C_6H_{10}O_3S$	
145.0151	7.32	negative	0.31	high lightxheat	decrease	$C_6H_{10}S_2$	alpha-Ketoglutaric acid
365.1835	5.51	negative	0.31	high lightxheat	decrease	$C_{22}H_{26}N_2O_3$	
191.0207	13.99	negative	0.31	high lightxheat	decrease	$C_6H_8O_7$	Citric acid
177.0414	7.83	negative	0.30	high lightxheat	decrease	$C_6H_{10}O_6$	
219.0154	7.28	negative	0.30	high lightxheat	decrease	$C_7H_8O_8$	
189.0891	11.01	negative	0.28	high lightxheat	decrease	$C_7H_{14}N_2O_4$	

138.0569	6.47	negative	0.28	high lightxheat	decrease	$C_7H_9NO_2$	
431.3182	1.06	negative	0.28	high lightxheat	decrease	$C_{27}H_{44}O_4$	
178.0519	5.17	negative	0.28	high lightxheat	decrease	$C_9H_9NO_3$	
176.1028	11.61	positive	0.28	high lightxheat	decrease	$C_6H_{13}N_3O_3$	Citrulline
159.0762	11.61	positive	0.28	high lightxheat	decrease	$C_6H_{10}N_2O_3$	
338.1227	8.18	positive	0.27	high lightxheat	decrease	$C_{16}H_{19}NO_7$	
327.0678	8.19	positive	0.27	high lightxheat	decrease	$C_{14}H_{14}O_9$	
322.1124	8.19	positive	0.27	high lightxheat	decrease	$C_{13}H_{23}NO_4S_2$	
457.1099	3.47	positive	0.26	high lightxheat	decrease	$C_{17}H_{21}N_4O_9P$	
191.1024	11.02	positive	0.26	high lightxheat	decrease	$C_7H_{14}N_2O_4$	
371.1360	5.87	negative	0.26	high lightxheat	decrease	$C_{17}H_{24}O_9$	
174.0893	11.61	negative	0.25	high lightxheat	decrease	$C_6H_{13}N_3O_3$	Citrulline
162.0781	11.66	negative	0.25	high lightxheat	decrease	$C_7H_9N_5$	
379.0991	6.02	positive	0.24	high lightxheat	decrease	$C_{17}H_{18}N_2O_6S$	
417.1510	5.41	positive	0.24	high lightxheat	decrease	$C_{22}H_{24}O_8$	
147.0475	6.76	positive	0.24	high lightxheat	decrease	$C_6H_{10}O_2S$	
122.0811	9.07	positive	0.24	high lightxheat	decrease	$C_4H_{11}NO_3$	
174.0758	11.01	positive	0.24	high lightxheat	decrease	$C_7H_{11}NO_4$	
145.1082	5.89	positive	0.23	high lightxheat	decrease	$C_5H_{12}N_4O$	
134.0446	12.03	positive	0.23	high lightxheat	decrease	$C_4H_7NO_4$	Aspartic acid
613.1557	17.01	positive	0.23	high lightxheat	decrease	$C_{20}H_{32}N_6O_{12}S_2$	GSSG
141.0202	3.90	negative	0.22	high lightxheat	decrease	$C_6H_6O_4$	
139.0749	10.48	positive	0.22	high lightxheat	decrease	$C_8H_{10}O_2$	
135.0480	12.03	positive	0.21	high lightxheat	decrease	$C_5H_{10}O_2S$	
124.0392	9.96	positive	0.21	high lightxheat	decrease	$C_6H_5NO_2$	
314.1079	11.99	positive	0.21	high lightxheat	decrease	$C_{17}H_{16}ClN_3O$	
132.0311	12.05	negative	0.21	high lightxheat	decrease	$C_4H_7NO_4$	Aspartic acid
297.0585	5.99	positive	0.21	high lightxheat	decrease	$C_{10}H_{20}N_2S_4$	
129.0202	7.25	negative	0.21	high lightxheat	decrease	$C_5H_6O_4$	
115.0865	14.72	positive	0.19	high lightxheat	decrease	$C_5H_{10}N_2O$	
187.0734	8.61	negative	0.19	high lightxheat	decrease	$C_7H_{12}N_2O_4$	
193.0366	7.18	negative	0.19	high lightxheat	decrease	$C_6H_{10}O_7$	
173.0919	11.02	positive	0.19	high lightxheat	decrease	$C_7H_{12}N_2O_3$	

146.0468	10.97	negative	0.19	high lightxheat	decrease	$C_5H_9NO_4$	Glutamic acid
133.0970	14.72	positive	0.18	high lightxheat	decrease	$C_5H_{12}N_2O_2$	Ornithine
139.0501	2.00	positive	0.18	high lightxheat	decrease	$C_6H_6N_2O_2$	
163.0752	5.90	positive	0.18	high lightxheat	decrease	$C_{10}H_{10}O_2$	
277.1671	5.82	positive	0.18	high lightxheat	decrease	$C_{14}H_{20}N_4O_2$	
177.0616	9.80	positive	0.17	high lightxheat	decrease	$C_4H_8N_4O_4$	
299.0522	4.40	positive	0.17	high lightxheat	decrease	$C_{16}H_{10}O_6$	
345.1145	5.85	positive	0.17	high lightxheat	decrease	$C_{22}H_{17}ClN_2$	
299.0783	7.26	negative	0.16	high lightxheat	decrease	$C_{13}H_{16}O_8$	
179.0359	6.04	negative	0.16	high lightxheat	decrease	$C_9H_8O_4$	
175.1074	8.25	positive	0.16	high lightxheat	decrease	$C_7H_{14}N_2O_3$	
148.0603	11.01	positive	0.15	high lightxheat	decrease	$C_5H_9NO_4$	Glutamic acid
141.0656	8.70	positive	0.15	high lightxheat	decrease	$C_6H_8N_2O_2$	
259.0226	19.06	negative	0.14	high lightxheat	decrease	$C_6H_{13}O_9P$	Glucose 6-phosphate
140.0115	8.39	negative	0.13	high lightxheat	decrease	$C_2H_8NO_4P$	
115.0865	6.90	positive	0.12	high lightxheat	decrease	$C_5H_{10}N_2O$	
229.0122	18.08	negative	0.12	high lightxheat	decrease	$C_5H_{11}O_8P$	Ribose 5-phosphate
209.0819	13.99	negative	0.12	high lightxheat	decrease	$C_{11}H_{14}O_4$	
111.0094	7.27	negative	0.11	high lightxheat	decrease	$C_5H_4O_3$	
203.1499	10.54	positive	0.11	high lightxheat	decrease	$C_8H_{18}N_4O_2$	
335.1355	6.52	negative	0.11	high lightxheat	decrease	$C_{18}H_{24}O_4S$	
93.0463	1.99	negative	0.11	high lightxheat	decrease	$C_5H_6N_2$	
286.0917	11.77	positive	0.10	high lightxheat	decrease	$C_{12}H_{15}NO_7$	
132.0423	9.82	negative	0.10	high lightxheat	decrease	$C_3H_7N_3O_3$	
251.0777	8.28	negative	0.10	high lightxheat	decrease	$C_{10}H_{12}N_4O_4$	
228.9940	7.23	negative	0.10	high lightxheat	decrease	$C_9H_8Cl_2N_2O$	
387.1310	5.91	negative	0.08	high lightxheat	decrease	$C_{18}H_{20}N_4O_6$	
175.0482	9.82	negative	0.08	high lightxheat	decrease	$C_4H_8N_4O_4$	
177.0545	7.07	positive	0.08	high lightxheat	decrease	$C_{10}H_8O_3$	
215.0176	9.80	positive	0.07	high lightxheat	decrease	$C_4H_9NO_7P$-	
275.0756	3.23	negative	0.07	high lightxheat	decrease	$C_{11}H_{16}O_8$	
409.1094	5.63	positive	0.06	high lightxheat	decrease	$C_{19}H_{20}O_{10}$	
283.0829	4.71	negative	0.05	high lightxheat	decrease	$C_{12}H_{17}N_2O_4P$	

385.1154	5.66	negative	0.05	high lightxheat	decrease	$C_{17}H_{22}O_{10}$	
168.0451	0.91	positive	0.05	high lightxheat	decrease	$C_3H_9N_3O_3S$	
351.1035	6.16	positive	0.04	high lightxheat	decrease	$C_{16}H_{18}N_2O_5S$	
207.0519	4.71	negative	0.04	high lightxheat	decrease	$C_8H_{16}O_2S_2$	
173.0101	7.27	negative	0.04	high lightxheat	decrease	$C_6H_6O_6$	
279.0274	10.85	negative	0.04	high lightxheat	decrease	$C_{14}H_{13}ClO_2S$	
145.1446	9.29	positive	0.03	high lightxheat	decrease	$C_8H_{18}NO$	
303.0489	9.66	positive	0.03	high lightxheat	decrease	$C_{15}H_{10}O_7$	
83.0141	7.27	negative	0.03	high lightxheat	decrease	$C_4H_4O_2$	
381.0936	5.90	positive	0.02	high lightxheat	decrease	$C_{21}H_{16}O_7$	
223.0618	5.90	negative	0.02	high lightxheat	decrease	$C_{11}H_{12}O_5$	
365.1193	5.90	positive	0.02	high lightxheat	decrease	$C_{17}H_{20}N_2O_5S$	
339.0736	5.91	negative	0.01	high lightxheat	decrease	$C_{15}H_{16}O_9$	
207.0650	5.88	positive	0.01	high lightxheat	decrease	$C_{11}H_{10}O_4$	
162.0241	6.47	negative	0.01	high lightxheat	decrease	$C_5H_9NO_3S$	
141.0657	5.66	positive	0.00	high lightxheat	decrease	$C_6H_8N_2O_2$	
225.0755	5.70	positive	0.00	high lightxheat	decrease	$C_{11}H_{12}O_5$	
308.0905	11.42	positive	0.00	high lightxheat	decrease	$C_{10}H_{17}N_3O_6S$	GSH
167.0220	9.37	negative	0.00	high lightxheat	decrease	$C_5H_4N_4O_3$	
311.1144	6.02	negative	211.51	high lightxsalinity	increase	$C_{15}H_{20}O_7$	
125.0363	10.83	negative	26.51	high lightxsalinity	increase	$C_5H_6N_2O_2$	
155.0360	6.72	negative	23.63	high lightxsalinity	increase	$C_7H_8O_4$	
130.0518	6.37	negative	16.90	high lightxsalinity	increase	$C_5H_9NO_3$	
147.0308	6.40	negative	13.88	high lightxsalinity	increase	$C_5H_8O_5$	
181.0152	6.57	negative	13.18	high lightxsalinity	increase	$C_8H_6O_5$	
93.0463	1.99	negative	12.53	high lightxsalinity	increase	$C_5H_6N_2$	
254.0843	11.66	positive	11.48	high lightxsalinity	increase	$C_{12}H_{15}NO_3S$	
209.0819	13.99	negative	10.54	high lightxsalinity	increase	$C_{11}H_{14}O_4$	
102.0549	10.49	positive	9.74	high lightxsalinity	increase	$C_4H_7NO_2$	
258.1098	12.64	positive	9.32	high lightxsalinity	increase	$C_{10}H_{15}N_3O_5$	
236.1135	11.06	positive	9.08	high lightxsalinity	increase	$C_9H_{17}NO_6$	
123.0440	8.94	positive	8.69	high lightxsalinity	increase	$C_7H_6O_2$	
285.1022	9.04	positive	8.61	high lightxsalinity	increase	$C_{12}H_{17}N_2O_4P$	

503.1611	14.65	negative	8.04	high lightxsalinity	increase	$C_{18}H_{32}O_{16}$	Raffinose
139.0501	2.00	positive	7.92	high lightxsalinity	increase	$C_6H_6N_2O_2$	
203.0835	7.20	negative	7.80	high lightxsalinity	increase	$C_{11}H_{12}N_2O_2$	
168.0654	12.05	positive	6.93	high lightxsalinity	increase	$C_8H_9NO_3$	
325.1121	12.05	positive	6.87	high lightxsalinity	increase	$C_{12}H_{20}O_{10}$	
293.2107	0.90	positive	6.71	high lightxsalinity	increase	$C_{18}H_{28}O_3$	
97.0284	12.06	positive	5.66	high lightxsalinity	increase	$C_5H_4O_2$	
109.0283	12.09	positive	5.54	high lightxsalinity	increase	$C_6H_4O_2$	
204.0865	12.03	positive	5.51	high lightxsalinity	increase	$C_8H_{13}NO_5$	
163.0599	12.04	positive	5.50	high lightxsalinity	increase	$C_6H_{10}O_5$	
214.0494	13.95	negative	5.36	high lightxsalinity	increase	$C_5H_{14}NO_6P$	
127.0389	12.07	positive	5.30	high lightxsalinity	increase	$C_6H_6O_3$	
217.0837	10.98	negative	5.09	high lightxsalinity	increase	$C_8H_{14}N_2O_5$	
145.0494	12.05	positive	4.86	high lightxsalinity	increase	$C_6H_8O_4$	
119.0347	12.03	negative	4.67	high lightxsalinity	increase	$C_4H_8O_4$	
252.1084	13.36	positive	4.45	high lightxsalinity	increase	$C_9H_{17}NO_7$	
254.9172	5.49	negative	4.41	high lightxsalinity	increase	$C_4H_8Cl_3O_4P$	
453.0928	12.08	negative	4.38	high lightxsalinity	increase	$C_{22}H_{18}N_2O_9$	
222.0978	11.36	positive	4.26	high lightxsalinity	increase	$C_8H_{15}NO_6$	
343.1153	12.04	negative	4.01	high lightxsalinity	increase	$C_8H_{21}N_6O_7P_2$	
341.1104	12.04	negative	3.97	high lightxsalinity	increase	$C_{12}H_{22}O_{11}$	Sucrose
389.1206	12.04	negative	3.83	high lightxsalinity	increase	$C_{20}H_{22}O_8$	
388.1191	12.04	negative	3.77	high lightxsalinity	increase	$C_{23}H_{19}NO_5$	
231.0154	5.74	negative	3.76	high lightxsalinity	increase	$C_9H_4N_4O_4$	
180.0868	12.10	positive	3.69	high lightxsalinity	increase	$C_6H_{13}NO_5$	
182.0810	8.96	positive	3.69	high lightxsalinity	increase	$C_9H_{11}NO_3$	Tyrosine
165.0544	8.96	positive	3.64	high lightxsalinity	increase	$C_9H_8O_3$	
259.0131	12.03	negative	3.48	high lightxsalinity	increase	$C_6H_{12}O_9S$	Fructose 6-phosphate
316.9492	5.43	negative	3.32	high lightxsalinity	increase	$C_{14}H_{10}Cl_4$	
136.0756	8.94	positive	3.25	high lightxsalinity	increase	C_8H_9NO	
213.0501	10.91	negative	3.03	high lightxsalinity	increase	$C_8H_{10}N_2O_5$	
89.0248	2.53	negative	2.80	high lightxsalinity	increase	$C_3H_6O_3$	
275.0215	7.34	negative	2.74	high lightxsalinity	increase	$C_{14}H_{12}O_2S_2$	

367.1093	12.03	positive	2.72	high lightxsalinity	increase	$C_{22}H_{19}ClO_3$	
365.1042	12.03	positive	2.71	high lightxsalinity	increase	$C_{21}H_{16}O_6$	Sucrose (M+Na)
61.0398	2.38	positive	2.68	high lightxsalinity	increase	CH_4N_2O	Urea
182.9920	5.75	negative	2.54	high lightxsalinity	increase	$C_7H_4O_6$	
279.0274	10.85	negative	2.49	high lightxsalinity	increase	$C_{14}H_{13}ClO_2S$	
111.0206	1.94	negative	2.48	high lightxsalinity	increase	$C_4H_4N_2O_2$	
162.0404	12.66	positive	2.46	high lightxsalinity	increase	$C_5H_7NO_5$	
309.2079	0.99	negative	2.38	high lightxsalinity	increase	$C_{18}H_{30}O_4$	
379.0991	6.02	positive	2.26	high lightxsalinity	increase	$C_{17}H_{18}N_2O_6S$	
85.0283	12.05	positive	2.18	high lightxsalinity	increase	$C_4H_4O_2$	
115.0043	5.74	negative	2.11	high lightxsalinity	increase	$C_4H_4O_4$	Fumaric acid
345.1145	5.85	positive	2.08	high lightxsalinity	increase	$C_{22}H_{17}ClN_2$	
188.0705	7.20	positive	2.01	high lightxsalinity	increase	$C_6H_{10}ClN_5$	
141.0656	8.70	positive	0.50	high lightxsalinity	decrease	$C_6H_8N_2O_2$	
457.1099	3.47	positive	0.49	high lightxsalinity	decrease	$C_{17}H_{21}N_4O_9P$	
138.0915	5.64	positive	0.49	high lightxsalinity	decrease	$C_8H_{11}NO$	
208.0623	9.19	negative	0.49	high lightxsalinity	decrease	$C_{10}H_{11}NO_4$	
205.0500	5.62	negative	0.49	high lightxsalinity	decrease	$C_{11}H_{10}O_4$	
145.0151	7.32	negative	0.48	high lightxsalinity	decrease	$C_6H_{10}S_2$	alpha-Ketoglutaric acid
275.0756	3.23	negative	0.48	high lightxsalinity	decrease	$C_{11}H_{16}O_8$	
133.0606	11.13	positive	0.48	high lightxsalinity	decrease	$C_4H_8N_2O_3$	Asparagine
113.0339	5.95	positive	0.48	high lightxsalinity	decrease	$C_4H_4N_2O_2$	
289.0686	4.63	positive	0.47	high lightxsalinity	decrease	$C_{15}H_{12}O_6$	
447.0548	13.82	negative	0.47	high lightxsalinity	decrease	$C_{16}H_{20}N_2O_9S_2$	
135.0647	11.13	positive	0.47	high lightxsalinity	decrease	$C_5H_{10}O_4$	
116.0341	11.13	positive	0.47	high lightxsalinity	decrease	$C_4H_5NO_3$	
176.1028	11.61	positive	0.45	high lightxsalinity	decrease	$C_6H_{13}N_3O_3$	Citrulline
115.0865	0.95	positive	0.45	high lightxsalinity	decrease	$C_5H_{10}N_2O$	
191.1024	11.02	positive	0.45	high lightxsalinity	decrease	$C_7H_{14}N_2O_4$	
159.0762	11.61	positive	0.45	high lightxsalinity	decrease	$C_6H_{10}N_2O_3$	
98.9840	14.99	positive	0.44	high lightxsalinity	decrease	$C_2H_3KO_2$	
174.0758	11.01	positive	0.43	high lightxsalinity	decrease	$C_7H_{11}NO_4$	
381.0936	5.90	positive	0.43	high lightxsalinity	decrease	$C_{21}H_{16}O_7$	

207.0584	13.80	positive	0.43	high lightxsalinity	decrease	$C_{10}H_{10}N_2OS$	
69.0335	6.65	positive	0.43	high lightxsalinity	decrease	C_4H_4O	
172.0625	4.45	negative	0.43	high lightxsalinity	decrease	$C_7H_{11}NO_4$	
146.0599	8.62	positive	0.42	high lightxsalinity	decrease	C_9H_7NO	
145.1446	9.29	positive	0.42	high lightxsalinity	decrease	$C_8H_{18}NO$	
96.9696	14.99	negative	0.42	high lightxsalinity	decrease	$C_2H_3KO_2$	
87.0440	6.65	positive	0.42	high lightxsalinity	decrease	$C_4H_6O_2$	
104.0704	6.65	positive	0.41	high lightxsalinity	decrease	$C_4H_9NO_2$	gamma-Aminobutyric acid
135.0480	12.03	positive	0.41	high lightxsalinity	decrease	$C_5H_{10}O_2S$	
134.0446	12.03	positive	0.41	high lightxsalinity	decrease	$C_4H_7NO_4$	Aspartic acid
184.0731	13.88	positive	0.41	high lightxsalinity	decrease	$C_5H_{14}NO_4P$	
187.0986	3.08	negative	0.41	high lightxsalinity	decrease	$C_9H_{16}O_4$	
105.0199	5.82	negative	0.40	high lightxsalinity	decrease	$C_3H_6O_4$	
174.0893	11.61	negative	0.40	high lightxsalinity	decrease	$C_6H_{13}N_3O_3$	Citrulline
215.0176	9.80	positive	0.40	high lightxsalinity	decrease	$C_4H_9NO_7P$-	
140.0115	8.39	negative	0.39	high lightxsalinity	decrease	$C_2H_8NO_4P$	
132.0423	9.82	negative	0.39	high lightxsalinity	decrease	$C_3H_7N_3O_3$	
124.0392	9.96	positive	0.39	high lightxsalinity	decrease	$C_6H_5NO_2$	
132.0311	12.05	negative	0.39	high lightxsalinity	decrease	$C_4H_7NO_4$	Aspartic acid
417.1510	5.41	positive	0.39	high lightxsalinity	decrease	$C_{22}H_{24}O_8$	
364.0647	18.38	positive	0.38	high lightxsalinity	decrease	$C_{10}H_{14}N_5O_8P$	Guanosine monophosphate
189.0415	6.34	negative	0.38	high lightxsalinity	decrease	$C_7H_{10}O_6$	
135.0461	6.05	negative	0.38	high lightxsalinity	decrease	$C_8H_8O_2$	
175.0482	9.82	negative	0.38	high lightxsalinity	decrease	$C_4H_8N_4O_4$	
116.0704	7.43	positive	0.38	high lightxsalinity	decrease	$C_5H_9NO_2$	Proline
173.0919	11.02	positive	0.38	high lightxsalinity	decrease	$C_7H_{12}N_2O_3$	
279.1182	11.50	positive	0.37	high lightxsalinity	decrease	$C_{22}H_{14}$	
141.0657	5.66	positive	0.36	high lightxsalinity	decrease	$C_6H_8N_2O_2$	
141.0202	6.67	negative	0.35	high lightxsalinity	decrease	$C_6H_6O_4$	
175.1186	14.01	positive	0.35	high lightxsalinity	decrease	$C_6H_{14}N_4O_2$	Arginine
140.0341	8.37	positive	0.34	high lightxsalinity	decrease	$C_6H_5NO_3$	
308.0905	11.42	positive	0.34	high lightxsalinity	decrease	$C_{10}H_{17}N_3O_6S$	GSH
160.0755	11.94	positive	0.33	high lightxsalinity	decrease	$C_{10}H_9NO$	

144.1018	5.50	positive	0.33	high lightxsalinity	decrease	$C_7H_{13}NO_2$	
197.0673	7.40	positive	0.33	high lightxsalinity	decrease	$C_6H_{12}O_7$	
150.0582	7.25	positive	0.32	high lightxsalinity	decrease	$C_5H_{11}NO_2S$	
253.0933	4.42	negative	0.32	high lightxsalinity	decrease	$C_9H_{18}O_8$	
259.0226	19.06	negative	0.32	high lightxsalinity	decrease	$C_6H_{13}O_9P$	Glucose 6-phosphate
175.1073	9.56	positive	0.32	high lightxsalinity	decrease	$C_7H_{14}N_2O_3$	
115.0865	14.72	positive	0.30	high lightxsalinity	decrease	$C_5H_{10}N_2O$	
88.0756	5.12	positive	0.30	high lightxsalinity	decrease	C_4H_9NO	
133.0970	14.72	positive	0.30	high lightxsalinity	decrease	$C_5H_{12}N_2O_2$	Ornithine
229.1443	5.58	positive	0.29	high lightxsalinity	decrease	$C_{12}H_{20}O_4$	
207.0308	6.05	negative	0.29	high lightxsalinity	decrease	$C_{10}H_8O_5$	
163.0752	5.90	positive	0.29	high lightxsalinity	decrease	$C_{10}H_{10}O_2$	
162.0781	11.66	negative	0.29	high lightxsalinity	decrease	$C_7H_9N_5$	
151.0623	7.23	positive	0.28	high lightxsalinity	decrease	$C_6H_{14}S_2$	
437.2046	6.62	negative	0.28	high lightxsalinity	decrease	$C_{25}H_{30}N_2O_5$	
229.0867	1.15	positive	0.28	high lightxsalinity	decrease	$C_{14}H_{12}O_3$	
179.0359	6.04	negative	0.26	high lightxsalinity	decrease	$C_9H_8O_4$	
228.9940	7.23	negative	0.26	high lightxsalinity	decrease	$C_9H_8Cl_2N_2O$	
161.0918	7.24	positive	0.26	high lightxsalinity	decrease	$C_6H_{12}N_2O_3$	
233.1493	6.64	positive	0.25	high lightxsalinity	decrease	$C_{10}H_{20}N_2O_4$	
133.0317	7.24	positive	0.25	high lightxsalinity	decrease	$C_5H_8O_2S$	
341.1103	12.66	negative	0.25	high lightxsalinity	decrease	$C_{12}H_{22}O_{11}$	Maltose
70.0652	14.01	positive	0.24	high lightxsalinity	decrease	C_4H_7N	
124.9922	12.86	negative	0.24	high lightxsalinity	decrease	$C_2H_6O_4S$	
311.1265	7.41	positive	0.23	high lightxsalinity	decrease	$C_{20}H_{14}N_4$	
76.0757	5.16	positive	0.23	high lightxsalinity	decrease	C_3H_9NO	
112.0868	14.01	positive	0.22	high lightxsalinity	decrease	$C_5H_9N_3$	
228.0650	13.85	negative	0.21	high lightxsalinity	decrease	$C_{13}H_{11}NO_3$	
116.0361	7.06	negative	0.21	high lightxsalinity	decrease	$C_4H_7NO_3$	
289.0847	6.57	negative	0.21	high lightxsalinity	decrease	$C_{14}H_{14}N_2O_5$	
251.0777	8.28	negative	0.21	high lightxsalinity	decrease	$C_{10}H_{12}N_4O_4$	
182.0469	6.45	negative	0.20	high lightxsalinity	decrease	$C_8H_9NO_4$	
95.0599	14.01	positive	0.20	high lightxsalinity	decrease	$C_5H_6N_2$	

265.0718	5.60	negative	0.19	high lightxsalinity	decrease	$C_{16}H_{12}NO_3$	
138.0569	6.47	negative	0.19	high lightxsalinity	decrease	$C_7H_9NO_2$	
149.0465	7.25	negative	0.18	high lightxsalinity	decrease	$C_6H_{14}S_2$	Xylose
229.0122	18.08	negative	0.17	high lightxsalinity	decrease	$C_5H_{11}O_8P$	Ribose 5-phosphate
163.0622	6.53	negative	0.16	high lightxsalinity	decrease	$C_6H_{12}O_5$	
191.0571	6.49	negative	0.15	high lightxsalinity	decrease	$C_7H_{12}O_6$	
189.1231	6.38	positive	0.15	high lightxsalinity	decrease	$C_8H_{16}N_2O_3$	
122.0257	6.21	negative	0.14	high lightxsalinity	decrease	$C_6H_5NO_2$	
136.0617	6.00	positive	0.13	high lightxsalinity	decrease	$C_5H_5N_5$	Adenine
140.0361	6.47	negative	0.13	high lightxsalinity	decrease	$C_6H_7NO_3$	
164.0738	12.52	positive	0.13	high lightxsalinity	decrease	$C_6H_{13}NO_2S$	
191.0207	13.99	negative	0.13	high lightxsalinity	decrease	$C_6H_8O_7$	Citric acid
154.0156	6.20	negative	0.12	high lightxsalinity	decrease	$C_6H_5NO_4$	
177.0545	7.07	positive	0.11	high lightxsalinity	decrease	$C_{10}H_8O_3$	
231.1004	5.12	positive	0.11	high lightxsalinity	decrease	$C_{14}H_{14}O_3$	
142.0519	6.62	negative	0.10	high lightxsalinity	decrease	$C_6H_9NO_3$	
103.0043	6.69	negative	0.10	high lightxsalinity	decrease	$C_3H_4O_4$	
196.0294	13.37	negative	0.09	high lightxsalinity	decrease	$C_5H_{11}NO_5S$	
165.0203	6.45	negative	0.09	high lightxsalinity	decrease	$C_8H_6O_4$	
145.0991	14.13	negative	0.09	high lightxsalinity	decrease	$C_6H_{14}N_2O_2$	Lysine
193.0366	7.18	negative	0.09	high lightxsalinity	decrease	$C_6H_{10}O_7$	
62.0602	6.00	positive	0.08	high lightxsalinity	decrease	C_2H_7NO	
335.1355	6.52	negative	0.06	high lightxsalinity	decrease	$C_{18}H_{24}O_4S$	
162.0241	6.47	negative	0.05	high lightxsalinity	decrease	$C_5H_9NO_3S$	
146.0922	6.20	positive	0.05	high lightxsalinity	decrease	$C_5H_{11}N_3O_2$	
100.0410	6.61	negative	0.05	high lightxsalinity	decrease	$C_4H_7NO_2$	
293.0541	14.01	negative	0.05	high lightxsalinity	decrease	$C_9H_{15}N_2O_7P$	
188.0575	6.42	negative	0.03	high lightxsalinity	decrease	$C_7H_{11}NO_5$	
128.0705	6.63	positive	0.03	high lightxsalinity	decrease	$C_6H_9NO_2$	
211.0257	6.82	negative	0.02	high lightxsalinity	decrease	$C_9H_8O_6$	
147.0475	6.76	positive	0.02	high lightxsalinity	decrease	$C_6H_{10}O_2S$	
175.1074	8.25	positive	0.02	high lightxsalinity	decrease	$C_7H_{14}N_2O_3$	
145.1082	5.89	positive	0.00	high lightxsalinity	decrease	$C_5H_{12}N_4O$	

236.1135	11.06	positive	17.41	salinity	increase	$C_9H_{17}NO_6$
254.0843	11.66	positive	13.84	salinity	increase	$C_{12}H_{15}NO_3S$
252.1084	13.36	positive	11.94	salinity	increase	$C_9H_{17}NO_7$
293.2107	0.90	positive	8.64	salinity	increase	$C_{18}H_{28}O_3$
222.0978	11.36	positive	7.19	salinity	increase	$C_8H_{15}NO_6$
130.0862	6.83	positive	6.31	salinity	increase	$C_6H_{11}NO_2$
93.0463	1.99	negative	5.65	salinity	increase	$C_5H_6N_2$
231.0154	5.74	negative	4.19	salinity	increase	$C_9H_4N_4O_4$
162.0241	6.47	negative	3.87	salinity	increase	$C_5H_9NO_3S$
351.1035	6.16	positive	3.43	salinity	increase	$C_{16}H_{18}N_2O_5S$
139.0501	2.00	positive	3.40	salinity	increase	$C_6H_6N_2O_2$
158.0832	5.75	negative	3.22	salinity	increase	$C_7H_{13}NO_3$
161.0465	5.61	negative	3.12	salinity	increase	$C_6H_{10}O_5$
595.2917	12.05	negative	2.83	salinity	increase	$C_{34}H_{44}O_9$
311.1144	6.02	negative	2.70	salinity	increase	$C_{15}H_{20}O_7$
162.0759	9.98	positive	2.52	salinity	increase	$C_6H_{11}NO_4$
225.0755	5.70	positive	2.46	salinity	increase	$C_{11}H_{12}O_5$
139.0501	6.84	positive	2.32	salinity	increase	$C_6H_6N_2O_2$
162.0404	12.66	positive	2.29	salinity	increase	$C_5H_7NO_5$
207.0650	5.88	positive	2.26	salinity	increase	$C_{11}H_{10}O_4$
121.0303	5.56	negative	2.25	salinity	increase	$C_7H_6O_2$
124.9558	6.49	negative	2.19	salinity	increase	$C_2H_6S_3$
163.0752	5.90	positive	2.09	salinity	increase	$C_{10}H_{10}O_2$
339.0736	5.91	negative	2.08	salinity	increase	$C_{15}H_{16}O_9$
325.1121	12.05	positive	0.49	salinity	decrease	$C_{12}H_{20}O_{10}$
116.0341	11.13	positive	0.49	salinity	decrease	$C_4H_5NO_3$
168.0654	12.05	positive	0.49	salinity	decrease	$C_8H_9NO_3$
191.1024	11.02	positive	0.48	salinity	decrease	$C_7H_{14}N_2O_4$
134.0639	11.12	positive	0.48	salinity	decrease	$C_5H_{11}NOS$
311.1265	7.41	positive	0.48	salinity	decrease	$C_{20}H_{14}N_4$
199.0346	11.16	negative	0.47	salinity	decrease	$C_{11}H_8N_2S$
114.0204	11.13	negative	0.47	salinity	decrease	$C_4H_5NO_3$
134.0481	6.05	negative	0.47	salinity	decrease	$C_5H_5N_5$

259.0131	12.03	negative	0.46	salinity	decrease	$C_6H_{12}O_9S$	Fructose 6-phosphate
453.0928	12.08	negative	0.45	salinity	decrease	$C_{22}H_{18}N_2O_9$	
193.0366	7.18	negative	0.45	salinity	decrease	$C_6H_{10}O_7$	
154.0156	6.20	negative	0.44	salinity	decrease	$C_6H_5NO_4$	
124.9922	12.86	negative	0.44	salinity	decrease	$C_2H_6O_4S$	
145.1082	5.89	positive	0.44	salinity	decrease	$C_5H_{12}N_4O$	
131.0471	11.19	negative	0.42	salinity	decrease	$C_4H_8N_2O_3$	Asparagine
135.0647	11.13	positive	0.39	salinity	decrease	$C_5H_{10}O_4$	
365.1193	5.90	positive	0.38	salinity	decrease	$C_{17}H_{20}N_2O_5S$	
197.0673	7.40	positive	0.38	salinity	decrease	$C_6H_{12}O_7$	
297.0585	5.99	positive	0.35	salinity	decrease	$C_{10}H_{20}N_2S_4$	
189.0891	11.01	negative	0.35	salinity	decrease	$C_7H_{14}N_2O_4$	
173.0919	11.02	positive	0.35	salinity	decrease	$C_7H_{12}N_2O_3$	
335.1355	6.52	negative	0.34	salinity	decrease	$C_{18}H_{24}O_4S$	
409.1094	5.63	positive	0.33	salinity	decrease	$C_{19}H_{20}O_{10}$	
275.1348	11.15	positive	0.33	salinity	decrease	$C_{10}H_{18}N_4O_5$	
191.0207	13.99	negative	0.32	salinity	decrease	$C_6H_8O_7$	Citric acid
203.1499	10.54	positive	0.29	salinity	decrease	$C_8H_{18}N_4O_2$	
98.0236	11.15	positive	0.29	salinity	decrease	$C_4H_3NO_2$	
182.9920	5.75	negative	0.28	salinity	decrease	$C_7H_4O_6$	
160.0755	11.94	positive	0.28	salinity	decrease	$C_{10}H_9NO$	
146.0599	8.62	positive	0.27	salinity	decrease	C_9H_7NO	
196.0294	13.37	negative	0.24	salinity	decrease	$C_5H_{11}NO_5S$	
175.1074	8.25	positive	0.21	salinity	decrease	$C_7H_{14}N_2O_3$	
277.1671	5.82	positive	0.20	salinity	decrease	$C_{14}H_{20}N_4O_2$	
217.0837	10.98	negative	0.14	salinity	decrease	$C_8H_{14}N_2O_5$	
209.0819	13.99	negative	0.14	salinity	decrease	$C_{11}H_{14}O_4$	
308.0905	11.42	positive	0.12	salinity	decrease	$C_{10}H_{17}N_3O_6S$	GSH
231.1004	5.12	positive	0.08	salinity	decrease	C14H14O3	
279.0274	10.85	negative	0.01	salinity	decrease	C14H13ClO2S	

Supplemental Table 3-3. Metabolites identified with reference standard with *m/z*, retention time, and fragmentation

Identity	**Polarity**	***M/z***	**Retention time (min)**	**Molecular formula**	**Monoisotopic Mass**	**Adduct**	**Theoretical exact mass (Da)**	**Mass accuracy (ppm)**	**Fragment ions**
Adenine	positive	136.0617	6.00	$C_5H_5N_5$	135.0545	M+H	136.062	0	119.04, 94.04, 92.03
Adenosine	positive	268.1038	5.50	$C_{10}H_{13}N_5O_4$	267.0968	M+H	268.104	0	136.06
Alanine	positive	90.0548	8.59	$C_3H_7NO_2$	89.0477	M+H	90.055	1	74.10, 72.08, 72.04, 60.08, 54.00
alpha-Ketoglutaric acid	negative	145.0151	7.32	$C_5H_6O_5$	146.0215	M-H	145.014	6	118.04, 101.06, 77.01, 64.02
Arginine	positive	175.1186	14.01	$C_6H_{14}N_4O_2$	174.1117	M+H	175.119	1	158.09, 141.07, 130.10, 116.07, 112.09, 97.08, 72.08, 70.07, 60.06
Asparagine	positive	133.0606	11.13	$C_4H_8N_2O_3$	132.0535	M+H	133.061	1	116.03, 88.04, 87.06, 74.02, 70.03, 60.04
Aspartic acid	positive	134.0446	12.03	$C_4H_7NO_4$	133.0375	M+H	134.045	1	116.03, 88.04, 74.02, 70.03
Citric acid	negative	191.0207	13.99	$C_6H_8O_7$	192.0270	M-H	191.02	5	129.02, 111.01, 102.95, 87.01, 57.03
Citrulline	negative	174.0893	11.61	$C_6H_{13}N_3O_3$	175.0957	M-H	174.088	5	131.08
Dihydroxyacetone phosphate	negative	168.9915	16.50	$C_3H_7O_6P$	169.9980	M-H	168.991	4	96.97, 78.96
Fructose	negative	179.0570	7.84	$C_6H_{12}O_6$	180.0634	M-H	179.056	5	168.89, 122.89, 89.02, 69.00
Fructose 6-phosphate	negative	259.0131	12.03	$C_6H_{13}O_9P$	260.0297	M-H	259.022	0	223, 199, 168.99, 138.98, 96.97, 78.96
Fumaric acid	negative	115.0043	5.74	$C_4H_4O_4$	116.0110	M-H	115.004	5	72.02, 71.01, 69.00
gamma-Aminobutyric acid	positive	104.0704	6.65	$C_4H_9NO_2$	103.0633	M+H	104.071	1	87.04, 86.06, 69.03
Glucose	negative	179.0570	9.82	$C_6H_{12}O_6$	180.0634	M-H	179.056	5	163.04, 119.04, 113.02, 101.02, 89.02, 85.03, 71.01, 59.01
Glucose 6-phosphate	negative	259.0226	19.06	$C_6H_{13}O_9P$	260.0297	M-H	259.022	0	199.00, 168.99, 138.98, 101.02, 96.97, 78.96
Glutamic acid	positive	148.0603	11.01	$C_5H_9NO_4$	147.0532	M+H	148.06	0	130.05, 102.06, 84.04
Glutamine	positive	147.0762	10.56	$C_5H_{10}N_2O_3$	146.0691	M+H	147.076	1	130.09, 123.96, 102,05, 84.08, 64.93
Glycine	positive	76.0393	9.69	$C_2H_5NO_2$	75.0320	M+H	76.0393	0	57.05, 58.04, 75.06
GSH	positive	308.0905	11.42	$C_{10}H_{17}N_3O_6S$	307.0838	M+H	308.091	1	291.06, 245.06, 233.06, 179.05, 162.02, 130.05, 84.04, 76.02
GSSG	positive	613.1557	17.01	$C_{20}H_{32}N_6O_{12}S_2$	612.1520	M+H	613.159	5	538.13, 484.12, 466.11, 409.09, 355.08, 288.07, 324.04, 177.03, 130.05
Guanine	positive	152.0566	9.00	$C_5H_5N_5O$	151.0494	M+H	152.057	0	108.52, 99.51, 97.01, 88.00, 87.00

Guanosine monophosphate	positive	364.0647	18.38	$C_{10}H_{14}N_5O_8P$	363.0580	M+H	364.065	2	152.06, 97.03
Histidine	negative	154.0631	14.24	$C_6H_9N_3O_2$	155.0695	M-H	154.062	5	137.04, 110.07, 96.96, 93.05, 81.05, 72.01
Leucine	positive	132.1018	6.47	$C_6H_{13}NO_2$	131.0946	M+H	132.102	1	86.10, 69.07
Lysine	positive	147.1126	14.14	$C_6H_{14}N_2O_2$	146.1055	M+H	147.113	1	130.09, 123.96, 102.05, 84.08
Malic acid	negative	133.0151	7.34	$C_4H_6O_5$	134.0215	M-H	133.014	6	115.00, 89.02, 72.99, 71.01
Maltose	negative	341.1103	12.66	$C_{12}H_{22}O_{11}$	342.1162	M-H	341.109	4	221.07, 119.04, 161.05, 119.04, 101.02, 89.02
Mannitol	positive	183.0844	8.95	$C_6H_{14}O_6$	182.0790	M+H	183.086	10	165.05, 147.04, 136.08, 123.04, 119.05, 113.96, 91.05
Ornithine	positive	133.0970	14.72	$C_5H_{12}N_2O_2$	132.0899	M+H	133.097	0	116.07, 115.09, 70.07
Phenylalanine	positive	166.0860	6.75	$C_9H_{11}NO_2$	165.0790	M+H	166.086	1	149.06, 131.05, 120.08, 103.05
Proline	positive	116.0704	7.43	$C_5H_9NO_2$	115.0633	M+H	116.071	1	70.07
Proline [M+1]	positive	117.0737							
Pyruvic acid	negative	87.0091	4.09	$C_3H_4O_3$	88.0160	M-H	87.0088	4	62.63, 59.01
Raffinose	negative	503.1611	14.65	$C_{18}H_{32}O_{16}$	504.1690	M-H	503.162	1	289.07, 272.09, 254.08, 228.10, 210.09, 179.05, 160.01, 143.05, 128.04, 74.02
Ribose 5-phosphate	negative	229.0122	18.08	$C_5H_{11}O_8P$	230.0192	M-H	229.012	1	138.98, 96.97, 78.96
Serine	positive	106.0498	11.45	$C_3H_7NO_3$	105.0426	M+H	106.05	0	88.04, 70.03, 60.04
Shikimic acid	negative	173.0471	6.71	$C_7H_{10}O_5$	174.0528	M-H	173.046	9	137.02, 129.02, 111.05, 99.05, 93.03, 83.05, 73.03, 71.01
Succinic acid	negative	117.0201	5.31	$C_4H_6O_4$	118.0266	M-H	117.019	6	99.01, 73.03
Sucrose	negative	341.1104	12.04	$C_{12}H_{22}O_{11}$	342.1162	M-H	341.109	4	221.07, 119.04, 101.02, 89.02, 71.01, 59.01
Sucrose (M+Na)	positive	365.1042	12.03	$C_{12}H_{22}O_{11}$	342.1162	M+Na	365.105	7	221.07, 119.04, 101.02, 89.02, 71.01, 59.01
Threonine	positive	120.0654	9.76	$C_4H_9NO_3$	119.0582	M+H	120.066	0	102.05, 84.04, 74.06, 56.05
Tryptophan	positive	205.0969	7.21	$C_{11}H_{12}N_2O_2$	204.0899	M+H	205.097	1	188.07, 170.06, 159.09, 146.06, 144.08, 132.08, 91.05, 74.02
Tyrosine	positive	182.0810	8.96	$C_9H_{11}NO_3$	181.0739	M+H	182.081	1	165.05, 147.04, 136.08, 123.04, 119.05, 113.96, 91.05
Urea	positive	61.0398	2.38	CH_4N_2O	60.0324	M+H	61.0396	2	60.04
Valine	positive	118.0861	6.96	$C_5H_{11}NO_2$	117.0790	M+H	118.086	1	72.08
Xylose	negative	149.0465	6.40	$C_5H_{10}O_5$	150.0528	M-H	149.046	6	89.02, 71.01, 59.01

Supplemental Table 3-4. Average fold change of all metabolic features in all treatments compared to control

M/z	Retention time	Polarity	Cold	Heat	Drought	Salinity	High light	Cold x drought	Heat x drought	High light x drought	Cold x salinity	Heat x salinity	High light x heat	High light x cold	High light x salinity
59.0137	7.81	negative	1.29	1.34	0.97	0.84	1.31	1.33	1.03	0.89	1.28	1.58	1.29	1.54	1.16
59.0137	9.82	negative	1.14	1.44	0.66	1.04	1.24	0.96	0.62	0.31	1.17	1.54	1.14	1.34	1.05
60.0559	6.01	positive	0.84	0.94	0.73	0.78	0.79	0.89	1.08	0.67	0.90	1.07	0.94	0.78	0.20
60.0809	1.00	positive	0.91	0.86	0.80	0.86	0.86	1.03	1.10	0.76	0.95	0.91	0.58	0.94	0.68
61.0398	2.38	positive	5.70	0.95	1.25	1.42	1.20	0.97	1.31	0.92	1.81	1.27	0.79	1.00	2.68
61.9882	10.57	negative	1.01	0.81	0.84	1.07	0.92	0.98	0.85	1.07	0.98	0.72	0.66	1.00	0.68
62.0602	6.00	positive	0.91	0.81	0.85	0.95	0.85	1.05	0.93	0.73	0.92	0.86	0.61	0.92	0.08
63.9925	10.56	negative	1.01	0.94	0.95	0.98	0.87	1.00	0.98	0.94	0.97	1.00	0.79	0.91	0.56
64.0159	1.09	positive	0.93	0.89	1.00	0.94	0.98	1.00	1.05	0.99	1.00	0.93	0.85	0.92	0.93
64.0159	5.57	positive	1.21	0.77	0.95	0.69	0.86	0.73	0.81	0.89	1.15	0.78	0.54	0.72	1.08
65.0145	1.75	negative	0.72	0.95	0.91	0.90	1.04	0.82	0.84	0.61	1.19	0.86	0.81	0.98	0.87
65.0605	14.01	positive	0.72	0.94	0.79	0.52	0.65	0.68	0.76	0.83	0.89	1.59	0.63	0.59	0.21
66.0339	1.93	positive	0.76	0.86	0.84	1.06	0.94	0.77	0.79	0.64	0.88	0.91	0.79	0.97	0.97
66.0683	12.22	positive	0.66	0.79	0.70	0.65	0.69	0.69	0.78	0.68	0.83	1.11	0.36	0.58	0.46
67.0292	1.93	positive	0.82	0.87	0.83	1.04	0.96	0.83	0.86	0.72	0.86	0.92	0.82	0.99	1.03
67.0542	14.14	positive	0.90	3.66	1.60	1.04	1.04	1.04	2.04	1.77	0.97	4.00	3.55	0.88	0.76
68.0495	6.64	positive	0.85	1.21	2.19	1.38	1.35	1.75	3.58	1.89	0.90	1.10	3.13	1.17	0.27
68.9958	9.12	negative	1.08	1.07	1.21	1.28	1.32	1.01	0.94	1.17	1.06	0.91	1.37	1.26	1.18
68.9958	7.55	negative	1.40	1.24	0.50	1.43	1.41	1.55	1.22	1.46	1.53	0.65	0.08	1.44	1.40
69.0335	6.65	positive	0.86	1.25	2.18	1.38	1.33	1.80	3.72	1.91	0.86	1.11	3.29	1.12	0.43
69.9992	9.12	negative	1.09	1.06	1.21	1.29	1.34	1.02	0.97	1.16	1.07	0.90	1.37	1.25	1.18
70.0288	11.14	positive	0.88	1.28	0.80	0.40	0.69	0.89	1.13	0.90	0.76	1.53	0.43	0.75	0.52
70.0651	7.43	positive	0.95	2.51	1.85	1.04	1.26	1.01	2.32	1.92	0.75	2.66	1.50	1.07	0.90
70.0652	14.01	positive	0.75	0.93	0.80	0.56	0.66	0.70	0.79	0.83	0.88	1.51	0.66	0.61	0.24
71.0139	5.78	negative	1.25	2.61	0.88	1.59	3.97	1.36	1.44	1.32	1.04	2.39	1.94	2.89	1.70
71.0139	9.83	negative	1.12	1.38	0.67	1.02	1.27	0.97	0.63	0.33	1.11	1.52	1.11	1.28	0.99
71.0139	7.84	negative	1.25	1.42	0.97	0.89	1.46	1.28	1.08	0.94	1.24	1.59	1.29	1.57	1.22
71.0291	4.94	positive	1.10	1.08	1.26	1.38	1.27	1.03	1.22	1.22	1.17	1.19	1.20	1.21	1.30
71.0491	9.58	positive	0.97	1.08	0.92	0.93	1.10	0.97	1.04	0.86	1.08	1.30	0.74	1.04	0.67
71.0685	7.43	positive	0.99	2.73	2.03	1.06	1.26	1.06	2.46	2.01	0.76	2.91	1.44	1.08	0.91

