IN SILICO MODELING AND "-OMICS" DATA ANALYSIS FOR RICE SYSTEMS AGROBIOTECHOLOGY

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NATIONAL UNIVERSITY OF SINGAPORE

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சுழன்றும்ஏர்ப் பின்னது உலகம் அதனால்

உழந்தும் உழவே தலை. *(குறள் 1031)*

Transliteration

Agriculture, though laborious, is the most excellent (form of labour);

for people, though they go about (in search of various employments),

have at last to resort to the farmer.

Dedicated:

To the World farming community

DECLARATION

I hereby declare that the thesis is my original work and it has been written by me in its entirety.

I have duly acknowledged all the sources of information which have been used in the thesis.

This thesis has also not been submitted for any degree in any university previously.

Meiyappan Lakshmanan

27 March 2014

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எந்நன்றி கொன்றார்க்கும் உய்வுண்டாம் உய்வில்லை

செய்ந்நன்றி கொன்ற மகற்கு. *(குறள் 110)*

Transliteration

He who has killed every virtue may yet escape;

there is no escape for him who has killed a benefit.

As per this famous Tamil adage, it is imperative for me to start the dissertation with this section where I can thank one and all who have helped me in the last four years and even before that, laying the foundations for my research career.

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Summary

Rice is one of the major food crops in the world, especially in Asia. Although the overall yield of rice has been increasing since the Green Revolution in 1960s, the growing population and adverse climatic changes pose huge challenges for its sustained production in the future. Moreover, several biotic and abiotic stresses such as drought, flooding and salinity affect the rice production significantly. Therefore, in order to improve the crop yield and enhance the stress resistance, it is imperative to analyse the possible biochemical adaptations of rice to several abiotic stresses.

Despite several decades of research, still, a clear understanding on how the cellular phenotype of rice varies across various stress conditions remains elusive. Such situations exist even with the availability of multiple high throughput data such as metabolomics, proteomics and transcriptomics mainly due to the lack of systematic approaches. To this end, the current work aims to initiate a systems approach to characterise the rice cellular physiology under various stresses by combining the mathematical network models and highthroughput data through an integrative *in silico* framework.

This thesis contains three major parts. The first part describes and reviews the methods for developing and analysing constraints-based metabolic models, and the software tools available to implement such methods. Next, to initiate the systems analysis of rice, a central regulatory/metabolic model representing the rice coleoptile and leaf was developed based on the available genomics and biochemical data. Notably, this central model accounts for 52 direct and indirect regulatory interactions using 12 regulatory proteins for the discrimination between the photosynthetic and non-photosynthetic cells. Subsequently, the metabolic model was also utilised for elucidating the metabolic characteristics of rice cells under flooding stress. The relevant transcriptome data was utilised to further unravel the possible transcriptionally regulated reactions and the po-

tential transcription factors controlling their expression under anoxic stress. The same metabolic model was also used to characterise the cellular behaviour of rice leaves under drought stress. Additionally, the essential genes of rice photorespiratory pathway during drought stress were also identified as this pathway wastes significant amount of carbon under such conditions.

Although the central metabolic/regulatory model was able to characterise the overall cellular behaviours under various stress conditions, still the finer details of metabolic and transcriptional adaptations were not unravelled as it does not cover the secondary metabolism. Therefore, the central model was expanded into a high-quality, fully-compartmentalised, genome-scale model by taking into account all the known metabolic genes in rice. The resulting model, named as *i*OS2164, includes 2164 genes, 2284 reactions and 2001 metabolites localised across seven intracellular compartments: cytosol, plastid, mitochondrion, peroxisome, vacuole, thylakoid and endoplasmic reticulum. It should be noted that the light-driven photophosphorylation reactions in this *i*OS2164 were modelled in a wavelength specific manner, thereby enabling us to simulate the exact metabolic behaviour of rice at various coloured lights in the visible spectrum. Subsequently, this metabolic model was utilised in combination with transcriptome and metabolome data for analysing the cellular behaviour under five different light treatments: blue, red, green, white and dark, highlighting several light sensitive signalling cascades and the responsive metabolic pathways in rice. The knowledge obtained from such large-scale combined study has several potential applications including crop improvement and synthetic gene circuit design. Overall, this work provides a systematic computational framework by combining the constraints-based metabolic modelling and "-omics" data for the analysis of rice physiology under various abiotic stresses. In general, with the ever increasing "-omics" data, the developed framework could be applied to any cellular organism for analysing its metabolic behaviour in a systematic manner.

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Nomenclature

Roman Symbols

C_i	Specific concentration of metabolite i (mmol/gDCW)
c_j	Weighting factor for each reaction j in objective function
S_{ij}	Stocihiometric matrix of dimension i x j
t	Time (hr)
$v_{j,diff}$	Flux difference sample of reaction, j (mmol/gDCW-hr)
v_j	Metabolic flux through specific reaction, j (mmol/gDCW-hr)
v_j^{max}	Upper limits for the metabolic flux of reaction j (mmol/gDCW-hr)
v_j^{min}	Lower limits for the metabolic flux of reaction j (mmol/gDCW-hr)

Greek Symbols

μ_j	Mean of flux difference sample $v_{j,diff}$ (mmol/gDCW-hr)
ϕ_i	Flux-sum of metabolite i (mmol/gDCW-hr)
σ_j	Standard deviation of flux difference sample $v_{j,diff}$ (mmol/gDCW-hr)

Abbreviations

α-KG	alpha-ketoglutarate
QH_2	Ubiquinol
V_C/V_O ratio	The carboxylation-to-oxygenation flux ratio of ribulose-1,5-bisphosphate carboxylase/oxygenase (RuBisCO)

$Z_{metabolite}$	Z-score of metabolites in reporter metabolite analysis
1,3-PGA	1,3-diphosphoglycerate
2-PGA	2-phosphoglycerate
3-PGA	3-phosphoglycerate
AA	Amino acid
ABA	Abscisic acid
Ac-CoA	Acetyl-coenzyme A
Acald	Acetaldehyde
ACHR	Artifcial centering hit-and-run
ACO	Aconitase
ADH	Alcohol dehydrogenase
ADP-G	ADP-glucose
Ala	Alanine
ALAAT	Alanine aminotransferase
ALD	Aldolase
ALDH	Aldehyde dehydrogenase
APS	Glucose-1-phosphate adenylyltransferase
Asn	Asparagine
Asp	Aspartate
ASP1	Aspartate aminotransferase
ASPG	Asparaginase
ATPS	ATP synthase
C/bf6	Cytochrome b_6f complex

CBM	Constraints-based modeling
CellML	Cell markup language
CMA	Cofactor modification analysis
COX	Cytochrome C oxidase
CSY	Citrate synthase
DCW	Dry cell weight
DHAP	Dihydroxyacetone phosphate
E-4-P	Erythrose-4-phosphate
EFM	Elementary flux modes
ExPa	Extreme pathways
F-1,6-bP	Fructose-1,6-bisphosphate
F-6-P	Fructose-6-phosphate
FBA	Flux balance analysis
FBP	Fructose-bisphosphatase
FCA	Flux coupling analysis
Fd	Ferredoxin
Fd-GOGAT	Ferredoxin-dependent glutamate synthase
FDR	False discovery rate
FK	Fructokinase
FNR	Ferredoxin-NADP+ reductase
FUM	Fumarase
FVA	Flux variability analysis
G-1-P	Glucose-1-phosphate

G-6-P	Glucose-6-phosphate
G3P	Glyceraldehyde-3-phosphate
GA	Gibberellic acid
GABA	gamma-Aminobutyrate
GABA-TP	gamma-aminobutyrate aminotransferase
GAD	Glutamate decarboxylase
GAPDH	Glyceraldehyde phosphate dehydrogenase
GDC	Glycine decarboxylase
GEO	Gene expression omnibus
GGAT	Glycine aminotransferase
GIMME	Gene inactivity moderated by metabolism and expression
Gln	Glutamine
GLN1	Glutamate-ammonia ligase
Glu	Glutamate
GLYK	Glycerate kinase
GO	Gene ontology
GOX	Glycolate oxidase
GPR	Gene-protein-reaction
GS	Glutamine synthase
HP	Hydroxypyruvate
HPR	Hydroxypyruvate reductase
HXK	Hexokinase
IAA	Indole acetic acid

IDP	Isocitrate dehydrogenase (NADP-dependent)
iMAT	Integrative metabolic analysis tool
LED	Light emitting diode
LP	Linear programming
MCMC	Markov chain Monte Carlo
MDH	Malate dehydrogenase
MFAML	Metabolic flux analysis markup language
MOMA	Minimization of metabolic adjustment
NAD9	NADH dehydrogenase
NDH	NAD(P)H dehydrogenase
NDPK	Nucleoside diphosphate kinase
OAA	Oxaloacetate
pc	Plastocyanin
PDC	Pyruvate decarboxylase
PDH	Pyruvate dehydrogenase
PEP	Phosphoenolpyruvate
PEPE	Phosphoenolpyruvate enolase
PFK	6-phosphofructokinase
PFP	PPi dependent phosphofructokinase
PGI	Phosphoglucoisomerase
PGK	Phosphoglycerate kinase
PGLYCM	Phosphoglucomutase
PGP	Phosphoglycolate phosphatase

PhPP	Phenotypic phase plane
PPC	Phosphoenolpyruvate carboxylase
PPDK	Pyruvate orthophosphate dikinase
PPF	Photosynthetic photon flux
PPi	Pyrophosphate
PPP	Pentose phosphate pathway
PPS	Pyruvate-water dikinase
pq	Plastoquinone
PRK	Phosphoribulokinase
PROM	Probabilistic regulation of metabolism
PRPP	Phosphoribosyl pyrophosphate
PRS	Ribose-phosphate diphosphokinase
PSI	Photosystem I
PSII	Photosystem II
PSLR	Photosynthetic light reaction
PTOX	Plastid terminal oxidase
PYK	Pyruvate kinase
Q	Ubiquinone
QP	Quadratic programming
R-5-P	Ribose-5-phosphate
R/P ratio	Ratio of respiration-to-photosynthesis
RBCS-C	Ribulose-1,5-bisphosphate carboxylase
RBCS-O	Ribulose-1,5-bisphosphate oxygenase

rFBA	Regulatory flux balance analysis
ROOM	Regulatory on-off minimization of metabolic flux changes
ROS	Reactive oxygen species
RPD	Rice proteome database
RPE	Ribose-5-phosphate epimerase
Ru-1,5-bP	Ribulose-1,5-bisphosphate
Ru-5-P	Ribulose-5-phosphate
RuBisCO	Ribulose-1,5-bisphosphate carboxylase/oxygenase
S-1,7-bP	Sedoheptulose-1,7-bisphosphate
S-6-P	Sucrose-6-phosphate
S-7-P	Sedoheptulose-7-phosphate
SBML	Systems biology markup language
SBP	Sedoheptulose-bisphosphatase
SBPGL	Sedoheptulose 1,7-bisphosphate D-glyceraldehyde-3-phosphate-lyase
SDH	Succinate dehydrogenase
SGAT	Serine-glyoxylate aminotransferase
SHM1	Serine hydroxymethyltransferase
SL	Synthetic lethal
SPP	Sucrose phosphatase
SPS	Sucrose phosphate synthase
SSA	Succinic semialdehyde
SSADH	Succinic semialdehyde dehydrogenase
SSI	Starch synthase

SUCLG	Succinyl-coA ligase
SUS	Sucrose synthase
TCA	Tricarboxylic acid
TF	Transcription factor
TKT	Transketolase
TPI	Triose phosphate isomerase
UDP-G	UDP-glucose
UDP-Glc	UDP-Glucose
UGPP	UDP-Glucose pyrophosphorylase
UI	User interface
X-5-P	D-xylulose-5-phosphate
Xu-5-P	Xylulose-5-phosphate

Chapter 1

Introduction

1.1 Rice

1.1.1 A major food source of the world

Rice is one of the major staple foods of the world, especially in Asia: each person consumes more than 100 kg of rice per year, on an average (Nelson, 2011). It is one of the three major cereal grains along with maize and wheat. As of 2012, with an annual production of 719 million tons, rice is the second most-produced cereal grain, next to maize (872 million tons)[1]. Nevertheless, since maize is also used for non-edible purposes, rice could be the cereal that supplies the world's most nutritional and calorific requirements. Furthermore, unlike maize or wheat, rice is primarily consumed as whole cereal without further treatments.

Rice has been domesticated thousands of years ago, and is considered as one of the important events in human civilization. The recent genetic analysis of rice have suggested that it has been domesticated long ago than expected, approximately 8200–13500 years ago in the Pearl River valley region of China, and from which it could have spread to Southeast Asia and to South Asia (Molina *et al*, 2011; Huang *et al*, 2012). Based on archeological evidences, it was introduced to Southern Europe during the early Middle Ages and to the United States in the 17^{th} century (Taylor, 1990). Today, rice is grown all over the world except Antarctica.

[1]FAOSTAT (http://faostat.fao.org/site/567/DesktopDefault.aspx). Retrieved: March 14, 2014.

1.1.2 Botanical aspects and varieties

The two common rice varieties that are cultivated, Asian rice (*Oryza sativa*) and African rice (*Oryza glaberrima*), belong to the *Oryza* genus under the grass (*Poaceae*) family within the *Plantae* kingdom. Apart from these two major varieties, approximately 20 more species of rice are known to exist, possibly due to its long history of cultivation and selection under diverse environments (Christou, 1994). Both *O. sativa* and *O. glaberrima* are diploid (2n=24) whereas other varieties could be even tetraploid. Among the two major groups, *O. sativa* is the most cultivated, almost all over the world. On the other hand, *O. glaberrima* is grown only in parts of Africa, which is also currently being gradually changed to *O. sativa* due to better yields. *O. sativa* is again subdivided into two major subspecies: indica and japonica. Indica varieties are generally tall with considerable drought tolerance and resistance to insects and pests than other subclasses (Christou, 1994). It is primarily grown in Indian subcontinent, Southern China and in Americas. Japonica varieties are mostly grown on Southern Europe and Japan since it requires temperate climates. These varieties are more responsive to fertilisers but less resistant to insects and pests (Christou, 1994). Further, since the amylose content is lesser in these varieties, they tend to be stickier and glossier upon cooking.

1.1.3 Rice production: Current status and future challenges

Rice is normally grown as an annual plant in lowlands, either irrigated or rain-fed, as it requires sufficient amount of water. The overall yield of rice has been increasing since the 1900's. From an annual production of 2639 kg/ha in the year 1930, it has almost doubled in 1980 (Christou, 1994). A major reason for such dramatic increase in rice yield is mainly because of the Green Revolution in 1960s: the annual rice yield increased by 40% during 1960s and 30% in 1970s (Juliano, 1985). Since then, there has been a progressive increase in the yield and production of rice (Fig. 1.1). However, despite such increasing production trends, the problem of food security has now become alarming with the world population propelling beyond 7 billion[2]. Such growing population is also expected to impact the available arable land, and thus posing serious concerns towards world food production.

[2]World Population Clock (http://www.worldometers.info/world-population/). Retrieved: March 14, 2014.

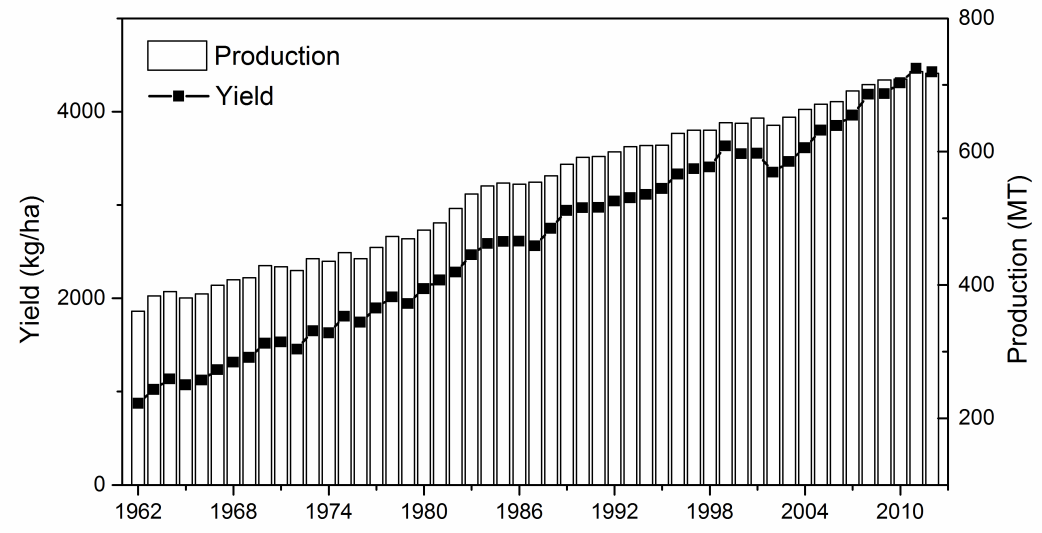


Figure 1.1: World rice yield and production from 1962 to 2012. Data retrieved from FAOSTAT (http://faostat.fao.org/site/567/DesktopDefault.aspx) on March 14, 2014.

1.1.4 Factors affecting rice productivity

Besides growing food demand and shrinking arable lands, rice production also faces serious challenges by several other environmental stressors, often simultaneously. Broadly, such stressors can be classified into two major classes: abiotic and biotic.

Abiotic stressors include drought, flooding, salinity, cold and light. Among these, drought stress is considered as the main abiotic stressor, which can reduce the crop yields drastically even under ideal cultivation conditions (Hadiarto and Tran, 2011). During water scarcity, the stomata in plant leaves close due to the passive loss of turgor in guard cells. As a result, the CO_2 uptake decreases dramatically and the excess light energy which cannot fix any carbon is dissipated in the form of reactive oxygen species (ROS), such as superoxides and peroxides (de Carvalho, 2008). Such toxic compounds can damage the DNA and proteins, and thus, possibly leading to several lethal effects on cellular metabolism. Similar to drought stress, flooding stress is also considered as one of the critical abiotic stressor of food crop productivity as nearly one third of the crop loss is directly attributed to excess water (Blom and Voesenek, 1996). During flooding, typically, plants are water-logged and surrounded by water, restricting the O_2 diffusion and thus severely inhibit the aerobic respiration. However, unlike many other food crops, rice is unique in its ability to survive oxygen stress through several adaptive mechanisms including fermentative energy generation (Alpi and Beevers, 1983;

Guglielminetti *et al*, 1995; Perata and Alpi, 1993). Therefore, rice has been often considered as a model plant for studying flooding stress. However, rice is a salt-sensitive crop as salinity impacts the plant growth significantly at the seedling stage (Negrao *et al*, 2011). Under salt stress, the osmotic stress gradually develops and slows down the transpiration and leaf expansion. Concurrent to these changes, the abnormality in root Na^+ transporters cause the leaves to prematurely senesce and die. Collectively, salinity reduces the photosynthesis greatly, and thus reducing the plant growth. Light also affects plant growth significantly: both light intensity (fluence) and quality (wavelength) impacts plant development in several ways. Similar to drought stress, high light intensities also severely inhibit photosynthesis, and hence crop productivity (Osakabe and Osakabe, 2012). Another important consideration is that light quality affects various morphological processes in plants (Neff *et al*, 2000).

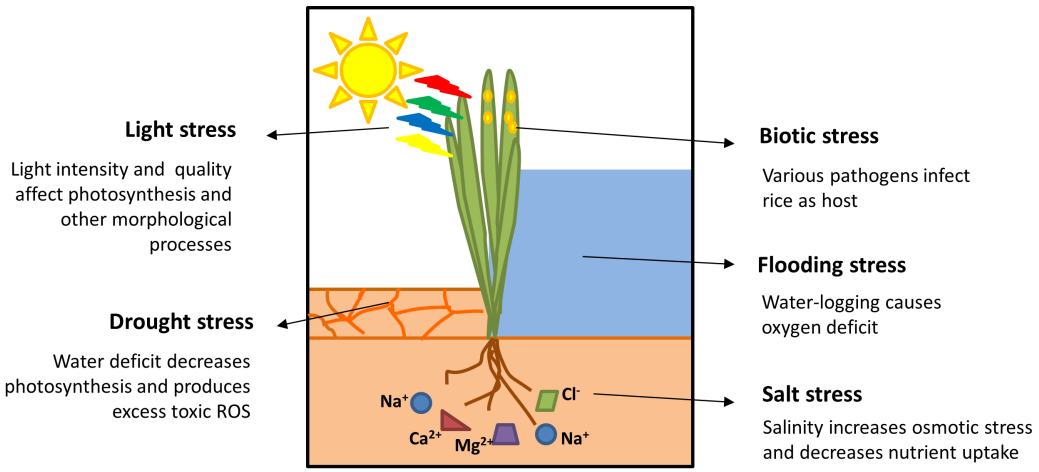


Figure 1.2: Factors affecting rice productivity. Both abiotic and biotic stress limits rice productivity tremendously.

Similar to abiotic stressors, plant development is also affected by insects and diseases, i.e. biotic stressors, particularly during grain development and germination. Nearly 25% of the production losses in rice have been accounted by diseases and insects (Van Nguyen and Ferrero, 2006). Among several pathogens, rice growth is severely affected by the bacteria *Xanthomonas oryzae*, pv. *oryzae*, which causes a bacterial leaf blight disease and the fungus *Magnaporthe grisea*, which induces a blast disease (Van Nguyen and Ferrero, 2006).

1.1.5 Rice research: past, present and future

Technically, rice research has been initiated thousands of years ago when it was first domesticated. Most of the early research was involved with rice cultivation techniques and breeding. These include: (i) selection of rice varieties with suitable characteristics as progenitors and their preservation for subsequent generations, (ii) selection of suitable lands, (iii) water management and (iv) determination of optimal cultivation and harvestation times (Christou, 1994). In terms of scientific research, it could have possibly started during the European Renaissance, i.e. 14^{th}- 17^{th} century. It was during this period that plant anatomy was identified with the invention of microscopes and the general concepts of plant physiology such as uptake of CO_2 and release of O_2, water and nutrient absorption through roots and plant sexuality was unravelled (Browne, 2007).

In terms of molecular biology research, although the exact date of origin could not be pinpointed, most of them could have started in the 19^{th} century following the landmark discoveries such as the structure of plant cell and principles of light utilization in photosynthesis. The legacy of these discoveries was utilised in early 20^{th} century for various molecular analyses to study about the plant cells as a separate entity. Further, the advent of plant suspension cell cultures also fuelled such progress. Several biochemical analyses were conducted to identify the individual compounds involved in cellular growth. The details of photosynthesis, metabolism and transport were elucidated more precisely and by the mid-20^{th} century the molecular basis of plant cellular growth and reproduction was firmly established (Lack and Evans, 2005). Later, with the arrival of recombinant DNA techniques, plant scientists have utilised them in combination with molecular biology methods for gaining detailed insights into genes and gene products in several plant processes.

In the modern genomic era, the genome sequence and large-scale datasets of plants have now become available. Arabidopsis is the first plant genome to be sequenced completely in 2000 (The Arabidopsis Initiative, 2000). Among cereal crops, interestingly, rice was the first plant to get its genome sequenced through International Rice Genome Sequencing Project (2005). Concurrently, the developments in high-throughput technologies have helped generating large amounts of cellular component data at the genome-scale from plant samples grown under a wide variety of conditions. Please note

that a detailed coverage of these developments will be provided later in Section 1.3. However, despite the availability of such large compendium of cellular data, still the complete characterization of rice cellular responses is impossible as most of such data are largely underutilised. In this regard, the field of systems biology offers immense promise to integrate every piece of biological information available into a whole knowledge-base for the improved understanding of the organism at the molecular level, and thus could be considered as the next revolution in plant research.

The following section discuss the basics of systems biology, its practice methods and tools and how it can be utilised for analysing rice cellular behaviour.

1.2 Systems Biology

1.2.1 A new paradigm in biological research

Biological systems are enormously complex, still, organised and coordinated at various levels, performing a wide range of activities. The past century has made tremendous progress towards the understanding of such complex systems, however in parts: majority of the research in 20^{th} century were focused on the chemistry of biological molecules, their structure, and the elemental analysis of machineries which synthesise and utilise them. The major breakthrough in such progressive path was made with the identification of DNA, the centrepiece of all living systems, and its central role in controlling the functioning of biological systems at various levels. Since then, the development of nucleotide sequencing and other high-throughput technologies have now made us to assimilate huge amounts of component data at different levels of the cellular hierarchy, and thereby, allowing us to possibly identify all the components of cellular system. Nevertheless, despite the acquisition of enormous amounts of data, the question of how cellular systems interact among these components is far from being answered with the traditional reductionist approach. Typically, a large number of these parts interact at various levels and varying scales of time and space in cells. Such enormous complexity of cellular organisms have motivated researchers to look them in a different manner by abstracting the biological processes as mathematical models using the vast experimental data. This approach has been later formally known as “systems biology” . Therefore, the field of systems biology is merely biology, however studies the living systems in terms of

mathematical representations.

Systems biology first formally came into existence in the late 1990's. However, since then its widespread has been tremendous. What made systems biology to spread in such a rapid manner? One can say, more than scientists' curiosity, systems biology has been mainly driven because of its potential applications. A few examples of systems biology applications include the development of individualised and predictive medicine for health care, improvement of yield in microbial cell factories for biotechnological industries, unravelling of cell-to-cell communication and cellular evolution.

1.2.2 Establishing the parts: generating components data

Systems biology, essentially aims to integrate various parts of the biological system for understanding the cellular functioning. In order to do so, the establishment of individual parts, i.e. components data, which details the molecular content of the cell is preliminary. The recent advances in highthroughput experimental technologies have now made it possible to generate large amounts such component data at each level of cellular hierarchy, i.e. from DNA to metabolites, at the entire genome-scale. Such large-scale biological datasets are associated with a generic term called "-omics". A brief description of each of these "-omics" technologies are provided in the following sub-sections.

1.2.2.1 Genomics

Genomics is the "-omics" field which involves the sequencing of DNAs at the entire genome-scale and the study of information contained therein. The complete sequence of a genome was first published for *Haemophilus influenzae* in 1995, and since then more than 300 genome sequences have been completed until 2006 (Liolios *et al*, 2006). In terms of plants, the genome sequences are currently available for more than 20 species including the major crops such as rice, maize and barley (Bolger *et al*, 2014). The whole genome sequences has multiple uses: (i) the sequence data, as it is, can be used to identify gene-regulatory networks, and (ii) genome sequences of multiple species to understand speciation via comparative genomics techniques. Genome annotation is another significant research area where genome sequences play a crucial role. It involves the identification of coding parts of the sequence and thereby predicting its biological function by complementing the sequence information with known proteins or RNAs

that are present in the cell. Finally, another overwhelming use of crop genomes is the quantitative trait locus mapping of desirable traits and to identify candidate genes of interest.

1.2.2.2 Transcriptomics

Transcriptomics is associated with large-scale RNA transcript profiling, providing information on either its presence/absence or abundance levels. Among all "-omics" data, transcriptomics is the most abundant. It generally gives a snapshot of the functionally active part in entire genome which has been transcribed at any given instance. Therefore, it is very much useful in comparative studies such as the comparison of plants grown under normal and stressed conditions to identify which part of sub-cellular machinery is markedly different between them, and thereby paving ways for improvement.

Currently, two major technologies, microarrays (Hardiman, 2004) and serial analysis of gene expression (SAGE) (Harbers and Carninci, 2005), are available for transcript profiling. Microarray is a chip which contains a collection a small quantity (picomoles) of various microscopic DNA sequences with flourescent tags as spots attached to a solid surface. Depending on the transcription of each gene, the corresponding DNA sequence gets hybridised which can be later scanned for the intensity. Depending on the expression levels, the intensity strength of each gene varies. SAGE, on the other hand, is a technique where the RNA levels are measured through a sequential analysis of short cDNA sequence tags corresponding to each transcript.

1.2.2.3 Proteomics

Proteomics is a field aimed at identifying and or quantifying the levels of individual proteins available in the cell. Similar to transciptome, the proteome data also provide us information about the active part of genome at any given instance based on the presence/absence calls of individual proteins. When compared to transcriptome technology, proteomics requires significant efforts and resources for the improved detection of proteins as protein detection is severely hampered by the differences in overall protein levels.

Some of the commonly used method in proteomics are gel electrophoresis and mass spectrometry (MS) (Patterson and Aebersold, 2003). Gel electrophoresis separates or

identifies the proteins based on size and charge. Smaller proteins move faster than the larger ones through the gel pores. MS, on the other hand, separates or identifies proteins based on their mass and charge. In MS, first the protein is ionised and then the mass-to-charge ratios is measured from which the protein can be detected.

1.2.2.4 Metabolomics

Metabolomics seeks to identify or quantify the levels of all intracellular metabolites of the cell at a given instance. Similar to transcriptomics and proteomics, the relative levels of metabolome to an environmental stimuli or genetic perturbation can be quantified using metabolomics. However, unlike transcriptomics, the detection and quantification of metabolites is often challenging because of their diverse range.

Metabolomics uses two major techniques to quantify and detect various metabolites: MS and nuclear magnetic resonance (NMR) spectroscopy (Dunn *et al*, 2005). In NMR spectroscopy, the intramolecular magnetic field is perturbed according to the resonance frequency, and thus giving an account of the corresponding molecule's electronic state.

1.2.3 Connecting the dots: integrating various "-omics" data

Once the parts of a system are established, it is then important to integrate these components into biologically meaningful correlations. In this regard, the ability to represent biological parts and their interactions in the form of a mathematical model, and to investigate them via appropriate *in silico* analysis techniques is considered as a key achievement of systems biology (Kitano, 2002a,b). In general, mathematical modelling in systems biology involves two steps: 1) system identification and 2) development and *in silico* analysis of mathematical model.

System identification involves the identification of the list of biological components, i.e. gene, protein or metabolite, and their interactions for representing the biological process of interest. As mentioned earlier, biological systems and processes operate and interact at various levels. Therefore, the system of interest could be on any of these levels or even across levels. For example, models can be made at the core level using various genes as the biological components and their interactions. Similarly, a protein-protein interaction could also be made at another level. On the other hand, models such as biochemical reaction networks can be developed by integrating the interactions within and

across various genes and gene products, i.e. transcripts, proteins and metabolites. Furthermore, systems biology models can be made by completely abstracting the biological activities of a organism, tissue or organs.

Following the system identification, the next step is to mathematically represent them. Again, as mentioned earlier, since biological activities take place at various levels and varying scales of time and space, the type of model can be plural: it can be either 1) microscopic or macroscopic, 2) deterministic or stochastic, 3) discrete or continuous, and 4) steady-state, temporal, spatial or spatio-temporal. The choice of modelling and simulation is mainly based on the data available and the type of system being studied. For example, a Boolean model can be used to describe the biological events such as metabolic regulation in a discrete manner using just the information of interactions between involved components. On the other hand, when the mechanistic details and kinetic parameters are available for a system, differential equation-based dynamic models can be used. Here, it should be noted that this thesis will entirely deal with a particular deterministic, steady-state modelling approach called constraints-based modelling. More details of this approach will be presented in the next chapter.

Once a mathematical model is developed, the *in silico* predictions must be compared with actual experimental outcomes. This step allows us to close the gap in abstracting the actual process more reliably via mathematical models; model predictions will fail only if there is a incomplete or missing feature exist in the model. Once reliable and accurate models are established, they can be further utilised to suggest novel hypotheses for new experimental horizons, leading to an iterative knowledge discovery process (Fig. 1.3).

1.3 Rice systems biology

1.3.1 Overview of rice "-omics" data wealth

As mentioned earlier, the availability of components data is the key requirement in systems biology. In this regard, the recent advances in genome sequencing and high-throughput experimental techniques have resulted in accumulation of large rice specific data at various levels of cellular hierarchy, providing unprecedented opportunities for systems biologists to initiate a systems analysis of rice cellular metabolism. The follow-

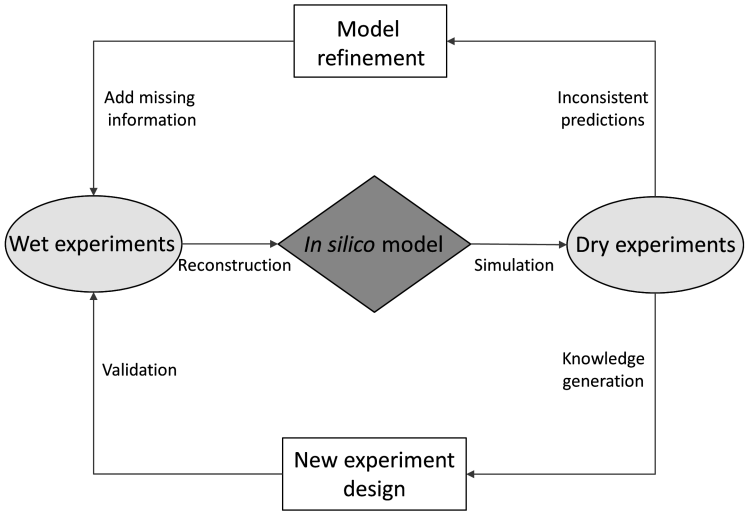


Figure 1.3: The iterative model building procedure in systems biology. Initially, an *in silico* model is reconstructed based on available data. The *in silico* predictions are then tested and the model is refined continuously. Once reliable model is established, it is then used for *de novo* experiment design (Kitano, 2002b).

ing section summarises the current wealth of rice highthroughput data.

Genome: Following its draft sequence in 2002 (Goff *et al*, 2002; Yu *et al*, 2002), the rice genome is being annotated continuously by two groups, Rice Annotation Project (RAP) (Tanaka *et al*, 2008) and MSU Rice Genome Annotation Project (MSU-RGAP) (Ouyang *et al*, 2007), improving our understanding about the gene products. At present, the functions of at least 30,000 genes are annotated[3].

Transcriptome: A tremendous progress has been made in the field of rice microarray data analysis. Currently, over 7000 gene expression datasets are publicly available in the Gene Expression Omnibus (GEO)[4].

Proteome: Similar to transcriptome data, huge amounts of proteome data are now available for rice. The Rice Proteome Database (RPD) maintained by National Institute of Agrobiological Sciences, Japan, currently has more than 13129 proteins obtained from various tissues and organelles[5].

Metabolome: Although the field of metabolome has not generated vast amounts of data in rice as it is in other "-omics" technologies, still considerable amount of work has been done, revealing characteristic traits of cellular metabolism under various circum-

[3]RAP-DB (http://rapdb.dna.affrc.go.jp/rice_docs/docs_genome_statistics.html) and MSU-RGAP-DB (http://rice.plantbiology.msu.edu/). Retrieved: March 15, 2014.
[4]GEO (http://www.ncbi.nlm.nih.gov/geo/). Retrieved: March 15, 2014.
[5]RPD (http://gene64.dna.affrc.go.jp/RPD/) Retrieved: March 15, 2014

stances (Oikawa *et al*, 2008).

1.3.2 Systems biology approaches towards understanding rice abiotic stress responses

In the previous section, an overview of all available rice highthroughput data has been provided. The current section will specifically focus on the past researches which has been devoted to analyse the rice abiotic stress responses through systems biology approaches, especially "-omics" data generation.

With the rapid advancements in highthroughput experimental techniques, the "-omics" has been increasingly applied to rice for unravelling the stress response modulators. Table 1.1 summarises the list of "-omics" based studies on rice which focused on understanding the abiotic stresses such as flooding, drought and salinity. In general, the number of available transcriptome studies are much higher than the proteome and metabolome analysis as the development of whole genome microarrays has now become easier with the availability of rice whole genome sequence. Typically, these analyses compare the gene expression profiles of the stressed plants, i.e. flooding, drought or salinity, with the control and identifies the key stress-responsive genes based on differential expression patterns (Table 1.1). Similar approaches have also been adopted for proteomic and metabolomic analyses where the protein abundance and metabolite levels are used as markers for rice stress response. Interestingly, some studies have also compared the "-omics" responses between stresses, i.e. drought and salinity, or even between rice and other plants which may be tolerant to such abiotic stresses (Table 1.1).

In terms of flooding stress, the transcriptomic analyses of Lasanthi-Kudahettige *et al* (2007) and Narsai *et al* (2009) identified several genes of carbohydrate metabolism, lipid metabolism and ethylene response factors to be modulated under anoxia in rice as it is in Arabidopsis. Additionally, these studies also pinpointed that fermentation metabolism plays a critical role in rice anoxic adaptation as some of those genes were found to be upregulated dramatically. The comparative proteome and metabolome analysis of Shingaki-Wells *et al* (2011) compared the molecular mechanisms of rice, an anoxia tolerant plant, with wheat, an intolerant one. Their findings highlighted that the functioning of amino acid synthetic pathways is the primary difference between rice and wheat during anoxic adaptation where the former was able to successfully synthesise

amino acids even under complete anoxia whereas the latter does not. They further showed that when certain amino acids are exogenously fed, even wheat coleoptiles can grow under anoxia.

Table 1.1: Application of "-omics" techniques to unravel rice stress response

Type of abiotic stress	"-omics" type	Research summary	References
Flooding (Anoxic germination)	Transcriptome	Microarray analysis of rice seed germinated in air and anoxia	Lasanthi-Kudahettige *et al* (2007)
		Transcriptome and metabolome analysis of rice seed germinated in anoxia and anoxia at 9 different time points	Narsai *et al* (2009)
		Transcript profiling of alcohol dehydrogenase 1 (ADH1)-deficient mutant. ADH1 is one of the key enzyme involved in survival of rice under anoxia	Takahashi *et al* (2011)
	Proteome	Comparative proteome and metabolome analysis of rice and wheat during anoxic germination	Shingaki-Wells *et al* (2011)
	Metabolome	Metabolome analysis of rice coleoptile under air and anoxia	Fan *et al* (2003)
		Transcriptome and metabolome analysis of rice seed germinated in anoxia and anoxia at 9 different time points	Narsai *et al* (2009)
		Comparative proteome and metabolome analysis of rice and wheat during anoxic germination	Shingaki-Wells *et al* (2011)
Drought	Transcriptome	A comparative transcriptome analysis of rice under cold, drought and high-salinity stresses	Rabbani *et al* (2003)
		Microarray analysis of upland, drought-tolerant, and lowland, drought-intolerant, rice varieties	Wang *et al* (2007)
		EST-based analysis of drought stress related genes in rice	Gorantla *et al* (2007)
		Microarray analysis of drought and salt stress induced genes in rice shoot, flag leaf and panicle	Zhou *et al* (2007)
		Transcriptome analysis of drought-tolerant and drought-sensitive rice varieties	Degenkolbe *et al* (2009)
	Proteome	Proteomic analysis of three week old rice seedlings grown under normal and drought stress conditions	Salekdeh *et al* (2002)
		Proteomic analysis of rice 2 to 6 days old rice between under normal and drought stress conditions	Ali and Komatsu (2006)

Type of abiotic stress	"-omics" type	Research summary	References
Salinity	Transcriptome	Transcriptome analysis of rice plants experiencing salt stress between 15 min to 1 week from induction	Kawasaki *et al* (2001)
		A comparative transcriptome analysis of rice under cold, drought and high-salinity stresses	Rabbani *et al* (2003)
		Identification of salt stress related genes through comparative microarray analysis	Dai Yin *et al* (2005)
		Comparison of transcriptional responses between a recombinant, salt tolerant and a wild type salt intolerant	Walia *et al* (2005)
		Comparative transcriptome analysis of rice and barley during salt stress	Ueda *et al* (2006)
		Microarray analysis of drought and salt stress induced genes in rice shoot, flag leaf and panicle	Zhou *et al* (2007)
	Proteome	Proteomic analysis of rice seedlings grown under normal and salt stress conditions	Kim *et al* (2005)
		Proteomic analysis of three week old rice seedlings grown under normal and salt stress conditions	Yan *et al* (2005)
		Comparative analysis of rice proteome between control and salt stressed rice panicles	Dooki *et al* (2006)
		Proteomic analysis of short- and long-term salt-stress-responsive proteins in the rice leaf lamina	Parker *et al* (2006)
	Metabolome	Metabolome analysis of rice leaf and root under control and salt stressed conditions	Zuther *et al* (2007)

Regarding drought and salinity stress, the transcriptome analyses of Zhou *et al* (2007) identified several specific genes from the carbohydrate metabolism. In addition, they also reported the possible role of several transcription factors including AP2/EREBP-, bZIP, NAC and MYB in drought response. More specific to drought stress, Wang *et al* (2007) identified several genes involved in the detoxification or protection against oxidative stress to be upregulated in the drought resistant variety. With regards to salt stress, the proteomic analysis of Yan *et al* (2005) confirmed the Zhou *et al* (2007) tranascriptomic analysis results that the carbohydrate metabolism is indeed significantly altered under stressed conditions. Additionally, they also specifically identified three metabolic proteins, namely, UDP-glucose pyrophosphorylase, cytochrome C oxidase and glutamine synthetase, to be salt-stress specific.

In general, the availability of such large amounts of "-omics" data, especially under abiotic stresses, has provided us enormous opportunities to unravel the stress responsive mechanisms in rice. However, the intrinsic complexity of plant systems and the large volume of data pose huge challenges in integrating and analysing them systematically. To this end, as mentioned earlier, mathematical modelling offers the potential to integrate genome-wide data into mathematical models, enabling large-scale systems analysis. In fact, such approaches have been successfully applied to several microbes and animals, and to Arabidopsis for a certain extent (Coruzzi and Gutierrez, 2009). Therefore, it is highly required to initiate the systems analysis of rice by integrating the abundant highthroughput "-omics" data sets in combination with *in silico* modelling.

1.4 Scope of the thesis

1.4.1 Objectives

As mentioned earlier, several abiotic and biotic factors significantly influence the productivity of rice. Over the last few decades, numerous researches have been conducted to understand the cellular behavior of rice including highthroughput experimental approaches. However, despite such efforts, still the adaptive mechanisms of rice under different stress conditions remain poorly characterised. Therefore, in order to better understand the cellular behavior of rice under such stressful conditions, this thesis aims to propose an integrative analysis framework involving *in silico* modelling and highthroughput experimental data. It should be noted that large part of the dissertation focuses on the rice metabolism due to the legacy of biochemical information about metabolites and enzymes, and in some cases the transcription regulation. The knowledge obtained from such integrative analysis will enable us to understand the cellular mechanisms more precisely, and to propose design strategies for crop improvement.

The major objectives of the current study are:

- To review the metabolic network reconstruction and analysis methods, and the software applications available to perform them
- To develop reliable mathematical model(s) representing rice cellular metabolism
- To develop an *in silico* model-driven analysis framework for analyzing rice metabolism

under various stressful conditions

- To integrate multiple "-omics" data and mathematical model(s) of rice to improve the current understanding on its cellular behaviour

1.4.2 Organization

This thesis is organised into eight chapters. As seen already, Chapter 1 introduced rice, its current production status, future challenges and the factors affecting its productivity. It also discussed the advent of systems biology, its elite nature, potential applications and the need for systems-level approaches to study rice metabolism during various stresses. The rest of this thesis is organised as follows (Fig. 1.4):

Chapter 2 provides the overview of constraints-based modelling (CBM) framework. Further, it also documents all the individual CBM methods and the software tools available for implementing such analysis, and benchmarks each tool based on certain predefined measures. It should be noted that the contents of this chapter, in part, has been published in the journal, *Briefings in Bioinformatics* (Lakshmanan *et al*, 2014a).

Chapter 3 describes the reconstruction of the central metabolic/regulatory model of rice cells. Detailed procedure of model reconstruction and simulation methods for analysing two different tissue types, germinating seeds and photorespiring leaves, are provided. The model predictions are then validated with experimental data to test its predictive ability. It should be noted that the contents of this chapter, in part, has been published in the journal, *Plant Physiology* (Lakshmanan *et al*, 2013c).

Chapter 4 elaborates the *in silico* analysis of germinating rice seed cells during flooding stress and highlights the metabolic adaptations between normal and stress conditions. The simulated metabolic flux states were then compared with gene expression levels of corresponding enzymes between normal and stressed conditions to identify the putative transcriptionally regulated reactions. Further, the key transcription factors (TFs) involved in the transcriptional control are also summarised. It should be noted that the first and second parts of this chapter has been published in the journal, *Plant Physiology* (Lakshmanan *et al*, 2013c), and *AoB Plants* (Lakshmanan *et al*, 2014b), respectively.

Chapter 5 discusses the computational model-driven analysis of photorespiring leaf

cells under normal and drought stress. The essential enzymes/genes of the central metabolism under both normal and stressed conditions are also presented. It should be noted that the first and second parts of the chapter has been published in the journals, *Plant Physiology* (Lakshmanan *et al*, 2013c), and *Rice* (Lakshmanan *et al*, 2013b), respectively.

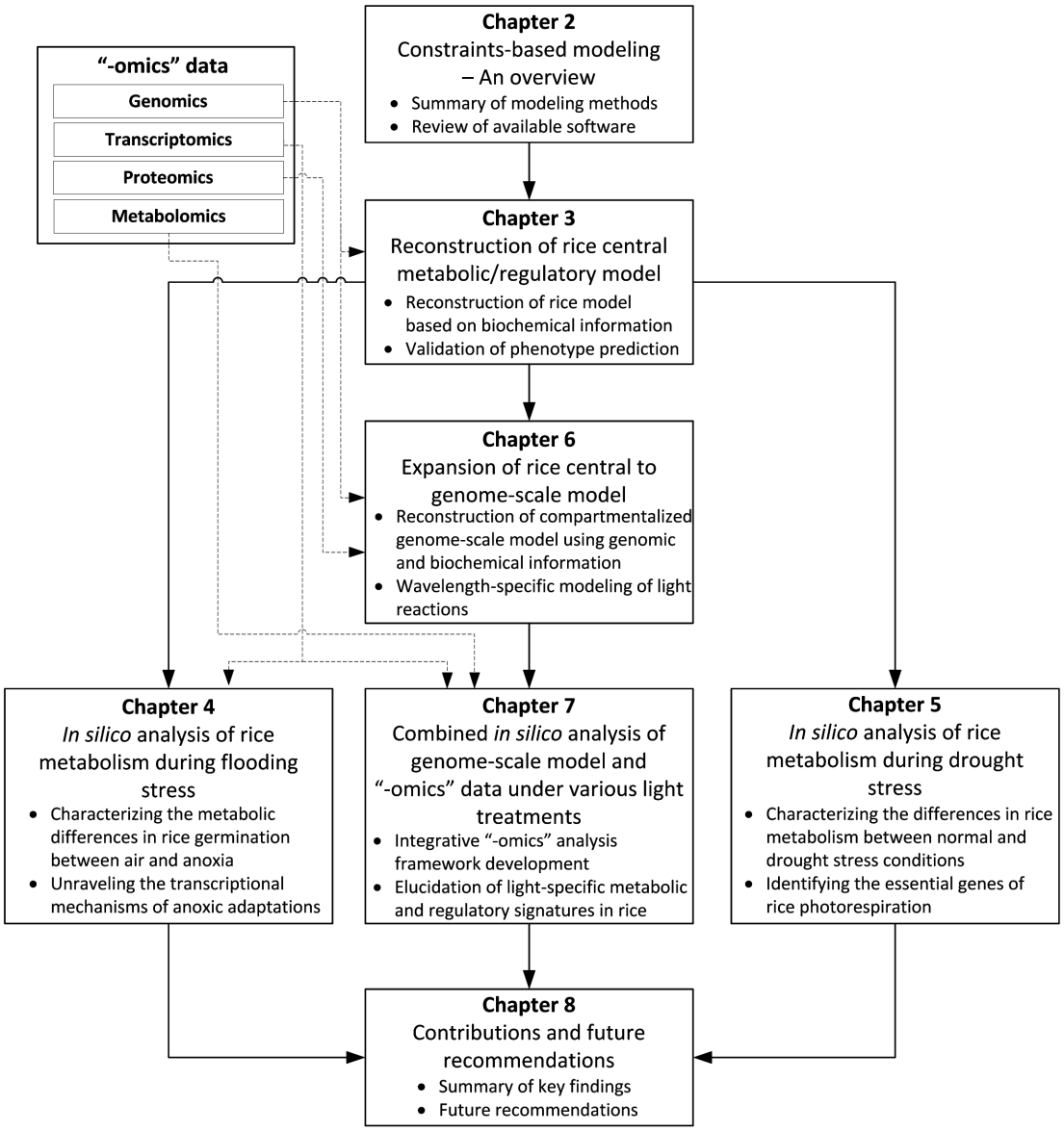


Figure 1.4: Flow chart showing the organization of thesis and the major research issues addressed in each of the following chapters.

Chapter 6 details the expansion of central metabolic model into a genome-scale model based on the genome annotation and other biochemical information. It should be noted that this chapter also provides the method to model the metabolic utilization

of light. Moreover, the model's predictive ability is tested using various qualitative and quantitative tests. It should be noted that the contents of this chapter is being prepared as manuscript for publication.

Chapter 7 presents the combined *in silico* analysis framework involving genome-scale metabolic model and multiple "-omics" data for the characterization of various metabolic and regulatory adaptations in rice based on light quality. This chapter combines various statistical data analysis methods and *in silico* modelling techniques in an integrative manner at various levels of cellular hierarchy: global-network-level, pathway-level and individual reactions and metabolite-level. In addition, it also presents the major light-specific TFs which orchestrate the light signalling in rice. It should be noted that the contents of this chapter is being prepared as manuscript for publication.

Chapter 8 summarises the key findings and highlights the major contributions of the current thesis. Possible extensions and future recommendations for an improved rice systems biological research are also discussed.

Chapter 2

Constraints-based modelling - An overview[1]

2.1 Introduction

As seen in the previous chapter, the key step in systems biology is to represent the biological process of interest in the mathematical form. Several approaches have been proposed in the past for modelling cellular processes. In terms of metabolic modelling, kinetic modelling (Steuer *et al*, 2006), cybernetic modelling (Kompala *et al*, 1984), metabolic control analysis (Reder, 1988) and constraints-based modelling (CBM) (Price *et al*, 2004a), are the four major approaches suggested. Among these, almost all the earlier metabolic networks were analysed using kinetic modelling framework. Typically, such models represent a part of the metabolism using a set of equations where each equation capture the dynamic changes in the concentration of metabolites involved. The rate of formation or depletion of a metabolite by an enzyme is usually represented using Michaelis-Menten kinetics or Hill equation. Although these models provide deep insights about the process, it is practically impossible to model large-scale networks using this method as the kinetic variables are often difficult to measure, and are not available for many of the biochemical reactions. In this regard, the constraints-based modelling has a clear advantage over the kinetic models as they require only the information on metabolic reaction stoichiometry, flux capacity and significantly lesser experimental data (Raman and Chandra, 2009). Several genome-scale metabolic networks have been successfully

[1]Excerpts of this chapter, in part, is a reprint of previous publication, Lakshmanan et al. (2014) Software applications for flux balance analysis, Briefings in Bioinformatics, 15(1):108-22, PMID: 23131418.

reconstructed for a myriad of microbes, and to a handful of animals and plants using such an approach (Kim *et al*, 2012b). Therefore, this thesis will also use constraints-based modelling techniques as it provides sufficient insights into rice cellular metabolism, at the same time, it also circumvents the issue of kinetic parameters scarcity. Accordingly, in this chapter, first, the theory of constraints-based modelling is presented. This is followed by a detailed discussion of the various constraints-based modelling methods and the software tools available for implementing such analysis.

2.2 Constraints-based modelling

2.2.1 System definition

The prerequisite of CBM is to reconstruct the metabolic network consisting of metabolic reactions with their stoichiometry clearly defined. Typically, metabolic network reconstruction starts with the collection of information available from the numerous genomic (e.g. NCBI, GeneDB, TIGR, etc.) and biochemical databases (e.g. BRENDA, ENZYME, KEGG, etc.), resulting into a draft network. The collected information is then manually curated by checking individual reactions for elemental and charge balancing, cofactor specificity and reaction directionality. Manual curation is followed by gap-filling, in which, the missing links are connected through addition of new reactions based on literature evidences. Additionally, transport reactions are also added to the network, facilitating the input and output from the system. The detailed procedure for reconstructing a genome-scale metabolic network can be found elsewhere (Thiele and Palsson, 2010).

2.2.2 Model development

Once the network is reconstructed, it is then converted into a mathematical model. It can be achieved by applying the first principle of mass conservation of internal metabolites within the network (Kauffman *et al*, 2003). In any metabolic network, the metabolites are continuously transformed into others through a series of enzyme catalysed reactions (Fig. 2.1). Therefore, the general equation for mass conservation of internal metabolites is given by:

$$\frac{dC_i}{dt} = \sum_j S_{ij} v_j \tag{2.1}$$

where C_i denotes the concentration of metabolite i, v_j represents the flux or specific rate of metabolic reaction j, and t is time. S is a stoichiometric matrix of dimension $i \times j$ whose rows correspond to metabolites and columns correspond to reactions.

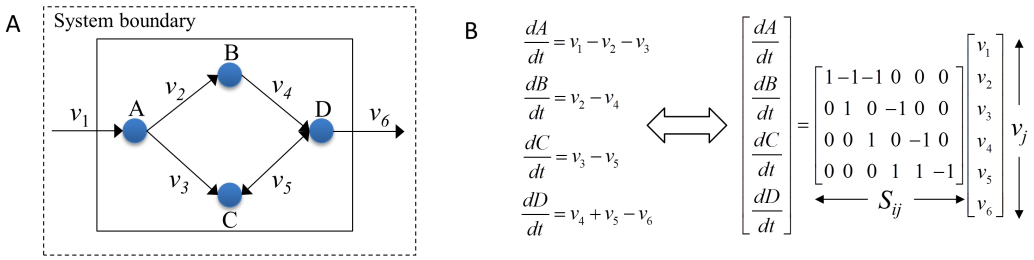


Figure 2.1: "S" matrix development. A. Definition of system boundary. B. Mass balance equations of all metabolites and the formation of "S" matrix.

During analysis, CBM assumes steady state; because the rates of intracellular reactions are much faster (in the order of milliseconds to tens of seconds) than the changes in cellular phenotype such as cell growth (in the order of hours to days) (Kauffman *et al*, 2003). Therefore, the steady state assumption modifies equation (2.1) as follows:

$$\sum_j S_{ij} v_j = 0 \tag{2.2}$$

When eq. (2.2) is visualised graphically where each flux representing individual axes, it resembles a hyperplane in the solution space (Fig. 2.2A). In a mathematical point of view, it is impossible to find the exact solution of such a system as it has both allowable and non-allowable solutions in its space. Therefore, in order to solve such system, additional constraints are needed to shrink the solution space into a smaller one. Flux limits are the most commonly applied additional constraints in CBM. Generally, the maximal values are applied for internal reactions and the exact values are constrained for input and output of the system.

$$v_j^{min} < v_j < v_j^{max} \tag{2.3}$$

where v_j^{min} and v_j^{max} are upper and lower limits of flux v_j, respectively.

Similarly, thermodynamic constraints, representing the reaction directionality, i.e. reversible or irreversible, can also be applied. Once the constraints are applied, a convex feasible solution space of steady state fluxes is obtained (Fig. 2.2A). Compared to previous step, it now becomes relatively easier to obtain steady state flux distributions from such convex space. Two main approaches are available for exploring and obtaining the possible solution from the convex space: biased and unbiased. Biased methods identifies the best solution based on a particular bias whereas unbiased methods enumerate all possible steady state solutions of the convex space. The following sections will detail the different methods available under each of such approach.

2.2.3 Unbiased solution methods - Global characterization of solution space

Unbiased methods surveys the entire convex solution space and identifies all possible solutions. The following subsections will briefly discuss about each of the method.

2.2.3.1 Extreme pathway and elementary flux modes

Extreme pathway (ExPa) analysis and elementary flux mode (EFM) analysis are the two methods which globally characterise the solution space by identifying certain reaction sets, i.e. ExPa or EFM, which represent specific metabolic functions (Fig. 2.2B). Collectively, the combinations of all such sets describe the entire space. More specifically, EFM are "the minimal set of irreversible reactions which could operate in a particular direction" whereas ExPa are "the minimal set of irreversible reactions that lies at the corners of the convex solution space". Both approaches have been utilised to explore the core metabolic network of *E. coli*. However, although these analysis characterises the entire solution space, it is often difficult to implement these for large-scale networks as it is computationally intensive and thus, it will not be utilised in this dissertation. The detailed procedure of computing ExPa and EFM of a metabolic network can be found elsewhere (Schuster and Hilgetag, 1994)(Schilling *et al*, 2000).

2.2.3.2 Sampling solution spaces

Similar to ExPa and EFM, random uniform sampling can identify all possible solutions of the convex space. However, due to its stochastic nature, random sampling is not

computationally intensive and can be successfully applied even to large-scale networks. Briefly, in random sampling, first, the flux intersects in the convex space are transformed into parallelepipeds. Subsequently, the parallelepipeds are uniformly sampled using Markov chain Monte Carlo (MCMC) sampling methods and a set of possible candidate solutions within the convex solution space is obtained and the probability distributions of the flux through each reaction is computed (Fig. 2.2) (Price *et al*, 2004b)(Wiback *et al*, 2004). It should be noted that as this method provides a set of solution with probability distributions, it is statistically more meaningful than other methods as it sufficiently accounts for the uncertainty. With sufficient constraints and adequate sampling, this is an effective method to characterise the metabolic states of an organism between any two conditions such as wild-type and mutant or glucose-grown and xylose-grown.

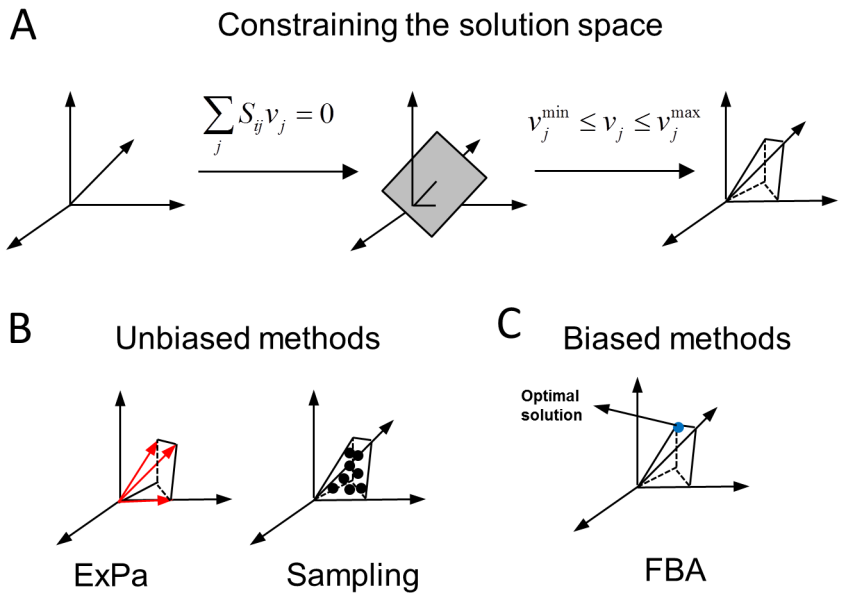


Figure 2.2: A. Constraining of solution space using sequential application of constraints. B. Biased solution methods. These methods characterises the entire solution space. C. Biased methods. These methods find the optimal solution of the network.

2.2.4 Biased solution methods - Finding the optimal solution

As seen above, EFM or ExPa can enumerate all possible solutions of the metabolic network. However, cells most often attain only one particular state and not all states suggested by such analysis. Therefore, in order to find the best possible solution which can be attained by the cells, optimization techniques are used.

2.2.4.1 Constraints-based flux analysis

Among several optimization-based methods, the most basic technique is the constraints-based flux analysis, also known as flux balance analysis (FBA). It uses linear programming (LP) to find the optimal solution of the network by either maximizing or minimizing a particular cellular objective while satisfying the constraints imposed by equations 2.2 and 2.3 (Fig. 2.2C) (Orth *et al*, 2010). Mathematically, the problem specific for maximizing a particular objective can be represented as follows:

$$\begin{aligned} \text{(P1)} \qquad & \max\ Z = \sum_j c_j v_j \\ & \text{s.t. } \sum_j S_{ij} v_j = 0 \\ & v_j^{min} < v_j < v_j^{max} \end{aligned}$$

where Z corresponds to the cellular objective and is represented as a linear function of certain metabolic reactions where the relative weights are determined by the coefficient c_j.

In constraints-based flux analysis, several objective functions such as biomass maximization or cell growth, maximization of any particular product or intracellular ATP and minimization of any particular substrate uptake have been used in the past (Schuetz *et al*, 2007). Among them, the "cellular biomass maximization" is the most widely used objective function for analysing metabolic models, following its initial success in predicting *E. coli*'s growth accurately (Feist and Palsson, 2010). Typically, most of the previous studies maximises the biomass while constraining the uptake of particular substrate(s).

Several extensions to constraints-based flux analysis framework has been suggested for a variety of purposes including exploration of metabolic networks, incorporation of regulatory mechanisms, mutant phenotype analysis and for strain design. The following subsections detail some of them.

2.2.4.2 Exploration of metabolic network using optimization

Flux variability analysis: As constraints-based flux analysis is an optimization-based approach, it is often possible to obtain multiple equivalent optimal solutions. Therefore, in order to identify all the active fluxes and their possible ranges during a particular state, flux variability analysis (FVA) has been proposed (Mahadevan and Schilling,

2003). Mathematically, it can be represented as:

$$\begin{aligned} \text{(P2)} \qquad & \max/\min\ v_j \\ & \text{s.t. } \sum_j S_{ij} v_j = 0 \\ & v_j^{min} < v_j < v_j^{max} \\ & \sum_j c_j v_j = Z_{obj} \text{ for } j = 1, 2..., n \end{aligned}$$

where Z_{obj} is the value of objective calculated from FBA and n is the number of fluxes. The upper range of fluxes is identified by maximizing the objective whereas the lower range is obtained by minimizing the same.

Flux sum analysis: The resultant fluxes from constraints-based flux analysis will just indicate the rates of consumption/generation of the metabolites for each of the respective metabolic reactions but not the overall turnover rates. Therefore, the concept of "flux-sum" was proposed to quantify the metabolite turnover rates (Kim *et al*, 2007)(Chung and Lee, 2009). Since the overall consumption and generation rates are equal under the steady-state assumption, the flux-sum, Φ_i of metabolite i can be formulated as:

$$\text{(P3)} \qquad \Phi_i = 0.5 \sum_j |S_{ij} v_j|$$

Here, it should be noted that each $|S_{ij} v_j|$ term in this summation series gives us the absolute rate of consumption/generation of metabolite i due to reaction j and thus by halving the sum of these terms, the overall turnover rate for metabolite i can be obtained.

Flux coupling analysis: The concept of FVA was further extended as flux coupling analysis (FCA) to analyse the correlation between any two fluxes and the blocked reactions, i.e. reaction which cannot carry any flux, in the metabolic network (Burgard *et al*, 2004).

Phenotypic phase plane analysis: Since FBA is an optimization-based approach, it is possible to analyse the shadow prices, i.e. sensitivities, of the objective with respect to a particular variable. Such an approach was termed as phenotypic phase plane (PhPP) analysis and was demonstrated using *E. coli* metabolic network, analysing the sensitivities of growth under varying carbon and/or oxygen uptake rates as phase planes (Edwards *et al*, 2002).

2.2.4.3 Incorporation of regulatory mechanisms

Regulatory flux balance analysis (rFBA): It is a variant of constraints-based flux analysis where the metabolic regulation of reactions are used as additional constraints based on Boolean logics (Covert *et al*, 2001). In rFBA, before simulating a particular state, the regulatory rules are applied to determine the presence or absence of individual reaction in the network.

Probabilistic regulation of metabolism: Since rFBA is formulated in a binary manner, i.e. ON or OFF, an alternative method known as probabilistic regulation of metabolism (PROM) has been suggested which can apply intermediate responses using the conditional probabilities of regulatory - metabolic network model (Chandrasekaran and Price, 2010). In this method, first, a probabilistic model of the transcription-regulatory network is built based on the transcriptomic data and regulatory interactions, and then merges it with the metabolic network to yield a regulatory - metabolic network model.

2.2.4.4 Mutant phenotype analysis

Gene deletion analysis: Interestingly, constraints-based flux analysis can be utilised to identify essential genes and/or reactions by just constraining the flux values of relevant reactions to zero in an iterative manner (Varma and Palsson, 1993)(Förster *et al*, 2003). Such method has been applied to the genome-scale metabolic networks of several organisms to identify essential genes and/or reactions. At times, such method has been used to screen mutants that can overproduce the product of interest.

Minimization of metabolic adjustment: Although constraints-based flux analysis can predict the essentiality of a particular gene/reaction, it may not accurately predict the optimal metabolic state of the corresponding mutant. Therefore, in order to address this limitation, minimization of metabolic adjustment (MOMA) was proposed. It utilises the quadratic programming (QP) to identify the closest point in solution space to that of wild type while considering the deletion constraint simultaneously (Segre *et al*, 2002).

Regulatory on-off minimization: Similar to MOMA, regulatory on-off minimization (ROOM) identifies the metabolic state closest to that of wild type. However, it uses a mixed-integer linear programming (MILP) framework which minimises the number of

significant flux changes with respect to the wild type upon gene deletion (Shlomi *et al*, 2005).

2.2.4.5 Integration of "-omics" data as constraints

Gene inactivity moderated by metabolism and expression (GIMME): In this method, the gene expression data is used to determine the reaction activity during simulation. The reaction activity is determined based on a particular predefined threshold expression value, above which the reaction is considered as present or else absent (Becker and Palsson, 2008).

Integrative metabolic analysis tool (iMAT): This method combines the transcriptomic and proteomic data with metabolic models using a MILP framework where the reaction presence is determined based on basal expression levels comparative to that of a global reference (Shlomi *et al*, 2008).

2.2.4.6 Strain design algorithms

OptKnock: OptKnock is a bi-level MILP optimization problem based on FBA where the inner optimization problem maximises the biomass production, i.e. same as FBA, and outer problem maximises the desired product (Burgard *et al*, 2003). Using such an approach, it reports the best gene knockout candidates which satisfies both the objectives.

OptGene: Although OptKnock is successful in identifying suitable strain designs, it is often computationally intensive to solve due to the bi-level framework. Therefore, to address this limitation, an evolutionary based algorithm is proposed (Patil *et al*, 2005), where initially a set of population with certain genes are scored for fitness based on either FBA or MOMA. Next, based on the fitness score, they are allowed to mate and produce new offspring with mutations introduced in them. This cycle is continued until the identification of certain mutant which overproduces the desired product.

Genetic design through local search: Similar to OptGene, this is also a heuristic based search approach which employs a local search with multiple search paths, and thus obtains efficient solutions with less computational time (Lun *et al*, 2009).

OptStrain: Although gene deletion is the common method used to improve microbial product synthesis, OptStrain suggests intelligent gene additions from other organisms

(Pharkya *et al*, 2004). This method is based on the assumption that addition of new reactions expands solution space, and thus product synthesis ability.

Cofactor modification analysis: Unlike previous methods, which identifies gene knockout or addition candidates, this method identifies best reaction targets whose cofactor specificity engineering would improve microbial product synthesis. Cofactor modification analysis (CMA) is also a bi-level optimization algorithm in which the outer level maximises the product synthesis and inner level maximises biomass while simultaneously considering the cofactor engineering (Lakshmanan *et al*, 2013a). The efficacy of this method has been demonstrated in *E. coli* for producing a wide range of native and non-native products.

2.3 Software applications for constraints-based modelling

As mentioned earlier, CBM has been one of the most widely employed computational techniques for systems-level analysis of living organisms due to its simplicity and extensibility (Raman and Chandra, 2009). However, although the theoretical formulation for CBM is simple and well established, still, it may not be easy for researchers to implement it without the familiarity in computational coding and basic programming skills since a large number of metabolites and reactions should be properly handled to quantify the metabolic fluxes. Particularly, recent genome-scale models for a variety of species involve more than 1,000 reactions and metabolites (Kim *et al*, 2012b). So, it is often cumbersome and error-prone to manually define stoichiometrically balanced model equation and constraints, and manipulate them for subsequent optimization using LP solver. Clearly, this has motivated systems biologists, bioinformaticians and bioengineers to develop specialised CBM software packages. Initially, such applications were designed to perform only FBA on the given network models. They simply re-formulate the network specifications in certain formats (e.g. text files and spreadsheets) into their LP equivalents for subsequent execution of the solvers. However, with the increasing advancements in software technologies and algorithm development, newer tools have improved/added some of the features, e.g., enhanced graphical user-interfaces to view and manipulate network models, implemented algorithms for more advanced analyses such as strain design methods, and recently, adopted platform-independent web-technologies.

Remarkably, since 2000, there has been a steady increase in the number of CBM software, and currently there are already more than 20 applications available (Fig. 2.3). The following subsections will provide a comprehensive review on their strengths and weaknesses to guide the potential users in selecting the suitable tool for their project requirements as well as to developers for improving the CBM tools. Toward this end, all currently available CBM tools under academic free license will be surveyed, and compared using various features such as operating platforms, ease of use, model creation facilities, additionally supported flux analysis techniques, visualization of network models and model exchange capabilities. Based on the comparison, some of the notable limitations in current software are discussed and future perspectives on CBM tool development is also provided.

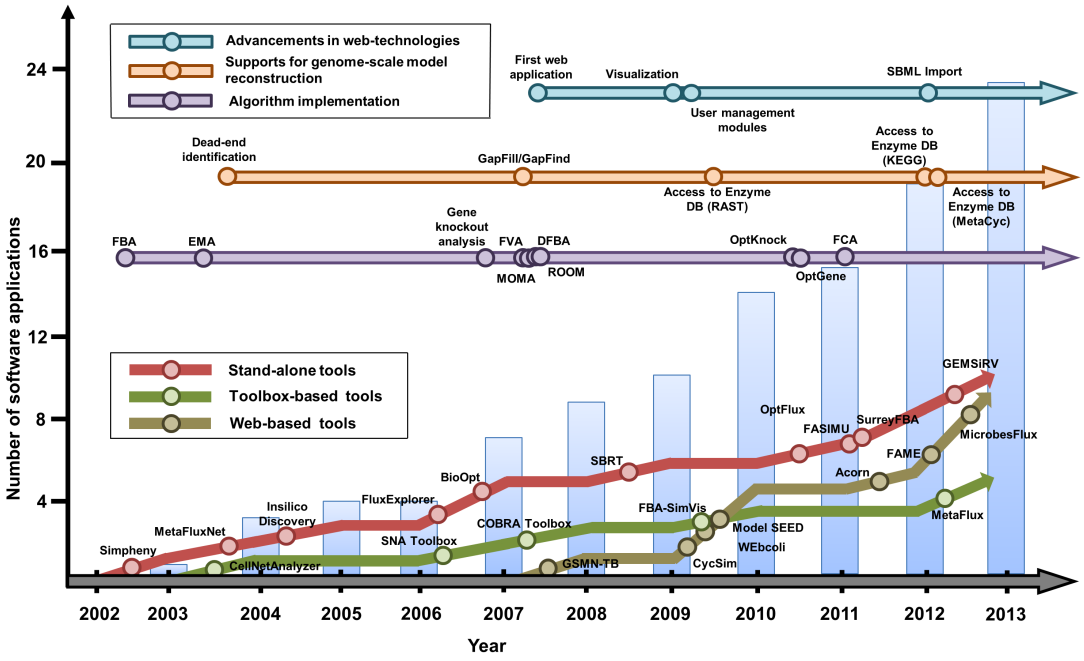


Figure 2.3: Timeline and development of FBA software. Timeline showing the launch of FBA software tools and the milestones of key features implemented in them. Software tools are classified into any one of the three categories: stand-alone, web-based and toolbox-based. Milestones are grouped into three classes: advancements in web-technologies, supports for genome-scale model reconstruction and algorithm implementation. The vertical bars at the background denote the number of available software at the end of each year.

2.3.1 Evaluation of software applications

The surveyed applications herein can be grouped into any one of three classes, i.e. (i) stand-alone, (ii) toolbox-based library, and (iii) web-based, on the basis of their plat-

form and software dependencies (Table 2.1). Stand-alone applications are independently installed onto the users' computers and executed locally. Toolbox-based applications, on the other hand, are not self-contained software, but add-on libraries installed in the general-purpose computation or network visualization tools such as MATLAB[2], Mathematica[3] or VANTED (Junker *et al*, 2006), leveraging upon their existing capabilities, e.g. matrix computations, data manipulation and/or visualization. The third class is web-based applications which are accessible online regardless of the users' platform, only requiring a web-browser with moderately fast internet connection to build models and conduct FBA simulations. Considering the differences among the classes, the CBM software applications was evaluated using a set of test models including a genome-scale metabolic model of *E. coli* (Reed *et al*, 2003) (Appendix A), in terms of five distinct characteristics: platform and software requirements, user friendliness nature, model reconstruction and analysis, visualization and model exchange formats (Fig. 2.4). The resultant comparisons of their unique and common features are summarised in Tables 2.2 to 2.4.

2.3.1.1 Usability

Usability can be defined as a measure of how easy it is to use the FBA software for building and analysing metabolic models. Availability of intuitive user interface (UI), comprehensive user documentation and other user friendly attributes can enhance this characteristic of the software considerably.

User interface: Invariably, users need some forms of interface to interact with the software application. In this aspect, the models can be defined through (i) script/console, (ii) forms or tables, and/or (iii) drag-and-drop operations on a graphical canvas. Script-based applications e.g. BioOpt, SBRT, COBRA toolbox, FASIMU, MetaFlux and GSMN, require users to specify models in flat files that list down all the molecules, reactions and/or their stoichiometric matrices. Ensuring model correctness could be often a tedious task in this approach since it is easy to commit typographical mistakes, especially for large network models. On the other hand, form-based software applications, including MetaFluxNet, OptFlux, SurreyFBA with JyMet GUI, CellNetanalyzer,

[2]MATLAB: (http://www.mathworks.com/products/matlab/)
[3]Mathematica: (http://www.wolfram.com/mathematica/)

Table 2.1: List of software applications evaluated in this study and their general characteristics

Type of the software application	Name	Tested version	URL	References
Stand-alone	OptFlux	2.1	http://www.optflux.org/	(Rocha *et al*, 2010)
	SBRT	2.0.0	http://www.bioc.uzh.ch/wagner/software/SBRT/	(Wright and Wagner, 2008)
	MetaFluxNet	1.8	http://metafluxnet.kaist.ac.kr/	(Lee *et al*, 2003a)(Lee *et al*, 2003b)
	BioOpt	-	http://129.16.106.142/tools.php?c=bioopt	(Cvijovic *et al*, 2010)
	SurreyFBA	-	http://sysbio3.fhms.surrey.ac.uk/	(Gevorgyan *et al*, 2011)
	FASIMU	2.3.1	http://www.bioinformatics.org/fasimu/downloads/	(Hoppe *et al*, 2011)
	GEMSiRV	-	http://sb.nhri.org.tw/GEMSiRV/en/	(Liao *et al*, 2012)
Toolbox-based	CellNetanalyzer/ FluxAnalyzer	9.5	http://www.mpi-magdeburg.mpg.de/projects/cna/cna.html	(Klamt *et al*, 2003)(Klamt *et al*, 2007)
	COBRAToolbox	2.0	http://opencobra.sourceforge.net/	(Becker *et al*, 2007)(Schellenberger *et al*, 2011)
	SNAToolbox	1.0	http://bioinformatics.org/project/?group_id¼546	(Urbanczik, 2006)
	FBA-SimVis	-	http://fbasimvis.ipk-gatersleben.de/	(Grafahrend-Belau *et al*, 2009a)
	MetaFlux	-	http://www.biocyc.org/download.shtml	(Latendresse *et al*, 2012)
Web-based	CycSim	1.0.0	http://www.biocyc.org/download.shtml	(Le Fèvre *et al*, 2009)
	WEbcoli	1.5	http://webcoli.org/	(Jung *et al*, 2009)
	GSMN-TB	-	http://sysbio3.fhms.surrey.ac.uk/cgi-bin/fba/fbapy	(Beste *et al*, 2007)
	Acorn	-	http://sysbio3.fhms.surrey.ac.uk:8080/acorn/homepage.jsf	(Sroka *et al*, 2011)
	Model SEED	-	http://seed-viewer.theseed.org/seedviewer.cgi?page=ModelView	(Henry *et al*, 2010)
	FAME	-	http://f-a-m-e.org/	(Boele *et al*, 2012)
	MicrobesFlux	-	http://tanglab.engineering.wustl.edu/static/MicrobesFlux.html	(Feng *et al*, 2012)

Table 2.2: Dependency and usability features of FBA applications

Software applications	Required software environment			Type of UI provided	User documentation rating
	Platforms supported	Additional software requirements	Optimization solver used		
OptFlux	Windows and Linux	Java JRE 1.6.x	GLPK	Wizard/Script	E
SBRT	Windows, Linux and Mac OS X	≥Java JRE 1.5.x	GLPK	Script	P
MetaFluxNet	Windows	≥.NET framework 1.1, Java JRE 1.4.2	Qsopt, LP_SOLVE	Wizard	E
BioOpt	Windows	NA	GLPK	Script	G
SurreyFBA	Windows, Linux and Mac OS X	Java JRE 1.6.x (4)	GLPK	Wizard[a]/Script	P
FASIMU[b]	Linux and Mac OS X	Optimization solver	GLPK, CPLEX, LINDO, LP_SOLVE	Script	F
GEMSiRV	Windows, Linux and Mac OS X	≥Java JRE 1.7.x	GLPK	Wizard	E
CellNetAnalyzer/ FluxAnalyzer[b]	Windows, Linux and Mac OS X	≥MATLAB 7.1, Optimization solver, SBMLToolbox 3.0.0	GLPK, OptimizationToolbox[c]	Wizard/Script	G
COBRAToolbox[b]	Windows and Mac OS X	≥MATLAB 6.5, Optimization solver, ≥libSBML 4.0, ≥SBML Toolbox 3.0.0	GLPK, TOMLAB_CPLEX[d], LINDO, Gurobi[d]	Script	F
SNAToolbox	Linux	≥Mathematica 5	-	Script	P
FBA-SimVis	Windows	≥VANTED1.8, Java JRE 1.6.x	GLPK	Pictorial	E
MetaFlux	Linux and Mac OS X	PathwayTools	SCIP	Wizard/Script	F
CycSim	-	Web Browser: ≥Firefox 2.0[e]		Wizard	F
WEbcoli	-	Web Browser: ≥IE 6.0[e] or ≥Firefox 2.0[e]	ILOG_CPLEX	Wizard/ Script	E
GSMN-TB	-	Web Browser	GLPK	Script	P
Acorn	-	Web Browser: ≥Firefox 2.0[e]	ILOG_CPLEX	Wizard	G
Model SEED	-	Web Browser, Java JRE 1.6.x	GLPK	Wizard	G
FAME	-	Web Browser: Google Chrome[e], Firefox[e]	GLPK/ILOG_CPLEX	Wizard	E
MicrobesFlux	-	Web Browser	IPOPT	Wizard	G

[a]Form-based interface is available through a separate program called 'JyMet', a GUI designed to access all routines of SurreyFBA; [b]Requires separate LP solver installation and configuration; [c]Optimization toolbox of MATLAB can be used for some functionality instead of GLPK; however developers recommend use of GLPK; [d]COBRA toolbox recommends TOMLAB CPLEX and Gurobi as fast and accurate solvers; [e]Recommended Web Browsers for accessing the application; User documentation rating: E-Excellent, G-Good, F-Fair and P-Poor.

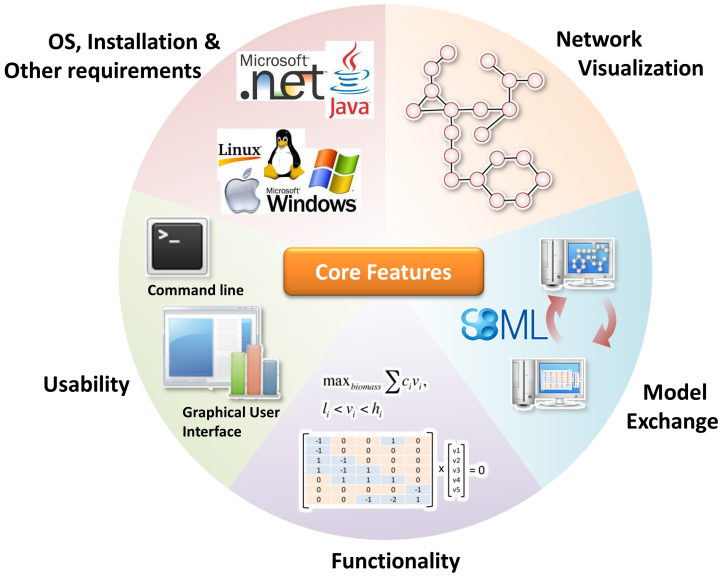


Figure 2.4: Core features of FBA software. The five core features of any FBA software include the following: (i) OS, installation and other requirements, (ii) usability, (iii) functionality, (iv) model exchange and (v) network visualization.

WEbcoli and CycSim, alleviate this issue by providing more error detection features as the user can input the various elements of the model using interactive screens which contain specified forms or tables. The last type of interface, i.e. the diagrammatic UI is more sophisticated, allowing users to create network models by visually dragging and dropping nodes (metabolites or compounds) and edges (reactions or interactions) onto a canvas. This is, indeed, an intuitive approach for model creation: users can quickly glance at the network topology and infer the correctness of the model. However, one severe problem with the interface is the proper layout of large-size network diagrams as it becomes very random and cluttered. In addition, the visualization of metabolic networks with hundreds to thousands of nodes remains a big challenge. Currently, among all surveyed applications, FBA-SimVis is the distinct tool to provide the drag-and-drop UI. Apart from model specification, UI is also critical in FBA simulations and the subsequent analysis of results. In this regard, script-based applications execute FBA upon a command line call and generates some specific file formats (e.g. text files and spreadsheets) containing the quantified metabolic flux values while form-based applications provide specific buttons/tabs within the software environment for FBA execution and employ grids to display the results. Detailed evaluation on the user-friendliness nature of UIs is provided in Appendix B.

User documentation and miscellaneous features: User manuals and documentations are available in the form of online help or separate documents detailing the implementation and execution methods of the FBA software. The availability of tutorials and case studies with relevant screenshots can also help the user acclimatise to the software much faster. The quality of user documentations provided in all applications was evaluated according to three core criteria: completeness, understandability and availability of case studies/tutorials (Table 2.2). The user manuals in most of the applications contain comprehensive information about 5 major components: (i) installation and software requirements, (ii) steps to create or edit models, (iii) FBA simulation procedures, (iv) network visualization methods and (v) export/import of model and analysis results. Interestingly, along with the typical user manuals, Acorn, FBA-SimVis, MicrobesFlux and WEbcoli also include the multi-media as a part of their documentation by providing video demos for tutorials. Obviously, the presence of such materials could reduce the user's learning curve through more interactive communication than normal text documents. However, despite these intuitive contents, none of the tools provides additional information such as troubleshooting steps for commonly encountered errors or exceptions. Furthermore, the help documents in SBRT, SurreyFBA and CycSim are relatively poor with little/no screenshots and illustrations; the documentation of SNA Toolbox contains many technical terms related to Mathematica without proper explanation. Therefore, it is believed that most tools require substantial improvement in the user documentation. More detailed evaluation result can be found in Appendix B. In addition to UI and help documents, availability of certain miscellaneous features can also enhance the usability of software applications. For example, the tooltips/succinct descriptions on the buttons/tabs inside a software environment are currently available in Acorn, GEMSiRV, MetaFluxNet and OptFlux. Similarly, Acorn, GEMSiRV, MetaFluxNet, OptFlux and SurreyFBA support the option to store, navigate, sort and/or filter the model information and analysis results.

2.3.1.2 Functionality

Functionality of a CBM software application can be defined as its capability to support various functional *in silico* analyses for cellular phenotype prediction and strain design under perturbed environmental and/or genetic conditions. The advanced features for

model reconstruction and evaluation was also considered as one of the relevant attributes in this facet.

Analytical algorithms for phenotype prediction and strain design: As seen in previous section, several CBM-based analytical algorithms have been developed to incorporate additional constraints, analyse the network flexibility, predict the cellular phenotype under perturbed conditions, and to postulate strain design strategies (Kim *et al*, 2012b; Lewis *et al*, 2012). The capabilities of the applications supporting such algorithms was evaluated by performing various *in silico* analyses using *E. coli* genome-scale model (Reed *et al*, 2003) as summarised in table 2.3. Details on evaluation methods and results can be found in Appendix C. Currently, only COBRA toolbox, FASIMU and OptFlux offer various functional analysis for predicting the phenotype of genetically perturbed strains using MOMA and ROOM. COBRA toolbox and OptFlux also provide some strain design algorithms, such as OptKnock and OptGene. Interestingly, COBRA toolbox and FASIMU can incorporate the available "-omics" datasets such as gene expression data for analysing environment- and tissue-specific metabolisms using GIMME and iMAT algorithms, respectively.

Supports for genome-scale model reconstruction and evaluation: As mentioned earlier, metabolic reconstruction is a prerequisite for CBM. It is initiated by collecting metabolic reactions of any specific organism from various biochemical databases such as KEGG[4], MetaCyc[5], and BRENDA[6] based on their genome annotation (Thiele and Palsson, 2010). It is followed by assembling of the reactions, resulting in the draft network model which can be further improved by manual curation via dead-end identification, reaction balance checking and gap filling. Currently, some of the applications have such facilities in automating the data collection from different databases (Table 2.3). FBA-SimVis, FAME and MicrobesFlux can import organism-specific pathway information from KEGG while MetaFlux and Model SEED can obtain relevant reaction data from MetaCyc and RAST server (Aziz *et al*, 2008), respectively. As an alternative, genome-scale models can even be drafted from the existing models, based on sequence homology between the genes of target and query organisms. Currently, GEMSiRV supports this approach to reconstruct metabolic models, connecting to the model repository from BiGG

[4]KEGG: (http://www.genome.jp/kegg/)
[5]MetaCyc: (http://www.metacyc.org/)
[6]BRENDA: (http://www.brenda-enzymes.info/)

Table 2.3: Functionalities supported by FBA applications

	Model reconstruction support		FBA and other phenotype prediction analyses								Strain design algorithms			EFM
				Knockout analysis			'omics' data inclusion		FCA	FVA				
	Pathway import	Gap-filling	FBA	FBA	MOMA	ROOM	GIMME	iMAT			OptKnock	OptGene	GDLS	
OptFlux			✓	✓	✓	✓				✓	✓	✓		✓
SBRT			✓	✓						✓				✓
MetaFluxNet		✓	✓	✓										
BioOpt			✓	✓[a]						✓				
SurreyFBA			✓	✓[a,b]						✓				✓
FASIMU		✓	✓	✓	✓	✓	✓	✓	✓	✓				
GEMSiRV	✓[c,d,e]	✓	✓	✓[f]						✓				
CellNetAnalyzer			✓	✓						✓				
COBRA toolbox		✓	✓	✓[a,g]	✓		✓	✓		✓	✓	✓	✓	
SNA toolbox				✓										✓
FBA-SimVis	✓[c,h]			✓	✓					✓				
MetaFlux	✓[d]	✓	✓	✓[a,f]										
CycSim			✓	✓										✓
WEbcoli			✓	✓										
GSMN-TB			✓	✓[g]						✓				
Model SEED	✓[i,j]	✓	✓											
Acorn			✓	✓[g]						✓				
FAME	✓[d]		✓	✓						✓				
MicrobesFlux	✓[d]		✓											

[a]Can perform in automated format, i.e. run simulations by knocking out each reaction/gene at a single instance in continuous format. [b]Both gene essentiality and reaction essentiality is available separately. [c]Connects with KEGG. [d]Connects with MetaCyc. [e]Contains even a reference DB of certain existing genome-scale models to support AUTOGRAPH method. [f]Can compare the predictions with available experimental datasets in PGDBs. [g]Based on the gene-reaction association; therefore, requires a mention of gene-reaction association. [h]When tested for the import of reactions from KEGG, failed due to the new licensing policy of KEGG, i.e. no free data download through FTP. [i]Automatically curates for network gaps and other inconsistencies. [j]Connects with RAST.

(Schellenberger *et al*, 2010). Apart from the support to automate the reconstruction of draft genome-scale models, software applications may also assist users in evaluating the networks connectivity and their gaps (Table 2.3). Currently, MetaFluxNet, MetaFlux, COBRA toolbox, GEMSiRV and FASIMU helps the user identify the dead-end/blocked metabolites in the model. Similarly, COBRA toolbox and FASIMU also allows the user to check the ability of any particular metabolite for its synthesis or degradation. Interestingly, MetaFlux, Model SEED and COBRA toolbox implement the MILP-based analytical algorithms - GapFind and/or GapFill (Kumar *et al*, 2007) for gap filling process.

2.3.1.3 Network visualization

Metabolic networks can be intuitively viewed as graphs where the metabolites and their interactions are represented by nodes and edges linking them, respectively. Most of applications provide basic static images to visualise the networks. However, laying out large-scale networks, e.g., genome-scale models, and magnifying any particular pathway are often cumbersome in such static maps because of their intractable nature. Therefore, dynamic network visualization features, supported by FBA-SimVis, remedy this issue by offering sophisticated graphical interfaces where users can re-align the nodes and edges, adjust their sizes, and interestingly allow users to visualise sub-networks of certain pathways from a large model for a biologically intuitive network analysis. In addition to the basic network visualization feature, some of the tools also offer advanced facilities such as incorporation of resultant flux values onto the network map either by simply overlaying the values itself or by providing additional visual cues via variations in the thickness of edges based on flux values (Table 2.4). Interestingly, some tools accommodate this function by exploiting specific plug-ins under network visualization environments such as Cytoscape (Shannon *et al*, 2003) and BiNA (Küntzer *et al*, 2006). For example, FASIMU can export compatible model formats to Cytoscape and BiNA, which can further link the resulting fluxes using its corresponding plug-ins FluxViz (Holzhutter, 2010) and faBiNA (Küntzer *et al*, 2006), respectively. Similarly, Model SEED generates models which can be visualised under Cytoscape environment, followed by flux mapping using its plug-in, CytoSEED (DeJongh *et al*, 2012). Remarkably, among all applications, FBA-SimVis is a unique tool in flux visualization as it enables the user to even perform flux perturba-

tion analysis through the network diagram. Thus, the network map of the perturbed state can be instantaneously visualised while manipulating the flux of a certain reaction. It should be highlighted that except a few features such as automatic re-alignment of networks based on layout algorithms and filtering option based on sub-networks available in FBA-SimVis, none of the tools can handle large-scale models. In this regard, availability of options to visualise interactive multiple sub-networks of a large-size model with appropriate links among them will improve the intuitive understanding of overall functional interactions along with their organization. Detailed information on network visualization evaluation procedure and results could be found in Appendix D.

2.3.1.4 Model exchange

The model exchange via standardised formats across different FBA applications allows us to fully utilise all the unique features supported in each application. Systems biology markup language (SBML) (Hucka *et al*, 2003)(Hucka *et al*, 2004) is one of the most widely accepted standards for model representation. Other formats include the metabolic flux analysis markup language (MFAML) (Yun *et al*, 2005) and cell markup language (CellML) (Lloyd *et al*, 2004). The model exchange feature in various formats is summarised in table 2.4 and figure 2.5.

SBML compatibility: Most of the stand-alone and toolbox-based applications support the import and/or export of SBML files although BioOpt, FASIMU and SBRT require additional step by the translator to convert them into compatible formats (Fig. 2.5). However, none of the web-based applications, except FAME, have SBML import function as they can conduct in silico analysis only on the existing pre-defined models. The SBML compatibility was tested for all the applications using test models (Appendix A) by validating generated SBML files through the online SBML validator[7] and the ability of all software applications to recognise the SBML exported by other software, i.e. the readiness of the application to perform FBA upon import of SBML. Here, it should be noted that some of the compatibility issues should be properly addressed for ensuring model consistency. The results revealed that SBML generated by COBRA toolbox and OptFlux are readily inter-transferable between them. However, certain FBA specific information such as reaction bounds and objective function are missing in the SBML

[7]SBML validator: (http://sbml.org/validator/)

Table 2.4: Network visualization and model-exchange supports of FBA applications

Software applications	Network visualization		Model-exchange			
			SBML		Others	
	Visulaization type	Flux visualization	Import	Export	Import	Export
OptFlux	S[a]	✓	✓	✓	Text files, MetaTool	Text files
SBRT	-		✓		Text files	
MetaFluxNet	S	✓	✓	✓	MFAML	MFAML, GAMS, LINDO, LP_SOLVE, CPLEX
BioOpt	-		✓[b]		Text files	
SurreyFBA	S[c]	✓	✓		Text files	
FASIMU	-	✓[N]	✓	✓	Text files, FA format[d]	MetaTool, Expa
GEMSiRV	S[a]	✓	✓	✓	Microsoft Excel	Microsoft Excel
CellNetAnalyzer	S[a]	✓	✓	✓	Text files, MetaTool	Text files, MetaTool
COBRA toolbox	S[a]	✓	✓	✓	Microsoft Excel, SimPheny, Text files	Text files, Microsoft Excel
SNA toolbox	-	-			Text files	Text files
FBA-SimVis	D	✓	✓	✓	GML, KGML, GraphML, XGMML	Text files
MetaFlux	S	✓		✓	Text files	Text files
CycSim	S	✓		✓		Text files
WEbcoli	D	✓		✓		Text files
GSMN-TB	-	-		✓		Text files
Model SEED	-	✓[N]		✓		Microsoft Excel, LP format
Acorn	D[e]	✓	✓			Text files
FAME	S	✓	✓	✓		
MicrobesFlux	-	-		✓		

[a]Requires a user supplied 'map' file to execute generate network topology; GEMSiRV can use even KGML/CellDesigner formats whereas OptFlux can use CellDesigner format. [b]Through another program/separate utility (available online at http://129.16.106.142/toolbox.php). [c]Available only while accessing through its GUI: 'JyMet'. [d]FluxAnalyzer format: a format that can be exported from CellNetAnalyzer. [e]Implemented through separate program which runs on desktop PC locally. S, static image; D, dynamic interface; [N]through specialised network visualization software such as Cytoscape.

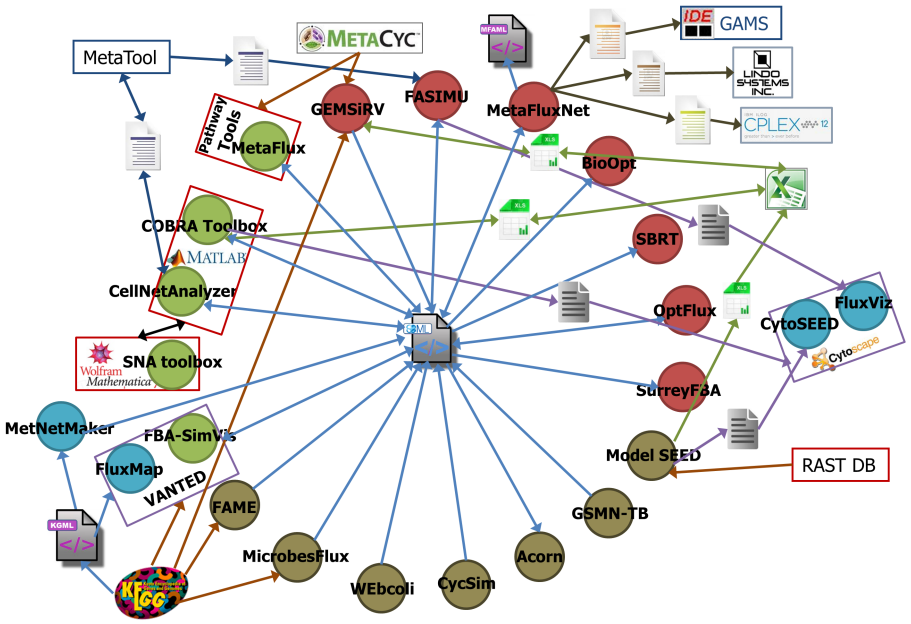


Figure 2.5: Model exchange capabilities of FBA applications. Brown-, green- and tan-coloured nodes represent the stand-alone, web-based and toolbox-based applications. Nodes with aquatic blue colour represent the software which cannot implement FBA but can help converting model format from one to another. The nodes inside rectangular represents the toolbox-based (red-coloured rectangles) or plug-in based (purple-coloured rectangles) software where the boxes denote base software and nodes inside them represent the additional libraries.

created by all other applications. Detailed discussion on the SBML issues can be found in Appendix E.

Compatibility in other formats: For the exchange of FBA models among different applications, other than SBML, a similar XML-based standard, MFAML, was specifically designed with relevant XML tags for reaction bounds and objective functions (Yun *et al*, 2005). Unfortunately, it is not widely adopted and currently, MetaFluxNet is the only tool that supports this format. The ability of software applications to create programming scripts/computer codes that represent the models in other general computational or optimization software was also analysed (Table 4). In this aspect, MetaFluxNet is the most versatile software as it can generate various scripts which are compatible with MATLAB, GAMS[8], LP SOLVE[9], IBM ILOG CPLEX[10] and LINDO[11] for the given FBA problem. Availability of such options certainly provides more flex-

[8]GAMS: (http://www.gams.com/)
[9]LP SOLVE: (http://lpsolve.sourceforge.net/)
[10]IBM ILOG CPLEX: (http://www.ibm.com/software/integration/optimization/cplex-optimizer/)
[11]LINDO: (http://www.lindo.com)

ibility in implementing complex algorithms which are currently not supported by any of the software applications surveyed. Similarly, OptFlux and FASIMU can generate MetaTool format (Pfeiffer *et al*, 1999), thus enabling EFM analysis.

2.3.2 Improvement suggestions and future perspectives

2.3.2.1 Genome-scale model reconstruction

As one of important features, the current applications can provide functional environment to accelerate the reconstruction of genome-scale metabolic models which is otherwise too laborious, requiring substantial time and manual efforts (Thiele and Palsson, 2010). Thus, it is highly required to implement specific functions for (semi-)automatically gathering information from various online enzyme databases and subsequently refining them with the help of network evaluation algorithms such as GapFill/GapFind, GrowMatch (Kumar and Maranas, 2009), and GeneForce (Barua *et al*, 2010). In this regard, as highlighted before, most recent applications, FAME, GEMSiRV, MetaFlux, MicrobesFlux and Model SEED, have already incorporated certain features in facilitating the reconstruction process by importing reaction data from KEGG, MetaCyc or RAST and improving the network connectivity using GapFill/GapFind. Nonethless, in order to improve the quality of such draft models, additional model curation steps such as elemental and charge balance check in reactions, verification of reaction directionality from more specific enzymatic databases, e.g., BRENDA and UniProt, assignment of reactions to appropriate cellular compartments based on the protein subcellular localization prediction software, e.g., PSORT (Nakai and Kanehisa, 1991) and MultiLoc (Höglund *et al*, 2006), and inclusion of transport reactions from TCDB database (Saier *et al*, 2006), are required. Moreover, software applications can also consider linking them with biological model storage database such as BiGG, Model SEED (Henry *et al*, 2010), BioMet toolbox (Cvijovic *et al*, 2010), and BioModels (Le Novere *et al*, 2006) since this support will not only allow users to directly perform simulations on existing models but can also help them reconstruct new genome-scale models using the AUTOGRAPH method (Notebaart *et al*, 2006). It should be noticed that the data from multiple-sources may often conflict with each other or even miss several information from one another. These issues can be appropriately resolved by implementing methods for data

integration and standardization. In such an attempt, a new knowledgebase, MetRxn, has been recently developed, integrating the data from 4 biochemical databases and 44 genome-scale metabolic models available from literature (Kumar *et al*, 2012). Therefore, utilization of this knowledgebase for integrating the data collected from different data sources would be an interesting option for model reconstruction.

2.3.2.2 FBA-based functional algorithms

Another critical functionality feature along with model reconstruction is to support various analytical algorithms for phenotype prediction and strain design. Although COBRA toolbox, FASIMU and OptFlux have already incorporated basic algorithms for mutant phenotype analysis such as MOMA and ROOM, a multitude of other FBA-based *in silico* techniques can be considered to enhance the functionality and broaden the analytical capability. For example, incorporation of regulatory constraints into the FBA framework via Boolean logic representation, e.g. rFBA, or by integrating the transcriptomic and/or proteomic datasets using various algorithms such as GIMME, E-Flux (Colijn *et al*, 2009), INIT (Agren *et al*, 2012), MBA (Jerby *et al*, 2010) and MADE (Jensen and Papin, 2011), offers a wide variety of applications. They include environment-specific phenotype prediction (Becker and Palsson, 2008; Covert *et al*, 2008; Jensen and Papin, 2011), development of tissue-specific sub-network models in higher organisms (Agren *et al*, 2012; Jerby *et al*, 2010; Mintz-Oron *et al*, 2012), identification of drug-targets (Colijn *et al*, 2009)(Folger *et al*, 2011) and the analysis of host-pathogen interactions (Bordbar *et al*, 2010). In terms of strain design, OptKnock, OptGene, GDLS, OptReg (Pharkya and Maranas, 2006), OptORF (Kim *et al*, 2011), RobustKnock (Tepper and Shlomi, 2010) and OptForce (Ranganathan *et al*, 2010) could help to devise novel strain engineering strategies by identifying the gene/reaction targets to be manipulated for the improved productivity. It should be highlighted that such advanced algorithms are mostly formulated as MILP problem (Park *et al*, 2009), whereby the combinatorial explosion as a result of the huge metabolic network models may lead to inefficient solving of the optimization problem based on default solver settings (Atamtürk and Savelsbergh, 2005). In this regard, it is desirable to have flexible options in selecting the solver algorithms and specifying the corresponding parameters.

2.3.2.3 Flexible and extensible software design

As stated earlier, it is highly necessary to standardise model exchange format across different applications in order to utilise various interesting features which are unique in each tool. However, the widely accepted SBML standard currently may not capture some of the key information for FBA, thus initiating community discussion and proposal to include additional attributes for better representing FBA models[12]. Alternatively, such interesting functions can be additionally implemented to a flexible and extensible software environment via plug-ins/add-ons as it is successfully adopted by Cytoscape, VANTED and CellDesigner (Funahashi *et al*, 2003). Interestingly, Microsoft Excel[13], the commonly used spreadsheet package for storing metabolic models, has all the necessary components to create and analyse FBA models including well-designed form-based interface, plotting and drawing facilities, in-built optimization solvers and scripting language for automating tasks (i.e. MACROS). It should be noticed that Excel-based FBA application may face technical challenges in handling large-size models due to the limitation in its in-built optimization solver. However, this issue can be appropriately resolved by using relevant software technologies such as OpenSolver[14], an open-source optimization solver for Excel that runs on advanced COIN-OR CBC optimization engine[15], and SolverStudio[16], a software framework that can integrate Excel with other open sources as well as commercial solvers, e.g., GLPK[17], COIN CLP [18], CPLEX, and GUROBI[19].

2.3.2.4 Web-based applications: Future outlook

Figure 2.3 clearly indicates the increasing popularity of web-based FBA applications. Such an augmented interest towards web applications is mainly attributable to their multiple advantages over the stand-alone or toolbox-based applications: it provides not only distributed computing for implementing complex analytical frameworks but a medium for collaborative research where the combined efforts of scientific community could be facilitated. Importantly, rich user interfaces and enhanced interoperability can be man-

[12]Proposal: (http://sbml.org/Community/Wiki/SBML_Level_3_Proposals/Flux_Constraints_Proposal)
[13]Microsoft Excel: (http://office.microsoft.com/en-us/excel/)
[14]OpenSolver (http://opensolver.org)
[15] COIN-OR: (https://projects.coin-or.org/Cbc)
[16]SolverStudio: (http://solverstudio.org)
[17]GLPK: (http://www.gnu.org/software/glpk/)
[18]COIN CLP: (http://www.coin-or.org/Clp/)
[19]GUROBI: (http://www.gurobi.com/)

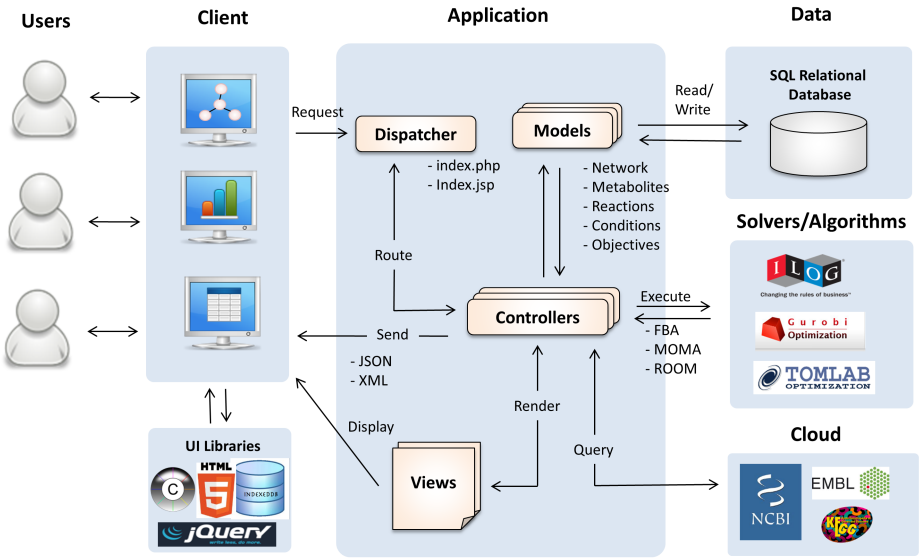


Figure 2.6: Typical architecture of web application. A typical three-tier architecture of web applications that incorporates the Model-View-Controller pattern for application design.

ifested by resorting to recent web-technologies, e.g., Ajax, service-oriented architecture and Semantic Web, adopting three-tier Model-View-Controller architecture as depicted in figure 2.6. Additionally, the use of Javascript libraries such as Cytoscape web and ExtJS can also improve interactivity, mimicking a desktop application within a web browser. For example, Discovery Studio provides a thin-client local front-end for users to interact with their models while performing expensive operations at the backend server. However, despite the recent technology improvements, web applications still suffer a major disadvantage in the form of the necessity of being online always. Therefore, future web applications should possibly allow us to perform at least few functions such as model construction offline. Implementation of this facility is very much plausible with the help of offline application cache (appcache) or cache manifest from the emerging HTML5 framework and Indexed database; the information can be temporarily cached in the client browser through their cookies while updating the transaction information from client-to-server and vice versa upon availability of the network connection. Finally, web-based FBA tools could even consider developing specialised applications (Apps) for smartphones so that the users could conduct FBA via portable devices.

Chapter 3

Reconstruction of rice central metabolic/regulatory model[1]

3.1 Introduction

Rice is truly a global food crop, and is considered as a major staple food in many Asian countries: each person consumes more than 100 kg of rice per year, on average (Nelson, 2011). Since the Green Revolution in 1960, there has been a progressive increase in the yield of rice. However, the growing population and adverse climatic changes pose huge challenges to sustaining the growing demand for rice. Moreover, several abiotic stresses also influence the annual yield significantly (Van Nguyen and Ferrero, 2006).

Over the last few decades, several efforts have been made to understand the cellular metabolism of rice by conventional experimental approaches. However, its metabolic adaptations under different stress conditions remain poorly characterised. Thus, with recent advancements in the modern genomic era, a systematic approach is required to improve our understanding of the metabolic changes of rice. In the postgenomic era, it can be achieved by utilizing the abundant highthroughput "omics" data sets in combination with *in silico* metabolic modelling. To this end, the development of a predictive in silico model based on the available biochemical, genomic, and regulatory information, and its subsequent examination by the well-established computational framework of constraints-based flux analysis, is highly desired.

Interestingly, flux-based metabolic modelling of plant systems has recently gained

[1]Excerpts of this chapter, in part, is a reprint of previous publication, Lakshmanan et al. (2013) Elucidating rice cell metabolism under flooding and drought stresses using flux-based modelling and analysis, Plant Physiology, 162:2140–2150, PMID: 23753178.

more attention following its tremendous success in elucidating the metabolic capabilities of myriad microbial and mammalian species and rationally engineering them to achieve desirable phenotypes. In this regard, metabolic network models for several plants, such as Arabidopsis (Poolman *et al*, 2009; de Oliveira Dal'Molin *et al*, 2010a; Saha *et al*, 2011; Chung *et al*, 2013; Mintz-Oron *et al*, 2012), barley (Grafahrend-Belau *et al*, 2009b), rapeseed (Hay and Schwender, 2011; Pilalis *et al*, 2011), maize (Saha *et al*, 2011), and a general C4 plant model (de Oliveira Dal'Molin *et al*, 2010b) have already been developed, and some of them are even in genome scale. Nevertheless, the metabolic model of rice is not available to date. Therefore, in this chapter, a combined metabolic/regulatory network model representing the central metabolism of rice cells is reconstructed. Subsequently, its *in silico* predictions are validated using rice suspension culture cells.

3.2 Materials and methods

3.2.1 Cell line and media conditions

Rice suspension cells were obtained from calli induced by rice seed (*Oryza sativa* L.) on amino acid callus induction (AACI) medium containing 2,4-dichlorophenoxyacetic acid (2 mg/L), sucrose (30 g/L) and Gelrite (2 g/L) for 2 months. The calli were then sieved for the establishment of suspension cells using a stainless screen mesh with a pore size of 1 mm. The suspension cells were cultured in 500-mL Erlenmeyer flasks. An Erlenmeyer flask containing 126 mL of AA medium consisted of 30 g/L of sucrose, 2 mg/L of 2,4-dichlorophenoxyacetic acid, 0.02 mg/L of kinetin. After sterilization, 14 mL of a 10-fold concentrated amino acid mixture was sterilised using 0.22-μm syringe filters with 0.1 mg/L of gibberellic acid. Subculture was performed every 9 days. Both aerobic and anaerobic cell cultures were performed at 120 rpm and 28 ^{0}C in a gyratory shaking incubator. For the cultivation under anaerobic conditions, a disposable bag chamber was designed. To apply anaerobic conditions, nitrogen gas was supplied through an air-filter (Sartorius AG, Germany) and dissolved oxygen levels were monitored using a DO electrode (Mettler-Toledo Process Analytical Inc., USA). In both conditions, 1 g of fresh cells was inoculated in 100-mL Erlenmeyer flasks with 30 mL of AA medium containing either 87.6 mmol sucrose or 175.3 mmol glucose as carbon source. Here, it

should be noted that these experiments was conducted by Dr. Jun-Young Kwon and his research team at the Cell Culture Engineering Laboratory, Inha University, Republic of Korea.

3.2.2 Analytical techniques

After sampling every 4 days, the suspension cells in cultured broth were filtered using Whatman No. 1 filter paper. The rice cells were washed three times using distilled water to remove remaining sugar on the cell surface, and the cells were then measured to determine fresh cell weight on a pre-weighed dish. To confirm dry cell weight (DCW), fresh cells were dried at 60 ^{0}C for 2 days and then weighed. Extracellular sucrose, glucose and fructose concentrations were measured using an HPLC (Young Lin Instrument, Republic of Korea) with Zorbax Carbohydrate Analysis column (Agilent Technologies, USA). The mobile phase was an acetonitrile/water mixture (75/25) and the column temperature was maintained at 40 ^{0}C. Samples were filtered with 0.45-μm syringe filters (Millipore, USA). The sugars were detected with a refractive index (RI) detector (Waters, USA). Sugar concentration was estimated from a standard curve with known concentrations of glucose, fructose and sucrose, respectively.

3.2.3 Metabolic network reconstruction

The central metabolic network of rice cells (*Oryza sativa*) was reconstructed based on the information collected from various biological and genomic databases such as KEGG (Kanehisa and Goto, 2000), RiceCyc and MetaCyc (Caspi *et al*, 2008). Initially, the biochemical reactions of the primary metabolism, which are necessary to generate the biomass precursors, were identified and included into the preliminary draft model. These reactions were then corrected for any stoichometrical imbalances, mapped with appropriate genes to devise proper gene-reaction relationships, and assigned to respective cellular compartments based on extensive literature studies. Additionally, some spontaneous as well as non-gene-associated reactions including that of metabolite transport were also incorporated into the model based on the physiological relevance from literature and databases. Once the draft model was assembled with all necessary reactions, it was then checked for any connectivity issue, i.e., dead-ends or blocked metabolites, by maximizing the production of individual metabolite precursors upon feeding it with various carbon

sources such as sucrose, glucose and fructose. The identified missing links were then filled either by introducing sink reactions to allow for material exchange between the cell and its surrounding environment or by adding reactions from other similar plants to close in the knowledge gaps.

Following the reconstruction of metabolic network, an extensive literature search was performed for collecting information on the regulatory mechanisms of all the reactions in primary metabolic pathways. Finally, this information was represented as a set of regulatory rules using the Boolean formalism which can guide whether relevant reactions are either active (ON) or not (OFF) (Covert *et al*, 2001). Specifically, the activity/inactivity of a particular reaction in the presence of certain regulatory protein(s) can be described using various logical operators such as IF, AND, OR and NOT. For example, if a reaction, rxn1, is activated by either regulatory protein A or B, then the corresponding rule can be formulated as "IF (A OR B)". Similarly, if a reaction, rxn2, is inactivated in the presence of both proteins C and D, the regulatory rule can be written as "IF NOT (C AND D)".

3.2.4 Constraints-based regulatory flux analysis

In this study, constraints-based flux analysis was utilised to simulate the rice metabolism under varying environmental conditions by manipulating the constraints. The biomass equation was maximised to obtain the optimal solution of the metabolic network as detailed in chapter 2 (Section 2.2.4.1, Problem P1).

In order to simulate the cellular metabolism of the seed-derived rice cells growing on either sucrose or glucose, the regulatory constraints were first applied to the network under steady-state conditions by evaluating whether metabolic enzymes were active or not for the given conditions using the Boolean rules, and by constraining the fluxes of repressed enzymes to zero. If an enzyme is available, then its flux value was allowed to be determined by FBA. In the case of exchange reactions, just the carbon source uptake rates were constrained at the experimentally measured values. Additionally, for the aerobic simulations, the oxygen exchange reaction was constrained at 3.312 mmol g^{-1} DCW day^{-1} based on literature (Wen and Zhong, 1995). For simulating the photorespiring metabolism of rice leaf cells, a similar procedure was followed by first constraining the fluxes of dark reactions to zero using Boolean regulatory rules as mentioned above.

Subsequently, the leaf cell growth was simulated by maximizing the leaf biomass while constraining the photon uptake at 100 mmol g^{-1} DCW day^{-1}. In addition, the ratio of flux through ribulose-1,5-bisphosphate carboxylase/oxygenase (RuBisCO) was set with a value between one and ten for simulating the photorespiratory behaviour at different carboxylation to oxygenation ratios (V_C/V_O) (Weber, 2007). In this study, all simulations were implemented by General Algebraic modelling System (GAMS) Integrated Development Environment (IDE) version 23.9. In order to compute the regulatory rules for each condition, the Microsoft EXCEL spread sheet package was used.

3.3 Results and discussion

3.3.1 Reconstruction of the rice central metabolic model

The central metabolic network of rice cells was reconstructed through a three-step process: (1) compilation of genes, reactions and related information on rice metabolism from enzyme databases and literature, (2) verification of elemental balances in reactions and assignment of compartments, and (3) dead-end identification and network gap-filling (see Materials and methods). Steps 1 and 2 in the reconstruction process gave rise to a draft network model consisting of 298 reactions with several missing links mainly in amino acid biosynthetic pathways. Such gaps could be filled by adding new reactions derived from other plants. For example, a metabolic gap existed in the histidine biosynthetic pathway of the draft model since the gene coding for the enzyme, histidinol-phosphatase (E.C. 3.1.3.15), was not found in the rice genome. Thus, it was manually included based on published references supporting its existence in Arabidopsis and plausibly in rice (Petersen *et al*, 2010). Similarly, 9 more reactions were added in the amino acid biosynthetic pathways and 7 reactions in the folates metabolism to improve the network connectivity (see Appendix F). Furthermore, several inter-compartmental transport reactions (48 between plastid and cytosol, and 27 between mitochondrion and plastid) were also added along with their transport systems such as free diffusion or proton symport.

The resulting metabolic network of rice accounts for 248 enzymes, catalysing 326 reactions in the rice central metabolism, primarily from the pathways: glycolysis and gluconeogenesis, tricarboxylic acid (TCA) cycle, pentose phosphate pathway (PPP),

Calvin cycle, photorespiratory pathway, glyoxylate cycle, oxidative phosphorylation, starch and sucrose metabolism, fermentation, cell wall metabolism, amino acid synthesis and fatty acid synthesis.

It should be noted that 52 direct and indirect regulatory interactions using 12 regulatory proteins for the discrimination between the photosynthetic and non-photosynthetic cells under normal and stressed conditions were also incorporated into the model using Boolean logic formalism, on the basis of established procedures (Covert *et al*, 2001)(see Materials and methods). As a result, the activation of 40 light-specific metabolic reactions in the model can be controlled by a relevant logic statement. Table 3.1 summarises the general features of the reconstructed rice network; Appendix F provides complete details on the model, which is also available as Systems Biology Markup Language (SBML) file (level 2, version 1, http://sbml.org) in Appendix G.

Table 3.1: Properties of the reconstructed rice central metabolic network

Features	Cytosol	Plastid	Mitochondria	Total
Metabolic reactions	139	153	34	326
Transport and exchange reactions	16[a]	48[b]	27[b]	91
Gene-enzyme-reaction associations	130	145	30	305
Reactions with regulatory rules	15	19	6	40
Metabolites	156	162	53	371

[a]exchange reactions; [b]inter-compartmental transport reactions

3.3.2 Biomass composition

Cellular biomass composition is also an important prerequisite for subsequent *in silico* flux analysis since the primary cellular objective is to maximise the cell growth. Thus, two separate biomass equations were developed for describing the cellular growth of two tissue types. The biomass equation for the germinating cells of rice seeds was derived from the macromolecular composition of rice coleoptiles (Edwards *et al*, 2012) while the other biomass equation representing the photo-respiring cells of rice leaves was developed using the rice straw composition (Juliano, 1985). The details of biomass compositions can be found in Appendix F.

3.3.3 Model validation

3.3.3.1 Seed-derived cells

The reconstructed rice metabolic model was first utilised to simulate the phenotypic behaviour of seed-derived cells in response to varying levels of oxygen. To do so, the coleoptile biomass equation was maximised, while simultaneously constraining the uptake rate of sucrose at 1 mmol g^{-1} DCW day^{-1} and varying oxygen uptake rates gradually from 0 to 4 mmol g^{-1} DCW day^{-1} (see Materials and methods). It should be noted that the Boolean gene regulatory rules were utilised to consider active reactions in seed-derived cells (see Appendix H for details). The model simulations show a linear decrease in biomass growth and increase in ethanol fermentation with decreasing levels of oxygen supply, suggesting the predominance of ethanol fermentation in the absence of cellular respiration (Fig. 3.1). It should be highlighted that these observations are in good agreement with the previous reports (Mohanty *et al*, 1993; Gibbs *et al*, 2000; Edwards *et al*, 2012). The model also predicted a sharp decline in the cell growth without any production of ethanol beyond a certain value of oxygen influx (3.35 mmol g^{-1} DCW day^{-1}), demarking the stoichiometric optimal value of oxygen uptake to maximise cell growth for the imposed restriction in sucrose uptake (Fig. 3.1). Any excess oxygen above this value resulted in futile energy cycle involving several redundant pathways to utilise the excess ATP produced, and thus, decreasing the cellular growth.

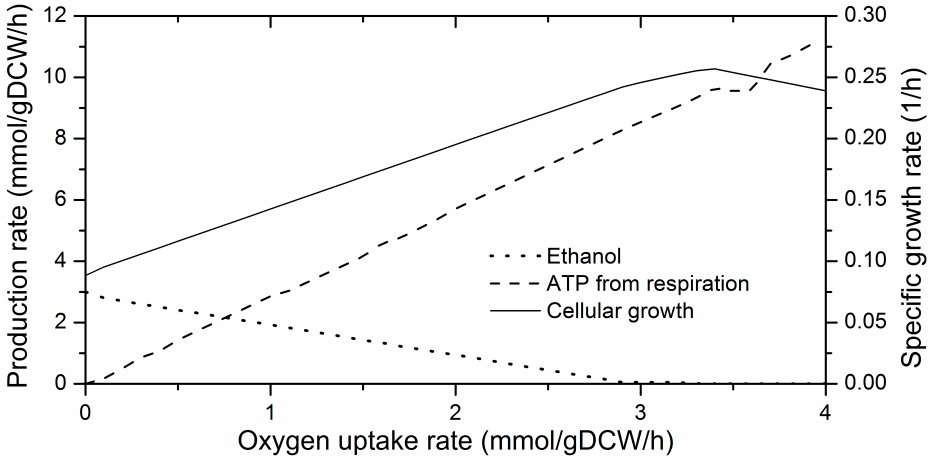


Figure 3.1: The effect of oxygen uptake rate on cellular growth, ATP synthesis from respiration and ethanolic fermentation in germinating rice seed cells

In order to further validate the model quantitatively, batch cultures of rice cells

growing on various carbon sources including sucrose and glucose in the presence and absence of oxygen were conducted. The residual concentrations of supplemented sugars in the medium as well as the dry cell weight (DCW) were monitored (Fig. 3.2). In case of sucrose, a lag phase of 2 days was observed under both aerobic and anaerobic conditions (Fig. 3.2A and 3.2B). Subsequently, the supplemented sucrose was sharply consumed as well as hydrolysed into glucose and fructose in the culture medium under aerobic conditions (Fig. 3.2A).

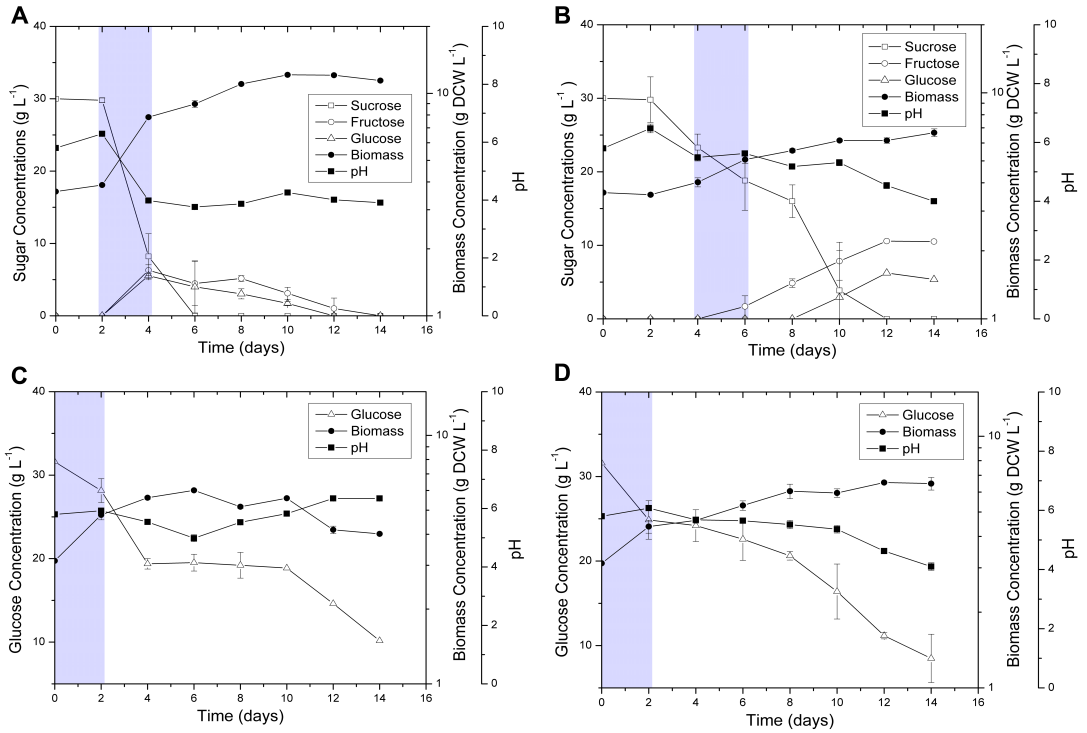


Figure 3.2: Profiles of cell biomass and residual concentration of the carbon nutrient components in the batch cultures of aerobic-sucrose (A), anaerobic-sucrose (B), aerobic-glucose (C) and anaerobic-glucose (D). Highlighted regions correspond to exponential growth phases of the cultures.

This external accumulation of hexose sugars was also accompanied by a sharp decrease in medium pH, dropping from 6.3 to 4.0 at day 4, and was maintained for the remaining 10 days (Fig. 3.2A). Collectively, these results demonstrate the acidification of culture medium, thus promoting the cell growth by increased cell wall-associated invertase activity (Amino and Tazawa, 1988; Shimon-Kerner *et al*, 2000). On the other hand, cells supplemented with sucrose under anoxia showed a delayed increase in pH of the medium (Fig. 3.2B), possibly suggesting that the external invertase activity is

dependent upon the presence of oxygen (Kwon *et al*, 2012). To explain this phenomenon clearly, further studies are required where the correlations among the cell growth, invertase activity and energy consumption must be investigated thoroughly. In case of glucose, rice cells grew without a lag phase under both aerobic and anaerobic conditions albeit a short exponential growth in the former (Fig. 3.2C and 3.2D). The supplemented glucose was steadily consumed in anoxia whereas the concentration did not decline in aerobic conditions from day 4 to day 10 (Fig. 3.2C). Despite these differences in cell growth behaviour, both sucrose and glucose supplemented cells grew faster under aerobic conditions than those in anaerobic conditions (3.20- and 1.33-fold higher, respectively), confirming the earlier simulation results. Nevertheless, in order to examine the quantitative agreement between experimental and simulated growth rates, the coleoptile biomass equation was again maximised while constraining the uptake rate of carbon source, i.e. sucrose or glucose, at experimentally measured values in both aerobic and anaerobic conditions. Here, it should be noted that the carbon source uptake rates from the exponential phase of the cell cultures were used for simulations since it is believed that cells typically evolve towards maximal growth in this phase (Schuster *et al*, 2008). Notably, the simulation results show good agreement between the *in silico* simulated growth rates and experimental observations within the acceptable error range for all four cases (Fig. 3.3).

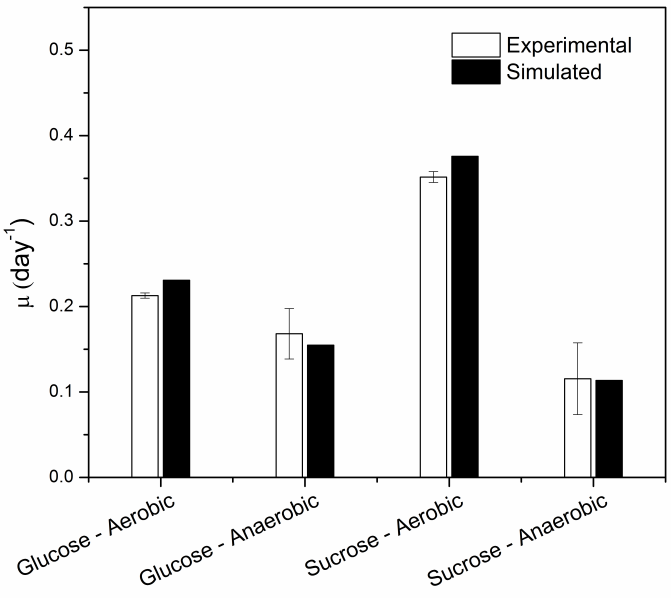


Figure 3.3: Experimental and simulated growth rates during exponential phase on different batch cultures.

3.3.3.2 Leaf cells

Photorespiration in rice leaf cells was simulated by maximizing the straw biomass equation, while constraining the photon uptake rate at 100 mmol g^{-1} DCW day^{-1} and fixing the carboxylation-to-oxygenation flux ratio (V_C/V_O) of ribulose-1,5-bisphosphate carboxylase/oxygenase (RuBisCO) with a value between one and ten. Here, it should be noted that the simulations with V_C/V_O ratios greater than or equal to three represent the photorespiration under normal conditions while any lesser value corresponds to the drought conditions (Jordan and Ogren, 1984).

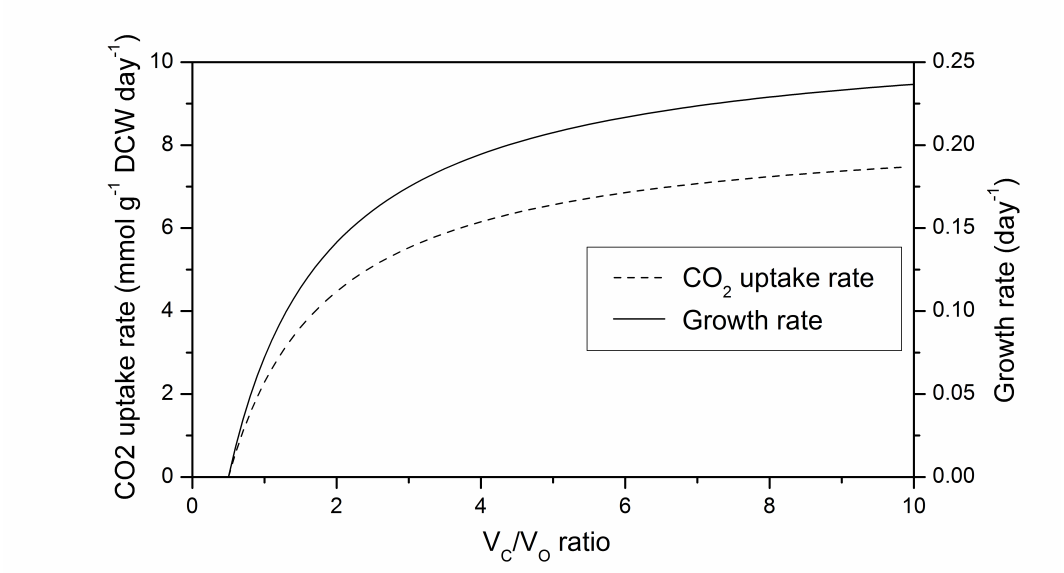


Figure 3.4: The effect of carboxylation-to-oxygenation ratio of RuBisCO on leaf cellular growth and CO_2 uptake while absorbing equal amounts of photon.

Again, the Boolean gene regulatory rules were also utilised to consider active reactions in the leaf cells (see Appendix H for details). Model simulations indicated a significant reduction in the CO_2 uptake rates and leaf growth rates as V_C/V_O decreases, and eventually reached zero at the compensation point (V_C/V_O =0.5) (Fig. 3.4). At severe photorespiration conditions, the carbon fixation rate reduces significantly (decreases by 40% at V_C/V_O =2 when compared to V_C/V_O =10) while absorbing same amounts of photon since most of the energy is wasted in recycling the 2-PG. Overall, these results are highly consistent with the theoretical calculations by Heldt and Piechulla (2011), who suggested that "more than one third of the captured photons will be wasted because of photorespiration".

3.3.4 Comparison of current model with existing plant models and future directions for further improvement

In the current work, the central metabolic/regulatory network of rice cells was developed. Compared to the existing plant models, the current model is unique in incorporating the regulatory information into FBA framework for investigating the effect of external signals on plant metabolic behaviours. This can be well exemplified while simulating the growth of germinating seed cells on starch as carbon source under aerobic and anaerobic conditions. Generally, when plant seeds germinate, they require the reserve carbohydrates such as starch to be metabolised for fuelling the synthetic pathways of biomass precursors. In this regard, rice is a unique plant due to its ability to metabolise starch via alpha-amylase even under anaerobic conditions. It should be highlighted that this model clearly differentiated the induction of alpha-amylase by different regulatory routes, via gibberellic acid (GA) response elements and the calcineurin B-like protein-interacting protein kinases under aerobic and anaerobic conditions, respectively (See Appendix H). Furthermore, the incorporation of regulatory information also allowed us to simulate photosynthetic metabolism by eliminating non-active enzymes under light conditions; the leaf simulations successfully eliminated the PFP and chose FBP for the synthesis of fructose-6-phosphate during photorespiration/photosynthesis as PFP is controlled by allosteric regulator, fructose-2,6-bisphosphate, which is produced only under dark conditions. In addition, the newly reconstructed model is also distinct from other plant models in terms of representing the inter-compartment metabolite transporters: it clearly presents the transport details of almost all the metabolites such as free diffusion, proton symport/antiport and redox shuttles based on extensive literature searches. Thus, translocation of various metabolites across compartments can be properly described along with the relevant redox balance and energy requirements.

Unlike microbes or animals, the secondary metabolism of plants plays significant role in orchestrating the cellular phenotype in response to the abiotic stresses (Ramakrishna and Ravishankar, 2011). For example, ascorbic acid, glutathione and ∝-tocopherol have been recognised for their role as antioxidants against the reactive oxygen species (ROS) which are produced during increased photorespiration (Jogaiah *et al*, 2013). Thus, it is highly required to expand the scope of the current model into the genome-scale model

of rice metabolism in order to better understand its metabolic characteristics. However, the reconstruction of such large-scale plant metabolic network could be challenging, which is mainly attributable to the physiological differences in their tissues, subcellular localization of reactions and the annotation of genomic content whose functions remain unidentified (Seaver *et al*, 2012; Sweetlove and Ratcliffe, 2011). These issues can be appropriately resolved by resorting to transcriptomic and/or proteomic datasets as surrogate for transcriptional regulation in developing tissue-specific models (Mintz-Oron *et al*, 2012), subcellular localization prediction software for compartmentalizing metabolic reactions (Mintz-Oron *et al*, 2012) and comparative genomics for annotating undiscovered genomic content (Seaver *et al*, 2012). Therefore, the comprehensive model developed in such a pipeline can be exploited to further enhance our understanding of the complex metabolic behaviour of rice and potentially help in rationally designing the modified crops in the future.

3.4 Summary

In this study, the first ever metabolic network of rice cells was reconstructed to elucidate the cellular phenotype of two different rice tissues via intracellular metabolic flux profiles during abiotic stresses. Using the model, the current chapter showed how the regulatory information in plants can be accounted for simulating tissue-specific and/or condition specific metabolic behaviour of rice cells. The phenotypic behaviour and metabolic states simulated by the model are highly consistent with the suspension culture experiments as well as previous reports. Therefore, it is now appropriate to utilise the reconstructed model for simulating the metabolic states upon various abiotic stresses.

Chapter 4

InCombined *in silico* modelling and microarray data analysis during flooding stress[1]

4.1 Introduction

Annual rice production is significantly affected due to several abiotic stresses. Among them, flooding stress tremendously limits rice productivity (Xu *et al*, 2006), particularly in the rain-fed lowlands of Southeast Asia. In general, when plants are water-logged by flooding, they experience a lower oxygen availability (hypoxia) or total absence of oxygen (anoxia), thus severely impairing the energy generation through reduced/eliminated mitochondrial respiration. Nevertheless, rice is unique in its ability to survive up to two weeks in complete submergence conditions by prolonged flood (Jackson and Ram, 2003; Bailey-Serres and Voesenek, 2008). Rice seeds can germinate and grow up to coleoptile even in anoxia through its distinctive metabolic adaptations. Under such conditions, predominant amounts of energy required for survival are produced by fermentative pathways, especially ethanolic fermentation (Atwell *et al*, 1982; Alpi and Beevers, 1983; Guglielminetti *et al*, 1995; Gibbs *et al*, 2000; Magneschi and Perata, 2009).

Several researches were focussed on understanding the biochemical adaptations of rice under anoxia in the past decade, including two large-scale microarray data analyses

[1]Excerpts of this chapter, in part, is a reprint of previous publication, Lakshmanan et al. (2013) Elucidating rice cell metabolism under flooding and drought stresses using flux-based modelling and nnalysis, Plant Physiology, 162:2140–2150, PMID: 23753178, and Lakshmanan et al (2014) Metabolic and transcriptional regulatory mechanisms underlying the anoxic adaptation of rice coleoptile, AoB Plants, 6:plu026. PMID: 24894389.

(Lasanthi-Kudahettige *et al*, 2007; Narsai *et al*, 2009). However, despite such efforts, the current knowledge on how oxygen deficiency is sensed and the regulatory cascades which fine-tunes the transcriptional and metabolism is still very limited. To date, the induction of ethylene-responsive *SUB1* locus under hypoxic conditions (Xu *et al*, 2006) and the induction of GA-response-free *RAmy3D* under anoxic conditions (Loreti *et al*, 2003) are the only two notable traits unravelled at the molecular level. Even with the availability of abundant high-throughput data, such limitations still exist mainly due to the lack of systematic frameworks to analyse and derive valid hypothesis from them. In this regard, as mentioned earlier, constraints-based *in silico* metabolic modelling and analysis is a useful approach as it not only predicts the physiological behaviour and metabolic states of an organism upon various environmental/genetic changes but also serves as a scaffold to contextualise the multiple "-omics" data, thereby enabling us to decipher biologically meaningful correlations (Lewis *et al*, 2012). Several frameworks are now available to integrate the metabolic models and high-throughput data such as gene expression (Becker and Palsson, 2008; Colijn *et al*, 2009; Bordel *et al*, 2010), metabolomics (Mo *et al*, 2009; Selvarasu *et al*, 2012) and proteomics (Shlomi *et al*, 2008) within the context of systems biology. Therefore, in order to understand the metabolic and transcriptional changes in rice during flooding stress, it is now imperative to utilise such an systems approach by combining the *in silico* modelling and "-omics" data. Accordingly, in this study, the metabolic adaptations of rice were first identified using the rice central metabolic/regulatory model reconstructed in previous chapter. Subsequently, the differences in flux levels are compared with gene expression data between air and anoxia to identify the possible reactions which are transcriptionally regulated. Furthermore, in order to gain a deeper insight into the key regulatory mechanisms during anoxic adaptation, the possible transcription factors (TFs) of transcriptionally regulated enzymes are also identified by analysing the distribution of putative cis-elements in their promoter regions.

4.2 Materials and methods

4.2.1 Microarray data

The raw transcriptome data generated by Lasanthi-Kudahettige *et al* (2007) was first downloaded from the Gene Expression Omnibus (accession no. GSE6908) and normalised using the quantile method (Bolstad *et al*, 2003). Differentially expressed genes were then identified by performing a linear model (Wettenhall and Smyth, 2004). The resulting p-values were also corrected for multiple testing using Benjamini-Hochberg correction.

4.2.2 Constraints-based regulatory flux analysis

In this study, constraints-based flux analysis was utilised to simulate the rice metabolism under varying environmental conditions by manipulating the constraints. The biomass equation was maximised to obtain the optimal solution of the metabolic network as detailed in chapter 2 (Section 2.2.4.1, Problem P1). The cellular metabolism of the seed-derived rice cells growing on either sucrose or glucose was simulated as mentioned in previous chapter (see Section 3.2.4).

4.2.3 Flux variability analysis

Since FBA is an optimization based technique, it is often possible to have multiple solutions attaining the same objective value. Therefore, in order to confirm the phenotypic and metabolic state predicted by FBA, flux variability analysis (FVA) was performed as described in chapter 2 (Section 2.2.4.2, Problem P2).

4.2.4 Flux sampling

The artificial centering hit-and-run (ACHR) Monte Carlo sampling was utilised to uniformly sample the metabolic flux solution space under aerobic and anaerobic conditions with appropriate flux constraints. In both conditions, the sucrose uptake rate, oxygen uptake rate and cell growth rates were constrained with experimentally measured values reported in previous chapter. To make fair comparison between both the conditions, the oxygen uptake and growth rates were normalised with respect to sucrose uptake rate.

The solution space was sampled with 100,000 randomly distributed points for 10,000 iterations in each simulation. In this study, COBRA toolbox (Schellenberger *et al*, 2011) was utilised to implement the random flux sampling. The differences in flux samples between aerobic and anaerobic conditions was quantified using a Z-score approach as described previously (Mo *et al*, 2009). In such approach, first, two random flux vectors, v_j , one from each sample, i.e. aerobic and anaerobic, was chosen and the difference is calculated as follows:

$$v_{j,diff} = v_{j,aerobic} - v_{j,anaerobic} \tag{4.1}$$

This approach was repeated for 10,000 times to create a new flux differences sample, $v_{j,diff}$, with 10,000 points. Next, from this flux difference sample, the sample mean, μ_j and standard deviation, σ_j was computed to calculate the Z-score as follows:

$$Z_j = \frac{\mu_j}{(\sigma_j/\sqrt{10000})} \tag{4.2}$$

Finally, the absolute Z-scores were translated to p-values using normal cumulative distribution function and the reactions with p-values less than 0.05 were deemed as statistically different between the aerobic and anaerobic conditions.

4.2.5 Identification of transcriptionally regulated enzymes

Using the p-values of transcriptome data and flux sampling, the reactions that are transcriptionally regulated were identified (Bordel *et al*, 2010). Briefly, if the flux and gene expression (for both up and downregulated genes) is significantly changed in same direction, then the corresponding enzyme is classified as "transcriptionally regulated". On the other hand, if the values significantly change in opposite direction, then the enzyme is classified as "metabolically regulated". In case of reactions with multiple isozymes, the gene expression was considered to be up- or down-regulated based on the expression values of majority of transcripts. For example, if a gene has more number of transcripts up-regulated than down-regulated, then it is considered as up-regulated.

4.2.6 Motif detection and identification of putative transcription factors

The promoter sequences [-1000, +200 nt] relative to the experimentally verified TSS for transcriptionally up and downregulated genes of the rice central metabolism were extracted from the in-house rice promoter sequence database. Known and novel promoter motifs were detected using the Dragon Motif Builder program with EM2 option (Huang *et al*, 2005). Thirty motifs were detected each time having a length of 8-10 nucleotides per detection at a threshold value of 0.875. Motifs occurrence in over 50% of the sequences at a threshold e value of $\leq 10^{-3}$ were considered as statistically overrepresented. Motif classes were identified by their matches in different plant Transcription Factor Binding databases such as TRANSFAC (Matys *et al*, 2003), PLACE database (Higo *et al*, 1999), AGRIS (Yilmaz *et al*, 2011) and Osiris (Morris *et al*, 2008).

4.3 Results and discussion

4.3.1 *In silico* flux analysis of seed-derived rice cells under normal and flooded conditions

In order to understand the metabolic differences in rice cells under air and anoxia, constraints-based flux analysis was performed by maximizing the coleoptile biomass equation while constraining the uptake rate of carbon source, i.e. sucrose or glucose, at experimentally measured values in both aerobic and anaerobic conditions. Further, to understand how oxygen influences the cellular growth, the internal flux distributions under aerobic and anaerobic conditions were examined. Significant difference among several metabolic pathways including glycolysis, tricarboxylic acid (TCA) cycle, fermentation and glutaminolysis was observed (Fig. 4.1A and 4.1B). In order to re-assure the confidence of the simulated metabolic states, FVA (Mahadevan and Schilling, 2003) was conducted for both conditions, thereby identifying commonly activated reactions, indicating the plausibility of such internal metabolic utilization (see Appendix I for complete results). The characteristic differences in flux distribution across various metabolic pathways between aerobic and anaerobic conditions are presented below.

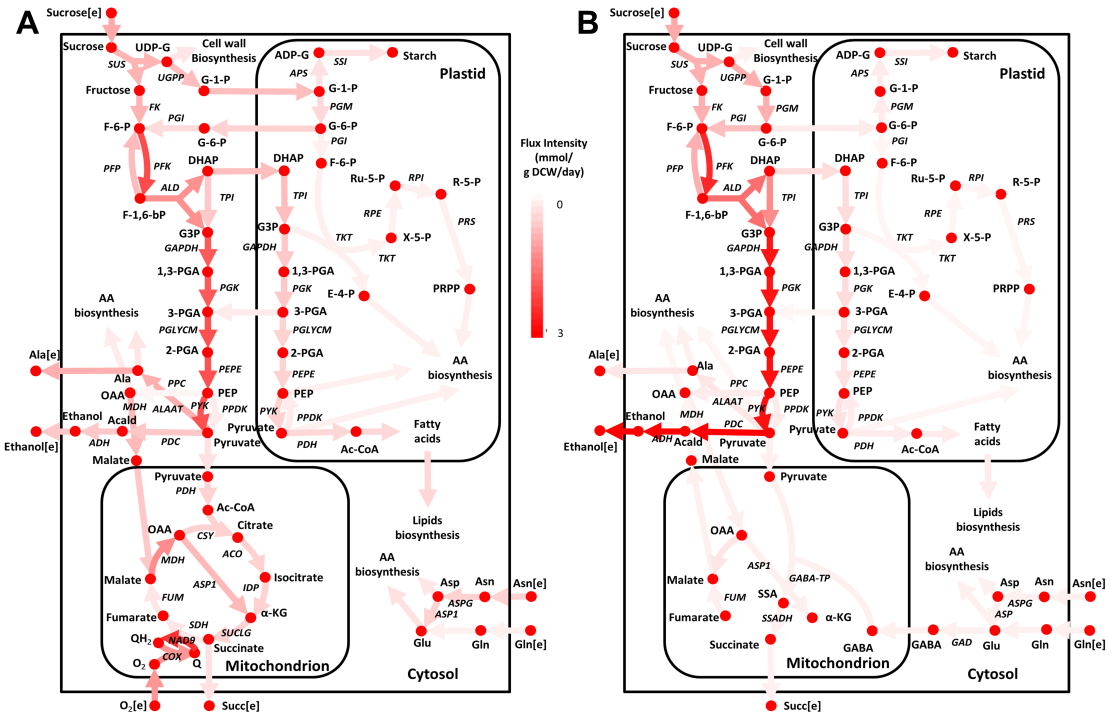


Figure 4.1: *In silico* flux-maps of seed-derived suspension culture rice cells grown on sucrose under aerobic (A) and anaerobic (B) conditions. The colour intensity of the lines in the central carbon metabolic network corresponds to the normalised flux values with respect to the sucrose uptake rates in each condition. Metabolite abbreviations are as follows: α-KG, α-ketoglutarate; 1,3-PGA, 1,3-diphosphoglycerate; 2-PGA, 2-phosphoglycerate; 3-PGA, 3-phosphoglycerate; AA, amino acids; Acald, acetaldehyde; Ac-CoA, acetyl-coenzyme A; ADP-G, ADP-glucose; Ala, Alanine; Asn, Asparagine; Asp, Aspartate; DHAP, dihydroxyacetone phosphate; E-4-P, erthrose-4-phosphate; F-6-P, fructose-6-phosphate; F-1,6-bP, fructose-1,6-bisphosphate; G-1-P, glucose-1-phosphate; G3P, glyceraldehyde-3-phosphate; G-6-P, glucose-6-phosphate; GABA, γ-aminobutyrate; Gln, glutamine; Glu – glutamate; OAA, oxaloacetate; PEP, phosphoenolpyruvate; PRPP- phosphoribosyl pyrophosphate; Q, ubiquinone; QH2, ubiquinol; R-5-P, ribose-5-phosphate; Ru-5-P, ribulose-5-phosphate; SSA, succinic semialdehyde; UDP-G, UDP-glucose, X-5-P, D-xylulose-5-phosphate. Enzyme abbreviations are as follows: ACO, aconitase; ADH, alcohol dehydrogenase; ALAAT, alanine aminotransferase; ALD, aldolase; APS, glucose-1-phosphate adenylyltransferase; ASP1, aspartate aminotransferase; ASPG, asparaginase; COX, cytochrome C oxidase; CSY, citrate synthase; FK, fructokinase; FUM, fumarase; GABA-TP, γ-aminobutyrate aminotransferase; GAD, glutamate decarboxylase; GAPDH, glyceraldehyde phosphate dehydrogenase; IDP, isocitrate dehydrogenase (NADP-dependent); MDH, malate dehydrogenase; NAD9, NADH dehydrogenase; PDC, pyruvate decarboxylase; PDH, pyruvate dehydrogenase; PEPE, phosphoenolpyruvate enolase; PFK, 6-phosphofructokinase; PFP, PPi-dependent phosphofructokinase; PGI, phosphoglucoisomerase; PGK, phosphoglycerate kinase; PGLYCM, phosphoglucomutase; PGM, phosphoglucomutase; PPC, phosphoenolpyruvate carboxylase; PPDK, pyruvate orthophosphate dikinase; PRS, ribose-phosphate diphosphokinase; PYK, pyruvate kinase; RPE, ribose-5-phosphate epimerase; TKT, transketolase; TPI, triose phosphate isomerase; SDH, succinate dehydrogenase; SSADH, succinic semialdehyde dehydrogenase; SSI, starch synthase; SUCLG, succinyl-coA ligase; SUS, sucrose synthase; UGPP, UDP-Glucose pyrophosphorylase.

4.3.1.1 Sucrose metabolism

In both aerobic and anaerobic conditions, sucrose synthase (SUS) was utilised for degrading sucrose into fructose and UDP-Glucose (UDP-Glc) (Fig. 4.1A and 4.1B), which is consistent with the previous experimental suggestions (Mohanty *et al*, 1993; Guglielminetti *et al*, 1995). The *in silico* analysis also confirmed the recycling of UTP to SUS which occurs through the nucleoside diphosphate kinase (NDPK) and the UDP-Glucose pyrophosphorylase (UGPP). Although the supply of UTP to SUS from UGPP was proposed by (Guglielminetti *et al*, 1995), they did not clearly reveal the source of PPi, rather just hypothesised its origin from PPi dependent phosphofructokinase (PFP). In this regard, the simulation results suggested that the PPi could be produced towards the gluconeogenesis direction via reactions catalysed by either PFP or pyruvate orthophosphate dikinase (PPDK), forming a substrate cycle in glycolysis. Such combined utilization of SUS, NDPK, UGPP and PFP/PPDK for the break-down of sucrose is energetically efficient than invertase since they consume one mole of ATP lesser for each mole of sucrose degraded (Guglielminetti *et al*, 1995; Magneschi and Perata, 2009).

4.3.1.2 Glycolysis

Compared to aerobic conditions, anaerobic glycolytic fluxes in cytosol showed a significant increase (by more than 42%), where the majority (97.5%) was fermented to ethanol (Fig. 4.1B). Notably, such an increase in carbon flux through glycolysis and a sharp decline in coleoptile growth have already been reported (Mohanty *et al*, 1993; Magneschi and Perata, 2009), highlighting the importance of ethanolic fermentation in combination with glycolysis for energy production under anaerobiosis. On the other hand, aerobic glycolysis showed that significant amounts of pyruvate was utilised in the oxidative conversion to acetyl-coA, thus enabling its entry into the TCA cycle for energy production (Fig. 4.1A). Furthermore, the simulations also indicated a certain amount of pyruvate (22%) being fermented into ethanol in aerobic conditions, in agreement with earlier reports (Edwards *et al*, 2012). In general, ethanol fermentation under aerobic conditions occurs mainly due to high glycolytic fluxes and/or limited oxygen availability where the excess pyruvate that cannot be oxidised, is fermented to regenerate the NAD^+ lost in glycolysis. It should be noted that glycolytic fluxes are regulated by the

hexokinase (HXK) activity in plants, which is determined by the supernatant hexose concentrations (Lalonde *et al*, 1999). Therefore, it is possible that the excessive hexose concentrations resulting from the sucrose breakdown via SUS/invertase may have led to higher activity of hexokinase enzyme, thereby resulting in an overflow metabolism via the glycolytic pathway. In plants, the plastidic glycolysis is more crucial than the cytosolic one as most of the amino acids and fatty acids are synthesised in plastids. In this regard, flux analysis results indicated anaerobic glycolysis with highly reduced fluxes (by 46%); most of the carbon source is channelled via cytosolic glycolysis to feed fermentative pathways for energy generation as mentioned earlier.

4.3.1.3 TCA cycle

Under anoxic conditions, simulation results revealed a truncated TCA cycle operation between fumarate and oxaloacetate (OAA), mainly due to the limited regeneration of redox cofactors since the mitochondrial respiration is impaired (Fig. 4.1A). These observations are in good agreement with earlier reports on plants, suggesting a partial TCA cycle activity under hypoxia and anoxia (Sweetlove *et al*, 2010). On the other hand, a fully operational TCA cycle was characterised under aerobic conditions where the carbon flux enters the cycle at three different points: (i) acetyl-CoA from pyruvate, (ii) malate from OAA and (iii) alpha-ketoglutarate (α-KG) from Glutaminolysis (Fig. 4.1B). It should be noted that a part of this α-KG was also withdrawn from the cycle and utilised in amino acid biosynthesis to keep the cycle balanced as any additional α-KG above the acetyl-CoA influx would cause an imbalance. Interestingly, the flux analysis also suggested the possibility of gamma-aminobutyric acid (GABA) shunt to be operational for the conversion of α-KG to succinate instead of α-KG dehydrogenase and succinate-CoA ligase (Fig. 4.1B). However, further analysis revealed that the operation of GABA shunt is just an alternate solution as confirmed by FVA (see Appendix I). Thus, the final determination of actual or plausible flux distributions in this case must await experimental verification through isotope-based internal flux measurements.

4.3.1.4 Glutaminolysis & amino acids biosynthesis

During the model simulations, the rice cells were freely allowed to consume glutamine and asparagine as nitrogen sources for the amino acid biosynthesis (Bewley and Black,

1994). Under both aerobic and anaerobic conditions, the consumed glutamine and asparagine was completely converted into glutamate and aspartate, and subsequently, into α-KG and OAA for amino acid synthesis. Furthermore, the amounts of asparagine consumed in aerobic conditions were reasonably higher since enhanced pyruvate pool facilitated the amino acid biosynthesis. The simulation results also highlighted the functional ability of rice to synthesise all amino acids via biosynthetic pathways even under anoxia rather than the protein degradation as often speculated. Interestingly, the flux analysis also suggested the possibility of GABA, a non-protein amino acid, to be synthesised under both aerobic and anaerobic conditions. As mentioned previously, although the synthesis of GABA and its subsequent utilization in GABA shunt did not influence the cellular growth under aerobic conditions, it enhanced the growth rate slightly under anaerobic conditions owing to the crucial role in glycine biosynthesis. Under anoxia, GABA is first synthesised from glutamate by glutamate decarboxylase (GAD), and then converted into succinate via 4-aminobutyrate aminotransferase (GABA-TP) and succinic semialdehyde dehydrogenase (SSADH). During these conversions, NADH is liberated in the SSADH step and recycled via a series of enzymes including the serine hydroxymethyltransferase (SHM1), producing net amounts of glycine. These observations are in very good agreement with earlier experiments by Shingaki-Wells *et al* (2011) who reported the anaerobic accumulation of GABA along with an increase in the expression of SHM1.

4.3.2 Random sampling of seed-derived rice cells under air and anoxia

Although FBA can simulate the metabolic differences between air and anoxia, a statistical measure cannot be achieved for the observed differences. Therefore, in order to reassure the observed differences with statistical confidence, random sampling was performed. The plausible metabolic states of rice coleoptile under air and anoxia were sampled using ACHR Monte Carlo sampling to estimate the range of possible steady-state flux values through each of the reaction in the rice model (see Materials and methods). The resulting probability distributions of individual reaction fluxes revealed significant differences in central metabolic pathways such as glycolysis, TCA cycle, pentose phosphate pathway and oxidative phosphorylation between aerobic and anaerobic conditions (Appendix J).

Under anoxia, the TCA cycle, pentose phosphate pathway and oxidative phosphorylation reactions have only a small range of fluxes where some of them even have zero flux due to the imposed capacity constraints, i.e. the absence of oxygen exchange. As a result, the fluxes across various amino acid and lipid synthetic pathways were also severely restricted under anoxic conditions. On the other hand, random sampling allowed us to observe the possibility of high fluxes through cytosolic glycolysis and fermentation, mainly to produce all the ATP required for cell growth as other energy producing pathways such as oxidative phosphorylation and TCA cycle are grossly impaired under such conditions. Overall, random sampling also highlighted the same metabolic differences which are simulated by FBA but with a statistical measure to each of the reaction.

4.3.3 Transcriptionally regulated reactions during anaerobic adaptation

The differences in flux samples were compared against gene expression data between air and anoxia, thereby identifying the reactions that are being likely transcriptionally regulated (see Materials and methods). Overall, among the 63 reactions in rice central metabolism, 37 and 5 exhibit transcriptional and metabolic regulation, respectively. The remaining 38 reactions could not be classified in any of these categories as they had insignificant change either in flux or gene expression. The complete list of transcriptionally and metabolically regulated reactions are provided in Appendix K.

Most of the reactions in TCA cycle, oxidative phosphorylation and pentose phosphate pathway show down-regulation in both flux and gene expression under anaerobic conditions while several reactions of the sucrose metabolism including SUS, FK, and NDPK are significantly upregulated at the transcriptional level. Only invertase in sucrose metabolism showed down-regulation in both flux and gene expression, confirming that rice preferably utilise SUS for metabolizing sucrose under anaerobic conditions to conserve the ATP usage. All the reactions in fermentation pathway including PDC, ADH and ALDH are up-regulated. In rice, both alcohol and aldehyde dehydrogenases have multiple isozymes and few of them such as *ADH1*, *ADH2* and *ALDH2a* showed a drastic increase in gene expression (Lasanthi-Kudahettige *et al*, 2007). Interestingly, the up-regulation of ALDH in both flux and transcript level is in very good agreement with earlier experimental reports on both tolerant and intolerant lines of rice under hypoxic

conditions during submergence (Nakazono *et al*, 2000; Ismail *et al*, 2012), indicating that ALDH is likely to play a key role in detoxifying the excess acetaldehyde from PDC that cannot be metabolised via ADH. In this regard, (Lasanthi-Kudahettige *et al*, 2007) have earlier hypothesised that the acetate resulting from ALDH can enter TCA cycle to further fuel amino acid biosynthetic pathways. However, the flux analysis revealed that the acetate from ALDH primarily fuels the lipid biosynthesis in plastid, as the fatty acid synthesis needs sufficient carbon flux to synthesise the required saturated fatty acids under anoxia.

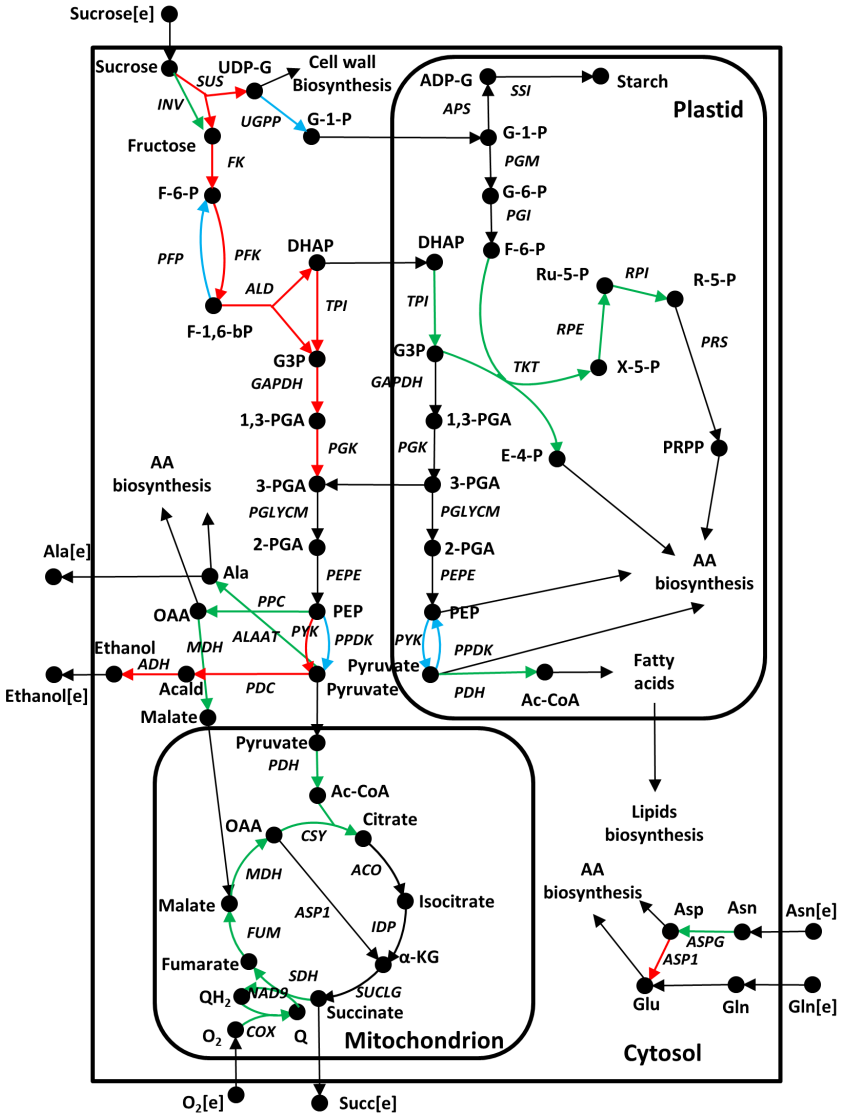


Figure 4.2: Central metabolic reactions of rice showing transcriptional and metabolic regulation under anoxia. Green, red and blue colours indicate the transcriptionally up-, down- and metabolically regulated enzymes, respectively. Reactions with black arrows represent the enzymes whose regulation mechanism is not investigated or identified in this study. Metabolite abbreviations are same as Fig. 4.1.

Unlike other central metabolic pathways, the glycolytic reactions did not show an overall up or downregulation in gene transcription and fluxes. Out of total 25 reactions, only 11 showed transcriptional regulation. Among the remaining 14, five were oppositely correlated between flux and gene expression, indicating that these enzymes are most likely to be metabolically regulated. Plastidic PK, UGPP, PFP, and cytosolic and plastidic PPDK are the five enzymes with metabolic regulation. Such observations are in good agreement with earlier hypothesis by Plaxton (1996), who suggested that PK, PPDK, PFK and PFP are possibly involved in the fine control of plant glycolysis and are most likely to be regulated based on the variation in substrate(s) and cofactor concentrations, pH and other metabolite effectors.

4.3.4 TFs associated with transcriptionally regulated genes

To identify the potential TFs involved in the transcriptional control of the transcriptionally regulated reactions, promoter analysis of the corresponding genes was performed. In total, promoter sequences for 26 transcriptionally up-regulated genes and 27 down-regulated genes were used for cis-element detection (see Appendix K). This analysis identified several highly enriched putative cis-elements associated with different potential TFs for both up and downregulated transcriptionally controlled genes (Tables 4.1 and 4.2). A high enrichment of putative cis-elements such as AT-hook/PE-1-like, GT element-like, pyrimidine-box-like, GARE-like and MYb-box-like associated with MYB TFs was observed among both up and downregulated genes. However, the high enrichment of these cis-elements in the upregulated genes signifies that MYB TFs especially play an important role in the transcriptional control of upregulated genes under anoxia. Similarly, putative cis-elements such as AS-1/ocs-like and ABRE-like associated with bZIP TFs were also found in both up- and down-regulated genes but with a high percentage of occurrences only in upregulated genes. Besides, a number of other putative cis-elements such as ERE-like/GCC-boxlike and zinc finger binding element-like associated with ERF and ZnF TFs were also more overrepresented in the upregulated genes albeit being present in both up- and down-regulated genes. Furthermore, a moderate enrichment of other ERE like-elements such as JA response element-like elements was also noticed among the upregulated genes (Table 4.1). Collectively, these results indicate that all these TFs, i.e. MYB, bZIP, ERF and ZnF, may work together in the transcriptional

Table 4.1: Potential cis-elements identified in the promoters of transcriptionally controlled up-regulated genes of rice seeds germinated under anoxia

Cis-elements	Motifs	Associated TFs	% (TIC), e-value
AT-hook/PE1-like	TTTTTTCA	MYB (PF1)	73 (12.78), 2e-004
	AATTTTTTT	MYB (PF1)	65 (16.05), 3e-005
	ATAAAAAAAA	MYB (PF1)	58 (16.67), 0e+00
	AAGAAAAAG	MYB (PF1)	58 (13.91), 1e-004
	AAAAATAC	MYB (PF1)	54 (13.32), 1e-004
	TTTTTTCTTT	MYB (PF1)	50(16.74), 3e-005
GT-element-like	TGGTTTGT	MYB (GT-1/GT-3b)	81 (12.15), 1e-004
	TTTTTTCA	MYB (GT-1/GT-3b)	73(12.78), 2e-004
	GGCTTGTG	MYB (GT-1/GT-3b)	69 (11.62), 2e-000
	AGGAAAAAG	MYB (GT-1/GT-3b)	58 (13.91), 1e-004
	AAATCATA	MYB (GT-1)	62 (12.80), 8e-005
	AAATCAAAT	MYB (GT-1)	62 (13.69), 1e-004
	TTTTTTCTTT	MYB (GT-1)	50 (16.74), 3e-005
Pyrimidine-box -like	TTTTTTCA	MYB (R1, R2R3)	73 (12.78), 2e-004
	CTTTTGCT	MYB (R1, R2R3)	65 (12.33), 9e-005
GARE-like	AAAACAAA	MYB (R1, R2R3)	58 (12.66), 2e-004
MYB-box-like	TGGTTTAT	MYB (R2R3)	81 (12.15), 1e-004
	TGGTTTGT	MYB (R2R3)	81 (12.15), 1e-004
	AACTTGTT	MYB (R2R3)	54 (13.18), 3e-005
As-1/ocs-like	TTTTTTCA	bZIP (Gr. D, I, S)	73 (12.78), 2e-004
	AAATCATA	bZIP (Gr. D, I, S)	62 (12.80), 8e-005
	ATGAAAAAG	bZIP (Gr. D, I, S)	58 (13.91), 1e-004
ABRE-like	AAATCAAAT	bZIP (Gr. A)	62 (12.80), 8e-005
	CTTTGCCA	bZIP (Gr. A)	58 (13.43), 1e-004
	GAGCGCCA	bZIP (Gr. A)	54 (12.18), 3e-004
RSG binding element like	AACTTGTT	bZIP	54 (13.18), 3e-005
CAMTA3 binding site-like	GAAGAAAA	bZIP	63 (14.30), 2e-004
RISbZ1 binding site-like	AAAACAAA	bZIP (RISbZ1)	58 (12.66), 2e-004
CAMTA3 binding site-like	GAGAAAGAA	bZIP	58 (14.52), 1e-004
	AAGAAGAG	bZIP	50 (13.41), 2e-004
Zinc finger binding element-like	AAGAAGAG	ZnF	62 (13.69), 1e-004
	AAATCATA	ZnF	62 (12.80), 8e-005
	AAATCAAAT	ZnF	50 (13.41), 2e-004
ERE-like (JA response element-like)	AAATCATA	ERF (Gr. VI, VIII, IX)	62 (12.80), 8e-005
	AAATCAAAT	ERF (Gr. VI, VIII, IX)	50 (13.41), 2e-004
GCC-box-like	CTCCGCCGC	ERF (I, IV, VII, X)	50 (15.38), 2e-005
AuxRe-like	CTTTTGCT	ARF	65 (12.33), 9e-005
	CTTTGCCA	ARF	58 (13.43), 1e-004
AAAAG/-element-like	CTTTTGCT	DOF (Dof1/4/11/22)	65 (12.33), 9e-005
	AAGAAAAAG	DOF (Dof1/4/11/22)	58 (13.43), 1e-004
MYC-box-ike	TGCTACTC	bHLH (JAMYC2)	65 (11.96), 1e-004
ARR10 binding element	AAATCATA	ARR-B (ARR10)	62 (13.69), 1e-004
TATA-box-like	TATAAATT	TBP	96 (12.32), 3e-005
DBP element-like	AAAAATAC	DBP	54 (13.32), 1e-004
DBP1 element-like	AATATATTA	DBP1	50 (15.09), 8e-005

control of the upregulated genes in rice central metabolism. Interestingly, the enrichment of MBF1C binding element and CRT/DRE-like elements associated with MBF1C and CBF/DREB TFs were noticed only in downregulated genes. This highlights the possibility that this TF could be involved in transcriptional control of downregulated genes under anoxia (Table 4.2).

Table 4.2: Potential cis-elements identified in the promoters of transcriptionally controlled down-regulated genes of rice seeds germinated under anoxia

Cis-elements	Motifs	Associated TFs	% (TIC), e-value
AT-hook/PE1-like	ATATTTTTAT	MYB (PF1)	59 (16.39), 6e-005
	TTTAAAAAA	MYB (PF1)	59 (16.42), 2e-005
GT-element-like	ATTGGCTA	MYB (GT-1)	56 (12.42), 2e-004
MYB-box-like	AAAATCCA	MYB (R2R3, MCB1/2)	70 (13.11), 2e-004
As-1/ocs-like	TCGTCGCG	bZIP (Gr. D, I, S)	63 (13.21), 0e+000
	ACGTGTCA	bZIP (Gr. D, I, S)	59 (11.79), 3e-004
	AGACGTTG	bZIP (Gr. D, I, S)	56 (11.91), 3e-005
ABRE-like	ATTGGCTA	bZIP (Gr. A)	59 (11.79), 3e-004
	TCGCCGGC	bZIP (Gr. A)	59 (13.20), 5e-005
ER stress RE-like	AACTTGTT	bZIP (Gr. D)	56 (12.42), 2e-004
RISbZ1 binding site-like	AAAACAAA	bZIP (RISbZ1)	58 (12.66), 2e-004
AuxRe-like	ACTACTAT	ARF1	67 (12.28), 9e-005
	TCGTCGCG	ARF1	63 (13.21), 0e+000
	ACGTGACA	ARF1	59 (11.79), 3e-004
	AATCCTTT	ARF1	56 (13.21), 9e-005
GAGA element-like	CTCCTCTC	GAGA-binding factor BBR/BPC2	63 (14.39), 7e-004
	TCCTCTAT	GAGA-binding factor BBR/BPC2	52 (13.62), 4e-004
	GGGAGAGGG	GAGA-binding factor BBR/BPC2	52 (15.63), 3e-005
DBP1 element-like	TTTATTTT	DBP1	85 (13.63), 2e-004
	ACATTAAA	DBP1	78 (12.88), 2e-004
	AAATAATA	DBP1	62 (13.44), 9e-005
GCC-box-like	GGCGGCGGC	ERF (I, IV, VII, X)	70 (15.92), 1e-004
	CCGCCGCC	ERF (I, IV, VII, X)	56 (13.95), 3e-004
ARR10 binding element like	AAAATCCA	ARR-B (ARR10)	70 (13.11), 2e-004
	AATCCTTT	ARR-B (ARR10, ARR5, ARR1)	56 (13.21), 9e-005
CRT/DRE-like	TCGTCGCG	CBF1/DREB	63 (13.21), 0e+000
AAAGG element-like	AATCCTTT	DOF	56 (13.21), 9e-005
	ATTTAAAGA	DOF (Dof1/4/11/22)	52 (14.11), 9e-005
Zinc finger binding element-like	GAGGAGGAG	ZnF	56 (16.04), 6e-005
MBF1C binding element like	GAGGAGGAG	MBF1C	56 (16.04), 6e-005
TATA-box-like	TTTTATATA	TBP	63 (15.28), 2e-004
DBP element-like	ATATTTTTAT	DBP	59 (16.39), 6e-005

4.3.4.1 MYB family TFs

Among all the putative cis-elements identified, the elements associated with MYB family TFs were found to be highly enriched in transcriptionally upregulated genes. Coincident with these observations a number of MYB family genes are also up-regulated under anoxia (Table 4.3). MYB proteins represent important plant TFs and are found to be involved in various developmental and physiological processes including transcriptional activation, kinase activity, protein binding and transcription repressor activation under abiotic and biotic stresses (Dubos *et al*, 2010). In rice, a recent analysis highlighted that 98.70 % of total MYB proteins are fully involved in transcriptional activation (Katiyar *et al*, 2012). Furthermore, the role of MYB TFs that bind specifically to MYB box/GT element during hypoxic and anoxic responses has already been reported through promoter analysis, both computationally and experimentally (Dolferus *et al*, 2003; Mohanty *et al*, 2005, 2012). Specifically, the *AtMYB2* in Arabidopsis has been shown to be a key regulator of the *ADH1* promoter under low oxygen conditions (Hoeren *et al*, 1998). When this *AtMYB2* was driven by a constitutive promoter, it was able to transactivate *ADH1* expression not only in Arabidopsis but also in *Nicotiana plumbaginifolia* and *Pisum sativum*. Collectively, these results fully support the hypothesis that MYB TFs play an important role in the upregulation of sucrose metabolism and fermentation enzymes at the transcriptional level.

4.3.4.2 bZIP, ERF and ZnF TFs

As mentioned above, the promoter analysis also highlighted significant overrepresentation of several other motifs associated with bZIP, ERF and ZnF TFs in the transcriptionally upregulated genes. In this regard, an increase in transcript levels of bZIP TF (*AtbZIP50*) in anoxia-exposed root cultures of Arabidopsis (Klok et al. 2002), the up-regulation of an ABRE-binding bZIP TF (*OsABF1*) in rice shoot and root under anoxic treatment (Hossain *et al*, 2010) and the upregulation of a number of bZIP TFs in rice anoxic coleoptile (Table 4.3) support the view that bZIP could orchestrate the transcription of upregulated genes upon anoxic stress. The major role of ERF TF has been identified as a positive regulator of *Sub1A* expression in a flood-tolerant rice variety during hypoxic conditions caused by submergence (Xu *et al*, 2006). However, the

Table 4.3: List of anoxia stressed up-regulated transcription factors with potential significance to the pattern of cis-element enrichment among the up-regulated genes

Family	Locus ID (Annotation)	Fold change
MYB/MYB-related	Os02g0706400 (Myb-related, similar to Radialis)	9
	Os06g0728700 (Homeodomain-like protein)	7
	Os08g0151000 (Myb-like, SHAQKYF class)	7
	Os01g0524500 (Myb-like, SHAQKYF class)	6
	Os01g0863300 (Similar to MCB2 protein)	4
	Os08g0549000 (Similar to MybHv5)	3
	Os05g0459000 (c-Myb protein)	2
	Os04g0480300 (Myb-like protein)	2
bZIP	Os09g0306400 (bZIP-1 domain protein)	16
	Os03g0336200 (RF2b transcription factor)	6
	Os06g0662200 (bZIP-1 domain protein)	4
	Os01g0867300 (G-box binding factor)	3
	Os05g0489700 (Similar to BZO2H3)	2
	Os05g0129300 (bZIP protein)	2
	Os05g0569300 (G-box binding factor)	2
ERF	Os03g0341000 (Similar to RAP2.2)	29
	Os01g0131600 (Similar to PTI6, pathogenesis-related)	3
	Os06g0604000 (Similar to ERF1 and ERF3)	3
ZnF	Os05g0525900 (Similar to Zing finger transcription factor PEI1)	21
	Os09g0560900 (Zinc finger, C2H2-like domain containing protein)	2
	Os02g0672100 (Zinc finger, C2H2-type domain containing protein)	2
	Os09g0560900 (Zinc finger, C2H2-like domain containing protein)	2
ARF	Os04g0671900 (Similar to auxin response factor)	2
	Os06g0677800 (Similar to auxin response factor)	2
DOF	Os05g0112200 (Dof domain, zinc finger family protein, expressed)	2
bHLH	Os11t0523700 (Basic helix- loop-helix protein 116) (bHLH116)	3
	Os02t0433600 (Helix-loop-helix DNA-binding domain containing protein)	2
Psedo-ARR-B	Os11t0157600 (Similar to Timing of CAB expression)	3

anoxia-tolerant rice variety '*Nipponbare*' that germinates and elongates under anoxia does not have this gene. Surprisingly, the presence of highly enriched putative GCC-box-like/ERE-like cis-elements in the promoters of all anoxia up-regulated genes in this variety of rice highlights the possibility that these TFs might also control the transcription of relevant genes as it is in Arabidopsis under hypoxic conditions (Hinz *et al*, 2010; Licausi *et al*, 2010, 2011). Unlike the ERF TFs, the role of ZnF TF in response to submergence/anoxia is not yet known. However, matching with the identification of ZnF binding site-like elements in transcriptionally upregulated genes, the increase in expression of ZnF TF genes (Table 4.3) in response to hypoxia/anoxia in both rice and Arabidopsis indicates the potential regulatory role in transcriptional control under oxygen stress (Loreti *et al*, 2005; Pandey and Kim, 2012).

4.3.5 Motif detection in negative sets

To ensure that the cis-element analysis did not identify an excessive number of false positives, motifs from the promoters of a similar number of genes that are not anoxia-specific were also analysed using the same protocol (see Materials and Methods). For this purpose, two negative datasets was used: (i) randomly selected genes from the non-differentially expressed gene list under anoxia (Lasanthi-Kudahettige *et al*, 2007) (negative set 1) and (ii) upregulated genes associated with drought response in rice (Zhang *et al*, 2012) (negative set 2). The list of genes from the negative sets and the results of this analysis are provided in Appendix L. Using the negative control Set 1, although a few common motifs such as MYB, bZIP and DOF was identified, their total enrichment was much lower compared with the motifs detected in transcriptionally up or downregulated genes of anoxia (Tables 4.1, 4.2 and Appendix M). Similarly, the motif analysis of negative Set 2 also revealed a significantly different cis-element enrichment pattern where most of the identified TFs such as MYB, bZIP, ERF, NAC and MYC have been experimentally confirmed to play a regulatory role in drought stress response (Shinozaki and Yamaguchi-Shinozaki, 2007; Zhang *et al*, 2012). Collectively, these results clearly demonstrate that the cis-element analysis identifies reasonably precise motifs that are specific to anoxic stress.

4.3.6 Comparison of proposed method and existing promoter analysis techniques

As mentioned earlier, the promoter sequences of 26 transcriptionally up-regulated and 27 down-regulated genes was utilised for the cis-element detection in this study. When compared with the normal promoter analysis method that considers the whole set of differentially expressed genes, the current study takes into account relatively few genes. Therefore, in order to argue that this small set of genes is sufficient to generate biologically meaningful results, the TFs identified in this study was compared with previous work which considered the whole list of upregulated (842) and downregulated (1794) genes during anoxic adaptation (Mohanty *et al*, 2012). Interestingly, the comparison result revealed that the TFs associated with up and downregulated genes are the same between two studies where the motif enrichment scores of certain TFs such as MYB, bZIP, ZnF and ERF are much higher in the current study, highlighting that their role could be more specific to anoxic adaptation. To further confirm these findings, the individual promoter sequences of four of the key transcriptionally regulated enzymes, i.e. SUS, PDC, ADH and ALDH, was also analysed and identified the same TFs as fully responsible for their transcription (Fig. 4.3). Therefore, based on these motif analysis results and experimental evidence from the literature, a positive role of MYB together with bZIP, ERF and ZnF in the transcriptional control of sucrose metabolism and fermentation during germination and coleoptile elongation of rice under anoxia can be hypothesised.

The methods used in the current study successfully identified several transcriptionally regulated reactions and their related TFs, where some of which are experimentally confirmed. However, the overall results of this approach await experimental validation since the current prediction relies on several assumptions concerning model completeness, constraints used during simulation and the statistical cutoff values chosen for comparative analysis. In the current work, the central model was utilised to simulate the differences in metabolic fluxes between air and anoxia. It should be noted that although this model predicts the overall cellular phenotype quite accurately (Lakshmanan et al. 2013), it may not capture the global changes in cellular metabolism. This reservation is needed since the model does not take account of the secondary metabolic pathways.

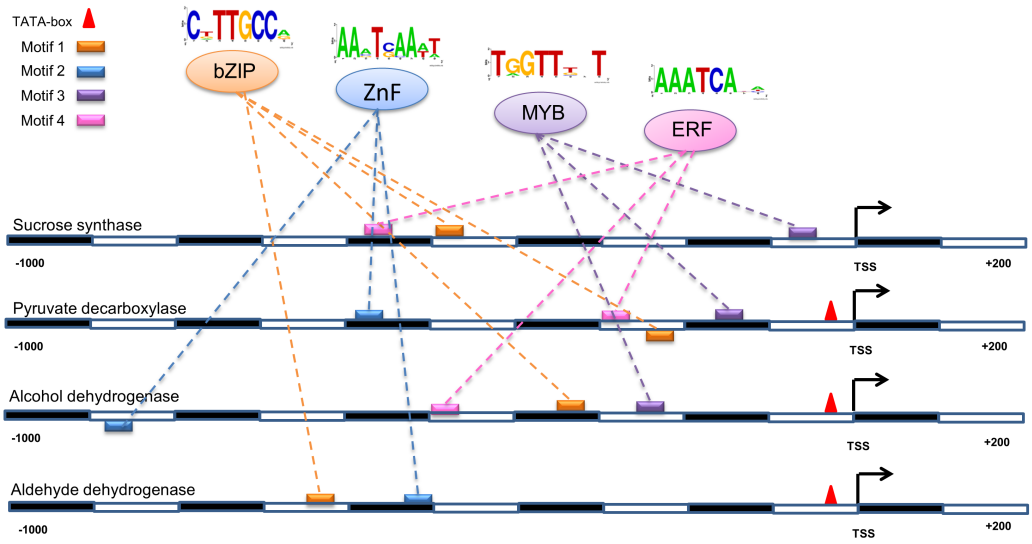


Figure 4.3: Presence of common putative cis-elements in the key transcriptionally regulated genes. The presence of potential putative cis-elements and their cognate known TFs are shown in different strands of the promoter region (21000, +200 nt relative to TSS) of the key genes. Each putative cis-element/motif is represented by its consensus logo. TATA boxes are located between 25 and 30 nt upstream from the TSS.

Moreover, only a few external fluxes, i.e. sucrose uptake, O_2 uptake and growth yield, was utilised as the sole constraints to identify the internal flux distributions during flux sampling simulations. In such cases, the internal fluxes of some reactions are determined with statistically low confidence scores due to the possibility of multiple flux solutions. Such limitations can be overcome by the use of C_{13} flux measurements as constraints to the internal reactions. Therefore, the list of transcriptionally regulated reactions and the TFs identified in this study need further confirmation by direct experiments.

4.4 Summary

The flux analysis of seed-derived rice cells revealed the importance of ethanolic fermentation together with glycolysis for ATP production under anaerobic growth conditions. The simulations also confirmed the crucial role of SUS ahead of invertase for breaking down sucrose in an energetically efficient manner while growing under both aerobic and anaerobic conditions. Moreover, the rice model even suggested the possible role of GABA in glycine synthesis via SHM1 under anaerobic conditions. The subsequent comparative analysis of changes in flux levels and gene expression between aerobic conditions identified 37 reactions from these pathways to be regulated at the transcriptional

level. The motif enrichment analysis of transcriptionally regulated enzymes highlighted a potential involvement of transcription factors such as MYB, bZIP, ERF and ZnF in controlling the transcription of sucrose metabolism and fermentation genes under anaerobic conditions. In future, the integrative *in silico* modelling and gene expression data analysis framework as described in this work can become a useful tool to analyse the adaptive mechanisms of plants under various stress conditions.

Chapter 5

In silico flux analysis of rice metabolism during drought stress[1]

5.1 Introduction

Drought stress is one of the major environmental factors affecting the growth and development of rice due to high levels of photorespiration. Thus, in order to investigate how this abiotic stress affects the rice physiology via metabolic adaptations, it is essential to characterise the cellular behaviour during the photorespiration. The process is initiated by the oxygenase side reaction of the bifunctional ribulose-1,5-bisphosphate carboxylase/oxygenase (RuBisCO), producing equimolar amounts of 3-phosphoglycerate (3-PGA) and unwanted 2-phosphoglycolate (2-PG) for each molecule of O_2 fixed (Jordan and Ogren, 1984). It is followed by the salvage of 2-PG into 3-PGA via photorespiratory pathways, requiring significant amount of cellular energy, i.e. ATP, in C_3 plants such as rice. In general, the ratio of carboxylase/oxygenase reactions (V_C/V_O) is three under normal conditions, however, can drop even below one and may reach the compensation point (V_C/V_O=0.5) at which the net CO_2 uptake rate becomes zero under drought conditions (Heldt and Piechulla, 2011). Therefore, the control of photorespiration has always been a main focus for improving rice productivity.

To date, a number of mutational studies have been performed in many C_3 plants, mainly in Arabidopsis and barley, to understand the photorespiratory pathway, but

[1]Excerpts of this chapter, in part, is a reprint of previous publications, Lakshmanan et al. (2013) Elucidating rice cell metabolism under flooding and drought stresses using flux-based modelling and analysis. Plant Physiology, 162:2140–2150. PMID: 23753178, and Lakshmanan et al (2013). Identifying essential genes/reactions of the rice photorespiration by *in silico* model-based analysis. Rice, 6:20. PMID: 24280628.

identified only a handful of essential enzymes including serine-glyoxylate aminotransferase (SGAT), glycine decarboxylase (GDC), ferredoxin-dependent glutamate synthase (Fd-GOGAT) and glutamine synthase (GS) (Foyer *et al*, 2009) due to the limitations in mutant isolation process and the possible involvement of alternate pathways and genetic redundancy of the relevant enzymes (Reumann, 2004; Timm *et al*, 2008). Thus, it is highly required to exploit more systematic approaches for improving the current understanding of the rice photorespiration. In this regard, *in silico* metabolic modelling and analysis allow us to predict the cellular behaviour and metabolic states globally upon various environmental/genetic changes (Lewis *et al*, 2012). For example, *in silico* knock-out mutant studies and comparative analysis have provided the conditionally essential gene sets and corresponding functional modules under various growth conditions in *E. coli* and *S. cerevisiae* (Segre *et al*, 2005; Joyce *et al*, 2006).

In this work, the rice photorespiration under ambient and drought conditions will be elucidated by first comparing the corresponding metabolic flux distributions, and then by identifying essential genes of rice during photorespiration.

5.2 Methods

5.2.1 Constraints-based regulatory flux analysis

In this study, constraints-based flux analysis was utilised to simulate the rice metabolism under varying environmental conditions by manipulating the constraints. The biomass equation was maximised to obtain the optimal solution of the metabolic network as detailed in chapter 2 (Section 2.2.4.1, Problem P1). The cellular metabolism of the photorespiring rice leaf cells was simulated as mentioned in previous chapter (see Section 3.2.4).

5.2.2 Flux variability analysis

Since FBA is an optimization based technique, it is often possible to have multiple solutions attaining the same objective value. Therefore, in order to confirm the phenotypic and metabolic state predicted by FBA, flux variability analysis (FVA) was performed as described in chapter 2 (Section 2.2.4.2, Problem P2).

5.2.3 Gene deletion analysis

Again, constraints-based flux analysis to identify the essential genes/reactions in the rice metabolism under varying environmental conditions by manipulating the constraints. The biomass equation was maximised to obtain the optimal solution of the metabolic network as detailed in chapter 2 (Section 2.2.4.1, Problem P1). In order to simulate the reaction deletions under photorespiration, the regulatory constraints was first applied to the network under steady-state conditions by evaluating whether metabolic enzymes were active or not for the given conditions using the Boolean rules, and by constraining the fluxes of repressed enzymes to zero as mentioned in chapter 3. Subsequently, the leaf cell growth was simulated by maximizing the leaf biomass while constraining flux through the corresponding reaction to be zero under a defined the photon uptake at 100 mmol g^{-1} DCW day^{-1}. In addition, the ratio of flux through RuBisCO was set with a value of either three or one representing the normal and stressed conditions (Weber, 2007). In this study, all simulations were implemented by General Algebraic Modeling System (GAMS) Integrated Development Environment (IDE) version 23.9.

5.3 Results and discussion

5.3.1 *In silico* flux analysis of photorespiring rice leaf cells under normal and stressed conditions

The reconstructed metabolic model was used to understand metabolic behaviours of photorespiring rice leaf cells under normal and drought-stressed conditions. Photorespiration in rice leaf cells was simulated by maximizing the straw biomass equation, while constraining the photon uptake rate at 100 mmol g^{-1} DCW day^{-1} and fixing the carboxylation-to-oxygenation flux ratio (V_C/V_O) of RuBisCO with a value between one and ten. Here, it should be noted that the simulations with V_C/V_O ratios greater than or equal to three represent the photorespiration under normal conditions while any lesser value corresponds to the drought conditions (Jordan and Ogren, 1984). Model simulations indicated a significant reduction in the CO_2 uptake rates and leaf growth rates as V_C/V_O decreases, and eventually reached zero at the compensation point (V_C/V_O =0.5) (Fig. 5.1A). At severe photorespiration conditions, the carbon fixation rate re-

duces significantly (decreases by 40% at V_C/V_O =2 when compared to V_C/V_O =10) while absorbing same amounts of photon since most of the energy is wasted in recycling the 2-PG. The resultant flux distributions in Figure 5.1B illustrate the classical photorespiratory metabolism linked to glycolysis, TCA cycle, Calvin cycle, photorespiratory cycle, and glutaminolysis reactions. To support this simulated metabolic behaviour, flux variability analysis was conducted in photorespiring rice leaf cells (see Methods for details), confirming the possible metabolic state (see Appendix I for complete results). Figure 5.1C depicts the flux changes through several important metabolic pathways under normal (V_C/V_O = 3) and drought-stressed conditions (V_C/V_O = 1).

5.3.1.1 Calvin cycle

Despite the large differences in CO_2 uptake between normal and drought-stressed photorespiration, the Calvin cycle did not exhibit any appreciable differences in terms of fluxes (Fig. 5.1C). In either case, it was driven by the supply of 3-PGA and CO_2 from cytosol to plastid through triose phosphate/phosphate translocator, and subsequently withdrawn in the form of dihydroxyacetone phosphate (DHAP) through a similar phosphate translocator, back to cytosol (Fig. 5.1B). The remaining DHAP in cytosol was utilised in two routes: (1) carbon storage via sucrose synthesis, and (2) energy production and biomass synthesis via cytosolic glycolysis and TCA cycle, in agreement with earlier reports (Weber, 2007). The bifurcation of DHAP between carbon storage and energy production was regulated by fructose 1,6-bisphosphate, which is recognised as a check point for the conversion of DHAP into sucrose or starch under dark conditions by a marked increase in its concentrations (Stitt, 1987).

5.3.1.2 Photorespiratory pathway

The flux analysis also successfully simulated the utilization of photorespiratory cycle from RuBisCO oxygenase to glycerate kinase, recycling the 2-PG back to 3-PGA (Fig. 5.1B). A sharp increase in fluxes along these pathways was observed with increasing levels of drought-stress (Fig. 5.1C). Such enormous increase in the fluxes within photorespiratory pathways release large amounts of ammonia in the mitochondria during the glycine oxidation via glycine decarboxylase (GDC) and SHM1. Even though this excess ammonia can be recovered within mitochondria via glutamate dehydrogenase, the

glutamine synthetase - glutamine oxoglutarate aminotransferase (GS-GOGAT) cycle in plastids is utilised with the help of malate transporters to maintain the redox balance of plastids (Atkin and Macherel, 2009); the excessive amounts of NADPH generated from photosynthetic light reactions in plastids under drought conditions also need to be recycled.

5.3.1.3 TCA cycle and oxidative phosphorylation

Unlike seed-derived rice cells, the model simulation observed a truncated TCA cycle operation between malate and OAA via malate dehydrogenase (MDH) during photorespiration (Fig. 5.1B), mainly to recycle the redox cofactors (Hanning and Heldt, 1993). Under such conditions, the redox cofactors generated from photosynthesis light reactions cannot be utilised in plastid due to the reduction in Calvin cycle fluxes. Thus, the cofactors are exported out of cytosol in the form of DHAP and glutamate, so that they can be further transmitted to mitochondrion via malate transporters for eventual utilization in oxidative phosphorylation. As photorespiration increased, the flux through MDH decreased accordingly since the glycine oxidation predominantly supplies the required redox cofactors to mitochondrial respiration (Fig. 5.1C). On the other hand, interestingly, the flux through oxidative phosphorylation did not change much with increasing levels of photorespiration, and indicated a sharp increase in the ratio of respiration-to-photosynthesis (R/P). This R/P ratio is a common denominator for analysing the magnitude of negative impact caused by photorespiration (Atkin and Macherel, 2009); it is important for plants to ensure a balance between respiration and photosynthesis so that the carbon balance can be maintained. Furthermore, this result complements the experimental observations by Flexas et al., 2005, highlighting that respiration cannot be impaired during drought stress albeit the differences in magnitude of fluxes. The simulation results also indicated that the ATP generated from respiration, i.e., oxidative phosphorylation, was exported to the plastids through ATP/ADP translocator to feed the photorespiratory pathways, GS-GOGAT cycle and the Calvin cycle. Such behaviour is essential to maintain the cellular haemostasis as the amounts of ATP generated from reduced photosynthesis under drought conditions are not sufficient (Keck and Boyer, 1974). In addition, the ATP transported from mitochondrion to plastid increases considerably in drought-stressed cells. Collectively, these observations on TCA cycle and

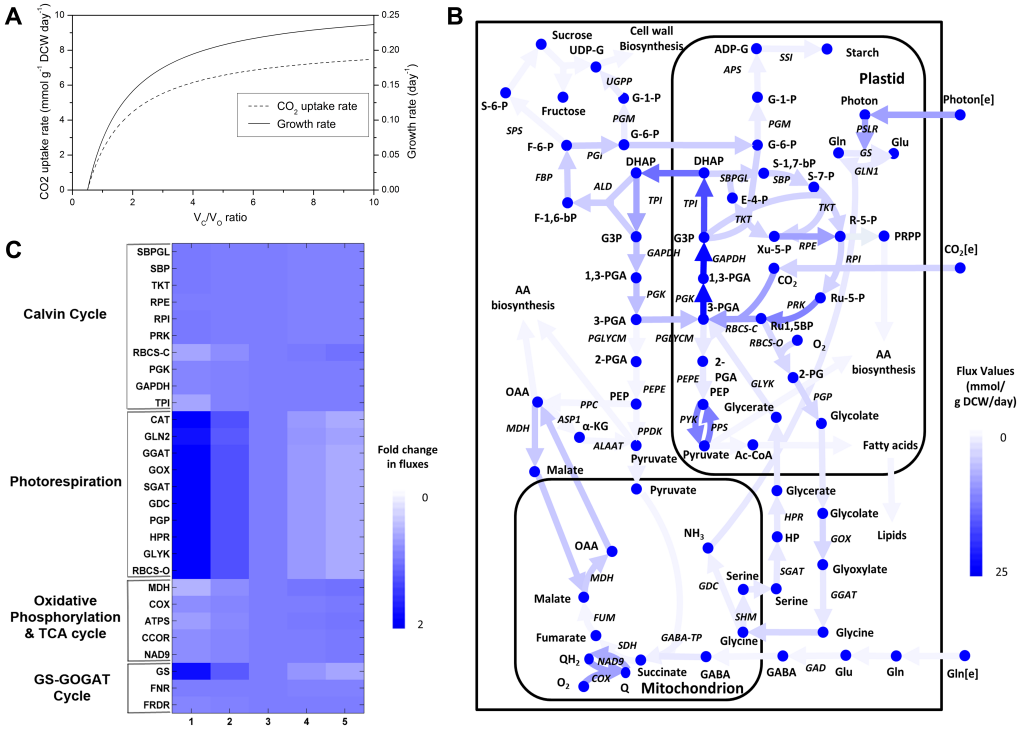


Figure 5.1: The effect of carboxylation-to-oxygenation ratio of RuBisCO on leaf cellular growth and CO_2 uptake while absorbing equal amounts of photon (A). Flux-map of the central metabolism in photorespiring leaves under normal conditions (V_C/V_O=3). The variation in fluxes through key enzymes upon varying levels of V_C/V_O (C). The colour intensity of the lines in the central carbon metabolic network figure B corresponds to the flux values obtained from simulations. Figure C is drawn by normalizing the flux values with respect to V_C/V_O=3. Metabolite abbreviations are as follows: α-KG, α-ketoglutarate; 1,3-PGA, 1,3-diphosphoglycerate; 2-PG, 2-phosphoglycololate; 2-PGA, 2-phosphoglycerate; 3-PGA, 3-phosphoglycerate; Ac-CoA, acetyl-coenzyme A; ADP-G, ADP-glucose; DHAP, dihydroxyacetone phosphate; E-4-P, D-erythrose-4-phosphate; F-1,6-bP, fructose-1,6-bisphosphate; F-6-P, fructose-6-phosphate; G-1-P, glucose-1-phosphate; G3P, glyceraldehyde-3-phosphate; G-6-P, glucose-6-phosphate; GABA, γ-aminobutyrate; Gln, glutamine; Glu – glutamate; HP, hydroxypyruvate; OAA, oxaloacetate; PEP, phosphophenolpyruvate; PRPP- phosphoribosyl pyrophosphate; Q, ubiquinone; QH2, ubiquinol; S-6-P, sucrose-6-phosphate; R-5-P, ribose-5-phosphate; Ru-1,5-bP, ribulose-1,5-bisphosphate; Ru-5-P, ribulose-5-phosphate; S-1,7-bP, sedoheptulose-1,7-bisphosphate; S-7-P, sedoheptulose-7-phosphate; Xu-5-P, xylulose-5-phosphate; UDP-G, UDP-glucose. Enzyme abbreviations are as follows: ACO, aconitase; ALAAT, alanine aminotransferase; ALD, aldolase; APS, glucose-1-phosphate adenylyltransferase; ASP1, aspartate aminotransferase; COX, cytochrome C oxidase; CSY, citrate synthase; FBP, fructose-bisphosphatase; FK, fructokinase; FUM, fumarase; GABA-TK, γ-aminobutyrate aminotransferase; GAD, glutamate decarboxylase; GAPDH, glyceraldehyde phosphate dehydrogenase; GDC, glycine decarboxylase; GGAT, glycine aminotransferase; GLYK, glycerate kinase; GLN1, glutamate-ammonia ligase; GOX, glycolate oxidase; GS, Glutamate synthase (ferredoxin-dependent); HPR, hydroxypyruvate reductase; MDH, malate dehydrogenase; NAD9, NADH dehydrogenase; PEPE, phosphoenolpyruvate enolase; PFK, phosphofructokinase; PGI, glucose-6-phosphate isomerase; PGK, phosphoglycerate kinase; PGLYCM, phosphoglucomutase; PGM, phosphoglucomutase; PGP, phosphoglycolate phosphatase; PPC, phosphoenolpyruvate carboxylase; PPDK, pyruvate orthophosphate dikinase; PPS, pyruvate-water dikinase; PRK, phosphoribulokinase; PSLR, photosynthetic light reaction; PYK, pyruvate kinase; RBCS-C, ribulose-1,5-bisphosphate carboxylase; RBCS-O, ribulose-1,5-bisphosphate oxygenase; RPE, ribose-5-phosphate epimerase; SBP, sedoheptulose-bisphosphatase; SBPGL, sedoheptulose 1,7-bisphosphate D-glyceraldehyde-3-phosphate-lyase; SDH, succinate dehydrogenase; SGAT, serine-glyoxylate aminotransferase; SHM, serine hydroxymethyltransferase; SPS, sucrose phosphate synthase; SPP, sucrose phosphatase; SSADH, succinic semialdehyde dehydrogenase; SSI, starch synthase; SUS, sucrose synthase; TKT, transketolase; TPI, triose phosphate isomerase; UGPP, UDP-Glucose pyrophosphorylase.

oxidative phosphorylation suggest that they are essential for producing energy rather than providing carbon skeletons for biomass synthesis under drought-stressed conditions.

5.3.2 Identification of essential genes in rice photorespiration

Both normal (V_C/V_O=3) and stressed (V_C/V_O=1) conditions during the rice photorespiration were simulated to evaluate the gene essentiality for cell growth by resorting to constraints-based flux analysis (see Methods). The results revealed about 60% of the reactions in the model are non-essential under both conditions while 25% were completely essential and distributed across various pathways of rice central metabolism as illustrated in figure 5.2. Most of the essential genes were identified in photosynthetic pathways such as photorespiratory cycle (10 genes) and Calvin cycle (7 genes), indicating the rigidity of CO_2 fixing mechanism in plants. Generally, these observations are in good agreement with the existing experimental evidences available on other plants such as Arabidopsis, pea, barley and maize (Table 5.1). The first enzyme of the photorespiratory pathway, phosphoglycolate phosphatase (PGLP) metabolise the toxic 2-PG which accumulates as a result of ribulose-1,5-bisphosphate (RuBP) oxygenase activity. If this 2-PG is not scavenged, it will inhibit the key glycolytic enzyme, triose phosphate isomerase (TPI), and thus eliminates photosynthesis even under ambient air (Somerville and Ogren, 1979). Likewise, other photorespiratory enzymes such as glycolate oxidase (GOX) and SGAT are also essential under both normal and stressed conditions for degrading the toxic metabolites, glycolate and glyoxylate, respectively (Wingler *et al*, 2000; Zelitch *et al*, 2009). Interestingly, serine hydroxymethyltransferase (mitochondrial) (SHM1: EC. 2.1.2.1), on the other hand, was found to be essential only under dry and hot condition, which is highly consistent with the experiments by Voll *et al* (2006), who reported the conditional viability of the SHM1 mutant of Arabidopsis thaliana. In order to further verify the results in rice, such predicted genes on Calvin cycle, photorespiratory pathway and GS-GOGAT cycle were compared with the essential genes of Arabidopsis and maize (Wang *et al*, 2012). Again, most of essential enzymes are common across all three plants, except PGLP with supporting experiments for current prediction (Somerville and Ogren, 1979).

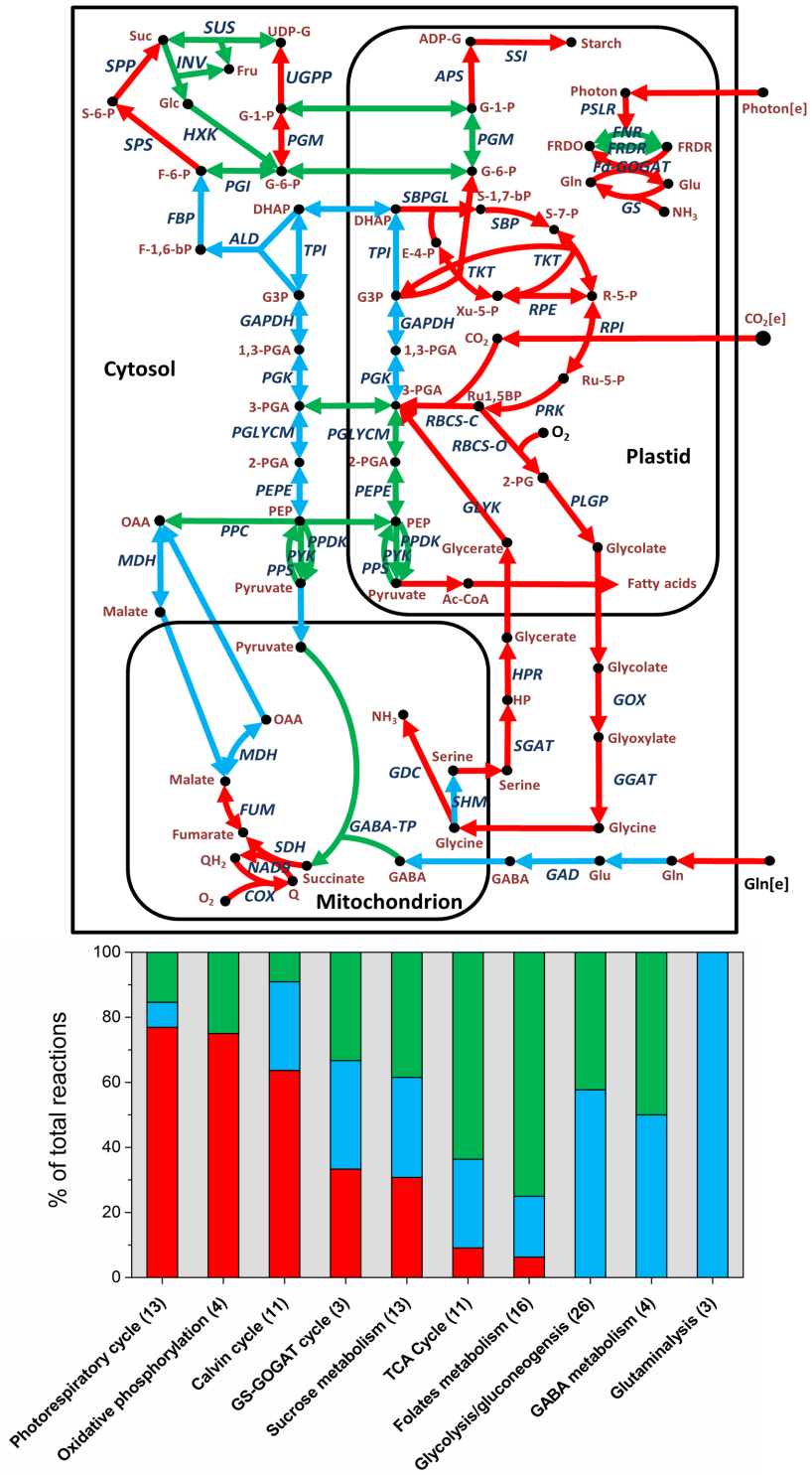


Figure 5.2: Distribution of the essential genes across rice central metabolism in photorespiring rice leaf cells. All the reactions corresponding to a certain E. C. number were deleted and the growth was maximised in both normal (V_C/V_O=3) and stressed (V_C/V_O=1) conditions. The genes were classified as essential – no growth (green); sub essential– reduced growth rate (blue) and non-essential (green) based on the extent at which its deletion influences the growth upon deletion of the gene.

Table 5.1: Comparison of essential genes/reactions in rice, Arabidopsis and maize during photorespiration

Enzyme	EC number	Pathway	Rice (C3)	Arabidopsis (C3)	Maize (C4)	Experimental studies
			(This study)	Wang *et al* (2012)		
RuBisCO	4.1.1.39	Calvin cycle	✓	✓	✓	Sicher and Bunce (1997)
PRK	2.7.1.19	Calvin cycle	✓	✓	✓	Moll and Levine (1970)
RPE	5.3.1.6	Calvin cycle	✓	✓	✓	
RPI	5.1.3.1	Calvin cycle	✓	✓	✓	
TKT	2.2.1.1	Calvin cycle	✓	✓	✓	
SBPase	3.1.3.37	Calvin cycle	✓	NA	NA	Liu *et al* (2012)
PLGP	3.1.3.18	Photorespiratory cycle	✓	X	X	Somerville and Ogren (1979)
SHM	2.1.2.1	Photorespiratory cycle	✓*	NA	NA	Voll *et al* (2006)
GLYK	2.7.1.31	Photorespiratory cycle	✓	NA	NA	Boldt *et al* (2005)
GDC		Photorespiratory cycle	✓	NA	NA	Wingler *et al* (1997)
Catalase	1.11.1.6	Photorespiratory cycle	✓	NA	NA	
GAL	6.3.1.2	Photorespiratory cycle	✓	NA	NA	
SGAT	2.6.1.45	Photorespiratory cycle	✓	NA	NA	Wingler *et al* (1999)
GOX	1.1.3.15	Photorespiratory cycle	✓	✓	✓	Zelitch *et al* (2009)
GS	4.2.1.2	GS-GOGAT cycle	✓	NA	NA	Blackwell *et al* (1987)
Fd-GOGAT	3.1.3.24	GS-GOGAT cycle	✓	NA	NA	Somerville and Ogren (1980)
GLBE	2.4.1.18	Starch biosynthesis	✓	✓	✓	
PPC	4.1.1.31		X	X	NA	

✓– essential gene; X – non-essential gene; NA – essentiality not reported/investigated; * - essential only under drought conditions

In addition to essential metabolic genes, the dispensability of inter-compartmental metabolite transporters was also analysed since the mechanism of photorespiration is quite intricate, involving three major organelles, chloroplast, mitochondria and peroxisomes. In this regard, a number of essential inter-compartmental transporters including mitochondrial and plastidic malate/fumarate/succinate redox shuttles was identified in both conditions. Malate transporters play an essential role in transmitting the excess

redox cofactors from plastid to mitochondria for their eventual utilization in oxidative phosphorylation while plastidic glycolate/glycerate transporter (PLGG) was reported as the core photorespiratory transporter (Pick *et al*, 2013). Additionally, a few unique mitochondrial transporters such as serine translocator, alpha-ketoglutarate/malate and glutamate/malate redox shuttles were identified to be essential only under stressed conditions, emphasizing their crucial roles in transporting the high fluxes of photorespiratory intermediates such as glycolate, glycerate, glutamate, oxoglutarate, glycine, and serine (Reumann and Weber, 2006)(see Appendix N for the entire list of essential transporters). From current analysis, it is evident that most of the photorespiratory enzymes including PGLP, GOX and SGAT are required for degrading the toxic metabolites and synthesizing signalling metabolites such as H_2O_2 and glutathione (Wingler *et al*, 1997). Therefore, in order to control photorespiration, attenuating photorespiratory fluxes by improving CO_2 concentration around RuBisCO is better than eliminating the entire pathway.

5.3.3 SL screening of non-essential gene pairs in rice photorespiration

Besides identifying essential genes/reactions, the synthetic lethal (SL) gene pairs of rice central metabolism were also screened under normal and stressed conditions to better characterise the functional interaction between the non-essential genes (see Methods). Note that SLs are pair of non-essential genes whose simultaneous removal can lead to zero growth (Suthers *et al*, 2009). Such lethality arises due to several reasons including interchangeable gene products with respect to an essential function (isozymes/isoforms), their existence in the same essential pathway or sharing of complementary essential function(s) (Suthers *et al*, 2009). Here, it should be noted that the inter-compartmental transporters were excluded during SL screening since the deletion of most of the transporters coupled with metabolic genes resulted in no growth. A total of 226 and 229 SLs were identified in the normal and stressed conditions, respectively. Interestingly, of the total 226 SLs the ferredoxin-$NADP^+$ reductase (FNR) in GS-GOGAT cycle, and the mitochondrial ATP synthase (ATPS) in oxidative phosphorylation were paired with 83 and 82 other genes of rice central metabolism, respectively. FNR is involved in reassimilating the ammonia released during photorespiration via Fd-GOGAT and maintaining the redox balance of plastids (Foyer *et al*, 2009) whereas ATPS is utilised to generate

necessary energy for the cell growth via mitochondrial respiration. Several SLs also contained the isoforms of same enzymes across different compartments. Such examples include the cytosolic and plastidic isoforms of enolase, phosphoglycerate kinase, glyceraldehyde-3-phosphate dehydrogenase and triosephosphate isomerase, and the cytosolic and mitochondrial isoforms of malate dehydrogenase (see Appendix N for the entire list of SLs).

5.3.4 Summary

In this chapter, the cellular metabolism of rice during drought stress was analysed. The flux analysis elucidated the crucial role of plastid-cytosol and mitochondrion-cytosol malate transporters in recycling the ammonia liberated during photorespiration and in exporting the excess redox cofactors, respectively. The model simulations also unravelled the essential role of mitochondrial respiration during drought stress. The gene deletion analysis identified a number of essential genes for the cell growth across various functional pathways such as photorespiratory cycle, Calvin cycle, GS-GOGAT cycle and sucrose metabolism as well as certain inter-compartmental transporters, which are mostly in good agreement with previous experiments. SL screening was also performed to identify the pair of non-essential genes whose simultaneous deletion become lethal, revealing the existence of more than 220 pairs of SLs on rice central metabolism. Overall, the gene deletion and synthetic lethal analyses highlighted the rigid nature of rice photosynthetic pathways and characterised functional interactions between central metabolic genes respectively. However, it also should be noted that gene essentiality results are condition-specific and sensitive to the model completeness. Therefore, the list of essential genes presented in the current study should be further confirmed with enhanced model predictability and subsequent experimental validations.

Chapter 6

Genome-scale reconstruction and analysis of rice metabolism[1]

6.1 Introduction

The previous chapters utilised the rice central metabolic/regulatory model to simulate rice metabolism under flooding and drought stresses. Although this model characterised the rice cellular behaviour under both the stresses, still, it is insufficient to analyse the global effects in rice. As mentioned earlier, the secondary metabolism of plants is crucial to sense various environmental signals and regulate various growth morphological process. For example, gibberallins, auxins, abscisic acid and brassinosteroids are known as growth regulators. Terpenoids such as carotenoids are associated with the photosynthetic machinery. Phenolic compounds such as flavonoids and anthocyanins play an important role in reproductive processes. Therefore, in order to understand the rice metabolism in a more detailed manner, it is imperative to expand the current model into the genome-scale model. Accordingly, the current chapter will first detail the procedure of reconstructing the genome-scale model. Then, it discusses the characteristics of resulting model and compares the *in silico* model predictions with literature data and rice suspension culture experiments.

[1]Excerpts of this chapter, in part, is a reprint of manuscript in preparation, Lakshmanan et al. (2014) Unravelling the light-specific metabolic and regulatory signatures of rice through combined *in silico* modeling and "-omics" analysis.

6.2 Methods

6.2.1 Metabolic network reconstruction

The genome-scale metabolic network of rice (*Oryza sativa* L. ssp. japonica (cv. *Nippon-bare*)) was reconstructed by expanding the previously published central model using the genome annotation (Goff *et al*, 2002) and the information collected from various biological and genomic databases on the basis of the established procedure. First, an initial draft consensus model was constructed by compiling the annotated metabolic genes and their corresponding biochemical reactions from RiceCyc (Dharmawardhana *et al*, 2013) and KEGG (Kanehisa and Goto, 2000). Subsequently, each reaction in the draft network was corrected for reaction directionalities based on information from BRENDA (Schomburg *et al*, 2002) and MetaCyc (Caspi *et al*, 2008), elemental and charge balanced, and mapped with appropriate genes to devise proper gene-protein-reaction (GPR) relationships. Charge balancing was done for each reaction based on their chemical formula and charge using the corresponding pKa value for a pH of 7.2. Next, each pathway in the draft network was manually curated using available literature sources for establishing the presence of particular enzymes and associated reactions in rice. Accordingly, the reactions which did not have sufficient literature evidence were removed from the metabolic network. Additionally, few rice-specific reactions such as oryzanol and oryzalaexin biosynthesis from published articles as the draft network did not contain these pathways. Literature sources were again used to localise the individual reactions in draft network to appropriate subcellular compartments. If the subcellular localizations of certain reactions are not available in published articles, then, the Plant-mPLoc (Chou and Shen, 2010) localization prediction software was used to predict putative cellular compartment. Once each reaction in the draft network was assigned to a certain subcellular compartment, the intracellular metabolite transport reactions were then added based on the evidences found in literature and TransportDB database (Ren *et al*, 2004). The connectivity of the draft network was then checked using the GapFind algorithm to find the gaps (Kumar *et al*, 2007). The identified missing links were filled either by adding reactions from other plants to close the knowledge gaps or by addition of sink reactions to allow the material exchange between the cell and its surrounding environment. Here, it should be noted that, new reactions were added during gap-filling only if sufficient

literature evidence was available to substantiate the presence of the enzymes or else left the gap unclosed. Further, in order to confirm the presence of added reactions in rice metabolic network, a BLASTp search in NCBI database was also performed for the enzymes added during gap-filling using their amino acid sequences collected from various other organisms against the non-redundant protein sequences of *Oryza sativa* L. ssp. japonica (cv. Nipponbare) genome. Finally, apart from the manual quality control steps for network connectivity, modelling-based gap-filling was also performed using constraints-based flux analysis, adding few reactions essential for *in silico* growth.

6.2.2 modelling of light utilizing metabolic reactions

The light utilizing metabolic reactions are modelled in a wavelength specific manner using a method described earlier (Chang *et al*, 2011) with slight modifications. In this method, first the photosynthetically active light spectrum, i.e. 400-700 nm, was divided into 15 parts each denoting a cumulative region. For example, the first part denoted by 410 nm covers the region 400-420 nm, the second part denoted by 430 nm covers 420-440nm and so on. Such breakdown of active spectrum allows us to accurately model the effective range of photon wavelengths capable of driving the associated reaction in rice network. Next, the prism reactions denoting the photon content equivalent of input light source was next reconstructed based on the method suggested by previous publication. It involves digitization of light intensity data for each light source and the integration of are under the curve in above mention 15 parts of the photosynthetically active light spectrum. Such reactions denote the distribution of available photons in any of the 15 parts of light spectra. Mathematically, it can be represented as follows:

$$\begin{aligned}
&\text{PhotonVis} \rightarrow \mathrm{C}^{420}_{400}\text{photon410} + \mathrm{C}^{440}_{420}\text{photon430} + \mathrm{C}^{460}_{440}\text{photon450} + \mathrm{C}^{480}_{460}\text{photon470} \\
&+\mathrm{C}^{500}_{480}\text{photon490} + \mathrm{C}^{520}_{500}\text{photon510} + \mathrm{C}^{540}_{520}\text{photon530} + \mathrm{C}^{560}_{540}\text{photon550} \\
&+\mathrm{C}^{580}_{560}\text{photon570} + \mathrm{C}^{600}_{580}\text{photon590} + \mathrm{C}^{620}_{600}\text{photon610} + \mathrm{C}^{640}_{620}\text{photon630} \\
&+\mathrm{C}^{660}_{640}\text{photon650} + \mathrm{C}^{680}_{660}\text{photon670} + \mathrm{C}^{700}_{680}\text{photon690}
\end{aligned}$$

where C is the coefficient of photon available in that particular range is calculated by integration of total area under the curve as described previously (Chang *et al*, 2011). Once the prism reactions are modelled, the “photon absorbance reactions” were then

drafted to provide the actual metabolic reaction with usable photons. This was done by analysing the absorbance spectrum of the metabolic reactions which involve photons, i.e. photosystem I and II, and calculated the amount of incident photons are absorbed. For example, the photon absorbance reaction at 410 nm for PSI can be written as follows:

$$\text{photon410} \rightarrow \text{xphotonPSI} + (1 - \text{x})\text{photonDrain}$$

where x is the ratio of incident photon absorbed by PSI at 410 nm. In such a way, the PSI and PSII were modelled. It should be noted that the protochlorophyllide oxidoreductase reaction was modelled in a slightly different manner as no absorbance spectra was available for the same. To model the protochlorophyllide oxidoreductase reaction, the action spectra, which denote the maximum activity of the corresponding enzyme throughout the visible spectra, was utilised. Accordingly, the reaction was written for all 15 regions between 400 and 700 nm with photon specific to that region and the activity at each level was multiplied with the whole reaction, reflecting the possible differences in reaction conversion across wavelengths.

6.2.3 Biomass composition

The two biomass equations, one representing the germinating cells of rice seeds and the other representing the photo-respiring cells of rice leaves, used in constraints-based flux analysis simulations is adopted from the central model with slight modifications by accounting for nucleotides and fatty acids composition. Lipid and fatty acid compositions were obtained from previous publications (Brown and Beevers, 1987). The overall DNA and RNA composition was also obtained from literature. The individual weights of nucleotides in the DNA and RNA were calculated based on the reported G+C content of 69.4% (Goff *et al*, 2002). Detailed information on biomass composition calculations could be found in Appendix O.

6.2.4 Constraints-based flux analysis

In this study, constraints-based flux analysis was utilised to simulate the rice metabolism under varying environmental conditions by manipulating the constraints. The biomass equation was maximised to obtain the optimal solution of the metabolic network as

detailed in chapter 2 (Section 2.2.4.1, Problem P1). In this study, the constraints-based flux analysis problems were solved using COBRA toolbox (Schellenberger *et al*, 2011).

In order to simulate the seed-derived rice cells growth on either sucrose or glucose, the regulatory constraints and proteome data were applied to the network using the Boolean rules as described previously. The carbon source uptake rate was constrained at the experimentally measured values. Additionally, for the aerobic simulations, the oxygen exchange reaction was constrained at 3.312 mmol g^{-1} DCW day^{-1} based on literature (Wen and Zhong, 1995). To simulate the photorespiring rice leaf cells growth, a similar procedure was followed by first constraining the fluxes of dark reactions to zero using Boolean regulatory rules. Subsequently, the leaf cell growth was simulated by maximizing the leaf biomass while constraining the photon uptake at 100 mmol g^{-1} DCW day^{-1}. Further, to simulate the photorespiratory behavior at different carboxylation to oxygenation ratios (V_C/V_O), the ratio of flux through RuBisCO was varied between between one and ten as described previously in chapter 3 (See Section 3.2.4).

6.3 Results and discussion

6.3.1 Reconstruction of rice genome-scale model

The genome-scale metabolic network of rice cells was reconstructed by expanding the previously reconstructed central model. It involved three key steps: (a) compilation of metabolic genes and related reactions from RiceCyc, PlantCyc, KEGG, TransportDB, in-house metabolome data and literature, (b) manual curation of metabolic reactions by verifying elemental balances, reaction directionalities, developing gene-protein-reaction (GPR) mappings and assigning proper subcellular compartments, and (c) dead-end identification and manual network gap-filling based on literature sources (see Materials and methods for details). The final reconstructed genome-scale metabolic network of rice, *i*OS2164, accounts for 2164 unique genes, 2284 reactions and 2001 metabolites localised across seven intracellular compartments: cytosol, plastid, mitochondrion, peroxisome, endoplasmic reticulum, vacuole and thylakoid (Fig. 6.1). The detailed list of completely curated *i*OS2164 metabolic network containing the various genes, reactions, and metabolites can be obtained from Appendix P.

During the reconstruction process, significant efforts were required in the gap-filling

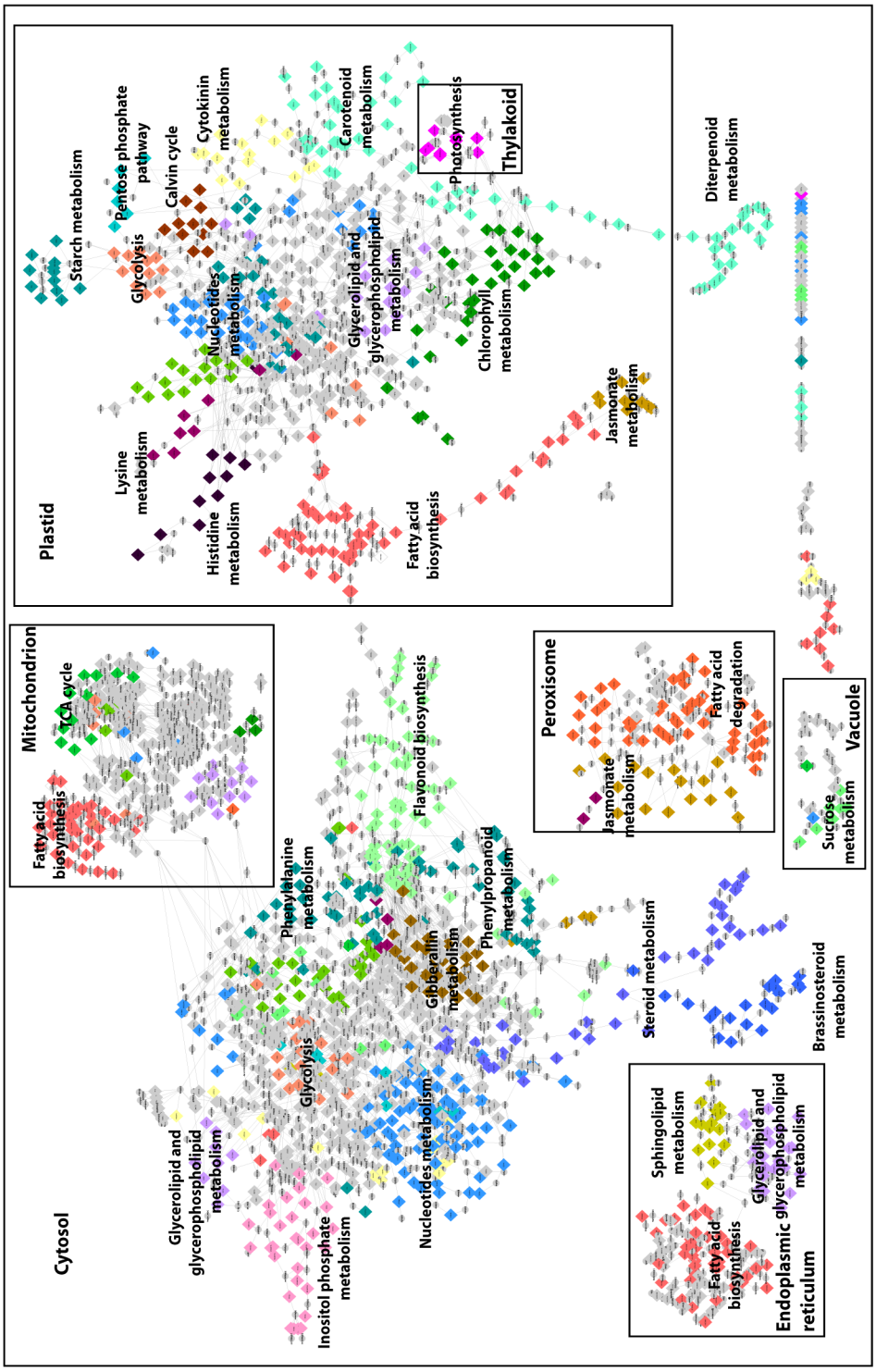


Figure 6.1: Compartmentalised network diagram of *i*OS2164 showing the distribution of major metabolic pathways across different cellular compartments.

process. A large number of gaps were identified in the draft reconstruction and were subsequently filled in the final model. In order to fill the gaps in a systematic manner, the identified gaps were classified into either knowledge or scope gaps. Knowledge gaps arise because of the limited knowledge of any particular pathway in the metabolic network whereas the scope gaps exist mainly due to the scope of reconstruction procedure, although its synthetic and consumption routes are known (Orth *et al*, 2011). In order to resolve these network gaps, several new reactions were added based on the information obtained from literature or inferred by the genome annotation of other organisms. Likewise, 145 new reactions were added, improving the network connectivity significantly. Additionally, sequence-based homology searches was performed to find genetic evidence for the newly added enzymes and identified putative locus for 15 of them. It should be noted that despite these efforts, the final reconstructed rice genome-scale model still has 10% of its metabolites as blocked under all conditions due to gaps, and thus highlights the further need of experiments to resolve these gaps.

6.3.2 Network characteristics of *i*OS2164

*i*OS2164 is a comprehensive representation of rice metabolism as it accounts for 2164 genes, 2284 reactions and 2001 metabolites classified into 59 major metabolic subsystems (Fig. 6.2A). Notably, it accounts for all the possible electron transport reactions in mitochondrion, plastid and thylakoid with curated stoichiometry obtained from literature and pathway database. The plastidic electron transport chain contains eight separate reactions: five represent the light-driven photophosphorylation reactions, including photosystem II (PS II), photosystem I (PS I), Z-scheme based electron transfer between the two photosystems, cyclic electron transfer around PS I, and Mehler's reaction for dissipating excess O_2; two represent the non-light specific oxidative phosphorylation reactions, which are NADH dehydrognease and plastidic terminal oxidase; and the last one represent the ATP synthase. Figure 6.2B provides the schematic illustration of both light-driven and non-light driven electron transport chain in thylakoid and plastid. Moreover, the light driven photophosphorylation reactions are modelled in a wavelength specific manner such that the model can predict the relative photosynthetic efficiency at all possible wavelengths in the visible spectra. Photosynthesis at various wavelengths in the visible spectrum is modeled using the approach proposed by Chang *et al* (2011)

in *Chlamydomonas reinhardtii* model, (*i*RC1080), with appropriate modifications to the photon absorbing metabolic reactions. In *i*RC1080, the photon absorbing metabolic reactions such as photosystem I (PSI), photosystem II (PSII) and protochlorophyllide oxidoreductase consider only the photons in the red and blue range based on the peak absorption pattern, and thus cannot simulate cellular growth appropriately in lights which does not fall in blue or red regions such as green and yellow. Further, it also assumes that all the photons present in these two peak regions are absorbed completely by corresponding metabolic reactions. However, the absorption spectra of both photosystems show light absorption do occur at all wavelengths in visible spectrum with maximum but not 100% absorption in blue and red regions. Therefore, in order to reflect this scenario exactly, in *i*OS2164, a new set of reactions called "photon absorbance reactions" were added between the prism reaction and actual photon utilizing metabolic reaction which filters the available photon from incident photons based on the absorbtivity data (see Materials and Methods for details).

Apart from the accurate modelling of electron transport reactions, another significant achievement of *i*OS2164 is the detailed coverage of fatty acid metabolism, lipid metabolism and intracellular transport of metabolites. In plants, de novo fatty acid synthesis is known to occur in both plastid and mitochondrion. However, most of the current plant models have assumed it to be completely synthesised in plastid due to the lack of information on mitochondrial pathways. In this regard, the fatty acid biosynthesis and degradation reactions has been modelled in appropriate subcellular compartments based on literature references in *i*OS2164. Similarly, the lipid biosynthetic pathways were modelled in plastid, mitochondrion and endoplasmic reticulum, based on existing literature sources (Li-Beisson *et al*, 2013). For modelling transport reactions, we once again leveraged on literature sources to replicate their exact translocation mechanisms in *i*OS2164. Accordingly, several intracellular transport reactions including the amino acid and nucleotides transport (Linka and Weber, 2009), malate shuttles between plastid/cytosol and mitochondrion/cytosol (Taniguchi and Miyake, 2012), ATP/ADP translocators between plastid/cytosol and mitochondrion/cytosol (Taniguchi and Miyake, 2012), triose phosphate transporters between plastid and cytosol (Taniguchi and Miyake, 2012; Linka and Weber, 2009), dicarboxylate transport between cytosol/mitochondrion (Picault *et al*, 2004), and fatty acid transport between plastid-cytosol-peroxisome are modelled

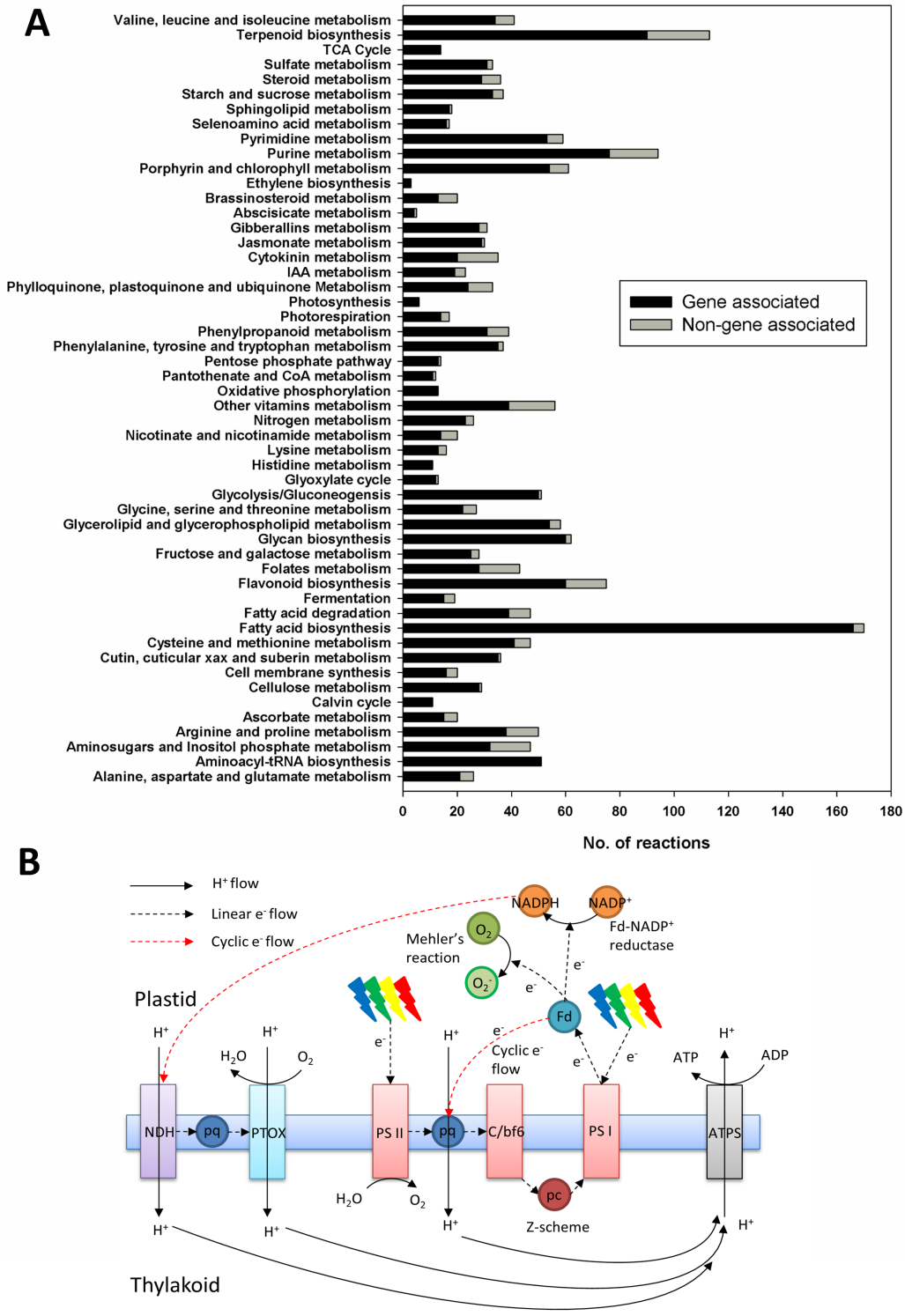
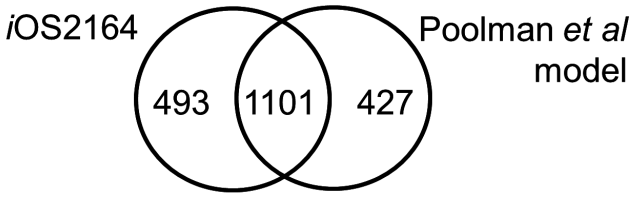


Figure 6.2: Network characteristics of *i*OS2164. (A) Reaction distribution across various pathways. (B) Schematic illustration of plastidic/thylakoidal membrane electron transport chain. Abbreviations are as follows: C/bf6 - cytochrome b6f complex, Fd - ferredoxin, NDH - NAD(P)H dehydrogenase, pc - plastocyanin, pq - plastoquinone, PTOX – plastid terminal oxidase, PS I - photosystem I and PS II - photosystem II.

based on known transport mechanisms (Li-Beisson *et al*, 2013).

6.3.3 Comparison of *i*OS2164 with previously published large-scale rice model



Properties	*i*OS2164	Poolman *et al* model
No. of ORFs included	**2164**	**NA**
Reactions	**2283**	**1735**
Metabolic reactions	**1900**	**1667**
Cytoplasmic	884	1620
Plastidic	545	28
Mitochondrial	242	15
Peroxisomal	84	0
Endoplasmic reticular	118	0
Vacuolar	18	0
Thylakoid Lumenal	9	0
Unique metabolic reactions	**1594**	**1528**
Transport reactions	**349**	**68**
Cytoplasm to Extracellular	41	45
Cytoplasm to plastid	111	14
Cytoplasm to mitochondrion	93	9
Cytoplasm to ER	47	0
Cytoplasm to peroxisome	43	0
Cytoplasm to vacuole	14	0
Spectral decomposition reactions	**34**	**NA**
Gene-reaction associations	**1707**	**NA**
Metabolic reactions	1629	NA
Transport reactions	78	NA
Metabolites	**2001**	**1535**
Unique metabolites	1310	1452

Figure 6.3: Comparison of *i*OS2164 with previous rice genome-scale model. The numbers in Venn diagram represent the number of unique metabolic reactions.

Figure 6.3 presents the comparison of *i*OS2164 and the previously published large-scale rice model (Poolman *et al*, 2013). From the comparison, it was found that *i*OS2164 to be a superior model in several aspects. First, *i*OS2164 is a fully compartmentalised model as all the metabolic reactions are appropriately assigned to any of the six subcellular compartments: cytosol, plastid, mitochondrion, peroxisome, endoplasmic reticulum, vacuole and thylakoid. It should be noted that a large number of reactions were present in more than one subcellular compartments (approx. 8% of total reactions) in *i*OS2164,

highlighting the importance of subcellular localization in plant GSMN. Reactions of glycolysis, pentose phosphate pathway, fatty acid metabolism and amino acid metabolism are the few examples of such multi-compartment reactions. Secondly, *i*OS2164 includes photosynthetic electron transport reactions including the photophosphorylation in a wavelength-specific manner as mentioned earlier. Thirdly, *i*OS2164 is more accurate in terms of metabolic pathway coverage and network connectivity than the earlier model. This can be well exemplified by the comparison of *i*OS2164 with the previously published model. Interestingly, the comparison revealed a large number of reactions unique to each of the model despite the fact, both models represent rice metabolism. A closer examination of these unique reactions shows that the previous model has lot of generic metabolic reactions from RiceCyc such as menthol synthesis, reticuline biosynthesis and methanogenesis which does not exist in rice. On the other hand, most of the unique reactions in *i*OS2164 were largely literature-based rice-specific reactions such as oryzanol synthesis, flavonoid synthesis and oryzalexin synthesis, highlighting the differences in quality between both the models.

6.3.4 Model validation

Following the reconstruction of *i*OS2164, several tests were performed to validate its predictive ability. First, the model was tested by simulating known metabolic functions including the biosynthesis and degradation of amino acids and secondary metabolites such as terpenoids and alkaloids. Second, the model predictions were validated using the batch cultures of rice cells (data presented in Chapter 3, section 3.3.3.1) growing on various sucrose and glucose under aerobic and anaerobic conditions (Fig. 6.4A). Third, the cell growth in photorespiring leaves were simulated at various carboxylation-to-oxygenation flux ratio (V_C/V_O) of RuBisCO, representing the intensity of photorespiration. The simulation results indicated a significant reduction in the CO_2 uptake rates and leaf growth rates at high photoprespiration, i.e. at low V_C/V_O ratios, and eventually reached zero at the compensation point (V_C/V_O =0.5) (Fig. 6.4B), agreeing well with the earlier theoretical calculations (Heldt and Piechulla, 2011). Finally, the ability of model to simulate the relative photosynthetic efficiency at all possible wavelengths in the visible spectra was also tested. The simulation results highlighted that the model indeed can predict such characteristics within acceptable error range, i.e. <25%

(Fig. 6.4C).

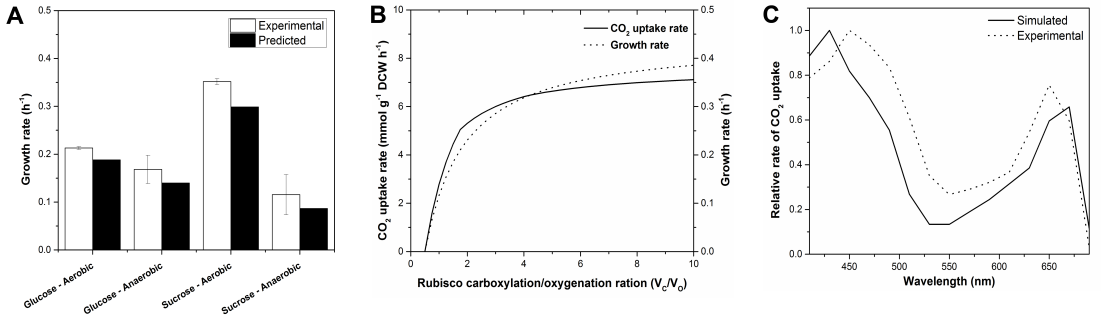


Figure 6.4: Validation of *i*OS2158 predictions. (A) Comparison between *in silico* and experimental growth of germinating seed cells. (B) CO_2 uptake and leaf growth rate at varying levels of photorespiration. (C) Comparison of simulated and experimental action spectrum (Bowsher *et al*, 2008).

6.4 Summary

In this study, a completely curated, high-quality, compartmentalised genome-scale metabolic model of rice cells, *i*OS2164, was reconstructed. The reconstructed model accounts for 2164 unique genes, 2284 reactions and 2001 unique metabolites localised across seven intracellular compartments: cytosol, plastid, mitochondrion, peroxisome, endoplasmic reticulum, vacuole and thylakoid. Notably, the light-driven photophosphorylation reactions in *i*OS2164 are modelled in a wavelength specific manner such that it can simulate the relative efficiency of photosynthesis based on light quality. The phenotypic behaviour and metabolic states simulated by the model are highly consistent with the suspension culture experiments as well as previous reports.

Chapter 7

Combined analysis of light-specific changes in rice metabolism and transcription using *i*OS2164 and "-omics" data[1]

7.1 Introduction

Light is the primary energy source as well as a key signalling element for plant growth and development. Although both light quantity (fluence) and quality (wavelength) are important for plant life, the latter is a crucial environmental indicator for plants to modulate their growth and morphological processes such as seed germination, stem elongation, phototropism, chloroplast development, shade avoidance, circadian rhythms and flowering induction (Neff *et al*, 2000). Since the discovery of red light stimulated seed germination in lettuce (Borthwick *et al*, 1952), several studies have been focussed on investigating the influence of individual light quality on plant growth and development. Earlier studies in this regard utilised the classical genetic and molecular approaches such as the use of light-signalling deficient mutants, measurement of enzyme activities and enzyme/metabolite levels of certain pathway(s). However, since the transitions of light quality perception and the orchestration of signalling cascades are likely to affect several metabolic effectors at almost all levels of cellular hierarchy, these studies are not sufficient to understand the overall changes. Therefore, to address this limitation, plant

[1]Excerpts of this chapter, in part, is a reprint of manuscript in preparation, Lakshmanan et al. (2014) Unravelling the light-specific metabolic and regulatory signatures of rice through combined *in silico* modeling and "-omics" analysis.

biologists in the modern genomic era have adopted the multiple "-omics" technologies such as transcriptomics (Wang *et al*, 2001; Tepperman *et al*, 2001), proteomics (Kim *et al*, 2006), and metabolomics (Jänkänpää *et al*, 2012)(Jung *et al*, 2013) for analysing the light controlled cellular processes in plants at a global level. Of several "-omics" techniques, genome-wide transcript profiling has been most widely applied in plants, mainly in Arabidopsis (Wang *et al*, 2001; Tepperman *et al*, 2001; Ma *et al*, 2001) and rice (Jiao *et al*, 2005), and have highlighted several noticeable traits including massive reprogramming of gene expression between photomorphogenesis and skotomorphogenesis, i.e. plant growth in the presence and absence of light, coordinated regulation of gene expression among several cellular pathways on different lights and significant differences among light-regulated gene expression across various organelles.

Concurrent to the development of highthroughput experimental techniques, the advances in genomic technologies have also enabled the development of large-scale computational models and related simulation methods for analysing the cellular behaviour at the systems level (Price *et al*, 2003; Lee *et al*, 2005b). In this regard, constraints-based *in silico* metabolic modelling and analysis is one of the well established techniques to elucidate the physiological behaviour and metabolic states of an organism upon various environmental/genetic changes as they systematically capture the genotype-phenotype relationships from the genome annotation, biochemical and cell physiological data (Lewis *et al*, 2012). As a result, several constraints-based models are developed at the genome-scale for a wide range of microbes and mammals (Kim *et al*, 2012b), and for few plants such as Arabidopsis (Poolman *et al*, 2009; de Oliveira Dal'Molin *et al*, 2010a; Mintz-Oron *et al*, 2012), maize (Saha *et al*, 2011) and rice (Poolman *et al*, 2013). Moreover, most importantly, these models are also utilised in contextualizing multiple "-omics" data through several integrative analysis, and thus providing novel biological insights at the systems-level (Shlomi *et al*, 2008; Selvarasu *et al*, 2012; Becker and Palsson, 2008). Among them, noticeably, the combined *in silico* analysis of human metabolic model and highthroughput data have been successfully exploited for characterizing the key metabolic and regulatory features of several diseases (Zelezniak *et al*, 2010; Hu *et al*, 2013; Mardinoglu *et al*, 2013, 2014). Similarly, it is now possible to combine the *in silico* metabolic models of plants with omics data for better understanding the effect of light quality on plant growth and development.

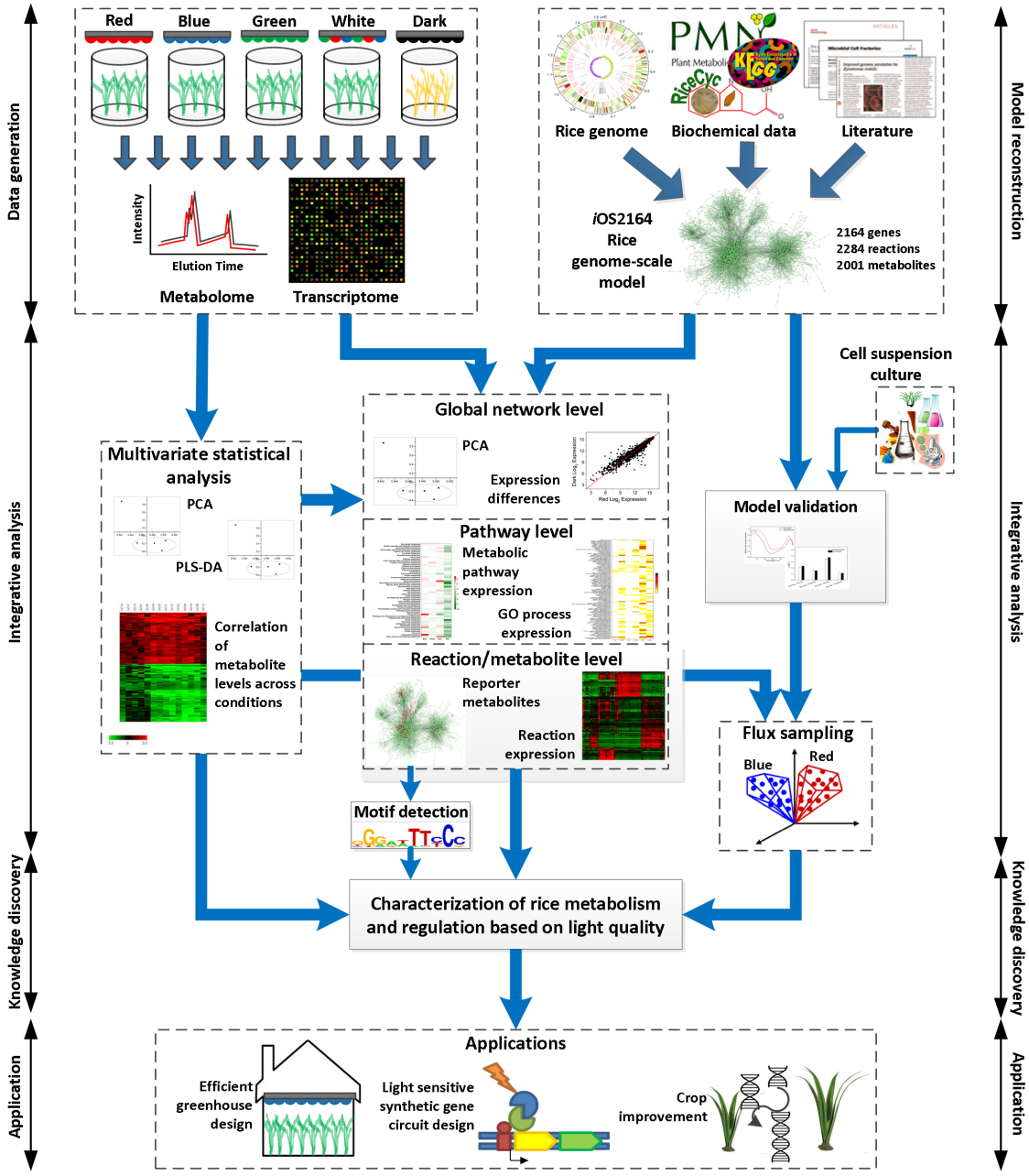


Figure 7.1: Schematic illustration of combined framework involving *in silico* modelling and "-omics" data analysis. Rice plants were grown in 5 different light treatments and the metabolome and transcriptome was profiled. Concurrently, the rice genome-scale metabolic model was reconstructed based on genome annotation, biochemical data and literature sources. Subsequently, the model and transcriptome data was utilised in the integrative analysis. The key light-specific regulatory and metabolic signatures identified from this study are further expected to be used in several potential applications.

The overall approach of the current study is illustrated in Figure 7.1. The gene expression of rice plants grown under different LED light illumination and in dark were first profiled. Subsequently, the reconstructed metabolic model was integrated with gene expression data to characterise the behavioural differences in rice plants grown under different light colours and in dark at several levels of cellular hierarchy: global network-level, individual pathway-level and at the level of individual reactions and metabolites. Further, by analysing the key putative cis-acting regulatory elements (CREs) of certain differentially expressed genes, the potential transcription factors (TFs) that are sensitive to specific light qualities were also identified. Collectively, the knowledge obtained from such large-scale integrative analysis has numerous potential basic and applied uses: (a) development of appropriate crop productive environment in greenhouses, (b) engineering of relevant light signal transduction pathways to improve agronomic traits of food crops, (c) design of synthetic gene circuits using light-sensitive transcription factors and (d) postulation of metabolic engineering strategies for improving the synthesis of secondary metabolites such terpenoids and phenolics.

7.2 Methods

7.2.1 Plant materials and growth conditions

Oryza sativa japonica rice cultivar 'Ilmi' were used in this study. Seed sterilization and stratification treatment was performed as previously described. The sterilised seeds were then inoculated on Murashige and Skoog (MS) medium solidified with 0.2% agar. Rice seedlings was cultivated for 7 days in an LED Chamber System (SJ I&C Co. Ltd., Korea) under a single LED light for 16-h photoperiod per day and at a temperature of 25±2 ^{0}C. The rice plants were grown in LED chambers with 3 W LED devices (Osram, Munich, Germany) under five different conditions: blue (B, 450 nm), green (G, 530 nm), red (R, 660 nm), and white (W, mixture of blue, green, and red lights), and dark (D, no light treatment). The photosynthetic photon flux (PPF) at the top of plants was 94 µmol m^{-2} s^{-1} in all light such that the photon fluence rate was distributed differently in the four conditions, the B condition with 100% blue light, R condition with 100% red light, G condition with 100% green light, W condition with equal amounts of each red, green, and blue light.

7.2.2 RNA isolation and labelling of probes

Total RNA was extracted from the aerial parts of rice plants using the Qiagen RNeasy Plant Mini Prep kit. For the synthesis of double strand cDNAs, RevertAidTM H Minus First Strand cDNA Synthesis Kit (Fermentas, Lithuania) was used. Briefly, 1 ml of oligo dT primer(100 µM) and 10 µl (10 µg) of total RNA were combined and denatured at 70 ^{0}C for 5 minutes and renatured by cooling the mixture in ice. First strand DNA was synthesised by adding 4 µl of 5X First Strand Buffer, 1µl RiboLockTM Ribonuclease Inhibitor, 2µl of 10mM dNTP mix and 1 µl of RevertAidTM H Minus M-MuLV Reverse Tranase enzyme and by incubating at 42 ^{0}C for 1 hour. The reaction was stopped by heating at 70 ^{0}C for 10min. To synthesise the second strand, 66.7µl of nuclease free water, 5µl of 10X reaction buffer for DNA Polymerase I (Fermentas, Lithuania), 5µl of 10X T4 DNA ligase buffer (Takara, Japan), 3µl of 10U/ul DNA Polymersase I (Fermentas, Lithuania), 0.2ml of 5U/ul Ribonuclease H (Fermentas, Lithuania) and 0.1ml of 350U/ul T4 DNA ligase (Takara, Japan) were added to the first strand reaction mixture and the reaction was proceeded at 15 ^{0}C for two hours. The double stranded cDNA mixture was purified using MinElute Reaction Cleanup Kit (QIAGEN, U.S.A.). For the synthesis of Cy3-labeled target DNA fragments, 1 mg of double strand cDNA was mixed with 30ml (1OD) of Cy3-9mer primers (Sigma-Aldrich, U.S.A.) and denatured by heating at 98 ^{0}C for 10 min. The reaction was further proceeded by adding 10µl of 50X dNTP mix (10mM each), 8µl of deionised water, 2µl of Klenow fragment (50 U/ml, Takara, Japan) and incubating at 37 ^{0}C for 2 hours. DNA was precipitated by centrifugation at 12,000 x g force after adding 11.5µl of 5M NaCl and adding 110µl of isopropanol. Precipitated samples were rehydrated with 13µl of water. To assess the reproducibility of the microarray analysis, the experiments were repeated three times with independently prepared RNA.