72.0808	6.93	positive	1.63	5.61	2.27	1.05	2.22	1.88	2.52	2.59	1.19	5.33	4.14	1.82	0.98
72.0808	12.22	positive	0.72	0.82	0.74	0.70	0.74	0.75	0.84	0.56	0.85	1.12	0.48	0.65	0.56
72.9932	7.32	negative	1.11	1.63	1.09	1.30	1.71	0.90	1.69	0.80	1.08	1.56	0.94	1.61	0.91
73.0296	5.34	negative	0.69	1.29	1.37	1.82	1.58	1.39	1.61	1.29	0.72	1.09	3.70	1.85	0.72
73.0841	6.87	positive	1.59	5.62	2.25	1.01	2.26	1.84	2.47	2.59	1.15	5.34	4.05	1.81	0.94
73.5317	4.93	positive	1.14	1.00	1.59	1.78	1.65	1.01	1.16	1.41	1.31	1.16	1.50	1.55	1.62
74.0236	11.20	positive	0.92	1.31	0.82	0.67	0.70	0.91	1.13	0.89	0.76	1.55	0.52	0.74	0.50
75.0089	3.66	negative	1.63	0.96	0.97	0.63	1.45	1.16	4.66	1.49	0.85	0.88	3.72	1.17	1.74
76.0393	9.69	positive	1.33	1.63	0.69	0.92	3.01	0.88	1.37	1.24	1.31	2.26	1.05	2.39	1.57
76.0757	5.16	positive	0.79	2.51	0.31	0.80	1.37	0.93	2.23	0.65	1.00	2.78	2.48	0.81	0.23
78.9593	14.99	negative	0.84	0.93	0.70	0.67	0.75	0.91	0.99	0.77	0.78	1.00	0.87	0.90	0.42
79.9569	7.41	negative	0.75	0.80	0.62	0.41	0.57	0.76	0.56	0.79	0.76	1.08	0.75	0.67	0.48
79.9572	10.58	negative	0.98	1.11	1.05	0.91	1.29	1.02	1.03	1.16	0.95	0.93	1.64	1.20	1.53
81.0447	1.94	positive	0.73	0.86	0.83	1.14	0.91	0.92	0.73	0.62	0.91	0.89	0.69	1.03	0.87
82.0525	1.93	positive	0.68	0.88	0.80	0.85	0.89	0.70	0.74	0.62	0.88	0.84	0.72	0.91	0.95
82.5370	4.94	positive	1.08	1.00	1.40	1.59	1.41	1.00	1.16	1.30	1.19	1.14	1.44	1.33	1.43
83.0141	7.27	negative	0.99	0.93	1.04	1.01	0.85	1.09	0.33	0.76	0.93	0.94	0.03	0.88	0.72
83.5358	4.94	positive	1.08	1.00	1.42	1.57	1.43	0.99	1.18	1.33	1.20	1.14	1.42	1.35	1.45
84.0443	10.68	positive	0.94	1.11	0.86	0.84	1.02	0.96	1.40	1.06	0.94	1.27	0.49	1.71	1.35
84.0807	0.95	positive	0.73	0.77	0.66	1.00	1.00	0.91	1.11	0.78	0.81	1.04	0.87	1.09	0.66
84.0807	14.14	positive	0.87	3.13	1.40	0.93	0.95	0.98	1.74	1.55	0.90	3.41	3.14	0.83	0.71
85.0283	7.81	positive	1.26	1.43	0.96	0.83	1.51	1.32	0.88	0.66	1.33	1.81	1.28	1.76	1.00
85.0283	12.05	positive	1.48	2.10	1.44	0.63	1.89	1.38	1.57	2.09	1.65	2.64	2.51	1.49	2.18
85.0298	7.26	negative	1.00	0.95	1.04	1.04	0.88	1.10	0.48	0.87	0.96	0.90	0.34	0.94	0.99
85.0477	10.55	positive	0.93	1.35	0.87	0.84	1.26	0.96	1.35	1.05	0.93	1.28	0.50	1.68	0.44
85.0760	1.02	positive	0.78	0.84	0.76	0.84	0.95	1.03	1.04	0.80	0.87	0.97	0.34	0.87	0.57
86.0600	6.60	positive	0.85	4.82	2.26	1.39	1.36	1.81	3.84	1.96	0.86	4.93	4.76	1.13	0.54
86.0712	12.22	positive	0.68	0.81	0.71	0.68	0.70	0.71	0.83	0.67	0.82	1.11	0.38	0.60	0.49
87.0091	4.09	negative	1.49	1.56	0.52	1.03	1.23	0.63	0.78	0.50	1.48	2.25	3.14	1.47	1.04
87.0440	6.65	positive	0.86	1.28	2.27	1.39	1.36	1.81	3.86	1.97	0.86	1.14	3.42	1.13	0.42
87.0552	11.13	positive	0.89	1.29	0.82	0.52	0.70	0.91	1.11	0.91	0.76	1.55	0.49	0.75	0.49
88.0125	4.08	negative	1.68	1.80	0.31	0.98	1.33	0.46	0.67	1.16	2.15	2.77	4.02	1.73	1.12
88.0392	11.48	positive	1.19	1.21	0.79	0.65	0.73	0.93	1.11	0.97	1.04	1.44	0.50	0.86	1.00

88.0473	6.65	positive	0.83	1.29	2.28	1.36	1.34	1.82	3.90	1.99	0.86	1.03	3.46	1.12	0.27
88.0756	5.12	positive	1.05	0.53	0.91	0.58	0.63	1.07	0.69	0.83	0.80	0.46	0.38	0.84	0.30
88.1120	0.97	positive	0.89	0.93	0.88	1.03	0.90	1.07	1.16	0.84	0.96	1.04	0.59	0.97	0.76
89.0248	2.53	negative	5.98	0.69	1.45	0.98	1.01	0.63	1.21	1.39	2.30	0.68	1.12	0.64	2.80
89.0248	9.82	negative	0.52	1.36	0.57	1.01	1.25	0.95	0.51	0.34	0.51	1.46	1.09	1.31	1.05
89.0248	7.84	negative	1.23	1.31	0.94	0.81	1.26	1.26	0.97	0.70	1.25	1.51	1.23	1.46	1.12
89.0483	6.64	positive	0.90	1.19	2.77	1.56	1.65	2.19	4.87	2.40	1.02	0.91	3.94	1.28	0.36
89.0789	5.12	positive	1.04	0.52	0.90	0.57	0.60	1.06	0.69	0.83	0.79	0.44	0.05	0.84	0.29
90.0282	2.53	negative	6.02	0.68	1.44	0.96	1.00	0.62	1.20	1.41	2.32	0.67	1.10	0.63	2.84
90.0548	8.59	positive	2.22	5.69	1.26	1.15	2.15	2.29	4.47	2.66	2.10	6.15	5.31	1.82	1.25
90.0913	5.60	positive	0.89	0.90	0.86	0.51	0.77	0.89	0.94	0.89	0.60	0.85	0.37	1.08	0.21
90.9766	1.09	positive	0.92	1.05	1.19	1.14	1.17	1.10	1.23	1.16	1.05	0.92	1.15	0.96	1.37
90.9766	5.51	positive	1.20	0.76	0.88	0.40	0.90	0.84	0.33	1.09	1.03	0.77	0.75	0.76	1.89
91.0582	8.59	positive	2.24	5.87	1.30	1.15	2.19	2.34	4.57	2.72	2.12	6.35	5.47	1.83	1.26
91.5423	4.93	positive	1.04	0.96	1.37	1.44	1.30	0.96	1.16	1.26	1.16	1.11	1.25	1.20	1.38
93.0463	1.99	negative	109.55	0.32	3.11	5.65	1.29	0.43	0.30	0.20	6.82	1.61	0.11	1.21	12.53
94.0450	4.94	positive	1.13	0.98	1.68	1.95	1.73	0.98	1.17	1.48	1.34	1.16	1.68	1.53	1.71
94.9814	12.44	negative	0.99	0.95	0.97	1.03	0.98	0.95	0.99	1.08	0.96	0.87	1.42	0.96	0.66
95.0257	11.14	negative	0.85	1.36	0.63	0.13	0.71	0.83	1.10	0.76	0.66	1.70	0.25	0.76	0.32
95.0438	4.94	positive	1.11	1.00	1.73	1.97	1.73	0.99	1.21	1.49	1.35	1.18	1.72	1.60	1.74
95.0599	14.01	positive	0.73	0.92	0.76	0.56	0.68	0.67	0.77	0.81	0.85	1.47	0.65	0.61	0.20
95.0603	1.94	positive	0.64	0.83	0.96	0.80	0.90	0.66	0.68	0.57	0.90	0.84	0.61	1.03	0.81
95.9525	10.75	negative	1.00	0.94	1.09	1.08	1.06	0.98	0.97	1.10	1.09	0.86	1.25	1.04	1.03
96.0807	6.93	positive	1.28	6.17	2.51	0.71	2.47	1.92	2.51	2.74	1.42	5.59	4.32	1.58	0.04
96.9696	14.99	negative	0.83	0.93	0.70	0.67	0.76	0.90	0.99	0.78	0.78	1.01	0.88	0.89	0.42
97.0284	12.06	positive	1.55	2.17	1.44	0.65	1.96	1.41	1.61	2.12	1.64	2.71	2.63	1.53	5.66
98.0236	11.15	positive	0.93	1.42	0.70	0.29	0.65	0.91	1.18	0.95	0.73	1.80	0.51	0.79	1.81
98.0474	1.91	positive	0.71	0.85	0.93	0.72	0.91	0.69	0.70	0.58	0.89	0.90	0.68	1.00	0.87
98.0600	6.93	positive	1.06	0.34	0.78	1.13	0.95	1.15	1.15	1.09	1.39	0.36	0.17	1.29	0.82
98.9840	14.99	positive	0.84	0.92	0.71	0.66	0.77	0.91	0.96	0.78	0.79	0.99	0.86	0.90	0.44
99.0093	7.27	negative	0.98	0.92	1.00	0.93	0.80	1.05	0.40	0.82	0.90	0.88	0.07	0.87	0.72
99.0916	0.95	positive	0.77	0.76	0.68	0.50	0.63	0.98	1.28	0.73	0.70	0.91	0.15	0.66	0.36
100.0410	6.61	negative	0.83	1.08	1.08	1.02	1.09	1.17	1.09	0.87	0.83	0.73	0.50	1.04	0.05

100.1120	4.59	positive	0.94	0.98	1.02	1.01	1.03	0.93	0.94	1.01	0.98	0.93	1.03	1.03	0.92
100.9342	1.17	negative	0.84	0.91	1.01	0.96	0.98	0.92	1.06	1.00	1.00	0.94	1.00	0.90	1.00
101.0249	7.31	negative	0.82	0.76	0.85	1.16	0.97	0.63	0.52	0.61	1.43	0.76	0.48	0.91	0.81
101.0249	9.86	negative	1.13	1.36	0.35	1.04	1.27	0.96	0.65	0.16	1.15	1.49	1.16	1.30	1.10
101.0709	10.54	positive	0.95	1.42	0.87	0.83	1.26	0.97	1.37	0.92	0.94	1.04	0.49	1.32	1.16
102.0549	10.49	positive	7.64	17.63	0.86	0.79	13.80	0.95	19.65	6.99	0.91	6.30	0.43	10.97	9.74
102.0549	12.57	positive	0.99	1.75	1.23	0.66	0.64	0.98	1.09	1.16	1.09	2.07	0.90	0.77	0.88
102.9574	13.59	negative	0.99	0.95	0.89	0.69	0.84	0.96	0.89	0.92	0.96	1.08	0.63	0.89	1.18
103.0043	6.69	negative	1.15	1.45	1.34	1.36	1.42	1.31	1.60	1.33	1.02	1.24	1.21	1.20	0.10
103.0407	2.08	negative	1.71	0.94	1.41	0.79	1.23	1.13	4.34	1.52	1.00	0.91	1.25	1.04	1.14
103.0542	6.64	positive	2.55	5.92	2.07	1.60	2.22	2.95	2.78	2.39	2.11	5.79	7.16	3.01	1.72
103.0576	1.05	positive	0.80	0.47	0.67	0.65	0.58	0.84	0.65	0.43	0.64	0.47	0.09	0.81	0.30
104.0359	11.45	negative	0.78	1.03	0.90	0.88	0.81	1.06	1.04	1.06	0.77	1.19	0.68	0.69	1.31
104.0704	6.65	positive	0.85	1.30	2.29	1.38	1.36	1.80	3.86	2.00	0.87	1.14	3.42	1.14	0.41
104.1068	0.99	positive	0.98	0.81	0.76	0.85	0.74	1.05	1.25	0.69	0.94	1.01	0.49	0.81	0.56
105.0199	5.82	negative	1.30	0.62	0.68	1.71	1.78	1.17	1.72	0.71	1.13	0.48	0.67	2.08	0.40
105.0393	11.44	negative	0.62	1.10	0.92	0.84	0.77	1.26	1.03	1.19	0.66	1.34	0.57	0.57	1.44
105.0738	6.65	positive	0.85	1.30	2.28	1.38	1.36	1.81	3.89	2.00	0.86	1.12	3.41	1.13	0.40
105.1102	0.99	positive	0.97	0.81	0.76	0.84	0.73	1.05	1.24	0.68	0.94	1.00	0.48	0.81	0.55
105.9611	7.62	negative	1.02	1.05	0.97	1.02	0.99	1.05	0.93	0.97	0.96	0.97	1.07	1.03	0.75
106.0233	5.81	negative	1.29	0.60	0.70	1.81	1.88	1.16	1.60	1.25	1.51	0.41	0.95	2.19	1.98
106.0498	11.45	positive	0.74	1.03	0.88	0.86	0.78	1.03	1.04	1.09	0.73	1.24	0.63	0.67	1.29
107.0531	11.45	positive	0.73	1.04	0.88	0.86	0.77	1.04	1.05	1.09	0.72	1.26	0.62	0.66	1.28
107.0603	1.93	positive	0.75	0.87	0.85	0.95	0.94	0.77	0.78	0.66	0.90	0.90	0.74	0.95	0.93
108.0210	5.38	negative	1.19	0.99	1.04	1.20	1.14	1.02	0.87	1.27	1.26	0.75	1.18	1.09	1.32
108.0681	1.94	positive	0.87	0.98	0.97	0.90	0.89	0.78	0.73	0.56	0.90	1.11	0.76	1.17	0.86
109.0283	12.09	positive	1.58	2.23	1.45	0.76	1.99	1.49	1.71	2.05	1.52	2.83	2.99	1.67	5.54
109.0413	10.49	negative	0.99	1.37	0.85	0.79	0.86	0.81	0.93	0.97	0.84	1.18	0.48	1.08	1.37
110.0086	4.94	positive	1.08	0.96	1.11	1.26	1.03	0.98	1.21	1.16	1.06	1.20	0.75	1.12	1.01
110.0255	6.56	negative	0.92	1.02	0.77	0.68	0.77	1.08	0.93	1.08	0.92	1.09	4.46	0.82	0.80
110.0712	14.25	positive	1.20	2.01	1.09	0.73	1.29	1.04	1.24	1.23	0.96	2.37	0.87	1.14	0.84
110.9763	10.75	negative	0.97	0.94	1.07	1.08	1.00	0.99	0.91	1.04	1.03	0.88	1.23	0.98	1.03
111.0094	7.27	negative	0.98	0.92	0.99	0.97	0.85	1.04	0.43	0.84	0.88	0.90	0.11	0.90	0.65

111.0101	5.76	negative	0.93	2.99	2.14	3.35	3.95	2.24	1.34	1.96	1.07	1.72	6.97	3.83	0.92
111.0206	1.94	negative	1.16	1.41	4.93	1.22	1.27	1.06	12.12	7.43	0.98	1.66	6.46	0.96	2.48
111.9798	10.75	negative	0.95	0.93	1.07	1.01	1.00	0.96	0.86	1.05	1.05	0.87	1.16	1.00	0.98
112.0070	4.96	positive	0.97	0.95	1.13	1.15	1.06	0.93	1.12	1.32	1.08	1.09	1.15	1.07	0.99
112.0505	9.17	positive	0.84	0.81	0.72	1.33	1.34	0.80	0.87	0.34	1.06	0.85	14.34	1.16	1.17
112.0868	14.01	positive	0.73	0.93	0.80	0.53	0.66	0.68	0.77	0.83	0.88	1.54	0.64	0.60	0.22
112.9722	10.75	negative	0.97	0.94	1.07	1.05	1.00	0.98	0.89	1.03	1.03	0.87	1.20	0.97	1.00
112.9862	9.14	negative	1.08	1.06	1.19	1.25	1.29	1.01	0.94	1.15	1.07	0.90	1.32	1.24	1.15
112.9862	7.82	negative	1.05	1.01	0.92	1.44	1.42	1.56	0.57	1.48	0.48	0.01	0.48	1.45	0.01
113.0339	5.95	positive	2.17	1.52	0.98	0.75	1.29	1.24	1.05	1.08	1.41	0.99	0.35	1.19	0.48
113.0708	11.61	positive	1.07	0.37	0.61	0.68	0.57	0.80	0.66	0.82	0.98	0.61	0.29	1.09	0.45
113.0906	14.01	positive	0.73	0.93	0.79	0.57	0.65	0.65	0.76	0.80	0.94	1.53	0.61	0.62	0.21
113.9896	9.12	negative	1.08	1.06	1.20	1.26	1.29	1.01	0.95	1.16	1.07	0.91	1.32	1.26	1.15
113.9896	7.62	negative	1.08	1.20	0.51	1.46	1.07	1.56	0.69	1.48	1.33	0.58	0.09	1.46	1.03
114.0204	11.13	negative	0.90	1.28	0.78	0.47	0.75	0.89	1.10	0.86	0.79	1.49	0.57	0.81	0.56
114.0550	11.60	positive	1.08	0.42	0.72	0.69	0.61	0.88	0.86	1.14	0.94	0.67	0.37	1.05	0.53
114.1025	12.22	positive	0.71	0.83	0.72	0.68	0.72	0.73	0.84	0.70	0.85	1.13	0.44	0.62	0.57
114.9369	1.11	negative	0.29	0.51	0.61	0.38	0.86	0.57	0.59	0.78	0.87	0.63	0.39	0.92	0.53
114.9904	9.12	negative	1.07	1.04	1.17	1.23	1.28	1.02	0.92	1.14	1.06	0.89	1.33	1.24	1.12
115.0043	5.74	negative	1.37	3.35	0.74	1.69	6.02	1.26	1.62	1.41	1.04	2.99	2.94	3.84	2.11
115.0044	7.34	negative	1.18	1.41	0.87	1.16	1.57	0.91	1.18	0.89	1.05	1.56	0.86	1.48	0.81
115.0865	14.72	positive	0.81	0.46	0.55	0.55	0.61	0.68	0.57	0.68	1.06	1.13	0.19	0.48	0.30
115.0865	6.90	positive	0.95	0.24	0.85	0.99	0.92	1.03	1.21	0.98	1.52	0.22	0.12	1.30	1.36
115.0865	0.95	positive	0.68	0.70	0.94	0.73	0.54	1.58	1.63	0.79	0.89	0.99	0.35	0.58	0.45
115.1058	12.22	positive	0.70	0.81	0.72	0.68	0.71	0.72	0.84	0.70	0.84	1.14	0.43	0.62	0.55
116.0341	11.13	positive	0.89	1.29	0.82	0.49	0.70	0.89	1.11	0.92	0.76	1.53	0.47	0.73	0.47
116.0361	7.06	negative	1.01	1.04	0.87	0.76	1.47	1.03	0.90	1.17	0.98	1.33	0.59	1.09	0.21
116.0512	5.07	negative	1.24	1.05	0.70	1.07	1.10	0.87	0.19	0.69	1.21	1.14	3.03	1.23	1.19
116.0704	7.43	positive	0.93	2.48	1.80	0.98	1.23	0.98	2.23	1.90	0.74	2.64	1.42	1.06	0.38
116.0818	5.78	positive	1.06	0.98	0.72	0.84	0.90	1.00	1.03	0.84	0.88	0.62	0.02	0.86	0.00
117.0201	5.31	negative	0.98	2.00	1.51	1.26	1.45	0.92	2.58	1.58	0.69	1.71	5.35	1.10	0.98
117.0294	9.80	positive	0.77	0.94	0.82	0.80	0.87	0.85	0.69	0.62	0.95	0.98	0.16	0.75	0.54
117.0375	11.13	positive	0.88	1.32	0.73	0.25	0.65	0.84	1.18	0.87	0.73	1.60	0.38	0.73	0.78

117.0737	7.43	positive	0.94	2.49	1.79	0.98	1.23	0.98	2.25	1.89	0.74	2.68	1.42	1.06	0.84
118.0055	7.26	negative	1.23	1.17	1.62	1.65	1.50	1.11	1.43	1.48	1.15	1.21	1.76	1.36	0.86
118.0234	5.31	negative	0.98	2.78	1.59	1.34	1.56	0.95	3.00	1.89	0.68	1.80	5.81	1.11	0.98
118.0517	9.77	negative	1.06	1.83	1.16	1.05	1.81	0.95	1.37	1.24	0.93	2.09	1.93	1.16	1.47
118.0861	6.96	positive	1.48	4.72	2.01	1.02	1.99	1.67	2.19	2.30	1.17	4.45	3.47	1.69	1.01
119.0161	8.03	positive	0.54	3.87	1.88	1.32	6.90	0.70	1.08	0.94	0.56	3.81	11.18	1.54	3.47
119.0347	12.03	negative	1.16	2.46	1.35	0.54	2.31	1.11	1.52	2.21	1.26	2.91	2.96	1.69	4.67
119.0357	9.81	negative	1.13	1.39	0.67	1.01	1.27	0.98	0.65	0.37	1.12	1.53	1.15	1.32	1.03
119.0522	5.82	positive	0.76	0.95	0.66	0.33	0.64	0.98	0.93	0.79	0.72	1.21	1.56	0.72	0.00
119.0894	6.92	positive	1.51	4.88	2.06	1.01	2.04	1.70	2.25	2.37	1.18	4.66	3.53	1.71	1.02
120.0556	1.96	positive	0.62	0.84	0.83	0.79	0.93	0.66	0.67	0.54	0.92	0.84	0.57	0.91	0.80
120.0654	9.76	positive	1.00	1.77	1.02	0.94	1.83	0.89	1.28	1.14	0.93	2.18	1.54	1.21	1.37
120.0807	6.75	positive	2.56	5.99	2.13	1.20	2.21	2.98	2.78	2.42	2.09	5.90	7.34	3.01	1.23
120.9973	7.88	negative	1.04	1.12	0.94	0.62	0.73	1.17	1.20	0.70	1.10	1.35	0.15	0.64	0.48
121.0303	5.56	negative	0.94	1.26	2.24	2.25	1.63	1.39	1.44	0.97	1.04	1.22	1.49	1.71	0.84
121.0396	1.99	positive	85.78	0.22	2.74	4.14	0.96	0.24	0.12	0.28	5.87	0.85	0.19	0.91	21.47
121.0687	9.76	positive	1.00	1.79	1.03	0.94	1.86	0.86	1.32	1.16	0.93	2.28	1.57	1.21	1.41
121.0743	6.65	positive	2.64	6.12	2.13	1.20	2.25	3.04	2.80	2.48	2.11	6.09	7.56	3.06	2.88
122.0257	6.21	negative	0.90	1.50	1.43	1.94	1.45	1.35	1.28	1.10	0.96	1.38	1.43	1.42	0.14
122.0712	1.94	positive	0.60	0.84	0.98	0.79	0.89	0.65	0.65	0.55	0.92	0.84	0.60	0.97	0.79
122.0811	9.07	positive	4.48	0.65	0.89	1.76	0.83	0.45	0.38	0.36	2.70	1.20	0.24	2.25	1.95
123.0403	5.13	positive	1.10	0.99	1.43	1.50	1.35	1.01	1.16	1.34	1.25	1.15	1.45	1.29	1.39
123.0440	8.94	positive	1.44	8.97	2.02	1.16	1.57	1.35	3.20	2.87	1.13	8.91	11.30	1.13	8.69
123.0461	6.39	negative	1.17	10.31	0.95	0.95	2.09	1.20	2.21	1.59	0.80	7.32	0.81	1.15	0.79
124.0392	9.96	positive	0.92	0.92	0.77	0.94	0.77	0.95	0.96	0.67	1.01	1.11	0.21	0.74	0.39
124.0392	8.53	positive	0.92	1.12	1.22	1.31	1.20	1.59	2.03	0.75	1.14	1.26	6.38	1.19	1.06
124.0869	1.11	positive	0.66	0.76	0.70	0.90	0.99	0.87	1.01	0.75	0.80	0.90	0.86	1.09	0.75
124.9558	8.18	negative	1.10	1.14	1.04	1.18	1.14	1.10	1.04	1.05	1.06	1.00	1.18	1.15	0.97
124.9558	6.49	negative	1.01	1.08	1.37	2.19	2.21	0.78	0.08	1.64	1.09	0.16	1.09	2.19	1.65
124.9922	12.86	negative	0.88	0.85	0.66	0.44	0.67	0.82	0.61	0.77	0.76	1.00	0.54	0.71	0.24
125.0363	10.83	negative	1.56	17.09	1.00	0.00	9.17	0.00	5.15	0.25	4.29	17.13	0.00	8.94	26.51
125.0378	4.93	positive	1.07	0.98	1.41	1.52	1.29	1.02	1.14	1.35	1.23	1.17	1.11	1.25	1.32
126.0548	5.66	positive	0.69	0.67	0.75	1.06	1.06	0.78	0.75	0.72	0.86	0.87	1.27	0.95	0.89

126.9058	8.22	negative	1.24	1.25	0.56	0.54	0.90	1.41	0.99	0.87	0.56	0.61	0.22	1.00	0.53
127.0389	12.07	positive	1.40	2.12	1.43	0.69	1.96	1.33	1.60	2.03	1.47	2.67	2.75	1.57	5.30
127.0521	10.50	negative	0.96	1.50	0.87	0.70	1.25	0.91	1.25	0.93	0.79	1.24	0.48	1.31	1.27
127.0977	5.15	positive	0.93	0.87	0.91	0.68	0.72	1.02	1.36	1.43	0.88	0.94	0.40	0.69	0.35
128.0191	4.94	positive	1.05	1.02	1.24	1.40	1.22	1.01	1.21	1.22	1.14	1.18	1.17	1.18	1.23
128.0361	4.44	negative	2.64	2.20	0.94	0.94	0.97	1.11	3.37	1.58	0.94	2.39	2.89	0.81	1.46
128.0361	11.02	negative	1.23	1.43	0.85	0.75	1.21	1.27	1.32	1.04	0.84	1.48	0.39	1.13	1.25
128.0422	12.08	positive	1.58	2.56	1.64	0.90	2.37	1.54	1.83	2.47	1.53	3.12	3.44	1.75	6.59
128.0705	6.63	positive	0.95	1.21	2.05	1.27	1.34	1.66	3.17	1.86	0.77	1.09	2.45	1.17	0.03
129.0202	7.25	negative	0.99	0.95	0.98	0.98	0.86	1.07	0.45	0.83	0.92	0.90	0.21	0.90	0.71
129.0395	4.42	negative	2.86	2.34	1.00	0.97	1.01	1.13	3.57	1.66	0.97	2.56	3.06	0.85	1.52
129.0396	11.02	negative	1.31	1.54	0.77	0.62	1.27	1.28	17.59	1.01	0.72	1.64	13.86	1.14	1.29
129.0656	10.55	positive	0.94	1.13	0.80	0.77	0.95	0.86	0.71	0.77	0.84	1.05	0.35	0.77	1.00
129.0657	6.88	positive	1.07	1.29	1.04	0.86	1.03	1.06	1.61	1.20	0.89	1.26	2.09	0.95	0.54
130.0497	10.55	positive	0.93	1.46	0.86	0.82	1.32	0.96	1.47	0.97	0.93	1.15	0.48	1.37	1.21
130.0518	6.37	negative	0.86	1.12	1.06	1.07	1.10	1.10	1.11	0.84	0.94	1.23	2.25	0.94	16.90
130.0650	11.96	positive	0.86	7.93	31.44	1.25	0.84	26.98	60.49	32.11	1.38	2.51	10.53	0.83	1.16
130.0650	5.13	positive	1.31	0.98	1.45	0.64	1.01	1.20	2.48	1.63	1.36	1.06	2.26	1.32	0.59
130.0862	6.83	positive	1.01	1.22	1.07	6.31	1.09	1.12	1.50	0.89	5.32	6.52	0.37	2.60	1.93
130.0890	14.10	positive	0.83	2.69	1.22	0.78	0.84	0.87	1.97	1.35	0.85	3.12	2.63	0.70	0.71
131.0357	4.65	negative	1.11	1.05	1.00	1.10	0.90	1.07	1.34	0.96	1.37	1.77	0.61	0.84	1.06
131.0471	11.19	negative	0.70	1.31	0.47	0.42	0.53	0.61	1.09	0.61	0.55	1.51	0.45	0.82	0.57
131.0530	10.54	positive	0.93	1.46	0.86	0.82	1.31	0.95	1.46	0.96	0.93	1.15	0.48	1.35	1.21
131.0722	1.23	negative	2.87	1.30	1.19	1.02	1.20	1.09	2.02	1.52	1.28	1.48	2.26	0.89	1.55
131.0834	14.01	negative	0.79	0.96	0.80	0.60	0.71	0.75	0.80	0.83	0.91	1.41	0.71	0.65	0.64
131.0895	6.85	positive	0.90	0.93	1.06	9.09	0.86	1.04	1.72	0.61	7.66	9.17	0.18	3.32	1.67
131.1290	12.21	positive	0.91	0.97	0.83	0.72	0.86	0.88	0.92	0.84	1.07	1.27	0.70	0.74	1.10
132.0311	12.05	negative	1.24	0.56	0.72	0.76	0.48	0.85	0.67	0.71	1.10	0.64	0.21	0.90	0.39
132.0423	9.82	negative	0.74	0.79	0.94	0.78	0.59	0.85	0.78	0.72	0.85	0.83	0.10	0.55	0.39
132.0504	11.13	negative	0.95	1.40	0.79	0.37	0.76	0.93	1.12	0.90	0.79	1.57	0.51	0.85	0.54
132.0653	10.44	positive	0.90	1.10	0.85	0.80	0.90	0.96	0.24	0.68	0.91	1.11	0.45	0.43	0.55
132.1018	6.47	positive	1.27	11.42	2.70	1.20	2.40	1.63	4.30	3.47	1.01	11.45	11.37	1.46	1.19
133.0151	7.34	negative	1.16	1.39	0.85	1.13	1.52	0.90	1.16	0.84	1.04	1.54	0.87	1.46	0.83

133.0317	7.24	positive	0.92	0.92	0.65	0.98	1.29	1.13	0.66	0.66	0.89	1.09	0.45	1.13	0.25
133.0515	3.54	negative	0.95	0.80	0.73	0.77	0.86	0.95	1.06	0.78	0.85	1.01	0.40	0.90	0.50
133.0606	11.13	positive	0.88	1.28	0.82	0.51	0.69	0.89	1.10	0.91	0.76	1.53	0.47	0.74	0.48
133.0970	14.72	positive	0.82	0.45	0.53	0.54	0.61	0.66	0.57	0.70	1.04	1.14	0.18	0.48	0.30
133.1050	6.47	positive	1.25	11.44	2.66	1.19	2.36	1.58	4.26	3.48	1.00	11.54	11.47	1.44	1.19
134.0446	12.03	positive	1.26	0.59	0.75	0.74	0.50	0.86	0.67	0.75	1.13	0.63	0.23	0.94	0.41
134.0481	6.05	negative	1.29	0.38	0.48	0.47	0.37	0.67	1.21	0.34	1.30	0.65	2.27	0.39	0.62
134.0639	11.12	positive	0.87	1.26	0.80	0.48	0.67	0.88	1.07	0.90	0.75	1.51	0.47	0.72	0.54
134.0810	9.60	positive	0.97	1.10	0.92	0.93	1.17	0.96	1.13	0.79	1.13	1.40	0.69	1.02	0.52
134.1053	6.46	positive	0.94	6.25	1.58	0.88	1.29	0.94	2.24	2.02	0.94	6.29	6.20	1.06	0.74
134.1175	5.04	positive	2.18	0.95	1.12	1.75	2.55	1.55	2.76	3.35	2.94	2.05	0.00	1.01	2.40
135.0280	7.61	negative	1.01	1.24	1.14	1.11	1.61	1.26	2.10	1.40	1.05	1.37	5.96	1.28	1.02
135.0461	6.05	negative	0.89	0.92	1.05	1.62	0.76	1.36	0.69	0.49	1.00	0.73	1.02	1.07	0.38
135.0480	12.03	positive	1.35	0.59	0.78	0.77	0.51	0.89	0.68	0.78	1.16	0.66	0.21	0.98	0.41
135.0647	11.13	positive	0.89	1.28	0.83	0.39	0.66	0.87	1.07	0.89	0.76	1.46	0.43	0.73	0.47
135.0790	1.94	positive	0.67	0.87	0.82	0.83	0.95	0.72	0.70	0.56	0.92	0.90	0.63	0.97	0.85
136.0617	6.00	positive	0.84	0.71	0.70	1.50	1.20	1.00	1.09	0.41	0.97	0.64	4.89	1.17	0.13
136.0756	8.94	positive	1.61	11.81	2.45	1.28	1.70	1.58	4.01	3.47	1.20	11.87	14.66	1.28	3.25
136.0868	1.94	positive	0.63	0.85	0.99	0.78	0.93	0.67	0.68	0.55	0.91	0.88	0.61	0.95	0.84
137.0253	2.13	negative	8.60	1.06	0.94	0.85	0.61	1.24	3.20	1.50	1.27	1.16	1.47	1.02	1.12
137.0477	5.48	negative	0.90	0.75	1.01	0.83	0.82	0.76	0.69	0.89	0.90	0.62	0.78	0.81	1.02
137.0650	5.99	positive	0.89	0.76	0.62	1.29	1.10	1.05	1.05	0.54	1.00	0.78	4.39	1.03	0.39
138.0398	1.99	negative	11.41	1.01	0.91	1.10	0.52	1.19	3.91	1.45	1.28	1.14	1.40	0.90	1.23
138.0569	6.47	negative	0.88	1.09	0.94	0.84	1.09	1.06	1.17	0.98	0.83	1.11	0.28	1.07	0.19
138.0915	5.64	positive	0.94	1.21	0.95	0.95	0.95	0.96	1.07	1.02	0.90	1.27	0.76	0.96	0.49
138.1025	1.94	positive	0.76	0.93	0.92	0.91	0.98	0.76	0.78	0.63	0.95	0.99	1.00	0.95	1.08
139.0079	9.13	negative	1.44	0.81	48.27	48.27	42.42	1.01	0.68	1.36	24.48	0.89	22.97	21.80	0.88
139.0501	2.00	positive	70.12	0.29	2.31	3.40	1.06	0.34	0.51	0.48	4.68	0.85	0.18	0.85	7.92
139.0501	6.84	positive	75.33	0.25	1.76	2.32	1.06	0.31	0.34	0.44	2.63	0.95	2.43	0.98	0.62
139.0749	10.48	positive	0.90	1.00	0.79	0.86	0.53	0.75	0.52	0.74	1.00	0.75	0.22	0.59	0.88
140.0115	8.39	negative	1.08	0.96	0.62	1.29	1.09	1.27	0.35	1.29	0.81	0.29	0.13	1.20	0.39
140.0115	9.85	negative	0.95	1.02	1.07	1.00	1.12	0.93	0.92	1.04	1.06	0.98	1.42	1.09	1.00
140.0341	8.37	positive	0.76	0.82	0.72	0.55	0.79	0.99	0.96	0.87	0.76	0.79	0.00	0.73	0.34

140.0361	6.47	negative	0.90	1.12	0.95	0.82	1.06	1.15	1.18	1.02	0.82	1.13	1.94	1.10	0.13
140.0681	5.79	positive	1.27	0.69	0.76	0.42	0.49	0.57	1.19	0.98	1.15	0.92	0.21	0.50	0.81
140.0819	1.90	positive	0.66	0.82	0.85	0.81	0.91	0.70	0.72	0.59	0.95	0.90	0.66	0.94	0.84
141.0037	8.23	negative	1.17	1.13	0.90	1.13	0.98	1.10	0.69	1.11	1.05	0.79	0.22	1.05	0.34
141.0037	9.85	negative	0.98	1.03	1.06	1.01	1.12	0.93	0.91	1.02	1.07	0.99	1.43	1.09	1.00
141.0202	3.90	negative	0.83	1.35	0.67	0.81	1.48	1.03	1.15	0.86	1.51	2.38	0.22	0.78	1.24
141.0202	6.67	negative	0.97	1.05	0.82	0.67	1.17	1.31	1.24	1.11	1.14	1.28	0.41	0.96	0.35
141.0656	8.70	positive	1.33	1.36	0.96	0.70	1.01	1.40	1.66	1.12	0.78	1.18	0.15	1.15	0.50
141.0657	5.66	positive	1.19	0.75	0.76	0.55	1.09	1.21	0.85	0.80	0.78	1.03	0.00	0.98	0.36
142.0519	6.62	negative	0.86	0.98	1.06	0.95	0.97	1.07	1.11	0.84	0.81	0.74	0.65	0.98	0.10
142.9994	7.28	negative	0.98	0.93	0.97	0.94	0.77	1.13	0.34	0.77	0.87	0.90	0.05	0.84	0.73
142.9995	3.51	negative	0.99	0.98	0.85	0.90	0.76	1.07	0.34	0.65	0.87	1.14	0.05	0.84	0.51
143.0358	7.84	negative	1.25	1.35	0.96	0.83	1.28	1.31	0.97	0.68	1.28	1.54	1.26	1.51	1.14
143.0358	9.80	negative	1.15	1.42	0.67	1.02	1.29	0.97	0.62	0.32	1.20	1.49	1.09	1.30	1.00
143.0813	6.84	positive	1.05	1.02	1.07	0.64	1.01	1.04	1.06	1.17	1.00	1.38	0.62	0.86	1.10
144.0029	7.27	negative	0.97	0.88	1.00	0.96	0.77	1.17	0.26	0.75	0.86	0.90	0.01	0.82	0.72
144.0464	0.93	negative	1.93	0.81	0.94	1.02	0.88	1.01	1.79	4.10	1.43	0.86	7.04	1.11	0.83
144.0807	7.28	positive	1.61	5.52	0.94	0.61	1.47	1.24	2.02	1.53	1.39	6.04	3.25	1.27	1.16
144.1018	5.50	positive	0.88	1.04	0.90	1.03	0.78	1.03	1.22	0.76	1.02	0.99	0.37	0.84	0.33
145.0151	7.32	negative	0.83	0.80	0.67	1.12	0.92	0.66	0.47	0.52	0.96	0.79	0.31	0.88	0.48
145.0494	12.05	positive	1.49	2.03	1.37	0.62	1.90	1.35	1.49	1.93	1.71	2.42	2.43	1.49	4.86
145.0627	10.50	negative	0.96	1.28	0.88	0.70	1.26	0.92	1.26	0.97	0.81	1.23	0.49	1.33	1.26
145.0991	14.13	negative	0.78	5.14	1.97	0.91	0.97	0.94	2.66	2.07	0.81	5.60	5.34	0.62	0.09
145.1082	5.89	positive	0.94	0.91	0.63	0.44	0.67	0.71	1.08	0.71	0.87	1.13	0.23	0.66	0.00
145.1335	0.99	positive	0.99	0.69	0.89	0.45	0.59	1.04	1.19	0.84	0.59	0.73	0.01	0.68	0.26
145.1446	9.29	positive	0.84	0.82	0.60	0.74	0.63	0.86	0.93	0.64	0.87	1.06	0.03	0.54	0.42
146.0185	7.29	negative	0.72	0.71	0.62	1.28	1.00	0.48	0.37	0.32	1.01	0.65	77.34	0.92	0.48
146.0468	10.97	negative	1.07	0.90	0.89	0.67	1.06	1.15	1.02	1.14	0.85	0.85	0.19	0.85	0.68
146.0599	8.62	positive	1.04	1.02	0.59	0.27	0.77	0.86	0.89	1.02	0.80	1.70	1.02	0.75	0.42
146.0633	0.90	positive	1.03	0.97	0.48	0.78	0.83	0.92	0.57	0.33	0.77	1.02	0.07	1.21	0.71
146.0922	6.20	positive	0.89	1.35	1.13	1.23	1.06	1.10	1.61	0.88	0.83	1.17	1.12	1.02	0.05
147.0308	6.40	negative	1.10	2.06	1.34	1.56	1.78	1.31	2.75	1.61	0.87	1.61	1.70	1.37	13.88
147.0475	6.76	positive	1.11	1.45	0.96	0.97	1.52	1.25	1.35	0.90	0.80	1.59	0.24	1.23	0.02

147.0500	11.01	negative	1.07	0.88	0.88	0.64	1.05	1.16	1.03	1.15	0.81	0.85	1.10	0.87	0.66
147.0672	2.75	negative	0.94	0.97	0.78	0.70	0.83	0.99	1.33	0.91	0.98	1.31	0.59	0.87	0.54
147.0762	10.56	positive	1.04	1.79	0.84	0.79	1.23	0.93	1.32	0.90	0.92	1.09	0.45	1.29	1.13
147.1126	14.14	positive	0.87	4.43	1.67	0.94	0.97	1.01	2.19	1.88	0.87	4.78	4.32	0.76	1.01
148.0511	11.03	negative	1.15	1.04	0.87	0.40	1.23	1.20	1.06	1.27	0.78	0.81	0.04	0.82	0.54
148.0603	11.01	positive	1.04	0.84	0.87	0.61	1.04	1.16	1.02	1.19	0.81	0.79	0.15	0.78	0.60
148.0704	2.75	negative	0.91	0.98	0.77	0.67	0.83	1.01	1.34	0.92	0.98	1.30	0.58	0.90	0.52
148.0868	1.94	positive	0.64	0.83	0.83	0.81	0.92	0.67	0.68	0.55	0.91	0.88	0.62	1.00	0.81
148.0974	9.05	positive	0.94	1.06	0.84	0.89	1.04	0.95	0.94	0.75	0.99	1.32	21.09	1.07	1.32
148.9534	7.89	negative	1.03	1.02	1.04	1.06	1.02	1.02	0.99	1.02	1.01	1.01	1.06	1.02	0.92
149.0252	5.93	negative	1.47	1.07	0.72	1.10	1.16	1.06	0.53	1.25	0.98	0.79	5.73	1.14	1.91
149.0465	7.25	negative	1.13	1.58	0.93	1.07	1.42	1.30	1.32	1.01	1.00	1.50	0.83	1.10	0.18
149.0635	11.00	positive	1.03	0.82	0.87	0.60	1.02	1.15	1.01	1.18	0.79	0.77	0.14	0.77	0.58
150.0430	8.17	negative	0.52	0.52	0.08	1.48	0.76	0.40	0.05	0.00	0.87	0.38	3.41	0.63	0.71
150.0497	6.40	negative	1.23	1.70	1.00	1.18	1.60	1.05	1.37	0.97	0.86	1.61	0.92	1.19	0.16
150.0582	7.25	positive	0.95	0.97	0.65	0.97	1.29	1.10	0.66	0.68	0.92	1.12	0.47	1.18	0.32
150.0947	5.56	positive	0.90	0.94	0.81	0.31	0.54	0.87	1.17	0.72	0.60	1.39	0.46	0.72	0.24
151.0271	5.41	negative	1.07	1.03	1.01	1.11	1.09	0.92	0.95	1.04	1.10	1.00	1.17	1.00	1.23
151.0351	4.94	positive	1.04	0.96	1.12	1.15	1.06	0.98	1.18	1.14	1.07	1.16	0.73	1.08	0.95
151.0620	6.19	negative	1.10	1.15	0.78	0.81	0.92	1.03	1.11	0.79	0.91	1.21	0.57	0.69	0.55
151.0623	7.23	positive	0.95	1.01	0.66	0.99	1.41	1.16	0.67	0.72	0.94	1.14	0.50	1.23	0.28
151.0977	1.98	positive	0.69	0.89	0.90	0.85	0.96	0.68	0.71	0.58	0.83	0.96	0.67	0.89	0.97
152.0162	5.42	negative	0.58	0.83	0.59	1.05	0.98	0.86	0.70	0.62	0.67	0.41	4.14	1.37	0.61
152.0357	4.94	positive	1.07	0.95	1.12	1.14	1.05	0.97	1.18	1.16	1.06	1.17	0.67	1.07	0.95
152.0566	9.00	positive	0.94	0.79	0.68	1.26	1.40	0.93	1.08	0.30	1.11	0.85	24.16	1.12	0.96
152.0817	1.94	positive	0.58	0.80	0.80	0.73	0.90	0.61	0.67	0.53	0.90	0.86	0.55	0.88	0.77
152.9873	13.63	negative	1.08	1.05	0.97	1.05	1.03	0.96	1.15	1.00	0.97	1.34	0.99	1.00	1.05
153.0326	4.94	positive	1.06	0.97	1.09	1.12	1.04	0.99	1.17	1.15	1.06	1.15	0.69	1.08	0.92
154.0156	6.20	negative	0.37	0.91	0.42	0.44	1.18	0.53	0.84	0.80	0.66	0.75	0.79	0.94	0.12
154.0631	14.24	negative	1.26	2.19	1.13	0.72	1.32	1.06	1.29	1.27	1.02	2.63	0.86	1.18	1.51
154.0952	5.29	positive	1.07	1.09	0.62	0.59	0.40	1.00	1.21	0.85	0.84	1.19	0.51	0.61	0.45
154.9196	13.61	negative	0.95	0.93	0.76	0.64	0.77	0.87	0.83	0.86	0.90	1.12	0.50	0.78	1.97
155.0360	6.72	negative	1.12	1.38	0.95	1.02	1.33	1.19	0.84	0.75	0.97	1.32	0.65	1.02	23.63

155.0425	11.19	positive	0.92	0.94	0.95	1.27	0.86	0.85	0.82	0.86	0.97	0.94	1.15	0.88	0.86
155.0789	14.72	positive	0.79	0.28	0.48	0.53	0.50	0.58	0.42	0.61	1.05	0.71	0.11	0.39	0.25
156.0766	14.25	positive	1.19	2.01	1.08	0.72	1.28	1.02	1.20	1.23	0.96	2.37	0.84	1.12	0.84
156.0788	14.01	negative	0.75	0.99	0.80	0.57	0.66	0.72	0.74	0.83	0.89	1.46	0.65	0.60	0.62
156.9166	13.61	negative	0.94	0.92	0.72	0.61	0.73	0.92	0.79	0.90	0.94	1.16	0.44	0.77	1.72
156.9540	10.64	positive	1.10	0.60	2.05	2.21	0.74	0.67	0.55	0.87	1.32	0.58	3.03	0.63	1.55
156.9870	1.42	positive	0.70	0.58	0.87	0.90	0.99	0.92	2.35	1.01	0.81	0.63	0.53	0.69	0.83
157.0128	2.51	negative	1.81	0.73	1.25	1.00	1.02	0.73	1.04	1.08	1.75	0.70	0.99	0.73	1.88
157.0152	5.05	negative	1.14	0.94	0.77	1.00	1.96	0.81	0.05	0.28	1.19	1.03	1.15	1.18	1.22
157.0387	7.10	negative	0.88	1.15	1.03	0.80	0.80	0.94	1.06	0.96	0.81	1.20	0.79	0.74	0.47
157.0801	14.25	positive	1.22	2.06	1.09	0.68	1.35	1.03	1.26	1.30	0.96	2.46	0.81	1.14	0.84
158.0416	5.95	positive	1.12	0.75	0.48	1.08	0.65	0.33	1.16	0.08	1.20	1.10	1.56	1.08	1.23
158.0832	5.75	negative	0.90	2.80	1.43	3.22	5.37	1.71	1.11	1.98	0.77	1.16	2.95	4.73	0.63
158.0922	14.01	positive	0.75	0.93	0.78	0.52	0.65	0.66	0.78	0.80	0.86	1.75	0.62	0.57	0.32
158.9639	5.57	positive	1.59	0.58	1.04	0.55	0.86	0.55	1.81	1.78	1.21	0.66	1.90	0.69	9.21
158.9639	1.10	positive	0.09	0.13	0.15	0.13	0.96	0.11	0.21	0.20	0.09	0.09	0.19	0.09	0.29
158.9794	4.92	negative	1.00	0.99	0.76	0.71	0.68	1.02	1.16	0.93	0.90	1.12	0.40	0.82	0.52
159.0309	6.54	negative	1.46	2.03	1.12	1.87	1.45	1.54	2.86	1.07	1.30	1.93	1.75	1.25	0.61
159.0762	11.61	positive	1.05	0.36	0.61	0.66	0.55	0.81	0.68	0.80	0.95	0.61	0.28	1.07	0.45
160.0755	11.94	positive	0.88	2.04	7.71	0.28	0.38	6.83	13.84	7.82	1.10	0.61	2.21	1.04	0.33
160.0966	7.77	positive	1.20	1.18	0.90	0.81	1.03	1.08	1.10	0.94	1.04	1.42	0.70	1.07	0.65
161.0465	5.61	negative	1.05	1.78	1.80	3.12	2.81	1.45	1.27	1.24	0.90	1.14	0.62	2.31	0.55
161.0465	12.72	negative	34.63	2.05	0.96	0.91	1.38	23.87	6.14	1.96	34.45	2.26	2.49	4.95	1.66
161.0821	1.94	positive	0.64	0.83	0.78	0.81	0.93	0.69	0.70	0.55	0.90	0.86	0.62	0.93	0.83
161.0829	2.29	negative	1.06	1.05	0.87	1.02	0.84	1.11	1.52	1.03	1.25	1.38	0.69	0.96	0.76
161.0916	9.05	positive	1.12	2.20	1.11	0.91	1.31	1.05	1.31	1.04	0.93	2.11	1.13	1.16	0.72
161.0918	7.24	positive	0.80	0.72	0.74	0.86	0.83	1.11	0.67	0.45	1.00	0.84	1.81	0.94	0.26
162.0241	6.47	negative	0.98	1.41	1.02	3.87	1.62	1.10	1.30	1.01	0.74	1.07	0.01	1.44	0.05
162.0404	12.66	positive	1.51	9.84	44.61	2.29	1.35	35.69	108.97	96.66	0.70	3.45	5.46	0.70	2.46
162.0759	9.98	positive	0.72	2.97	0.77	2.52	1.25	0.91	0.96	0.59	1.78	4.35	0.87	0.72	1.61
162.0781	11.66	negative	0.97	0.66	0.64	0.67	0.62	0.70	0.76	0.79	0.91	1.48	0.25	0.53	0.29
162.9834	8.41	negative	1.06	0.98	1.02	1.10	1.62	1.05	0.90	1.07	1.04	1.77	1.03	1.11	1.64
163.0422	9.22	positive	0.83	1.11	0.97	0.99	1.10	0.90	0.92	0.71	1.19	1.64	0.32	0.88	0.92

163.0599	12.04	positive	1.49	2.25	1.51	0.50	2.05	1.40	1.60	2.24	1.94	2.64	2.63	1.66	5.50
163.0622	6.53	negative	1.04	1.20	1.01	0.86	0.99	1.23	1.18	1.07	0.83	0.94	0.37	0.93	0.16
163.0752	5.90	positive	0.84	1.50	1.69	2.09	2.21	2.27	1.26	1.29	0.68	0.54	0.18	2.01	0.29
163.0977	1.93	positive	0.68	0.85	0.81	0.84	0.92	0.86	0.70	0.59	0.93	0.86	0.65	0.98	0.84
164.0690	6.61	negative	1.77	3.22	1.47	1.06	1.56	2.14	1.67	1.91	1.37	2.95	3.70	1.98	1.24
164.0738	12.52	positive	0.94	1.75	1.22	0.64	0.60	0.93	1.05	1.15	1.04	2.08	0.87	0.75	0.13
164.1102	5.17	positive	0.83	0.79	0.83	0.41	0.62	0.88	0.90	0.82	0.62	0.89	0.30	0.85	0.08
164.9203	1.11	positive	0.80	1.21	1.44	1.20	1.26	1.50	1.74	1.55	1.08	0.80	1.66	1.00	1.85
164.9349	4.09	positive	1.55	1.63	0.44	1.02	1.29	0.55	0.75	0.42	1.57	2.45	2.86	1.54	1.06
165.0203	6.45	negative	1.10	1.45	1.29	1.54	1.51	1.30	0.79	0.74	1.00	0.79	1.87	1.45	0.09
165.0414	8.55	negative	1.19	1.74	0.95	0.94	1.04	1.29	1.85	1.24	1.06	1.79	0.71	1.00	0.61
165.0544	8.96	positive	1.64	11.39	2.47	1.26	1.71	1.54	3.88	3.47	1.17	11.37	14.18	1.30	3.64
166.0236	6.43	negative	1.02	1.93	1.78	2.28	2.22	1.78	0.95	1.62	1.22	1.27	2.97	2.07	0.01
166.0447	8.59	negative	1.45	2.49	0.99	1.04	1.32	1.65	2.73	1.70	1.15	2.42	0.67	1.02	0.42
166.0530	11.02	positive	1.02	1.02	0.79	1.01	0.82	0.99	1.77	1.10	1.39	1.89	1.73	0.70	0.94
166.0860	6.75	positive	2.51	5.96	2.11	1.18	2.19	2.93	2.71	2.43	2.07	5.82	7.27	3.01	1.19
166.9333	4.93	negative	1.01	1.02	0.75	0.77	0.72	1.00	1.10	0.93	0.85	1.08	0.47	0.90	0.56
166.9505	2.55	positive	4.22	0.64	1.39	0.92	1.03	0.64	1.03	1.25	2.16	0.62	0.99	0.65	2.46
166.9971	7.26	negative	0.97	0.84	0.98	1.47	0.94	0.90	0.48	0.72	1.01	0.62	0.18	0.90	4.13
167.0220	9.37	negative	0.97	1.40	0.87	0.80	0.88	1.01	1.04	0.92	0.93	1.51	0.00	0.89	0.83
167.0359	6.40	negative	1.04	7.93	0.98	0.97	2.20	1.19	2.07	1.57	0.84	5.98	0.67	1.14	0.75
167.0894	6.75	positive	2.63	6.30	2.17	1.22	2.27	3.05	2.77	2.53	2.15	6.12	7.72	3.16	1.22
168.0288	10.98	negative	1.14	0.68	0.87	0.69	1.09	1.11	0.90	1.13	0.93	0.87	0.84	0.88	0.81
168.0441	13.81	negative	0.99	1.66	0.86	0.66	0.62	0.93	1.00	1.17	0.93	1.89	0.67	0.88	0.68
168.0451	0.91	positive	1.11	1.06	0.56	0.78	0.98	0.93	0.01	0.06	0.80	0.95	0.05	1.33	0.92
168.0654	12.05	positive	1.37	2.55	1.65	0.49	2.23	1.30	1.86	2.53	1.60	3.29	3.27	1.76	6.93
168.0765	14.73	positive	201.30	0.50	1.86	1.34	0.44	2.50	3.32	0.81	0.91	1.65	5.11	1.34	17.41
168.0920	6.74	positive	3.56	8.71	2.78	3.90	2.97	4.07	3.35	3.13	4.18	8.74	10.65	4.36	1.42
168.9915	16.50	negative	6.33	0.97	0.74	1.65	1.46	1.06	0.72	0.95	3.11	1.13	1.76	3.62	0.91
169.0152	7.89	negative	0.59	0.45	0.97	0.58	0.46	0.64	0.70	0.92	0.81	0.59	0.80	0.41	1.26
169.0355	9.35	positive	1.04	1.51	0.93	0.85	0.96	1.05	1.05	0.96	1.01	1.61	0.00	0.97	0.84
169.0455	4.94	positive	1.08	0.98	1.54	1.66	1.47	0.98	1.17	1.37	1.28	1.13	1.68	1.36	1.62
169.0582	10.59	positive	1.00	1.00	0.75	0.63	0.96	0.96	0.88	0.93	0.93	1.02	0.52	0.98	0.70

170.0469	6.41	negative	1.45	0.36	0.78	1.02	0.79	1.79	0.67	1.09	1.26	0.28	0.60	1.24	0.00
170.9710	4.09	negative	1.57	1.67	0.44	1.05	1.28	0.58	0.75	0.42	1.59	2.44	2.68	1.57	1.09
171.0308	5.81	negative	1.21	1.88	1.25	1.56	2.32	1.76	1.67	1.79	1.07	1.67	6.60	2.20	0.86
171.0759	10.55	positive	0.95	1.39	0.86	0.77	1.49	0.92	1.43	0.97	0.92	1.15	0.42	0.85	1.22
172.0625	4.45	negative	0.95	0.83	0.63	0.57	0.78	0.89	0.85	0.83	0.96	1.42	0.40	0.77	0.43
172.0989	5.59	negative	1.01	1.17	1.08	1.60	1.67	1.11	1.19	1.00	0.97	1.11	1.17	1.53	0.74
172.9867	2.54	negative	1.42	0.70	1.27	0.99	1.07	0.72	1.04	1.14	1.85	0.66	0.99	0.73	2.08
173.0101	7.27	negative	0.94	0.87	0.98	0.92	0.70	1.11	0.29	0.76	0.86	0.83	0.04	0.78	0.55
173.0501	6.71	negative	1.16	1.20	0.94	0.86	1.06	1.21	1.52	0.95	0.79	1.08	0.42	1.05	0.23
173.0678	4.97	positive	1.09	1.00	1.47	1.39	1.35	0.99	1.10	1.37	1.28	1.12	1.16	1.28	1.41
173.0781	1.07	positive	1.61	1.10	1.37	1.16	1.12	1.09	1.29	1.12	1.09	1.28	1.30	1.15	1.23
173.0919	11.02	positive	0.76	1.11	0.83	0.35	0.63	0.84	1.33	1.01	0.84	1.83	0.19	0.52	0.38
173.1053	14.01	negative	0.77	0.95	0.81	0.60	0.70	0.74	0.80	0.84	0.91	1.40	0.70	0.64	0.65
174.0418	6.78	negative	1.19	1.17	1.04	0.93	1.06	1.20	1.94	1.23	0.85	1.00	0.42	0.98	1.08
174.0758	11.01	positive	0.76	1.08	0.88	0.58	0.74	0.82	1.20	1.03	0.81	1.67	0.24	0.62	0.43
174.0893	11.61	negative	1.04	0.32	0.57	0.68	0.53	0.79	0.61	0.73	0.98	0.55	0.25	1.11	0.40
174.0899	1.93	positive	0.82	0.96	0.97	0.86	0.92	0.73	0.69	0.54	0.93	1.11	0.70	1.21	0.77
175.0258	5.07	negative	1.15	0.97	0.61	0.96	1.00	0.79	0.79	1.16	1.14	1.09	1.10	1.16	1.04
175.0482	9.82	negative	0.73	0.78	0.89	0.73	0.59	0.86	0.80	0.73	0.83	0.86	0.08	0.53	0.38
175.1073	9.56	positive	1.47	0.90	0.49	0.94	0.86	0.54	0.57	0.55	1.32	1.86	0.40	3.27	0.32
175.1074	8.25	positive	0.97	0.07	0.12	0.21	0.16	0.43	0.14	0.30	0.89	0.31	0.16	0.63	0.02
175.1186	14.01	positive	0.74	0.96	0.78	0.53	0.65	0.67	0.77	0.82	0.87	1.68	0.64	0.58	0.35
175.1439	12.19	positive	1.00	1.03	0.79	0.65	0.78	0.94	1.01	0.90	1.19	1.64	0.57	0.76	1.10
176.1028	11.61	positive	1.02	0.36	0.60	0.66	0.55	0.80	0.66	0.80	0.95	0.61	0.28	1.07	0.45
176.1221	14.01	positive	0.75	0.95	0.78	0.53	0.65	0.67	0.78	0.83	0.87	1.69	0.64	0.58	0.35
176.9369	14.99	negative	0.71	0.86	0.50	0.48	0.58	0.85	0.94	0.60	0.60	0.99	0.76	0.81	0.19
177.0414	7.83	negative	0.98	1.05	0.94	0.73	0.77	1.12	1.09	0.91	0.96	1.08	0.30	0.81	0.63
177.0414	6.47	negative	1.82	1.78	1.19	1.46	1.63	1.85	2.74	1.07	1.16	1.74	2.17	1.33	1.52
177.0545	7.07	positive	1.07	1.09	1.04	0.98	0.96	1.24	1.30	0.93	0.77	0.71	0.08	1.00	0.11
177.0616	9.80	positive	0.77	0.92	0.81	0.78	0.84	0.82	0.66	0.62	0.92	0.99	0.17	0.73	0.55
177.1062	11.61	positive	1.05	0.35	0.60	0.66	0.53	0.81	0.87	0.79	0.96	0.60	0.27	1.06	4.11
177.1238	13.99	positive	0.70	0.90	0.76	0.52	0.61	0.67	0.76	0.78	0.83	1.64	0.61	0.56	0.25
178.0519	5.17	negative	0.97	1.01	0.69	0.62	0.56	1.14	1.14	0.80	0.83	1.21	0.28	0.67	0.57

178.0585	14.26	positive	1.22	1.64	1.06	0.83	1.37	1.08	1.08	1.18	0.96	1.64	0.76	1.24	1.24
178.1258	5.14	positive	0.81	0.77	0.84	0.42	0.66	0.90	0.90	0.85	0.61	0.81	0.29	0.94	0.27
179.0029	6.80	negative	1.28	1.47	1.07	1.20	1.54	1.16	1.02	1.11	0.99	1.27	0.36	1.37	0.01
179.0359	6.04	negative	0.77	0.94	0.99	1.53	1.04	1.29	0.49	0.46	0.70	0.65	0.16	1.12	0.26
179.0570	9.82	negative	1.14	1.40	0.68	1.02	1.29	0.98	0.65	0.37	1.13	1.52	1.10	1.34	1.02
179.0570	7.84	negative	1.22	1.29	0.98	0.81	1.18	1.31	1.05	0.72	1.19	1.43	1.06	1.38	0.99
179.0678	1.09	positive	1.10	1.19	1.31	1.20	1.39	1.28	1.30	1.11	1.33	1.09	1.40	1.34	1.62
179.1294	5.24	positive	0.90	0.79	0.83	0.52	0.71	0.88	0.93	0.84	0.85	0.88	0.55	0.92	0.19
180.0666	8.95	negative	1.62	5.40	1.17	0.89	1.37	1.92	1.66	1.74	1.69	5.15	5.42	1.28	1.88
180.0868	12.10	positive	1.04	1.96	1.08	0.52	1.71	1.77	10.81	1.47	1.23	2.35	1.86	1.36	3.69
180.0878	8.15	positive	1.01	1.04	0.89	0.80	0.86	1.00	1.06	0.77	0.96	1.16	0.52	0.84	0.51
180.1216	5.21	positive	0.84	0.63	0.91	0.00	0.00	0.81	0.89	0.84	0.48	0.85	0.00	0.25	0.00
180.9740	1.12	negative	0.94	1.10	1.24	1.10	0.82	1.13	0.95	1.25	0.95	0.88	1.45	1.01	1.53
180.9740	5.40	negative	0.91	0.94	1.10	1.15	1.38	1.06	0.26	0.81	0.60	0.34	0.14	1.27	0.10
181.0152	6.57	negative	0.93	1.00	0.90	0.97	1.39	1.09	0.97	2.11	1.09	0.91	1.74	1.15	13.18
181.0614	7.87	negative	2.51	1.28	1.04	0.41	0.83	1.23	1.10	0.42	1.23	1.44	6.29	1.06	0.90
181.9387	1.34	negative	0.50	0.76	1.02	0.52	0.83	0.67	0.80	1.35	0.88	0.58	0.80	0.74	0.80
182.0469	6.45	negative	0.95	1.32	1.00	0.96	1.16	1.19	1.52	1.05	0.88	1.29	0.60	1.09	0.20
182.0810	8.96	positive	1.61	11.48	2.51	1.26	1.72	1.56	3.94	3.52	1.18	11.53	13.84	1.32	3.69
182.9491	5.53	positive	0.91	0.59	0.88	0.42	0.84	0.41	0.98	0.60	1.42	0.72	0.01	0.81	1.61
182.9920	5.75	negative	1.47	1.11	0.46	0.28	0.51	0.73	1.32	0.69	1.30	1.90	0.50	0.35	2.54
183.0112	8.13	negative	1.19	1.06	0.89	1.19	0.97	1.12	0.88	1.12	1.05	0.89	1.13	1.12	0.89
183.0844	8.95	positive	1.69	13.22	2.58	1.26	1.76	1.67	4.47	3.94	1.15	13.15	15.69	1.40	4.07
184.0731	13.88	positive	0.94	1.78	0.89	0.63	0.61	0.89	1.07	1.24	0.95	2.00	0.71	0.84	0.41
185.0077	5.32	negative	1.19	1.79	0.83	1.83	2.21	0.96	0.13	2.34	0.73	0.08	2.28	1.81	1.93
185.0762	13.88	positive	0.92	1.84	0.87	0.58	0.57	0.86	1.06	1.26	0.94	2.07	0.70	0.84	0.36
186.0761	12.05	positive	1.48	2.68	1.63	0.47	2.20	1.49	2.05	2.49	1.67	3.41	3.19	1.59	7.25
186.9305	5.94	negative	2.40	1.96	1.88	0.19	0.81	1.39	0.01	6.12	0.04	1.29	1.63	1.34	23.93
187.0734	8.61	negative	0.96	1.23	1.00	0.99	0.89	1.18	1.77	0.99	1.18	2.11	0.19	0.83	0.66
187.0986	3.08	negative	1.39	0.37	0.45	0.56	0.81	0.54	0.62	0.42	0.60	0.47	0.38	0.66	0.41
187.1075	6.82	positive	0.74	0.54	0.58	1.21	0.79	0.86	1.97	0.03	0.74	0.57	2.62	0.82	0.44
188.0575	6.42	negative	1.16	0.18	0.67	0.81	0.58	1.49	0.57	0.98	1.03	0.24	0.39	1.01	0.03
188.0705	7.20	positive	2.63	11.39	1.77	1.01	2.68	1.97	4.00	2.80	1.82	12.40	5.79	2.35	2.01

189.0415	6.34	negative	1.37	1.50	1.09	1.50	1.24	1.48	1.02	1.06	1.16	0.94	1.38	1.43	0.38
189.0891	11.01	negative	0.71	1.18	0.84	0.35	0.76	0.78	1.15	0.98	0.85	1.85	0.28	0.62	0.57
189.1231	6.38	positive	0.78	0.74	0.83	1.19	0.88	1.10	0.73	0.37	0.89	0.74	3.30	0.99	0.15
189.1345	12.19	positive	0.92	0.96	0.72	0.53	0.67	0.80	0.84	0.78	0.96	1.58	0.54	0.63	1.00
190.1631	11.26	positive	0.87	1.25	0.71	0.50	0.68	0.98	1.21	0.68	0.74	1.61	0.18	0.71	0.41
190.9118	5.35	positive	1.32	1.02	0.67	0.85	0.72	1.24	0.75	1.03	1.07	0.89	0.50	0.90	1.42
191.0207	13.99	negative	0.88	1.26	0.88	0.32	0.59	0.70	0.73	0.82	0.69	2.09	0.31	0.62	0.13
191.0571	6.49	negative	1.11	1.24	1.05	0.98	1.09	1.32	1.28	1.14	0.89	1.02	0.68	1.06	0.15
191.1024	11.02	positive	0.72	1.07	0.86	0.48	0.71	0.78	1.16	1.00	0.81	1.65	0.26	0.56	0.45
192.1059	11.02	positive	0.73	1.08	0.86	0.43	0.66	0.81	1.21	1.06	0.84	1.67	0.20	0.51	0.35
192.1415	4.99	positive	0.84	0.70	0.87	0.39	0.66	0.91	0.95	0.84	0.59	0.74	0.40	0.99	0.30
193.0366	7.18	negative	0.87	0.77	0.75	0.45	0.43	1.06	0.60	0.76	0.74	0.77	0.19	0.53	0.09
193.0549	4.34	negative	0.94	0.93	0.89	0.90	0.71	0.95	1.56	0.72	0.76	1.03	10.77	0.78	0.55
193.0709	12.23	positive	1.03	0.63	0.72	1.07	1.09	0.87	1.27	1.05	1.10	0.81	0.80	1.07	1.05
193.1451	4.98	positive	0.82	0.68	0.87	0.35	0.65	0.91	0.96	0.83	0.52	0.75	0.39	0.98	0.26
193.9298	14.99	positive	0.94	0.95	0.75	0.81	0.80	1.00	1.07	0.80	0.78	1.05	0.99	0.90	0.55
194.0501	7.42	negative	0.79	0.83	0.58	0.38	0.59	0.80	0.54	0.83	0.77	1.09	0.75	0.66	0.45
194.1373	4.98	positive	0.80	0.71	0.91	0.37	0.66	0.93	0.96	0.82	0.57	0.77	0.37	1.00	0.29
194.9374	15.01	negative	0.81	0.91	0.67	0.58	0.71	0.88	0.94	0.74	0.75	1.00	0.75	0.89	0.27
194.9455	5.30	positive	0.75	1.95	1.17	0.31	0.34	0.91	4.80	0.56	0.64	3.15	0.39	0.34	0.11
195.0538	7.42	negative	0.79	0.84	0.58	0.38	0.58	0.78	0.53	0.81	0.77	1.09	0.76	0.66	0.44
195.1225	0.99	positive	1.47	0.90	0.95	0.67	0.71	0.98	0.97	0.80	0.99	1.46	0.79	0.80	0.73
196.0294	13.37	negative	0.84	0.85	0.54	0.24	0.57	0.81	0.52	0.73	0.65	1.02	0.65	0.64	0.09
196.0460	7.42	negative	0.79	0.83	0.58	0.38	0.59	0.79	0.53	0.84	0.77	1.09	0.76	0.66	0.50
196.0635	7.40	positive	0.77	0.86	0.54	0.38	0.66	0.74	0.51	0.78	0.76	1.13	0.74	0.73	0.33
196.9479	5.37	negative	1.30	1.12	0.72	0.60	0.96	1.25	0.93	0.99	1.29	1.08	1.00	0.84	0.43
197.0230	3.85	negative	1.07	0.82	0.80	0.72	0.93	1.02	1.15	0.84	0.82	0.78	2.64	0.81	2.16
197.0493	7.41	negative	0.69	0.74	0.57	0.32	0.57	0.70	0.45	0.81	0.71	1.10	0.73	0.64	0.57
197.0673	7.40	positive	0.77	0.86	0.54	0.38	0.66	0.74	0.51	0.78	0.76	1.12	0.75	0.73	0.33
198.0594	7.40	positive	0.77	0.87	0.55	0.38	0.65	0.74	0.51	0.77	0.77	1.12	0.74	0.73	0.33
198.0758	6.51	negative	2.06	14.20	3.34	1.12	3.16	1.97	4.76	6.68	1.72	14.01	20.49	1.38	50.74
198.0852	11.64	positive	1.03	0.46	0.63	0.72	0.67	0.80	0.59	0.67	1.31	1.80	0.35	1.10	0.47
199.0081	9.63	negative	1.32	1.62	1.26	1.50	1.89	1.15	1.02	0.85	1.60	2.03	3.30	1.31	0.61

199.0346	11.16	negative	0.95	1.17	0.82	0.47	0.79	0.89	0.99	0.85	0.87	1.30	0.79	0.89	0.77
199.0436	9.79	positive	0.74	0.82	1.00	0.84	0.76	0.84	0.77	0.83	0.90	0.87	0.16	0.67	0.60
200.0574	5.50	negative	0.82	0.65	0.82	1.54	1.04	1.14	1.22	0.64	1.07	0.65	9.29	1.01	0.83
200.9816	5.32	negative	0.57	1.38	1.26	0.18	0.40	0.77	3.59	0.77	0.89	2.62	0.52	0.24	1.55
200.9872	11.41	negative	0.99	0.84	0.97	1.11	1.05	0.89	1.06	0.85	1.00	0.82	1.12	1.00	1.06
201.0390	2.49	negative	12.29	0.38	2.01	0.87	0.89	0.35	0.89	1.93	4.01	0.38	1.12	0.40	5.52
202.1086	1.94	positive	0.66	0.85	0.79	0.82	0.89	0.69	0.70	0.56	0.89	0.87	0.65	0.93	0.86
202.9974	5.14	negative	0.83	0.98	0.55	0.10	0.13	1.24	1.54	0.80	0.71	1.36	0.04	0.29	0.05
203.0525	7.86	positive	1.45	1.41	1.08	0.88	1.71	1.41	0.85	0.68	1.32	1.78	1.46	1.97	3.59
203.0835	7.20	negative	3.52	14.21	2.30	1.15	2.79	2.52	8.62	5.31	2.37	16.58	16.33	2.36	7.80
203.1041	6.56	positive	1.12	1.01	1.17	1.07	1.08	1.10	1.08	1.06	0.95	0.86	0.96	1.07	0.92
203.1499	10.54	positive	0.94	0.98	0.56	0.29	0.54	0.85	0.70	0.65	0.87	1.39	0.11	0.43	0.65
204.0865	7.85	positive	1.19	1.41	0.90	0.82	1.32	1.24	0.93	0.60	1.18	1.73	1.29	1.46	0.99
204.0865	12.03	positive	1.33	2.34	1.47	0.58	2.04	1.25	1.79	2.23	1.52	2.88	2.57	1.54	5.51
205.0500	5.62	negative	0.85	0.73	0.71	0.63	0.41	0.82	0.86	0.82	0.89	1.02	0.00	0.49	0.49
205.0816	12.07	positive	1.25	1.44	1.20	0.41	2.12	0.97	1.10	2.93	0.99	1.75	1.81	1.07	3.12
205.0969	7.21	positive	2.58	11.23	1.79	0.99	2.66	1.94	3.95	2.85	1.85	12.17	5.70	2.35	1.92
205.9614	4.42	positive	2.55	2.15	0.90	0.85	0.93	1.03	3.30	1.56	0.91	2.36	1.60	0.76	1.25
206.0550	13.77	positive	1.02	1.50	0.78	0.71	0.67	0.86	0.69	0.95	0.94	1.61	0.67	0.94	0.47
207.0308	6.05	negative	0.69	1.14	1.11	1.69	1.00	1.38	0.76	0.60	0.68	0.76	0.71	1.23	0.29
207.0519	4.71	negative	0.97	0.75	1.17	1.39	0.56	1.20	1.19	0.78	1.51	1.41	0.04	0.88	0.59
207.0584	13.80	positive	1.01	7.13	17.77	0.84	0.48	12.88	57.98	35.58	0.45	2.05	6.26	0.54	0.43
207.0650	5.88	positive	0.82	2.03	1.49	2.26	2.45	1.75	0.89	1.33	0.92	1.28	0.01	2.33	0.57
208.0623	9.19	negative	0.96	1.07	1.16	1.37	1.41	1.17	1.18	0.95	0.98	0.80	0.41	0.84	0.49
208.9440	10.75	negative	0.94	0.90	1.08	1.11	0.95	0.95	0.81	0.90	1.07	0.91	0.99	0.97	0.89
209.0675	7.70	negative	0.98	0.99	0.98	0.82	0.78	1.13	1.13	0.83	0.94	1.09	0.55	0.81	0.54
209.0819	13.99	negative	0.61	0.73	0.53	0.14	0.35	0.40	0.65	0.54	0.65	1.77	0.12	0.25	10.54
209.1395	4.80	positive	1.38	1.01	1.84	1.92	0.67	1.23	2.66	1.10	1.04	0.95	0.34	0.47	0.53
209.1397	1.06	positive	1.16	1.01	1.85	1.91	0.72	1.10	2.71	1.16	0.96	0.86	0.53	0.52	0.70
210.0707	7.85	negative	0.95	0.98	0.95	0.74	0.74	1.11	1.12	0.84	0.93	1.11	0.53	0.76	0.53
210.0759	9.20	positive	0.95	1.03	1.05	1.17	1.09	1.10	1.19	0.82	0.96	0.82	0.42	0.82	0.52
211.0021	13.77	negative	0.90	1.13	0.57	0.88	0.68	0.80	0.31	0.18	0.90	1.31	0.56	0.75	0.95
211.0257	6.82	negative	0.99	0.95	0.99	1.11	1.16	1.06	0.89	0.86	0.77	0.56	0.69	0.95	0.02

211.0486	8.73	negative	0.79	0.68	0.49	0.46	0.63	0.81	0.51	0.76	0.66	0.75	0.33	0.69	0.21
211.9975	4.44	negative	2.48	2.22	0.94	0.93	0.99	1.10	3.29	1.60	0.97	2.39	1.20	0.81	1.20
212.0585	8.72	positive	0.83	1.10	0.57	0.41	0.74	0.89	0.72	0.89	0.73	1.22	0.71	0.77	0.27
213.0413	8.29	negative	1.36	1.27	1.12	1.24	1.47	1.50	1.31	1.21	1.32	0.94	0.37	1.23	0.78
213.0501	10.91	negative	0.98	2.00	0.90	0.71	1.99	0.87	1.60	1.55	0.77	1.94	0.69	1.94	3.03
213.0622	8.72	positive	0.81	1.09	0.57	0.39	0.74	0.89	0.72	0.88	0.72	1.22	0.70	0.77	0.25
214.0341	11.02	negative	1.07	0.70	0.90	0.76	1.11	1.20	0.87	1.17	0.81	0.59	0.10	0.96	0.82
214.0494	13.95	negative	0.79	5.16	3.13	0.79	5.79	0.94	6.08	5.16	0.64	6.76	0.99	0.94	5.36
215.0176	9.80	positive	0.75	0.83	0.90	0.71	0.65	0.87	0.77	0.75	0.80	0.96	0.07	0.61	0.40
215.0336	7.85	negative	1.23	1.10	1.10	0.86	0.94	1.44	0.99	0.82	1.43	1.07	1.56	1.21	0.76
215.1386	5.77	positive	0.76	1.01	0.64	1.44	1.10	1.19	2.25	0.53	0.83	0.81	5.19	1.08	0.74
217.0128	2.51	negative	14.53	0.40	2.02	0.88	0.92	0.37	0.91	2.01	4.14	0.38	1.16	0.41	5.85
217.0295	6.75	negative	0.94	1.08	1.08	0.99	0.92	0.87	1.22	1.14	0.86	1.26	0.65	0.96	0.26
217.0837	10.98	negative	1.57	7.07	1.10	0.14	4.47	1.42	12.13	5.58	0.70	6.93	13.08	2.53	5.09
217.1044	0.99	positive	1.58	0.96	1.03	0.70	0.71	1.03	0.91	0.85	0.95	1.47	0.89	0.85	0.84
217.1282	7.46	positive	0.98	0.47	0.47	0.70	1.64	0.86	0.92	0.64	0.82	0.68	1.35	1.32	1.55
217.1544	5.37	positive	0.08	0.85	0.37	1.60	0.99	1.56	0.21	0.28	0.40	0.33	8.85	1.31	0.00
218.0454	7.41	positive	0.85	0.85	0.60	0.45	0.71	0.77	0.53	0.81	0.83	1.06	0.78	0.78	1.38
218.1079	0.99	positive	1.62	0.97	1.06	0.73	0.77	1.04	0.89	0.86	0.97	1.49	0.88	0.88	0.85
219.0154	3.41	negative	1.30	0.90	1.50	1.32	0.92	1.62	1.75	1.74	1.11	1.12	0.64	0.85	0.64
219.0154	7.28	negative	0.95	1.01	0.93	0.94	0.88	1.01	0.38	0.78	0.89	0.90	0.30	0.90	0.72
219.0492	7.39	positive	0.88	0.88	0.57	0.64	0.71	0.76	0.54	0.83	0.81	1.05	1.66	0.77	1.39
219.0972	10.97	positive	1.00	2.35	1.05	0.75	1.89	1.16	4.26	2.24	0.84	2.39	3.46	1.22	1.93
221.0497	6.01	negative	0.74	1.98	1.85	2.61	2.11	2.11	1.18	1.31	1.01	1.72	0.60	2.50	0.45
221.0674	12.74	negative	55.35	2.41	1.03	0.66	1.45	37.61	8.77	2.12	54.50	3.08	3.41	6.86	1.43
222.0978	11.36	positive	2.27	26.24	112.75	7.19	1.30	88.27	230.47	170.94	3.16	7.72	11.60	0.86	4.26
223.0618	5.90	negative	0.93	1.91	1.36	1.99	2.11	1.95	1.02	1.37	1.01	1.43	0.02	2.12	0.65
223.9854	11.46	negative	0.82	1.01	0.92	1.01	0.90	1.07	0.98	1.08	0.86	1.12	0.81	0.79	1.43
224.0652	5.90	negative	0.93	1.90	1.36	1.99	2.12	1.97	1.03	1.37	0.99	1.44	0.01	2.14	0.64
224.9485	2.56	negative	4.00	0.71	1.42	1.07	1.10	0.71	1.10	1.35	2.26	0.82	1.11	0.60	2.68
225.0623	9.83	negative	1.16	1.41	0.69	1.04	1.31	0.97	0.63	0.35	1.17	1.52	1.11	1.39	1.08
225.0623	11.47	negative	1.22	1.60	0.77	0.90	0.85	1.20	1.27	0.71	0.90	1.38	0.83	1.08	0.60
225.0672	5.90	negative	0.94	1.89	1.34	2.01	2.08	1.94	1.03	1.35	1.00	1.37	0.23	2.10	0.63

225.0755	5.70	positive	0.96	1.55	1.48	2.46	1.86	1.45	0.93	1.48	1.03	1.09	0.00	2.09	0.61
226.0707	10.47	positive	1.03	1.08	1.01	0.98	0.99	1.09	1.28	0.91	0.92	1.01	0.55	0.96	0.74
226.1799	1.09	positive	2.03	1.27	1.11	1.44	0.91	2.11	0.95	0.97	1.34	1.58	0.88	0.95	0.96
226.9792	9.12	negative	1.10	1.07	1.41	1.52	1.58	1.01	0.80	1.29	1.12	0.73	1.52	1.42	1.28
226.9971	7.23	negative	0.91	0.72	1.39	1.09	0.64	1.11	0.36	1.04	0.93	0.57	0.11	0.72	0.30
227.0205	5.77	negative	0.73	4.21	2.68	4.44	5.82	3.01	1.58	2.32	1.08	1.45	3.65	5.52	0.79
227.0660	11.80	positive	1.13	1.28	1.31	1.09	1.22	1.18	1.54	1.03	1.04	1.20	0.58	1.10	0.76
228.0650	13.85	negative	1.05	1.84	0.94	0.81	0.75	0.98	1.07	1.27	1.02	1.82	0.86	1.03	0.21
228.0993	12.05	positive	1.08	1.44	1.01	0.70	1.52	0.96	1.08	1.23	1.17	1.40	1.08	1.28	1.54
228.9940	7.23	negative	0.88	0.72	1.39	1.11	0.63	1.08	0.30	1.01	0.87	0.56	0.10	0.73	0.26
229.0122	18.08	negative	1.39	0.74	0.72	0.62	0.73	1.06	0.23	0.37	1.19	0.86	0.12	1.21	0.17
229.0867	1.15	positive	0.90	0.41	0.44	0.72	0.71	0.68	0.51	0.24	0.75	1.40	0.35	0.71	0.28
229.1029	12.02	positive	1.13	1.71	1.07	0.61	1.82	0.98	1.17	1.43	1.28	1.49	1.19	1.43	1.90
229.1443	5.58	positive	0.49	0.80	0.35	0.93	0.99	0.81	0.81	0.86	0.41	0.77	1.52	0.87	0.29
230.0973	5.00	positive	0.91	0.70	0.90	0.35	0.60	0.97	1.16	0.75	0.63	0.87	0.29	0.85	0.24
230.9258	10.73	negative	0.97	1.00	0.97	0.94	0.99	0.98	0.95	0.98	0.99	0.96	0.86	1.00	0.79
231.0154	5.74	negative	1.74	11.59	0.62	4.19	29.55	1.86	2.34	2.94	0.98	7.60	11.39	15.78	3.76
231.0605	11.45	negative	0.59	1.01	0.88	0.83	0.66	1.07	1.04	1.12	0.57	1.35	0.48	0.38	1.80
231.1004	5.12	positive	0.80	0.72	0.82	0.08	0.15	0.96	1.24	0.80	0.57	0.94	10.29	0.87	0.11
232.9355	9.14	negative	0.97	0.92	1.27	1.22	1.14	1.05	0.91	1.16	0.98	0.79	1.25	1.10	1.24
233.0673	3.52	negative	1.06	1.00	0.88	0.93	0.80	1.12	0.35	0.69	0.86	1.19	0.01	0.89	0.58
233.1131	8.87	positive	1.08	2.10	0.93	1.16	1.56	1.01	1.52	0.84	0.92	2.26	1.85	1.78	1.35
233.1493	6.64	positive	0.86	0.94	0.90	1.40	0.85	1.19	1.27	0.37	1.03	0.91	6.58	0.99	0.25
234.0194	7.40	positive	0.76	0.81	0.48	0.32	0.52	0.74	0.54	0.63	0.72	1.19	0.36	0.60	0.19
236.1135	11.06	positive	2.24	64.27	326.28	17.41	1.79	329.94	593.92	487.02	9.24	11.96	12.82	1.92	9.08
236.9750	9.85	negative	0.80	0.85	0.71	0.77	0.87	0.78	0.60	0.64	0.88	0.90	0.52	0.84	0.64
237.0411	5.58	negative	1.28	1.65	2.93	3.06	2.04	1.46	2.00	1.23	1.43	1.71	2.10	2.23	1.14
238.9372	5.30	negative	0.56	1.59	1.24	0.14	0.14	0.84	5.07	0.24	0.69	3.60	0.22	0.15	0.19
239.0600	7.86	negative	1.09	1.00	0.86	0.70	0.84	1.13	1.21	0.74	0.97	1.16	0.19	0.83	0.61
239.1486	0.95	positive	2.02	1.27	0.65	1.27	0.83	1.21	1.40	0.77	1.46	2.22	0.94	1.05	1.24
241.0335	6.70	negative	1.07	1.32	0.51	0.99	1.17	0.92	1.51	1.08	0.99	1.29	0.54	0.97	1.85
242.0786	12.06	positive	1.02	1.78	0.93	0.67	2.06	0.89	1.01	1.28	1.08	1.27	1.01	1.66	1.81
242.0788	11.79	negative	1.11	1.22	1.25	1.11	1.19	1.19	1.48	1.02	1.03	1.15	0.59	1.07	0.76

242.9404	4.94	negative	0.97	0.99	0.42	0.32	0.36	1.02	1.13	0.74	0.72	1.09	0.06	0.60	0.05
243.0542	3.23	negative	0.82	0.92	0.48	0.95	0.55	0.76	0.09	0.25	0.82	0.96	0.05	0.66	0.49
243.0628	5.51	negative	0.84	0.66	0.85	1.56	1.05	1.16	1.15	0.67	1.11	0.70	9.14	1.04	0.86
243.0824	11.79	negative	1.12	1.23	1.32	1.13	1.24	1.21	1.50	0.97	1.01	1.13	0.51	1.07	0.72
244.0620	5.05	negative	1.19	1.03	0.66	0.99	1.01	0.84	0.02	0.16	1.18	1.13	2.73	1.16	1.09
244.0924	11.80	positive	1.10	1.26	1.30	1.08	1.24	1.16	1.54	1.06	1.04	1.18	0.60	1.08	0.76
244.1283	7.68	positive	0.81	0.73	1.31	0.88	1.31	1.04	2.15	1.34	0.84	1.09	65.52	1.28	10.75
244.9412	10.73	negative	0.94	1.03	0.93	0.86	1.01	0.93	0.95	1.00	0.95	1.05	0.80	1.03	0.71
245.0657	5.05	negative	1.20	1.03	0.70	0.99	1.07	0.84	1.44	0.24	1.20	1.14	3.32	1.15	1.14
245.0963	11.80	positive	1.10	1.25	1.30	1.07	1.23	1.17	1.54	1.05	1.03	1.18	0.58	1.08	0.76
247.1286	7.98	positive	1.10	0.75	0.73	1.12	0.85	1.05	1.06	0.47	0.97	0.83	4.33	1.05	1.00
248.0804	16.06	negative	1.00	1.08	1.02	1.13	0.83	0.97	0.99	0.89	0.98	1.05	0.97	0.88	1.10
248.1660	4.76	negative	1.17	1.07	1.00	1.23	1.21	1.13	0.78	1.12	1.02	0.74	0.98	1.18	0.77
248.9608	1.12	negative	0.97	1.15	1.28	1.17	1.13	1.20	1.44	1.33	0.97	0.89	1.60	1.00	1.67
248.9608	5.41	negative	1.22	0.85	1.12	1.05	1.32	0.95	0.29	1.52	1.22	0.30	1.22	1.18	9.96
249.0984	6.37	negative	1.09	0.98	0.88	1.04	0.85	0.97	0.51	1.00	0.67	0.71	0.69	1.16	0.04
249.1079	11.31	positive	1.06	4.73	2.71	1.28	3.08	1.80	22.13	5.84	1.13	6.50	1.13	2.37	1.63
249.1095	1.10	positive	1.13	1.14	1.25	1.18	1.22	1.03	1.09	1.27	1.08	1.02	1.32	1.01	1.34
250.0143	8.71	positive	0.77	0.76	0.53	0.36	0.56	0.85	0.62	0.70	0.68	0.95	0.28	0.65	0.18
250.9959	11.20	negative	0.97	1.24	0.82	0.53	0.80	0.92	1.03	0.88	0.88	1.39	0.79	0.93	0.76
251.0777	8.28	negative	1.09	0.94	0.94	1.03	0.75	1.02	1.17	1.07	1.07	1.18	0.10	0.83	0.21
251.0781	12.27	positive	0.88	0.88	0.82	1.00	0.83	0.82	0.78	0.74	0.89	0.79	0.38	0.78	0.31
251.9988	11.19	negative	1.01	1.24	0.52	0.12	0.55	0.73	0.96	0.51	0.59	1.44	0.39	0.88	0.47
252.1084	13.36	positive	4.29	17.28	45.95	11.94	3.75	35.66	100.96	49.72	5.71	14.98	15.95	2.75	4.45
253.0933	4.42	negative	1.03	0.78	0.67	0.59	0.64	0.80	0.58	0.95	0.61	0.37	0.36	0.86	0.32
253.1044	5.57	positive	1.29	0.78	0.95	0.74	0.90	0.75	0.84	0.90	1.16	0.77	0.83	0.75	1.22
253.1045	1.11	positive	1.08	1.05	1.12	1.03	1.13	1.06	1.06	1.17	1.06	1.01	1.18	1.04	1.15
254.0003	5.74	negative	2.04	3.45	6.91	0.60	3.30	0.85	1.99	0.83	1.39	5.45	1.32	1.25	5.77
254.0843	11.66	positive	4.82	31.90	114.05	13.84	4.84	62.23	287.25	188.28	3.42	17.73	38.43	1.44	11.48
254.1616	5.81	positive	0.99	0.86	0.87	0.80	0.78	0.91	1.16	0.70	0.84	0.82	0.20	0.68	0.51
254.9171	1.12	negative	0.90	1.11	1.27	1.09	1.06	1.23	1.51	1.32	0.91	0.83	1.64	0.95	1.68
254.9172	5.49	negative	1.23	0.70	0.80	0.74	0.98	0.82	0.24	2.07	1.17	0.56	0.42	0.89	4.41
255.0973	5.79	positive	0.92	0.75	0.90	1.06	0.86	1.25	1.04	0.36	1.22	1.08	1.49	0.76	0.40