7.2.3 Microarray hybridisation, washing and scanning

Ten milligrams of DNA was used for microarray hybridization. The collected samples was mixed with 19.5 µl of 2X hybridization buffer (Nimblegen, U.S.A.) and finalised to 39 µl with deionised water. Hybridization was performed with MAUI chamber (Biomicro, U.S.A.) at 42 ^{0}C for 16-18 hours. After the hybridization, the microarray was washed

thrice and dried in a centrifuge for 1 minute at 500g. Hybridized microarray slides were scanned using GenePix scanner 4000B (Axon, U.S.A.) preset with a 5 um resolution and for Cy3 signal. Scanned signals were then digitized and analysed by Nimblescan (Nimblegen, U.S.A.). The grid was aligned to the image with a chip design file, NDF file. The alignment was checked by ensuring that the grid's corners are overlaid on the images corners. This was further checked by uniformity scores in the program. The analysis was performed in a two-part process. First pair reports (.pair) files were generated in which sequence, probe, and signal intensity information for Cy3 channel were collected. Data-based background subtraction using a local background estimator was performed to improve fold change estimates on arrays with high background signal. The data were normalized and processed with cubic spline normalization using quantiles to adjust signal variations between chips (Workman *et al*, 2002). A probe-level summarization by Robust Multi-Chip Analysis (RMA) using a median polish algorithm implemented in NimbleScan was used to produce call files in order to improve the sensitivity and reproducibility of microarray results (Irizarry *et al*, 2003). Here, it should be noted that these microarray experiments were conducted by Dr. Sun-Hwa Ha and her research team at the National Academy of Agricultural Science, Rural Development Administration, Republic of Korea.

7.2.4 Measurement of carotenoid contents

Carotenoids were extracted and measured using HPLC, as described previously (Kim *et al*, 2012a). Briefly, the carotenoids were extracted from rice samples (0.12 g) by adding 3 mL ethanol containing 0.1% ascorbic acid (w/v), vortex mixing for 20 s and placing in a water bath at 85 ^{0}C for 5 min. The carotenoid extract was saponified with potassium hydroxide (120 µL, 80% w/v) in a water bath at 85 ^{0}C for 10 min. After saponification, the samples were immediately placed on ice, and cold deionized water (1.5 mL) was added. To separate the layers, carotenoids were extracted twice with hexane (1.5 mL) by centrifugation at 1,200 x g. Aliquots of the extracts were dried under a stream of nitrogen and redissolved in 50:50 (v/v) dichloromethane/methanol before HPLC analysis. The carotenoids were then separated in a C30 YMC column (250 × 4.6 mm, 3 µm; YMC Co., Kyoto, Japan) by an Agilent 1100 HPLC instrument (Massy, France) equipped with a photodiode array detector. Chromatograms were generated

at 450 nm. Solvent A consisted of methanol/water (92:8 v/v) with 10 mM ammonium acetate; solvent B consisted of 100% methyl tert-butyl ether. Gradient elution was performed at 1 mL/min under the following conditions: 0 min, 90% A/10% B; 20 min, 83% A/17% B; 29 min, 75% A/25% B; 35 min, 30% A/70% B; 40 min, 30% A/70% B; 42 min, 25% A/75% B; 45 min, 90% A/10% B; and 55 min, 90% A/10% B. Carotenoid standards were purchased from CaroteNature (Lupsingen, Switzerland). Calibration curves were drawn for quantification by plotting four concentrations of the carotenoid standards.

7.2.5 Measurement of total phenolic contents

The phenols in rice leaf were extracted by the ultrasound-assisted method (Kim *et al*, 2004). The powdered samples (0.1 g) were extracted twice with 80% methanol (2 mL) by water-based sonication for 20 min which were filled with nitrogen gas to provide an oxygen-free environment. Supernatants were collected by centrifuging at 13,000 x g for 20 min at 4^0C and diluted to a final volume of 4 mL with distilled water (DW). The crude extracts were filtered using 0.45 mm poly tetrafluoroethylene (PTFE). The total phenolic contents of rice leaf extracts were determined by spectrophotometric method using Folin-Ciocalteu's phenol reagent (Singleton and Rossi, 1965) with some minor modifications. Diluted extracts (0.2 mL) were mixed with 2.6 mL DW and a reagent blank using 2.8 mL DW was prepared. Folin-Ciocalteu reagent (0.2 mL) was added to the mixtures. After 6 min, 2 mL of 7% Na_2CO_3 solution was added and the mixtures were allowed to stand for 1 h at 23^0C. The absorbance was read against the prepared blank at 750 nm. Total phenolic concentrations expressed as micrograms of gallic acid equivalents (GAE) / mg of rice leaf.

7.2.6 Analysis of differentially expressed genes

Differentially expressed genes between any two conditions, i.e. B-W, R-W, D-W and G-W, was identified using limma package in R computing environment, which is based on a modified t-statistic (Wettenhall and Smyth, 2004). Subsequently, the p-values were adjusted for multiple hypotheses testing using Benjamini and Hochberg's method (Benjamini and Hochberg, 1995) and the False Discovery Rate (FDR) was controlled at 5%.

7.2.7 Analysis of differentially expressed metabolic pathways

In order to analyse the differential expression of individual metabolic pathways in *i*OS2164, first the genes from microarray data was mapped with the rice model. A total of 1915 genes from *i*OS2164 were mapped with gene expression data spanning across various pathways. Subsequently, the differential expression of metabolic pathways was estimated using the method previously described (Hu *et al*, 2013). Briefly, the expression change of each gene in a particular light treatment relative to the W was first estimated as follows:

$$\Delta E_a^i = \log_2 x_a^i - \log_2 y_a^W \tag{7.1}$$

where x_a^i is the expression of gene a in i light treatment other than W, i.e. R, G, B or D, y_a^W and is the expression of corresponding gene in W. Next, the Wilcoxon signed-rank test of ΔE_a^i for all genes within a metabolic pathway in i light treatment was calculated to determine the significance of up or downregulation of the particular pathway in comparison with W.

7.2.8 Identification of reporter metabolites

The reporter metabolites in D, W, R and B light treatments were identified based on previous publication (Patil and Nielsen, 2005). Briefly, each metabolite in the *i*OS2164 was scored based on the p-values of neighbouring differentially expressed enzyme. For this purpose, first each enzyme in *i*OS2164 was assigned with a p-value based on the corresponding genes differential expression. In case of isozymes or enzyme complexes, the lowest p-value of the isozyme or enzyme subunit was utilised. Then, the p-values are converted into Z-scores for each enzyme i using inverse normal cumulative distribution (CDF) as follows:

$$Z_i = \theta^{-1}(1 - p_i) \tag{7.2}$$

Once each enzyme is Z-scored, then, the Z-score for each metabolite ($Z_{metabolite}$) in *i*OS2164 was calculated using the aggregated Z-scores of k neighbouring enzymes as follows:

$$Z_{metabolite} = \frac{1}{\sqrt{k}} \sum Z_i \tag{7.3}$$

The metabolite Z-scores are corrected for background distribution by subtracting mean (μ_k) and dividing by standard deviation (σ_k) from the original Z-score, $Z_{metabolite}$.

$$Z^{corrected}_{metabolite} = \left(\frac{Z_{metabolite} - \mu_k}{\sigma_k} \right) \tag{7.4}$$

Finally, the corrected Z-scores are transformed into p-values using normal CDF and metabolites with p-value less than 0.05 are classified as reporter metabolites.

7.2.9 Motif detection and identification of putative transcription factors

The promoter sequences [-1000, +200 nt] relative to the transcription start site for the up and downregulated genes which are neighbouring to reporter metabolites were extracted from the in-house rice promoter sequence database. Known and novel promoter motifs were detected using the Dragon Motif Builder program (Huang *et al*, 2005). At each time, thirty motifs were detected with a length of 8-10 nucleotides at a threshold value of 0.875. Motifs occurrence in over 50% of the sequences and a threshold e value of $\leq 10^{-3}$ were considered as statistically overrepresented. Different motif classes were identified using several plant Transcription Factor Binding databases such as TRANSFAC (Matys *et al*, 2003), PLACE database (Higo *et al*, 1999), AGRIS (Yilmaz *et al*, 2011) and Osiris (Morris *et al*, 2008). The total enrichment score was calculated by adding up the percentage occurrences of all motifs belonging to the same TF family.

7.2.10 Random sampling

Artificial centering hit-and-run (ACHR) Monte Carlo sampling (Price *et al*, 2004b) was utilised to uniformly sample the metabolic flux solution space in different light treatments with appropriate flux constraints. In all treatments, a PPF of 200 mmol g^{-1} DCW hr^{-1} was constrained in each of the simulation and the solution space was sampled with 100,000 randomly distributed points for 10,000 iterations. It should be noted that the internal reaction were constrained in each simulation based on the corresponding transcriptome data via E-Flux approach (Colijn *et al*, 2009). In this study, COBRA

toolbox (Schellenberger *et al*, 2011) was utilised to implement the random flux sampling. Once the metabolic network is sampled in each light treatment, the differences in flux samples between any pair of conditions was quantified using a Z-score approach as described previously (Mo *et al*, 2009). First, two random flux vectors, v_j, one from each sample was chosen and the difference is calculated as follows:

$$v_{j,diff} = v_{j,blue} - v_{j,red} \tag{7.5}$$

This approach was repeated for 10,000 times to flux difference sample, $v_{j,diff}$, with 10,000 points. Subsequently, the sample mean, μ_j and standard deviation, σ_j was computed to calculate the Z-score as follows:

$$Z_j = \frac{\mu_j}{(\sigma_j/\sqrt{10000})} \tag{7.6}$$

The absolute Z-scores were then translated to p-values using normal cumulative distribution function and the reactions with p-values less than 0.05 were classified as statistically different between the two conditions analysed.

7.3 Results

7.3.1 Transcript profiling and secondary metabolites content analysis of rice plants grown under various LED light sources

To compare the effects of different light quality on plant growth and development, rice plants were grown in LED chambers under five different conditions: blue (B, 450 nm), green (G, 530 nm), red (R, 660 nm), and white (W, mixture of blue, green, and red lights), and dark (D, no light treatment) (Fig. 7.1). In each light treatment, the photosynthetic photon flux (PPF) at the top of plants was maintained at 94 µmol m^{-2} s^{-1}. The photon fluence rate was distributed differently in the four conditions such that the B condition with 100% blue light, R condition with 100% red light, G condition with 100% green light and W condition with equal amounts of each red, green, and blue light (see Materials and Methods). Interestingly, the plants grown under different lights showed diverse phenotypes: shorter plant with wider leaf blades were observed in B, pale yellow plant with long coleoptile length in D and plants with comparatively identical structure

W and G (Fig. 7.2A). Furthermore, in order to understand the possible intracellular metabolic differences which cause the phenotypic diversity, we also quantified the intracellular content of secondary metabolites such as terpenoids and phenolic compounds. The results from these analyses results suggested that the terpenoid content was highest in B and lowest in D, and thus, possibly linking it to the shorter plant phenotype in B and pale yellow colour in D. The terpenoid contents in different light followed the order B>W>G>R>D (Fig. 7.2B) and the abundance of phenolic compounds was observed in B>W>R>G>D order (Fig. 7.2B).

In order to identify the differences in gene expression patterns across different conditions, the samples from the aerial parts of rice plants were collected and the transcripts were profiled. The gene expression profiling was conducted with the Rice 3'Tiling Microarray (Roche NimbleGen, Inc.) designed from the 27,448 genes deposited at IRGSP, RAP1 database (http://rapdb.lab.nig.ac.jp). Among the 27,448 transcripts, 20,507 genes are based on the full cDNA/EST supports in RAP1 database and the remaining 6,941 genes just have the partial cDNA/EST sequences. The scanned microarray hybridization signals were digitised and analysed by Nimblescan (Nimblegen, U.S.A.). Finally, the data was manually inspected and normalised to minimise the experimental variations and eliminate noisy data before being further processed (see Materials and Methods).

7.3.2 Global analysis of metabolic gene expression

To understand the differences in global metabolic gene expression pattern across different light treatments, the transcriptome data was first integrated with *i*OS2164. A total of 1915 genes, corresponding to 1659 reactions, in *i*OS2164 could be mapped with gene expression data spanning across various pathways. The differences in global expression profiles of all the 1915 metabolic genes was then analysed by two different metrics: a) plotting the $\log_2$ expression values of any two conditions pair-wise and b) principal component analysis (PCA). Overall, the relative differences between any two conditions were consistently identified by both the methods (Fig. 7.3). The global analysis indicated that the expression pattern of D is markedly different from all other light treatments. Among the light treatments, B and R showed the most divergent expression pattern (R^2=0.9406). On the other hand, G and W showed the minimal changes in expression

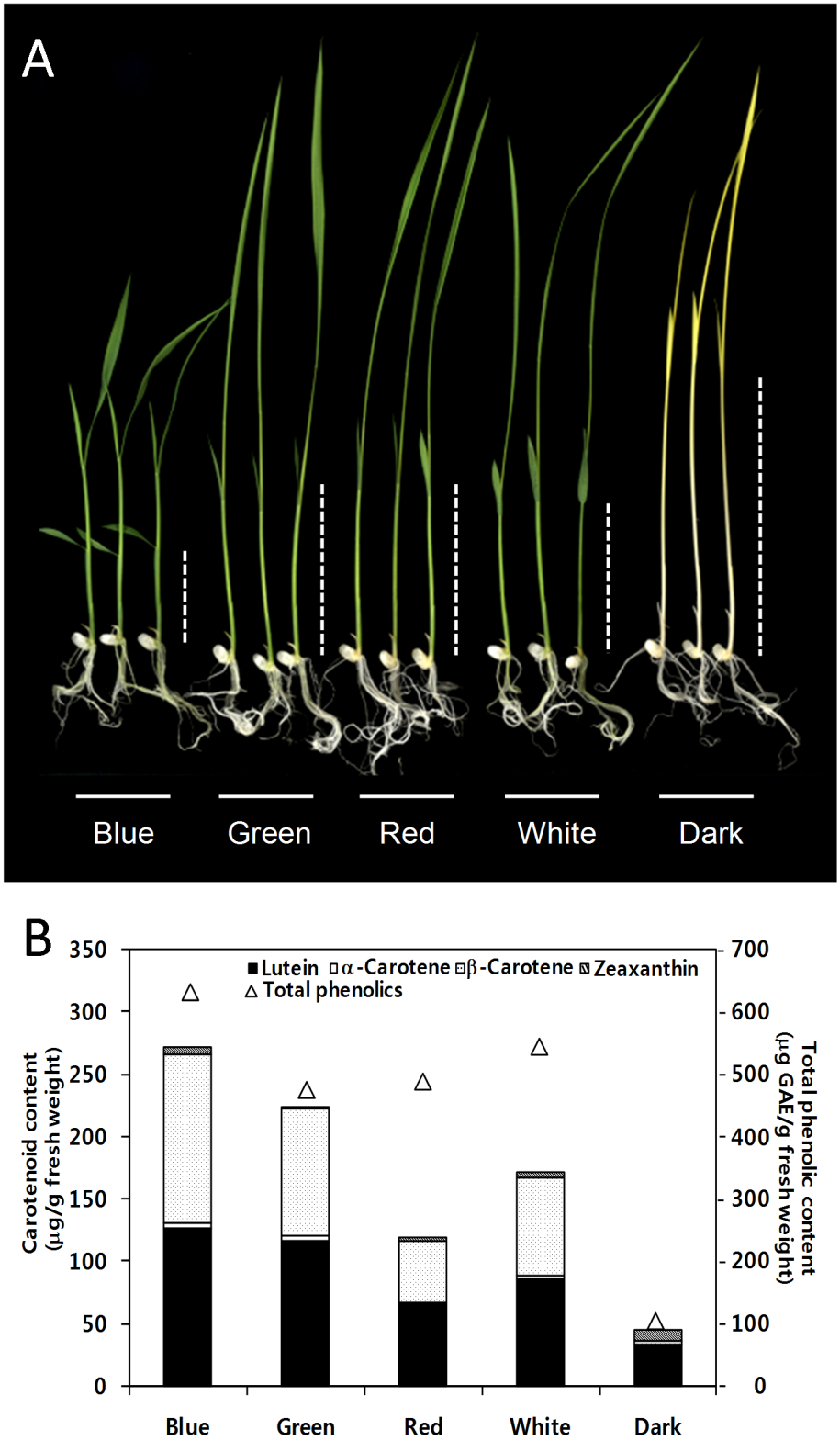


Figure 7.2: (A) Rice plants grown under different light treatments, (B) Total carotenoids and (C)Total phenolic compounds

(R^2=0.9919) between them. A closer examination of $\log_2$ expression plots (Fig. 7.3A) has further highlighted the specific patterns of up or downregulation between any two conditions. For example, in R-W comparison, most of the genes are overexpressed in W, whereas in B-R, genes are mostly underexpressed in R. Notably, the PCA of metabolome from similar experimental setup also revealed comparable groupings as identified by the PCA of metabolic gene expression data (Jung *et al*, 2013), indicating that the global transcript profile and metabolite profile are potentially correlated to each other.

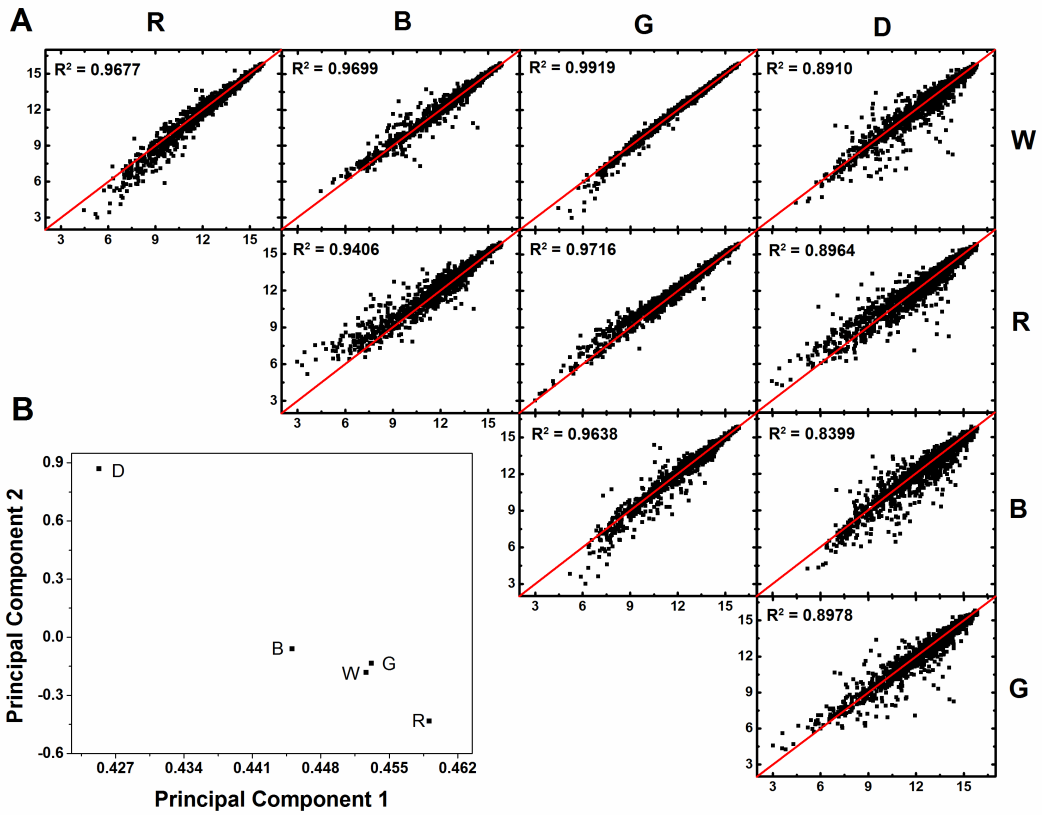


Figure 7.3: Global analysis of metabolic gene expression. (A) Pairwise comparison of $\log_2$ gene expression values between various light treatments. (B) Principal component analysis of expression values in each condition.

As mentioned earlier, since *i*OS2164 is a compartmentalised metabolic model, a compartment-wise analysis of metabolic gene expression using PCA was performed and observed unique trends of gene expression in few compartments (see Appendix Q). The expression pattern of cytosolic genes in R was clearly different from other light treatments. Similarly, the plastidic genes showed a distinct expression pattern in B when compared to other light treatments. Moreover, the endoplasmic reticulum showed the

most divergent gene expression pattern among all light treatments, suggesting that some genes in this compartment are indeed differentially expressed across all light treatments (see Appendix Q).

The overall gene expression pattern of rice transcripts including genes that are not metabolic was then analysed using PCA. These analyses once again highlighted that the expression pattern of G, B, R and W is very different from D (see Appendix Q). Among different light treatments, again, B and R had the most divergent expression pattern as it is in metabolic genes. However, the difference between W and G expression pattern is appreciable while considering all genes, revealing that most of the transcriptional changes between W and G may occur in non-metabolic genes.

7.3.3 Expression changes of individual metabolic pathways

Subsequent to the global analysis of metabolic genes, the expression changes of individual metabolic pathways in rice was analysed using *i*OS2164. The up and downregulation of each metabolic pathway in G, B, R and D treatments were examined relative to that of W. Here, it should be noted that white was used as reference since it contains most of the colours in visible spectra, i.e. R, G and B, and is the closest to plants natural energy source, i.e. sunlight. The significance of expression changes in metabolic pathways was calculated using Wilcoxon signed rank test, adjusted for multiple hypothesis testing (see Materials and Methods). The results are presented in figure 7.4A where the colour intensity denotes the statistical significance of differential expression.

The individual pathway analysis unravelled that several plastidic pathways such as photosynthesis, terpenoids biosynthesis, starch and sucrose metabolism, Calvin cycle, gibberellins metabolism and abscisicate biosynthesis are upregulated in B (Fig. 7.4A). It should be noted that the upregulation of terpenoids biosynthesis and phenylalanine, tyrosine and tryptophan metabolism are consistent with our secondary metabolites analysis which indicated a higher terpenoids and phenolic compounds synthesis in B. Similarly, the overexpression of gibberellins metabolism in B is also in good agreement with earlier report (Zhao *et al*, 2007), confirming that gibberellins homeostasis plays a key role in the inhibition of hypocotyl elongation as the plants grown in B were shorter than other conditions. In R treatment, several pathways including photosynthesis and Calvin cycle showed significant downregulation when compared to W. Again these ob-

servations are consistent with earlier experiments which showed that these pathways are upregulated in R supplemented with B rather than R only (Brown *et al*, 1995; Goins *et al*, 1997). Unlike R or B, which showed a clear up or downregulation of metabolic pathways, a mixed pattern was observed in D (Fig. 7.4A). Notably, photosynthesis is significantly downregulated whereas the amino acid metabolism, fatty acid degradation, starch and sucrose metabolism and oxidative phosphorylation were up-regulated in D, indicating that in the absence of photosynthesis, plant may degrade the available storage carbon to survive such stressful conditions as identified by previous studies (Kunz *et al*, 2009). Further, the flavonoid biosynthesis was significantly downregulated in D (Fig. 7.4A), agreeing well with earlier studies which reported the marked decrease in flavonoid accumulation under dark in Arabidopsis (Pandey *et al*, 2014).

Since the analysis of gene expression using *i*OS2164 reveals only the changes in metabolic pathways, the enrichment of differentially expressed genes for biological process Gene Ontology (BP:GO) terms were analysed using DAVID (Alvord *et al*, 2007) to get a general overview of changes in gene expression among different light treatments (see Materials and Methods for details). The results indicated a significant enrichment of carbohydrate catabolic processes (GO:0016311, GO:0044036, GO:0006022, GO:0006026, GO:0006030, GO:0006032) among the upregulated genes in D and isoprenoid biosynthetic process (GO:0008299) in B (Appendix R), which are highly consistent with earlier metabolic pathway analysis. Interestingly, the cellular process such as transcription (GO:0006350) and regulation of transcription (GO:0006355) were enriched in the downregulated genes of B, possibly suggesting that most of the phenotypic changes in B could be attributed to the differences in transcription.

7.3.4 Expression changes of individual biochemical reactions and reporter metabolites

The expression changes in individual biochemical reactions were identified using the available GPR relationships in *i*OS2164. The differential expression of each reaction under various light treatments was analysed in a pairwise manner using modified t-statistic, adjusted for multiple hypothesis testing (see Materials and Methods for details). When W is used as reference, most of the reactions in B is upregulated whereas D and R had a large number of reactions downregulated (Fig. 7.4B). Interestingly, this analysis also

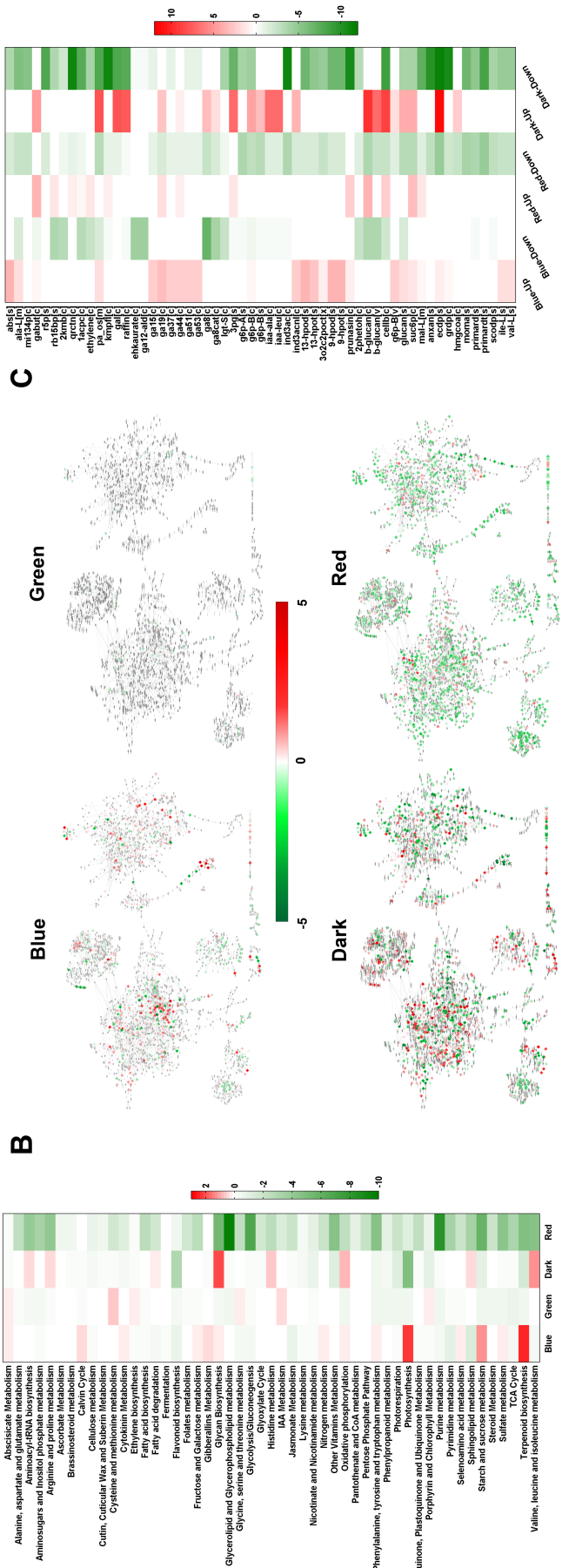


Figure 7.4: Differential expression patterns identified using *i*OS2164 in rice. (A) Expression levels of individual pathways, (B) Differential expression of individual reactions and (C) Enrichment of top 20 reporter metabolites in up and down regulated genes. The up and downregulation in each condition was identified using white colour as reference. The colour intensity in the heatmap and network diagram indicates the significance of up or downregulation and not fold change. For visualization purposes, the negative or positive logarithm of the p-value is presented.

highlighted that few reactions in R are significantly upregulated albeit the corresponding pathway showing an overall downregulation. Such examples include the 1,3-beta-glucan synthase and sucrose-phosphate synthase reactions from starch and sucrose metabolism which showed a significant upregulation despite the overall pathway is downregulated. It should be noted that although the cellulose and sucrose synthesis in R is upregulated but the corresponding catabolic pathways are more significantly downregulated, the pathway shows an overall downregulation. Collectively, these observations show the importance of analysing the gene expression data not only at the pathway level but also at individual reaction level.

With the differentially expressed reaction data, the metabolic hotspots in rice network was identified using the reporter metabolites algorithm (Patil and Nielsen, 2005) (see Materials and Methods for details). This analysis identifies the metabolites around which the most significant transcriptional changes occur from a topological point of view. The top 20 statistically significant reporter metabolites in R, B and D are provided in figure 7.4C (see Appendix S for reporter metabolite enrichment scores of all relevant metabolites). Notably, the reporter metabolite enrichment scores for G-W comparison was very large (p-value>0.2) as none of the metabolic genes were significantly differentially expressed under such conditions. Overall, the top-ranked reporter metabolites were mainly identified in terpenoids biosynthesis, gibberellin metabolism, IAA biosynthesis, amino acid metabolism and sucrose and starch metabolism. In B vs W comparison, this analysis also revealed that the most significant gene expression changes occur around phytohormones such as gibberallins, abscisate and ethylene as these metabolites are significantly enriched (Fig. 7.4C). Similarly, reporter metabolites of R vs W are mainly associated with terpenoids metabolism, IAA biosynthesis and gibberellins metabolism where most of the genes are grossly downregulated. Here, it should be noted that these observations are highly consistent with earlier reports which indicated an overall decrease in the level of auxins under R treatment (Jones *et al*, 1991). Appendix T provides the network visualization of top-ranked reporter metabolites and their neighbouring genes expression.

Next, the overlap of top ranked reporter metabolites (p-value<0.05) among different light treatments was analysed to identify the common indicators of transcriptional regulation. From this comparison, 32 metabolites were identified as mutual markers in

all three conditions (see Appendix U). Notably, most of these metabolites are from the IAA biosynthesis, jasmonate biosynthesis and gibberallins biosynthesis, indicating the key role of phytohormones in transcriptional orchestration across different light treatments. Further, a large number of metabolites were also found to be common between D-W and R-W, and just two metabolites to be shared between B-W and R-W. Interestingly, the plastidic and cytosolic glucans were the two metabolites in common between B-W and R-W, highlighting that the common transcriptional changes occur in starch and sucrose metabolism. The unique reporter metabolites of B-W was mainly from gibberellin biosynthesis and ethylene metabolism, which is consistent with earlier reports (Zhao *et al*, 2007; Vandenbussche *et al*, 2007) and the observed phenotype, i.e. shorter plants. Similarly, the identification of a large number of reporter metabolites in D-W comparison confirms the global rearrangement in cellular metabolism.

7.3.5 Motif analysis of differentially expressed metabolic reactions

The promoter regions of up and downregulated neighbouring genes of top ranked reporter metabolites (p-value<0.05) of B, R and D in comparison with W was then analysed for known transcription factor binding motifs (see Materials and Methods). Because, it has been hypothesised that these enzymes could be regulated by common transcription factors (Zelezniak *et al*, 2010). The promoter analysis revealed a number of unique motifs that are specific to upregulated genes of B, R and D, in addition to the certain common putative CREs among all of them (Table 7.1). Specifically, this analysis identified 62 and 65 unique TFs in the upregulated genes of R vs W and B vs W, where some of them were specific to both. In order to further asses the validity of our promoter analysis, we compared our results with literature evidences. These comparisons revealed that 9 and 25 TFs identified in our study are either directly or indirectly linked with the red and blue lights, respectively (see Dataset S2 for comparison results). On the other hand, we also found contradicting evidences on the light specificity of two of the TFs, highlighting the need of further experiments to confirm the exact role of such TFs.

In both B vs W and R vs W comparisons, several putative CREs of common plant TF families such as MYB, bZIP, bHLH and ZnF were enriched in the upregulated genes. More specifically, the R2R3 MYB TFs such as MYB1, MYB2, MYB5, MYB15 and MYB30 were found only in upregulated genes of R vs W (Table 7.1). Among these,

Table 7.1: List of TFs with total enrichment scores of target motifs among the upregulated and downregulated genes

TFs	Total enrichment score*					
	Upregulated			Downregulated		
	B	R	D	B	R	D
MYB	**925**	**1629**	**604**	**1233**	**1053**	**876**
MYB1		71	121	67		
MYB2, MYB5, MYB15, MYB30		86				
MYB80				91		
bZIP	**1037**	**401**	**269**	**175**	**403**	**397**
As1/ocs/TGA	337	57	196	117	197	222
ABRE	700	344	73	58	206	175
SBZ1/G/HBF-1	75					
GBF1, GBF2	75					
CPRF5,CPRF6, CPRF7	75					
HY5	131					
DPBF-1/DPBF-2	75					
ABI3	**152**	**86**	**53**	**108**		
ERF	**231**	**557**	**203**	**191**	**249**	**172**
bHLH	**225**	**229**	**126**	**292**	**116**	**50**
PIF1, PIF3, PIF4, PIF7	75					
WRKY	**56**					**62**
ZnF	**200**	**228**		**67**		**154**
ZCT1 , ZCT2 , ZCT3	56					
MBF1	**63**	**214**			**74**	**56**
ARF	**69**	**228**	**191**	**92**		**162**
DOF	**169**	**228**		**217**	**168**	
FUS3, LEC2 (ABA)	**75**	**172**	**53**	**108**	**-**	**-**
DBP	**369**	**186**	**141**	**166**	**122**	**205**
ARR-B	**56**	**71**	**121**		**68**	**125**
WOX		**86**	**53**			
BES1	**75**					
CA1	**81**			**75**		
EIL		**86**				
HD-ZIP				**83**		
BPC				**67**		
HD (WUSCHEL)				**75**		
ASIL1, S1F				**50**		
CAN	**75**					
Cysteine Protease		**71**				
GCBP-1, SP1, HSF		**100**				

*Total target motif enrichment score = sum of the % occurrences of all motifs belonging to the same TF family in the upregulated (UR) and downregulated (DR) groups of genes.

although MYB1 has shown to be having a light-specific response by earlier studies, this study has characterised that these TFs are possibly specific to R light. Promoter analysis also identified several bZIP TFs such as HY5, CPRF5, CPRF6, CPRF7, GBF1 and GBF2, and few bHLH TFs such as PIF1, PIF3, PIF4 and PIF7, only in the upregulated genes of B vs W, suggesting that these TFs are specific to B. It should be noted that these observations are highly consistent with earlier studies which had shown that these TFs are indeed B-responsive (Jiao *et al*, 2007). Motif analysis further unravelled the high enrichment of jasmonate (JA) response element-like motifs associated with JA responsive ERF TFs in D vs W, and thus highlighting that these TFs could be specific to dark-mediated transcriptional response (Table 7.1). In addition, several putative CREs associated with potential TFs were identified to be highly enriched in upregulated genes of B vs W or R vs W alone (Table 7.1).

7.3.6 Integrative analysis of rice metabolism through metabolome, transcriptome and constraints-based modelling

In order to better understand the physiological and biochemical differences among various light treatments, the changes in metabolite levels and the adjacent flux levels between B and R treatment were compared through an integrative analysis of metabolomics, transcriptomics and constraints-based modelling as these two conditions showed the marked differences in terms of transcript and metabolite levels. For this purpose, the differences in metabolites levels between the two conditions was analysed using the previously published metabolome data (Jung *et al*, 2013). Of the total 43 metabolites measured, 30 are accounted in *i*OS2164. Among which, the levels of 18 metabolites were significantly different between B and R (p-value$<$0.05). It could be observed from figure 7.5A that all the amino acids and fatty acids are higher in B whereas the sugars such as glucose, sucrose and fructose are higher in R.

Next, to unravel the possible metabolic flux distribution which could result in such diverse metabolite levels, the solution space of *i*OS2164 was sampled while simultaneously constraining the allowable fluxes through internal reactions based on transcriptome data and fixing the R and B specific spectral decomposition reactions at 196 mmol g^{-1} DCW^{-1} (Colijn *et al*, 2009). The plausible metabolic states of rice leaves under B and R treatments were sampled using artificial centering hit and run Monte Carlo sampling

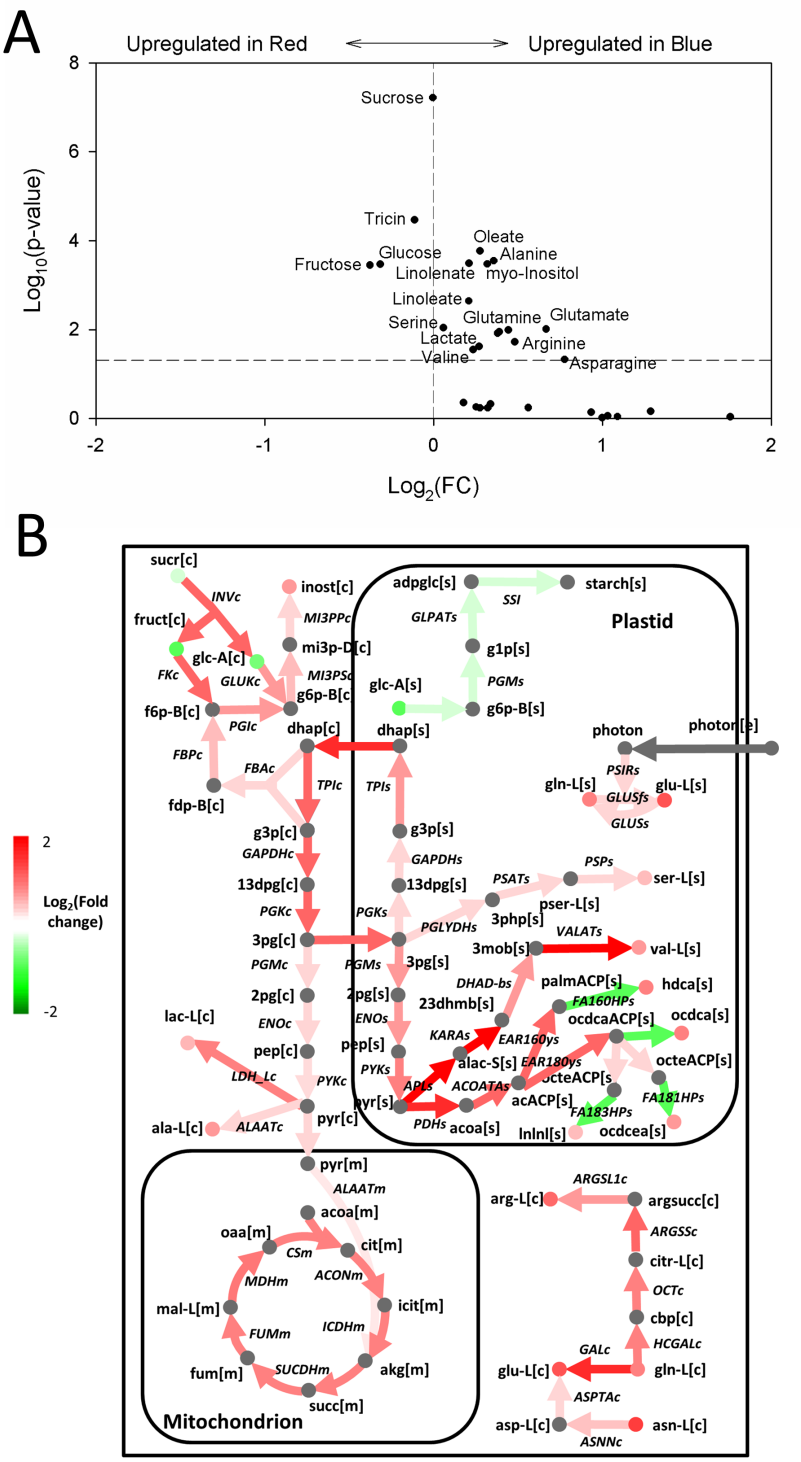


Figure 7.5: Regulatory and metabolic signatures of rice central pathways in blue when compared to red. (A) Comparison of metabolite levels in red and blue. Metabolites with a significant change ($p<0.05$) are highlighted above the dotted line. (B) The rice central metabolic map showing the fold change in metabolic fluxes obtained through random sampling and the fold change in metabolite levels. The fold changes in both metabolite levels and fluxes are calculated using red as reference.

(Price *et al*, 2004b), and the fold change between the two conditions was then estimated using the range of possible steady-state flux values which were identified via random sampling (see Materials and Methods). This analysis revealed that although the fluxes through the Calvin cycle and photosynthetic pathways do not change between B and R, the fluxes through glycolysis, TCA cycle, amino acid metabolism and fatty acid biosynthesis are significantly upregulated in B as indicated by the corresponding metabolite levels (Fig. 7.5B). On the other hand, the starch and other cell wall synthetic pathways was downregulated in B, agreeing well with the metabolome data which showed the carbohydrate levels to be slightly lower in B than R. Collectively, these observations highlight that although both B and R light are comparatively efficient for photosynthesis, B drains the fixed carbohydrates much faster than R into the amino acids and fatty acids synthesis first, and then to secondary metabolites, and thus yielding plants with wider leaf blades which photosynthesise even more efficiently.

7.4 Discussion

Till date, several studies have focussed on light signal perception and their subsequent control mechanisms in plants including large-scale transcript profiling experiments in Arabidopsis (Ma *et al*, 2001) and rice (Jiao *et al*, 2005). While these studies provided us various clues about the vast extent of light regulation on gene expression and global rearrangement of cellular metabolism, a more in-depth analysis of what pathways/enzymes/metabolites/TFs control which part of the intracellular mechanism in relation to plant growth and devolepment processes were largely missing. Such situations still exist even with the availability of abundant highthroughput data mainly because of the lack of systematic frameworks to analyse them. As such, the major contributions of the current work are not only the transcript profiling of rice plants grown under different light treatments but also the development of an integrative analysis framework combining the highthoughput data and genome-scale reconstruction at several levels of cellular hierarchy to derive new hypothesis and correlate them with observed plant phenotypes. To achieve this goal, a completely curated, high-quality, compartmentalised genome-scale metabolic model of rice cells was also reconstructed describing its metabolic organization.

As mentioned earlier, light affects plant growth and development in several ways. Accordingly, the gene expression patterns of different light treatments showed dissimilar effects across conditions. The gene expression pattern of rice under dark was markedly different from all other light treatments, an observation consistent from previous studies (Jiao *et al*, 2005), confirming light induces significant changes in gene expression. The transcriptome analysis of B vs W further indicated an up and downregulation of gibberellin metabolism and ethylene metabolism, respectively, providing insights about the rice cellular metabolism responsible for the observed plant phenotype, i.e. shorter with wider leaf blades. It is known that the accumulation of inactive gibberellin affects hypocotyl elongation negatively whereas ethylene regulates it positively (Vandenbussche *et al*, 2007; Zhao *et al*, 2007). Therefore, it is evident that the increased gibberellin metabolism and decreased ethylene biosynthesis are accountable for the reduced stem length under B. Moreover, the gene expression analysis also indicated that B favour terpenoids and phenolic compounds synthesis than other light qualities as most of the genes in these pathways were significantly upregulated under B. The secondary metabolite content analysis of rice leaves have further confirmed that B indeed have the highest carotenoid and phenolic compounds. Plants grown under D were pale yellow, indicating that they are devoid of chlorophylls in their leaves. Coincide with these observations, the gene expression analysis indicated the downregulation of several secondary metabolite pathways including chlorophyll metabolism. On the other hand, amino acid metabolism, fatty acid degradation, starch and sucrose metabolism and oxidative phosphorylation were up-regulated in D, suggesting that in the absence of photosynthesis, plant may degrade the available storage carbon to survive such stressful conditions as shown by previous studies (Kunz *et al*, 2009). Finally, the G treatment did not show any appreciable differences in both phenotype and gene expression when compared to W. Interestingly, these observations are quite different from earlier perceptions about G light which is mainly considered as a negative effector of plant growth that antogonises the effects of R and B light (Folta and Maruhnich, 2007). However, few other studies have showed that G light may also has positive effects on plant growth, particularly in hypocotyl elongation and stem growth (Folta, 2004). These diverse observations could be possibly due to the differences in cultivation conditions such as wavelength and photon fluence rates or may be even specific to certain plants. Therefore, further studies

focussing on minute morphological differences are required to substantiate the role of green light in rice growth and development.

In the current study, the promoter regions of differentially expressed genes which are neighbouring to top-ranked reporter metabolites ($p<0.05$) was also analysed. Overall, this analysis revealed several light quality specific TFs. Notably, this analysis confirmed the blue light responsiveness of the bZIP proteins, especially HY5. Several reports have earlier identified that HY5 responds positively to both B and R light through a specific interaction with the G-box motif having the pattern CACGTG and mediates the light control of gene expressions (Chattopadhyay *et al*, 1998). Besides HY5, numerous other group G type bZIP TFs were also identified as B specific, where some of them such as GBF1, GBF2, CPRF5, CPRF6 and CPRF7 have been shown to be involved in ultraviolet and blue light signal transduction in parsley and Arabidopsis by binding specific to the G-box of the light-responsive promoters (Schindler *et al*, 1992; Kircher *et al*, 1998). The promoter analysis indicated a high enrichment of ABRE-like motifs associated with bZIP TFs in response to B. ABRE-binding bZIP TFs are shown to positively modulate the light harvesting complex B (LHCB) expression by repressing the WRKY40 transcription, which other ways will repress LHCB (Liu *et al*, 2013). Accordingly, the gene expression analysis also suggested an upregulation of abscisate biosynthesis in B and thus, it could possibly play a similar role in rice leaves. The motif enrichment patterns asscoiated with TF bHLH family suggests that this family of TFs could be specific to both B and R light treatment which is consistent with earlier reports (Jiao *et al*, 2007; Casal *et al*, 2005). Finally, it should be noted that the promoter analysis also indicated several ZnF and WRKY TFs to be B responsive (Table 7.1). Among which, the WRKY TFs are known to play a critical role in secondary metabolites accumulation (Li *et al*, 2013; Suttipanta *et al*, 2011). In this regard, as mentioned earlier the blue light showed a significantly higher secondary metabolite contents than other colours. Collectively, these observations suggest that WRKY and ZnF TFs could play a critical role in blue light mediated secondary metabolite synthesis.

In this study, the transcriptome data was integrated with genome-scale constraints-based model of rice, providing mechanistic insights into the behavioural differences under various light treatments. When compared to the previous work involving the genome-wide transcript profiling of rice plants (Jiao *et al*, 2005), the current work represent

a significant expansion both in terms of analysis technique and knowledge discovered. The earlier work utilised classical statistical methods for analysing gene expression data and had largely reported the transcriptional differences between light and dark albeit profiling the transcripts at various light qualities. In this regard, the current work reports not only the functional differences between light and dark but also across various light qualities, thus deepening current knowledge on how different light qualities, either independently or cooperatively, orchestrate plant morphogenesis. The insights gained from such analysis could possibly help engineer plants to improve their agronomic traits by modulating their light perception pathways. Moreover, the promoter analysis of reporter metabolites neighbouring differentially expressed genes have revealed several new potential blue-, red- and common light-specifc TFs in addition to the well established ones. The identification of such new light-specific TFs provides us unprecedented oppurtunities in the emerging field of optogenetics; several light-sensitive synthetic circuits utilizing light-specific TFs have been successfully constructed and applied in microbial and mammalian systems including biomedical processes (Bacchus *et al*, 2013). The use of light-specific TFs in synthetic circuits, particularly in mammalian systems, are preferred for a myriad of reasons: precise, spatiotemporally controllable and no potential pharmacologic side effects. In this regard, some of the light-specific TF families identified in this study such as DOF, bZIP, bHLH and MYB are known to exist even in mammalian species. Therefore, it will be interesting to first test whether these homologs in mammalian systems respond in a similar fashion such that they can be later exploited in constructing relevant synthetic gene circuits. Taken together, this study represents a step towards the understanding of light quality perception and relevant transcriptional and metabolic changes in plants within the context of systems biology. In future, the integrative framework presented in this study can be leveraged to improve plant traits towards better productivity.

7.5 Summary

In this work, the transcripts of rice leaves were profiled at genome-scale under four different light treatments: blue (B), green (G), red (R), white (W), dark (D). Subsequently, the transcriptome data was utilised for characterizing the behavioural differ-

ences through a combined framework involving the *in silico* metabolic modelling. A significant rearrangement in global gene expression pattern across different light treatments was identified. Several metabolic pathways responded in specific manner based on the light quality: photosynthesis and secondary metabolite synthesis was upregulated in B, reserve carbohydrates degradation was pronounced in D. Additionally, the cis-acting elements analysis of certain differentially expressed genes revealed several putative TFs which are sensitive to specific light qualities. Moving forward, the framework proposed in the current study could serve as a promising approach for unravelling the light-specific control of relevant transcriptional and metabolic changes in plants and the knowledge discovered could possibly be applied towards engineering crop plants for better productivity.

Chapter 8

Contributions and future recommendations

8.1 Summary of contributions

Rice is a major food crop, supplementing the nutritional requirements for billions of people around the world. However, its sustained production faces huge challenges on account of various abiotic and biotic stresses. Thus, it is important to understand the intrinsic stress response mechanisms of rice so as to improve its stress tolerance and enhance the yield. With such motivation, the current work has initiated a systems approach to analyse the molecular mechanisms of rice under various stressed conditions. The following section presents some of the key contributions from this work.

Combined regulatory and metabolic modelling of rice cells

In this work, the reconstruction of rice central metabolic model of rice showed how regulatory information can be combined with this model to simulate tissue specific characteristics of rice cell. It should be noted that the central model developed in this study was also the first to represent rice metabolism. The model simulations were compared with suspension cell culture experiments where the *in silico* simulated growth rates are in good agreement with experimental observations.

***In silico* analysis of rice metabolism under flooding and drought stresses**

The developed central model was later utilised to analyse the rice cell metabolism under

drought and flooding stresses, respectively. The flux analysis of seed-derived rice cells revealed the importance of ethanolic fermentation together with glycolysis for ATP production under anaerobic conditions, i.e. flooding stress. The simulations also confirmed the crucial role of SUS ahead of invertase for breaking down sucrose in an energetically efficient manner while growing under both aerobic and anaerobic conditions. Moreover, the central model even suggested the possible role of GABA in glycine synthesis via serine-hydroxy methyltransferase under anaerobic conditions. Similarly, flux analysis of photorespiring leaves highlighted the important role of malate transporters in balancing the redox cofactors across compartments and the active engagement of respiration in generating the required ATP for biosynthetic processes during the reduction in photosynthesis. Further, the gene deletion and synthetic lethal analyses highlighted the rigid nature of rice photosynthetic pathways and characterised functional interactions between central metabolic genes, respectively. A number of essential genes for the cell growth across various functional pathways such as photorespiratory cycle, Calvin cycle, GS-GOGAT cycle and sucrose metabolism as well as certain inter-compartmental transporters were identified, which are mostly in good agreement with previous experiments.

Reconstruction rice genome-scale metabolic network

A genome-scale metabolic network of rice, *i*OS2164, was also reconstructed by expanding the central model. *i*OS2164 is a completely curated, high-quality, compartmentalised genome-scale metabolic model of rice cells and is most comprehensive in terms of possible metabolic pathway inclusion, appropriate subcellular localization of reactions, detailed accounting of electron transport metabolism in both plastid and mitochondrion, and network connectivity. Further, the light specific reactions in *i*OS2164 are modelled in a wavelength specific manner such that it can accurately simulate the photosynthetic behaviour for a particular light quality.

Characterization of light-specific metabolic and transcriptional changes

Using the reconstructed genome-scale model and transcriptome data of rice plants grown under various light treatments, the light-specific metabolic and transcriptional changes in rice were analysed. The integrative analysis indicated a significant rearrangement in global gene expression pattern across different light treatments. Several metabolic pathways responded in specific manner based on the light quality: photosynthesis and

secondary metabolite synthesis was upregulated in B, reserve carbohydrates degradation was pronounced in D. Additionally, the cis-acting elements analysis of certain differentially expressed genes revealed several light-specific transcription factors (TFs) such as MYB, bZIP, bHLH and Znf.

Development of an integrative *in silico* analysis framework

As a part of current work, a systematic *in silico* framework has been developed to analyse the cellular mechanisms of rice under various stress conditions. The proposed framework integrates the transcriptome data and metabolic modelling in a systematic way to derive new hypotheses, which cannot be attained by either of them alone. Chapters 4 and 7 have demonstrated the applicability of proposed algorithm by analysing the metabolic adaptations in rice during flooding stress and different light treatments, respectively. It should be noted that, although the current work has demonstrated the proposed framework in rice, it can be applied to any other cellular systems including microbial and mammalian organisms.

8.2 Future recommendations

Development of root specific rice model to investigate salt stress

Similar to drought and flooding stresses, salt stress also severely affects rice productivity. Therefore, the expansion of current work to investigate the effects of salt stress on rice roots will be appropriate. In order to do so, the approach proposed in current work can be utilised to develop a root specific model (Lakshmanan *et al*, 2013c). Further, such a model will also provide novel insights about the nitrate and sulphate assimilation in plants; both nitrogen and sulphur are essential compounds for amino acids synthesis and is primarily assimilated through the roots in the form of mineral salts. Therefore, it is highly required develop a root specific model as it, together with the leaf and seed specific models, will provide us global insights into rice metabolism.

Model-driven alternative pathway design

As mentioned earlier, photorespiration in plants represent a major energy drain, and is essential to eliminate or minimise it to improve crop yield. In this regard, the metabolic simulations indicated that the photorespiratory pathway is quite rigid and any gene

knockout in this pathway will affect the plant in a lethal manner (Lakshmanan *et al*, 2013b). Therefore, to minimise photorepiration, two options are available: 1) increasing CO_2 concentration around RuBisCO or 2) designing alternative bypass pathways to reduce the flux through photorespiratory pathway (Peterhansel *et al*, 2013). Among these, the plants with alternative pathways have been tried in Arabidopsis and have shown good results (Kebeish *et al*, 2007; Maier *et al*, 2012). Similarly, to design a transgenic rice plant with alternative pathway, the presented rice model can be utilised to asses the performance of all possible metabolic routes which are available for the salvage of 2-PG into 3-PGA. Therefore, the rice model can be utilised appropriately for suggesting viable design strategies to guide crop improvement in an efficient way.

In silico analysis of biotic stresses

The current work presented the *in silico* framework for analysing rice metabolism under abiotic stresses. However, as mentioned earlier, rice productivity is also affected severely by biotic stresses. Among several pathogens, the bacterium *Xanthomonas oryzae*, pv. *oryzae* (Xoo), is considered to be most lethal as it can cause yield losses as high as 50% at fully infected fields (Ezuka *et al*, 2000). Therefore, it is important to study the molecular basis of its interactions with rice to develop new varieties with enhanced resistance. In this regard, as the genome annotation of Xoo is currently available (Lee *et al*, 2005a), the development of genome-scale metabolic model would be rational beginning to initiate the systems analysis of rice-Xoo interactions. Once the model has been developed, it can be combined with the rice genome-scale model based on the approaches proposed for studying host - microbe metabolic interactions between human and other infectious microbes such as *Mycobacterium tuberculosis* (Bordbar *et al*, 2010), *Plasmodium falciparum* (Huthmacher *et al*, 2010) and *Bacteroides thetaiotaomicron* (Heinken *et al*, 2013).

Multi-tissue type whole plant modelling

In the current work, the cellular metabolism in different tissues were mostly analysed in an individual manner. However, most of the plant metabolic functions occur across different tissues and organs in a co-ordinated manner. Therefore, it is necessary to model the plant systems on a whole-plant scale. Recently, Grafahrend-Belau *et al* (2013) have suggested a multiscale metabolic modelling (MMM) approach to integrate the

individual organ-specific models of barley into a whole-plant dynamic model. Using similar approach, the integration of multiple tissue type rice static models will also provide novel insights into its stress response mechanisms at a global-level.

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Appendices

The Appendices associated with previously published materials, i.e. Appendix A-N, are available online:

Appendix A:

http://bib.oxfordjournals.org/content/suppl/2012/10/12/bbs069.DC1/Supplementary_Note_1.doc

Appendix B:

http://bib.oxfordjournals.org/content/suppl/2012/10/12/bbs069.DC1/Supplementary_Note_2.pdf

Appendix C:

http://bib.oxfordjournals.org/content/suppl/2012/10/12/bbs069.DC1/Supplementary_Note_3.pdf

Appendix D:

http://bib.oxfordjournals.org/content/suppl/2012/10/12/bbs069.DC1/Supplementary_Note_4.pdf

Appendix E:

http://bib.oxfordjournals.org/content/suppl/2012/10/12/bbs069.DC1/Supplementary_Note_5.pdf

Appendix F:

http://www.plantphysiol.org/content/suppl/2013/06/10/pp.113.220178.DC1/220178S1.xls

Appendix G:

http://www.plantphysiol.org/content/suppl/2013/06/10/pp.113.220178.DC1/220178S2.zip

Appendix H:

http://www.plantphysiol.org/content/suppl/2013/06/10/pp.113.220178.DC1/220178S3.xls

Appendix I:

http://www.plantphysiol.org/content/suppl/2013/06/10/pp.113.220178.DC1/220178S4.xls

Appendix J:

http://aobpla.oxfordjournals.org/content/suppl/2014/06/03/plu026.DC1/plu026supp_data2.doc

Appendix K:

http://aobpla.oxfordjournals.org/content/suppl/2014/06/03/plu026.DC1/plu026supp_data3.doc

Appendix L:

http://aobpla.oxfordjournals.org/content/suppl/2014/06/03/plu026.DC1/plu026supp_data4.doc

Appendix M:

http://aobpla.oxfordjournals.org/content/suppl/2014/06/03/plu026.DC1/plu026supp_data5.doc

Appendix N:

http://www.biomedcentral.com/content/supplementary/1939-8433-6-20-S2.pdf

Appendix O:

Seed-derived cells biomass composition

Overall Composition (Colmer et al. (2001) J Exp Bot 52, 1507-1517 & http://archive.gramene.org/newsletters/rice_genetics/rgn6/v6p163.html)

Components	Wt %
Proteins	14.4
Carbohydrates - monosaccharides	19.08
DNA	0.12
RNA	1.2
Lipids	9.9
Carbohydrates - polysaccharides	55.3

Carbohydrates Composition (Cho et al (2008) J Crop Sci Biotech, 11: 181-186)

Components	MW	Wt %	g/gDCW	mmol/gDCW	Moles	Mol frac	MW Contribution
Glucose	180.16	2.50000	0.00477	0.0265	0.000026	0.0458	8.2450
Sucrose	342.3	96.00000	0.18299	0.5346	0.000535	0.9249	316.6088
Fructose	180.16	1.60000	0.00305	0.0169	0.000017	0.0293	5.2768

Polysaccharides Composition (Cho et al (2008) J Crop Sci Biotech, 11: 181-186)

Components	MW	Wt %	g/g DCW	mmol/gDCW	Moles	Mol frac	MW Contribution
Cellulose	162.14	21.70000	0.120	0.740107315	0.000740107	0.2196	35.6104
Hemicellulose	171.6015992	21.70000	0.120	0.69930001	0.0006993	0.2075	35.6104
Starch	162.14	56.60000	0.313	1.930418157	0.001930418	0.5729	92.8826

Hemicellulose Composition (Saha et al (2011) PLoS ONE 6: e21784)

Components	MW	Wt %	g/gDCW	mmol/gDCW	Moles	Mol frac	MW Contribution
Arabinose	150.13	6.75876	0.0081	0.0540	0.0001	0.0773	11.5981
Xylose	150.13	30.78441	0.0369	0.2461	0.0002	0.3519	52.8265
Galactose	180.156	1.48002	0.0018	0.0099	0.0000	0.0141	2.5397
Glucose	180.16	25.94968	0.0311	0.1728	0.0002	0.2472	44.5301
Uronic acid	194.14	35.02713	0.0420	0.2165	0.0002	0.3096	60.1071

DNA (Goff et al (2002) Science 296: 92-100)

Nucleotide	DNA (mol/mol)	MW (g/mol)	DNA (g/mol)	DNA (g/g)	g/gDCW	mmol/ gDCW
dATP	0.28	487.15100	136.4023	0.2827	0.0003	0.0007
dCTP	0.22	461.10900	101.4440	0.2103	0.0003	0.0005

dTTP	0.28	478.13600	133.8781	0.2775	0.0003	0.0007
dGTP	0.22	503.15000	110.6930	0.2295	0.0003	0.0005

RNA (Individual nucleotide distribution assumed same as G+C of DNA)

RNA	RNA (mol/mol)	MW (g/mol)	RNA (g/mol)	RNA (g/g)	g/gDCW	mmol/ gDCW
ATP	0.28	503.15000	140.8820	0.3031	0.0036	0.0072
CTP	0.22	479.12400	105.4073	0.2268	0.0027	0.0057
UTP	0.28	480.10800	134.4302	0.2892	0.0035	0.0072
GTP	0.22	519.14900	114.2128	0.2457	0.0029	0.0057

Lipids (Cho et al (2008) J Crop Sci Biotech, 11: 181-186)

Lipid	content (wt %)	MW	mmol/g DCW
TAG	64.70	**851.5714286**	0.075217413
Free FA	20.40	**273.1904762**	0.073926442
Phospholipids	12.60	**301.62066**	0.041356584

Fatty acid (Brown and Beevers (1987) Plant Physiol. 84: 555-559)

Fatty acid	Content (mol)	Mole fraction	MW
16:00	11.7000	0.2532	255
16:10	1.9000	0.0411	253
18:10	15.7000	0.3398	282
18:20	15.8000	0.3420	280
18:30	1.1000	0.0238	278
Total	46.2000		273.1905

Phospholipids (Brown and Beevers (1987) Plant Physiol. 84: 555-559)

Phospholipid	Moles	Mole fraction	MW	No. of FA	mmol/g DCW
PC	10.8000	0.5902	312.2300	2	0.024407164
PE	5.6000	0.3060	269.1500	2	0.012655567
PI	1.3000	0.0710	388.2200	2	0.002937899
PA	0.6000	0.0328	226.0800	2	0.001355954
Total	18.3000		301.62066		0.041356584

Amino acids (Juliano (1985) Rice: Chemistry and Technology, 2nd ed)

Amino acids	MW	Wt %	Mol/g Protein	mmol/gDCW	Mol Frac	MW Contribution
Alanine	89.05	5.65	0.00063	0.0914	0.0821	7.3065
Arginine	174.11	8.6	0.00049	0.0711	0.0639	11.1214
Aspartic acid	133.04	9.1	0.00068	0.0985	0.0885	11.7680
Cystine	240.02	2.1	0.00009	0.0126	0.0113	2.7157

Glutamic acid	147.05	17.95	0.00122	0.1758	0.1579	23.2126
Glycine	75.03	4.9	0.00065	0.0940	0.0845	6.3366
Histidine	155.07	2.25	0.00015	0.0209	0.0188	2.9097
Isoleucine	131.09	4.1	0.00031	0.0450	0.0404	5.3020
Leucine	131.09	8.2	0.00063	0.0901	0.0809	10.6041
Lysine	146.11	4.15	0.00028	0.0409	0.0367	5.3667
Methionine	149.05	2.6	0.00017	0.0251	0.0226	3.3623
Phenylalanine	165.08	4.7	0.00028	0.0410	0.0368	6.0780
Proline	115.06	5.1	0.00044	0.0638	0.0573	6.5952
Serine	105.04	5.1	0.00049	0.0699	0.0628	6.5952
Threonine	119.06	3.95	0.00033	0.0478	0.0429	5.1081
Tryptophan	204.09	1.7	0.00008	0.0120	0.0108	2.1984
Tyrosine	181.07	4.85	0.00027	0.0386	0.0346	6.2719
Valine	117.08	6.1	0.00052	0.0750	0.0674	7.8884

Appendix P:

Genome-scale model of rice

Abbreviation	Name	Reaction Equation	GPR (MSU)	Subsystem	EC Number
Coleoptile_Biomass	Coleoptile Biomass reaction	0.0914 ala-L[c] + 0.0639 arg-L[c] + 0.0985 asp-L[c] + 0.0126 cys-L[c] + 0.1758 glu-L[c] + 0.094 gly[c] + 0.021 his-L[c] + 0.045 ile-L[c] + 0.0901 leu-L[c] + 0.0409 lys-L[c] + 0.0251 met-L[c] + 0.0410 phe-L[c] + 0.0638 pro-L[c] + 0.0699 ser-L[c] + 0.0478 thr-L[c] + 0.0120 trp-L[c] + 0.0386 tyr-L[c] + 0.075 val-L[c] + 0.0265 glc-A[c] + 0.5346 sucr[c] + 0.0169 fru-B[c] + 1.93 starch[s] + 0.74 cellulose[c] + 0.054 udparab[c] + 0.246 udpxyl[c] + 0.0099 udpgal[c] + 0.1728 udpg[c] + 0.2165 udpglcur[c] + 0.0007 datp[c] + 0.0005 dctp[c] + 0.0007 dttp[c] + 0.0005 dgtp[c] + 0.0072 utp[c] + 0.0057 ctp[c] + 0.0057 gtp[c] + 0.0012 fa_os[r] + 0.0752 triglyc_os[r] + 0.001356 pa_os[r] + 0.0244 pc_os[r] + 0.01265 pe_os[r] + 0.00293 ptd1ino_os[r] + 33.2572 atp[c] -> 33.2572 adp[c] + 33.2572 pi[c] + 0.6992 udp[c] + 0.6992 h[c]		biomass	
Straw_Biomass	Straw Biomass reaction	0.0321 ala-L[c] + 0.0123 arg-L[c] + 0.0417 asp-L[c] + 0.0033 cys-L[c] + 0.0385 glu-L[c] + 0.0282 gly[c] + 0.057 his-L[c] + 0.0140 ile-L[c] + 0.0234 leu-L[c] + 0.0153 lys-L[c] + 0.0076 met-L[c] + 0.0133 phe-L[c] + 0.0225 pro-L[c] + 0.0219 ser-L[c] + 0.0192 thr-L[c] + 0.0016 trp-L[c] + 0.0077 tyr-L[c] + 0.0225 val-L[c] + 0.0546 glc-A[c] + 0.1049 sucr[c] + 0.0643 fru-B[c] + 0.3249 starch[s] + 0.74 cellulose[c] + 0.054 udparab[c] + 0.246 udpxyl[c] + 0.0099 udpgal[c] + 0.1728 udpg[c] + 0.2165 udpglcur[c] + 0.0007 datp[c] + 0.0072 utp[c] + 0.0057 ctp[c] + 0.0057 gtp[c] + 0.0005 dctp[c] + 0.0005 dgtp[c] + 0.0007 dttp[c] + 0.0012 fa_os[r] + 0.0752 triglyc_os[r] + 0.001356 pa_os[r] + 0.0244 pc_os[r] + 0.01265 pe_os[r] + 0.00293 ptd1ino_os[r] + 33.87297 atp[c] -> 33.87297 adp[c] + 33.87297 pi[c] + 0.6992 udp[c] + 0.6992 h[c]		biomass	
ACCOAC_OSc	Acyl-CoA composition	0.2532 pmtcoa[c] + 0.0411 hdcoa[c] + 0.3398 odecoa[c] + 0.3420 ocdycacoa[c] + 0.0238 lnlncoa[c] <=> acylcoa_os[c]		Unassigned	
ACCOAC_Osr	Acyl-CoA composition	0.2532 pmtcoa[r] + 0.0411 hdcoa[r] + 0.3398 odecoa[r] + 0.3420 ocdycacoa[r] + 0.0238 lnlncoa[r] <=> acylcoa_os[r]		Unassigned	
ACPC_OSs	ACP composition	0.2532 palmACP[s] + 0.0411 hdeACP[s] + 0.3398 octeACP[s] + 0.3420 ocdcyaACP[s] + 0.0238 lnlnlACP[s] <=> ACP_os[s]		Unassigned	
ACPC_OSm	ACP composition	0.2532 palmACP[m] + 0.0411 hdeACP[m] + 0.3398 octeACP[m] + 0.3420 ocdcyaACP[m] + 0.0238 lnlnlACP[m] <=> ACP_os[m]		Unassigned	
FAC_Osc	Fatty acid composition	fa_os[c] <=> 0.2532 hdca[c] + 0.0411 hdcea[c] + 0.3398 ocdcea[c] + 0.3420 ocdcya[c] + 0.0238 lnlnl[c]		Unassigned	
FAC_Osr	Fatty acid composition	fa_os[r] <=> 0.2532 hdca[r] + 0.0411 hdcea[r] + 0.3398 ocdcea[r] + 0.3420 ocdcya[r] + 0.0238 lnlnl[r]		Unassigned	
EX_co2(e)	CO2 exchange	co2[e] <=>		Exchange Reactions	
EX_h2o(e)	H2O exchange	h2o[e] <=>		Exchange Reactions	
EX_h(e)	H+ exchange	h[e] <=>		Exchange Reactions	
EX_no3(e)	nitrate exchange	no3[e] <=>		Exchange Reactions	
EX_o2(e)	O2 exchange	o2[e] <=>		Exchange Reactions	
EX_pi(e)	Phosphate exchange	pi[e] <=>		Exchange Reactions	
EX_sucr(e)	Sucrose exchange	sucr[e] <=>		Exchange Reactions	
EX_fru-B(e)	Fructose exchange	fru-B[e] <=>		Exchange Reactions	
EX_glc-A(e)	Glucose exchange	glc-A[e] <=>		Exchange Reactions	
EX_so4(e)	Sulfate exchange	so4[e] <=>		Exchange Reactions	
EX_hco3(e)	Bicarbonate exchange	hco3[e] <=>		Exchange Reactions	

EX_so3(e)	Sulfite exchange	hso3[e] <=>		Exchange Reactions	
EX_h2s(e)	Hydrogen sulfide exchange	h2s[e] <=>		Exchange Reactions	
EX_nh4(e)	Ammonia exchange	nh4[e] <=>		Exchange Reactions	
EX_asn-L(e)	L-Asparagine exchange	asn-L[e] <=>		Exchange Reactions	
EX_gln-L(e)	L-Glutamine exchange	gln-L[e] <=>		Exchange Reactions	
EX_etoh(e)	Ethanol exchange	etoh[e] <=>		Exchange Reactions	
EX_ac(e)	Acetate exchange	ac[e] <=>		Exchange Reactions	
EX_lac-L(e)	L-Lactate exchange	lac-L[e] <=>		Exchange Reactions	
EX_tsul(e)	Thiosulfate exchange	tsul[e] <=>		Exchange Reactions	
EX_fe2(e)	Fe2+ exchange	fe2[e] <=>		Exchange Reactions	
EX_fe3(e)	Fe3+ exchange	fe3[e] <=>		Exchange Reactions	
EX_mg2(e)	Magnesium exchange	mg2[e] <=>		Exchange Reactions	
EX_ala-L(e)	L-Alanine exchange	ala-L[e] <=>		Exchange Reactions	
EX_arg-L(e)	L-Arginine exchange	arg-L[e] <=>		Exchange Reactions	
EX_asp-L(e)	L-Aspartate exchange	asp-L[e] <=>		Exchange Reactions	
EX_cys-L(e)	L-Cysteine exchange	cys-L[e] <=>		Exchange Reactions	
EX_glu-L(e)	L-Glutamate exchange	glu-L[e] <=>		Exchange Reactions	
EX_gly(e)	Glycine exchange	gly[e] <=>		Exchange Reactions	
EX_his-L(e)	L-Histidine exchange	his-L[e] <=>		Exchange Reactions	
EX_ile-L(e)	L-Isoleucine exchange	ile-L[e] <=>		Exchange Reactions	
EX_leu-L(e)	L-Leucine exchange	leu-L[e] <=>		Exchange Reactions	
EX_lys-L(e)	L-Lysine exchange	lys-L[e] <=>		Exchange Reactions	
EX_met-L(e)	L-Methionine exchange	met-L[e] <=>		Exchange Reactions	
EX_phe-L(e)	L-Phenylalanine exchange	phe-L[e] <=>		Exchange Reactions	
EX_pro-L(e)	L-Proline exchange	pro-L[e] <=>		Exchange Reactions	
EX_ser-L(e)	L-Serine exchange	ser-L[e] <=>		Exchange Reactions	
EX_thr-L(e)	L-Threonine exchange	thr-L[e] <=>		Exchange Reactions	
EX_trp-L(e)	L-Tryptophan exchange	trp-L[e] <=>		Exchange Reactions	
EX_tyr-L(e)	L-Tyrosine exchange	tyr-L[e] <=>		Exchange Reactions	
EX_val-L(e)	L-Valine exchange	val-L[e] <=>		Exchange Reactions	
EX_coa[c]	demand removing excess coa	coa[c] ->		Demand	
EX_photonVis(e)	photon emission	photon690[u] <=>		Exchange Reactions	
DM_photon410(u)	demand removing photon298 from system	photonDrain[u] ->		Demand	
PRISM_blue_LED	spectral decomposition of white LED	photonVis[e] -> 0.009290386222 photon430[u] + 0.370517176 photon450[u] + 0.520401408 photon470[u] + 0.094361569 photon490[u] + 0.00457897551 photon510[u]		Spectral decomposition	
PRISM_red_LED	spectral decomposition of red LED (674nm)	photonVis[e] -> 0.002879576 photon610[u] + 0.003855380193 photon630[u] + 0.483357529 photon650[u] + 0.456570768 photon670[u] + 0.010829504 photon690[u]		Spectral decomposition	
PRISM_white_LED	spectral decomposition of red LED (674nm)	photonVis[e] -> 0.002723395 photon430[u] + 0.135928126 photon450[u] + 0.189971935 photon470[u] + 0.050389911 photon490[u] + 0.147583919 photon510[u] + 0.132047235 photon530[u] + 0.03140161 photon550[u] + 0.004592156577 photon570[u] + 0.00058518 photon590[u] + 0.0008778146299 photon610[u] + 0.01410125 photon630[u] + 0.140107154 photon650[u] + 0.146392098 photon670[u] + 0.003258373729 photon690[u]		Spectral decomposition	
PRISM_green_LED	spectral decomposition of red LED (674nm)	photonVis[e] -> 0.072259765 photon490[u] + 0.432884077 photon510[u] + 0.376758388 photon530[u] + 0.102672594 photon550[u] + 0.0013448784 photon570[u]		Spectral decomposition	
RPSI_410(u)	Photosystem I 410 specific reaction	photon410[u] -> 0.700028 photonPSI[u] + 0.299972 photonDrain[u]		Spectral decomposition	
RPSI_430(u)	Photosystem I 430 specific reaction	photon430[u] -> 0.796708442 photonPSI[u] + 0.203291558 photonDrain[u]		Spectral decomposition	
RPSI_450(u)	Photosystem I 450 specific reaction	photon450[u] -> 0.617580018 photonPSI[u] + 0.382419982		Spectral decomposition	

		photonDrain[u]			
RPSI_470(u)	Photosystem I 470 specific reaction	photon470[u] -> 0.524710291 photonPSI[u] + 0.475289709 photonDrain[u]		Spectral decomposition	
RPSI_490(u)	Photosystem I 490 specific reaction	photon490[u] -> 0.399317934 photonPSI[u] + 0.600682066 photonDrain[u]		Spectral decomposition	
RPSI_510(u)	Photosystem I 510 specific reaction	photon510[u] -> 0.18437505 photonPSI[u] + 0.81562495 photonDrain[u]		Spectral decomposition	
RPSI_530(u)	Photosystem I 530 specific reaction	photon530[u] -> 0.092758148 photonPSI[u] + 0.907241852 photonDrain[u]		Spectral decomposition	
RPSI_550(u)	Photosystem I 550 specific reaction	photon550[u] -> 0.098111892 photonPSI[u] + 0.901888108 photonDrain[u]		Spectral decomposition	
RPSI_570(u)	Photosystem I 570 specific reaction	photon570[u] -> 0.152178 photonPSI[u] + 0.847822 photonDrain[u]		Spectral decomposition	
RPSI_590(u)	Photosystem I 590 specific reaction	photon590[u] -> 0.191296711 photonPSI[u] + 0.808703289 photonDrain[u]		Spectral decomposition	
RPSI_610(u)	Photosystem I 610 specific reaction	photon610[u] -> 0.258195936 photonPSI[u] + 0.741804064 photonDrain[u]		Spectral decomposition	
RPSI_630(u)	Photosystem I 630 specific reaction	photon630[u] -> 0.322072036 photonPSI[u] + 0.677927964 photonDrain[u]		Spectral decomposition	
RPSI_650(u)	Photosystem I 630 specific reaction	photon650[u] -> 0.552832539 photonPSI[u] + 0.447167461 photonDrain[u]		Spectral decomposition	
RPSI_670(u)	Photosystem I 670 specific reaction	photon670[u] -> 0.490895969 photonPSI[u] + 0.509104031 photonDrain[u]		Spectral decomposition	
RPSI_690(u)	Photosystem I 690 specific reaction	photon690[u] -> 0.068254056 photonPSI[u] + 0.931745944 photonDrain[u]		Spectral decomposition	
RPSII_410(u)	Photosystem II 410 specific reaction	photon410[u] -> 0.768811 photonPSII[u] + 0.231189 photonDrain[u]		Spectral decomposition	
RPSII_430(u)	Photosystem II 430 specific reaction	photon430[u] -> 0.852685475 photonPSII[u] + 0.14731525 photonDrain[u]		Spectral decomposition	
RPSII_450(u)	Photosystem II 450 specific reaction	photon450[u] -> 0.791244063 photonPSII[u] + 0.208755937 photonDrain[u]		Spectral decomposition	
RPSII_470(u)	Photosystem II 470 specific reaction	photon470[u] -> 0.685799028 photonPSII[u] + 0.314200972 photonDrain[u]		Spectral decomposition	
RPSII_490(u)	Photosystem II 490 specific reaction	photon490[u] -> 0.612537409 photonPSII[u] + 0.387462591 photonDrain[u]		Spectral decomposition	
RPSII_510(u)	Photosystem II 510 specific reaction	photon510[u] -> 0.348632042 photonPSII[u] + 0.651367958 photonDrain[u]		Spectral decomposition	
RPSII_530(u)	Photosystem II 530 specific reaction	photon530[u] -> 0.167573364 photonPSII[u] + 0.832426636 photonDrain[u]		Spectral decomposition	
RPSII_550(u)	Photosystem II 550 specific reaction	photon550[u] -> 0.141326491 photonPSII[u] + 0.858673509 photonDrain[u]		Spectral decomposition	
RPSII_570(u)	Photosystem II 570 specific reaction	photon570[u] -> 0.157294434 photonPSII[u] + 0.842705566 photonDrain[u]		Spectral decomposition	
RPSII_590(u)	Photosystem II 590 specific reaction	photon590[u] -> 0.216296356 photonPSII[u] + 0.783703644 photonDrain[u]		Spectral decomposition	
RPSII_610(u)	Photosystem II 610 specific reaction	photon610[u] -> 0.25191974 photonPSII[u] + 0.748080254 photonDrain[u]		Spectral decomposition	
RPSII_630(u)	Photosystem II 630 specific reaction	photon630[u] -> 0.298803678 photonPSII[u] + 0.701196322 photonDrain[u]		Spectral decomposition	
RPSII_650(u)	Photosystem II 630 specific reaction	photon650[u] -> 0.390343412 photonPSII[u] + 0.609656588 photonDrain[u]		Spectral decomposition	
RPSII_670(u)	Photosystem II 670 specific reaction	photon670[u] -> 0.65691013 photonPSII[u] + 0.34308987 photonDrain[u]		Spectral decomposition	
RPSII_690(u)	Photosystem II 690 specific reaction	photon690[u] -> 0.367269367 photonPSII[u] + 0.632730633 photonDrain[u]		Spectral decomposition	
CO2tex	CO2 transport (extracellular to cytosol)	co2[e] <=> co2[c]		Transport (Extracellular)	

H2Otex	H2O transport (extracellular to cytosol)	h2o[e] <=> h2o[c]		Transport (Extracellular)	
Htex	proton transport via diffusion (extracellular to cytosol)	h[e] <=> h[c]		Transport (Extracellular)	
NO3tex	nitrate transport (extracellular to cytosol)	no3[e] <=> no3[c]		Transport (Extracellular)	
O2tex	O2 transport in via diffusion (extracellular to cytosol)	o2[e] <=> o2[c]		Transport (Extracellular)	
Pitex	PI transport in via diffusion (extracellular to cytosol)	pi[e] <=> pi[c]		Transport (Extracellular)	
SUCRtex	sucrose transport transport via diffusion (extracellular to cytosol)	sucr[e] <=> sucr[c]		Transport (Extracellular)	
FRUtex	D-fructose transport via diffusion (extracellular to cytosol)	fru-B[e] <=> fru-B[c]		Transport (Extracellular)	
GLCtex	glucose transport via diffusion (extracellular to cytosol)	glc-A[e] <=> glc-A[c]		Transport (Extracellular)	
SO4tex	sulfate transport via diffusion (extracellular to cytosol)	so4[e] <=> so4[c]		Transport (Extracellular)	
SO3tex	sulfite transport via diffusion (extracellular to cytosol)	hso3[e] <=> hso3[c]		Transport (Extracellular)	
HCO3tex	bicarbonate transport via diffusion (extracellular to cytosol)	hco3[e] <=> hco3[c]		Transport (Extracellular)	
H2Stex	hydrogen sulfide transport via diffusion (extracellular to cytosol)	h2s[e] <=> h2s[c]		Transport (Extracellular)	
NH4tex	ammonia transport via diffusion (extracellular to cytosol)	nh4[e] <=> nh4[c]		Transport (Extracellular)	
ASNtex	L-asparagine transport via diffusion (extracellular to cytosol)	asn-L[e] <=> asn-L[c]		Transport (Extracellular)	
GLNtex	L-glutamine transport via diffusion (extracellular to cytosol)	gln-L[e] <=> gln-L[c]		Transport (Extracellular)	
ETOHtex	ethanol transport via diffusion (extracellular to cytosol)	etoh[c] -> etoh[e]		Transport (Extracellular)	
ACtex	Acetate transport via diffusion (extracellular to cytosol)	ac[c] -> ac[e]		Transport (Extracellular)	
LACtex	L-lactate transport via diffusion (extracellular to cytosol)	lac-L[c] -> lac-L[e]		Transport (Extracellular)	
TSULtex	Thiosulfate transport via diffusion (extracellular to cytosol)	tsul[e] <=> tsul[c]		Transport (Extracellular)	
FE2tex	Fe2+ transport via diffusion (extracellular to cytosol)	fe2[e] <=> fe2[c]		Transport (Extracellular)	
FE3tex	Fe3+ transport via diffusion (extracellular to cytosol)	fe3[e] <=> fe3[c]		Transport (Extracellular)	
MG2tex	Mg2 transport via diffusion (extracellular to cytosol)	mg2[e] <=> mg2[c]		Transport (Extracellular)	
ALAtex	L-alanine transport via diffusion (extracellular to cytosol)	ala-L[e] <=> ala-L[c]		Transport (Extracellular)	
ARGtex	L-arginine transport via diffusion (extracellular to cytosol)	arg-L[e] <=> arg-L[c]		Transport (Extracellular)	
ASPtex	L-aspartate transport via diffusion (extracellular to cytosol)	asp-L[e] <=> asp-L[c]		Transport (Extracellular)	
CYStex	L-cysteine transport via diffusion (extracellular to cytosol)	cys-L[e] <=> cys-L[c]		Transport (Extracellular)	
GLUtex	L-glutamate transport via diffusion (extracellular to cytosol)	glu-L[e] <=> glu-L[c]		Transport (Extracellular)	
GLYtex	Glycine transport via diffusion (extracellular to cytosol)	gly[e] <=> gly[c]		Transport (Extracellular)	
HIStex	L-histidine transport via diffusion (extracellular to cytosol)	his-L[e] <=> his-L[c]		Transport (Extracellular)	

ILEtex	L-isoleucine transport via diffusion (extracellular to cytosol)	ile-L[e] <=> ile-L[c]		Transport (Extracellular)	
LEUtex	L-leucine transport via diffusion (extracellular to cytosol)	leu-L[e] <=> leu-L[c]		Transport (Extracellular)	
LYStex	L-lysine transport via diffusion (extracellular to cytosol)	lys-L[e] <=> lys-L[c]		Transport (Extracellular)	
METtex	L-methionine transport via diffusion (extracellular to cytosol)	met-L[e] <=> met-L[c]		Transport (Extracellular)	
PHEtex	L-phenylalanine transport via diffusion (extracellular to cytosol)	phe-L[e] <=> phe-L[c]		Transport (Extracellular)	
PROtex	L-proline transport via diffusion (extracellular to cytosol)	pro-L[e] <=> pro-L[c]		Transport (Extracellular)	
SERtex	L-serine transport via diffusion (extracellular to cytosol)	ser-L[e] <=> ser-L[c]		Transport (Extracellular)	
THRtex	L-threonine transport via diffusion (extracellular to cytosol)	thr-L[e] <=> thr-L[c]		Transport (Extracellular)	
TRPtex	L-tryptophan transport via diffusion (extracellular to cytosol)	trp-L[e] <=> trp-L[c]		Transport (Extracellular)	
TYRtex	L-tyrosine transport via diffusion (extracellular to cytosol)	tyr-L[e] <=> tyr-L[c]		Transport (Extracellular)	
VALtex	L-valine transport via diffusion (extracellular to cytosol)	val-L[e] <=> val-L[c]		Transport (Extracellular)	
PPASc	Soluble inorganic pyrophosphatase, cytosol	h2o[c] + ppi[c] -> h[c] + 2 pi[c]	(LOC_Os01g64670 or LOC_Os02g47600 or LOC_Os04g59040 or LOC_Os05g02310 or LOC_Os05g36260 or LOC_Os10g26600)	Starch and sucrose metabolism (Sucrose)	3.6.1.1
PPASs	Soluble inorganic pyrophosphatase, plastidic	h2o[s] + ppi[s] -> h[s] + 2 pi[s]	LOC_Os02g52940	Starch and sucrose metabolism (Sucrose)	3.6.1.1
PPASm	Soluble inorganic pyrophosphatase, mitochondrial	h2o[m] + ppi[m] -> h[m] + 2 pi[m]	(LOC_Os01g64670 or LOC_Os02g47600 or LOC_Os04g59040 or LOC_Os05g02310 or LOC_Os05g36260 or LOC_Os10g26600)	Starch and sucrose metabolism (Sucrose)	3.6.1.1
PPASx	Soluble inorganic pyrophosphatase, peroxisomal	h2o[x] + ppi[x] -> h[x] + 2 pi[x]	(LOC_Os01g64670 or LOC_Os02g47600 or LOC_Os04g59040 or LOC_Os05g02310 or LOC_Os05g36260 or LOC_Os10g26600)	Starch and sucrose metabolism (Sucrose)	3.6.1.1
PPASv	Soluble inorganic pyrophosphatase, vacuolar	h2o[v] + ppi[v] -> h[v] + 2 pi[v]	(LOC_Os01g64670 or LOC_Os02g47600 or LOC_Os04g59040 or LOC_Os05g02310 or LOC_Os05g36260 or LOC_Os10g26600)	Starch and sucrose metabolism (Sucrose)	3.6.1.1
PPAIcxc	Membrane -bound H+-inorganic pyrophosphatase, peroxisomal	h2o[c] + ppi[c] -> h[x] + 2 pi[c]	(LOC_Os01g23580 or LOC_Os02g55890 or LOC_Os05g06480 or LOC_Os06g08080 or LOC_Os06g43660)	Oxidative phosphorylation	3.6.1.1
PPAIcvc	Membrane -bound H+-inorganic pyrophosphatase, vacuolar	h2o[c] + ppi[c] -> h[v] + 2 pi[c]	(LOC_Os02g33490 or LOC_Os01g23580 or LOC_Os02g55890 or LOC_Os05g06480 or LOC_Os06g08080 or LOC_Os06g43660)	Oxidative phosphorylation	3.6.1.1
APLs	Acetolactate synthase, plastidic	pyr[s] + 2ahethmpp[s] -> alac-S[s] + thmpp[s]	(LOC_Os02g30630 or LOC_Os02g39570)	Valine, leucine and isoleucine metabolism	2.2.1.6
APLm	Acetolactate synthase, mitochondrial	pyr[m] + 2ahethmpp[m] -> alac-S[m] + thmpp[m]		Valine, leucine and isoleucine metabolism	2.2.1.6
CATv	Catalase, vacuolar	2 h2o2[v] -> 2 h2o[v] + o2[v]	(LOC_Os08g43560 or LOC_Os04g14680)	Glyoxylate Cycle	1.11.1.6
CATs	Catalase, plastidic	2 h2o2[s] -> 2 h2o[s] + o2[s]	(LOC_Os08g43560 or LOC_Os04g14680)	Glyoxylate Cycle	1.11.1.6
CATx	Catalase, peroxisomal	2 h2o2[x] -> 2 h2o[x] + o2[x]	(LOC_Os08g43560 or LOC_Os04g14680 or LOC_Os02g02400 or LOC_Os06g51150)	Glyoxylate Cycle	1.11.1.6

CATm	Catalase, mitochondrial	2 h2o2[m] -> 2 h2o[m] + o2[m]	(LOC_Os08g43560 or LOC_Os04g14680)	Glyoxylate Cycle	1.11.1.6
GLUSfm	Glutamate synthase (ferredoxin), mitochondrial	gln-L[m] + akg[m] + 2 fdxrd[m] -> 2 glu-L[m] + 2 fdxox[m] + 2 h[m]	LOC_Os07g46460	Nitrogen metabolism; GS-GOGAT Cycle	1.4.7.1
GLUSfs	Glutamate synthase (ferredoxin), plastidic	gln-L[s] + akg[s] + 2 fdxrd[s] -> 2 glu-L[s] + 2 fdxox[s] + 2 h[s]	LOC_Os07g46460	Nitrogen metabolism; GS-GOGAT Cycle	1.4.7.1
RBPCs	Ribulose-bisphosphate carboxylase	3 co2[s] + o2[s] + 3 h2o[s] + 4 rb15bp[s] -> 7 3pg[s] + 2pglyc[s]	(LOC_Os01g58020 and LOC_Os05g35330 and LOC_Os11g32770 and LOC_Os12g10580 and LOC_Os10g21280) and (LOC_Os12g19394 and LOC_Os02g05830 and LOC_Os12g17600 and LOC_Os12g19381 and LOC_Os12g19470)	Calvin cycle	4.1.1.39
CYOO6m	Cytochrome c oxidase (complex IV)	4 focytc[m] + 8 h[m] + o2[m] -> 4 ficytc[m] + 4 h[c] + 2 h2o[m]	(LOC_Osm1g00550 and LOC_Osm1g00330 and LOC_Osm1g00110 and LOC_Os01g42650 and LOC_Os08g38720 and LOC_Os03g50940)	Oxidative phosphorylation	1.9.3.1
NO3Rm	Nitrate reductase (Ubiquinol-8), mitochondrial	2 h[c] + no3[c] + q8h2[m] -> h2o[m] + q8[m] + 2 h[c] + no2[c]	LOC_Os10g17780	Oxidative phosphorylation	1.7.99.4
AOXm	Alternative oxidase	4 h[m] + o2[m] + q8h2[m] -> 2 h2o[m] + q8[m] + 2 h[c]	(LOC_Os04g51150 or LOC_Os04g51160 or LOC_Os04g46770 or LOC_Os03g63010)	Oxidative phosphorylation	1.10.3.11
ATPPHc	ATP phosphohydrolase, cytosolic	atp[c] + h2o[c] -> adp[c] + pi[c] + h[c]	(LOC_Os01g49000 or LOC_Os06g03940)	Purine metabolism	3.6.1.3
ATPPHm	ATP phosphohydrolase, mitochondrial	atp[m] + h2o[m] -> adp[m] + pi[m] + h[m]	(LOC_Os01g49000 or LOC_Os06g03940)	Purine metabolism	3.6.1.3
ATPPHs	ATP phosphohydrolase, plastidic	atp[s] + h2o[s] -> adp[s] + pi[s] + h[s]	(LOC_Os01g49000 or LOC_Os06g03940)	Purine metabolism	3.6.1.3
ATPSs	ATP synthase (complex V), plastidic	adp[s] + 4 h[u] + pi[s] -> atp[s] + 3 h[s] + h2o[u]	((LOC_Osp1g00280 and LOC_Osp1g00300 and LOC_Osp1g00290) and (LOC_Osp1g00310 and LOC_Osp1g00410 and LOC_Osp1g00400 and LOC_Os10g17280) and (LOC_Os02g51470 or LOC_Os02g51470) and LOC_Os07g32880)	Photosynthesis; Photophosphorylation	3.6.3.14
ATPSm	ATP synthase (complex V), mitochondrial	adp[m] + 3 h[c] + pi[m] -> atp[m] + 2 h[m] + h2o[m]	((LOC_Os05g47980 and LOC_Os07g31300 and LOC_Os08g15170 and LOC_Os08g37320 and LOC_Os10g17280) and (LOC_Osm1g00580 and LOC_Osm1g00370 and LOC_Osm1g00430))	Oxidative phosphorylation	3.6.3.14
ATPSv	ATP synthase (complex V-type), vacuolar	adp[v] + 3 h[c] + pi[v] -> atp[v] + 2 h[v] + h2o[v]	(LOC_Os01g73130 and LOC_Os01g41610 and LOC_Os01g12260 and LOC_Os01g46980 and LOC_Os01g61780 and LOC_Os01g40470 and LOC_Os01g42430 and LOC_Os01g51380 and LOC_Os02g07870 and LOC_Os02g34510 and LOC_Os02g57850 and LOC_Os03g14690 and LOC_Os04g05080 and LOC_Os04g51270 and LOC_Os04g55040 and LOC_Os04g56540 and LOC_Os05g01560 and LOC_Os05g40230 and LOC_Os05g51530 and LOC_Os06g37180 and LOC_Os06g45120 and LOC_Os11g06890)	Oxidative phosphorylation	3.6.3.14
GLUSs	Glutamate synthase (NADH)	gln-L[s] + akg[s] + nadh[s] + h[s] -> 2 glu-L[s] + nad[s]	LOC_Os01g48960	Nitrogen metabolism; GS-GOGAT Cycle	1.4.1.14
GLUSys	Glutamate synthase (NADPH)	gln-L[s] + akg[s] + nadph[s] + h[s] -> 2 glu-L[s] + nadp[s]	LOC_Os01g48960	Nitrogen metabolism; GS-GOGAT Cycle	1.4.1.13
GTHRc	Glutathione reductase (NADPH), cytosolic	gthox[c] + nadph[c] + h[c] -> 2 gthrd[c] + nadp[c]	(LOC_Os02g56850 or None)	Sulfate metabolism	1.8.1.7

				(Glutathione)	
GTHRs	Glutathione reductase (NADPH), plastidic	gthox[s] + nadph[s] + h[s] -> 2 gthrd[s] + nadp[s]	LOC_Os03g06740 or LOC_Os10g28000	Sulfate metabolism (Glutathione)	1.8.1.7
GTHRm	Glutathione reductase (NADPH), mitochondrial	gthox[m] + nadph[m] + h[m] -> 2 gthrd[m] + nadp[m]	LOC_Os03g06740	Sulfate metabolism (Glutathione)	1.8.1.7
ADK1c	Adenylate kinase, cytosolic	atp[c] + amp[c] -> 2 adp[c]	(None or LOC_Os12g13380)	Purine metabolism	2.7.4.3
ADK1m	Adenylate kinase, mitochondrial	atp[m] + amp[m] -> 2 adp[m]	(None or LOC_Os12g13380)	Purine metabolism	2.7.4.3
ADK1s	Adenylate kinase, plastidic	atp[s] + amp[s] -> 2 adp[s]	(LOC_Os03g03820 or LOC_Os07g22950 or LOC_Os08g01770 or LOC_Os08g19140)	Purine metabolism	2.7.4.3
ATPAPc	Apyrase	atp[c] + 2 h2o[c] -> amp[c] + ppi[c] + 6 h[c]	(LOC_Os03g03820 or LOC_Os07g22950 or LOC_Os08g01770 or LOC_Os08g19140)	Purine metabolism	2.7.4.3
ADPAc	ADP-Apyrase	adp[c] + h2o[c] -> amp[c] + pi[c] + h[c]	(LOC_Os07g48430 or LOC_Os03g21120)	Purine metabolism	3.6.1.5
GAL1PUTc	galactose-1-phosphate uridylyltransferase	gal1p[c] + utp[c] + h[c] -> udpgal[c] + ppi[c]		Primary Cell Wall Metabolism (Galactose metabolism)	2.7.7.10
DPCOAKc	Dephospho-CoA kinase	atp[c] + dpcoa[c] -> adp[c] + coa[c] + h[c]	LOC_Os01g25880	Pantothenate and CoA metabolism	2.7.1.24
URIKGc	uridine kinase (GTP), cytosolic	uri[c] + gtp[c] -> ump[c] + gdp[c] + h[c]	(LOC_Os02g17320 or LOC_Os11g16370)	Pyrimidine metabolism	2.7.1.48
URIKGs	uridine kinase (GTP), plastidic	uri[s] + gtp[s] -> ump[s] + gdp[s] + h[s]	(LOC_Os02g47020 or LOC_Os04g50880)	Pyrimidine metabolism	2.7.1.48
DHDHc	Dihydropyrimidine dehydrogenase (NADP+)	56dura[c] + nadp[c] + h[c] <=> ura[c] + nadph[c]	LOC_Os02g50350	Pyrimidine metabolism	1.3.1.2
BUPNc	beta-ureidopropionase	cala[c] + h2o[c] + h[c] -> ala-B[c] + co2[c] + nh4[c]	LOC_Os07g30170	Pantothenate and CoA metabolism	3.5.1.6
DHPDc	Dihydropyrimidinase	56dura[c] + h2o[c] <=> cala[c] + h[c]	LOC_Os01g59340	Pantothenate and CoA metabolism	3.5.2.2
TMDSc	Thymidylate synthase	dump[c] + mlthf[c] <=> dhf[c] + dtmp[c]	(LOC_Os12g26060 or LOC_Os11g29390)	Pyrimidine metabolism	2.1.1.45
CYTDc	Cytidine deaminase	cytd[c] + h2o[c] + h[c] -> uri[c] + nh4[c]	(LOC_Os01g51540 or LOC_Os06g40910)	Pyrimidine metabolism	3.5.4.5
GTPCYTDPTc	GTP:cytidine 5-phosphotransferase, cytosolic	cytd[c] + gtp[c] <=> gdp[c] + cmp[c]	(LOC_Os02g17320 or LOC_Os11g16370)	Pyrimidine metabolism	2.7.1.48
GTPCYTDPTs	GTP:cytidine 5-phosphotransferase, plastidic	cytd[s] + gtp[s] <=> gdp[s] + cmp[s]	(LOC_Os02g47020 or LOC_Os04g50880)	Pyrimidine metabolism	2.7.1.48
DCTPDAc	deoxycytidine triphosphate deaminase	dctp[c] + h2o[c] -> nh4[c] + dutp[c]		Pyrimidine metabolism	3.5.4.13
CTPRc	ribonucleoside-triphosphate reductase (CTP)	ctp[c] + fadh2[c] -> fad[c] + h2o[c] + dctp[c]		Pyrimidine metabolism	1.17.4.2
UTPRc	ribonucleoside-triphosphate reductase (UTP)	utp[c] + fadh2[c] -> fad[c] + h2o[c] + dutp[c]		Pyrimidine metabolism	1.17.4.2
ATPRc	ribonucleoside-triphosphate reductase (ATP)	atp[c] + fadh2[c] -> fad[c] + h2o[c] + datp[c]		Pyrimidine metabolism	1.17.4.2
GTPRc	ribonucleoside-triphosphate reductase (GTP)	gtp[c] + fadh2[c] -> fad[c] + h2o[c] + dgtp[c]		Pyrimidine metabolism	1.17.4.2
DCAHc	Deoxycytidine aminohydrolase	dcyt[c] + h2o[c] + h[c] -> duri[c] + nh4[c]	(LOC_Os01g51540 or LOC_Os06g40910)	Pyrimidine metabolism	3.5.4.5
UPRTs	Uracil phosphoribosyltransferase, plastidic	ump[s] + ppi[s] <=> ura[s] + prpp[s]	LOC_Os05g38170	Pyrimidine metabolism	2.4.2.9
UPRTc	Uracil phosphoribosyltransferase, cytosolic	ump[c] + ppi[c] <=> ura[c] + prpp[c]	(LOC_Os11g16370 or LOC_Os02g17320)	Pyrimidine metabolism	2.4.2.9
UPHc	Uridine phosphorylase, cytosolic	pi[c] + uri[c] <=> r1p[c] + ura[c]	LOC_Os08g44370	Pyrimidine metabolism	2.4.2.3
UPHs	Uridine phosphorylase, plastidic	pi[s] + uri[s] <=> r1p[s] + ura[s]		Pyrimidine metabolism	2.4.2.3
DURIKc	ATP:deoxyuridine 5-phosphotransferase	atp[c] + duri[c] -> adp[c] + dump[c] + h[c]	LOC_Os03g02200	Pyrimidine metabolism	2.7.1.21
TMDKc	Thymidine kinase	atp[c] + thymd[c] -> adp[c] + dtmp[c] + h[c]	LOC_Os03g02200	Pyrimidine metabolism	2.7.1.21
ATCYc	ATP:cytidine 5-phosphotransferase, cytosolic	atp[c] + cytd[c] -> adp[c] + cmp[c] + h[c]	(LOC_Os02g17320 or LOC_Os11g16370)	Pyrimidine metabolism	2.7.1.48
ATCYs	ATP:cytidine 5-phosphotransferase, plastidic	atp[s] + cytd[s] -> adp[s] + cmp[s] + h[s]	(LOC_Os02g47020 or LOC_Os04g50880)	Pyrimidine metabolism	2.7.1.48
AUPTc	Uridine kinase, cytosolic	atp[c] + uri[c] -> adp[c] + ump[c] + h[c]	(LOC_Os02g17320 or LOC_Os11g16370)	Pyrimidine metabolism	2.7.1.48
AUPTs	Uridine kinase, plastidic	atp[s] + uri[s] -> adp[s] + ump[s] + h[s]	(LOC_Os02g47020 or LOC_Os04g50880)	Pyrimidine metabolism	2.7.1.48
TPHc	Thymidylate 5-phosphohydrolase, cytosolic	dtmp[c] + h2o[c] -> thymd[c] + pi[c]	LOC_Os01g51280	Pyrimidine metabolism	3.1.3.5
TPHs	Thymidylate 5-phosphohydrolase, plastidic	dtmp[s] + h2o[s] -> thymd[s] + pi[s]	LOC_Os03g44660	Pyrimidine metabolism	3.1.3.5
DUMPc	2-Deoxyuridine 5-monophosphate phosphohydrolase	dump[c] + h2o[c] -> duri[c] + pi[c]	LOC_Os01g51280	Pyrimidine metabolism	3.1.3.5
DCMPc	2-Deoxycytidine 5-monophosphate phosphohydrolase	dcmp[c] + h2o[c] -> dcyt[c] + pi[c]	LOC_Os01g51280	Pyrimidine metabolism	3.1.3.5
CMPc	Cytidine-5-monophosphate phosphohydrolase	cmp[c] + h2o[c] -> cytd[c] + pi[c]	LOC_Os01g51280	Pyrimidine metabolism	3.1.3.5
CMPs	Cytidine-5-monophosphate phosphohydrolase	cmp[s] + h2o[s] -> cytd[s] + pi[s]	LOC_Os03g44660	Pyrimidine metabolism	3.1.3.5
UMPc	Uridine 5-monophosphate phosphohydrolase,	ump[c] + h2o[c] -> uri[c] + pi[c]	LOC_Os01g51280	Pyrimidine metabolism	3.1.3.5

	cytosolic				
UMPs	Uridine 5-monophosphate phosphohydrolase, plastidic	ump[s] + h2o[s] -> uri[s] + pi[s]	LOC_Os03g44660	Pyrimidine metabolism	3.1.3.5
CTPSc	CTP synthetase	atp[c] + utp[c] + gln-L[c] + h2o[c] -> adp[c] + pi[c] + ctp[c] + glu-L[c] + 2 h[c]	(LOC_Os05g49770 or LOC_Os12g36950 or LOC_Os01g43020 or LOC_Os01g46570)	Pyrimidine metabolism	6.3.4.2
DUTNHc	dUTP pyrophosphatase	dutp[c] + h2o[c] -> dump[c] + ppi[c] + h[c]	LOC_Os03g46640	Pyrimidine metabolism	3.6.1.23
DCDTc	2-Deoxycytidine diphosphate:oxidized-thioredoxin 2-oxidoreductase	trdrd[c] + cdp[c] -> dcdp[c] + trdox[c] + h2o[c]	((LOC_Os02g56100 or LOC_Os06g03720) and (LOC_Os06g14620 or LOC_Os06g07210))	Pyrimidine metabolism	1.17.4.1
DUDTc	2-Deoxyuridine 5-diphosphate:oxidized-thioredoxin 2-oxidoreductase	trdrd[c] + udp[c] -> dudp[c] + trdox[c] + h2o[c]	((LOC_Os02g56100 or LOC_Os06g03720) and (LOC_Os06g14620 or LOC_Os06g07210))	Pyrimidine metabolism	1.17.4.1
TDSRs	Thioredoxin reductase (NADPH), plastidic	trdox[s] + nadph[s] + h[s] <=> trdrd[s] + nadp[s]	(LOC_Os07g46410 or LOC_Os06g22140 or LOC_Os02g48290)	Pyrimidine metabolism	1.8.1.9
TDSRc	Thioredoxin reductase (NADPH), cytosolic	trdox[c] + nadph[c] + h[c] <=> trdrd[c] + nadp[c]	(LOC_Os06g22140 or LOC_Os02g48290)	Pyrimidine metabolism	1.8.1.9
TDSRm	Thioredoxin reductase (NADPH), mitochondrial	trdox[m] + nadph[m] + h[m] <=> trdrd[m] + nadp[m]	(LOC_Os06g22140 or LOC_Os02g48290)	Pyrimidine metabolism	1.8.1.9
ATDTDc	ATP:dTDP phosphotransferase	atp[c] + dtdp[c] -> adp[c] + dttp[c]	(LOC_Os10g41410 or LOC_Os02g35700 or LOC_Os12g36194 or LOC_Os05g51700)	Pyrimidine metabolism	2.7.4.6
DTMPKc	dTMP kinase	atp[c] + dtmp[c] -> adp[c] + dtdp[c]	(LOC_Os01g70950 or LOC_Os07g44630)	Pyrimidine metabolism	2.7.4.9
ATDUDc	ATP:dUDP phosphotransferase	atp[c] + dudp[c] -> adp[c] + dutp[c]	(LOC_Os10g41410 or LOC_Os02g35700 or LOC_Os12g36194 or LOC_Os05g51700)	Pyrimidine metabolism	2.7.4.6
DUMPKc	dUMP kinase	atp[c] + dump[c] <=> adp[c] + dudp[c]	(LOC_Os04g33300 or LOC_Os06g02000)	Pyrimidine metabolism	2.7.4.22
ATDCDc	ATP:dCDP phosphotransferase	atp[c] + dcdp[c] -> adp[c] + dctp[c]	(LOC_Os10g41410 or LOC_Os02g35700 or LOC_Os12g36194 or LOC_Os05g51700)	Pyrimidine metabolism	2.7.4.6
DCMPKc	dCMP kinase	atp[c] + dcmp[c] <=> adp[c] + dcdp[c]	LOC_Os07g43170	Pyrimidine metabolism	2.7.4.14
ATCDc	ATP:CDP phosphotransferase, cytosolic	atp[c] + cdp[c] -> adp[c] + ctp[c]	(LOC_Os10g41410 or LOC_Os02g35700 or LOC_Os12g36194 or LOC_Os05g51700)	Pyrimidine metabolism	2.7.4.6
ATCDs	ATP:CDP phosphotransferase, plastidic	atp[s] + cdp[s] -> adp[s] + ctp[s]	(LOC_Os07g30970 or LOC_Os12g36194 or LOC_Os05g51700)	Pyrimidine metabolism	2.7.4.6
CMPKc	CMP kinase, cytosolic	atp[c] + cmp[c] <=> adp[c] + cdp[c]	LOC_Os07g43170	Pyrimidine metabolism	2.7.4.14
CMPKs	CMP kinase, plastidic	atp[s] + cmp[s] <=> adp[s] + cdp[s]	LOC_Os02g53790	Pyrimidine metabolism	2.7.4.14
ATUDc	ATP:UDP phosphotransferase, cystosolic	atp[c] + udp[c] -> adp[c] + utp[c]	(LOC_Os10g41410 or LOC_Os02g35700 or LOC_Os12g36194 or LOC_Os05g51700)	Pyrimidine metabolism	2.7.4.6
ATUDs	ATP:UDP phosphotransferase, plastidic	atp[s] + udp[s] -> adp[s] + utp[s]	(LOC_Os07g30970 or LOC_Os12g36194 or LOC_Os05g51700)	Pyrimidine metabolism	2.7.4.6
ATUDv	ATP:UDP phosphotransferase, vacuolar	atp[v] + udp[v] -> adp[v] + utp[v]	LOC_Os07g30970	Pyrimidine metabolism	2.7.4.6
UMPKc	ATP:UMP phosphotransferase	atp[c] + ump[c] -> adp[c] + udp[c]	(LOC_Os04g33300 or LOC_Os06g02000)	Pyrimidine metabolism	2.7.4.22
MATc	Methionine adenosyltransferase	atp[c] + met-L[c] + h2o[c] -> pi[c] + ppi[c] + amet[c]	(LOC_Os01g18860 or LOC_Os07g29440 or LOC_Os06g11180 or LOC_Os01g22010 or LOC_Os05g04510 or LOC_Os01g10940)	Phytohormones biosynthesis (Ethylene)	2.5.1.6
AMPDc	AMP deaminase	amp[c] + h2o[c] + h[c] -> imp[c] + nh4[c]	(LOC_Os07g49270 or LOC_Os05g28180)	Purine metabolism	3.5.4.6
AMPPc	Adenosine 5-monophosphate phosphohydrolase	amp[c] + h2o[c] -> adn[c] + pi[c]	(LOC_Os01g51280 or LOC_Os03g44660 or LOC_Os07g10460)	Purine metabolism	3.1.3.5
ADNKc	Adenosine kinase	atp[c] + adn[c] -> adp[c] + amp[c] + h[c]	(LOC_Os02g41590 or LOC_Os04g43750)	Purine metabolism	2.7.1.20
APPRTc	Adenine phosphoribosyltransferase, cytosolic	ade[c] + prpp[c] <=> amp[c] + ppi[c]	(LOC_Os02g40010 or LOC_Os04g42520 or LOC_Os12g39860 or LOC_Os07g30150 or LOC_Os12g40130)	Purine metabolism	2.4.2.7
APPRTs	Adenine phosphoribosyltransferase, plastidic	ade[s] + prpp[s] <=> amp[s] + ppi[s]	(LOC_Os12g39860 or LOC_Os05g38170 or LOC_Os12g40130)	Purine metabolism	2.4.2.7

ADSHc	Adenosylhomocysteinase	ahcys[c] + h2o[c] <=> adn[c] + hcys-L[c]	LOC_Os11g26850	Cysteine and methionine metabolism	3.3.1.1
PEPSs	PEP synthetase	h2o[s] + pyr[s] + atp[s] -> pi[s] + pep[s] + amp[s]	LOC_Os06g30310	Glycolysis/Gluconeogensis	2.7.9.2
PYKc	Pyruvate kinase, cytosolic	adp[c] + h[c] + pep[c] -> atp[c] + pyr[c]	(LOC_Os01g16960 or LOC_Os03g20880 or LOC_Os11g10980)	Glycolysis/Gluconeogensis	2.7.1.40
PYKs	Pyruvate kinase, plastidic	adp[s] + h[s] + pep[s] -> atp[s] + pyr[s]	(LOC_Os01g16960 or LOC_Os01g47080 or LOC_Os03g20880 or LOC_Os03g46910 or LOC_Os07g08340 or LOC_Os10g42100 or LOC_Os11g05110 or LOC_Os11g10980 or LOC_Os12g05110)	Glycolysis/Gluconeogensis	2.7.1.40
PPDKs	Pyruvate phosphate dikinase, plastidic	atp[s] + pyr[s] + pi[s] -> ppi[s] + pep[s] + amp[s]	LOC_Os03g31750	Glycolysis/Gluconeogensis	2.7.9.1
PPDKc	Pyruvate phosphate dikinase, cytosolic	atp[c] + pyr[c] + pi[c] -> ppi[c] + pep[c] + amp[c]	LOC_Os05g33570	Glycolysis/Gluconeogensis	2.7.9.1
MDH2c	Malate dehydrogenase (oxaloacetate decarboxylating) (NADP+), cytosolic	mal-L[c] + nadp[c] -> co2[c] + nadph[c] + pyr[c]	LOC_Os05g09440	Glycolysis/Gluconeogensis	1.1.1.40
MDH2s	Malate dehydrogenase (oxaloacetate decarboxylating) (NADP+), plastidic	mal-L[s] + nadp[s] -> co2[s] + nadph[s] + pyr[s]	(LOC_Os01g52500 or LOC_Os01g54030 or LOC_Os01g09320 or LOC_Os05g09440)	Glycolysis/Gluconeogensis	1.1.1.40
PDCm	pyruvate decarboxylase, mitochondrial	2ahethmpp[m] -> acald[m] + thmpp[m]		Fermentation	4.1.1.1
PDCs	pyruvate decarboxylase, plastidic	2ahethmpp[s] -> acald[s] + thmpp[s]	(LOC_Os01g06660 or LOC_Os05g39310 or LOC_Os03g18220 or LOC_Os05g39320 or LOC_Os07g49250)	Fermentation	4.1.1.1
ACSc	acetate--CoA ligase, cytosolic	coa[c] + ac[c] + atp[c] -> accoa[c] + ppi[c] + amp[c]	(LOC_Os02g32490 or LOC_Os04g33190)	Fermentation	6.2.1.1
ACSx	acetate--CoA ligase, peroxisomal	coa[x] + ac[x] + atp[x] -> accoa[x] + ppi[x] + amp[x]		Fermentation	6.2.1.1
ACSs	acetate--CoA ligase, plastidic	coa[s] + ac[s] + atp[s] -> accoa[s] + ppi[s] + amp[s]	LOC_Os02g32490	Fermentation	6.2.1.1
GLU5Kc	Glutamate 5-kinase, cytosolic	atp[c] + glu-L[c] -> adp[c] + glu5p[c]		Arginine and proline metabolism	2.7.2.11
GLU5Ks	Glutamate 5-kinase, plastidic	atp[s] + glu-L[s] -> adp[s] + glu5p[s]	(LOC_Os01g55890 or LOC_Os01g73450)	Arginine and proline metabolism	2.7.2.11
GDHym	Glutamate dehydrogenase (NADP+)	glu-L[m] + nadp[m] + h2o[m] <=> akg[m] + nh4[m] + nadph[m] + h[m]	LOC_Os01g37760	Alanine, aspartate and glutamate metabolism	1.4.1.4
GDHm	Glutamate dehydrogenase (NAD+)	glu-L[m] + nad[m] + h2o[m] <=> akg[m] + nh4[m] + nadh[m] + h[m]	(LOC_Os02g43470 or LOC_Os03g58040 or LOC_Os04g45970)	Alanine, aspartate and glutamate metabolism	1.4.1.2
PYR5CDm	1-pyrroline-5-carboxylate dehydrogenase (NAD), mitochondrial	glu5sa[m] + h2o[m] + nad[m] -> glu-L[m] + 2 h[m] + nadh[m]	(LOC_Os06g36850 or LOC_Os06g36820 or LOC_Os01g74650 or LOC_Os06g05700 or LOC_Os03g50510 or LOC_Os06g42560 or LOC_Os01g59920 or LOC_Os06g36880 or LOC_Os12g42980 or LOC_Os04g08350 or LOC_Os06g05690 or LOC_Os02g12900 or LOC_Os06g36840 or LOC_Os04g32010 or LOC_Os03g53650)	Arginine and proline metabolism	1.2.1.88
PYR5CDs	1-pyrroline-5-carboxylate dehydrogenase (NAD), plastidic	glu5sa[s] + h2o[s] + nad[s] -> glu-L[s] + 2 h[s] + nadh[s]	(LOC_Os06g36850 or LOC_Os06g36820 or LOC_Os01g74650 or LOC_Os06g05700 or LOC_Os03g50510 or LOC_Os06g42560 or LOC_Os01g59920 or LOC_Os06g36880 or LOC_Os12g42980 or LOC_Os04g08350 or LOC_Os06g05690 or LOC_Os02g12900 or LOC_Os06g36840 or LOC_Os04g32010 or LOC_Os03g53650)	Arginine and proline metabolism	1.2.1.88
PYR5CDym	1-pyrroline-5-carboxylate dehydrogenase (NADP), mitochondrial	glu5sa[m] + h2o[m] + nadp[m] -> glu-L[m] + 2 h[m] + nadph[m]	(LOC_Os06g36850 or LOC_Os06g36820 or LOC_Os01g74650 or LOC_Os06g05700 or LOC_Os03g50510 or LOC_Os06g42560 or LOC_Os01g59920 or LOC_Os06g36880 or LOC_Os12g42980 or LOC_Os04g08350 or LOC_Os06g05690 or LOC_Os02g12900 or LOC_Os06g36840 or LOC_Os04g32010 or LOC_Os03g53650)	Arginine and proline metabolism	1.2.1.88

PYR5CDys	1-pyrroline-5-carboxylate dehydrogenase (NADP), plastidic	glu5sa[s] + h2o[s] + nadp[s] -> glu-L[s] + 2 h[s] + nadph[s]	(LOC_Os06g36850 or LOC_Os06g36820 or LOC_Os01g74650 or LOC_Os06g05700 or LOC_Os03g50510 or LOC_Os06g42560 or LOC_Os01g59920 or LOC_Os06g36880 or LOC_Os12g42980 or LOC_Os04g08350 or LOC_Os06g05690 or LOC_Os02g12900 or LOC_Os06g36840 or LOC_Os04g32010 or LOC_Os03g53650)	Arginine and proline metabolism	1.2.1.88
GALc	Glutamate--ammonia ligase, cytosolic	atp[c] + glu-L[c] + nh4[c] -> adp[c] + pi[c] + gln-L[c] + h[c]	(LOC_Os02g50240 or LOC_Os03g12290 or LOC_Os03g50490)	Alanine, aspartate and glutamate metabolism	6.3.1.2
GALm	Glutamate--ammonia ligase, mitochondrial	atp[m] + glu-L[m] + nh4[m] -> adp[m] + pi[m] + gln-L[m] + h[m]	LOC_Os04g56400	Alanine, aspartate and glutamate metabolism	6.3.1.2
GALs	Glutamate--ammonia ligase, plastidic	atp[s] + glu-L[s] + nh4[s] -> adp[s] + pi[s] + gln-L[s] + h[s]	LOC_Os04g56400	Photorespiration	6.3.1.2
AGATm	Alanine--glyoxylate aminotransferase, mitochondrial	glx[m] + ala-L[m] <=> gly[m] + pyr[m]	(LOC_Os03g07570 or LOC_Os03g21960 or LOC_Os05g39770)	Glycine, serine and threonine metabolism	2.6.1.44
AGATx	Alanine--glyoxylate aminotransferase, peroxisomal	glx[x] + ala-L[x] <=> gly[x] + pyr[x]	LOC_Os08g39300	Glycine, serine and threonine metabolism	2.6.1.44
AGATs	Alanine--glyoxylate aminotransferase, plastidic	glx[s] + ala-L[s] <=> gly[s] + pyr[s]	LOC_Os07g01760	Glycine, serine and threonine metabolism	2.6.1.44
ALAATc	Alanine aminotransferase, cytosolic	akg[c] + ala-L[c] <=> glu-L[c] + pyr[c]		Alanine, aspartate and glutamate metabolism	2.6.1.2
ALAATm	Alanine aminotransferase, mitochondrial	akg[m] + ala-L[m] <=> glu-L[m] + pyr[m]	(LOC_Os09g26380 or LOC_Os10g25130 or LOC_Os10g25140)	Alanine, aspartate and glutamate metabolism	2.6.1.2
ALAATs	Alanine aminotransferase, plastidic	akg[s] + ala-L[s] <=> glu-L[s] + pyr[s]	(LOC_Os07g01760 or LOC_Os09g26380 or LOC_Os10g25130 or LOC_Os10g25140)	Alanine, aspartate and glutamate metabolism	2.6.1.2
AAATc	Amino-acid N-acetyltransferase	accoa[c] + glu-L[c] -> coa[c] + acglu[c] + h[c]	(LOC_Os03g31690 or LOC_Os07g39690)	Arginine and proline metabolism	2.3.1.1
ARGDs	Glutamate decarboxylase, plastidic	glu-L[s] + h[s] -> 4abut[s] + co2[s]	LOC_Os04g37500	Alanine, aspartate and glutamate metabolism	4.1.1.15
ARGDc	Glutamate decarboxylase, cytosolic	glu-L[c] + h[c] -> 4abut[c] + co2[c]	LOC_Os03g13300	Alanine, aspartate and glutamate metabolism	4.1.1.15
ARGDm	Glutamate decarboxylase, mitochondrial	glu-L[m] + h[m] -> 4abut[m] + co2[m]	(LOC_Os03g51080 or LOC_Os04g37460 or LOC_Os04g37500 or LOC_Os08g36320)	Alanine, aspartate and glutamate metabolism	4.1.1.15
ASPCLc	L-aspartate 1-carboxy-lyase (beta-alanine-forming)	asp-L[c] <=> ala-B[c] + co2[c]		Alanine, aspartate and glutamate metabolism	4.1.1.16
ICDHc	Isocitrate dehydrogenase (NADP+), cytosolic	icit[c] + nadp[c] <=> akg[c] + co2[c] + nadph[c]	(LOC_Os01g46610 or LOC_Os04g42920 or LOC_Os05g49760)	Sulfate metabolism (Glutathione)	1.1.1.42
ICDHm	Isocitrate dehydrogenase (NADP+), mitochondrial	icit[m] + nadp[m] <=> akg[m] + co2[m] + nadph[m]	(LOC_Os02g38200 or LOC_Os04g40310)	TCA Cycle	1.1.1.42
GTHPs	glutathione peroxidase, plastidic	h2o2[s] + 2 gthrd[s] -> gthox[s] + 2 h2o[s]	(LOC_Os04g46960 or LOC_Os02g44500 or LOC_Os06g08670)	Sulfate metabolism (Glutathione)	1.11.1.9
GTHPc	glutathione peroxidase, cytosolic	h2o2[c] + 2 gthrd[c] -> gthox[c] + 2 h2o[c]	LOC_Os03g24380	Sulfate metabolism (Glutathione)	1.11.1.9
GTHPm	glutathione peroxidase, mitochondrial	h2o2[m] + 2 gthrd[m] -> gthox[m] + 2 h2o[m]	LOC_Os11g18170	Sulfate metabolism (Glutathione)	1.11.1.9
UPGCDc	UDP-glucose 6-dehydrogenase	udpg[c] + h2o[c] + 2 nad[c] -> udpglcur[c] + 2 nadh[c] + 3 h[c]	(LOC_Os03g55070 or LOC_Os12g25700 or LOC_Os12g25690)	Primary Cell Wall Metabolism (Galactose metabolism)	1.1.1.22
GALKc	Galactokinase	atp[c] + gal[c] <=> adp[c] + gal1p[c] + h[c]	(LOC_Os03g61710 or LOC_Os02g04840 or LOC_Os11g11060 or LOC_Os04g51880 or LOC_Os06g48940 or LOC_Os10g18220 or LOC_Os03g02410)	Primary Cell Wall Metabolism (Galactose metabolism)	2.7.1.6
UGLTc	UDP-glucose--hexose-1-phosphate uridylyltransferase	gal1p[c] + udpg[c] <=> g1p[c] + udpgal[c]	LOC_Os07g07550	Primary Cell Wall Metabolism (Galactose	2.7.7.12

				metabolism)	
THAc	alpha,alpha-trehalase	tre[c] + h2o[c] -> 2 glc-B[c]	LOC_Os10g37660	Starch and sucrose metabolism (Sucrose)	3.2.1.28
THPc	Trehalose-phosphatase	tre6p[c] + h2o[c] -> tre[c] + pi[c]	(LOC_Os02g44230 or LOC_Os07g30160 or LOC_Os04g46760 or LOC_Os12g32130 or LOC_Os03g12360 or LOC_Os09g23350 or LOC_Os05g03810 or LOC_Os10g40550 or LOC_Os12g09060)	Starch and sucrose metabolism (Sucrose)	3.1.3.12
TPSc	alpha,alpha-trehalose-phosphate synthase (UDP-forming)	udpg[c] + g6p-A[c] -> udp[c] + tre6p[c] + h[c]	LOC_Os05g44210	Starch and sucrose metabolism (Sucrose)	2.4.1.15
GLCNSc	1,3-beta-glucan synthase	2 udpg[c] + h2o[c] -> b-glucan[c] + 2 udp[c]	(LOC_Os03g03610 or LOC_Os01g34880 or LOC_Os01g34890 or LOC_Os01g34930 or LOC_Os01g48200 or LOC_Os01g55040 or LOC_Os02g14900 or LOC_Os02g58560 or LOC_Os03g02756 or LOC_Os06g02260 or LOC_Os06g08380 or LOC_Os06g51270)	Starch and sucrose metabolism (Cellulose)	2.4.1.34
GLCNGBc	Glucan endo-1,3-beta-D-glucosidase	b-glucan[c] + h2o[c] <=> 2 glc-B[c]	(LOC_Os01g58730 or LOC_Os01g71350 or LOC_Os01g71380 or LOC_Os01g71400 or LOC_Os01g71400 or LOC_Os01g71474 or LOC_Os01g71650 or LOC_Os01g71670 or LOC_Os01g71680 or LOC_Os01g71810 or LOC_Os01g71820 or LOC_Os01g71830 or LOC_Os01g71860 or LOC_Os03g40330 or LOC_Os03g56130)	Starch and sucrose metabolism (Cellulose)	3.2.1.39
GLCNGBv	Glucan endo-1,3-beta-D-glucosidase	b-glucan[v] + h2o[v] <=> 2 glc-B[v]	(LOC_Os01g58730 or LOC_Os01g71350 or LOC_Os01g71380 or LOC_Os01g71400 or LOC_Os01g71400 or LOC_Os01g71474 or LOC_Os01g71650 or LOC_Os01g71670 or LOC_Os01g71680 or LOC_Os01g71810 or LOC_Os01g71820 or LOC_Os01g71830 or LOC_Os01g71860 or LOC_Os03g40330 or LOC_Os03g56130)	Starch and sucrose metabolism (Cellulose)	3.2.1.39
GLCNGAc	Glucan 1,3-beta-glucosidase	b-glucan[c] + h2o[c] <=> 2 glc-A[c]	(LOC_Os01g58730 or LOC_Os01g71350 or LOC_Os01g71380 or LOC_Os01g71400 or LOC_Os01g71400 or LOC_Os01g71474 or LOC_Os01g71650 or LOC_Os01g71670 or LOC_Os01g71680 or LOC_Os01g71810 or LOC_Os01g71820 or LOC_Os01g71830 or LOC_Os01g71860 or LOC_Os03g40330 or LOC_Os03g56130)	Starch and sucrose metabolism (Cellulose)	3.2.1.58
GLCNGAv	Glucan 1,3-beta-glucosidase	b-glucan[v] + h2o[v] <=> 2 glc-A[v]	(LOC_Os01g58730 or LOC_Os01g71350 or LOC_Os01g71380 or LOC_Os01g71400 or LOC_Os01g71400 or LOC_Os01g71474 or LOC_Os01g71650 or LOC_Os01g71670 or LOC_Os01g71680 or LOC_Os01g71810 or LOC_Os01g71820 or LOC_Os01g71830 or LOC_Os01g71860 or LOC_Os03g40330 or LOC_Os03g56130)	Starch and sucrose metabolism (Cellulose)	3.2.1.58
GALUic	UTP--glucose-1-phosphate uridylyltransferase	utp[c] + g1p[c] + h[c] -> ppi[c] + udpg[c]	(LOC_Os02g02560 or LOC_Os09g38030)	Starch and sucrose metabolism (Sucrose)	2.7.7.9
GALUiv	UTP--glucose-1-phosphate uridylyltransferase	utp[v] + g1p[v] + h[v] -> ppi[v] + udpg[v]		Starch and sucrose metabolism (Sucrose)	2.7.7.9
MTGHc	manninotriose galactohydrolase	mnt[c] + h2o[c] -> gal[c] + melib[c]	LOC_Os07g48160	Primary Cell Wall Metabolism (Galactose metabolism)	3.2.1.22
MGHAc	melibiose galactohydrolase (glc-A)	melib[c] + h2o[c] -> gal[c] + glc-A[c]	LOC_Os07g48160	Primary Cell Wall	3.2.1.22