255.1080	9.64	positive	1.01	0.95	0.44	1.18	1.35	0.91	0.88	0.77	1.62	1.77	0.59	1.42	1.58
256.0813	9.95	positive	0.91	0.92	0.77	0.93	0.77	0.93	0.93	0.67	1.00	1.11	1.99	0.73	0.48
258.1098	12.64	positive	1.67	5.58	3.93	1.08	9.64	1.51	5.08	6.23	1.50	8.72	0.38	1.49	9.32
258.9565	9.85	negative	1.00	0.96	1.02	0.99	1.10	0.97	0.92	1.06	1.05	0.87	0.98	1.05	0.94
259.0131	12.03	negative	1.36	2.11	1.48	0.46	1.86	1.23	1.62	2.08	1.52	2.54	2.10	1.58	3.48
259.0226	19.06	negative	1.82	0.85	0.38	0.66	0.58	1.27	0.48	0.35	1.42	0.88	0.14	1.35	0.32
259.1135	12.63	positive	1.75	5.36	3.76	1.07	9.19	1.48	4.87	6.07	1.43	8.34	1.57	1.41	4.33
260.1966	11.22	positive	0.46	0.61	0.61	0.85	0.60	0.83	0.18	0.03	0.71	0.93	4.30	0.65	0.89
261.1305	0.97	positive	2.07	1.32	0.75	1.22	0.80	1.29	1.32	0.89	1.47	2.13	0.86	1.08	1.25
261.1441	7.39	positive	0.76	0.72	0.84	1.15	0.77	1.14	1.05	0.50	1.00	0.69	3.77	0.94	0.73
262.0503	13.84	positive	0.85	1.41	0.90	0.65	0.62	0.83	1.04	1.19	0.97	1.53	0.64	0.83	0.31
264.9885	9.36	negative	1.06	1.56	1.09	0.96	1.08	1.03	0.99	0.96	1.03	1.70	0.00	1.09	0.95
265.0113	10.91	negative	1.10	2.67	0.95	0.77	2.10	0.99	1.76	1.39	0.83	2.51	0.75	2.28	4.03
265.0718	5.60	negative	0.65	0.50	0.69	0.66	0.68	0.57	0.52	0.47	0.47	0.89	0.91	0.66	0.19
265.1045	1.11	positive	1.01	1.01	1.12	1.06	1.05	1.03	1.05	1.11	0.99	0.96	1.35	1.00	1.20
265.1141	11.14	positive	0.86	1.29	0.60	0.19	0.68	0.75	0.99	0.87	0.73	1.48	0.31	0.69	0.35
265.9953	11.05	negative	1.10	0.88	0.91	0.71	1.11	1.12	0.95	1.12	0.87	0.75	0.27	0.95	0.82
266.0745	11.77	positive	1.08	1.15	1.01	1.17	1.15	1.01	0.95	0.81	1.03	1.06	0.63	1.05	0.90
266.1596	5.80	positive	0.63	0.54	1.25	0.86	0.56	1.15	3.60	0.94	0.85	0.85	0.26	0.64	0.33
267.0781	11.77	positive	1.09	1.14	1.00	1.15	1.19	0.99	1.00	0.80	1.06	1.13	0.59	1.04	0.88
267.0923	5.47	negative	0.77	0.26	0.64	0.56	0.55	0.74	0.73	0.26	0.94	0.60	2.94	0.57	0.81
267.1630	5.88	positive	0.53	0.68	1.25	0.87	0.41	1.19	3.76	0.92	0.87	0.88	0.62	0.65	0.94
268.1038	5.50	positive	1.02	0.58	0.80	1.71	1.25	1.02	0.85	0.49	1.20	0.58	24.08	1.33	1.20
269.1077	5.48	positive	1.04	0.50	0.76	1.75	1.27	1.04	0.82	0.43	1.23	0.51	26.89	1.39	1.21
270.0970	8.83	positive	1.01	1.09	0.81	0.86	0.75	1.03	1.16	0.80	1.01	1.30	0.47	0.75	0.53
270.8909	5.40	negative	1.28	1.05	0.52	1.16	1.06	1.25	0.46	1.27	1.16	0.38	0.29	1.28	1.19
271.0716	13.99	negative	0.70	0.89	0.71	0.44	0.55	0.61	0.71	0.70	0.84	1.60	0.53	0.49	1.40
271.2279	1.04	negative	3.06	1.16	1.00	1.20	0.81	0.92	1.13	0.78	0.74	1.16	1.94	0.72	0.80
273.0616	5.05	negative	0.85	0.85	1.09	0.71	0.61	1.12	1.22	0.92	0.92	0.97	0.02	0.70	0.45
274.0721	3.24	negative	0.84	0.93	0.49	0.96	0.60	0.78	0.14	0.30	0.84	0.99	0.10	0.71	0.49
274.8731	5.27	positive	1.23	1.02	1.00	0.72	0.84	1.17	0.81	1.09	1.25	0.65	0.51	0.78	1.52
275.0215	7.34	negative	2.01	2.92	0.71	1.42	3.31	0.82	2.14	0.95	1.57	3.74	1.08	3.21	2.74
275.0756	3.23	negative	0.85	0.92	0.50	0.92	0.59	0.75	0.11	0.28	0.82	0.99	0.07	0.71	0.48

275.1348	11.15	positive	0.69	1.02	1.92	0.33	0.67	1.15	3.41	3.60	0.61	1.92	0.40	0.67	1.36
276.1185	13.05	positive	0.76	2.94	1.09	0.75	0.93	0.94	1.67	1.15	0.71	3.32	1.47	0.86	0.94
276.8708	5.29	positive	1.40	1.11	0.62	0.63	0.59	1.44	0.69	1.04	1.48	0.73	0.59	0.91	1.87
277.0240	7.87	negative	1.27	1.29	1.02	0.86	1.17	1.37	0.83	0.67	1.33	1.40	1.53	1.54	0.92
277.0889	9.62	positive	0.91	0.73	0.61	1.29	0.92	0.95	0.79	0.79	1.41	1.20	0.90	0.95	1.27
277.1671	5.82	positive	0.85	0.43	0.34	0.20	1.16	0.60	0.61	0.67	0.94	0.66	0.18	1.25	0.54
279.0274	10.85	negative	1.15	1.97	0.50	0.01	1.91	0.98	1.59	1.25	0.64	1.86	0.04	1.88	2.49
279.1182	11.50	positive	0.77	0.75	1.03	0.86	0.86	1.09	12.13	2.08	0.72	0.84	0.61	0.95	0.37
280.0267	13.84	negative	1.02	1.75	0.92	0.74	0.70	0.96	1.00	1.22	0.98	1.77	0.78	0.99	0.40
280.9089	5.27	negative	1.37	1.22	1.21	0.63	0.86	1.57	1.17	1.03	1.67	0.95	0.73	0.84	2.08
280.9854	10.93	negative	1.36	5.81	0.85	0.07	3.90	0.79	3.61	1.25	0.60	6.49	0.20	3.67	7.16
281.0884	12.72	negative	197.85	3.41	0.77	1.01	0.66	135.38	16.74	3.55	206.92	4.32	3.06	13.01	1.11
281.1255	3.55	negative	0.84	0.66	0.92	1.58	0.81	0.52	0.77	0.72	1.63	1.20	0.57	0.99	1.12
283.0829	4.71	negative	0.94	0.84	1.16	1.43	0.70	1.17	1.17	0.88	1.60	1.45	0.05	0.88	0.58
283.2240	1.11	positive	0.99	1.05	1.05	1.04	1.09	1.04	1.01	1.05	0.98	1.00	1.06	1.01	1.10
283.2240	5.64	positive	1.31	0.79	0.68	0.75	0.91	0.74	0.83	0.93	1.19	0.79	0.59	0.76	1.29
283.2647	1.84	negative	0.48	0.65	0.88	0.55	0.85	0.55	0.59	1.10	1.00	0.49	0.39	0.88	0.51
284.0985	9.05	positive	0.92	0.77	0.70	1.24	1.42	0.94	1.08	0.30	1.13	0.84	23.23	1.13	1.38
285.0620	7.43	negative	1.22	1.03	1.30	2.45	1.14	1.25	1.43	0.99	2.10	2.03	0.39	1.23	1.12
285.1022	9.04	positive	0.82	0.48	0.46	1.36	1.43	0.92	1.03	0.08	1.09	0.46	30.59	1.00	8.61
286.0917	11.77	positive	0.90	0.92	0.92	0.89	0.79	1.01	1.16	0.80	1.01	1.11	0.10	0.71	0.54
287.0777	4.89	negative	0.94	1.01	0.86	0.63	0.75	0.94	1.00	0.85	0.86	1.02	0.47	0.78	0.56
287.9775	11.04	negative	1.07	1.01	0.87	0.56	1.19	1.13	0.95	1.17	0.85	0.83	0.12	1.01	1.02
288.9875	7.28	negative	1.04	1.00	1.03	1.12	1.03	1.12	0.40	0.86	0.95	0.87	0.10	1.08	0.41
289.0686	4.63	positive	1.13	0.97	0.88	0.89	0.71	0.94	0.95	0.80	0.92	1.10	0.32	0.82	0.47
289.0847	6.57	negative	1.05	1.08	1.05	1.00	0.95	1.09	1.15	0.91	1.02	1.10	0.85	0.97	0.21
289.0914	12.03	positive	1.26	2.33	1.48	0.47	2.17	1.12	1.56	2.26	1.43	2.84	2.82	1.60	6.17
289.1392	6.83	positive	1.07	1.18	0.73	0.49	0.96	1.06	1.05	1.05	0.70	1.12	0.01	0.96	0.38
291.0973	6.57	positive	1.02	0.97	0.97	0.88	0.84	0.95	0.97	0.74	0.99	1.07	0.54	0.86	1.43
291.1297	15.85	positive	1.13	0.78	1.15	0.89	1.29	1.22	2.17	1.78	1.20	1.12	1.30	1.72	1.19
293.0541	14.01	negative	0.77	0.95	0.84	0.68	0.79	0.78	0.81	0.85	0.95	1.28	0.79	0.73	0.05
293.1452	10.64	positive	0.98	1.53	0.74	0.57	1.27	0.91	1.03	0.88	0.83	1.59	0.40	1.33	1.05
293.1762	1.01	negative	1.44	0.77	0.69	0.79	0.84	0.80	4.50	1.13	1.26	1.19	2.43	0.47	1.32

293.1794	6.64	negative	1.42	0.63	1.43	1.98	1.11	0.53	0.07	0.79	1.10	0.74	0.89	0.77	1.11
293.2107	0.90	positive	4.46	5.17	16.72	8.64	5.67	3.43	157.88	61.23	5.05	6.46	136.76	1.95	6.71
294.9975	9.82	negative	0.76	0.83	0.90	0.89	0.64	0.90	0.59	0.53	0.86	0.91	0.08	0.56	0.44
295.0348	4.41	negative	14.07	6.72	0.86	0.83	0.98	1.33	16.11	3.20	1.00	7.81	9.82	0.59	2.83
295.0675	14.04	positive	0.90	0.80	0.88	0.85	0.99	0.87	0.72	0.89	1.03	0.79	0.82	0.93	0.61
295.1045	6.38	negative	1.02	0.83	0.76	0.81	0.73	0.84	0.67	0.94	0.67	0.74	0.54	1.00	0.20
296.0970	12.02	positive	1.53	0.93	1.02	0.49	0.76	1.01	0.83	1.22	1.46	1.19	0.38	1.32	0.94
297.0585	5.99	positive	1.32	0.75	1.44	0.35	0.56	0.57	1.31	1.30	1.01	1.04	0.21	0.49	1.22
297.1201	5.57	negative	1.08	0.76	0.75	0.69	0.49	0.83	0.76	0.85	0.74	1.81	0.44	0.68	0.48
297.1539	8.23	negative	1.17	1.12	1.00	1.18	1.10	1.10	0.87	1.14	1.06	0.95	1.42	1.12	0.85
297.2447	0.96	negative	1.17	0.89	0.87	1.15	0.76	0.81	1.27	0.80	1.05	1.55	1.06	0.62	1.00
298.0955	14.04	positive	0.85	6.18	1.16	0.67	0.72	0.91	2.54	1.41	0.70	7.46	3.57	0.68	0.62
298.1571	8.25	negative	1.16	1.13	1.00	1.19	1.12	1.09	0.90	1.14	1.05	0.93	1.08	1.12	0.83
299.0522	4.40	positive	0.93	0.90	0.92	0.72	0.77	1.06	1.20	1.05	0.84	1.06	0.17	0.90	0.64
299.0783	7.26	negative	0.94	1.09	1.27	1.31	0.91	1.22	1.61	1.23	1.32	1.50	0.16	1.17	1.19
299.0993	9.63	negative	0.94	0.76	0.67	1.36	0.92	1.04	0.95	0.95	1.43	1.09	0.89	0.92	1.11
301.0938	4.71	negative	0.87	0.74	0.83	0.98	0.70	0.91	0.99	0.93	1.09	1.24	0.31	0.81	0.62
301.1057	8.67	positive	2.68	14.06	1.40	0.97	4.94	3.16	6.91	5.36	2.71	15.53	9.59	3.34	1.36
302.1019	12.65	negative	0.69	5.53	3.75	1.13	9.72	0.61	3.73	5.13	0.54	8.08	0.19	1.37	8.33
303.0037	10.78	negative	3.58	0.50	4.81	1.37	1.23	3.66	82.12	11.26	1.24	1.13	66.47	0.37	1.99
303.0489	9.66	positive	1.17	1.25	0.90	0.82	1.19	1.13	1.19	0.95	0.89	0.97	0.03	1.26	0.74
303.0730	8.24	negative	0.97	1.04	0.81	0.86	1.20	1.08	1.15	0.90	1.67	2.08	0.26	0.86	0.70
305.0134	7.30	negative	1.21	1.05	0.26	0.09	0.17	1.70	0.73	1.07	1.17	1.04	0.00	0.23	0.51
305.0886	4.40	negative	0.96	1.03	1.03	0.87	0.86	1.16	1.30	1.08	0.97	1.18	0.19	1.01	0.79
305.0992	3.55	positive	1.01	0.95	0.88	0.82	0.84	0.99	1.11	0.90	0.88	1.03	0.46	0.81	0.65
305.1566	0.94	positive	1.38	1.39	0.76	1.33	0.97	1.51	0.93	0.77	1.59	2.16	0.81	1.19	1.41
306.0167	7.27	negative	1.33	0.98	0.22	0.00	0.00	2.09	0.78	1.03	1.42	0.67	0.00	0.10	0.67
307.1405	6.47	negative	1.13	1.19	1.25	1.01	1.08	1.22	1.43	0.98	0.86	0.82	0.21	1.07	0.38
308.0123	8.74	negative	0.84	0.65	0.56	0.41	0.63	0.90	0.45	0.82	0.69	0.66	0.35	0.73	0.20
308.0905	11.42	positive	0.46	2.12	0.17	0.12	1.08	0.28	0.12	1.00	0.32	1.09	0.00	1.26	0.34
309.1199	4.13	negative	0.95	0.92	0.87	0.89	0.70	0.94	0.95	0.85	0.97	1.11	0.18	0.78	0.53
309.1301	5.60	positive	1.19	0.90	0.78	0.82	0.83	0.87	0.64	1.01	1.11	0.96	0.47	0.85	1.48
309.1302	1.11	positive	1.02	1.04	1.13	1.06	1.08	1.01	0.96	1.12	0.94	0.93	1.18	1.07	1.22

309.2079	0.99	negative	1.63	1.11	2.50	1.75	1.45	0.84	10.71	4.39	1.79	1.49	3.08	1.11	2.38
311.1144	6.02	negative	0.88	2.28	1.82	2.70	1.52	1.77	1.78	1.39	1.21	98.16	0.85	1.55	211.51
311.1265	7.41	positive	0.76	1.42	0.86	0.48	0.85	0.78	0.87	1.15	0.67	1.81	0.83	0.84	0.23
311.1459	5.70	positive	1.24	0.76	0.74	0.77	0.78	0.76	0.91	1.04	1.34	0.86	0.54	0.79	1.52
311.1461	1.11	positive	1.04	1.03	1.04	1.03	1.05	0.96	0.98	1.10	0.97	0.91	1.14	1.02	1.19
311.1693	8.15	negative	1.17	1.13	0.99	1.15	1.07	1.13	0.93	1.12	1.04	0.99	1.47	1.10	0.88
311.2237	0.99	negative	1.66	1.22	1.65	1.74	1.37	0.87	19.30	4.55	1.51	1.61	5.98	1.04	1.58
312.0956	5.48	negative	0.88	0.47	0.62	0.70	0.66	0.83	0.95	0.40	1.12	0.60	2.93	0.71	1.07
312.1298	7.41	positive	0.75	1.40	0.85	0.47	0.84	0.77	0.86	1.15	0.66	1.79	0.81	0.84	0.22
312.1726	8.16	negative	1.18	1.13	0.99	1.17	1.06	1.13	0.91	1.11	1.04	0.99	1.46	1.11	0.88
313.0991	5.48	negative	0.89	0.49	0.62	0.69	0.64	0.82	0.95	0.39	1.10	0.93	2.93	0.72	1.09
313.1205	7.39	positive	0.77	1.43	0.87	0.46	0.85	0.77	0.87	1.17	0.67	1.80	0.82	0.84	0.27
313.1635	8.17	negative	1.12	1.10	0.94	1.13	1.01	1.10	0.84	1.06	1.01	0.95	1.38	1.07	0.82
313.2731	9.04	positive	0.98	0.98	0.85	0.84	0.79	0.98	1.18	0.93	0.94	1.25	0.80	0.81	0.61
314.1079	11.99	positive	1.16	0.87	0.88	0.58	0.71	0.86	0.81	0.96	1.21	1.16	0.21	1.00	0.70
315.1091	4.09	negative	0.83	0.85	1.27	1.21	0.73	1.00	1.49	1.04	1.10	1.27	0.42	0.89	0.87
315.1268	10.68	positive	1.08	1.02	0.70	0.57	1.13	1.09	0.98	1.07	0.92	0.98	0.51	1.16	0.60
316.9491	1.12	negative	0.97	1.16	1.31	1.17	1.14	1.21	1.49	1.35	0.96	0.85	1.65	0.96	1.67
316.9492	5.43	negative	1.10	0.87	1.06	1.11	1.49	0.97	0.21	2.07	1.40	0.54	1.33	1.29	3.32
319.0684	5.06	negative	0.84	0.84	1.07	0.68	0.60	1.12	1.18	0.91	0.91	0.95	0.02	0.68	0.44
319.1143	3.52	positive	0.81	0.78	0.88	0.53	0.79	0.91	0.98	0.98	0.51	0.66	0.21	0.83	0.35
321.1203	6.77	negative	0.96	1.23	0.87	0.47	0.94	1.04	0.89	1.03	0.57	0.73	0.09	0.92	3.33
322.1124	8.19	positive	0.94	1.02	0.83	0.88	1.43	1.09	1.07	0.94	1.92	2.28	0.27	0.94	0.68
322.9055	1.12	negative	0.93	1.14	1.34	1.18	1.12	1.29	1.69	1.37	0.93	0.84	1.78	0.96	1.84
323.1359	7.52	negative	1.07	0.92	0.99	0.96	0.85	1.08	1.23	0.96	1.03	1.21	0.77	0.85	0.52
323.1359	5.85	negative	0.87	0.88	1.05	1.96	1.10	0.95	1.08	1.23	1.75	1.83	0.70	1.40	1.33
323.1457	5.72	positive	1.41	0.75	0.72	0.48	0.73	0.76	1.11	1.04	1.27	1.02	0.41	0.61	1.65
323.1458	1.11	positive	1.04	1.04	1.07	0.99	1.05	0.99	1.00	1.16	0.92	0.93	1.24	0.94	1.23
324.0926	12.66	positive	3.38	38.86	206.32	6.40	3.00	177.43	603.92	489.35	2.20	12.06	17.52	1.17	7.31
325.1121	12.05	positive	1.85	2.45	1.53	0.49	2.26	1.61	1.61	2.34	2.09	2.92	3.09	1.70	6.87
325.1853	8.07	negative	1.16	1.14	1.00	1.12	1.05	1.12	0.95	1.11	1.05	1.02	1.46	1.08	0.88
326.1887	8.08	negative	1.16	1.13	0.98	1.13	1.06	1.13	0.95	1.11	1.05	1.02	1.46	1.07	0.88
326.9023	4.94	negative	0.98	0.99	0.38	0.26	0.31	1.02	1.13	0.70	0.71	1.07	0.02	0.56	0.02

327.0678	8.19	positive	0.92	0.95	0.73	0.87	1.24	1.00	0.87	0.77	1.75	2.07	0.27	0.82	0.66
327.1128	3.65	negative	0.99	1.02	0.73	0.70	0.77	0.97	0.60	0.67	0.77	0.94	0.19	1.03	0.60
327.1801	8.08	negative	1.14	1.10	0.69	0.77	1.01	1.13	0.90	1.07	1.03	1.00	1.17	1.12	0.88
329.0889	4.68	negative	0.95	0.84	1.17	1.42	0.71	1.19	1.18	0.89	1.62	1.46	0.04	0.89	0.56
329.1097	11.09	negative	1.15	0.90	0.94	1.24	0.73	1.15	1.08	0.95	1.11	1.20	0.75	1.18	0.65
330.0922	4.70	negative	0.94	0.84	1.16	1.41	0.70	1.18	1.18	0.87	1.61	1.46	0.02	0.88	0.55
330.1386	9.73	positive	1.05	1.00	0.40	1.16	1.49	0.89	0.91	0.75	1.68	1.92	0.49	1.59	1.06
332.1697	8.57	positive	1.73	3.27	1.04	1.04	1.76	1.73	2.52	1.94	1.63	3.16	2.83	1.49	1.04
332.8570	4.08	positive	1.49	1.56	0.39	0.98	1.22	0.53	0.72	0.36	1.52	2.32	2.30	1.48	1.03
333.0836	4.92	negative	1.35	1.17	1.06	1.08	0.75	0.91	0.98	0.84	0.91	1.06	1.46	1.31	0.52
335.1302	6.09	positive	1.63	0.85	4.14	5.07	4.06	2.68	0.92	5.27	8.80	7.95	6.84	0.65	8.04
335.1355	6.52	negative	0.92	1.41	1.02	0.34	1.03	1.24	1.19	1.11	0.97	1.78	0.11	0.91	0.06
337.0784	11.66	negative	0.95	0.91	0.92	0.70	0.80	1.01	1.07	0.87	0.81	1.12	0.32	0.87	0.57
337.1098	11.88	positive	1.08	0.98	0.85	1.03	0.86	1.00	1.02	0.83	0.98	1.06	2.10	0.94	0.81
338.1227	8.18	positive	1.21	1.09	0.90	0.82	1.35	1.21	1.21	0.83	0.78	0.81	0.27	1.16	0.69
338.3410	0.99	positive	4.88	0.67	0.70	0.69	0.35	2.10	0.70	0.18	1.68	1.01	0.13	0.54	0.25
338.8945	4.09	negative	1.56	1.73	0.45	1.06	1.37	0.58	0.75	0.56	1.63	2.46	2.49	1.62	1.10
339.0736	5.91	negative	0.85	2.07	1.36	2.08	2.33	1.99	0.93	1.33	0.99	1.53	0.01	2.25	0.60
339.1402	1.10	positive	1.03	1.09	1.18	1.05	1.09	1.01	1.03	1.24	1.01	0.95	1.31	0.99	1.33
339.1404	5.79	positive	1.46	0.73	0.72	0.32	0.48	0.66	1.10	1.02	1.32	1.02	0.50	0.39	1.79
339.2015	8.01	negative	1.11	1.09	0.98	1.08	1.01	1.09	0.97	1.07	1.04	1.00	1.42	1.05	0.86
340.0472	11.79	negative	1.11	1.21	1.22	1.13	1.21	1.18	1.42	0.99	1.04	1.14	0.57	1.08	0.75
340.0770	5.91	negative	0.86	2.08	1.36	2.09	2.31	2.00	0.92	1.34	0.99	1.52	0.01	2.25	0.15
340.2048	8.01	negative	1.13	1.10	1.00	1.06	1.01	1.10	0.97	1.07	1.04	1.00	1.41	1.06	0.87
341.0788	5.90	negative	1.09	2.75	1.77	2.70	3.03	2.60	1.18	1.69	1.29	1.99	1.51	2.95	0.77
341.1103	12.66	negative	23.67	1.06	0.63	1.02	0.52	25.47	5.11	0.94	37.85	0.72	1.17	3.99	0.25
341.1104	12.04	negative	1.30	1.98	1.41	0.63	1.79	1.21	1.49	1.92	1.42	2.40	2.12	1.49	3.97
341.1972	8.01	negative	1.15	1.00	0.84	0.87	0.96	1.04	0.88	1.05	0.97	0.95	1.40	0.91	0.78
342.1031	12.63	positive	3.66	49.90	290.16	5.85	38.49	214.59	854.78	741.06	0.53	130.46	172.75	0.63	635.95
342.1139	12.04	negative	1.30	1.96	1.38	0.62	1.78	1.20	1.48	1.89	1.40	2.40	2.14	1.49	3.96
342.1396	8.03	positive	0.98	1.05	0.90	0.76	0.87	1.03	1.06	0.77	0.99	1.18	0.45	0.82	0.45
343.1153	12.04	negative	1.28	1.97	1.40	0.60	1.82	1.19	1.48	1.89	1.43	2.39	2.13	1.47	4.01
345.1145	5.85	positive	1.34	0.60	0.78	0.80	0.48	0.59	1.45	0.87	2.35	2.11	0.17	0.45	2.08

348.8972	5.37	negative	1.28	1.07	0.73	0.79	0.76	1.23	0.77	1.09	1.15	0.62	1.35	1.15	1.38
349.1519	6.32	negative	0.99	1.73	1.26	0.42	1.07	1.44	1.47	1.19	0.43	0.70	0.07	1.03	0.16
349.1819	0.93	positive	1.47	1.05	0.70	1.04	0.77	1.10	0.88	0.63	1.28	2.11	0.70	0.87	1.06
351.1035	6.16	positive	0.63	0.83	0.60	3.43	0.41	0.74	0.92	0.54	4.57	7.34	0.04	0.55	1.15
351.1674	5.59	negative	1.08	1.05	1.72	1.45	0.88	1.12	1.53	1.09	1.05	1.20	2.27	1.10	0.94
357.1204	6.02	negative	0.86	1.11	1.45	1.61	0.89	1.16	1.35	1.05	1.18	1.53	0.43	1.03	0.88
358.1843	13.98	positive	0.89	1.30	0.83	0.66	0.65	0.83	3.35	1.00	0.93	1.87	0.66	0.77	0.50
359.1480	0.95	positive	0.67	0.54	0.95	1.11	0.62	0.73	0.75	0.93	1.16	1.35	0.49	0.71	1.15
360.1492	12.03	positive	1.19	2.05	1.32	0.53	1.95	1.16	1.35	1.96	1.50	2.28	2.31	1.50	3.95
361.1515	6.27	negative	0.99	1.65	1.23	0.78	1.05	1.39	1.33	1.15	0.79	1.10	0.58	1.04	0.37
363.1671	6.14	negative	0.92	1.93	1.52	0.41	1.08	1.80	1.96	1.46	0.48	0.63	0.32	1.17	0.43
364.0647	18.38	positive	0.89	0.44	0.32	0.64	0.93	0.60	0.48	0.22	0.80	0.59	1.87	0.77	0.38
364.8716	5.31	negative	1.41	1.23	1.45	0.41	0.33	1.79	1.48	1.06	1.98	1.18	0.05	0.72	2.29
365.1042	12.03	positive	1.28	1.53	1.16	0.69	1.47	1.11	1.10	1.45	1.34	1.69	1.74	1.31	2.71
365.1193	5.90	positive	1.71	0.48	0.95	0.38	0.43	0.59	1.78	0.77	0.98	0.48	0.02	0.38	0.74
365.1835	5.51	negative	0.99	1.07	1.39	1.24	0.98	1.10	1.37	1.12	1.04	1.07	0.31	0.98	0.97
366.1078	12.03	positive	1.28	1.54	1.14	0.70	1.46	1.10	1.10	1.45	1.34	1.69	1.75	1.31	2.74
367.1093	12.03	positive	1.26	1.53	1.11	0.67	1.47	1.06	1.06	1.43	1.30	1.66	1.77	1.33	2.72
367.1715	1.11	positive	1.01	1.04	1.11	0.99	1.05	0.97	0.99	1.09	0.96	0.94	1.31	1.02	1.26
369.0410	14.01	negative	0.82	0.96	0.83	0.71	0.80	0.80	0.79	0.85	0.93	1.23	0.79	0.74	0.53
369.0779	6.18	positive	1.56	1.03	1.09	0.98	1.15	1.04	1.18	1.68	1.60	1.43	0.36	1.08	2.12
371.1360	5.87	negative	0.92	0.94	1.25	1.06	0.78	1.01	1.20	1.03	0.85	0.85	0.26	0.93	0.57
375.2041	6.06	negative	0.87	1.29	1.33	1.27	1.05	1.31	1.37	1.16	0.89	1.12	1.06	1.05	0.73
376.1956	8.61	positive	1.85	3.31	1.14	1.23	1.87	1.86	2.72	2.04	1.72	3.36	3.39	1.66	1.30
377.9951	13.79	negative	1.02	1.52	0.77	0.68	0.66	0.85	0.79	1.00	0.90	1.68	0.65	0.93	0.54
379.0991	6.02	positive	1.69	0.61	1.47	1.39	0.73	0.60	1.62	1.14	2.53	2.58	0.24	0.62	2.26
379.1576	8.10	negative	1.07	1.12	0.73	1.00	0.57	0.96	0.66	1.39	1.18	0.60	1.30	0.99	1.56
379.1989	5.45	negative	0.74	0.66	1.08	0.94	0.83	0.94	1.33	0.97	0.94	0.70	0.23	0.71	0.45
381.0784	12.04	positive	1.19	1.48	1.01	0.59	1.23	1.04	1.11	1.24	1.19	1.81	1.11	1.15	1.89
381.0936	5.90	positive	1.20	0.72	1.04	0.76	0.76	1.19	1.46	0.78	0.75	0.49	0.02	0.82	0.43
381.1298	0.95	positive	0.70	0.60	1.06	1.13	0.65	0.76	0.74	1.11	1.05	1.34	0.62	0.78	1.33
381.3389	1.00	negative	0.84	0.94	0.95	1.50	0.79	0.96	1.17	0.63	0.89	1.17	4.02	0.78	0.84
382.1332	0.95	positive	0.74	0.60	1.08	1.08	0.64	0.78	0.67	1.10	1.04	1.32	0.62	0.77	1.35

383.1668	1.12	positive	1.08	1.13	1.12	1.15	1.18	1.91	1.55	1.21	1.01	0.98	1.33	1.06	1.31
383.1669	5.80	positive	1.81	0.61	0.62	0.45	0.39	0.57	0.94	1.01	1.42	0.90	0.34	0.26	1.84
384.9366	1.12	negative	1.01	1.20	1.40	1.19	1.19	1.26	1.69	1.42	0.98	0.91	1.86	0.95	1.86
384.9367	3.42	negative	2.95	0.51	0.39	0.00	0.35	0.82	0.75	0.36	1.03	1.08	65.87	1.16	0.10
385.1154	5.66	negative	0.88	0.77	0.74	0.74	0.49	0.82	0.90	0.85	0.91	1.06	0.05	0.57	0.50
386.1187	5.62	negative	0.87	0.77	0.73	0.74	0.49	0.81	0.90	0.84	0.90	1.04	0.00	0.57	0.50
387.1156	12.04	negative	1.28	1.94	1.39	0.61	1.75	1.19	1.44	1.90	1.41	2.33	2.03	1.47	3.76
387.1310	5.91	negative	1.36	0.65	0.98	0.67	0.61	0.92	1.49	0.87	0.88	0.47	0.08	0.61	0.61
388.1191	12.04	negative	1.28	1.95	1.37	0.62	1.74	1.16	1.43	1.87	1.40	2.36	2.02	1.46	3.77
389.1206	12.04	negative	1.32	1.98	1.41	0.62	1.77	1.19	1.47	1.93	1.43	2.37	2.05	1.50	3.83
389.1367	5.90	negative	1.54	0.51	1.15	0.66	0.50	1.02	1.75	0.97	1.03	0.28	0.06	0.59	0.67
390.2113	8.57	positive	1.42	2.57	1.10	1.10	1.46	1.44	2.07	1.69	1.45	2.64	2.49	1.38	1.05
390.8930	1.12	negative	0.99	1.28	1.50	1.34	1.19	1.40	2.01	1.54	0.97	0.90	2.11	0.98	2.15
391.1194	7.38	positive	0.74	0.72	0.31	0.17	0.47	0.59	0.25	0.60	0.65	1.02	0.63	0.59	0.11
391.1986	6.62	negative	0.93	1.02	1.40	1.03	0.89	1.12	1.26	1.06	0.73	0.70	0.80	0.96	0.42
393.1328	4.70	positive	0.90	0.97	0.72	0.85	0.66	0.89	0.96	0.76	0.85	1.04	0.28	0.78	0.34
393.1729	8.02	negative	1.31	1.00	0.76	0.60	0.47	1.20	0.78	1.29	0.92	0.81	1.10	0.87	1.23
399.1708	4.71	negative	0.92	1.03	0.77	0.91	0.66	0.93	0.97	0.74	0.87	0.98	0.39	0.76	0.42
401.1817	5.45	negative	1.17	1.30	0.78	1.17	1.17	1.18	0.54	1.55	1.27	0.52	0.25	1.13	1.37
403.1635	6.42	negative	1.04	1.28	1.01	0.38	1.14	1.10	1.17	1.01	0.22	0.20	0.36	1.09	0.09
405.2147	6.47	negative	1.08	1.07	1.57	1.13	0.88	1.15	1.31	1.06	0.74	0.76	0.84	1.08	0.28
406.2062	8.58	positive	1.82	3.65	1.23	1.13	1.91	1.83	3.03	2.05	1.73	3.93	3.60	1.64	1.22
409.1094	5.63	positive	1.16	0.89	0.56	0.33	0.48	1.03	0.82	1.26	1.23	0.83	0.06	0.33	0.88
410.8641	4.94	negative	0.95	0.97	0.35	0.23	0.28	1.02	1.09	0.69	0.68	1.06	0.01	0.53	0.00
413.1011	7.39	positive	0.77	0.75	0.40	0.24	0.55	0.65	0.33	0.67	0.70	1.06	0.62	0.64	0.34
415.1470	13.39	negative	0.89	1.21	0.66	1.52	1.03	1.03	0.80	0.24	1.25	1.55	0.67	1.01	1.00
415.1987	3.34	negative	1.21	1.31	0.84	0.99	1.04	1.10	1.27	0.98	1.08	1.67	1.15	1.00	0.95
417.1510	5.41	positive	0.70	0.84	1.08	0.81	0.68	0.89	1.60	0.69	0.87	1.36	0.24	0.62	0.39
417.2117	8.05	negative	1.15	1.13	1.00	1.18	1.09	1.17	0.99	1.07	1.09	0.97	1.17	1.06	0.87
420.0473	12.65	negative	1.18	7.52	39.59	1.78	1.40	27.97	120.42	96.33	0.77	2.84	3.50	0.72	1.42
421.1880	5.79	negative	0.84	1.07	1.19	1.19	0.87	1.13	1.31	1.10	0.96	1.10	0.91	0.86	0.75
423.1527	8.02	negative	1.11	1.13	1.11	1.23	0.88	1.00	0.46	0.93	1.08	0.86	1.46	1.11	0.60
425.0836	5.62	positive	0.70	0.76	0.72	0.77	0.48	0.67	0.96	0.69	0.74	1.26	0.00	0.56	0.28

431.1940	4.66	negative	1.14	1.10	0.90	0.94	0.89	1.07	1.14	0.95	0.98	1.23	0.77	0.97	0.71
431.2220	8.51	negative	1.08	1.16	2.34	1.21	0.90	1.60	3.57	2.79	0.97	1.40	2.41	0.99	0.64
431.3182	1.06	negative	1.15	0.66	0.88	1.14	0.81	0.99	1.10	1.02	0.96	0.63	0.28	0.96	0.68
433.1114	7.71	positive	1.07	1.17	0.83	0.70	1.19	1.05	0.94	0.91	0.96	1.21	0.89	1.33	0.55
433.2094	4.19	negative	1.00	1.02	0.78	0.86	0.86	1.00	1.02	0.90	1.00	1.36	0.71	0.91	0.74
436.0427	15.70	negative	1.23	3.31	8.75	1.15	0.83	5.28	35.70	21.60	0.43	1.85	6.02	0.74	1.44
437.2046	6.62	negative	0.93	1.00	1.44	0.98	0.85	1.13	1.24	1.04	0.69	0.74	0.70	0.96	0.28
439.0775	12.05	negative	1.40	1.84	1.33	0.60	1.69	1.24	1.35	1.77	1.51	2.20	1.87	1.45	3.15
439.1411	13.40	positive	0.90	1.25	0.64	1.35	1.08	1.00	0.81	0.28	1.27	1.58	0.62	1.01	1.18
440.0809	12.05	negative	1.39	1.83	1.30	0.61	1.67	1.22	1.33	1.75	1.49	2.18	1.87	1.44	3.13
441.0771	12.06	negative	1.39	1.83	1.34	0.59	1.68	1.25	1.34	1.76	1.48	2.20	1.84	1.44	3.11
447.0548	13.82	negative	1.01	6.94	17.74	0.94	0.50	13.02	57.93	34.80	0.41	1.95	6.66	0.56	0.47
450.2322	8.60	positive	1.81	3.39	1.12	1.13	1.94	1.81	2.89	2.11	1.70	3.59	3.42	1.67	1.27
453.0928	12.08	negative	1.36	1.83	1.26	0.45	1.54	1.09	1.20	1.73	1.77	2.54	1.49	1.38	4.38
455.1027	12.06	negative	1.40	1.79	1.32	0.65	1.68	1.25	1.38	1.74	1.50	2.14	1.85	1.47	3.05
457.1099	3.47	positive	1.08	0.91	1.27	1.66	1.42	1.41	1.34	0.73	0.84	0.51	0.26	0.81	0.49
457.2043	1.12	positive	1.03	1.13	1.13	1.15	1.12	1.09	1.06	1.26	1.00	1.01	1.42	1.06	1.39
458.8798	1.12	negative	0.84	1.29	1.62	1.22	1.22	1.50	2.07	1.67	1.01	0.74	2.31	0.93	2.47
461.1518	13.39	negative	0.89	1.20	0.63	1.44	1.02	0.96	0.73	0.22	1.21	1.50	0.65	0.98	0.98
463.1463	3.47	negative	1.08	0.95	1.27	1.74	1.41	1.45	1.41	0.75	0.86	0.54	0.29	0.85	0.53
464.2473	8.56	positive	1.49	2.93	1.17	1.12	1.57	1.55	2.41	1.87	1.51	3.05	2.17	1.48	1.21
476.1600	12.06	positive	1.49	0.87	0.95	0.52	0.74	0.97	0.81	1.11	1.46	1.07	0.39	1.25	0.85
476.2761	7.71	positive	2.29	2.09	6.64	2.61	2.82	3.09	22.83	15.61	1.57	2.42	15.95	3.53	1.26
477.0651	11.95	negative	0.43	21.52	105.08	2.32	0.54	95.33	189.85	93.24	3.20	4.88	24.99	0.75	1.26
478.2629	6.75	positive	0.96	1.19	0.97	1.03	1.22	1.16	1.21	1.24	1.05	1.07	2.25	1.08	0.44
479.2503	7.08	negative	0.90	1.03	1.01	0.86	0.92	1.05	1.18	0.88	0.77	0.86	0.11	0.75	0.33
480.2428	8.58	positive	1.80	3.71	1.21	1.13	1.96	1.86	3.01	2.05	1.71	3.91	3.51	1.66	1.27
482.2224	6.04	positive	0.25	1.55	1.54	1.71	1.34	1.41	1.09	1.05	0.41	0.92	1.56	1.30	0.01
487.1790	6.01	positive	1.41	0.65	1.04	0.64	0.51	0.67	1.39	1.17	1.34	1.11	0.55	0.51	1.44
492.1039	13.34	negative	3.83	14.14	39.25	10.69	2.96	29.74	83.93	42.75	4.57	11.78	14.53	2.41	3.38
494.2581	6.70	positive	0.85	1.07	1.23	1.14	1.18	1.26	1.63	1.26	1.03	1.03	2.64	1.16	0.00
503.1611	14.65	negative	2.15	13.55	3.79	1.13	7.73	3.16	9.27	7.36	1.86	19.59	2.27	1.89	8.04
505.2470	7.98	negative	1.42	2.23	1.10	0.91	1.97	1.66	0.70	0.88	1.60	3.02	4.33	2.79	1.53

505.2566	10.05	negative	1.66	0.23	1.07	1.56	1.02	0.79	17.16	5.86	1.02	0.91	62.75	1.19	1.23
513.1133	13.39	negative	0.90	1.22	0.63	1.39	1.02	0.99	0.73	0.22	1.23	1.56	0.62	1.00	1.09
525.2453	3.84	positive	1.09	0.76	1.10	0.75	0.83	1.86	2.66	2.71	0.94	1.32	1.83	0.94	0.76
527.1577	12.02	positive	1.44	2.77	1.55	0.36	2.59	1.21	1.43	2.46	1.71	3.50	3.32	1.95	6.46
539.2247	4.47	positive	1.98	0.80	1.70	2.35	1.49	0.71	0.91	3.53	3.00	1.55	0.03	1.19	0.73
539.2880	9.03	positive	1.00	1.02	0.86	0.86	0.85	1.01	1.22	0.94	1.00	1.31	0.88	0.86	0.53
571.4702	8.37	positive	1.12	1.05	0.84	0.83	0.89	1.06	0.88	1.12	0.87	1.16	0.69	0.99	0.68
573.4853	8.36	positive	1.17	1.10	0.92	0.93	0.96	1.01	0.95	1.26	0.94	1.25	0.75	1.04	0.72
573.4857	10.36	positive	1.00	1.14	0.96	0.80	1.02	1.02	1.34	1.22	0.94	1.22	0.94	1.02	0.95
575.5012	10.34	positive	1.08	1.13	1.01	0.87	1.06	1.03	1.33	1.23	1.00	1.28	0.99	1.04	0.94
576.5047	10.34	positive	1.07	1.13	1.01	0.84	1.06	0.99	1.35	1.27	0.97	1.28	0.99	1.04	0.95
577.5167	8.34	positive	1.09	0.91	0.77	0.93	0.87	0.90	0.95	1.06	0.91	0.93	0.80	0.98	0.58
585.4498	1.11	positive	0.98	0.91	0.58	0.56	0.75	1.24	0.76	0.58	0.67	0.92	0.80	0.88	0.56
591.1749	3.15	negative	0.89	0.94	0.86	0.91	0.71	0.93	0.97	0.74	0.87	0.67	0.00	0.73	0.58
593.2742	6.69	positive	0.87	1.07	0.84	1.02	1.08	1.06	1.83	0.39	0.84	1.38	0.43	1.18	0.28
593.2759	12.14	negative	0.48	1.42	1.49	1.68	0.75	1.16	9.02	1.00	0.83	2.53	23.54	0.53	0.72
595.1644	8.44	positive	1.25	1.20	1.00	0.87	1.12	1.31	1.34	1.18	0.98	1.02	0.32	1.19	0.65
595.2917	12.05	negative	1.36	2.97	1.83	2.83	1.29	2.07	9.23	1.13	1.41	3.03	22.77	1.53	0.77
596.1678	8.43	positive	2.11	0.00	1.09	0.00	2.78	3.28	2.33	1.01	0.00	1.17	0.73	2.94	0.00
611.1573	9.66	positive	1.13	1.18	0.89	0.79	1.12	1.13	1.15	0.95	0.87	0.91	0.00	1.20	0.67
613.1557	17.01	positive	1.22	1.22	1.28	0.81	0.94	1.31	1.84	1.56	1.15	1.26	0.23	1.16	0.70
669.4559	6.87	negative	1.08	1.00	1.01	1.08	0.98	1.18	1.19	0.90	0.97	1.11	0.82	0.90	0.61
671.4711	6.85	negative	1.12	0.83	1.00	1.15	0.99	1.18	1.06	0.83	1.01	0.93	0.67	0.92	0.60
672.4748	6.85	negative	1.13	0.82	1.00	1.16	0.99	1.19	1.07	0.84	1.02	0.93	0.67	0.93	0.56
693.4624	6.82	negative	1.19	0.82	0.94	1.05	0.89	1.20	0.89	0.72	1.00	0.91	0.54	0.93	0.49
695.4777	6.80	negative	1.19	0.73	0.87	1.13	0.90	1.18	0.87	0.67	1.05	0.84	0.50	0.97	0.51
696.4814	6.80	negative	1.20	0.72	0.86	1.13	0.89	1.17	0.86	0.66	1.05	0.84	0.50	0.96	0.46
707.1257	9.65	negative	1.10	1.11	0.89	0.76	0.91	1.19	1.24	0.95	0.84	0.82	0.02	1.04	0.51

Supplemental Table 3-5. Average fold change of metabolites identified with reference standard in all treatments compared to control

Metabolites	Cold	Heat	Drought	Salinity	High light	Cold x drought	Heat x drought	High light x drought	Cold x salinity	Heat x salinity	High light x heat	High light x cold	High light x salinity
Adenine	0.84	0.71	0.70	1.50	1.20	1.00	1.09	0.41	0.97	0.64	4.89	1.17	0.13
Adenosine	1.02	0.58	0.80	1.71	1.25	1.02	0.85	0.49	1.20	0.58	24.08	1.33	1.20
Alanine	2.22	5.69	1.26	1.15	2.15	2.29	4.47	2.66	2.10	6.15	5.31	1.82	1.25
alpha-Ketoglutaric acid	0.83	0.80	0.67	1.12	0.92	0.66	0.47	0.52	0.96	0.79	0.31	0.88	0.48
Arginine	0.74	0.96	0.78	0.53	0.65	0.67	0.77	0.82	0.87	1.68	0.64	0.58	0.35
Asparagine	0.88	1.28	0.82	0.51	0.69	0.89	1.10	0.91	0.76	1.53	0.47	0.74	0.48
Aspartic acid	1.26	0.59	0.75	0.74	0.50	0.86	0.67	0.75	1.13	0.63	0.23	0.94	0.41
Citric acid	0.88	1.26	0.88	0.32	0.59	0.70	0.73	0.82	0.69	2.09	0.31	0.62	0.13
Citrulline	1.04	0.32	0.57	0.68	0.53	0.79	0.61	0.73	0.98	0.55	0.25	1.11	0.40
Dihydroxyacetone phosphate	6.33	0.97	0.74	1.65	1.46	1.06	0.72	0.95	3.11	1.13	1.76	3.62	0.91
Fructose	1.22	1.29	0.98	0.81	1.18	1.31	1.05	0.72	1.19	1.43	1.06	1.38	0.99
Fructose 6-phosphate	1.36	2.11	1.48	0.46	1.86	1.23	1.62	2.08	1.52	2.54	2.10	1.58	3.48
Fumaric acid	1.37	3.35	0.74	1.69	6.02	1.26	1.62	1.41	1.04	2.99	2.94	3.84	2.11
gamma-Aminobutyric acid	0.85	1.30	2.29	1.38	1.36	1.80	3.86	2.00	0.87	1.14	3.42	1.14	0.41
Glucose	1.14	1.40	0.68	1.02	1.29	0.98	0.65	0.37	1.13	1.52	1.10	1.34	1.02
Glucose 6-phosphate	1.82	0.85	0.38	0.66	0.58	1.27	0.48	0.35	1.42	0.88	0.14	1.35	0.32
Glutamic acid	1.04	0.84	0.87	0.61	1.04	1.16	1.02	1.19	0.81	0.79	0.15	0.78	0.60
Glutamine	1.04	1.79	0.84	0.79	1.23	0.93	1.32	0.90	0.92	1.09	0.45	1.29	1.13
Glycine	1.33	1.63	0.69	0.92	3.01	0.88	1.37	1.24	1.31	2.26	1.05	2.39	1.57
GSH	0.46	2.12	0.17	0.12	1.08	0.28	0.12	1.00	0.32	1.09	0.00	1.26	0.34
GSSG	1.22	1.22	1.28	0.81	0.94	1.31	1.84	1.56	1.15	1.26	0.23	1.16	0.70
Guanine	0.94	0.79	0.68	1.26	1.40	0.93	1.08	0.30	1.11	0.85	24.16	1.12	0.96
Guanosine monophosphate	0.89	0.44	0.32	0.64	0.93	0.60	0.48	0.22	0.80	0.59	1.87	0.77	0.38
Histidine	1.26	2.19	1.13	0.72	1.32	1.06	1.29	1.27	1.02	2.63	0.86	1.18	1.51
Leucine	1.27	11.42	2.70	1.20	2.40	1.63	4.30	3.47	1.01	11.45	11.37	1.46	1.19
Lysine	0.87	4.43	1.67	0.94	0.97	1.01	2.19	1.88	0.87	4.78	4.32	0.76	1.01
Malic acid	1.16	1.39	0.85	1.13	1.52	0.90	1.16	0.84	1.04	1.54	0.87	1.46	0.83
Maltose	23.67	1.06	0.63	1.02	0.52	25.47	5.11	0.94	37.85	0.72	1.17	3.99	0.25
Mannitol	1.69	13.22	2.58	1.26	1.76	1.67	4.47	3.94	1.15	13.15	15.69	1.40	4.07

Ornithine	0.82	0.45	0.53	0.54	0.61	0.66	0.57	0.70	1.04	1.14	0.18	0.48	0.30
Phenylalanine	2.51	5.96	2.11	1.18	2.19	2.93	2.71	2.43	2.07	5.82	7.27	3.01	1.19
Proline	0.93	2.48	1.80	0.98	1.23	0.98	2.23	1.90	0.74	2.64	1.42	1.06	0.38
Pyruvic acid	1.49	1.56	0.52	1.03	1.23	0.63	0.78	0.50	1.48	2.25	3.14	1.47	1.04
Raffinose	2.15	13.55	3.79	1.13	7.73	3.16	9.27	7.36	1.86	19.59	2.27	1.89	8.04
Ribose 5-phosphate	1.39	0.74	0.72	0.62	0.73	1.06	0.23	0.37	1.19	0.86	0.12	1.21	0.17
Serine	0.74	1.03	0.88	0.86	0.78	1.03	1.04	1.09	0.73	1.24	0.63	0.67	1.29
Shikimic acid	1.16	1.20	0.94	0.86	1.06	1.21	1.52	0.95	0.79	1.08	0.42	1.05	0.23
Succinic acid	0.98	2.00	1.51	1.26	1.45	0.92	2.58	1.58	0.69	1.71	5.35	1.10	0.98
Sucrose	1.30	1.98	1.41	0.63	1.79	1.21	1.49	1.92	1.42	2.40	2.12	1.49	3.97
Threonine	1.00	1.77	1.02	0.94	1.83	0.89	1.28	1.14	0.93	2.18	1.54	1.21	1.37
Tryptophan	2.58	11.23	1.79	0.99	2.66	1.94	3.95	2.85	1.85	12.17	5.70	2.35	1.92
Tyrosine	1.61	11.48	2.51	1.26	1.72	1.56	3.94	3.52	1.18	11.53	13.84	1.32	3.69
Urea	5.70	0.95	1.25	1.42	1.20	0.97	1.31	0.92	1.81	1.27	0.79	1.00	2.68
Valine	1.48	4.72	2.01	1.02	1.99	1.67	2.19	2.30	1.17	4.45	3.47	1.69	1.01
Xylose	1.13	1.58	0.93	1.07	1.42	1.30	1.32	1.01	1.00	1.50	0.83	1.10	0.18

Supplemental Table 3-6. Standard compounds used for feature identification

Adenine
Adenosine
Citric acid
D-(−)-Fructose
D-(+)-Glucose
D-(+)-Maltose monohydrate
D-(+)-Raffinose pentahydrate
D-(+)-Xylose
D-Fructose 6-phosphate disodium salt hydrate
D-Glucose 6-phosphate sodium salt
Dihydroxyacetone phosphate dilithium salt
D-Mannitol
D-Ribose 5-phosphate disodium salt hydrate
Fumaric acid
Glycine
Guanine
Guanosine 3′-monophosphate disodium salt
L-Alanine
L-Arginine
L-Asparagine
L-Aspartic acid
L-Citrulline
L-Cysteine
L-Glutamic acid
L-Glutamine
L-Glutathione oxidized
L-Glutathione reduced
L-Histidine
L-Leucine
L-Lysine
L-Ornithine monohydrochloride
L-Phenylalanine

L-Proline
L-Serine
L-Threonine
L-Tryptophan
L-Tyrosine
L-Valine
Malic acid
Pyruvic acid
Shikimic acid
Succinic acid
Sucrose
Urea
α-Ketoglutaric acid
γ-Aminobutyric acid

Chapter 4. Conclusion: the use of metabolomics for plant abiotic stress responses

The goal of this thesis research has been to understand how plant respond to different abiotic stresses and to do this a metabolomics approach was used, as metabolomics is one of the most frequently used and powerful tools of systems biology. In Chapter 1, I investigated *Arabidopsis thaliana*'s priming effect from temperature stresses and plant memory during the recovery phase between different stresses as elicited by heat, cold, drought, and high light in a standardized reference system. We found many metabolites in central metabolism, including amino acid metabolism, sugar metabolism, glycolysis, TCA cycle, GABA shunt, glutathione metabolism, purine metabolism, and the urea cycle, showed shared stress response patterns across different stresses. However, cysteine, GSH, and maltose showed unique and dramatic patterns, demonstrating unique and large changes in glutathione biosynthesis, GSH oxidation, and starch degradation. The similar response patterns between cold and high light, heat and drought may predict their potential cross stress tolerance. During recovery, plants subjected to basal heat and drought showed an overcompensation behavior. Priming treatment had a greater impact on cold stress as contrasted with heat stress. Entire metabolic pathways were monitored from precursors and intermediates to their products simultaneously. The subtle interplay of functionally related metabolites and the important transitions that regulate stress and recovery processes were revealed.

In Chapter 2, the LC-MS based metabolomics approach developed in Chapter 1 were employed to further study *Arabidopsis thaliana* in response to a combination of abiotic stresses that better mimics field conditions, a model approach which is surprisingly rarely studied. Both untargeted and targeted metabolomics approaches were employed to investigate the relationship between combined stress with metabolic responses to each single stress elicited by heat, cold, drought, salinity, and high light in *Arabidopsis thaliana* 11-day-old seedlings. Interestingly, only two combined stresses, including high light x cold and cold x salinity, had metabolic effects from both of their individual stresses. Most of the combined stresses exhibited one dominant stress response. Among them, drought stress was the dominant stress for all its combined stresses and the dominant effect was not caused by the more severe experimental conditions tested in our study, indicating that water deficiency may either be a more important stress responded to by plant or, alternatively, the one stress that metabolic intervention can partially alleviate. The metabolic response of plants to the combined stresses of high light and heat, and high light and salinity are unique in that they cannot be simply explained by linear combinations of the corresponding single stress responses. Most of metabolic features are specifically changed in these two combined stresses that should be considered as novel stress conditions. Many identified stress signatures contributed to the differences between stress and control showed shared patterns across different abiotic treatments. However, maltose and GSH showed unique stress response patterns, which was consistent with the results in Chapter 1.

Altogether, the metabolomics methods used in this study provided results that are a direct indication of the biochemical adaptations of a stress-responding plant. Shared and unique stress signatures were identified in a single platform to eliminate other factors in addition to stress. To my knowledge, this is the first metabolomics study that comprehensively investigated combinations of abiotic stresses that plants are more often to encounter in field and natural environments. In addition to the combined responses and the dominant effects from two individual stresses, combined stresses including high light x heat and high light x salinity showed unique responses that should be considered as novel stress condition responses. This study highlights the importance of studying plants that are subjected to combined stresses and thus these results may potentially contribute to future research designed to enhance crop plant tolerance to field stress conditions. In conclusion, the efforts at characterizing plant abiotic stress responses in this thesis have provided significant insights to a number of important biological questions. The untargeted metabolomics approach developed in this study shall be a valuable tool for future plant metabolomics studies into plant environmental adaptation. The metabolic abundance changes for decreased precursors and increased products in this study may be related to their different metabolic flux. Therefore, this work may lay the foundation for future dynamic metabolic flux analyses, within the entire plant and in specific tissues, to better understand the kinetics of metabolic response networks that facilitate a plant’s adaptation to abiotic stress events.

Bibliography

Ahmad, P. and Prasad, M.N. V (2012). Abiotic stress responses in plants: Metabolism, productivity and sustainability.

Allwood, J.W., Ellis, D.I., and Goodacre, R. (2008). Metabolomic technologies and their application to the study of plants and plant-host interactions. Physiol. Plant. **132**: 117–135.

Alonso, J.M. et al. (2003). Genome-wide insertional mutagenesis of *Arabidopsis thaliana*. Science (80-.). **301**: 653–657.

Alscher, R.G. (1989). Biosynthesis and antioxidant function of glutathione in plants. Physiol. Plant. **77**: 457–464.

Anderson, J.P. (2004). Antagonistic Interaction between Abscisic Acid and Jasmonate-Ethylene Signaling Pathways Modulates Defense Gene Expression and Disease Resistance in *Arabidopsis*. PLANT CELL ONLINE **16**: 3460–3479.

Avramova, Z. (2015). Transcriptional "memory" of a stress: Transient chromatin and memory (epigenetic) marks at stress-response genes. Plant J. **83**: 149–159.

Bateman, R.J., Munsell, L.Y., Chen, X., Holtzman, D.M., and Yarasheski, K.E. (2007). Stable Isotope Labeling Tandem Mass Spectrometry (SILT) to Quantify Protein Production and Clearance Rates. J. Am. Soc. Mass Spectrom. **18**: 997–1006.

Bino, R.J. et al. (2004). Potential of metabolomics as a functional genomics tool. Trends Plant Sci. **9**: 418–425.

Bonham-Smith, P.C., Kapoor, M., and Bewley, J.D. (1987). Establishment of thermotolerance in maize by exposure to stresses other than a heat shock does not require heat shock protein synthesis. Plant Physiol. **85**: 575–580.

Bowler, C. and Fluhr, R. (2000). The role of calcium and activated oxygens as signals for controlling cross-tolerance. Trends Plant Sci. **5**: 241–246.

Cajka, T. and Fiehn, O. (2016). Toward Merging Untargeted and Targeted Methods in Mass Spectrometry-Based Metabolomics and Lipidomics. Anal. Chem. **88**: 524–545.

Cakmak, I. and Marschner, H. (1992). Magnesium deficiency and high light intensity enhance activities of superoxide dismutase, ascorbate peroxidase, and glutathione reductase in bean leaves. Plant Physiol. **98**: 1222–1227.

Caldana, C., Degenkolbe, T., Cuadros-Inostroza, A., Klie, S., Sulpice, R., Leisse, A., Steinhauser, D., Fernie, A.R., Willmitzer, L., and Hannah, M.A. (2011). High-density kinetic analysis of the metabolomic and transcriptomic response of *Arabidopsis* to eight environmental conditions. Plant J. **67**: 869–884.

Cardinale, F., Meskiene, I., Ouaked, F., and Hirt, H. (2002). Convergence and Divergence of Stress-Induced Mitogen-Activated Protein Kinase Signaling Pathways at the Level of Two Distinct Mitogen-Activated Protein Kinase Kinases. Plant Cell **14**: 703–711.

Chambers, M.C. et al. (2012). A cross-platform toolkit for mass spectrometry and proteomics. Nat. Biotechnol. **30**: 918–920.

Chen, J. and Goldsbrough, P.B. (1994). Increased Activity of [gamma]-Glutamylcysteine Synthetase in Tomato Cells Selected for Cadmium Tolerance. Plant Physiol. **106**: 233–239.

Chiang, Y., Stushnoff, C., Mcsay, a E., Jones, M.L., and Bohnert, H.J. (2005). Overexpression of Mannitol-1-Phosphate Dehydrogenase Increases Mannitol Accumulation and Adds Protection against chilling injury in Petunia. J. Am. Soc. Hort.

Sci. **130**: 605–610.

Chinnusamy, V., Ohta, M., Kanrar, S., Lee, B. ha, Hong, X., Agarwal, M., and Zhu, J.K. (2003). ICE1: A regulator of cold-induced transcriptome and freezing tolerance in *Arabidopsis*. Genes Dev. **17**: 1043–1054.

Chiou, T.J. and Bush, D.R. (1998). Sucrose is a signal molecule in assimilate partitioning. Proc. Natl. Acad. Sci. U. S. A. **95**: 4784–4788.

Cloutier, Y. and Andrews, C.J. (1984). Efficiency of cold hardiness induction by desiccation stress in four winter cereals. Plant Physiol. **76**: 595–598.

Craufurd, P.Q. and Peacock, J.M. (1993). Effect of heat and drought stress on sorghum (Sorghum bicolor). II. Grain yield. Exp. Agric. **29**: 77–86.

Crisp, P.A., Ganguly, D., Eichten, S.R., Borevitz, J.O., and Pogson, B.J. (2016). Reconsidering plant memory: Intersections between stress recovery, RNA turnover, and epigenetics. Sci. Adv. **2**: e1501340–e1501340.

Dettmer, K., Aronov, P.A., and Hammock, B.D. (2007). Mass spectrometry-based metabolomics. Mass Spectrom. Rev. **26**: 51–78.

Dietz, K.-J. and Sunkar, R. (2010). Plant Stress Tolerance. Methods Mol. Biol. **639**: 291–297.

Dixon, R.A. (2001). Natural products and plant disease resistance. Nature **411**: 843–847.

Dreier, W., Schnarrenberger, C., and Börner, T. (1995). Light- and Stress-Dependent Enhancement of Amylolytic Activities in White and Green Barley Leaves: β-Amylases are Stress-Induced Proteins. J. Plant Physiol. **145**: 342–348.

Dudley, E., Yousef, M., Wang, Y., and Griffiths, W.J. (2010). Targeted metabolomics and mass spectrometry. Adv. Protein Chem. Struct. Biol. **80**: 45–83.

Edelbrock, C. (1979). Mixture model tests of hierarchical clustering algorithms: The problem of classifying everybody. Multiva. Behav. Res. **14**: 367–384.

Fan, K.T., Rendahl, A.K., Chen, W.P., Freund, D.M., Gray, W.M., Cohen, J.D., and Hegeman, A.D. (2016). Proteome Scale-Protein Turnover Analysis Using High Resolution Mass Spectrometric Data from Stable-Isotope Labeled Plants. J. Proteome Res. **15**: 851–867.

Fernie, A.R., Carrari, F., and Sweetlove, L.J. (2004). Respiratory metabolism: glycolysis, the TCA cycle and mitochondrial electron transport. Curr Opin Plant biol **7**: 254–261.

Firtzlaff, V., Oberländer, J., Geiselhardt, S., Hilker, M., and Kunze, R. (2016). Pre-exposure of *Arabidopsis* to the abiotic or biotic environmental stimuli “chilling” or “insect eggs” exhibits different transcriptomic responses to herbivory. Sci. Rep. **6**: 28544.

Foster, J.G. and Hess, J.L. (1980). Responses of superoxide dismutase and glutathione reductase activities in cotton leaf tissue exposed to an atmosphere enriched in oxygen. Plant Physiol. **66**: 482–7.

Foyer, C.H., LopezDelgado, H., Dat, J.F., and Scott, I.M. (1997). Hydrogen peroxide- and glutathione-associated mechanisms of acclimatory stress tolerance and signalling. Physiol. Plant. **100**: 241–254.

Freund, D.M. and Hegeman, A.D. (2017). Recent advances in stable isotope-enabled mass spectrometry-based plant metabolomics. Curr. Opin. Biotechnol. **43**: 41–48.

Gamble, P.E. and Burke, J.J. (1984). Effect of Water-Stress on the Chloroplast Antioxidant System .1. Alterations in Glutathione-Reductase Activity. Plant Physiol. **76**: 615–621.

Gao, A.G., Hakimi, S.M., Mittanck, C.A., Wu, Y., Woerner, B.M., Stark, D.M., Shah, D.M., Liang, J., and Rommens, C.M.T. (2000). Fungal pathogen protection in potato by expression of a plant defensin peptide. Nat. Biotechnol. **18**: 1307–1310.

Giacomoni, F. et al. (2015). Workflow4Metabolomics: A collaborative research infrastructure for computational metabolomics. Bioinformatics **31**: 1493–1495.

Gilmour, S.J., Sebolt, A.M., Salazar, M.P., Everard, J.D., and Thomashow, M.F. (2000). Overexpression of the *Arabidopsis* CBF3 transcriptional activator mimics multiple biochemical changes associated with cold acclimation. Plant Physiol. **124**: 1854–1865.

Guitton, Y. et al. (2017). Create, run, share, publish, and reference your LC–MS, FIA–MS, GC–MS, and NMR data analysis workflows with the Workflow4Metabolomics 3.0 Galaxy online infrastructure for metabolomics. Int. J. Biochem. Cell Biol. **93**: 89–101.

Guy, C. (1999). Molecular responses of plants to cold shock and cold acclimation. J. Mol. Microbiol. Biotechnol. **1**: 231–42.

Hallberg, R.L., Kraus, K.W., and Hallberg, E.M. (1985). Induction of acquired thermotolerance in Tetrahymena thermophila: effects of protein synthesis inhibitors. Mol Cell Biol **5**: 2061–2069.

Hannah, M.A. (2006). Natural Genetic Variation of Freezing Tolerance in *Arabidopsis*. Plant Physiol. **142**: 98–112.

Hare, P.D. and Cress, W.A. (1997). Metabolic implications of stress-induced proline accumulation in plants. Plant Growth Regul. **21**: 79–102.

Heilmann, I. (2004). Identification of the *Arabidopsis* Palmitoyl-Monogalactosyldiacylglycerol 7-Desaturase Gene FAD5, and Effects of Plastidial Retargeting of *Arabidopsis* Desaturases on the fad5 Mutant Phenotype. Plant Physiol. **136**: 4237–4245.

Hirayama, T. and Shinozaki, K. (2010). Research on plant abiotic stress responses in the post-genome era: Past, present and future. Plant J. **61**: 1041–1052.

Hoekstra, F.A., Golovina, E.A., and Buitink, J. (2001). Mechanisms of plant desiccation tolerance. Trends Plant Sci. **6**: 431–438.

Horai, H. et al. (2010). MassBank: A public repository for sharing mass spectral data for life sciences. J. Mass Spectrom. **45**: 703–714.

Huang, T. and Jander, G. (2017). Abscisic acid-regulated protein degradation causes osmotic stress-induced accumulation of branched-chain amino acids in *Arabidopsis thaliana*. Planta **246**: 737–747.

Iba, K., Gibson, S., Nishiuchi, T., Fuse, T., Nishimura, M., Arondel, V., Hugly, S., and Somerville, C. (1993). A gene encoding a chloroplast ω-3 fatty acid desaturase complements alterations in fatty acid desaturation and chloroplast copy number of the fad7 mutant of *Arabidopsis thaliana*. J. Biol. Chem. **268**: 24099–24105.

Jaglo-Ottosen, K.R., Gilmour, S.J., Zarka, D.G., Schabenberger, O., and Thomashow, M.F. (1998). *Arabidopsis* CBF1 overexpression induces COR genes and enhances freezing tolerance. Science (80-.). **280**: 104–106.

Johnson, C.H., Ivanisevic, J., Benton, H.P., and Siuzdak, G. (2015). Bioinformatics: The next frontier of metabolomics. Anal. Chem. **87**: 147–156.

Kanehisa, M., Furumichi, M., Tanabe, M., Sato, Y., and Morishima, K. (2017). KEGG: New perspectives on genomes, pathways, diseases and drugs. Nucleic Acids Res. **45**: D353–D361.

Kang, J., Choi, H., Im, M., and Kim, S.Y. (2002). *Arabidopsis* basic leucine zipper proteins that mediate stress-responsive abscisic acid signaling. Plant Cell **14**: 343–357.
Kaplan, F. and Guy, C.L. (2005). RNA interference of *Arabidopsis* beta-amylase8 prevents maltose accumulation upon cold shock and increases sensitivity of PSII photochemical efficiency to freezing stress. Plant J. **44**: 730–743.
Kaplan, F., Kopka, J., Haskell, D.W., Zhao, W., Schiller, K.C., Gatzke, N., Sung, D.Y., Guy, C.L., Molecular, P., Program, C.B., and K, E.H.F. (2004). Exploring the Temperature-Stress Metabolome. Plant Physiol. **136**: 4159–4168.
Kaplan, F., Kopka, J., Sung, D.Y., Zhao, W., Popp, M., Porat, R., and Guy, C.L. (2007). Transcript and metabolite profiling during cold acclimation of *Arabidopsis* reveals an intricate relationship of cold-regulated gene expression with modifications in metabolite content. Plant J. **50**: 967–981.
Keleş, Y. and Öncel, I. (2002). Response of antioxidative defence system to temperature and water stress combinations in wheat seedlings. Plant Sci. **163**: 783–790.
Kind, T. and Fiehn, O. (2006). Metabolomic database annotations via query of elemental compositions: Mass accuracy is insufficient even at less than 1 ppm. BMC Bioinformatics **7**.
Kinnersley, A.M. and Turano, F.J. (2000). Gamma aminobutyric acid (GABA) and plant responses to stress. CRC. Crit. Rev. Plant Sci. **19**: 479–509.
Knight, H. and Knight, M.R. (2001). Abiotic stress signalling pathways: Specificity and cross-talk. Trends Plant Sci. **6**: 262–267.
Koch, K.E. (1996). Carbohydrate-Modulated Gene Expression in Plants. Annu. Rev. Plant Physiol. Plant Mol. Biol. **47**: 509–540.
Korn, M., Gärtner, T., Erban, A., Kopka, J., Selbig, J., and Hincha, D.K. (2010). Predicting *Arabidopsis* freezing tolerance and heterosis in freezing tolerance from metabolite composition. Mol. Plant **3**: 224–235.
Leung, J., Bouvier-Durand, M., Morris, P., Guerrier, D., Chefdor, F., and Giraudat, J. (1994). *Arabidopsis* ABA response gene ABI1: features of a calcium-modulated protein phosphatase. Science (80-.). **264**: 1448–1452.
Li, X. and Liu, F. (2016). Drought Stress Tolerance in Plants, Vol 1. **1**: 17–45.
Loreto, F. and Bongi, G. (1989). Combined Low Temperature-High Light Effects on Gas Exchange Properties of Jojoba Leaves. Plant Physiol **91**: 1580–1585.
Lu, Y. and Sharkey, T.D. (2004). The role of amylomaltase in maltose metabolism in the cytosol of photosynthetic cells. Planta **218**: 466–473.
Markley, J.L., Ulrich, E.L., Berman, H.M., Henrick, K., Nakamura, H., and Akutsu, H. (2008). BioMagResBank (BMRB) as a partner in the Worldwide Protein Data Bank (wwPDB): New policies affecting biomolecular NMR depositions. J. Biomol. NMR **40**: 153–155.
Marrs, K.A. (1996). The finctions and regulation of glutathione S-transferases in plants. Annu. Rev. Plant Physiol. Plant Mol. Biol. **47**: 127–158.
McKersie, B.D., Bowley, S.R., and Jones, K.S. (1999). Winter Survival of Transgenic Alfalfa Overexpressing Superoxide Dismutase1. Plant Physiol. **119**: 839–848.
Mittler, R. (2006). Abiotic stress, the field environment and stress combination. Trends Plant Sci. **11**: 15–19.
Mittler, R. (2002). Oxidative stress, antioxidants and stress tolerance. Trends Plant Sci. **7**: 405–410.

Mittler, R., Merquiol, E., Hallak-Herr, E., Rachmilevitch, S., Kaplan, A., and Cohen, M. (2001). Living under a “dormant” canopy: A molecular acclimation mechanism of the desert plant Retama raetam. Plant J. **25**: 407–416.

Mohamed, R., Meilan, R., Ostry, M.E., Michler, C.H., and Strauss, S.H. (2001). Bacterio-opsin gene overexpression fails to elevate fungal disease resistance in transgenic poplar (*Populus*). Can. J. For. Res. **31**: 268–275.

Nieto-Sotelo, J., Kannan, K.B., Martínez, L.M., and Segal, C. (1999). Characterization of a maize heat-shock protein 101 gene, HSP101, encoding a ClpB/Hsp 100 protein homologue. Gene **230**: 187–195.

Nishizawa, A., Yabuta, Y., and Shigeoka, S. (2008). Galactinol and Raffinose Constitute a Novel Function to Protect Plants from Oxidative Damage. PLANT Physiol. **147**: 1251–1263.

Obata, T. and Fernie, A.R. (2012). The use of metabolomics to dissect plant responses to abiotic stresses. Cell. Mol. Life Sci. **69**: 3225–3243.

Ogata, H., Goto, S., Sato, K., Fujibuchi, W., Bono, H., and Kanehisa, M. (1999). KEGG: Kyoto encyclopedia of genes and genomes. Nucleic Acids Res. **27**: 29–34.

Pandey, P., Irulappan, V., Bagavathiannan, M. V., and Senthil-Kumar, M. (2017). Impact of Combined Abiotic and Biotic Stresses on Plant Growth and Avenues for Crop Improvement by Exploiting Physio-morphological Traits. Front. Plant Sci. **8**: 1–15.

Patti, G.J. et al. (2012). Innovation: Metabolomics: the apogee of the omics trilogy. Nat. Rev. Mol. Cell Biol. **13**: 263–269.

Pratt, J.M., Petty, J., Riba-Garcia, I., Robertson, D.H.L., Gaskell, S.J., Oliver, S.G., and Beynon, R.J. (2002). Dynamics of Protein Turnover, a Missing Dimension in Proteomics. Mol. Cell. Proteomics **1**: 579–591.

Qiu, Q.-S., Guo, Y., Dietrich, M.A., Schumaker, K.S., and Zhu, J.-K. (2002). Regulation of SOS1, a plasma membrane Na+/H+ exchanger in *Arabidopsis thaliana*, by SOS2 and SOS3. Proc. Natl. Acad. Sci. **99**: 8436–8441.

Rajashekar, C.B. and Panda, M. (2014). Water stress is a component of cold acclimation process essential for inducing full freezing tolerance in strawberry. Sci. Hortic. (Amsterdam). **174**: 54–59.

Rizhsky, L. (2004). When Defense Pathways Collide. The Response of *Arabidopsis* to a Combination of Drought and Heat Stress. Plant Physiol. **134**: 1683–1696.

Rizhsky, L., Liang, H., and Mittler, R. (2002). The Combined Effect of Drought Stress and Heat Shock on Gene Expression in Tobacco\r10.1104/pp.006858. Plant Physiol. **130**: 1143–1151.

Roitsch, T. (1999). Source-sink regulation by sugar and stress. Curr. Opin. Plant Biol. **2**: 198–206.

Roscher, a, Kruger, N.J., and Ratcliffe, R.G. (2000). Strategies for metabolic flux analysis in plants using isotope labelling. J. Biotechnol. **77**: 81–102.

Roxas, V.P., Smith, R.K., Allen, E.R., and Allen, R.D. (1997). Overexpression of glutathione S-transferase/glutathioneperoxidase enhances the growth of transgenic tobacco seedlings during stress. Nat. Biotechnol. **15**: 988–991.

Sakuma, Y., Maruyama, K., Osakabe, Y., Qin, F., Seki, M., Shinozaki, K., and Yamaguchi-Shinozaki, K. (2006). Functional analysis of an *Arabidopsis* transcription factor, DREB2A, involved in drought-responsive gene expression. Plant Cell **18**: 1292–309.

Sanchez, D.H., Siahpoosh, M.R., Roessner, U., Udvardi, M., and Kopka, J. (2008). Plant metabolomics reveals conserved and divergent metabolic responses to salinity. Physiol. Plant. **132**: 209–219.

Savin, R. and Nicolas, M. (1996). Effects of Short Periods of Drought and High Temperature on Grain Growth and Starch Accumulation of Two Malting Barley Cultivars. Aust. J. Plant Physiol. **23**: 201.

Schachtman, D.P. and Schroeder, J.I. (1994). Structure and transport mechanism of a high-affinity potassium uptake transporter from higher plants. Nature **370**: 655–658.

Schrimpe-Rutledge, A.C., Codreanu, S.G., Sherrod, S.D., and McLean, J.A. (2016). Untargeted Metabolomics Strategies—Challenges and Emerging Directions. J. Am. Soc. Mass Spectrom. **27**: 1897–1905.

Seki, M. et al. (2002). Monitoring the expression profiles of 7000 *Arabidopsis* genes under drought, cold and high-salinity stresses using a full-length cDNA microarray. Plant J. **31**: 279–292.

Shahjee, H.M., Banerjee, K., and Ahmad, F. (2002). Comparative analysis of naturally occurring L-amino acid osmolytes and their D-isomers on protection of Escherichia coli against environmental stresses. J. Biosci. **27**: 515–20.

Shen, Q. and Ho, T.H. (1995). Functional dissection of an abscisic acid (ABA)-inducible gene reveals two independent ABA-responsive complexes each containing a G-box and a novel cis-acting element. Plant Cell Online **7**: 295–307.

Shi, H., Ishitani, M., Kim, C., and Zhu, J.-K. (2000). The *Arabidopsis thaliana* salt tolerance gene SOS1 encodes a putative Na+/H+ antiporter. Proc. Natl. Acad. Sci. **97**: 6896–6901.

Shi, H., Lee, B., Wu, S.-J., and Zhu, J.-K. (2002). Overexpression of a plasma membrane Na+/H+ antiporter gene improves salt tolerance in *Arabidopsis thaliana*. Nat. Biotechnol. **21**: 81–85.

Shou, H., Bordallo, P., Fan, J.-B., Yeakley, J.M., Bibikova, M., Sheen, J., and Wang, K. (2004). Expression of an active tobacco mitogen-activated protein kinase kinase kinase enhances freezing tolerance in transgenic maize. Proc. Natl. Acad. Sci. U. S. A. **101**: 3298–303.

Shulaev, V., Cortes, D., Miller, G., and Mittler, R. (2008). Metabolomics for plant stress response. Physiol. Plant. **132**: 199–208.

Smith, A., O ’maille, G., Want, E.J., Qin, C., Trauger, S.A., Brandon, T.R., Custodio, D.E., Abagyan, R., and Siuzdak, G. (2005). METLIN A Metabolite Mass Spectral Database. Proc. 9Th Int. Congr. Ther. Drug Monit. Clin. Toxicol. **27**: 747–751.

Smith, A.B. and Matthews, J.L. (2015). Quantifying uncertainty and variable sensitivity within the US billion-dollar weather and climate disaster cost estimates. Nat. Hazards **77**: 1829–1851.

De Souza, D.P., Saunders, E.C., McConville, M.J., and Likić, V.A. (2006). Progressive peak clustering in GC-MS Metabolomic experiments applied to Leishmania parasites. Bioinformatics **22**: 1391–1396.

Strid, Å., Chow, W.S., and Anderson, J.M. (1994). UV-B damage and protection at the molecular level in plants. Photosynth. Res. **39**: 475–489.

Strohm, M., Jouanin, L., Kunert, K.J., Pruvost, C., Polle, A., Foyer, C.H., and Rennenberg, H. (1995). Regulation of glutathione synthesis in leaves of transgenic poplar (Populus tremula X P. alba) overexpressing glutathione synthetase. Plant J. **7**:

141–145.

Su, L., Dai, Z., Li, S., and Xin, H. (2015). A novel system for evaluating drought-cold tolerance of grapevines using chlorophyll fluorescence. BMC Plant Biol. **15**.

Suzuki, N. (2005). Enhanced Tolerance to Environmental Stress in Transgenic Plants Expressing the Transcriptional Coactivator Multiprotein Bridging Factor 1c. PLANT Physiol. **139**: 1313–1322.

Suzuki, N., Rivero, R.M., Shulaev, V., Blumwald, E., and Mittler, R. (2014). Abiotic and biotic stress combinations. New Phytol. **203**: 32–43.

Thévenot, E.A., Roux, A., Xu, Y., Ezan, E., and Junot, C. (2015). Analysis of the Human Adult Urinary Metabolome Variations with Age, Body Mass Index, and Gender by Implementing a Comprehensive Workflow for Univariate and OPLS Statistical Analyses. J. Proteome Res. **14**: 3322–3335.

Tolleter, D., Jaquinod, M., Mangavel, C., Passirani, C., Saulnier, P., Manon, S., Teyssier, E., Payet, N., Avelange-Macherel, M.-H., and Macherel, D. (2007). Structure and Function of a Mitochondrial Late Embryogenesis Abundant Protein Are Revealed by Desiccation. PLANT CELL ONLINE **19**: 1580–1589.

Trygg, J., Kettaneh-Wold, N., and Wallbäcks, L. (2001). Interpretation of regression coefficients under a latent variable regression model. J. Chemom. **15**: 265–284.

Urano, K., Maruyama, K., Ogata, Y., Morishita, Y., Takeda, M., Sakurai, N., Suzuki, H., Saito, K., Shibata, D., Kobayashi, M., Yamaguchi-Shinozaki, K., and Shinozaki, K. (2009). Characterization of the ABA-regulated global responses to dehydration in *Arabidopsis* by metabolomics. Plant J. **57**: 1065–1078.

Vera-Estrella, R. (2004). Novel Regulation of Aquaporins during Osmotic Stress. PLANT Physiol. **135**: 2318–2329.

Vetter, J. (2000). Plant cyanogenic glycosides. Toxicon **38**: 11–36.

Vinaixa, M., Samino, S., Saez, I., Duran, J., Guinovart, J.J., and Yanes, O. (2012). A Guideline to Univariate Statistical Analysis for LC/MS-Based Untargeted Metabolomics-Derived Data. Metabolites **2**: 775–795.

Vinocur, B. and Altman, A. (2005). Recent advances in engineering plant tolerance to abiotic stress: Achievements and limitations. Curr. Opin. Biotechnol. **16**: 123–132.

De Vos, R.C., Moco, S., Lommen, A., Keurentjes, J.J., Bino, R.J., and Hall, R.D. (2007). Untargeted large-scale plant metabolomics using liquid chromatography coupled to mass spectrometry. Nat. Protoc. **2**: 778–791.

Wang, W., Vinocur, B., and Altman, A. (2003). Plant responses to drought, salinity and extreme temperatures: Towards genetic engineering for stress tolerance. Planta **218**: 1–14.

Wang, W., Vinocur, B., Shoseyov, O., and Altman, A. (2004). Role of plant heat-shock proteins and molecular chaperones in the abiotic stress response. Trends Plant Sci. **9**: 244–252.

Wang, X. et al. (2012). Urine Metabolomics Analysis for Biomarker Discovery and Detection of Jaundice Syndrome in Patients With Liver Disease. Mol. Cell. Proteomics **11**: 370–380.

Wardlaw, I.F. (1972). Responses of Plants to Environmental Stresses. J. Levitt. Academic Press, New York, 1972. xiv, 698 pp., illus. $32.50. Physiological Ecology. Science (80-.). **177**: 786–786.

Weigelt, K., Küster, H., Radchuk, R., Müller, M., Weichert, H., Fait, A., Fernie,

A.R., Saalbach, I., and Weber, H. (2008). Increasing amino acid supply in pea embryos reveals specific interactions of N and C metabolism, and highlights the importance of mitochondrial metabolism. Plant J. **55**: 909–926.
Wen, X., Qiu, N., Lu, Q., and Lu, C. (2005). Enhanced thermotolerance of photosystem II in salt-adapted plants of the halophyte Artemisia anethifolia. Planta **220**: 486–497.
Wiklund, S., Johansson, E., Sjöström, L., Mellerowicz, E.J., Edlund, U., Shockcor, J.P., Gottfries, J., Moritz, T., and Trygg, J. (2008). Visualization of GC/TOF-MS-based metabolomics data for identification of biochemically interesting compounds using OPLS class models. Anal. Chem. **80**: 115–122.
Wingate, V.P., Lawton, M. a, and Lamb, C.J. (1988). Glutathione causes a massive and selective induction of plant defense genes. Plant Physiol. **87**: 206–210.
Wishart, D.S. et al. (2013). HMDB 3.0-The Human Metabolome Database in 2013. Nucleic Acids Res. **41**.
Wold, S., Esbensen, K., and Geladi, P. (1987). Principal component analysis. Chemom. Intell. Lab. Syst. **2**: 37–52.
Wulff-Zottele, C., Gatzke, N., Kopka, J., Orellana, A., Hoefgen, R., Fisahn, J., and Hesse, H. (2010). Photosynthesis and metabolism interact during acclimation of *Arabidopsis thaliana* to high irradiance and sulphur depletion. Plant, Cell Environ. **33**: 1974–1988.
Xiong, L. (2003). Disease Resistance and Abiotic Stress Tolerance in Rice Are Inversely Modulated by an Abscisic Acid-Inducible Mitogen-Activated Protein Kinase. PLANT CELL ONLINE **15**: 745–759.
Yancey, P., Clark, M., Hand, S., Bowlus, R., and Somero, G. (1982). Living with water stress: evolution of osmolyte systems. Science (80-.). **217**: 1214–1222.
Yang, X.Y., Chen, W.P., Rendahl, A.K., Hegeman, A.D., Gray, W.M., and Cohen, J.D. (2010). Measuring the turnover rates of *Arabidopsis* proteins using deuterium oxide: An auxin signaling case study. Plant J. **63**: 680–695.
Yoshiba, Y., Nanjo, T., Miura, S., Yamaguchi-Shinozaki, K., and Shinozaki, K. (1999). Stress-responsive and developmental regulation of Δ1-Pyrroline-5-carboxylate synthetase 1 (P5CS1) gene expression in *Arabidopsis thaliana*. Biochem. Biophys. Res. Commun. **261**: 766–772.
Yoshimura, K., Miyao, K., Gaber, A., Takeda, T., Kanaboshi, H., Miyasaka, H., and Shigeoka, S. (2004). Enhancement of stress tolerance in transgenic tobacco plants overexpressing Chlamydomonas glutathione peroxidase in chloroplasts or cytosol. Plant J. **37**: 21–33.
Yu, B., Wakao, S., Fan, J., and Benning, C. (2004). Loss of plastidic lysophosphatidic acid acyltransferase causes embryo-lethality in *Arabidopsis*. Plant Cell Physiol. **45**: 503–510.
Zhang, J.Z., Creelman, R. a, and Zhu, J.-K. (2004). From laboratory to field. Using information from *Arabidopsis* to engineer salt, cold, and drought tolerance in crops. Plant Physiol. **135**: 615–621.
Zhang, T. and Watson, D.G. (2015). A short review of applications of liquid chromatography mass spectrometry based metabolomics techniques to the analysis of human urine. Analyst **140**: 2907–2915.

Appendix 1. Metabolomics study of *Arabidopsis thaliana* abiotic stress related mutants in relation to cold and drought treatments

Background

Nine important stress related mutants, including *abi1*, *dreb2a*, *fab1*, *fad5*, *fad7*, *lea*, *lpat1*, *p5cs1*, *sos1* described in (**Table 1**) and wild-type Col-0, were studied in control, cold, and drought treated plants. ABA INSENSITIVE 1 (ABI1) is a negative regulator of the ABA signal transduction cascade and of ABA promotion of stomatal closure (Leung et al., 1994). The transcription factor DEHYDRATION-RESPONSIVE ELEMENT-BINDING PROTEIN2A (DREB2A) specifically binds to the cis-acting dehydration-responsive element/C-repeat (DRE/CRT) involved in gene expression responses to drought and low-temperature stress (Sakuma et al., 2006). *ARABIDOPSIS* BETA-KETOACYL-ACP SYNTHETASE 2 (FAB1) encodes a β-ketoacyl-acyl carrier protein (ACP) synthase II (KASII) that is involved in 16:0-ACP to 18:0-ACP fatty acid elongation (Alonso et al., 2003). FATTY ACID DESATURASE 5 (FAD5) encodes a chloroplastic enzyme involved in 16:1 fatty acids synthesis from galactolipids and sulpholipids (Heilmann, 2004). FATTY ACID DESATURASE 7 (FAD7) encodes a chloroplastic enzyme that participates in the synthesis of 16:3 and 18:3 fatty acids from galactolipids, sulpholipids and phosphatidylglycerol (Iba et al., 1993). LATE-EMBRYOGENESIS ABUNDANT (LEA) genes encode a large and diverse group of proteins that accumulate during plant seed dehydration, at the maturation phase of seed development (Tolleter et al., 2007). LYSOPHOSPHATIDIC ACID ACYLTRANSFERASE 1 (LPAT1) encodes lysophosphatidic acid acyltransferase (LPAAT) that is involved in chloroplastic phosphatidic acid biosynthesis (Yu et al., 2004). DELTA1-PYRROLINE-5-CARBOXYLATE SYNTHASE 1 (P5CS1) encodes a delta-1-pyrroline-5-carboxylate synthase that is the key enzyme in proline biosynthesis (Yoshiba et al., 1999). SALT OVERLY SENSITIVE 1 (SOS1) encodes a plasma membrane-localized Na+/H+ antiporter that is essential for cell toxic Na^+ extrusion which is a key determinant for plant salt tolerance (Shi et al., 2000).

Results

Multivariate statistical comparisons using principle components analysis (PCA) and orthogonal projections to latent structures discriminant analysis (OPLS-DA)

A comprehensive characterization of *Arabidopsis thaliana* metabolome variations between stress related mutants and wild-type under control conditions and abiotic stress treatments, including cold and drought, was addressed. The most statistically significant metabolic differences between stressed and control plants, with both mutants and wild-type plants were identified using an untargeted metabolomics approach. Multivariate statistics modeling PCA and OPLS-DA were performed.

PCA was generated for all ten genotypes in control, cold, and drought conditions (**Figure A-1**). In control conditions, mutants including *lea*, *dreb2a*, *fad7*, and *abi1* are separated from Col-0, indicting their different metabolic phenotype without stress treatment. In contrast, *sos1* and *dreb2a* are clustered together with control, indicating these two mutants showed similar metabolic phenotype with wild-type during control conditions. With drought treatment, most mutants, including *fad5*, *lpat1*, *fab1*, *p5cs1*, *fad7,* clustered together with their corresponding control, indicating these mutants are not, at the metabolic level, drought stress related. However, *sos1* and *abi1* separated between drought stress and control in PC1 (25%), indicating these two mutants have a drought related metabolic phenotype. With cold stress treatment, most mutants, including *lea*, *p5cs1*, *dreb2a*, *sos1*, *fad7*, *abi1*, are well separated from their corresponding control, suggesting they may have a cold stress related metabolic phenotype. By comparison, *lpat1* and *fad5,* with cold conditions, are clustered together with their corresponding control, indicating these two mutants are not, at the metabolic level, cold related. In summary, cold stress induced a stronger metabolic profile change for most of the mutants tested in our study when compared to drought stress.

The OPLS-DA were then performed between both stress and control, mutant and wild-type, to identify important metabolic feature drivers of differentiation. The OPLS-DA score plot and s-plot, for comparison between stress and control *in the same genotype*, are shown in **Figure A-2** and **Figure A-3**. For comparison, the OPLS-DA score plot and s-plot, for comparison between mutant and wild-type *in the same treatment*, are shown in **Figure A-4** and **Figure A-5**. The top ten metabolic features with the highest and lowest

OPLS-DA S-plot covariance value in the different treatments compared to control and different mutants compared to wild-type are reported in **Table A-2** and **Table A-3**.

Hierarchical clustering analysis (HCA) for all the metabolic features

The measured metabolome is represented by the total of the metabolic features detected. The HCA results for the average abundance of all the features from the ten genotypes in the three treatments is reported in **Figure A-6**. *Abi1* under cold conditions and *sos1* under drought conditions formed two single clusters, 1 and 7, highlighting their specific response patterns across all the samples. The HCA results for the ratio changes for all the features in the different treatments compared to control in the same genotype is reported in **Figure A-7**. *Lea* under drought treatment and cold treatment, as well as *sos1* under cold treatment formed their own single clusters, 3 and 4. This result suggested that *lea* has a specific metabolic response in both drought and cold stress, whereas *sos1* has a specific metabolic response in cold stress only. The HCA results for the ratio changes of all the features in different mutant compared to wild-type in the same treatment is reported in **Figure A-8**. *Fad7* in control conditions, *sos1* in drought treatment, and *lea* in cold treatment formed their own single clusters, 6, 7, and 4. This result indicated that *fad7* has large and specific metabolic changes when compared to wild-type without stress treatment. *Sos1* showed a specific metabolic difference compared to wild-type during drought treatment, and showed specific metabolic changes compared to wild-type with cold conditions.

Materials and Methods

Plant materials, growth conditions, and treatments

Arabidopsis thaliana wild-type (Col-0) was obtained from Lehle Seeds. *Abi1, dreb2a, fab1, fad5, fad7, lea, lpat1, p5cs1, sos1* seeds were obtained from the *Arabidopsis* Biological Resource Center. Seeds were sterilized with 30% (v/v) bleach containing 0.1% (v/v) Triton X-100 and vernalized at 4 °C for 2 days. Seedlings were germinated on 1/2 x MS media made from MS Salts (PhytoTechnology Laboratories, M524 Murashige & Skoog (MS) Basal Salt Mixture, 4.33 g/L for 1 x MS) with 1.5% agar. Plants were grown prior to stress, during recovery, and as unstressed controls, vertically, at 22°C under a 16-

h-light/8-h-dark photoperiod, with ~80 μmol m-2 s-1 illumination from cool-white fluorescent tube lights (control conditions). Eleven-day-old seedlings were treated with cold (4°C for 2h) and drought (plants moved to desiccate in air for 2h) conditions. Whole seedlings were harvested, frozen in liquid nitrogen, and stored at -80°C. Experiments were performed using three biological replicates.

Sample extraction and LC-HRMS analysis

Seedlings were lyophilized, weighed, and extracted in 70% isopropanol alcohol with one 2.5 mm tungsten carbide ball in a Geno/Grinder™ (OPS Diagnostics) for 7 minutes at an intensity of 10,956 x g on -20°C chilled blocks to make a final concentration of 10 mg/ml (dry weight). After centrifugation for 10 minutes at 100,956 x g, 1 μL of supernatant was injected onto a UHPLC (Ultimate 3000, Dionex) with a ZIC-cHILIC column (100 mm ×2.1 mm, 3 μm particle size, EMD Millipore Corporation, Billerica, MA). Solvents A (0.1% (v/v) formic acid in water) and B (0.1% (v/v) formic acid in acetonitrile) were used as mobile phases for gradient separation. An extract corresponding to 100 µg of plant material (fresh weight) was loaded onto the column with at a flow rate of 0.4 mL/min, followed by the following gradient separation: 1 min from 98% B, 17 min to 65% B and maintained for 2 min, then 95% B and maintained for 1.5 min. The column was equilibrated for 1 min with 98% B prior to the next run. The samples were analyzed using a hybrid quadrupole Orbitrap mass spectrometer (Q Exactive, Thermo Fisher Scientific, San Jose CA). Full scan MS (range 50−750 *m/z*) were acquired with 35 k resolution for both positive and negative mode in polarity switching. The target value based on predictive automatic gain control was 1.0 × 106 with 200 ms of maximum injection time. The flow rate for sheath gas, aux gas, and sweep gas was 50, 20, and 1 ml/min, respectively. The capillary temperature was 350 °C. The S-lens RF was set to 55. The Aux gas heater temperature was 300 °C. Targeted MS/MS acquisition was used during metabolite identification with an inclusion list of ions of interest. Briefly, the precursor ions were sequentially fragmented in the HCD collision cell with normalized collision energy of 10%, 20%, 40%. MS/MS scans were acquired with 17.5 k resolution and the target value was 2.0 × 105 with 100 ms of maximum injection time. An isolation width of 2.0 *m/z* was used for precursor ion selection in MS/MS mode.