				Metabolism (Galactose metabolism)	
MGHBc	melibiose galactohydrolase (glc-B)	melib[c] + h2o[c] -> gal[c] + glc-B[c]	LOC_Os07g48160	Primary Cell Wall Metabolism (Galactose metabolism)	3.2.1.22
SFHc	stachyose fructohydrolase	stc[c] + h2o[c] -> mnt[c] + fru-B[c]	LOC_Os01g73580	Primary Cell Wall Metabolism (Galactose metabolism)	3.2.1.26
RGHc	Raffinose galactohydrolase	raffin[c] + h2o[c] -> gal[c] + sucr[c]	LOC_Os07g48160	Primary Cell Wall Metabolism (Galactose metabolism)	3.2.1.22
SYGHc	stachyose galactohydrolase	stc[c] + h2o[c] -> raffin[c] + gal[c]	LOC_Os07g48160	Primary Cell Wall Metabolism (Galactose metabolism)	3.2.1.22
GRGTc	galactinol---raffinose galactosyltransferase	1Dgali[c] + raffin[c] -> inost[c] + stc[c]	LOC_Os01g07530	Primary Cell Wall Metabolism (Galactose metabolism)	2.4.1.67
RAFFINSc	raffinose synthase	1Dgali[c] + sucr[c] -> inost[c] + raffin[c]	LOC_Os01g07530	Primary Cell Wall Metabolism (Galactose metabolism)	2.4.1.82
IAGTc	inositol 3-alpha-galactosyltransferase	udpgal[c] + inost[c] -> udp[c] + 1Dgali[c] + h[c]	LOC_Os07g48830	Primary Cell Wall Metabolism (Galactose metabolism)	2.4.1.123
UDPG4Ec	UDP-glucose 4-epimerase	udpg[c] <=> udpgal[c]	(LOC_Os05g51670 or LOC_Os08g28730 or LOC_Os09g15420 or LOC_Os09g35800)	Primary Cell Wall Metabolism (Galactose metabolism)	5.1.3.2
ATGDc	ATP:GDP phosphotransferase, cytosolic	atp[c] + gdp[c] -> adp[c] + gtp[c]	(LOC_Os10g41410 or LOC_Os02g35700 or LOC_Os12g36194 or LOC_Os05g51700)	Purine metabolism	2.7.4.6
ATGDs	ATP:GDP phosphotransferase, plastidic	atp[s] + gdp[s] -> adp[s] + gtp[s]	(LOC_Os07g30970 or LOC_Os12g36194 or LOC_Os05g51700)	Purine metabolism	2.7.4.6
GTPDPKs	GTP diphosphokinase	atp[s] + gtp[s] -> amp[s] + gdptp[s]	(LOC_Os08g35620 or LOC_Os09g27050)	Purine metabolism	2.7.6.5
GBDPs	Guanosine-3,5-bis(diphosphate) 3-pyrophosphohydrolase	ppgpp[s] + h2o[s] -> gdp[s] + ppi[s]	LOC_Os02g47120	Purine metabolism	3.1.7.2
GDTPs	Guanosine-5-triphosphate,3-diphosphate pyrophosphatase	gdptp[s] + h2o[s] -> ppgpp[s] + pi[s] + h[s]	LOC_Os04g58900	Purine metabolism	3.6.1.40
UMPKs	ATP:UMP phosphotransferase	atp[s] + ump[s] -> adp[s] + udp[s]	(LOC_Os04g33300 or LOC_Os06g02000)	Pyrimidine metabolism	2.7.4.22
ATDADc	ATP:dADP phosphotransferase	atp[c] + dadp[c] -> adp[c] + datp[c]	(LOC_Os10g41410 or LOC_Os02g35700 or LOC_Os12g36194 or LOC_Os05g51700)	Purine metabolism	2.7.4.6
ATDGDc	ATP:dGDP phosphotransferase	atp[c] + dgdp[c] -> adp[c] + dgtp[c]	(LOC_Os10g41410 or LOC_Os02g35700 or LOC_Os12g36194 or LOC_Os05g51700)	Purine metabolism	2.7.4.6
PPCKc	Phosphoenolpyruvate carboxykinase (ATP)	oaa[c] + atp[c] -> co2[c] + pep[c] + adp[c]	(LOC_Os03g15050 or LOC_Os10g13700 or LOC_Os04g50208)	Glycolysis/Gluconeogensis	4.1.1.49
MDHys	malate dehydrogenase (NADP+), plastidic	mal-L[s] + nadp[s] <=> oaa[s] + nadph[s] + h[s]	LOC_Os08g44810	Fermentation	1.1.1.82
MDHs	Malate dehydrogenase, plastidic	mal-L[s] + nad[s] <=> oaa[s] + nadh[s] + h[s]	(LOC_Os05g49880 or LOC_Os03g56280 or LOC_Os01g61380 or LOC_Os01g46070 or LOC_Os07g43700 or LOC_Os04g46560 or LOC_Os08g33720 or LOC_Os12g43630)	Glycolysis/Gluconeogensis	1.1.1.37
MDHc	Malate dehydrogenase, cytosolic	mal-L[c] + nad[c] <=> oaa[c] + nadh[c] + h[c]	LOC_Os10g33800	Glyoxylate Cycle	1.1.1.37
MDHx	Malate dehydrogenase, peroxisomal	mal-L[x] + nad[x] <=> oaa[x] + nadh[x] + h[x]	(LOC_Os03g56280 or LOC_Os12g43630)	Glyoxylate Cycle	1.1.1.37
MDHm	Malate dehydrogenase, mitochondrial	mal-L[m] + nad[m] <=> oaa[m] + nadh[m] + h[m]	(LOC_Os05g49880 or LOC_Os01g61380 or LOC_Os01g46070 or LOC_Os07g43700 or LOC_Os08g33720)	TCA Cycle	1.1.1.37

MDHv	Malate dehydrogenase, vacuolar	mal-L[v] + nad[v] <=> oaa[v] + nadh[v] + h[v]	(LOC_Os03g56280 or LOC_Os12g43630)	TCA Cycle	1.1.1.37
PPCc	Phosphoenolpyruvate carboxylase	co2[c] + h2o[c] + pep[c] <=> h[c] + oaa[c] + pi[c]	(LOC_Os01g02050 or LOC_Os08g43710 or LOC_Os01g55350 or LOC_Os01g11054 or LOC_Os09g14670 or LOC_Os08g27840 or LOC_Os02g14770 or LOC_Os01g73970)	Glycolysis/Gluconeogensis	4.1.1.31
ATPCSc	ATP-citrate (pro-S-)-lyase	cit[c] + coa[c] + atp[c] -> oaa[c] + accoa[c] + pi[c] + adp[c]	(LOC_Os01g19450 or LOC_Os12g37870)	TCA Cycle	2.3.3.8
CSx	Citrate synthase, peroxisomal	oaa[x] + accoa[x] + h2o[x] <=> cit[x] + coa[x] + h[x]	LOC_Os02g13840	Glyoxylate Cycle	2.3.3.1
CSm	Citrate synthase, mitochondrial	oaa[m] + accoa[m] + h2o[m] <=> cit[m] + coa[m] + h[m]	(LOC_Os02g10070 or LOC_Os11g33240)	TCA Cycle	2.3.3.1
ASPO1s	L-aspartate oxidase	asp-L[s] + o2[s] -> h[s] + h2o2[s] + iasp[s]	LOC_Os02g04170	Nicotinate and Nicotinamide metabolism	1.4.3.16
NNDPRs	Nicotinate-nucleotide pyrophosphorylase (carboxylating)	2 h[s] + prpp[s] + quln[s] -> co2[s] + nicrnt[s] + ppi[s]	LOC_Os09g38060	Nicotinate and Nicotinamide metabolism	2.4.2.19
NNATc	Nicotinate-nucleotide adenylyltransferase	atp[c] + h[c] + nicrnt[c] <=> dnad[c] + ppi[c]	LOC_Os02g56980	Nicotinate and Nicotinamide metabolism	2.7.7.18
NADS(nh4)c	NAD(+) synthetase	atp[c] + dnad[c] + nh4[c] -> amp[c] + h[c] + nad[c] + ppi[c]	LOC_Os07g07260	Nicotinate and Nicotinamide metabolism	6.3.1.5
NADS(gln-L)c	NAD(+) synthetase (glutamine-hydrolysing)	atp[c] + dnad[c] + gln-L[c] + h2o[c] -> amp[c] + ppi[c] + nad[c] + glu-L[c] + h[c]	LOC_Os07g07260	Nicotinate and Nicotinamide metabolism	6.3.5.1
QULNSs	quinolinate synthase	dhap[s] + iasp[s] -> 2 h2o[s] + pi[s] + quln[s]	LOC_Os12g19304	Nicotinate and Nicotinamide metabolism	2.5.1.72
NAMNPPc	Nicotinate phosphoribosyltransferase	atp[c] + h2o[c] + nac[c] + prpp[c] -> adp[c] + nicrnt[c] + pi[c] + ppi[c]	(LOC_Os03g62110 or LOC_Os04g35060)	Nicotinate and Nicotinamide metabolism	6.3.4.21
NNAMc	nicotinamidase	h2o[c] + ncam[c] -> nac[c] + nh4[c] + h[c]	LOC_Os02g39400	Nicotinate and Nicotinamide metabolism	3.5.1.19
NMNDAc	Nicotinamide-nucleotide amidase	h2o[c] + nmn[c] -> nh4[c] + nicrnt[c] + h[c]		Nicotinate and Nicotinamide metabolism	3.5.1.42
NMNNc	NMN nucleosidase	h2o[c] + nmn[c] <=> h[c] + ncam[c] + r5p[c]		Nicotinate and Nicotinamide metabolism	3.2.2.14
NMNATc	Nicotinamide-nucleotide adenylyltransferase	atp[c] + h[c] + nmn[c] -> nad[c] + ppi[c]	(LOC_Os02g56980 or LOC_Os09g17870)	Nicotinate and Nicotinamide metabolism	2.7.7.1
N2PHs	NADP phosphatase, plastidic	pi[s] + nad[s] -> nadp[s] + h2o[s]		Nicotinate and Nicotinamide metabolism	3.1.3.-
N2PHc	NADP phosphatase, cytosolic	pi[c] + nad[c] -> nadp[c] + h2o[c]	(LOC_Os01g56880 or LOC_Os12g44010)	Nicotinate and Nicotinamide metabolism	3.1.3.-
NADKc	NAD(+) kinase, cytosolic	atp[c] + nad[c] -> adp[c] + h[c] + nadp[c]	LOC_Os09g17680	Nicotinate and Nicotinamide metabolism	2.7.1.23
NADKs	NAD(+) kinase, plastidic	atp[s] + nad[s] -> adp[s] + h[s] + nadp[s]	(LOC_Os11g08670 or LOC_Os05g32210 or LOC_Os01g72690)	Nicotinate and Nicotinamide metabolism	2.7.1.23
NADKm	NAD(+) kinase, mitochondrial	atp[m] + nad[m] -> adp[m] + h[m] + nadp[m]		Nicotinate and Nicotinamide metabolism	2.7.1.23
NADHKc	NADH kinase, cytosolic	atp[c] + nadh[c] -> adp[c] + h[c] + nadph[c]	LOC_Os09g17680	Nicotinate and Nicotinamide metabolism	2.7.1.86
NADHKs	NADH kinase, plastidic	atp[s] + nadh[s] -> adp[s] + h[s] + nadph[s]	(LOC_Os11g08670 or LOC_Os05g32210 or LOC_Os01g72690)	Nicotinate and Nicotinamide metabolism	2.7.1.86
NADHKm	NADH kinase, mitochondrial	atp[m] + nadh[m] -> adp[m] + h[m] + nadph[m]		Nicotinate and Nicotinamide metabolism	2.7.1.86
ASPTAc	Aspartate aminotransferase, cytosolic	akg[c] + asp-L[c] <=> glu-L[c] + oaa[c]	LOC_Os01g55540	Nitrogen metabolism	2.6.1.1
ASPTAm	Aspartate aminotransferase, mitochondrial	akg[m] + asp-L[m] <=> glu-L[m] + oaa[m]	(LOC_Os02g14110 or LOC_Os06g35540)	Nitrogen metabolism	2.6.1.1
ASPTAs	Aspartate aminotransferase, plastidic	akg[s] + asp-L[s] <=> glu-L[s] + oaa[s]	(LOC_Os01g65090 or LOC_Os02g55420)	Nitrogen metabolism	2.6.1.1
GLYTAx	Glycine aminotransferase	glx[x] + glu-L[x] -> gly[x] + akg[x]	LOC_Os07g01760	Photorespiration	2.6.1.4
SUCL(GDP)m	Succinate--CoA ligase (GDP-forming)	succ[m] + coa[m] + gtp[m] <=> succoa[m] + gdp[m] + pi[m]	LOC_Os02g40830	TCA Cycle	6.2.1.4
SUCL(ADP)m	Succinate--CoA ligase (ADP-forming)	succ[m] + coa[m] + atp[m] <=> succoa[m] + adp[m] + pi[m]	LOC_Os02g40830	TCA Cycle	6.2.1.5
CTPCHc	GTP cyclohydrolase I	gtp[c] + h2o[c] -> ahdt[c] + for[c] + 2 h[c]	LOC_Os04g56710	Folates metabolism	3.5.4.16
LYSDCs	Lysine decarboxylase	lys-L[s] + h[s] <=> co2[s] + cadaverine[s]	LOC_Os05g46360	Lysine metabolism	4.1.1.18
AASADc	alpha-aminoadipate reductase	L2aadp[c] + h[c] + nadh[c] <=> L2aadp6sa[c] + nad[c] + h2o[c]	LOC_Os09g26880	Lysine metabolism	1.2.1.31

SACCDyc	Saccharopine dehydrogenase (NADP+, L-lysine forming)	h2o[c] + nadp[c] + saccrp-L[c] <=> akg[c] + lys-L[c] + nadph[c] + h[c]	LOC_Os02g54254	Lysine metabolism	1.5.1.8
SACCDc	Saccharopine dehydrogenase (NAD+, L-glutamate forming)	L2aadp6sa[c] + glu-L[c] + h[c] + nadh[c] <=> h2o[c] + nad[c] + saccrp-L[c]	LOC_Os02g54254	Lysine metabolism	1.5.1.9
AATAc	2-aminoadipate aminotransferase	2oxoadp[c] + glu-L[c] <=> L2aadp[c] + akg[c]		Lysine metabolism	2.6.1.39
PDHam1m	Pyruvate dehydrogenase (lipoamide) (reaction 1), mitochondrial	pyr[m] + thmpp[m] + h[m] -> 2ahethmpp[m] + co2[m]	((LOC_Os09g33500 and LOC_Os08g42410) and (LOC_Os06g13720 and LOC_Os02g50620))	Glycolysis/Gluconeogensis	1.2.4.1
PDHam2m	Pyruvate dehydrogenase (lipoamide) (reaction 2), mitochondrial	2ahethmpp[m] + lpam[m] -> adhlam[m] + thmpp[m]	((LOC_Os09g33500 and LOC_Os08g42410) and (LOC_Os06g13720 and LOC_Os02g50620))	Glycolysis/Gluconeogensis	1.2.4.1
PDHe2m	Dihydrolipoamide S-acetyltransferase, mitochondrial	adhlam[m] + coa[m] <=> accoa[m] + dhlam[m]	(LOC_Os06g30460 or LOC_Os06g01630 or LOC_Os02g01500 or LOC_Os07g22720)	Glycolysis/Gluconeogensis	2.3.1.12
PDHe3m	dihydrolipoyl dehydrogenase, mitochondrial	dhlam[m] + nad[m] <=> h[m] + lpam[m] + nadh[m]	(LOC_Os01g22520 or LOC_Os05g06750)	Glycolysis/Gluconeogensis	1.8.1.4
PDHam1s	Pyruvate dehydrogenase (lipoamide) (reaction 1), plastidic	pyr[s] + thmpp[s] + h[s] -> 2ahethmpp[s] + co2[s]	(LOC_Os04g02900 and (LOC_Os03g44300 and LOC_Os12g42230))	Glycolysis/Gluconeogensis	1.2.4.1
PDHam2s	Pyruvate dehydrogenase (lipoamide) (reaction 2), plastidic	2ahethmpp[s] + lpam[s] -> adhlam[s] + thmpp[s]	(LOC_Os04g02900 and (LOC_Os03g44300 and LOC_Os12g42230))	Glycolysis/Gluconeogensis	1.2.4.1
PDHe2s	Dihydrolipoamide S-acetyltransferase, plastidic	adhlam[s] + coa[s] <=> accoa[s] + dhlam[s]	LOC_Os12g08170	Glycolysis/Gluconeogensis	2.3.1.12
PDHe3s	dihydrolipoyl dehydrogenase, plastidic	dhlam[s] + nad[s] <=> h[s] + lpam[s] + nadh[s]	(LOC_Os01g23610 or LOC_Os05g06460)	Glycolysis/Gluconeogensis	1.8.1.4
AKGDHam1m	2-oxoglutarate dehydrogenase (lipoamide) (reaction 1), mitochondrial	akg[m] + thmpp[m] + h[m] -> 3chpthmpp[m] + co2[m]	(LOC_Os07g49520 or LOC_Os04g32020)	Glycolysis/Gluconeogensis	1.2.4.2
AKGDHam2m	2-oxoglutarate dehydrogenase (lipoamide) (reaction 2), mitochondrial	3chpthmpp[m] + h[m] + lpam[m] -> co2[m] + sdhlam[m]	(LOC_Os07g49520 or LOC_Os04g32020)	TCA Cycle	1.2.4.2
AKGDHe2m	2-oxoglutarate dehydrogenase E2 component	coa[m] + sdhlam[m] + h[m] <=> dhlam[m] + succoa[m]	LOC_Os04g32330	TCA Cycle	2.3.1.61
OXADH1m	2-oxoadipate dehydrogenase E1 component	2oxoadp[m] + h[m] + lpam[m] -> co2[m] + gdhlam[m]	LOC_Os07g49520	Lysine metabolism	1.2.4.2
OXADH2m	2-oxoadipate dehydrogenase E2 component	coa[m] + gdhlam[m] + h[m] <=> dhlam[m] + gcoa[m]	LOC_Os04g32330	Lysine metabolism	2.3.1.61
DAPDCs	Diaminopimelate decarboxylase	26dap-M[s] + h[s] -> lys-L[s] + co2[s]	LOC_Os02g24354	Lysine metabolism	4.1.1.20
MALSs	Malate synthase, plastidic	accoa[s] + glx[s] + h2o[s] -> coa[s] + h[s] + mal-L[s]	LOC_Os04g40990	Photorespiration	2.3.3.9
MALSx	Malate synthase, peroxisomal	accoa[x] + glx[x] + h2o[x] -> coa[x] + h[x] + mal-L[x]		Glyoxylate Cycle	2.3.3.9
GOXx	glycolate oxidase	glyclt[x] + o2[x] -> glx[x] + h2o2[x]	(LOC_Os03g57220 or LOC_Os04g53210 or LOC_Os04g53214 or LOC_Os07g05820)	Photorespiration	1.1.3.15
ICLx	Isocitrate lyase	icit[x] -> glx[x] + succ[x]	LOC_Os07g34520	Glyoxylate Cycle	4.1.3.1
AMOx	aminoacetone:oxygen oxidoreductase(deaminating)	aact[x] + h2o[x] + o2[x] -> mthgxl[x] + nh4[x] + h2o2[x]	LOC_Os04g40040	Glycine, serine and threonine metabolism	1.4.3.21
AOBUTDx	(No enzyme)	2aobut[x] + 2 h[x] -> aact[x] + co2[x]		Glycine, serine and threonine metabolism	spontaneous
THR3DHx	L-threonine 3-dehydrogenase	thr-L[x] + nad[x] -> 2aobut[x] + nadh[x] + 2 h[x]	(LOC_Os01g54940 or LOC_Os04g30420 or LOC_Os08g01760 or LOC_Os08g29170 or LOC_Os05g24880 or LOC_Os09g28570)	Glycine, serine and threonine metabolism	1.1.1.103
GLYATx	Glycine C-acetyltransferase	accoa[x] + gly[x] <=> coa[x] + 2aobut[x] + h[x]		Glycine, serine and threonine metabolism	2.3.1.29
ASPKs	Aspartate kinase	atp[s] + asp-L[s] -> adp[s] + 4pasp[s]	(LOC_Os07g20544 or LOC_Os09g12290 or LOC_Os01g70300 or LOC_Os03g63330 or LOC_Os08g25390)	Glycine, serine and threonine metabolism	2.7.2.4
ASPALs	Aspartate--ammonia ligase	asp-L[s] + atp[s] + nh4[s] -> amp[s] + asn-L[s] + h[s] + ppi[s]	LOC_Os03g18130	Nitrogen metabolism	6.3.1.1
ASPALc	Aspartate--ammonia ligase	asp-L[c] + atp[c] + nh4[c] -> amp[c] + asn-L[c] + h[c] + ppi[c]	LOC_Os06g15420	Nitrogen metabolism	6.3.1.1
ASNNc	Asparaginase	asn-L[c] + h2o[c] -> asp-L[c] + nh4[c]	(LOC_Os04g58600 or LOC_Os04g46370)	Nitrogen metabolism	3.5.1.1
FDHm	Formate dehydrogenase, mitochondrial	for[m] + nad[m] -> co2[m] + nadh[m]	(LOC_Os06g29180 or LOC_Os06g29220)	Folates metabolism	1.2.1.2

FDHNc	Formate dehydrogenase-N	for[c] + q8[m] + 2 h[m] -> q8h2[m] + h[c] + co2[c]	(LOC_Os06g29180 or LOC_Os06g29220)	Folates metabolism	1.2.1.2
SULOx	sulfite oxidase, peroxisomal	hso3[x] + o2[x] + h2o[x] -> so4[x] + h2o2[x] + h[x]	(LOC_Os08g41830 or LOC_Os12g25630)	Sulfate metabolism	1.8.3.1
SULOm	sulfite oxidase, mitochondrial	hso3[m] + o2[m] + h2o[m] -> so4[m] + h2o2[m] + h[m]	(LOC_Os08g41830 or LOC_Os12g25630)	Sulfate metabolism	1.8.3.1
SUATc	Sulfate adenylyltransferase, cytosolic	atp[c] + so4[c] + h[c] -> ppi[c] + aps[c]	(LOC_Os04g02050 or LOC_Os03g53230)	Sulfate metabolism	2.7.7.4
SUATs	Sulfate adenylyltransferase, plastidic	atp[s] + so4[s] + h[s] -> ppi[s] + aps[s]	(LOC_Os04g02050 or LOC_Os03g53230)	Sulfate metabolism	2.7.7.4
ARGNc	Arginase	h2o[c] + arg-L[c] -> orn[c] + urea[c]	LOC_Os04g01590	Arginine and proline metabolism	3.5.3.1
PTORc	putrescine oxidase	ptrc[c] + o2[c] + h2o[c] <=> 4abutn[c] + nh4[c] + h2o2[c]	(LOC_Os06g23114 or LOC_Os06g23140)	Arginine and proline metabolism	1.4.3.10
PAOc	primary-amine oxidase	13dampp[c] + o2[c] + h2o[c] -> bamppald[c] + nh4[c] + h2o2[c]	LOC_Os04g40040	Alanine, aspartate and glutamate metabolism	1.4.3.21
AMPORc	3-aminopropanal:NAD+ oxidoreductase	bamppald[c] + nad[c] + h2o[c] -> ala-B[c] + nadh[c] + 2 h[c]	(LOC_Os11g08300 or LOC_Os09g26880 or LOC_Os04g45720 or LOC_Os02g43280 or LOC_Os02g43194)	Alanine, aspartate and glutamate metabolism	1.2.1.3
SPMDDHc	Spermidine dehydrogenase	spmd[c] + o2[c] + h2o[c] -> 13dampp[c] + 4abutn[c] + h2o2[c]	LOC_Os02g43220	Arginine and proline metabolism	1.5.99.6
ABORc	4-aminobutanal:NAD+ 1-oxidoreductase	4abutn[c] + nad[c] + h2o[c] -> 4abut[c] + nadh[c] + 2 h[c]	(LOC_Os11g08300 or LOC_Os09g26880 or LOC_Os04g45720 or LOC_Os02g43280 or LOC_Os02g43194)	Arginine and proline metabolism	1.2.1.3
ARG2MO	arginine 2-monooxygenase	o2[c] + arg-L[c] -> gabut[c] + co2[c] + h2o[c]	(LOC_Os08g33620 or LOC_Os06g04070 or LOC_Os04g01690)	Arginine and proline metabolism	1.13.12.1
GABUTAHc	4-Guanidinobutanamide amidohydrolase	gabut[c] + h2o[c] -> gabutn + nh4[c]	(LOC_Os04g10434 or LOC_Os06g16030 or LOC_Os11g06900 or LOC_Os12g07150 or LOC_Os04g02754 or LOC_Os04g02780 or LOC_Os04g10410 or LOC_Os04g10460 or LOC_Os04g10530 or LOC_Os04g55050 or LOC_Os10g06710 or LOC_Os11g33090)	Arginine and proline metabolism	3.5.1.4
GABUTNAHc	4-Guanidinobutanoate amidinohydrolase	gabutn[c] + h2o[c] -> 4abut[c] + urea[c]		Arginine and proline metabolism	3.5.3.7
CMPAc	N-carbamoylputrescine amidase	cbmp[c] + h2o[c] + h[c] -> ptrc[c] + co2[c] + nh4[c]	LOC_Os02g33080	Arginine and proline metabolism	3.5.1.53
AGDIc	Agmatine deiminase	agm[c] + h2o[c] -> cbmp[c] + nh4[c]	LOC_Os04g39210	Arginine and proline metabolism	3.5.3.12
AGMTc	Agmatinase	agm[c] + h2o[c] -> ptrc[c] + urea[c]	LOC_Os04g01590	Arginine and proline metabolism	3.5.3.11
ARDCc	Arginine decarboxylase	arg-L[c] + h[c] -> agm[c] + co2[c]	(LOC_Os08g33620 or LOC_Os06g04070 or LOC_Os04g01690)	Arginine and proline metabolism	4.1.1.19
NOSc	Nitric-oxide synthase	arg-L[c] + o2[c] + nadph[c] -> no[c] + citr-L[c] + nadp[c]	LOC_Os03g17170	Arginine and proline metabolism	1.14.13.39
ARGDIc	Arginine deiminase	arg-L[c] + h2o[c] -> citr-L[c] + nh4[c]	LOC_Os11g44860	Arginine and proline metabolism	3.5.3.6
HCGALc	carbamoyl-phosphate synthetase (glutamine-hydrolysing)	2 atp[c] + gln-L[c] + hco3[c] + h2o[c] -> 2 adp[c] + pi[c] + glu-L[c] + cbp[c] + 2 h[c]	(LOC_Os01g68320 or LOC_Os02g47850)	Arginine and proline metabolism	6.3.5.5
ASNS1c	asparagine synthetase (glutamine-hydrolysing), cytosolic	gln-L[c] + h2o[c] -> glu-L[c] + nh4[c]	LOC_Os03g18130	Nitrogen metabolism	6.3.5.4
ASNS1s	asparagine synthetase (glutamine-hydrolysing), plstidic	asp-L[s] + atp[s] + gln-L[s] + h2o[s] -> amp[s] + asn-L[s] + glu-L[s] + h[s] + ppi[s]	LOC_Os06g15420	Nitrogen metabolism	6.3.5.4
PSPs	Phosphoserine phosphatase	pser-L[s] + h2o[s] -> ser-L[s] + pi[s]	(LOC_Os12g31820 or LOC_Os11g41160)	Glycine, serine and threonine metabolism	3.1.3.3
CYSTGLs	Cystathionine gamma-lyase	cyst-L[s] + h2o[s] -> 2obut[s] + cys-L[s] + nh4[s]	LOC_Os01g74650	Cysteine and methionine metabolism	4.4.1.1
CYSTBSs	Cystathionine beta-synthase	hcys-L[s] + ser-L[s] -> cyst-L[s] + h2o[s]	(LOC_Os03g50510 or LOC_Os12g42980 or LOC_Os03g11660 or LOC_Os03g53650)	Cysteine and methionine metabolism	4.2.1.22
SATc	Serine O-acetyltransferase, cytosolic	ser-L[c] + accoa[c] -> acser[c] + coa[c]	(LOC_Os05g45710 or LOC_Os03g04140	Cysteine and methionine	2.3.1.30

			or LOC_Os01g52260)	metabolism	
SATs	Serine O-acetyltransferase, plastidic	ser-L[s] + accoa[s] -> acser[s] + coa[s]	(LOC_Os03g08660 or LOC_Os03g10050)	Cysteine and methionine metabolism	2.3.1.30
SATm	Serine O-acetyltransferase, mitochondrial	ser-L[m] + accoa[m] -> acser[m] + coa[m]	LOC_Os03g10050	Cysteine and methionine metabolism	2.3.1.30
SGATs	Serine--glyoxylate aminotransferase, plastidic	ser-L[s] + glx[s] <=> hpyr[s] + gly[s]		Photorespiration	2.6.1.45
SGATx	Serine--glyoxylate aminotransferase, peroxisomal	ser-L[x] + glx[x] <=> hpyr[x] + gly[x]	LOC_Os08g39300	Photorespiration	2.6.1.45
METSMTc	Methionine S-methyltransferase	met-L[c] + amet[c] -> ahcys[c] + mmet[c]	LOC_Os05g01470	Cysteine and methionine metabolism	2.1.1.12
HCYSMTc	Homocysteine S-methyltransferase (acetylhomocysteine forming)	amet[c] + hcys-L[c] -> ahcys[c] + h[c] + met-L[c]	(LOC_Os12g41390 or LOC_Os01g56610 or LOC_Os03g12110 or LOC_Os10g28630)	Cysteine and methionine metabolism	2.1.1.10
AMETAHYCSTc	S-adenosyl-L-methionine:L-histidine N-methyltransferase	amet[c] <=> ahcys[c]	LOC_Os10g01550	Cysteine and methionine metabolism	2.1.1.37
HCYSMT2c	Homocysteine S-methyltransferase (methionine forming)	mmet[c] + hcys-L[c] -> 2 met-L[c]	(LOC_Os12g41390 or LOC_Os01g56610 or LOC_Os03g12110 or LOC_Os10g28630)	Cysteine and methionine metabolism	2.1.1.10
MSx	5-methyltetrahydropteroyltriglutamate—homocysteine S-methyltransferase, peroxisomal	5mthglu[x] + hcys-L[x] -> met-L[x] + thglu[x]	(LOC_Os12g42876 or LOC_Os12g42884)	Cysteine and methionine metabolism	2.1.1.14
MSv	5-methyltetrahydropteroyltriglutamate—homocysteine S-methyltransferase, vacuolor	5mthglu[v] + hcys-L[v] -> met-L[v] + thglu[v]	(LOC_Os12g42876 or LOC_Os12g42884)	Cysteine and methionine metabolism	2.1.1.14
MSc	5-methyltetrahydropteroyltriglutamate—homocysteine S-methyltransferase, cytosolic	5mthglu[c] + hcys-L[c] -> met-L[c] + thglu[c]	(LOC_Os12g42876 or LOC_Os12g42884)	Cysteine and methionine metabolism	2.1.1.14
ACDOc	acireductone dioxygenase [iron(II)-requiring]	12dmpo[c] + o2[c] -> 2kmb[c] + for[c] + h[c]	(LOC_Os03g06620 or LOC_Os10g28350)	Cysteine and methionine metabolism	1.13.11.54
METLc	Methionine gamma-lyase	met-L[c] + h2o[c] <=> nh4[c] + 2obut[c] + ch4s[c]	(LOC_Os10g37340 or LOC_Os03g06620)	Cysteine and methionine metabolism	4.4.1.11
ACHYSLc	O-Acetyl-L-homoserine acetate-lyase (adding methanethiol)	ch4s[c] + achms[c] <=> met-L[c] + ac[c]		Cysteine and methionine metabolism	2.5.1.49
MOTAc	methionine--phenylpyruvate transaminase	2kmb[c] + glu-L[c] -> met-L[c] + akg[c]	(LOC_Os02g19970 or LOC_Os06g23684 or LOC_Os11g35040 or LOC_Os11g42510)	Cysteine and methionine metabolism	2.6.1.5
M5TRKc	5-methylthioribose kinase	atp[c] + 5mtr[c] -> adp[c] + 5mdr1p[c] + h[c]	LOC_Os04g57400	Cysteine and methionine metabolism	2.7.1.100
MTANc	Methylthioadenosine nucleosidase	5mta[c] + h2o[c] -> ade[c] + 5mtr[c]	LOC_Os06g02220	Cysteine and methionine metabolism	3.2.2.16
SPRMSc	Spermine synthase	5mta[c] + sprm[c] + h[c] <=> ametam[c] + spmd[c]	LOC_Os02g14190	Cysteine and methionine metabolism	2.5.1.22
ORDCc	Ornithine decarboxylase	orn[c] + h[c] -> ptrc[c] + co2[c]	LOC_Os04g04980	Arginine and proline metabolism	4.1.1.17
SPMSc	Spermidine synthase	ametam[c] + ptrc[c] -> 5mta[c] + spmd[c] + h[c]	(LOC_Os02g15550 or LOC_Os06g33710 or LOC_Os07g22600)	Cysteine and methionine metabolism	2.5.1.16
AMCLc	Adenosylmethionine decarboxylase	amet[c] + h[c] -> ametam[c] + co2[c]	(LOC_Os05g04990 or LOC_Os05g13480 or LOC_Os09g24600)	Cysteine and methionine metabolism	4.1.1.50
ACPCSc	1-aminocyclopropane-1-carboxylate synthase	amet[c] -> 1acpc[c] + 5mta[c] + h[c]	(LOC_Os01g09700 or LOC_Os04g48850 or LOC_Os03g51740)	Phytohormones biosynthesis (Ethylene)	4.4.1.14
AMCPCOc	aminocyclopropanecarboxylate oxidase	ascb-L[c] + 1acpc[c] + o2[c] + h[c] -> 2 h2o[c] + dhdascb[c] + co2[c] + cyan[c] + ethylene[c]	(LOC_Os09g27750 or LOC_Os01g39860 or LOC_Os02g53180 or LOC_Os06g37590 or LOC_Os09g27820 or LOC_Os05g05680 or LOC_Os11g08380)	Phytohormones biosynthesis (Ethylene)	1.14.17.4
M5TRPIc	5-methylthioribose-1-phosphate isomerase	5mdr1p[c] -> 5mdru1p[c]	LOC_Os11g11050	Cysteine and methionine metabolism	5.3.1.23
M5TRPHc	methylthioribulose 1-phosphate dehydratase	5mdru1p[c] <=> dkmpp[c] + h2o[c]	LOC_Os11g29370	Cysteine and methionine metabolism	4.2.1.109
ACRSPc	acireductone synthase, phosphate forming	dkmpp[c] + h2o[c] -> 12dmpo[c] + pi[c] + h[c]	(LOC_Os01g01120 or LOC_Os11g29370)	Cysteine and methionine	3.1.3.77

				metabolism	
ENOc	enolase, cytosolic	2pg[c] <=> h2o[c] + pep[c]	(LOC_Os03g15950 or LOC_Os03g14450 or LOC_Os06g04510 or LOC_Os10g08550)	Glycolysis/Gluconeogensis	4.2.1.11
ENOs	enolase, plastidic	2pg[s] <=> h2o[s] + pep[s]	LOC_Os09g20820	Glycolysis/Gluconeogensis	4.2.1.11
ORNTAm	Ornithine--oxo-acid aminotransferase, mitochondrial	orn[m] + akg[m] <=> glu5sa[m] + glu-L[m]	LOC_Os03g44150	Arginine and proline metabolism	2.6.1.13
ORNTAc	Ornithine--oxo-acid aminotransferase, cytosolic	orn[c] + akg[c] <=> glu5sa[c] + glu-L[c]		Arginine and proline metabolism	2.6.1.13
TRPMOc	tryptophan N-monooxygenase	trp-L[c] + 2 nadph[c] + 2 o2[c] + 2 h[c] -> ind3acetaldoxime[c] + co2[c] + 2 nadp[c] + 3 h2o[c]	LOC_Os04g08824	Phytohormones biosynthesis (IAA)	1.14.13.125
IAOc	Indole-3-acetaldehyde oxidase	id3acald[c] + o2[c] + h2o[c] -> ind3ac[c] + h2o2[c] + h[c]	(LOC_Os03g57690 or LOC_Os10g04860)	Phytohormones biosynthesis (IAA)	1.2.3.7
TOORc	Tryptamine:oxygen oxidoreductase(deaminating)	tryptamine[c] + h2o[c] + o2[c] -> nh4[c] + h2o2[c] + id3acald[c]	(LOC_Os06g23140 or LOC_Os06g23114)	Phytohormones biosynthesis (IAA)	1.4.3.6
TRPTAc	Tryptophan aminotransferase	akg[c] + trp-L[c] <=> glu-L[c] + indpyr[c]	(LOC_Os05g07720 or LOC_Os01g07500)	Phytohormones biosynthesis (IAA)	2.6.1.27
ALAADc	Aromatic-L-amino-acid decarboxylase	h[c] + trp-L[c] -> co2[c] + tryptamine[c]	(LOC_Os10g26110 or LOC_Os08g04560 or LOC_Os08g04540)	Phytohormones biosynthesis (IAA)	4.1.1.28
INDPYRDc	Indolepyruvate decarboxylase	h[c] + indpyr[c] <=> co2[c] + id3acald[c]	(LOC_Os01g06660 or LOC_Os07g49250 or LOC_Os05g39320 or LOC_Os05g39310 or LOC_Os03g18220)	Phytohormones biosynthesis (IAA)	4.1.1.74
IAOHLc	3-Indoleacetaldoxime hydro-lyase	ind3acetaldoxime[c] -> h2o[c] + ind3acnl[c]	(LOC_Os01g12740 or LOC_Os01g12750 or LOC_Os01g12770 or LOC_Os01g12760)	Phytohormones biosynthesis (IAA)	4.99.1.6
TRYPTORc	Tryptamine 5-hydroxylase	tryptamine[c] + o2[c] + nadph[c] -> srntn[c] + h2o[c] + nadp[c]	(LOC_Os07g19210 or LOC_Os07g19130)	Phytohormones biosynthesis (IAA)	1.14.13.-
NTRLASEc	nitrilase	2 h2o[c] + ind3acnl[c] -> ind3ac[c] + nh4[c]	(LOC_Os02g42350 or LOC_Os02g42330)	Phytohormones biosynthesis (IAA)	3.5.5.1
TRP2MOc	Tryptophan 2-monooxygenase	trp-L[c] + o2[c] -> h2o[c] + iad[c] + co2[c]		Phytohormones biosynthesis (IAA)	1.13.12.3
AMID3c	indole acetamide hydrolase	h2o[c] + iad[c] -> ind3ac[c] + nh4[c]	(LOC_Os04g02754 or LOC_Os04g02780 or LOC_Os11g06900 or LOC_Os10g06710 or LOC_Os04g55050 or LOC_Os04g10530 or LOC_Os04g10460 or LOC_Os04g10410)	Phytohormones biosynthesis (IAA)	3.5.1.4
IAAGTc	indole-3-acetate beta-glucosyltransferase	ind3ac[c] + udpg[c] -> ind3acg[c] + udp[c]	LOC_Os03g48740	Phytohormones biosynthesis (IAA)	2.4.1.121
IAAINOSTc	IAA-myo-inositol synthase	ind3acg[c] + inost[c] -> iaainost[c] + glc-B[c]		Phytohormones biosynthesis (IAA)	2.3.1.72
IAAIGSc	indol-3-ylacetyl-myo-inositol galactoside synthase	iaainost[c] + udpgal[c] -> iaainostgal[c] + udp[c]		Phytohormones biosynthesis (IAA)	2.4.1.156
IAAIASc	indol-3-ylacetyl-myo-inositol arabinoside synthase	iaainost[c] + udparab[c] -> iaainostarab[c] + udp[c]		Phytohormones biosynthesis (IAA)	2.4.2.34
IAAALASc	indole-3-acetic acid amido synthetase (ala-L)	ind3ac[c] + ala-L[c] + atp[c] -> iaa-ala[c] + amp[c] + ppi[c] + h[c]	(LOC_Os07g47490 or LOC_Os01g55940 or LOC_Os07g40290 or LOC_Os05g42150 or LOC_Os01g57610)	Phytohormones biosynthesis (IAA)	6.3.-.-
IAALEUSc	indole-3-acetic acid amido synthetase (leu-L)	ind3ac[c] + leu-L[c] + atp[c] -> iaa-leu[c] + amp[c] + ppi[c] + h[c]	(LOC_Os07g47490 or LOC_Os01g55940 or LOC_Os07g40290 or LOC_Os05g42150 or LOC_Os01g57610)	Phytohormones biosynthesis (IAA)	6.3.-.-
IAAASPSc	indole-3-acetic acid amido synthetase (asp-L)	ind3ac[c] + asp-L[c] + atp[c] -> iaa-asp[c] + amp[c] + ppi[c] + h[c]	(LOC_Os07g47490 or LOC_Os01g55940 or LOC_Os07g40290 or LOC_Os05g42150 or LOC_Os01g57610)	Phytohormones biosynthesis (IAA)	6.3.-.-
IAAGLUSc	indole-3-acetic acid amido synthetase (glu-L)	ind3ac[c] + glu-L[c] + atp[c] -> iaa-glu[c] + amp[c] + ppi[c] + h[c]	(LOC_Os07g47490 or LOC_Os01g55940 or LOC_Os07g40290 or LOC_Os05g42150 or LOC_Os01g57610)	Phytohormones biosynthesis (IAA)	6.3.-.-

IAAGLNSc	indole-3-acetic acid amido synthetase (gln-L)	ind3ac[c] + gln-L[c] + atp[c] -> iaa-gln[c] + amp[c] + ppi[c] + h[c]	(LOC_Os07g47490 or LOC_Os01g55940 or LOC_Os07g40290 or LOC_Os05g42150 or LOC_Os01g57610)	Phytohormones biosynthesis (IAA)	6.3.-.-
IAAALAHc	IAA-amino acid conjugate hydrolase (iaa-ala)	iaa-ala[c] + h2o[c] -> ind3ac[c] + ala-L[c]	(LOC_Os03g62070 or LOC_Os06g47620 or LOC_Os01g51060 or LOC_Os07g14600 or LOC_Os07g14590 or LOC_Os03g62060 or LOC_Os04g44110 or LOC_Os01g37960)	Phytohormones biosynthesis (IAA)	3.5.1.-
IAALEUHc	IAA-amino acid conjugate hydrolase (iaa-leu)	iaa-leu[c] + h2o[c] -> ind3ac[c] + leu-L[c]	(LOC_Os03g62070 or LOC_Os06g47620 or LOC_Os01g51060 or LOC_Os07g14600 or LOC_Os07g14590 or LOC_Os03g62060 or LOC_Os04g44110 or LOC_Os01g37960)	Phytohormones biosynthesis (IAA)	3.5.1.-
IAAAMYHc	indole-3-acetyl-myo-inositol hydrolase	iaainost[c] + h2o[c] -> inost[c] + ind3ac[c]	(LOC_Os06g44270 or LOC_Os06g44260)	Phytohormones biosynthesis (IAA)	
SERHs	Tryptophan synthase (indoleglycerol phosphate)	ser-L[s] + 3ig3p[s] -> trp-L[s] + g3p[s] + h2o[s]	(LOC_Os03g58260 or LOC_Os07g08430) and (LOC_Os08g04180 or LOC_Os06g42560)	Phenylalanine, tyrosine and tryptophan metabolism	4.2.1.20
TRPS2s	Tryptophan synthase (indole)	ser-L[s] + indole[s] -> trp-L[s] + h2o[s]	(LOC_Os03g58260 or LOC_Os07g08430) and (LOC_Os08g04180 or LOC_Os06g42560)	Phenylalanine, tyrosine and tryptophan metabolism	4.2.1.20
PPDHc	Prephenate dehydratase, cytosolic	pphn[c] + h[c] -> phpyr[c] + h2o[c] + co2[c]		Phenylalanine, tyrosine and tryptophan metabolism	4.2.1.51
PPDHs	Prephenate dehydratase, plastidic	pphn[s] + h[s] -> phpyr[s] + h2o[s] + co2[s]	(LOC_Os07g32774 or LOC_Os04g33390 or LOC_Os09g39260 or LOC_Os09g39230 or LOC_Os08g33260 or LOC_Os10g37980)	Phenylalanine, tyrosine and tryptophan metabolism	4.2.1.51
LDH_Lc	L-lactate dehydrogenase	nadh[c] + pyr[c] + h[c] -> nad[c] + lac-L[c]	(LOC_Os02g01510 or LOC_Os06g01590)	Fermentation	1.1.1.27
MALCOADCc	Malonyl-CoA decarboxylase	co2[c] + accoa[c] -> malcoa[c] + h[c]	LOC_Os09g23070	Alanine, aspartate and glutamate metabolism	4.1.1.9
MALSADHm	malonate-semialdehyde dehydrogenase (acetylating)	nad[m] + msa[m] + coa[m] -> accoa[m] + nadh[m] + co2[m]	LOC_Os07g09060	Alanine, aspartate and glutamate metabolism	1.2.1.18
MALSADHym	malonate-semialdehyde dehydrogenase (acetylating)	nadp[m] + msa[m] + coa[m] -> accoa[m] + nadph[m] + co2[m]	LOC_Os07g09060	Alanine, aspartate and glutamate metabolism	1.2.1.18
ICHDxm	Isocitrate dehydrogenase (NAD+)	icit[m] + nad[m] -> akg[m] + co2[m] + nadh[m]	(LOC_Os04g40320 or LOC_Os02g38200 or LOC_Os01g16900)	TCA Cycle	1.1.1.41
ACALDHc	acetaldehyde dehydrogenase, cytosolic	acald[c] + nad[c] + h2o[c] -> nadh[c] + ac[c] + 2 h[c]	(LOC_Os11g08300 or LOC_Os09g26880 or LOC_Os04g45720 or LOC_Os02g43280 or LOC_Os02g43194)	Fermentation	1.2.1.3
ACALDHs	acetaldehyde dehydrogenase, plastidic	acald[s] + nad[s] + h2o[s] -> nadh[s] + ac[s] + 2 h[s]	(LOC_Os06g15990 or LOC_Os11g08300)	Fermentation	1.2.1.3
ACALDHm	acetaldehyde dehydrogenase, mitochondrial	acald[m] + nad[m] + h2o[m] -> nadh[m] + ac[m] + 2 h[m]	LOC_Os02g49720 or LOC_Os06g15990	Fermentation	1.2.1.3
GLYCRORc	Glycerol:NAD+ oxidoreductase	glyc[c] + nad[c] <=> glyald[c] + nadh[c] + h[c]	(LOC_Os11g08300 or LOC_Os09g26880 or LOC_Os04g45720 or LOC_Os02g43280 or LOC_Os02g43194)	Fermentation	1.2.1.3
GLYCORc	Glycerol:NADP+ oxidoreductase	glyald[c] + nadph[c] + h[c] -> glyc[c] + nadp[c]	LOC_Os05g38230	Fermentation	1.1.1.2
SSNOm	Succinate-semialdehyde dehydrogenase, mitochondrial	sucsal[m] + nad[m] + h2o[m] -> succ[m] + nadh[m] + 2 h[m]	LOC_Os02g07760	Alanine, aspartate and glutamate metabolism	1.2.1.24
TYRDCc	Tyrosine decarboxylase	tyr-L[c] + h[c] -> co2[c] + tyramine[c]	LOC_Os07g25590	Phenylalanine, tyrosine and tryptophan metabolism	4.1.1.25
34HPPORc	3,4-hydroxyphenylpyruvate dioxygenase, cytosolic	34hpp[c] + o2[c] -> hgentis[c] + co2[c]	LOC_Os02g07160	Phenylalanine, tyrosine and tryptophan metabolism	1.13.11.27
34HPPORs	3,4-hydroxyphenylpyruvate dioxygenase, plastidic	34hpp[s] + o2[s] -> hgentis[s] + co2[s]	(LOC_Os02g17920 or LOC_Os05g14194 or LOC_Os08g09250)	Phenylalanine, tyrosine and tryptophan metabolism	1.13.11.27
HGDOc	Homogentisate 1,2-dioxygenase	hgentis[c] + o2[c] -> 4mlacac[c] + h[c]	LOC_Os06g01360	Phenylalanine, tyrosine and tryptophan metabolism	1.13.11.5
PPORs	Prephenate dehydrogenase (NADP+)	pphn[s] + nadp[s] <=> 34hpp[s] + nadph[s] + co2[s]	(LOC_Os06g35050 or LOC_Os06g49520)	Phenylalanine, tyrosine and	1.3.1.13

				tryptophan metabolism	
TYRTAc	Tyrosine aminotransferase, cytosolic	akg[c] + tyr-L[c] -> 34hpp[c] + glu-L[c]	LOC_Os02g20360	Phenylalanine, tyrosine and tryptophan metabolism	2.6.1.5
TYRTAs	Tyrosine aminotransferase, plastidic	akg[s] + tyr-L[s] -> 34hpp[s] + glu-L[s]	(None or LOC_Os02g19970 or LOC_Os06g23684 or LOC_Os11g35040)	Phenylalanine, tyrosine and tryptophan metabolism	2.6.1.5
FAAc	Fumarylacetoacetase	4fumacac[c] + h2o[c] -> acac[c] + fum[c] + h[c]	LOC_Os02g10310	Phenylalanine, tyrosine and tryptophan metabolism	3.7.1.2
MAAIc	Maleylacetoacetate isomerase	4mlacac[c] -> 4fumacac[c]	LOC_Os02g35590	Phenylalanine, tyrosine and tryptophan metabolism	5.2.1.2
ARGDHTs	arogenate dehydratase	arogenate[s] + h[s] -> co2[s] + h2o[s] + phe-L[s]	(LOC_Os03g17730 or LOC_Os04g33390 or LOC_Os07g49390 or LOC_Os09g39230)	Phenylalanine, tyrosine and tryptophan metabolism	4.2.1.91
ARGOAT1s	L-arogenate:oxaloacetate aminotransferase	pphn[s] + asp-L[s] <=> oaa[s] + arogenate[s]	LOC_Os01g65090	Phenylalanine, tyrosine and tryptophan metabolism	2.6.1.78
ARGOAT2s	L-arogenate:2-oxoglutarate aminotransferase	pphn[s] + glu-L[s] <=> akg[s] + arogenate[s]	LOC_Os01g65090	Phenylalanine, tyrosine and tryptophan metabolism	2.6.1.78
ARGDHs	arogenate dehydrogenase	arogenate[s] + nadp[s] -> tyr-L[s] + nadph[s] + co2[s]	LOC_Os06g49520	Phenylalanine, tyrosine and tryptophan metabolism	1.3.1.78
ALCDx2c	alcohol dehydrogenase (NAD)	chol[c] + nad[c] -> betald[c] + nadh[c] + h[c]	(LOC_Os02g42520 or LOC_Os02g57040 or LOC_Os03g08999 or LOC_Os03g09020 or LOC_Os07g42924 or LOC_Os10g07229 or LOC_Os11g10480 or LOC_Os11g10510 or LOC_Os11g10520)	Glycine, serine and threonine metabolism	1.1.1.1
BETALDDHc	Betaine-aldehyde dehydrogenase	betald[c] + nad[c] + h2o[c] -> glybet[c] + nadh[c] + 2 h[c]	(LOC_Os08g32870 or LOC_Os04g39020 or LOC_Os09g26880)	Glycine, serine and threonine metabolism	1.2.1.8
BETHCYSs	Betaine--homocysteine S-methyltransferase	glybet[s] + hcys-L[s] -> met-L[s] + dmetgly[s]		Glycine, serine and threonine metabolism	2.1.1.5
DMTGDHs	dimethylglycine dehydrogenase	dmetgly[s] + fad[s] + h2o[s] -> fadh2[s] + fald[s] + sarc[s]		Glycine, serine and threonine metabolism	1.5.8.4
SARCOs	Sarcosine oxidase	sarc[s] + o2[s] + h2o[s] -> h2o2[s] + fald[s] + gly[s]	LOC_Os12g35890	Glycine, serine and threonine metabolism	1.5.3.1
GLYDHDm	Glycine dehydrogenase (decarboxylating)	gly[m] + lpro[m] <=> alpro[m] + co2[m]	(LOC_Os06g45670 or LOC_Os02g07410 or LOC_Os06g40940 or LOC_Os01g51410 or LOC_Os10g37180)	Photorespiration	1.4.4.2
DHLDHm	dihydrolipoylprotein:NAD+ oxidoreductase	dhlpro[m] + nad[m] <=> lpro[m] + nadh[m] + h[m]	(LOC_Os01g22520 or LOC_Os01g23610 or LOC_Os05g06750)	Photorespiration	1.8.1.4
MTAMnh4m	Aminomethyltransferase	alpro[m] + thf[m] + h[m] <=> dhlpro[m] + mlthf[m] + nh4[m]	(LOC_Os06g04380 or LOC_Os04g53230)	Photorespiration	2.1.2.10
THRAc	L-threonine aldolase	thr-L[c] -> acald[c] + gly[c]	LOC_Os04g43650	Glycine, serine and threonine metabolism	4.1.2.5
ALCDx1c	alcohol dehydrogenase	acald[c] + nadh[c] + h[c] <=> etoh[c] + nad[c]	(LOC_Os02g42520 or LOC_Os02g57040 or LOC_Os03g08999 or LOC_Os03g09020 or LOC_Os07g42924 or LOC_Os10g07229 or LOC_Os11g10480 or LOC_Os11g10510 or LOC_Os11g10520)	Fermentation	1.1.1.1
MAN6PIc	Mannose-6-phosphate isomerase	man6p[c] <=> f6p-B[c]	(LOC_Os11g38810 or LOC_Os09g22090 or LOC_Os01g03710)	Primary Cell Wall Metabolism (Fructose)	5.3.1.8
PMANMc	Phosphomannomutase	man1p[c] <=> man6p[c]	(LOC_Os06g28194 or LOC_Os04g58580 or LOC_Os07g26610)	Primary Cell Wall Metabolism (Fructose)	5.4.2.8
MANKINc	Hexokinase (D-mannose)	man[c] + atp[c] -> man6p[c] + adp[c]	(LOC_Os06g45980 or LOC_Os05g31110 or LOC_Os01g71320)	Primary Cell Wall Metabolism (Fructose)	2.7.1.7
MDHARc	Monodehydroascorbate reductase (NADH), cytosolic	2 mhdascb[c] + nadh[c] + h[c] -> 2 ascb-L[c] + nad[c]	LOC_Os08g44340	Ascorbate Metabolism	1.6.5.4
MDHARs	Monodehydroascorbate reductase (NADH), plastidic	2 mhdascb[s] + nadh[s] + h[s] -> 2 ascb-L[s] + nad[s]		Ascorbate Metabolism; Water-water cycle	1.6.5.4
MDHARm	Monodehydroascorbate reductase (NADH), mitochondrial	2 mhdascb[m] + nadh[m] + h[m] -> 2 ascb-L[m] + nad[m]	LOC_Os09g39380	Ascorbate Metabolism	1.6.5.4

MDHARyc	Monodehydroascorbate reductase (NADPH), cytosolic	2 mhdascb[c] + nadph[c] + h[c] -> 2 ascb-L[c] + nadp[c]	(LOC_Os02g47790 or LOC_Os08g44340)	Ascorbate Metabolism	1.6.5.-
MDHARys	Monodehydroascorbate reductase (NADPH), plastidic	2 mhdascb[s] + nadph[s] + h[s] -> 2 ascb-L[s] + nadp[s]	LOC_Os09g39380	Ascorbate Metabolism; Water-water cycle	1.6.5.-
MDHARym	Monodehydroascorbate reductase (NADPH), mitochondrial	2 mhdascb[m] + nadph[m] + h[m] -> 2 ascb-L[m] + nadp[m]		Ascorbate Metabolism	1.6.5.-
ASCOXc	L-ascorbate oxidase	o2[c] + 4 ascb-L[c] + 4 h[c] -> 2 h2o[c] + 4 mhdascb[c]	LOC_Os06g37150	Ascorbate Metabolism	1.10.3.3
ASCPO1c	L-ascorbate peroxidase (reaction 1), cytosolic	2 ascb-L[c] + h2o2[c] + 2 h[c] -> 2 mhdascb[c] + 2 h2o[c]	(LOC_Os03g17690 or LOC_Os07g49400)	Ascorbate Metabolism	1.11.1.11
ASCPO1s	L-ascorbate peroxidase (reaction 1), plastidic	2 ascb-L[s] + h2o2[s] + 2 h[s] -> 2 mhdascb[s] + 2 h2o[s]	(LOC_Os12g07830 or LOC_Os12g07820)	Ascorbate Metabolism; Water-water cycle	1.11.1.11
ASCPO2c	L-ascorbate peroxidase (reaction 2), cytosolic	2 mhdascb[c] + 2 h[c] -> ascb-L[c] + dhdascb[c]		Ascorbate Metabolism	spontaneous
ASCPO2s	L-ascorbate peroxidase (reaction 2), plastidic	2 mhdascb[s] + 2 h[s] -> dhdascb[s] + ascb-L[s]		Ascorbate Metabolism; Water-water cycle	spontaneous
GGTv	gamma-glutamyltransferase	h2o[v] + gthrd[v] <=> glu-L[v] + cgly[v]	(LOC_Os01g05810 or LOC_Os01g05820 or LOC_Os04g38450)	Sulfate metabolism (Glutathione)	2.3.2.2
CYSGLYv	cysteinylglycinase	cgly[v] + h2o[v] -> cys-L[v] + gly[v]	LOC_Os08g44860	Sulfate metabolism (Glutathione)	3.4.11.2
GLUCYSs	Glutamate--cysteine ligase, plastidic	atp[s] + cys-L[s] + glu-L[s] -> adp[s] + glucys[s] + h[s] + pi[s]	LOC_Os05g03820	Sulfate metabolism (Glutathione)	6.3.2.2
GLUCYSm	Glutamate--cysteine ligase, mitochondrial	atp[m] + cys-L[m] + glu-L[m] -> adp[m] + glucys[m] + h[m] + pi[m]	LOC_Os07g27790	Sulfate metabolism (Glutathione)	6.3.2.2
GTHSs	glutathione synthetase, plastidic	atp[s] + glucys[s] + gly[s] -> adp[s] + gthrd[s] + h[s] + pi[s]	(LOC_Os12g16200 or LOC_Os12g34380 or LOC_Os11g42350)	Sulfate metabolism (Glutathione)	6.3.2.3
GTHSm	glutathione synthetase, mitochondrial	atp[m] + glucys[m] + gly[m] -> adp[m] + gthrd[m] + h[m] + pi[m]		Sulfate metabolism (Glutathione)	6.3.2.3
GTHDHc	Glutathione dehydrogenase (ascorbate), cytosolic	dhdascb[c] + 2 gthrd[c] -> gthox[c] + ascb-L[c]	LOC_Os02g34530	Ascorbate Metabolism	1.8.5.1
GTHDHs	Glutathione dehydrogenase (ascorbate), plastidic	dhdascb[s] + 2 gthrd[s] -> gthox[s] + ascb-L[s]	LOC_Os06g12630	Ascorbate Metabolism; Water-water cycle	1.8.5.1
GALLDHm	Galactonolactone dehydrogenase, mitochondrial	focytc[m] + gallac[c] <=> ficytc[m] + ascb-L[c] + h[m]	(LOC_Os11g04740 or LOC_Os12g04520)	Ascorbate Metabolism	1.3.2.3
GALDHc	L-galactose 1-dehydrogenase	gal-L[c] + nad[c] -> gallac[c] + nadh[c] + h[c]	LOC_Os12g29760	Ascorbate Metabolism	1.1.1.-
GDPGPc	GDP-L-galactose phosphorylase	gdpgal[c] + h2o[c] -> gdp[c] + h[c] + gal-L[c]	LOC_Os12g08810	Ascorbate Metabolism	2.7.7.69
GDPME1c	GDP-mannose 3,5-epimerase	gdpmann[c] <=> gdpgal[c]	LOC_Os10g28200	Ascorbate Metabolism	5.1.3.18
GDPME3c	GDP-D-galactose:GDP-L-gulose epimerase	gdpgal[c] <=> gdpgul[c]	LOC_Os10g28200	Ascorbate Metabolism	5.1.3.18
GAMPGc	Mannose-1-phosphate guanylyltransferase	gtp[c] + man1p[c] + h[c] -> ppi[c] + gdpmann[c]	(LOC_Os01g62840 or LOC_Os03g16150 or LOC_Os08g13930)	Primary Cell Wall Metabolism (Fructose)	2.7.7.13
GMANDc	GDP-D-mannose dehydratase	gdpmann[c] -> h2o[c] + gdpddman[c]	LOC_Os06g04620	Primary Cell Wall Metabolism (Fructose)	4.2.1.47
GOFUCRc	GDP-4-oxo-L-fucose reductase	gdpddman[c] + h[c] + nadph[c] -> gdpfuc[c] + nadp[c]	LOC_Os06g44270	Primary Cell Wall Metabolism (Fructose)	1.1.1.271
FUCPGTc	fucose-1-phosphate guanylyltransferase	gdpfuc[c] + ppi[c] <=> gtp[c] + h[c] + fuc1p[c]	LOC_Os03g02410	Primary Cell Wall Metabolism (Fructose)	2.7.7.30
LACDHc	Lactaldehyde dehydrogenase	h2o[c] + nad[c] + lald[c] -> nadh[c] + lac-L[c] + 2 h[c]	(LOC_Os01g40860 or LOC_Os01g40870 or LOC_Os02g07760 or LOC_Os02g49720 or LOC_Os05g45960 or LOC_Os06g15990 or LOC_Os06g39230 or LOC_Os06g39230 or LOC_Os09g26880 or LOC_Os02g43280 or LOC_Os02g43194 or LOC_Os11g08300 or LOC_Os12g07810)	Fermentation	1.2.1.22
FCPAc	L-fuculose-phosphate aldolase	fc1p[c] -> lald[c] + dhap[c]		Fermentation	4.1.2.17
FCKc	L-fuculokinase	atp[c] + fcl-L[c] -> adp[c] + fc1p[c] + h[c]		Primary Cell Wall Metabolism (Fructose)	2.7.1.51
FCIc	L-fucose isomerase	fuc-L[c] <=> fcl-L[c]	LOC_Os04g05880	Primary Cell Wall Metabolism (Fructose)	5.3.1.25
FUKc	fucokinase	fuc-L[c] + atp[c] <=> h[c] + fuc1p[c] + adp[c]	LOC_Os03g02410	Primary Cell Wall Metabolism (Fructose)	2.7.1.52

FBPc	Fructose-bisphosphatase, cytosolic	fdp-B[c] + h2o[c] -> f6p-B[c] + pi[c]	(LOC_Os01g64660 or LOC_Os03g18310)	Glycolysis/Gluconeogensis	3.1.3.11
FBPs	Fructose-bisphosphatase, plastidic	fdp-B[s] + h2o[s] -> f6p-B[s] + pi[s]	LOC_Os03g16050	Glycolysis/Gluconeogensis	3.1.3.11
SPSc	Sucrose-phosphate synthase, cytosol	udpg[c] + f6p-B[c] -> suc6p[c] + udp[c] + h[c]	(LOC_Os11g12810 or LOC_Os02g09170 or LOC_Os08g20660 or LOC_Os01g69030 or LOC_Os06g43630)	Starch and sucrose metabolism (Sucrose)	2.4.1.14
SPSv	Sucrose-phosphate synthase, vacuolar	udpg[v] + f6p-B[v] -> suc6p[v] + udp[v] + h[v]		Starch and sucrose metabolism (Sucrose)	2.4.1.14
PGI1c	Glucose-6-phosphate isomerase (g6p-A), cytoslic	g6p-A[c] <=> f6p-B[c]	(LOC_Os03g56460 or LOC_Os06g14510)	Glycolysis/Gluconeogensis	5.3.1.9
PGI1s	Glucose-6-phosphate isomerase (g6p-A), plastidic	g6p-A[s] <=> f6p-B[s]	(LOC_Os08g37380 or LOC_Os09g29070)	Glycolysis/Gluconeogensis	5.3.1.9
PGI2c	Glucose-6-phosphate isomerase (g6p-B), cytoslic	g6p-B[c] <=> f6p-B[c]	(LOC_Os03g56460 or LOC_Os06g14510)	Glycolysis/Gluconeogensis	5.3.1.9
PGI2s	Glucose-6-phosphate isomerase (g6p-B), plastidic	g6p-B[s] <=> f6p-B[s]	(LOC_Os08g37380 or LOC_Os09g29070)	Glycolysis/Gluconeogensis	5.3.1.9
NO2Rs	Ferredoxin--nitrite reductase	no2[s] + 6 fdxrd[s] + 7 h[s] -> nh4[s] + 6 fdxox[s] + 2 h2o[s]	(LOC_Os01g25520 or LOC_Os01g25520)	Nitrogen metabolism	1.7.7.1
NODOx	nitric oxide, NADH2:oxygen oxidoreductase	2 no[c] + 2 o2[c] + nadh[c] -> 2 no3[c] + nad[c] + h[c]		Nitrogen metabolism	1.14.12.17
NODOy	nitric oxide, NADPH2:oxygen oxidoreductase	2 no[c] + 2 o2[c] + nadph[c] -> 2 no3[c] + nadp[c] + h[c]		Nitrogen metabolism	1.14.12.17
NITRc	nitrate reductase (NADH), cytosolic	no3[c] + nadh[c] + h[c] -> no2[c] + nad[c] + h2o[c]	(LOC_Os02g53130 or LOC_Os08g36480 or LOC_Os08g36500)	Nitrogen metabolism	1.7.1.1
NITRv	nitrate reductase (NADH), vacuolar	no3[v] + nadh[v] + h[v] -> no2[v] + nad[v] + h2o[v]	(LOC_Os02g53130 or LOC_Os08g36480 or LOC_Os08g36500)	Nitrogen metabolism	1.7.1.1
BFFSc	Beta-fructofuranosidase, cytoslic	suc6p[c] + h2o[c] -> fru-B[c] + g6p-B[c]	(LOC_Os04g56920 or LOC_Os02g01590 or LOC_Os01g73580 or LOC_Os04g45290 or LOC_Os02g33110 or LOC_Os11g07440 or LOC_Os03g20020 or LOC_Os02g34560 or LOC_Os02g03320 or LOC_Os01g22900)	Starch and sucrose metabolism (Sucrose)	3.2.1.26
BFFSv	Beta-fructofuranosidase, vacuolar	suc6p[v] + h2o[v] -> fru-B[v] + g6p-B[v]	(LOC_Os04g56920 or LOC_Os02g01590 or LOC_Os01g73580 or LOC_Os04g45290 or LOC_Os02g33110 or LOC_Os11g07440 or LOC_Os03g20020 or LOC_Os02g34560 or LOC_Os02g03320 or LOC_Os01g22900)	Starch and sucrose metabolism (Sucrose)	3.2.1.26
INVc	Invertase, cytosolic	sucr[c] + h2o[c] -> fru-B[c] + glc-A[c]	(LOC_Os04g56920 or LOC_Os02g01590 or LOC_Os01g73580 or LOC_Os04g45290 or LOC_Os02g33110 or LOC_Os11g07440 or LOC_Os03g20020 or LOC_Os02g34560 or LOC_Os02g03320 or LOC_Os01g22900)	Starch and sucrose metabolism (Sucrose)	3.2.1.26
INVv	Invertase, vacuolar	sucr[v] + h2o[v] -> fru-B[v] + glc-A[v]	(LOC_Os04g56920 or LOC_Os02g01590 or LOC_Os01g73580 or LOC_Os04g45290 or LOC_Os02g33110 or LOC_Os11g07440 or LOC_Os03g20020 or LOC_Os02g34560 or LOC_Os02g03320 or LOC_Os01g22900)	Starch and sucrose metabolism (Sucrose)	3.2.1.26
SPPc	Sucrose-phosphatase, cytosolic	suc6p[c] + h2o[c] -> sucr[c] + pi[c]	(LOC_Os01g27880 or LOC_Os02g05030 or LOC_Os05g05270)	Starch and sucrose metabolism (Sucrose)	3.1.3.24
SPPv	Sucrose-phosphatase, vacuolar	suc6p[v] + h2o[v] -> sucr[v] + pi[v]		Starch and sucrose metabolism (Sucrose)	3.1.3.24
SUSc	Sucrose synthase, cytosolic	udpg[c] + fru-B[c] <=> sucr[c] + udp[c] + h[c]	(LOC_Os03g22120 or LOC_Os02g58480 or LOC_Os04g17650 or LOC_Os04g24430)	Starch and sucrose metabolism (Sucrose)	2.4.1.13
SUSv	Sucrose synthase, vacuolar	udpg[v] + fru-B[v] <=> sucr[v] + udp[v] + h[v]	(LOC_Os03g28330 or LOC_Os06g09450 or LOC_Os07g42490)	Starch and sucrose metabolism (Sucrose)	2.4.1.13
MI3PSc	myo-inositol-1-phosphate synthase	g6p-B[c] -> mi3p-D[c]	(LOC_Os10g22450 or LOC_Os03g09250)	Primary Cell Wall	5.5.1.4

				Metabolism (Inositol phosphate)	
SULRs	Sulfite reductase (ferredoxin)	hso3[s] + 3 fdxrd[s] + 6 h[s] -> h2s[s] + 3 fdxox[s] + 3 h2o[s]	LOC_Os05g42350	Sulfate metabolism	1.8.7.1
XYL2c	Xylose isomerase, cytosolic	glc-A[c] <=> fru-B[c]	LOC_Os12g42900	Primary Cell Wall Metabolism (Fructose)	5.3.1.5
XYL2v	Xylose isomerase, vacuolar	glc-A[v] <=> fru-B[v]	LOC_Os07g47290	Primary Cell Wall Metabolism (Fructose)	5.3.1.5
UDPACGEc	UDP-N-acetylglucosamine 4-epimerase	uacgam[c] -> uacmam[c]		Primary Cell Wall Metabolism (Amino sugars)	5.1.3.7
UDPACGLPc	UDP-N-acetylglucosamine pyrophosphorylase	utp[c] + acgam1p[c] + h[c] -> ppi[c] + uacgam[c]	LOC_Os03g52460	Primary Cell Wall Metabolism (Amino sugars)	2.7.7.23
ACGAMPMc	Phosphoacetylglucosamine mutase	acgam6p[c] <=> acgam1p[c]	LOC_Os07g09720	Primary Cell Wall Metabolism (Amino sugars)	5.4.2.3
ACGAM6PSic	Glucosamine-phosphate N-acetyltransferase	accoa[c] + gam6p[c] -> coa[c] + acgam6p[c] + h[c]	LOC_Os09g31310	Primary Cell Wall Metabolism (Amino sugars)	2.3.1.4
GAMPTc	ATP:D-glucosamine 6-phosphotransferase	atp[c] + gam[c] <=> gam6p[c] + adp[c]	LOC_Os01g52450	Primary Cell Wall Metabolism (Amino sugars)	2.7.1.1
GAMACTc	glucosamine acetyltransferase	accoa[c] + gam[c] <=> coa[c] + acgam[c] + h[c]	LOC_Os09g31310	Primary Cell Wall Metabolism (Amino sugars)	2.3.1.4
ACGAMKc	N-acetylglucosamine kinase	atp[c] + acgam[c] <=> adp[c] + acgam6p[c]		Primary Cell Wall Metabolism (Amino sugars)	2.7.1.59
CAGHc	chitobiose N-acetylglucosaminohydrolase	chitb[c] + h2o[c] -> 2 acgam[c]	(LOC_Os01g66700 or LOC_Os03g11980 or LOC_Os05g02510 or LOC_Os05g34320 or LOC_Os07g38790)	Primary Cell Wall Metabolism (Amino sugars)	3.2.1.52
CHITNc	chitinase	chitin[c] + h2o[c] -> acgam[c]	(LOC_Os01g66700 or LOC_Os03g11980 or LOC_Os05g02510 or LOC_Os05g34320 or LOC_Os07g38790)	Primary Cell Wall Metabolism (Amino sugars)	3.2.1.14
ACGAM2Ec	N-acetylglucosamine 2-epimerase	acgam[c] <=> acmana[c]		Primary Cell Wall Metabolism (Amino sugars)	5.1.3.8
UAG2EMAic	UDP-N-acetyl-D-glucosamine 2-epimerase (Hydrolysis)	h2o[c] + uacgam[c] -> acmana[c] + h[c] + udp[c]		Primary Cell Wall Metabolism (Amino sugars)	5.1.3.14
ACNMLc	N-Acetylneuraminate lyase	acnam[c] <=> acmana[c] + pyr[c]		Primary Cell Wall Metabolism (Amino sugars)	4.1.3.3
CMPSASc	CMP sialic acid synthase	acnam[c] + ctp[c] -> cmpacna[c] + ppi[c]		Primary Cell Wall Metabolism (Amino sugars)	2.7.7.43
GF6PTAc	Glucosamine--fructose-6-phosphate aminotransferase (isomerizing)	gln-L[c] + f6p-B[c] -> glu-L[c] + gam6p[c]	(LOC_Os11g03900 or LOC_Os12g03720)	Primary Cell Wall Metabolism (Amino sugars)	2.6.1.16
FKc	Fructokinase	fru-B[c] + atp[c] -> f6p-B[c] + adp[c] + h[c]	(LOC_Os01g66940 or LOC_Os08g02120)	Starch and sucrose metabolism (Sucrose)	2.7.1.4
MCPSTm	3-mercaptopyruvate sulfurtransferase	cyan[m] + mercppyr[m] -> pyr[m] + tcynt[m] + h[m]	(LOC_Os12g41500 or LOC_Os02g07044)	Cysteine and methionine metabolism	2.8.1.2
TSSTm	Thiosulfate sulfurtransferase	tsul[m] + cyan[m] <=> tcynt[m] + h[m] + hso3[m]	(LOC_Os12g41500 or LOC_Os02g07044)	Cysteine and methionine metabolism	2.8.1.1
MCPSTs	3-mercaptopyruvate sulfurtransferase	cyan[s] + mercppyr[s] -> pyr[s] + tcynt[s] + h[s]	(LOC_Os12g41500 or LOC_Os02g07044)	Cysteine and methionine metabolism	2.8.1.2
TSSTs	Thiosulfate sulfurtransferase	tsul[s] + cyan[s] <=> tcynt[s] + h[s] + hso3[s]	(LOC_Os12g41500 or LOC_Os02g07044)	Cysteine and methionine metabolism	2.8.1.1
SOXs	sulfite oxidase	hso3[s] + o2[s] + h2o[s] <=> so4[s] + h2o2[s]	(LOC_Os08g41830 or LOC_Os12g25630)	Sulfate metabolism	1.8.3.1
CYSATs	aspartate aminotransferase, cysteine forming, plastidic	mercppyr[s] + glu-L[s] -> cys-L[s] + akg[s]	LOC_Os02g55420	Cysteine and methionine metabolism	2.6.1.1
CYSATm	aspartate aminotransferase, cysteine forming, mitochondrial	mercppyr[m] + glu-L[m] -> cys-L[m] + akg[m]	(LOC_Os02g14110 or LOC_Os06g35540)	Cysteine and methionine metabolism	2.6.1.1
AATCs	aspartate aminotransferase, cysteate forming, plastidic	3sala[s] + akg[s] <=> 3spyr[s] + glu-L[s]	LOC_Os02g55420	Cysteine and methionine metabolism	2.6.1.1
AATCm	aspartate aminotransferase, cysteate forming, mitochondrial	3sala[m] + akg[m] <=> 3spyr[m] + glu-L[m]	(LOC_Os02g14110 or LOC_Os06g35540)	Cysteine and methionine metabolism	2.6.1.1

3SPYRSPs	3-sulfinopyruvate hydrolase (spontaneous), plastidic	3spyr[s] + h2o[s] -> hso3[s] + pyr[s]		Cysteine and methionine metabolism	
3SPYRSPm	3-sulfinopyruvate hydrolase (spontaneous), mitochondrial	3spyr[m] + h2o[m] -> hso3[m] + pyr[m]		Cysteine and methionine metabolism	
LCYSTSs	cysteine dioxygenase, plastid	cys-L[s] + o2[s] -> 3sala[s]		Cysteine and methionine metabolism	1.13.11.20
LCYSTSm	cysteine dioxygenase, mitochondrial	cys-L[m] + o2[m] -> 3sala[m]		Cysteine and methionine metabolism	1.13.11.20
CYSSc	Cysteine synthase, cytosolic	acser[c] + h2s[c] -> cys-L[c] + ac[c] + h[c]	(LOC_Os02g12900 or LOC_Os03g53650 or LOC_Os12g42980)	Cysteine and methionine metabolism	2.5.1.47
CYSSm	Cysteine synthase, mitochondrial	acser[m] + h2s[m] -> cys-L[m] + ac[m] + h[m]	LOC_Os01g74650	Cysteine and methionine metabolism	2.5.1.47
CYSSs	Cysteine synthase, plastidic	acser[s] + h2s[s] -> cys-L[s] + ac[s] + h[s]	(LOC_Os01g59920 or LOC_Os06g05690 or LOC_Os04g08350 or LOC_Os03g50510)	Cysteine and methionine metabolism	2.5.1.47
ALABATc	b-alanine-pyruvate aminotransferase	msa[c] + ala-L[c] -> ala-B[c] + pyr[c]		Alanine, aspartate and glutamate metabolism	2.6.1.18
DHFRc	Dihydrofolate reductase, cytosolic	dhf[c] + h[c] + nadph[c] <=> nadp[c] + thf[c]	(LOC_Os12g26060 or LOC_Os11g29390)	Folates metabolism	1.5.1.3
DHFRm	Dihydrofolate reductase, mitochondrial	dhf[m] + h[m] + nadph[m] <=> nadp[m] + thf[m]		Folates metabolism	1.5.1.3
FPGSc	folylpolyglutamate synthetase	atp[c] + 10fthf[c] + glu-L[c] -> adp[c] + pi[c] + 10fthglu[c]	(LOC_Os03g02030 or LOC_Os10g35940 or LOC_Os10g40130 or LOC_Os12g42870)	Folates metabolism	6.3.2.17
FTHFLc	Formate--tetrahydrofolate ligase, cytosolic	atp[c] + for[c] + thf[c] <=> 10fthf[c] + adp[c] + pi[c]		Folates metabolism	6.3.4.3
FTHFLm	Formate--tetrahydrofolate ligase, mitochondrial	atp[m] + for[m] + thf[m] <=> 10fthf[m] + adp[m] + pi[m]		Folates metabolism	6.3.4.3
FTHFLs	Formate--tetrahydrofolate ligase, plastidic	atp[s] + for[s] + thf[s] <=> 10fthf[s] + adp[s] + pi[s]	LOC_Os09g27420	Folates metabolism	6.3.4.3
CALANc	beta-cyanoalanine nitrilase	asp-L[c] + nh4[c] <=> cala-L[c] + 2 h2o[c]	LOC_Os02g42350	Nitrogen metabolism	3.5.5.4
CALASc	beta-cyanoalanine synthetase	cys-L[c] + cyan[c] <=> cala-L[c] + h2s[c]	LOC_Os04g08350	Nitrogen metabolism	4.4.1.9
MANITL	(R)-mandelonitrile lyase	cyan[c] + benzald[c] <=> manit[c]	LOC_Os06g44540	Nitrogen metabolism	4.1.2.10
BG1c	beta-glucosidase (prunasin forming)	manit[c] + glc-B[c] <=> prunasin[c] + h2o[c]	(LOC_Os01g32364 or LOC_Os02g03870 or LOC_Os03g11420 or LOC_Os03g49600 or LOC_Os03g53790 or LOC_Os03g53800 or LOC_Os04g39900 or LOC_Os04g43360 or LOC_Os05g30350 or LOC_Os08g39860 or LOC_Os09g31430 or LOC_Os10g17650)	Nitrogen metabolism	3.2.1.21
BG2c	beta-glucosidase (amyloglucoside forming)	prunasin[c] + glc-B[c] <=> amygd[c] + h2o[c]	(LOC_Os01g32364 or LOC_Os02g03870 or LOC_Os03g11420 or LOC_Os03g49600 or LOC_Os03g53790 or LOC_Os03g53800 or LOC_Os04g39900 or LOC_Os04g43360 or LOC_Os05g30350 or LOC_Os08g39860 or LOC_Os09g31430 or LOC_Os10g17650)	Nitrogen metabolism	3.2.1.21
FORAc	Formamidase	frmd[c] + h2o[c] <=> for[c] + nh4[c] + h[c]	LOC_Os01g55950	Folates metabolism	3.5.1.49
FORMHLc	formamide hydro-lyase (cyanide-forming)	frmd[c] -> h2o[c] + cyan[c]		Nitrogen metabolism	4.2.1.66
FTHDFc	Formyltetrahydrofolate deformylase, cytosolic	10fthf[c] + h2o[c] -> for[c] + h[c] + thf[c]	LOC_Os01g49330	Folates metabolism	3.5.1.10
FTHDFm	Formyltetrahydrofolate deformylase, mitochondrial	10fthf[m] + h2o[m] -> for[m] + h[m] + thf[m]	LOC_Os03g01222	Folates metabolism	3.5.1.10
FTHDFs	Formyltetrahydrofolate deformylase, plastidic	10fthf[s] + h2o[s] -> for[s] + h[s] + thf[s]	(LOC_Os05g18790 or LOC_Os08g39160 or LOC_Os06g22560)	Folates metabolism	3.5.1.10
SHMTs	Serine hydroxymethyltransferase, plastidic	mlthf[s] + gly[s] + h2o[s] <=> thf[s] + ser-L[s]	(LOC_Os01g70380 or LOC_Os01g70370)	Glycine, serine and threonine metabolism	2.1.2.1
SHMTm	Serine hydroxymethyltransferase, mitochondrial	mlthf[m] + gly[m] + h2o[m] <=> thf[m] + ser-L[m]	(LOC_Os03g52840 or LOC_Os11g26860 or LOC_Os01g65410 or LOC_Os12g22030 or LOC_Os05g35440)	Photorespiration	2.1.2.1
MLTHFRc	methylenetetrahydrofolate reductase, cytosolic	mlthf[c] + nadph[c] + h[c] <=> nadp[c] + 5mthf[c]	LOC_Os03g60090	Folates metabolism	1.5.1.20
MLTHFRs	methylenetetrahydrofolate reductase, plastidic	mlthf[s] + nadph[s] + h[s] <=> nadp[s] + 5mthf[s]		Folates metabolism	1.5.1.20

METSc	5-methyltetrahydrofolate--homocysteine S-methyltransferase, cytosolic	5mthf[c] + hcys-L[c] <=> thf[c] + met-L[c]		Folates metabolism	2.1.1.13
METSs	5-methyltetrahydrofolate--homocysteine S-methyltransferase, plastidic	5mthf[s] + hcys-L[s] <=> thf[s] + met-L[s]	LOC_Os01g56610	Folates metabolism	2.1.1.13
MLTHFR_Fs	methylenetetrahydrofolate reductase (ferredoxin), cytosolic	mlthf[c] + 2 fdxrd[c] + 2 h[c] <=> 2 fdxox[c] + 5mthf[c]		Folates metabolism	1.5.7.1
MLTHFR_Fc	methylenetetrahydrofolate reductase (ferredoxin), plastidic	mlthf[s] + 2 fdxrd[s] + 2 h[s] <=> 2 fdxox[s] + 5mthf[s]		Folates metabolism	1.5.7.1
GLPATs	Glucose-1-phosphate adenylyltransferase	atp[s] + g1p[s] -> adpglc[s] + ppi[s]	(LOC_Os05g50380 or LOC_Os03g52460 or LOC_Os09g12660 or LOC_Os01g44220 or LOC_Os07g13980 or LOC_Os08g25734)	Starch and sucrose metabolism (Starch)	2.7.7.27
HCGALm	carbamoyl-phosphate synthetase (glutamine-hydrolysing)	2 atp[m] + gln-L[m] + hco3[m] + h2o[m] -> 2 adp[m] + pi[m] + glu-L[m] + cbp[m] + 2 h[m]	(LOC_Os03g57980 or LOC_Os01g68320 or LOC_Os07g07920 or LOC_Os02g47850)	Arginine and proline metabolism	6.3.5.5
ORPDCs	Orotidine-5-phosphate decarboxylase	orot5p[s] + h[s] -> ump[s] + co2[s]	(LOC_Os01g72250 or LOC_Os01g72240)	Pyrimidine metabolism	4.1.1.23
ATNSs	Anthranilate synthase	chor[s] + gln-L[s] -> anth[s] + pyr[s] + glu-L[s] + h[s]	((LOC_Os03g61120 and LOC_Os06g48620) and (LOC_Os04g38950 and LOC_Os03g50880))	Phenylalanine, tyrosine and tryptophan metabolism	4.1.3.27
TALc	Threonine dehydratase	thr-L[c] -> 2obut[c] + nh4[c]	LOC_Os03g50510	Valine, leucine and isoleucine metabolism	4.3.1.19
TPIc	Triosephosphate isomerase, cytosolic	dhap[c] <=> g3p[c]	(LOC_Os01g05490 or LOC_Os01g62420)	Glycolysis/Gluconeogensis	5.3.1.1
TPIs	Triosephosphate isomerase, plastidic	dhap[s] <=> g3p[s]	LOC_Os09g36450	Calvin Cycle	5.3.1.1
RPDPKc	ribose-phosphate diphosphokinase, cytosolic	atp[c] + r5p[c] -> amp[c] + prpp[c] + h[c]	LOC_Os02g48390	Purine metabolism	2.7.6.1
RPDPKs	ribose-phosphate diphosphokinase, plastidic	atp[s] + r5p[s] -> amp[s] + prpp[s] + h[s]	LOC_Os02g03540	Purine metabolism	2.7.6.1
PPMc	Phosphopentosemutase, cytosolic	r5p[c] <=> r1p[c]	(LOC_Os03g50480 or LOC_Os07g26610)	Pentose Phosphate Pathway	5.4.2.2
PPMs	Phosphopentosemutase, plastidic	r5p[s] <=> r1p[s]	LOC_Os10g11140	Pentose Phosphate Pathway	5.4.2.2
RBKc	Ribokinase, cytosolic	atp[c] + rib-D[c] -> adp[c] + h[c] + r5p[c]		Pentose Phosphate Pathway	2.7.1.15
RBKs	Ribokinase, plastidic	atp[s] + rib-D[s] -> adp[s] + h[s] + r5p[s]	(LOC_Os05g09370 or LOC_Os10g42240 or LOC_Os08g45180 or LOC_Os10g32830)	Pentose Phosphate Pathway	2.7.1.15
AUNORs	5-amino-6-(5-phosphoribosylamino)uracil reductase	5apru[s] + nadph[s] + h[s] -> 5aprbu[s] + nadp[s]	(LOC_Os02g27340 or LOC_Os04g09810 or LOC_Os03g02600)	Other Vitamins Metabolism (Riboflavin)	1.1.1.193
RIBFSs	Riboflavin synthase	2 dmlz[s] + h[s] -> ribflv[s] + 4r5au[s]	LOC_Os04g42000	Other Vitamins Metabolism (Riboflavin)	2.5.1.9
RIBFKc	Riboflavin kinase	atp[c] + ribflv[c] -> adp[c] + fmn[c] + h[c]	(LOC_Os10g14814 or LOC_Os10g32730 or LOC_Os03g58710)	Other Vitamins Metabolism (Riboflavin)	2.7.1.26
FMNATs	FMN adenylyltransferase, plastidic	atp[s] + fmn[s] + 2 h[s] -> ppi[s] + fad[s]	LOC_Os03g58710	Other Vitamins Metabolism (Riboflavin)	2.7.7.2
FMNATc	FMN adenylyltransferase, cytosolic	atp[c] + fmn[c] + 2 h[c] -> ppi[c] + fad[c]		Other Vitamins Metabolism (Riboflavin)	2.7.7.2
FMNATm	FMN adenylyltransferase, mitochondrial	atp[m] + fmn[m] + 2 h[m] -> ppi[m] + fad[m]		Other Vitamins Metabolism (Riboflavin)	2.7.7.2
GTPDHs	GTP cyclohydrolase II	gtp[s] + 3 h2o[s] -> for[s] + 25dhpp[s] + ppi[s] + 2 h[s]	(LOC_Os05g38570 or LOC_Os02g36340)	Other Vitamins Metabolism (Riboflavin)	3.5.4.25
DHPAHs	diaminohydroxyphosphoribosylaminopyrimidine deaminase	25dhpp[s] + h2o[s] -> 5apru[s] + nh4[s]	(LOC_Os04g09810 or LOC_Os03g02600)	Other Vitamins Metabolism (Riboflavin)	3.5.4.26
R5PFLs	3,4-dihydroxy-2-butanone-4-phosphate synthase	r5p[s] -> db4p[s] + for[s] + h[s]	(LOC_Os02g36340 or LOC_Os05g38570 or LOC_Os08g37605)	Other Vitamins Metabolism (Riboflavin)	4.1.99.12
DLDLBTs	6,7-dimethyl-8-ribityllumazine synthase	4r5au[s] + db4p[s] -> dmlz[s] + 2 h2o[s] + pi[s] + h[s]	LOC_Os04g42000	Other Vitamins Metabolism (Riboflavin)	2.5.1.78
AUSs	5-amino-6-(5-phosphoribitylamino)uracil phosphatase	5aprbu[s] + h2o[s] -> 4r5au[s] + pi[s]		Other Vitamins Metabolism (Riboflavin)	3.1.3.-
RPIc	ribose-5-phosphate isomerase, cytosolic	r5p[c] <=> ru5p-D[c]	(LOC_Os04g24140 or LOC_Os01g36090)	Pentose Phosphate Pathway	5.3.1.6
RPIs	ribose-5-phosphate isomerase, plastidic	r5p[s] <=> ru5p-D[s]	(LOC_Os03g56869 or LOC_Os07g08030)	Calvin cycle	5.3.1.6

GAPDHys	Glyceraldehyde-3-phosphate dehydrogenase (NADP+), plastidic	g3p[s] + nadp[s] + h2o[s] -> 3pg[s] + nadph[s] + 2 h[s]	LOC_Os03g03720	Glycolysis/Gluconeogensis	1.2.1.9
GAPDH1c	Glyceraldehyde-3-phosphate dehydrogenase (NAD+), cytsolic	g3p[c] + nad[c] + h2o[c] -> 3pg[c] + nadh[c] + 2 h[c]	(LOC_Os11g08300 or LOC_Os09g26880 or LOC_Os04g45720 or LOC_Os02g43280 or LOC_Os02g43194)	Glycolysis/Gluconeogensis	1.2.1.3
GAPDH2s	Glyceraldehyde-3-phosphate dehydrogenase (NAD+), plastidic	g3p[s] + nad[s] + h2o[s] -> 3pg[s] + nadh[s] + 2 h[s]	(LOC_Os06g15990 or LOC_Os11g08300)	Glycolysis/Gluconeogensis	1.2.1.3
GAPDHc	Glyceraldehyde 3-phosphate dehydrogenase (phosphorylating), cytosolic	g3p[c] + nad[c] + pi[c] <=> 13dpg[c] + h[c] + nadh[c]	(LOC_Os08g03290 or LOC_Os04g40950 or LOC_Os02g38920)	Glycolysis/Gluconeogensis	1.2.1.12
GAPDHs	Glyceraldehyde 3-phosphate dehydrogenase (phosphorylating), plastidic	g3p[s] + nad[s] + pi[s] <=> 13dpg[s] + h[s] + nadh[s]	(LOC_Os04g38600 or LOC_Os02g38920)	Calvin Cycle	1.2.1.12
KHKc	ketohexokinase	atp[c] + fru-B[c] -> adp[c] + f1p[c] + h[c]		Primary Cell Wall Metabolism (Fructose)	2.7.1.3
FBA2c	Fructose-bisphosphate aldolase	f1p[c] <=> dhap[c] + glyald[c]	(LOC_Os05g33380 or LOC_Os01g02880)	Primary Cell Wall Metabolism (Fructose)	4.1.2.13
FALDTKc	Formaldehyde transketolase, cytosolic	fald[c] + xu5p-D[c] -> dha[c] + g3p[c]		Glycerolipid and Glycerophospholipid metabolism	2.2.1.3
FALDTKs	Formaldehyde transketolase, plastidic	fald[s] + xu5p-D[s] -> dha[s] + g3p[s]		Glycerolipid and Glycerophospholipid metabolism	2.2.1.3
GLYCNKc	Glycerone kinase, cytsosolic	dha[c] + atp[c] <=> dhap[c] + adp[c] + h[c]	LOC_Os03g51000	Glycerolipid and Glycerophospholipid metabolism	2.7.1.29
GLYCNKs	Glycerone kinase, plastidic	dha[s] + atp[s] <=> dhap[s] + adp[s] + h[s]		Glycerolipid and Glycerophospholipid metabolism	2.7.1.29
FBAc	Fructose-bisphosphate aldolase, cytosolic	fdp-B[c] <=> dhap[c] + g3p[c]	(LOC_Os05g33380 or LOC_Os01g02880)	Glycolysis/Gluconeogensis	4.1.2.13
FBAs	Fructose-bisphosphate aldolase, plastidic	fdp-B[s] <=> dhap[s] + g3p[s]	(LOC_Os11g07020 or LOC_Os08g02700)	Glycolysis/Gluconeogensis	4.1.2.13
HDCs	Histidine decarboxylase	his-L[s] + h[s] <=> hista[s] + co2[s]	LOC_Os04g04640	Histidine metabolism	4.1.1.22
ADPARTs	ATP phosphoribosyltransferase	prpp[s] + atp[s] -> prbatp[s] + ppi[s]	LOC_Os03g04169	Histidine metabolism	2.4.2.17
PRDPARs	Amidophosphoribosyltransferase	gln-L[s] + prpp[s] + h2o[s] -> pram[s] + ppi[s] + glu-L[s]	(LOC_Os01g65260 or LOC_Os05g35580)	Purine metabolism	2.4.2.14
ANTPPTs	Anthranilate phosphoribosyltransferase	anth[s] + prpp[s] -> pran[s] + ppi[s]	(LOC_Os06g41090 or LOC_Os02g03850 or LOC_Os04g39680 or LOC_Os03g03450 or LOC_Os05g30750)	Phenylalanine, tyrosine and tryptophan metabolism	2.4.2.18
FUMm	Fumarate hydratase, mitochondrial	mal-L[m] <=> fum[m] + h2o[m]	LOC_Os03g21950	TCA Cycle	4.2.1.2
ADSALc	Adenylosuccinate lyase, cytosolic	dcamp[c] -> fum[c] + amp[c]		Purine metabolism	4.3.2.2
ADSALs	Adenylosuccinate lyase, plastidic	dcamp[s] -> fum[s] + amp[s]	(LOC_Os03g19280 or LOC_Os03g19930)	Purine metabolism	4.3.2.2
ARGSL1c	Argininosuccinate lyase	argsuc[c] <=> fum[c] + arg-L[c]	LOC_Os03g19280	Arginine and proline metabolism	4.3.2.1
LATs	L-leucine aminotransferase, plastidic	leu-L[s] + akg[s] <=> 4mop[s] + glu-L[s]	(LOC_Os02g17330 or LOC_Os03g01600 or LOC_Os10g40200 or LOC_Os03g12890 or LOC_Os03g24460 or LOC_Os05g48450 or LOC_Os04g47190)	Valine, leucine and isoleucine metabolism	2.6.1.42
LATm	L-leucine aminotransferase, cytosolic	leu-L[m] + akg[m] <=> 4mop[m] + glu-L[m]		Valine, leucine and isoleucine metabolism	2.6.1.42
GSNPc	guanosine phosphorylase	gsn[c] + pi[c] <=> gua[c] + r1p[c]		Purine metabolism	2.4.2.15
ADNPc	adenosine phosphorylase	adn[c] + pi[c] <=> ade[c] + r1p[c]		Purine metabolism	2.4.2.1
INSPc	inosine phosphorylase	ins[c] + pi[c] <=> hxan[c] + r1p[c]		Purine metabolism	2.4.2.1
ADNDAc	adenosine deaminase (polypeptide)	adn[c] + h2o[c] + h[c] -> ins[c] + nh4[c]	(LOC_Os04g58690 or LOC_Os07g46630 or LOC_Os05g28180)	Purine metabolism	3.5.4.4
IMPc	Inosine 5-monophosphate phosphohydrolase	imp[c] + h2o[c] -> ins[c] + pi[c]	(LOC_Os01g51280 or LOC_Os03g44660 or LOC_Os07g10460)	Purine metabolism	3.1.3.5
GMPRc	GMP reductase	gmp[c] + 2 h[c] + nadph[c] <=> imp[c] + nadp[c] + nh4[c]	LOC_Os03g56800	Purine metabolism	1.7.1.7
IMPCs	IMP cyclohydrolase	fprica[s] <=> imp[s] + h2o[s]	LOC_Os08g10570	Purine metabolism	3.5.4.10
GMPS2c	GMP synthetase (glutamine-hydrolysing)	atp[c] + xmp[c] + gln-L[c] + h2o[c] -> amp[c] + ppi[c] + gmp[c] +	(LOC_Os02g08270 or LOC_Os02g03740	Purine metabolism	6.3.5.2

		glu-L[c] + 2 h[c]	or LOC_Os09g25610 or LOC_Os08g23730 or LOC_Os02g47850)		
GMPS1c	GMP synthetase	atp[c] + xmp[c] + nh4[c] -> amp[c] + ppi[c] + gmp[c] + 2 h[c]	(LOC_Os02g08270 or LOC_Os09g25610 or LOC_Os08g23730 or LOC_Os02g47850)	Purine metabolism	6.3.4.1
GDKc	Guanylate kinase	atp[c] + gmp[c] -> adp[c] + gdp[c]	LOC_Os03g20460	Purine metabolism	2.7.4.8
ATDGMc	ATP:dGMP phosphotransferase	atp[c] + dgmp[c] -> adp[c] + dgdp[c]	LOC_Os03g20460	Purine metabolism	2.7.4.12
ATDAMc	ATP:dAMP phosphotransferase	atp[c] + damp[c] -> adp[c] + dadp[c]	(LOC_Os10g07010 or LOC_Os02g49920 or LOC_Os07g15190 or LOC_Os06g15170 or LOC_Os06g14810 or LOC_Os04g02640 or LOC_Os03g14170 or LOC_Os01g34560 or LOC_Os06g15020 or LOC_Os05g49290 or LOC_Os03g12030 or LOC_Os06g15250)	Purine metabolism	2.7.4.3
DGDTc	2-Deoxyadenosine 5-diphosphate (GDP):oxidized-thioredoxin 2-oxidoreductase	gdp[c] + trdrd[c] -> dgdp[c] + trdox[c] + h2o[c]	((LOC_Os02g56100 and LOC_Os06g03720) and (LOC_Os06g14620 and LOC_Os06g07210))	Purine metabolism	1.17.4.1
DADTc	2-Deoxyadenosine 5-diphosphate (ADP):oxidized-thioredoxin 2-oxidoreductase	trdrd[c] + adp[c] -> dadp[c] + trdox[c] + h2o[c]	((LOC_Os02g56100 and LOC_Os06g03720) and (LOC_Os06g14620 and LOC_Os06g07210))	Purine metabolism	1.17.4.1
IMPDc	IMP dehydrogenase	imp[c] + nad[c] + h2o[c] -> xmp[c] + nadh[c] + h[c]	(LOC_Os01g73040 or LOC_Os03g56800 or LOC_Os01g69900 or LOC_Os11g06930 or LOC_Os12g07190)	Purine metabolism	1.1.1.205
INSKc	Inosine kinase	atp[c] + ins[c] -> adp[c] + h[c] + imp[c]		Purine metabolism	2.7.1.73
HXPRTc	Hypoxanthine phosphoribosyltransferase	hxan[c] + prpp[c] -> imp[c] + ppi[c]	LOC_Os05g08950	Purine metabolism	2.4.2.8
ADSSc	adenylosuccinate synthetase, cytosolic	asp-L[c] + gtp[c] + imp[c] -> dcamp[c] + gdp[c] + 2 h[c] + pi[c]	(LOC_Os02g01220 or LOC_Os04g17660)	Purine metabolism	6.3.4.4
ADSSs	adenylosuccinate synthetase, plastidic	asp-L[s] + gtp[s] + imp[s] -> dcamp[s] + gdp[s] + 2 h[s] + pi[s]	(LOC_Os03g07840 or LOC_Os03g49220)	Purine metabolism	6.3.4.4
MIOORc	Myo-inositol oxygenase	inost[c] + o2[c] -> glcur[c] + h2o[c] + h[c]	LOC_Os06g36560	Primary Cell Wall Metabolism (Inositol phosphate)	1.13.99.1
PI45PLCc	1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase	h2o[c] + pail45p[c] -> 12dgr_os[c] + h[c] + mi145p[c]	(LOC_Os05g03610 or LOC_Os03g18010 or LOC_Os12g37560 or LOC_Os07g49330)	Primary Cell Wall Metabolism (Inositol phosphate)	3.1.4.11
PI5P4Kc	1-phosphatidylinositol-5-phosphate 4-kinase	atp[c] + pail5p[c] <=> adp[c] + h[c] + pail45p[c]	LOC_Os09g28060	Primary Cell Wall Metabolism (Inositol phosphate)	2.7.1.149
PI4P5Kc	1-phosphatidylinositol-4-phosphate kinase	atp[c] + pail4p[c] <=> adp[c] + h[c] + pail45p[c]	(LOC_Os12g13440 or LOC_Os09g10650 or LOC_Os08g01390 or LOC_Os04g59540 or LOC_Os03g49510)	Primary Cell Wall Metabolism (Inositol phosphate)	2.7.1.68
PIK4c	1-phosphatidylinositol 4-kinase	atp[c] + ptd1ino_os[c] <=> adp[c] + h[c] + pail4p[c]	LOC_Os03g50320	Primary Cell Wall Metabolism (Inositol phosphate)	2.7.1.67
PIK3c	1-phosphatidylinositol 3-kinase	atp[c] + ptd1ino_os[c] -> adp[c] + h[c] + pail3p[c]	(LOC_Os05g08810 or LOC_Os08g21590)	Primary Cell Wall Metabolism (Inositol phosphate)	2.7.1.137
PI3P5Kc	1-phosphatidylinositol-3-phosphate 5-kinase	atp[c] + pail3p[c] -> pail35p[c] + adp[c] + h[c]	LOC_Os01g01689	Primary Cell Wall Metabolism (Inositol phosphate)	2.7.1.150
MI34Pc	Inositol-3-phosphate 4-kinase	mi3p-D[c] + atp[c] -> mi34p[c] + adp[c]	(LOC_Os02g26720 or LOC_Os03g12840 or LOC_Os03g51610 or LOC_Os10g01480 or LOC_Os10g42550)	Primary Cell Wall Metabolism (Inositol phosphate)	2.7.1.-
MI346Pc	Inositol-3,4-diphosphate 6-kinase	mi34p[c] + atp[c] -> mi346p[c] + adp[c]	(LOC_Os02g26720 or LOC_Os03g12840 or LOC_Os03g51610 or LOC_Os10g01480 or LOC_Os10g42550)	Primary Cell Wall Metabolism (Inositol phosphate)	2.7.1.-

MI3456Pc	Inositol-3,4,6-triphosphate 5-kinase	mi346p[c] + atp[c] -> mi3456p[c] + adp[c]	(LOC_Os02g26720 or LOC_Os03g12840 or LOC_Os03g51610 or LOC_Os10g01480 or LOC_Os10g42550)	Primary Cell Wall Metabolism (Inositol phosphate)	2.7.1.-
IBPHc	Inositol-3,4-bisphosphate 4-phosphatase	mi34p[c] + h2o[c] -> mi3p-D[c] + pi[c]		Primary Cell Wall Metabolism (Inositol phosphate)	3.1.3.66
MI14PPc	D-myo-Inositol-1,4-bisphosphate 1-phosphohydrolase	h2o[c] + mi14p[c] -> mi4p-D[c] + pi[c]	(LOC_Os12g08270 or LOC_Os12g08280)	Primary Cell Wall Metabolism (Inositol phosphate)	3.1.3.57
MI134PPc	D-myo-Inositol 1,3,4-trisphosphate 1-phosphohydrolase	h2o[c] + mi134p[c] -> mi34p[c] + pi[c]	(LOC_Os12g08270 or LOC_Os12g08280)	Primary Cell Wall Metabolism (Inositol phosphate)	3.1.3.57
MI145PPc	Inositol-1,4,5-trisphosphate 5-phosphatase	h2o[c] + mi145p[c] -> mi14p[c] + pi[c]	(LOC_Os09g32440 or LOC_Os08g41270 or LOC_Os05g45900 or LOC_Os01g51890)	Primary Cell Wall Metabolism (Inositol phosphate)	3.1.3.56
MI1456PKc	inositol-polyphosphate multikinase	2 atp[c] + mi145p[c] -> 2 adp[c] + 2 h[c] + mi13456p[c]	LOC_Os02g32370	Primary Cell Wall Metabolism (Inositol phosphate)	2.7.1.151
MI145PKc	1D-myo-inositol-trisphosphate 3-kinase	atp[c] + mi145p[c] <=> adp[c] + h[c] + mi1345p[c]		Primary Cell Wall Metabolism (Inositol phosphate)	2.7.1.127
MI134PK1c	Inositol-1,3,4-trisphosphate 5/6-kinase 1	mi134p[c] + atp[c] <=> adp[c] + h[c] + mi1345p[c]	(LOC_Os02g26720 or LOC_Os03g12840 or LOC_Os03g51610 or LOC_Os10g01480 or LOC_Os10g42550)	Primary Cell Wall Metabolism (Inositol phosphate)	2.7.1.159
MI134PK2c	Inositol-1,3,4-trisphosphate 5/6-kinase 2	mi134p[c] + atp[c] <=> adp[c] + h[c] + mi1346p[c]	(LOC_Os02g26720 or LOC_Os03g12840 or LOC_Os03g51610 or LOC_Os10g01480 or LOC_Os10g42550)	Primary Cell Wall Metabolism (Inositol phosphate)	2.7.1.159
MI1346PK1c	inositol-tetrakisphosphate 5-kinase	atp[c] + mi1346p[c] -> adp[c] + h[c] + mi13456p[c]	LOC_Os02g32370	Primary Cell Wall Metabolism (Inositol phosphate)	2.7.1.140
MI1346PK2c	inositol-tetrakisphosphate 5-kinase	atp[c] + mi1346p[c] -> adp[c] + h[c] + mi12346p[c]		Primary Cell Wall Metabolism (Inositol phosphate)	2.7.1.-
IPKK2c	Inositol-pentakisphosphate 2-kinase	mi13456p[c] + atp[c] -> minohp[c] + adp[c] + h[c]	LOC_Os04g56580	Primary Cell Wall Metabolism (Inositol phosphate)	2.7.1.158
IPKK5c	Inositol-pentakisphosphate 5-kinase	mi12346p[c] + atp[c] -> minohp[c] + adp[c] + h[c]		Primary Cell Wall Metabolism (Inositol phosphate)	2.7.1.-
IPKK4c	Inositol-pentakisphosphate 4-kinase	mi12356p[c] + atp[c] -> minohp[c] + adp[c] + h[c]		Primary Cell Wall Metabolism (Inositol phosphate)	2.7.1.-
IPKK6c	Inositol-pentakisphosphate 6-kinase	mi12345p[c] + atp[c] -> minohp[c] + adp[c] + h[c]		Primary Cell Wall Metabolism (Inositol phosphate)	2.7.1.-
PHYTASEc	6-phytase	minohp[c] + h2o[c] -> mi12345p[c] + 2 h[c] + pi[c]		Primary Cell Wall Metabolism (Inositol phosphate)	3.1.3.26
MIHPPc	myo-inositol-hexakisphosphate 4-phosphohydrolase	minohp[c] + h2o[c] -> mi12356p[c] + 2 h[c] + pi[c]		Primary Cell Wall Metabolism (Inositol phosphate)	3.1.3.26
MI1345PPc	inositol (1,3,4,5)-tetrakisphosphate 3-phosphatase	mi1345p[c] + h2o[c] -> mi145p[c] + 2 h[c] + pi[c]	LOC_Os03g60370	Primary Cell Wall Metabolism (Inositol phosphate)	3.1.3.62
MI1345PP2c	D-myo-inositol(1,4,5)/(1,3,4,5)-polyphosphate 5-phosphatase	mi1345p[c] + h2o[c] -> mi134p[c] + 2 h[c] + pi[c]	(LOC_Os09g32440 or LOC_Os08g41270 or LOC_Os05g45900 or	Primary Cell Wall Metabolism (Inositol	3.1.3.56

			LOC_Os01g51890)	phosphate)	
ITK1Kc	1D-myo-inositol-tetrakisphosphate 1-kinase	atp[c] + mi3456p[c] <=> adp[c] + mi13456p[c] + h[c]	(LOC_Os02g26720 or LOC_Os03g12840 or LOC_Os03g51610 or LOC_Os10g01480 or LOC_Os10g42550)	Primary Cell Wall Metabolism (Inositol phosphate)	2.7.1.134
MI4PPc	Myo-inositol-1(or 4)-monophosphatase	mi4p-D[c] + h2o[c] -> inost[c] + pi[c]	(LOC_Os02g07350 or LOC_Os03g39000)	Primary Cell Wall Metabolism (Inositol phosphate)	3.1.3.25
MI3PPc	Myo-inositol-1(or 4)-monophosphatase	mi3p-D[c] + h2o[c] -> inost[c] + pi[c]	(LOC_Os02g07350 or LOC_Os03g39000)	Primary Cell Wall Metabolism (Inositol phosphate)	3.1.3.25
DHAD-bs	Dihydroxy-acid dehydratase	23dhmb[s] -> 3mob[s] + h2o[s]	LOC_Os08g44530	Valine, leucine and isoleucine metabolism	4.2.1.9
HMGCOASc	Hydroxymethylglutaryl-CoA synthase, cytosolic	accoa[c] + h2o[c] + aacoa[c] -> hmgcoa[c] + coa[c]	(LOC_Os08g43170 or LOC_Os03g02710 or LOC_Os09g34960)	Terpenoid biosynthesis (MVA Pathway)	2.3.3.10
HMGCOASm	Hydroxymethylglutaryl-CoA synthase, mitochondrial	accoa[m] + h2o[m] + aacoa[m] -> hmgcoa[m] + coa[m]		Terpenoid biosynthesis (MVA Pathway)	2.3.3.10
GCOADx	glutaryl-CoA degradation	gcoa[x] + fad[x] -> fadh2[x] + gccoa[x]		Lysine metabolism	1.3.8.-
GCOADCx	Glutaconyl-CoA decarboxylase	gccoa[x] -> co2[x] + b2coa[x]	LOC_Os02g17390	Lysine metabolism	4.1.1.70
ACACTx	Acetyl-CoA C-acetyltransferase, peroxisomal	2 accoa[x] <=> aacoa[x] + coa[x]	(LOC_Os01g02020 or LOC_Os09g07830)	Fermentation	2.3.1.9
ACACTs	Acetyl-CoA C-acetyltransferase, plastidic	2 accoa[s] <=> aacoa[s] + coa[s]		Lysine metabolism	2.3.1.9
ACACTc	Acetyl-CoA C-acetyltransferase, cytosol	2 accoa[c] <=> aacoa[c] + coa[c]		Terpenoid biosynthesis (MVA Pathway)	2.3.1.9
ACACTm	Acetyl-CoA C-acetyltransferase, mitochondrial	2 accoa[m] <=> aacoa[m] + coa[m]		Valine, leucine and isoleucine metabolism	2.3.1.9
IPMSs	2-isopropylMalate synthase	accoa[s] + 3mob[s] + h2o[s] -> 3c3hmp[s] + coa[s] + h[s]	(LOC_Os11g04670 or LOC_Os12g04440)	Valine, leucine and isoleucine metabolism	2.3.3.13
HMNOm	3-hydroxyisobutyrate dehydrogenase	3hib[m] + nad[m] <=> mmsa[m] + nadh[m] + h[m]	(LOC_Os06g46372 or LOC_Os02g35500)	Valine, leucine and isoleucine metabolism	1.1.1.31
MOD	3-methyl-2-oxobutanoate dehydrogenase	3mob[m] + thmpp[m] + h[m] -> 2mhop[m] + co2[m]	(LOC_Os12g08260 and LOC_Os07g07470)	Valine, leucine and isoleucine metabolism	1.2.4.4
MOD(2mhop)	3-methyl-2-oxobutanoate dehydrogenase, 2-Methyl-1-hydroxypropyl-ThPP transforming	2mhop[m] + lpam[m] -> 2mpdhl[m] + thmpp[m]	(LOC_Os12g08260 and LOC_Os07g07470)	Valine, leucine and isoleucine metabolism	1.2.4.4
DHRT(ibcoa)	dihydrolipoyllysine-residue (2-methylpropanoyl)transferase, 2-Methylbutanoyl-CoA forming	coa[m] + 2mpdhl[m] -> ibcoa[m] + dhlam[m]	LOC_Os01g21160	Valine, leucine and isoleucine metabolism	2.3.1.168
MMSDm	Methylmalonate-semialdehyde dehydrogenase (acylating)	mmsa[m] + coa[m] + nad[m] -> ppcoa[m] + co2[m] + nadh[m]	LOC_Os07g09060	Valine, leucine and isoleucine metabolism	1.2.1.27
MCDH1m	2-methylacyl-CoA dehydrogenase	ibcoa[m] + fad[m] -> 2mp2coa[m] + fadh2[m]	LOC_Os07g47820	Valine, leucine and isoleucine metabolism	1.3.99.12
HIBHm	3-hydroxyisobutyryl-CoA hydrolase	3hibutcoa[m] + h2o[m] -> coa[m] + 3hib[m] + h[m]	(LOC_Os01g54860 or LOC_Os10g42220 or LOC_Os06g39344 or LOC_Os10g40540 or LOC_Os12g16350)	Valine, leucine and isoleucine metabolism	3.1.2.4
ECH1m	Enoyl-CoA hydratase	2mp2coa[m] + h2o[m] -> 3hibutcoa[m]	(LOC_Os02g43720 or LOC_Os05g29880 or LOC_Os02g17390 or LOC_Os05g06300 or LOC_Os02g43710 or LOC_Os01g24680 or LOC_Os01g70090)	Valine, leucine and isoleucine metabolism	4.2.1.17
DHADm	Dihydroxy-acid dehydratase	23dhmb[m] -> 3mob[m] + h2o[m]	LOC_Os08g44530	Valine, leucine and isoleucine metabolism	4.2.1.9
VALATs	L-valine aminotransferase, plastidic	val-L[s] + akg[s] <=> 3mob[s] + glu-L[s]	(LOC_Os02g17330 or LOC_Os03g01600 or LOC_Os10g40200 or LOC_Os03g12890 or LOC_Os03g24460 or LOC_Os05g48450 or LOC_Os04g47190)	Valine, leucine and isoleucine metabolism	2.6.1.42
VALATm	L-valine aminotransferase, mitochondrial	val-L[m] + akg[m] <=> 3mob[m] + glu-L[m]		Valine, leucine and isoleucine metabolism	2.6.1.42
MTHFDm	Methylenetetrahydrofolate dehydrogenase (NAD+)	mlthf[m] + nad[m] <=> methf[m] + nadh[m]		Folates metabolism	1.5.1.15

MTHFDs	Methylenetetrahydrofolate dehydrogenase (NAD+)	mlthf[s] + nad[s] <=> methf[s] + nadh[s]	LOC_Os09g15810	Folates metabolism	1.5.1.15
MTHFDc	Methylenetetrahydrofolate dehydrogenase (NAD+)	mlthf[c] + nad[c] <=> methf[c] + nadh[c]		Folates metabolism	1.5.1.15
FTHFCLc	5-formyltetrahydrofolate cyclo-ligase, cytosolic	atp[c] + 5fthf[c] + h[c] <=> adp[c] + pi[c] + methf[c]		Folates metabolism	6.3.3.2
FTHFCLm	5-formyltetrahydrofolate cyclo-ligase, mitochondrial	atp[m] + 5fthf[m] + h[m] <=> adp[m] + pi[m] + methf[m]	LOC_Os07g39070	Folates metabolism	6.3.3.2
FTHFCLs	5-formyltetrahydrofolate cyclo-ligase, plastidic	atp[s] + 5fthf[s] + h[s] <=> adp[s] + pi[s] + methf[s]	LOC_Os12g07020	Folates metabolism	6.3.3.2
MTHFDym	Methylenetetrahydrofolate dehydrogenase (NADP+)	mlthf[m] + nadp[m] <=> methf[m] + nadph[m]		Folates metabolism	1.5.1.5
MTHFDys	Methylenetetrahydrofolate dehydrogenase (NADP+)	mlthf[s] + nadp[s] <=> methf[s] + nadph[s]		Folates metabolism	1.5.1.5
MTHFDyc	Methylenetetrahydrofolate dehydrogenase (NADP+)	mlthf[c] + nadp[c] <=> methf[c] + nadph[c]	LOC_Os03g60090	Folates metabolism	1.5.1.5
MOHMTm	5,10-Methylenetetrahydrofolate:3-methyl-2-oxobutanoate hydroxymethyltransferase	3mob[m] + h2o[m] + mlthf[m] -> 2dhp[m] + thf[m]	LOC_Os01g12560	Pantothenate and CoA metabolism	2.1.2.11
GMPc	Guanosine 5-monophosphate phosphohydrolase	h2o[c] + gmp[c] -> pi[c] + gsn[c]	(LOC_Os01g51280 or LOC_Os03g44660 or LOC_Os07g10460)	Purine metabolism	3.1.3.5
GNSKc	Guanosine 5-phosphotransferase	gsn[c] + atp[c] -> gmp[c] + adp[c] + h[c]		Purine metabolism	2.7.1.73
GUAPRTc	guanine phosphoribosyltransferase	gua[c] + prpp[c] -> gmp[c] + ppi[c]	LOC_Os05g08950	Purine metabolism	2.4.2.8
DAD2DAc	Deoxyadenosine aminohydrolase	dad-2[c] + h2o[c] + h[c] -> din[c] + nh4[c]	(LOC_Os07g46630 or LOC_Os05g28180 or LOC_Os04g58690)	Purine metabolism	3.5.4.4
DINSPc	Deoxyinosine:orthophosphate ribosyltransferase	din[c] + pi[c] -> hxan[c] + 2dr1p[c]		Purine metabolism	2.4.2.1
DURIPP	deoxyuridine phosphorylase	duri[c] + pi[c] <=> 2dr1p[c] + ura[c]		Purine metabolism	2.4.2.1
DAD2NPc	Deoxyadenosine:orthophosphate ribosyltransferase	dad-2[c] + pi[c] <=> 2dr1p[c] + ade[c]		Purine metabolism	2.4.2.1
DAMPHc	2-Deoxyadenosine 5-monophosphate phosphohydrolase	damp[c] + h2o[c] <=> dad-2[c] + pi[c]	(LOC_Os01g51280 or LOC_Os03g44660 or LOC_Os07g10460)	Purine metabolism	3.1.3.5
ADEDAc	adenine deaminase	ade[c] + h2o[c] <=> nh4[c] + hxan[c]	(LOC_Os07g46630 or LOC_Os05g28180 or LOC_Os04g58690)	Purine metabolism	3.5.4.2
ADNRHc	Adenosine ribohydrolase	h2o[c] + adn[c] -> rib-D[c] + ade[c]	LOC_Os09g39440	Purine metabolism	3.2.2.1
GTPDPKc	GTP diphosphokinase	gtp[c] + atp[c] <=> pppgpp[c] + amp[c]	(LOC_Os09g27050 or LOC_Os08g35620)	Purine metabolism	2.7.6.5
PPPGPPPc	guanosine-5-triphosphate, 3-diphosphate pyrophosphatase	pppgpp[c] + h2o[c] -> ppgpp[c] + pi[c] + h[c]		Purine metabolism	3.6.1.40
PRODHm	Proline dehydrogenase	pro-L[m] + fad[m] -> 1pyr5c[m] + fadh2[m] + h[m]	LOC_Os10g40360	Arginine and proline metabolism	1.5.99.8
P5CRc	Pyrroline-5-carboxylate reductase (NADH), cytosolic	1pyr5c[c] + nadh[c] + 2 h[c] -> pro-L[c] + nad[c]	LOC_Os01g71990	Arginine and proline metabolism	1.5.1.2
P5CRs	Pyrroline-5-carboxylate reductase (NADH), plastidic	1pyr5c[s] + nadh[s] + 2 h[s] -> pro-L[s] + nad[s]		Arginine and proline metabolism	1.5.1.2
P5CRyc	Pyrroline-5-carboxylate reductase (NADPH), cytosolic	1pyr5c[c] + nadph[c] + 2 h[c] -> pro-L[c] + nadp[c]	LOC_Os01g71990	Arginine and proline metabolism	1.5.1.2
P5CRys	Pyrroline-5-carboxylate reductase (NADPH), plastidic	1pyr5c[s] + nadph[s] + 2 h[s] -> pro-L[s] + nadp[s]		Arginine and proline metabolism	1.5.1.2
CYSTALs	Cystathionine beta-lyase	cyst-L[s] + h2o[s] -> hcys-L[s] + nh4[s] + pyr[s]	LOC_Os06g07860	Cysteine and methionine metabolism	4.4.1.8
GCALDDc	Glycolaldehyde dehydrogenase	gcald[c] + h2o[c] + nad[c] -> glyclt[c] + 2 h[c] + nadh[c]	LOC_Os07g48920	Folates metabolism	1.2.1.21
PGLYCPs	Phosphoglycolate phosphatase	2pglyc[s] + h2o[s] -> glyclt[s] + pi[s]	LOC_Os04g41340	Photorespiration	3.1.3.18
GLCRPUic	Glucuronate-1-phosphate uridylyltransferase	glcur1p[c] + utp[c] + h[c] -> udpglcur[c] + ppi[c]	LOC_Os06g48760	Primary Cell Wall Metabolism (Membrane)	2.7.7.44
XYLXYLc	xylan 1,4-beta-xylosidase	xylan[c] + h2o[c] -> 2 xyl-D[c]	LOC_Os11g18690	Starch and sucrose metabolism (Starch)	3.2.1.37
XSc	1,4-beta-D-xylan synthase	2 udpxyl[c] + h2o[c] -> xylan[c] + 2 udp[c]	LOC_Os03g17850	Starch and sucrose metabolism (Starch)	2.4.2.24
UGEc	UDP-glucuronate 4-epimerase	udpglcur[c] <=> udpgalur[c]	LOC_Os02g54890	Starch and sucrose metabolism (Cellulose)	5.1.3.6