Data analysis

Thermo RAW files were converted to mzXML format using MSConvert (Chambers et al., 2012). Preprocessing including peak detection, grouping, and retention time correction and statistics analysis including multivariate modeling PCA, OPLS-DA and hierarchical clustering analysis were performed in Workflow4Metabolomics.org online resource for computational metabolomics (Giacomoni et al., 2015). Annotation was first performed from databases including BMRB (Markley et al., 2008), METLIN (Smith et al., 2005), and HMDB (Wishart et al., 2013) public databases, and identities were confirmed with authentic standards for accurate mass measurement, retention time, and fragmentation data. S-plots of OPLS-DA were generated to select variables with both high covariance and correlation values as metabolic signature candidates (Wiklund et al., 2008). To generate these S-plots the covariance was plotted on the x-axis whereas the correlation profile is plotted on the y-axis; the most positive and negative loadings in covariance and correlation represent variables with both high magnitude and high reliability. The S-plots for all the treatment compared to control and all the mutant compared to wild-type are performed. The top 10 most positive and negative loadings in the S-plot of the different groups were reported.

Tables

Table A-1. Stress related mutants

Mutant name	Gene other names	Stress phenotype	Germplasm / Stock	Locus	Description	Reference
abi1	ABA INSENSITIVE 1, ABI1, ATABI1	osmotic susceptible salinity susceptible	CS22	AT4G26080	Involved in abscisic acid (ABA) signal transduction. Negative regulator of ABA promotion of stomatal closure.	Leung et al., 1994)
dreb2a	DEHYDRATION-RESPONSIVE ELEMENT BINDING PROTEIN 2, DRE-BINDING PROTEIN 2A, DREB2, DREB2A	cold susceptible drought susceptible salinity susceptible	SALK_097569C	AT5G05410	Encodes a transcription factor that specifically binds to DRE/CRT cis elements (responsive to drought and low-temperature stress). Belongs to the DREB subfamily A-2 of ERF/AP2 transcription factor family (DREB2A). There are eight members in this subfamily including DREB2B. The protein contains one AP2 domain. Overexpression of transcriptional activation domain of DREB2A resulted in significant drought stress tolerance but only slight freezing tolerance in transgenic *Arabidopsis* plants. Microarray and RNA gel blot analyses revealed that DREB2A regulates expression of many water stress–inducible genes.	Sakuma et al., 2006
fab1	*ARABIDOPSIS* BETA-KETOACYL-ACP SYNTHETASE 2, ATKAS2, BETA-KETOACYL-ACP SYNTHETASE 2, FAB1, FATTY ACID BIOSYNTHESIS 1, KAS2	cold susceptible heat resistant high light susceptible	SALK_018337C	AT1G74960	Encodes a plastidic beta-ketoacyl-ACP synthase II, involved in fatty acid elongation from 16:0-ACP to 18:0-ACP. Homozygous knock-out mutants are embryo lethal, indicating early embryo development is sensitive to elevated 16:0.	Alonso et al., 2003
fad5	ADS3, ATADS3, FAD5, FADB, FATTY ACID DESATURASE 5, FATTY ACID DESATURASE B, JB67	high light susceptible	CS23879	AT3G15850	Chloroplastic enzyme responsible for the synthesis of 16:1 fatty acids from galactolipids and sulpholipids. Uses ferredoxin as electron donor.	Heilmann, 2004

				AT2G 37290	Ypt/Rab-GAP domain of gyp1p superfamily protein; FUNCTIONS IN: RAB GTPase activator activity; INVOLVED IN: regulation of Rab GTPase activity; CONTAINS InterPro DOMAIN/s: RabGAP/TBC (InterPro:IPR000195); BEST *Arabidopsis thaliana* protein match is: Ypt/Rab-GAP domain of gyp1p superfamily protein (TAIR:AT3G55020.1).	
fad7	ATFAD7, FAD7, FADD, FATTY ACID DESATURASE 7, FATTY ACID DESATURASE D	heat resistant cold susceptible	CS803 6	AT3G 11170	Chloroplastic enzyme responsible for the synthesis of 16:3 and 18:3 fatty acids from galactolipids, sulpholipids and phosphatidylglycerol. Uses ferredoxin as electron donor. Gene expression is induced by wounding in shoot and root. The wound-response in shoot is independent of jasmonic acid mediated pathway whereas the root response is mediated by jasmonic acid.	Iba et al., 1993
lea	DEHYDRIN LEA, LEA	salinity susceptible drought susceptible	SALK _1495 21C	AT2G 21490	Dehydrin LEA (LEA); FUNCTIONS IN: molecular_function unknown; INVOLVED IN: response to water, response to stress; LOCATED IN: cellular_component unknown; EXPRESSED IN: petal, leaf whorl, sepal, flower; EXPRESSED DURING: 4 anthesis, petal differentiation and expansion stage; CONTAINS InterPro DOMAIN/s: Dehydrin (InterPro:IPR000167); BEST *Arabidopsis thaliana* protein match is: Dehydrin family protein (TAIR:AT4G39130.1); Has 1372 Blast hits to 1173 proteins in 160 species: Archae - 0; Bacteria - 7; Metazoa - 17; Fungi - 21; Plants - 1314; Viruses - 2; Other Eukaryotes - 11 (source: NCBI BLink).	Tolleter et al., 2007
lpat1	ATS2, EMB1995, EMBRYO DEFECTIVE 1995, LPAT1, LYSOPHOSPHATIDIC ACID ACYLTRANSFERASE 1	cold resistant heat susceptible high light resistant	SALK _1338 05C	AT4G 30580	Encodes a plastidic lysophosphatidic acid acyltransferase (LPAAT). Is critical for chloroplasts phosphatidic acid biosynthesis. The null allele is embryo lethal.	Yu et al., 2004
p5cs1	ATP5CS, DELTA1-PYRROLINE-5-CARBOXYLATE SYNTHASE 1, P5CS1	salinity susceptible	SALK _0635 17C	AT2G 39800	Encodes a delta1-pyrroline-5-carboxylate synthase that catalyzes the rate-limiting enzyme in the biosynthesis of proline. Gene is expressed in reproductive organs and tissues under non-stress conditions but in the whole plant under water-limiting condition. Expression is also induced by abscisic acid and salt stress in a light-dependent manner. encodes a delta1-pyrroline-5-carboxylate synthase that catalyzes the rate-limiting enzyme in the biosynthesis of proline. Gene is expressed in reproductive organs and tissues under non-stress conditions but in the whole plant under water-limiting condition. Expression is also induced by abscisic acid and salt stress in a light-dependent manner. P5CS1 appears to be involved in salt stress responses related to proline accumulation, including	Yoshiba et al., 1999

					protection from reactive oxidative species. P5CS1 appears to be present in different cells and/or different subcellular locations from P5CS2 in a tissue-dependent manner.	
sos1	ATGL1, ATMYB0, GL1, GLABRA 1, MYB DOMAIN PROTEIN 0, MYB0	salinity susceptible	CS3862	AT3G27920	Encodes GL1, a Myb-like protein that is required for induction of trichome development. Interacts with JAZ and DELLA proteins to regulate trichome initiation.	Shi et al., 2000

Table A-2. Metabolic features with top 10 most positive and negative covariance loadings for the OPLS-DA S-plot for the treatment as compared to control

M/z	**Retention time**	**Polarity**	**Covariance**	**Correlation**	**Vip_prediction**	**Genotype**	**Treatment**	**Identified with reference standard**
147.0759	624.87	positive	2975	0.60	0.89	abi1	cold	Glutamine
130.0494	626.99	positive	2211	0.56	0.83	abi1	cold	
90.0546	507.61	positive	1809	0.98	1.44	abi1	cold	Alanine
148.0599	655.96	positive	1433	0.92	1.35	abi1	cold	Glutamic acid
145.0696	625.01	negative	1105	0.86	1.26	abi1	cold	Glutamine
116.0702	439.21	positive	1099	0.90	1.33	abi1	cold	Proline
439.0847	715.38	negative	1073	0.96	1.42	abi1	cold	
104.1066	56.07	positive	1027	0.88	1.29	abi1	cold	
133.0603	660.77	positive	939	0.76	1.12	abi1	cold	Asparagine
133.0185	449.98	negative	917	0.97	1.44	abi1	cold	Malic acid
110.0083	289.70	positive	-228	-0.83	1.22	abi1	cold	
82.5369	289.37	positive	-256	-0.80	1.19	abi1	cold	
112.9827	455.41	negative	-263	-0.23	0.35	abi1	cold	
74.0963	213.33	positive	-276	-0.78	1.15	abi1	cold	
132.0535	621.06	positive	-315	-0.97	1.43	abi1	cold	
253.1289	348.78	positive	-337	-0.92	1.36	abi1	cold	
381.1283	55.17	positive	-425	-0.97	1.43	abi1	cold	
148.0790	623.73	positive	-498	-0.88	1.30	abi1	cold	Glutamine [M+1]
106.0495	680.89	positive	-524	-0.77	1.13	abi1	cold	Serine
118.0857	424.74	positive	-652	-0.71	1.04	abi1	cold	Valine
90.0546	507.61	positive	1053	0.99	1.31	Col_0	cold	Alanine
118.0857	424.74	positive	932	1.00	1.32	Col_0	cold	Valine
166.0856	394.32	positive	718	0.98	1.29	Col_0	cold	Phenylalanine
439.0847	715.38	negative	687	0.96	1.26	Col_0	cold	
104.0702	381.14	positive	663	0.90	1.18	Col_0	cold	gamma-Aminobutyric acid
76.0391	577.83	positive	616	0.97	1.28	Col_0	cold	Glycine
81.0445	105.70	positive	594	1.00	1.32	Col_0	cold	
387.1207	715.25	negative	540	0.95	1.26	Col_0	cold	
120.0804	394.32	positive	513	0.97	1.28	Col_0	cold	
147.0759	624.87	positive	473	0.20	0.27	Col_0	cold	Glutamine

114.1022	717.99	positive	-455	-0.83	1.09	Col_0	cold	
196.0632	438.06	positive	-460	-0.54	0.71	Col_0	cold	
194.0625	438.17	negative	-471	-0.66	0.88	Col_0	cold	
116.0702	439.21	positive	-493	-0.48	0.63	Col_0	cold	Proline
88.0754	286.44	positive	-754	-0.84	1.11	Col_0	cold	
133.0603	660.77	positive	-848	-0.97	1.28	Col_0	cold	Asparagine
106.0495	680.89	positive	-906	-0.99	1.31	Col_0	cold	Serine
112.9827	455.41	negative	-942	-1.00	1.32	Col_0	cold	
148.0599	655.96	positive	-1044	-0.89	1.18	Col_0	cold	Glutamic acid
61.9896	629.65	negative	-2146	-0.95	1.26	Col_0	cold	
96.9625	908.66	negative	1467	0.45	0.68	dreb2a	cold	
148.0599	655.96	positive	1327	0.94	1.42	dreb2a	cold	Glutamic acid
106.0495	680.89	positive	1062	0.91	1.37	dreb2a	cold	Serine
74.0963	213.33	positive	939	0.99	1.50	dreb2a	cold	
175.1182	828.03	positive	883	0.46	0.70	dreb2a	cold	Arginine
133.0603	660.77	positive	733	0.70	1.06	dreb2a	cold	Asparagine
114.1022	717.99	positive	680	0.68	1.03	dreb2a	cold	
194.0625	438.17	negative	542	0.56	0.85	dreb2a	cold	
234.0189	438.75	positive	533	0.58	0.88	dreb2a	cold	
66.0681	718.06	positive	532	0.64	0.97	dreb2a	cold	
112.9827	540.78	negative	-623	-0.90	1.37	dreb2a	cold	
387.1207	715.25	negative	-666	-0.95	1.43	dreb2a	cold	
133.0185	449.98	negative	-734	-0.82	1.24	dreb2a	cold	Malic acid
76.0391	577.83	positive	-758	-0.95	1.45	dreb2a	cold	Glycine
81.0445	105.70	positive	-783	-0.96	1.46	dreb2a	cold	
104.0702	381.14	positive	-873	-0.59	0.89	dreb2a	cold	gamma-Aminobutyric acid
166.0856	394.32	positive	-887	-0.98	1.49	dreb2a	cold	Phenylalanine
439.0847	715.38	negative	-938	-0.99	1.50	dreb2a	cold	
147.0759	624.87	positive	-1353	-0.38	0.57	dreb2a	cold	Glutamine
90.0546	507.61	positive	-1440	-0.97	1.48	dreb2a	cold	Alanine
106.0495	680.89	positive	836	0.98	1.40	fab1	cold	Serine
61.9896	629.65	negative	749	0.45	0.64	fab1	cold	
74.0963	213.33	positive	691	0.99	1.41	fab1	cold	

114.1022	717.99	positive	313	0.73	1.03	fab1	cold	
457.1086	197.05	positive	274	0.92	1.32	fab1	cold	
447.0494	827.34	negative	261	0.89	1.27	fab1	cold	
194.0625	438.17	negative	256	0.38	0.54	fab1	cold	
104.0291	678.70	negative	233	0.99	1.41	fab1	cold	Serine
385.1228	329.16	negative	233	1.00	1.42	fab1	cold	
176.1024	691.43	positive	222	0.85	1.21	fab1	cold	Citrulline
133.0185	449.98	negative	-707	-0.96	1.37	fab1	cold	Malic acid
387.1207	715.25	negative	-721	-0.99	1.41	fab1	cold	
76.0391	577.83	positive	-732	-0.98	1.40	fab1	cold	Glycine
81.0445	105.70	positive	-772	-1.00	1.42	fab1	cold	
130.0494	626.99	positive	-785	-0.48	0.68	fab1	cold	
104.1066	56.07	positive	-838	-0.90	1.28	fab1	cold	
166.0856	394.32	positive	-871	-1.00	1.42	fab1	cold	Phenylalanine
439.0847	715.38	negative	-897	-0.99	1.41	fab1	cold	
147.0759	624.87	positive	-1166	-0.80	1.15	fab1	cold	Glutamine
90.0546	507.61	positive	-1330	-1.00	1.42	fab1	cold	Alanine
106.0495	680.89	positive	1156	1.00	1.44	fad5	cold	Serine
148.0599	655.96	positive	1018	0.90	1.29	fad5	cold	Glutamic acid
104.0702	381.14	positive	736	0.95	1.37	fad5	cold	gamma-Aminobutyric acid
194.0625	438.17	negative	545	0.82	1.18	fad5	cold	
116.0702	439.21	positive	526	0.81	1.17	fad5	cold	Proline
175.1182	828.03	positive	450	0.31	0.45	fad5	cold	Arginine
87.0438	381.14	positive	394	0.96	1.38	fad5	cold	
86.0598	381.14	positive	361	0.96	1.38	fad5	cold	
146.0532	648.68	negative	345	0.93	1.35	fad5	cold	Glutamic acid
98.9838	908.56	positive	327	0.54	0.78	fad5	cold	
76.0391	577.83	positive	-639	-0.99	1.42	fad5	cold	Glycine
341.1180	715.28	negative	-645	-0.99	1.43	fad5	cold	Sucrose
110.9735	638.84	negative	-656	-1.00	1.44	fad5	cold	
166.0856	394.32	positive	-771	-0.99	1.43	fad5	cold	Phenylalanine
387.1207	715.25	negative	-818	-0.99	1.43	fad5	cold	
130.0494	626.99	positive	-891	-0.83	1.20	fad5	cold	

439.0847	715.38	negative	-1001	-0.99	1.43	fad5	cold	
90.0546	507.61	positive	-1176	-1.00	1.44	fad5	cold	Alanine
147.0759	624.87	positive	-1285	-0.87	1.26	fad5	cold	Glutamine
61.9896	629.65	negative	-2012	-0.67	0.96	fad5	cold	
175.1182	828.03	positive	1192	0.66	0.91	fad7	cold	Arginine
106.0495	680.89	positive	499	0.72	0.99	fad7	cold	Serine
94.0448	289.23	positive	468	0.80	1.11	fad7	cold	
65.0603	828.64	positive	404	0.64	0.88	fad7	cold	
82.5369	289.37	positive	379	0.81	1.12	fad7	cold	
176.1024	691.43	positive	327	0.69	0.96	fad7	cold	Citrulline
173.1183	827.89	negative	311	0.74	1.03	fad7	cold	Arginine
176.1217	828.09	positive	300	0.66	0.91	fad7	cold	Arginine [M+1]
70.0650	828.64	positive	283	0.70	0.97	fad7	cold	
129.0405	253.59	negative	277	0.28	0.39	fad7	cold	
439.0847	715.38	negative	-906	-0.94	1.31	fad7	cold	
133.0185	449.98	negative	-967	-0.89	1.23	fad7	cold	Malic acid
116.0702	439.21	positive	-971	-0.88	1.22	fad7	cold	Proline
104.1066	56.07	positive	-1000	-0.91	1.26	fad7	cold	
104.0702	381.14	positive	-1111	-0.92	1.27	fad7	cold	gamma-Aminobutyric acid
136.0615	342.73	positive	-1164	-0.92	1.27	fad7	cold	Adenine
90.0546	507.61	positive	-1291	-0.91	1.26	fad7	cold	Alanine
148.0599	655.96	positive	-1409	-0.82	1.14	fad7	cold	Glutamic acid
130.0494	626.99	positive	-2234	-0.84	1.17	fad7	cold	
147.0759	624.87	positive	-2496	-0.79	1.09	fad7	cold	Glutamine
106.0495	680.89	positive	1063	0.99	1.35	lea	cold	gamma-Aminobutyric acid [M+1]
175.1182	828.03	positive	1012	0.63	0.86	lea	cold	
194.0625	438.17	negative	547	0.75	1.02	lea	cold	
339.1034	348.29	negative	540	0.95	1.30	lea	cold	
133.0603	660.77	positive	431	0.52	0.72	lea	cold	Leucine
148.0790	623.73	positive	375	0.92	1.26	lea	cold	Lysine
223.0671	347.80	negative	366	0.93	1.27	lea	cold	
88.0754	286.44	positive	339	0.30	0.41	lea	cold	
176.1024	691.43	positive	332	0.86	1.18	lea	cold	Arginine

173.1183	827.89	negative	322	0.82	1.12	lea	cold	Arginine
145.0696	625.01	negative	-813	-0.91	1.25	lea	cold	Glutamine
166.0856	394.32	positive	-826	-1.00	1.36	lea	cold	
116.0702	439.21	positive	-834	-0.93	1.27	lea	cold	
76.0391	577.83	positive	-907	-1.00	1.36	lea	cold	
387.1207	715.25	negative	-932	-1.00	1.37	lea	cold	
439.0847	715.38	negative	-1130	-1.00	1.37	lea	cold	
90.0546	507.61	positive	-1166	-0.99	1.36	lea	cold	
104.1066	56.07	positive	-1259	-0.97	1.34	lea	cold	
130.0494	626.99	positive	-2430	-0.91	1.25	lea	cold	
147.0759	624.87	positive	-2836	-0.88	1.20	lea	cold	
61.9896	629.65	negative	1305	0.94	1.31	lpat1	cold	
106.0495	680.89	positive	964	1.00	1.38	lpat1	cold	Serine
194.0625	438.17	negative	561	0.79	1.09	lpat1	cold	
98.9838	908.56	positive	482	0.86	1.19	lpat1	cold	
96.9625	908.66	negative	373	0.78	1.08	lpat1	cold	
196.0632	438.06	positive	365	0.47	0.65	lpat1	cold	
74.0963	213.33	positive	349	0.98	1.36	lpat1	cold	
234.0189	438.75	positive	280	0.79	1.09	lpat1	cold	
104.0291	678.70	negative	266	0.99	1.38	lpat1	cold	Serine
447.0494	827.34	negative	245	0.84	1.17	lpat1	cold	
110.9735	638.84	negative	-604	-0.99	1.37	lpat1	cold	
341.1180	715.28	negative	-611	-0.99	1.37	lpat1	cold	Sucrose
104.1066	56.07	positive	-710	-0.91	1.25	lpat1	cold	
76.0391	577.83	positive	-736	-1.00	1.38	lpat1	cold	Glycine
387.1207	715.25	negative	-746	-0.99	1.37	lpat1	cold	
166.0856	394.32	positive	-747	-0.99	1.37	lpat1	cold	Phenylalanine
439.0847	715.38	negative	-962	-1.00	1.38	lpat1	cold	
130.0494	626.99	positive	-1005	-0.97	1.34	lpat1	cold	
90.0546	507.61	positive	-1332	-1.00	1.38	lpat1	cold	Alanine
147.0759	624.87	positive	-1338	-0.97	1.34	lpat1	cold	Glutamine
61.9896	629.65	negative	968	0.40	0.57	p5cs1	cold	
106.0495	680.89	positive	868	0.98	1.40	p5cs1	cold	Serine

74.0963	213.33	positive	491	0.94	1.34	p5cs1	cold	
104.0702	381.14	positive	474	0.55	0.78	p5cs1	cold	gamma-Aminobutyric acid
94.0448	289.23	positive	363	0.65	0.93	p5cs1	cold	
87.0438	381.14	positive	348	0.74	1.06	p5cs1	cold	
82.5369	289.37	positive	316	0.74	1.05	p5cs1	cold	
86.0598	381.14	positive	313	0.73	1.04	p5cs1	cold	
447.0494	827.34	negative	242	0.83	1.18	p5cs1	cold	
104.0291	678.70	negative	237	0.99	1.42	p5cs1	cold	Serine
133.0185	449.98	negative	-803	-0.94	1.34	p5cs1	cold	Malic acid
166.0856	394.32	positive	-853	-0.96	1.38	p5cs1	cold	Phenylalanine
145.0696	625.01	negative	-868	-0.92	1.32	p5cs1	cold	Glutamine
76.0391	577.83	positive	-893	-0.99	1.41	p5cs1	cold	Glycine
439.0847	715.38	negative	-994	-0.98	1.40	p5cs1	cold	
175.1182	828.03	positive	-994	-0.75	1.07	p5cs1	cold	Arginine
104.1066	56.07	positive	-1045	-0.78	1.12	p5cs1	cold	
90.0546	507.61	positive	-1462	-0.97	1.38	p5cs1	cold	Alanine
130.0494	626.99	positive	-2116	-0.76	1.08	p5cs1	cold	
147.0759	624.87	positive	-2756	-0.80	1.14	p5cs1	cold	Glutamine
61.9896	629.65	negative	2412	0.91	1.28	sos1	cold	
148.0599	655.96	positive	1181	0.87	1.23	sos1	cold	Glutamic acid
112.9827	455.41	negative	992	1.00	1.40	sos1	cold	
106.0495	680.89	positive	974	0.95	1.34	sos1	cold	Serine
133.0603	660.77	positive	881	0.89	1.24	sos1	cold	Asparagine
104.0702	381.14	positive	816	0.64	0.91	sos1	cold	gamma-Aminobutyric acid
98.9838	908.56	positive	755	0.98	1.37	sos1	cold	
96.9625	908.66	negative	585	0.98	1.38	sos1	cold	
175.1182	828.03	positive	474	0.35	0.49	sos1	cold	Arginine
194.0625	438.17	negative	418	0.75	1.05	sos1	cold	
387.1207	715.25	negative	-507	-0.97	1.36	sos1	cold	
120.0804	394.32	positive	-529	-0.99	1.39	sos1	cold	
76.0391	577.83	positive	-533	-0.92	1.30	sos1	cold	Glycine
147.0759	624.87	positive	-585	-0.32	0.44	sos1	cold	Glutamine
130.0494	626.99	positive	-615	-0.35	0.49	sos1	cold	

439.0847	715.38	negative	-676	-0.98	1.38	sos1	cold	
166.0856	394.32	positive	-703	-0.99	1.39	sos1	cold	Phenylalanine
110.9735	638.84	negative	-722	-0.97	1.36	sos1	cold	
118.0857	424.74	positive	-798	-0.83	1.17	sos1	cold	Valine
90.0546	507.61	positive	-1236	-0.99	1.40	sos1	cold	Alanine
104.0702	381.14	positive	1146	0.77	1.16	abi1	drought	gamma-Aminobutyric acid
87.0438	381.14	positive	546	0.75	1.13	abi1	drought	
86.0598	381.14	positive	506	0.76	1.13	abi1	drought	
110.9735	638.84	negative	439	0.85	1.28	abi1	drought	
94.0448	289.23	positive	433	0.82	1.23	abi1	drought	
325.1991	476.30	negative	406	0.69	1.03	abi1	drought	
447.0494	827.34	negative	365	0.94	1.41	abi1	drought	
311.1682	479.61	negative	361	0.66	0.99	abi1	drought	
118.0857	424.74	positive	309	0.36	0.54	abi1	drought	Valine
148.0790	623.73	positive	297	0.87	1.31	abi1	drought	Glutamine [M+1]
192.1411	281.27	positive	-613	-0.97	1.45	abi1	drought	
106.0495	680.89	positive	-648	-0.73	1.09	abi1	drought	Serine
209.1391	62.38	positive	-657	-0.99	1.49	abi1	drought	
145.0696	625.01	negative	-726	-0.83	1.24	abi1	drought	Glutamine
175.1182	828.03	positive	-899	-0.74	1.11	abi1	drought	Arginine
209.1390	270.29	positive	-999	-0.97	1.46	abi1	drought	
88.0754	286.44	positive	-1088	-0.97	1.46	abi1	drought	
148.0599	655.96	positive	-1121	-0.83	1.25	abi1	drought	Glutamic acid
61.9896	629.65	negative	-1462	-0.56	0.84	abi1	drought	
130.0494	626.99	positive	-1661	-0.44	0.66	abi1	drought	
104.0702	381.14	positive	2717	0.97	1.49	Col-0	drought	gamma-Aminobutyric acid
147.0759	624.87	positive	2308	0.73	1.12	Col-0	drought	Glutamine
116.0702	439.21	positive	1685	0.91	1.40	Col-0	drought	Proline
130.0494	626.99	positive	1354	0.56	0.85	Col-0	drought	
87.0438	381.14	positive	1331	0.97	1.49	Col-0	drought	
86.0598	381.14	positive	1225	0.97	1.49	Col-0	drought	
61.9896	629.65	negative	1217	0.73	1.12	Col-0	drought	
132.1015	375.46	positive	1213	0.97	1.49	Col-0	drought	Leucine

90.0546	507.61	positive	1015	0.99	1.52	Col-0	drought	Alanine
104.1066	56.07	positive	882	0.96	1.48	Col-0	drought	
112.9827	455.41	negative	-266	-0.87	1.33	Col-0	drought	
115.0033	334.72	negative	-267	-0.73	1.12	Col-0	drought	Fumaric acid
82.5369	289.37	positive	-287	-0.61	0.94	Col-0	drought	
151.0347	289.20	positive	-290	-0.64	0.98	Col-0	drought	
105.0161	348.07	negative	-297	-0.91	1.39	Col-0	drought	
173.0231	429.81	negative	-303	-0.97	1.48	Col-0	drought	
209.1390	270.29	positive	-341	-0.86	1.32	Col-0	drought	
106.0495	680.89	positive	-404	-0.71	1.08	Col-0	drought	Serine
94.0448	289.23	positive	-454	-0.72	1.10	Col-0	drought	
148.0599	655.96	positive	-753	-0.69	1.05	Col-0	drought	Glutamic acid
104.0702	381.14	positive	2134	0.95	1.49	dreb2a	drought	gamma-Aminobutyric acid
116.0702	439.21	positive	1450	0.86	1.35	dreb2a	drought	Proline
132.1015	375.46	positive	1064	0.95	1.48	dreb2a	drought	Leucine
87.0438	381.14	positive	1049	0.95	1.48	dreb2a	drought	
90.0546	507.61	positive	976	0.96	1.49	dreb2a	drought	Alanine
86.0598	381.14	positive	967	0.95	1.48	dreb2a	drought	
439.0847	715.38	negative	870	0.97	1.51	dreb2a	drought	
387.1207	715.25	negative	740	0.93	1.45	dreb2a	drought	
196.0632	438.06	positive	623	0.95	1.49	dreb2a	drought	
311.1256	438.39	positive	602	0.87	1.36	dreb2a	drought	
130.0494	626.99	positive	-465	-0.14	0.22	dreb2a	drought	
98.9838	908.56	positive	-530	-0.71	1.10	dreb2a	drought	
146.0532	648.68	negative	-555	-0.77	1.20	dreb2a	drought	Glutamic acid
104.1066	56.07	positive	-604	-0.69	1.08	dreb2a	drought	
339.1034	348.29	negative	-618	-0.78	1.22	dreb2a	drought	
88.0754	286.44	positive	-697	-0.88	1.38	dreb2a	drought	
133.0185	449.98	negative	-800	-1.00	1.56	dreb2a	drought	Malic acid
106.0495	680.89	positive	-815	-0.80	1.26	dreb2a	drought	Serine
96.9625	908.66	negative	-1483	-0.44	0.69	dreb2a	drought	
148.0599	655.96	positive	-1658	-0.95	1.48	dreb2a	drought	Glutamic acid
175.1182	828.03	positive	693	0.75	1.02	fab1	drought	Arginine

148.0599	655.96	positive	525	0.67	0.91	fab1	drought	Glutamic acid
133.0185	449.98	negative	373	0.77	1.05	fab1	drought	Malic acid
74.0963	213.33	positive	359	0.85	1.15	fab1	drought	
112.9827	540.78	negative	329	0.65	0.88	fab1	drought	
209.1390	270.29	positive	321	1.00	1.35	fab1	drought	
105.0161	348.07	negative	296	0.90	1.22	fab1	drought	
98.9838	908.56	positive	287	0.56	0.76	fab1	drought	
118.0857	424.74	positive	283	0.42	0.57	fab1	drought	Valine
106.0495	680.89	positive	281	0.67	0.92	fab1	drought	Serine
387.1207	715.25	negative	-691	-0.99	1.35	fab1	drought	
439.0847	715.38	negative	-722	-0.99	1.34	fab1	drought	
104.1066	56.07	positive	-885	-0.93	1.26	fab1	drought	
90.0546	507.61	positive	-991	-1.00	1.36	fab1	drought	Alanine
132.1015	375.46	positive	-1039	-1.00	1.36	fab1	drought	Leucine
86.0598	381.14	positive	-1048	-1.00	1.36	fab1	drought	
87.0438	381.14	positive	-1134	-1.00	1.36	fab1	drought	
61.9896	629.65	negative	-1239	-0.66	0.90	fab1	drought	
116.0702	439.21	positive	-1688	-0.99	1.34	fab1	drought	Proline
104.0702	381.14	positive	-2301	-1.00	1.36	fab1	drought	gamma-Aminobutyric acid
148.0599	655.96	positive	1416	0.96	1.31	fad5	drought	Glutamic acid
175.1182	828.03	positive	747	0.48	0.66	fad5	drought	Arginine
106.0495	680.89	positive	681	0.97	1.33	fad5	drought	Serine
98.9838	908.56	positive	577	0.82	1.12	fad5	drought	
196.0632	438.06	positive	576	0.65	0.89	fad5	drought	
133.0185	449.98	negative	563	0.88	1.21	fad5	drought	Malic acid
194.0625	438.17	negative	496	0.67	0.92	fad5	drought	
114.1022	717.99	positive	480	0.82	1.12	fad5	drought	
133.0603	660.77	positive	431	0.61	0.84	fad5	drought	Asparagine
96.9625	908.66	negative	429	0.84	1.15	fad5	drought	
387.1207	715.25	negative	-576	-0.99	1.36	fad5	drought	
72.0806	406.23	positive	-588	-1.00	1.36	fad5	drought	
104.1066	56.07	positive	-823	-0.95	1.30	fad5	drought	
86.0598	381.14	positive	-925	-0.99	1.36	fad5	drought	

90.0546	507.61	positive	-969	-0.98	1.35	fad5	drought	Alanine
87.0438	381.14	positive	-1002	-0.99	1.36	fad5	drought	
132.1015	375.46	positive	-1166	-1.00	1.37	fad5	drought	Leucine
116.0702	439.21	positive	-1534	-0.98	1.34	fad5	drought	Proline
104.0702	381.14	positive	-2036	-0.99	1.36	fad5	drought	gamma-Aminobutyric acid
61.9896	629.65	negative	-2336	-0.77	1.06	fad5	drought	
94.0448	289.23	positive	404	0.78	1.20	fad7	drought	
105.0161	348.07	negative	348	0.97	1.50	fad7	drought	
95.0435	289.05	positive	157	0.78	1.20	fad7	drought	
95.0600	828.77	positive	101	0.94	1.46	fad7	drought	
96.0441	210.07	positive	66	0.99	1.53	fad7	drought	
104.0291	678.70	negative	53	0.28	0.43	fad7	drought	Serine
101.0194	578.29	negative	42	0.72	1.12	fad7	drought	
101.0193	437.59	negative	34	0.30	0.47	fad7	drought	
98.0598	396.50	positive	24	0.66	1.03	fad7	drought	
105.0354	678.20	negative	6	0.17	0.26	fad7	drought	Serine [M+1]
98.0233	661.85	positive	-3	-0.14	0.22	fad7	drought	
98.9838	908.56	positive	-6	-0.01	0.02	fad7	drought	
102.9510	814.22	negative	-21	-0.54	0.83	fad7	drought	
108.0022	309.96	negative	-37	-0.36	0.56	fad7	drought	
106.0190	348.39	negative	-49	-0.53	0.82	fad7	drought	
103.0343	116.36	negative	-49	-0.83	1.28	fad7	drought	
98.0710	109.39	positive	-57	-0.83	1.29	fad7	drought	
99.0913	59.13	positive	-78	-0.74	1.14	fad7	drought	
97.0282	717.74	positive	-96	-0.86	1.33	fad7	drought	
102.9979	410.69	negative	-158	-0.78	1.20	fad7	drought	
175.1182	828.03	positive	1410	0.86	1.11	lea	drought	
148.0599	655.96	positive	1402	0.99	1.28	lea	drought	Lysine
147.0759	624.87	positive	1151	0.79	1.02	lea	drought	
130.0494	626.99	positive	916	0.78	1.01	lea	drought	
106.0495	680.89	positive	828	0.99	1.29	lea	drought	
133.0603	660.77	positive	805	0.91	1.18	lea	drought	
196.0632	438.06	positive	706	0.78	1.01	lea	drought	

98.9838	908.56	positive	643	0.86	1.11	lea	drought	
114.1022	717.99	positive	607	0.92	1.20	lea	drought	
194.0625	438.17	negative	593	0.80	1.03	lea	drought	
387.1207	715.25	negative	-594	-0.95	1.23	lea	drought	
104.1066	56.07	positive	-678	-0.88	1.14	lea	drought	gamma-Aminobutyric acid
112.9827	455.41	negative	-923	-1.00	1.29	lea	drought	
132.1015	375.46	positive	-1025	-0.97	1.26	lea	drought	
90.0546	507.61	positive	-1048	-0.99	1.29	lea	drought	
86.0598	381.14	positive	-1056	-0.99	1.28	lea	drought	
87.0438	381.14	positive	-1144	-0.99	1.28	lea	drought	
61.9896	629.65	negative	-1420	-0.55	0.71	lea	drought	
116.0702	439.21	positive	-1514	-0.86	1.11	lea	drought	
104.0702	381.14	positive	-2318	-0.99	1.28	lea	drought	
61.9896	629.65	negative	1730	0.63	0.84	lpat1	drought	
148.0599	655.96	positive	713	0.91	1.22	lpat1	drought	Glutamic acid
106.0495	680.89	positive	429	0.95	1.29	lpat1	drought	Serine
136.0615	342.73	positive	334	0.90	1.21	lpat1	drought	Adenine
112.9827	455.41	negative	304	0.93	1.25	lpat1	drought	
115.0033	334.72	negative	303	0.97	1.30	lpat1	drought	Fumaric acid
133.0185	449.98	negative	264	0.82	1.10	lpat1	drought	Malic acid
105.0161	348.07	negative	242	0.91	1.23	lpat1	drought	
74.0963	213.33	positive	217	0.73	0.99	lpat1	drought	
146.0532	648.68	negative	213	0.92	1.24	lpat1	drought	Glutamic acid
387.1207	715.25	negative	-731	-1.00	1.34	lpat1	drought	
104.1066	56.07	positive	-773	-0.91	1.23	lpat1	drought	
439.0847	715.38	negative	-780	-0.99	1.34	lpat1	drought	
147.0759	624.87	positive	-885	-0.96	1.30	lpat1	drought	Glutamine
86.0598	381.14	positive	-972	-0.99	1.33	lpat1	drought	
90.0546	507.61	positive	-989	-0.99	1.33	lpat1	drought	Alanine
87.0438	381.14	positive	-1053	-0.99	1.33	lpat1	drought	
132.1015	375.46	positive	-1081	-0.99	1.34	lpat1	drought	Leucine
116.0702	439.21	positive	-1850	-0.96	1.29	lpat1	drought	Proline
104.0702	381.14	positive	-2156	-0.99	1.33	lpat1	drought	gamma-Aminobutyric acid

61.9896	629.65	negative	1125	0.48	0.70	p5cs1	drought	
148.0599	655.96	positive	971	0.90	1.33	p5cs1	drought	Glutamic acid
106.0495	680.89	positive	490	0.77	1.14	p5cs1	drought	Serine
196.0632	438.06	positive	483	0.62	0.91	p5cs1	drought	
98.9838	908.56	positive	414	0.77	1.14	p5cs1	drought	
391.1180	437.14	positive	348	0.78	1.15	p5cs1	drought	
74.0963	213.33	positive	303	0.77	1.13	p5cs1	drought	
136.0615	342.73	positive	300	0.83	1.23	p5cs1	drought	Adenine
194.0625	438.17	negative	297	0.55	0.81	p5cs1	drought	
84.0441	649.02	positive	287	0.92	1.36	p5cs1	drought	
72.0806	406.23	positive	-613	-0.97	1.43	p5cs1	drought	
387.1207	715.25	negative	-705	-1.00	1.47	p5cs1	drought	
439.0847	715.38	negative	-739	-1.00	1.47	p5cs1	drought	
147.0759	624.87	positive	-844	-0.70	1.03	p5cs1	drought	Glutamine
90.0546	507.61	positive	-948	-1.00	1.47	p5cs1	drought	Alanine
86.0598	381.14	positive	-1072	-0.99	1.46	p5cs1	drought	
87.0438	381.14	positive	-1162	-0.99	1.45	p5cs1	drought	
132.1015	375.46	positive	-1185	-0.97	1.43	p5cs1	drought	Leucine
116.0702	439.21	positive	-1400	-0.92	1.36	p5cs1	drought	Proline
104.0702	381.14	positive	-2385	-0.99	1.46	p5cs1	drought	gamma-Aminobutyric acid
61.9896	629.65	negative	1678	0.84	1.02	sos1	drought	
112.9827	455.41	negative	848	1.00	1.21	sos1	drought	
339.1034	348.29	negative	653	0.99	1.19	sos1	drought	
112.9827	540.78	negative	635	0.96	1.16	sos1	drought	
94.0448	289.23	positive	520	0.86	1.04	sos1	drought	
223.0671	347.80	negative	440	0.98	1.18	sos1	drought	
82.5369	289.37	positive	366	0.82	1.00	sos1	drought	
68.9956	513.43	negative	328	0.97	1.17	sos1	drought	
110.9735	638.84	negative	303	0.86	1.04	sos1	drought	
105.0161	348.07	negative	286	0.87	1.05	sos1	drought	
114.1022	717.99	positive	-1091	-0.97	1.18	sos1	drought	
87.0438	381.14	positive	-1097	-0.99	1.19	sos1	drought	
132.1015	375.46	positive	-1198	-0.99	1.20	sos1	drought	Leucine

148.0599	655.96	positive	-1360	-0.94	1.14	sos1	drought	Glutamic acid
104.1066	56.07	positive	-1404	-0.96	1.17	sos1	drought	
133.0603	660.77	positive	-1493	-0.99	1.19	sos1	drought	Asparagine
130.0494	626.99	positive	-1724	-0.65	0.79	sos1	drought	
116.0702	439.21	positive	-1939	-0.99	1.19	sos1	drought	Proline
147.0759	624.87	positive	-2182	-0.68	0.82	sos1	drought	Glutamine
104.0702	381.14	positive	-2255	-0.99	1.19	sos1	drought	gamma-Aminobutyric acid

Table A-3. Metabolic features with the top 10 most positive and negative covariance loadings for the OPLS-DA S-plot for the mutant as compared to wildtype

M/z	Retention time	Polarity	Covariance	Correlation	Vip_prediction	Mutant	Identified with reference standard
61.9896	10.49	negative	1721	0.90	1.23	abi1	
98.9838	15.14	positive	769	0.93	1.27	abi1	
116.0702	7.32	positive	738	0.64	0.87	abi1	Proline
339.1034	5.80	negative	618	0.83	1.13	abi1	
96.9625	15.14	negative	595	0.95	1.29	abi1	
148.0599	10.93	positive	472	0.54	0.74	abi1	Glutamic acid
106.0495	11.35	positive	460	0.84	1.15	abi1	Serine
223.0671	5.80	negative	453	0.84	1.14	abi1	
94.0448	4.82	positive	432	0.84	1.14	abi1	
104.0702	6.35	positive	416	0.58	0.79	abi1	gamma-Aminobutyric acid
209.1391	1.04	positive	-598	-0.99	1.35	abi1	
118.0857	7.08	positive	-604	-0.71	0.96	abi1	Valine
192.1411	4.69	positive	-659	-0.98	1.33	abi1	
84.0441	10.82	positive	-755	-0.77	1.04	abi1	
209.1390	4.50	positive	-843	-0.97	1.33	abi1	
145.0696	10.42	negative	-1033	-0.97	1.32	abi1	Glutamine
133.0603	11.01	positive	-1213	-0.98	1.33	abi1	Asparagine
175.1182	13.80	positive	-1392	-0.87	1.18	abi1	Arginine
130.0494	10.45	positive	-1501	-0.43	0.59	abi1	
147.0759	10.41	positive	-2407	-0.55	0.75	abi1	Glutamine
147.0759	10.41	positive	1547	0.41	0.64	dreb2a	Glutamine
96.9625	15.14	negative	1474	0.44	0.68	dreb2a	
148.0599	10.93	positive	1297	0.88	1.36	dreb2a	Glutamic acid
104.0702	6.35	positive	1127	0.88	1.36	dreb2a	gamma-Aminobutyric acid
104.1066	0.93	positive	1103	0.95	1.46	dreb2a	
175.1182	13.80	positive	1075	0.54	0.83	dreb2a	Arginine
130.0494	10.45	positive	910	0.29	0.45	dreb2a	
114.1022	11.97	positive	748	0.71	1.09	dreb2a	
196.0632	7.30	positive	724	0.69	1.06	dreb2a	

194.0625	7.30	negative	712	0.70	1.08	dreb2a	
138.0624	6.39	negative	-279	-0.88	1.35	dreb2a	
95.0435	4.82	positive	-287	-0.96	1.48	dreb2a	
123.0401	4.92	positive	-288	-0.96	1.48	dreb2a	
133.0185	7.50	negative	-296	-0.89	1.37	dreb2a	Malic acid
85.0758	1.45	positive	-328	-0.93	1.43	dreb2a	
151.0347	4.82	positive	-462	-0.91	1.41	dreb2a	
112.9827	9.01	negative	-481	-0.81	1.25	dreb2a	
82.5369	4.82	positive	-543	-0.97	1.49	dreb2a	
94.0448	4.82	positive	-748	-0.96	1.48	dreb2a	
88.0754	4.77	positive	-974	-0.89	1.37	dreb2a	
61.9896	10.49	negative	1054	0.54	0.86	fab1	
175.1182	13.80	positive	684	0.52	0.82	fab1	Arginine
192.1411	4.69	positive	471	0.97	1.53	fab1	
194.0625	7.30	negative	449	0.53	0.83	fab1	
244.0919	11.74	positive	423	0.91	1.44	fab1	
196.0632	7.30	positive	419	0.41	0.64	fab1	
118.0857	7.08	positive	381	0.48	0.76	fab1	Valine
303.0805	8.13	negative	302	0.94	1.48	fab1	
74.0963	3.56	positive	286	0.91	1.44	fab1	
327.0666	8.11	positive	276	0.96	1.50	fab1	
84.0441	10.82	positive	-608	-0.61	0.96	fab1	
116.0702	7.32	positive	-648	-0.52	0.82	fab1	Proline
133.0185	7.50	negative	-677	-0.96	1.50	fab1	Malic acid
148.0599	10.93	positive	-686	-0.63	1.00	fab1	Glutamic acid
104.0702	6.35	positive	-723	-0.91	1.43	fab1	gamma-Aminobutyric acid
145.0696	10.42	negative	-923	-0.93	1.46	fab1	Glutamine
133.0603	11.01	positive	-967	-0.95	1.50	fab1	Asparagine
88.0754	4.77	positive	-1367	-0.96	1.52	fab1	
130.0494	10.45	positive	-2417	-0.83	1.30	fab1	
147.0759	10.41	positive	-2477	-0.77	1.21	fab1	Glutamine
148.0599	10.93	positive	1044	0.89	1.18	fad5	Glutamic acid
116.0702	7.32	positive	829	0.72	0.96	fad5	Proline

196.0632	7.30	positive	679	0.72	0.95	fad5	
106.0495	11.35	positive	676	0.98	1.30	fad5	Serine
194.0625	7.30	negative	662	0.81	1.07	fad5	
175.1182	13.80	positive	647	0.44	0.59	fad5	Arginine
115.0033	5.58	negative	503	0.95	1.26	fad5	Fumaric acid
234.0189	7.31	positive	416	0.93	1.23	fad5	
244.0919	11.74	positive	393	1.00	1.32	fad5	
112.9827	7.59	negative	383	0.96	1.27	fad5	
148.0790	10.40	positive	-518	-0.99	1.30	fad5	Glutamine [M+1]
104.0702	6.35	positive	-600	-0.90	1.19	fad5	gamma-Aminobutyric acid
112.9827	9.01	negative	-650	-0.99	1.31	fad5	
94.0448	4.82	positive	-686	-0.97	1.28	fad5	
145.0696	10.42	negative	-887	-0.95	1.26	fad5	Glutamine
133.0603	11.01	positive	-907	-0.96	1.28	fad5	Asparagine
88.0754	4.77	positive	-1109	-0.96	1.27	fad5	
61.9896	10.49	negative	-1900	-0.96	1.28	fad5	
130.0494	10.45	positive	-2437	-0.89	1.17	fad5	
147.0759	10.41	positive	-2721	-0.87	1.15	fad5	Glutamine
175.1182	13.80	positive	1338	0.84	1.02	fad7	Arginine
129.0405	4.23	negative	595	0.70	0.85	fad7	
65.0603	13.81	positive	497	0.88	1.07	fad7	
118.0857	7.08	positive	414	0.70	0.84	fad7	Valine
176.1217	13.80	positive	335	0.84	1.02	fad7	Arginine [M+1]
381.1283	0.92	positive	327	0.84	1.02	fad7	
70.0650	13.81	positive	306	0.87	1.06	fad7	
173.1183	13.80	negative	304	0.86	1.04	fad7	Arginine
112.9827	9.01	negative	269	0.91	1.11	fad7	
112.0866	13.81	positive	230	0.87	1.06	fad7	
145.0696	10.42	negative	-730	-0.93	1.13	fad7	Glutamine
133.0185	7.50	negative	-816	-0.98	1.19	fad7	Malic acid
112.9827	7.59	negative	-869	-1.00	1.21	fad7	
88.0754	4.77	positive	-942	-0.94	1.14	fad7	
133.0603	11.01	positive	-1087	-1.00	1.21	fad7	Asparagine

116.0702	7.32	positive	-1109	-0.88	1.07	fad7	Proline
148.0599	10.93	positive	-1369	-0.95	1.15	fad7	Glutamic acid
61.9896	10.49	negative	-2024	-0.95	1.16	fad7	
130.0494	10.45	positive	-2073	-0.86	1.04	fad7	
147.0759	10.41	positive	-2226	-0.83	1.01	fad7	Glutamine
175.1182	13.80	positive	1510	0.91	1.14	lea	Arginine
148.0599	10.93	positive	1100	0.93	1.16	lea	Glutamic acid
196.0632	7.30	positive	861	0.80	1.00	lea	
106.0495	11.35	positive	763	0.98	1.23	lea	Serine
194.0625	7.30	negative	758	0.84	1.06	lea	
98.9838	15.14	positive	701	0.93	1.17	lea	
234.0189	7.31	positive	576	0.95	1.19	lea	
114.1022	11.97	positive	537	0.88	1.11	lea	
96.9625	15.14	negative	505	0.92	1.15	lea	
116.0702	7.32	positive	502	0.52	0.65	lea	Proline
209.1390	4.50	positive	-429	-0.97	1.22	lea	
87.0438	6.35	positive	-461	-0.98	1.22	lea	
94.0448	4.82	positive	-617	-0.95	1.19	lea	
112.9827	9.01	negative	-677	-1.00	1.25	lea	
145.0696	10.42	negative	-697	-0.91	1.14	lea	Glutamine
104.0702	6.35	positive	-892	-0.97	1.22	lea	gamma-Aminobutyric acid
112.9827	7.59	negative	-893	-1.00	1.25	lea	
147.0759	10.41	positive	-1713	-0.70	0.87	lea	Glutamine
130.0494	10.45	positive	-1753	-0.78	0.98	lea	
61.9896	10.49	negative	-1782	-0.97	1.21	lea	
61.9896	10.49	negative	2187	0.98	1.35	lpat1	
196.0632	7.30	positive	749	0.71	0.97	lpat1	
194.0625	7.30	negative	673	0.77	1.06	lpat1	
98.9838	15.14	positive	522	0.79	1.09	lpat1	
115.0033	5.58	negative	427	0.96	1.31	lpat1	Fumaric acid
234.0189	7.31	positive	388	0.87	1.18	lpat1	
244.0919	11.74	positive	380	0.98	1.34	lpat1	
96.9625	15.14	negative	377	0.73	1.00	lpat1	

391.1180	7.29	positive	348	0.73	1.00	lpat1	
106.0495	11.35	positive	329	0.78	1.07	lpat1	Serine
148.0790	10.40	positive	-501	-0.99	1.36	lpat1	Glutamine [M+1]
209.1390	4.50	positive	-501	-0.98	1.34	lpat1	
104.0702	6.35	positive	-512	-0.54	0.74	lpat1	gamma-Aminobutyric acid
112.9827	9.01	negative	-563	-0.99	1.36	lpat1	
94.0448	4.82	positive	-677	-0.96	1.31	lpat1	
145.0696	10.42	negative	-877	-0.94	1.28	lpat1	Glutamine
133.0603	11.01	positive	-925	-0.99	1.35	lpat1	Asparagine
88.0754	4.77	positive	-1114	-0.95	1.30	lpat1	
130.0494	10.45	positive	-2428	-0.87	1.19	lpat1	
147.0759	10.41	positive	-2651	-0.85	1.16	lpat1	Glutamine
61.9896	10.49	negative	1551	0.89	1.37	p5cs1	
104.0702	6.35	positive	709	0.81	1.26	p5cs1	gamma-Aminobutyric acid
196.0632	7.30	positive	639	0.58	0.90	p5cs1	
194.0625	7.30	negative	519	0.61	0.94	p5cs1	
104.1066	0.93	positive	473	0.73	1.13	p5cs1	
192.1411	4.69	positive	421	0.96	1.49	p5cs1	
87.0438	6.35	positive	364	0.83	1.28	p5cs1	
391.1180	7.29	positive	356	0.67	1.05	p5cs1	
244.0919	11.74	positive	350	0.92	1.43	p5cs1	
62.0600	5.65	positive	342	0.87	1.35	p5cs1	
110.9735	10.65	negative	-453	-0.93	1.44	p5cs1	
209.1390	4.50	positive	-495	-0.97	1.50	p5cs1	
133.0185	7.50	negative	-502	-0.85	1.32	p5cs1	Malic acid
84.0441	10.82	positive	-541	-0.56	0.87	p5cs1	
116.0702	7.32	positive	-909	-0.70	1.08	p5cs1	Proline
145.0696	10.42	negative	-918	-0.92	1.43	p5cs1	Glutamine
133.0603	11.01	positive	-1006	-0.96	1.49	p5cs1	Asparagine
88.0754	4.77	positive	-1213	-0.93	1.45	p5cs1	
130.0494	10.45	positive	-2391	-0.81	1.26	p5cs1	
147.0759	10.41	positive	-2509	-0.77	1.20	p5cs1	Glutamine
104.0702	6.35	positive	1376	0.79	1.36	sos1	gamma-Aminobutyric acid

61.9896	10.49	negative	700	0.33	0.57	sos1	
87.0438	6.35	positive	671	0.78	1.35	sos1	
86.0598	6.35	positive	614	0.78	1.34	sos1	
244.0919	11.74	positive	450	0.87	1.49	sos1	
118.0857	7.08	positive	397	0.44	0.75	sos1	Valine
126.9077	8.49	negative	393	0.91	1.56	sos1	
175.1182	13.80	positive	391	0.29	0.50	sos1	Arginine
192.1411	4.69	positive	371	0.89	1.52	sos1	
136.0615	5.71	positive	347	0.62	1.07	sos1	Adenine
94.0448	4.82	positive	-360	-0.53	0.92	sos1	
90.0546	8.46	positive	-373	-0.79	1.36	sos1	Alanine
209.1390	4.50	positive	-392	-0.82	1.41	sos1	
131.0526	10.61	positive	-420	-0.65	1.12	sos1	
84.0441	10.82	positive	-605	-0.57	0.98	sos1	
116.0702	7.32	positive	-797	-0.57	0.98	sos1	Proline
145.0696	10.42	negative	-906	-0.90	1.55	sos1	Glutamine
88.0754	4.77	positive	-1326	-0.93	1.60	sos1	
147.0759	10.41	positive	-2227	-0.68	1.16	sos1	Glutamine
130.0494	10.45	positive	-2396	-0.79	1.35	sos1	
118.0857	7.08	positive	889	1.00	1.26	cold_abi1	Valine
98.9838	15.14	positive	545	0.87	1.10	cold_abi1	
94.0448	4.82	positive	448	0.79	1.00	cold_abi1	
96.9625	15.14	negative	414	0.89	1.13	cold_abi1	
81.0445	1.76	positive	370	0.92	1.17	cold_abi1	
82.5369	4.82	positive	305	0.83	1.05	cold_abi1	
115.0033	5.58	negative	246	0.96	1.21	cold_abi1	Fumaric acid
146.0630	0.86	positive	244	0.92	1.17	cold_abi1	
168.0448	0.85	positive	241	0.93	1.18	cold_abi1	
151.0347	4.82	positive	225	0.70	0.88	cold_abi1	
84.0441	10.82	positive	-929	-0.96	1.21	cold_abi1	
196.0632	7.30	positive	-970	-0.85	1.08	cold_abi1	
90.0546	8.46	positive	-1247	-0.96	1.21	cold_abi1	Alanine
145.0696	10.42	negative	-1385	-0.96	1.21	cold_abi1	Glutamine

61.9896	10.49	negative	-1506	-0.78	0.98	cold_abi1	
148.0599	10.93	positive	-1521	-0.95	1.21	cold_abi1	Glutamic acid
133.0603	11.01	positive	-1659	-0.97	1.22	cold_abi1	Asparagine
175.1182	13.80	positive	-1668	-0.92	1.17	cold_abi1	Arginine
130.0494	10.45	positive	-3355	-0.96	1.22	cold_abi1	
147.0759	10.41	positive	-4263	-0.96	1.21	cold_abi1	Glutamine
147.0759	10.41	positive	2527	0.86	1.16	cold_dreb2a	Glutamine
61.9896	10.49	negative	2085	0.88	1.19	cold_dreb2a	
130.0494	10.45	positive	1575	0.86	1.16	cold_dreb2a	
104.0702	6.35	positive	1139	0.78	1.06	cold_dreb2a	gamma-Aminobutyric acid
148.0599	10.93	positive	1100	0.95	1.28	cold_dreb2a	Glutamic acid
104.1066	0.93	positive	1040	0.84	1.14	cold_dreb2a	
116.0702	7.32	positive	1039	0.83	1.12	cold_dreb2a	Proline
196.0632	7.30	positive	844	0.76	1.03	cold_dreb2a	
112.9827	7.59	negative	676	0.69	0.94	cold_dreb2a	
90.0546	8.46	positive	636	0.78	1.05	cold_dreb2a	Alanine
209.1391	1.04	positive	-160	-0.66	0.89	cold_dreb2a	
138.0624	6.39	negative	-173	-0.79	1.07	cold_dreb2a	
381.1283	0.92	positive	-174	-0.77	1.04	cold_dreb2a	
139.0132	9.09	negative	-196	-0.74	1.01	cold_dreb2a	
82.5369	4.82	positive	-213	-0.65	0.88	cold_dreb2a	
94.0448	4.82	positive	-315	-0.61	0.82	cold_dreb2a	
110.9735	10.65	negative	-494	-0.96	1.30	cold_dreb2a	
88.0754	4.77	positive	-524	-0.81	1.10	cold_dreb2a	
118.0857	7.08	positive	-540	-0.56	0.76	cold_dreb2a	Valine
74.0963	3.56	positive	-676	-0.98	1.33	cold_dreb2a	
61.9896	10.49	negative	2356	0.96	1.33	cold_fab1	
112.9827	7.59	negative	1003	1.00	1.37	cold_fab1	
196.0632	7.30	positive	901	0.87	1.20	cold_fab1	
175.1182	13.80	positive	871	0.78	1.08	cold_fab1	Arginine
148.0599	10.93	positive	759	0.86	1.18	cold_fab1	Glutamic acid
194.0625	7.30	negative	670	0.86	1.18	cold_fab1	
104.1066	0.93	positive	657	0.74	1.01	cold_fab1	

90.0546	8.46	positive	537	0.84	1.15	cold_fab1	Alanine
439.0847	11.92	negative	486	0.84	1.16	cold_fab1	
311.1256	7.31	positive	475	0.91	1.26	cold_fab1	
87.0438	6.35	positive	-352	-0.76	1.04	cold_fab1	
94.0448	4.82	positive	-384	-0.69	0.96	cold_fab1	
110.9735	10.65	negative	-400	-0.90	1.23	cold_fab1	
74.0963	3.56	positive	-550	-0.96	1.32	cold_fab1	
84.0441	10.82	positive	-574	-0.72	0.99	cold_fab1	
145.0696	10.42	negative	-664	-0.87	1.20	cold_fab1	Glutamine
88.0754	4.77	positive	-664	-0.89	1.22	cold_fab1	
104.0702	6.35	positive	-689	-0.73	1.01	cold_fab1	gamma-Aminobutyric acid
130.0494	10.45	positive	-1544	-0.76	1.05	cold_fab1	
147.0759	10.41	positive	-2262	-0.91	1.25	cold_fab1	Glutamine
61.9896	10.49	negative	1981	0.73	0.89	cold_fad5	
148.0599	10.93	positive	1090	0.95	1.16	cold_fad5	Glutamic acid
116.0702	7.32	positive	997	0.97	1.18	cold_fad5	Proline
112.9827	7.59	negative	951	1.00	1.22	cold_fad5	
196.0632	7.30	positive	904	0.97	1.19	cold_fad5	
175.1182	13.80	positive	737	0.88	1.08	cold_fad5	Arginine
194.0625	7.30	negative	691	0.96	1.18	cold_fad5	
439.0847	11.92	negative	629	0.93	1.14	cold_fad5	
311.1256	7.31	positive	575	0.99	1.21	cold_fad5	
387.1207	11.92	negative	556	0.95	1.16	cold_fad5	
87.0438	6.35	positive	-521	-0.99	1.21	cold_fad5	
112.9827	9.01	negative	-589	-0.96	1.18	cold_fad5	
94.0448	4.82	positive	-636	-0.93	1.13	cold_fad5	
88.0754	4.77	positive	-680	-0.91	1.12	cold_fad5	
84.0441	10.82	positive	-698	-0.99	1.21	cold_fad5	
145.0696	10.42	negative	-803	-0.99	1.21	cold_fad5	Glutamine
118.0857	7.08	positive	-864	-1.00	1.22	cold_fad5	Valine
104.0702	6.35	positive	-1077	-0.99	1.21	cold_fad5	gamma-Aminobutyric acid
130.0494	10.45	positive	-2043	-0.97	1.19	cold_fad5	
147.0759	10.41	positive	-2578	-0.97	1.18	cold_fad5	Glutamine

136.0615	5.71	positive	1440	1.00	1.68	cold_fad7	Adenine
148.0599	10.93	positive	1047	0.61	1.04	cold_fad7	Glutamic acid
175.1182	13.80	positive	836	0.44	0.74	cold_fad7	Arginine
112.9827	7.59	negative	788	0.70	1.18	cold_fad7	
381.1283	0.92	positive	727	0.95	1.60	cold_fad7	
104.0702	6.35	positive	695	0.80	1.35	cold_fad7	gamma-Aminobutyric acid
325.1991	7.94	negative	623	0.72	1.22	cold_fad7	
110.9735	10.65	negative	596	0.96	1.62	cold_fad7	
89.0180	2.40	negative	509	0.90	1.53	cold_fad7	
129.0405	4.23	negative	477	0.47	0.79	cold_fad7	
268.1034	5.33	positive	-404	-0.98	1.66	cold_fad7	Adenosine
96.9625	15.14	negative	-417	-0.68	1.15	cold_fad7	
118.0857	7.08	positive	-420	-0.40	0.68	cold_fad7	Valine
147.0759	10.41	positive	-492	-0.16	0.26	cold_fad7	Glutamine
133.0603	11.01	positive	-556	-0.61	1.04	cold_fad7	Asparagine
82.5369	4.82	positive	-557	-0.87	1.47	cold_fad7	
98.9838	15.14	positive	-565	-0.72	1.22	cold_fad7	
151.0347	4.82	positive	-574	-0.90	1.52	cold_fad7	
81.0445	1.76	positive	-645	-0.99	1.67	cold_fad7	
94.0448	4.82	positive	-824	-0.89	1.51	cold_fad7	
148.0599	10.93	positive	1542	0.98	1.18	cold_lea	Glutamic acid
116.0702	7.32	positive	1187	0.97	1.17	cold_lea	Proline
104.1066	0.93	positive	1107	0.94	1.13	cold_lea	
130.0494	10.45	positive	1079	0.60	0.72	cold_lea	
196.0632	7.30	positive	994	0.97	1.17	cold_lea	
175.1182	13.80	positive	943	0.69	0.84	cold_lea	Arginine
147.0759	10.41	positive	930	0.42	0.50	cold_lea	Glutamine
439.0847	11.92	negative	849	0.99	1.19	cold_lea	
98.9838	15.14	positive	835	0.91	1.09	cold_lea	
61.9896	10.49	negative	790	0.61	0.74	cold_lea	
136.0615	5.71	positive	-323	-0.83	1.01	cold_lea	Adenine
87.0438	6.35	positive	-344	-0.75	0.90	cold_lea	
209.1390	4.50	positive	-346	-0.89	1.07	cold_lea	

110.9735	10.65	negative	-414	-0.97	1.17	cold_lea	
82.5369	4.82	positive	-417	-0.94	1.13	cold_lea	
339.1034	5.80	negative	-504	-0.99	1.19	cold_lea	
94.0448	4.82	positive	-622	-0.93	1.12	cold_lea	
104.0702	6.35	positive	-717	-0.76	0.91	cold_lea	gamma-Aminobutyric acid
112.9827	9.01	negative	-721	-1.00	1.20	cold_lea	
118.0857	7.08	positive	-846	-1.00	1.20	cold_lea	Valine
61.9896	10.49	negative	2569	0.98	1.21	cold_lpat1	
148.0599	10.93	positive	999	0.95	1.17	cold_lpat1	Glutamic acid
112.9827	7.59	negative	912	1.00	1.23	cold_lpat1	
196.0632	7.30	positive	848	0.94	1.16	cold_lpat1	
116.0702	7.32	positive	747	0.90	1.11	cold_lpat1	Proline
194.0625	7.30	negative	657	0.95	1.17	cold_lpat1	
90.0546	8.46	positive	582	0.91	1.13	cold_lpat1	Alanine
175.1182	13.80	positive	582	0.82	1.01	cold_lpat1	Arginine
439.0847	11.92	negative	575	0.92	1.14	cold_lpat1	
311.1256	7.31	positive	505	0.96	1.19	cold_lpat1	
81.0445	1.76	positive	-492	-0.99	1.22	cold_lpat1	
112.9827	9.01	negative	-531	-0.98	1.21	cold_lpat1	
88.0754	4.77	positive	-602	-0.90	1.11	cold_lpat1	
94.0448	4.82	positive	-621	-0.92	1.14	cold_lpat1	
104.0702	6.35	positive	-669	-0.86	1.06	cold_lpat1	gamma-Aminobutyric acid
84.0441	10.82	positive	-689	-0.98	1.21	cold_lpat1	
145.0696	10.42	negative	-716	-0.95	1.17	cold_lpat1	Glutamine
118.0857	7.08	positive	-869	-1.00	1.23	cold_lpat1	Valine
130.0494	10.45	positive	-1949	-0.96	1.19	cold_lpat1	
147.0759	10.41	positive	-2468	-0.96	1.18	cold_lpat1	Glutamine
61.9896	10.49	negative	1831	0.72	0.93	cold_p5cs1	
148.0599	10.93	positive	1290	0.92	1.20	cold_p5cs1	Glutamic acid
196.0632	7.30	positive	1043	0.96	1.25	cold_p5cs1	
104.1066	0.93	positive	995	0.78	1.02	cold_p5cs1	
112.9827	7.59	negative	983	1.00	1.30	cold_p5cs1	
175.1182	13.80	positive	863	0.72	0.94	cold_p5cs1	Arginine

194.0625	7.30	negative	781	0.96	1.25	cold_p5cs1	
90.0546	8.46	positive	706	0.77	1.01	cold_p5cs1	Alanine
114.1022	11.97	positive	599	0.88	1.14	cold_p5cs1	
439.0847	11.92	negative	598	0.87	1.13	cold_p5cs1	
209.1391	1.04	positive	-275	-0.92	1.19	cold_p5cs1	
116.0702	7.32	positive	-374	-0.56	0.72	cold_p5cs1	Proline
82.5369	4.82	positive	-380	-0.88	1.14	cold_p5cs1	
74.0963	3.56	positive	-380	-0.88	1.15	cold_p5cs1	
110.9735	10.65	negative	-446	-0.94	1.22	cold_p5cs1	
112.9827	9.01	negative	-450	-0.74	0.96	cold_p5cs1	
104.0702	6.35	positive	-490	-0.63	0.82	cold_p5cs1	gamma-Aminobutyric acid
94.0448	4.82	positive	-556	-0.85	1.10	cold_p5cs1	
88.0754	4.77	positive	-621	-0.82	1.06	cold_p5cs1	
118.0857	7.08	positive	-918	-1.00	1.30	cold_p5cs1	Valine
110.9735	10.65	negative	847	0.97	1.64	cold_sos1	
196.0632	7.30	positive	451	0.58	0.99	cold_sos1	
244.0919	11.74	positive	448	0.98	1.67	cold_sos1	
129.0405	4.23	negative	430	0.40	0.68	cold_sos1	
148.0790	10.40	positive	398	0.85	1.44	cold_sos1	Glutamine [M+1]
114.1022	11.97	positive	350	0.68	1.15	cold_sos1	
90.0546	8.46	positive	348	0.55	0.93	cold_sos1	Alanine
457.1086	3.28	positive	338	0.71	1.20	cold_sos1	
194.0625	7.30	negative	334	0.66	1.12	cold_sos1	
126.9077	8.49	negative	327	0.96	1.63	cold_sos1	
96.9625	15.14	negative	-464	-0.89	1.50	cold_sos1	
94.0448	4.82	positive	-466	-0.65	1.10	cold_sos1	
98.9838	15.14	positive	-588	-0.87	1.47	cold_sos1	
81.0445	1.76	positive	-629	-0.98	1.67	cold_sos1	
84.0441	10.82	positive	-655	-0.64	1.08	cold_sos1	
145.0696	10.42	negative	-708	-0.79	1.34	cold_sos1	Glutamine
116.0702	7.32	positive	-713	-0.79	1.34	cold_sos1	Proline
88.0754	4.77	positive	-911	-0.89	1.51	cold_sos1	
130.0494	10.45	positive	-1537	-0.63	1.07	cold_sos1	

147.0759	10.41	positive	-2332	-0.77	1.30	cold_sos1	Glutamine
61.9896	10.49	negative	2678	0.86	1.20	drought_abi1	
104.0702	6.35	positive	2195	0.94	1.31	drought_abi1	gamma-Aminobutyric acid
116.0702	7.32	positive	1936	0.97	1.35	drought_abi1	Proline
130.0494	10.45	positive	1137	0.52	0.72	drought_abi1	
132.1015	6.26	positive	1121	0.97	1.36	drought_abi1	Leucine
87.0438	6.35	positive	1086	0.94	1.31	drought_abi1	
86.0598	6.35	positive	998	0.94	1.31	drought_abi1	
98.9838	15.14	positive	930	0.95	1.33	drought_abi1	
148.0599	10.93	positive	887	0.76	1.06	drought_abi1	Glutamic acid
104.1066	0.93	positive	876	0.77	1.07	drought_abi1	
94.0448	4.82	positive	-356	-0.65	0.91	drought_abi1	
145.0696	10.42	negative	-369	-0.54	0.75	drought_abi1	Glutamine
325.1991	7.94	negative	-378	-0.69	0.96	drought_abi1	
381.1283	0.92	positive	-409	-0.96	1.35	drought_abi1	
112.9827	9.01	negative	-449	-0.89	1.24	drought_abi1	
133.0603	11.01	positive	-535	-0.39	0.55	drought_abi1	Asparagine
110.9735	10.65	negative	-574	-0.95	1.33	drought_abi1	
175.1182	13.80	positive	-802	-0.64	0.89	drought_abi1	Arginine
118.0857	7.08	positive	-854	-0.95	1.33	drought_abi1	Valine
147.0759	10.41	positive	-1602	-0.45	0.63	drought_abi1	Glutamine
175.1182	13.80	positive	1274	0.73	1.22	drought_dreb2a	Arginine
196.0632	7.30	positive	864	0.68	1.14	drought_dreb2a	
114.1022	11.97	positive	818	0.84	1.42	drought_dreb2a	
194.0625	7.30	negative	780	0.71	1.20	drought_dreb2a	
66.0681	11.97	positive	663	0.84	1.41	drought_dreb2a	
244.0919	11.74	positive	623	0.97	1.63	drought_dreb2a	
131.1287	11.96	positive	605	0.85	1.43	drought_dreb2a	
118.0857	7.08	positive	532	0.45	0.76	drought_dreb2a	Valine
439.0847	11.92	negative	484	0.79	1.33	drought_dreb2a	
311.1256	7.31	positive	447	0.71	1.20	drought_dreb2a	
76.0391	9.63	positive	-430	-0.99	1.67	drought_dreb2a	Glycine
87.0438	6.35	positive	-435	-0.49	0.83	drought_dreb2a	

223.0671	5.80	negative	-463	-0.89	1.51	drought_dreb2a	
61.9896	10.49	negative	-516	-0.22	0.37	drought_dreb2a	
339.1034	5.80	negative	-657	-0.90	1.51	drought_dreb2a	
133.0185	7.50	negative	-881	-0.81	1.36	drought_dreb2a	Malic acid
130.0494	10.45	positive	-885	-0.31	0.53	drought_dreb2a	
104.0702	6.35	positive	-951	-0.52	0.88	drought_dreb2a	gamma-Aminobutyric acid
147.0759	10.41	positive	-1021	-0.29	0.50	drought_dreb2a	Glutamine
88.0754	4.77	positive	-1289	-0.95	1.60	drought_dreb2a	
175.1182	13.80	positive	1274	0.73	1.22	drought_fab1	Arginine
196.0632	7.30	positive	864	0.68	1.14	drought_fab1	
114.1022	11.97	positive	818	0.84	1.42	drought_fab1	
194.0625	7.30	negative	780	0.71	1.20	drought_fab1	
66.0681	11.97	positive	663	0.84	1.41	drought_fab1	
244.0919	11.74	positive	623	0.97	1.63	drought_fab1	
131.1287	11.96	positive	605	0.85	1.43	drought_fab1	
118.0857	7.08	positive	532	0.45	0.76	drought_fab1	Valine
439.0847	11.92	negative	484	0.79	1.33	drought_fab1	
311.1256	7.31	positive	447	0.71	1.20	drought_fab1	
76.0391	9.63	positive	-430	-0.99	1.67	drought_fab1	Glycine
87.0438	6.35	positive	-435	-0.49	0.83	drought_fab1	
223.0671	5.80	negative	-463	-0.89	1.51	drought_fab1	
61.9896	10.49	negative	-516	-0.22	0.37	drought_fab1	
339.1034	5.80	negative	-657	-0.90	1.51	drought_fab1	
133.0185	7.50	negative	-881	-0.81	1.36	drought_fab1	Malic acid
130.0494	10.45	positive	-885	-0.31	0.53	drought_fab1	
104.0702	6.35	positive	-951	-0.52	0.88	drought_fab1	gamma-Aminobutyric acid
147.0759	10.41	positive	-1021	-0.29	0.50	drought_fab1	Glutamine
88.0754	4.77	positive	-1289	-0.95	1.60	drought_fab1	
116.0702	7.32	positive	859	0.74	1.01	drought_fad5	Proline
61.9896	10.49	negative	579	0.24	0.32	drought_fad5	
115.0033	5.58	negative	523	0.88	1.20	drought_fad5	Fumaric acid
106.0495	11.35	positive	395	0.74	1.01	drought_fad5	Serine
62.0600	5.65	positive	302	0.82	1.11	drought_fad5	

173.0231	7.16	negative	298	1.00	1.36	drought_fad5	
143.0072	7.16	negative	255	1.00	1.36	drought_fad5	
70.0650	7.32	positive	245	0.73	1.00	drought_fad5	
335.1084	3.71	positive	243	0.85	1.15	drought_fad5	
126.9077	8.49	negative	243	0.96	1.31	drought_fad5	
741.6599	8.32	negative	236	0.99	1.34	drought_fad5	
86.0598	6.35	positive	-611	-0.81	1.11	drought_fad5	
87.0438	6.35	positive	-671	-0.82	1.11	drought_fad5	
131.0526	10.61	positive	-690	-0.99	1.35	drought_fad5	
84.0441	10.82	positive	-982	-0.99	1.35	drought_fad5	
88.0754	4.77	positive	-1068	-0.96	1.31	drought_fad5	
145.0696	10.42	negative	-1074	-0.99	1.34	drought_fad5	Glutamine
133.0603	11.01	positive	-1230	-0.94	1.29	drought_fad5	Asparagine
104.0702	6.35	positive	-1357	-0.81	1.11	drought_fad5	gamma-Aminobutyric acid
130.0494	10.45	positive	-3072	-0.99	1.35	drought_fad5	
147.0759	10.41	positive	-3773	-0.99	1.35	drought_fad5	Glutamine
118.0857	7.08	positive	843	0.98	1.23	drought_fad7	Valine
381.1283	0.92	positive	639	0.99	1.25	drought_fad7	
112.9827	9.01	negative	396	0.90	1.13	drought_fad7	
397.1016	0.95	positive	359	0.98	1.24	drought_fad7	
139.0132	9.09	negative	342	0.97	1.22	drought_fad7	
110.9735	10.65	negative	329	0.96	1.21	drought_fad7	
359.1467	0.92	positive	315	0.99	1.25	drought_fad7	
129.0405	4.23	negative	304	0.36	0.45	drought_fad7	
382.1317	0.99	positive	300	0.99	1.25	drought_fad7	
89.0180	2.40	negative	196	0.69	0.87	drought_fad7	
104.1066	0.93	positive	-967	-0.96	1.21	drought_fad7	
145.0696	10.42	negative	-1007	-0.98	1.24	drought_fad7	Glutamine
148.0599	10.93	positive	-1138	-0.89	1.12	drought_fad7	Glutamic acid
88.0754	4.77	positive	-1147	-0.97	1.22	drought_fad7	
133.0603	11.01	positive	-1316	-0.97	1.22	drought_fad7	Asparagine
116.0702	7.32	positive	-1520	-0.93	1.17	drought_fad7	Proline
104.0702	6.35	positive	-1646	-0.90	1.14	drought_fad7	gamma-Aminobutyric acid

61.9896	10.49	negative	-2343	-0.97	1.23	drought_fad7	
130.0494	10.45	positive	-2945	-0.99	1.24	drought_fad7	
147.0759	10.41	positive	-3621	-0.98	1.24	drought_fad7	Glutamine
116.0702	7.32	positive	866	0.51	0.79	drought_lea	Proline
90.0546	8.46	positive	556	0.83	1.29	drought_lea	Alanine
115.0033	5.58	negative	499	0.92	1.42	drought_lea	Fumaric acid
194.0625	7.30	negative	433	0.47	0.73	drought_lea	
311.1256	7.31	positive	365	0.62	0.97	drought_lea	
62.0600	5.65	positive	353	0.83	1.29	drought_lea	
106.0495	11.35	positive	331	0.66	1.03	drought_lea	Serine
196.0632	7.30	positive	327	0.31	0.48	drought_lea	
234.0189	7.31	positive	267	0.59	0.91	drought_lea	
112.9827	7.59	negative	266	0.84	1.30	drought_lea	
88.0754	4.77	positive	-668	-0.65	1.01	drought_lea	
112.9827	9.01	negative	-680	-0.96	1.49	drought_lea	
61.9896	10.49	negative	-713	-0.24	0.38	drought_lea	
104.0702	6.35	positive	-767	-0.46	0.72	drought_lea	gamma-Aminobutyric acid
131.0526	10.61	positive	-771	-0.92	1.43	drought_lea	
133.0603	11.01	positive	-1052	-0.88	1.36	drought_lea	Asparagine
84.0441	10.82	positive	-1103	-0.99	1.54	drought_lea	
145.0696	10.42	negative	-1160	-0.98	1.53	drought_lea	Glutamine
130.0494	10.45	positive	-3259	-0.98	1.52	drought_lea	
147.0759	10.41	positive	-3987	-0.98	1.52	drought_lea	Glutamine
116.0702	7.32	positive	1106	0.79	1.06	drought_lpat1	Proline
196.0632	7.30	positive	888	0.78	1.05	drought_lpat1	
194.0625	7.30	negative	773	0.81	1.09	drought_lpat1	
98.9838	15.14	positive	653	0.98	1.32	drought_lpat1	
311.1256	7.31	positive	615	0.91	1.23	drought_lpat1	
96.9625	15.14	negative	471	0.95	1.27	drought_lpat1	
115.0033	5.58	negative	403	0.97	1.30	drought_lpat1	Fumaric acid
244.0919	11.74	positive	398	0.98	1.32	drought_lpat1	
234.0189	7.31	positive	389	0.84	1.13	drought_lpat1	
439.0847	11.92	negative	389	0.91	1.22	drought_lpat1	

129.0405	4.23	negative	-535	-0.72	0.97	drought_lpat1	
131.0526	10.61	positive	-653	-0.99	1.33	drought_lpat1	
61.9896	10.49	negative	-726	-0.29	0.39	drought_lpat1	
133.0603	11.01	positive	-904	-0.89	1.21	drought_lpat1	Asparagine
84.0441	10.82	positive	-955	-0.99	1.34	drought_lpat1	
104.0702	6.35	positive	-1027	-0.68	0.92	drought_lpat1	gamma-Aminobutyric acid
145.0696	10.42	negative	-1027	-0.98	1.32	drought_lpat1	Glutamine
88.0754	4.77	positive	-1045	-0.95	1.28	drought_lpat1	
130.0494	10.45	positive	-2914	-0.99	1.33	drought_lpat1	
147.0759	10.41	positive	-3556	-0.98	1.33	drought_lpat1	Glutamine
192.1411	4.69	positive	432	0.99	1.64	drought_p5cs1	
244.0919	11.74	positive	305	0.87	1.44	drought_p5cs1	
303.0805	8.13	negative	276	0.94	1.56	drought_p5cs1	
212.0582	8.63	positive	274	0.83	1.37	drought_p5cs1	
178.1254	4.76	positive	256	0.99	1.64	drought_p5cs1	
166.0856	6.57	positive	250	0.65	1.08	drought_p5cs1	Phenylalanine
327.0666	8.11	positive	245	0.98	1.62	drought_p5cs1	
194.0625	7.30	negative	245	0.27	0.44	drought_p5cs1	
131.0514	11.12	negative	244	0.46	0.77	drought_p5cs1	Asparagine
322.1111	8.09	positive	206	0.97	1.60	drought_p5cs1	
129.0405	4.23	negative	-646	-0.71	1.18	drought_p5cs1	
131.0526	10.61	positive	-741	-0.99	1.63	drought_p5cs1	
61.9896	10.49	negative	-998	-0.38	0.63	drought_p5cs1	
133.0603	11.01	positive	-1153	-0.90	1.49	drought_p5cs1	Asparagine
145.0696	10.42	negative	-1183	-0.98	1.63	drought_p5cs1	Glutamine
84.0441	10.82	positive	-1192	-1.00	1.65	drought_p5cs1	
88.0754	4.77	positive	-1256	-0.93	1.54	drought_p5cs1	
116.0702	7.32	positive	-1325	-0.80	1.32	drought_p5cs1	Proline
130.0494	10.45	positive	-3311	-0.99	1.63	drought_p5cs1	
147.0759	10.41	positive	-4031	-0.98	1.63	drought_p5cs1	Glutamine
148.0599	10.93	positive	1676	0.99	1.24	drought_sos1	Glutamic acid
133.0603	11.01	positive	1386	0.97	1.23	drought_sos1	Asparagine
104.1066	0.93	positive	1235	0.93	1.17	drought_sos1	

104.0702	6.35	positive	1170	0.77	0.97	drought_sos1	gamma-Aminobutyric acid
114.1022	11.97	positive	1159	0.98	1.23	drought_sos1	
116.0702	7.32	positive	1134	0.86	1.08	drought_sos1	Proline
66.0681	11.97	positive	1048	0.99	1.24	drought_sos1	
196.0632	7.30	positive	942	0.83	1.04	drought_sos1	
244.0919	11.74	positive	926	0.97	1.22	drought_sos1	
106.0495	11.35	positive	813	0.96	1.21	drought_sos1	Serine
147.0759	10.41	positive	-368	-0.13	0.16	drought_sos1	Glutamine
130.0494	10.45	positive	-406	-0.17	0.21	drought_sos1	
223.0671	5.80	negative	-432	-0.95	1.20	drought_sos1	
94.0448	4.82	positive	-474	-0.83	1.05	drought_sos1	
129.0405	4.23	negative	-480	-0.70	0.88	drought_sos1	
112.9827	9.01	negative	-622	-0.97	1.23	drought_sos1	
339.1034	5.80	negative	-625	-0.96	1.20	drought_sos1	
112.9827	7.59	negative	-857	-1.00	1.26	drought_sos1	
88.0754	4.77	positive	-896	-0.92	1.15	drought_sos1	
61.9896	10.49	negative	-2027	-0.96	1.21	drought_sos1	

Figures

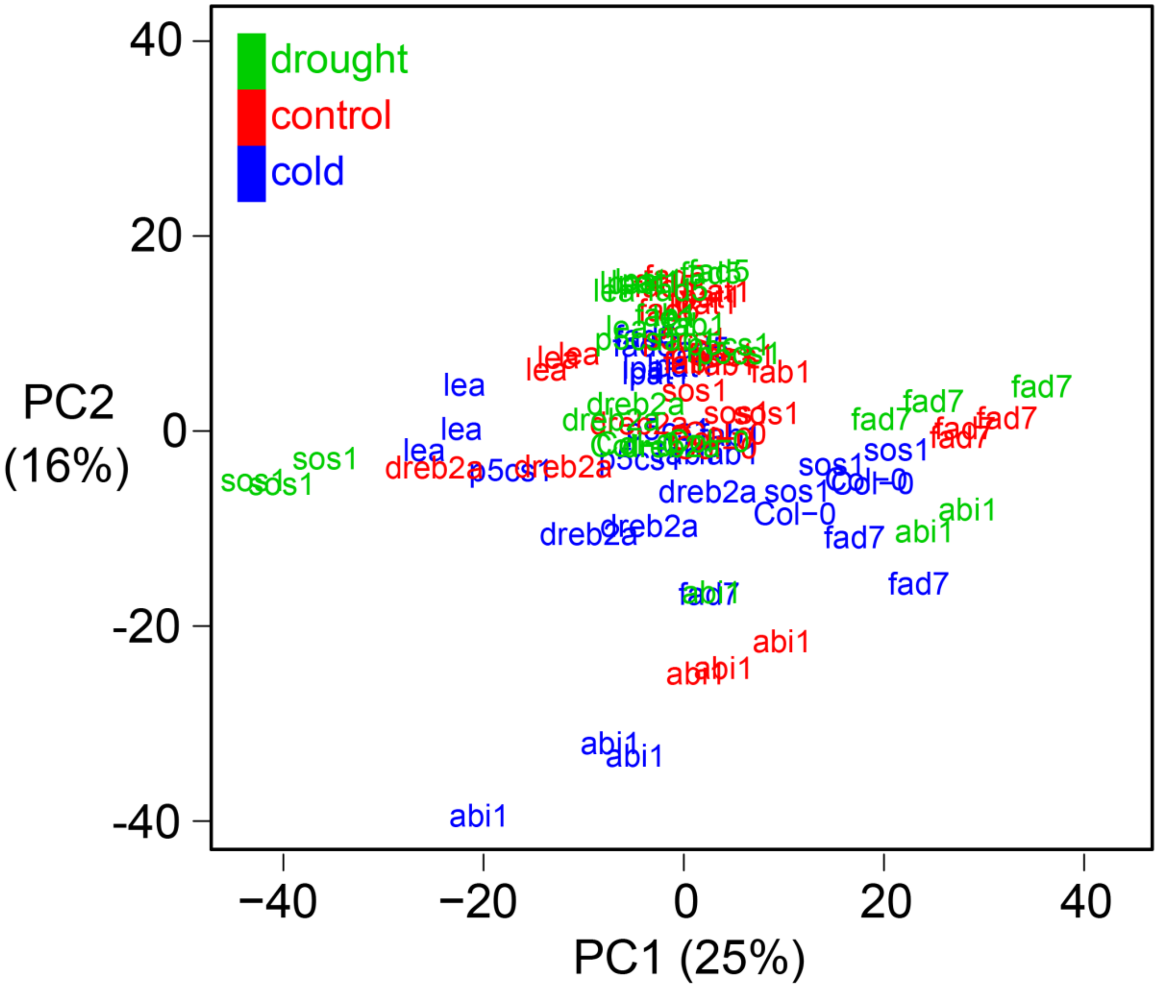


Figure A-1. PCA score plots of stress resistant or susceptible mutants and wild-type in control, cold, and drought treatments.

In the score plot, the names and colors corresponded to different genotypes (Col-0, *abi1*, *dreb2a*, *fab1*, *fad5*, *fad7*, *lea*, *lpat1*, *p5cs1*, *sos1*) and treatments (control, cold, drought).

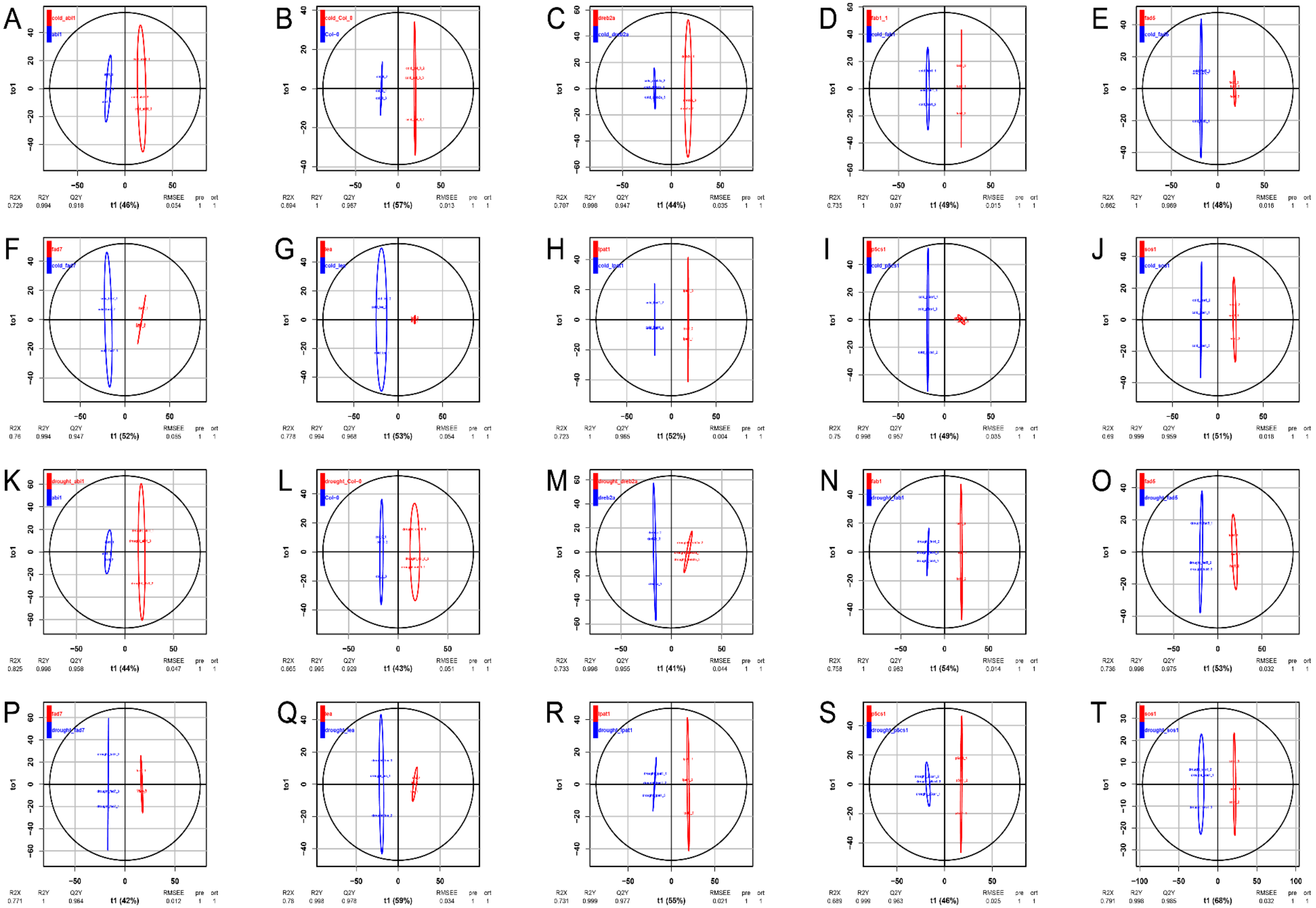

A
cold_abi1
abi1
R2X 0.729 R2Y 0.994 Q2Y 0.918 t1 (46%) RMSEE 0.054 pre 1 ort 1
B
cold_Col_0
Col-0
R2X 0.694 R2Y 1 Q2Y 0.987 t1 (57%) RMSEE 0.013 pre 1 ort 1
C
dreb2a
cold_dreb2a
R2X 0.707 R2Y 0.998 Q2Y 0.947 t1 (44%) RMSEE 0.035 pre 1 ort 1
D
fab1_1
cold_fab1
R2X 0.735 R2Y 1 Q2Y 0.97 t1 (49%) RMSEE 0.015 pre 1 ort 1
E
fad6
cold_fad6
R2X 0.662 R2Y 1 Q2Y 0.969 t1 (48%) RMSEE 0.016 pre 1 ort 1
F
fad7
cold_fad7
R2X 0.76 R2Y 0.994 Q2Y 0.947 t1 (52%) RMSEE 0.055 pre 1 ort 1
G
lea
cold_lea
R2X 0.778 R2Y 0.994 Q2Y 0.968 t1 (53%) RMSEE 0.054 pre 1 ort 1
H
ipat1
cold_ipat1
R2X 0.723 R2Y 1 Q2Y 0.985 t1 (52%) RMSEE 0.004 pre 1 ort 1
I
p5cs1
cold_p5cs1
R2X 0.75 R2Y 0.998 Q2Y 0.957 t1 (49%) RMSEE 0.035 pre 1 ort 1
J
sos1
cold_sos1
R2X 0.69 R2Y 0.999 Q2Y 0.959 t1 (51%) RMSEE 0.018 pre 1 ort 1
K
drought_abi1
abi1
R2X 0.825 R2Y 0.998 Q2Y 0.958 t1 (44%) RMSEE 0.047 pre 1 ort 1
L
drought_Col-0
Col-0
R2X 0.665 R2Y 0.995 Q2Y 0.929 t1 (43%) RMSEE 0.051 pre 1 ort 1
M
drought_dreb2a
dreb2a
R2X 0.733 R2Y 0.996 Q2Y 0.955 t1 (41%) RMSEE 0.044 pre 1 ort 1
N
fab1
drought_fab1
R2X 0.758 R2Y 1 Q2Y 0.983 t1 (54%) RMSEE 0.014 pre 1 ort 1
O
fad6
drought_fad6
R2X 0.736 R2Y 0.998 Q2Y 0.975 t1 (53%) RMSEE 0.032 pre 1 ort 1
P
fad7
drought_fad7
R2X 0.771 R2Y 1 Q2Y 0.964 t1 (42%) RMSEE 0.012 pre 1 ort 1
Q
lea
drought_lea
R2X 0.78 R2Y 0.998 Q2Y 0.978 t1 (59%) RMSEE 0.034 pre 1 ort 1
R
ipat1
drought_ipat1
R2X 0.731 R2Y 0.999 Q2Y 0.977 t1 (55%) RMSEE 0.021 pre 1 ort 1
S
p5cs1
drought_p5cs1
R2X 0.689 R2Y 0.999 Q2Y 0.963 t1 (46%) RMSEE 0.025 pre 1 ort 1
T
sos1
drought_sos1
R2X 0.791 R2Y 0.998 Q2Y 0.985 t1 (68%) RMSEE 0.032 pre 1 ort 1
to1

Figure A-2. OPLS-DA score plots of treatment compared to corresponding control.
Figure A-J show different genotypes in cold treatment compared to control. (A) *abi1*, (B) Col-0, (C) *dreb2a*, (D) *fab1*, (E) *fad5*, (F) *fad7*, (G) *lea*, (H) *lpat1*, (I) *p5cs1*, (J) *sos1*. Figure K-T show different genotypes in drought treatment compared to control. (K) *abi1*, (L) Col-0, (M) *dreb2a*, (N) *fab1*, (O) *fad5*, (P) *fad7*, (Q) *lea*, (R) *lpat1*, (S) *p5cs1*, (T) *sos1*.