UG46DHc	UDP-glucose 4,6-dehydratase	udpg[c] <=> udpddg[c] + h2o[c]	LOC_Os03g17000	Starch and sucrose metabolism (Cellulose)	4.2.1.76
PECTNc	Pectinesterase	3 udpgalur[c] + 2 h2o[c] -> pect[c] + 3 udp[c]	(LOC_Os01g20980 or LOC_Os01g21034 or LOC_Os01g44340 or LOC_Os01g53990 or LOC_Os01g57854 or LOC_Os05g44600 or LOC_Os08g34900 or LOC_Os10g26680 or LOC_Os12g37660)	Starch and sucrose metabolism (Cellulose)	3.1.1.11 or 2.4.1.43 or 3.2.1.15
UDDGEc	UDP-4-dehydro-6-deoxy-glucose 3,5-epimerase	udpddg[c] <=> udpkrmn[c]	LOC_Os02g45540	Starch and sucrose metabolism (Cellulose)	1.1.1.- or 5.1.3.-
URMNORc	UDP-L-rhamnose:NADP+ 4-oxidoreductase	udpkrmn[c] + nadph[c] + h[c] <=> udprmn[c] + nadp[c]	LOC_Os02g45540	Starch and sucrose metabolism (Cellulose)	1.1.1.- or 5.1.3.-
UGDCc	UDP-glucuronate decarboxylase	udpglcur[c] + h[c] -> udpxyl[c] + co2[c]	(LOC_Os01g21320 or LOC_Os03g17230)	Starch and sucrose metabolism (Cellulose)	4.1.1.35
HPRs	Hydroxypyruvate reductase (NAD), plastidic	h[s] + hpyr[s] + nadh[s] -> glyc-R[s] + nad[s]		Photorespiration	1.1.1.29
HPRx	Hydroxypyruvate reductase (NAD), peroxisomal	h[x] + hpyr[x] + nadh[x] -> glyc-R[x] + nad[x]	LOC_Os02g01150	Photorespiration	1.1.1.29
HPRys	Hydroxypyruvate reductase (NADP), plastidic	h[s] + hpyr[s] + nadph[s] -> glyc-R[s] + nadp[s]	LOC_Os04g01650	Photorespiration	1.1.1.79
HPRyx	Hydroxypyruvate reductase (NADP), peroxisomal	h[x] + hpyr[x] + nadph[x] -> glyc-R[x] + nadp[x]	LOC_Os04g01650	Photorespiration	1.1.1.79
ASPCT1c	Aspartate carbamoyltransferase (asp-L)	cbp[c] + asp-L[c] -> pi[c] + cbasp[c]	(LOC_Os08g15030 or LOC_Os02g47590)	Pyrimidine metabolism	2.1.3.2
THRSs	Threonine synthase	phom[s] + h2o[s] -> thr-L[s] + pi[s]	(LOC_Os03g50510 or LOC_Os05g47640 or LOC_Os03g11660 or LOC_Os01g49890)	Glycine, serine and threonine metabolism	4.2.3.1
AAPTc	L-arabinokinase	atp[c] + arab-L[c] -> adp[c] + B-ara1p[c] + h[c]	(LOC_Os02g04840 or LOC_Os06g48940)	Starch and sucrose metabolism (Cellulose)	2.7.1.46
UTPUc	UTP-monosaccharide-1-phosphate uridylyltransferase	utp[c] + B-ara1p[c] + h[c] -> ppi[c] + udparab[c]	LOC_Os06g48760	Starch and sucrose metabolism (Cellulose)	2.7.7.64
UMPUc	beta-L-arabinose-1-phosphate uridylyltransferase	udp[c] + B-ara1p[c] + h[c] -> pi[c] + udparab[c]	LOC_Os06g48760	Starch and sucrose metabolism (Cellulose)	2.7.7.37
ARABFv	alpha-L-arabinofuranosidase, vacuolar	udparab[v] + h2o[v] -> arab-L[v] + udp[v] + h[v]	(LOC_Os12g03470 or LOC_Os11g03730)	Starch and sucrose metabolism (Cellulose)	3.2.1.55
ARABFc	alpha-L-arabinofuranosidase, cytosolic	udparab[c] + h2o[c] -> arab-L[c] + udp[c] + h[c]	(LOC_Os12g03470 or LOC_Os11g03730)	Starch and sucrose metabolism (Cellulose)	3.2.1.55
UA4Ec	UDP-arabinose 4-epimerase	udpxyl[c] <=> udparab[c]	LOC_Os07g04690	Starch and sucrose metabolism (Cellulose)	5.1.3.5
GLCURKc	Glucuronokinase	glcur[c] + atp[c] -> glcur1p[c] + adp[c] + h[c]	LOC_Os11g11060	Starch and sucrose metabolism (Cellulose)	2.7.1.43
PGKc	Phosphoglycerate kinase	13dpg[c] + adp[c] <=> 3pg[c] + atp[c]		Glycolysis/Gluconeogensis	2.7.2.3
PGKs	Phosphoglycerate kinase	13dpg[s] + adp[s] <=> 3pg[s] + atp[s]	(LOC_Os01g58610 or LOC_Os02g07260 or LOC_Os05g41640 or LOC_Os06g45710 or LOC_Os10g30550)	Glycolysis/Gluconeogensis	2.7.2.3
PGLYDHs	Phosphoglycerate dehydrogenase	3pg[s] + nad[s] -> 3php[s] + nadh[s] + h[s]	(LOC_Os06g44460 or LOC_Os08g34720 or LOC_Os04g55720)	Glycine, serine and threonine metabolism	1.1.1.95
GLYK1s	Glycerate kinase (3-PG)	atp[s] + glyc-R[s] <=> adp[s] + 3pg[s] + h[s]	LOC_Os01g48990	Photorespiration	2.7.1.31
GLYK2s	Glycerate kinase (2-PG)	atp[s] + glyc-R[s] <=> adp[s] + 2pg[s] + h[s]		Photorespiration	2.7.1.165
PGMc	Phosphoglycerate mutase, cytosolic	3pg[c] <=> 2pg[c]	(LOC_Os01g60190 or LOC_Os03g21260 or LOC_Os05g40420)	Glycolysis/Gluconeogensis	5.4.2.1
PGMs	Phosphoglycerate mutase, plastidic	3pg[s] <=> 2pg[s]	(LOC_Os11g05260 or LOC_Os08g37140)	Glycolysis/Gluconeogensis	5.4.2.1
G6PEc	glucose-6-phosphate 1-epimerase, cytosolic	g6p-A[c] <=> g6p-B[c]	(LOC_Os01g46950 or LOC_Os04g56290 or LOC_Os08g14330)	Glycolysis/Gluconeogensis	5.1.3.15
G6PEs	glucose-6-phosphate 1-epimerase, plastidic	g6p-A[s] <=> g6p-B[s]	(LOC_Os01g46950 or LOC_Os08g14330)	Glycolysis/Gluconeogensis	5.1.3.15
PRUKs	Phosphoribulokinase	atp[s] + ru5p-D[s] -> adp[s] + h[s] + rb15bp[s]	(LOC_Os02g47020 or LOC_Os04g50880 or LOC_Os08g41790)	Calvin cycle	2.7.1.19
GLNKc	Gluconokinase, cytosolic	atp[c] + glcn[c] -> 6pgc[c] + adp[c] + h[c]	LOC_Os06g02430	Pentose Phosphate Pathway	2.7.1.12
GLNKs	Gluconokinase, plastidic	atp[s] + glcn[s] -> 6pgc[s] + adp[s] + h[s]	LOC_Os06g02430	Pentose Phosphate Pathway	2.7.1.12
GNDc	Phosphogluconate dehydrogenase (decarboxylating), cytosolic	6pgc[c] + nadp[c] -> co2[c] + nadph[c] + ru5p-D[c]	LOC_Os06g02144	Pentose Phosphate Pathway	1.1.1.44

GNDs	Phosphogluconate dehydrogenase (decarboxylating), plastidic	6pgc[s] + nadp[s] -> co2[s] + nadph[s] + ru5p-D[s]	LOC_Os11g29400	Pentose Phosphate Pathway	1.1.1.44
XYLIc	Xylose isomerase	xyl-D[c] <=> xylu-D[c]	LOC_Os07g47290	Starch and sucrose metabolism (Cellulose)	5.3.1.5
XYLKc	Xylulokinase	atp[c] + xylu-D[c] -> adp[c] + h[c] + xu5p-D[c]	(LOC_Os07g22650 or LOC_Os07g44660)	Starch and sucrose metabolism (Cellulose)	2.7.1.17
RPEc	ribulose phosphate 3-epimerase, cytosolic	ru5p-D[c] <=> xu5p-D[c]	LOC_Os09g32810	Pentose Phosphate Pathway	5.1.3.1
RPEs	ribulose phosphate 3-epimerase, plastidic	ru5p-D[s] <=> xu5p-D[s]	LOC_Os03g07300	Calvin cycle	5.1.3.1
3HPPDc	3-hydroxypropionate dehydrogenase	3hpp[c] + nad[c] <=> h[c] + msa[c] + nadh[c]		Alanine, aspartate and glutamate metabolism	1.1.1.59
TKT1s	Transketolase	r5p[s] + xu5p-D[s] <=> g3p[s] + s7p[s]	(LOC_Os04g19740 or LOC_Os06g04270)	Calvin cycle	2.2.1.1
ABTA1m	4-aminobutyrate aminotransferase (GABA-TK)	4abut[m] + akg[m] -> glu-L[m] + sucsal[m]	(LOC_Os08g10510 or LOC_Os03g44150 or LOC_Os08g41990)	Alanine, aspartate and glutamate metabolism	2.6.1.19
ABTA2m	4-aminobutyrate aminotransferase (GABA-TP)	ala-B[m] + akg[m] -> glu-L[m] + msa[m]	(LOC_Os08g10510 or LOC_Os03g44150 or LOC_Os08g41990)	Alanine, aspartate and glutamate metabolism	2.6.1.19
MOPCs	leucine biosynthesis; spontaneous reaction	3c4mop[s] + h[s] -> 4mop[s] + co2[s]		Valine, leucine and isoleucine metabolism	spontaneous
MTHFCc	Methenyltetrahydrofolate cyclohydrolase, cytosolic	h2o[c] + methf[c] <=> 10fthf[c] + h[c]		Folates metabolism	3.5.4.9
MTHFCs	Methenyltetrahydrofolate cyclohydrolase, plastidic	h2o[s] + methf[s] <=> 10fthf[s] + h[s]	LOC_Os02g02850	Folates metabolism	3.5.4.9
MTHFCm	Methenyltetrahydrofolate cyclohydrolase, mitochondrial	h2o[m] + methf[m] <=> 10fthf[m] + h[m]		Folates metabolism	3.5.4.9
GUADc	Guanine deaminase	gua[c] + h[c] + h2o[c] -> nh4[c] + xan[c]	LOC_Os03g61810	Purine metabolism	3.5.4.3
GSNRHc	Guanosine ribohydrolase	h2o[c] + gsn[c] -> rib-D[c] + gua[c]	(LOC_Os08g44370 or LOC_Os09g39440)	Purine metabolism	3.2.2.1
CHRSs	Chorismate synthase	3psme[s] -> chor[s] + pi[s]	LOC_Os03g14990	Phenylalanine, tyrosine and tryptophan metabolism	4.2.3.5
CHRMs	Chorismate mutase	chor[s] -> pphn[s]	(LOC_Os08g34290 or LOC_Os02g08410 or LOC_Os12g38900 or LOC_Os01g55870)	Phenylalanine, tyrosine and tryptophan metabolism	5.4.99.5
ADCSs	Aminodeoxychorismate synthase	chor[s] + gln-L[s] -> 4adcho[s] + glu-L[s]	LOC_Os06g48620	Folates metabolism	2.6.1.85
UREASEc	Urease	h2o[c] + urea[c] -> 2 nh4[c] + co2[c]	LOC_Os01g60250	Purine metabolism	3.5.1.5
ATAHc	Allantoicase	alltt[c] + h2o[c] + h[c] <=> urdglyc[c] + urea[c]		Purine metabolism	3.5.3.4
ATNAHc	Allantoinase	alltn[c] + h2o[c] -> alltt[c] + h[c]	LOC_Os04g58390	Purine metabolism	3.5.2.5
ATSc	allantoin synthetase	5houdic[c] + h[c] -> alltn[c] + co2[c]	LOC_Os03g27320	Purine metabolism	4.1.1.-
HIUHc	Hydroxyisourate hydrolase	5hiu[c] + h2o[c] -> 5houdic[c] + h[c]	LOC_Os03g27320	Purine metabolism	3.5.2.17
UROc	Urate oxidase	urate[c] + o2[c] + h2o[c] -> 5hiu[c] + h2o2[c] + h[c]	LOC_Os01g64520	Purine metabolism	1.7.3.3
XANDHc	Xanthine dehydrogenase	xan[c] + nad[c] + h2o[c] -> urate[c] + nadh[c] + h[c]	LOC_Os03g31550	Purine metabolism	1.17.1.4
HXANORc	hypoxanthine oxidoreductase	hxan[c] + nad[c] + h2o[c] -> xan[c] + nadh[c] + h[c]	LOC_Os03g31550	Purine metabolism	1.17.1.4
INSRHc	Inosine ribohydrolase	ins[c] + h2o[c] -> hxan[c] + rib-D[c]	(LOC_Os08g44370 or LOC_Os09g39440)	Purine metabolism	3.2.2.2
HOMATs	Homoserine O-acetyltransferase	accoa[s] + hom-L[s] -> achms[s] + coa[s]	LOC_Os02g47780	Glycine, serine and threonine metabolism	2.3.1.31
HOMSTs	Homoserine O-succinyltransferase	succoa[s] + hom-L[s] -> suchms[s] + coa[s]		Cysteine and methionine metabolism	2.3.1.46
AHSLs	O-Acetyl-L-homoserine succinate-lyase (adding cysteine)	achms[s] + cys-L[s] -> cyst-L[s] + ac[s] + h[s]	LOC_Os10g25950	Cysteine and methionine metabolism	2.5.1.48
SHSL4s	O-Succinyl-L-homoserine succinate-lyase	suchms[s] + h2o[s] <=> 2obut[s] + succ[s] + nh4[s] + h[s]	LOC_Os03g25940	Cysteine and methionine metabolism	2.5.1.48
SHSL1s	O-succinylhomoserine (thiol)-lyase	suchms[s] + cys-L[s] -> cyst-L[s] + succ[s] + h[s]	(LOC_Os10g25950 or LOC_Os03g25940)	Cysteine and methionine metabolism	2.5.1.48
HSKs	Homoserine kinase	atp[s] + hom-L[s] -> adp[s] + phom[s] + h[s]	(LOC_Os04g58720 or LOC_Os02g58510)	Glycine, serine and threonine metabolism	2.7.1.39
HSDHs	Homoserine dehydrogenase (NADH)	aspsa[s] + nadh[s] + h[s] -> hom-L[s] + nad[s]	(LOC_Os09g12290 or LOC_Os08g25390)	Glycine, serine and threonine metabolism	1.1.1.3
HSDHys	Homoserine dehydrogenase (NADPH)	aspsa[s] + nadph[s] + h[s] -> hom-L[s] + nadp[s]	(LOC_Os09g12290 or LOC_Os08g25390)	Glycine, serine and threonine	1.1.1.3

				metabolism	
GLUKAc	Glucokinase (glc-A), cytosolic	atp[c] + glc-A[c] -> adp[c] + g6p-A[c] + h[c]	(LOC_Os07g26540 or LOC_Os05g45590 or LOC_Os05g09500 or LOC_Os01g71320 or LOC_Os01g09460)	Glycolysis/Gluconeogensis	2.7.1.1
GLUKAs	Glucokinase (glc-A), plastidic	atp[s] + glc-A[s] -> adp[s] + g6p-A[s] + h[s]	(LOC_Os01g52450 or LOC_Os01g53930 or LOC_Os05g44760 or LOC_Os07g09890)	Glycolysis/Gluconeogensis	2.7.1.1
ADE1c	Aldose 1-epimerase, cytosolic	glc-A[c] <=> glc-B[c]	(LOC_Os02g36600 or LOC_Os03g26430 or LOC_Os04g38530 or LOC_Os04g38540 or LOC_Os09g02140 or LOC_Os10g06720)	Glycolysis/Gluconeogensis	5.1.3.3
ADE1s	Aldose 1-epimerase, plastidic	glc-A[s] <=> glc-B[s]	(LOC_Os04g38540 or LOC_Os10g06720)	Glycolysis/Gluconeogensis	5.1.3.3
GLUKBc	Hexokinase (glc-B), cytosolic	atp[c] + glc-B[c] -> adp[c] + g6p-B[c] + h[c]	(LOC_Os07g26540 or LOC_Os05g45590 or LOC_Os05g09500 or LOC_Os01g71320 or LOC_Os01g09460)	Glycolysis/Gluconeogensis	2.7.1.1
GLUKBs	Hexokinase (glc-B), plastidic	atp[s] + glc-B[s] -> adp[s] + g6p-B[s] + h[s]	(LOC_Os01g52450 or LOC_Os01g53930 or LOC_Os05g44760 or LOC_Os07g09890)	Glycolysis/Gluconeogensis	2.7.1.1
BAMYLs	beta-amylase	starch[s] + h2o[s] -> 2 malt[s]	(LOC_Os10g41550 or LOC_Os03g04770 or LOC_Os07g35880 or LOC_Os07g35940 or LOC_Os03g22790 or LOC_Os05g38250 or LOC_Os07g47120 or LOC_Os02g03690 or LOC_Os09g39570 or LOC_Os01g13550 or LOC_Os10g32810 or LOC_Os01g62850 or LOC_Os09g07480)	Starch and sucrose metabolism (Starch)	3.2.1.2
GGSs	Glucan 1,4-alpha-glucosidase	starch[s] + 3 h2o[s] -> 4 glc-A[s]	LOC_Os05g43870	Starch and sucrose metabolism (Starch)	3.2.1.3
MGHs	maltose glucohydrolase	malt[s] + h2o[s] -> 2 glc-A[s]	LOC_Os06g46284	Starch and sucrose metabolism (Starch)	3.2.1.20
SPPAs	starch phosphorylase	starch[s] + 2 pi[s] -> glucan[s] + 2 g1p[s]	(LOC_Os01g63270 or LOC_Os03g55090)	Starch and sucrose metabolism (Starch)	2.4.1.1
DPHSs	2-dehydro-3-deoxyphosphoheptonate aldolase	pep[s] + e4p[s] + h2o[s] -> 2dda7p[s] + pi[s]	(LOC_Os10g41480 or LOC_Os08g37790 or LOC_Os03g27230 or LOC_Os07g42960)	Phenylalanine, tyrosine and tryptophan metabolism	2.5.1.54
TALAs	Transaldolase	g3p[s] + s7p[s] <=> e4p[s] + f6p-B[s]	(LOC_Os08g05830 or LOC_Os01g70170)	Calvin cycle	2.2.1.2
FBA3s	Sedoheptulose 1,7-bisphosphate D-glyceraldehyde-3-phosphate-lyase	dhap[s] + e4p[s] -> s17bp[s]	LOC_Os01g67860	Calvin cycle	4.1.2.13
TKT2s	Transketolase	e4p[s] + xu5p-D[s] <=> f6p-B[s] + g3p[s]	(LOC_Os04g19740 or LOC_Os06g04270)	Calvin cycle	2.2.1.1
SBPs	Sedoheptulose-bisphosphatase	h2o[s] + s17bp[s] -> pi[s] + s7p[s]	LOC_Os04g16680	Calvin cycle	3.1.3.37
ASPCTs	Aspartate carbamoyltransferase	cbp[s] + asp-L[s] -> pi[s] + cbasp[s]	(LOC_Os08g15030 or LOC_Os02g47590)	Pyrimidine metabolism	2.1.3.2
ORPRTs	Orotate phosphoribosyltransferase	orot5p[s] + ppi[s] <=> orot[s] + prpp[s]	LOC_Os01g72240	Pyrimidine metabolism	2.4.2.10
ACONTc	Aconitate hydratase, cytosolic	acon-C[c] + h2o[c] <=> icit[c]	LOC_Os08g09200	Glyoxylate Cycle	4.2.1.3
ACONc	Aconitase, cytosolic	cit[c] <=> acon-C[c] + h2o[c]	LOC_Os08g09200	Glyoxylate Cycle	4.2.1.3
ACONTm	Aconitate hydratase, mitochondrial	acon-C[m] + h2o[m] <=> icit[m]	(LOC_Os02g03260 or LOC_Os06g19960 or LOC_Os03g04410)	TCA Cycle	4.2.1.3
ACONm	Aconitase, mitochondrial	cit[m] <=> acon-C[m] + h2o[m]	(LOC_Os02g03260 or LOC_Os06g19960 or LOC_Os03g04410)	TCA Cycle	4.2.1.3
ARGSSs	argininosuccinate synthetase, plastidic	atp[s] + citr-L[s] + asp-L[s] -> amp[s] + ppi[s] + argsuc[s] + h[s]	(LOC_Os11g19770 or LOC_Os12g13320)	Arginine and proline metabolism	6.3.4.5
ARGSSc	argininosuccinate synthetase, cytosolic	atp[c] + citr-L[c] + asp-L[c] -> amp[c] + ppi[c] + argsuc[c] + h[c]		Arginine and proline metabolism	6.3.4.5
DHRs	Dihydroorotase	cbasp[s] + h[s] <=> dhor-S[s] + h2o[s]	LOC_Os01g54370	Pyrimidine metabolism	3.5.2.3
PGLc	6-phosphogluconolactonase, cytosolic	6pgl[c] + h2o[c] -> 6pgc[c] + h[c]	(LOC_Os07g41280 or LOC_Os03g30300)	Pentose Phosphate Pathway	3.1.1.31
PGLs	6-phosphogluconolactonase, plastidic	6pgl[s] + h2o[s] -> 6pgc[s] + h[s]	(LOC_Os09g35970 or LOC_Os08g43370)	Pentose Phosphate Pathway	3.1.1.31
PFPc	Diphosphate--fructose-6-phosphate 1-phosphotransferase	f6p-B[c] + ppi[c] -> pi[c] + fdp-B[c] + h[c]	((LOC_Os06g22060 or LOC_Os08g25720 or LOC_Os02g48360 or	Glycolysis/Gluconeogensis	2.7.1.90

			LOC_Os09g12650) and LOC_Os06g13810)		
AGSs	Amylo-1,6-glucosidase	2 glucan[s] -> starch[s] + h2o[s]	(LOC_Os06g26234 or LOC_Os06g51084 or LOC_Os02g32660 or LOC_Os08g40930 or LOC_Os09g29404)	Starch and sucrose metabolism (Starch)	2.4.1.18
XTSNPc	Xanthosine phosphorylase	xtsn[c] + pi[c] <=> xan[c] + r1p[c]		Purine metabolism	2.4.2.1
XSTNRHc	Xanthosine ribohydrolase	xtsn[c] + h2o[c] -> xan[c] + rib-D[c]	LOC_Os09g39440	Purine metabolism	3.2.2.1
GSNDc	Guanosine deaminase	h2o[c] + gsn[c] -> nh4[c] + xtsn[c]		Purine metabolism	3.5.4.15
CYORm	Q-cytochrome c oxidoreductase (complex III)	2 ficytc[m] + 2 h[m] + q8h2[m] -> 2 focytc[m] + 4 h[c] + q8[m]	((LOC_Os03g59220 or LOC_Os08g14860 or LOC_Os07g10500) and (LOC_Os06g07969 or LOC_Os06g07869))	Oxidative phosphorylation	1.10.2.2
NADORm	NADH-coenzyme Q oxidoreductase (complex I)	h[m] + nadh[m] + q8[m] -> nad[m] + q8h2[m]	(LOC_Os02g57180 and LOC_Os03g03770 and LOC_Os03g09210 and LOC_Os03g18420 and LOC_Os03g19890 and LOC_Os03g22950 and LOC_Os03g50540 and LOC_Os03g56300 and LOC_Os04g24520 and LOC_Os05g40300 and LOC_Os05g43360 and LOC_Os05g45730 and LOC_Os06g50000 and LOC_Os07g12150 and LOC_Os07g39710 and LOC_Os07g44650 and LOC_Os08g06430 and LOC_Os08g44250 and LOC_Os10g42840 and LOC_Osm1g00210 and LOC_Osm1g00640 and LOC_Osm1g00280 and LOC_Osm1g00320 and LOC_Osm1g00460 and LOC_Osm1g00190 and LOC_Osm1g00230 and LOC_Osm1g00590)	Oxidative phosphorylation	1.6.5.3 and 1.6.99.3
NADORFu	NADH-dehydrogenase (complex I-like)	h[u] + fdxrd[u] + pq[u] -> fdxox[u] + pqh2[u]	(LOC_Osp1g00960 and (LOC_Osp1g00810 or LOC_Osp1g01060) and LOC_Osp1g00390 and LOC_Osp1g00910 and LOC_Osp1g00930 and LOC_Osp1g00880 and LOC_Osp1g00940 and LOC_Osp1g00970 and LOC_Osp1g00950 and LOC_Osp1g00370 and LOC_Osp1g00380)	Chlororespiration; Oxidative Phosphorylation	1.6.5.3
PTOXs	Plastid terminal oxidase	4 h[s] + pqh2[u] + o2[s] -> 2 h2o[s] + pq[u] + 2 h[u]	LOC_Os04g57320	Chlororespiration; Oxidative Phosphorylation	
NADOR2u	NAD(P)H-dehydrogenase (complex I-like)	h[u] + nadph[s] + pq[u] -> nadp[s] + pqh2[u]	(LOC_Osp1g00960 and (LOC_Osp1g00810 or LOC_Osp1g01060) and LOC_Osp1g00390 and LOC_Osp1g00910 and LOC_Osp1g00930 and LOC_Osp1g00880 and LOC_Osp1g00940 and LOC_Osp1g00970 and LOC_Osp1g00950 and LOC_Osp1g00370 and LOC_Osp1g00380)	Chlororespiration; Oxidative Phosphorylation	
NADOR1u	NAD(P)H-dehydrogenase (complex I-like)	h[u] + nadh[s] + pq[u] -> nad[s] + pqh2[u]	(LOC_Osp1g00960 and (LOC_Osp1g00810 or LOC_Osp1g01060) and LOC_Osp1g00390 and LOC_Osp1g00910 and LOC_Osp1g00930 and LOC_Osp1g00880 and LOC_Osp1g00940 and LOC_Osp1g00970 and LOC_Osp1g00950 and LOC_Osp1g00370 and LOC_Osp1g00380)	Chlororespiration; Oxidative Phosphorylation	1.6.5.3
SUCDH1m	Succinate-Q oxidoreductase (complex II)	q8[m] + succ[m] -> q8h2[m] + fum[m]	(LOC_Os07g04240 and LOC_Os07g33680 and LOC_Os09g20440 and	TCA Cycle	1.3.5.1

			LOC_Os02g02940)		
BCTA3s	Branched-chain amino acid (ile-L) aminotransferase, plastidic	3mop[s] + glu-L[s] <=> ile-L[s] + akg[s]	(LOC_Os02g17330 or LOC_Os03g01600 or LOC_Os10g40200 or LOC_Os03g12890 or LOC_Os03g24460 or LOC_Os05g48450 or LOC_Os04g47190)	Valine, leucine and isoleucine metabolism	2.6.1.42
BCTA3m	Branched-chain amino acid (ile-L) aminotransferase, mitochondrial	3mop[m] + glu-L[m] <=> ile-L[m] + akg[m]		Valine, leucine and isoleucine metabolism	2.6.1.42
DHFSm	dihydrofolate synthetase	atp[m] + dhpt[m] + glu-L[m] -> adp[m] + pi[m] + dhf[m] + h[m]	LOC_Os12g42870	Folates metabolism	6.3.2.12
GACTs	Glutamate N-acetyltransferase	acorn[s] + glu-L[s] <=> orn[s] + acglu[s]	LOC_Os03g17120	Arginine and proline metabolism	2.3.1.35
AOTAs	Acetylornithine aminotransferase	acg5sa[s] + glu-L[s] <=> acorn[s] + akg[s]	(LOC_Os05g03830 or LOC_Os07g27780)	Arginine and proline metabolism	2.6.1.11
AODAAc	Acetylornithine deacetylase	acorn[c] + h2o[c] -> ac[c] + orn[c]	LOC_Os02g46520	Arginine and proline metabolism	3.5.1.16
OCTs	Ornithine carbamoyltransferase, plastidic	cbp[s] + orn[s] <=> pi[s] + citr-L[s] + h[s]	(LOC_Os08g15030 or LOC_Os02g47590)	Arginine and proline metabolism	2.1.3.3
OCTc	Ornithine carbamoyltransferase, cytosolic	cbp[c] + orn[c] <=> pi[c] + citr-L[c] + h[c]		Arginine and proline metabolism	2.1.3.3
ASADHs	Aspartate-semialdehyde dehydrogenase	4pasp[s] + nadph[s] + h[s] -> aspsa[s] + pi[s] + nadp[s]	(LOC_Os03g42110 or LOC_Os10g35170 or LOC_Os03g55280)	Glycine, serine and threonine metabolism	1.2.1.11
DHDPSs	dihydrodipicolinate synthase	aspsa[s] + pyr[s] -> 23dhdp[s] + h2o[s] + h[s]	(LOC_Os04g18200 or LOC_Os04g48540)	Lysine metabolism	4.3.3.7
G3PLs	Indole-3-glycerol-phosphate lyase	3ig3p[s] -> indole[s] + g3p[s]	LOC_Os03g58300	Phenylalanine, tyrosine and tryptophan metabolism	4.1.2.8
SKKs	shikimate-kinase	atp[s] + skm[s] -> adp[s] + skm5p[s] + h[s]	(LOC_Os10g42700 or LOC_Os02g46220 or LOC_Os10g41580 or LOC_Os02g51410 or LOC_Os06g12150 or LOC_Os04g54800 or LOC_Os01g01302)	Phenylalanine, tyrosine and tryptophan metabolism	2.7.1.71
SKDHs	Shikimate 5-dehydrogenase	3dhsk[s] + nadph[s] + h[s] -> skm[s] + nadp[s]	(LOC_Os01g27750 or LOC_Os12g34874)	Phenylalanine, tyrosine and tryptophan metabolism	1.1.1.25
SSs	Starch (bacterial glycogen) synthase	2 adpglc[s] + h2o[s] -> 2 adp[s] + glucan[s]	(LOC_Os04g56920 or LOC_Os11g07440 or LOC_Os02g01590 or LOC_Os01g73580 or LOC_Os03g20020 or LOC_Os02g34560 or LOC_Os04g45290 or LOC_Os02g03320 or LOC_Os01g22900 or LOC_Os02g33110)	Starch and sucrose metabolism (Starch)	2.4.1.21
DPRm	2-dehydropantoate 2-reductase	2dhp[m] + h[m] + nadph[m] -> nadp[m] + pant-R[m]	LOC_Os08g16570	Pantothenate and CoA metabolism	1.1.1.169
PANTSc	pantothenate synthetase	ala-B[c] + atp[c] + pant-R[c] -> amp[c] + h[c] + pnto-R[c] + ppi[c]	LOC_Os03g63490	Pantothenate and CoA metabolism	6.3.2.1
AGKc	Acetylglutamate kinase	atp[c] + acglu[c] -> adp[c] + acg5p[c]	(LOC_Os04g46460 or LOC_Os03g31690 or LOC_Os07g39690 or LOC_Os02g44000)	Arginine and proline metabolism	2.7.2.8
PRPNCOAHYDm	3-hydroxyacyl-CoA dehydrogenase	h2o[m] + prpncoa[m] -> 3hpcoa[m]	LOC_Os02g17390	Alanine, aspartate and glutamate metabolism	4.2.1.17
XMPc	Xanthosine 5-phosphate phosphohydrolase	xmp[c] + h2o[c] -> xtsn[c] + pi[c]	(LOC_Os01g51280 or LOC_Os03g44660 or LOC_Os07g10460)	Purine metabolism	3.1.3.5
DAPEPs	Diaminopimelate epimerase	26dap-LL[s] -> 26dap-M[s]	LOC_Os12g37960	Lysine metabolism	5.1.1.7
G6PDHc	Glucose-6-phosphate 1-dehydrogenase, cytosolic	g6p-B[c] + nadp[c] -> 6pgl[c] + h[c] + nadph[c]	(LOC_Os04g40874 or LOC_Os02g38840)	Pentose Phosphate Pathway	1.1.1.49
G6PDHs	Glucose-6-phosphate 1-dehydrogenase, plastidic	g6p-B[s] + nadp[s] -> 6pgl[s] + h[s] + nadph[s]	(LOC_Os03g29950 or LOC_Os03g20300 or LOC_Os07g22350)	Pentose Phosphate Pathway	1.1.1.49
CELLBGc	cellobiose beta-glucosidase	cellb[c] + h2o[c] -> 2 glc-B[c]	(LOC_Os01g32364 or LOC_Os02g03870 or LOC_Os03g11420 or LOC_Os03g49600 or LOC_Os03g53790 or LOC_Os03g53800 or LOC_Os04g39900 or LOC_Os04g43360 or LOC_Os05g30350 or LOC_Os08g39860	Starch and sucrose metabolism (Cellulose)	3.2.1.21

			or LOC_Os09g31430 or LOC_Os10g17650)		
CELLc	cellulase	cellulose[c] -> cellb[c]	(LOC_Os05g03840 or LOC_Os01g71650 or LOC_Os03g52630 or LOC_Os02g50040 or LOC_Os01g71820 or LOC_Os03g56130 or LOC_Os03g21210 or LOC_Os04g36610 or LOC_Os01g71474 or LOC_Os01g71340 or LOC_Os01g12070 or LOC_Os01g71400 or LOC_Os01g71830 or LOC_Os03g40330 or LOC_Os01g71860 or LOC_Os09g36060 or LOC_Os06g14540 or LOC_Os10g22570 or LOC_Os01g71810 or LOC_Os01g71350 or LOC_Os01g21070 or LOC_Os05g15510 or LOC_Os01g51570 or LOC_Os01g71410 or LOC_Os01g71670 or LOC_Os01g71680 or LOC_Os01g71380 or LOC_Os05g31140 or LOC_Os02g53820)	Starch and sucrose metabolism (Cellulose)	3.2.1.4
CELLSc	Cellulose synthase (UDP-forming)	2 udpg[c] + h2o[c] -> cellulose[c] + 2 udp[c]	(LOC_Os01g56130 or LOC_Os02g09930 or LOC_Os05g43530 or LOC_Os09g25900 or LOC_Os02g51060)	Starch and sucrose metabolism (Cellulose)	2.4.1.12
HDHs	Histidinol dehydrogenase	histd[s] + nad[s] -> histda[s] + nadh[s] + 2 h[s]	LOC_Os01g13190	Histidine metabolism	
HDAHs	Histidinal dehydrogenase	histda[s] + nad[s] + h2o[s] -> his-L[s] + nadh[s] + 2 h[s]	LOC_Os01g13190	Histidine metabolism	1.1.1.23
HPs	Histidinol-phosphatase	hisp[s] + h2o[s] -> histd[s] + pi[s]	(LOC_Os09g15400 or LOC_Os07g09330)	Histidine metabolism	3.1.3.15
PNTKc	Pantothenate kinase	atp[c] + pnto-R[c] -> 4ppan[c] + adp[c] + h[c]	(LOC_Os06g10520 or LOC_Os09g36270 or LOC_Os06g21980)	Pantothenate and CoA metabolism	2.7.1.33
PTPATic	Pantetheine-phosphate adenylyltransferase	atp[c] + h[c] + pan4p[c] -> dpcoa[c] + ppi[c]	LOC_Os07g08210	Pantothenate and CoA metabolism	2.7.7.3
KARAm	Ketol-acid reductoisomerase, mitochondrial	alac-S[m] + nadph[m] + h[m] -> 23dhmb[m] + nadp[m]		Pantothenate and CoA metabolism	1.1.1.86
KARAs	Ketol-acid reductoisomerase, plastidic	alac-S[s] + nadph[s] + h[s] -> 23dhmb[s] + nadp[s]	(LOC_Os05g49800 or LOC_Os01g46380)	Pantothenate and CoA metabolism	1.1.1.86
DHPSm	Dihydropteroate synthase	2ahhmd[m] + 4abz[m] -> dhpt[m] + ppi[m]	LOC_Os10g35250	Folates metabolism	2.5.1.15
DHQSs	3-dehydroquinate synthase	2dda7p[s] -> 3dhq[s] + pi[s]	LOC_Os09g36800	Phenylalanine, tyrosine and tryptophan metabolism	4.2.3.4
DQDHs	3-dehydroquinate dehydratase	3dhq[s] -> 3dhsk[s] + h2o[s]	(LOC_Os12g34874 or LOC_Os01g27750)	Phenylalanine, tyrosine and tryptophan metabolism	4.2.1.10
3HPCOAHYDc	3-hydroxyisobutyryl-CoA hydrolase	3hpcoa[c] + h2o[c] -> 3hpp[c] + coa[c] + h[c]	LOC_Os01g54860	Alanine, aspartate and glutamate metabolism	3.1.2.4
AOOAs	Histidinol-phosphate aminotransferase	hisp[s] + akg[s] <=> imacp[s] + glu-L[s]	(LOC_Os11g41900 or LOC_Os01g70570 or LOC_Os05g38350 or LOC_Os01g57360 or LOC_Os07g34730 or LOC_Os11g45400 or LOC_Os05g28960 or LOC_Os01g63580 or LOC_Os05g37600 or LOC_Os10g35390 or LOC_Os05g42270 or LOC_Os02g02340 or LOC_Os06g49790 or LOC_Os04g32010 or LOC_Os03g53650 or LOC_Os04g57150)	Histidine metabolism	2.6.1.9
PPCDCc	Phosphopantothenoylcysteine decarboxylase	4ppcys[c] + h[c] -> co2[c] + pan4p[c]	LOC_Os06g09910	Pantothenate and CoA metabolism	4.1.1.36
G5DHc	Glutamate-5-semialdehyde dehydrogenase, cytosolic	glu5p[c] + nadph[c] + h[c] -> glu5sa[c] + pi[c] + nadp[c]	(LOC_Os05g38150 or LOC_Os01g62900)	Arginine and proline metabolism	1.2.1.41
G5DHs	Glutamate-5-semialdehyde dehydrogenase, plastidic	glu5p[s] + nadph[s] + h[s] -> glu5sa[s] + pi[s] + nadp[s]		Arginine and proline metabolism	1.2.1.41
GSCc	Proline biosynthesis; spontaneous reaction, cytosolic	glu5sa[c] <=> 1pyr5c[c] + h2o[c] + h[c]		Arginine and proline metabolism	spontaneous
GSCm	Proline biosynthesis; spontaneous reaction,	glu5sa[m] <=> 1pyr5c[m] + h2o[m] + h[m]		Arginine and proline	spontaneous

	mitochondrial			metabolism	
GSCs	Proline biosynthesis; spontaneous reaction, plastidic	glu5sa[s] <=> 1pyr5c[s] + h2o[s] + h[s]		Arginine and proline metabolism	spontaneous
AGGPRc	N-acetyl-gamma-glutamyl-phosphate reductase	acg5p[c] + nadph[c] + h[c] -> acg5sa[c] + pi[c] + nadp[c]	(LOC_Os03g42110 or LOC_Os10g35170)	Arginine and proline metabolism	1.2.1.38
IGPDs	Imidazoleglycerol-phosphate dehydratase	eig3p[s] -> imacp[s] + h2o[s]	LOC_Os04g52710	Histidine metabolism	4.2.1.19
PSCITs	3-phosphoshikimate 1-carboxyvinyltransferase	pep[s] + skm5p[s] -> pi[s] + 3psme[s]	LOC_Os06g04280	Phenylalanine, tyrosine and tryptophan metabolism	2.5.1.19
HPPKm	2-amino-4-hydroxy-6-hydroxymethyldihydropteridine pyrophosphokinase	atp[m] + 2ahhmp[m] -> amp[m] + 2ahhmd[m]	(LOC_Os07g42632 or LOC_Os11g03680)	Folates metabolism	2.7.6.3
PYAM5POc	Pyridoxamine-phosphate oxidase	pyam5p[c] + h2o[c] + o2[c] -> pydx5p[c] + nh4[c] + h2o2[c]	(LOC_Os02g05500 or LOC_Os03g02450 or LOC_Os10g23120)	Other Vitamins Metabolism (B6)	1.4.3.5
PDX5POic	Pyridoxine 5-phosphate:oxygen oxidoreductase	pdx5p[c] + o2[c] -> h2o2[c] + pydx5p[c]	(LOC_Os02g05500 or LOC_Os03g02450 or LOC_Os10g23120)	Other Vitamins Metabolism (B6)	1.4.3.5
PYDXNOc	Pyridoxine:oxygen oxidoreductase (deaminating)	pydxn[c] + o2[c] -> pydx[c] + h2o2[c]	(LOC_Os02g05500 or LOC_Os03g02450 or LOC_Os10g23120)	Other Vitamins Metabolism (B6)	1.4.3.5
PYDXOc	Pyridoxamine:oxygen oxidoreductase (deaminating)	pydam[c] + h2o[c] + o2[c] -> pydx[c] + nh4[c] + h2o2[c]	(LOC_Os02g05500 or LOC_Os03g02450 or LOC_Os10g23120)	Other Vitamins Metabolism (B6)	1.4.3.5
PYDXNKc	pyridoxine 5-phosphotransferase	atp[c] + pydxn[c] -> adp[c] + pdx5p[c] + h[c]	LOC_Os12g40830	Other Vitamins Metabolism (B6)	2.7.1.35
PYDAMKc	pyridoxal 5-phosphotransferase	atp[c] + pydam[c] -> adp[c] + pyam5p[c] + h[c]	LOC_Os12g40830	Other Vitamins Metabolism (B6)	2.7.1.35
PYDXKc	Pyridoxal kinase	atp[c] + pydx[c] -> adp[c] + pydx5p[c] + h[c]	LOC_Os12g40830	Other Vitamins Metabolism (B6)	2.7.1.35
PYDMPATc	Pyridoxamine--pyruvate aminotransferase	pyr[c] + pydam[c] <=> ala-L[c] + pydx[c]		Other Vitamins Metabolism (B6)	2.6.1.30
PYDXNSc	Pyridoxine synthase	gcald[c] + 2obut[c] + ala-L[c] -> pydxn[c] + co2[c] + 2 h2o[c] + 2 h[c]		Other Vitamins Metabolism (B6)	
DHNPTAc	Dihydroneopterin aldolase	dhnpt[c] -> gcald[c] + 2ahhmp[c]	(LOC_Os08g44210 or LOC_Os06g06100 or LOC_Os09g38759)	Folates metabolism	4.1.2.25
IGPSs	indole-3-glycerol-phosphate synthase	2cpr5p[s] + h[s] -> 3ig3p[s] + co2[s] + h2o[s]	LOC_Os09g08130	Phenylalanine, tyrosine and tryptophan metabolism	4.1.1.48
PRAIs	Phosphoribosylanthranilate isomerase	pran[s] -> 2cpr5p[s]	LOC_Os02g16630	Phenylalanine, tyrosine and tryptophan metabolism	5.3.1.24
IMDHTs	3-isopropylMalate dehydratase	3c3hmp[s] <=> 3c2hmp[s]	(LOC_Os02g43830 or LOC_Os02g03260 or LOC_Os03g04410)	Valine, leucine and isoleucine metabolism	4.2.1.33
PRADPs	Phosphoribosyl-ATP pyrophosphatase	prbatp[s] + h2o[s] -> prbamp[s] + ppi[s] + h[s]	LOC_Os01g16940	Histidine metabolism	3.6.1.31
PRACHs	Phosphoribosyl-AMP cyclohydrolase	prbamp[s] + h2o[s] -> prfp[s]	LOC_Os01g16940	Histidine metabolism	3.5.4.19
PPRGLs	Phosphoribosylamine--glycine ligase	atp[s] + pram[s] + gly[s] -> adp[s] + pi[s] + gar[s] + h[s]	(LOC_Os08g09210 or LOC_Os12g09540)	Purine metabolism	6.3.4.13
PSATs	Phosphoserine aminotransferase	3php[s] + glu-L[s] -> pser-L[s] + akg[s]	LOC_Os03g06200	Glycine, serine and threonine metabolism	2.6.1.52
DHPRs	Dihydrodipicolinate reductase	23dhdp[s] + nadh[s] + h[s] -> thdp[s] + nad[s] + h2o[s]	(LOC_Os02g24020 or LOC_Os03g14120)	Lysine metabolism	1.17.1.8
DHPRys	Dihydrodipicolinate reductase	23dhdp[s] + nadph[s] + h[s] -> thdp[s] + nadp[s] + h2o[s]	(LOC_Os02g24020 or LOC_Os03g14120)	Lysine metabolism	1.17.1.8
TMMPKs	thiamin-monophosphate kinase	thmmp[s] + atp[s] -> thmpp[s] + adp[s]		Other Vitamins Metabolism (Thiamine)	2.7.4.16
DXPSs	1-deoxy-D-xylulose-5-phosphate synthase	g3p[s] + h[s] + pyr[s] -> co2[s] + dxyl5p[s]	(LOC_Os06g05100 or LOC_Os05g33840)	Other Vitamins Metabolism (Thiamine)	2.2.1.7
TMPPPs	Thiamine-phosphate pyrophosphorylase	2mahmp[s] + 4mpetz[s] + h[s] -> ppi[s] + thmmp[s]	LOC_Os12g09000	Other Vitamins Metabolism (Thiamine)	2.5.1.3
HMPKs	Hydroxymethylpyrimidine kinase	4ahmmp[s] + atp[s] -> 4ampm[s] + adp[s] + h[s]	LOC_Os12g09000	Other Vitamins Metabolism (Thiamine)	2.7.1.49
THMKs	Thiamine kinase	atp[s] + thm[s] -> adp[s] + h[s] + thmmp[s]		Other Vitamins Metabolism (Thiamine)	2.7.1.89
PMPKs	Phosphomethylpyrimidine kinase	4ampm[s] + atp[s] -> 2mahmp[s] + adp[s]	LOC_Os12g09000	Other Vitamins Metabolism (Thiamine)	2.7.4.7

THICs	thiamine biosynthesis protein (ThiC)	air[s] + 2 h2o[s] -> 4ahmmp[s] + pi[s] + 2 co2[s] + 7 h[s]	LOC_Os03g47610	Other Vitamins Metabolism (Thiamine)	
THZPSN3s	thiazole phosphate synthesis	atp[s] + dhgly[s] + dxyl5p[s] + h[s] + iscssh[s] + nadph[s] -> 4mpetz[s] + amp[s] + co2[s] + 2 h2o[s] + iscs[s] + nadp[s] + ppi[s]		Other Vitamins Metabolism (Thiamine)	
TYRLs	tyrosine lyase	amet[s] + nadph[s] + tyr-L[s] -> 4crsol[s] + dad-5[s] + dhgly[s] + h[s] + met-L[s] + nadp[s]		Other Vitamins Metabolism (Thiamine)	
ICYSDSs	ISC Cysteine desulfuration	cys-L[s] + iscs[s] -> ala-L[s] + iscssh[s]		Other Vitamins Metabolism (Thiamine)	
THMPs	thiamin phosphatase	h2o[s] + thmmp[s] -> pi[s] + thm[s]		Other Vitamins Metabolism (Thiamine)	3.6.1.-
TMDPKc	Thiamine pyrophosphokinase	atp[c] + thm[c] -> amp[c] + thmpp[c]	(LOC_Os05g30454 or LOC_Os01g25440 or LOC_Os01g70580)	Other Vitamins Metabolism (Thiamine)	2.7.6.2
PRFGCLs	phosphoribosylformylglycinamidine cyclo-ligase	atp[s] + fpram[s] -> adp[s] + pi[s] + air[s] + h[s]	LOC_Os03g61600	Purine metabolism	6.3.3.1
PRAICs	Phosphoribosylaminoimidazole carboxylase	air[s] + co2[s] <=> 5aizc[s] + 2 h[s]	LOC_Os01g10280	Purine metabolism	4.1.1.21
PPNCL2c	Phosphopantothenate--cysteine ligase	4ppan[c] + ctp[c] + cys-L[c] -> 4ppcys[c] + cmp[c] + h[c] + ppi[c]	(LOC_Os02g36550 or LOC_Os08g07880)	Pantothenate and CoA metabolism	6.3.2.5
FPGFTs	Phosphoribosylglycinamide formyltransferase	10fthf[s] + gar[s] <=> thf[s] + fgam[s] + h[s]	(LOC_Os08g39160 or LOC_Os05g18790 or LOC_Os06g22560)	Purine metabolism	2.1.2.2
FGFTs	N2-Formyl-N1-(5-phospho-D-ribosyl)glycinamide formyltransferase, chloroplast	fgam[s] + thf[s] + 3 h[s] -> gar[s] + methf[s] + h2o[s]	(LOC_Os08g39160 or LOC_Os05g18790 or LOC_Os06g22560)	Purine metabolism	2.1.2.2
IMDHs	3-isopropylMalate dehydrogenase	3c2hmp[s] + nad[s] -> 3c4mop[s] + nadh[s] + h[s]	LOC_Os03g45320	Valine, leucine and isoleucine metabolism	1.1.1.85
MOD(4mop)	3-methyl-2-oxobutanoate dehydrogenase, 4-Methyl-2-oxopentanoate transforming	4mop[m] + thmpp[m] + h[m] -> 3mhtpp[m] + co2[m]	(LOC_Os12g08260 and LOC_Os07g07470)	Valine, leucine and isoleucine metabolism	1.2.4.4
MOD(3mhtpp)	3-methyl-2-oxobutanoate dehydrogenase, 3-Methyl-1-hydroxybutyl-ThPP transforming	3mhtpp[m] + lpam[m] -> 3mbdhl[m] + thmpp[m]	(LOC_Os12g08260 and LOC_Os07g07470)	Valine, leucine and isoleucine metabolism	1.2.4.4
DHRT(ivcoa)	dihydrolipoyllysine-residue (2-methylpropanoyl)transferase, Isovaleryl-CoA forming	coa[m] + 3mbdhl[m] -> ivcoa[m] + dhlam[m]	LOC_Os01g21160	Valine, leucine and isoleucine metabolism	2.3.1.168
IVCDHm	Isovaleryl-CoA dehydrogenase	ivcoa[m] + fad[m] -> 3mb2coa[m] + fadh2[m]	LOC_Os07g47820	Valine, leucine and isoleucine metabolism	1.3.8.4
MCTCm	Methylcrotonyl-CoA carboxylase	atp[m] + 3mb2coa[m] + hco3[m] -> adp[m] + pi[m] + 3mgcoa[m] + h[m]	LOC_Os12g41250	Valine, leucine and isoleucine metabolism	6.4.1.4
MGCm	Methylglutaconyl-CoA hydratase	hmgcoa[m] <=> 3mgcoa[m] + h2o[m]	LOC_Os02g43720	Valine, leucine and isoleucine metabolism	4.2.1.18
HMGLm	Hydroxymethylglutaryl-CoA lyase	hmgcoa[m] -> accoa[m] + acac[m]	(LOC_Os12g04020 or LOC_Os11g04210 or LOC_Os01g16350)	Valine, leucine and isoleucine metabolism	4.1.3.4
PPCOAOc	Propanoyl-CoA:(acceptor) 2,3-oxidoreductase	ppcoa[m] + fad[m] -> fadh2[m] + prpncoa[m]	LOC_Os07g47820	Alanine, aspartate and glutamate metabolism	1.3.8.7
FPGFTm	Phosphoribosylglycinamide formyltransferase	10fthf[m] + gar[m] <=> thf[m] + fgam[m] + h[m]	(LOC_Os08g39160 or LOC_Os05g18790 or LOC_Os06g22560)	Purine metabolism	2.1.2.2
FGFTm	N2-Formyl-N1-(5-phospho-D-ribosyl)glycinamide formyltransferase, mitochondria	fgam[m] + thf[m] + 3 h[m] -> gar[m] + methf[m] + h2o[m]	(LOC_Os08g39160 or LOC_Os05g18790 or LOC_Os06g22560)	Purine metabolism	2.1.2.2
PRFGSs	phosphoribosylformylglycinamidine synthetase	atp[s] + fgam[s] + gln-L[s] + h2o[s] -> adp[s] + pi[s] + fpram[s] + glu-L[s] + h[s]	(LOC_Os05g01440 or LOC_Os01g66500)	Purine metabolism	6.3.5.3
IMGPSs	Imidazole glycerol phosphate synthase	prlp[s] + gln-L[s] -> eig3p[s] + aicar[s] + glu-L[s] + h[s]	(LOC_Os05g33260 or LOC_Os03g15120)	Histidine metabolism	2.4.2.-
AIALs	Adenylosuccinate lyase	25aics[s] <=> fum[s] + aicar[s]	(LOC_Os03g19280 or LOC_Os03g19930 or LOC_Os03g21950)	Purine metabolism	4.3.2.2
FPAIFs	Phosphoribosylaminoimidazolecarboxamide formyltransferase	10fthf[s] + aicar[s] <=> thf[s] + fprica[s]	LOC_Os08g10570	Purine metabolism	2.1.2.3
PRAISs	Phosphoribosylaminoimidazole-succinocarboxamide synthetase	atp[s] + 5aizc[s] + asp-L[s] -> adp[s] + pi[s] + 25aics[s] + h[s]	LOC_Os09g29190	Purine metabolism	6.3.2.6
DNMPPAc	Dihydroneopterin monophosphate	dhpmp[c] + h2o[c] -> dhnpt[c] + pi[c]	LOC_Os02g37910	Folates metabolism	3.6.1.-

	dephosphorylase				
DNTPPAc	dihydroneopterin triphosphate diphosphatase	ahdt[c] + h2o[c] -> dhpmp[c] + ppi[c]	LOC_Os02g37910	Folates metabolism	3.6.1.-
PRICIs	N-(5-phospho-D-ribosylformimino)-5-amino-1-(5-phosphoribosyl)-4- imidazole carboxamide isomerase	prfp[s] -> prlp[s]	LOC_Os05g33260	Histidine metabolism	5.3.1.16
PFKc	6-phosphofructokinase, cytosolic	atp[c] + f6p-B[c] -> adp[c] + fdp-B[c] + h[c]	(LOC_Os04g39420 or LOC_Os08g34050 or LOC_Os09g30240 or LOC_Os01g09570 or LOC_Os09g24910 or LOC_Os05g44922)	Glycolysis/Gluconeogensis	2.7.1.11
PFKs	6-phosphofructokinase, plastidic	atp[s] + f6p-B[s] -> adp[s] + fdp-B[s] + h[s]	LOC_Os10g26570	Glycolysis/Gluconeogensis	2.7.1.11
KARA2is	Ketol-acid reductoisomerase	2ahbut[s] + h[s] + nadph[s] -> 23dhmp[s] + nadp[s]	(LOC_Os05g49800 or LOC_Os01g46380)	Valine, leucine and isoleucine metabolism	1.1.1.86
DHAD-ps	Dihydroxy-acid dehydratase	23dhmp[s] -> 3mop[s] + h2o[s]	LOC_Os08g44530	Valine, leucine and isoleucine metabolism	4.2.1.9
GLDPs	4-alpha-glucanotransferase	glucan[s] + h2o[s] -> 2 glc-A[s]	(LOC_Os07g43390 or LOC_Os07g46790)	Starch and sucrose metabolism (Starch)	2.4.1.25
ADCLs	Aminodeoxychorismate lyase	4adcho[s] -> 4abz[s] + pyr[s] + h[s]	(LOC_Os01g13690 or LOC_Os02g17330 or LOC_Os05g15530)	Folates metabolism	4.1.3.38
BPNTs	3-Phospho-5-adenylyl sulfate 3-phosphohydrolase	paps[s] + h2o[s] -> aps[s] + pi[s]	(LOC_Os03g39000 or LOC_Os12g08270 or LOC_Os12g08280 or LOC_Os02g56170)	Sulfate metabolism (Glutathione)	3.1.3.7
BPNT2s	3(2),5-bisphosphate nucleotidase	pap[s] + h2o[s] -> amp[s] + pi[s]	(LOC_Os03g39000 or LOC_Os12g08270 or LOC_Os12g08280 or LOC_Os02g56170)	Sulfate metabolism (Glutathione)	3.1.3.7
ADSKs	Adenylylsulfate kinase	aps[s] + atp[s] <=> adp[s] + h[s] + paps[s]	(LOC_Os03g53230 or LOC_Os07g38560 or LOC_Os11g41650)	Sulfate metabolism (Glutathione)	2.7.1.25
ADSKc	Adenylylsulfate kinase, cytosolic	aps[c] + atp[c] <=> adp[c] + h[c] + paps[c]	(LOC_Os03g53230 or LOC_Os07g38560 or LOC_Os11g41650)	Sulfate metabolism (Glutathione)	2.7.1.25
PAPSRs	Phosphoadenylyl-sulfate reductase (thioredoxin)	paps[s] + trdrd[s] <=> h[s] + pap[s] + hso3[s] + trdox[s]	(LOC_Os07g32570 or LOC_Os01g15490)	Sulfate metabolism (Glutathione)	1.8.4.8
ASRGs	Adenylyl-sulfate reductase (glutathione)	amp[s] + hso3[s] + gthox[s] + h[s] <=> aps[s] + 2 gthrd[s]	LOC_Os07g32570	Sulfate metabolism (Glutathione)	1.8.4.9; 1.8.99.2
AAs	alpha-amylase	starch[s] + h2o[s] -> 2 glucan[s]	(LOC_Os01g51754 or LOC_Os02g52700 or LOC_Os02g52710 or LOC_Os04g33040 or LOC_Os05g32710 or LOC_Os06g26234 or LOC_Os06g49970 or LOC_Os08g36900 or LOC_Os08g36910 or LOC_Os09g28400 or LOC_Os09g28420 or LOC_Os09g28430 or LOC_Os09g29404 or LOC_Os04g08270)	Starch and sucrose metabolism (Starch)	3.2.1.1;3.2.1.41
PHETAs	L-phenylalanine transferase, plastidic	akg[s] + phe-L[s] <=> glu-L[s] + phpyr[s]	(LOC_Os11g35040 or LOC_Os06g23684 or LOC_Os02g19970 or LOC_Os02g19924 or LOC_Os01g65090)	Phenylalanine, tyrosine and tryptophan metabolism	2.6.1.57
PHETAc	L-phenylalanine transferase, cytosolic	akg[c] + phe-L[c] <=> glu-L[c] + phpyr[c]	(LOC_Os11g35040 or LOC_Os06g23684 or LOC_Os02g20360 or LOC_Os02g19970 or LOC_Os02g19924 or LOC_Os01g65090)	Phenylalanine, tyrosine and tryptophan metabolism	2.6.1.57
PPYRDCc	Phenylpyruvate decarboxylase	h[c] + phpyr[c] -> co2[c] + pacald[c]		Phenylalanine, tyrosine and tryptophan metabolism	4.1.1.43
ALCD25c	Phenylethylalcohol:NAD+ oxidoreductase	h[c] + nadh[c] + pacald[c] -> 2phetoh[c] + nad[c]	(LOC_Os03g12270 or LOC_Os04g52280 or LOC_Os08g16910 or LOC_Os09g23530 or LOC_Os09g23540 or LOC_Os09g23550 or LOC_Os10g29470)	Phenylalanine, tyrosine and tryptophan metabolism	1.1.1.90
DAPATs	LL-2,6-diaminoheptanedioate aminotransferase	thdp[s] + glu-L[s] + h2o[s] + h[s] <=> 26dap-LL[s] + akg[s]	LOC_Os03g09910	Lysine metabolism	2.6.1.83
PGMTc	Phosphoglucomutase, cytosolic	g1p[c] <=> g6p-A[c]	LOC_Os03g50480	Starch and sucrose metabolism (Sucrose)	5.4.2.2

PGMTv	Phosphoglucomutase, cytosolic	g1p[v] <=> g6p-A[v]		Starch and sucrose metabolism (Sucrose)	5.4.2.2
PGMTs	Phosphoglucomutase, plastidic	g1p[s] <=> g6p-A[s]	(LOC_Os06g28194 or LOC_Os07g26610 or LOC_Os10g11140)	Starch and sucrose metabolism (Starch)	5.4.2.2
ACHBSs	Acetolactate synthase	2ahethmpp[s] + 2obut[s] + h[s] -> 2ahbut[s] + thmpp[s]	(LOC_Os06g51450 or LOC_Os02g34630 or LOC_Os11g14950 or LOC_Os02g30630 or LOC_Os04g31960 or LOC_Os02g39570 or LOC_Os03g52690 or LOC_Os03g21080 or LOC_Os04g32010)	Valine, leucine and isoleucine metabolism	2.2.1.6
MOD(3mop)	3-methyl-2-oxobutanoate dehydrogenase, 3-Methyl-2-oxopentanoate transforming	3mop[m] + thmpp[m] + h[m] -> 2mhob[m] + co2[m]	(LOC_Os12g08260 and LOC_Os07g07470)	Valine, leucine and isoleucine metabolism	1.2.4.4
MOD(2mbdhl)	3-methyl-2-oxobutanoate dehydrogenase, 2-Methyl-1-hydroxybutyl-ThPP transforming	2mhob[m] + lpam[m] -> 2mbdhl[m] + thmpp[m]	(LOC_Os12g08260 and LOC_Os07g07470)	Valine, leucine and isoleucine metabolism	1.2.4.4
DHRT(2mbcoa)	dihydrolipoyllysine-residue (2-methylpropanoyl)transferase, 2-Methylbutanoyl-CoA forming	coa[m] + 2mbdhl[m] -> 2mbcoa[m] + dhlam[m]	LOC_Os01g21160	Valine, leucine and isoleucine metabolism	2.3.1.168
MCDH2m	2-methyl-branched-chain-enoyl-CoA reductase	2mbcoa[m] + fad[m] -> 2mb2coa[m] + fadh2[m]	LOC_Os07g47820	Valine, leucine and isoleucine metabolism	1.3.99.12
ECH2m	Tiglyl-CoA hydratase	2mb2coa[m] + h2o[m] -> 3hmbcoa[m]	(LOC_Os05g29880 or LOC_Os05g06300 or LOC_Os01g24680 or LOC_Os02g43720 or LOC_Os01g70090 or LOC_Os02g43710 or LOC_Os02g17390)	Valine, leucine and isoleucine metabolism	4.2.1.17
HMNOSm	3-hydroxy-2-methylbutyryl-CoA dehydrogenase	3hmbcoa[m] + nad[m] <=> 2maacoa[m] + nadh[m] + h[m]		Valine, leucine and isoleucine metabolism	1.1.1.178
ACCATm	2-methylacetoacetyl-CoA thiolase	coa[m] + 2maacoa[m] -> ppcoa[m] + accoa[m]	(LOC_Os02g57260 or LOC_Os10g31950)	Valine, leucine and isoleucine metabolism	2.3.1.9
CYSTS_Gs	Cystathionine gamma-synthase	phom[s] + cys-L[s] -> cyst-L[s] + pi[s]	LOC_Os10g25950	Cysteine and methionine metabolism	2.5.1.48
DHRDHm	Dihydroorotate dehydrogenase	dhor-S[c] + q8[m] -> orot[c] + q8h2[m]	LOC_Os04g57950	Pyrimidine metabolism	1.3.5.2
CBMKs	Carbamate kinase	atp[s] + co2[s] + nh4[s] <=> adp[s] + cbp[s] + h[s]	(LOC_Os06g14370 or LOC_Os02g44000)	Purine metabolism	2.7.2.2
CBPSs	carbamoyl-phosphate synthase (ammonia)	2 atp[s] + co2[s] + nh4[s] + h2o[s] -> cbp[s] + 2 adp[s] + pi[s]	LOC_Os01g38970	Purine metabolism	6.3.4.16
HCO3Es	carbonic anhydrase, plastidic	h[s] + hco3[s] -> co2[s] + h2o[s]	(LOC_Os01g45274 or LOC_Os02g33030 or LOC_Os08g32750 or LOC_Os08g32840 or LOC_Os09g28910 or LOC_Os12g05730)	Nitrogen metabolism	4.2.1.1
HCO3Ec	carbonic anhydrase, cytosolic	h[c] + hco3[c] -> co2[c] + h2o[c]	(LOC_Os04g33660 or LOC_Os08g32750 or LOC_Os08g32840 or LOC_Os08g36630 or LOC_Os11g05510 or LOC_Os12g05730)	Nitrogen metabolism	4.2.1.1
HCO3Em	carbonic anhydrase, mitochondrial	co2[m] + h2o[m] <=> h[m] + hco3[m]	LOC_Os08g32750	Nitrogen metabolism	4.2.1.1
ACCOACs	Acetyl-CoA carboxylase, plastidic	accoa[s] + atp[s] + hco3[s] -> adp[s] + h[s] + malcoa[s] + pi[s]	LOC_Osp1g00440	Fermentation	6.4.1.2
ACCOACc	Acetyl-CoA carboxylase, cytosolic	accoa[c] + atp[c] + hco3[c] -> adp[c] + h[c] + malcoa[c] + pi[c]	LOC_Os05g22940	Fermentation	6.4.1.2
PHENH4Lc	Phenylalanine ammonia-lyase	phe-L[c] <=> nh4[c] + t-cinn[c] + h[c]	(LOC_Os02g41630 or LOC_Os04g43760)	Phenylpropanoid metabolism	4.3.1.5
TYRNH4Lc	Tyrosine ammonia-lyase	tyr-L[c] <=> nh4[c] + coum[c] + h[c]	(LOC_Os04g43760 or LOC_Os02g41630)	Phenylpropanoid metabolism	4.3.1.25
COUMCOARc	4-coumaryl-CoA reductase	coumcoa[c] + nadph[c] + h[c] -> coumald[c] + nadp[c] + coa[c]	(LOC_Os09g31518 or LOC_Os09g31502 or LOC_Os09g31490 or LOC_Os03g60380 or LOC_Os03g60279)	Phenylpropanoid metabolism	1.2.1.44
COUMCOALc	4-coumarate--CoA ligase	coa[c] + coum[c] + atp[c] -> coumcoa[c] + ppi[c] + amp[c]	(LOC_Os08g34790 or LOC_Os08g04770 or LOC_Os06g44620 or LOC_Os03g05780 or LOC_Os02g08100 or LOC_Os08g14760 or LOC_Os02g46970)	Phenylpropanoid metabolism	6.2.1.12
CAFFCMTc	Caffeoyl-CoA O-methyltransferase	caffcoa[c] + amet[c] -> ahcys[c] + fercoa[c] + h[c]	(LOC_Os09g30360 or LOC_Os06g06980 or LOC_Os08g38900)	Phenylpropanoid metabolism	2.1.1.104
CAFFQTc	Caffeoyl-CoA:quinate O-(3,4-dihydroxycinnamoyl)transferase	caffqnt[c] + coa[c] -> caffcoa[c] + qnt[c]	(LOC_Os02g39850 or LOC_Os04g42251)	Phenylpropanoid metabolism	3.1.2.-
FERCOARc	feruloyl-CoA reductase	fercoa[c] + nadph[c] + h[c] -> conald[c] + nadp[c] + coa[c]	(LOC_Os09g31518 or LOC_Os09g31502	Phenylpropanoid metabolism	1.2.1.44

			or LOC_Os09g31490 or LOC_Os03g60380 or LOC_Os03g60279)		
TCMO4c	Trans-cinnamate 4-monooxygenase	t-cinn[c] + o2[c] + nadph[c] + h[c] -> h2o[c] + nadp[c] + coum[c]	(LOC_Os01g60450 or LOC_Os05g25640)	Phenylpropanoid metabolism	1.14.13.11
TCMO2c	Trans-cinnamate 2-monooxygenase	t-cinn[c] + o2[c] + nadph[c] + h[c] -> h2o[c] + nadp[c] + 2-coum[c]	(LOC_Os01g60450 or LOC_Os05g25640)	Phenylpropanoid metabolism	1.14.13.14
SKMHCTc	Shikimate O-hydroxycinnamoyltransferase	coumcoa[c] + skm[c] -> coumskm[c] + coa[c]	LOC_Os04g42250	Phenylpropanoid metabolism	2.3.1.133
CONOHDHc	coniferyl-alcohol dehydrogenase	conald[c] + nadph[c] + h[c] -> conoh[c] + nadp[c]	LOC_Os02g09490	Phenylpropanoid metabolism	1.1.1.195
SINOHDHc	sinapyl-alcohol dehydrogenase	sinald[c] + nadph[c] + h[c] -> sinoh[c] + nadp[c]	LOC_Os02g09490	Phenylpropanoid metabolism	1.1.1.195
COUMQMOc	coumaroylquinate 3-monooxygenase	coumqnt[c] + nadph[c] + o2[c] + h[c] -> caffqnt[c] + nadp[c] + h2o[c]	LOC_Os05g41440	Phenylpropanoid metabolism	1.14.13.36
FERH2c	ferulate 5-hydroxylase	conald[c] + nadph[c] + o2[c] + h[c] -> hconald[c] + nadp[c] + h2o[c]	(LOC_Os03g02180 or LOC_Os10g36848)	Phenylpropanoid metabolism	1.14.13.-
CONCMTc	S-adenosyl-L-methionine:3,4-dihydroxy-trans-cinnamate 3-O-methyltransferase	hconald[c] + amet[c] -> ahcys[c] + sinald[c] + h[c]	(LOC_Os08g06100 or LOC_Os02g57760 or LOC_Os04g01470 or LOC_Os12g13800)	Phenylpropanoid metabolism	2.1.1.68
COUMSKMMOc	coumaroylshikimate 3-monooxygenase	coumskm[c] + nadph[c] + o2[c] + h[c] -> caffskm[c] + nadp[c] + h2o[c]	LOC_Os05g41440	Phenylpropanoid metabolism	1.14.13.36
COUMCQHc	p-coumaroyl-CoA:quinate hydroxycinnamoyltransferase	coumcoa[c] + qnt[c] -> coumqnt[c] + coa[c]	LOC_Os04g42250	Phenylpropanoid metabolism	2.3.1.133
HCCSHCTc	Hydroxycinnamoyl-CoA:shikimate hydroxycinnamoyltransferase	caffskm[c] + coa[c] -> caffcoa[c] + skm[c]	(LOC_Os02g39850 or LOC_Os04g42251)	Phenylpropanoid metabolism	3.1.2.-
COUMOHDHc	4-coumaryl-alcohol dehydrogenase	coumald[c] + nadph[c] + h[c] -> coumoh[c] + nadp[c]	LOC_Os02g09490	Phenylpropanoid metabolism	1.1.1.195
CINNCOARc	Cinnamoyl-CoA reductase	cinncoa[c] + nadph[c] + h[c] -> cinnald[c] + nadp[c] + coa[c]	(LOC_Os09g31518 or LOC_Os09g31502 or LOC_Os09g31490 or LOC_Os03g60380 or LOC_Os03g60279)	Phenylpropanoid metabolism	1.2.1.44
CINNCOALc	cinnamate:CoA ligase	coa[c] + t-cinn[c] + atp[c] -> cinncoa[c] + ppi[c] + amp[c]	(LOC_Os02g08100 or LOC_Os02g46970 or LOC_Os03g05780 or LOC_Os06g44620 or LOC_Os08g14760 or LOC_Os08g34790)	Phenylpropanoid metabolism	6.2.1.12
CINNALDOc	cinnamaldehyde oxidase	cinnald[c] + o2[c] + h2o[c] <=> t-cinn[c] + h2o2[c] + h[c]	(LOC_Os10g04860 or LOC_Os07g18162 or LOC_Os07g18158 or LOC_Os07g18154 or LOC_Os07g18120 or LOC_Os07g07050 or LOC_Os03g57720 or LOC_Os03g57690 or LOC_Os03g57680)	Phenylpropanoid metabolism	1.2.3.9
CINNOHDHc	cinnamyl-alcohol dehydrogenase	nadp[c] + cinnoh[c] <=> nadph[c] + cinnald[c] + h[c]	(LOC_Os11g40690 or LOC_Os10g11810 or LOC_Os02g09490)	Phenylpropanoid metabolism	1.1.1.195
TFCOASc	trans-feruloyl-CoA synthase	fer[c] + coa[c] + atp[c] -> fercoa[c] + amp[c] + ppi[c]	(LOC_Os02g08100 or LOC_Os02g46970 or LOC_Os03g05780 or LOC_Os06g44620 or LOC_Os08g14760 or LOC_Os08g34790)	Phenylpropanoid metabolism	6.2.1.12
COUMGUTFc	2-coumarate O-beta-glucosyltransferase	udpg[c] + 2-coum[c] <=> coumghcinn[c] + udp[c] + h[c]		Phenylpropanoid metabolism	2.4.1.114
COUMGUIc	2-coumarate beta-D-glucoside isomerase	coumghcinn[c] <=> coumntg[c]		Phenylpropanoid metabolism	5.2.1.-
EBGLCSc	exo-beta-glucanse	coumntg[c] + h2o[c] <=> coumnt[c] + glc-B[c]	LOC_Os03g49600	Phenylpropanoid metabolism	3.2.1.21
COUMNSc	coumarin synthase	coumnt[c] + h[c] -> coumn[c] + h2o[c]		Phenylpropanoid metabolism	spontaneous
COUMHYc	4-coumaroyl 2-hydroxylase	coumcoa[c] + akg[c] + o2[c] -> co2[c] + succ[c] + dhcinncoa[c]		Phenylpropanoid metabolism	1.14.11.-
UMBLFSc	umbelliferone biosynthesis	dhcinncoa[c] -> coa[c] + umblf[c]		Phenylpropanoid metabolism	spontaneous
PRENTc	prenyltransferase	umblf[c] + dmpp[c] <=> dmsbs[c] + ppi[c]	(LOC_Os08g29970 or LOC_Os08g29910 or LOC_Os08g23320)	Phenylpropanoid metabolism	2.5.1.-
MARMSc	marmesin synthase	dmsbs[c] + nadph[c] + o2[c] -> marm[c] + nadp[c] + h2o[c]		Phenylpropanoid metabolism	
PSORSc	psoralen synthase	marm[c] + nadph[c] + o2[c] + h[c] -> psor[c] + act[c] + nadp[c] + 2 h2o[c]	(LOC_Os01g36350 or LOC_Os05g43910 or LOC_Os06g15680)	Phenylpropanoid metabolism	1.14.13.102
PSORMOc	psoralen 5-monooxygenase	psor[c] + nadph[c] + o2[c] + h[c] -> bgptl[c] + nadp[c] + h2o[c]		Phenylpropanoid metabolism	
BGPTLMTc	bergaptol O-methyltransferase	bgptl[c] + amet[c] -> bgptn[c] + ahcys[c] + h[c]		Phenylpropanoid metabolism	2.1.1.69
PINCAOc	Pinocembrin,2-oxoglutarate:oxygen oxidoreductase (3-hydroxylating)	pincem[c] + o2[c] + akg[c] -> pinban[c] + co2[c] + succ[c]	LOC_Os04g56700	Flavonoid biosynthesis	1.14.11.9
MALCINNMTc	malonyl-CoA:cinnamoyl-CoA	3 malcoa[c] + cinncoa[c] + 3 h[c] -> pinchal[c] + 4 coa[c] + 3	(LOC_Os11g32650 or LOC_Os07g11440)	Flavonoid biosynthesis	2.3.1.-

	malonyltransferase (cyclizing)	co2[c]			
PINCLc	Pinocembrin chalcone lyase (decyclizing)	pinchal[c] -> pincem[c] + h[c]	(LOC_Os03g60509 or LOC_Os02g21520)	Flavonoid biosynthesis	5.5.1.6
NRGNDOc	Naringenin 3-dioxygenase	nrgn[c] + o2[c] + akg[c] -> co2[c] + succ[c] + dhk[c]	LOC_Os04g56700	Flavonoid biosynthesis	1.14.11.9
DCHALSc	6-deoxychalcone synthase	coumcoa[c] + 3 malcoa[c] + nadph[c] + 4 h[c] -> isoqtgn[c] + 4 coa[c] + 3 co2[c] + nadp[c] + h2o[c]	LOC_Os07g11440	Flavonoid biosynthesis	2.3.1.170
NRGCSc	Naringenin-chalcone synthase	coumcoa[c] + 3 malcoa[c] + 3 h[c] -> nrgchal[c] + 3 co2[c] + 4 coa[c]	(LOC_Os11g32650 or LOC_Os07g11440)	Flavonoid biosynthesis	2.3.1.74
CHALIc	Chalcone isomerase	nrgchal[c] -> nrgn[c] + h[c]	(LOC_Os03g60509 or LOC_Os02g21520)	Flavonoid biosynthesis	5.5.1.6
NRGNAORc	naringenin 2-oxoglutarate oxygen oxidoreductase	nrgn[c] + akg[c] + o2[c] -> apgn[c] + succ[c] + co2[c] + h2o[c]	LOC_Os04g56700	Flavonoid biosynthesis	1.14.11.22
NRGNNORc	naingenin, NADPH:oxygen osidoreductase	nrgn[c] + h[c] + nadph[c] + o2[c] -> apgn[c] + 2 h2o[c] + nadp[c]	LOC_Os06g01250	Flavonoid biosynthesis	1.14.13.-
APG3Hc	apigenin 3-hydroxylase	apgn[c] + nadph[c] + h[c] + o2[c] -> ltln[c] + nadp[c] + h2o[c]	LOC_Os03g25150	Flavonoid biosynthesis	1.14.13.88
ERDTLHc	eriodictyol 2-hydroxylase	erdtl[c] + h[c] + o2[c] + nadph[c] -> 2herdtl[c] + h2o[c] + nadp[c]	LOC_Os06g01250	Flavonoid biosynthesis	1.14.13.-
2HEDBTSc	2-hydroxyeriodictyol dibenzoylmethane tautomer synthase	2herdtl[c] <=> erdtlt[c]		Flavonoid biosynthesis	
2HEDBT6GTc	2-hydroxyeriodictyol dibenzoylmethane tautomer 6C-glucosyltransferase	erdtlt[c] + udpg[c] -> 2herdtl6g[c] + udp[c] + h[c]	LOC_Os06g18010	Flavonoid biosynthesis	2.4.1.-
2HEDGDHc	2-hydroxyeriodictyol-C-glucoside dehydratase	2herdtl6g[c] <=> iorntn[c] + h[c] + h2o[c]		Flavonoid biosynthesis	4.2.1.-
2HEDBT8GTc	2-hydroxyeriodictyol dibenzoylmethane tautomer 8C-glucosyltransferase	erdtlt[c] + udpg[c] -> 2herdtl8g[c] + udp[c]	LOC_Os06g18010	Flavonoid biosynthesis	2.4.1.-
ORNTNSc	orientin synthase (spontaneous)	2herdtl8g[c] -> orntn[c] + h2o[c]		Flavonoid biosynthesis	spontaneous
NRGNHc	naringenin 2-hydroxylase	nrgn[c] + h[c] + o2[c] + nadph[c] -> 2hnrgn[c] + nadp[c] + h2o[c]	LOC_Os06g01250	Flavonoid biosynthesis	1.14.13.-
2HNDBTSc	2-hydroxynaringenin dibenzoylmethane tautomer synthase	2hnrgn[c] <=> nrgnt[c]		Flavonoid biosynthesis	
2HNDBT6GTc	2-hydroxynaringenin dibenzoylmethane tautomer 6C-glucosyltransferase	nrgnt[c] + udpg[c] -> 2hnrgn6g[c] + udp[c] + h[c]	LOC_Os06g18010	Flavonoid biosynthesis	2.4.1.-
2HNDGDHc	2-hydroxynaringenin-C-glucoside dehydratase	2hnrgn6g[c] <=> ivtxn[c] + h2o[c]		Flavonoid biosynthesis	4.2.1.-
2HNDBT8GTc	2-hydroxynaringenin dibenzoylmethane tautomer 8C-glucosyltransferase	nrgnt[c] + udpg[c] -> 2hnrgn8g[c] + udp[c] + 2 h[c]	LOC_Os06g18010	Flavonoid biosynthesis	2.4.1.-
VTXNSc	vitexin synthase (spontaneous)	2hnrgn8g[c] -> vtxn[c] + h2o[c]		Flavonoid biosynthesis	spontaneous
ISVTXNGTc	isovitexin beta-glucosyltransferase	udpg[c] + ivtxn[c] -> ivtxn2g[c] + udp[c] + h[c]		Flavonoid biosynthesis	2.4.1.106
IORNTNMTc	isoorientin 3-methyltransferase	iorntn[c] + amet[c] -> ahcys[c] + iscprn[c] + h[c]		Flavonoid biosynthesis	2.1.1.78
ISCPRNGTc	Isoscoparin beta-glucosyltransferase	udpg[c] + iscprn[c] -> iscprn2g[c] + udp[c] + h[c]		Flavonoid biosynthesis	2.4.1.-
LTLNHOc	luteolin 3-hydroxylase	ltln[c] + nadph[c] + h[c] + o2[c] -> trctn[c] + nadp[c] + h2o[c]	LOC_Os03g25150	Flavonoid biosynthesis	1.14.13.88
TRICINS1c	tricin synthase 1	amet[c] + trctn[c] -> ahcys[c] + mtrctn[c]	LOC_Os08g06100	Flavonoid biosynthesis	2.1.1.175
TRICINS2c	tricin synthase 2	mtrctn[c] + amet[c] -> ahcys[c] + tricin[c]	LOC_Os08g06100	Flavonoid biosynthesis	2.1.1.175
ISQTGNLc	Isoliquiritigenin lyase (decyclizing)	isoqtgn[c] -> lqtgn[c]	(LOC_Os03g60509 or LOC_Os02g21520)	Flavonoid biosynthesis	5.5.1.6
LQTGN6Hc	Liquiritigenin 6-hydroxylase	lqtgn[c] + nadph[c] + o2[c] + h[c] -> butin[c] + nadp[c] + h2o[c]	LOC_Os10g17260	Flavonoid biosynthesis	1.14.13.-
NRGNMOc	Naringenin 3-monooxygenase	nrgn[c] + nadph[c] + o2[c] + h[c] -> erdtl[c] + nadp[c] + h2o[c]	(LOC_Os10g17260 or LOC_Os10g16974 or LOC_Os08g35510)	Flavonoid biosynthesis	1.14.13.21
DHKFORc	Dihydrokaempferol,2-oxoglutarate:oxygen oxidoreductase	dhk[c] + akg[c] + o2[c] -> kmpfl[c] + succ[c] + co2[c] + h2o[c]	(LOC_Os08g15149 or LOC_Os02g52840)	Flavonoid biosynthesis	1.14.11.23
DHQORc	Dihydroquercetin,2-oxoglutarate:oxygen oxidoreductase	dhqrctn[c] + akg[c] + o2[c] -> qrctn[c] + succ[c] + co2[c] + h2o[c]	(LOC_Os08g15149 or LOC_Os02g52840)	Flavonoid biosynthesis	1.14.11.23
DHKMOc	Dihydrokaempferol 3-monooxygenase	dhk[c] + nadph[c] + o2[c] + h[c] -> dhqrctn[c] + nadp[c] + h2o[c]	(LOC_Os10g17260 or LOC_Os10g16974 or LOC_Os08g35510)	Flavonoid biosynthesis	1.14.13.21
KMPFLMOc	Kaempferol 3-monooxygenase	kmpfl[c] + nadph[c] + o2[c] + h[c] -> qrctn[c] + nadp[c] + h2o[c]	(LOC_Os10g17260 or LOC_Os10g16974 or LOC_Os08g35510)	Flavonoid biosynthesis	1.14.13.21
QRCTNGLT3c	Quercetin 3-O-glucosyltransferase	qrctn[c] + udpg[c] -> udp[c] + qrctn3g[c]	(LOC_Os05g45100 or LOC_Os01g64910 or LOC_Os07g32010 or LOC_Os01g53370 or LOC_Os07g32630 or LOC_Os05g45180)	Flavonoid biosynthesis	2.4.1.-
KMPFLGLT3c	Kaempferol 3-O-glucosyltransferase	kmpfl[c] + udpg[c] -> udp[c] + kmpfl3g[c]	(LOC_Os05g45100 or LOC_Os01g64910 or LOC_Os07g32010 or LOC_Os01g53370 or LOC_Os07g32630 or	Flavonoid biosynthesis	2.4.1.-

			LOC_Os05g45180)		
DHKRc	dihydrokaempferol 4-reductase	dhk[c] + nadph[c] + 2 h[c] -> lplg[c] + nadp[c]	LOC_Os01g44260	Flavonoid biosynthesis	1.1.1.219
LCYCORc	leucocyanidin:NADP+ 4-oxidoreductase	dhqrctn[c] + nadph[c] + 2 h[c] -> lcyc[c] + nadp[c]	LOC_Os01g44260	Flavonoid biosynthesis	1.1.1.219
ERYORc	Eriodictyol 2-oxoglutarate:oxygen oxidoreductase (3-hydroxylating)	erdtl[c] + o2[c] + akg[c] -> dhqrctn[c] + co2[c] + succ[c]	LOC_Os04g56700	Flavonoid biosynthesis	1.14.11.9
LPLGRc	leucopelargonidin reductase	lplg[c] + nadph[c] + h[c] -> afzl[c] + nadp[c] + h2o[c]	(LOC_Os01g01650 or LOC_Os01g01660 or LOC_Os06g27770)	Flavonoid biosynthesis	1.17.1.3
LCYCRc	leucoanthocyanidin reductase	lcyc[c] + nadph[c] + h[c] -> catcn[c] + nadp[c] + h2o[c]	(LOC_Os01g01650 or LOC_Os01g01660 or LOC_Os06g27770)	Flavonoid biosynthesis	1.17.1.3
LPLGDOc	leucopelargonidin dioxygenase	lplg[c] + akg[c] + o2[c] + h[c] -> plgn[c] + succ[c] + co2[c] + 2 h2o[c]	(LOC_Os06g42130 or LOC_Os01g27490)	Flavonoid biosynthesis	1.14.11.-
PNGLTc	Pelargonidin 3-O-glucosyltransferase	plgn[c] + udpg[c] -> udp[c] + plgng[c]	(LOC_Os06g09240 or LOC_Os07g05420 or LOC_Os08g15330)	Flavonoid biosynthesis	2.4.1.115
PLGNRc	Pelargonidin reductase	plgn[c] + 2 nadp[c] -> epflzn[c] + 2 nadph[c] + h[c]	LOC_Os04g53850	Flavonoid biosynthesis	1.3.1.77
CNDNRc	Cyanidin reductase	cndn[c] + 2 nadp[c] -> epctcn[c] + 2 nadph[c] + h[c]	LOC_Os04g53850	Flavonoid biosynthesis	1.3.1.77
CNDNGLTc	Cyanidin 3-O-glucosyltransferase	cndn[c] + udpg[c] -> udp[c] + cndng[c]	(LOC_Os06g09240 or LOC_Os07g05420 or LOC_Os08g15330)	Flavonoid biosynthesis	2.4.1.115
CNDNGLT5c	Cyanidin 5-O-glucosyltransferase	cndn[c] + udpg[c] -> udp[c] + cndn5g[c]	(LOC_Os05g45100 or LOC_Os01g64910 or LOC_Os07g32010 or LOC_Os01g53370 or LOC_Os07g32630 or LOC_Os05g45180)	Flavonoid biosynthesis	2.4.1.-
CNDNG3Gc	Cyanidin 5-O-glucoside: 3-O-glucosyltransferase	cndn5g[c] + udpg[c] -> udp[c] + cndn35dg[c]	(LOC_Os05g45100 or LOC_Os01g64910 or LOC_Os07g32010 or LOC_Os01g53370 or LOC_Os07g32630 or LOC_Os05g45180)	Flavonoid biosynthesis	2.4.1.-
CNDNG5Gc	Cyanidin 3-O-glucoside: 5-O-glucosyltransferase	cndng[c] + udpg[c] -> udp[c] + cndn35dg[c]	(LOC_Os05g45100 or LOC_Os01g64910 or LOC_Os07g32010 or LOC_Os01g53370 or LOC_Os07g32630 or LOC_Os05g45180)	Flavonoid biosynthesis	2.4.1.-
LCYCDOc	Leucoanthocyanidin dioxygenase	lcyc[c] + akg[c] + o2[c] + h[c] -> cndn[c] + succ[c] + co2[c] + 2 h2o[c]	(LOC_Os06g42130 or LOC_Os01g27490)	Flavonoid biosynthesis	1.14.11.-
GLUTRRs	glutamyl-tRNA reductase	glutrna[s] + h[s] + nadph[s] -> glu1sa[s] + nadp[s] + trnaglu[s]	LOC_Os10g35840	Phylloquinone, Plastoquinone and Ubiquinone Metabolism	1.2.1.70
HMBSs	Hydroxymethylbilane synthase	h2o[s] + 4 ppbng[s] -> hmbil[s] + 4 nh4[s]	(LOC_Os02g48670 or LOC_Os11g32030 or LOC_Os09g31190)	Phylloquinone, Plastoquinone and Ubiquinone Metabolism	2.5.1.61
PPBNGSs	Porphobilinogen synthase	2 5aop[s] -> h[s] + 2 h2o[s] + ppbng[s]	LOC_Os06g49110	Phylloquinone, Plastoquinone and Ubiquinone Metabolism	4.2.1.24
UPP3Ss	uroporphyrinogen-III synthase	hmbil[s] -> h2o[s] + uppg3[s]	LOC_Os03g08730	Phylloquinone, Plastoquinone and Ubiquinone Metabolism	4.2.1.75
G1SATs	Glutamate-1-semialdehyde 2,1-aminomutase	glu1sa[s] <=> 5aop[s]	(LOC_Os03g44150 or LOC_Os08g41990)	Phylloquinone, Plastoquinone and Ubiquinone Metabolism	5.4.3.8
GLUTRSs	Glutamate--tRNA ligase	atp[s] + glu-L[s] + trnaglu[s] -> amp[s] + glutrna[s] + ppi[s]	(LOC_Os10g22380 or LOC_Os01g16520 or LOC_Os05g08990 or LOC_Os02g02860 or LOC_Os01g09000)	Phylloquinone, Plastoquinone and Ubiquinone Metabolism	6.1.1.17
UPP3MTs	uroporphyrinogen-III methyltransferase	2 amet[s] + uppg3[s] -> 2 ahcys[s] + dscl[s] + h[s]	LOC_Os01g44050	Phylloquinone, Plastoquinone and Ubiquinone Metabolism	2.1.1.107
PC2Ds	precorrin 2 dehydrogenase	dscl[s] + nadp[s] + h[s] <=> scl[s] + nadph[s]		Porphyrin and Chlorophyll Metabolism	1.3.1.76
SHCHFs	sirohydrochlorin ferrochelatase	fe2[s] + scl[s] -> sheme[s]	LOC_Os02g19440	Porphyrin and Chlorophyll Metabolism	4.99.1.4
MPMECY1s	magnesium-protoporphyrin IX monomethyl ester (oxidative) cyclase	mppp9me[s] + nadph[s] + h[s] + o2[s] -> hmppp9me[s] + nadp[s] + h2o[s]	LOC_Os01g17170	Porphyrin and Chlorophyll Metabolism	1.14.13.81
MPMECY2s	magnesium-protoporphyrin IX monomethyl ester (oxidative) cyclase	hmppp9me[s] + nadph[s] + 2 h[s] + o2[s] -> omppp9me[s] + nadp[s] + 2 h2o[s]	LOC_Os01g17170	Porphyrin and Chlorophyll Metabolism	1.14.13.81
MPMECY3s	magnesium-protoporphyrin IX monomethyl ester (oxidative) cyclase	omppp9me[s] + nadph[s] + o2[s] -> dvpchlda[s] + nadp[s] + 2 h2o[s]	LOC_Os01g17170	Porphyrin and Chlorophyll Metabolism	1.14.13.81

CHLOR410s	chlorophyllide-a:NADP+ oxidoreductase (photon410)	0.26485 pchlda[s] + 0.26485 nadph[s] + 0.26485 h[s] + 0.26485 photon410[u] -> 0.26485 chlda[s] + 0.26485 nadp[s]	(LOC_Os10g35370 or LOC_Os04g58200 or LOC_Os03g05310)	Porphyrin and Chlorophyll Metabolism	1.3.1.33
CHLOR430s	chlorophyllide-a:NADP+ oxidoreductase (photon430)	0.56582 pchlda[s] + 0.56582 nadph[s] + 0.56582 h[s] + 0.56582 photon430[u] -> 0.56582 chlda[s] + 0.56582 nadp[s]	(LOC_Os10g35370 or LOC_Os04g58200 or LOC_Os03g05310)	Porphyrin and Chlorophyll Metabolism	1.3.1.33
CHLOR450s	chlorophyllide-a:NADP+ oxidoreductase (photon450)	0.8139 pchlda[s] + 0.8139 nadph[s] + 0.8139 h[s] + 0.8139 photon450[u] -> 0.8139 chlda[s] + 0.8139 nadp[s]	(LOC_Os10g35370 or LOC_Os04g58200 or LOC_Os03g05310)	Porphyrin and Chlorophyll Metabolism	1.3.1.33
CHLOR470s	chlorophyllide-a:NADP+ oxidoreductase (photon470)	0.4478 pchlda[s] + 0.4478 nadph[s] + 0.4478 h[s] + 0.4478 photon470[u] -> 0.4478 chlda[s] + 0.4478 nadp[s]	(LOC_Os10g35370 or LOC_Os04g58200 or LOC_Os03g05310)	Porphyrin and Chlorophyll Metabolism	1.3.1.33
CHLOR490s	chlorophyllide-a:NADP+ oxidoreductase (photon490)	0.1840 pchlda[s] + 0.1840 nadph[s] + 0.1840 h[s] + 0.1840 photon490[u] -> 0.1840 chlda[s] + 0.1840 nadp[s]	(LOC_Os10g35370 or LOC_Os04g58200 or LOC_Os03g05310)	Porphyrin and Chlorophyll Metabolism	1.3.1.33
CHLOR510s	chlorophyllide-a:NADP+ oxidoreductase (photon510)	0.1382 pchlda[s] + 0.1382 nadph[s] + 0.1382 h[s] + 0.1382 photon510[u] -> 0.1382 chlda[s] + 0.1382 nadp[s]	(LOC_Os10g35370 or LOC_Os04g58200 or LOC_Os03g05310)	Porphyrin and Chlorophyll Metabolism	1.3.1.33
CHLOR530s	chlorophyllide-a:NADP+ oxidoreductase (photon530)	0.2080 pchlda[s] + 0.2080 nadph[s] + 0.2080 h[s] + 0.2080 photon530[u] -> 0.2080 chlda[s] + 0.2080 nadp[s]	(LOC_Os10g35370 or LOC_Os04g58200 or LOC_Os03g05310)	Porphyrin and Chlorophyll Metabolism	1.3.1.33
CHLOR550s	chlorophyllide-a:NADP+ oxidoreductase (photon550)	0.24811 pchlda[s] + 0.24811 nadph[s] + 0.24811 h[s] + 0.24811 photon550[u] -> 0.24811 chlda[s] + 0.24811 nadp[s]	(LOC_Os10g35370 or LOC_Os04g58200 or LOC_Os03g05310)	Porphyrin and Chlorophyll Metabolism	1.3.1.33
CHLOR570s	chlorophyllide-a:NADP+ oxidoreductase (photon570)	0.3014 pchlda[s] + 0.3014 nadph[s] + 0.3014 h[s] + 0.3014 photon570[u] -> 0.3014 chlda[s] + 0.3014 nadp[s]	(LOC_Os10g35370 or LOC_Os04g58200 or LOC_Os03g05310)	Porphyrin and Chlorophyll Metabolism	1.3.1.33
CHLOR590s	chlorophyllide-a:NADP+ oxidoreductase (photon590)	0.3447 pchlda[s] + 0.3447 nadph[s] + 0.3447 h[s] + 0.3447 photon590[u] -> 0.3447 chlda[s] + 0.3447 nadp[s]	(LOC_Os10g35370 or LOC_Os04g58200 or LOC_Os03g05310)	Porphyrin and Chlorophyll Metabolism	1.3.1.33
CHLOR610s	chlorophyllide-a:NADP+ oxidoreductase (photon610)	0.5565 pchlda[s] + 0.5565 nadph[s] + 0.5565 h[s] + 0.5565 photon610[u] -> 0.5565 chlda[s] + 0.5565 nadp[s]	(LOC_Os10g35370 or LOC_Os04g58200 or LOC_Os03g05310)	Porphyrin and Chlorophyll Metabolism	1.3.1.33
CHLOR630s	chlorophyllide-a:NADP+ oxidoreductase (photon630)	0.8377 pchlda[s] + 0.8377 nadph[s] + 0.8377 h[s] + 0.8377 photon630[u] -> 0.8377 chlda[s] + 0.8377 nadp[s]	(LOC_Os10g35370 or LOC_Os04g58200 or LOC_Os03g05310)	Porphyrin and Chlorophyll Metabolism	1.3.1.33
CHLOR650s	chlorophyllide-a:NADP+ oxidoreductase (photon650)	pchlda[s] + nadph[s] + h[s] + photon650[u] -> chlda[s] + nadp[s]	(LOC_Os10g35370 or LOC_Os04g58200 or LOC_Os03g05310)	Porphyrin and Chlorophyll Metabolism	1.3.1.33
CHLOR670s	chlorophyllide-a:NADP+ oxidoreductase (photon670)	0.4324 pchlda[s] + 0.4324 nadph[s] + 0.4324 h[s] + 0.4324 photon670[u] -> 0.4324 chlda[s] + 0.4324 nadp[s]	(LOC_Os10g35370 or LOC_Os04g58200 or LOC_Os03g05310)	Porphyrin and Chlorophyll Metabolism	1.3.1.33
CHLOR690s	chlorophyllide-a:NADP+ oxidoreductase (photon690)	0.1455 pchlda[s] + 0.1455 nadph[s] + 0.1455 h[s] + 0.1455 photon690[u] -> 0.1455 chlda[s] + 0.1455 nadp[s]	(LOC_Os10g35370 or LOC_Os04g58200 or LOC_Os03g05310)	Porphyrin and Chlorophyll Metabolism	1.3.1.33
DVCHLOR410s	divinyl chlorophyllide-a:NADP+ oxidoreductase (photon410)	0.26485 dvpchlda[s] + 0.26485 nadph[s] + 0.26485 h[s] + 0.26485 photon410[u] -> 0.26485 chlda[s] + 0.26485 nadp[s]	(LOC_Os10g35370 or LOC_Os04g58200 or LOC_Os03g05310)	Porphyrin and Chlorophyll Metabolism	1.3.1.33
DVCHLOR430s	divinyl chlorophyllide-a:NADP+ oxidoreductase (photon430)	0.56582 dvpchlda[s] + 0.56582 nadph[s] + 0.56582 h[s] + 0.56582 photon430[u] -> 0.56582 chlda[s] + 0.56582 nadp[s]	(LOC_Os10g35370 or LOC_Os04g58200 or LOC_Os03g05310)	Porphyrin and Chlorophyll Metabolism	1.3.1.33
DVCHLOR450s	divinyl chlorophyllide-a:NADP+ oxidoreductase (photon450)	0.8139 dvpchlda[s] + 0.8139 nadph[s] + 0.8139 h[s] + 0.8139 photon450[u] -> 0.8139 chlda[s] + 0.8139 nadp[s]	(LOC_Os10g35370 or LOC_Os04g58200 or LOC_Os03g05310)	Porphyrin and Chlorophyll Metabolism	1.3.1.33
DVCHLOR470s	divinyl chlorophyllide-a:NADP+ oxidoreductase (photon470)	0.4478 dvpchlda[s] + 0.4478 nadph[s] + 0.4478 h[s] + 0.4478 photon470[u] -> 0.4478 chlda[s] + 0.4478 nadp[s]	(LOC_Os10g35370 or LOC_Os04g58200 or LOC_Os03g05310)	Porphyrin and Chlorophyll Metabolism	1.3.1.33
DVCHLOR490s	divinyl chlorophyllide-a:NADP+ oxidoreductase (photon490)	0.1840 dvpchlda[s] + 0.1840 nadph[s] + 0.1840 h[s] + 0.1840 photon490[u] -> 0.1840 chlda[s] + 0.1840 nadp[s]	(LOC_Os10g35370 or LOC_Os04g58200 or LOC_Os03g05310)	Porphyrin and Chlorophyll Metabolism	1.3.1.33
DVCHLOR510s	divinyl chlorophyllide-a:NADP+ oxidoreductase (photon510)	0.1382 dvpchlda[s] + 0.1382 nadph[s] + 0.1382 h[s] + 0.1382 photon510[u] -> 0.1382 chlda[s] + 0.1382 nadp[s]	(LOC_Os10g35370 or LOC_Os04g58200 or LOC_Os03g05310)	Porphyrin and Chlorophyll Metabolism	1.3.1.33
DVCHLOR530s	divinyl chlorophyllide-a:NADP+ oxidoreductase (photon530)	0.2080 dvpchlda[s] + 0.2080 nadph[s] + 0.2080 h[s] + 0.2080 photon530[u] -> 0.2080 chlda[s] + 0.2080 nadp[s]	(LOC_Os10g35370 or LOC_Os04g58200 or LOC_Os03g05310)	Porphyrin and Chlorophyll Metabolism	1.3.1.33
DVCHLOR550s	divinyl chlorophyllide-a:NADP+ oxidoreductase (photon550)	0.24811 dvpchlda[s] + 0.24811 nadph[s] + 0.24811 h[s] + 0.24811 photon550[u] -> 0.24811 chlda[s] + 0.24811 nadp[s]	(LOC_Os10g35370 or LOC_Os04g58200 or LOC_Os03g05310)	Porphyrin and Chlorophyll Metabolism	1.3.1.33
DVCHLOR570s	divinyl chlorophyllide-a:NADP+ oxidoreductase (photon570)	0.3014 dvpchlda[s] + 0.3014 nadph[s] + 0.3014 h[s] + 0.3014 photon570[u] -> 0.3014 chlda[s] + 0.3014 nadp[s]	(LOC_Os10g35370 or LOC_Os04g58200 or LOC_Os03g05310)	Porphyrin and Chlorophyll Metabolism	1.3.1.33
DVCHLOR590s	divinyl chlorophyllide-a:NADP+ oxidoreductase (photon590)	0.3447 dvpchlda[s] + 0.3447 nadph[s] + 0.3447 h[s] + 0.3447 photon590[u] -> 0.3447 chlda[s] + 0.3447 nadp[s]	(LOC_Os10g35370 or LOC_Os04g58200 or LOC_Os03g05310)	Porphyrin and Chlorophyll Metabolism	1.3.1.33
DVCHLOR610s	divinyl chlorophyllide-a:NADP+ oxidoreductase (photon610)	0.5565 dvpchlda[s] + 0.5565 nadph[s] + 0.5565 h[s] + 0.5565 photon610[u] -> 0.5565 chlda[s] + 0.5565 nadp[s]	(LOC_Os10g35370 or LOC_Os04g58200 or LOC_Os03g05310)	Porphyrin and Chlorophyll Metabolism	1.3.1.33
DVCHLOR630s	divinyl chlorophyllide-a:NADP+ oxidoreductase (photon630)	0.8377 dvpchlda[s] + 0.8377 nadph[s] + 0.8377 h[s] + 0.8377 photon630[u] -> 0.8377 chlda[s] + 0.8377 nadp[s]	(LOC_Os10g35370 or LOC_Os04g58200 or LOC_Os03g05310)	Porphyrin and Chlorophyll Metabolism	1.3.1.33
DVCHLOR650s	divinyl chlorophyllide-a:NADP+ oxidoreductase (photon650)	dvpchlda[s] + nadph[s] + h[s] + photon650[u] -> chlda[s] + nadp[s]	(LOC_Os10g35370 or LOC_Os04g58200 or LOC_Os03g05310)	Porphyrin and Chlorophyll Metabolism	1.3.1.33

DVCHLOR670s	divinyl chlorophyllide-a:NADP+ oxidoreductase (photon670)	0.4324 dvpchlda[s] + 0.4324 nadph[s] + 0.4324 h[s] + 0.4324 photon670[u] -> 0.4324 chlda[s] + 0.4324 nadp[s]	(LOC_Os10g35370 or LOC_Os04g58200 or LOC_Os03g05310)	Porphyrin and Chlorophyll Metabolism	1.3.1.33
DVCHLOR690s	divinyl chlorophyllide-a:NADP+ oxidoreductase (photon690)	0.1455 dvpchlda[s] + 0.1455 nadph[s] + 0.1455 h[s] + 0.1455 photon690[u] -> 0.1455 chlda[s] + 0.1455 nadp[s]	(LOC_Os10g35370 or LOC_Os04g58200 or LOC_Os03g05310)	Porphyrin and Chlorophyll Metabolism	1.3.1.33
CPPPGOs	Coproporphyrinogen oxidase	cpppg3[s] + 2 h[s] + o2[s] -> 2 co2[s] + 2 h2o[s] + pppg9[s]	(LOC_Os12g17070 or LOC_Os04g52130)	Porphyrin and Chlorophyll Metabolism	1.3.3.3
PPPGOs	Protoporphyrinogen oxidase	3 o2[s] + pppg9[s] -> 3 h2o2[s] + ppp9[s]	(LOC_Os02g54254 or LOC_Os07g23190 or LOC_Os05g01760 or LOC_Os02g19510 or LOC_Os06g51520 or LOC_Os01g69050 or LOC_Os07g37760 or LOC_Os01g73970)	Porphyrin and Chlorophyll Metabolism	1.3.3.4
MPMTs	Magnesium-protoporphyrin O-methyltransferase	amet[s] + mppp9[s] <=> ahcys[s] + mppp9me[s] + h[s]	LOC_Os06g04150	Porphyrin and Chlorophyll Metabolism	2.1.1.11
UPP1Rs	uroporphyrinogen I reductase	uppg1[s] + nadph[s] <=> upp1[s] + nadp[s] + 7 h[s]		Porphyrin and Chlorophyll Metabolism	
UPP1Ss	uroporphyrinogen I synthase, spontaneous	hmbil[s] -> uppg1[s] + h2o[s]		Porphyrin and Chlorophyll Metabolism	spontaneous
UPPDC1s	Uroporphyrinogen decarboxylase	4 h[s] + uppg3[s] -> 4 co2[s] + cpppg3[s]	(LOC_Os03g22060 or LOC_Os01g43390 or LOC_Os03g21900)	Porphyrin and Chlorophyll Metabolism	4.1.1.37
UPPDC2s	uroporphyrinogen decarboxylase (uroporphyrinogen I)	uppg1[s] + 4 h[s] -> cpppg1[s] + 4 co2[s]	(LOC_Os03g22060 or LOC_Os01g43390 or LOC_Os03g21900)	Porphyrin and Chlorophyll Metabolism	4.1.1.37
CPP1Os	coproporphyrinogen I oxidase	cpppg1[s] + nadp[s] <=> cpp1[s] + nadph[s] + 5 h[s]		Porphyrin and Chlorophyll Metabolism	
UPP3Os	uroporphyrinogen III oxidase	uppg3[s] + nadp[s] <=> upp3[s] + 5 h[s] + nadph[s]		Porphyrin and Chlorophyll Metabolism	
FCLTs	Ferrochelatase	fe2[s] + ppp9[s] -> 2 h[s] + pheme[s]	(LOC_Os05g29760 or LOC_Os09g12560)	Porphyrin and Chlorophyll Metabolism	4.99.1.1
MGCHLs	Magnesium chelatase	atp[s] + ppp9[s] + mg2[s] + h2o[s] -> adp[s] + pi[s] + mppp9[s] + h[s]	(LOC_Os03g59640 and LOC_Os03g36540 and LOC_Os03g20700)	Porphyrin and Chlorophyll Metabolism	6.6.1.1
DVCHLDRs	divinyl chlorophyllide a 8-vinyl-reductase	dvchlda[s] + nadph[s] + h[s] <=> chlda[s] + nadp[s]	LOC_Os03g22780	Porphyrin and Chlorophyll Metabolism	1.3.1.75
DVPCHLDRs	divinylprotochlorophyllide vinyl-reductase	dvpchlda[s] + nadph[s] + h[s] <=> pchlda[s] + nadp[s]	LOC_Os03g22780	Porphyrin and Chlorophyll Metabolism	1.3.1.75
FCRs	Ferric-chelate reductase	2 fe2[s] + nad[s] + h[s] <=> 2 fe3[s] + nadh[s]	LOC_Os04g48930	Porphyrin and Chlorophyll Metabolism	1.16.1.7
HEMEOSm	heme o biosynthesis	frdp[m] + h2o[m] + pheme[m] -> hemeO[m] + ppi[m]	(LOC_Os08g29970 or LOC_Os08g29910 or LOC_Os08g23320)	Porphyrin and Chlorophyll Metabolism	2.5.1.-
HEMELs	heme c ligase (chloroplast)	apocytc[s] + pheme[s] <=> cytc[s]		Porphyrin and Chlorophyll Metabolism	4.4.1.17
HEMELm	heme c ligase (mitochondria)	apocytc[m] + pheme[m] <=> cytc[m]		Porphyrin and Chlorophyll Metabolism	4.4.1.17
HEMEASm	heme a synthase (mitochondria)	h2o[m] + hemeO[m] -> 5 h[m] + hemeA[m]	LOC_Os08g38720	Porphyrin and Chlorophyll Metabolism	1.-.-.-
HOXGs	Heme oxygenase (decyclizing)	3 h[s] + 3 nadph[s] + 3 o2[s] + pheme[s] <=> biliverd[s] + co[s] + fe2[s] + 3 h2o[s] + 3 nadp[s]	LOC_Os06g40080	Porphyrin and Chlorophyll Metabolism	1.14.99.3
CHLBSEs	Chlorophyllase	chlb[s] + h2o[s] -> chldb[s] + phytol[s]	(LOC_Os10g28370 or LOC_Os02g18500)	Porphyrin and Chlorophyll Metabolism	3.1.1.14
CHLBSNs	chlorophyll synthase	chldb[s] + pdp[s] -> chlb[s] + ppi[s] + h[s]	LOC_Os05g28200	Porphyrin and Chlorophyll Metabolism	2.5.1.62
CHLDAOs	chlorophyllide-a oxygenase (CHLDA)	chlda[s] + 2 nadph[s] + 2 o2[s] + 2 h[s] <=> chldb[s] + 2 nadp[s] + 3 h2o[s]	LOC_Os10g41760	Porphyrin and Chlorophyll Metabolism	1.14.13.122
CHLAOs	chlorophyllide-a oxygenase (CHLA)	chla[s] + 2 nadph[s] + 2 o2[s] + 2 h[s] <=> chlb[s] + 2 nadp[s] + 3 h2o[s]	LOC_Os10g41760	Porphyrin and Chlorophyll Metabolism	1.14.13.122
CHLASEs	Chlorophyllase	chla[s] + h2o[s] <=> chlda[s] + phytol[s]	(LOC_Os10g28370 or LOC_Os02g18500)	Porphyrin and Chlorophyll Metabolism	3.1.1.14
CHLASNs	chlorophyll synthase	chlda[s] + pdp[s] -> chla[s] + ppi[s] + h[s]	LOC_Os05g28200	Porphyrin and Chlorophyll	2.5.1.62

				Metabolism	
FERO	ferroxidase	o2[s] + 4 fe2[s] + 4 h[s] -> 4 fe3[s] + 2 h2o[s]	(LOC_Os01g57460 or LOC_Os12g01530 or LOC_Os01g57460)	Porphyrin and Chlorophyll Metabolism	1.16.3.1
FRDPFTm	(2E,6E)-farnesyl-diphosphate:isopentenyl-diphosphate farnesyltranstransferase	frdp[m] + 5 ipdp[m] -> octdp[m] + 5 ppi[m]	LOC_Os12g17320	Phylloquinone, Plastoquinone and Ubiquinone Metabolism	2.5.1.90
CHORLm	chorismate lyase	chor[m] -> pyr[m] + 4hbz[m]		Phylloquinone, Plastoquinone and Ubiquinone Metabolism	4.1.3.40
HBZOPT8m	4-hydroxybenzoate octaprenyltransferase	4hbz[m] + octdp[m] -> 3ophb[m] + ppi[m]	LOC_Os08g23320	Phylloquinone, Plastoquinone and Ubiquinone Metabolism	2.5.1.39
3OPHBH2m	Hydroxylation of 3-Decaprenyl-4-hydroxybenzoate (NADPH)	3ophb[m] + h[m] + nadph[m] + o2[m] -> 3opdhb[m] + h2o[m] + nadp[m]		Phylloquinone, Plastoquinone and Ubiquinone Metabolism	
3OPHBH1m	Hydroxylation of 3-Decaprenyl-4-hydroxybenzoate (NADPH)	3ophb[m] + h[m] + nadh[m] + o2[m] -> 3opdhb[m] + h2o[m] + nad[m]		Phylloquinone, Plastoquinone and Ubiquinone Metabolism	
DHOPBMTm	dihydroxydecaprenylbenzoate methyltransferase	3opdhb[m] + amet[m] -> 3opdhmb[m] + ahcys[m] + h[m]	LOC_Os06g05900	Phylloquinone, Plastoquinone and Ubiquinone Metabolism	2.1.1.114
OPHMBDCm	3-Decaprenyl-4-hydroxy-5-methoxybenzoate decarboxylation	3opdhmb[m] + h[m] -> 2omph[m] + co2[m]		Phylloquinone, Plastoquinone and Ubiquinone Metabolism	
COQ6m	Ubiquinone biosynthesis monooxgenase COQ6	2omph[m] + h[m] + nadph[m] + o2[m] -> 2ombzl[m] + h2o[m] + nadp[m]	(LOC_Os03g62250 or LOC_Os03g62260)	Phylloquinone, Plastoquinone and Ubiquinone Metabolism	1.14.13.-
COQ5m	Ubiquinone biosynthesis methyltransferase COQ5	2ombzl[m] + amet[m] -> 2ommbl[m] + ahcys[m] + h[m]	LOC_Os01g74520	Phylloquinone, Plastoquinone and Ubiquinone Metabolism	2.1.1.201
COQ7m	Ubiquinone biosynthesis COQ7	2ommbl[m] + h[m] + nadph[m] + o2[m] -> 2omhmbl[m] + h2o[m] + nadp[m]		Phylloquinone, Plastoquinone and Ubiquinone Metabolism	1.14.13.-
COQ3m	methyltransferase COQ3	2omhmbl[m] + amet[m] -> ahcys[m] + h[m] + q8h2[m]		Phylloquinone, Plastoquinone and Ubiquinone Metabolism	2.1.1.114
DHNCOASs	1,4-dihydroxy-2-naphthoyl-CoA synthase	2sbzcoa[s] -> h2o[s] + dhncoa[s]	LOC_Os01g47350	Phylloquinone, Plastoquinone and Ubiquinone Metabolism	4.1.3.36
DHNCOAHs	1,4-dihydroxy-2-naphthoyl-CoA hydrolase	dhncoa[s] + h2o[s] -> dhn[s] + coa[s]	(LOC_Os03g48480 or LOC_Os05g04660)	Phylloquinone, Plastoquinone and Ubiquinone Metabolism	3.1.2.28
ICHORMs	Isochorismate mutase	chor[s] <=> ichor[s]	LOC_Os09g19734	Phylloquinone, Plastoquinone and Ubiquinone Metabolism	5.4.4.2
2SBZCOALs	o-succinylbenzoate—CoA ligase	atp[s] + 2sbz[s] + coa[s] -> 2sbzcoa[s] + amp[s] + ppi[s]	LOC_Os08g03630	Phylloquinone, Plastoquinone and Ubiquinone Metabolism	6.2.1.26
SBZSs	o-succinylbenzoate synthase	sephchc[s] -> 2sbz[s] + h2o[s]	LOC_Os04g57810	Phylloquinone, Plastoquinone and Ubiquinone Metabolism	4.2.1.113
DHNPPTs	1,4-dihydroxy-2-naphthoate polyprenyltransferase	dhn[s] + pdp[s] -> pnq[s] + co2[s] + ppi[s]	LOC_Os03g09060	Phylloquinone, Plastoquinone and Ubiquinone Metabolism	2.5.1.-
DMPPTs	demethylphylloquinone phytyltransferase	pnq[s] + amet[s] -> pqnne[s] + ahcys[s]	LOC_Os04g42870	Phylloquinone, Plastoquinone and Ubiquinone Metabolism	2.1.1.163
DHNOPTs	1,4-dihydroxy-2-naphthoate octaprenyltransferase	dhn[s] + octdp[s] -> dmq[s] + ppi[s] + co2[s]	LOC_Os03g09060	Phylloquinone, Plastoquinone and Ubiquinone Metabolism	2.5.1.74
DMPQMTs	demethylphylloquinone methyltransferase	dmq[s] + amet[s] -> mnqnne[s] + ahcys[s]	LOC_Os04g42870	Phylloquinone, Plastoquinone and Ubiquinone Metabolism	2.1.1.163
SEPHCHCSs	2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene-1-carboxylic-acid synthase	akg[s] + ichor[s] + h[s] -> sephhc[s] + co2[s]		Phylloquinone, Plastoquinone and Ubiquinone Metabolism	2.2.1.9
SEPHHCSs	2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate synthase	sephhc[s] -> sephchc[s] + pyr[s]		Phylloquinone, Plastoquinone and Ubiquinone Metabolism	4.2.99.20
MPQMTs	2-methyl-6-phytylquinol methyltransferase	mpq[s] + amet[s] -> dmpq[s] + ahcys[s] + h[s]	LOC_Os12g42090	Other Vitamins Metabolism (Vitamin E)	2.1.1.-
TMTDs	delta-tocopherol methyltransferase	dvite[s] + amet[s] -> bvite[s] + ahcys[s] + h[s]	LOC_Os02g47310	Other Vitamins Metabolism (Vitamin E)	2.1.1.95
TMTBs	Tocopherol O-methyltransferase	bvite[s] + amet[s] -> avite1[s] + ahcys[s] + h[s]	LOC_Os02g47310	Other Vitamins Metabolism (Vitamin E)	2.1.1.95
HPTs	phytyl-diphosphate:homogentisate phytyltransferase (decarboxylating)	pdp[s] + hgentis[s] -> mpq[s] + ppi[s] + co2[s]	LOC_Os06g44840	Other Vitamins Metabolism (Vitamin E)	2.5.1.-
FRDPFTs	(2E,6E)-farnesyl-diphosphate:isopentenyl-	frdp[s] + 5 ipdp[s] -> octdp[s] + 5 ppi[s]		Phylloquinone, Plastoquinone	2.5.1.90

	diphosphate farnesyltranstransferase			and Ubiquinone Metabolism	
OCTDPOTs	(E)-octaprenyl-diphosphate:isopentenyl-diphosphate octaprenyltranstransferase	octdp[s] + ipdp[s] -> npdp[s] + ppi[s]	LOC_Os12g17320	Phylloquinone, Plastoquinone and Ubiquinone Metabolism	2.5.1.85
HGENTISSTs	homogentisate solanesyltransferase	hgentis[s] + npdp[s] -> msbq[s] + ppi[s] + co2[s]	LOC_Os02g39290	Phylloquinone, Plastoquinone and Ubiquinone Metabolism	
MSBQMTs	MPBQ/MSBQ methyltransferase	msbq[s] + amet[s] -> plast[s] + ahcys[s]	LOC_Os12g42090	Phylloquinone, Plastoquinone and Ubiquinone Metabolism	2.1.1.-
TYCGs	tocopherol cyclase	dmpq[s] -> yvite[s]	LOC_Os02g17650	Other Vitamins Metabolism (Vitamin E)	
TYCDs	tocopherol cyclase	mpq[s] -> dvite[s]	LOC_Os02g17650	Other Vitamins Metabolism (Vitamin E)	
HMGCOARc	Hydroxymethylglutaryl-CoA reductase (NADPH)	coa[c] + mev-R[c] + 2 nadp[c] <=> 2 h[c] + hmgcoa[c] + 2 nadph[c]	(LOC_Os08g40180 or LOC_Os09g31970 or LOC_Os02g48330)	Terpenoid biosynthesis (MVA Pathway)	1.1.1.34
HMGCOARyc	Hydroxymethylglutaryl-CoA reductase (NADH)	coa[c] + mev-R[c] + 2 nad[c] <=> 2 h[c] + hmgcoa[c] + 2 nadh[c]	(LOC_Os08g40180 or LOC_Os09g31970 or LOC_Os02g48330)	Terpenoid biosynthesis (MVA Pathway)	1.1.1.88
MEVKc	Mevalonate kinase	atp[c] + mev-R[c] -> 5pmev[c] + adp[c] + h[c]	LOC_Os10g18220	Terpenoid biosynthesis (MVA Pathway)	2.7.1.36
PMEVKc	Phosphomevalonate kinase	5pmev[c] + atp[c] -> 5dpmev[c] + adp[c]	LOC_Os03g14830	Terpenoid biosynthesis (MVA Pathway)	2.7.4.2
DPMVDc	Diphosphomevalonate decarboxylase	5dpmev[c] + atp[c] -> adp[c] + co2[c] + ipdp[c] + pi[c]	(LOC_Os02g01760 or LOC_Os02g01920)	Terpenoid biosynthesis (MVA Pathway)	4.1.1.33
IPDDIc	Isopentenyl-diphosphate delta-isomerase, cytosolic	ipdp[c] <=> dmpp[c]	(LOC_Os05g34180 or LOC_Os07g36190)	Terpenoid biosynthesis (MEP Pathway, MVA Pathway)	5.3.3.2
IPDDIm	Isopentenyl-diphosphate delta-isomerase, mitochondrial	ipdp[m] <=> dmpp[m]	(LOC_Os05g34180 or LOC_Os07g36190)	Terpenoid biosynthesis (MEP Pathway, MVA Pathway)	5.3.3.2
IPDDIs	Isopentenyl-diphosphate delta-isomerase, plastidic	ipdp[s] <=> dmpp[s]	(LOC_Os05g34180 or LOC_Os07g36190)	Terpenoid biosynthesis (MEP Pathway, MVA Pathway)	5.3.3.2
DXPRIis	1-deoxy-D-xylulose-5-phosphate reductoisomerase	dxyl5p[s] + h[s] + nadph[s] -> 2me4p[s] + nadp[s]	LOC_Os01g01710	Terpenoid biosynthesis (MEP Pathway)	1.1.1.267
IPDPS2s	1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate reductase (ipdp, nadph)	h[s] + h2mb4p[s] + nadh[s] -> h2o[s] + ipdp[s] + nad[s]	LOC_Os03g52170	Terpenoid biosynthesis (MEP Pathway)	1.17.1.2
IPDPS1s	1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate reductase (ipdp, nadh)	h[s] + h2mb4p[s] + nadph[s] -> h2o[s] + ipdp[s] + nadp[s]	LOC_Os03g52170	Terpenoid biosynthesis (MEP Pathway)	1.17.1.2
DMPPS2s	1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate reductase (dmpp, nadph)	h[s] + h2mb4p[s] + nadh[s] -> dmpp[s] + h2o[s] + nad[s]	LOC_Os03g52170	Terpenoid biosynthesis (MEP Pathway)	1.17.1.2
DMPPS1s	1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate reductase (dmpp, nadh)	h[s] + h2mb4p[s] + nadph[s] -> dmpp[s] + h2o[s] + nadp[s]	LOC_Os03g52170	Terpenoid biosynthesis (MEP Pathway)	1.17.1.2
MECDPDH5s	(E)-4-hydroxy-3-methylbut-2-enyl-diphosphate synthase	2mecdp[s] + 2 fdxrd[s] + h[s] -> 2 fdxox[s] + h2mb4p[s] + h2o[s]	LOC_Os02g39160	Terpenoid biosynthesis (MEP Pathway)	1.17.7.1
CDPMEKs	4-(cytidine 5-diphospho)-2-C-methyl-D-erythritol kinase	4c2me[s] + atp[s] -> 2p4c2me[s] + adp[s] + h[s]	LOC_Os01g58790	Terpenoid biosynthesis (MEP Pathway)	2.7.1.148
MEPCTs	2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase	2me4p[s] + ctp[s] + h[s] -> 4c2me[s] + ppi[s]	LOC_Os01g66360	Terpenoid biosynthesis (MEP Pathway)	2.7.7.60
MECDPSs	2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase	2p4c2me[s] -> 2mecdp[s] + cmp[s]	(LOC_Os02g45660 or LOC_Os07g40260)	Terpenoid biosynthesis (MEP Pathway)	4.6.1.12
DMATTs	Dimethylallyltransferase, plastidic	dmpp[s] + ipdp[s] -> grdp[s] + ppi[s]	(LOC_Os02g44780 or LOC_Os07g39270 or LOC_Os01g14630)	Terpenoid biosynthesis (Monoterpenoid biosynthesis)	2.5.1.1
DMATTm	Dimethylallyltransferase, mitochondrial	dmpp[m] + ipdp[m] -> grdp[m] + ppi[m]	(LOC_Os01g50760 or LOC_Os05g46580 or LOC_Os06g46450)	Terpenoid biosynthesis (Monoterpenoid biosynthesis)	2.5.1.1
GRTTs	geranyltranstransferase, plastidic	grdp[s] + ipdp[s] -> frdp[s] + ppi[s]	(LOC_Os02g44780 or LOC_Os07g39270 or LOC_Os01g14630)	Terpenoid biosynthesis (Monoterpenoid biosynthesis)	2.5.1.10
GRTTm	geranyltranstransferase, mitochondrial	grdp[m] + ipdp[m] -> frdp[m] + ppi[m]	(LOC_Os01g50760 or LOC_Os05g46580 or LOC_Os06g46450)	Terpenoid biosynthesis (Monoterpenoid biosynthesis)	2.5.1.10
FRTTs	Farnesyltranstransferase	frdp[s] + ipdp[s] -> ggdp[s] + ppi[s]	(LOC_Os02g44780 or LOC_Os07g39270 or LOC_Os01g14630)	Terpenoid biosynthesis (Monoterpenoid biosynthesis)	2.5.1.29
DMATTc	Dimethylallyltransferase, cytosolic	dmpp[c] + ipdp[c] -> grdp[c] + ppi[c]	(LOC_Os04g56210 or LOC_Os04g56230)	Terpenoid biosynthesis	2.5.1.1

				(Monoterpenoid biosynthesis)	
GRTTc	geranyltranstransferase, cytosolic	grdp[c] + ipdp[c] -> frdp[c] + ppi[c]	(LOC_Os04g56210 or LOC_Os04g56230)	Terpenoid biosynthesis (Monoterpenoid biosynthesis)	2.5.1.10
GGDRc	geranylgeranyl diphosphate reductase	ggdp[s] + 3 h[s] + 3 nadph[s] <=> pdp[s] + 3 nadp[s]	LOC_Os02g51080	Terpenoid biosynthesis (Monoterpenoid biosynthesis)	1.3.1.83
LIMSs	(4S)-limonene synthase	grdp[s] -> lim[s] + ppi[s]	(LOC_Os01g45350 or LOC_Os01g01780)	Terpenoid biosynthesis (Monoterpenoid biosynthesis)	4.2.3.16
PSPPSc	Farnesyl-diphosphate farnesyltransferase	2 frdp[c] -> ppi[c] + psqldp[c]	(LOC_Os03g59040 or LOC_Os07g10130)	Terpenoid biosynthesis (Sesquiterpenoid/Triterpenoid biosynthesis)	2.5.1.21
SQLSc	squalene synthase	psqldp[c] + nadph[c] + h[c] -> ppi[c] + sql[c] + nadp[c]	(LOC_Os03g59040 or LOC_Os07g10130)	Terpenoid biosynthesis (Sesquiterpenoid/Triterpenoid biosynthesis)	2.5.1.21
SQLMOc	squalene monooxygenase	sql[c] + nadph[c] + o2[c] + h[c] <=> Ssq23epx[c] + nadp[c] + h2o[c]	LOC_Os03g12910	Terpenoid biosynthesis (Sesquiterpenoid/Triterpenoid biosynthesis)	1.14.13.132
PRIMARTSc	9-beta-pimara-7,15-diene oxidase	primard[s] + 3 nadph[s] + 3 o2[s] + 2 h[s] -> primardt[s] + 3 nadp[s] + 3 h2o[s]	LOC_Os04g10160	Terpenoid biosynthesis (Diterpenoid biosynthesis)	1.14.14.1
SCODPSs	syn-copalyl-diphosphate synthase	ggdp[s] -> scodp[s]	LOC_Os04g09900	Terpenoid biosynthesis (Diterpenoid biosynthesis)	5.5.1.14
PRIMARDSs	syn-pimara-7,15-diene synthase	scodp[s] -> primard[s] + ppi[s]	LOC_Os04g10060	Terpenoid biosynthesis (Diterpenoid biosynthesis)	4.2.3.35
MOMASys	momilactone-A synthase	primardt[s] + nadp[s] -> moma[s] + nadph[s] + h[s]	LOC_Os04g10010	Terpenoid biosynthesis (Diterpenoid biosynthesis)	1.1.1.295
MOMASs	momilactone-A synthase	primardt[s] + nad[s] -> moma[s] + nadh[s] + h[s]	LOC_Os04g10010	Terpenoid biosynthesis (Diterpenoid biosynthesis)	1.1.1.295
STEMSs	stemar-13-ene synthase	scodp[s] -> stem[s] + ppi[s]	LOC_Os11g28530	Terpenoid biosynthesis (Diterpenoid biosynthesis)	4.2.3.33
STEMOc	stemar-13-ene oxidase	stem[c] + o2[c] + nadph[c] -> h2o[c] + nadp[c] + stemol[c]	LOC_Os06g37300	Terpenoid biosynthesis (Diterpenoid biosynthesis)	
P450MO1c	cytochrome P450 monooxygenase	stemol[c] + o2[c] + nadph[c] -> h2o[c] + nadp[c] + ozln-S[c]		Terpenoid biosynthesis (Diterpenoid biosynthesis)	
ESANDSs	ent-sandaracopimaradiene synthase	ecdp[s] -> esand[s] + ppi[s]	LOC_Os12g30824	Terpenoid biosynthesis (Diterpenoid biosynthesis)	4.2.3.29
ESANDO1c	ent-cassa-12,15-diene oxidase	esand[c] + o2[c] + nadph[c] -> h2o[c] + nadp[c] + esandol[c]	LOC_Os06g37300	Terpenoid biosynthesis (Diterpenoid biosynthesis)	
P450MO4c	cytochrome P450 monooxygenase	esandol[c] + o2[c] + nadph[c] -> ozln-D[c] + nadp[c] + h2o[c]		Terpenoid biosynthesis (Diterpenoid biosynthesis)	
P450MO5c	cytochrome P450 monooxygenase	esandol[c] + o2[c] + nadph[c] -> ozln-E[c] + nadp[c] + h2o[c]		Terpenoid biosynthesis (Diterpenoid biosynthesis)	
P450MO6c	cytochrome P450 monooxygenase	esandol[c] + o2[c] + nadph[c] -> ozln-F[c] + nadp[c] + h2o[c]		Terpenoid biosynthesis (Diterpenoid biosynthesis)	
OZLNDO1c	Oryzalexin D oxidase	ozln-D[c] + o2[c] + nadph[c] + h[c] -> ozln-A[c] + nadp[c] + 2 h2o[c]		Terpenoid biosynthesis (Diterpenoid biosynthesis)	
OZLNDO2c	Oryzalexin D oxidase	ozln-D[c] + o2[c] + nadph[c] + h[c] -> ozln-B[c] + nadp[c] + 2 h2o[c]		Terpenoid biosynthesis (Diterpenoid biosynthesis)	
OZLNAOc	Oryzalexin A oxidase	ozln-A[c] + o2[c] + nadph[c] + h[c] -> ozln-C[c] + nadp[c] + 2 h2o[c]		Terpenoid biosynthesis (Diterpenoid biosynthesis)	
OZLNBOc	Oryzalexin B oxidase	ozln-B[c] + o2[c] + nadph[c] + h[c] -> ozln-C[c] + nadp[c] + 2 h2o[c]		Terpenoid biosynthesis (Diterpenoid biosynthesis)	
PRIMADNSs	ent-pimara-8(14),15-diene synthase	ecdp[s] -> primardn[s] + ppi[s]	LOC_Os02g36220	Terpenoid biosynthesis (Diterpenoid biosynthesis)	4.2.3.30
EIKAURSs	ent-isokaurene synthase	ecdp[s] -> eikaur[s] + ppi[s]	LOC_Os02g36264	Terpenoid biosynthesis (Diterpenoid biosynthesis)	4.2.3.103
EIKAUROc	ent-isokaurene C2-hydroxylase	eikaur[c] + o2[c] + nadph[c] -> eihkaur[c] + h2o[c] + nadp[c]	LOC_Os02g36150	Terpenoid biosynthesis (Diterpenoid biosynthesis)	1.14.13.143

ECASDSs	ent-cassa-12,15-diene synthase	ecdp[s] -> ecasd[s] + ppi[s]	LOC_Os02g36140	Terpenoid biosynthesis (Diterpenoid biosynthesis)	4.2.3.28
ECASDO1c	ent-cassa-12,15-diene oxidase	ecasd[c] + o2[c] + nadph[c] -> h2o[c] + nadp[c] + ecasdol[c]	LOC_Os06g37300	Terpenoid biosynthesis (Diterpenoid biosynthesis)	
ECASDO2c	ent-cassa-12,15-diene oxidase	ecasdol[c] + o2[c] + nadph[c] + h[c] -> 2 h2o[c] + nadp[c] + ecasdal[c]	LOC_Os06g37300	Terpenoid biosynthesis (Diterpenoid biosynthesis)	
ECASDO3c	ent-cassa-12,15-diene oxidase	ecasdal[c] + o2[c] + nadph[c] -> h2o[c] + nadp[c] + ecasdate[c]	LOC_Os06g37300	Terpenoid biosynthesis (Diterpenoid biosynthesis)	
ECASDATEO1c	ent-cassa-12,15-diene-3alpha-ol-11-keto oxidase	ecasdate[c] + o2[c] + nadph[c] -> phtc-C[c] + nadp[c] + h2o[c]		Terpenoid biosynthesis (Diterpenoid biosynthesis)	
ECASDATEO2c	ent-cassa-12,15-diene-3alpha-ol-11-keto oxidase	phtc-C[c] + o2[c] + nadph[c] + h[c] -> phtc-E[c] + nadp[c] + 2 h2o[c]		Terpenoid biosynthesis (Diterpenoid biosynthesis)	
P450MO2c	cytochrome P450 monooxygenase	phtc-C[c] + o2[c] + nadph[c] -> phtc-B[c] + nadp[c] + h2o[c]		Terpenoid biosynthesis (Diterpenoid biosynthesis)	
ECASDATEO3c	ent-cassa-12,15-diene-3alpha-ol-11-keto oxidase	ecasdate[c] + o2[c] + nadph[c] -> ecasd2ate[c] + nadp[c] + h2o[c]	LOC_Os06g37300	Terpenoid biosynthesis (Diterpenoid biosynthesis)	
ECASD2ATEO1c	ent-cassa-12,15-diene-2,3alpha-ol-11-keto oxidase	ecasd2ate[c] + o2[c] + nadph[c] + h[c] -> phtc-D[c] + nadp[c] + 2 h2o[c]		Terpenoid biosynthesis (Diterpenoid biosynthesis)	
ECASD2ATEO2c	ent-cassa-12,15-diene-2,3alpha-ol-11-keto oxidase	ecasd2ate[c] + o2[c] + nadph[c] + h[c] -> phtc-A[c] + nadp[c] + 2 h2o[c]		Terpenoid biosynthesis (Diterpenoid biosynthesis)	
P450MO3c	cytochrome P450 monooxygenase	ecasd2ate[c] + o2[c] + nadph[c] -> phtc-B[c] + nadp[c] + h2o[c]		Terpenoid biosynthesis (Diterpenoid biosynthesis)	
EKAURSs	Ent-kaurene synthase	ecdp[s] -> ppi[s] + ekaur[s]	(LOC_Os04g52240 or LOC_Os04g52230 or LOC_Os04g52210)	Terpenoid biosynthesis (Diterpenoid biosynthesis)	4.2.3.19
ECPDs	ent-copalyl diphosphate synthase	ggdp[s] -> ecdp[s]	(LOC_Os09g15050 or LOC_Os02g17780 or LOC_Os02g36210)	Terpenoid biosynthesis (Diterpenoid biosynthesis)	5.5.1.13
EKAURO1c	Ent-kaurene oxidase	ekaur[c] + o2[c] + nadph[c] + h[c] -> h2o[c] + nadp[c] + ekaurol[c]	LOC_Os06g37224	Phytohormones biosynthesis (Gibberallins)	1.14.13.78
EKAURO2c	Ent-kaurene oxidase	ekaurol[c] + o2[c] + nadph[c] + h[c] -> 2 h2o[c] + nadp[c] + ekaural[c]	LOC_Os06g37224	Phytohormones biosynthesis (Gibberallins)	1.14.13.78
EKAURO3c	Ent-kaurene oxidase	ekaural[c] + o2[c] + nadph[c] -> h2o[c] + nadp[c] + ekaurate[c]	LOC_Os06g37224	Phytohormones biosynthesis (Gibberallins)	1.14.13.78
EKAURATEO1c	Ent-kaurenoic acid oxidase	ekaurate[c] + o2[c] + nadph[c] + h[c] -> ehkaurate[c] + nadp[c] + h2o[c]	LOC_Os06g02019	Phytohormones biosynthesis (Gibberallins)	1.14.13.79
EKAURATEO2c	Ent-kaurenoic acid oxidase	ehkaurate[c] + nadph[c] + h[c] + o2[c] -> ga12-ald[c] + nadp[c] + 2 h2o[c]	LOC_Os06g02019	Phytohormones biosynthesis (Gibberallins)	1.14.13.79
EKAURATEO3c	Ent-kaurenoic acid oxidase	ga12-ald[c] + nadph[c] + o2[c] -> ga12[c] + nadp[c] + h2o[c]	LOC_Os06g02019	Phytohormones biosynthesis (Gibberallins)	1.14.13.79
GADO12c	(gibberellin-12),2-oxoglutarate:oxygen oxidoreductase	ga12[c] + o2[c] + akg[c] -> ga53[c] + co2[c] + succ[c]	(LOC_Os01g09300 or LOC_Os07g01340)	Phytohormones biosynthesis (Gibberallins)	1.14.11.12
GAAKGOR1c	(gibberellin-12),2-oxoglutarate:oxygen oxidoreductase	ga12[c] + o2[c] + akg[c] -> ga15[c] + co2[c] + succ[c]	(LOC_Os01g09300 or LOC_Os07g01340)	Phytohormones biosynthesis (Gibberallins)	1.14.11.12
GAAKGOR2c	(gibberellin-15),2-oxoglutarate:oxygen oxidoreductase	ga15[c] + o2[c] + akg[c] -> ga24[c] + co2[c] + succ[c] + h2o[c]	(LOC_Os01g09300 or LOC_Os07g01340)	Phytohormones biosynthesis (Gibberallins)	1.14.11.12
GAAKGOR3c	(gibberellin-24),2-oxoglutarate:oxygen oxidoreductase	ga24[c] + o2[c] + akg[c] -> ga9[c] + 2 co2[c] + succ[c] + h[c]	(LOC_Os01g09300 or LOC_Os07g01340)	Phytohormones biosynthesis (Gibberallins)	1.14.11.12
GADO1c	gibberellin 3beta-dioxygenase	ga9[c] + o2[c] + akg[c] -> ga4[c] + co2[c] + succ[c]	LOC_Os05g08540	Phytohormones biosynthesis (Gibberallins)	1.14.11.15
GAAKORG12c	(gibberellin-4),2-oxoglutarate:oxygen oxidoreductase	ga4[c] + o2[c] + akg[c] -> ga34[c] + co2[c] + succ[c] + h[c]	(LOC_Os01g09300 or LOC_Os07g01340)	Phytohormones biosynthesis (Gibberallins)	1.14.11.-
GAAKORG10c	(gibberellin-9),2-oxoglutarate:oxygen oxidoreductase	ga9[c] + o2[c] + akg[c] -> ga51[c] + co2[c] + succ[c] + h[c]	(LOC_Os01g09300 or LOC_Os07g01340)	Phytohormones biosynthesis (Gibberallins)	1.14.11.-
GAAKORG11c	(gibberellin-51),2-oxoglutarate:oxygen oxidoreductase	ga51[c] + o2[c] + akg[c] -> ga51cat[c] + co2[c] + succ[c] + h[c]	(LOC_Os01g09300 or LOC_Os07g01340)	Phytohormones biosynthesis (Gibberallins)	1.14.11.-
GAAKGOR4c	(gibberellin-24),2-oxoglutarate:oxygen oxidoreductase	ga24[c] + o2[c] + akg[c] -> ga25[c] + co2[c] + succ[c] + h[c]	(LOC_Os01g09300 or LOC_Os07g01340)	Phytohormones biosynthesis (Gibberallins)	1.14.11.12

GADO2c	gibberellin 3beta-dioxygenase	ga24[c] + o2[c] + akg[c] -> ga36[c] + co2[c] + succ[c]		Phytohormones biosynthesis (Gibberallins)	1.14.11.-
GADO3c	gibberellin 3beta-dioxygenase	ga25[c] + o2[c] + akg[c] -> ga13[c] + co2[c] + succ[c]		Phytohormones biosynthesis (Gibberallins)	1.14.11.-
GADO4c	gibberellin 3beta-dioxygenase	ga12[c] + o2[c] + akg[c] -> ga14[c] + co2[c] + succ[c]		Phytohormones biosynthesis (Gibberallins)	1.14.11.-
GADO5c	gibberellin 3beta-dioxygenase	ga14[c] + o2[c] + akg[c] -> ga37[c] + co2[c] + succ[c]	(LOC_Os01g09300 or LOC_Os07g01340)	Phytohormones biosynthesis (Gibberallins)	1.14.11.-
GAAKGOR5c	(gibberellin-37),2-oxoglutarate:oxygen oxidoreductase	ga37[c] + o2[c] + akg[c] -> ga36[c] + co2[c] + succ[c] + h2o[c]	(LOC_Os01g09300 or LOC_Os07g01340)	Phytohormones biosynthesis (Gibberallins)	1.14.11.-
GAAKGOR6c	(gibberellin-36),2-oxoglutarate:oxygen oxidoreductase	ga36[c] + o2[c] + akg[c] -> ga4[c] + 2 co2[c] + succ[c] + h[c]	(LOC_Os01g09300 or LOC_Os07g01340)	Phytohormones biosynthesis (Gibberallins)	1.14.11.-
GADO6c	gibberellin 3beta-dioxygenase	ga53[c] + o2[c] + akg[c] -> ga44[c] + succ[c] + co2[c]	(LOC_Os01g09300 or LOC_Os07g01340)	Phytohormones biosynthesis (Gibberallins)	1.14.11.-
GAAKORG7c	(gibberellin-19),2-oxoglutarate:oxygen oxidoreductase	ga19[c] + o2[c] + akg[c] -> ga20[c] + 2 co2[c] + succ[c] + h[c]	(LOC_Os01g09300 or LOC_Os07g01340)	Phytohormones biosynthesis (Gibberallins)	1.14.11.-
GAAKORG15c	(gibberellin-19),2-oxoglutarate:oxygen oxidoreductase	ga19[c] + o2[c] + akg[c] -> ga17[c] + co2[c] + succ[c] + h[c]	(LOC_Os01g09300 or LOC_Os07g01340)	Phytohormones biosynthesis (Gibberallins)	1.14.11.-
GAAKORG8c	(gibberellin-20),2-oxoglutarate:oxygen oxidoreductase	ga20[c] + o2[c] + akg[c] -> ga29[c] + co2[c] + succ[c] + h[c]	(LOC_Os01g09300 or LOC_Os07g01340)	Phytohormones biosynthesis (Gibberallins)	1.14.11.-
GAAKORG9c	(gibberellin-29),2-oxoglutarate:oxygen oxidoreductase	ga29[c] + o2[c] + akg[c] -> ga29cat[c] + co2[c] + succ[c] + h[c]	(LOC_Os01g09300 or LOC_Os07g01340)	Phytohormones biosynthesis (Gibberallins)	1.14.11.-
GADO7c	gibberellin-44 dioxygenase	ga44[c] + akg[c] + o2[c] -> ga19[c] + succ[c] + co2[c] + h2o[c]	(LOC_Os01g09300 or LOC_Os07g01340 or LOC_Os03g63970)	Phytohormones biosynthesis (Gibberallins)	1.14.11.12
GA3DOc	gibberellin 3 beta-dioxygenase	ga20[c] + akg[c] + o2[c] -> ga1[c] + succ[c] + co2[c]	(LOC_Os01g08220 or LOC_Os05g08540 or LOC_Os07g07420 or LOC_Os03g63970 or LOC_Os05g34854 or LOC_Os01g66100)	Phytohormones biosynthesis (Gibberallins)	1.14.11.15
GA2DOc	gibberellin 2 beta-dioxygenase	ga1[c] + akg[c] + o2[c] -> ga8[c] + succ[c] + co2[c]	(LOC_Os01g55240 or LOC_Os05g43880 or LOC_Os05g06670)	Phytohormones biosynthesis (Gibberallins)	1.14.11.13
GA4DOc	gibberellin 2 beta-dioxygenase	ga8[c] + akg[c] + o2[c] -> ga8cat[c] + succ[c] + co2[c]	(LOC_Os01g55240 or LOC_Os05g43880 or LOC_Os05g06670)	Phytohormones biosynthesis (Gibberallins)	1.14.11.-
VLXANDEOs	violaxanthin de-epoxidase	vlxan[s] + ascb-L[s] + h[s] -> anxan[s] + dhdascb[s] + h2o[s]	(LOC_Os01g51860 or LOC_Os04g31040)	Terpenoid biosynthesis (Carotenoid biosynthesis)	1.10.99.3
ANXANDEOs	antheraxanthin de-epoxidase	anxan[s] + ascb-L[s] + h[s] -> zxan[s] + dhdascb[s] + h2o[s]	LOC_Os04g31040	Terpenoid biosynthesis (Carotenoid biosynthesis)	1.10.99.3
ZXANEOys	zeaxanthin epoxidase (nadph)	zxan[s] + nadph[s] + o2[s] + h[s] -> anxan[s] + nadp[s] + h2o[s]	LOC_Os04g37619	Terpenoid biosynthesis (Carotenoid biosynthesis)	1.14.13.90
ZXANEOs	zeaxanthin epoxidase (nadh)	zxan[s] + nadh[s] + o2[s] + h[s] -> anxan[s] + nad[s] + h2o[s]	LOC_Os04g37619	Terpenoid biosynthesis (Carotenoid biosynthesis)	1.14.13.90
ANXANEOys	antheraxanthin epoxidase (nadph)	anxan[s] + nadph[s] + o2[s] + h[s] -> vlxan[s] + nadp[s] + h2o[s]	LOC_Os04g37619	Terpenoid biosynthesis (Carotenoid biosynthesis)	1.14.13.90
ANXANEOs	antheraxanthin epoxidase (nadh)	anxan[s] + nadh[s] + o2[s] + h[s] -> vlxan[s] + nad[s] + h2o[s]	LOC_Os04g37619	Terpenoid biosynthesis (Carotenoid biosynthesis)	1.14.13.90
ACAROTORs	alpha-carotene,NADH:oxygen 3-oxidoreductase	a-carot[s] + nadph[s] + o2[s] + h[s] -> znxan[s] + nadp[s] + h2o[s]		Terpenoid biosynthesis (Carotenoid biosynthesis)	1.14.99.-
CAROTEMOs	carotene epsilon-monooxygenase	a-carot[s] + nadph[s] + o2[s] + h[s] -> a-cptxan[s] + nadp[s] + h2o[s]	LOC_Os10g39930	Terpenoid biosynthesis (Carotenoid biosynthesis)	1.14.99.45
CPTXANORs	alpha-cryptoxanthin,NADH:oxygen 3-oxidoreductase	a-cptxan[s] + nadh[s] + o2[s] + h[s] -> lutein[s] + nad[s] + h2o[s]	(LOC_Os03g03370 or LOC_Os04g48880 or LOC_Os10g38940)	Terpenoid biosynthesis (Carotenoid biosynthesis)	1.14.13.129
ZNXANMOs	zeinoxanthin epsilon-monooxygenase	znxan[s] + nadph[s] + o2[s] + h[s] -> lutein[s] + nadp[s] + h2o[s]	LOC_Os10g39930	Terpenoid biosynthesis (Carotenoid biosynthesis)	1.14.99.-
PHYTDSs	15-cis-phytoene desaturase	phyt[s] + fad[s] <=> phytfl[s] + fadh2[s]	LOC_Os03g08570	Terpenoid biosynthesis (Carotenoid biosynthesis)	1.3.5.5
PHYTFLDSs	all-trans phytofluene desaturase	phytfl[s] + fad[s] <=> z-carot[s] + fadh2[s]	LOC_Os03g08570	Terpenoid biosynthesis (Carotenoid biosynthesis)	1.3.5.5

BCAROTHs	beta-carotene 3-hydroxylase	b-carot[s] + nadh[s] + o2[s] + h[s] -> b-cptxan[s] + nad[s] + h2o[s]	LOC_Os02g57290	Terpenoid biosynthesis (Carotenoid biosynthesis)	1.14.99.-
BCPTXANHs	beta-cryptoxanthin 3-hydroxylase	b-cptxan[s] + nadh[s] + o2[s] + h[s] -> zxan[s] + nad[s] + h2o[s]		Terpenoid biosynthesis (Carotenoid biosynthesis)	1.14.99.-
CAROTDSs	Carotene 7,8-desaturase	nrsprn[s] + fad[s] <=> lycop[s] + fadh2[s]	LOC_Os07g10490	Terpenoid biosynthesis (Carotenoid biosynthesis)	1.3.5.6
ZCARTDSs	all-trans-zeta-carotene desaturase	z-carot[s] + fad[s] <=> nrsprn[s] + fadh2[s]	LOC_Os07g10490	Terpenoid biosynthesis (Carotenoid biosynthesis)	1.3.5.6
CBGL1s	carotenoid beta-end group lyase (decyclizing), nrsprn	nrsprn[s] <=> b-zcarot[s]	LOC_Os02g09750	Terpenoid biosynthesis (Carotenoid biosynthesis)	5.5.1.19
CBGL2s	carotenoid beta-end group lyase (decyclizing), z-carot	b-zcarot[s] <=> dhbzcarot[s]	LOC_Os02g09750	Terpenoid biosynthesis (Carotenoid biosynthesis)	5.5.1.19
PHYTS1s	phytoene synthase (phdp forming)	2 ggdp[s] -> phdp[s] + ppi[s]	LOC_Os06g51290	Terpenoid biosynthesis (Carotenoid biosynthesis)	2.5.1.32
PHYTS2s	phytoene synthase (phyt forming)	phdp[s] -> phyt[s] + ppi[s]	LOC_Os06g51290	Terpenoid biosynthesis (Carotenoid biosynthesis)	2.5.1.32
NXANSs	neoxanthin synthase	vlxan[s] -> nxan[s]	LOC_Os01g39960	Terpenoid biosynthesis (Carotenoid biosynthesis)	5.3.99.9
LYCOPEC1s	lycopene epsilon-cyclase	lycop[s] -> d-carot[s]	LOC_Os01g39960	Terpenoid biosynthesis (Carotenoid biosynthesis)	5.5.1.18
LYCOPBC1s	lycopene beta-cyclase (a-carot)	d-carot[s] -> a-carot[s]	LOC_Os02g09750	Terpenoid biosynthesis (Carotenoid biosynthesis)	5.5.1.19
LYCOPBC2s	lycopene beta-cyclase (g-carot)	lycop[s] -> g-carot[s]	LOC_Os02g09750	Terpenoid biosynthesis (Carotenoid biosynthesis)	5.5.1.-
LYCOPBC3s	lycopene beta-cyclase (b-carot)	g-carot[s] -> b-carot[s]	LOC_Os02g09750	Terpenoid biosynthesis (Carotenoid biosynthesis)	5.5.1.-
NXANIs	neoxanthin isomerase	nxan[s] -> cnxan[s]		Terpenoid biosynthesis (Carotenoid biosynthesis)	5.2.1.-
XANXNDHs	Xanthoxin dehydrogenase	xanxn[s] + nad[s] -> absald[s] + nadh[s] + h[s]	LOC_Os03g59610	Phytohormones biosynthesis (Abscisic acid)	1.1.1.288
EPCDOs	9-cis-epoxycarotenoid dioxygenase	cnxan[s] + o2[s] -> xanxn[s] + acrtnl[s]	LOC_Os04g46470	Phytohormones biosynthesis (Abscisic acid)	1.13.11.51
ABSALDOs	Abscisic-aldehyde oxidase	absald[s] + h2o[s] + o2[s] -> abs[s] + h2o2[s] + h[s]	(LOC_Os10g04860 or LOC_Os03g57690)	Phytohormones biosynthesis (Abscisic acid)	1.2.3.14
ABSH1s	abscisic acid 8-hydroxylase	abs[s] + nadph[s] + o2[s] + h[s] -> habs[s] + nadp[s] + h2o[s]	(LOC_Os02g47470 or LOC_Os09g28390)	Phytohormones biosynthesis (Abscisic acid)	1.14.13.93
ABSH2s	phaseic acid synthase	habs[s] -> phas[s]		Phytohormones biosynthesis (Abscisic acid)	
ECAROTHs	epsilon-carotene hydroxylase	ee-carotl[s] + o2[s] + fad[s] <=> lacxan[s] + h2o[s] + fadh2[s]	LOC_Os10g39930	Terpenoid biosynthesis (Carotenoid biosynthesis)	1.14.99.-
EECAROTLHs	apsilon,epsilon-carotene-3-diol hydroxylase	e-carot[s] + o2[s] + fad[s] <=> ee-carotl[s] + h2o[s] + fadh2[s]	LOC_Os10g39930	Terpenoid biosynthesis (Carotenoid biosynthesis)	1.14.99.-
LYCOPEC2s	lycopene epsilon-cyclase	d-carot[s] -> e-carot[s]	LOC_Os01g39960	Terpenoid biosynthesis (Carotenoid biosynthesis)	5.5.1.18
HSTDHc	3-beta-hydroxysteroid dehydrogenase	campst43l[c] + nad[c] -> campst43e[c] + nadh[c] + h[c]	LOC_Os03g32170	Phytohormones biosynthesis (Brassinosteroids)	1.1.1.145
DXCSTNMOc	3-epi-6-deoxocathasterone 23-monooxygenase	dxcstn[c] + o2[c] + 2 h[c] -> dxstn[c] + h2o[c]	LOC_Os01g10040	Phytohormones biosynthesis (Brassinosteroids)	1.14.13.112
DXSTNORc	6-Deoxoteasterone:brassinosteroid C3-oxidoreductase	dxstn[c] -> dhdxstn[c] + 2 h[c]	LOC_Os01g10040	Phytohormones biosynthesis (Brassinosteroids)	1.14.-.-
DXTSTc	6-Deoxotyphasterol:brassinosteroid C3-oxidoreductase	dhdxstn[c] + 2 h[c] -> dxtst[c]		Phytohormones biosynthesis (Brassinosteroids)	1.14.-.-
DXTSTOc	6-Deoxotyphasterol:brassinosteroid C6-oxidase	dxtst[c] + o2[c] -> tpst[c] + h2o[c]	LOC_Os03g40540	Phytohormones biosynthesis (Brassinosteroids)	1.14.-.-
DXSTNOc	6-Deoxoteasterone:brassinosteroid C6-oxidase	dxstn[c] + o2[c] -> tstn[c] + h2o[c]	LOC_Os03g40540	Phytohormones biosynthesis (Brassinosteroids)	

DHDXSTNOc	3-Dehydro-6-deoxoteasterone:brassinosteroid C6-oxidase	dhdxstn[c] + o2[c] -> dhtstn[c] + h2o[c]	LOC_Os03g40540	Phytohormones biosynthesis (Brassinosteroids)	
TSTNORc	Teasterone:brassinosteroid C3-oxidoreductase	tstn[c] -> dhtstn[c] + 2 h[c]		Phytohormones biosynthesis (Brassinosteroids)	
BRS1c	Typhasterol synthase	dhtstn[c] + 2 h[c] -> tpst[c]		Phytohormones biosynthesis (Brassinosteroids)	
BRS2c	Castasterone synthase	tpst[c] + o2[c] + nadph[c] -> cstn[c] + h2o[c] + nadp[c]		Phytohormones biosynthesis (Brassinosteroids)	
BRS3c	Brassinolide synthase	cstn[c] + o2[c] -> brsnl[c] + h2o[c]	LOC_Os03g40540	Phytohormones biosynthesis (Brassinosteroids)	
CAMPSTHc	Campesterol,NADPH:brassinosteroid C22alpha-hydroxylase	campst[c] + o2[c] + nadph[c] + h[c] -> 22hcampst[c] + h2o[c] + nadp[c]	LOC_Os03g12660	Phytohormones biosynthesis (Brassinosteroids)	1.14.13.-
22HCAMHc	5alpha-Campestan-3-one,NADPH:brassinosteroid C22alpha-hydroxylase	5camp3e[c] + o2[c] + nadph[c] + h[c] -> 22h5camp3e[c] + h2o[c] + nadp[c]	LOC_Os03g12660	Phytohormones biosynthesis (Brassinosteroids)	1.14.13.-
CAMPST43EHc	Campest-4-en-3-one,NADPH:brassinosteroid C22alpha-hydroxylase	campst43e[c] + o2[c] + nadph[c] + h[c] -> 22h5camp43e[c] + h2o[c] + nadp[c]	LOC_Os03g12660	Phytohormones biosynthesis (Brassinosteroids)	1.14.13.-
CAMPSTLHc	Campesterol,NADPH:brassinosteroid C22alpha-hydroxylase	campstl[c] + o2[c] + nadph[c] + h[c] -> dxcstn[c] + h2o[c] + nadp[c]	LOC_Os03g12660	Phytohormones biosynthesis (Brassinosteroids)	1.14.13.-
22HCAM43Rc	22alpha-Hydroxy-campest-4-en-3-one;NADPH:steroid 5alpha-reductase	22h5camp43e[c] + nadph[c] + h[c] -> 22h5camp3e[c] + nadp[c]	(LOC_Os07g31140 or LOC_Os07g06800 or LOC_Os04g48750 or LOC_Os01g05670 or LOC_Os01g63260)	Phytohormones biosynthesis (Brassinosteroids)	1.3.99.-
CAM43Rc	Campest-4-en-3-one,NADPH:steroid 5alpha-reductase	campst43e[c] + nadph[c] + h[c] -> 5camp3e[c] + nadp[c]	(LOC_Os07g31140 or LOC_Os07g06800 or LOC_Os04g48750 or LOC_Os01g05670 or LOC_Os01g63260)	Phytohormones biosynthesis (Brassinosteroids)	1.3.99.-
DKSTIc	Delta5-3-ketosteroid isomerase	campst[c] -> campst43l[c]		Phytohormones biosynthesis (Brassinosteroids)	5.3.3.1
BRS5c	6-Deoxocathasterone synthase	22h5camp3e[c] + 2 h[c] -> dxcstn[c]		Phytohormones biosynthesis (Brassinosteroids)	
BRS4c	Campestanol synthase	5camp3e[c] + 2 h[c] -> campstl[c]		Phytohormones biosynthesis (Brassinosteroids)	
STR14DMc	sterol 14alpha-demethylase	obfool[c] + 3 o2[c] + 3 nadph[c] + 2 h[c] -> mergtrol[c] + for[c] + 3 nadp[c] + 4 h2o[c]	(LOC_Os07g28110 or LOC_Os07g37980 or LOC_Os05g34380 or LOC_Os07g37970 or LOC_Os07g28160)	Steroid Metabolism	1.14.13.70
CAMPSTc	Campesterol synthase	mchsterol[c] + nadph[c] + h[c] -> campst[c] + nadp[c]		Steroid Metabolism	1.3.-.-
STISTSc	Stigmasterol synthase	sitst[c] + o2[c] + nadph[c] + h[c] -> stist[c] + 2 h2o[c] + nadp[c]		Steroid Metabolism	1.3.1.-
DHAVESTRc	5-dehydroavenasterol reductase	dhavest[c] + 2 nadph[c] -> isfst[c] + 2 nadp[c]	LOC_Os02g26650	Steroid Metabolism	1.3.1.21
DHEPISTRc	5-Dehydroepisterol reductase	dhepist[c] + 2 nadph[c] -> mchsterol[c] + 2 nadp[c]	LOC_Os02g26650	Steroid Metabolism	1.3.1.21
MERGRc	4alpha-methyl-5alpha-ergosta-8,14,24(28)-trien-3beta-ol delta14 reductase	mergtrol[c] + nadph[c] + h[c] -> mfecostrl[c] + nadp[c]	(LOC_Os09g39220 or LOC_Os01g25189)	Steroid Metabolism	1.3.1.70
DHAVESTSc	5-dehydroavenasterol synthase	avest[c] -> dhavest[c] + 2 h[c]	LOC_Os01g04260	Steroid Metabolism	1.14.21.6
DHEPISTSc	5-Dehydroepisterol synthase	epist[c] -> dhepist[c] + 2 h[c]	LOC_Os01g04260	Steroid Metabolism	1.14.21.6
CYEUOLSc	cycloeucalenol synthase	menecyart[c] + nadph[c] + 2 o2[c] + 2 h[c] <=> cyeuol[c] + for[c] + nadp[c] + 2 h2o[c]		Steroid Metabolism	2.1.1.-
AVESTSc	avenasterol synthase	edenelo[c] + 3 h[c] + 3 nadph[c] + 3 o2[c] <=> avest[c] + for[c] + 4 h2o[c] + 3 nadp[c]	LOC_Os07g01150	Steroid Metabolism	1.14.13.72
METMTc	24-methylenesterol C-methyltransferase	metphnl[c] + amet[c] -> edenelo[c] + ahcys[c] + h[c]	LOC_Os03g04340	Steroid Metabolism	2.1.1.143
CYARTMTc	sterol 24-C-methyltransferase	cyart[c] + amet[c] <=> menecyart[c] + ahcys[c] + h[c]	LOC_Os07g10600	Steroid Metabolism	2.1.1.41
CSTLIc	cholestenol Delta-isomerase	mfecostrl[c] -> metphnl[c]	LOC_Os01g01369	Steroid Metabolism	5.3.3.5
CASc	Cycloartenol synthase	Ssq23epx[c] -> cyart[c]	(LOC_Os05g14800 or LOC_Os11g18310 or LOC_Os02g04760 or LOC_Os11g18340)	Steroid Metabolism	5.4.99.8
CYECYCIc	Cycloeucalenol cycloisomerase	cyeuol[c] <=> obfool[c]	LOC_Os11g19700	Steroid Metabolism	5.5.1.9
DSTRc	delta24-sterol reductase	isfst[c] + nadph[c] + h[c] -> sitst[c] + nadp[c]	LOC_Os10g25780	Steroid Metabolism	1.3.1.72
IPDPT1s	2-Isopentenyl-diphosphate:ATP delta2-isopentenyltransferase	dmpp[s] + atp[s] + h[s] -> ipatp[s] + ppi[s]	(LOC_Os07g09220 or LOC_Os07g11050)	Phytohormones biosynthesis (Zeatin)	2.5.1.-

IPDPT2s	2-Isopentenyl-diphosphate:ADP delta2-isopentenyltransferase	dmpp[s] + adp[s] -> ipadp[s] + ppi[s]	(LOC_Os07g09220 or LOC_Os07g11050)	Phytohormones biosynthesis (Zeatin)	2.5.1.-
ADMATs	adenylate dimethylallyltransferase	dmpp[s] + amp[s] -> ipamp[s] + ppi[s]	(LOC_Os07g09220 or LOC_Os07g11050)	Phytohormones biosynthesis (Zeatin)	2.5.1.27
CYTTHs	cytokinin trans-hydroxylase	ipatp[s] + h2o[s] + nadph[s] -> nadp[s] + t-ztnrtp[s]		Phytohormones biosynthesis (Zeatin)	
TZTNS1s	trans zeatin synthesis 1	t-ztnrtp[s] + h2o[s] -> t-ztnrdp[s] + pi[s] + 2 h[s]		Phytohormones biosynthesis (Zeatin)	
TZTNS2s	trans zeatin synthesis 2	t-ztnrdp[s] + h2o[s] -> t-ztnrp[s] + pi[s] + h[s]		Phytohormones biosynthesis (Zeatin)	
IPAMRPs	N6-(delta2-isopentenyl)-adenosine 5-monophosphate phosphoribohydrolase	ipamp[s] + h2o[s] -> ipadne[s] + r5p[s]	LOC_Os01g40630	Phytohormones biosynthesis (Zeatin)	
TZTNS3s	trans zeatin synthesis 3	ipamp[s] + h2o[s] -> ipadn[s] + pi[s]		Phytohormones biosynthesis (Zeatin)	3.2.2.-
TZTNS4s	trans zeatin synthesis 4	ipadne[s] + h2o[s] -> 2 h[s] + t-ztn[s]		Phytohormones biosynthesis (Zeatin)	3.2.2.-
TZTNS5s	trans zeatin synthesis 5	ipadn[s] + h2o[s] -> 2 h[s] + t-ztnr[s]		Phytohormones biosynthesis (Zeatin)	3.2.2.-
TZTNS6s	trans zeatin synthesis 6	t-ztnr[s] + h2o[s] -> rib-D[s] + t-ztn[s]		Phytohormones biosynthesis (Zeatin)	3.2.2.-
IPADEDHs	Isopentenyladenosine-5-diphosphate-hydroxylase	ipadp[s] + nadph[s] + h2o[s] -> t-ztnrdp[s] + nadp[s] + 3 h[s]		Phytohormones biosynthesis (Zeatin)	
IPADETHs	Isopentenyladenosine-5-triphosphate-hydroxylase	ipamp[s] + nadph[s] + h2o[s] -> t-ztnrp[s] + nadp[s] + 3 h[s]		Phytohormones biosynthesis (Zeatin)	
CKTHs	cytokinin trans-hydroxylase	t-ztnrp[s] + h2o[s] -> t-ztn[s] + r5p[s]	LOC_Os01g40630	Phytohormones biosynthesis (Zeatin)	
ZTNRs	zeatin reductase	t-ztn[s] + nadph[s] + h[s] <=> dhz[s] + nadp[s]		Phytohormones biosynthesis (Zeatin)	1.3.1.69
P450MOc	P-450 monooxygenase	t-ztn[c] + fad[c] + h2o[c] <=> ipadne[c] + fadh2[c] + o2[c]		Phytohormones biosynthesis (Zeatin)	1.3.1.69
CKDH3c	cytokinin dehydrogenase	t-ztn[c] + h2o[c] + fad[c] + h[c] -> ade[c] + fadh2[c] + 34hb[c]	(None or LOC_Os01g71310 or LOC_Os05g31040 or LOC_Os01g10110 or LOC_Os01g56810)	Phytohormones biosynthesis (Zeatin)	1.5.99.12
CKDH2c	cytokinin dehydrogenase	ipadn[c] + h2o[c] + fad[c] + h[c] -> adn[c] + fadh2[c] + 33dma[c]	(None or LOC_Os01g71310 or LOC_Os05g31040 or LOC_Os01g10110 or LOC_Os01g56810)	Phytohormones biosynthesis (Zeatin)	1.5.99.12
CKDH1c	cytokinin dehydrogenase	ipadne[c] + h2o[c] + fad[c] + h[c] -> ade[c] + fadh2[c] + 33dma[c]	(None or LOC_Os01g71310 or LOC_Os05g31040 or LOC_Os01g10110 or LOC_Os01g56810)	Phytohormones biosynthesis (Zeatin)	1.5.99.12
TRNAIPTc	tRNA isopentenyltransferase	dmpp[c] + trna[c] -> ptrna[c] + ppi[c]	(LOC_Os07g11050 or LOC_Os06g51350 or LOC_Os05g24660 or LOC_Os03g24240 or LOC_Os03g24440 or LOC_Os03g59570)	Phytohormones biosynthesis (Zeatin)	2.5.1.8
cZTNS1c	cis-zeatin synthesis, 1	ptrna[c] <=> ctrna[c]		Phytohormones biosynthesis (Zeatin)	
cZTNS2c	cis-zeatin synthesis, 2	ctrna[c] <=> c-ztnrp[c]		Phytohormones biosynthesis (Zeatin)	
CKPc	cytokinin phosphohydrolase	c-ztnrp[c] + h2o[c] -> c-ztnr[c] + pi[c]		Phytohormones biosynthesis (Zeatin)	
cZTNS3c	cis-zeatin synthesis, 3	c-ztnr[c] + h2o[c] -> c-ztn[c] + rib-D[c]		Phytohormones biosynthesis (Zeatin)	
CKGT1c	cytokinin N-glucosyltransferase	c-ztn[c] + udpg[c] -> c-ztn7g[c] + udp[c]	(LOC_Os11g25730 or LOC_Os11g25454 or LOC_Os07g13940 or LOC_Os07g13810 or LOC_Os07g13800 or LOC_Os07g13634 or LOC_Os03g60960 or LOC_Os01g59100)	Phytohormones biosynthesis (Zeatin)	2.4.1.-

CKGT2c	cytokinin N-glucosyltransferase	t-ztn[c] + udpg[c] -> t-ztn7g[c] + udp[c]	(LOC_Os11g25730 or LOC_Os11g25454 or LOC_Os07g13940 or LOC_Os07g13810 or LOC_Os07g13800 or LOC_Os07g13634 or LOC_Os03g60960 or LOC_Os01g59100)	Phytohormones biosynthesis (Zeatin)	2.4.1.-
CKGT3c	cytokinin N-glucosyltransferase	dhz[c] + udpg[c] -> dhz7g[c] + udp[c]	(LOC_Os11g25730 or LOC_Os11g25454 or LOC_Os07g13940 or LOC_Os07g13810 or LOC_Os07g13800 or LOC_Os07g13634 or LOC_Os03g60960 or LOC_Os01g59100)	Phytohormones biosynthesis (Zeatin)	2.4.1.-
CKGT4c	cytokinin N-glucosyltransferase	ipadne[c] + udpg[c] -> ipadne7g[c] + udp[c]	(LOC_Os11g25730 or LOC_Os11g25454 or LOC_Os07g13940 or LOC_Os07g13810 or LOC_Os07g13800 or LOC_Os07g13634 or LOC_Os03g60960 or LOC_Os01g59100)	Phytohormones biosynthesis (Zeatin)	2.4.1.-
CKGT5c	cytokinin N-glucosyltransferase	c-ztn[c] + udpg[c] -> c-ztn9g[c] + udp[c]	(LOC_Os11g25730 or LOC_Os11g25454 or LOC_Os07g13940 or LOC_Os07g13810 or LOC_Os07g13800 or LOC_Os07g13634 or LOC_Os03g60960 or LOC_Os01g59100)	Phytohormones biosynthesis (Zeatin)	2.4.1.-
CKGT6c	cytokinin N-glucosyltransferase	t-ztn[c] + udpg[c] -> t-ztn9g[c] + udp[c]	(LOC_Os11g25730 or LOC_Os11g25454 or LOC_Os07g13940 or LOC_Os07g13810 or LOC_Os07g13800 or LOC_Os07g13634 or LOC_Os03g60960 or LOC_Os01g59100)	Phytohormones biosynthesis (Zeatin)	2.4.1.-
CKGT7c	cytokinin N-glucosyltransferase	dhz[c] + udpg[c] -> dhz9g[c] + udp[c]	(LOC_Os11g25730 or LOC_Os11g25454 or LOC_Os07g13940 or LOC_Os07g13810 or LOC_Os07g13800 or LOC_Os07g13634 or LOC_Os03g60960 or LOC_Os01g59100)	Phytohormones biosynthesis (Zeatin)	2.4.1.-
CKGT8c	cytokinin N-glucosyltransferase	ipadne[c] + udpg[c] -> ipadne9g[c] + udp[c]	(LOC_Os11g25730 or LOC_Os11g25454 or LOC_Os07g13940 or LOC_Os07g13810 or LOC_Os07g13800 or LOC_Os07g13634 or LOC_Os03g60960 or LOC_Os01g59100)	Phytohormones biosynthesis (Zeatin)	2.4.1.-
CKOGT1c	cytokinin O-glucosyltransferase	t-ztn[c] + udpg[c] -> t-ztng[c] + udp[c]	(LOC_Os10g09990 or LOC_Os09g16030 or LOC_Os09g03140 or LOC_Os08g38160 or LOC_Os08g38130 or LOC_Os08g38110)	Phytohormones biosynthesis (Zeatin)	2.4.1.203
CKOGT2c	cytokinin O-glucosyltransferase	c-ztn[c] + udpg[c] -> c-ztng[c] + udp[c]	(LOC_Os10g09990 or LOC_Os09g16030 or LOC_Os09g03140 or LOC_Os08g38160 or LOC_Os08g38130 or LOC_Os08g38110)	Phytohormones biosynthesis (Zeatin)	2.4.1.215
CKOGT3c	cytokinin O-glucosyltransferase	dhz[c] + udpg[c] -> dhzg[c] + udp[c]	(LOC_Os10g09990 or LOC_Os09g16030 or LOC_Os09g03140 or LOC_Os08g38160 or LOC_Os08g38130 or LOC_Os08g38110)	Phytohormones biosynthesis (Zeatin)	2.4.1.-
C3STDH2c	C-3 sterol dehydrogenase (zymosterol)	nad[c] + 4mzym_int1[c] -> co2[c] + h[c] + nadh[c] + 4mzym_int2[c]	LOC_Os03g29170	Steroid Metabolism	1.1.1.170
C3STDH1c	C-3 sterol dehydrogenase (zymosterol)	nad[c] + zym_int1[c] -> co2[c] + h[c] + nadh[c] + zym_int2[c]	LOC_Os03g29170	Steroid Metabolism	1.1.1.170
C3STKR2c	C-3 sterol keto reductase (zymosterol)	h[c] + nadph[c] + zym_int2[c] -> nadp[c] + zymst[c]		Steroid Metabolism	1.1.1.270
C3STKR1c	C-3 sterol keto reductase (4-methylzymosterol)	4mzym_int2[c] + h[c] + nadph[c] -> 4mzym[c] + nadp[c]		Steroid Metabolism	1.1.1.270
LNS14DMc	lanosterol 14-demethylase	2 h[c] + lanost[c] + 3 nadph[c] + 3 o2[c] -> 44mctr[c] + for[c] + 4 h2o[c] + 3 nadp[c]	LOC_Os02g02230	Steroid Metabolism	1.14.13.70
C4STMO1c	C-4 sterol methyl oxidase (4,4-dimethylzymosterol)	44mzym[c] + 3 h[c] + 3 nadph[c] + 3 o2[c] -> 4mzym_int1[c] + 4 h2o[c] + 3 nadp[c]	(LOC_Os11g48020 or LOC_Os07g01150)	Steroid Metabolism	1.14.13.72
C4STMO2c	C-4 sterol methyl oxidase (4,4-	4mzym[c] + 3 h[c] + 3 nadph[c] + 3 o2[c] -> zym_int1[c] + 4	(LOC_Os11g48020 or LOC_Os07g01150)	Steroid Metabolism	1.14.13.72

	dimethylzymosterol)	h2o[c] + 3 nadp[c]			
LTHSTRLOc	lathosterol oxidase	lthstrl[c] + nadph[c] + h[c] + o2[c] -> 7dhchsterol[c] + nadp[c] + 2 h2o[c]	LOC_Os01g04260	Steroid Metabolism	1.14.21.6
7DHCSRc	7-dehydrocholesterol reductase	7dhchsterol[c] + nadph[c] + h[c] -> chsterol[c] + nadp[c]	LOC_Os02g26650	Steroid Metabolism	1.3.1.21
C14STRc	C-14 sterol reductase	44mctr[c] + h[c] + nadph[c] -> 44mzym[c] + nadp[c]	LOC_Os09g39220	Steroid Metabolism	1.3.1.70
CHLSTRc	lanosterol D24-reductase	chlstol[c] + nadph[c] + h[c] -> lthstrl[c] + nadp[c]	(LOC_Os11g48020 or LOC_Os07g01150)	Steroid Metabolism	1.3.1.72
CHLSTIc	delta 8,24-Cholestadien-3beta-ol delta7-delta8-isomerase	zymst[c] -> chlstol[c]	LOC_Os01g01369	Steroid Metabolism	5.3.3.5
D24STR1c	delta 24-sterol reductase	zymst[c] + nadph[c] + h[c] -> chlestol[c] + nadp[c]	(LOC_Os11g48020 or LOC_Os07g01150)	Steroid Metabolism	1.3.1.72
CHLSDDIc	5alpha-Cholest-7-en-3beta-ol delta7-delta8-isomerase	chlestol[c] -> lthstrl[c]	LOC_Os01g01369	Steroid Metabolism	5.3.3.5
LNSTLSc	lanosterol synthase	Ssq23epx[c] -> lanost[c]	(LOC_Os02g04690 or LOC_Os02g04710 or LOC_Os11g08569 or LOC_Os11g18194 or LOC_Os11g18366 or LOC_Os11g35710)	Steroid Metabolism	5.4.99.7
SAM24MTc	sterol 24-C-methyltransferase	amet[c] + zymst[c] -> ahcys[c] + fecost[c] + h[c]	LOC_Os07g10600	Steroid Metabolism	2.1.1.41
C8STIc	C-8 sterol isomerase	fecost[c] -> epist[c]	LOC_Os03g53580	Steroid Metabolism	
LATOXc	lathosterol oxidase	epist[c] + nadp[c] <=> ergstt[c] + nadph[c] + h[c]	LOC_Os01g04260	Steroid Metabolism	1.14.21.6
C22SDc	C-22 sterol desaturase	ergstt[c] + nadp[c] <=> ergsttt[c] + nadph[c] + h[c]		Steroid Metabolism	1.14.14.-
D24STRc	delta 24(24(1))-sterol reductase	ergsttt[c] + nadph[c] + h[c] <=> ergtrol[c] + nadp[c]		Steroid Metabolism	1.3.1.71
THFGLUHv	gamma-glutamyl hydrolase	thglu[v] + 2 h2o[v] -> 2 glu-L[v] + thf[v] + 2 h[v]	LOC_Os05g44130	Folates metabolism	3.4.19.9
URDGLLc	Ureidoglycolate lyase	urdglyc[c] -> glx[c] + urea[c]		Purine metabolism	4.3.2.3
ALTNDAc	allantoate deiminase	alltt[c] + h2o[c] -> urdgly[c] + nh4[c] + co2[c]	LOC_Os06g45480	Purine metabolism	3.5.3.9
URDGLAHc	Ureidoglycine aminohydrolase	urdgly[c] + h2o[c] <=> urdglyc[c] + nh4[c] + h[c]	LOC_Os07g31270	Purine metabolism	3.5.3.-
PYDXSc	Pyridoxal 5-phosphate synthase	g3p[c] + ru5p-D[c] + gln-L[c] -> pydx5p[c] + glu-L[c] + pi[c] + 3 h2o[c] + h[c]	(LOC_Os02g03740 or LOC_Os07g01020 or LOC_Os10g01080 or LOC_Os11g48080)	Other Vitamins Metabolism (B6)	4.-.-.-
PYAMPPc	Pyridoxamine-5-phosphate phosphohydrolase	pyam5p[c] + h2o[c] -> pydam[c] + pi[c]		Other Vitamins Metabolism (B6)	3.1.3.74
PDXPPc	Pyridoxine-5-phosphate phosphohydrolase	pdx5p[c] + h2o[c] -> pydxn[c] + pi[c]		Other Vitamins Metabolism (B6)	3.1.3.74
PYDXPPc	Pyridoxal-5-phosphate phosphohydrolase	pydx5p[c] + h2o[c] -> pydx[c] + pi[c]		Other Vitamins Metabolism (B6)	3.1.3.74
MCOATAs	malonyl-CoA:[acyl-carrier-protein] S-malonyltransferase	ACP[s] + malcoa[s] + h[s] <=> coa[s] + malACP[s]	LOC_Os03g18590	Fatty acid biosynthesis	2.3.1.39
ACOATAs	beta-ketoacyl-acyl-carrier-protein synthase III	accoa[s] + ACP[s] -> coa[s] + acACP[s]	LOC_Os04g55060	Fatty acid biosynthesis	2.3.1.38
MACPCLs	malonyl-[acyl-carrier-protein] carboxy-lyase	malACP[s] -> co2[s] + acACP[s]	LOC_Os04g55060	Fatty acid biosynthesis	2.3.1.41
ACMAT1s	Acyl-[acyl-carrier-protein]:malonyl-[acyl-carrier-protein] C-acyltransferase (decarboxylating)	acACP[s] + h[s] + malACP[s] -> ACP[s] + actACP[s] + co2[s]	LOC_Os04g36800	Fatty acid biosynthesis	2.3.1.180
3OAR40s	3-oxoacyl-[acyl-carrier-protein] reductase (n-C4:0)	actACP[s] + h[s] + nadph[s] -> 3hbutACP[s] + nadp[s]	(LOC_Os02g30060 or LOC_Os03g53690 or LOC_Os04g30760 or LOC_Os06g08600 or LOC_Os07g07440 or LOC_Os07g37420 or LOC_Os10g31780 or LOC_Os12g13930)	Fatty acid biosynthesis	1.1.1.100
3HAD40s	3-hydroxyacyl-[acyl-carrier-protein] dehydratase (n-C4:0)	3hbutACP[s] -> but2eACP[s] + h2o[s]	LOC_Os05g36000	Fatty acid biosynthesis	4.2.1.59
EAR40ys	enoyl-[acyl-carrier-protein] reductase (NADPH) (n-C4:0)	but2eACP[s] + h[s] + nadph[s] -> butACP[s] + nadp[s]	(LOC_Os08g23810 or LOC_Os09g10600)	Fatty acid biosynthesis	1.3.1.10
3OAS60s	3-oxoacyl-[acyl-carrier-protein] synthase (n-C6:0)	butACP[s] + h[s] + malACP[s] -> 3ohexACP[s] + ACP[s] + co2[s]	LOC_Os04g36800	Fatty acid biosynthesis	2.3.1.180
3OAR60s	3-oxoacyl-[acyl-carrier-protein] reductase (n-C6:0)	3ohexACP[s] + h[s] + nadph[s] -> 3hhexACP[s] + nadp[s]	(LOC_Os02g30060 or LOC_Os03g53690 or LOC_Os04g30760 or LOC_Os06g08600 or LOC_Os07g07440 or LOC_Os07g37420 or LOC_Os10g31780 or LOC_Os12g13930)	Fatty acid biosynthesis	1.1.1.100

3HAD60s	3-hydroxyacyl-[acyl-carrier-protein] dehydratase (n-C6:0)	3hhexACP[s] -> thex2eACP[s] + h2o[s]	LOC_Os05g36000	Fatty acid biosynthesis	4.2.1.59
EAR60ys	enoyl-[acyl-carrier-protein] reductase (NADPH) (n-C6:0)	thex2eACP[s] + h[s] + nadph[s] -> hexACP[s] + nadp[s]	(LOC_Os08g23810 or LOC_Os09g10600)	Fatty acid biosynthesis	1.3.1.10
3OAS80s	3-oxoacyl-[acyl-carrier-protein] synthase (n-C8:0)	h[s] + hexACP[s] + malACP[s] -> 3ooctACP[s] + ACP[s] + co2[s]	LOC_Os04g36800	Fatty acid biosynthesis	2.3.1.180
3OAR80s	3-oxoacyl-[acyl-carrier-protein] reductase (n-C8:0)	3ooctACP[s] + h[s] + nadph[s] -> 3hoctACP[s] + nadp[s]	(LOC_Os02g30060 or LOC_Os03g53690 or LOC_Os04g30760 or LOC_Os06g08600 or LOC_Os07g07440 or LOC_Os07g37420 or LOC_Os10g31780 or LOC_Os12g13930)	Fatty acid biosynthesis	1.1.1.100
3HAD80s	3-hydroxyacyl-[acyl-carrier-protein] dehydratase (n-C8:0)	3hoctACP[s] -> toct2eACP[s] + h2o[s]	LOC_Os05g36000	Fatty acid biosynthesis	4.2.1.59
EAR80ys	enoyl-[acyl-carrier-protein] reductase (NADPH) (n-C8:0)	toct2eACP[s] + h[s] + nadph[s] -> nadp[s] + ocACP[s]	(LOC_Os08g23810 or LOC_Os09g10600)	Fatty acid biosynthesis	1.3.1.10
3OAS100s	3-oxoacyl-[acyl-carrier-protein] synthase (n-C10:0)	h[s] + malACP[s] + ocACP[s] -> 3odecACP[s] + ACP[s] + co2[s]	LOC_Os04g36800	Fatty acid biosynthesis	2.3.1.180
3OAR100s	3-oxoacyl-[acyl-carrier-protein] reductase (n-C10:0)	3odecACP[s] + h[s] + nadph[s] -> 3hdecACP[s] + nadp[s]	(LOC_Os02g30060 or LOC_Os03g53690 or LOC_Os04g30760 or LOC_Os06g08600 or LOC_Os07g07440 or LOC_Os07g37420 or LOC_Os10g31780 or LOC_Os12g13930)	Fatty acid biosynthesis	1.1.1.100
3HAD100s	3-hydroxyacyl-[acyl-carrier-protein] dehydratase (n-C10:0)	3hdecACP[s] -> tdec2eACP[s] + h2o[s]	LOC_Os05g36000	Fatty acid biosynthesis	4.2.1.59
EAR100ys	enoyl-[acyl-carrier-protein] reductase (NADPH) (n-C10:0)	tdec2eACP[s] + h[s] + nadph[s] -> dcaACP[s] + nadp[s]	(LOC_Os08g23810 or LOC_Os09g10600)	Fatty acid biosynthesis	1.3.1.10
3OAS120s	3-oxoacyl-[acyl-carrier-protein] synthase (n-C12:0)	dcaACP[s] + h[s] + malACP[s] -> 3oddecACP[s] + ACP[s] + co2[s]	LOC_Os04g36800	Fatty acid biosynthesis	2.3.1.180
3OAR120s	3-oxoacyl-[acyl-carrier-protein] reductase (n-C12:0)	3oddecACP[s] + h[s] + nadph[s] -> 3hddecACP[s] + nadp[s]	(LOC_Os02g30060 or LOC_Os03g53690 or LOC_Os04g30760 or LOC_Os06g08600 or LOC_Os07g07440 or LOC_Os07g37420 or LOC_Os10g31780 or LOC_Os12g13930)	Fatty acid biosynthesis	1.1.1.100
3HAD120s	3-hydroxyacyl-[acyl-carrier-protein] dehydratase (n-C12:0)	3hddecACP[s] -> tddec2eACP[s] + h2o[s]	LOC_Os05g36000	Fatty acid biosynthesis	4.2.1.59
EAR120ys	enoyl-[acyl-carrier-protein] reductase (NADPH) (n-C12:0)	tddec2eACP[s] + h[s] + nadph[s] -> ddcaACP[s] + nadp[s]	(LOC_Os08g23810 or LOC_Os09g10600)	Fatty acid biosynthesis	1.3.1.10
3OAS140s	3-oxoacyl-[acyl-carrier-protein] synthase (n-C14:0)	ddcaACP[s] + h[s] + malACP[s] -> 3omrsACP[s] + ACP[s] + co2[s]	LOC_Os04g36800	Fatty acid biosynthesis	2.3.1.180
3OAR140s	3-oxoacyl-[acyl-carrier-protein] reductase (n-C14:0)	3omrsACP[s] + h[s] + nadph[s] -> 3hmrsACP[s] + nadp[s]	(LOC_Os02g30060 or LOC_Os03g53690 or LOC_Os04g30760 or LOC_Os06g08600 or LOC_Os07g07440 or LOC_Os07g37420 or LOC_Os10g31780 or LOC_Os12g13930)	Fatty acid biosynthesis	1.1.1.100
3HAD140s	3-hydroxyacyl-[acyl-carrier-protein] dehydratase (n-C14:0)	3hmrsACP[s] -> h2o[s] + tmrs2eACP[s]	LOC_Os05g36000	Fatty acid biosynthesis	4.2.1.59
EAR140ys	enoyl-[acyl-carrier-protein] reductase (NADPH) (n-C14:0)	h[s] + nadph[s] + tmrs2eACP[s] -> myrsACP[s] + nadp[s]	(LOC_Os08g23810 or LOC_Os09g10600)	Fatty acid biosynthesis	1.3.1.10
3OAS160s	3-oxoacyl-[acyl-carrier-protein] synthase (n-C16:0)	h[s] + malACP[s] + myrsACP[s] -> 3opalmACP[s] + ACP[s] + co2[s]	LOC_Os04g36800	Fatty acid biosynthesis	2.3.1.180
3OAR160s	3-oxoacyl-[acyl-carrier-protein] reductase (n-C16:0)	3opalmACP[s] + h[s] + nadph[s] -> 3hpalmACP[s] + nadp[s]	(LOC_Os02g30060 or LOC_Os03g53690 or LOC_Os04g30760 or LOC_Os06g08600 or LOC_Os07g07440 or LOC_Os07g37420 or LOC_Os10g31780 or LOC_Os12g13930)	Fatty acid biosynthesis	1.1.1.100
3HAD160s	3-hydroxyacyl-[acyl-carrier-protein] dehydratase	3hpalmACP[s] -> h2o[s] + tpalm2eACP[s]	LOC_Os05g36000	Fatty acid biosynthesis	4.2.1.59

	(n-C16:0)				
EAR160ys	enoyl-[acyl-carrier-protein] reductase (NADPH) (n-C16:0)	h[s] + tpalm2eACP[s] + nadph[s] -> nadp[s] + palmACP[s]	(LOC_Os08g23810 or LOC_Os09g10600)	Fatty acid biosynthesis	1.3.1.10
3OAS180s	3-oxoacyl-[acyl-carrier-protein] synthase (n-C18:0)	h[s] + malACP[s] + palmACP[s] -> 3ooctdACP[s] + ACP[s] + co2[s]	LOC_Os04g36800	Fatty acid biosynthesis	2.3.1.180
3OAR180s	3-oxoacyl-[acyl-carrier-protein] reductase (n-C18:0)	3ooctdACP[s] + h[s] + nadph[s] -> 3hoctaACP[s] + nadp[s]	(LOC_Os02g30060 or LOC_Os03g53690 or LOC_Os04g30760 or LOC_Os06g08600 or LOC_Os07g07440 or LOC_Os07g37420 or LOC_Os10g31780 or LOC_Os12g13930)	Fatty acid biosynthesis	1.1.1.100
3HAD180s	3-hydroxyacyl-[acyl-carrier-protein] dehydratase (n-C18:0)	3hoctaACP[s] -> toctd2eACP[s] + h2o[s]	LOC_Os05g36000	Fatty acid biosynthesis	4.2.1.59
EAR180ys	enoyl-[acyl-carrier-protein] reductase (NADPH) (n-C18:0)	toctd2eACP[s] + h[s] + nadph[s] -> nadp[s] + ocdcaACP[s]	(LOC_Os08g23810 or LOC_Os09g10600)	Fatty acid biosynthesis	1.3.1.10
FAS161ACP_Ls	fatty acyl-ACP synthase (n-C16:1ACP)	palmACP[s] + o2[s] + nadph[s] -> 2 h2o[s] + hdeACP[s] + nadp[s]	(LOC_Os01g65830 or LOC_Os01g69080 or LOC_Os02g30200 or LOC_Os03g30950 or LOC_Os04g31070 or LOC_Os08g09950 or LOC_Os08g10010)	Fatty acid biosynthesis	1.14.19.2
FAS181ACP_Ls	fatty acyl-ACP synthase (n-C18:1ACP)	ocdcaACP[s] + o2[s] + nadph[s] -> 2 h2o[s] + octeACP[s] + nadp[s]	(LOC_Os01g65830 or LOC_Os01g69080 or LOC_Os02g30200 or LOC_Os03g30950 or LOC_Os04g31070 or LOC_Os08g09950 or LOC_Os08g10010)	Fatty acid biosynthesis	1.14.19.2
FAS182ACP_Ls	fatty acyl-ACP synthase (n-C18:2ACP)	octeACP[s] + o2[s] + nadph[s] -> 2 h2o[s] + ocdcyaACP[s] + nadp[s]	(LOC_Os01g65830 or LOC_Os01g69080 or LOC_Os02g30200 or LOC_Os03g30950 or LOC_Os04g31070 or LOC_Os08g09950 or LOC_Os08g10010)	Fatty acid biosynthesis	1.14.19.2
FAS183ACP_Ls	fatty acyl-ACP synthase (n-C18:3ACP)	ocdcyaACP[s] + o2[s] + nadph[s] -> 2 h2o[s] + lnlnlACP[s] + nadp[s]	(LOC_Os01g65830 or LOC_Os01g69080 or LOC_Os02g30200 or LOC_Os03g30950 or LOC_Os04g31070 or LOC_Os08g09950 or LOC_Os08g10010)	Fatty acid biosynthesis	1.14.19.2
FA140ACPHs	fatty-acyl-ACP hydrolase (n-C14:0)	h2o[s] + myrsACP[s] -> ACP[s] + h[s] + ttdca[s]	((LOC_Os06g39520 or LOC_Os06g05130) or (LOC_Os09g32760 or LOC_Os11g43820))	Fatty acid biosynthesis	3.1.2.14
FA160ACPHs	fatty-acyl-ACP hydrolase (n-C16:0)	h2o[s] + palmACP[s] -> ACP[s] + h[s] + hdca[s]	((LOC_Os06g39520 or LOC_Os06g05130) or (LOC_Os09g32760 or LOC_Os11g43820))	Fatty acid biosynthesis	3.1.2.14
FA161ACPHs	fatty-acyl-ACP hydrolase (n-C16:1)	h2o[s] + hdeACP[s] -> ACP[s] + h[s] + hdcea[s]	((LOC_Os06g39520 or LOC_Os06g05130) or (LOC_Os09g32760 or LOC_Os11g43820))	Fatty acid biosynthesis	3.1.2.14
FA180ACPHs	fatty-acyl-ACP hydrolase (n-C18:0)	h2o[s] + ocdcaACP[s] -> ACP[s] + h[s] + ocdca[s]	((LOC_Os06g39520 or LOC_Os06g05130) or (LOC_Os09g32760 or LOC_Os11g43820))	Fatty acid biosynthesis	3.1.2.14
FA181ACPHs	fatty-acyl-ACP hydrolase (n-C18:1)	h2o[s] + octeACP[s] -> ACP[s] + h[s] + ocdcea[s]	((LOC_Os06g39520 or LOC_Os06g05130) or (LOC_Os09g32760 or LOC_Os11g43820))	Fatty acid biosynthesis	3.1.2.14
FA182ACPHs	fatty-acyl-ACP hydrolase (n-C18:2)	h2o[s] + ocdcyaACP[s] -> ACP[s] + h[s] + ocdcya[s]	((LOC_Os06g39520 or LOC_Os06g05130) or (LOC_Os09g32760 or LOC_Os11g43820))	Fatty acid biosynthesis	3.1.2.14
FA183ACPHs	fatty-acyl-ACP hydrolase (n-C18:3)	h2o[s] + lnlnlACP[s] -> ACP[s] + h[s] + lnlnl[s]	((LOC_Os06g39520 or LOC_Os06g05130) or (LOC_Os09g32760 or LOC_Os11g43820))	Fatty acid biosynthesis	3.1.2.14

FACOAL140r	fatty-acid--CoA ligase (tetradecanoate), endoplasmic reticular	atp[r] + coa[r] + ttdca[r] <=> amp[r] + ppi[r] + tdcoa[r]	(LOC_Os01g46750 or LOC_Os01g48910 or LOC_Os03g62850 or LOC_Os05g04170 or LOC_Os05g25310 or LOC_Os06g06350 or LOC_Os11g04980 or LOC_Os11g06880 or LOC_Os11g35400 or LOC_Os12g04990 or LOC_Os12g07110)	Fatty acid biosynthesis	6.2.1.3
FACOAL160r	fatty-acid--CoA ligase (hexadecanoate), endoplasmic reticular	atp[r] + coa[r] + hdca[r] <=> amp[r] + ppi[r] + pmtcoa[r]	(LOC_Os01g46750 or LOC_Os01g48910 or LOC_Os03g62850 or LOC_Os05g04170 or LOC_Os05g25310 or LOC_Os06g06350 or LOC_Os11g04980 or LOC_Os11g06880 or LOC_Os11g35400 or LOC_Os12g04990 or LOC_Os12g07110)	Fatty acid biosynthesis	6.2.1.3
FACOAL161r	fatty-acid--CoA ligase (hexadecenoate), endoplasmic reticular	atp[r] + coa[r] + hdcea[r] <=> amp[r] + ppi[r] + hdcoa[r]	(LOC_Os01g46750 or LOC_Os01g48910 or LOC_Os03g62850 or LOC_Os05g04170 or LOC_Os05g25310 or LOC_Os06g06350 or LOC_Os11g04980 or LOC_Os11g06880 or LOC_Os11g35400 or LOC_Os12g04990 or LOC_Os12g07110)	Fatty acid biosynthesis	6.2.1.3
FACOAL180r	fatty-acid--CoA ligase (octadecanoate), endoplasmic reticular	atp[r] + coa[r] + ocdca[r] <=> amp[r] + ppi[r] + stcoa[r]	(LOC_Os01g46750 or LOC_Os01g48910 or LOC_Os03g62850 or LOC_Os05g04170 or LOC_Os05g25310 or LOC_Os06g06350 or LOC_Os11g04980 or LOC_Os11g06880 or LOC_Os11g35400 or LOC_Os12g04990 or LOC_Os12g07110)	Fatty acid biosynthesis	6.2.1.3
FACOAL181r	fatty-acid--CoA ligase (octadecenoate), endoplasmic reticular	atp[r] + coa[r] + ocdcea[r] <=> amp[r] + ppi[r] + odecoa[r]	(LOC_Os01g46750 or LOC_Os01g48910 or LOC_Os03g62850 or LOC_Os05g04170 or LOC_Os05g25310 or LOC_Os06g06350 or LOC_Os11g04980 or LOC_Os11g06880 or LOC_Os11g35400 or LOC_Os12g04990 or LOC_Os12g07110)	Fatty acid biosynthesis	6.2.1.3
FACOAL182r	fatty-acid--CoA ligase (octadecynoate), endoplasmic reticular	atp[r] + coa[r] + ocdcya[r] <=> amp[r] + ppi[r] + ocdycacoa[r]	(LOC_Os01g46750 or LOC_Os01g48910 or LOC_Os03g62850 or LOC_Os05g04170 or LOC_Os05g25310 or LOC_Os06g06350 or LOC_Os11g04980 or LOC_Os11g06880 or LOC_Os11g35400 or LOC_Os12g04990 or LOC_Os12g07110)	Fatty acid biosynthesis	6.2.1.3
FACOAL183r	fatty-acid--CoA ligase (linolenoate), endoplasmic reticular	atp[r] + coa[r] + lnlnl[r] <=> amp[r] + ppi[r] + lnlncoa[r]	(LOC_Os01g46750 or LOC_Os01g48910 or LOC_Os03g62850 or LOC_Os05g04170 or LOC_Os05g25310 or LOC_Os06g06350 or LOC_Os11g04980 or LOC_Os11g06880 or LOC_Os11g35400 or LOC_Os12g04990 or LOC_Os12g07110)	Fatty acid biosynthesis	6.2.1.3
FA200COAHr	Long-chain fatty-acyl-CoA hydrolase (arachidate), endoplasmic reticular	h2o[r] + araccoa[r] -> coa[r] + arac[r]	LOC_Os09g34190	Fatty acid biosynthesis	3.1.2.2
FA220COAHr	Long-chain fatty-acyl-CoA hydrolase (behenate), endoplasmic reticular	h2o[r] + behcoa[r] -> coa[r] + beh[r]	LOC_Os09g34190	Fatty acid biosynthesis	3.1.2.2
FA240COAHr	Long-chain fatty-acyl-CoA hydrolase (lignocerate), endoplasmic reticular	h2o[r] + lgnccoa[r] -> coa[r] + lgnc[r]	LOC_Os09g34190	Fatty acid biosynthesis	3.1.2.2
FA260COAHr	Long-chain fatty-acyl-CoA hydrolase (cerotate), endoplasmic reticular	h2o[r] + cercoa[r] -> coa[r] + cero[r]	LOC_Os09g34190	Fatty acid biosynthesis	3.1.2.2
FA280COAHr	Long-chain fatty-acyl-CoA hydrolase (montanate), endoplasmic reticular	h2o[r] + mntcoa[r] -> coa[r] + mntt[r]	LOC_Os09g34190	Fatty acid biosynthesis	3.1.2.2
FA300COAHr	Long-chain fatty-acyl-CoA hydrolase (melissate), endoplasmic reticular	h2o[r] + mlscoa[r] -> coa[r] + mls[r]	LOC_Os09g34190	Fatty acid biosynthesis	3.1.2.2
FACOAL200r	fatty-acid--CoA ligase (arachidate), endoplasmic reticular	amp[r] + ppi[r] + araccoa[r] <=> atp[r] + coa[r] + arac[r]	(LOC_Os01g46750 or LOC_Os01g48910 or LOC_Os03g62850 or LOC_Os05g04170 or LOC_Os05g25310 or LOC_Os06g06350	Fatty acid biosynthesis	6.2.1.3

			or LOC_Os11g04980 or LOC_Os11g06880 or LOC_Os11g35400 or LOC_Os12g04990 or LOC_Os12g07110)		
FACOAL220r	fatty-acid--CoA ligase (behenate), endoplasmic reticular	amp[r] + ppi[r] + behcoa[r] <=> atp[r] + coa[r] + beh[r]	(LOC_Os01g46750 or LOC_Os01g48910 or LOC_Os03g62850 or LOC_Os05g04170 or LOC_Os05g25310 or LOC_Os06g06350 or LOC_Os11g04980 or LOC_Os11g06880 or LOC_Os11g35400 or LOC_Os12g04990 or LOC_Os12g07110)	Fatty acid biosynthesis	6.2.1.3
FACOAL240r	fatty-acid--CoA ligase (lignocerate), endoplasmic reticular	amp[r] + ppi[r] + lgnccoa[r] <=> atp[r] + coa[r] + lgnc[r]	(LOC_Os01g46750 or LOC_Os01g48910 or LOC_Os03g62850 or LOC_Os05g04170 or LOC_Os05g25310 or LOC_Os06g06350 or LOC_Os11g04980 or LOC_Os11g06880 or LOC_Os11g35400 or LOC_Os12g04990 or LOC_Os12g07110)	Fatty acid biosynthesis	6.2.1.3
FACOAL260r	fatty-acid--CoA ligase (cerotate), endoplasmic reticular	amp[r] + ppi[r] + cercoa[r] <=> atp[r] + coa[r] + cero[r]	(LOC_Os01g46750 or LOC_Os01g48910 or LOC_Os03g62850 or LOC_Os05g04170 or LOC_Os05g25310 or LOC_Os06g06350 or LOC_Os11g04980 or LOC_Os11g06880 or LOC_Os11g35400 or LOC_Os12g04990 or LOC_Os12g07110)	Fatty acid biosynthesis	6.2.1.3
FACOAL280r	fatty-acid--CoA ligase (montanate), endoplasmic reticular	amp[r] + ppi[r] + mntcoa[r] <=> atp[r] + coa[r] + mntt[r]	(LOC_Os01g46750 or LOC_Os01g48910 or LOC_Os03g62850 or LOC_Os05g04170 or LOC_Os05g25310 or LOC_Os06g06350 or LOC_Os11g04980 or LOC_Os11g06880 or LOC_Os11g35400 or LOC_Os12g04990 or LOC_Os12g07110)	Fatty acid biosynthesis	6.2.1.3
FACOAL300r	fatty-acid--CoA ligase (melissate), endoplasmic reticular	amp[r] + ppi[r] + mlscoa[r] <=> atp[r] + coa[r] + mls[r]	(LOC_Os01g46750 or LOC_Os01g48910 or LOC_Os03g62850 or LOC_Os05g04170 or LOC_Os05g25310 or LOC_Os06g06350 or LOC_Os11g04980 or LOC_Os11g06880 or LOC_Os11g35400 or LOC_Os12g04990 or LOC_Os12g07110)	Fatty acid biosynthesis	6.2.1.3
ALFACOAR200r	alcohol-forming fatty acyl-CoA reductase (n-C20:0CoA)	araccoa[r] + 2 nadph[r] + 2 h[c] <=> coa[r] + 2 nadp[r] + aracol[r]	LOC_Os03g07140	Secondary Cell Wall Metabolism (Cuticular Wax)	1.2.1-
ALFACOAR220r	alcohol-forming fatty acyl-CoA reductase (n-C22:0CoA)	behcoa[r] + 2 nadph[r] + 2 h[c] <=> coa[r] + 2 nadp[r] + behol[r]	LOC_Os03g07140	Secondary Cell Wall Metabolism (Cuticular Wax)	1.2.1-
ALFACOAR240r	alcohol-forming fatty acyl-CoA reductase (n-C24:0CoA)	lgnccoa[r] + 2 nadph[r] + 2 h[c] <=> coa[r] + 2 nadp[r] + lgncol[r]	LOC_Os03g07140	Secondary Cell Wall Metabolism (Cuticular Wax)	1.2.1-
ALFACOAR260r	alcohol-forming fatty acyl-CoA reductase (n-C26:0CoA)	cercoa[r] + 2 nadph[r] + 2 h[c] <=> coa[r] + 2 nadp[r] + cerool[r]	LOC_Os03g07140	Secondary Cell Wall Metabolism (Cuticular Wax)	1.2.1-
ALFACOAR280r	alcohol-forming fatty acyl-CoA reductase (n-C28:0CoA)	mntcoa[r] + 2 nadph[r] + 2 h[c] <=> coa[r] + 2 nadp[r] + mntol[r]	LOC_Os03g07140	Secondary Cell Wall Metabolism (Cuticular Wax)	1.2.1-
ALFACOAR300r	alcohol-forming fatty acyl-CoA reductase (n-C30:0CoA)	mlscoa[r] + 2 nadph[r] + 2 h[c] <=> coa[r] + 2 nadp[r] + mlsol[r]	LOC_Os03g07140	Secondary Cell Wall Metabolism (Cuticular Wax)	1.2.1-
ALFAACT200r	long-chain-alcohol O-fatty-acyltransferase (n-C20:0CoA)	aracol[r] + hdcoa[r] <=> aracpalm[r] + coa[r]	LOC_Os04g20880	Secondary Cell Wall Metabolism (Cuticular Wax)	2.3.1.75
ALFAACT220r	long-chain-alcohol O-fatty-acyltransferase (n-C22:0CoA)	behol[r] + hdcoa[r] <=> behpalm[r] + coa[r]	LOC_Os04g20880	Secondary Cell Wall Metabolism (Cuticular Wax)	2.3.1.75
PALMH1r	palmitate omega-hydroxylase	hdca[r] + nadph[r] + o2[r] + h[r] -> nadp[r] + h2o[r] + hydro16[r]	LOC_Os01g58990	Secondary Cell Wall Metabolism (Cutin wax)	1.14.13.-
FAOH1r	fatty acid omega-hydroxylase	hydro16[r] + nadph[r] + o2[r] + h[r] -> nadp[r] + h2o[r] + dhydro1016[r]	LOC_Os02g44654	Secondary Cell Wall Metabolism (Cutin wax)	1.14.13.-
HPALMDHr	16-hydroxypalmitate dehydrogenase	hydro16[r] + nadp[r] -> nadph[r] + h[r] + 16opalm[r]	LOC_Os04g48400	Secondary Cell Wall Metabolism (Cutin wax)	1.1.1.-

OOFADH1r	omega-oxo fatty acid dehydrogenase	16opalm[r] + h2o[r] + nadp[r] -> 2 h[r] + nadph[r] + hddt[r]	LOC_Os04g39020	Secondary Cell Wall Metabolism (Cutin wax)	1.1.1.-
OLEHr	oleate omega-hydroxylase	ocdcea[r] + 2 nadph[r] + o2[r] -> 2 nadp[r] + h2o[r] + hydro18[r]	LOC_Os01g63540	Secondary Cell Wall Metabolism (Cutin wax)	1.14.13.-
HOLEDHr	18-hydroxyoleate dehydrogenase	hydro18[r] + nadp[r] -> nadph[r] + h[r] + 18oole[r]	LOC_Os04g48400	Secondary Cell Wall Metabolism (Cutin wax)	1.1.1.-
OOFADH2r	omega-oxo fatty acid dehydrogenase	18oole[r] + h2o[r] + nadp[r] -> 2 h[r] + nadph[r] + oddt[r]	LOC_Os04g39020	Secondary Cell Wall Metabolism (Cutin wax)	1.1.1.-
FAOH2r	fatty acid omega-hydroxylase	hydro18[r] + nadph[r] + o2[r] + h[r] -> nadp[r] + h2o[r] + dhydro1018[r]	LOC_Os02g44654	Secondary Cell Wall Metabolism (Cutin wax)	1.14.13.-
THYDRO91018Sc	9,10,18-trihydroxystearate synthesis	dhydro1018[r] + h2o[r] -> thydro91018[r]		Secondary Cell Wall Metabolism (Cutin wax)	3.3.2.-
OFAFTc	omega-fatty acid O-feruloyl transferase	hydro16[c] + hydro18[c] + dhydro1016[c] + dhydro1018[c] + thydro91018[c] + 5 fercoa[c] <=> 5 coa[c] + 5 feralk[c]	LOC_Os11g31090	Secondary Cell Wall Metabolism (Cutin wax)	2.3.1.188
FAOH3r	fatty acid (arachidate) omega-hydroxylase	arac[r] + nadph[r] + o2[r] + h[r] -> nadp[r] + h2o[r] + hydro20[r]	(LOC_Os01g63540 or LOC_Os02g44654 or LOC_Os04g47250 or LOC_Os10g34480)	Secondary Cell Wall Metabolism (Suberin)	1.14.13.-
FAOH4r	fatty acid (behenate) omega-hydroxylase	beh[r] + nadph[r] + o2[r] + h[r] -> nadp[r] + h2o[r] + hydro22[r]	(LOC_Os01g63540 or LOC_Os02g44654 or LOC_Os04g47250 or LOC_Os10g34480)	Secondary Cell Wall Metabolism (Suberin)	1.14.13.-
FAOH5r	fatty acid (lignocerate) omega-hydroxylase	lgnc[r] + nadph[r] + o2[r] + h[r] -> nadp[r] + h2o[r] + hydro24[r]	(LOC_Os01g63540 or LOC_Os02g44654 or LOC_Os04g47250 or LOC_Os10g34480)	Secondary Cell Wall Metabolism (Suberin)	1.14.13.-
FAOH6r	fatty acid (cerotate) omega-hydroxylase	cero[r] + nadph[r] + o2[r] + h[r] -> nadp[r] + h2o[r] + hydro26[r]	(LOC_Os01g63540 or LOC_Os02g44654 or LOC_Os04g47250 or LOC_Os10g34480)	Secondary Cell Wall Metabolism (Suberin)	1.14.13.-
FAOH7r	fatty acid (montanate) omega-hydroxylase	mntt[r] + nadph[r] + o2[r] + h[r] -> nadp[r] + h2o[r] + hydro28[r]	(LOC_Os01g63540 or LOC_Os02g44654 or LOC_Os04g47250 or LOC_Os10g34480)	Secondary Cell Wall Metabolism (Suberin)	1.14.13.-
FAOH8r	fatty acid (melissate) omega-hydroxylase	mls[r] + nadph[r] + o2[r] + h[r] -> nadp[r] + h2o[r] + hydro30[r]	(LOC_Os01g63540 or LOC_Os02g44654 or LOC_Os04g47250 or LOC_Os10g34480)	Secondary Cell Wall Metabolism (Suberin)	1.14.13.-
HARACDHr	20-hydroxyarachidate dehydrogenase	hydro20[r] + nadp[r] -> nadph[r] + h[r] + 20oarac[r]	LOC_Os04g48400	Secondary Cell Wall Metabolism (Suberin)	1.1.1.-
HBEHDHr	22-hydroxybehenate dehydrogenase	hydro22[r] + nadp[r] -> nadph[r] + h[r] + 22obeh[r]	LOC_Os04g48400	Secondary Cell Wall Metabolism (Suberin)	1.1.1.-
HLGNCDHr	24-hydroxylignocerate dehydrogenase	hydro24[r] + nadp[r] -> nadph[r] + h[r] + 24olgnc[r]	LOC_Os04g48400	Secondary Cell Wall Metabolism (Suberin)	1.1.1.-
HCERODHr	26-hydroxycerotate dehydrogenase	hydro26[r] + nadp[r] -> nadph[r] + h[r] + 26ocero[r]	LOC_Os04g48400	Secondary Cell Wall Metabolism (Suberin)	1.1.1.-
HMNTDHr	28-hydroxymontanate dehydrogenase	hydro28[r] + nadp[r] -> nadph[r] + h[r] + 28omntt[r]	LOC_Os04g48400	Secondary Cell Wall Metabolism (Suberin)	1.1.1.-
HMLSDHr	30-hydroxymelissate dehydrogenase	hydro30[r] + nadp[r] -> nadph[r] + h[r] + 30omls[r]	LOC_Os04g48400	Secondary Cell Wall Metabolism (Suberin)	1.1.1.-
OOFADH3r	omega-oxo fatty acid dehydrogenase	20oarac[r] + h2o[r] + nadp[r] -> 2 h[r] + nadph[r] + ardt[r]	LOC_Os04g39020	Secondary Cell Wall Metabolism (Suberin)	1.1.1.-
OOFADH4r	omega-oxo fatty acid dehydrogenase	22obeh[r] + h2o[r] + nadp[r] -> 2 h[r] + nadph[r] + behdt[r]	LOC_Os04g39020	Secondary Cell Wall Metabolism (Suberin)	1.1.1.-
OOFADH5r	omega-oxo fatty acid dehydrogenase	24olgnc[r] + h2o[r] + nadp[r] -> 2 h[r] + nadph[r] + lgndt[r]	LOC_Os04g39020	Secondary Cell Wall Metabolism (Suberin)	1.1.1.-
OOFADH6r	omega-oxo fatty acid dehydrogenase	26ocero[r] + h2o[r] + nadp[r] -> 2 h[r] + nadph[r] + cerdt[r]	LOC_Os04g39020	Secondary Cell Wall Metabolism (Suberin)	1.1.1.-
OOFADH7r	omega-oxo fatty acid dehydrogenase	28omntt[r] + h2o[r] + nadp[r] -> 2 h[r] + nadph[r] + mntdt[r]	LOC_Os04g39020	Secondary Cell Wall Metabolism (Suberin)	1.1.1.-
OOFADH8r	omega-oxo fatty acid dehydrogenase	30omls[r] + h2o[r] + nadp[r] -> 2 h[r] + nadph[r] + mlsdt[r]	LOC_Os04g39020	Secondary Cell Wall Metabolism (Suberin)	1.1.1.-

FACOAL140c	fatty-acid--CoA ligase (tetradecanoate)	atp[c] + coa[c] + ttdca[c] <=> amp[c] + ppi[c] + tdcoa[c]	(LOC_Os01g46750 or LOC_Os01g48910 or LOC_Os03g62850 or LOC_Os05g04170 or LOC_Os05g25310 or LOC_Os06g06350 or LOC_Os11g04980 or LOC_Os11g06880 or LOC_Os11g35400 or LOC_Os12g04990 or LOC_Os12g07110)	Fatty acid biosynthesis	6.2.1.3
FACOAL160c	fatty-acid--CoA ligase (hexadecanoate)	atp[c] + coa[c] + hdca[c] <=> amp[c] + ppi[c] + pmtcoa[c]	(LOC_Os01g46750 or LOC_Os01g48910 or LOC_Os03g62850 or LOC_Os05g04170 or LOC_Os05g25310 or LOC_Os06g06350 or LOC_Os11g04980 or LOC_Os11g06880 or LOC_Os11g35400 or LOC_Os12g04990 or LOC_Os12g07110)	Fatty acid biosynthesis	6.2.1.3
FACOAL161c	fatty-acid--CoA ligase (hexadecenoate)	atp[c] + coa[c] + hdcea[c] <=> amp[c] + ppi[c] + hdcoa[c]	(LOC_Os01g46750 or LOC_Os01g48910 or LOC_Os03g62850 or LOC_Os05g04170 or LOC_Os05g25310 or LOC_Os06g06350 or LOC_Os11g04980 or LOC_Os11g06880 or LOC_Os11g35400 or LOC_Os12g04990 or LOC_Os12g07110)	Fatty acid biosynthesis	6.2.1.3
FACOAL180c	fatty-acid--CoA ligase (octadecanoate)	atp[c] + coa[c] + ocdca[c] <=> amp[c] + ppi[c] + stcoa[c]	(LOC_Os01g46750 or LOC_Os01g48910 or LOC_Os03g62850 or LOC_Os05g04170 or LOC_Os05g25310 or LOC_Os06g06350 or LOC_Os11g04980 or LOC_Os11g06880 or LOC_Os11g35400 or LOC_Os12g04990 or LOC_Os12g07110)	Fatty acid biosynthesis	6.2.1.3
FACOAL181c	fatty-acid--CoA ligase (octadecenoate)	atp[c] + coa[c] + ocdcea[c] <=> amp[c] + ppi[c] + odecoa[c]	(LOC_Os01g46750 or LOC_Os01g48910 or LOC_Os03g62850 or LOC_Os05g04170 or LOC_Os05g25310 or LOC_Os06g06350 or LOC_Os11g04980 or LOC_Os11g06880 or LOC_Os11g35400 or LOC_Os12g04990 or LOC_Os12g07110)	Fatty acid biosynthesis	6.2.1.3
FACOAL182c	fatty-acid--CoA ligase (octadecynoate)	atp[c] + coa[c] + ocdcya[c] <=> amp[c] + ppi[c] + ocdycacoa[c]	(LOC_Os01g46750 or LOC_Os01g48910 or LOC_Os03g62850 or LOC_Os05g04170 or LOC_Os05g25310 or LOC_Os06g06350 or LOC_Os11g04980 or LOC_Os11g06880 or LOC_Os11g35400 or LOC_Os12g04990 or LOC_Os12g07110)	Fatty acid biosynthesis	6.2.1.3
FACOAL183c	fatty-acid--CoA ligase (linolenoate)	atp[c] + coa[c] + lnlnl[c] <=> amp[c] + ppi[c] + lnlncoa[c]	(LOC_Os01g46750 or LOC_Os01g48910 or LOC_Os03g62850 or LOC_Os05g04170 or LOC_Os05g25310 or LOC_Os06g06350 or LOC_Os11g04980 or LOC_Os11g06880 or LOC_Os11g35400 or LOC_Os12g04990 or LOC_Os12g07110)	Fatty acid biosynthesis	6.2.1.3
FAS161COA_Lc	fatty acyl-CoA synthase (n-C16:1CoA)	pmtcoa[c] + o2[c] + nadph[c] -> 2 h2o[c] + hdcoa[c] + nadp[c]		Fatty acid biosynthesis (desaturation)	
FAS181COA_Lc	fatty acyl-CoA synthase (n-C18:1CoA)	stcoa[c] + o2[c] + nadph[c] -> 2 h2o[c] + odecoa[c] + nadp[c]		Fatty acid biosynthesis (desaturation)	
FAS182COA_Lc	fatty acyl-CoA synthase (n-C18:2CoA)	odecoa[c] + o2[c] + nadph[c] -> 2 h2o[c] + ocdycacoa[c] + nadp[c]		Fatty acid biosynthesis (desaturation)	
FAS183COA_Lc	fatty acyl-CoA synthase (n-C18:3CoA)	ocdycacoa[c] + o2[c] + nadph[c] -> 2 h2o[c] + lnlncoa[c] + nadp[c]		Fatty acid biosynthesis (desaturation)	
3OCS200r	3-oxoacyl-CoA synthase (n-C20:0)	h[r] + malcoa[r] + stcoa[r] -> 3oaraccoa[r] + coa[r] + co2[r]	(LOC_Os02g10320 or LOC_Os04g36800 or LOC_Os07g42420)	Fatty acid biosynthesis (Very long chain)	2.3.1.199
3OCR200r	3-oxoacyl-CoA reductase (n-C20:0)	3oaraccoa[r] + h[r] + nadph[r] -> 3haraccoa[r] + nadp[r]	LOC_Os04g40730	Fatty acid biosynthesis (Very long chain)	1.1.1.330
3HCD200r	3-hydroxyacyl-CoA dehydratase (n-C20:0)	3haraccoa[r] -> tarac2ecoa[r] + h2o[r]	(LOC_Os01g05694 or LOC_Os01g05720 or LOC_Os01g05744 or LOC_Os04g20280 or LOC_Os05g38590)	Fatty acid biosynthesis (Very long chain)	4.2.1.134

ECR200yr	enoyl-CoA reductase (NADPH) (n-C20:0)	tarac2ecoa[r] + h[r] + nadph[r] -> nadp[r] + araccoa[r]	LOC_Os01g05670	Fatty acid biosynthesis (Very long chain)	1.3.1.93
3OCS220r	3-oxoacyl-CoA synthase (n-C22:0)	h[r] + malcoa[r] + araccoa[r] -> 3obehcoa[r] + coa[r] + co2[r]	(LOC_Os02g10320 or LOC_Os04g36800 or LOC_Os07g42420)	Fatty acid biosynthesis (Very long chain)	2.3.1.199
3OCR220r	3-oxoacyl-CoA reductase (n-C22:0)	3obehcoa[r] + h[r] + nadph[r] -> 3hbehcoa[r] + nadp[r]	LOC_Os04g40730	Fatty acid biosynthesis (Very long chain)	1.1.1.330
3HCD220r	3-hydroxyacyl-CoA dehydratase (n-C22:0)	3hbehcoa[r] -> tbeh2ecoa[r] + h2o[r]	(LOC_Os01g05694 or LOC_Os01g05720 or LOC_Os01g05744 or LOC_Os04g20280 or LOC_Os05g38590)	Fatty acid biosynthesis (Very long chain)	4.2.1.134
ECR220yr	enoyl-CoA reductase (NADPH) (n-C22:0)	tbeh2ecoa[r] + h[r] + nadph[r] -> nadp[r] + behcoa[r]	LOC_Os01g05670	Fatty acid biosynthesis (Very long chain)	1.3.1.93
3OCS240r	3-oxoacyl-CoA synthase (n-C24:0)	h[r] + malcoa[r] + behcoa[r] -> 3olgnccoa[r] + coa[r] + co2[r]	(LOC_Os02g10320 or LOC_Os04g36800 or LOC_Os07g42420)	Fatty acid biosynthesis (Very long chain)	2.3.1.199
3OCR240r	3-oxoacyl-CoA reductase (n-C24:0)	3olgnccoa[r] + h[r] + nadph[r] -> 3hlgnccoa[r] + nadp[r]	LOC_Os04g40730	Fatty acid biosynthesis (Very long chain)	1.1.1.330
3HCD240r	3-hydroxyacyl-CoA dehydratase (n-C24:0)	3hlgnccoa[r] -> tlgnc2ecoa[r] + h2o[r]	(LOC_Os01g05694 or LOC_Os01g05720 or LOC_Os01g05744 or LOC_Os04g20280 or LOC_Os05g38590)	Fatty acid biosynthesis (Very long chain)	4.2.1.134
ECR240yr	enoyl-CoA reductase (NADPH) (n-C24:0)	tlgnc2ecoa[r] + h[r] + nadph[r] -> nadp[r] + lgnccoa[r]	LOC_Os01g05670	Fatty acid biosynthesis (Very long chain)	1.3.1.93
3OCS260r	3-oxoacyl-CoA synthase (n-C26:0)	h[r] + malcoa[r] + lgnccoa[r] -> 3ocercoa[r] + coa[r] + co2[r]	(LOC_Os02g10320 or LOC_Os04g36800 or LOC_Os07g42420)	Fatty acid biosynthesis (Very long chain)	2.3.1.199
3OCR260r	3-oxoacyl-CoA reductase (n-C26:0)	3ocercoa[r] + h[r] + nadph[r] -> 3hcercoa[r] + nadp[r]	LOC_Os04g40730	Fatty acid biosynthesis (Very long chain)	1.1.1.330
3HCD260r	3-hydroxyacyl-CoA dehydratase (n-C26:0)	3hcercoa[r] -> tcer2ecoa[r] + h2o[r]	(LOC_Os01g05694 or LOC_Os01g05720 or LOC_Os01g05744 or LOC_Os04g20280 or LOC_Os05g38590)	Fatty acid biosynthesis (Very long chain)	4.2.1.134
ECR260yr	enoyl-CoA reductase (NADPH) (n-C26:0)	tcer2ecoa[r] + h[r] + nadph[r] -> nadp[r] + cercoa[r]	LOC_Os01g05670	Fatty acid biosynthesis (Very long chain)	1.3.1.93
3OCS280r	3-oxoacyl-CoA synthase (n-C28:0)	h[r] + malcoa[r] + cercoa[r] -> 3omntcoa[r] + coa[r] + co2[r]	(LOC_Os02g10320 or LOC_Os04g36800 or LOC_Os07g42420)	Fatty acid biosynthesis (Very long chain)	2.3.1.199
3OCR280r	3-oxoacyl-CoA reductase (n-C28:0)	3omntcoa[r] + h[r] + nadph[r] -> 3hmntcoa[r] + nadp[r]	LOC_Os04g40730	Fatty acid biosynthesis (Very long chain)	1.1.1.330
3HCD280cr	3-hydroxyacyl-CoA dehydratase (n-C28:0)	3hmntcoa[r] -> tmnt2ecoa[r] + h2o[r]	(LOC_Os01g05694 or LOC_Os01g05720 or LOC_Os01g05744 or LOC_Os04g20280 or LOC_Os05g38590)	Fatty acid biosynthesis (Very long chain)	4.2.1.134
ECR280yr	enoyl-CoA reductase (NADPH) (n-C28:0)	tmnt2ecoa[r] + h[r] + nadph[r] -> nadp[r] + mntcoa[r]	LOC_Os01g05670	Fatty acid biosynthesis (Very long chain)	1.3.1.93
3OCS300r	3-oxoacyl-CoA synthase (n-C30:0)	h[r] + malcoa[r] + mntcoa[r] -> 3omlscoa[r] + coa[r] + co2[r]	(LOC_Os02g10320 or LOC_Os04g36800 or LOC_Os07g42420)	Fatty acid biosynthesis (Very long chain)	2.3.1.199
3OCR300r	3-oxoacyl-CoA reductase (n-C30:0)	3omlscoa[r] + h[r] + nadph[r] -> 3hmlscoa[r] + nadp[r]	LOC_Os04g40730	Fatty acid biosynthesis (Very long chain)	1.1.1.330
3HCD300r	3-hydroxyacyl-CoA dehydratase (n-C30:0)	3hmlscoa[r] -> tmls2ecoa[r] + h2o[r]	(LOC_Os01g05694 or LOC_Os01g05720 or LOC_Os01g05744 or LOC_Os04g20280 or LOC_Os05g38590)	Fatty acid biosynthesis (Very long chain)	4.2.1.134
ECR300yr	enoyl-CoA reductase (NADPH) (n-C30:0)	tmls2ecoa[r] + h[r] + nadph[r] -> nadp[r] + mlscoa[r]	LOC_Os01g05670	Fatty acid biosynthesis (Very long chain)	1.3.1.93
FA140ACOASc	long-chain-fatty-acid-CoA ligase (n-C14:0)	ACP[s] + h[s] + ttdca[s] -> h2o[s] + myrsACP[s]	LOC_Os03g62850	Fatty acid biosynthesis	6.2.1.20
FA160ACOASc	long-chain-fatty-acid-CoA ligase (n-C16:0)	ACP[s] + h[s] + hdca[s] -> h2o[s] + palmACP[s]	LOC_Os03g62850	Fatty acid biosynthesis	6.2.1.20
FA161ACOASc	long-chain-fatty-acid-CoA ligase (n-C16:1)	ACP[s] + h[s] + hdcea[s] -> h2o[s] + hdeACP[s]	LOC_Os03g62850	Fatty acid biosynthesis	6.2.1.20
FA180ACOASc	long-chain-fatty-acid-CoA ligase (n-C18:0)	ACP[s] + h[s] + ocdca[s] -> h2o[s] + ocdcaACP[s]	LOC_Os03g62850	Fatty acid biosynthesis	6.2.1.20
FA181ACOASc	long-chain-fatty-acid-CoA ligase (n-C18:1)	ACP[s] + h[s] + ocdcea[s] -> h2o[s] + octeACP[s]	LOC_Os03g62850	Fatty acid biosynthesis	6.2.1.20
FA182ACOASc	long-chain-fatty-acid-CoA ligase (n-C18:2)	ACP[s] + h[s] + ocdcya[s] -> h2o[s] + ocdcyaACP[s]	LOC_Os03g62850	Fatty acid biosynthesis	6.2.1.20
FA183ACOASc	long-chain-fatty-acid-CoA ligase (n-C18:3)	ACP[s] + h[s] + lnlnl[s] -> h2o[s] + lnlnlACP[s]	LOC_Os03g62850	Fatty acid biosynthesis	6.2.1.20
FACOAL140x	fatty-acid--CoA ligase (tetradecanoate)	atp[x] + coa[x] + ttdca[x] <=> amp[x] + ppi[x] + tdcoa[x]	(LOC_Os01g46750 or LOC_Os01g48910 or LOC_Os03g62850 or LOC_Os05g04170	Fatty acid degradation	6.2.1.3

			or LOC_Os05g25310 or LOC_Os06g06350 or LOC_Os11g04980 or LOC_Os11g06880 or LOC_Os11g35400 or LOC_Os12g04990 or LOC_Os12g07110)		
FACOAL160x	fatty-acid--CoA ligase (hexadecanoate)	atp[x] + coa[x] + hdca[x] <=> amp[x] + ppi[x] + pmtcoa[x]	(LOC_Os01g46750 or LOC_Os01g48910 or LOC_Os03g62850 or LOC_Os05g04170 or LOC_Os05g25310 or LOC_Os06g06350 or LOC_Os11g04980 or LOC_Os11g06880 or LOC_Os11g35400 or LOC_Os12g04990 or LOC_Os12g07110)	Fatty acid degradation	6.2.1.3
FACOAL161x	fatty-acid--CoA ligase (hexadecenoate)	atp[x] + coa[x] + hdcea[x] <=> amp[x] + ppi[x] + hdcoa[x]	(LOC_Os01g46750 or LOC_Os01g48910 or LOC_Os03g62850 or LOC_Os05g04170 or LOC_Os05g25310 or LOC_Os06g06350 or LOC_Os11g04980 or LOC_Os11g06880 or LOC_Os11g35400 or LOC_Os12g04990 or LOC_Os12g07110)	Fatty acid degradation	6.2.1.3
FACOAL180x	fatty-acid--CoA ligase (octadecanoate)	atp[x] + coa[x] + ocdca[x] <=> amp[x] + ppi[x] + stcoa[x]	(LOC_Os01g46750 or LOC_Os01g48910 or LOC_Os03g62850 or LOC_Os05g04170 or LOC_Os05g25310 or LOC_Os06g06350 or LOC_Os11g04980 or LOC_Os11g06880 or LOC_Os11g35400 or LOC_Os12g04990 or LOC_Os12g07110)	Fatty acid degradation	6.2.1.3
FACOAL181x	fatty-acid--CoA ligase (octadecenoate)	atp[x] + coa[x] + ocdcea[x] <=> amp[x] + ppi[x] + odecoa[x]	(LOC_Os01g46750 or LOC_Os01g48910 or LOC_Os03g62850 or LOC_Os05g04170 or LOC_Os05g25310 or LOC_Os06g06350 or LOC_Os11g04980 or LOC_Os11g06880 or LOC_Os11g35400 or LOC_Os12g04990 or LOC_Os12g07110)	Fatty acid degradation	6.2.1.3
FACOAL182x	fatty-acid--CoA ligase (octadecynoate)	atp[x] + coa[x] + ocdcya[x] <=> amp[x] + ppi[x] + ocdycacoa[x]	(LOC_Os01g46750 or LOC_Os01g48910 or LOC_Os03g62850 or LOC_Os05g04170 or LOC_Os05g25310 or LOC_Os06g06350 or LOC_Os11g04980 or LOC_Os11g06880 or LOC_Os11g35400 or LOC_Os12g04990 or LOC_Os12g07110)	Fatty acid degradation	6.2.1.3
FACOAL183x	fatty-acid--CoA ligase (linoleoate)	atp[x] + coa[x] + lnlnl[x] <=> amp[x] + ppi[x] + lnlncoa[x]	(LOC_Os01g46750 or LOC_Os01g48910 or LOC_Os03g62850 or LOC_Os05g04170 or LOC_Os05g25310 or LOC_Os06g06350 or LOC_Os11g04980 or LOC_Os11g06880 or LOC_Os11g35400 or LOC_Os12g04990 or LOC_Os12g07110)	Fatty acid degradation	6.2.1.3
ACOA80ORx	Octanoyl-CoA:oxygen 2-oxidoreductase	occoa[x] + fad[x] -> oc2coa[x] + fadh2[x]	(LOC_Os01g06600 or LOC_Os05g07090 or LOC_Os06g01390 or LOC_Os06g23780 or LOC_Os06g23870 or LOC_Os06g24704 or LOC_Os11g39220 or LOC_Os07g47820)	Fatty acid degradation (Beta oxidation)	1.3.3.6;1.3.8.7
ECOAH3x	(S)-Hydroxyoctanoyl-CoA hydro-lyase	oc2coa[x] + h2o[x] <=> 3hocoa[x]	(LOC_Os01g24680 or LOC_Os02g17390)	Fatty acid degradation (Beta oxidation)	4.2.1.17
HACD3x	(S)-hydroxyoctanoyl-CoA:NAD oxidoreductase	3hocoa[x] + nad[x] <=> 3oocoa[x] + nadh[x] + h[x]	(LOC_Os01g24680 or LOC_Os02g17390)	Fatty acid degradation (Beta oxidation)	1.1.1.35
ACACT3x	Hexanoyl-CoA:acetyl-CoA C-acyltransferase	coa[x] + 3oocoa[x] <=> hxcoa[x] + accoa[x]	(LOC_Os02g57260 or LOC_Os10g31950)	Fatty acid degradation (Beta oxidation)	2.3.1.16
ACOA60ORx	Hexanoyl-CoA:(acceptor) 2,3-oxidoreductase	hxcoa[x] + fad[x] -> hx2coa[x] + fadh2[x]	(LOC_Os01g06600 or LOC_Os05g07090 or LOC_Os06g01390 or LOC_Os06g23780 or LOC_Os06g23870 or LOC_Os06g24704 or LOC_Os11g39220 or LOC_Os07g47820)	Fatty acid degradation (Beta oxidation)	1.3.3.6;1.3.8.7
ECOAH2x	(S)-Hydroxyhexanoyl-CoA hydro-lyase	hx2coa[x] + h2o[x] <=> 3hhcoa[x]	(LOC_Os01g24680 or LOC_Os02g17390)	Fatty acid degradation (Beta	4.2.1.17

				oxidation)	
HACD2x	(S)-hydroxyhexanoyl-CoA:NAD oxidoreductase	3hhcoa[x] + nad[x] <=> 3ohcoa[x] + nadh[x] + h[x]	(LOC_Os01g24680 or LOC_Os02g17390)	Fatty acid degradation (Beta oxidation)	1.1.1.35
ACACT2x	butanoyl-CoA:acetyl-CoA C-butanoyltransferase	coa[x] + 3ohcoa[x] <=> accoa[x] + btcoa[x]	(LOC_Os02g57260 or LOC_Os10g31950)	Fatty acid degradation (Beta oxidation)	2.3.1.16
ACOA40ORx	Butanoyl-CoA:oxygen 2-oxidoreductase	btcoa[x] + fad[x] -> fadh2[x] + b2coa[x]	(LOC_Os01g06600 or LOC_Os05g07090 or LOC_Os06g01390 or LOC_Os06g23780 or LOC_Os06g23870 or LOC_Os06g24704 or LOC_Os11g39220 or LOC_Os07g47820)	Fatty acid degradation (Beta oxidation)	1.3.3.6;1.3.8.7
ECOAH1x	(S)-3-Hydroxybutanoyl-CoA hydro-lyase	b2coa[x] + h2o[x] <=> 3hbcoa[x]	(LOC_Os01g24680 or LOC_Os02g17390)	Fatty acid degradation (Beta oxidation)	4.2.1.17
HACD1x	(S)-3-Hydroxybutanoyl-CoA:NAD oxidoreductase	3hbcoa[x] + nad[x] <=> aacoa[x] + nadh[x] + h[x]	(LOC_Os01g24680 or LOC_Os02g17390)	Fatty acid degradation (Beta oxidation)	1.1.1.35
ACOA100ORx	Decanoyl-CoA:(acceptor) 2,3-oxidoreductase	dcacoa[x] + fad[x] -> dc2coa[x] + fadh2[x]	(LOC_Os01g06600 or LOC_Os05g07090 or LOC_Os06g01390 or LOC_Os06g23780 or LOC_Os06g23870 or LOC_Os06g24704 or LOC_Os11g39220 or LOC_Os07g47820)	Fatty acid degradation (Beta oxidation)	1.3.3.6;1.3.8.7
ECOAH4x	(S)-Hydroxydecanoyl-CoA hydro-lyase	dc2coa[x] + h2o[x] <=> 3hdcoa[x]	(LOC_Os01g24680 or LOC_Os02g17390)	Fatty acid degradation (Beta oxidation)	4.2.1.17
HACD4x	(S)-hydroxydecanoyl-CoA:NAD oxidoreductase	3hdcoa[x] + nad[x] <=> 3odcoa[x] + nadh[x] + h[x]	(LOC_Os01g24680 or LOC_Os02g17390)	Fatty acid degradation (Beta oxidation)	1.1.1.35
ACACT4x	Octanoyl-CoA:acetyl-CoA C-acyltransferase	coa[x] + 3odcoa[x] <=> occoa[x] + accoa[x]	(LOC_Os02g57260 or LOC_Os10g31950)	Fatty acid degradation (Beta oxidation)	2.3.1.16
ACOA120ORx	Lauroyl-CoA:(acceptor) 2,3-oxidoreductase	ddcacoa[x] + fad[x] -> dd2coa[x] + fadh2[x]	(LOC_Os01g06600 or LOC_Os05g07090 or LOC_Os06g01390 or LOC_Os06g23780 or LOC_Os06g23870 or LOC_Os06g24704 or LOC_Os11g39220 or LOC_Os07g47820)	Fatty acid degradation (Beta oxidation)	1.3.3.6;1.3.8.7
ECOAH5x	(S)-3-Hydroxydodecanoyl-CoA hydro-lyase	dd2coa[x] + h2o[x] <=> 3hddcoa[x]	(LOC_Os01g24680 or LOC_Os02g17390)	Fatty acid degradation (Beta oxidation)	4.2.1.17
HACD5x	(S)-3-hydroxydodecanoyl-CoA:NAD oxidoreductase	3hddcoa[x] + nad[x] <=> 3oddcoa[x] + nadh[x] + h[x]	(LOC_Os01g24680 or LOC_Os02g17390)	Fatty acid degradation (Beta oxidation)	1.1.1.35
ACACT5x	Decanoyl-CoA:acetyl-CoA C-acyltransferase	coa[x] + 3oddcoa[x] <=> dcacoa[x] + accoa[x]	(LOC_Os02g57260 or LOC_Os10g31950)	Fatty acid degradation (Beta oxidation)	2.3.1.16
ACOA140ORx	Tetradecanoyl-CoA:(acceptor) 2,3-oxidoreductase	tdcoa[x] + fad[x] -> td2coa[x] + fadh2[x]	(LOC_Os01g06600 or LOC_Os05g07090 or LOC_Os06g01390 or LOC_Os06g23780 or LOC_Os06g23870 or LOC_Os06g24704 or LOC_Os11g39220 or LOC_Os07g47820)	Fatty acid degradation (Beta oxidation)	1.3.3.6;1.3.8.7
ECOAH6x	(S)-3-Hydroxytetradecanoyl-CoA hydro-lyase	td2coa[x] + h2o[x] <=> 3htdcoa[x]	(LOC_Os01g24680 or LOC_Os02g17390)	Fatty acid degradation (Beta oxidation)	4.2.1.17
HACD6x	(S)-3-Hydroxytetradecanoyl-CoA:NAD oxidoreductase	3htdcoa[x] + nad[x] <=> 3otdcoa[x] + nadh[x] + h[x]	(LOC_Os01g24680 or LOC_Os02g17390)	Fatty acid degradation (Beta oxidation)	1.1.1.35
ACACT6x	Lauroyl-CoA:acetyl-CoA C-acyltransferase	coa[x] + 3otdcoa[x] <=> ddcacoa[x] + accoa[x]	(LOC_Os02g57260 or LOC_Os10g31950)	Fatty acid degradation (Beta oxidation)	2.3.1.16
ACOA160ORx	Palmitoyl-CoA:oxygen 2-oxidoreductase	pmtcoa[x] + fad[x] -> hdd2coa[x] + fadh2[x]	(LOC_Os01g06600 or LOC_Os05g07090 or LOC_Os06g01390 or LOC_Os06g23780 or LOC_Os06g23870 or LOC_Os06g24704 or LOC_Os11g39220 or LOC_Os07g47820)	Fatty acid degradation (Beta oxidation)	1.3.3.6;1.3.8.7
ECOAH7x	(S)-3-Hydroxyhexadecanoyl-CoA hydro-lyase	hdd2coa[x] + h2o[x] <=> 3hhdcoa[x]	(LOC_Os01g24680 or LOC_Os02g17390)	Fatty acid degradation (Beta oxidation)	4.2.1.17
HACD7x	(S)-3-Hydroxyhexadecanoyl-CoA:NAD oxidoreductase	3hhdcoa[x] + nad[x] <=> 3ohdcoa[x] + nadh[x] + h[x]	(LOC_Os01g24680 or LOC_Os02g17390)	Fatty acid degradation (Beta oxidation)	1.1.1.35

ACACT7x	myristoyl-CoA:acetylCoA C-myristoyltransferase	coa[x] + 3ohdcoa[x] <=> tdcoa[x] + accoa[x]	(LOC_Os02g57260 or LOC_Os10g31950)	Fatty acid degradation (Beta oxidation)	2.3.1.16
ACOA180ORx	Octadecanoyl-CoA::oxygen 2-oxidoreductase	stcoa[x] + fad[x] -> toctd2ecoa[x] + fadh2[x]	(LOC_Os01g06600 or LOC_Os05g07090 or LOC_Os06g01390 or LOC_Os06g23780 or LOC_Os06g23870 or LOC_Os06g24704 or LOC_Os11g39220 or LOC_Os07g47820)	Fatty acid degradation (Beta oxidation)	1.3.3.6;1.3.8.7
ECOAH8x	(3R)-3-Hydroxyoctadecanoyl-CoA hydro-lyase	toctd2ecoa[x] + h2o[x] <=> 3hoctacoa[x]	(LOC_Os01g24680 or LOC_Os02g17390)	Fatty acid degradation (Beta oxidation)	4.2.1.17
HCAD8x	(3R)-3-Hydroxyoctadecanoyl-CoA:NAD+ oxidoreductase	3hoctacoa[x] + nad[x] <=> 3ooctdcoa[x] + nadh[x] + h[x]	(LOC_Os01g24680 or LOC_Os02g17390)	Fatty acid degradation (Beta oxidation)	1.1.1.35
ACAT8x	HexadecanoylCoA:acetyl-CoA C-acyltransferase	coa[x] + 3ooctdcoa[x] <=> pmtcoa[x] + accoa[x]	(LOC_Os02g57260 or LOC_Os10g31950)	Fatty acid degradation (Beta oxidation)	2.3.1.16
FAOS183yx	fatty acid oxidation saturation (C18)	lnlncoa[x] + nadph[x] + h[x] -> ocdycacoa[x] + nadp[x]		Fatty acid degradation	
FAOS182yx	fatty acid oxidation saturation (C18)	ocdycacoa[x] + nadph[x] + h[x] -> odecoa[x] + nadp[x]		Fatty acid degradation	
FAOS181yx	fatty acid oxidation saturation (C18)	odecoa[x] + nadph[x] + h[x] -> stcoa[x] + nadp[x]		Fatty acid degradation	
FAOS161yx	fatty acid oxidation saturation (C16)	hdcoa[x] + nadph[x] + h[x] -> pmtcoa[x] + nadp[x]		Fatty acid degradation	
FAOS183x	fatty acid oxidation saturation (C18)	lnlncoa[x] + h2o2[x] -> ocdycacoa[x] + o2[x]		Fatty acid degradation	
FAOS182x	fatty acid oxidation saturation (C18)	ocdycacoa[x] + h2o2[x] -> odecoa[x] + o2[x]		Fatty acid degradation	
FAOS181x	fatty acid oxidation saturation (C18)	odecoa[x] + h2o2[x] -> stcoa[x] + o2[x]		Fatty acid degradation	
FAOS161x	fatty acid oxidation saturation (C16)	hdcoa[x] + h2o2[x] -> pmtcoa[x] + o2[x]		Fatty acid degradation	
3OCS60m	3-oxoacyl-CoA synthase (n-C6:0)	coa[m] + 3ohcoa[m] <=> accoa[m] + btcoa[m]	(LOC_Os02g57260 or LOC_Os10g31950)	Fatty acid biosynthesis (elongation in mitochondrion)	2.3.1.16
3OCR60m	3-oxoacyl-CoA reductase (n-C6:0)	3hhcoa[m] + nad[m] <=> 3ohcoa[m] + nadh[m] + h[m]	(LOC_Os01g24680 or LOC_Os02g17390)	Fatty acid biosynthesis (elongation in mitochondrion)	1.1.1.35
3HCD60m	3-hydroxyacyl-CoA dehydratase (n-C6:0)	hx2coa[m] + h2o[m] <=> 3hhcoa[m]	(LOC_Os01g24680 or LOC_Os02g17390)	Fatty acid biosynthesis (elongation in mitochondrion)	4.2.1.17
ECR60ym	enoyl-CoA reductase (NADPH) (n-C6:0)	hx2coa[m] + nadph[m] + h[m] -> hxcoa[m] + nadp[m]	LOC_Os12g01160	Fatty acid biosynthesis (elongation in mitochondrion)	1.1.1.38
3OCS80m	3-oxoacyl-CoA synthase (n-C8:0)	coa[m] + 3oocoa[m] <=> hxcoa[m] + accoa[m]	(LOC_Os02g57260 or LOC_Os10g31950)	Fatty acid biosynthesis (elongation in mitochondrion)	2.3.1.16
3OCR80m	3-oxoacyl-CoA reductase (n-C8:0)	3hocoa[m] + nad[m] <=> 3oocoa[m] + nadh[m] + h[m]	(LOC_Os01g24680 or LOC_Os02g17390)	Fatty acid biosynthesis (elongation in mitochondrion)	1.1.1.35
3HCD80m	3-hydroxyacyl-CoA dehydratase (n-C8:0)	oc2coa[m] + h2o[m] <=> 3hocoa[m]	(LOC_Os01g24680 or LOC_Os02g17390)	Fatty acid biosynthesis (elongation in mitochondrion)	4.2.1.17
ECR80ym	enoyl-CoA reductase (NADPH) (n-C8:0)	oc2coa[m] + nadph[m] + h[m] -> occoa[m] + nadp[m]	LOC_Os12g01160	Fatty acid biosynthesis (elongation in mitochondrion)	1.1.1.38
3OCS100m	3-oxoacyl-CoA synthase (n-C10:0)	coa[m] + 3odcoa[m] <=> occoa[m] + accoa[m]	(LOC_Os02g57260 or LOC_Os10g31950)	Fatty acid biosynthesis (elongation in mitochondrion)	2.3.1.16
3OCR100m	3-oxoacyl-CoA reductase (n-C10:0)	3hdcoa[m] + nad[m] <=> 3odcoa[m] + nadh[m] + h[m]	(LOC_Os01g24680 or LOC_Os02g17390)	Fatty acid biosynthesis (elongation in mitochondrion)	1.1.1.35
3HCD100m	3-hydroxyacyl-CoA dehydratase (n-C10:0)	dc2coa[m] + h2o[m] <=> 3hdcoa[m]	(LOC_Os01g24680 or LOC_Os02g17390)	Fatty acid biosynthesis (elongation in mitochondrion)	4.2.1.17
ECR100ym	enoyl-CoA reductase (NADPH) (n-C10:0)	dc2coa[m] + nadph[m] + h[m] -> dcacoa[m] + nadp[m]	LOC_Os12g01160	Fatty acid biosynthesis (elongation in mitochondrion)	1.1.1.38
3OCS120m	3-oxoacyl-CoA synthase (n-C12:0)	coa[m] + 3oddcoa[m] <=> dcacoa[m] + accoa[m]	(LOC_Os02g57260 or LOC_Os10g31950)	Fatty acid biosynthesis (elongation in mitochondrion)	2.3.1.16
3OCR120m	3-oxoacyl-CoA reductase (n-C12:0)	3hddcoa[m] + nad[m] <=> 3oddcoa[m] + nadh[m] + h[m]	(LOC_Os01g24680 or LOC_Os02g17390)	Fatty acid biosynthesis (elongation in mitochondrion)	1.1.1.35
3HCD120m	3-hydroxyacyl-CoA dehydratase (n-C12:0)	dd2coa[m] + h2o[m] <=> 3hddcoa[m]	(LOC_Os01g24680 or LOC_Os02g17390)	Fatty acid biosynthesis (elongation in mitochondrion)	4.2.1.17
ECR120ym	enoyl-CoA reductase (NADPH) (n-C12:0)	dd2coa[m] + nadph[m] + h[m] -> ddcacoa[m] + nadp[m]	LOC_Os12g01160	Fatty acid biosynthesis (elongation in mitochondrion)	1.1.1.38
3OCS140m	3-oxoacyl-CoA synthase (n-C14:0)	coa[m] + 3otdcoa[m] <=> ddcacoa[m] + accoa[m]	(LOC_Os02g57260 or LOC_Os10g31950)	Fatty acid biosynthesis (elongation in mitochondrion)	2.3.1.16
3OCR140m	3-oxoacyl-CoA reductase (n-C14:0)	3htdcoa[m] + nad[m] <=> 3otdcoa[m] + nadh[m] + h[m]	(LOC_Os01g24680 or LOC_Os02g17390)	Fatty acid biosynthesis	1.1.1.35