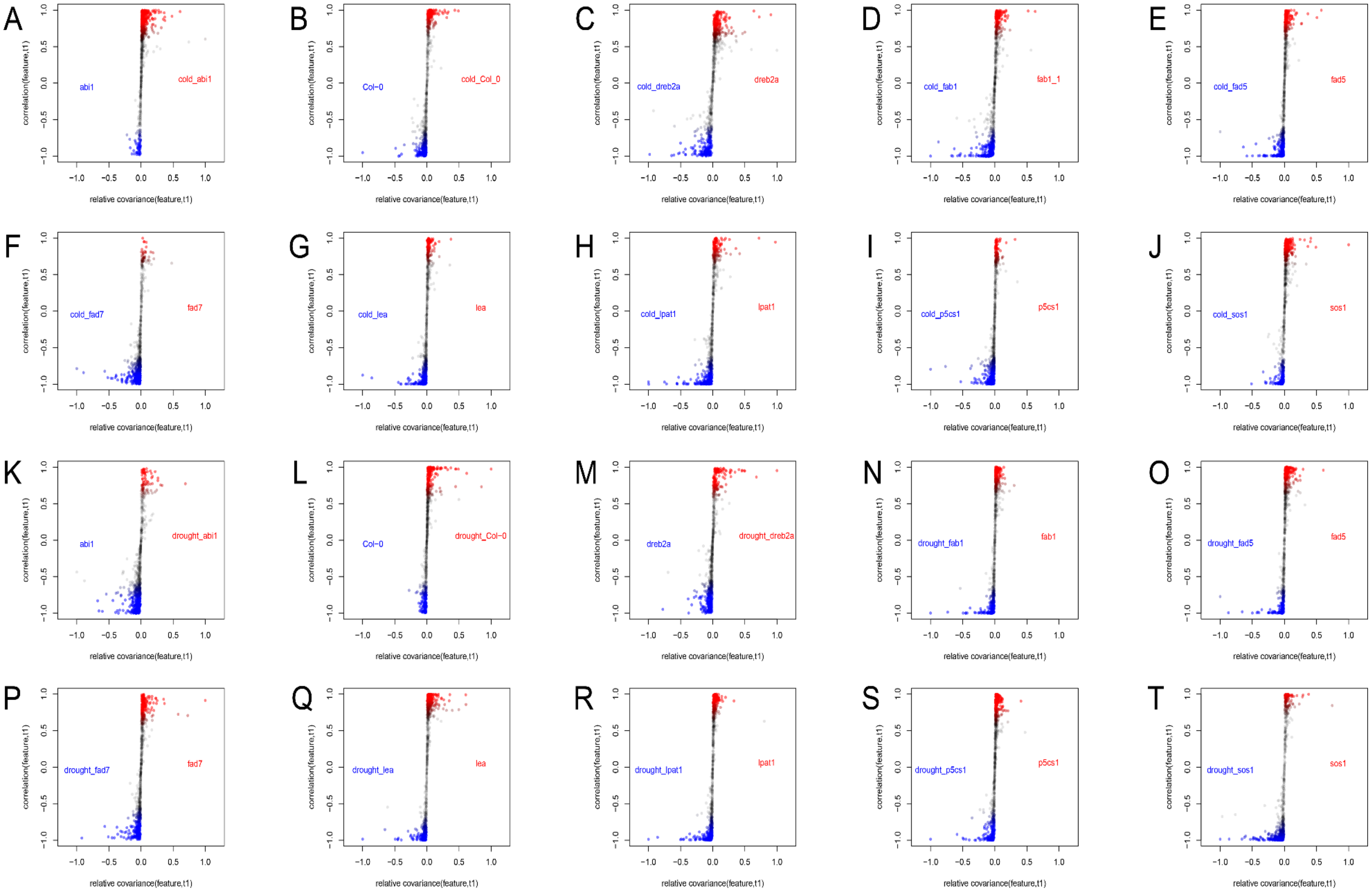
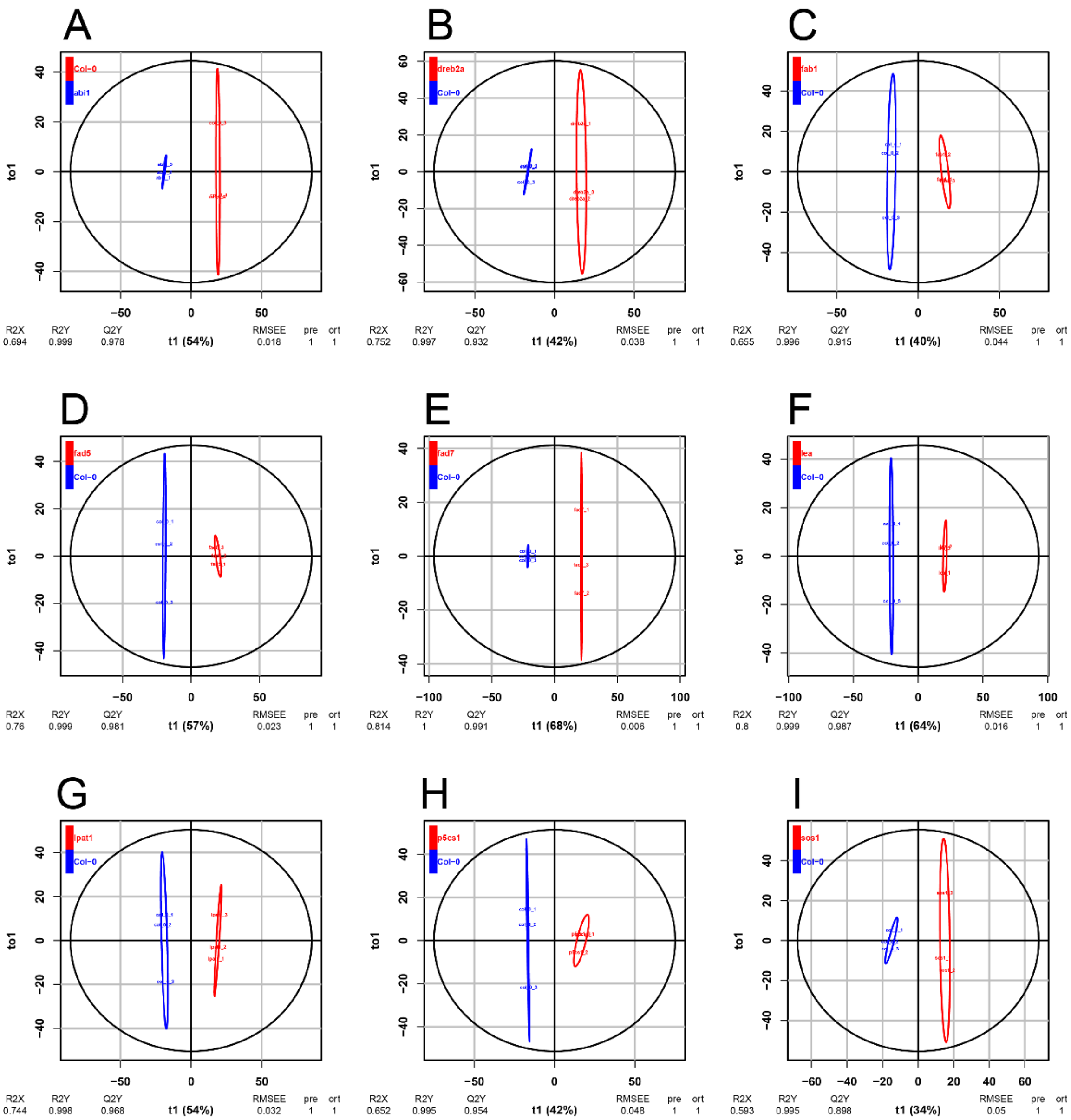

A
abi1
cold_abi1
B
Col−0
cold_Col_0
C
cold_dreb2a
dreb2a
D
cold_fab1
fab1_1
E
cold_fad5
fad5
F
cold_fad7
fad7
G
cold_lea
lea
H
cold_lpat1
lpat1
I
cold_p5cs1
p5cs1
J
cold_sos1
sos1
K
abi1
drought_abi1
L
Col−0
drought_Col−0
M
dreb2a
drought_dreb2a
N
drought_fab1
fab1
O
drought_fad5
fad5
P
drought_fad7
fad7
Q
drought_lea
lea
R
drought_lpat1
lpat1
S
drought_p5cs1
p5cs1
T
drought_sos1
sos1
correlation(feature,t1)
relative covariance(feature,t1)
−1.0
−0.5
0.0
0.5
1.0

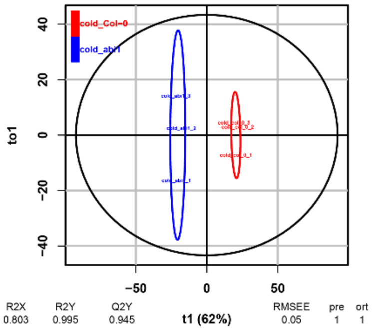
Figure A-3. OPLS-DA S-plots of treatment compared to corresponding control.

Figure A-J show different genotypes in cold treatment compared to control. (A) *abi1*, (B) Col-0, (C) *dreb2a*, (D) *fab1*, (E) *fad5*, (F) *fad7*, (G) *lea*, (H) *lpat1*, (I) *p5cs1*, (J) *sos1*. Figure K-T show different genotypes in drought treatment compared to control. (K) *abi1*, (L) Col-0, (M) *dreb2a*, (N) *fab1*, (O) *fad5*, (P) *fad7*, (Q) *lea*, (R) *lpat1*, (S) *p5cs1*, (T) *sos1*.



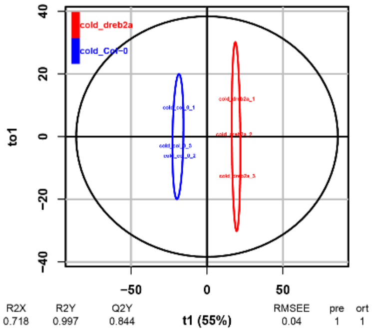
A
Col−0
abi1
to1
t1 (54%)
R2X 0.694
R2Y 0.999
Q2Y 0.978
RMSEE 0.018
pre 1
ort 1
B
dreb2a
Col−0
to1
t1 (42%)
R2X 0.752
R2Y 0.997
Q2Y 0.932
RMSEE 0.038
pre 1
ort 1
C
fab1
Col−0
to1
t1 (40%)
R2X 0.655
R2Y 0.996
Q2Y 0.915
RMSEE 0.044
pre 1
ort 1
D
fad5
Col−0
to1
t1 (57%)
R2X 0.76
R2Y 0.999
Q2Y 0.981
RMSEE 0.023
pre 1
ort 1
E
fad7
Col−0
to1
t1 (68%)
R2X 0.814
R2Y 1
Q2Y 0.991
RMSEE 0.006
pre 1
ort 1
F
lea
Col−0
to1
t1 (64%)
R2X 0.8
R2Y 0.999
Q2Y 0.987
RMSEE 0.016
pre 1
ort 1
G
lpat1
Col−0
to1
t1 (54%)
R2X 0.744
R2Y 0.998
Q2Y 0.968
RMSEE 0.032
pre 1
ort 1
H
p5cs1
Col−0
to1
t1 (42%)
R2X 0.652
R2Y 0.995
Q2Y 0.954
RMSEE 0.048
pre 1
ort 1
I
sos1
Col−0
to1
t1 (34%)
R2X 0.593
R2Y 0.995
Q2Y 0.898
RMSEE 0.05
pre 1
ort 1

J



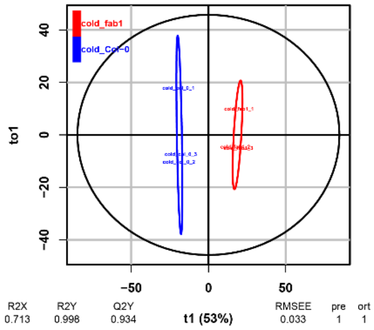
cold_Col-0
cold_abi1
to1
40
20
0
-20
-40
-50
0
50
t1 (62%)
R2X 0.803
R2Y 0.995
Q2Y 0.945
RMSEE 0.05
pre 1
ort 1

K



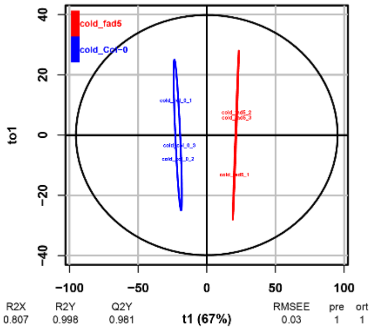
cold_dreb2a
cold_Col-0
to1
40
20
0
-20
-40
-50
0
50
t1 (55%)
R2X 0.718
R2Y 0.997
Q2Y 0.844
RMSEE 0.04
pre 1
ort 1

L



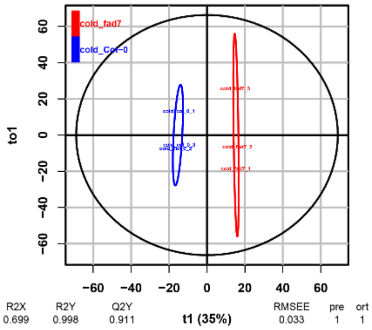
cold_fab1
cold_Col-0
to1
40
20
0
-20
-40
-50
0
50
t1 (53%)
R2X 0.713
R2Y 0.998
Q2Y 0.934
RMSEE 0.033
pre 1
ort 1

M



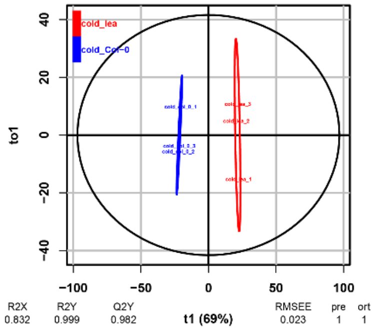
cold_fad5
cold_Col-0
to1
40
20
0
-20
-40
-100
-50
0
50
100
t1 (67%)
R2X 0.807
R2Y 0.998
Q2Y 0.981
RMSEE 0.03
pre 1
ort 1

N



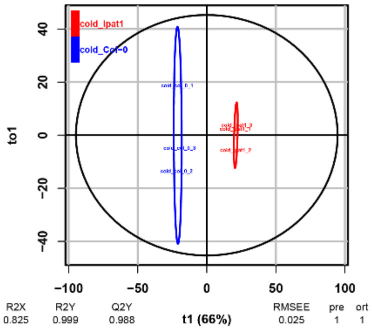
cold_fad7
cold_Col-0
to1
60
40
20
0
-20
-40
-60
-60
-40
-20
0
20
40
60
t1 (35%)
R2X 0.699
R2Y 0.998
Q2Y 0.911
RMSEE 0.033
pre 1
ort 1

O



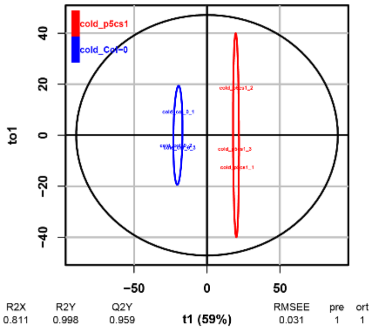
cold_lea
cold_Col-0
to1
40
20
0
-20
-40
-100
-50
0
50
100
t1 (69%)
R2X 0.832
R2Y 0.999
Q2Y 0.982
RMSEE 0.023
pre 1
ort 1

P



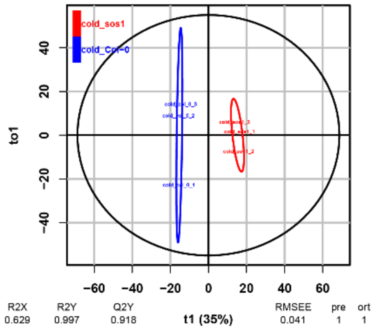
cold_lpat1
cold_Col-0
to1
40
20
0
-20
-40
-100
-50
0
50
100
t1 (66%)
R2X 0.825
R2Y 0.999
Q2Y 0.988
RMSEE 0.025
pre 1
ort 1

Q



cold_p5cs1
cold_Col-0
to1
40
20
0
-20
-40
-50
0
50
t1 (59%)
R2X 0.811
R2Y 0.998
Q2Y 0.959
RMSEE 0.031
pre 1
ort 1

R



cold_sos1
cold_Col-0
to1
40
20
0
-20
-40
-60
-40
-20
0
20
40
60
t1 (35%)
R2X 0.629
R2Y 0.997
Q2Y 0.918
RMSEE 0.041
pre 1
ort 1

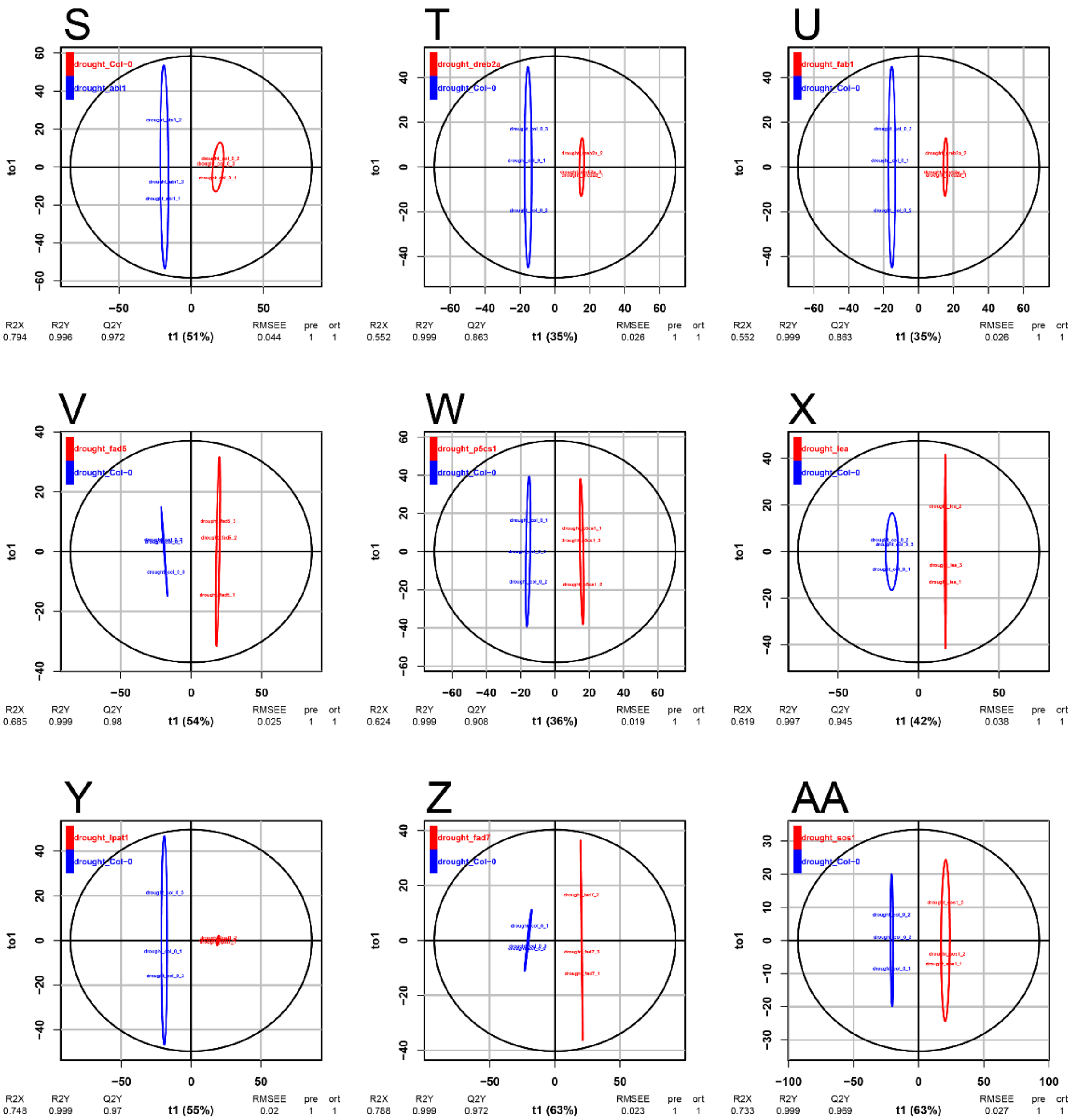
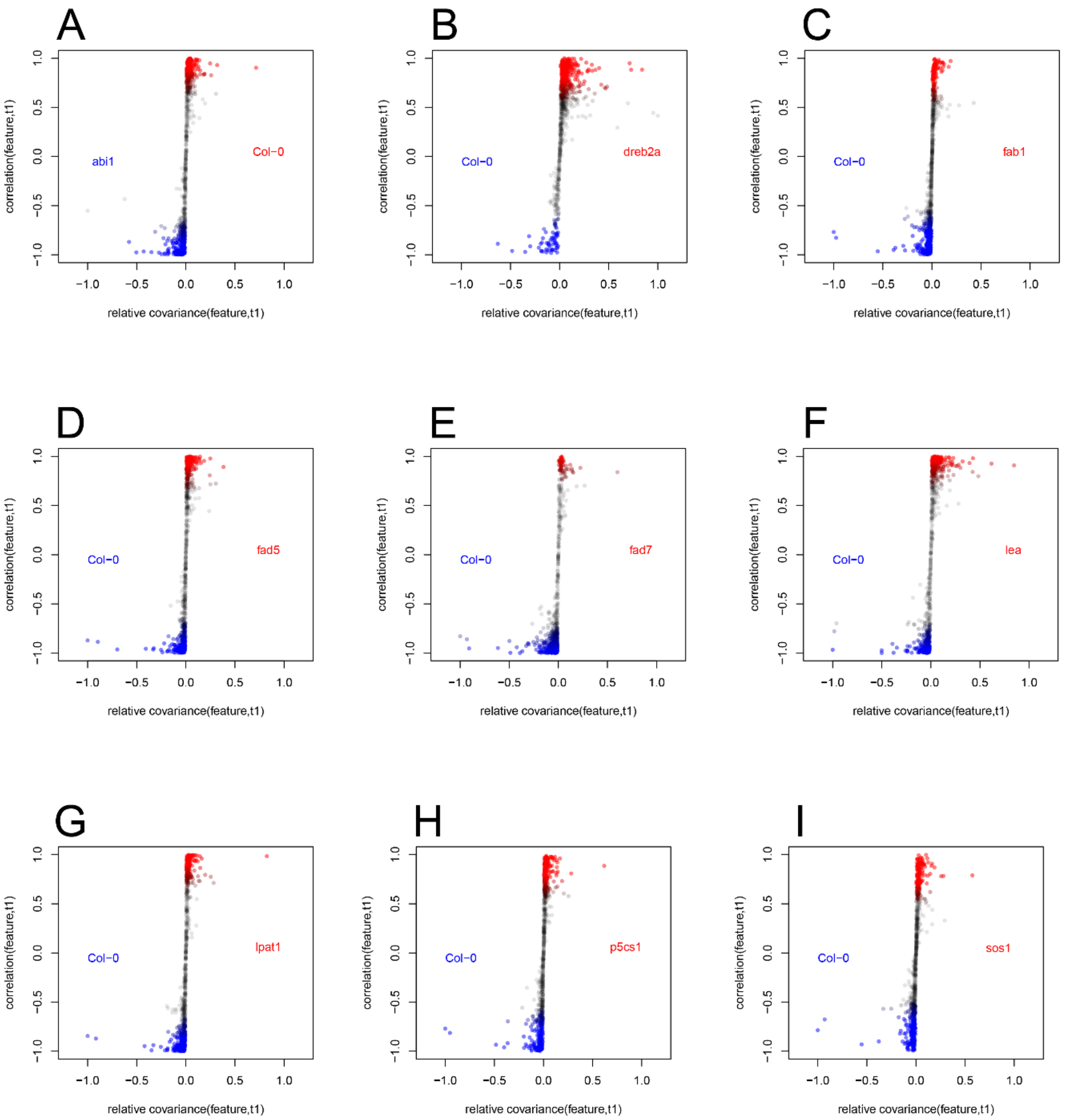
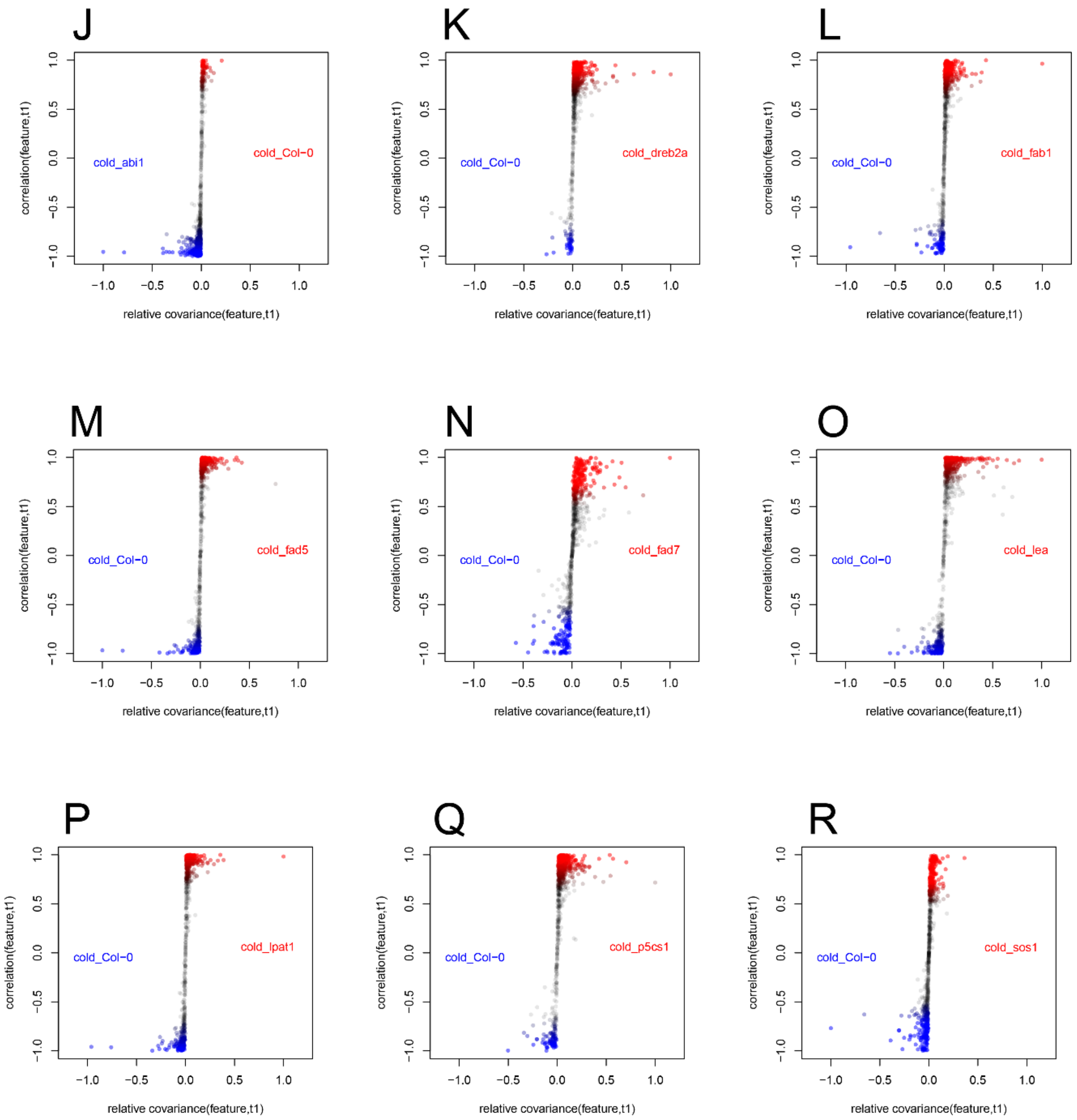


Figure A-4. OPLS-DA score plots for mutant compared to corresponding wild-type. Figure A-I show different mutants compared to wild-type in control conditions. (A) *abi1* and Col-0, (B) *dreb2a* and Col-0, (C) *fab1* and Col-0, (D) *fad5* and Col-0, (E) *fad7* and Col-0, (F) *lea* and Col-0, (G) *lpat1* and Col-0, (H) *p5cs1* and Col-0, (I) *sos1* and Col-0. Figure J-R show different mutants compared to wild-type in cold treatment. (J) *abi1* and Col-0, (K) *dreb2a* and Col-0, (L) *fab1* and Col-0, (M) *fad5* and Col-0, (N) *fad7* and Col-0, (O) *lea* and Col-0, (P) *lpat1* and Col-0, (Q) *p5cs1* and Col-0, (R) *sos1* and Col-0. Figure S-AA show different mutants compared to wild-type in control conditions. (S) *abi1* and Col-0, (T), *dreb2a* and Col-0, (U) *fab1* and Col-0, (V) *fad5* and Col-0, (W) *fad7* and Col-0, (X) *lea* and Col-0, (Y) *lpat1* and Col-0, (Z) *p5cs1* and Col-0, (AA) *sos1* and Col-0.


A
abi1
Col−0
B
Col−0
dreb2a
C
Col−0
fab1
D
Col−0
fad5
E
Col−0
fad7
F
Col−0
lea
G
Col−0
lpat1
H
Col−0
p5cs1
I
Col−0
sos1
correlation(feature,t1)
relative covariance(feature,t1)
−1.0
−0.5
0.0
0.5
1.0


J
cold_abi1
cold_Col−0
K
cold_Col−0
cold_dreb2a
L
cold_Col−0
cold_fab1
M
cold_Col−0
cold_fad5
N
cold_Col−0
cold_fad7
O
cold_Col−0
cold_lea
P
cold_Col−0
cold_lpat1
Q
cold_Col−0
cold_p5cs1
R
cold_Col−0
cold_sos1
correlation(feature,t1)
relative covariance(feature,t1)
−1.0
−0.5
0.0
0.5
1.0

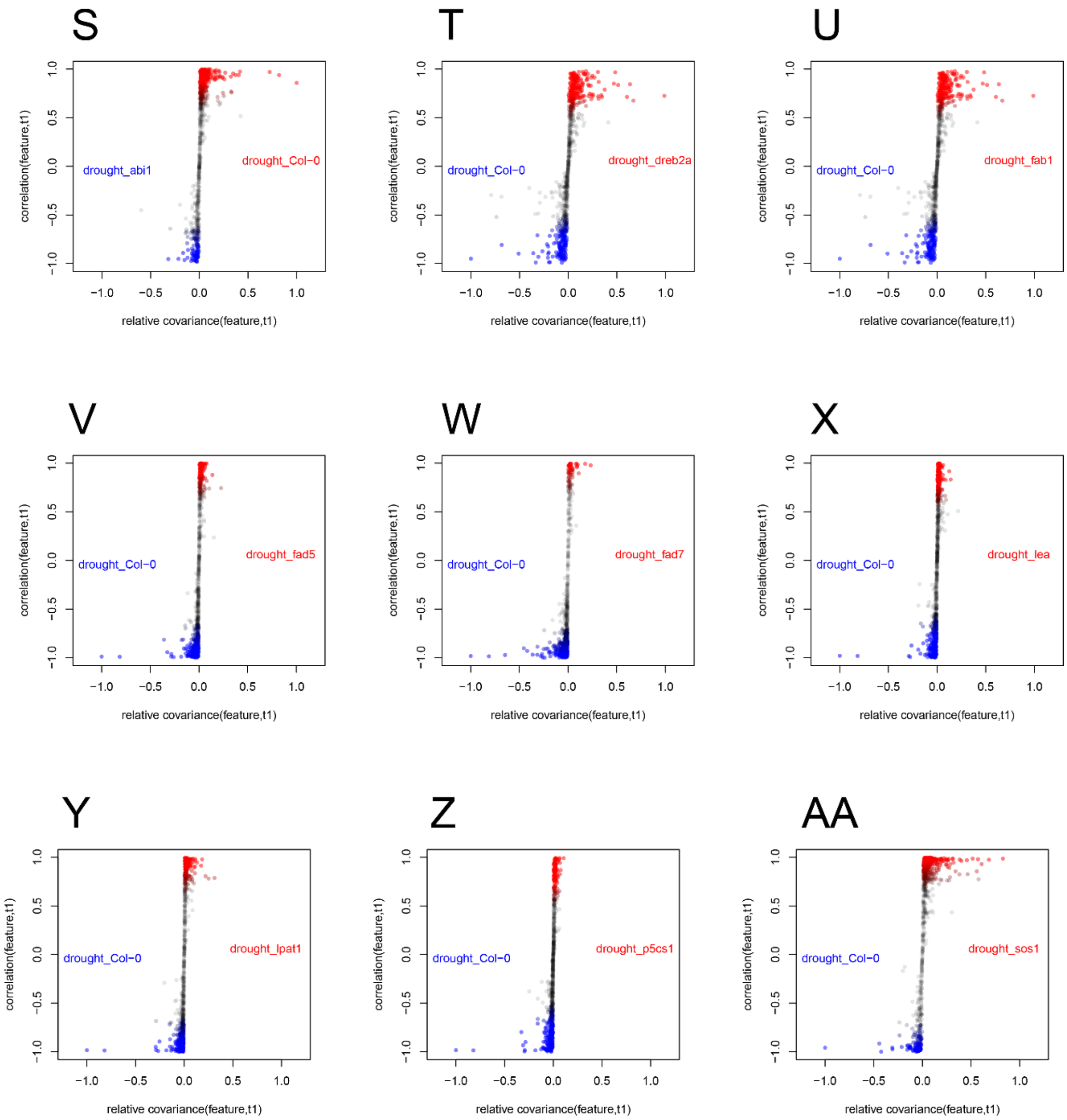


Figure A-5. OPLS-DA S-plots for mutants compared to corresponding wild-type. Figure A-I show different mutants compared to wild-type in control conditions. (A) *abi1* and Col-0, (B) *dreb2a* and Col-0, (C) *fab1* and Col-0, (D) *fad5* and Col-0, (E) *fad7* and Col-0, (F) *lea* and Col-0, (G) *lpat1* and Col-0, (H) *p5cs1* and Col-0, (I) *sos1* and Col-0. Figure J-R show different mutants compared to wild-type in cold treatment. (J) *abi1* and Col-0, (K) *dreb2a* and Col-0, (L) *fab1* and Col-0, (M) *fad5* and Col-0, (N) *fad7* and Col-0, (O) *lea* and Col-0, (P) *lpat1* and Col-0, (Q) *p5cs1* and Col-0, (R) *sos1* and Col-0. Figure S-AA show different mutants compared to wild-type in control conditions. (S) *abi1* and Col-0, (T), *dreb2a* and Col-0, (U) *fab1* and Col-0, (V) *fad5* and Col-0, (W) *fad7* and Col-0, (X) *lea* and Col-0, (Y) *lpat1* and Col-0, (Z) *p5cs1* and Col-0, (AA) *sos1* and Col-0.

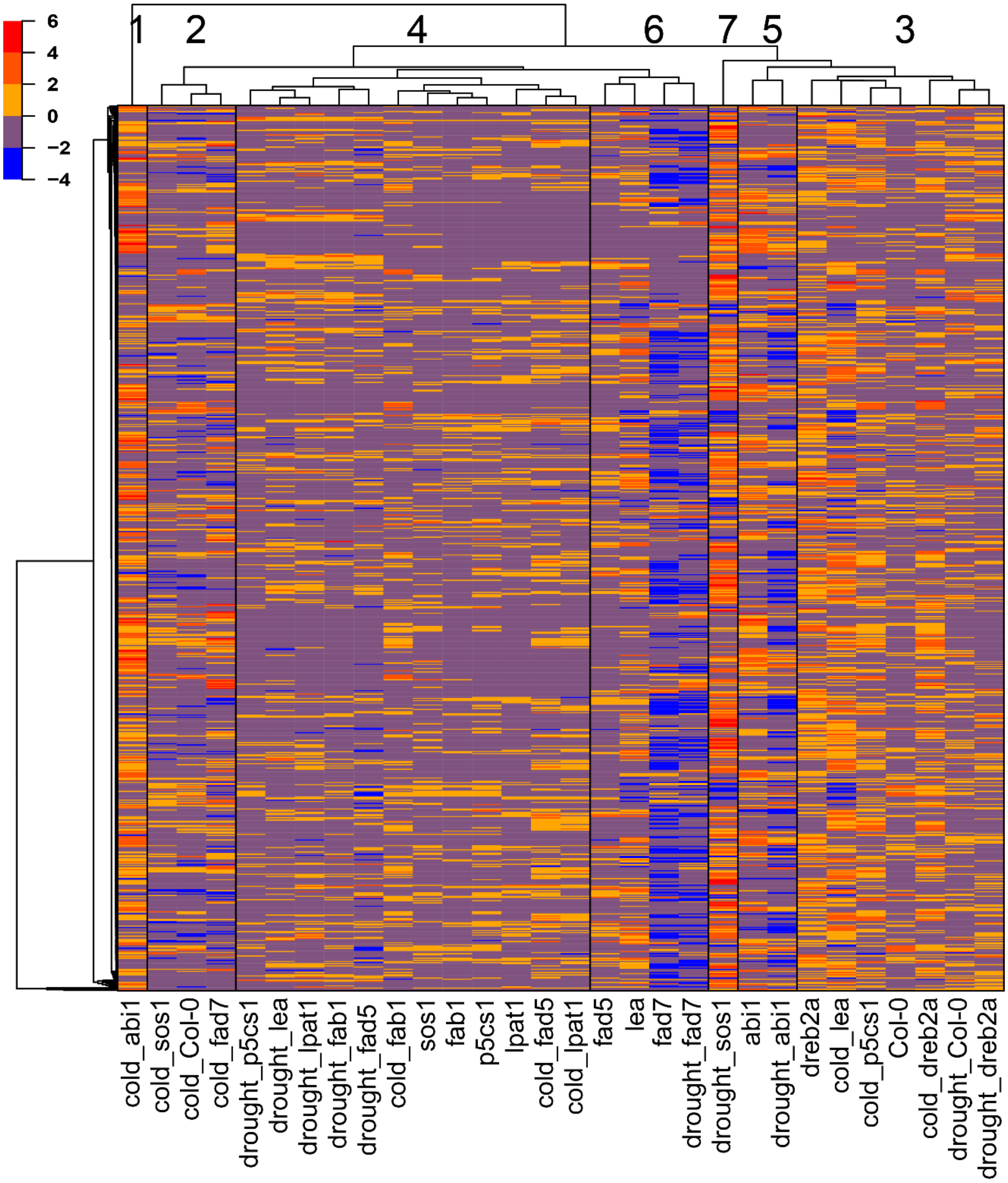


Figure A-6. HCA for average abundance of all the metabolic features for all ten genotypes with all three treatments.

The top horizontal side bar reflects the $\log_2$-transformed average abundance of all metabolic features for all genotypes in all treatments. Clusters were generated using the Mcquitty method and Euclidean distance function. Seven clusters of treatments are labeled 1-7.

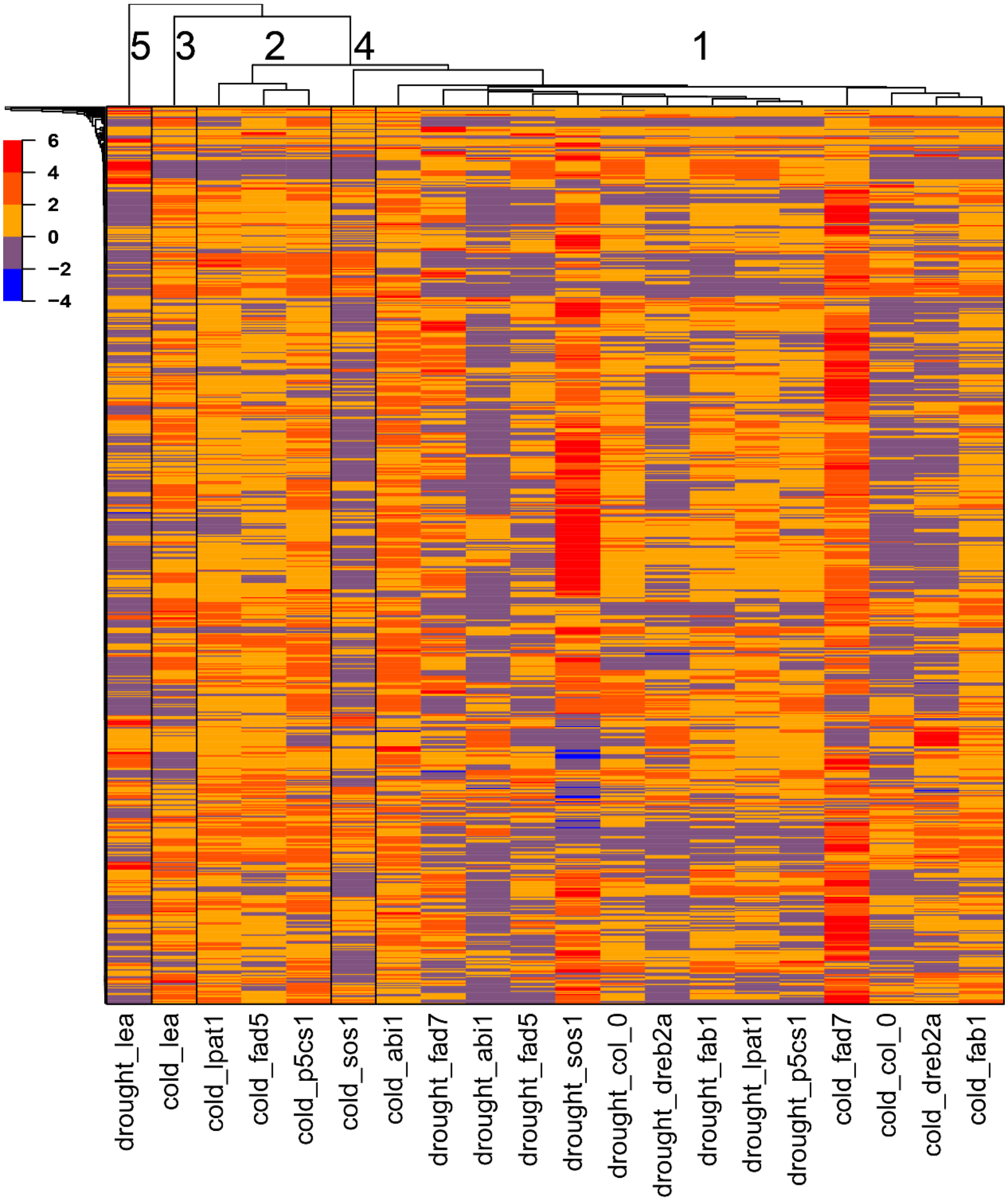


Figure A-7. HCA for ratios of all the metabolic features in treatment compared to the corresponding control.

The top horizontal side bar reflects the $\log_2$-transformed average abundance of all metabolic features for all genotypes in all treatments. Clusters were generated using the Mcquitty method and Euclidean distance function. Five clusters of treatments are labeled 1-5.

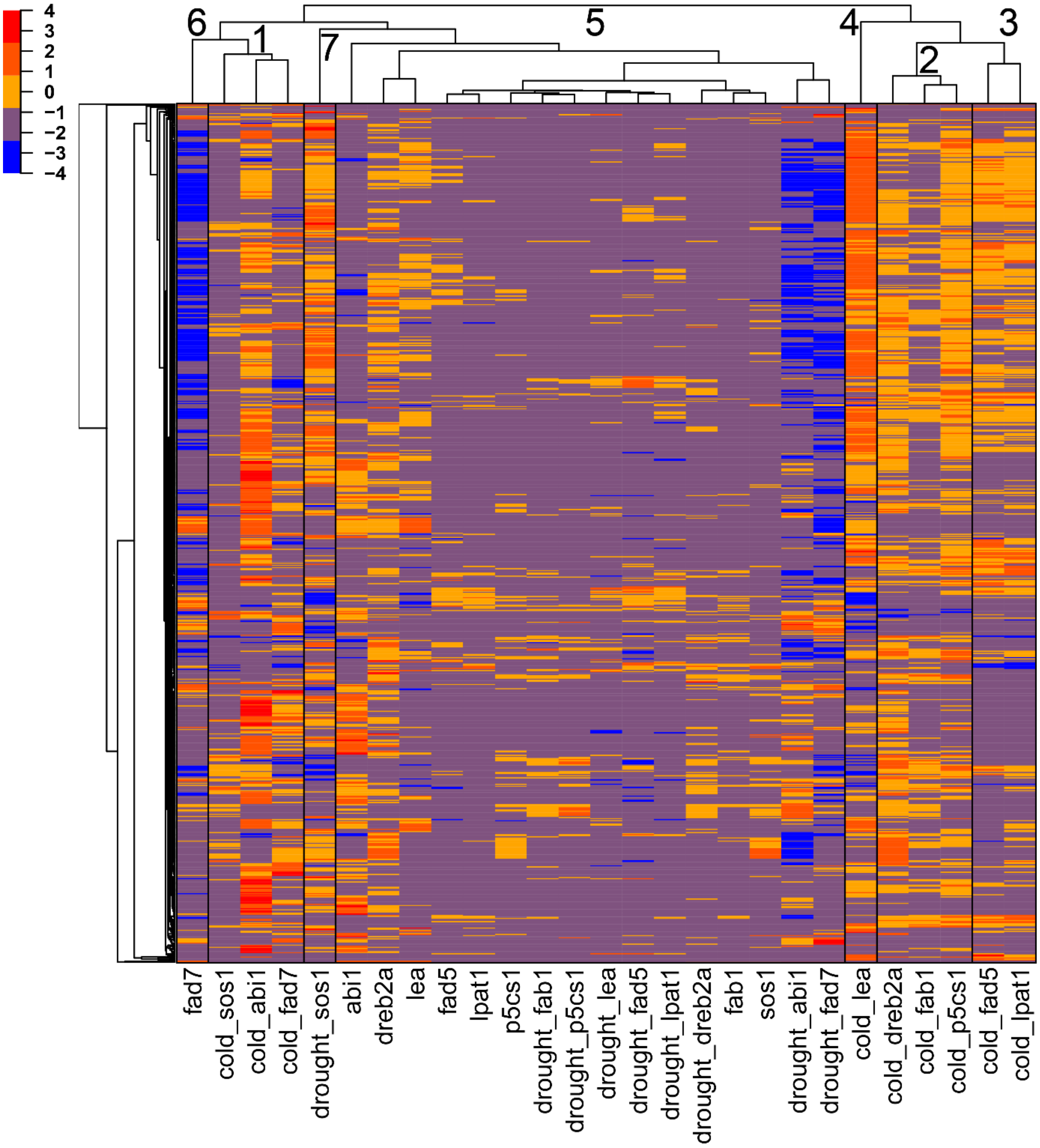


Figure A-8. HCA for ratios of all the metabolic features in mutants compared to the corresponding wildtype.

The top horizontal side bar reflects the $\log_2$-transformed average abundance of all metabolic features for all genotypes in all treatments. Clusters were generated using the Mcquitty method and Euclidean distance function. Seven clusters of treatments are labeled 1-7.