				(elongation in mitochondrion)	
3HCD140m	3-hydroxyacyl-CoA dehydratase (n-C14:0)	td2coa[m] + h2o[m] <=> 3htdcoa[m]	(LOC_Os01g24680 or LOC_Os02g17390)	Fatty acid biosynthesis (elongation in mitochondrion)	4.2.1.17
ECR140ym	enoyl-CoA reductase (NADPH) (n-C14:0)	td2coa[m] + nadph[m] + h[m] -> tdcoa[m] + nadp[m]	LOC_Os12g01160	Fatty acid biosynthesis (elongation in mitochondrion)	1.1.1.38
3OCS160m	3-oxoacyl-CoA synthase (n-C16:0)	coa[m] + 3ohdcoa[m] <=> tdcoa[m] + accoa[m]	(LOC_Os02g57260 or LOC_Os10g31950)	Fatty acid biosynthesis (elongation in mitochondrion)	2.3.1.16
3OCR160m	3-oxoacyl-CoA reductase (n-C16:0)	3hhdcoa[m] + nad[m] <=> 3ohdcoa[m] + nadh[m] + h[m]	(LOC_Os01g24680 or LOC_Os02g17390)	Fatty acid biosynthesis (elongation in mitochondrion)	1.1.1.35
3HCD160m	3-hydroxyacyl-CoA dehydratase (n-C16:0)	hdd2coa[m] + h2o[m] <=> 3hhdcoa[m]	(LOC_Os01g24680 or LOC_Os02g17390)	Fatty acid biosynthesis (elongation in mitochondrion)	4.2.1.17
ECR160ym	enoyl-CoA reductase (NADPH) (n-C16:0)	hdd2coa[m] + nadph[m] + h[m] -> pmtcoa[m] + nadp[m]	LOC_Os12g01160	Fatty acid biosynthesis (elongation in mitochondrion)	1.1.1.38
MTE160m	mitochondrial acyl-CoA thioesterase	h2o[m] + pmtcoa[m] -> coa[m] + h[m] + hdca[m]	(LOC_Os03g01150 or LOC_Os10g41340)	Fatty acid degradation	3.1.2.22
MCOATAc	malonyl-CoA:[acyl-carrier-protein] S-malonyltransferase	ACP[c] + malcoa[c] + h[c] <=> coa[c] + malACP[c]	LOC_Os03g18590	Fatty acid biosynthesis	2.3.1.39
MCOATAm	malonyl-CoA:[acyl-carrier-protein] S-malonyltransferase	ACP[m] + malcoa[m] + h[m] <=> coa[m] + malACP[m]	LOC_Os03g18590	Fatty acid biosynthesis (in mitochondrion)	2.3.1.39
ACOATAm	beta-ketoacyl-acyl-carrier-protein synthase III	accoa[m] + ACP[m] -> coa[m] + acACP[m]	LOC_Os02g10320	Fatty acid biosynthesis (in mitochondrion)	2.3.1.41
MACPCLm	malonyl-[acyl-carrier-protein] carboxy-lyase	2 malACP[m] -> 2 co2[m] + actACP[m] + ACP[m]	LOC_Os05g36000	Fatty acid biosynthesis (in mitochondrion)	
3OAR40m	3-oxoacyl-[acyl-carrier-protein] reductase (n-C4:0)	actACP[m] + h[m] + nadph[m] -> 3hbutACP[m] + nadp[m]	(LOC_Os08g23810 or LOC_Os09g10600)	Fatty acid biosynthesis (in mitochondrion)	1.3.1.10
3HAD40m	3-hydroxyacyl-[acyl-carrier-protein] dehydratase (n-C4:0)	3hbutACP[m] -> but2eACP[m] + h2o[m]	LOC_Os02g10320	Fatty acid biosynthesis (in mitochondrion)	2.3.1.41
EAR40ym	enoyl-[acyl-carrier-protein] reductase (NADPH) (n-C4:0)	but2eACP[m] + h[m] + nadph[m] -> butACP[m] + nadp[m]	LOC_Os06g09630	Fatty acid biosynthesis (in mitochondrion)	1.1.1.100
3OAS60m	3-oxoacyl-[acyl-carrier-protein] synthase (n-C6:0)	butACP[m] + h[m] + malACP[m] -> 3ohexACP[m] + ACP[m] + co2[m]	LOC_Os05g36000	Fatty acid biosynthesis (in mitochondrion)	4.2.1.59
3OAR60m	3-oxoacyl-[acyl-carrier-protein] reductase (n-C6:0)	3ohexACP[m] + h[m] + nadph[m] -> 3hhexACP[m] + nadp[m]	(LOC_Os08g23810 or LOC_Os09g10600)	Fatty acid biosynthesis (in mitochondrion)	1.3.1.10
3HAD60m	3-hydroxyacyl-[acyl-carrier-protein] dehydratase (n-C6:0)	3hhexACP[m] -> thex2eACP[m] + h2o[m]	LOC_Os02g10320	Fatty acid biosynthesis (in mitochondrion)	2.3.1.41
EAR60ym	enoyl-[acyl-carrier-protein] reductase (NADPH) (n-C6:0)	thex2eACP[m] + h[m] + nadph[m] -> hexACP[m] + nadp[m]	LOC_Os06g09630	Fatty acid biosynthesis (in mitochondrion)	1.1.1.100
3OAS80m	3-oxoacyl-[acyl-carrier-protein] synthase (n-C8:0)	h[m] + hexACP[m] + malACP[m] -> 3ooctACP[m] + ACP[m] + co2[m]	LOC_Os05g36000	Fatty acid biosynthesis (in mitochondrion)	4.2.1.59
3OAR80m	3-oxoacyl-[acyl-carrier-protein] reductase (n-C8:0)	3ooctACP[m] + h[m] + nadph[m] -> 3hoctACP[m] + nadp[m]	(LOC_Os08g23810 or LOC_Os09g10600)	Fatty acid biosynthesis (in mitochondrion)	1.3.1.10
3HAD80m	3-hydroxyacyl-[acyl-carrier-protein] dehydratase (n-C8:0)	3hoctACP[m] -> toct2eACP[m] + h2o[m]	LOC_Os02g10320	Fatty acid biosynthesis (in mitochondrion)	2.3.1.41
EAR80ym	enoyl-[acyl-carrier-protein] reductase (NADPH) (n-C8:0)	toct2eACP[m] + h[m] + nadph[m] -> nadp[m] + ocACP[m]	LOC_Os06g09630	Fatty acid biosynthesis (in mitochondrion)	1.1.1.100
3OAS100m	3-oxoacyl-[acyl-carrier-protein] synthase (n-C10:0)	h[m] + malACP[m] + ocACP[m] -> 3odecACP[m] + ACP[m] + co2[m]	LOC_Os05g36000	Fatty acid biosynthesis (in mitochondrion)	4.2.1.59
3OAR100m	3-oxoacyl-[acyl-carrier-protein] reductase (n-C10:0)	3odecACP[m] + h[m] + nadph[m] -> 3hdecACP[m] + nadp[m]	(LOC_Os08g23810 or LOC_Os09g10600)	Fatty acid biosynthesis (in mitochondrion)	1.3.1.10
3HAD100m	3-hydroxyacyl-[acyl-carrier-protein] dehydratase (n-C10:0)	3hdecACP[m] -> tdec2eACP[m] + h2o[m]	LOC_Os02g10320	Fatty acid biosynthesis (in mitochondrion)	2.3.1.41
EAR100ym	enoyl-[acyl-carrier-protein] reductase (NADPH) (n-C10:0)	tdec2eACP[m] + h[m] + nadph[m] -> dcaACP[m] + nadp[m]	LOC_Os06g09630	Fatty acid biosynthesis (in mitochondrion)	1.1.1.100
3OAS120m	3-oxoacyl-[acyl-carrier-protein] synthase (n-C12:0)	dcaACP[m] + h[m] + malACP[m] -> 3oddecACP[m] + ACP[m] + co2[m]	LOC_Os05g36000	Fatty acid biosynthesis (in mitochondrion)	4.2.1.59
3OAR120m	3-oxoacyl-[acyl-carrier-protein] reductase (n-C12:0)	3oddecACP[m] + h[m] + nadph[m] -> 3hddecACP[m] + nadp[m]	(LOC_Os08g23810 or LOC_Os09g10600)	Fatty acid biosynthesis (in mitochondrion)	1.3.1.10

3HAD120m	3-hydroxyacyl-[acyl-carrier-protein] dehydratase (n-C12:0)	3hddecACP[m] -> tddec2eACP[m] + h2o[m]	LOC_Os02g10320	Fatty acid biosynthesis (in mitochondrion)	2.3.1.41
EAR120ym	enoyl-[acyl-carrier-protein] reductase (NADPH) (n-C12:0)	tddec2eACP[m] + h[m] + nadph[m] -> ddcaACP[m] + nadp[m]	LOC_Os06g09630	Fatty acid biosynthesis (in mitochondrion)	1.1.1.100
3OAS140m	3-oxoacyl-[acyl-carrier-protein] synthase (n-C14:0)	ddcaACP[m] + h[m] + malACP[m] -> 3omrsACP[m] + ACP[m] + co2[m]	LOC_Os05g36000	Fatty acid biosynthesis (in mitochondrion)	4.2.1.59
3OAR140m	3-oxoacyl-[acyl-carrier-protein] reductase (n-C14:0)	3omrsACP[m] + h[m] + nadph[m] -> 3hmrsACP[m] + nadp[m]	(LOC_Os08g23810 or LOC_Os09g10600)	Fatty acid biosynthesis (in mitochondrion)	1.3.1.10
3HAD140m	3-hydroxyacyl-[acyl-carrier-protein] dehydratase (n-C14:0)	3hmrsACP[m] -> h2o[m] + tmrs2eACP[m]	LOC_Os02g10320	Fatty acid biosynthesis (in mitochondrion)	2.3.1.41
EAR140ym	enoyl-[acyl-carrier-protein] reductase (NADPH) (n-C14:0)	h[m] + nadph[m] + tmrs2eACP[m] -> myrsACP[m] + nadp[m]	LOC_Os06g09630	Fatty acid biosynthesis (in mitochondrion)	1.1.1.100
3OAS160m	3-oxoacyl-[acyl-carrier-protein] synthase (n-C16:0)	h[m] + malACP[m] + myrsACP[m] -> 3opalmACP[m] + ACP[m] + co2[m]	LOC_Os05g36000	Fatty acid biosynthesis (in mitochondrion)	4.2.1.59
3OAR160m	3-oxoacyl-[acyl-carrier-protein] reductase (n-C16:0)	3opalmACP[m] + h[m] + nadph[m] -> 3hpalmACP[m] + nadp[m]	(LOC_Os08g23810 or LOC_Os09g10600)	Fatty acid biosynthesis (in mitochondrion)	1.3.1.10
3HAD160m	3-hydroxyacyl-[acyl-carrier-protein] dehydratase (n-C16:0)	3hpalmACP[m] -> h2o[m] + tpalm2eACP[m]	LOC_Os02g10320	Fatty acid biosynthesis (in mitochondrion)	2.3.1.41
EAR160ym	enoyl-[acyl-carrier-protein] reductase (NADPH) (n-C16:0)	h[m] + tpalm2eACP[m] + nadph[m] -> nadp[m] + palmACP[m]	LOC_Os06g09630	Fatty acid biosynthesis (in mitochondrion)	1.1.1.100
3OAS180m	3-oxoacyl-[acyl-carrier-protein] synthase (n-C18:0)	h[m] + malACP[m] + palmACP[m] -> 3ooctdACP[m] + ACP[m] + co2[m]	LOC_Os05g36000	Fatty acid biosynthesis (in mitochondrion)	4.2.1.59
3OAR180m	3-oxoacyl-[acyl-carrier-protein] reductase (n-C18:0)	3ooctdACP[m] + h[m] + nadph[m] -> 3hoctaACP[m] + nadp[m]	(LOC_Os08g23810 or LOC_Os09g10600)	Fatty acid biosynthesis (in mitochondrion)	1.3.1.10
3HAD180m	3-hydroxyacyl-[acyl-carrier-protein] dehydratase (n-C18:0)	3hoctaACP[m] -> toctd2eACP[m] + h2o[m]	LOC_Os02g10320	Fatty acid biosynthesis (in mitochondrion)	2.3.1.41
EAR180ym	enoyl-[acyl-carrier-protein] reductase (NADPH) (n-C18:0)	toctd2eACP[m] + h[m] + nadph[m] -> nadp[m] + ocdcaACP[m]	LOC_Os06g09630	Fatty acid biosynthesis (in mitochondrion)	1.1.1.100
FAS161ACP_Lm	fatty acyl-ACP synthase (n-C16:1ACP)	palmACP[m] + o2[m] + nadph[m] -> 2 h2o[m] + hdeACP[m] + nadp[m]	(LOC_Os01g65830 or LOC_Os01g69080 or LOC_Os02g30200 or LOC_Os03g30950 or LOC_Os04g31070 or LOC_Os08g09950 or LOC_Os08g10010)	Fatty acid biosynthesis (in mitochondrion)	1.14.19.2
FAS181ACP_Lm	fatty acyl-ACP synthase (n-C18:1ACP)	ocdcaACP[m] + o2[m] + nadph[m] -> 2 h2o[m] + octeACP[m] + nadp[m]	(LOC_Os01g65830 or LOC_Os01g69080 or LOC_Os02g30200 or LOC_Os03g30950 or LOC_Os04g31070 or LOC_Os08g09950 or LOC_Os08g10010)	Fatty acid biosynthesis (in mitochondrion)	1.14.19.2
FAS182ACP_Lm	fatty acyl-ACP synthase (n-C18:2ACP)	octeACP[m] + o2[m] + nadph[m] -> 2 h2o[m] + ocdcyaACP[m] + nadp[m]	(LOC_Os01g65830 or LOC_Os01g69080 or LOC_Os02g30200 or LOC_Os03g30950 or LOC_Os04g31070 or LOC_Os08g09950 or LOC_Os08g10010)	Fatty acid biosynthesis (in mitochondrion)	1.14.19.2
FAS183ACP_Lm	fatty acyl-ACP synthase (n-C18:3ACP)	ocdcyaACP[m] + o2[m] + nadph[m] -> 2 h2o[m] + lnlnlACP[m] + nadp[m]	(LOC_Os01g65830 or LOC_Os01g69080 or LOC_Os02g30200 or LOC_Os03g30950 or LOC_Os04g31070 or LOC_Os08g09950 or LOC_Os08g10010)	Fatty acid biosynthesis (in mitochondrion)	1.14.19.2
G3PDc	glycerol-3-phosphate dehydrogenase	glyc3p[m] + q8[m] <=> dhap[m] + q8h2[m]	LOC_Os04g14790	Glycerolipid and Glycerophospholipid metabolism	1.1.5.3
GLYCKr	Glycerol kinase, cytosolic	atp[c] + glyc[c] -> adp[c] + glyc3p[c] + h[c]	LOC_Os04g55410	Glycerolipid and Glycerophospholipid metabolism	2.7.1.30
GLYCKs	Glycerol kinase, plastidic	atp[s] + glyc[s] -> adp[s] + glyc3p[s] + h[s]	LOC_Os02g08130	Glycerolipid and Glycerophospholipid metabolism	2.7.1.30
GLYCKm	Glycerol kinase, mitochondrial	atp[m] + glyc[m] -> adp[m] + glyc3p[m] + h[m]		Glycerolipid and Glycerophospholipid metabolism	2.7.1.30

G3PDNc	glycerol-3-phosphate dehydrogenase (NAD+)	glyc3p[c] + nad[c] <=> dhap[c] + nadh[c] + h[c]	LOC_Os01g74000	Glycerolipid and Glycerophospholipid metabolism	1.1.1.8/1.1.1.94
G3PATr	Glycerol-3-phosphate O-acyltransferase, endoplasmic reticular	acylcoa_os[r] + glyc3p[r] -> 1ag3p_os[r] + coa[r]	(LOC_Os01g22560 or LOC_Os07g34730 or LOC_Os11g45400)	Glycerolipid and Glycerophospholipid metabolism	2.3.1.15
G3PATs	Glycerol-3-phosphate O-acyltransferase, plastidic	ACP_os[s] + glyc3p[s] -> 1ag3p_os[s] + ACP[s]	LOC_Os10g42720	Glycerolipid and Glycerophospholipid metabolism	2.3.1.15
G3PATm	Glycerol-3-phosphate O-acyltransferase, mitochondrial	ACP_os[m] + glyc3p[m] -> 1ag3p_os[m] + ACP[m]	(LOC_Os01g22560 or LOC_Os01g44069 or LOC_Os05g38350 or LOC_Os11g45400)	Glycerolipid and Glycerophospholipid metabolism	2.3.1.15
AGPATr	1-acylglycerol-3-phosphate O-acyltransferase, endoplasmic reticular	acylcoa_os[r] + 1ag3p_os[r] -> pa_os[r] + coa[r]	(LOC_Os11g41900 or LOC_Os01g57360 or LOC_Os07g34730 or LOC_Os11g45400 or LOC_Os05g28960 or LOC_Os01g63580 or LOC_Os05g37600 or LOC_Os10g35390 or LOC_Os05g42270 or LOC_Os06g49790 or LOC_Os04g32010 or LOC_Os03g53650)	Glycerolipid and Glycerophospholipid metabolism	2.3.1.51
AGPATs	1-acylglycerol-3-phosphate O-acyltransferase, plastidic	ACP_os[s] + 1ag3p_os[s] -> pa_os[s] + ACP[s]	(LOC_Os11g41900 or LOC_Os01g70570 or LOC_Os05g38350 or LOC_Os01g57360 or LOC_Os07g34730 or LOC_Os11g45400 or LOC_Os05g28960 or LOC_Os01g63580 or LOC_Os05g37600 or LOC_Os10g35390 or LOC_Os05g42270 or LOC_Os02g02340 or LOC_Os06g49790 or LOC_Os04g32010 or LOC_Os03g53650 or LOC_Os04g57150)	Glycerolipid and Glycerophospholipid metabolism	2.3.1.51
AGPATm	1-acylglycerol-3-phosphate O-acyltransferase, mitochondrial	ACP_os[m] + 1ag3p_os[m] -> pa_os[m] + ACP[m]	(LOC_Os11g41900 or LOC_Os01g70570 or LOC_Os05g38350 or LOC_Os01g57360 or LOC_Os07g34730 or LOC_Os11g45400 or LOC_Os05g28960 or LOC_Os01g63580 or LOC_Os05g37600 or LOC_Os10g35390 or LOC_Os05g42270 or LOC_Os02g02340 or LOC_Os06g49790 or LOC_Os04g32010 or LOC_Os03g53650 or LOC_Os04g57150)	Glycerolipid and Glycerophospholipid metabolism	2.3.1.51
PAPAr	Phosphatidate phosphatase, endoplasmic reticular	pa_os[r] + h2o[r] -> 12dgr_os[r] + pi[r]	(LOC_Os09g13870 or LOC_Os01g47580 or LOC_Os08g27040 or LOC_Os01g04660 or LOC_Os05g47660 or LOC_Os08g27030 or LOC_Os01g49820)	Glycerolipid and Glycerophospholipid metabolism	3.1.3.4
PAPAs	Phosphatidate phosphatase, plastidic	pa_os[s] + h2o[s] -> 12dgr_os[s] + pi[s]	(LOC_Os09g13870 or LOC_Os01g47580 or LOC_Os08g27040 or LOC_Os01g04660 or LOC_Os05g47660 or LOC_Os08g27030 or LOC_Os01g49820)	Glycerolipid and Glycerophospholipid metabolism	3.1.3.4
PAPAm	Phosphatidate phosphatase, mitochondrial	pa_os[m] + h2o[m] -> 12dgr_os[m] + pi[m]	(LOC_Os09g13870 or LOC_Os01g47580 or LOC_Os08g27040 or LOC_Os01g04660 or LOC_Os05g47660 or LOC_Os08g27030 or LOC_Os01g49820)	Glycerolipid and Glycerophospholipid metabolism	3.1.3.4
DAGKm	diacylglycerol kinase (ATP dependent), mitochondrial	atp[m] + 12dgr_os[m] -> adp[m] + pa_os[m] + h[m]	(LOC_Os08g05650 or LOC_Os07g37580 or LOC_Os03g03400 or LOC_Os01g57350 or LOC_Os10g37280 or LOC_Os08g08110 or LOC_Os04g54200 or LOC_Os04g45800 or LOC_Os02g54650 or LOC_Os01g57420 or LOC_Os12g38780 or LOC_Os12g12260 or LOC_Os12g12260 or LOC_Os03g31180 or LOC_Os02g43906 or	Glycerolipid and Glycerophospholipid metabolism	2.7.1.107

			LOC_Os08g15090)		
DAGACTr	diacylglycerol O-acyltransferase, endoplasmic reticular	acylcoa_os[r] + 12dgr_os[r] -> triglyc_os[r] + coa[r]	(LOC_Os05g10810 or LOC_Os06g36800)	Glycerolipid and Glycerophospholipid metabolism	2.3.1.20
TAGLc	triacylglycerol lipase	triglyc_os[c] + h2o[c] -> fa_os[c] + 12dgr_os[c] + h[c]	(LOC_Os01g55650 or LOC_Os03g59620)	Glycerolipid and Glycerophospholipid metabolism	3.1.1.3
DAGLc	diacylglycerol lipase	12dgr_os[c] + h2o[c] -> fa_os[c] + mgr_os[c] + h[c]	(LOC_Os01g55650 or LOC_Os03g59620)	Glycerolipid and Glycerophospholipid metabolism	3.1.1.3
MAGLc	monoacylglycerol lipase	mgr_os[c] + h2o[c] -> fa_os[c] + glyc[c] + h[c]	LOC_Os12g01030	Glycerolipid and Glycerophospholipid metabolism	3.1.1.23
CDPDAGSr	phosphatidate cytidylyltransferase, endoplasmic reticular	ctp[r] + h[r] + pa_os[r] <=> cdpdag_os[r] + ppi[r]	(LOC_Os04g56920 or LOC_Os11g07440 or LOC_Os02g01590 or LOC_Os01g73580 or LOC_Os03g20020 or LOC_Os02g34560 or LOC_Os04g45290 or LOC_Os02g03320 or LOC_Os01g22900 or LOC_Os02g33110)	Glycerolipid and Glycerophospholipid metabolism	2.7.7.41
CDPDAGSm	phosphatidate cytidylyltransferase, mitochondrial	ctp[m] + h[m] + pa_os[m] <=> cdpdag_os[m] + ppi[m]	(LOC_Os04g56920 or LOC_Os11g07440 or LOC_Os02g01590 or LOC_Os01g73580 or LOC_Os03g20020 or LOC_Os02g34560 or LOC_Os04g45290 or LOC_Os02g03320 or LOC_Os01g22900 or LOC_Os02g33110)	Glycerolipid and Glycerophospholipid metabolism	2.7.7.41
CDIPTr	phosphatidylinositol synthase, endoplasmic reticular	cdpdag_os[r] + inost[r] -> cmp[r] + ptd1ino_os[r] + h[r]	(LOC_Os06g29650 or LOC_Os02g03110)	Glycerolipid and Glycerophospholipid metabolism	2.7.8.11
PGPSr	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase, endoplasmic reticular	cdpdag_os[r] + glyc3p[r] -> cmp[r] + pgp_os[r] + h[r]	(LOC_Os03g17520 or LOC_Os01g57930)	Glycerolipid and Glycerophospholipid metabolism	2.7.8.5
PGPSm	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase, mitochondrial	cdpdag_os[m] + glyc3p[m] -> cmp[m] + pgp_os[m] + h[m]	(LOC_Os03g17520 or LOC_Os01g57930)	Glycerolipid and Glycerophospholipid metabolism	2.7.8.5
PGPPm	Phosphatidylglycerophosphatase, mitochondrial	h2o[m] + pgp_os[m] -> pg_os[m] + pi[m]	LOC_Os04g41340	Glycerolipid and Glycerophospholipid metabolism	3.1.3.27
CLPNSm	cardiolipin synthase, mitochondrial	cdpdag_os[m] + pg_os[m] -> clpn_os[m] + cmp[m] + h[m]	LOC_Os01g57930	Glycerolipid and Glycerophospholipid metabolism	2.7.8.-
PSSr	phosphatidylserine synthase, endoplasmic reticular	cdpdag_os[r] + ser-L[r] <=> cmp[r] + h[r] + ps_os[r]	(LOC_Os01g49024 or LOC_Os01g66900 or LOC_Os04g41810 or LOC_Os01g67030)	Glycerolipid and Glycerophospholipid metabolism	2.7.8.8
PSSm	phosphatidylserine synthase, mitochondrial	cdpdag_os[m] + ser-L[m] <=> cmp[m] + h[m] + ps_os[m]	(LOC_Os01g49024 or LOC_Os01g66900 or LOC_Os04g41810 or LOC_Os01g67030)	Glycerolipid and Glycerophospholipid metabolism	2.7.8.8
PEDCr	phosphatidylserine decarboxylase, endoplasmic reticular	h[r] + ps_os[r] -> co2[r] + pe_os[r]	(LOC_Os01g72940 or LOC_Os03g01216)	Glycerolipid and Glycerophospholipid metabolism	4.1.1.65
PEDCm	phosphatidylserine decarboxylase, mitochondrial	h[m] + ps_os[m] -> co2[m] + pe_os[m]	(LOC_Os01g72940 or LOC_Os03g01216)	Glycerolipid and Glycerophospholipid metabolism	4.1.1.65
ETHAPTr	Ethanolaminephosphotransferase, endoplasmic reticular	12dgr_os[r] + cdpea[r] <=> cmp[r] + h[r] + pe_os[r]	LOC_Os02g02750	Glycerolipid and Glycerophospholipid metabolism	2.7.8.1
PETHACTr	phosphoethanolamine cytidyltransferase	ctp[r] + ethamp[r] + h[r] -> cdpea[r] + ppi[r]	(LOC_Os12g02820 or LOC_Os11g03050)	Glycerolipid and	2.7.7.14

				Glycerophospholipid metabolism	
ETHAKr	Ethanolamine kinase, endoplasmic reticular	atp[r] + etha[r] -> adp[r] + ethamp[r] + h[r]	LOC_Os09g26700	Glycerolipid and Glycerophospholipid metabolism	2.7.1.82
ETHAKs	Ethanolamine kinase, plastidic	atp[s] + etha[s] -> adp[s] + ethamp[s] + h[s]	LOC_Os09g26700	Glycerolipid and Glycerophospholipid metabolism	2.7.1.82
SERDCr	serine decarboxylase, endoplasmic reticular	ser-L[r] + h[r] <=> etha[r] + co2[r]	LOC_Os02g33710	Glycerolipid and Glycerophospholipid metabolism	4.1.1.-
SERDCs	serine decarboxylase, plastidic	ser-L[s] + h[s] <=> etha[s] + co2[s]	LOC_Os02g33710	Glycerolipid and Glycerophospholipid metabolism	4.1.1.-
PETHAMTr	phosphoethanolamine N-methyltransferase , endoplasmic reticular	ethamp[r] + 3 amet[r] -> 3 ahcys[r] + 3 h[r] + cholp[r]	LOC_Os01g50030	Glycerolipid and Glycerophospholipid metabolism	2.1.1.103
PETHAMTs	phosphoethanolamine N-methyltransferase, plastidic	ethamp[s] + 3 amet[s] -> 3 ahcys[s] + 3 h[s] + cholp[s]	LOC_Os01g50030	Glycerolipid and Glycerophospholipid metabolism	2.1.1.103
CHOLKr	choline kinase, endoplasmic reticular	chol[r] + atp[r] -> cholp[r] + adp[r] + h[r]	(LOC_Os05g45880 or LOC_Os01g51920 or LOC_Os01g08760)	Glycerolipid and Glycerophospholipid metabolism	2.7.1.32
CHOLKs	choline kinase, plastidic	chol[s] + atp[s] -> cholp[s] + adp[s] + h[s]	(LOC_Os05g45880 or LOC_Os01g51920 or LOC_Os01g08760)	Glycerolipid and Glycerophospholipid metabolism	2.7.1.32
PCHOLPPr	phocholine phosphatase, endoplasmic reticular	cholp[r] + h2o[r] -> chol[r] + pi[r]	LOC_Os01g52230	Glycerolipid and Glycerophospholipid metabolism	3.1.3.75
PCHOLPPs	phocholine phosphatase, plastidic	cholp[s] + h2o[s] -> chol[s] + pi[s]	LOC_Os01g52230	Glycerolipid and Glycerophospholipid metabolism	3.1.3.75
CHOLPCTr	choline phosphate cytididyltransferase, endoplasmic reticular	cholp[r] + ctp[r] + h[r] -> cdpchol[r] + ppi[r]	LOC_Os02g07720	Glycerolipid and Glycerophospholipid metabolism	2.7.7.15
CHOLPCTs	choline phosphate cytididyltransferase, plastidic	cholp[s] + ctp[s] + h[s] -> cdpchol[s] + ppi[s]	LOC_Os02g07720	Glycerolipid and Glycerophospholipid metabolism	2.7.7.15
DAGCPr	diacylglycerol cholinephosphotransferase, endoplasmic reticular	12dgr_os[r] + cdpchol[r] -> cmp[r] + h[r] + pc_os[r]	LOC_Os02g02750	Glycerolipid and Glycerophospholipid metabolism	2.7.8.2
DAGCPs	diacylglycerol cholinephosphotransferase, plastidic	12dgr_os[s] + cdpchol[s] -> cmp[s] + h[s] + pc_os[s]	LOC_Os02g02750	Glycerolipid and Glycerophospholipid metabolism	2.7.8.2
PLCr	Phospholipase C	pc_os[r] + h2o[r] -> chol[r] + 12dgr_os[r] + h[r]	(LOC_Os12g37560 or LOC_Os09g02729 or LOC_Os08g01310 or LOC_Os07g49330 or LOC_Os05g03610 or LOC_Os04g35100 or LOC_Os03g18010)	Glycerolipid and Glycerophospholipid metabolism	3.1.4.3
PLAr	Phospholipase A	pc_os[r] + h2o[r] -> 1agpc_os[r] + fa_os[r] + h[r]	(LOC_Os05g51520 or LOC_Os02g58500 or LOC_Os01g09220 or LOC_Os11g34440 or LOC_Os05g09150 or LOC_Os05g09240 or LOC_Os05g09280 or LOC_Os03g50030)	Glycerolipid and Glycerophospholipid metabolism	3.1.1.4
LPPr	Lysophospholipase	1agpc_os[r] + h2o[r] -> g3pc[r] + fa_os[r] + h[r]	(LOC_Os06g44060 or LOC_Os01g21580 or LOC_Os01g21560 or LOC_Os01g20860)	Glycerolipid and Glycerophospholipid metabolism	3.1.1.5

GPEPEr	Glycerophosphodiester phosphodiesterase (Glycerophosphocholine)	g3pc[r] + h2o[r] -> chol[r] + glyc3p[r] + h[r]	(LOC_Os09g17000 or LOC_Os07g41150 or LOC_Os04g32320 or LOC_Os08g42390 or LOC_Os11g12800 or LOC_Os08g39350 or LOC_Os12g27102 or LOC_Os02g09450 or LOC_Os02g31030 or LOC_Os02g37590 or LOC_Os01g55780 or LOC_Os04g39610 or LOC_Os03g40670)	Glycerolipid and Glycerophospholipid metabolism	3.1.4.46
MGDGSs	monogalactosyldiacylglycerol synthase	udpgal[s] + 12dgr_os[s] -> udp[s] + mgdg_os[s]	(LOC_Os02g55910 or LOC_Os08g20420 or LOC_Os09g25580)	Glycerolipid and Glycerophospholipid metabolism	2.4.1.46
DGDGSs	digalactosyldiacylglycerol synthase	udpgal[s] + mgdg_os[s] -> dgdg_os[s] + udp[s]	(LOC_Os02g33580 or LOC_Os03g11560 or LOC_Os03g16140 or LOC_Os04g34000)	Glycerolipid and Glycerophospholipid metabolism	2.4.1.141
SQTs	sulfoquinovosyltransferase	udpsq[s] + 12dgr_os[s] -> udp[s] + sq12dgr_os[s]	(LOC_Os01g04920 or LOC_Os03g15840)	Glycerolipid and Glycerophospholipid metabolism	2.4.1.-
UDPSQSs	UDP-sulfoquinovose synthase	udpg[s] + hso3[s] -> udpsq[s] + h2o[s]	LOC_Os05g32140	Glycerolipid and Glycerophospholipid metabolism	3.13.1.1
LNL9LOs	linolenate 9-lipoxygenase	o2[s] + lnlnl[s] -> 9-hpot[s]	(LOC_Os12g26290 or LOC_Os12g37260 or LOC_Os12g37320 or LOC_Os12g37350 or LOC_Os11g36719 or LOC_Os08g39840 or LOC_Os08g39850 or LOC_Os05g23880 or LOC_Os04g37430 or LOC_Os03g08220 or LOC_Os03g49260 or LOC_Os03g49350 or LOC_Os03g49380 or LOC_Os03g52860 or LOC_Os02g10120)	Phytohormones biosynthesis (Jasmonic acid)	1.13.11.12
OCDCYA9LOs	linoleate 9-lipoxygenase	o2[s] + ocdcya[s] -> 9-hpod[s]	(LOC_Os12g26290 or LOC_Os12g37260 or LOC_Os12g37320 or LOC_Os12g37350 or LOC_Os11g36719 or LOC_Os08g39840 or LOC_Os08g39850 or LOC_Os05g23880 or LOC_Os04g37430 or LOC_Os03g08220 or LOC_Os03g49260 or LOC_Os03g49350 or LOC_Os03g49380 or LOC_Os03g52860 or LOC_Os02g10120)	Phytohormones biosynthesis (Jasmonic acid)	1.13.11.-
LNL13LOs	linolenate 13-lipoxygenase	o2[s] + lnlnl[s] -> 13-hpot[s]	(LOC_Os12g26290 or LOC_Os12g37260 or LOC_Os12g37320 or LOC_Os12g37350 or LOC_Os11g36719 or LOC_Os08g39840 or LOC_Os08g39850 or LOC_Os05g23880 or LOC_Os04g37430 or LOC_Os03g08220 or LOC_Os03g49260 or LOC_Os03g49350 or LOC_Os03g49380 or LOC_Os03g52860 or LOC_Os02g10120)	Phytohormones biosynthesis (Jasmonic acid)	1.13.11.12
OCDCYA13LOs	linoleate 13-lipoxygenase	o2[s] + ocdcya[s] -> 13-hpod[s]	(LOC_Os12g26290 or LOC_Os12g37260 or LOC_Os12g37320 or LOC_Os12g37350 or LOC_Os11g36719 or LOC_Os08g39840 or LOC_Os08g39850 or LOC_Os05g23880 or LOC_Os04g37430 or LOC_Os03g08220 or LOC_Os03g49260 or LOC_Os03g49350 or LOC_Os03g49380 or LOC_Os03g52860 or LOC_Os02g10120)	Phytohormones biosynthesis (Jasmonic acid)	1.13.11.-
LNL9HPLs	linolenate 9-hydroperoxide lyase	9-hpot[s] -> 3-non[s] + 9-nonan[s]	(LOC_Os03g12500 or LOC_Os03g55800 or LOC_Os02g12690 or LOC_Os02g12680 or LOC_Os02g02000)	Phytohormones biosynthesis (Jasmonic acid)	
OCDCYA9HPLs	linoleate 9-hydroperoxide lyase	9-hpod[s] -> 3-nond[s] + 9-nonan[s]	(LOC_Os03g12500 or LOC_Os03g55800 or LOC_Os02g12690 or LOC_Os02g12680 or LOC_Os02g02000)	Phytohormones biosynthesis (Jasmonic acid)	

LNL13HPLs	linolenate 13-hydroperoxide lyase	13-hpot[s] -> hxnl[s] + 12o9dd[s]	(LOC_Os03g12500 or LOC_Os03g55800 or LOC_Os02g12690 or LOC_Os02g12680 or LOC_Os02g02000)	Phytohormones biosynthesis (Jasmonic acid)	
OCDCYA13HPLs	linoleate 13-hydroperoxide lyase	13-hpod[s] -> hxndl[s] + 12o9dd[s]	(LOC_Os03g12500 or LOC_Os03g55800 or LOC_Os02g12690 or LOC_Os02g12680 or LOC_Os02g02000)	Phytohormones biosynthesis (Jasmonic acid)	
HPDHs	hydroperoxide dehydratase	13-hpot[s] -> h2o[s] + 1213s-epoxlin[s]	LOC_Os03g55800	Phytohormones biosynthesis (Jasmonic acid)	4.2.1.92
ALOCs	allene-oxide cyclase	1213s-epoxlin[s] -> 12oxophyt[s]	LOC_Os03g32314	Phytohormones biosynthesis (Jasmonic acid)	5.3.99.6
OPRx	12-oxophytodienoate reductase	nadph[x] + 12oxophyt[x] + h[x] -> nadp[x] + 3o2c2poct[x]	(LOC_Os06g11290 or LOC_Os08g35740 or LOC_Os06g11280 or LOC_Os02g35310 or LOC_Os06g11200 or LOC_Os06g11240 or LOC_Os06g11210)	Phytohormones biosynthesis (Jasmonic acid)	1.3.1.42
3OOPCOALx	3-oxo-2-(2-[Z]-pentenyl)cyclopentane-1-octanoate CoA ligase	3o2c2poct[x] + atp[x] + coa[x] -> opc8coa[x] + amp[x] + ppi[x]	LOC_Os01g67530	Phytohormones biosynthesis (Jasmonic acid)	6.2.1.-
OPC8ACOx	OPC8 acyl-CoA oxidase	opc8coa[x] + o2[x] -> ocp8t2ecoa[x] + h2o2[x]	(LOC_Os06g23780 or LOC_Os01g06600 or LOC_Os11g39220 or LOC_Os06g01390 or LOC_Os06g24704 or LOC_Os05g07090 or LOC_Os06g23870 or LOC_Os06g23760)	Phytohormones biosynthesis (Jasmonic acid)	1.3.3.6
OPC8T2ECHx	OPC8-trans-2-enoyl-CoA hydratase	ocp8t2ecoa[x] + h2o[x] <=> opc8hacoa[x]	(LOC_Os02g43720 or LOC_Os05g29880 or LOC_Os02g17390 or LOC_Os05g06300 or LOC_Os02g43710 or LOC_Os01g24680 or LOC_Os01g70090)	Phytohormones biosynthesis (Jasmonic acid)	4.2.1.17
OPC8HACDHx	OPC8-3-hydroxyacyl-CoA dehydrogenase	opc8hacoa[x] + nad[x] -> oopc8coa[x] + nadh[x] + h[x]	(LOC_Os01g24680 or LOC_Os02g17390)	Phytohormones biosynthesis (Jasmonic acid)	1.1.1.35
OOPC8CTx	OPC8-3-ketoacyl-CoA thiolase	oopc8coa[x] + coa[x] -> accoa[x] + opc6coa[x]	(LOC_Os10g31950 or LOC_Os02g57260)	Phytohormones biosynthesis (Jasmonic acid)	2.3.1.16
OPC6ACOx	OPC6 acyl-CoA oxidase	opc6coa[x] + o2[x] -> ocp6t2ecoa[x] + h2o2[x]	(LOC_Os06g23780 or LOC_Os01g06600 or LOC_Os11g39220 or LOC_Os06g01390 or LOC_Os06g24704 or LOC_Os05g07090 or LOC_Os06g23870 or LOC_Os06g23760)	Phytohormones biosynthesis (Jasmonic acid)	1.3.3.6
OPC6T2ECHx	OPC6-trans-2-enoyl-CoA hydratase	ocp6t2ecoa[x] + h2o[x] <=> opc6hacoa[x]	(LOC_Os02g43720 or LOC_Os05g29880 or LOC_Os02g17390 or LOC_Os05g06300 or LOC_Os02g43710 or LOC_Os01g24680 or LOC_Os01g70090)	Phytohormones biosynthesis (Jasmonic acid)	4.2.1.17
OPC6HACDHx	OPC6-3-hydroxyacyl-CoA dehydrogenase	opc6hacoa[x] + nad[x] -> oopc6coa[x] + nadh[x] + h[x]	(LOC_Os01g24680 or LOC_Os02g17390)	Phytohormones biosynthesis (Jasmonic acid)	1.1.1.35
OOPC6CTx	OPC6-3-ketoacyl-CoA thiolase	oopc6coa[x] + coa[x] -> accoa[x] + opc4coa[x]	(LOC_Os10g31950 or LOC_Os02g57260)	Phytohormones biosynthesis (Jasmonic acid)	2.3.1.16
OPC4ACOx	OPC4 acyl-CoA oxidase	opc4coa[x] + o2[x] -> ocp4t2ecoa[x] + h2o2[x]	(LOC_Os06g23780 or LOC_Os01g06600 or LOC_Os11g39220 or LOC_Os06g01390 or LOC_Os06g24704 or LOC_Os05g07090 or LOC_Os06g23870 or LOC_Os06g23760)	Phytohormones biosynthesis (Jasmonic acid)	1.3.3.6
OPC4T2ECHx	OPC4-trans-2-enoyl-CoA hydratase	ocp4t2ecoa[x] + h2o[x] <=> opc4hacoa[x]	(LOC_Os02g43720 or LOC_Os05g29880 or LOC_Os02g17390 or LOC_Os05g06300 or LOC_Os02g43710 or LOC_Os01g24680 or LOC_Os01g70090)	Phytohormones biosynthesis (Jasmonic acid)	4.2.1.17
OPC4HACDHx	OPC4-3-hydroxyacyl-CoA dehydrogenase	opc4hacoa[x] + nad[x] -> oopc4coa[x] + nadh[x] + h[x]	(LOC_Os01g24680 or LOC_Os02g17390)	Phytohormones biosynthesis (Jasmonic acid)	1.1.1.35
OOPC4CTx	OPC4-3-ketoacyl-CoA thiolase	oopc4coa[x] + coa[x] -> accoa[x] + jascoa[x]	(LOC_Os10g31950 or LOC_Os02g57260)	Phytohormones biosynthesis (Jasmonic acid)	2.3.1.16
JASCHc	jasmonate coa hydrolase	jascoa[x] + h2o[x] -> coa[x] + h[x] + 7ijas[x]	LOC_Os09g34190	Phytohormones biosynthesis	3.1.2.20

				(Jasmonic acid)	
JASIc	jasmonate synthase, spontaneous	7ijas[x] <=> jas[x]		Phytohormones biosynthesis (Jasmonic acid)	Spontaneous
AMETJASMTc	S-adenosyl-L-methionine:jasmonate O-methyltransferase	jas[c] + amet[c] -> ahcys[c] + metjas[c]	LOC_Os01g50610	Phytohormones biosynthesis (Jasmonic acid)	2.1.1.141
JASVSc	jasmonic acid-valine synthetase	jas[c] + val-L[c] + atp[c] -> jasval[c] + amp[c] + ppi[c]	(LOC_Os11g08340 or LOC_Os01g12160 or LOC_Os05g50890)	Phytohormones biosynthesis (Jasmonic acid)	6.3.-.-
JASILSc	jasmonic acid-isoleucine synthetase	jas[c] + ile-L[c] + atp[c] -> jasile[c] + amp[c] + ppi[c]	(LOC_Os11g08340 or LOC_Os01g12160 or LOC_Os05g50890)	Phytohormones biosynthesis (Jasmonic acid)	6.3.-.-
JASLSc	jasmonic acid-leucine synthetase	jas[c] + leu-L[c] + atp[c] -> jasleu[c] + amp[c] + ppi[c]	(LOC_Os11g08340 or LOC_Os01g12160 or LOC_Os05g50890)	Phytohormones biosynthesis (Jasmonic acid)	6.3.-.-
SERPTr	Serine C-palmitoyltransferase	pmtcoa[r] + ser-L[r] + h[r] -> 3dsphgn[r] + coa[r] + co2[r]	(LOC_Os01g70360 or LOC_Os11g31640 or LOC_Os10g11200 or LOC_Os02g56300 or LOC_Os03g14800)	Sphingolipid metabolism	2.3.1.50
3DSPHRr	3-dehydrosphinganine reductase	3dsphgn[r] + nadph[r] + h[r] -> sphgn[r] + nadp[r]	LOC_Os02g47350	Sphingolipid metabolism	1.1.1.102
SLCBK1r	sphinganine kinase	atp[r] + sphgn[r] -> adp[r] + sph1p[r] + h[r]	LOC_Os01g57350	Sphingolipid metabolism	2.7.1.91
SGPL11r	sphinganine 1-phosphate aldolase	sph1p[r] -> ethamp[r] + hxdcal[r]	LOC_Os01g01080	Sphingolipid metabolism	4.1.2.27
SGPL12r	sphingosine 1-phosphate aldolase	sphs1p[r] -> ethamp[r] + hxdceal[r]	LOC_Os01g01080	Sphingolipid metabolism	4.1.2.27
SLCBK2r	sphingosine kinase	atp[r] + sphings[r] -> adp[r] + sphs1p[r] + h[r]	LOC_Os01g57350	Sphingolipid metabolism	2.7.1.91
ASPHGNAr	N-Acylsphingosine amidohydrolase	cer1_os[r] + h2o[r] -> sphgn[r] + fa_os[r]	LOC_Os01g43520	Sphingolipid metabolism	3.5.1.23
PCAHr	Phytoceramide amidohydrolase	cer2_os[r] + h2o[r] -> psphings[r] + fa_os[r]	LOC_Os01g43520	Sphingolipid metabolism	3.5.1.23
ASPHGNAHr	N-Acylsphingosine amidohydrolase	cer3_os[r] + h2o[r] -> sphings[r] + fa_os[r]	LOC_Os01g43520	Sphingolipid metabolism	3.5.1.23
SPHOORr	sphinganine oxygen oxidoreductase (NADPH, 4-hydroxylating)	h[r] + nadph[r] + o2[r] + sphgn[r] -> h2o[r] + nadp[r] + psphings[r]	LOC_Os02g51150	Sphingolipid metabolism	1.14.-.-
PCSr	dihydrosphinganine delta(4)-desaturase	h[r] + nadph[r] + o2[r] + sphgn[r] -> 2 h2o[r] + nadp[r] + sphings[r]	LOC_Os02g51150	Sphingolipid metabolism	1.14.-.-
DHCDSr	dihydroceramide delta(4)-desaturase	cer1_os[r] + fadh2[r] + o2[r] <=> cer3_os[r] + fad[r] + 2 h2o[r]	LOC_Os02g42660	Sphingolipid metabolism	1.14.-.-
ASPHGNAT1r	acyl-CoA:sphingosine N-acyltransferase	acylcoa_os[r] + sphgn[r] -> cer1_os[r] + coa[r] + h[r]	LOC_Os03g15750	Sphingolipid metabolism	2.3.1.24
ASPHGNAT2r	acyl-CoA:sphingosine N-acyltransferase	acylcoa_os[r] + sphings[r] -> cer3_os[r] + coa[r] + h[r]	LOC_Os03g15750	Sphingolipid metabolism	2.3.1.24
ASPHGNAT3r	acyl-CoA:sphingosine N-acyltransferase	acylcoa_os[r] + psphings[r] -> cer2_os[r] + coa[r] + h[r]	LOC_Os03g15750	Sphingolipid metabolism	2.3.1.24
UGCGr	Ceramide glucosyltransferase	cer3_os[r] + udpg[r] -> gluside[r] + h[r] + udp[r]	LOC_Os01g67920	Sphingolipid metabolism	2.4.1.80
UGALCGc	glucosylceramide beta-1,4-galactosyltransferase lactosylceramide synthase	gluside[c] + udpgal[c] -> galgluside[c] + h[c] + udp[c]		Sphingolipid metabolism	2.4.1.274
GLB1c	Beta-galactosidase	galgluside[c] + h2o[c] -> gal[c] + gluside[c]	(LOC_Os01g72340 or LOC_Os05g46200)	Sphingolipid metabolism	3.2.1.23
OACPSSTm	octanoyl-[acp]:sulfur sulfurtransferase	oclysLCP[m] + 2 amet[m] -> lipACP[m] + 2 met-L[m] + 2 dad-5[m]	(LOC_Os01g56310 or LOC_Os04g38330 or LOC_Os05g43576)	Glycolysis/Gluconeogensis	2.8.1.8
LACPLTm	lipoyl-[acp]:protein N6-lipoyltransferase	ocACP[m] + lipro[m] -> oclysLCP[m] + ACP[m]	(LOC_Os03g20560 or LOC_Os12g40440 or LOC_Os12g40450)	Glycolysis/Gluconeogensis	2.3.1.181
MCOAMTc	malonyl-CoA O-methyltransferase	malACP[c] + amet[c] -> ahcys[c] + malACPme[c]		Other Vitamins Metabolism (Biotin)	2.1.1.197
MACPMMEc	malonyl-[acyl-carrier protein]-methyl-ester:malonyl-[acyl-carrier protein] C-acyltransferase	malACPme[c] + malACP[c] -> akgACPme[c] + co2[c] + ACP[c]	(LOC_Os02g10320 or LOC_Os04g36800 or LOC_Os07g42420)	Other Vitamins Metabolism (Biotin)	2.3.1.179
3HGNORc	3-hydroxyglutaryl-[acp]-methyl-ester:NADP+ oxidoreductase	akgACPme[c] + nadph[c] + h[c] -> hakgACPme[c] + nadp[c]	(LOC_Os02g30060 or LOC_Os03g53690 or LOC_Os04g30760 or LOC_Os06g08600 or LOC_Os07g07440 or LOC_Os07g37420 or LOC_Os10g31780 or LOC_Os12g13930)	Other Vitamins Metabolism (Biotin)	1.1.1.100
3HGMELc	3-hydroxyglutaryl-[acp]-methyl-ester hydro-lyase	hakgACPme[c] <=> egluACPme[c] + h2o[c]	LOC_Os05g36000	Other Vitamins Metabolism (Biotin)	4.2.1.59
GLUACPMEORc	glutaryl-[acp]-methyl-ester:NADP+ oxidoreductase	egluACPme[c] + nadh[c] + h[c] -> gluACPme[c] + nadp[c]	(LOC_Os08g23810 or LOC_Os09g10600)	Other Vitamins Metabolism (Biotin)	1.3.1.10
GLUMEORc	glutaryl-[acp]-methyl-ester:malonyl-[acyl-carrier protein] C-acyltransferase (decarboxylating)	gluACPme[c] + malACP[c] -> kpimACPme[c] + co2[c] + ACP[c]	LOC_Os04g55060	Other Vitamins Metabolism (Biotin)	2.3.1.41
HPIMMEORc	3-hydroxypimeloyl-[acp]-methyl-ester:NADP+ oxidoreductase	kpimACPme[c] + nadph[c] + h[c] -> hpimACPme[c] + nadp[c]	(LOC_Os02g30060 or LOC_Os03g53690 or LOC_Os04g30760 or LOC_Os06g08600	Other Vitamins Metabolism (Biotin)	1.1.1.100

			or LOC_Os07g07440 or LOC_Os07g37420 or LOC_Os10g31780 or LOC_Os12g13930)		
HPIMMELc	3-hydroxypimeloyl-[acp]-methyl-ester hydro-lyase	hpimACPme[c] <=> epimACPme[c] + h2o[c]	LOC_Os05g36000	Other Vitamins Metabolism (Biotin)	4.2.1.59
PIMACPMEc	pimelyl-[acyl-carrier protein]-methyl-ester:NADP+ oxidoreductase	epimACPme[c] + nadph[c] + h[c] -> pimACPme[c] + nadp[c]	(LOC_Os08g23810 or LOC_Os09g10600)	Other Vitamins Metabolism (Biotin)	1.3.1.10
PACPMEEc	pimelyl-[acyl-carrier protein] methyl ester esterase	pimACPme[c] + h2o[c] -> pimACP[c] + h[c] + meoh[c]		Other Vitamins Metabolism (Biotin)	3.1.1.85
AONSc	8-amino-7-oxononanoate synthase	pimACP[c] + ala-L[c] + h[c] -> 8aonn[c] + co2[c] + ACP[c]	(LOC_Os11g31640 or LOC_Os10g11200 or LOC_Os04g43650 or LOC_Os03g14800 or LOC_Os02g56300 or LOC_Os01g70380 or LOC_Os01g70370 or LOC_Os01g70360)	Other Vitamins Metabolism (Biotin)	2.3.1.47
AMETAOTc	adenosylmethionine-8-amino-7-oxononanoate transaminase	8aonn[c] + amet[c] -> amob[c] + dann[c]	(LOC_Os08g14770 or LOC_Os08g10510 or LOC_Os05g39770 or LOC_Os03g44150 or LOC_Os03g21960)	Other Vitamins Metabolism (Biotin)	2.6.1.62
DTBTSc	dethiobiotin synthase	atp[c] + co2[c] + dann[c] <=> adp[c] + dtbt[c] + 3 h[c] + pi[c]		Other Vitamins Metabolism (Biotin)	6.3.3.3
BTNSc	biotin synthase	dtbt[c] + 2 amet[c] -> btn[c] + 2 met-L[c] + 2 dad-5[c] + h[c]	LOC_Os08g42730	Other Vitamins Metabolism (Biotin)	2.8.1.6
PFRTc	protein farnesyltransferase	frdp[c] + cys-prot[c] -> frprot[c] + ppi[c]	(LOC_Os01g53600 and LOC_Os09g33930)	Terpenoid biosynthesis (Monoterpenoid biosynthesis)	2.5.1.58
CAAPc	CAAX protease	frprot[c] + h2o[c] -> frcysprot[c]	LOC_Os02g45650	Terpenoid biosynthesis (Monoterpenoid biosynthesis)	3.4.24.84
PIOCMTc	protein-S-isoprenylcysteine O-methyltransferase	amet[c] + frcysprot[c] -> ahcys[c] + frcysmpest[c]	LOC_Os04g51380	Terpenoid biosynthesis (Monoterpenoid biosynthesis)	2.1.1.100
FRCYOc	farnesyl-L-cysteine oxidase	frcysmpest[c] + o2[c] + h2o[c] -> frnsl[c] + cys-L[c] + h2o2[c]	LOC_Os04g59630	Terpenoid biosynthesis (Monoterpenoid biosynthesis)	1.8.3.5;1.8.3.6
FRNCTIc	(2E,6E)-farnesol 2-cis-trans-isomerase	frnsl[c] <=> frnsol[c]		Terpenoid biosynthesis (Monoterpenoid biosynthesis)	5.2.1.9
FRORc	2-trans,6-trans-farnesol:NADP+ 1-oxidoreductase	frnsol[c] + nadp[c] -> frnsl[c] + nadph[c] + h[c]	LOC_Os03g08624	Terpenoid biosynthesis (Monoterpenoid biosynthesis)	1.1.1.216
FRPTc	CTP:2-trans,6-trans-farnesol O-phosphotransferase	ctp[c] + frnsol[c] -> frp[c] + cdp[c]	LOC_Os01g61560	Terpenoid biosynthesis (Monoterpenoid biosynthesis)	2.7.1.-
FRPPTc	CTP:farnesyl-phosphate phosphotransferase	ctp[c] + frp[c] -> frdp[c] + cdp[c]		Terpenoid biosynthesis (Monoterpenoid biosynthesis)	
DEDOLDPSc	dehydrodolichol diphosphate synthase	frdp[c] + 8 ipdp[c] -> dedoldp[c] + 8 ppi[c]	(LOC_Os01g63830 or LOC_Os03g10080 or LOC_Os06g07120 or LOC_Os07g41680)	Glycan Biosynthesis (N-Glycan)	2.5.1.87
DEDOLDPSATc	dehydrodolichol diphosphate saturase	dedoldp[c] + 2 nadh[c] -> doldp[c] + 2 nad[c]		Glycan Biosynthesis (N-Glycan)	
DOLDPPc	dolichyl-diphosphate phosphohydrolase	doldp[c] + h2o[c] -> dolp[c] + pi[c] + h[c]	LOC_Os03g17940	Glycan Biosynthesis (N-Glycan)	3.6.1.43
DOLKc	dolichol kinase	dolichol[c] + ctp[c] <=> cdp[c] + dolp[c]	LOC_Os02g05320	Glycan Biosynthesis (N-Glycan)	2.7.1.108
GLCNACPTc	UDP-GlcNAc:dolichyl-phosphate N-acetylglucosaminephosphotransferase	uacgam[c] + dolp[c] + 2 h[c] -> ump[c] + G00001[c]	LOC_Os07g46640	Glycan Biosynthesis (N-Glycan)	2.7.8.15
GLCNACTc	UDP-GlcNAc:dolichyl-pyrophosphoryl-GlcNAc GlcNAc transferase	uacgam[c] + G00001[c] -> udp[c] + G00002[c] + h[c]	LOC_Os02g26814	Glycan Biosynthesis (N-Glycan)	2.4.1.141
BDMTc	chitobiosyldiphosphodolichol beta-mannosyltransferase	gdpmann[c] + G00002[c] -> gdp[c] + G00003[c] + h[c]	LOC_Os03g08300	Glycan Biosynthesis (N-Glycan)	2.4.1.142
DOLPMTc	dolichyl-phosphate beta-D-mannosyltransferase	gdpmann[c] + dolp[c] -> gdp[c] + dolmanp[c]	LOC_Os03g60939	Glycan Biosynthesis (N-Glycan)	2.4.1.83
G13MTc	alpha-1,3-mannosyltransferase (G00003)	gdpmann[c] + G00003[c] -> gdp[c] + G00004[c] + h[c]	LOC_Os04g49960	Glycan Biosynthesis (N-Glycan)	2.4.1.132

G16MT1c	alpha-1,6-mannosyltransferase (G00004)	gdpmann[c] + G00004[c] -> gdp[c] + G00005[c] + h[c]	LOC_Os04g49960	Glycan Biosynthesis (N-Glycan)	2.4.1.257
G12MT1c	alpha-1,2-mannosyltransferase (G00005)	G00005[c] + gdpmann[c] -> G10526[c] + gdp[c] + h[c]	LOC_Os12g39340	Glycan Biosynthesis (N-Glycan)	2.4.1.131
G12MT2c	alpha-1,2-mannosyltransferase (G10526)	G10526[c] + gdpmann[c] -> G00006[c] + gdp[c] + h[c]	LOC_Os12g39340	Glycan Biosynthesis (N-Glycan)	2.4.1.131
DOLPMT1c	dolichyl-phosphate-mannose-glycolipid alpha-mannosyltransferase (G00006)	dolmanp[c] + G00006[c] -> dolp[c] + G10595[c] + h[c]	LOC_Os01g07720	Glycan Biosynthesis (N-Glycan)	2.4.1.258
G12MT3c	alpha-1,2-mannosyltransferase (G10595)	dolmanp[c] + G10595[c] -> dolp[c] + G10596[c] + h[c]	LOC_Os01g11070	Glycan Biosynthesis (N-Glycan)	2.4.1.259
G16MT2c	alpha-1,6-mannosyltransferase (G10596)	dolmanp[c] + G10596[c] -> dolp[c] + G10597[c] + h[c]	LOC_Os04g46050	Glycan Biosynthesis (N-Glycan)	2.4.1.260
G12MT4c	alpha-1,2-mannosyltransferase (G10597)	dolmanp[c] + G10597[c] -> dolp[c] + G00007[c] + h[c]	LOC_Os01g11070	Glycan Biosynthesis (N-Glycan)	2.4.1.261
UDPDOLPTc	dolichyl-phosphate beta-glucosyltransferase	udpg[c] + dolp[c] -> udp[c] + dolpglc[c]	LOC_Os03g60700	Glycan Biosynthesis (N-Glycan)	2.4.1.117
DOLPGT1c	alpha-1,3-glucosyltransferase (G10598)	dolpglc[c] + G00007[c] -> dolp[c] + G10598[c] + h[c]	LOC_Os07g07010	Glycan Biosynthesis (N-Glycan)	2.4.1.267
DOLPGT2c	alpha-1,3-glucosyltransferase (G10599)	dolpglc[c] + G10598[c] -> dolp[c] + G10599[c] + h[c]	LOC_Os02g46320	Glycan Biosynthesis (N-Glycan)	2.4.1.265
DOLPGT3c	alpha-1,2-glucosyltransferase (G00008)	dolpglc[c] + G10599[c] -> dolp[c] + G00008[c] + h[c]	LOC_Os04g42490	Glycan Biosynthesis (N-Glycan)	2.4.1.266
DOLASNTc	dolichyl-diphosphooligosaccharide-protein glycotransferase	Asn-X-Ser-FSLASH-Thr[c] + G00008[c] -> doldp[c] + G00009[c] + 3 h[c]	(LOC_Os04g57890 or LOC_Os04g32550)	Glycan Biosynthesis (N-Glycan)	2.4.99.18
MG1Ac	mannosyl-oligosaccharide glucosidase (G00171) (glc-A)	h2o[c] + G00009[c] -> glc-A[c] + G00171[c]	LOC_Os01g69210	Glycan Biosynthesis (N-Glycan)	3.2.1.106
MG1Bc	mannosyl-oligosaccharide glucosidase (G00171) (glc-B)	h2o[c] + G00009[c] -> glc-B[c] + G00171[c]	LOC_Os01g69210	Glycan Biosynthesis (N-Glycan)	3.2.1.106
MG2Ac	glucan 1,3-alpha-glucosidase (G00010) (glc-A)	h2o[c] + G00171[c] -> glc-A[c] + G00010[c]	LOC_Os03g11720	Glycan Biosynthesis (N-Glycan)	3.2.1.84
MG2Bc	glucan 1,3-alpha-glucosidase (G00010) (glc-B)	h2o[c] + G00171[c] -> glc-B[c] + G00010[c]	LOC_Os03g11720	Glycan Biosynthesis (N-Glycan)	3.2.1.84
MG3Ac	glucan 1,3-alpha-glucosidase (G00011) (glc-A)	h2o[c] + G00010[c] -> glc-A[c] + G00011[c]	LOC_Os03g11720	Glycan Biosynthesis (N-Glycan)	3.2.1.84
MG3Bc	glucan 1,3-alpha-glucosidase (G00011) (glc-B)	h2o[c] + G00010[c] -> glc-B[c] + G00011[c]	LOC_Os03g11720	Glycan Biosynthesis (N-Glycan)	3.2.1.84
MM1c	mannosyl-oligosaccharide 1,2-alpha-mannosidase (G00012)	G00011[c] + 4 h2o[c] -> G00012[c] + 4 man[c]	(LOC_Os04g51690 or LOC_Os05g11850)	Glycan Biosynthesis (N-Glycan)	3.2.1.113
MGAGT1c	alpha-1,3-mannosyl-glycoprotein 2-beta-N-acetylglucosaminyltransferase (G00013)	uacgam[c] + G00012[c] -> udp[c] + G00013[c]	LOC_Os02g58590	Glycan Biosynthesis (N-Glycan)	2.4.1.101
MM2c	mannosyl-oligosaccharide 1,3-1,6-alpha-mannosidase (G00014)	G00013[c] + 2 h2o[c] -> G00014[c] + 2 man[c]	LOC_Os06g13650	Glycan Biosynthesis (N-Glycan)	3.2.1.114
MGAGT2c	alpha-1,3-mannosyl-glycoprotein 2-beta-N-acetylglucosaminyltransferase (G00015)	uacgam[c] + G00014[c] -> udp[c] + G00015[c]	LOC_Os02g55470	Glycan Biosynthesis (N-Glycan)	2.4.1.143
MGAGT3c	alpha-1,3-mannosyl-glycoprotein 2-beta-N-acetylglucosaminyltransferase (G10619)	uacgam[c] + G00015[c] -> udp[c] + G00019[c]	(LOC_Os02g38140 or LOC_Os04g40150 or LOC_Os12g41780)	Glycan Biosynthesis (N-Glycan)	2.4.1.144
GPXTc	glycoprotein 2-beta-D-xylosyltransferase	udpxyl[c] + G00015[c] -> udp[c] + G00179[c]	LOC_Os08g39380	Glycan Biosynthesis (N-Glycan)	2.4.2.38
GPFTc	glycoprotein 3-alpha-L-fucosyltransferase	gdpfuc[c] + G00179[c] -> gdp[c] + G13056[c]	LOC_Os08g36840	Glycan Biosynthesis (N-Glycan)	2.4.1.214
PIACGTc	phosphatidylinositol N-acetylglucosaminyltransferase	ptd1ino_os[c] + uacgam[c] -> G00143[c] + udp[c]	LOC_Os07g16960	Glycan Biosynthesis (Glycolipids)	2.4.1.198
ACGPIDc	N-acetylglucosaminylphosphatidylinositol deacetylase	G00143[c] + h2o[c] -> ac[c] + G00144[c]	LOC_Os04g58210	Glycan Biosynthesis (Glycolipids)	3.5.1.89
GPIATc	glucosaminylphosphatidyl inositol acetyltransferase	G00144[c] + pmtcoa[c] -> coa[c] + G00145[c]	LOC_Os03g26090	Glycan Biosynthesis (Glycolipids)	2.3.-.-

GPIMTc	GlcN-acylPI mannosyltransferase	dolmanp[c] + G00145[c] -> dolp[c] + h[c] + G00146[c]	(LOC_Os03g46750 or LOC_Os12g40500)	Glycan Biosynthesis (Glycolipids)	2.4.1.-
H6ET3c	H6 phosphoethanolaminyl transferase	G00146[c] + pe_os[c] -> 12dgr_os[c] + G00147[c]	LOC_Os02g37050	Glycan Biosynthesis (Glycolipids)	2.7.-.-
H2MTc	H2 mannosyltransferase	dolmanp[c] + G00147[c] -> dolp[c] + h[c] + G00148[c]	LOC_Os12g31480	Glycan Biosynthesis (Glycolipids)	2.4.1.-
H3MTc	H3 mannosyltransferase	dolmanp[c] + G00148[c] -> dolp[c] + h[c] + G00149[c]	LOC_Os01g39810	Glycan Biosynthesis (Glycolipids)	2.4.1.-
H4ETc	H4 phosphoethanolaminyl transferase	G00149[c] + pe_os[c] -> 12dgr_os[c] + G13044[c]	(LOC_Os03g03690 or LOC_Os10g08940)	Glycan Biosynthesis (Glycolipids)	2.7.-.-
H6MTc	H6 mannosyltransferase	dolmanp[c] + G13044[c] -> dolp[c] + h[c] + G13045[c]	LOC_Os02g12740	Glycan Biosynthesis (Glycolipids)	2.6.-.-
A4GALTc	Lactosylceramide 4-alpha-galactosyltransferase	galgluside[c] + udpgal[c] -> h[c] + thcrm[c] + udp[c]	LOC_Os04g44740	Glycan Biosynthesis (Glycolipids)	2.4.1.228
B3GALT3c	Beta-1,3-galactosyltransferase 3	thcrm[c] + udpacgal[c] -> gbside[c] + h[c] + udp[c]	LOC_Os02g36770	Glycan Biosynthesis (Glycolipids)	2.4.1.79
AGALSc	alpha-galactosidase	thcrm[c] + h2o[c] -> gal[c] + galgluside[c]	(LOC_Os07g48160 or LOC_Os10g35110 or LOC_Os07g26900)	Glycan Biosynthesis (Glycolipids)	3.2.1.22
HXAMS1c	Hexaminadose	gbside[c] + h2o[c] -> thcrm[c] + galgluside[c]	(LOC_Os01g66700 or LOC_Os03g11980 or LOC_Os05g02510 or LOC_Os05g34320 or LOC_Os07g38790)	Glycan Biosynthesis (Glycolipids)	3.2.1.52
SIAT9c	Lactosylceramide alpha-2,3-sialyltransferase	cmpacna[c] + galgluside[c] -> cmp[c] + gm3[c] + h[c]		Glycan Biosynthesis (Glycolipids)	2.4.99.9
GALGT2c	Beta-1,4 N-acetylgalactosaminyltransferase	udpacgal[c] + gm3[c] -> udp[c] + gm2[c] + h[c]	LOC_Os05g35266	Glycan Biosynthesis (Glycolipids)	2.4.1.92
B3GALT42c	Beta-1,3-galactosyltransferase 4	udpgal[c] + gm2[c] -> udp[c] + gm1[c] + h[c]	LOC_Os05g35266	Glycan Biosynthesis (Glycolipids)	2.4.1.92
HXAMS2c	Hexaminadose	gm2[c] + h2o[c] -> gm3[c] + acgal[c]	(LOC_Os01g66700 or LOC_Os03g11980 or LOC_Os05g02510 or LOC_Os05g34320 or LOC_Os07g38790)	Glycan Biosynthesis (Glycolipids)	3.2.1.52
BGALSc	beta-galactosidase	gm1[c] + h2o[c] -> gal[c] + gm2[c]	LOC_Os05g46200	Glycan Biosynthesis (Glycolipids)	3.2.1.23
UDPACGALEc	UDP-N-acetylglucosamine 4-epimerase	udpacgal[c] <=> uacgam[c]		Primary Cell Wall Metabolism (Amino sugars)	5.1.3.7
ALATc	alanine---tRNA ligase, cytosolic	atp[c] + ala-L[c] + trnaala[c] -> amp[c] + ppi[c] + alatrna[c]	(LOC_Os10g10244 or LOC_Os07g15440 or LOC_Os06g13660 or LOC_Os01g03030)	Aminoacyl-tRNA biosynthesis	6.1.1.7
ALATs	alanine---tRNA ligase, plastidic	atp[s] + ala-L[s] + trnaala[s] -> amp[s] + ppi[s] + alatrna[s]	(LOC_Os10g10244 or LOC_Os07g15440 or LOC_Os06g13660 or LOC_Os01g03030)	Aminoacyl-tRNA biosynthesis	6.1.1.7
ALATm	alanine---tRNA ligase, mitochondrion	atp[m] + ala-L[m] + trnaala[m] -> amp[m] + ppi[m] + alatrna[m]	(LOC_Os10g10244 or LOC_Os07g15440 or LOC_Os06g13660 or LOC_Os01g03030)	Aminoacyl-tRNA biosynthesis	6.1.1.7
ARGTc	arginine---tRNA ligase, cytosolic	atp[c] + arg-L[c] + trnaarg[c] -> amp[c] + ppi[c] + argtrna[c]	(LOC_Os06g01400 or LOC_Os05g07030 or LOC_Os01g06510)	Aminoacyl-tRNA biosynthesis	6.1.1.19
ARGTs	arginine---tRNA ligase, plastidic	atp[s] + arg-L[s] + trnaarg[s] -> amp[s] + ppi[s] + argtrna[s]	(LOC_Os06g01400 or LOC_Os05g07030 or LOC_Os01g06510)	Aminoacyl-tRNA biosynthesis	6.1.1.19
CYSTLc	cysteine---tRNA ligase, cytosolic	atp[c] + cys-L[c] + trnacys[c] -> amp[c] + ppi[c] + cystrna[c]	(LOC_Os10g32570 or LOC_Os09g38420 or LOC_Os03g04960)	Aminoacyl-tRNA biosynthesis	6.1.1.16
CYSTLs	cysteine---tRNA ligase, plastidic	atp[s] + cys-L[s] + trnacys[s] -> amp[s] + ppi[s] + cystrna[s]	(LOC_Os10g32570 or LOC_Os09g38420 or LOC_Os03g04960)	Aminoacyl-tRNA biosynthesis	6.1.1.16
CYSTLm	cysteine---tRNA ligase, mitochondrial	atp[m] + cys-L[m] + trnacys[m] -> amp[m] + ppi[m] + cystrna[m]	(LOC_Os10g32570 or LOC_Os09g38420 or LOC_Os03g04960)	Aminoacyl-tRNA biosynthesis	6.1.1.16
GLNTLc	glutamine---tRNA ligase	atp[c] + gln-L[c] + trnagln[c] -> amp[c] + ppi[c] + glntrna[c]	(LOC_Os05g08990 or LOC_Os01g09000)	Aminoacyl-tRNA biosynthesis	6.1.1.18
GLUTLc	glutamate---tRNA ligase	atp[c] + glu-L[c] + trnaglu[c] -> amp[c] + ppi[c] + glutrna[c]	(LOC_Os10g22380 or LOC_Os05g08990	Aminoacyl-tRNA	6.1.1.17

			or LOC_Os02g02860 or LOC_Os01g09000 or LOC_Os01g16520)	biosynthesis	
LEUTLc	Leucine---tRNA ligase	atp[c] + leu-L[c] + trnaleu[c] -> amp[c] + ppi[c] + leutrna[c]	(LOC_Os10g36210 or LOC_Os07g06940 or LOC_Os06g43760 or LOC_Os05g15150 or LOC_Os03g48850 or LOC_Os03g21740 or LOC_Os03g11120 or LOC_Os03g02100 or LOC_Os02g53770 or LOC_Os02g09120 or LOC_Os02g09100 or LOC_Os09g21110 or LOC_Os09g32650 or LOC_Os01g03020)	Aminoacyl-tRNA biosynthesis	6.1.1.4
GLYTLc	glycine---tRNA ligase, cytsolic	atp[c] + gly[c] + trnagly[c] -> amp[c] + ppi[c] + glytrna[c]	(LOC_Os08g19850 or LOC_Os10g10080 or LOC_Os08g42560 or LOC_Os07g32020 or LOC_Os06g01400 or LOC_Os04g32650 or LOC_Os01g72970)	Aminoacyl-tRNA biosynthesis	6.1.1.14
GLYTLm	glycine---tRNA ligase, mitochondrial	atp[m] + gly[m] + trnagly[m] -> amp[m] + ppi[m] + glytrna[m]	(LOC_Os08g19850 or LOC_Os10g10080 or LOC_Os08g42560 or LOC_Os07g32020 or LOC_Os06g01400 or LOC_Os04g32650)	Aminoacyl-tRNA biosynthesis	6.1.1.14
GLYTLs	glycine---tRNA ligase, plastidic	atp[s] + gly[s] + trnagly[s] -> amp[s] + ppi[s] + glytrna[s]	(LOC_Os08g19850 or LOC_Os10g10080 or LOC_Os08g42560 or LOC_Os07g32020 or LOC_Os06g01400 or LOC_Os04g32650 or LOC_Os01g72970)	Aminoacyl-tRNA biosynthesis	6.1.1.14
SERTLc	serine---tRNA ligase, cytosolic	atp[c] + ser-L[c] + trnaser[c] -> amp[c] + ppi[c] + sertrna[c]	(LOC_Os02g54290 or LOC_Os02g54170 or LOC_Os02g38480 or LOC_Os11g39670 or LOC_Os03g10190 or LOC_Os01g37837)	Aminoacyl-tRNA biosynthesis	6.1.1.11
SERTLs	serine---tRNA ligase, plastidic	atp[s] + ser-L[s] + trnaser[s] -> amp[s] + ppi[s] + sertrna[s]	(LOC_Os02g54290 or LOC_Os02g54170 or LOC_Os02g38480 or LOC_Os11g39670 or LOC_Os03g10190 or LOC_Os01g37837)	Aminoacyl-tRNA biosynthesis	6.1.1.11
SERTLm	serine---tRNA ligase, mitochondrial	atp[m] + ser-L[m] + trnaser[m] -> amp[m] + ppi[m] + sertrna[m]	(LOC_Os02g54290 or LOC_Os02g54170 or LOC_Os02g38480 or LOC_Os11g39670 or LOC_Os03g10190 or LOC_Os01g37837)	Aminoacyl-tRNA biosynthesis	6.1.1.11
THRTLc	threonine---tRNA ligase, cytosolic	atp[c] + thr-L[c] + trnathr[c] -> amp[c] + ppi[c] + thrtrna[c]	(LOC_Os08g19850 or LOC_Os02g33500)	Aminoacyl-tRNA biosynthesis	6.1.1.3
THRTLm	threonine---tRNA ligase, mitochondrial	atp[m] + thr-L[m] + trnathr[m] -> amp[m] + ppi[m] + thrtrna[m]	LOC_Os08g19850	Aminoacyl-tRNA biosynthesis	6.1.1.3
LYSTLm	lysine---tRNA ligase, mitochondrial	atp[m] + lys-L[m] + trnalys[m] -> amp[m] + ppi[m] + lystrna[m]	LOC_Os02g41470	Aminoacyl-tRNA biosynthesis	6.1.1.6
LYSTLs	lysine---tRNA ligase, plastidic	atp[s] + lys-L[s] + trnalys[s] -> amp[s] + ppi[s] + lystrna[s]	LOC_Os02g41470	Aminoacyl-tRNA biosynthesis	6.1.1.6
LYSTLc	lysine---tRNA ligase, cytosolic	atp[c] + lys-L[c] + trnalys[c] -> amp[c] + ppi[c] + lystrna[c]	(LOC_Os03g38980 or LOC_Os03g38980)	Aminoacyl-tRNA biosynthesis	6.1.1.6
METTLc	methionine---tRNA ligase, cytosolic	atp[c] + met-L[c] + trnamet[c] -> amp[c] + ppi[c] + mettrna[c]	(LOC_Os06g31210 or LOC_Os03g11120 or LOC_Os10g26050)	Aminoacyl-tRNA biosynthesis	6.1.1.10
METTLm	methionine---tRNA ligase, mitochondrial	atp[m] + met-L[m] + trnamet[m] -> amp[m] + ppi[m] + mettrna[m]	(LOC_Os06g31210 or LOC_Os03g11120 or LOC_Os10g26050)	Aminoacyl-tRNA biosynthesis	6.1.1.10
METTLs	methionine---tRNA ligase, plastidic	atp[s] + met-L[s] + trnamet[s] -> amp[s] + ppi[s] + mettrna[s]	(LOC_Os06g31210 or LOC_Os03g11120 or LOC_Os10g26050)	Aminoacyl-tRNA biosynthesis	6.1.1.10
PHETLc	phenylalanine---tRNA ligase, cytosolic	atp[c] + phe-L[c] + trnaphe[c] -> amp[c] + ppi[c] + phetrna[c]	(LOC_Os10g26050 or LOC_Os07g41080 or LOC_Os06g31210 or LOC_Os01g49940 or LOC_Os12g34860 or LOC_Os10g26130 or LOC_Os05g48510)	Aminoacyl-tRNA biosynthesis	6.1.1.18
PHETLs	phenylalanine---tRNA ligase, plastidic	atp[s] + phe-L[s] + trnaphe[s] -> amp[s] + ppi[s] + phetrna[s]	(LOC_Os10g26050 or LOC_Os07g41080 or LOC_Os06g31210 or LOC_Os01g49940	Aminoacyl-tRNA biosynthesis	6.1.1.18

			or LOC_Os12g34860 or LOC_Os10g26130)		
PHETLm	phenylalanine---tRNA ligase, mitochondrial	atp[m] + phe-L[m] + trnaphe[m] -> amp[m] + ppi[m] + phetrna[m]	((LOC_Os12g34860 or LOC_Os10g26130) and LOC_Os05g48510)	Aminoacyl-tRNA biosynthesis	6.1.1.20
ASNTLc	asparagine---tRNA ligase, cytosolic	atp[c] + asn-L[c] + trnaasn[c] -> amp[c] + ppi[c] + asntrna[c]	(LOC_Os02g46130 or LOC_Os02g41470 or LOC_Os02g04700 or LOC_Os01g06020 or LOC_Os07g30200 or LOC_Os01g27520)	Aminoacyl-tRNA biosynthesis	6.1.1.22
ASNTLs	asparagine---tRNA ligase, plastidic	atp[s] + asn-L[s] + trnaasn[s] -> amp[s] + ppi[s] + asntrna[s]	(LOC_Os02g46130 or LOC_Os02g41470 or LOC_Os02g04700 or LOC_Os01g06020 or LOC_Os07g30200 or LOC_Os01g27520)	Aminoacyl-tRNA biosynthesis	6.1.1.22
ASNTLm	asparagine---tRNA ligase, mitochondrial	atp[m] + asn-L[m] + trnaasn[m] -> amp[m] + ppi[m] + asntrna[m]	(LOC_Os02g46130 or LOC_Os02g41470 or LOC_Os02g04700 or LOC_Os01g06020 or LOC_Os07g30200 or LOC_Os01g27520)	Aminoacyl-tRNA biosynthesis	6.1.1.22
ILETLc	isoleucine---tRNA ligase, cytosolic	atp[c] + ile-L[c] + trnaile[c] -> amp[c] + ppi[c] + iletrna[c]	(LOC_Os10g26050 or LOC_Os09g32650 or LOC_Os09g21110 or LOC_Os07g06940 or LOC_Os06g31210 or LOC_Os05g15150 or LOC_Os03g48850 or LOC_Os03g21740 or LOC_Os03g11120 or LOC_Os03g02100 or LOC_Os01g03020 or LOC_Os10g36210 or LOC_Os06g43760 or LOC_Os02g09100 or LOC_Os02g09120 or LOC_Os02g53770)	Aminoacyl-tRNA biosynthesis	6.1.1.5
ILETLs	isoleucine---tRNA ligase, plastidic	atp[s] + ile-L[s] + trnaile[s] -> amp[s] + ppi[s] + iletrna[s]	(LOC_Os10g26050 or LOC_Os09g32650 or LOC_Os09g21110 or LOC_Os07g06940 or LOC_Os06g31210 or LOC_Os05g15150 or LOC_Os03g48850 or LOC_Os03g21740 or LOC_Os03g11120 or LOC_Os03g02100 or LOC_Os01g03020 or LOC_Os10g36210 or LOC_Os06g43760 or LOC_Os02g09100 or LOC_Os02g09120 or LOC_Os02g53770)	Aminoacyl-tRNA biosynthesis	6.1.1.5
ILETLm	isoleucine---tRNA ligase, mitochondrial	atp[m] + ile-L[m] + trnaile[m] -> amp[m] + ppi[m] + iletrna[m]	(LOC_Os10g26050 or LOC_Os09g32650 or LOC_Os09g21110 or LOC_Os07g06940 or LOC_Os06g31210 or LOC_Os05g15150 or LOC_Os03g48850 or LOC_Os03g21740 or LOC_Os03g11120 or LOC_Os03g02100 or LOC_Os01g03020 or LOC_Os10g36210 or LOC_Os06g43760 or LOC_Os02g09100 or LOC_Os02g09120 or LOC_Os02g53770)	Aminoacyl-tRNA biosynthesis	6.1.1.5
VALTLs	valine---tRNA ligase, plastidic	atp[s] + val-L[s] + trnaval[s] -> amp[s] + ppi[s] + valtrna[s]	(LOC_Os03g48850 or LOC_Os03g21740 or LOC_Os03g02100 or LOC_Os06g43760 or LOC_Os10g36210 or LOC_Os02g53770 or LOC_Os07g06940)	Aminoacyl-tRNA biosynthesis	6.1.1.9
VALTLm	valine---tRNA ligase, mitochondrial	atp[m] + val-L[m] + trnaval[m] -> amp[m] + ppi[m] + valtrna[m]	(LOC_Os03g48850 or LOC_Os03g21740 or LOC_Os03g02100 or LOC_Os06g43760 or LOC_Os10g36210 or LOC_Os02g53770 or LOC_Os07g06940)	Aminoacyl-tRNA biosynthesis	6.1.1.9
ASPTLc	aspartate---tRNA ligase, cytosolic	atp[c] + asp-L[c] + trnaasp[c] -> amp[c] + ppi[c] + asptrna[c]	(LOC_Os12g22600 or LOC_Os07g30200 or LOC_Os03g38980 or LOC_Os02g04700 or LOC_Os02g41470 or LOC_Os02g46130 or LOC_Os01g06020 or LOC_Os01g27520)	Aminoacyl-tRNA biosynthesis	6.1.1.12
ASPTLs	aspartate---tRNA ligase, plastidic	atp[s] + asp-L[s] + trnaasp[s] -> amp[s] + ppi[s] + asptrna[s]	(LOC_Os12g22600 or LOC_Os07g30200	Aminoacyl-tRNA	6.1.1.12

			or LOC_Os03g38980 or LOC_Os02g04700 or LOC_Os02g41470 or LOC_Os02g46130 or LOC_Os01g06020 or LOC_Os01g27520)	biosynthesis	
ASPTLm	aspartate---tRNA ligase, mitochondrial	atp[m] + asp-L[m] + trnaasp[m] -> amp[m] + ppi[m] + asptrna[m]	(LOC_Os12g22600 or LOC_Os07g30200 or LOC_Os03g38980 or LOC_Os02g04700 or LOC_Os02g41470 or LOC_Os02g46130 or LOC_Os01g06020 or LOC_Os01g27520)	Aminoacyl-tRNA biosynthesis	6.1.1.12
TYRTLc	tyrosine---tRNA ligase, cytosolic	atp[c] + tyr-L[c] + trnatyr[c] -> amp[c] + ppi[c] + tyrtrna[c]	(LOC_Os08g09260 or LOC_Os07g47860 or LOC_Os08g05490 or LOC_Os01g31610)	Aminoacyl-tRNA biosynthesis	6.1.1.1
TYRTLs	tyrosine---tRNA ligase, plastidic	atp[s] + tyr-L[s] + trnatyr[s] -> amp[s] + ppi[s] + tyrtrna[s]	(LOC_Os08g09260 or LOC_Os07g47860 or LOC_Os08g05490 or LOC_Os01g31610)	Aminoacyl-tRNA biosynthesis	6.1.1.1
TYRTLm	tyrosine---tRNA ligase, mitochondrial	atp[m] + tyr-L[m] + trnatyr[m] -> amp[m] + ppi[m] + tyrtrna[m]	(LOC_Os08g09260 or LOC_Os07g47860 or LOC_Os08g05490 or LOC_Os01g31610)	Aminoacyl-tRNA biosynthesis	6.1.1.1
TRPTLc	tryptophan---tRNA ligase, cytosolic	atp[c] + trp-L[c] + trnatrp[c] -> amp[c] + ppi[c] + trptrna[c]	(LOC_Os08g09260 or LOC_Os07g47860 or LOC_Os04g58400 or LOC_Os12g35570 or LOC_Os08g05490 or LOC_Os08g23110 or LOC_Os07g17770 or LOC_Os01g54020)	Aminoacyl-tRNA biosynthesis	6.1.1.2
TRPTLs	tryptophan---tRNA ligase, plastidic	atp[s] + trp-L[s] + trnatrp[s] -> amp[s] + ppi[s] + trptrna[s]	(LOC_Os08g09260 or LOC_Os07g47860 or LOC_Os04g58400 or LOC_Os12g35570 or LOC_Os08g05490 or LOC_Os08g23110 or LOC_Os07g17770 or LOC_Os01g54020)	Aminoacyl-tRNA biosynthesis	6.1.1.2
TRPTLm	tryptophan---tRNA ligase, mitochondrial	atp[m] + trp-L[m] + trnatrp[m] -> amp[m] + ppi[m] + trptrna[m]	(LOC_Os08g09260 or LOC_Os07g47860 or LOC_Os04g58400 or LOC_Os12g35570 or LOC_Os08g05490 or LOC_Os08g23110 or LOC_Os07g17770 or LOC_Os01g54020)	Aminoacyl-tRNA biosynthesis	6.1.1.2
PROTLc	proline---tRNA ligase, cytosolic	atp[c] + pro-L[c] + trnapro[c] -> amp[c] + ppi[c] + protrna[c]	(LOC_Os07g07060 or LOC_Os12g25710 or LOC_Os08g42560 or LOC_Os04g32650)	Aminoacyl-tRNA biosynthesis	6.1.1.15
PROTLs	proline---tRNA ligase, plastidic	atp[s] + pro-L[s] + trnapro[s] -> amp[s] + ppi[s] + protrna[s]	(LOC_Os07g07060 or LOC_Os12g25710 or LOC_Os08g42560 or LOC_Os04g32650)	Aminoacyl-tRNA biosynthesis	6.1.1.15
PROTLm	proline---tRNA ligase, mitochondrial	atp[m] + pro-L[m] + trnapro[m] -> amp[m] + ppi[m] + protrna[m]	(LOC_Os07g07060 or LOC_Os12g25710 or LOC_Os08g42560 or LOC_Os04g32650)	Aminoacyl-tRNA biosynthesis	6.1.1.15
HISTLc	histidine---tRNA ligase, cytosolic	atp[c] + his-L[c] + trnahis[c] -> amp[c] + ppi[c] + histrna[c]	(LOC_Os04g41510 or LOC_Os05g05840 or LOC_Os02g51830)	Aminoacyl-tRNA biosynthesis	6.1.1.21
HISTLs	histidine---tRNA ligase, plastidic	atp[s] + his-L[s] + trnahis[s] -> amp[s] + ppi[s] + histrna[s]	(LOC_Os04g41510 or LOC_Os05g05840 or LOC_Os02g51830)	Aminoacyl-tRNA biosynthesis	6.1.1.21
HISTLm	histidine---tRNA ligase, mitochondrial	atp[m] + his-L[m] + trnahis[m] -> amp[m] + ppi[m] + histrna[m]	(LOC_Os04g41510 or LOC_Os05g05840 or LOC_Os02g51830)	Aminoacyl-tRNA biosynthesis	6.1.1.21
METTc	N-methyltransferase	ala-B[c] + amet[c] -> ahcys[c] + ala-B-bet[c] + h[c]	(LOC_Os12g01800 or LOC_Os11g01810 or LOC_Os10g32540 or LOC_Os09g29740 or LOC_Os09g29710 or LOC_Os09g29690 or LOC_Os07g49300 or LOC_Os07g42280 or LOC_Os06g38550 or LOC_Os06g06730 or LOC_Os06g06560 or LOC_Os04g21720 or LOC_Os03g58060 or LOC_Os03g53890 or LOC_Os03g29350 or LOC_Os03g20720 or LOC_Os03g12940 or LOC_Os03g02010	Alanine, aspartate and glutamate metabolism	2.1.1.49

			or LOC_Os02g37090 or LOC_Os02g35060)		
BETAHHs	betaine aldehyde hydrate hydratase	betaldh[s] -> betald[s] + h2o[s]		Glycine, serine and threonine metabolism	Spontaneous
CHOLMOs	choline monooxygenase	chol[s] + o2[s] + 2 fdxrd[s] -> betaldh[s] + h2o[s] + 2 fdxox[s]	LOC_Os06g48510	Glycine, serine and threonine metabolism	1.14.15.7
GLYB1s	Glycine betane biosynthesis, spontaneous reaction	betald[s] + h2o[s] + nad[s] -> nadh[s] + glybet[s]	(LOC_Os08g32870 or LOC_Os04g39020)	Glycine, serine and threonine metabolism	Spontaneous
ICHORSs	isochorismatase	ichor[s] + h2o[s] -> 23ddhb[s] + pyr[s]	(LOC_Os02g17640 or LOC_Os04g44420)	Primary Cell Wall Metabolism (Membrane)	3.3.2.1
23DDHBDHs	2,3-dihydro-2,3-dihydroxybenzoate dehydrogenase	23ddhb[s] + nad[s] -> 23dhb[s] + nadh[s] + h[s]	(LOC_Os12g13930 or LOC_Os12g27830)	Primary Cell Wall Metabolism (Membrane)	1.3.1.28
ENTBSs	enterobactin synthetase	6 atp[s] + 3 ser-L[s] + 3 23dhb[s] -> entb[s] + 6 ppi[s] + 6 amp[s]		Primary Cell Wall Metabolism (Membrane)	
GDPMDHc	GDP-mannose 4,6-dehydratase	g1p[c] + dttp[c] -> dtdpglu[c] + ppi[c]	(LOC_Os08g13930 or LOC_Os03g52460 or LOC_Os03g16150 or LOC_Os03g11050 or LOC_Os01g62840)	Primary Cell Wall Metabolism (Membrane)	2.7.7.24
TDPGDHc	dTDP-glucose 4,6-dehydratase	dtdpglu[c] -> dtdp4d6dg[c] + h2o[c]	(LOC_Os09g34090 or LOC_Os08g03570 or LOC_Os07g04690 or LOC_Os06g44270 or LOC_Os06g44260 or LOC_Os06g04620 or LOC_Os05g11360 or LOC_Os04g52730 or LOC_Os03g29170 or LOC_Os03g29150 or LOC_Os03g17000 or LOC_Os03g16980 or LOC_Os03g14540 or LOC_Os02g48460)	Primary Cell Wall Metabolism (Membrane)	4.2.1.46
TDPDREc	dTDP-4-dehydrorhamnose 3,5-epimerase	dtdp4d6dg[c] <=> dtdp4d6dm[c]		Primary Cell Wall Metabolism (Membrane)	5.1.3.13
DTDPDHRRc	dTDP-4-dehydrorhamnose reductase	dtdp4d6dm[c] + nadph[c] + h[c] -> dtdprmn[c] + nadp[c]	(LOC_Os03g29150 or LOC_Os08g03570 or LOC_Os06g04620 or LOC_Os06g44260 or LOC_Os06g44270 or LOC_Os04g52730 or LOC_Os03g14540 or LOC_Os03g17000 or LOC_Os03g29170 or LOC_Os02g48460 or LOC_Os02g57180 or LOC_Os02g57990)	Primary Cell Wall Metabolism (Membrane)	1.1.1.133
ARAB5PIc	arabinose-5-phosphate isomerase	r5p[c] <=> ara5p[c]	LOC_Os02g06360	Primary Cell Wall Metabolism (Membrane)	5.3.1.13
KDOPSc	3-deoxy-8-phosphooctulonate synthase	pep[c] + ara5p[c] + h2o[c] -> pi[c] + kdo8p[c]	LOC_Os12g10784	Primary Cell Wall Metabolism (Membrane)	2.5.1.55
KDOPPc	3-deoxy-manno-octulosonate-8-phosphatase	kdo8p[c] + h2o[c] -> kdo[c] + pi[c]		Primary Cell Wall Metabolism (Membrane)	3.1.3.45
KDOCTc	3-deoxy-manno-octulosonate cytidylyltransferase	ctp[c] + kdo[c] -> ppi[c] + ckdo[c]	LOC_Os05g48750	Primary Cell Wall Metabolism (Membrane)	2.7.7.38
UAGAATm	UDP-N-acetylglucosamine acyltransferase	3hmrsACP[m] + uacgam[m] <=> ACP[m] + u3aga[m]	LOC_Os01g52400	Primary Cell Wall Metabolism (Membrane)	2.3.1.129
UHGADAm	UDP-3-O-acetylglucosamine deacetylase	h2o[m] + u3aga[m] -> ac[m] + u3hga[m]	LOC_Os03g12320	Primary Cell Wall Metabolism (Membrane)	3.5.1.108
U23GAATm	UDP-3-O-(3-hydroxymyristoyl)glucosamine acyltransferase	3hmrsACP[m] + u3hga[m] -> ACP[m] + h[m] + u23ga[m]	LOC_Os07g04200	Primary Cell Wall Metabolism (Membrane)	2.3.1.191
USHDm	UDP-sugar hydrolase	h2o[m] + u23ga[m] -> 2 h[m] + lipidX[m] + ump[m]		Primary Cell Wall Metabolism (Membrane)	3.6.1.54
LPADSSm	Lipid A disaccaride synthase	lipidX[m] + u23ga[m] -> h[m] + lipidAds[m] + udp[m]	LOC_Os01g54900	Primary Cell Wall Metabolism (Membrane)	2.4.1.182
TDSKm	Tetraacyldisaccharide 4-kinase	atp[m] + lipidAds[m] -> adp[m] + h[m] + lipidA[m]	LOC_Os07g01200	Primary Cell Wall Metabolism (Membrane)	2.7.1.130
MOATm	3-deoxy-D-manno-octulosonic acid transferase	ckdo[m] + lipidA[m] -> cmp[m] + h[m] + kdolipid4[m]	LOC_Os01g63840	Primary Cell Wall Metabolism (Membrane)	2.4.99.12

MOAT2m	3-deoxy-D-manno-octulosonic acid transferase	ckdo[m] + kdolipid4[m] -> cmp[m] + h[m] + kdo2lipid4[m]	LOC_Os01g63840	Primary Cell Wall Metabolism (Membrane)	2.4.99.13
UACGAMCVTc	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	pep[c] + uacgam[c] -> uaccg[c] + pi[c]	(LOC_Os03g30934 and LOC_Os02g26814)	Glycan Biosynthesis (Peptidoglycan)	2.5.1.7
UACMDHc	UDP-N-acetylmuramate dehydrogenase	uaccg[c] + nadph[c] + h[c] -> uamr[c] + nadp[c]	LOC_Os10g34230	Glycan Biosynthesis (Peptidoglycan)	1.1.1.158
UAMASc	UDP-N-acetylmuramate---L-alanine ligase	uamr[c] + atp[c] + ala-L[c] -> adp[c] + pi[c] + uama[c]	LOC_Os10g40130	Glycan Biosynthesis (Peptidoglycan)	6.3.2.8
GLURc	glutamate racemase	glu-D[c] <=> glu-L[c]	LOC_Os01g37470	Glycan Biosynthesis (Peptidoglycan)	5.1.1.3
UAMAGSc	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase	atp[c] + glu-D[c] + uama[c] -> adp[c] + h[c] + pi[c] + uamag[c]	LOC_Os10g40130	Glycan Biosynthesis (Peptidoglycan)	6.3.2.9
UAAGDSc	UDP-N-acetylmuramoyl-L-alanyl-D-glutamyl-meso-2,6-diaminopimelate synthetase	26dap-M[c] + atp[c] + uamag[c] -> adp[c] + h[c] + pi[c] + ugmd[c]	LOC_Os10g40130	Glycan Biosynthesis (Peptidoglycan)	6.3.2.13
ALARc	alanine racemase	ala-L[c] <=> ala-D[c]		Alanine, aspartate and glutamate metabolism	5.1.1.1
ALAALAc	D-alanine-D-alanine ligase (reversible)	2 ala-D[c] + atp[c] <=> adp[c] + alaala[c] + h[c] + pi[c]	(LOC_Os07g49110 or LOC_Os07g49110)	Glycan Biosynthesis (Peptidoglycan)	6.3.2.4
UGMDDSc	UDP-N-acetylmuramoyl-L-alanyl-D-glutamyl-meso-2,6-diaminopimeloyl-D-alanyl-D-alanine synthetase	alaala[c] + atp[c] + ugmd[c] -> adp[c] + h[c] + pi[c] + ugmda[c]	LOC_Os10g40130	Glycan Biosynthesis (Peptidoglycan)	6.3.2.10
PAPPT3c	phospho-N-acetylmuramoyl-pentapeptide-transferase (meso-2,6-diaminopimelate)	udcpp[c] + ugmda[c] -> uagmda[c] + ump[c]	LOC_Os01g11260	Glycan Biosynthesis (Peptidoglycan)	2.7.8.13
UAGPT3c	UDP-N-acetyl-D-glucosamine:undecaprenyl-diphospho-N-acetylmuramoyl- L-alanyl-gamma-D-glutamyl-meso-2,6-diaminopimeloyl-D-alanyl-D- alanine 4-beta-N-acetylglucosaminlytransferase	uacgam[c] + uagmda[c] -> h[c] + uaagmda[c] + udp[c]	LOC_Os01g33230	Glycan Biosynthesis (Peptidoglycan)	2.4.1.227
STCSDSc	strictosidine synthase	tryptamine[c] + sclgn[c] -> stcsd[c] + h2o[c]	(LOC_Os12g04424 or LOC_Os11g04660 or LOC_Os10g39710 or LOC_Os09g20684 or LOC_Os09g20700 or LOC_Os09g20720 or LOC_Os09g20810 or LOC_Os08g07810 or LOC_Os08g34330 or LOC_Os07g35970 or LOC_Os07g35990 or LOC_Os07g36040 or LOC_Os07g36060 or LOC_Os07g42250 or LOC_Os06g41820 or LOC_Os06g41830 or LOC_Os06g41850 or LOC_Os03g15710 or LOC_Os03g53950 or LOC_Os01g50330)	Phenylalanine, tyrosine and tryptophan metabolism	4.3.3.2
TRPNRc	tropinone (psi-tropine-forming) reductase	pstrp[c] + nadp[c] -> trpn[c] + nadph[c] + h[c]	(LOC_Os11g25230 or LOC_Os04g22730)	Phenylalanine, tyrosine and tryptophan metabolism	1.1.1.236
CNLNSs	L-canaline synthase	hom-L[s] + nh4[s] -> cnln-L[s] + 2 h[s]		Arginine and proline metabolism	
ASPCT2s	Aspartate carbamoyltransferase 2	cnln-L[s] + cbp[s] -> pi[s] + uhom-L[s]	(LOC_Os08g15030 or LOC_Os02g47590)	Arginine and proline metabolism	2.1.3.3
CAVNS2s	argininosuccinate synthase	uhom-L[s] + atp[s] + asp-L[s] -> ppi[s] + amp[s] + cavsucc[s]	(LOC_Os12g13320 or LOC_Os11g19770)	Arginine and proline metabolism	6.3.4.5
ARGSL2s	argininosuccinate lyase	cavsucc[s] -> fum[s] + cav[s]	LOC_Os03g19280	Arginine and proline metabolism	4.3.2.1
ARGCAVs	arginase (cavanine)	cav[s] + h2o[s] -> cnln-L[s] + urea[s] + h[s]	LOC_Os04g01590	Arginine and proline metabolism	3.5.3.1
CC3H1c	p-coumarate:caffeate 3-hydroxylase	coum[c] + nadph[c] + o2[c] -> caff[c] + nadp[c] + h2o[c]	LOC_Os05g41440	Phenylpropanoid metabolism	
CAFFMTc	caffeate O-methyltransferase	amet[c] + caff[c] -> ahcys[c] + fer[c]	(LOC_Os08g06100 or LOC_Os02g57760 or LOC_Os04g01470 or LOC_Os12g13800)	Phenylpropanoid metabolism	2.1.1.68
FERHc	ferulate 5-hydroxylase	fer[c] + nadph[c] + o2[c] -> hfer[c] + nadp[c] + h2o[c]	(LOC_Os10g36848 or LOC_Os06g24180	Phenylpropanoid metabolism	

			or LOC_Os03g02180)		
HFERMTc	hydroxy-ferulate O-methyltransferase	amet[c] + hfer[c] -> ahcys[c] + sin[c]	(LOC_Os08g06100 or LOC_Os02g57760 or LOC_Os04g01470 or LOC_Os12g13800)	Phenylpropanoid metabolism	2.1.1.68
DHQRc	dihydroquercetin reductase	dhqrctn[c] + nadph[c] -> lcdpn[c] + nadp[c]	LOC_Os01g44260	Flavonoid biosynthesis	1.1.1.219
LCAKGORc	leucocyanidin,2-oxoglutarate:oxygen oxidoreductase	lcdpn[c] + akg[c] + o2[c] -> dlpdn[c] + succ[c] + co2[c] + 2 h2o[c]	LOC_Os01g27490	Flavonoid biosynthesis	1.14.11.19
UDPGATc	UDP-glucose:anthocyanidin 3-O-D-glucosyltransferase	udpg[c] + dlpdn[c] -> udp[c] + dldpng[c]	(LOC_Os06g09240 or LOC_Os07g05420 or LOC_Os08g15330)	Flavonoid biosynthesis	2.4.1.115
UDPGAGGc	UDP-glucose:anthocyanidin 3-glucoside-2-O-glucosyltransferase	dldpng[c] + udpg[c] -> udp[c] + dldpndg[c]	(LOC_Os01g08440 or LOC_Os02g10880 or LOC_Os06g39270 or LOC_Os06g39330)	Flavonoid biosynthesis	2.4.1.-
GENT1c	hydroxycinnamoyl-CoA:anthocyanidin 3,5-diglucoside 5-O-glucoside-6-O-hydroxycinnamoyltransferase	dldpndg[c] + caffcoa[c] -> dldpngcaff[c] + coa[c]	LOC_Os04g54570	Flavonoid biosynthesis	2.3.1.153
GENT2c	UDP-glucose:anthocyanidin-3-glucoside glucosyltransferase	dldpngcaff[c] + udpg[c] -> udp[c] + dlgcgg[c]	(LOC_Os06g09240 or LOC_Os07g05420 or LOC_Os08g15330)	Flavonoid biosynthesis	2.4.1.-
GENT3c	UDP-glucose:anthocyanidin-3-glucoside glucosyltransferase	dldpndg[c] + udpg[c] -> dldpntg[c] + udp[c]	(LOC_Os06g09240 or LOC_Os07g05420 or LOC_Os08g15330)	Flavonoid biosynthesis	2.4.1.38
GENT4c	anthocyanin 3-O-glucoside 6-O-hydroxycinnamoyltransferase	dldpntg[c] + caffcoa[c] -> dlgcgg[c] + coa[c]	LOC_Os04g54570	Flavonoid biosynthesis	2.3.1.-
GENT5c	anthocyanin 3-O-glucoside 6-O-hydroxycinnamoyltransferase	dlgcgg[c] + caffcoa[c] -> gentdp[c] + coa[c]	LOC_Os04g54570	Flavonoid biosynthesis	2.3.1.-
PLIVLPNSm	phloroisovalerophenone synthase	3 malcoa[m] + ivcoa[m] -> 4 coa[m] + 3 co2[m] + plivlpn[m]	LOC_Os11g32650	Terpenoid biosynthesis (Terpenophenolics biosynthesis)	2.3.1.156
PRET1c	prenyltransferase 1	plivlpn[c] + dmpp[c] -> pplivlpn[c] + ppi[c]	(LOC_Os12g08070 or LOC_Os08g29970 or LOC_Os08g29910 or LOC_Os08g23320 or LOC_Os05g23950 or LOC_Os04g14190 or LOC_Os04g14110 or LOC_Os03g09060 or LOC_Os02g39290)	Terpenoid biosynthesis (Terpenophenolics biosynthesis)	2.3.1.-
PRET2c	prenyltransferase 2	pplivlpn[c] + dmpp[c] -> dpplivlpn[c] + ppi[c]	(LOC_Os12g08070 or LOC_Os08g29970 or LOC_Os08g29910 or LOC_Os08g23320 or LOC_Os05g23950 or LOC_Os04g14190 or LOC_Os04g14110 or LOC_Os03g09060 or LOC_Os02g39290)	Terpenoid biosynthesis (Terpenophenolics biosynthesis)	2.3.1.-
HUMSc	humulone synthase	dpplivlpn[c] + o2[c] -> humu[c] + h2o[c]		Terpenoid biosynthesis (Terpenophenolics biosynthesis)	
PLIBTNSm	phloroisobutyrophenone synthase	3 malcoa[m] + ibcoa[m] -> 4 coa[m] + 3 co2[m] + plibtn[m]	LOC_Os11g32650	Terpenoid biosynthesis (Terpenophenolics biosynthesis)	2.3.1.156
PRET3c	prenyltransferase 3	plibtn[c] + dmpp[c] -> pplibtn[c] + ppi[c]	(LOC_Os12g08070 or LOC_Os08g29970 or LOC_Os08g29910 or LOC_Os08g23320 or LOC_Os05g23950 or LOC_Os04g14190 or LOC_Os04g14110 or LOC_Os03g09060 or LOC_Os02g39290)	Terpenoid biosynthesis (Terpenophenolics biosynthesis)	2.3.1.-
PRET4c	prenyltransferase 4	pplibtn[c] + dmpp[c] -> dpplibtn[c] + ppi[c]	(LOC_Os12g08070 or LOC_Os08g29970 or LOC_Os08g29910 or LOC_Os08g23320 or LOC_Os05g23950 or LOC_Os04g14190 or LOC_Os04g14110 or LOC_Os03g09060 or LOC_Os02g39290)	Terpenoid biosynthesis (Terpenophenolics biosynthesis)	2.3.1.-
CHUMSc	cohumulone synthase	dpplibtn[c] + o2[c] -> chumu[c] + h2o[c]		Terpenoid biosynthesis (Terpenophenolics biosynthesis)	
LGTHLc	lactoylglutathione lyase	gthrd[c] + mthgxl[c] -> lgt-S[c]	(LOC_Os07g46360 or LOC_Os07g06660	Sulfate metabolism	4.4.1.5

			or LOC_Os05g07940 or LOC_Os03g45720 or LOC_Os01g07850 or LOC_Os08g09250 or LOC_Os05g14194 or LOC_Os05g22970 or LOC_Os02g17920)	(Glutathione)	
GLYOXc	hydroxyacylglutathione hydrolase	h2o[c] + lgt-S[c] -> gthrd[c] + h[c] + lac-D[c]	(LOC_Os09g34100 or LOC_Os03g21460 or LOC_Os01g47690)	Sulfate metabolism (Glutathione)	3.1.2.6
LACRc	lactate racemase	lac-D[c] <=> lac-L[c]		Fermentation	5.1.2.1
HMGS_Ss	S-(hydroxymethyl)glutathione synthase (spontaneous)	fald[s] + gthrd[s] <=> hmglut-S[s]	(LOC_Os06g02620 or LOC_Os12g07060)	Sulfate metabolism (Glutathione)	4.4.1.22
HMGDys	S-(hydroxymethyl)glutathione dehydrogenase	hmglut-S[s] + nadp[s] -> fglut-S[s] + h[s] + nadph[s]	LOC_Os02g57040	Sulfate metabolism (Glutathione)	1.1.1.284
SFGTHs	S-Formylglutathione hydralase	fglut-S[s] + h2o[s] -> for[s] + gthrd[s] + h[s]	LOC_Os01g71300	Sulfate metabolism (Glutathione)	3.1.2.12
SODs	superoxide dismutase	2 suo2[s] + 2 h[s] -> h2o2[s] + o2[s]	(LOC_Os08g44770 or LOC_Os07g46990 or LOC_Os06g02500 or LOC_Os06g05110 or LOC_Os05g25850 or LOC_Os03g22810)	Ascorbate metabolism; Water-water cycle	1.15.1.1
MRs	Mehler reaction	fdxrd[u] + 2 o2[s] -> 2 suo2[s] + fdxox[u]		Ascorbate metabolism; Water-water cycle	
CBFCNCEFs	cytochrome b6/f complex	2 h[s] + 2 pccu2p[u] + pqh2[u] -> 4 h[u] + 2 pccu1p[u] + pq[u]	(LOC_Os07g37030 and LOC_Os01g57941 and LOC_Os03g55720 and LOC_Osp1g00530 and LOC_Osp1g00650 and LOC_Osp1g00640 and LOC_Osp1g00540 and LOC_Osp1g00480)	Photosynthesis; Photophosphorylation	1.10.9.1
CCEFs	Cyclic electron flow	fdxrd[u] + pq[u] -> fdxox[u] + pqh2[u]	(LOC_Os07g37030 and LOC_Os01g57941 and LOC_Os03g55720 and LOC_Osp1g00530 and LOC_Osp1g00650 and LOC_Osp1g00640 and LOC_Osp1g00540 and LOC_Osp1g00480)	Photosynthesis; Photophosphorylation	
FNORs	ferredoxin---NADP+ reductase	2 fdxrd[u] + nadp[s] + h[s] -> 2 fdxox[u] + nadph[s]	(LOC_Os02g01340 or LOC_Os06g01850 or LOC_Os07g05400)	Photosynthesis; GS-GOGAT Cycle	1.18.1.2
PSIMR1blue	photosystem I (blue light-activated)	fdxox[u] + 2 pccu1p[u] + 2 photonPSI[u] + 2 h[u] -> fdxrd[u] + 2 pccu2p[u]	(LOC_Osp1g00920 and LOC_Osp1g00450 and LOC_Osp1g00550 and LOC_Osp1g00350 and (LOC_Osp1g00340 and LOC_Osp1g00330) and LOC_Os06g21590 and LOC_Os07g38960 and LOC_Os08g33820 and LOC_Os09g26810 and LOC_Os04g38410 and LOC_Os09g17740 and LOC_Os01g41710 and LOC_Os09g12540 and LOC_Os08g44680 and LOC_Os07g25430 and LOC_Os03g56670 and LOC_Os09g30340 and LOC_Os05g48630 and LOC_Os07g05480 and LOC_Os12g23200 and LOC_Os12g08770 and LOC_Os04g33830)	Photosynthesis; Water-water cycle	
PSIINCblue	photosystem II (blue light-activated)	2 h2o[u] + 4 photonPSII[u] + 2 pq[u] -> o2[u] + 2 pqh2[u]	(LOC_Osp1g00110 and LOC_Osp1g00170 and LOC_Osp1g00150 and LOC_Osp1g00490 and LOC_Osp1g00140 and LOC_Osp1g00500 and LOC_Osp1g00630 and LOC_Osp1g00610 and LOC_Os04g57310 and LOC_Os07g37240 and LOC_Os11g13890 and LOC_Os04g38410 and LOC_Os01g52240 and LOC_Os03g39610 and LOC_Os07g37550 and LOC_Os09g12540 and LOC_Os09g17740	Photosynthesis	

			and LOC_Os01g41710 and LOC_Os01g52240 and LOC_Os03g39610 and LOC_Os04g38410 and LOC_Os01g71190 and LOC_Os01g31690 and LOC_Os12g37710 and LOC_Os04g35530 and LOC_Os08g40160 and LOC_Os12g08830 and LOC_Os01g43070 and LOC_Os01g59090 and LOC_Os04g44200 and LOC_Os07g36080 and LOC_Os02g36850 and LOC_Os07g01480 and LOC_Os07g05360 and LOC_Os01g64960 and LOC_Os01g56680 and LOC_Os08g02630)		
ACHMSSCc	O-Acetylhomoserine succinate-lyase (adding cysteine), cytosol	achms[c] + selcys[c] -> selcyst[c] + ac[c]	(LOC_Os03g25940 or LOC_Os10g25950 or LOC_Os10g26010)	Selenoamino acid metabolism	2.5.1.48
ACHMSSCs	O-Acetylhomoserine succinate-lyase (adding cysteine), chloroplast	achms[s] + selcys[s] -> selcyst[s] + ac[s]	(LOC_Os03g25940 or LOC_Os10g25950 or LOC_Os10g26010)	Selenoamino acid metabolism	2.5.1.48
ACSERLc	O3-Acetyl-L-serine acetate-lyase (adding hydrogen sulfide), cytosol	acser[c] + seln[c] <=> selcys[c] + ac[c] + 2 h[c]	(LOC_Os06g36850 or LOC_Os06g36820 or LOC_Os01g74650 or LOC_Os06g05700 or LOC_Os03g50510 or LOC_Os06g42560 or LOC_Os01g59920 or (LOC_Os06g36880 or LOC_Os12g42980 or LOC_Os04g08350 or LOC_Os06g05690 or LOC_Os02g12900 or LOC_Os06g36840 or LOC_Os04g32010 or LOC_Os03g53650))	Selenoamino acid metabolism	2.5.1.47
ACSERLs	O3-Acetyl-L-serine acetate-lyase (adding hydrogen sulfide), chloroplast	acser[s] + seln[s] <=> selcys[s] + ac[s] + 2 h[s]	(LOC_Os06g36850 or LOC_Os06g36820 or LOC_Os01g74650 or LOC_Os06g05700 or LOC_Os03g50510 or LOC_Os06g42560 or LOC_Os01g59920 or (LOC_Os06g36880 or LOC_Os12g42980 or LOC_Os04g08350 or LOC_Os06g05690 or LOC_Os02g12900 or LOC_Os06g36840 or LOC_Os04g32010 or LOC_Os03g53650))	Selenoamino acid metabolism	2.5.1.47
PHOMSCc	O-Phosphorylhomoserine succinate-lyase (adding cysteine), cytosol	phom[c] + selcys[c] + h[c] -> selcyst[c] + pi[c]	(LOC_Os03g25940 or LOC_Os10g25950 or LOC_Os10g26010)	Selenoamino acid metabolism	2.5.1.48
PHOMSCs	O-Phosphorylhomoserine succinate-lyase (adding cysteine), chloroplast	phom[s] + selcys[s] + h[s] -> selcyst[s] + pi[s]	(LOC_Os03g25940 or LOC_Os10g25950 or LOC_Os10g26010)	Selenoamino acid metabolism	2.5.1.48
SEAHCYSHYDc	Se-Adenosylselenohomocysteine hydrolase	seahcys[c] + h2o[c] <=> adn[c] + selhcys[c] + h[c]	LOC_Os11g26850	Selenoamino acid metabolism	3.3.1.1
SELCYSLY2	Selenocysteine reductase	selcys[c] + pdx5p[c] + h[c] -> seln[c] + ala-L[c] + pydx5p[c]	LOC_Os12g18900	Selenoamino acid metabolism	4.4.1.16
SELCYSTLc	Selenocystathionine L-homocysteine-lyase (deaminating), cytosol	selcyst[c] + h2o[c] -> selhcys[c] + nh4[c] + pyr[c] + h[c]	LOC_Os06g07860	Selenoamino acid metabolism	4.4.1.8
SELCYSTLs	Selenocystathionine L-homocysteine-lyase (deaminating), chloroplast	selcyst[s] + h2o[s] -> selhcys[s] + nh4[s] + pyr[s] + h[s]	LOC_Os06g07860	Selenoamino acid metabolism	4.4.1.8
SELTORc	Selenite:ferredoxin oxidoreductase, cytosol	selt[c] + 6 fdxrd[c] -> seln[c] + 6 fdxox[c] + 3 h2o[c] + 6 h[c]	LOC_Os05g42350	Selenoamino acid metabolism	1.8.7.1
SUCHMSSELCYSL	O-Succinyl-L-homoserine succinate-lyase (adding cysteine), cytosol	suchms[c] + selcys[c] -> selcyst[c] + succ[c]	(LOC_Os03g25940 or LOC_Os10g25950 or LOC_Os10g26010)	Selenoamino acid metabolism	2.5.1.48
SECYSTLc	selenocysteine---tRNA ligase	atp[c] + ser-L[c] + trnasecys[c] -> amp[c] + ppi[c] + sertrna(sec)[c]	(LOC_Os03g10190 or LOC_Os01g37837 or LOC_Os11g39670)	Selenoamino acid metabolism	6.1.1.11
METTSc	methionyl-tRNA synthetase	atp[c] + selmet[c] + trnasemet[c] -> amp[c] + ppi[c] + sertrna(met)[c]	(LOC_Os06g31210 or LOC_Os03g11120 or LOC_Os10g26050)	Selenoamino acid metabolism	6.1.1.10
METSMTFc	methionine S-methyltransferase	selmet[c] + amet[c] <=> semetselmet[c] + achms[c]	LOC_Os05g01470	Selenoamino acid metabolism	2.1.1.12
SELMETLs	Selenomethionine methanethiol-lyase (deaminating)	selmet[c] + h2o[c] <=> metsel[c] + nh4[c] + 2obut[c]	LOC_Os10g37340	Selenoamino acid metabolism	4.1.1.11

SELNPS	selenophosphate synthase	seln[c] + atp[c] + h2o[c] <=> selnp[c] + amp[c] + pi[c]		Selenoamino acid metabolism	2.7.9.3
MCFTc	24-methylenecycloartanyl feruloyltransferase	menecyart[c] + fercoa[c] -> mcfer[c] + coa[c]		Flavonoid biosynthesis	
CYARTFTc	Cycloartenol feruloyltransferase	cyart[c] + fercoa[c] -> cyartfer[c] + coa[c]		Flavonoid biosynthesis	
CAMPSTFTc	campesterol feruloyltransferase	campst[c] + fercoa[c] -> campstfer[c] + coa[c]		Flavonoid biosynthesis	
SITSTFTc	sitosterol feruloyltransferase	sitst[c] + fercoa[c] -> sitstfer[c] + coa[c]		Flavonoid biosynthesis	
LEVSc	levansucrase	1-kesttr[c] + sucr[c] -> 16-kesttt[c] + glc-B[c]	LOC_Os02g01590	Starch and sucrose metabolism (Cellulose)	2.4.1.10
SSFTc	sucrose:sucrose fructosyltransferase	2 sucr[c] -> 1-kesttr[c] + glc-B[c]	LOC_Os02g01590	Starch and sucrose metabolism (Cellulose)	2.4.1.99
FFFTc	2,1-fructan:2,1-fructan 1-fructosyltransferase	2 1-kesttr[c] -> 11-kesttt[c] + sucr[c]	LOC_Os02g01590	Starch and sucrose metabolism (Cellulose)	2.4.1.100
SFFTc	sucrose:fructan 6-fructosyltransferase	2 sucr[c] -> 6-kesttr[c] + glc-B[c]	LOC_Os02g01590	Starch and sucrose metabolism (Cellulose)	2.4.1.10
FRCEXHc	fructan exohydrolase	1-kesttr[c] + h2o[c] -> fru-B[c] + sucr[c]	LOC_Os01g73580	Starch and sucrose metabolism (Cellulose)	3.2.1.80
DGSNTTPc	diguanosinetetraphosphatase	gtp[c] + gmp[c] <=> h2o[c] + gppppg[c]	LOC_Os04g58900	Purine metabolism	3.6.1.17
ACPCDAc	1-aminocyclopropane-1-carboxylate deaminase	1acpc[c] + h2o[c] <=> nh4[c] + 2obut[c]	(LOC_Os01g50060 or LOC_Os02g53330)	Cysteine and methionine metabolism	3.5.99.7
AHCYSNc	adenosylhomocysteine nucleosidase	ahcys[c] + h2o[c] <=> ade[c] + rhcys-L[c]	LOC_Os06g02220	Purine metabolism	3.2.2.9
ADECYCc	adenylate cyclase	atp[c] <=> camp[c] + ppi[c]	LOC_Os08g20400	Purine metabolism	4.6.1.1
TYRMOc	tyrosine 3-monooxygenase	tyr-L[c] + thbpt[c] + o2[c] -> dopa-L[c] + 4hthbpt[c]	LOC_Os03g10060	Phenylalanine, tyrosine and tryptophan metabolism	1.14.16.2
4HTHBPTHLc	4a-hydroxytetrahydrobiopterin hydro-lyase	4hthbpt[c] <=> dhbpt[c] + h2o[c]	LOC_Os03g01030	Folates metabolism	4.2.1.96
THBPTDHc	5,6,7,8-tetrahydrobiopterin:NAD+ oxidoreductase	dhbpt[c] + nadh[c] + h[c] <=> thbpt[c] + nad[c]		Folates metabolism	1.5.1.34
PHENMUTc	phosphopentomutase	2dr1p[c] <=> 2dr5p[c]		Purine metabolism	5.4.2.7
DRPAc	deoxyribose-phosphate aldolase	2dr5p[c] -> acald[c] + g3p[c]		Purine metabolism	4.1.2.4
UDPGALMc	UDP-galactopyranose mutase	udpgal[c] <=> udpgalfur[c]		Starch and sucrose metabolism (Cellulose)	5.4.99.9
THD2c	NAD(P) transhydrogenase (mitochondrial)	nadh[m] + nadp[m] + 2 h[c] -> nadph[m] + nad[m] + 2 h[m]		Nicotinate and Nicotinamide metabolism	1.6.1.1
MALTDPs	maltodextrin phosphorylase	malttt[s] + pi[s] <=> maltt[s] + g1p[s]	(LOC_Os03g55090 or LOC_Os01g63270)	Starch and sucrose metabolism (Starch)	2.4.1.1
MALTGAMs	maltase-glucoamylase	maltt[s] + h2o[s] <=> malt[s] + glc-A[s]	LOC_Os06g46284	Starch and sucrose metabolism (Starch)	3.2.1.20
NRGNMTc	naringenin 7-O-methyltransferase	nrgn[c] + amet[c] -> sakur[c] + ahcys[c]	LOC_Os12g13810	Flavonoid biosynthesis	2.1.1.232
UDPGLTLNGc	UDP-glucose-luteolin beta-D-glucosyltransferase	ltln[c] + udpg[c] -> ltlng[c] + udp[c]	(LOC_Os08g38110 or LOC_Os06g17110 or LOC_Os01g41450 or LOC_Os06g39070 or LOC_Os06g08830)	Flavonoid biosynthesis	2.4.1.81
UDPRMNLc	UDP-L-rhamnose:luteolin-7-O-beta-D-glucoside 2-O-alpha-L-rhamnosyltransferase	ltlng[c] + udprmn[c] -> ltlnnp[c] + udp[c] + h[c]	LOC_Os07g47550	Flavonoid biosynthesis	2.4.1.236
UDPGAPGNGc	UDPglucose:apigenin 7-O-beta-D-glucosyltransferase	apgn[c] + udpg[c] -> apgng[c] + udp[c]	(LOC_Os08g38110 or LOC_Os06g17110 or LOC_Os01g41450 or LOC_Os06g39070 or LOC_Os06g08830)	Flavonoid biosynthesis	2.4.1.81
UDPRMNAc	UDP-L-rhamnose:apigenin 7-O-beta-D-glucoside 2-O-beta-L-rhamnosyltransferase	apgng[c] + udprmn[c] -> apgnnp[c] + udp[c] + h[c]	LOC_Os07g47550	Flavonoid biosynthesis	2.4.1.236
CRPESc	beta-caryophyllene synthase	frdp[c] -> crpe[c] + ppi[c]	LOC_Os01g23530	Terpenoid biosynthesis (Sesquiterpenoid/Triterpenoid biosynthesis)	4.2.3.57
HUMLSc	alpha-humulene synthase	frdp[c] -> huml[c] + ppi[c]	LOC_Os01g23530	Terpenoid biosynthesis (Sesquiterpenoid/Triterpenoid biosynthesis)	4.2.3.104
ELMSc	beta-elemene synthase	frdp[c] -> elm[c] + ppi[c]	LOC_Os01g23530	Terpenoid biosynthesis (Sesquiterpenoid/Triterpenoid biosynthesis)	4.2.3.-
GAAKORG4498c	(gibberellin-4),2-oxoglutarate:oxygen	ga44[c] + o2[c] + akg[c] + 2 h[c] -> ga98[c] + co2[c] + succ[c]	(LOC_Os01g09300 or LOC_Os07g01340)	Phytohormones biosynthesis	1.14.11.-

	oxidoreductase			(Gibberallins)	
NADtm	NAD transporter, mitochondrial	nad[c] <=> nad[m]		Transport (Mitochondrial)	
UACGAMtm	UDP-N-acetyl-D-glucosamine transport, mitochondrial	uacgam[c] <=> uacgam[m]		Transport (Mitochondrial)	
CKDOtm	CMPKDO transport, mitochondrial	ckdo[c] <=> ckdo[m]		Transport (Mitochondrial)	
THFtm	Tetrahydrofolate transport, diffusion, mitochondrial	thf[m] <=> thf[c]	(LOC_Os01g32980 or LOC_Os03g52430)	Transport (Mitochondrial)	
FORtm	formate transport out via proton symport, mitochondrial	for[m] + h[m] -> for[c] + h[c]		Transport (Mitochondrial)	
ADENm	adenine nucleotide carrier, mitochondrial	amp[m] + atp[c] + 2 h[c] -> amp[c] + atp[m] + 2 h[m]		Transport (Mitochondrial)	
PYRt2m	pyruvate mitochondrial transport via proton symport	pyr[c] + h[c] <=> pyr[m] + h[m]	(LOC_Os01g11160 or LOC_Os01g42234 or LOC_Os02g43860 or LOC_Os02g47210 or LOC_Os03g25820 or LOC_Os03g25840 or LOC_Os03g25869 or LOC_Os03g25920 or LOC_Os03g37984 or LOC_Os03g43970 or LOC_Os03g43980 or LOC_Os03g45170 or LOC_Os04g35540 or LOC_Os04g45950 or LOC_Os06g34830 or LOC_Os08g41370 or LOC_Os10g30090 or LOC_Os11g05690 or LOC_Os12g06060 or LOC_Os12g39080 or LOC_Os12g41890 or LOC_Os12g42850)	Transport (Mitochondrial)	
ASPt2m	Amino acid transporter (asp-L), mitochondrial	asp-L[m] + h[m] <=> asp-L[c] + h[c]	(LOC_Os01g11160 or LOC_Os01g42234 or LOC_Os02g43860 or LOC_Os02g47210 or LOC_Os03g25820 or LOC_Os03g25840 or LOC_Os03g25869 or LOC_Os03g25920 or LOC_Os03g37984 or LOC_Os03g43970 or LOC_Os03g43980 or LOC_Os03g45170 or LOC_Os04g35540 or LOC_Os04g45950 or LOC_Os06g34830 or LOC_Os08g41370 or LOC_Os10g30090 or LOC_Os11g05690 or LOC_Os12g06060 or LOC_Os12g39080 or LOC_Os12g41890 or LOC_Os12g42850)	Transport (Mitochondrial)	
CYSt2m	Amino acid transporter (cys-L), mitochondrial	cys-L[m] + h[m] <=> cys-L[c] + h[c]	(LOC_Os01g11160 or LOC_Os01g42234 or LOC_Os02g43860 or LOC_Os02g47210 or LOC_Os03g25820 or LOC_Os03g25840 or LOC_Os03g25869 or LOC_Os03g25920 or LOC_Os03g37984 or LOC_Os03g43970 or LOC_Os03g43980 or LOC_Os03g45170 or LOC_Os04g35540 or LOC_Os04g45950 or LOC_Os06g34830 or LOC_Os08g41370 or LOC_Os10g30090 or LOC_Os11g05690 or LOC_Os12g06060 or LOC_Os12g39080 or LOC_Os12g41890 or LOC_Os12g42850)	Transport (Mitochondrial)	
THRt2m	Amino acid transporter (thr-L), mitochondrial	thr-L[m] + h[m] <=> thr-L[c] + h[c]	(LOC_Os01g11160 or LOC_Os01g42234 or LOC_Os02g43860 or LOC_Os02g47210 or LOC_Os03g25820 or LOC_Os03g25840 or LOC_Os03g25869 or LOC_Os03g25920 or LOC_Os03g37984 or LOC_Os03g43970 or LOC_Os03g43980 or LOC_Os03g45170 or LOC_Os04g35540 or LOC_Os04g45950 or LOC_Os06g34830 or LOC_Os08g41370 or LOC_Os10g30090 or LOC_Os11g05690 or LOC_Os12g06060 or LOC_Os12g39080 or LOC_Os12g41890 or	Transport (Mitochondrial)	

			LOC_Os12g42850)		
LYSt2m	Amino acid transporter (lys-L), mitochondrial	lys-L[m] + h[m] <=> lys-L[c] + h[c]	(LOC_Os01g11160 or LOC_Os01g42234 or LOC_Os02g43860 or LOC_Os02g47210 or LOC_Os03g25820 or LOC_Os03g25840 or LOC_Os03g25869 or LOC_Os03g25920 or LOC_Os03g37984 or LOC_Os03g43970 or LOC_Os03g43980 or LOC_Os03g45170 or LOC_Os04g35540 or LOC_Os04g45950 or LOC_Os06g34830 or LOC_Os08g41370 or LOC_Os10g30090 or LOC_Os11g05690 or LOC_Os12g06060 or LOC_Os12g39080 or LOC_Os12g41890 or LOC_Os12g42850)	Transport (Mitochondrial)	
METt2m	Amino acid transporter (met-L), mitochondrial	met-L[m] + h[m] <=> met-L[c] + h[c]	(LOC_Os01g11160 or LOC_Os01g42234 or LOC_Os02g43860 or LOC_Os02g47210 or LOC_Os03g25820 or LOC_Os03g25840 or LOC_Os03g25869 or LOC_Os03g25920 or LOC_Os03g37984 or LOC_Os03g43970 or LOC_Os03g43980 or LOC_Os03g45170 or LOC_Os04g35540 or LOC_Os04g45950 or LOC_Os06g34830 or LOC_Os08g41370 or LOC_Os10g30090 or LOC_Os11g05690 or LOC_Os12g06060 or LOC_Os12g39080 or LOC_Os12g41890 or LOC_Os12g42850)	Transport (Mitochondrial)	
PHEt2m	Amino acid transporter (phe-L), mitochondrial	phe-L[m] + h[m] <=> phe-L[c] + h[c]	(LOC_Os01g11160 or LOC_Os01g42234 or LOC_Os02g43860 or LOC_Os02g47210 or LOC_Os03g25820 or LOC_Os03g25840 or LOC_Os03g25869 or LOC_Os03g25920 or LOC_Os03g37984 or LOC_Os03g43970 or LOC_Os03g43980 or LOC_Os03g45170 or LOC_Os04g35540 or LOC_Os04g45950 or LOC_Os06g34830 or LOC_Os08g41370 or LOC_Os10g30090 or LOC_Os11g05690 or LOC_Os12g06060 or LOC_Os12g39080 or LOC_Os12g41890 or LOC_Os12g42850)	Transport (Mitochondrial)	
ILEt2m	Amino acid transporter (ile-L), mitochondrial	ile-L[m] + h[m] <=> ile-L[c] + h[c]	(LOC_Os01g11160 or LOC_Os01g42234 or LOC_Os02g43860 or LOC_Os02g47210 or LOC_Os03g25820 or LOC_Os03g25840 or LOC_Os03g25869 or LOC_Os03g25920 or LOC_Os03g37984 or LOC_Os03g43970 or LOC_Os03g43980 or LOC_Os03g45170 or LOC_Os04g35540 or LOC_Os04g45950 or LOC_Os06g34830 or LOC_Os08g41370 or LOC_Os10g30090 or LOC_Os11g05690 or LOC_Os12g06060 or LOC_Os12g39080 or LOC_Os12g41890 or LOC_Os12g42850)	Transport (Mitochondrial)	
VALt2m	Amino acid transporter (val-L), mitochondrial	val-L[m] + h[m] <=> val-L[c] + h[c]	(LOC_Os01g11160 or LOC_Os01g42234 or LOC_Os02g43860 or LOC_Os02g47210 or LOC_Os03g25820 or LOC_Os03g25840 or LOC_Os03g25869 or LOC_Os03g25920 or LOC_Os03g37984 or LOC_Os03g43970 or LOC_Os03g43980 or LOC_Os03g45170 or LOC_Os04g35540 or LOC_Os04g45950 or LOC_Os06g34830 or LOC_Os08g41370	Transport (Mitochondrial)	

			or LOC_Os10g30090 or LOC_Os11g05690 or LOC_Os12g06060 or LOC_Os12g39080 or LOC_Os12g41890 or LOC_Os12g42850)		
TYRt2m	Amino acid transporter (tyr-L), mitochondrial	tyr-L[m] + h[m] <=> tyr-L[c] + h[c]	(LOC_Os01g11160 or LOC_Os01g42234 or LOC_Os02g43860 or LOC_Os02g47210 or LOC_Os03g25820 or LOC_Os03g25840 or LOC_Os03g25869 or LOC_Os03g25920 or LOC_Os03g37984 or LOC_Os03g43970 or LOC_Os03g43980 or LOC_Os03g45170 or LOC_Os04g35540 or LOC_Os04g45950 or LOC_Os06g34830 or LOC_Os08g41370 or LOC_Os10g30090 or LOC_Os11g05690 or LOC_Os12g06060 or LOC_Os12g39080 or LOC_Os12g41890 or LOC_Os12g42850)	Transport (Mitochondrial)	
PROt2m	Amino acid transporter (pro-L), mitochondrial	pro-L[m] + h[m] <=> pro-L[c] + h[c]	(LOC_Os01g11160 or LOC_Os01g42234 or LOC_Os02g43860 or LOC_Os02g47210 or LOC_Os03g25820 or LOC_Os03g25840 or LOC_Os03g25869 or LOC_Os03g25920 or LOC_Os03g37984 or LOC_Os03g43970 or LOC_Os03g43980 or LOC_Os03g45170 or LOC_Os04g35540 or LOC_Os04g45950 or LOC_Os06g34830 or LOC_Os08g41370 or LOC_Os10g30090 or LOC_Os11g05690 or LOC_Os12g06060 or LOC_Os12g39080 or LOC_Os12g41890 or LOC_Os12g42850)	Transport (Mitochondrial)	
HISt2m	Amino acid transporter (his-L), mitochondrial	his-L[m] + h[m] <=> his-L[c] + h[c]	(LOC_Os01g11160 or LOC_Os01g42234 or LOC_Os02g43860 or LOC_Os02g47210 or LOC_Os03g25820 or LOC_Os03g25840 or LOC_Os03g25869 or LOC_Os03g25920 or LOC_Os03g37984 or LOC_Os03g43970 or LOC_Os03g43980 or LOC_Os03g45170 or LOC_Os04g35540 or LOC_Os04g45950 or LOC_Os06g34830 or LOC_Os08g41370 or LOC_Os10g30090 or LOC_Os11g05690 or LOC_Os12g06060 or LOC_Os12g39080 or LOC_Os12g41890 or LOC_Os12g42850)	Transport (Mitochondrial)	
LEUt2m	Amino acid transporter (leu-L), mitochondrial	leu-L[m] + h[m] <=> leu-L[c] + h[c]	(LOC_Os01g11160 or LOC_Os01g42234 or LOC_Os02g43860 or LOC_Os02g47210 or LOC_Os03g25820 or LOC_Os03g25840 or LOC_Os03g25869 or LOC_Os03g25920 or LOC_Os03g37984 or LOC_Os03g43970 or LOC_Os03g43980 or LOC_Os03g45170 or LOC_Os04g35540 or LOC_Os04g45950 or LOC_Os06g34830 or LOC_Os08g41370 or LOC_Os10g30090 or LOC_Os11g05690 or LOC_Os12g06060 or LOC_Os12g39080 or LOC_Os12g41890 or LOC_Os12g42850)	Transport (Mitochondrial)	
TRPt2m	Amino acid transporter (trp-L), mitochondrial	trp-L[m] + h[m] <=> trp-L[c] + h[c]	(LOC_Os01g11160 or LOC_Os01g42234 or LOC_Os02g43860 or LOC_Os02g47210 or LOC_Os03g25820 or LOC_Os03g25840 or LOC_Os03g25869 or LOC_Os03g25920 or LOC_Os03g37984 or LOC_Os03g43970	Transport (Mitochondrial)	

			or LOC_Os03g43980 or LOC_Os03g45170 or LOC_Os04g35540 or LOC_Os04g45950 or LOC_Os06g34830 or LOC_Os08g41370 or LOC_Os10g30090 or LOC_Os11g05690 or LOC_Os12g06060 or LOC_Os12g39080 or LOC_Os12g41890 or LOC_Os12g42850)		
ASPGLU2m	Aspartate-glutamate transporter	asp-L[m] + glu-L[c] <=> asp-L[c] + glu-L[m]	(LOC_Os05g29860 or LOC_Os07g19460)	Transport (Mitochondrial)	
ALAt2m	Amino acid transporter (ala-L), mitochondrial	ala-L[m] + h[m] <=> ala-L[c] + h[c]	(LOC_Os01g11160 or LOC_Os01g42234 or LOC_Os02g43860 or LOC_Os02g47210 or LOC_Os03g25820 or LOC_Os03g25840 or LOC_Os03g25869 or LOC_Os03g25920 or LOC_Os03g37984 or LOC_Os03g43970 or LOC_Os03g43980 or LOC_Os03g45170 or LOC_Os04g35540 or LOC_Os04g45950 or LOC_Os06g34830 or LOC_Os08g41370 or LOC_Os10g30090 or LOC_Os11g05690 or LOC_Os12g06060 or LOC_Os12g39080 or LOC_Os12g41890 or LOC_Os12g42850)	Transport (Mitochondrial)	
H2Otm	H2O transport, mitochondrial	h2o[c] <=> h2o[m]		Transport (Mitochondrial)	
CO2tm	CO2 transport, mitochondrial	co2[c] <=> co2[m]		Transport (Mitochondrial)	
NH4tm	ammonia transport, mitochondrial	nh4[c] <=> nh4[m]		Transport (Mitochondrial)	
NO2tmr	O2 transport (diffusion)	no2[c] <=> no2[m]		Transport (Mitochondrial)	
NO3tmr	NO3 transport (diffusion)	no3[c] <=> no3[m]		Transport (Mitochondrial)	
O2tmr	O2 transport (diffusion)	o2[c] <=> o2[m]		Transport (Mitochondrial)	
FADH2tm	FADH2 transport, mitochondria	fadh2[c] <=> fadh2[m]		Transport (Mitochondrial)	
FADtm	FAD transport by free diffusion, mitochondria	fad[c] <=> fad[m]		Transport (Mitochondrial)	
PItm	phosphate transporter, mitochondrial	pi[c] + h[c] <=> pi[m] + h[m]	(LOC_Os02g52860 or LOC_Os03g15690 or LOC_Os04g37600 or LOC_Os06g10810 or LOC_Os09g28160 or LOC_Os09g38100)	Transport (Mitochondrial)	
H2O2tm	hydrogen peroxide transport via diffusion, mitochondria	h2o2[c] <=> h2o2[m]		Transport (Mitochondrial)	
ATPtm	ADP/ATP transporter, mitochondrial	atp[m] + adp[c] + h[c] -> atp[c] + adp[m] + h[m]	(LOC_Os05g23720 or LOC_Os05g46220 or LOC_Os11g43960)	Transport (Mitochondrial)	
4ABUTtmi	Gamma-aminobutyric acid permease, mitochondrial	4abut[c] + h[m] <=> 4abut[m] + h[c]	(LOC_Os01g71700 or LOC_Os01g71710 or LOC_Os01g71720 or LOC_Os01g71740 or LOC_Os01g71760)	Transport (Mitochondrial)	
SUCFUMtmr	Succinate/fumarate antiporter, mitochondrial	succ[m] + fum[c] <=> fum[m] + succ[c]	(LOC_Os03g18160 or LOC_Os04g44540)	Transport (Mitochondrial)	
GLYtm	Amino acid transporter (gly), mitochondrial	gly[m] + h[m] <=> gly[c] + h[c]	(LOC_Os01g11160 or LOC_Os01g42234 or LOC_Os02g43860 or LOC_Os02g47210 or LOC_Os03g25820 or LOC_Os03g25840 or LOC_Os03g25869 or LOC_Os03g25920 or LOC_Os03g37984 or LOC_Os03g43970 or LOC_Os03g43980 or LOC_Os03g45170 or LOC_Os04g35540 or LOC_Os04g45950 or LOC_Os06g34830 or LOC_Os08g41370 or LOC_Os10g30090 or LOC_Os11g05690 or LOC_Os12g06060 or LOC_Os12g39080 or LOC_Os12g41890 or LOC_Os12g42850)	Transport (Mitochondrial)	
SERtm	Amino acid transporter (ser-L), mitochondrial	ser-L[m] + h[m] <=> ser-L[c] + h[c]	(LOC_Os01g11160 or LOC_Os01g42234 or LOC_Os02g43860 or LOC_Os02g47210 or LOC_Os03g25820 or LOC_Os03g25840 or LOC_Os03g25869 or LOC_Os03g25920	Transport (Mitochondrial)	

			or LOC_Os03g37984 or LOC_Os03g43970 or LOC_Os03g43980 or LOC_Os03g45170 or LOC_Os04g35540 or LOC_Os04g45950 or LOC_Os06g34830 or LOC_Os08g41370 or LOC_Os10g30090 or LOC_Os11g05690 or LOC_Os12g06060 or LOC_Os12g39080 or LOC_Os12g41890 or LOC_Os12g42850)		
DICtm	dicarboxylate transport, mitochondrial	succ[c] + mal-L[m] -> succ[m] + mal-L[c]	(LOC_Os01g14520 or LOC_Os01g28840 or LOC_Os01g43460 or LOC_Os01g12680 or LOC_Os04g48530 or LOC_Os05g13320 or LOC_Os05g18670 or LOC_Os05g50770 or LOC_Os07g08350)	Transport (Mitochondrial)	
MALCITtm	Dicarboxylate/tricarboxylate carrier (mal:cit), mitochondrial	cit[m] + mal-L[c] -> cit[c] + mal-L[m]	(LOC_Os03g07890 or LOC_Os10g25830)	Transport (Mitochondrial)	
MALAKGtm	Malate/2-oxoglutarate carrier, mitochondrial	mal-L[c] + akg[m] -> mal-L[m] + akg[c]	(LOC_Os05g11780 or LOC_Os08g37370 or LOC_Os09g29050 or LOC_Os11g24450)	Transport (Mitochondrial)	
SO4AKGtm	Sulfate/2-oxoglutarate carrier, mitochondrial	so4[m] + akg[c] -> so4[c] + akg[m]	(LOC_Os05g11780 or LOC_Os08g37370 or LOC_Os09g29050 or LOC_Os11g24450)	Transport (Mitochondrial)	
AKGCITtm	Dicarboxylate/tricarboxylate carrier (akg:cit), mitochondrial	akg[c] + cit[m] <=> akg[m] + cit[c]	(LOC_Os03g07890 or LOC_Os10g25830)	Transport (Mitochondrial)	
AKGICITtm	Dicarboxylate/tricarboxylate carrier (akg:icit), mitochondrial	akg[c] + icit[m] <=> akg[m] + icit[c]	(LOC_Os03g07890 or LOC_Os10g25830)	Transport (Mitochondrial)	
MALICITtm	Dicarboxylate/tricarboxylate carrier (mal:icit), mitochondrial	mal-L[c] + icit[m] <=> mal-L[m] + icit[c]	(LOC_Os03g07890 or LOC_Os10g25830)	Transport (Mitochondrial)	
MALOAAtm	Dicarboxylate/tricarboxylate carrier (mal:oaa), mitochondrial	mal-L[m] + oaa[c] <=> mal-L[c] + oaa[m]	(LOC_Os03g07890 or LOC_Os10g25830)	Transport (Mitochondrial)	
OAAAKGtm	Dicarboxylate/tricarboxylate carrier (oaa:akg), mitochondrial	oaa[c] + akg[m] <=> oaa[m] + akg[c]	(LOC_Os03g07890 or LOC_Os10g25830)	Transport (Mitochondrial)	
OAACITtm	Dicarboxylate/tricarboxylate carrier (oaa:cit), mitochondrial	oaa[c] + cit[m] <=> oaa[m] + cit[c]	(LOC_Os03g07890 or LOC_Os10g25830)	Transport (Mitochondrial)	
OAAICITtm	Dicarboxylate/tricarboxylate carrier (oaa:icit), mitochondrial	oaa[c] + icit[m] <=> oaa[m] + icit[c]	(LOC_Os03g07890 or LOC_Os10g25830)	Transport (Mitochondrial)	
ASNtm	Asparagine/H+ symporter, mitochondrial	asn-L[c] + h[c] <=> asn-L[m] + h[m]	(LOC_Os01g11160 or LOC_Os01g42234 or LOC_Os02g43860 or LOC_Os02g47210 or LOC_Os03g25820 or LOC_Os03g25840 or LOC_Os03g25869 or LOC_Os03g25920 or LOC_Os03g37984 or LOC_Os03g43970 or LOC_Os03g43980 or LOC_Os03g45170 or LOC_Os04g35540 or LOC_Os04g45950 or LOC_Os06g34830 or LOC_Os08g41370 or LOC_Os10g30090 or LOC_Os11g05690 or LOC_Os12g06060 or LOC_Os12g39080 or LOC_Os12g41890 or LOC_Os12g42850)	Transport (Mitochondrial)	
ACACt2m	Acetoacetate transport via diffusion, mitochondria	acac[c] <=> acac[m]		Transport (Mitochondrial)	
ORNtm	mitochondrial basic amino acid transporter, orn for arg-L	orn[c] + arg-L[m] <=> orn[m] + arg-L[c]		Transport (Mitochondrial)	
CITRtm	mitochondrial basic amino acid transporter, orn for arg-L	citr-L[c] + arg-L[m] <=> citr-L[m] + arg-L[c]		Transport (Mitochondrial)	
ACtm	acetate transport, mitochondrial	ac[c] <=> ac[m]		Transport (Mitochondrial)	
COAtm	CoA transporter	coa[c] -> coa[m]		Transport (Mitochondrial)	
ACCOAtm	Acetyl-CoA:CoA antiporter, mitochondrial	accoa[c] + coa[m] <=> accoa[m] + coa[c]		Transport (Mitochondrial)	

AMETt2m	S-Adenosyl-L-methionine reversible transport, mitochondrial	ahcys[c] + amet[m] <=> ahcys[m] + amet[c]		Transport (Mitochondrial)	
IPDPtm	isopentenyl pyrophosphate transport, mitochondria	ipdp[c] <=> ipdp[m]		Transport (Mitochondrial)	dead-end
HCO3(h)tmi	hco3 transport, mitochondria	h[c] + hco3[c] -> h[m] + hco3[m]		Transport (Mitochondrial)	
GCOAtm	Glutaconyl-CoA reversible mitochondrial transport	gcoa[c] <=> gcoa[m]		Transport (Mitochondrial)	dead-end
GLXtm	glyoxylate transport, mitochondrial	glx[c] <=> glx[m]		Transport (Mitochondrial)	dead-end
3HPCOAtm	3-Hydroxypropionyl-CoA transport, mitochondria	3hpcoa[m] -> 3hpcoa[c]		Transport (Mitochondrial)	dead-end
CTPtm	CTP/CMP antiport	cmp[m] + ctp[c] + 2 h[c] <=> cmp[c] + ctp[m] + 2 h[m]		Transport (Mitochondrial)	
2AHHMPtm	2-Amino-4-hydroxy-6-hydroxymethyl-7,8-dihydropteridine transport	2ahhmp[c] -> 2ahhmp[m]		Transport (Mitochondrial)	dead-end
4ABZtm	4-Aminobenzoate mitochondrial transport via diffusion	4abz[c] <=> 4abz[m]		Transport (Mitochondrial)	dead-end
THMPPt2m	Thiamine diphosphate transport, mitochondria	thmpp[c] <=> thmpp[m]		Transport (Mitochondrial)	
FMNtm	FMN transport, mitochondrial	fmn[c] -> fmn[m]		Transport (Mitochondrial)	dead-end
PANTtm	pantothenate mitochondrial transport	pant-R[c] <=> pant-R[m]		Transport (Mitochondrial)	dead-end
2OXOADPTm	2-oxoadipate shuttle (cytosol/mitochondria)	2oxoadp[c] + akg[m] <=> 2oxoadp[m] + akg[c]		Transport (Mitochondrial)	
TSULtm	Thiosulfate porter, mitochondrial	tsul[c] + atp[c] + h2o[c] -> tsul[m] + adp[c] + pi[c] + h[c]	(LOC_Os06g03770 or LOC_Os07g28090)	Transport (Mitochondrial)	
5FTHFtm	5-Formyltetrahydrofolate uptake carrier, mitochondria	5fthf[c] + h[c] <=> 5fthf[m] + h[m]	(LOC_Os01g32980 or LOC_Os03g52430)	Transport (Mitochondrial)	
MLTHFtm	5,10-Methylenetetrahydrofolate uptake carrier, mitochondria	mlthf[c] + h[c] <=> mlthf[m] + h[m]	(LOC_Os01g32980 or LOC_Os03g52430)	Transport (Mitochondrial)	
ACSERtmi	efflux pump for O-acetylserine, mitochondria	acser[m] -> acser[c]		Transport (Mitochondrial)	
NA1ATPasem	Na+-translocating F-type ATPase, mitochondrial	na1[m] + atp[m] + h2o[m] -> na1[c] + adp[m] + pi[m] + h[m]	(LOC_Os10g17280 or LOC_Os03g55874 or LOC_Os07g31300 or LOC_Os12g19430 or LOC_Os10g21230 or LOC_Os04g16740 or LOC_Os07g31310 or LOC_Os12g23610 or LOC_Os10g21240 or LOC_Os05g35320 or LOC_Os08g15170 or LOC_Os12g23630 or LOC_Os01g08350 or LOC_Os10g21270 or LOC_Os09g08880 or LOC_Os05g47980 or LOC_Os12g34110 or LOC_Os01g49190 or LOC_Os10g38270 or LOC_Os09g08910 or LOC_Os06g02980 or LOC_Os01g58000 or LOC_Os12g10570)	Transport (Mitochondrial)	
NA1Htm	Na+/H+ antiporter, mitochondrial	h[m] + na1[c] <=> h[c] + na1[m]	(LOC_Os05g05590 or LOC_Os06g21360 or LOC_Os07g47100 or LOC_Os09g11450 or LOC_Os09g30446 or LOC_Os11g42790 or LOC_Os12g44360 or LOC_Os01g60140 or LOC_Os02g58660 or LOC_Os03g61290 or LOC_Os05g02240 or LOC_Os05g19500 or LOC_Os05g31730 or LOC_Os05g39600 or LOC_Os05g40650 or LOC_Os08g02450 or LOC_Os08g43690 or LOC_Os09g37300 or LOC_Os11g01820 or LOC_Os11g03070 or LOC_Os12g01820 or LOC_Os12g02840 or LOC_Os12g42200 or LOC_Os12g44300)	Transport (Mitochondrial)	
PI:natm	phosphate transporter, mitochondrial	pi[c] + na1[c] <=> pi[m] + na1[m]	LOC_Os02g38020	Transport (Mitochondrial)	
PHEMEtm	protoheme transport (mitochondrion)	pheme[m] <=> pheme[c]		Transport (Mitochondrial)	dead-end
FA40COAtm	butanoyl-CoA transport (mitochondria)	btcoa[c] <=> btcoa[m]		Transport (Mitochondrial)	dead-end
MSAtm	malonate-semialdehyde transport, mitochondria	msa[c] -> msa[m]		Transport (Mitochondrial)	dead-end
MHDASCBtm	Monodehydroascorbate transport, mitochondrial	mhdascb[c] -> mhdascb[m]		Transport (Mitochondrial)	dead-end
PINA1tm	Pi:Na+ symporter, mitochondrial	pi[m] + na1[m] -> pi[c] + na1[c]	LOC_Os02g38020	Transport (Mitochondrial)	

CHORtm	Chorismate transport, mitochondrial	chor[m] <=> chor[c]		Transport (Mitochondrial)	dead-end
SO3tm	sulfite transport, mitochondrial	hso3[c] <=> hso3[m]		Transport (Mitochondrial)	dead-end
GLYCtm	glycerol transport, mitochondrial	glyc[c] <=> glyc[m]		Transport (Mitochondrial)	dead-end
CDPDAGtm	CDP-diacylglycerol transport, mitochondrial	cdpdag_os[c] <=> cdpdag_os[m]		Transport (Mitochondrial)	
PTD1INOtm	1-Phosphatidyl-D-myo-inositol transport, Mitochondrial	ptd1ino_os[c] <=> ptd1ino_os[m]		Transport (Mitochondrial)	
PEtm	Phosphatidylethanolamine transport, Mitochondrial	pe_os[c] <=> pe_os[m]		Transport (Mitochondrial)	
PStm	PhosphatidylsMitochondrialine transport, Mitochondrial	ps_os[c] <=> ps_os[m]		Transport (Mitochondrial)	
PGPtm	PhosphatidylglycMitochondrialophosphate transport, Mitochondrial	pgp_os[c] <=> pgp_os[m]		Transport (Mitochondrial)	
PCtm	Phosphatidylcholine transport, Mitochondrial	pc_os[c] <=> pc_os[m]		Transport (Mitochondrial)	
ACALDtm	Acetaldehyde transport, diffusion	acald[c] <=> acald[m]		Transport (Mitochondrial)	
ACts	Acetate transporter, plastidic	ac[c] <=> ac[s]		Transport (Plastidic)	
NADts	NAD transporter, plastidic	nad[c] <=> nad[s]		Transport (Plastidic)	
5FTHFts	5-Formyltetrahydrofolate uptake carrier, plastid	5fthf[c] + h[c] <=> 5fthf[s] + h[s]	(LOC_Os01g32980 or LOC_Os03g52430)	Transport (Plastidic)	
5MTHFts	5-Methylenetetrahydrofolate uptake carrier, plastid	5mthf[c] + h[c] <=> 5mthf[s] + h[s]	(LOC_Os01g32980 or LOC_Os03g52430)	Transport (Plastidic)	
MHDASCBts	Monodehydroascorbate transport, plastidic	mhdascb[c] -> mhdascb[s]		Transport (Plastidic)	dead-end
DHORSts	(S)-Dihydroorotate transport via diffusion, plastid	dhor-S[c] <=> dhor-S[s] + h[s]		Transport (Plastidic)	
OROTts	Orotate transport via diffusion, plastidic	orot[c] <=> orot[s]		Transport (Plastidic)	
ACCOAts	Acetyl-CoA:CoA antiporter, plastidic	accoa[c] + coa[s] <=> accoa[s] + coa[c]		Transport (Plastidic)	
SUCCOAtz	Succinyl-CoA transport, plastid	succoa[c] <=> succoa[s]		Transport (Plastidic)	
TSULts	Thiosulfate porter, plastidic	tsul[c] + atp[c] + h2o[c] -> tsul[s] + adp[c] + pi[c] + h[c]		Transport (Plastidic)	
ASPts	Amino acid transporter (asp-L), plastidic	asp-L[c] + h[c] <=> asp-L[s] + h[s]		Transport (Plastidic)	
CYSts	cysteine transport, plastidic	cys-L[c] <=> cys-L[s]	(LOC_Os01g11160 or LOC_Os01g42234 or LOC_Os02g43860 or LOC_Os02g47210 or LOC_Os03g25820 or LOC_Os03g25840 or LOC_Os03g25869 or LOC_Os03g25920 or LOC_Os03g37984 or LOC_Os03g43970 or LOC_Os03g43980 or LOC_Os03g45170 or LOC_Os04g35540 or LOC_Os04g45950 or LOC_Os06g34830 or LOC_Os08g41370 or LOC_Os10g30090 or LOC_Os11g05690 or LOC_Os12g06060 or LOC_Os12g39080 or LOC_Os12g41890 or LOC_Os12g42850)	Transport (Plastidic)	
GLYts	Amino acid transporter (gly), plastidic	gly[c] + h[c] <=> gly[s] + h[s]	(LOC_Os01g11160 or LOC_Os01g42234 or LOC_Os02g43860 or LOC_Os02g47210 or LOC_Os03g25820 or LOC_Os03g25840 or LOC_Os03g25869 or LOC_Os03g25920 or LOC_Os03g37984 or LOC_Os03g43970 or LOC_Os03g43980 or LOC_Os03g45170 or LOC_Os04g35540 or LOC_Os04g45950 or LOC_Os06g34830 or LOC_Os08g41370 or LOC_Os10g30090 or LOC_Os11g05690 or LOC_Os12g06060 or LOC_Os12g39080 or LOC_Os12g41890 or LOC_Os12g42850)	Transport (Plastidic)	
HISts	Amino acid transporter (his-L), plastidic	his-L[c] + h[c] <=> his-L[s] + h[s]	(LOC_Os01g11160 or LOC_Os01g42234 or LOC_Os02g43860 or LOC_Os02g47210 or LOC_Os03g25820 or LOC_Os03g25840 or LOC_Os03g25869 or LOC_Os03g25920 or LOC_Os03g37984 or LOC_Os03g43970	Transport (Plastidic)	

			or LOC_Os03g43980 or LOC_Os03g45170 or LOC_Os04g35540 or LOC_Os04g45950 or LOC_Os06g34830 or LOC_Os08g41370 or LOC_Os10g30090 or LOC_Os11g05690 or LOC_Os12g06060 or LOC_Os12g39080 or LOC_Os12g41890 or LOC_Os12g42850)		
ILEts	Amino acid transporter (ile-L), plastidic	ile-L[c] + h[c] <=> ile-L[s] + h[s]	(LOC_Os01g11160 or LOC_Os01g42234 or LOC_Os02g43860 or LOC_Os02g47210 or LOC_Os03g25820 or LOC_Os03g25840 or LOC_Os03g25869 or LOC_Os03g25920 or LOC_Os03g37984 or LOC_Os03g43970 or LOC_Os03g43980 or LOC_Os03g45170 or LOC_Os04g35540 or LOC_Os04g45950 or LOC_Os06g34830 or LOC_Os08g41370 or LOC_Os10g30090 or LOC_Os11g05690 or LOC_Os12g06060 or LOC_Os12g39080 or LOC_Os12g41890 or LOC_Os12g42850)	Transport (Plastidic)	
LEUts	Amino acid transporter (leu-L), plastidic	leu-L[c] + h[c] <=> leu-L[s] + h[s]	(LOC_Os01g11160 or LOC_Os01g42234 or LOC_Os02g43860 or LOC_Os02g47210 or LOC_Os03g25820 or LOC_Os03g25840 or LOC_Os03g25869 or LOC_Os03g25920 or LOC_Os03g37984 or LOC_Os03g43970 or LOC_Os03g43980 or LOC_Os03g45170 or LOC_Os04g35540 or LOC_Os04g45950 or LOC_Os06g34830 or LOC_Os08g41370 or LOC_Os10g30090 or LOC_Os11g05690 or LOC_Os12g06060 or LOC_Os12g39080 or LOC_Os12g41890 or LOC_Os12g42850)	Transport (Plastidic)	
LYSts	Amino acid transporter (lys-L), plastidic	lys-L[s] + h[s] <=> lys-L[c] + h[c]	(LOC_Os01g11160 or LOC_Os01g42234 or LOC_Os02g43860 or LOC_Os02g47210 or LOC_Os03g25820 or LOC_Os03g25840 or LOC_Os03g25869 or LOC_Os03g25920 or LOC_Os03g37984 or LOC_Os03g43970 or LOC_Os03g43980 or LOC_Os03g45170 or LOC_Os04g35540 or LOC_Os04g45950 or LOC_Os06g34830 or LOC_Os08g41370 or LOC_Os10g30090 or LOC_Os11g05690 or LOC_Os12g06060 or LOC_Os12g39080 or LOC_Os12g41890 or LOC_Os12g42850)	Transport (Plastidic)	
METts	Amino acid transporter (met-L), plastidic	met-L[s] + h[s] <=> met-L[c] + h[c]	(LOC_Os01g11160 or LOC_Os01g42234 or LOC_Os02g43860 or LOC_Os02g47210 or LOC_Os03g25820 or LOC_Os03g25840 or LOC_Os03g25869 or LOC_Os03g25920 or LOC_Os03g37984 or LOC_Os03g43970 or LOC_Os03g43980 or LOC_Os03g45170 or LOC_Os04g35540 or LOC_Os04g45950 or LOC_Os06g34830 or LOC_Os08g41370 or LOC_Os10g30090 or LOC_Os11g05690 or LOC_Os12g06060 or LOC_Os12g39080 or LOC_Os12g41890 or LOC_Os12g42850)	Transport (Plastidic)	
PHEts	phenylalanine transport, plastidic	phe-L[c] <=> phe-L[s]	(LOC_Os01g11160 or LOC_Os01g42234 or LOC_Os02g43860 or LOC_Os02g47210	Transport (Plastidic)	

			or LOC_Os03g25820 or LOC_Os03g25840 or LOC_Os03g25869 or LOC_Os03g25920 or LOC_Os03g37984 or LOC_Os03g43970 or LOC_Os03g43980 or LOC_Os03g45170 or LOC_Os04g35540 or LOC_Os04g45950 or LOC_Os06g34830 or LOC_Os08g41370 or LOC_Os10g30090 or LOC_Os11g05690 or LOC_Os12g06060 or LOC_Os12g39080 or LOC_Os12g41890 or LOC_Os12g42850)		
PROts	Amino acid transporter (pro-L), plastidic	pro-L[s] + h[s] <=> pro-L[c] + h[c]	(LOC_Os01g11160 or LOC_Os01g42234 or LOC_Os02g43860 or LOC_Os02g47210 or LOC_Os03g25820 or LOC_Os03g25840 or LOC_Os03g25869 or LOC_Os03g25920 or LOC_Os03g37984 or LOC_Os03g43970 or LOC_Os03g43980 or LOC_Os03g45170 or LOC_Os04g35540 or LOC_Os04g45950 or LOC_Os06g34830 or LOC_Os08g41370 or LOC_Os10g30090 or LOC_Os11g05690 or LOC_Os12g06060 or LOC_Os12g39080 or LOC_Os12g41890 or LOC_Os12g42850)	Transport (Plastidic)	
SERts	Amino acid transporter (ser-L), plastidic	ser-L[c] + h[c] <=> ser-L[s] + h[s]	(LOC_Os01g11160 or LOC_Os01g42234 or LOC_Os02g43860 or LOC_Os02g47210 or LOC_Os03g25820 or LOC_Os03g25840 or LOC_Os03g25869 or LOC_Os03g25920 or LOC_Os03g37984 or LOC_Os03g43970 or LOC_Os03g43980 or LOC_Os03g45170 or LOC_Os04g35540 or LOC_Os04g45950 or LOC_Os06g34830 or LOC_Os08g41370 or LOC_Os10g30090 or LOC_Os11g05690 or LOC_Os12g06060 or LOC_Os12g39080 or LOC_Os12g41890 or LOC_Os12g42850)	Transport (Plastidic)	
THRts	Amino acid transporter (thr-L), plastidic	thr-L[c] + h[c] <=> thr-L[s] + h[s]	(LOC_Os01g11160 or LOC_Os01g42234 or LOC_Os02g43860 or LOC_Os02g47210 or LOC_Os03g25820 or LOC_Os03g25840 or LOC_Os03g25869 or LOC_Os03g25920 or LOC_Os03g37984 or LOC_Os03g43970 or LOC_Os03g43980 or LOC_Os03g45170 or LOC_Os04g35540 or LOC_Os04g45950 or LOC_Os06g34830 or LOC_Os08g41370 or LOC_Os10g30090 or LOC_Os11g05690 or LOC_Os12g06060 or LOC_Os12g39080 or LOC_Os12g41890 or LOC_Os12g42850)	Transport (Plastidic)	
TRPts	Tryptophan permease, plastidic	trp-L[c] + h[c] <=> trp-L[s] + h[s]	(LOC_Os01g11160 or LOC_Os01g42234 or LOC_Os02g43860 or LOC_Os02g47210 or LOC_Os03g25820 or LOC_Os03g25840 or LOC_Os03g25869 or LOC_Os03g25920 or LOC_Os03g37984 or LOC_Os03g43970 or LOC_Os03g43980 or LOC_Os03g45170 or LOC_Os04g35540 or LOC_Os04g45950 or LOC_Os06g34830 or LOC_Os08g41370 or LOC_Os10g30090 or LOC_Os11g05690 or LOC_Os12g06060 or LOC_Os12g39080 or LOC_Os12g41890 or	Transport (Plastidic)	

			LOC_Os12g42850)		
TYRts	Tyrosine permease, plastidic	tyr-L[c] + h[c] <=> tyr-L[s] + h[s]	(LOC_Os01g11160 or LOC_Os01g42234 or LOC_Os02g43860 or LOC_Os02g47210 or LOC_Os03g25820 or LOC_Os03g25840 or LOC_Os03g25869 or LOC_Os03g25920 or LOC_Os03g37984 or LOC_Os03g43970 or LOC_Os03g43980 or LOC_Os03g45170 or LOC_Os04g35540 or LOC_Os04g45950 or LOC_Os06g34830 or LOC_Os08g41370 or LOC_Os10g30090 or LOC_Os11g05690 or LOC_Os12g06060 or LOC_Os12g39080 or LOC_Os12g41890 or LOC_Os12g42850)	Transport (Plastidic)	
VALts	Amino acid transporter (val-L), plastidic	val-L[c] + h[c] <=> val-L[s] + h[s]	(LOC_Os01g11160 or LOC_Os01g42234 or LOC_Os02g43860 or LOC_Os02g47210 or LOC_Os03g25820 or LOC_Os03g25840 or LOC_Os03g25869 or LOC_Os03g25920 or LOC_Os03g37984 or LOC_Os03g43970 or LOC_Os03g43980 or LOC_Os03g45170 or LOC_Os04g35540 or LOC_Os04g45950 or LOC_Os06g34830 or LOC_Os08g41370 or LOC_Os10g30090 or LOC_Os11g05690 or LOC_Os12g06060 or LOC_Os12g39080 or LOC_Os12g41890 or LOC_Os12g42850)	Transport (Plastidic)	
ARGt2s	Amino acid transporter (arg-L), plastidic	arg-L[c] + h[c] <=> arg-L[s] + h[s]	(LOC_Os01g11160 or LOC_Os01g42234 or LOC_Os02g43860 or LOC_Os02g47210 or LOC_Os03g25820 or LOC_Os03g25840 or LOC_Os03g25869 or LOC_Os03g25920 or LOC_Os03g37984 or LOC_Os03g43970 or LOC_Os03g43980 or LOC_Os03g45170 or LOC_Os04g35540 or LOC_Os04g45950 or LOC_Os06g34830 or LOC_Os08g41370 or LOC_Os10g30090 or LOC_Os11g05690 or LOC_Os12g06060 or LOC_Os12g39080 or LOC_Os12g41890 or LOC_Os12g42850)	Transport (Plastidic)	
THFts	Tetrahydrofolate transport, diffusion, plastidic	thf[s] <=> thf[c]	(LOC_Os01g32980 or LOC_Os03g52430)	Transport (Plastidic)	dead-end
FORts	formate out via proton symport, plastidic	for[s] + h[s] -> for[c] + h[c]		Transport (Plastidic)	
G1P(pi)ts	Glucose 1-phosphate:pi antiporter, plastidic	g1p[c] + pi[s] <=> g1p[s] + pi[c]		Transport (Plastidic)	
G3P(pi)tsr	Glyceraldehyde 3-phosphate transport via triose-phosphate translocator (from plastid)	g3p[c] + pi[s] <=> g3p[s] + pi[c]		Transport (Plastidic)	
G6PA(pi)ts	alpha-glucose 6-phosphate:pi antiporter, plastidic	g6p-A[c] + pi[s] <=> g6p-A[s] + pi[c]	(LOC_Os01g07310 or LOC_Os01g07730 or LOC_Os01g60780 or LOC_Os02g41780 or LOC_Os02g49260 or LOC_Os04g59550 or LOC_Os05g07670 or LOC_Os05g07870 or LOC_Os06g19380 or LOC_Os06g30950 or LOC_Os07g33954 or LOC_Os07g34006 or LOC_Os07g33910 or LOC_Os08g01410 or LOC_Os08g01410 or LOC_Os10g33920 or LOC_Os12g05780 or LOC_Os12g05780)	Transport (Plastidic)	
G6PB(pi)ts	beta-glucose 6-phosphate:pi antiporter, plastidic	g6p-B[c] + pi[s] <=> g6p-B[s] + pi[c]	(LOC_Os01g07310 or LOC_Os01g07730 or LOC_Os01g60780 or LOC_Os02g41780 or LOC_Os02g49260 or LOC_Os04g59550 or LOC_Os05g07670 or LOC_Os05g07870 or LOC_Os06g19380 or LOC_Os06g30950	Transport (Plastidic)	

			or LOC_Os07g33954 or LOC_Os07g34006 or LOC_Os07g33910 or LOC_Os08g01410 or LOC_Os08g01410 or LOC_Os10g33920 or LOC_Os12g05780 or LOC_Os12g05780)		
DHAP(pi)tsr	Dihydroxyacetone phosphate transport via triose-phosphate translocator (from plastidic)	dhap[c] + pi[s] <=> dhap[s] + pi[c]	(LOC_Os01g13770 or LOC_Os05g15160)	Transport (Plastidic)	
3PG(pi)tsr	3-Phospho-D-glycerate transport via triose phosphate translocator (from plastidic)	3pg[c] + pi[s] <=> 3pg[s] + pi[c]	(LOC_Os01g13770 or LOC_Os05g15160)	Transport (Plastidic)	
PEPPIts	Phosphoenolpyruvate:Pi antiporter, plastidic	pep[c] + pi[s] -> pep[s] + pi[c]	(LOC_Os12g04170 or LOC_Os11g04380 or LOC_Os10g34490 or LOC_Os09g12600 or LOC_Os08g25624 or LOC_Os08g04110 or LOC_Os05g03070 or LOC_Os03g18990 or LOC_Os03g17740 or LOC_Os01g58870)	Transport (Plastidic)	
ATP2ts	AMP transporter, plastidic	amp[c] <=> amp[s]		Transport (Plastidic)	
FMNts	FMN transport, plastidic	fmn[c] -> fmn[s]		Transport (Plastidic)	dead-end
4ABZts	4-Aminobenzoate plastidic transport via diffusion	4abz[c] <=> 4abz[s]		Transport (Plastidic)	dead-end
NICRNTts	Nicotinate D-ribonucleotide plastidic transport via diffusion	nicrnt[s] -> nicrnt[c]		Transport (Plastidic)	dead-end
THMt2s	Thiamine diphosphate transport, plastidic	thm[c] <=> thm[s]		Transport (Plastidic)	dead-end
THMPPt2s	Thiamine diphosphate transport, plastidic	thmpp[c] <=> thmpp[s]		Transport (Plastidic)	dead-end
H2Ots	H2O transport, plastidic	h2o[c] <=> h2o[s]		Transport (Plastidic)	
CO2ts	CO2 plastidic transport	co2[c] <=> co2[s]		Transport (Plastidic)	
H2Sts	H2S plastidic transport	h2s[c] <=> h2s[s]		Transport (Plastidic)	
TCP32	Glutamate/Glutamine transporter	gln-L[s] + glu-L[c] -> glu-L[s] + gln-L[c]		Transport (Plastidic)	
NH4ts	ammonia transport, plastidic	nh4[c] <=> nh4[s]		Transport (Plastidic)	
O2tsr	O2 transport (diffusion), plastidic	o2[c] <=> o2[s]		Transport (Plastidic)	
Pits	phosphate transporter, plastidic	pi[c] + h[c] <=> pi[s] + h[s]		Transport (Plastidic)	
SO4ts	Sulfate transport, plastidic	so4[c] -> so4[s]		Transport (Plastidic)	
NO2ts	nitrite transport, plastidic	no2[c] -> no2[s]		Transport (Plastidic)	
HCYSts	homocysteine transport, chloropalst	hcys-L[s] <=> hcys-L[c]		Transport (Plastidic)	
ATPts	ADP/ATP transporter, plastidic	adp[c] + atp[s] + h[c] -> adp[s] + atp[c] + h[s]	(LOC_Os01g45910 or LOC_Os02g11740)	Transport (Plastidic)	
GLYCRts	Glycolate/Glycerate transport, plastidic	2 glyclt[s] + glyc-R[c] <=> 2 glyclt[c] + glyc-R[s]		Transport (Plastidic)	
MALFUMts	Malate/Fumarate transport, plastidic	mal-L[s] + fum[c] <=> fum[s] + mal-L[c]		Transport (Plastidic)	
MALOAAts	Oxaloacetate/Malate transport, plastidic	mal-L[s] + oaa[c] -> oaa[s] + mal-L[c]		Transport (Plastidic)	
MALAKGts	alpha-Ketoglutarate/Malate transport, plastidic	mal-L[s] + akg[c] -> akg[s] + mal-L[c]		Transport (Plastidic)	
MALGLUts	Glutamate/Malate transport, plastidic	mal-L[c] + glu-L[s] -> glu-L[c] + mal-L[s]		Transport (Plastidic)	
SUCFUMtsr	succinate-fumarate antiport, plastid	fum[s] + succ[c] <=> fum[c] + succ[s]		Transport (Plastidic)	
UDPGALts	UDP-galactose:UMP antiporter, plastid	udpgal[c] + ump[s] <=> udpgal[s] + ump[c]	(LOC_Os05g02490 or LOC_Os07g39280)	Transport (Plastidic)	
UDPGts	UDP-glucose antiporter, plastid	udpg[c] + udp[s] <=> udpg[s] + udp[c]		Transport (Plastidic)	
RIBFLVts	riboflavin transport, plastidic	ribflv[c] <=> ribflv[s]		Transport (Plastidic)	
IPDPts	Isopentenyl diphosphate transport, plastidic	ipdp[c] <=> ipdp[s]		Transport (Plastidic)	
EKAURts	ent-kaurene transport, plastidic	ekaur[s] -> ekaur[c]		Transport (Plastidic)	
UTPUMPts	UMP transporter	ump[s] <=> ump[c]		Transport (Plastidic)	
PPHNts	prephenate transport, plastidic	pphn[c] <=> pphn[s]		Transport (Plastidic)	
CHOLts	Choline transport, plastidic	chol[c] -> chol[s]		Transport (Plastidic)	
PCts	Phosphatidylcholine transport, plastidic	pc_os[c] <=> pc_os[s]		Transport (Plastidic)	
4ABUTts	Gamma-aminobutyric acid permease, plastidic	4abut[c] + h[c] <=> 4abut[s] + h[s]	(LOC_Os01g71700 or LOC_Os01g71710 or LOC_Os01g71720 or LOC_Os01g71740 or LOC_Os01g71760)	Transport (Plastidic)	
GLU4ABUTtsi	Glutamate:gamma-aminobutyrate antiporter, plastidic, irreversible	4abut[c] + glu-L[s] -> 4abut[s] + glu-L[c]	(LOC_Os01g42234 or LOC_Os04g35540)	Transport (Plastidic)	
GLYC3Pts	glycerol 3-phosphate transport (plastid)	glyc3p[s] <=> glyc3p[c]	(LOC_Os02g43620 or LOC_Os04g46880	Transport (Plastidic)	

			or LOC_Os06g08170 or LOC_Os08g06010)		
GLYCts	Glycerol:H+ symporter, plastidic	glyc[c] + h[c] <=> glyc[s] + h[s]	LOC_Os05g05200	Transport (Plastidic)	
CTPts	CDP/CTP transporter, plastidic	cdp[c] + ctp[s] + h[c] <=> cdp[s] + ctp[c] + h[s]		Transport (Plastidic)	
UTPts	UDP/UTP transporter, plastidic	udp[c] + utp[s] + h[c] <=> udp[s] + utp[c] + h[s]		Transport (Plastidic)	
FE2ts	ferrous iron transport, plastidic	fe2[c] -> fe2[s]		Transport (Plastidic)	
FE3abcs	ferric iron transport (ABC-type), plastidic	fe3[c] + atp[c] + h2o[c] -> fe3[s] + adp[c] + pi[c] + h[c]		Transport (Plastidic)	
HCO3(h)tsi	hco3 transport, plastid	h[c] + hco3[c] -> h[s] + hco3[s]		Transport (Plastidic)	
HGENTISts	homogentisate transport	hgentis[c] <=> hgentis[s]		Transport (Plastidic)	
PHEMEts	protoheme transport (plastid)	pheme[s] <=> pheme[c]		Transport (Plastidic)	
PINA1ts	Pi:Na+ symporter, plastid	pi[s] + na1[s] -> pi[c] + na1[c]	LOC_Os02g38020	Transport (Plastidic)	
MG2ts	Divalent cation (Mg2+) transport system, plastid	mg2[c] <=> mg2[s]	(LOC_Os04g35160 or LOC_Os04g42280 or LOC_Os06g44150)	Transport (Plastidic)	
METHFts	5,10-Methenyltetrahydrofolate uptake carrier, plastid	methf[c] + h[c] <=> methf[s] + h[s]	(LOC_Os01g14100 or LOC_Os03g58080 or LOC_Os04g42130 or LOC_Os05g32320 or LOC_Os06g08750 or LOC_Os07g24230 or LOC_Os07g07654 or LOC_Os09g25560)	Transport (Plastidic)	
NA1ATPases	Na+-translocating F-type ATPase, plastid	na1[s] + atp[s] + h2o[s] -> na1[c] + adp[s] + pi[s] + h[s]	(LOC_Os03g52660 or LOC_Os07g32880 or LOC_Os10g38292 or LOC_Os02g51470 or LOC_Os03g17070 or LOC_Os03g48471)	Transport (Plastidic)	
PYRts	pyruvate transport by free diffusion, plastid	pyr[c] <=> pyr[s]		Transport (Plastidic)	
NA1Hts	Na+/H+ antiporter, plastid	h[s] + na1[c] <=> h[c] + na1[s]	LOC_Os09g02214	Transport (Plastidic)	
SO3t	sulfite tranport, plastid	hso3[c] <=> hso3[s]		Transport (Plastidic)	
FA140s	fatty acid transport (14:0), plastidic	ttdca[s] <=> ttdca[c]		Transport (Plastidic)	
FA160s	fatty acid transport (16:0), plastidic	hdca[s] <=> hdca[c]		Transport (Plastidic)	
FA161s	fatty acid transport (16:1), plastidic	hdcea[s] <=> hdcea[c]		Transport (Plastidic)	
FA180s	fatty acid transport (18:0), plastidic	ocdca[s] <=> ocdca[c]		Transport (Plastidic)	
FA181s	fatty acid transport (18:1), plastidic	ocdcea[s] <=> ocdcea[c]		Transport (Plastidic)	
FA182s	fatty acid transport (18:2), plastidic	ocdcya[s] <=> ocdcya[c]		Transport (Plastidic)	
FA183s	fatty acid transport (18:3), plastidic	lnlnl[s] <=> lnlnl[c]		Transport (Plastidic)	
ARGSUCts	Argininosuccinate transport, plastid	argsuc[s] <=> argsuc[c]		Transport (Plastidic)	dead-end
ACGLUts	Acetylglutamate transport, plastid	acglu[s] <=> acglu[c]		Transport (Plastidic)	dead-end
GLYBETts	Glycine betaine transport, plastid	glybet[c] <=> glybet[s]		Transport (Plastidic)	dead-end
AMETt2s	S-Adenosyl-L-methionine reversible transport, plastidic	ahcys[c] + amet[s] <=> ahcys[s] + amet[c]		Transport (Plastidic)	
AC5GSAtr	N-Acetyl-L-glutamate 5-semialdehyde transport	acg5sa[c] <=> acg5sa[s]		Transport (Plastidic)	dead-end
ACORNts	N2-Acetyl-L-ornithine transport	acorn[c] <=> acorn[s]		Transport (Plastidic)	dead-end
CHORts	Chorismate transport	chor[c] <=> chor[s]		Transport (Plastidic)	dead-end
26dap-Mts	meso-2,6-Diaminoheptanedioate transport	26dap-M[c] <=> 26dap-M[s]		Transport (Plastidic)	dead-end
STEMts	Stemar-13-ene transport	stem[c] <=> stem[s]		Transport (Plastidic)	dead-end
EIHKAURts	ent-2alpha-Hydroxyisokaurene transport	eihkaur[c] <=> eihkaur[s]		Transport (Plastidic)	dead-end
ECASDts	ent-Cassa-12,15-diene transport	ecasd[c] <=> ecasd[s]		Transport (Plastidic)	dead-end
ESANDts	ent-Sandaracopimara-8(14),15-diene transport	esand[c] <=> esand[s]		Transport (Plastidic)	dead-end
DHZts	Dihydrozeatin transport	dhz[c] <=> dhz[s]		Transport (Plastidic)	dead-end
IPADNEts	N6-Dimethylallyladenine transport	ipadne[c] <=> ipadne[s]		Transport (Plastidic)	dead-end
TZTNRts	trans-zeatin riboside transport	t-ztnr[c] <=> t-ztnr[s]		Transport (Plastidic)	dead-end
TZTNts	trans-zeatin transport	t-ztn[c] <=> t-ztn[s]		Transport (Plastidic)	dead-end
IPADNts	Isopentenyl adenosine transport	ipadn[c] <=> ipadn[s]		Transport (Plastidic)	dead-end
COA(h)ts	CoA transport, plastid	coa[c] + h[c] <=> coa[s] + h[s]		Transport (Plastidic)	
PYRtv	pyruvate vacuolar transport	pyr[c] <=> pyr[v]		Transport (Vacuolar)	
SUCRtv	sucrsoe vacuolar transport via proton symport	sucr[c] + h[c] -> sucr[v] + h[v]		Transport (Vacuolar)	
FRUCtv	hexose vacuolar transport via proton symport	fru-B[v] + h[v] -> fru-B[c] + h[c]		Transport (Vacuolar)	
GLCAtv	hexose vacuolar transport via proton symport	glc-A[v] + h[v] -> glc-A[c] + h[c]		Transport (Vacuolar)	

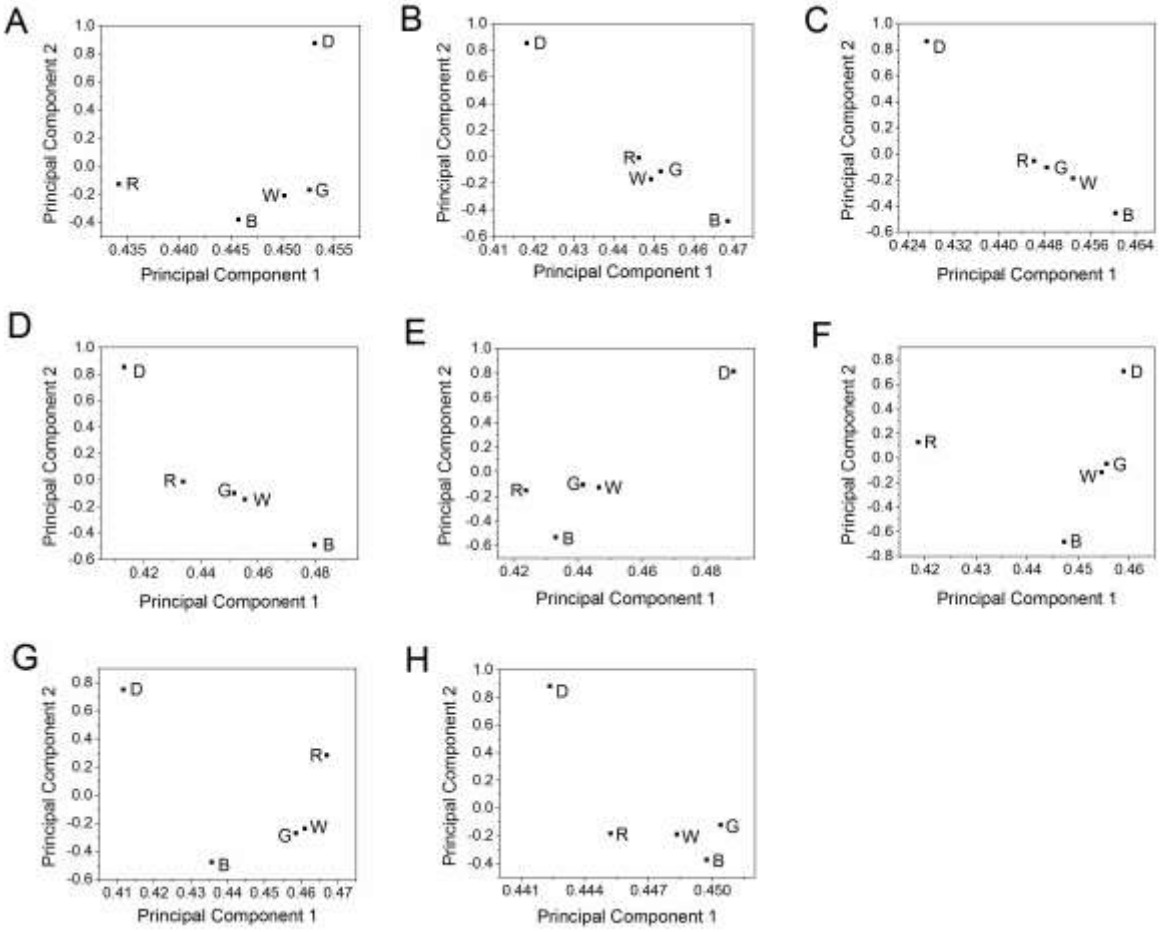
GLCBtv	hexose vacuolar transport via proton symport	glc-B[v] + h[v] -> glc-B[c] + h[c]		Transport (Vacuolar)	
GLYtv	Amino acid transporter (gly), vacuolar	gly[c] + h[c] <=> gly[v] + h[v]		Transport (Vacuolar)	
CYStv	cysteine transport, vacuolar	cys-L[c] <=> cys-L[v]		Transport (Vacuolar)	
H2Otv	H2O transport, vacuolar	h2o[c] <=> h2o[v]		Transport (Vacuolar)	
GTHRDabcv	Reduced glutathione via ABC system (vacuolar)	atp[v] + gthrd[c] + h2o[v] -> adp[v] + gthrd[v] + h[v] + pi[v]		Transport (Vacuolar)	
THFtv	Tetrahydrofolate transport, diffusion, vacuolar	thf[v] <=> thf[c]		Transport (Vacuolar)	
HPGLUtv	Tetrahydropteroyltri-L-glutamate transport, diffusion, vacuolar	thglu[c] -> thglu[v]		Transport (Vacuolar)	
NO2tvr	O2 transport (diffusion)	no2[c] <=> no2[v]		Transport (Vacuolar)	
NO3tvr	NO3 transport (diffusion)	no3[c] <=> no3[v]		Transport (Vacuolar)	
FA140COAabcx	fatty acyl-CoA transport via ABC system (14:0), peroxisomal	atp[x] + h2o[x] + tdcoa[c] -> adp[x] + h[x] + ttdca[x] + pi[x] + coa[c]		Transport (Peroxisomal)	
FA160COAabcx	fatty acyl-CoA transport via ABC system (16:0), peroxisomal	atp[x] + h2o[x] + pmtcoa[c] -> adp[x] + h[x] + hdca[x] + pi[x] + coa[c]		Transport (Peroxisomal)	
FA161COAabcx	fatty acyl-CoA transport via ABC system (16:1), peroxisomal	atp[x] + h2o[x] + hdcoa[c] -> adp[x] + h[x] + hdcea[x] + pi[x] + coa[c]		Transport (Peroxisomal)	
FA180COAabcx	fatty acyl-CoA transport via ABC system (18:0), peroxisomal	atp[x] + h2o[x] + stcoa[c] -> adp[x] + h[x] + ocdca[x] + pi[x] + coa[c]		Transport (Peroxisomal)	
FA181COAabcx	fatty acyl-CoA transport via ABC system (18:1), peroxisomal	atp[x] + h2o[x] + odecoa[c] -> adp[x] + h[x] + ocdcea[x] + pi[x] + coa[c]		Transport (Peroxisomal)	
FA182COAabcx	fatty acyl-CoA transport via ABC system (18:2), peroxisomal	atp[x] + h2o[x] + ocdycacoa[c] -> adp[x] + h[x] + ocdcya[x] + pi[x] + coa[c]		Transport (Peroxisomal)	
FA183COAabcx	fatty acyl-CoA transport via ABC system (18:3), peroxisomal	atp[x] + h2o[x] + lnlncoa[c] -> adp[x] + h[x] + lnlnl[x] + pi[x] + coa[c]		Transport (Peroxisomal)	
ATP2tx	AMP/ATP transporter, peroxisomal	amp[x] + atp[c] + h[x] -> amp[c] + atp[x] + h[c]		Transport (Peroxisomal)	
ATPtx	ADP/ATP transporter, peroxisomal	adp[x] + atp[c] + h[x] -> adp[c] + atp[x] + h[c]		Transport (Peroxisomal)	
GLYtx	Amino acid transporter (gly), peroxisomal	gly[c] + h[c] <=> gly[x] + h[x]		Transport (Peroxisomal)	
SERtx	Amino acid transporter (ser-L), peroxisomal	ser-L[c] + h[c] <=> ser-L[x] + h[x]		Transport (Peroxisomal)	
GLYCLTtx	glycolate transport, peroxisomal	glyclt[c] <=> glyclt[x]		Transport (Peroxisomal)	
MALOAAtx	malate/oxaloacetate shuttle	mal-L[x] + oaa[c] <=> mal-L[c] + oaa[x]		Transport (Peroxisomal)	
H2Otx	H2O transport, peroxisomal	h2o[c] <=> h2o[x]		Transport (Peroxisomal)	
CITx	citrate transport, peroxisomal	cit[c] <=> cit[x]		Transport (Peroxisomal)	
CO2tx	CO2 transport, peroxisomal	co2[c] <=> co2[x]		Transport (Peroxisomal)	
O2tx	O2 transport, peroxisomal	o2[c] <=> o2[x]		Transport (Peroxisomal)	
PItx	phosphate peroxisomal transport via proton symport	h[c] + pi[c] <=> h[x] + pi[x]		Transport (Peroxisomal)	
CITtcx	citrate/isocitrate antiport into peroxisome	cit[x] + icit[c] <=> cit[c] + icit[x]		Transport (Peroxisomal)	
ACtx	acetate transport, peroxisomal	ac[c] <=> ac[x]		Transport (Peroxisomal)	
ALAtx	Amino acid transporter (ala-L), peroxisomal	ala-L[c] + h[c] <=> ala-L[x] + h[x]		Transport (Peroxisomal)	
PYRt2x	pyruvate peroxisomal transport via proton symport	pyr[c] + h[c] <=> pyr[x] + h[x]		Transport (Peroxisomal)	
SUCCtx	succinate transporter, peroxisome	succ[c] <=> succ[x]		Transport (Peroxisomal)	
NH4tx	Ammonium transporter, peroxisomal	nh4[c] <=> nh4[x]	(LOC_Os01g50860 or LOC_Os01g65500 or LOC_Os02g35190 or LOC_Os03g48940 or LOC_Os04g55210 or LOC_Os08g20570 or LOC_Os08g38980 or LOC_Os12g25200)	Transport (Peroxisomal)	
THRtx	Amino acid transporter (thr-L), peroxisomal	thr-L[c] + h[c] <=> thr-L[x] + h[x]		Transport (Peroxisomal)	
ACCOAtx	Acetyl-CoA:CoA antiporter, peroxisomal	accoa[c] + coa[x] <=> accoa[x] + coa[c]		Transport (Peroxisomal)	
COA(h)tx	CoA transport, peroxisome	coa[c] + h[c] <=> coa[x] + h[x]		Transport (Peroxisomal)	
GLXtx	glyoxylate transport, peroxisomal	glx[c] <=> glx[x]		Transport (Peroxisomal)	
GLUtx	L-glutamate transport, peroxisome	glu-L[c] <=> glu-L[x]		Transport (Peroxisomal)	
AKGtx	alpha-Ketoglutarate transport, peroxisome	akg[c] <=> akg[x]		Transport (Peroxisomal)	
GCOAtx	Glutaryl-CoA transport, peroxisome	gcoa[c] <=> gcoa[x]		Transport (Peroxisomal)	
GLYCRtx	Glycerate transport, peroxisome	glyc-R[x] <=> glyc-R[c]		Transport (Peroxisomal)	

FADH2tx	FADH2 transport, peroxisome	fadh2[c] <=> fadh2[x]		Transport (Peroxisomal)	
FADtx	FAD transport by free diffusion, peroxisome	fad[c] <=> fad[x]		Transport (Peroxisomal)	
NADPH2tx	NADPH transport, peroxisome	nadph[c] <=> nadph[x]		Transport (Peroxisomal)	
NADPtx	NADP transport by free diffusion, peroxisome	nadp[c] <=> nadp[x]		Transport (Peroxisomal)	
MTHGXLtx	Methyl glyoxal transport via diffucision	mthgxl[c] <=> mthgxl[x]		Transport (Peroxisomal)	
B2COAtx	Crotonoyl-CoA transport	b2coa[x] <=> b2coa[c]		Transport (Peroxisomal)	
FA40COAtx	butanoyl-CoA transport (peroxisome)	btcoa[c] <=> btcoa[x]		Transport (Peroxisomal)	dead-end
JAStx	Jasmonate transport, peroxisomal	jas[c] <=> jas[x]		Transport (Peroxisomal)	dead-end
OPDAtx	OPDA transport, peroxisomal	12oxophyt[c] <=> 12oxophyt[x]		Transport (Peroxisomal)	dead-end
FA140CoAr	fatty acyl CoA transport (14:0), ER	tdcoa[r] <=> tdcoa[c]		Transport (ER)	
FA160CoAr	fatty acyl CoA transport (16:0), ER	pmtcoa[r] <=> pmtcoa[c]		Transport (ER)	
FA161CoAr	fatty acyl CoA transport (16:1), ER	hdcoa[r] <=> hdcoa[c]		Transport (ER)	
FA180CoAr	fatty acyl CoA transport (18:0), ER	stcoa[r] <=> stcoa[c]		Transport (ER)	
FA181CoAr	fatty acyl CoA transport (18:1), ER	odecoa[r] <=> odecoa[c]		Transport (ER)	
FA182CoAr	fatty acyl CoA transport (18:2), ER	ocdycacoa[r] <=> ocdycacoa[c]		Transport (ER)	
FA183CoAr	fatty acyl CoA transport (18:3), ER	lnlncoa[r] <=> lnlncoa[c]		Transport (ER)	
FA140r	fatty acid transport (14:0), ER	ttdca[r] <=> ttdca[c]		Transport (ER)	
FA160r	fatty acid transport (16:0), ER	hdca[r] <=> hdca[c]		Transport (ER)	
FA161r	fatty acid transport (16:1), ER	hdcea[r] <=> hdcea[c]		Transport (ER)	
FA180r	fatty acid transport (18:0), ER	ocdca[r] <=> ocdca[c]		Transport (ER)	
FA181r	fatty acid transport (18:1), ER	ocdcea[r] <=> ocdcea[c]		Transport (ER)	
FA182r	fatty acid transport (18:2), ER	ocdcya[r] <=> ocdcya[c]		Transport (ER)	
FA183r	fatty acid transport (18:3), ER	lnlnl[r] <=> lnlnl[c]		Transport (ER)	
NADPH2tr	NADPH transport, ER	nadph[c] <=> nadph[r]		Transport (ER)	
NADPtr	NADP transport by free diffusion, ER	nadp[c] <=> nadp[r]		Transport (ER)	
UDPGr	UDP-glucose transport, ER	udpg[c] <=> udpg[r]		Transport (ER)	
GLUSIDEr	Glucosylceramide transport, ER	gluside[c] <=> gluside[r]		Transport (ER)	
HYDRO16tr	16-Hydroxypalmitate transport, ER	hydro16[c] <=> hydro16[r]		Transport (ER)	
HYDRO18tr	18-Hydroxypalmitate transport, ER	hydro18[c] <=> hydro18[r]		Transport (ER)	
DHYDRO1016tr	10,16-dihydroxypalmitate transport, ER	dhydro1016[c] <=> dhydro1016[r]		Transport (ER)	
DHYDRO1018tr	9,10-epoxy-18-hydroxystearate transport, ER	dhydro1018[c] <=> dhydro1018[r]		Transport (ER)	
THYDRO91018tr	9,10,18-trihydroxystearate transport, ER	thydro91018[c] <=> thydro91018[r]		Transport (ER)	
AMETt2r	S-Adenosyl-L-methionine reversible transport, ER	ahcys[c] + amet[r] <=> ahcys[r] + amet[c]		Transport (ER)	
ATPtr	ADP/ATP transporter, ER	adp[r] + atp[c] + h[r] <=> adp[c] + atp[r] + h[c]		Transport (ER)	
ATP2tr	AMP/ATP transporter, ER	amp[r] + atp[c] + h[r] <=> amp[c] + atp[r] + h[c]		Transport (ER)	
H2Otr	H2O transport, ER	h2o[c] <=> h2o[r]		Transport (ER)	
CO2tr	CO2 transport, ER	co2[c] <=> co2[r]		Transport (ER)	
O2tr	O2 transport, ER	o2[c] <=> o2[r]		Transport (ER)	
MALCOAtr	Malonyl-CoA transport, ER	malcoa[r] <=> malcoa[c]		Transport (ER)	
Pitr	phosphate ER transport via proton symport	h[c] + pi[c] <=> h[r] + pi[r]		Transport (ER)	
SERtr	Amino acid transporter (ser-L), ER	ser-L[c] + h[c] <=> ser-L[r] + h[r]		Transport (ER)	
COA(h)tr	CoA transport, ER	coa[c] + h[c] <=> coa[r] + h[r]		Transport (ER)	
GLYC3Ptr	glycerol 3-phosphate transport (ER)	glyc3p[r] <=> glyc3p[c]	(LOC_Os02g43620 or LOC_Os04g46880 or LOC_Os06g08170 or LOC_Os08g06010)	Transport (ER)	
TRIGLYCtr	Triacylglycerol transport, ER	triglyc_os[c] <=> triglyc_os[r]		Transport (ER)	
CTPtr	CTP transport, ER	ctp[c] <=> ctp[r]		Transport (ER)	
CMPtr	CMP transport, ER	cmp[c] <=> cmp[r]		Transport (ER)	
CDPDAGtr	CDP-diacylglycerol transport, ER	cdpdag_os[c] <=> cdpdag_os[r]		Transport (ER)	
PTD1INOtr	1-Phosphatidyl-D-myo-inositol transport, ER	ptd1ino_os[c] <=> ptd1ino_os[r]		Transport (ER)	
PEtr	Phosphatidylethanolamine transport, ER	pe_os[c] <=> pe_os[r]		Transport (ER)	
PStr	Phosphatidylserine transport, ER	ps_os[c] <=> ps_os[r]		Transport (ER)	
PGPtr	Phosphatidylglycerophosphate transport, ER	pgp_os[c] <=> pgp_os[r]		Transport (ER)	

PCtr	Phosphatidylcholine transport, ER	pc_os[c] <=> pc_os[r]		Transport (ER)	
CHOLtr	Choline transport, ER	chol[c] <=> chol[r]		Transport (ER)	
INOSTtr	Inositol transport, ER	inost[c] <=> inost[r]		Transport (ER)	
FADH2tr	FADH2 transport, ER	fadh2[c] <=> fadh2[r]		Transport (ER)	
FADtr	FAD transport by free diffusion, ER	fad[c] <=> fad[r]		Transport (ER)	
O2tu	O2 thylakoid trnasport	o2[u] -> o2[s]		Transport (Thylakoid)	

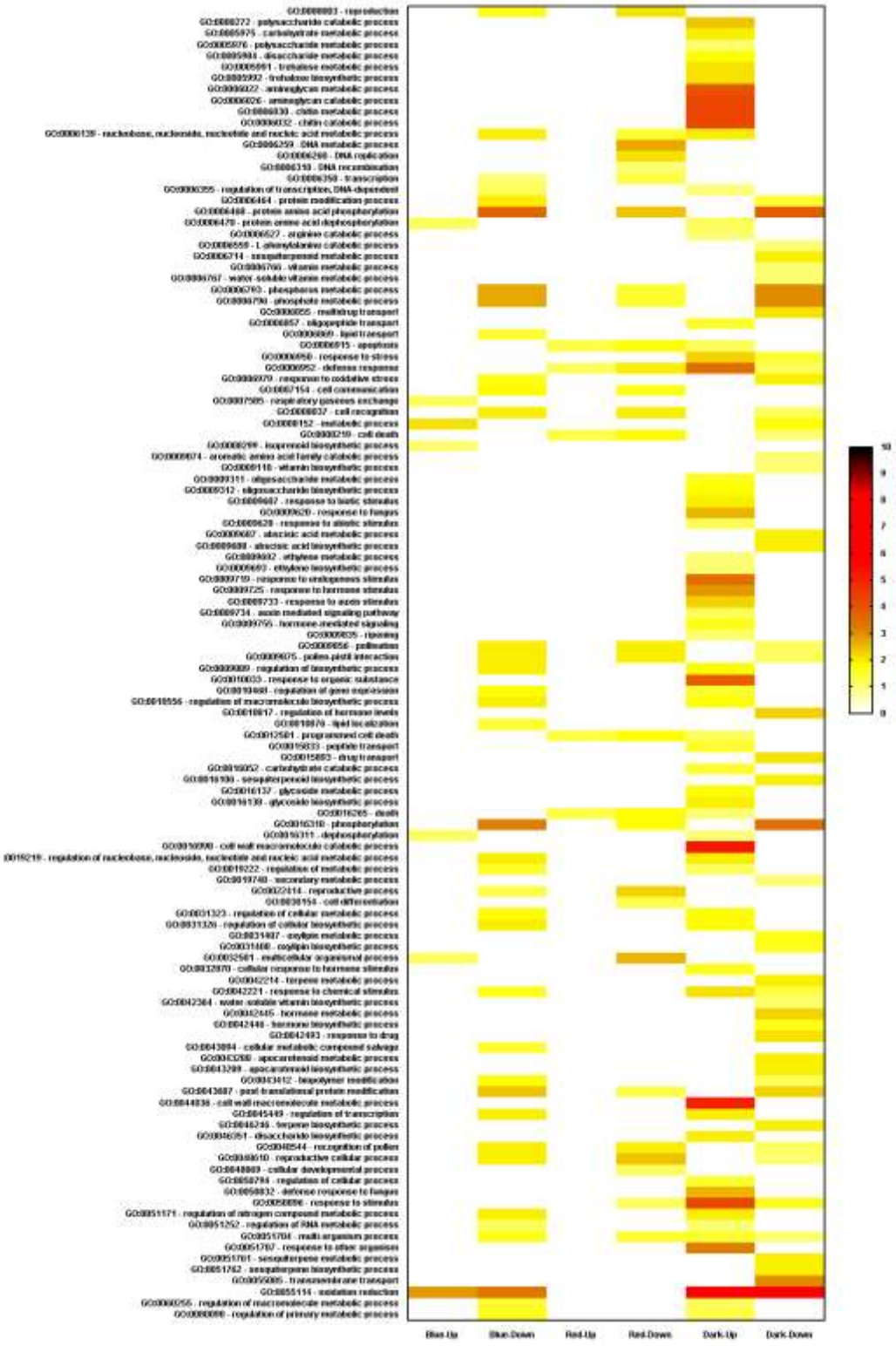
Appendix Q:

PCA of gene expression. (A) Cytosol. (B) Plastid. (C) Mitochondrion. (D) Peroxisome. (E) Vacuole. (F) Endoplasmic reticulum. (G) Thylakoid. (H) All genes including non-metabolic.



Appendix R:

Enrichment scores different GO:biological process. For visualization purposes, the negative logarithm of p-value is presented.



Appendix S:

Enrichment scores reporter metabolites in B vs W, R vs W and D vsW.

Blue/White			Red/White			Dark/White		
Metabolite	**norm score**	**p-value**	**Metabolite**	**norm score**	**p-value**	**Metabolite**	**norm score**	**p-value**
ga8[c]	5.12521	1.49E-07	ppi[r]	6.317324	1.33E-10	ind3ac[c]	9.133371	0
ehkaurate[c]	3.95149	3.88E-05	ecdp[s]	4.13463	1.78E-05	ecdp[s]	6.8501407	3.69E-12
ga12-ald[c]	3.95149	3.88E-05	primardt[s]	4.092839	2.13E-05	kmpfl[c]	6.7839152	5.85E-12
ga8cat[c]	3.62407	0.000145	moma[s]	3.653738	1.29E-04	qrctn[c]	6.7839152	5.85E-12
rb15bp[s]	3.53423	0.000204	ind3ac[c]	3.550409	1.92E-04	prunasin[c]	6.6255491	1.73E-11
abs[s]	3.52886	0.000209	primard[s]	3.43506	2.96E-04	grdp[c]	6.6055367	1.98E-11
b-glucan[c]	3.51988	0.000216	b-glucan[c]	3.418953	0.00031	ppi[r]	6.4840336	4.47E-11
b-glucan[v]	3.42215	0.000311	g6p-A[s]	3.400774	0.00034	anxan[s]	6.4046205	7.54E-11
9-hpot[s]	3.40647	0.000329	gabut[c]	3.389489	0.00035	b-glucan[c]	6.2724609	1.78E-10
9-hpod[s]	3.40647	0.000329	g6p-B[s]	3.299173	0.00048	na1[c]	6.0286042	8.27E-10
13-hpod[s]	3.40647	0.000329	glucan[s]	3.263788	0.00055	cellb[c]	5.8844109	2.00E-09
2kmb[c]	3.21599	0.00065	suc6p[c]	3.236109	0.00061	xmp[c]	5.7482096	4.51E-09
1acpc[c]	3.15788	7.95E-04	pa_os[m]	3.219282	0.00064	primardt[s]	5.7221954	5.26E-09
ga19[c]	3.10801	0.000942	trdrd[c]	3.164252	0.00078	gal[c]	5.6551853	7.78E-09
13-hpot[s]	2.83639	0.002281	trdox[c]	3.164252	0.00078	r5p[s]	5.6368209	8.66E-09
lgt-S[c]	2.73609	0.003109	anxan[s]	3.071198	1.07E-03	pa_os[m]	5.5782601	1.21E-08
ethylene[c]	2.62732	0.004303	scodp[s]	2.96814	0.0015	1acpc[c]	5.4941465	1.96E-08
ind3acnl[c]	2.58735	0.004836	g6p-B[c]	2.862971	0.0021	raffin[c]	5.4860003	2.06E-08
g6p-B[v]	2.58302	0.004897	xmp[c]	2.853403	0.00216	pep[c]	5.3351131	4.77E-08
2phetoh[c]	2.55562	0.0053	ala-L[m]	2.799192	2.56E-03	h2o[u]	5.3315143	4.87E-08
ga53[c]	2.53768	0.00558	val-L[s]	2.788639	0.00265	mal-L[m]	5.2877083	6.19E-08
ga15[c]	2.53768	5.58E-03	ile-L[s]	2.788639	0.00265	3pg[s]	5.1943927	1.03E-07
ga51[c]	2.53768	0.00558	mi134p[c]	2.787153	0.00266	b-glucan[v]	5.1432727	1.35E-07
ga37[c]	2.53768	0.00558	3o2c2poct[x]	2.745982	0.00302	iaa-ala[c]	5.1398311	1.37E-07
ga44[c]	2.53768	0.00558	hmgcoa[c]	2.724673	3.22E-03	iaa-leu[c]	5.1398311	1.37E-07
ga29[c]	2.53768	0.00558	ga8[c]	2.717891	0.00328	h2o2[s]	5.116731	1.55E-07
eikaur[s]	2.50394	0.006141	12dgr_os[s]	2.7063	0.0034	moma[s]	5.071138	1.98E-07
ppi[r]	2.38966	0.008432	thcrm[c]	2.632401	0.00424	cndn5g[c]	5.0139696	2.67E-07
amob[c]	2.38202	0.008609	3ig3p[s]	2.617616	0.00443	cndn35dg[c]	5.0139696	2.67E-07
cellb[c]	2.28592	0.01113	b-glucan[v]	2.61635	0.00444	t-cinn[c]	4.9959117	2.93E-07
ga1[c]	2.24998	0.012225	33dma[c]	2.614213	4.47E-03	9-hpot[s]	4.9435426	3.84E-07
phe-L[s]	2.18451	0.014462	cellb[c]	2.583828	0.00489	9-hpod[s]	4.9435426	3.84E-07
ind3acetaldoxime[c]	2.17832	0.014691	tryptamine[c]	2.579834	0.00494	13-hpod[s]	4.9435426	3.84E-07
acrtnl[s]	2.16014	0.015381	pep[s]	2.56275	0.00519	dhqrctn[c]	4.9350205	4.01E-07
glucan[s]	2.15302	0.015659	ACP[m]	2.56015	0.00523	aps[s]	4.9332622	4.04E-07
ala-L[m]	2.12523	0.016784	f6p-B[s]	2.558199	0.00526	dhk[c]	4.8787029	5.34E-07
lpam[m]	2.08483	0.018542	grdp[s]	2.551476	0.00536	id3acald[c]	4.8385597	6.54E-07
nad[v]	2.05576	0.019903	prunasin[c]	2.551307	0.00537	pccu2p[u]	4.7768859	8.90E-07
nadh[v]	2.05576	0.019903	ga1[c]	2.535587	0.00561	pccu1p[u]	4.7768859	8.90E-07
eikaur[c]	2.0481	0.020275	lplg[c]	2.534052	5.64E-03	tryptamine[c]	4.7600157	9.68E-07
33dma[c]	1.99382	2.31E-02	lcyc[c]	2.534052	0.00564	gtp[s]	4.7313846	1.11E-06
pa_os[m]	1.96375	0.024779	glyc3p[r]	2.485951	0.00646	ala-L[m]	4.7236291	1.16E-06
epflzn[c]	1.95511	0.025285	grdp[c]	2.459098	0.00696	phe-L[s]	4.7196731	1.18E-06
epctcn[c]	1.95511	0.025285	12dgr_os[m]	2.450886	0.00713	na1[m]	4.7057141	1.26E-06
primardn[s]	1.95511	0.025285	ekaurol[c]	2.447732	0.00719	f6p-B[c]	4.705329	1.27E-06
sclgn[c]	1.94151	0.026098	ekaural[c]	2.447732	0.00719	amygd[c]	4.6849707	1.40E-06
stcsd[c]	1.94151	0.026098	phe-L[s]	2.424367	0.00767	33dma[c]	4.6287679	1.84E-06
pser-L[s]	1.93954	0.026218	2cpr5p[s]	2.407155	0.00804	dtdpglu[c]	4.6169099	1.95E-06
8aonn[c]	1.89764	0.028872	B-ara1p[c]	2.378294	0.0087	mi134p[c]	4.5100567	3.24E-06
id3acald[c]	1.88906	0.029442	12dgr_os[r]	2.375745	0.00876	1Dgali[c]	4.4277281	4.76E-06
arg-L[s]	1.87053	0.030705	tre[c]	2.347775	0.00944	vlxan[s]	4.3818696	5.88E-06
val-L[s]	1.86347	0.031198	pro-L[m]	2.345712	0.0095	13-hpot[s]	4.3517701	6.75E-06
ile-L[s]	1.86347	0.031198	his-L[m]	2.328567	0.00994	pchlda[s]	4.3507894	6.78E-06
thr-L[s]	1.84059	0.032841	pran[s]	2.320108	0.01017	dvchlda[s]	4.3507894	6.78E-06
suc6p[c]	1.83515	0.033242	pa_os[s]	2.306213	0.01055	pa_os[s]	4.3342237	7.31E-06
ga9[c]	1.81675	0.034628	cinnald[c]	2.299963	0.01073	his-L[m]	4.2616075	1.01E-05
ga4[c]	1.81675	0.034628	pep[c]	2.293319	0.01091	primard[s]	4.2324269	1.16E-05
ga20[c]	1.81675	3.46E-02	mev-R[c]	2.280717	0.01128	oaa[m]	4.2055874	1.30E-05
ga34[c]	1.79441	3.64E-02	3chpthmpp[m]	2.274347	1.15E-02	mi346p[c]	4.1564709	1.62E-05
ga51cat[c]	1.79441	0.036374	trp-L[s]	2.263165	0.01181	mi3456p[c]	4.1564709	1.62E-05
ga17[c]	1.79441	3.64E-02	pchlda[s]	2.25157	0.01217	stc[c]	4.1518635	1.65E-05
ga29cat[c]	1.79441	0.036374	dvchlda[s]	2.25157	0.01217	butin[c]	4.1462261	1.69E-05
2pglyc[s]	1.71892	0.042815	hydro20[r]	2.250419	0.01221	3o2c2poct[x]	4.12459	1.86E-05
9-nonan[s]	1.66966	4.75E-02	hydro22[r]	2.250419	0.01221	ile-L[s]	4.1037381	2.03E-05
12o9dd[s]	1.66966	0.047493	hydro24[r]	2.250419	0.01221	val-L[s]	4.0782719	2.27E-05
			hydro26[r]	2.250419	0.01221	ga1[c]	4.0593044	2.46E-05

			hydro28[r]	2.250419	0.01221	trp-L[s]	4.0453458	2.61E-05
			hydro30[r]	2.250419	0.01221	9-nonan[s]	4.0402674	2.67E-05
			gbside[c]	2.237511	0.01263	12o9dd[s]	4.0402674	2.67E-05
			tdcoa[x]	2.237365	0.01263	gabut[c]	4.0169296	2.95E-05
			mi14p[c]	2.221712	0.01315	2pglyc[s]	4.0123371	3.01E-05
			dtmp[c]	2.21963	0.01322	gdp[c]	4.0045187	3.11E-05
			mgdg_os[s]	2.219539	0.01323	pro-L[m]	3.9834676	3.40E-05
			leu-L[s]	2.207776	0.01363	nad[v]	3.9665335	3.65E-05
			fer[c]	2.189281	0.01429	nadh[v]	3.9665335	3.65E-05
			chlda[s]	2.176291	0.01477	g6p-B[c]	3.9634185	3.69E-05
			5apru[s]	2.171001	0.01497	dtdprmn[c]	3.9579367	3.78E-05
			vlxan[s]	2.133101	0.01646	paps[s]	3.9486642	3.93E-05
			tre6p[c]	2.116183	0.01716	ACP[m]	3.9399469	4.07E-05
			hisp[s]	2.105538	0.01762	12dgr_os[m]	3.9065545	4.68E-05
			phpyr[s]	2.0979	0.01796	tre[c]	3.878066	5.26E-05
			asp-L[m]	2.094169	0.01812	met-L[m]	3.8517164	5.86E-05
			4ppcys[c]	2.092624	0.01819	dvpchlda[s]	3.8185103	6.71E-05
			h2o2[s]	2.086712	0.01846	pram[s]	3.7933894	7.43E-05
			asn-L[m]	2.066649	0.01938	leu-L[s]	3.7872477	7.62E-05
			opc8coa[x]	2.055779	0.0199	na1[s]	3.7751544	8.00E-05
			dadp[c]	2.054942	0.01994	lpam[m]	3.7692778	8.19E-05
			adpglc[s]	2.052313	0.02007	ethylene[c]	3.7676372	8.24E-05
			man6p[c]	2.042469	0.02055	uri[c]	3.7590378	8.53E-05
			anth[s]	2.033773	0.02099	ggdp[s]	3.7567947	8.61E-05
			glc-B[s]	2.028671	0.02125	suc6p[c]	3.7419026	9.13E-05
			8aonn[c]	2.027469	0.02131	f6p-B[s]	3.736456	9.33E-05
			34hpp[s]	2.025947	0.02139	glucan[s]	3.7257918	9.74E-05
			dhf[c]	2.021562	0.02161	man6p[c]	3.722457	9.86E-05
			arg-L[s]	2.014449	0.02198	scodp[s]	3.6987771	0.0001083
			9-hpot[s]	2.011894	0.02212	chlda[s]	3.6961802	0.0001094
			9-hpod[s]	2.011894	0.02212	12dgr_os[r]	3.6917406	0.0001114
			13-hpod[s]	2.011894	0.02212	tre6p[c]	3.6464738	0.0001329
			h2o[u]	2.006209	0.02242	lgt-S[c]	3.6230351	0.0001456
			pap[s]	2.005782	0.02244	g6p-A[s]	3.5835397	0.0001695
			xylan[c]	2.003947	0.02254	4adcho[s]	3.578869	0.0001725
			abs[s]	2.002141	0.02263	mgdg_os[s]	3.578696	0.0001727
			dvpchlda[s]	2.000533	0.02272	mi13456p[c]	3.576792	0.0001739
			ocp8t2ecoa[x]	1.997473	0.02289	coum[c]	3.5588031	0.0001863
			ocp6t2ecoa[x]	1.997473	0.02289	ind3acnl[c]	3.5544815	0.0001894
			ocp4t2ecoa[x]	1.997473	0.02289	gdp[s]	3.5515419	0.0001915
			f6p-B[c]	1.994624	0.02304	3ig3p[s]	3.546306	0.0001953
			lcdpn[c]	1.989156	0.02334	qrctn3g[c]	3.5454119	0.000196
			dlpdn[c]	1.973307	0.02423	kmpfl3g[c]	3.5454119	0.000196
			G00009[c]	1.972673	0.02427	melib[c]	3.5292951	0.0002083
			hconald[c]	1.963117	2.48E-02	lqtgn[c]	3.5235253	0.0002129
			hfer[c]	1.963117	0.02482	hisp[s]	3.5144419	0.0002203
			ind3acnl[c]	1.962154	0.02487	aps[c]	3.5122491	0.0002222
			indole[s]	1.95881	0.02507	rb15bp[s]	3.5106928	0.0002235
			13-hpot[s]	1.958089	0.02511	ser-L[m]	3.5030778	0.00023
			t-ztng[c]	1.95783	0.02512	sphgn[r]	3.4989751	0.0002335
			c-ztng[c]	1.95783	0.02512	selmet[c]	3.4916946	0.00024
			dhzg[c]	1.95783	0.02512	10fthglu[c]	3.4743985	0.000256
			mi13456p[c]	1.947156	0.02576	pap[s]	3.4644372	0.0002657
			g6p-A[c]	1.943833	0.02596	pep[s]	3.4639192	0.0002662
			thf[s]	1.929207	0.02685	seln[s]	3.4600874	0.00027
			sclgn[c]	1.925907	0.02706	abs[s]	3.4501392	0.0002801
			stcsd[c]	1.925907	0.02706	2ahethmpp[s]	3.4366033	0.0002945
			r5p[s]	1.922456	0.02727	fdp-B[s]	3.4109873	0.0003236
			ga8cat[c]	1.921839	0.02731	udpgal[s]	3.4108214	0.0003238
			ga19[c]	1.916405	0.02766	22h5camp43e[c]	3.4099991	0.0003248
			ga20[c]	1.916405	0.02766	asn-L[m]	3.4040468	0.000332
			acser[s]	1.915823	0.02769	cndng[c]	3.3945611	0.0003437
			g3pc[r]	1.887876	0.02952	opc8coa[x]	3.3813929	0.0003606
			akgACPme[c]	1.881704	0.02994	adpglc[s]	3.3538713	0.0003984
			hemeA[m]	1.861639	0.03133	arg-L[s]	3.3518468	0.0004014
			ga9[c]	1.85584	0.03174	thcrm[c]	3.3461963	0.0004096
			ga4[c]	1.85584	0.03174	g6p-B[s]	3.3294019	0.0004352
			34hb[c]	1.848528	0.03226	13dpg[s]	3.3240957	0.0004435
			paps[s]	1.831033	0.03355	12dgr_os[s]	3.322264	0.0004465
			dudp[c]	1.829643	0.03365	thr-L[s]	3.312901	0.0004617
			dhqrctn[c]	1.828001	0.03377	25dhpp[s]	3.3073517	0.0004709
			3dsphgn[r]	1.827233	0.03383	8aonn[c]	3.2973865	0.0004879
			sin[c]	1.824411	0.03404	1-kesttr[c]	3.2971614	0.0004883
			nh4[x]	1.822324	0.0342	cinnald[c]	3.296166	0.0004901
			3oaraccoa[r]	1.822225	0.03421	34hb[c]	3.2730331	0.000532

			3obehcoa[r]	1.822225	0.03421	trdrd[c]	3.2688823	0.0005399
			3olgnccoa[r]	1.822225	0.03421	trdox[c]	3.2688823	0.0005399
			3ocercoa[r]	1.822225	0.03421	psqldp[c]	3.2574076	0.0005622
			3omntcoa[r]	1.822225	0.03421	t-ztng[c]	3.2495199	0.000578
			3omlscoa[r]	1.822225	0.03421	c-ztng[c]	3.2495199	0.000578
			amygd[c]	1.804047	0.03561	dhzg[c]	3.2495199	0.000578
			malttt[s]	1.798183	0.03607	fer[c]	3.2463173	0.0005845
			h2mb4p[s]	1.791635	0.0366	metjas[c]	3.2412662	0.000595
			gar[m]	1.791529	0.0366	pg_os[m]	3.2398796	0.0005979
			fgam[m]	1.791529	0.0366	alpro[m]	3.1996253	0.000688
			4adcho[s]	1.784226	0.03719	fdp-B[c]	3.1932693	0.0007034
			4ppan[c]	1.782752	0.03731	acser[s]	3.1827205	0.0007295
			crpe[c]	1.76196	0.03904	gthrd[s]	3.170416	0.0007611
			huml[c]	1.76196	0.03904	erdtl[c]	3.1662021	0.0007722
			elm[c]	1.76196	0.03904	iaa-asp[c]	3.1647805	0.000776
			ga44[c]	1.761874	0.03905	iaa-glu[c]	3.1647805	0.000776
			hemeO[m]	1.759625	0.03924	iaa-gln[c]	3.1647805	0.000776
			agm[c]	1.757504	0.03942	glcur[c]	3.1632349	0.0007801
			G00171[c]	1.753811	0.03973	act[c]	3.1260026	0.000886
			tyr-L[m]	1.741692	0.04078	phpyr[s]	3.1256586	0.000887
			trp-L[m]	1.741692	0.04078	ga8[c]	3.1250282	0.0008889
			cndng[c]	1.741429	0.0408	2phetoh[c]	3.1210621	0.000901
			eikaur[c]	1.740256	0.04091	trdox[s]	3.1098639	0.0009359
			ser-L[m]	1.733499	0.0415	trdrd[s]	3.1098639	0.0009359
			1agpc_os[r]	1.733492	0.0415	ga44[c]	3.0820232	0.001028
			lim[s]	1.73346	0.04151	tyr-L[m]	3.0790892	0.0010382
			mi346p[c]	1.719917	0.04272	trp-L[m]	3.0790892	0.0010382
			mi3456p[c]	1.719917	0.04272	asp-L[m]	3.0398524	0.0011835
			trnaleu[c]	1.707797	0.04384	1ag3p_os[m]	3.0265435	0.0012368
			leutrna[c]	1.707797	0.04384	dgdg_os[s]	3.0197301	0.001265
			trnaile[c]	1.707797	0.04384	glyc3p[r]	3.0174066	0.0012747
			iletrna[c]	1.707797	0.04384	eikaur[s]	3.0173443	0.001275
			trnaile[s]	1.707797	0.04384	cholp[r]	3.0163148	0.0012793
			iletrna[s]	1.707797	0.04384	cholp[s]	3.0163148	0.0012793
			trnaile[m]	1.707797	0.04384	ga19[c]	2.994302	0.0013754
			iletrna[m]	1.707797	0.04384	ga20[c]	2.994302	0.0013754
			trnaval[s]	1.707797	4.38E-02	so4[m]	2.9567904	0.0015543
			valtrna[s]	1.707797	0.04384	2cpr5p[s]	2.9530707	0.0015731
			trnaval[m]	1.707797	0.04384	34hpp[s]	2.9383614	0.0016498
			valtrna[m]	1.707797	4.38E-02	anth[s]	2.9328951	0.0016791
			cndn5g[c]	1.707706	0.04385	ind3acetaldoxime[c]	2.9270033	0.0017112
			cndn35dg[c]	1.707706	4.38E-02	cytd[c]	2.9214126	0.0017422
			6pgl[s]	1.707298	0.04388	hpyr[x]	2.9202142	0.001749
			trdox[s]	1.70501	0.0441	glc-A[s]	2.9129344	0.0017902
			trdrd[s]	1.70501	0.0441	thr-L[m]	2.9121888	0.0017945
			2phetoh[c]	1.700409	0.04453	2ahbut[s]	2.8835246	0.0019663
			metjas[c]	1.697946	0.04476	glyald[c]	2.8786332	0.001997
			sdhlam[m]	1.694955	0.04504	phe-L[m]	2.8776333	0.0020034
			gdhlam[m]	1.694955	0.04504	ahdt[c]	2.8621502	0.0021039
			aps[s]	1.684769	0.04602	octdp[m]	2.8579626	0.0021319
			sprm[c]	1.665224	0.04793	3-non[s]	2.8569004	0.002139
			dmpp[c]	1.662468	0.04821	3-nond[s]	2.8569004	0.002139
			thr-L[s]	1.661608	0.0483	hxnl[s]	2.8569004	0.002139
			ala-B-bet[c]	1.657126	0.04875	hxndl[s]	2.8569004	0.002139
			cbp[s]	1.653388	0.04913	cndn[c]	2.856065	0.0021446
						malt[s]	2.8320241	0.0023127
						betald[c]	2.8185123	0.0024123
						aspsa[s]	2.8130803	0.0024535
						2sbzcoa[s]	2.8115447	0.0024652
						tdcoa[x]	2.8100994	0.0024763
						gthox[s]	2.792934	0.0026116
						dmpp[c]	2.7841604	0.0026833
						frdp[m]	2.7800391	0.0027176
						alltn[c]	2.7694266	0.0028078
						1ag3p_os[r]	2.7679458	0.0028205
						gdpgal[c]	2.7642678	0.0028525
						primardn[s]	2.7580911	0.002907
						tsul[m]	2.7558288	0.0029272
						B-ara1p[c]	2.7411574	0.0030612
						glu-L[v]	2.7274189	0.0031916
						hmgcoa[c]	2.7246733	0.0032183
						succ[m]	2.7243913	0.003221
						cmp[s]	2.7083028	0.0033814
						1ag3p_os[s]	2.6994245	0.003473
						2mp2coa[m]	2.6989267	0.0034782

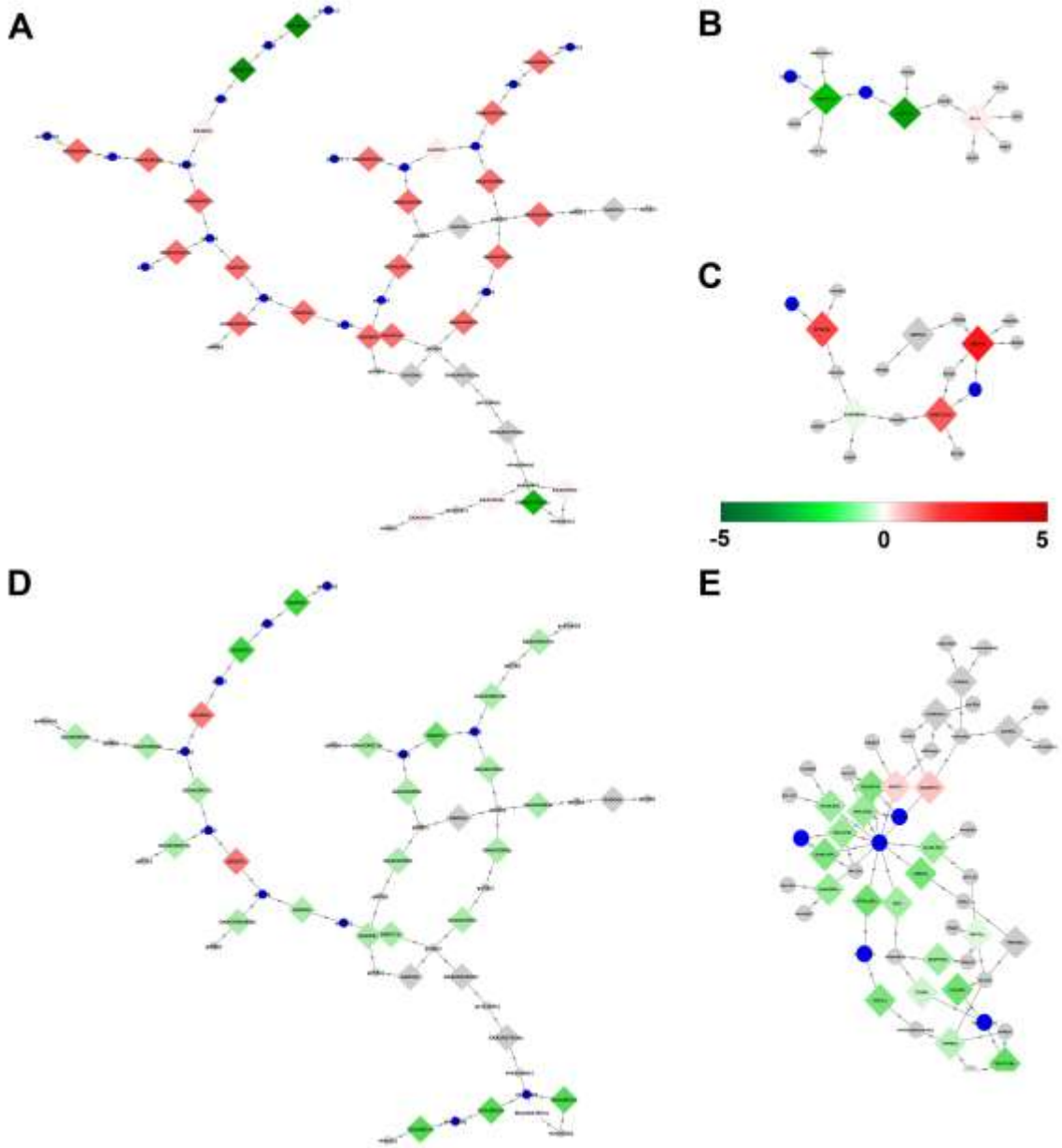
						2mb2coa[m]	2.6989267	0.0034782
						acg5p[c]	2.6890386	0.0035829
						phdp[s]	2.6801098	0.0036799
						nac[c]	2.6662407	0.0038352
						db4p[s]	2.6561086	0.0039524
						mnt[c]	2.6466142	0.0040651
						ekaurol[c]	2.6303325	0.0042651
						ekaural[c]	2.6303325	0.0042651
						psphings[r]	2.6215775	0.0043762
						bamppald[c]	2.6196424	0.0044011
						sphings[r]	2.6136327	0.0044793
						srntn[c]	2.6090273	0.00454
						mmet[c]	2.6072186	0.0045641
						5mta[c]	2.6025611	0.0046265
						g3pc[r]	2.5997622	0.0046644
						prpp[s]	2.5946225	0.0047347
						e4p[s]	2.5850411	0.0048684
						ptrc[c]	2.5780523	0.0049679
						imacp[s]	2.5742103	0.0050235
						grdp[s]	2.5514763	0.0053634
						indole[s]	2.5503032	0.0053815
						4ppan[c]	2.5388052	0.0055616
						icit[m]	2.5368892	0.0055921
						lplg[c]	2.5340523	0.0056376
						lcyc[c]	2.5340523	0.0056376
						4ppcys[c]	2.5098527	0.0060391
						ACP[c]	2.5045553	0.0061303
						Ssq23epx[c]	2.4965113	0.0062711
						semetselmet[c]	2.4665019	0.006822
						trnahis[c]	2.4633643	0.006882
						histrna[c]	2.4633643	0.006882
						trnahis[s]	2.4633643	0.006882
						histrna[s]	2.4633643	0.006882
						trnahis[m]	2.4633643	0.006882
						histrna[m]	2.4633643	0.006882
						2pg[c]	2.4556614	0.0070313
						cit[m]	2.4530749	0.007082
						6pgl[c]	2.4311642	0.0075252
						npdp[s]	2.4281443	0.0075882
						h2mb4p[s]	2.4060671	0.0080627
						lpro[m]	2.4054896	0.0080754
						cinncoa[c]	2.4031687	0.0081268
						oclysLCP[m]	2.398089	0.0082404
						cys-prot[c]	2.3967324	0.008271
						3mb2coa[m]	2.3925809	0.0083652
						s7p[s]	2.3908214	0.0084054
						gar[s]	2.3848204	0.0085437
						akgACPme[c]	2.3781329	0.0087003
						malACP[m]	2.3593993	0.0091523
						5apru[s]	2.357184	0.0092071
						xylu-D[c]	2.3421161	0.0095874
						fdxrd[m]	2.3280773	0.009954
						fdxox[m]	2.3280773	0.009954
						pran[s]	2.3201075	0.0101675
						g6p-A[c]	2.3023536	0.0106576
						adhlam[m]	2.2979726	0.0107817
						arab-L[c]	2.2943443	0.0108854
						2mecdp[s]	2.2894119	0.0110277
						focytc[m]	2.2888453	0.0110442
						ficytc[m]	2.2888453	0.0110442
						2kmb[c]	2.2885444	0.0110529
						2dhp[m]	2.2877427	0.0110763
						mev-R[c]	2.280717	0.0112826
						caff[c]	2.2753846	0.0114414
						3chpthmpp[m]	2.2743472	0.0114726
						obfool[c]	2.2600586	0.0119088
						gal-L[c]	2.2554125	0.0120537
						hydro20[r]	2.2504188	0.0122112
						hydro22[r]	2.2504188	0.0122112
						hydro24[r]	2.2504188	0.0122112
						hydro26[r]	2.2504188	0.0122112
						hydro28[r]	2.2504188	0.0122112
						hydro30[r]	2.2504188	0.0122112
						acald[s]	2.2489925	0.0122565
						gbside[c]	2.237511	0.0126265

						mi14p[c]	2.2217123	0.0131514
						dtmp[c]	2.2196299	0.013222
						dldpng[c]	2.2156323	0.0133583
						mergtrol[c]	2.2141966	0.0134076
						occoa[x]	2.2104384	0.0135374
						hxcoa[x]	2.2104384	0.0135374
						dcacoa[x]	2.2104384	0.0135374
						ddcacoa[x]	2.2104384	0.0135374
						ga8cat[c]	2.2097287	0.013562
						cytd[s]	2.2060621	0.0136898
						dudp[c]	2.2024758	0.0138159
						man1p[c]	2.1993555	0.0139263
						campst43e[c]	2.1993192	0.0139276
						frprot[c]	2.1989103	0.0139422
						lanost[c]	2.1891719	0.0142922
						g6p-B[v]	2.1717305	0.014938
						ocp8t2ecoa[x]	2.1681344	0.0150742
						ocp6t2ecoa[x]	2.1681344	0.0150742
						ocp4t2ecoa[x]	2.1681344	0.0150742
						gdpmann[c]	2.1654892	0.0151751
						mi4p-D[c]	2.1343209	0.0164083
						lys-L[m]	2.1325707	0.01648
						pail45p[c]	2.124834	0.0168002
						agm[c]	2.1152318	0.0172051
						maltt[s]	2.1096491	0.0174443
						dadp[c]	2.1017194	0.0177889
						1agpc_os[r]	2.0889886	0.0183544
						ru5p-D[c]	2.0663873	0.019396
						gm2[c]	2.0639081	0.0195132
						6pgc[c]	2.0625288	0.0195787
						4pasp[s]	2.0616141	0.0196222
						a-cptxan[s]	2.0480973	0.0202752
						lutein[s]	2.0480973	0.0202752
						gln-L[m]	2.0480267	0.0202787
						lipro[m]	2.0354064	0.020905
						c-ztn7g[c]	2.0347305	0.020939
						t-ztn7g[c]	2.0347305	0.020939
						dhz7g[c]	2.0347305	0.020939
						ipadne7g[c]	2.0347305	0.020939
						c-ztn9g[c]	2.0347305	0.020939
						t-ztn9g[c]	2.0347305	0.020939
						dhz9g[c]	2.0347305	0.020939
						ipadne9g[c]	2.0347305	0.020939
						glc-B[s]	2.028671	0.0212459
						dhf[c]	2.021562	0.0216108
						pect[c]	2.0096146	0.022236
						xylan[c]	2.0039467	0.0225379
						lcdpn[c]	1.9891556	0.023342
						22hcampst[c]	1.9881238	0.023399
						sclgn[c]	1.9843755	0.023607
						stcsd[c]	1.9843755	0.023607
						ala-B-bet[c]	1.9794443	0.023883
						dnad[c]	1.9792739	0.0238926
						dlpdn[c]	1.9733073	0.0242303
						G00009[c]	1.9726725	0.0242664
						12dgr_os[c]	1.9716909	0.0243225
						hconald[c]	1.9631171	0.0248163
						hfer[c]	1.9631171	0.0248163
						dkmpp[c]	1.9549946	0.0252919
						ACP[s]	1.9409998	0.0261292
						paps[c]	1.9398329	0.0262
						absald[s]	1.9394962	0.0262205
						thf[s]	1.9292068	0.0268526
						acgam1p[c]	1.9230989	0.0272338
						selcys[s]	1.9165608	0.0276469
						3hbutACP[s]	1.9144248	0.027783
						3hhexACP[s]	1.9144248	0.027783
						3hoctACP[s]	1.9144248	0.027783
						3hdecACP[s]	1.9144248	0.027783
						3hddecACP[s]	1.9144248	0.027783
						3hmrsACP[s]	1.9144248	0.027783
						3hpalmACP[s]	1.9144248	0.027783
						3hoctaACP[s]	1.9144248	0.027783
						hakgACPme[c]	1.9144248	0.027783
						hpimACPme[c]	1.9144248	0.027783

						2sbz[s]	1.9065445	0.0282898
						ppp9[s]	1.9039342	0.0284594
						selcys[c]	1.8864353	0.0296182
						mpq[s]	1.8674486	0.0309195
						hemeA[m]	1.8616389	0.031327
						ga9[c]	1.8558396	0.0317382
						ga4[c]	1.8558396	0.0317382
						mgr_os[c]	1.8529337	0.0319459
						malttt[s]	1.8491926	0.032215
						4abut[m]	1.8402945	0.0328625
						xyl-D[c]	1.8394183	0.0329268
						sql[c]	1.8357086	0.0332004
						3haraccoa[r]	1.831983	0.033477
						3hbehcoa[r]	1.831983	0.033477
						3hlgnccoa[r]	1.831983	0.033477
						3hcercoa[r]	1.831983	0.033477
						3hmntcoa[r]	1.831983	0.033477
						3hmlscoa[r]	1.831983	0.033477
						metsel[c]	1.8293847	0.033671
						3dsphgn[r]	1.8272331	0.0338324
						sin[c]	1.8244107	0.034045
						nh4[x]	1.8223244	0.0342029
						3oaraccoa[r]	1.8222246	0.0342105
						3obehcoa[r]	1.8222246	0.0342105
						3olgnccoa[r]	1.8222246	0.0342105
						3ocercoa[r]	1.8222246	0.0342105
						3omntcoa[r]	1.8222246	0.0342105
						3omlscoa[r]	1.8222246	0.0342105
						caffqnt[c]	1.8158404	0.0346974
						caffskm[c]	1.8158404	0.0346974
						cyan[m]	1.7975157	0.0361269
						tcynt[m]	1.7975157	0.0361269
						cyan[s]	1.7975157	0.0361269
						tcynt[s]	1.7975157	0.0361269
						gar[m]	1.791529	0.0366042
						fgam[m]	1.791529	0.0366042
						G00001[c]	1.7883685	0.0368583
						lthstrl[c]	1.7847744	0.037149
						ru5p-D[s]	1.7802207	0.0375199
						glcur1p[c]	1.776036	0.0378635
						alaala[c]	1.7719506	0.0382014
						prpncoa[m]	1.7636879	0.0388923
						oc2coa[x]	1.7636879	0.0388923
						hx2coa[x]	1.7636879	0.0388923
						dc2coa[x]	1.7636879	0.0388923
						dd2coa[x]	1.7636879	0.0388923
						td2coa[x]	1.7636879	0.0388923
						hdd2coa[x]	1.7636879	0.0388923
						toctd2ecoa[x]	1.7636879	0.0388923
						crpe[c]	1.7619603	0.039038
						huml[c]	1.7619603	0.039038
						elm[c]	1.7619603	0.039038
						hemeO[m]	1.7596248	0.0392357
						G00171[c]	1.7538106	0.0397315
						trnamet[c]	1.7519058	0.039895
						mettrna[c]	1.7519058	0.039895
						trnamet[m]	1.7519058	0.039895
						mettrna[m]	1.7519058	0.039895
						trnamet[s]	1.7519058	0.039895
						mettrna[s]	1.7519058	0.039895
						trnaphe[c]	1.7519058	0.039895
						phetrna[c]	1.7519058	0.039895
						trnaphe[s]	1.7519058	0.039895
						phetrna[s]	1.7519058	0.039895
						trnaile[c]	1.7519058	0.039895
						iletrna[c]	1.7519058	0.039895
						trnaile[s]	1.7519058	0.039895
						iletrna[s]	1.7519058	0.039895
						trnaile[m]	1.7519058	0.039895
						iletrna[m]	1.7519058	0.039895
						trnasemet[c]	1.7519058	0.039895
						sertrna(met)[c]	1.7519058	0.039895

Appendix T:

Visualization of individual metabolic pathways. (A) Gibberallins biosynthesis in B-W. (B) Ethylene biosynthesis in B-W. (C) Abcisate biosynthesis in B-W. (D) Gibberallins biosynthesis in R-W. (E) IAA biosynthesis in R-W.



Appendix U:

Common and unique reporter metabolites.

Unique in Blue	Unique in Dark	Common between Blue and Dark	Common between Red and Dark	Common between Blue and Red	Common in all
acrtnl[s]	10fthglu[c]	12o9dd[s]	12dgr_os[m]	b-glucan[c]	13-hpod[s]
amob[c]	12dgr_os[c]	1acpc[c]	12dgr_os[r]	glucan[s]	13-hpot[s]
ehkaurate[c]	13dpg[s]	2kmb[c]	12dgr_os[s]		2phetoh[c]
epctcn[c]	1ag3p_os[m]	2pglyc[s]	1agpc_os[r]		33dma[c]
epflzn[c]	1ag3p_os[s]	9-nonan[s]	2cpr5p[s]		8aonn[c]
ga12-ald[c]	1agpc_os[r]	eikaur[s]	34hb[c]		9-hpod[s]
ga15[c]	1Dgali[c]	ethylene[c]	34hpp[s]		9-hpot[s]
ga17[c]	1-kesttr[c]	g6p-B[v]	3chpthmpp[m]		abs[s]
ga29[c]	22h5camp43e[c]	id3acald[c]	3dsphgn[r]		ala-L[m]
ga29cat[c]	22hcampst[c]	ind3acetaldoxime[c]	3ig3p[s]		arg-L[s]
ga34[c]	25dhpp[s]	lgt-S[c]	3o2c2poct[x]		b-glucan[v]
ga37[c]	2ahbut[s]	lpam[m]	3oaraccoa[r]		cellb[c]
ga51[c]	2ahethmpp[s]	nad[v]	3obehcoa[r]		eikaur[c]
ga51cat[c]	2dhp[m]	nadh[v]	3ocercoa[r]		ga1[c]
ga53[c]	2mb2coa[m]	primardn[s]	3olgnccoa[r]		ga19[c]
	2mecdp[s]	psphings[r]	3omlscoa[r]		ga20[c]
	2mp2coa[m]	rb15bp[s]	3omntcoa[r]		ga4[c]
	2pg[c]		4adcho[s]		ga44[c]
	2sbz[s]		4ppan[c]		ga8[c]
	2sbzcoa[s]		4ppcys[c]		ga8cat[c]
	3haraccoa[r]		5apru[s]		ga9[c]
	3hbehcoa[r]		6pgl[s]		ile-L[s]
	3hbutACP[s]		ACP[m]		ind3acnl[c]
	3hcercoa[r]		acser[s]		pa_os[m]
	3hddecACP[s]		adpglc[s]		phe-L[s]
	3hdecACP[s]		agm[c]		ppi[r]
	3hhexACP[s]		akgACPme[c]		sclgn[c]
	3hlgnccoa[r]		ala-B-bet[c]		stcsd[c]
	3hmlscoa[r]		amygd[c]		suc6p[c]
	3hmntcoa[r]		anth[s]		thr-L[s]
	3hmrsACP[s]		anxan[s]		val-L[s]
	3hoctaACP[s]		aps[s]		
	3hoctACP[s]		asn-L[m]		
	3hpalmACP[s]		asp-L[m]		
	3mb2coa[m]		B-ara1p[c]		

	3-non[s]		cbp[s]			
	3-nond[s]		chlda[s]			
	3pg[s]		cinnald[c]			
	4abut[m]		cndn35dg[c]			
	4pasp[s]		cndn5g[c]			
	5mta[c]		cndng[c]			
	6pgc[c]		crpe[c]			
	6pgl[c]		c-ztng[c]			
	absald[s]		dadp[c]			
	acald[s]		dhf[c]			
	acg5p[c]		dhqrctn[c]			
	acgam1p[c]		dhzg[c]			
	ACP[c]		dlpdn[c]			
	ACP[s]		dmpp[c]			
	a-cptxan[s]		dtmp[c]			
	act[c]		dudp[c]			
	adhlam[m]		dvchlda[s]			
	ahdt[c]		dvpchlda[s]			
	alaala[c]		ecdp[s]			
	alltn[c]		ekaural[c]			
	alpro[m]		ekaurol[c]			
	aps[c]		elm[c]			
	arab-L[c]		f6p-B[c]			
	aspsa[s]		f6p-B[s]			
	bamppald[c]		fer[c]			
	betald[c]		fgam[m]			
	b-glucan[c]		G00009[c]			
	butin[c]		G00171[c]			
	caff[c]		g3pc[r]			
	caffqnt[c]		g6p-A[c]			
	caffskm[c]		g6p-A[s]			
	cala[c]		g6p-B[c]			
	campst43e[c]		g6p-B[s]			
	cer2_os[r]		gabut[c]			
	chlestol[c]		gar[m]			
	chlstol[c]		gbside[c]			
	cholp[r]		gdhlam[m]			
	cholp[s]		glc-B[s]			
	cinncoa[c]		glyc3p[r]			
	cit[m]		grdp[c]			
	cmp[s]		grdp[s]			
	cndn[c]		h2mb4p[s]			
	coum[c]		h2o[u]			

	cyan[m]		h2o2[s]			
	cyan[s]		hconald[c]			
	cys-prot[c]		hemeA[m]			
	cytd[c]		hemeO[m]			
	cytd[s]		hfer[c]			
	c-ztn7g[c]		his-L[m]			
	c-ztn9g[c]		hisp[s]			
	db4p[s]		hmgcoa[c]			
	dc2coa[x]		huml[c]			
	dcacoa[x]		hydro20[r]			
	dd2coa[x]		hydro22[r]			
	ddcacoa[x]		hydro24[r]			
	dgdg_os[s]		hydro26[r]			
	dhk[c]		hydro28[r]			
	dhlpro[m]		hydro30[r]			
	dhncoa[s]		iletrna[c]			
	dhz7g[c]		iletrna[m]			
	dhz9g[c]		iletrna[s]			
	dkmpp[c]		ind3ac[c]			
	dldpng[c]		indole[s]			
	dnad[c]		lcdpn[c]			
	dtdp[c]		lcyc[c]			
	dtdpglu[c]		leu-L[s]			
	dtdprmn[c]		leutrna[c]			
	dump[c]		lim[s]			
	e4p[s]		lplg[c]			
	erdtl[c]		malttt[s]			
	fdp-B[c]		man6p[c]			
	fdp-B[s]		metjas[c]			
	fdxox[m]		mev-R[c]			
	fdxrd[m]		mgdg_os[s]			
	ficytc[m]		mi13456p[c]			
	focytc[m]		mi134p[c]			
	frdp[m]		mi14p[c]			
	frprot[c]		mi3456p[c]			
	G00001[c]		mi346p[c]			
	gal[c]		moma[s]			
	gal-L[c]		nh4[x]			
	gar[s]		ocp4t2ecoa[x]			
	gdp[c]		ocp6t2ecoa[x]			
	gdp[s]		ocp8t2ecoa[x]			
	gdpgal[c]		opc8coa[x]			
	gdpmann[c]		pa_os[s]			

	ggdp[s]		pap[s]			
	glc-A[s]		paps[s]			
	glcur[c]		pchlda[s]			
	glcur1p[c]		pep[c]			
	gln-L[m]		pep[s]			
	glucan[s]		phpyr[s]			
	glu-L[v]		pran[s]			
	glyald[c]		primard[s]			
	gm2[c]		primardt[s]			
	gthox[s]		pro-L[m]			
	gthrd[s]		prunasin[c]			
	gtp[s]		r5p[s]			
	hakgACPme[c]		scodp[s]			
	hdd2coa[x]		sdhlam[m]			
	histrna[c]		ser-L[m]			
	histrna[m]		sin[c]			
	histrna[s]		sprm[c]			
	hpimACPme[c]		tdcoa[x]			
	hpyr[x]		thcrm[c]			
	hx2coa[x]		thf[s]			
	hxcoa[x]		trdox[c]			
	hxndl[s]		trdox[s]			
	hxnl[s]		trdrd[c]			
	iaa-ala[c]		trdrd[s]			
	iaa-asp[c]		tre[c]			
	iaa-gln[c]		tre6p[c]			
	iaa-glu[c]		trnaile[c]			
	iaa-leu[c]		trnaile[m]			
	icit[m]		trnaile[s]			
	imacp[s]		trnaleu[c]			
	ipadne7g[c]		trnaval[m]			
	ipadne9g[c]		trnaval[s]			
	jasile[c]		trp-L[m]			
	jasleu[c]		trp-L[s]			
	jasval[c]		tryptamine[c]			
	kmpfl[c]		tyr-L[m]			
	kmpfl3g[c]		t-ztng[c]			
	lanost[c]		valtrna[m]			
	lipro[m]		valtrna[s]			
	lpro[m]		vlxan[s]			
	lqtgn[c]		xmp[c]			
	lthstrl[c]		xylan[c]			
	lutein[s]					

	lys-L[m]					
	malACP[m]					
	mal-L[m]					
	malt[s]					
	maltt[s]					
	man1p[c]					
	melib[c]					
	mergtrol[c]					
	met-L[m]					
	metsel[c]					
	mettrna[c]					
	mettrna[m]					
	mettrna[s]					
	mgr_os[c]					
	mi4p-D[c]					
	mmet[c]					
	mnt[c]					
	mpq[s]					
	na1[c]					
	na1[m]					
	na1[s]					
	nac[c]					
	nad[x]					
	nadh[x]					
	npdp[s]					
	nrsprn[s]					
	oaa[m]					
	obfool[c]					
	oc2coa[x]					
	occoa[x]					
	ocdcaACP[s]					
	oclysLCP[m]					
	octdp[m]					
	opc4coa[x]					
	opc6coa[x]					
	pail45p[c]					
	paps[s]					
	pccu1p[u]					
	pccu2p[u]					
	pect[c]					
	pg_os[m]					
	phdp[s]					
	phe-L[m]					

	phetrna[c]					
	phetrna[s]					
	pnto-R[c]					
	ppp9[s]					
	pram[s]					
	prpncoa[m]					
	prpp[s]					
	psqldp[c]					
	ptrc[c]					
	qrctn[c]					
	qrctn3g[c]					
	raffin[c]					
	ru5p-D[c]					
	ru5p-D[s]					
	s7p[s]					
	selcys[c]					
	selcys[s]					
	selmet[c]					
	seln[s]					
	semetselmet[c]					
	sertrna(met)[c]					
	so4[m]					
	sphgn[r]					
	sphings[r]					
	sql[c]					
	srntn[c]					
	Ssq23epx[c]					
	stc[c]					
	succ[m]					
	t-cinn[c]					
	tcynt[m]					
	tcynt[s]					
	td2coa[x]					
	thr-L[m]					
	toctd2ecoa[x]					
	trnahis[c]					
	trnahis[m]					
	trnahis[s]					
	trnamet[c]					
	trnamet[m]					
	trnamet[s]					
	trnaphe[c]					
	trnaphe[s]					

	trnasemet[c] tsul[m] t-ztn7g[c] t-ztn9g[c] udpgal[s] urate[c] uri[c] xyl-D[c] xylu-D[c]				